



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 02:45 PM UTC

PDB ID : 3J6B / pdb_00003j6b
EMDB ID : EMD-2566
Title : Structure of the yeast mitochondrial large ribosomal subunit
Authors : Amunts, A.; Brown, A.; Bai, X.C.; Llacer, J.L.; Hussain, T.; Emsley, P.; Long, F.; Murshudov, G.; Scheres, S.H.W.; Ramakrishnan, V.
Deposited on : 2014-01-22
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

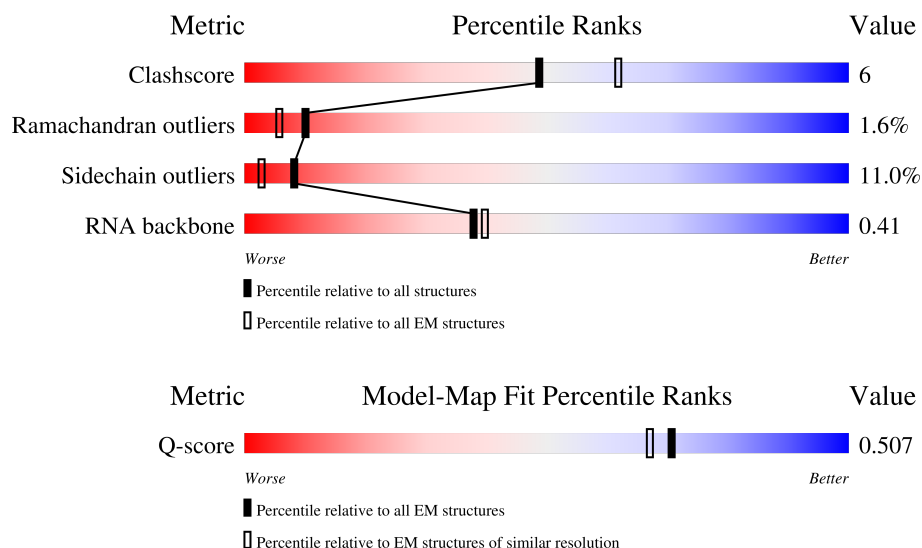
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



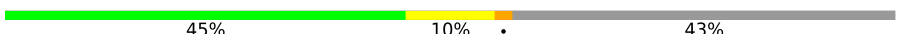
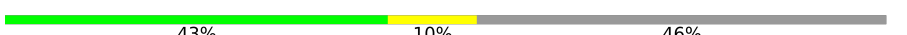
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	A	3296	
2	B	393	
3	C	269	

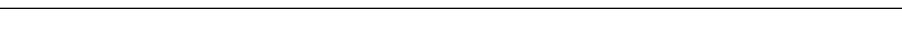
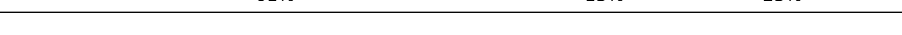
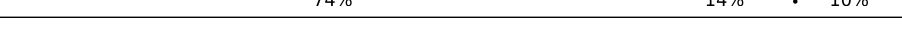
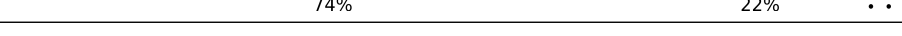
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Mol	Chain	Length	Quality of chain
4	D	286	
5	E	292	
6	F	214	
7	G	139	
8	H	163	
9	I	138	
10	J	322	
11	K	232	
12	L	238	
13	M	169	
14	N	161	
15	O	309	
16	P	263	
17	Q	297	
18	R	371	
19	S	258	
20	T	319	
21	U	86	
22	V	177	
23	W	183	
24	X	70	
25	Y	105	
26	Z	115	
27	0	93	
28	1	367	

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Mol	Chain	Length	Quality of chain
29	2	147	
30	3	146	
31	4	140	
32	5	390	
33	6	281	
34	7	146	
35	8	264	
36	9	253	
37	a	195	
38	b	157	
39	c	131	
40	d	226	
41	e	20	

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 195137 atoms, of which 83818 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 21S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2713	Total	C	H	N	O	P	0	0
			86569	25948	28898	10265	18752	2706		

- Molecule 2 is a protein called 54S ribosomal protein RML2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	295	Total	C	H	N	O	S	0	0
			4603	1405	2343	459	387	9		

- Molecule 3 is a protein called 54S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	249	Total	C	H	N	O	S	0	0
			3906	1217	1976	360	343	10		

- Molecule 4 is a protein called 54S ribosomal protein YmL6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	239	Total	C	H	N	O	S	0	0
			3780	1187	1914	337	339	3		

- Molecule 5 is a protein called 54S ribosomal protein L7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	274	Total	C	H	N	O	S	0	0
			4294	1363	2169	387	369	6		

- Molecule 6 is a protein called 54S ribosomal protein L6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	185	Total	C	H	N	O	S	0	0
			2747	870	1392	236	246	3		

- Molecule 7 is a protein called 54S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	55	Total	C	H	N	O	S	0	0
			929	293	471	86	78	1		

- Molecule 8 is a protein called 54S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	148	Total	C	H	N	O	S	0	0
			2394	742	1218	225	205	4		

- Molecule 9 is a protein called 54S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	125	Total	C	H	N	O	S	0	0
			1952	583	1015	175	168	11		

- Molecule 10 is a protein called 54S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	220	Total	C	H	N	O	S	0	0
			3555	1109	1828	325	290	3		

- Molecule 11 is a protein called 54S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	195	Total	C	H	N	O	S	0	0
			3208	1001	1635	297	270	5		

- Molecule 12 is a protein called 54S ribosomal protein L8, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	229	Total	C	H	N	O	S	0	0
			3698	1139	1883	333	335	8		

- Molecule 13 is a protein called 54S ribosomal protein IMG1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	151	Total	C	H	N	O	S	0	0
			2492	766	1286	220	217	3		

- Molecule 14 is a protein called 54S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	118	Total	C	H	N	O	S	0	0
			1958	598	1010	177	171	2		

- Molecule 15 is a protein called 54S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	223	Total	C	H	N	O	S	0	0
			3684	1147	1895	328	309	5		

- Molecule 16 is a protein called 54S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	207	Total	C	H	N	O	S	0	0
			3450	1101	1728	310	305	6		

- Molecule 17 is a protein called 54S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	279	Total	C	H	N	O	S	0	0
			4287	1368	2161	375	375	8		

- Molecule 18 is a protein called 54S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	318	Total	C	H	N	O	S	0	0
			4981	1571	2500	452	454	4		

- Molecule 19 is a protein called 54S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	S	146	Total	C	H	N	O	S	0	0
			2440	763	1249	220	207	1		

- Molecule 20 is a protein called 54S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	T	209	Total	C	H	N	O	S	0	0
			3264	1044	1618	307	292	3		

- Molecule 21 is a protein called 54S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	82	Total	C	H	N	O	0	0
			1341	410	702	116	113		

- Molecule 22 is a protein called 54S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
22	V	64	Total	C	H	N	O	S	0	0
			1083	332	555	105	90	1		

- Molecule 23 is a protein called 54S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	W	112	Total	C	H	N	O	S	0	0
			1922	587	985	181	163	6		

- Molecule 24 is a protein called 54S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	64	Total	C	H	N	O	0	0
			1077	330	565	96	86		

- Molecule 25 is a protein called 54S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	45	Total	C	H	N	O	0	0
			788	239	412	80	57		

- Molecule 26 is a protein called mitochondrial ribosomal protein YNL122C.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Z	62	Total	C	H	N	O	S	0	0
			1054	322	546	111	74	1		

- Molecule 27 is a protein called 54S ribosomal protein RTC6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
27	0	38	Total	C	H	N	O	S	0	0
			673	205	349	66	50	3		

- Molecule 28 is a protein called 54S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	1	332	Total	C	H	N	O	S	0	0
			5397	1744	2690	467	490	6		

- Molecule 29 is a protein called 54S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	2	113	Total	C	H	N	O	S	0	0
			1858	583	939	169	162	5		

- Molecule 30 is a protein called 54S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	3	126	Total	C	H	N	O	S	0	0
			2025	643	1030	181	168	3		

- Molecule 31 is a protein called 54S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	4	138	Total	C	H	N	O	S	0	0
			2263	700	1146	219	193	5		

- Molecule 32 is a protein called 54S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	5	326	Total	C	H	N	O	S	0	0
			5026	1596	2541	425	453	11		

- Molecule 33 is a protein called 54S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	6	209	Total	C	H	N	O	S	0	0
			3187	1046	1595	273	271	2		

- Molecule 34 is a protein called 54S ribosomal protein IMG2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	7	106	Total	C	H	N	O	S	0	0
			1755	550	901	150	152	2		

- Molecule 35 is a protein called 54S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	8	182	Total	C	H	N	O	S	0	0
			2829	898	1416	241	271	3		

- Molecule 36 is a protein called 54S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	9	195	Total	C	H	N	O	S	0	0
			2865	919	1437	250	254	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
9	169	GLY	ASP	conflict	UNP P36523

- Molecule 37 is a protein called 54S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	a	176	Total	C	H	N	O	S	0	0
			2882	898	1455	264	259	6		

- Molecule 38 is a protein called 54S ribosomal protein L25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	b	155	Total	C	H	N	O	S	0	0
			2671	850	1372	225	221	3		

- Molecule 39 is a protein called 54S ribosomal protein L31, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	c	118	Total	C	H	N	O	S	0	0
			2066	643	1066	190	163	4		

- Molecule 40 is a protein called Mitochondrial homologous recombination protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	d	204	Total	C	H	N	O	S	0	0
			3423	1099	1706	313	299	6		

- Molecule 41 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	e	20	Total	C	H	N	O	P	0	0
			648	191	221	81	136	19		

- Molecule 42 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
42	A	109	Total	Mg	0
			109	109	
42	N	1	Total	Mg	0
			1	1	

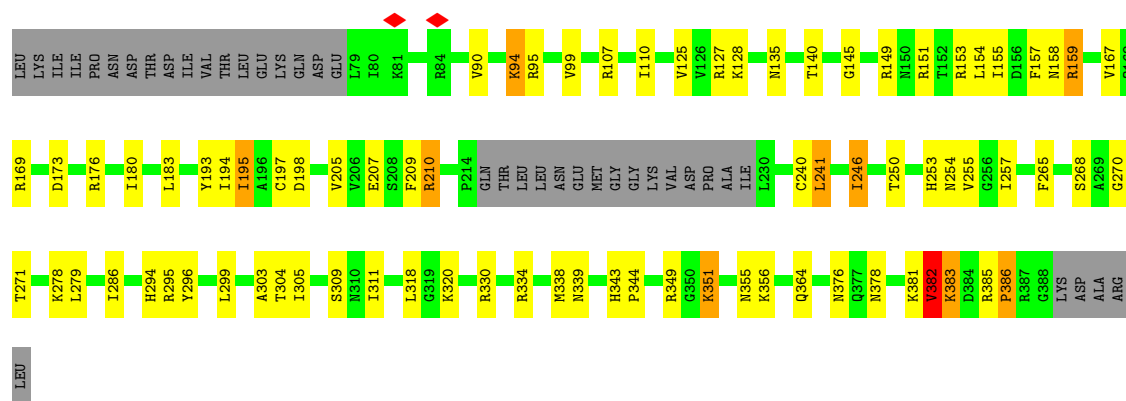
- Molecule 43 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
43	B	1	Total	Na	0
			1	1	

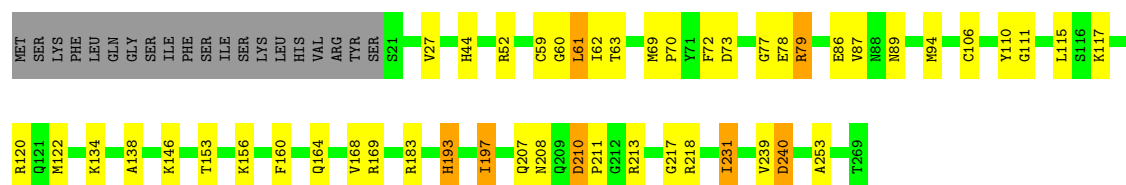
- Molecule 44 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
44	W	1	Total	Zn	0
			1	1	
44	0	1	Total	Zn	0
			1	1	

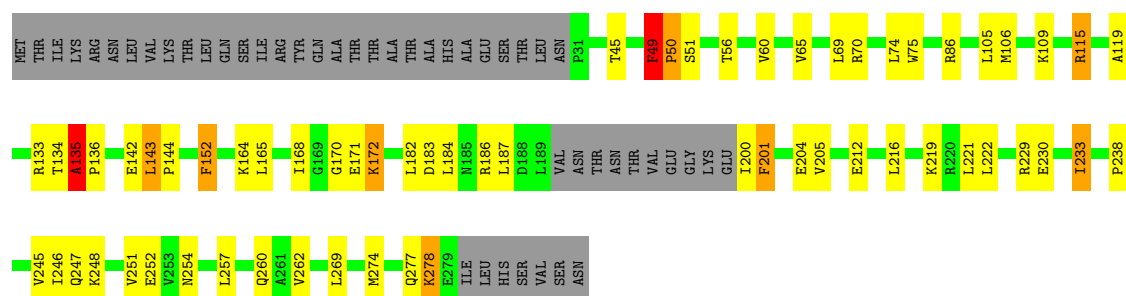




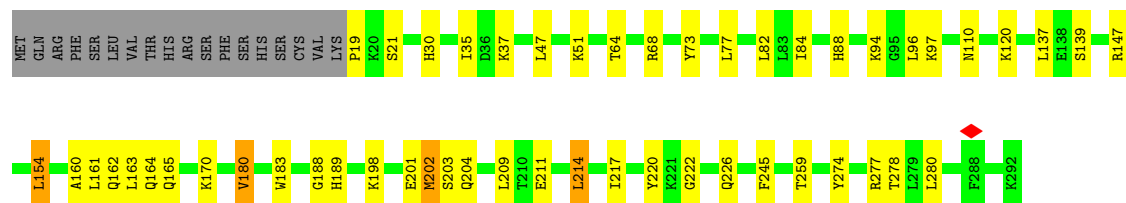
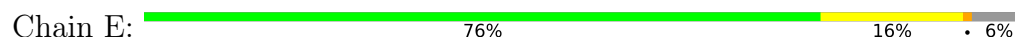
- Molecule 3: 54S ribosomal protein L9, mitochondrial



- Molecule 4: 54S ribosomal protein YmL6, mitochondrial

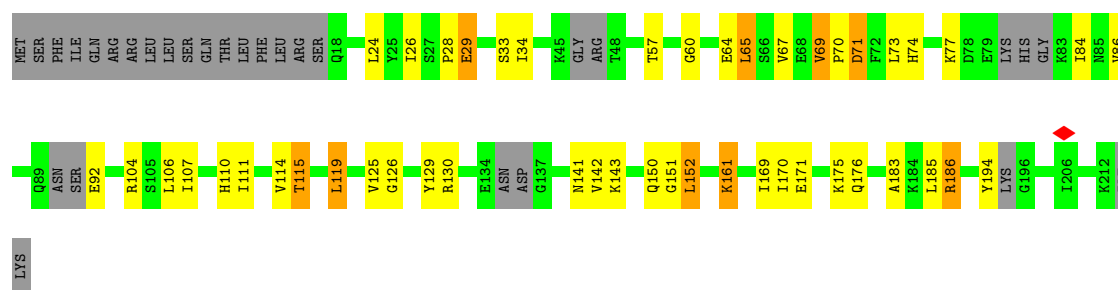


- Molecule 5: 54S ribosomal protein L7, mitochondrial



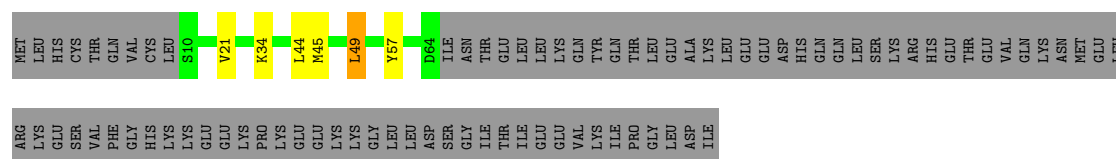
- Molecule 6: 54S ribosomal protein L6, mitochondrial





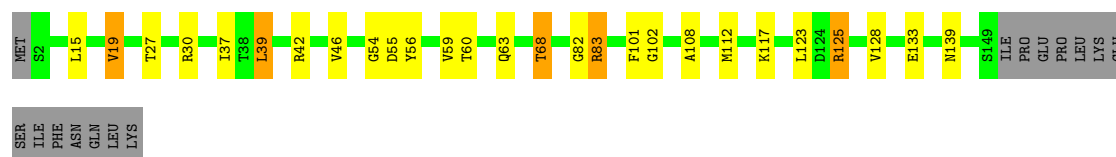
- Molecule 7: 54S ribosomal protein L50, mitochondrial

Chain G: 35% 60%



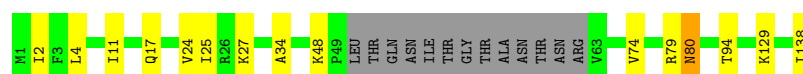
- Molecule 8: 54S ribosomal protein L23, mitochondrial

Chain H: 74% 13% 9%



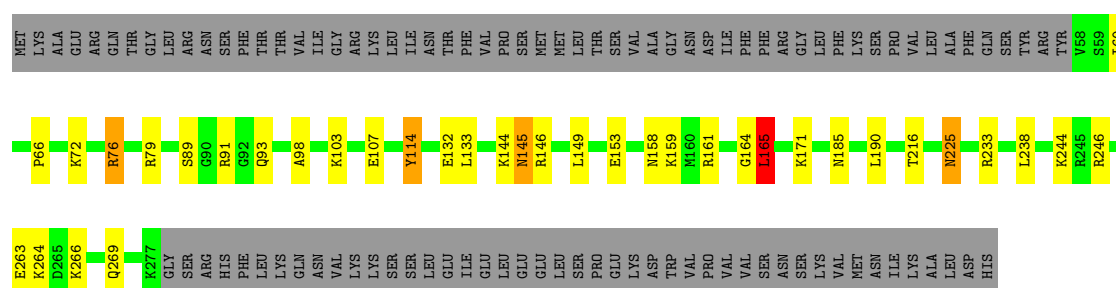
- Molecule 9: 54S ribosomal protein L38, mitochondrial

Chain I: 80% 10% 9%



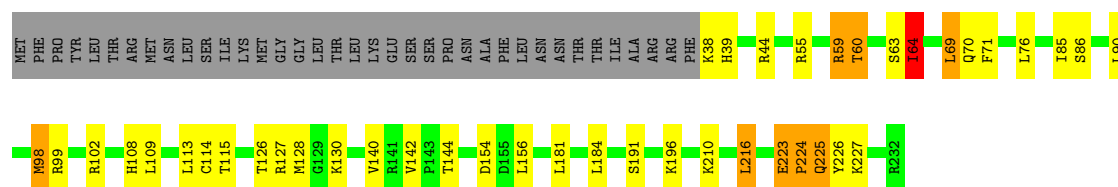
- Molecule 10: 54S ribosomal protein L10, mitochondrial

Chain J: 57% 10% 32%



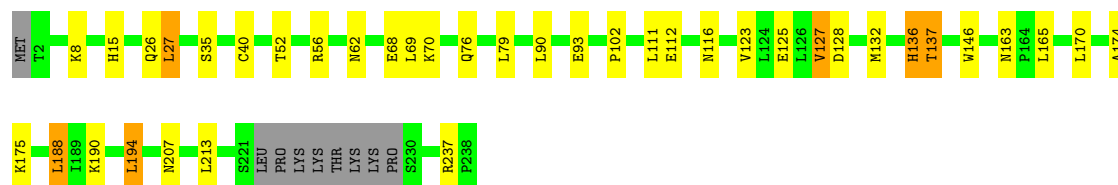
- Molecule 11: 54S ribosomal protein L16, mitochondrial

Chain K:  66% 15% 16%



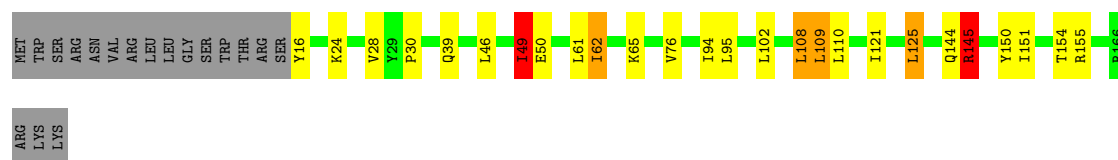
- Molecule 12: 54S ribosomal protein L8, mitochondrial

Chain L:  80% 14%



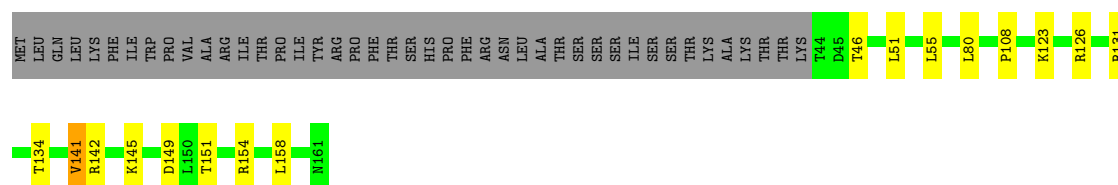
- Molecule 13: 54S ribosomal protein IMG1, mitochondrial

Chain M:  74% 12% 11%



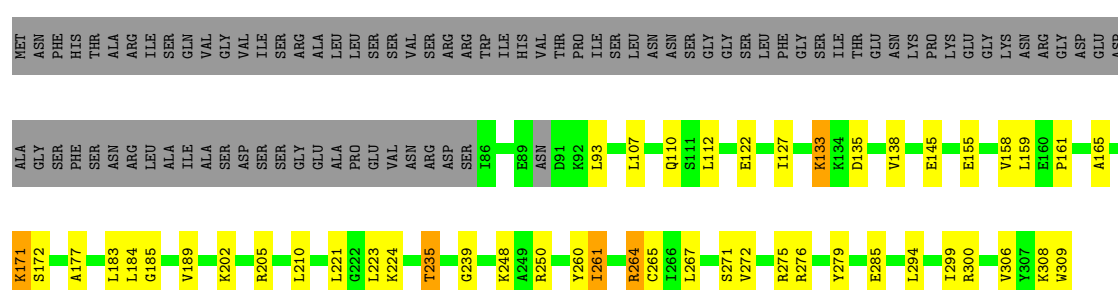
- Molecule 14: 54S ribosomal protein L49, mitochondrial

Chain N:  63% 9% 27%



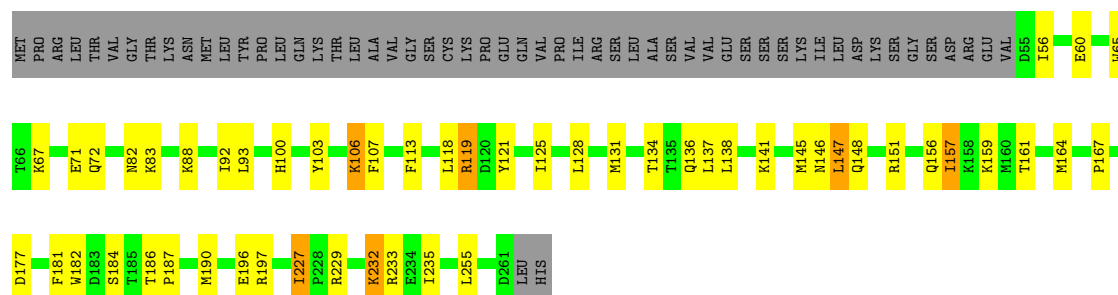
- Molecule 15: 54S ribosomal protein L22, mitochondrial

Chain O:  56% 14% 28%



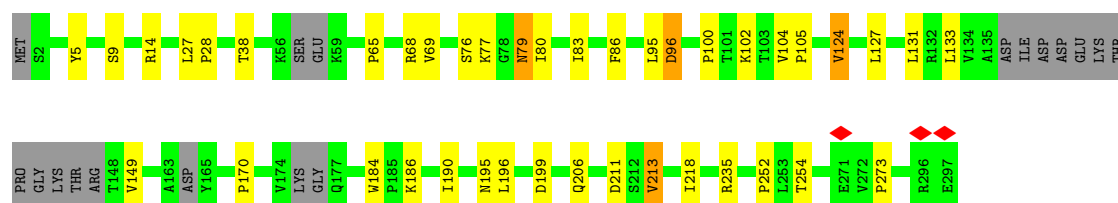
- Molecule 16: 54S ribosomal protein L41, mitochondrial

Chain P: 



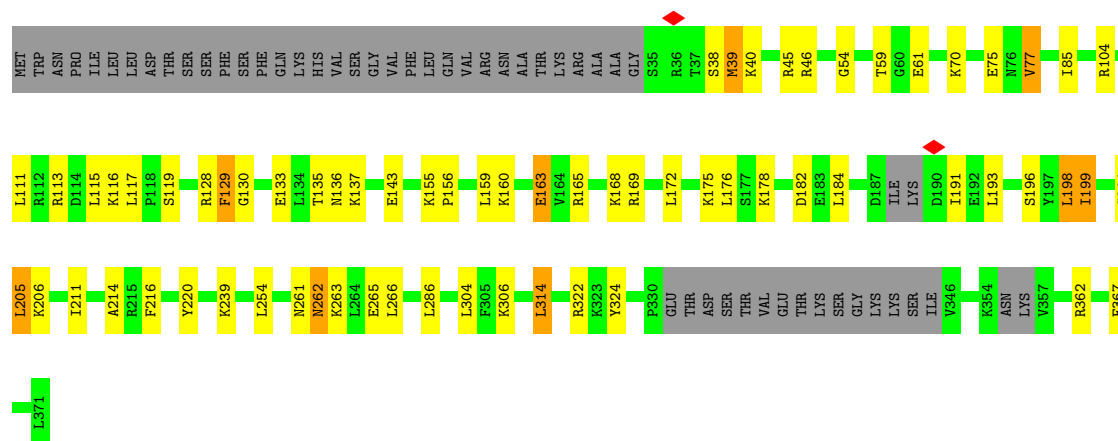
- Molecule 17: 54S ribosomal protein L40, mitochondrial

Chain Q: 

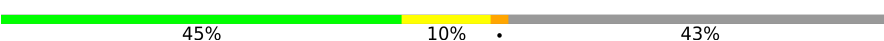


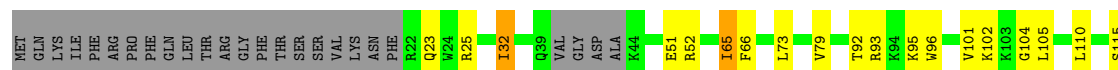
- Molecule 18: 54S ribosomal protein L2, mitochondrial

Chain R: 



- Molecule 19: 54S ribosomal protein L24, mitochondrial

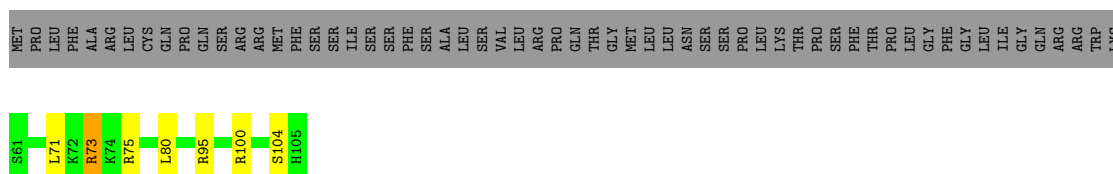
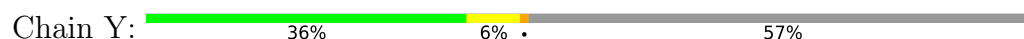
Chain S: 



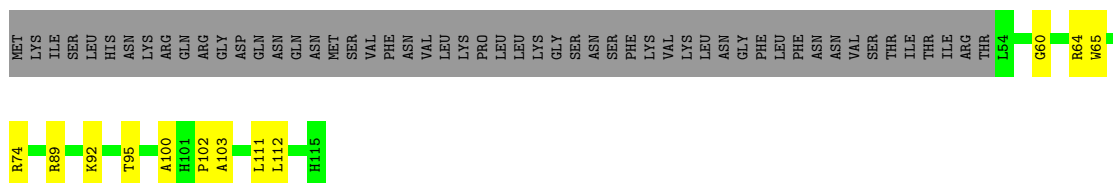
- Molecule 24: 54S ribosomal protein L39, mitochondrial



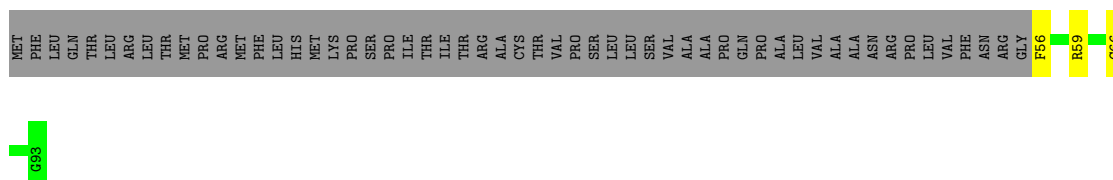
- Molecule 25: 54S ribosomal protein L34, mitochondrial



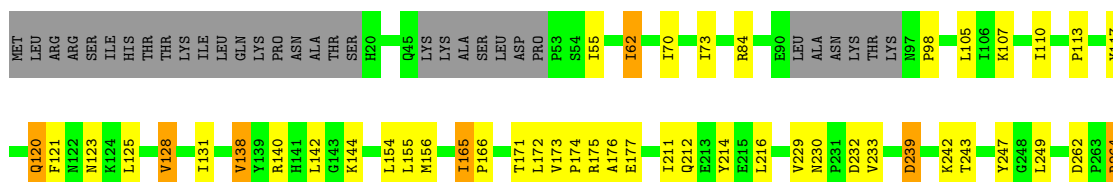
- Molecule 26: mitochondrial ribosomal protein YNL122C

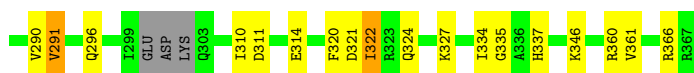


- Molecule 27: 54S ribosomal protein RTC6, mitochondrial



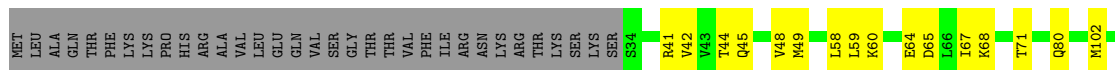
- Molecule 28: 54S ribosomal protein L35, mitochondrial





- Molecule 29: 54S ribosomal protein L28, mitochondrial

Chain 2: 59% 16% 23%



- Molecule 30: 54S ribosomal protein L27, mitochondrial

Chain 3: 77% 10% 14%



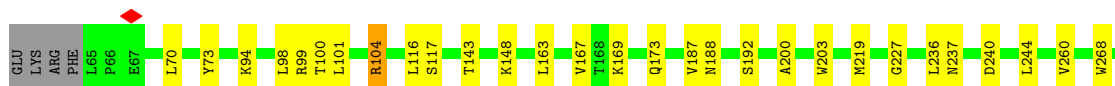
- Molecule 31: 54S ribosomal protein L51, mitochondrial

Chain 4: 76% 19% 5%



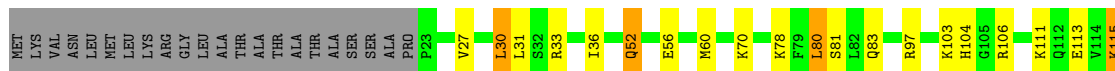
- Molecule 32: 54S ribosomal protein L3, mitochondrial

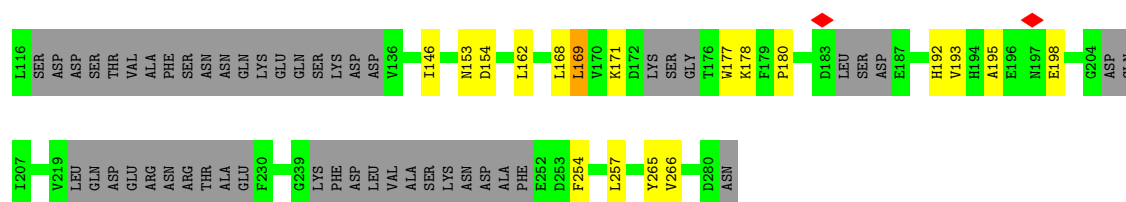
Chain 5: 68% 14% 16%



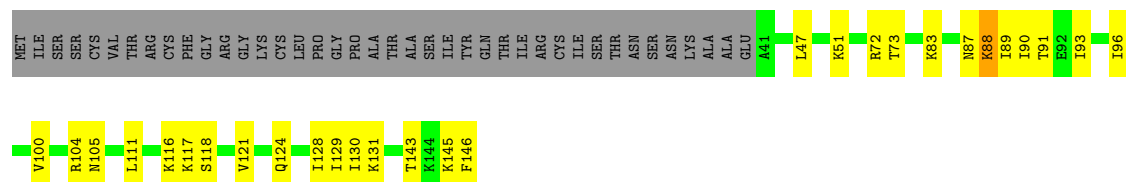
- Molecule 33: 54S ribosomal protein L17, mitochondrial

Chain 6: 61% 12% 26%

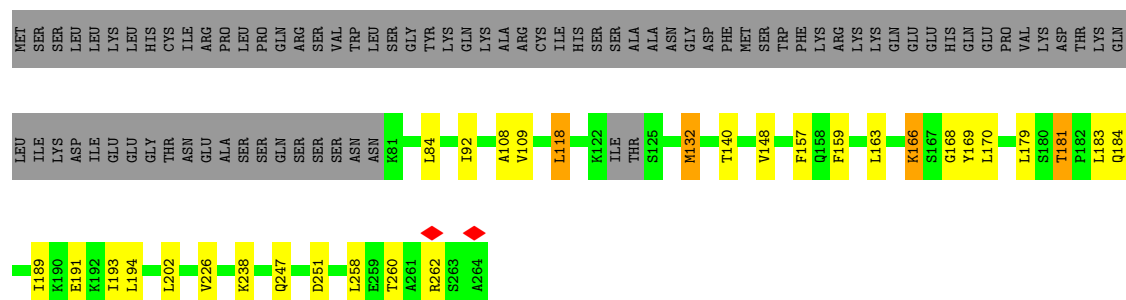




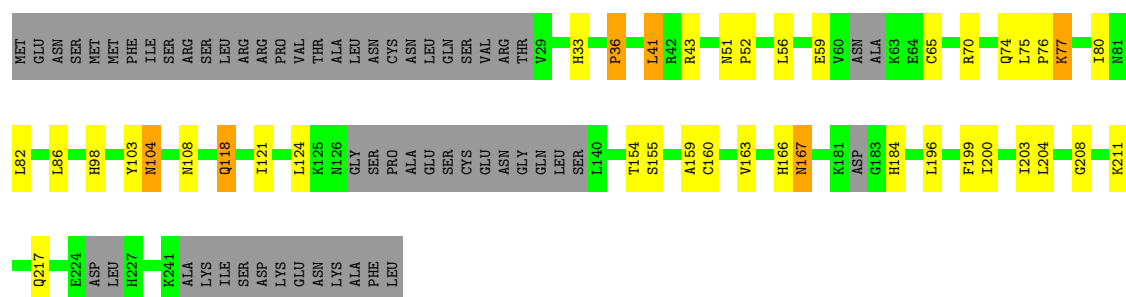
- Molecule 34: 54S ribosomal protein IMG2, mitochondrial



- Molecule 35: 54S ribosomal protein L13, mitochondrial



- Molecule 36: 54S ribosomal protein L15, mitochondrial



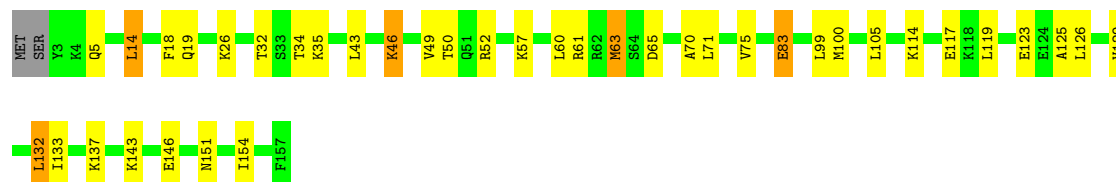
- Molecule 37: 54S ribosomal protein L20, mitochondrial





- Molecule 38: 54S ribosomal protein L25, mitochondrial

Chain b: 74% 22%



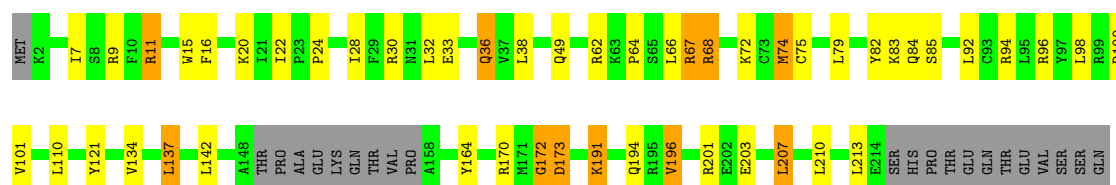
- Molecule 39: 54S ribosomal protein L31, mitochondrial

Chain c: 73% 15% 10%



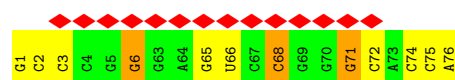
- Molecule 40: Mitochondrial homologous recombination protein 1

Chain d: 68% 18% 5% 10%



- Molecule 41: E-site tRNA

Chain e: 70% 40% 45% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	47124	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4700	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.687	Depositor
Minimum map value	-0.940	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.0681	Depositor
Map size ($\text{\AA}$)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NA, MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.37	0/64599	0.72	50/100487 (0.0%)
2	B	0.49	0/2305	0.84	0/3102
3	C	0.43	0/1973	0.76	0/2654
4	D	0.45	0/1904	0.90	2/2579 (0.1%)
5	E	0.42	0/2181	0.83	0/2955
6	F	0.47	0/1376	0.87	0/1869
7	G	0.41	0/468	0.82	0/628
8	H	0.47	0/1200	0.87	0/1610
9	I	0.41	0/943	0.76	1/1260 (0.1%)
10	J	0.42	0/1764	0.90	0/2360
11	K	0.43	0/1606	0.92	3/2148 (0.1%)
12	L	0.44	0/1843	0.97	0/2486
13	M	0.40	0/1224	0.84	1/1651 (0.1%)
14	N	0.40	0/961	0.73	0/1295
15	O	0.46	0/1821	0.97	0/2444
16	P	0.42	0/1766	0.89	0/2381
17	Q	0.44	0/2174	0.87	2/2946 (0.1%)
18	R	0.46	0/2522	1.01	3/3392 (0.1%)
19	S	0.43	0/1216	0.84	0/1626
20	T	0.48	0/1689	1.05	1/2297 (0.0%)
21	U	0.51	0/648	0.97	0/870
22	V	0.36	0/539	0.64	0/726
23	W	0.43	0/955	0.90	1/1273 (0.1%)
24	X	0.45	0/520	0.79	2/696 (0.3%)
25	Y	0.62	0/383	0.92	0/504
26	Z	0.56	0/522	0.96	0/695
27	0	0.40	0/329	0.59	0/432
28	1	0.42	0/2777	0.89	3/3772 (0.1%)
29	2	0.46	0/938	1.08	2/1264 (0.2%)
30	3	0.41	0/1018	0.77	0/1368
31	4	0.42	0/1138	0.87	1/1526 (0.1%)
32	5	0.44	0/2538	1.01	1/3451 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	6	0.41	0/1631	0.81	0/2214
34	7	0.42	0/869	0.80	0/1166
35	8	0.44	0/1438	0.98	0/1945
36	9	0.44	0/1453	1.04	1/1969 (0.1%)
37	a	0.43	0/1458	0.96	0/1961
38	b	0.41	0/1333	0.96	0/1783
39	c	0.45	0/1024	0.97	2/1367 (0.1%)
40	d	0.43	0/1762	0.96	1/2381 (0.0%)
41	e	0.38	0/476	0.76	1/739 (0.1%)
All	All	0.40	0/119284	0.80	78/174272 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	0
3	C	0	1
4	D	0	1
10	J	0	1
20	T	0	1
37	a	0	1
All	All	1	5

There are no bond length outliers.

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2897	A	C2'-C3'-O3'	11.55	126.83	109.50
1	A	1892	G	C2'-C3'-O3'	11.50	126.75	109.50
1	A	733	A	C2'-C3'-O3'	8.48	126.42	113.70
31	4	46	SER	N-CA-C	8.22	122.13	112.93
1	A	2586	U	C2'-C3'-O3'	8.18	121.77	109.50
1	A	3252	U	C2'-C3'-O3'	7.85	121.28	109.50
1	A	1306	A	C4'-C3'-O3'	7.75	121.02	109.40
1	A	2426	A	C2'-C3'-O3'	7.66	120.98	109.50
1	A	261	A	C4'-C3'-O3'	7.49	120.63	109.40
11	K	223	GLU	CA-C-N	7.49	129.20	119.84
11	K	223	GLU	C-N-CA	7.49	129.20	119.84
1	A	1706	G	C2'-C3'-O3'	7.41	120.61	109.50
1	A	276	U	C4'-C3'-O3'	7.36	120.44	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	R	199	ILE	N-CA-CB	7.12	118.88	110.55
1	A	2906	U	C2'-C3'-O3'	7.06	124.30	113.70
1	A	1312	G	C2'-C3'-O3'	6.95	124.13	113.70
1	A	307	G	C4'-C3'-O3'	6.93	119.80	109.40
1	A	3268	A	C2'-C3'-O3'	6.88	124.03	113.70
1	A	3122	U	C2'-C3'-O3'	6.67	119.51	109.50
1	A	1547	U	C4'-C3'-O3'	6.64	119.36	109.40
1	A	2329	A	C4'-C3'-O3'	6.58	119.27	109.40
1	A	1272	U	C4'-C3'-O3'	6.56	119.24	109.40
1	A	840	C	C2'-C3'-O3'	6.49	123.43	113.70
1	A	2373	U	C2'-C3'-O3'	6.46	119.19	109.50
1	A	3020	U	C2'-C3'-O3'	6.45	123.37	113.70
1	A	1409	C	C2'-C3'-O3'	6.37	123.26	113.70
1	A	44	U	C2'-C3'-O3'	6.36	123.24	113.70
32	5	279	VAL	CB-CA-C	-6.29	103.92	111.97
18	R	220	TYR	CA-C-O	-6.24	113.93	120.55
1	A	326	A	C2'-C3'-O3'	6.24	123.05	113.70
1	A	2941	A	C4'-C3'-O3'	-6.22	103.66	113.00
28	1	138	VAL	CB-CA-C	-6.21	104.02	111.97
41	e	1	G	C5'-C4'-C3'	6.17	125.25	116.00
1	A	2585	A	C2'-C3'-O3'	6.12	118.67	109.50
1	A	951	A	C4'-C3'-O3'	6.08	118.52	109.40
1	A	2316	A	C2'-C3'-O3'	5.97	118.46	109.50
1	A	28	U	C4'-C3'-O3'	5.88	118.22	109.40
1	A	3171	A	C4'-C3'-O3'	5.87	118.20	109.40
13	M	49	ILE	N-CA-CB	5.78	119.25	110.58
1	A	1355	G	C4'-C3'-O3'	5.66	117.89	109.40
28	1	173	VAL	CA-C-N	5.65	126.90	119.84
28	1	173	VAL	C-N-CA	5.65	126.90	119.84
24	X	40	ASP	CA-C-N	5.60	125.22	119.56
24	X	40	ASP	C-N-CA	5.60	125.22	119.56
1	A	1361	C	C4'-C3'-O3'	5.60	117.80	109.40
1	A	746	A	C2'-C3'-O3'	5.59	117.88	109.50
4	D	135	ALA	CA-C-N	-5.57	112.88	119.84
4	D	135	ALA	C-N-CA	-5.57	112.88	119.84
1	A	1064	A	C2'-C3'-O3'	5.57	117.85	109.50
20	T	155	VAL	N-CA-CB	5.52	118.04	110.54
39	c	116	VAL	CA-C-N	5.48	126.69	119.84
39	c	116	VAL	C-N-CA	5.48	126.69	119.84
1	A	2941	A	N9-C1'-C2'	5.47	120.21	112.00
1	A	3068	U	C4'-C3'-O3'	5.46	121.19	113.00
1	A	3135	U	C4'-C3'-O3'	5.45	117.58	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	680	A	C2'-C3'-O3'	-5.44	105.53	113.70
9	I	25	ILE	N-CA-C	5.44	115.69	110.74
1	A	2359	U	C2'-C3'-O3'	5.40	121.79	113.70
1	A	1665	G	N9-C1'-C2'	5.35	120.02	112.00
1	A	2437	U	C2'-C3'-O3'	5.32	117.48	109.50
11	K	144	THR	N-CA-C	5.32	117.08	111.28
1	A	2467	A	C2'-C3'-O3'	5.32	121.68	113.70
18	R	70	LYS	N-CA-C	-5.31	105.54	112.23
1	A	25	A	C2'-C3'-O3'	5.26	117.38	109.50
1	A	1093	A	C4'-C3'-O3'	5.26	117.29	109.40
1	A	1522	A	C2'-C3'-O3'	5.26	121.58	113.70
1	A	643	U	C4'-C3'-O3'	5.25	117.27	109.40
40	d	100	ASP	N-CA-C	5.23	116.67	110.97
1	A	158	C	C3'-C2'-O2'	5.18	118.47	110.70
1	A	3193	A	C2'-C3'-O3'	5.17	121.46	113.70
23	W	127	ILE	N-CA-CB	5.14	117.53	110.54
29	2	125	PHE	CA-C-N	5.11	126.22	119.84
29	2	125	PHE	C-N-CA	5.11	126.22	119.84
1	A	2446	U	C2'-C3'-O3'	5.10	117.15	109.50
36	9	155	SER	N-CA-C	5.09	117.10	110.43
1	A	615	U	C2'-C3'-O3'	5.07	121.31	113.70
17	Q	199	ASP	CA-C-N	5.00	124.44	119.24
17	Q	199	ASP	C-N-CA	5.00	124.44	119.24

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1665	G	C1'

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	210	ASP	Peptide
4	D	49	PHE	Peptide
10	J	93	GLN	Peptide
20	T	43	HIS	Peptide
37	a	87	MET	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	57671	28898	28934	636	0
2	B	2260	2343	2303	49	0
3	C	1930	1976	1964	21	0
4	D	1866	1914	1898	30	0
5	E	2125	2169	2125	26	0
6	F	1355	1392	1338	23	0
7	G	458	471	467	2	0
8	H	1176	1218	1210	19	0
9	I	937	1015	1013	10	0
10	J	1727	1828	1812	13	0
11	K	1573	1635	1629	11	0
12	L	1815	1883	1873	21	0
13	M	1206	1286	1283	13	0
14	N	948	1010	1006	2	0
15	O	1789	1895	1877	22	0
16	P	1722	1728	1718	24	0
17	Q	2126	2161	2092	20	0
18	R	2481	2500	2413	27	0
19	S	1191	1249	1234	17	0
20	T	1646	1618	1557	26	0
21	U	639	702	699	12	0
22	V	528	555	553	5	0
23	W	937	985	974	10	0
24	X	512	565	563	7	0
25	Y	376	412	410	3	0
26	Z	508	546	539	6	0
27	0	324	349	345	3	0
28	1	2707	2690	2661	27	0
29	2	919	939	923	15	0
30	3	995	1030	1012	10	0
31	4	1117	1146	1142	19	0
32	5	2485	2541	2488	29	0
33	6	1592	1595	1511	14	0
34	7	854	901	897	10	0
35	8	1413	1416	1381	15	0
36	9	1428	1437	1368	19	0
37	a	1427	1455	1449	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	b	1299	1372	1367	14	0
39	c	1000	1066	1062	12	0
40	d	1717	1706	1691	24	0
41	e	427	221	222	9	0
42	A	109	0	0	0	0
42	N	1	0	0	0	0
43	B	1	0	0	0	0
44	O	1	0	0	1	0
44	W	1	0	0	0	0
All	All	111319	83818	83003	1111	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 6.

All (1111) 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)
1:A:45:U:O4	1:A:2895:A:N1	1.58	1.36
1:A:114:U:O4	1:A:118:A:N1	1.68	1.25
1:A:1913:A:N1	1:A:2880:U:O4	1.73	1.21
1:A:122:A:N6	1:A:139:U:N3	1.91	1.19
1:A:274:U:O4	1:A:367:A:N1	1.78	1.15
1:A:1344:U:O4	1:A:1555:A:N1	1.85	1.09
1:A:1344:U:C4	1:A:1555:A:N1	2.23	1.06
1:A:45:U:H3	1:A:2895:A:H61	1.04	1.00
1:A:123:A:C2	1:A:139:U:O2	2.20	0.94
1:A:1689:U:H3	1:A:2853:A:H61	1.15	0.94
1:A:230:A:H8	1:A:588:C:HO2'	1.08	0.93
27:0:66:CYS:SG	44:0:100:ZN:ZN	1.57	0.92
1:A:1913:A:N6	1:A:2880:U:H3	1.68	0.91
1:A:1361:C:O2'	1:A:1362:C:H6	1.53	0.91
1:A:2941:A:H2'	1:A:2942:A:C8	2.06	0.91
1:A:45:U:H3	1:A:2895:A:N6	1.67	0.90
1:A:944:U:HO2'	1:A:946:A:H2	1.20	0.89
1:A:274:U:H3	1:A:367:A:N6	1.70	0.88
1:A:315:A:H4'	1:A:315:A:OP1	1.72	0.88
1:A:1360:G:C6	1:A:1361:C:N3	2.43	0.87
1:A:1689:U:H3	1:A:2853:A:N6	1.73	0.86
1:A:2949:C:O2	3:C:79:ARG:NH2	2.08	0.86
26:Z:60:GLY:O	26:Z:64:ARG:HD2	1.75	0.86
1:A:152:G:O2'	1:A:153:G:O5'	1.94	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1583:G:C2'	1:A:1585:G:H22	1.89	0.85
1:A:1361:C:O2'	1:A:1362:C:O5'	1.95	0.85
1:A:3160:U:H5''	12:L:52:THR:HG21	1.58	0.84
6:F:24:LEU:HD13	6:F:107:ILE:HD11	1.57	0.84
1:A:3242:A:H2'	1:A:3243:A:C8	2.14	0.82
1:A:1360:G:C5	1:A:1361:C:N3	2.48	0.82
32:5:104:ARG:NH1	32:5:203:TRP:O	2.13	0.82
1:A:274:U:H3	1:A:367:A:H61	1.24	0.81
1:A:2359:U:O3'	18:R:169:ARG:NH2	2.13	0.81
1:A:268:C:N4	1:A:2674:U:O2	2.13	0.81
1:A:122:A:N6	1:A:139:U:C2	2.48	0.81
1:A:3156:U:H2'	1:A:3157:A:C8	2.17	0.80
1:A:3162:U:H2'	1:A:3163:U:C6	2.15	0.80
1:A:114:U:C4	1:A:118:A:N1	2.50	0.80
1:A:45:U:O4	1:A:2895:A:C2	2.34	0.80
1:A:164:U:O2	16:P:82:ASN:HA	1.81	0.80
1:A:2792:G:HO2'	27:O:56:PHE:N	1.81	0.79
1:A:1913:A:N6	1:A:2880:U:N3	2.26	0.78
1:A:2612:A:C8	1:A:2648:A:H2'	2.18	0.78
1:A:164:U:O2'	1:A:165:A:OP1	2.00	0.78
13:M:144:GLN:O	13:M:145:ARG:HB2	1.83	0.78
1:A:238:C:H5	1:A:288:G:H1	1.32	0.78
1:A:1681:C:O2	1:A:1681:C:O5'	2.02	0.77
1:A:307:G:O2'	1:A:308:U:O5'	2.03	0.76
1:A:122:A:N6	1:A:139:U:H3	1.80	0.76
1:A:45:U:C4	1:A:2895:A:N1	2.53	0.76
1:A:1360:G:C2	1:A:1361:C:O2	2.39	0.76
33:6:36:ILE:HD11	33:6:162:LEU:HD22	1.68	0.75
1:A:849:U:H2'	1:A:850:A:C8	2.21	0.75
1:A:1583:G:H2'	1:A:1585:G:H22	1.54	0.73
1:A:307:G:HO2'	1:A:308:U:P	2.12	0.73
1:A:1913:A:N1	1:A:2880:U:C4	2.57	0.72
20:T:53:ILE:HD11	40:d:134:VAL:HG12	1.72	0.72
1:A:1313:G:H5'	1:A:1314:U:H2'	1.70	0.71
1:A:727:G:C6	1:A:728:C:N3	2.58	0.71
1:A:3159:G:N2	1:A:3248:C:C2	2.58	0.71
2:B:155:ILE:HD11	2:B:157:PHE:CZ	2.26	0.71
1:A:1344:U:C4	1:A:1555:A:C2	2.78	0.71
15:O:294:LEU:HD21	32:5:335:VAL:HG12	1.73	0.70
1:A:2373:U:O2'	1:A:2374:A:OP2	2.09	0.70
1:A:2597:G:N2	1:A:2652:C:C2	2.59	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3159:G:N2	12:L:102:PRO:O	2.24	0.70
1:A:2957:A:H1'	1:A:2958:U:H5''	1.74	0.70
1:A:3025:U:H2'	1:A:3026:A:C8	2.26	0.70
1:A:563:U:O2'	1:A:564:A:OP1	2.08	0.70
1:A:1583:G:H2'	1:A:1585:G:N2	2.06	0.70
1:A:1075:A:C6	1:A:1076:U:H1'	2.27	0.69
1:A:2913:U:O4	1:A:2941:A:N1	2.26	0.69
6:F:119:LEU:HD11	6:F:169:ILE:HD11	1.73	0.69
1:A:114:U:N3	1:A:118:A:N6	2.39	0.69
31:4:60:GLN:HB3	32:5:100:THR:HG21	1.74	0.68
1:A:1312:G:H2'	1:A:1313:G:H5''	1.74	0.68
1:A:2913:U:H3	1:A:2941:A:H2	1.42	0.68
1:A:616:A:O2'	1:A:617:A:OP1	2.09	0.68
1:A:841:G:OP1	5:E:110:ASN:HB2	1.94	0.68
1:A:2670:C:N3	1:A:2682:G:C2	2.62	0.67
1:A:2613:A:O2'	1:A:2614:U:OP1	2.12	0.67
1:A:1361:C:O2'	1:A:1362:C:C5'	2.42	0.67
9:I:2:ILE:HD11	9:I:94:THR:HG21	1.76	0.67
1:A:268:C:O2'	1:A:269:A:OP2	2.12	0.67
13:M:61:LEU:O	13:M:62:ILE:HB	1.95	0.67
40:d:74:MET:HE2	40:d:170:ARG:HD3	1.76	0.67
1:A:1361:C:O2'	1:A:1362:C:C6	2.33	0.67
1:A:2814:U:H5'	1:A:2833:A:C2	2.30	0.66
16:P:181:PHE:HB3	20:T:127:LEU:HD11	1.78	0.66
1:A:115:A:OP2	17:Q:9:SER:OG	2.14	0.66
1:A:1180:C:OP1	21:U:72:ARG:NH1	2.29	0.66
1:A:3247:A:C2	1:A:3250:A:N6	2.63	0.66
1:A:1892:G:O2'	1:A:1893:U:OP2	2.10	0.66
3:C:59:CYS:SG	3:C:60:GLY:N	2.68	0.66
1:A:486:G:H22	10:J:91:ARG:NE	1.94	0.66
1:A:2913:U:C5	1:A:3068:U:H2'	2.30	0.66
17:Q:27:LEU:N	17:Q:28:PRO:HD2	2.10	0.66
1:A:1913:A:C2	1:A:2880:U:O4	2.49	0.66
1:A:3160:U:C5'	12:L:52:THR:HG21	2.26	0.66
1:A:743:A:O2'	21:U:42:ALA:O	2.15	0.65
40:d:79:LEU:HD12	40:d:85:SER:HA	1.76	0.65
1:A:1424:U:H2'	1:A:1425:U:O4'	1.96	0.65
1:A:1312:G:O2'	1:A:1313:G:OP1	2.13	0.65
1:A:1343:U:H1'	1:A:1344:U:C5	2.32	0.65
4:D:133:ARG:O	4:D:134:THR:HG22	1.97	0.65
9:I:79:ARG:O	9:I:80:ASN:CB	2.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:151:GLN:O	20:T:155:VAL:HG13	1.97	0.65
1:A:1392:A:O2'	1:A:1393:U:O5'	2.13	0.64
1:A:275:A:C2	1:A:367:A:C2	2.86	0.64
1:A:2094:A:N6	1:A:2250:G:O2'	2.30	0.64
1:A:1064:A:O2'	1:A:1065:A:OP2	2.12	0.64
17:Q:83:ILE:HG22	17:Q:95:LEU:HD22	1.79	0.64
30:3:61:ILE:HG23	30:3:77:VAL:HG22	1.78	0.64
1:A:1696:A:OP2	2:B:334:ARG:NH1	2.31	0.64
24:X:16:THR:HG21	38:b:132:LEU:HD13	1.80	0.64
33:6:171:LYS:HA	33:6:177:TRP:HB2	1.79	0.64
40:d:92:LEU:HD21	40:d:137:LEU:HA	1.78	0.64
1:A:114:U:O4	1:A:118:A:C2	2.50	0.64
1:A:2612:A:N3	1:A:2612:A:H5''	2.13	0.64
1:A:3247:A:H2	1:A:3250:A:H61	1.46	0.64
12:L:190:LYS:O	12:L:194:LEU:HD22	1.98	0.64
1:A:608:A:C2	1:A:1585:G:H8	2.15	0.63
1:A:608:A:C2	1:A:1585:G:C8	2.87	0.63
24:X:17:ALA:HA	38:b:125:ALA:HB1	1.80	0.63
1:A:2601:A:HO2'	1:A:2602:A:H8	1.47	0.63
1:A:3159:G:C2	1:A:3248:C:N3	2.66	0.63
18:R:198:LEU:HD21	18:R:254:LEU:HD22	1.79	0.63
1:A:1344:U:O4	1:A:1555:A:C6	2.52	0.63
12:L:111:LEU:HD22	23:W:118:MET:HE1	1.80	0.63
5:E:84:ILE:HD11	29:2:123:LYS:CB	2.29	0.63
8:H:39:LEU:O	8:H:54:GLY:HA3	1.98	0.63
16:P:255:LEU:HD21	32:5:73:TYR:CE2	2.33	0.62
1:A:3242:A:H2'	1:A:3243:A:H8	1.60	0.62
14:N:80:LEU:HD12	14:N:151:THR:HG21	1.79	0.62
2:B:338:MET:HE2	2:B:343:HIS:HB2	1.80	0.62
1:A:1761:A:H2'	1:A:1762:A:C8	2.35	0.62
1:A:2331:U:O2	1:A:2367:A:H1'	1.99	0.62
11:K:63:SER:O	11:K:64:ILE:HG22	1.98	0.62
34:7:96:ILE:HG21	34:7:100:VAL:HG12	1.82	0.62
1:A:1343:U:C1'	1:A:1344:U:C5	2.83	0.62
31:4:13:ARG:NH1	32:5:289:SER:O	2.33	0.61
36:9:76:PRO:O	36:9:77:LYS:CB	2.48	0.61
1:A:2913:U:H5	1:A:3068:U:H2'	1.64	0.61
3:C:213:ARG:NH2	8:H:82:GLY:O	2.33	0.61
10:J:76:ARG:HG3	10:J:76:ARG:HH11	1.64	0.61
1:A:2446:U:O2'	1:A:2447:A:O5'	2.17	0.61
1:A:238:C:O2	1:A:238:C:O5'	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:227:ILE:HD13	16:P:232:LYS:HD3	1.82	0.61
1:A:314:A:N6	1:A:361:G:C8	2.69	0.61
28:1:243:THR:OG1	28:1:320:PHE:O	2.18	0.61
1:A:2670:C:C2	1:A:2682:G:N2	2.68	0.61
1:A:2958:U:H3'	1:A:2958:U:O2	2.00	0.61
1:A:271:A:H2'	1:A:272:G:O4'	2.01	0.61
6:F:69:VAL:HG11	6:F:73:LEU:HD23	1.83	0.61
15:O:177:ALA:HB3	15:O:235:THR:HG21	1.83	0.60
5:E:217:ILE:HG23	5:E:220:TYR:HB2	1.81	0.60
12:L:111:LEU:HD21	12:L:123:VAL:HG23	1.83	0.60
18:R:176:LEU:HD13	18:R:198:LEU:HB3	1.82	0.60
1:A:1696:A:H2'	1:A:1697:C:O4'	2.01	0.60
1:A:2913:U:N3	1:A:2941:A:C2	2.66	0.60
1:A:1361:C:O2	1:A:1361:C:O4'	2.19	0.60
18:R:77:VAL:HG13	18:R:85:ILE:HG23	1.84	0.60
1:A:486:G:H22	10:J:91:ARG:HE	1.48	0.60
1:A:274:U:C4	1:A:367:A:N1	2.66	0.60
1:A:3271:A:HO2'	13:M:16:TYR:N	2.00	0.59
31:4:99:LYS:O	31:4:102:LYS:HG3	2.02	0.59
1:A:1107:U:H2'	8:H:68:THR:HG21	1.84	0.59
1:A:34:U:O2'	1:A:35:U:P	2.60	0.59
1:A:549:U:O2	1:A:2635:C:O2'	2.16	0.59
1:A:671:G:H2'	1:A:673:A:N7	2.18	0.59
2:B:241:LEU:HD11	2:B:305:ILE:HD11	1.85	0.59
2:B:254:ASN:O	2:B:303:ALA:HA	2.02	0.59
1:A:346:G:C2	1:A:357:C:O2	2.55	0.59
1:A:2670:C:C2	1:A:2682:G:C2	2.91	0.59
24:X:35:THR:HB	24:X:48:LEU:HD11	1.85	0.59
1:A:1944:C:C2	1:A:2892:G:N2	2.71	0.59
1:A:461:U:H6	1:A:461:U:H5'	1.68	0.59
18:R:54:GLY:O	18:R:113:ARG:NH2	2.35	0.59
1:A:1358:C:H2'	1:A:1358:C:O2	2.03	0.59
1:A:2585:A:H4'	1:A:2586:U:OP1	2.03	0.59
1:A:1361:C:HO2'	1:A:1362:C:H6	0.72	0.58
1:A:1583:G:N3	1:A:1585:G:N2	2.51	0.58
2:B:278:LYS:HG2	2:B:299:LEU:HD11	1.85	0.58
16:P:227:ILE:HD12	16:P:227:ILE:O	2.03	0.58
1:A:1313:G:N2	1:A:1321:C:C2	2.71	0.58
20:T:56:THR:HG22	40:d:172:GLY:O	2.02	0.58
1:A:122:A:N6	1:A:140:U:C4	2.72	0.58
1:A:543:A:N1	1:A:550:A:N1	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:850:A:H2'	1:A:851:A:C8	2.39	0.58
1:A:1564:C:C2	1:A:1572:G:C2	2.92	0.58
1:A:615:U:C2'	1:A:616:A:OP1	2.51	0.58
1:A:331:A:O2'	1:A:332:A:P	2.62	0.58
1:A:2597:G:C2	1:A:2652:C:C2	2.92	0.58
1:A:1549:U:OP1	16:P:119:ARG:NH2	2.36	0.58
36:9:51:ASN:HB2	36:9:52:PRO:HD2	1.86	0.58
36:9:103:TYR:O	36:9:104:ASN:CB	2.51	0.58
1:A:1173:U:H2'	1:A:1174:G:O4'	2.04	0.57
1:A:966:A:C2	1:A:1059:A:C2	2.92	0.57
1:A:2835:U:H2'	1:A:2836:G:O4'	2.05	0.57
1:A:2593:A:H2'	1:A:2594:A:C8	2.39	0.57
7:G:21:VAL:HG12	7:G:57:TYR:HA	1.86	0.57
9:I:24:VAL:HG22	9:I:34:ALA:HB2	1.85	0.57
6:F:28:PRO:O	6:F:29:GLU:CB	2.51	0.57
38:b:75:VAL:HG12	38:b:75:VAL:O	2.04	0.57
1:A:122:A:C6	1:A:139:U:N3	2.62	0.57
1:A:1944:C:C2	1:A:2892:G:C2	2.92	0.57
11:K:85:ILE:HD12	11:K:142:VAL:HG21	1.87	0.57
20:T:95:ILE:N	20:T:96:PRO:CD	2.68	0.57
1:A:23:U:H2'	1:A:24:G:C8	2.40	0.57
12:L:170:LEU:HD13	12:L:213:LEU:HD11	1.85	0.57
1:A:1386:A:O2'	19:S:65:ILE:O	2.15	0.57
1:A:3107:U:OP1	3:C:52:ARG:NH1	2.37	0.57
1:A:2590:U:H3'	1:A:2591:A:H5'	1.86	0.57
1:A:1755:A:H2'	1:A:1756:U:C6	2.40	0.56
4:D:135:ALA:CB	4:D:136:PRO:CD	2.83	0.56
1:A:1360:G:N2	1:A:1552:C:C2	2.73	0.56
1:A:1074:U:O4	1:A:1075:A:N6	2.38	0.56
1:A:1344:U:H2'	1:A:1562:A:C2	2.40	0.56
1:A:2612:A:H2	1:A:2638:G:H1	1.52	0.56
1:A:3031:U:C4	1:A:3032:U:C4	2.92	0.56
1:A:3035:U:O2	1:A:3035:U:O4'	2.23	0.56
8:H:102:GLY:HA2	8:H:128:VAL:HG11	1.87	0.56
21:U:26:LEU:HD21	21:U:47:LEU:HD23	1.87	0.56
23:W:123:GLN:O	23:W:127:ILE:HG23	2.05	0.56
1:A:847:U:O2	1:A:847:U:O4'	2.23	0.56
1:A:2733:A:N6	1:A:2734:A:C6	2.73	0.56
16:P:184:SER:HA	20:T:131:VAL:HG23	1.86	0.56
31:4:27:THR:HB	31:4:73:ARG:HG3	1.87	0.56
15:O:133:LYS:HE3	15:O:279:TYR:CZ	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:2:117:ASN:O	29:2:118:ALA:C	2.48	0.56
1:A:1343:U:C2	1:A:1344:U:O4	2.59	0.56
1:A:1725:G:OP1	2:B:176:ARG:NH2	2.39	0.56
1:A:34:U:O2'	1:A:35:U:O5'	2.23	0.56
1:A:2335:U:O4'	1:A:2335:U:O2	2.23	0.56
6:F:152:LEU:HD21	6:F:185:LEU:HD23	1.88	0.56
1:A:1261:U:H5'	31:4:71:LEU:HD21	1.87	0.56
1:A:1362:C:H2'	1:A:1363:C:H6	1.70	0.56
1:A:1952:A:H4'	3:C:207:GLN:O	2.06	0.56
1:A:2958:U:O2'	1:A:2959:C:O4'	2.20	0.56
1:A:1344:U:C5	1:A:1555:A:C2	2.93	0.56
32:5:283:ILE:O	32:5:287:ILE:N	2.38	0.56
1:A:878:G:H22	1:A:891:A:H2	1.53	0.55
1:A:1360:G:C2	1:A:1552:C:C2	2.94	0.55
1:A:2711:G:OP1	4:D:115:ARG:NH2	2.38	0.55
8:H:108:ALA:O	8:H:112:MET:HG2	2.06	0.55
31:4:16:VAL:HG23	32:5:289:SER:HB2	1.88	0.55
1:A:23:U:HO2'	36:9:98:HIS:HD1	1.40	0.55
4:D:233:ILE:HG22	4:D:245:VAL:HG11	1.89	0.55
35:8:132:MET:SD	35:8:166:LYS:HB3	2.47	0.55
1:A:2597:G:C2	1:A:2652:C:N3	2.75	0.55
4:D:70:ARG:NH1	34:7:124:GLN:O	2.40	0.55
1:A:238:C:O2	1:A:238:C:O4'	2.24	0.55
1:A:386:U:O2	1:A:386:U:O4'	2.25	0.55
1:A:1833:G:C6	1:A:1834:C:C4	2.94	0.55
1:A:2360:U:P	18:R:169:ARG:HH22	2.30	0.55
1:A:2958:U:H2'	1:A:2959:C:C6	2.42	0.55
4:D:205:VAL:HG11	35:8:108:ALA:HB1	1.87	0.55
23:W:157:ARG:NH2	40:d:121:TYR:O	2.40	0.55
32:5:167:VAL:HG13	32:5:288:MET:HE1	1.89	0.55
19:S:132:ILE:HD12	19:S:132:ILE:N	2.22	0.55
37:a:66:VAL:HG12	37:a:66:VAL:O	2.06	0.55
1:A:595:U:O4	25:Y:73:ARG:HB2	2.05	0.54
20:T:144:SER:O	20:T:147:THR:OG1	2.22	0.54
1:A:1698:C:O3'	2:B:318:LEU:O	2.26	0.54
1:A:1743:G:N2	1:A:1744:C:C2	2.75	0.54
1:A:602:A:O2'	1:A:1366:A:N3	2.37	0.54
1:A:2426:A:O2'	1:A:2427:U:O5'	2.20	0.54
1:A:3279:U:H2'	1:A:3280:C:C6	2.43	0.54
17:Q:218:ILE:HG22	20:T:103:PHE:CD1	2.43	0.54
1:A:836:A:N3	1:A:2290:A:O2'	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:A:H2'	1:A:510:A:O4'	2.07	0.54
31:4:28:LEU:HD13	31:4:72:LEU:CD2	2.38	0.54
1:A:2707:G:N1	1:A:2708:C:C4	2.76	0.54
12:L:146:TRP:CZ3	23:W:127:ILE:HD11	2.43	0.54
3:C:62:ILE:HD11	3:C:138:ALA:HB3	1.90	0.54
1:A:906:A:OP1	39:c:18:LYS:HE2	2.07	0.54
1:A:1358:C:H5	1:A:1553:G:H1	1.56	0.54
8:H:37:ILE:HG23	8:H:42:ARG:HB2	1.90	0.54
1:A:857:U:O2	1:A:857:U:O4'	2.22	0.54
18:R:204:SER:CB	18:R:214:ALA:HB1	2.38	0.54
5:E:214:LEU:O	5:E:217:ILE:HG22	2.08	0.54
1:A:1313:G:C2	1:A:1321:C:C2	2.95	0.53
1:A:1561:G:H3'	1:A:1561:G:N3	2.22	0.53
6:F:125:VAL:HG12	6:F:125:VAL:O	2.09	0.53
1:A:1405:U:O4'	1:A:1405:U:O2	2.26	0.53
1:A:2720:G:C6	1:A:2765:C:N3	2.77	0.53
1:A:3160:U:H5''	12:L:52:THR:CG2	2.33	0.53
1:A:176:U:H2'	1:A:177:A:C8	2.44	0.53
1:A:2707:G:N2	1:A:2708:C:C2	2.77	0.53
6:F:65:LEU:N	6:F:65:LEU:HD22	2.24	0.53
39:c:47:LEU:O	39:c:51:VAL:HG13	2.08	0.53
1:A:3156:U:H2'	1:A:3157:A:H8	1.70	0.53
1:A:3264:C:O2'	32:5:332:LYS:O	2.26	0.53
32:5:163:LEU:HD12	32:5:283:ILE:HD11	1.90	0.53
1:A:536:A:H4'	1:A:537:U:OP1	2.07	0.53
8:H:27:THR:HG22	8:H:30:ARG:HD2	1.90	0.53
20:T:102:SER:N	20:T:105:ASP:OD2	2.42	0.53
1:A:331:A:O2'	1:A:332:A:OP2	2.25	0.53
1:A:554:U:H2'	1:A:556:A:C8	2.44	0.53
1:A:870:C:O2	1:A:870:C:O4'	2.22	0.53
1:A:2952:G:H1'	1:A:3062:A:C2	2.44	0.53
3:C:61:LEU:HD21	3:C:160:PHE:CE2	2.44	0.53
30:3:74:TRP:C	30:3:76:LYS:H	2.16	0.53
1:A:1750:G:C6	1:A:1751:C:C4	2.97	0.53
5:E:161:LEU:HD22	29:2:45:GLN:HB3	1.91	0.53
16:P:92:ILE:HG23	20:T:122:ARG:HA	1.91	0.53
1:A:595:U:H2'	1:A:595:U:O2	2.08	0.53
1:A:2287:A:OP1	18:R:45:ARG:NH2	2.41	0.53
1:A:2382:A:H4'	33:6:80:LEU:HD11	1.91	0.53
19:S:138:LYS:O	19:S:155:ARG:NH2	2.42	0.53
34:7:83:LYS:HB2	34:7:88:LYS:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:e:71:G:C6	41:e:72:C:C4	2.97	0.53
1:A:1373:U:O2	1:A:1373:U:O4'	2.25	0.52
1:A:2913:U:OP2	1:A:3069:A:OP1	2.27	0.52
15:O:172:SER:O	15:O:261:ILE:HG23	2.08	0.52
28:1:233:VAL:HG22	28:1:242:LYS:O	2.09	0.52
29:2:140:LEU:O	29:2:141:TRP:CB	2.56	0.52
32:5:324:VAL:HG21	32:5:339:HIS:ND1	2.24	0.52
16:P:186:THR:HG22	16:P:187:PRO:HD3	1.91	0.52
1:A:33:A:N6	1:A:34:U:C4	2.77	0.52
1:A:915:G:C5	21:U:13:ILE:HD12	2.44	0.52
1:A:1493:U:H2'	1:A:1494:A:C8	2.45	0.52
1:A:3247:A:H2	1:A:3250:A:N6	2.06	0.52
18:R:204:SER:HB3	18:R:214:ALA:HB1	1.91	0.52
1:A:1486:U:H2'	1:A:1487:A:C8	2.45	0.52
17:Q:213:VAL:HG22	30:3:122:ILE:HD13	1.91	0.52
20:T:57:THR:HG21	23:W:148:LEU:HD12	1.92	0.52
20:T:96:PRO:O	20:T:99:ARG:HB2	2.09	0.52
1:A:247:A:H2'	1:A:248:A:O4'	2.09	0.52
1:A:2913:U:N3	1:A:2941:A:H2	2.06	0.52
25:Y:71:LEU:HD11	25:Y:75:ARG:NH2	2.24	0.52
1:A:581:C:C2	1:A:700:G:C2	2.97	0.52
1:A:1392:A:HO2'	1:A:1393:U:C5'	2.22	0.52
32:5:188:ASN:O	32:5:192:SER:N	2.43	0.52
1:A:3162:U:N3	1:A:3163:U:C4	2.78	0.52
19:S:105:LEU:HD12	19:S:118:MET:HE3	1.91	0.52
3:C:240:ASP:OD1	3:C:240:ASP:N	2.43	0.52
10:J:76:ARG:HH11	10:J:76:ARG:CG	2.23	0.52
1:A:511:G:H2'	1:A:512:U:C6	2.46	0.51
1:A:1681:C:O2	1:A:1681:C:O4'	2.26	0.51
1:A:2720:G:C2	1:A:2765:C:O2	2.63	0.51
1:A:2741:G:N2	1:A:2796:G:H1	2.06	0.51
6:F:126:GLY:HA3	6:F:129:TYR:CD2	2.45	0.51
20:T:144:SER:O	20:T:148:THR:HG23	2.10	0.51
1:A:261:A:C4	1:A:307:G:N7	2.79	0.51
1:A:2427:U:H3'	1:A:2427:U:O2	2.10	0.51
1:A:2601:A:O2'	1:A:2602:A:C8	2.63	0.51
6:F:183:ALA:O	6:F:186:ARG:HG3	2.10	0.51
14:N:134:THR:HB	14:N:141:VAL:HG22	1.92	0.51
1:A:527:A:H62	1:A:539:U:H5'	1.74	0.51
1:A:2258:C:OP1	19:S:96:TRP:CZ3	2.64	0.51
1:A:2364:U:H2'	1:A:2365:A:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:202:MET:HG3	5:E:203:SER:N	2.24	0.51
11:K:98:MET:HA	11:K:98:MET:HE3	1.93	0.51
16:P:92:ILE:O	16:P:107:PHE:HA	2.11	0.51
1:A:441:A:N1	1:A:448:U:H5	2.09	0.51
15:O:155:GLU:O	15:O:158:VAL:HG12	2.10	0.51
20:T:89:HIS:O	30:3:96:ALA:HB2	2.11	0.51
1:A:23:U:O2'	36:9:98:HIS:ND1	2.33	0.51
1:A:3068:U:H4'	1:A:3069:A:OP2	2.10	0.51
40:d:7:ILE:HD11	40:d:49:GLN:HE22	1.76	0.51
1:A:27:A:OP1	37:a:105:SER:OG	2.15	0.51
1:A:904:G:C2	1:A:912:C:C2	2.98	0.51
1:A:2435:A:H3'	1:A:2436:A:H5''	1.91	0.51
1:A:1355:G:O2'	1:A:1356:U:P	2.69	0.51
1:A:1960:A:C2	1:A:1961:G:C8	2.99	0.51
1:A:2594:A:H2'	1:A:2595:U:C6	2.46	0.51
13:M:108:LEU:HG	13:M:125:LEU:HD23	1.93	0.51
32:5:169:LYS:O	32:5:173:GLN:HG2	2.11	0.51
36:9:82:LEU:HD11	36:9:203:ILE:HG22	1.92	0.51
1:A:834:A:HO2'	1:A:835:A:H8	1.58	0.51
17:Q:83:ILE:HG22	17:Q:95:LEU:CD2	2.41	0.51
23:W:124:ILE:O	23:W:127:ILE:HG12	2.10	0.51
37:a:66:VAL:O	37:a:66:VAL:CG1	2.59	0.51
1:A:122:A:N6	1:A:139:U:C4	2.56	0.51
1:A:1582:A:H2'	1:A:1583:G:O4'	2.11	0.51
4:D:70:ARG:HG2	4:D:70:ARG:HH11	1.76	0.51
11:K:69:LEU:HD23	11:K:69:LEU:H	1.76	0.51
19:S:105:LEU:HB3	19:S:132:ILE:HD11	1.93	0.51
24:X:16:THR:CG2	38:b:132:LEU:HD13	2.40	0.51
41:e:3:C:C2	41:e:71:G:N2	2.79	0.51
1:A:164:U:HO2'	1:A:165:A:P	2.30	0.51
1:A:1830:G:O2'	1:A:1868:G:N1	2.44	0.51
1:A:3233:A:O5'	1:A:3233:A:H8	1.94	0.51
1:A:117:U:O4'	1:A:117:U:O2	2.30	0.50
9:I:79:ARG:O	9:I:80:ASN:HB3	2.10	0.50
28:1:120:GLN:HB3	28:1:121:PHE:CD1	2.47	0.50
37:a:189:LYS:HD3	37:a:192:TRP:CZ2	2.46	0.50
1:A:1392:A:O2'	1:A:1393:U:P	2.69	0.50
11:K:223:GLU:HG2	11:K:224:PRO:HD2	1.93	0.50
15:O:127:ILE:HD12	15:O:138:VAL:HG23	1.93	0.50
16:P:138:LEU:HD11	16:P:159:LYS:HD2	1.92	0.50
32:5:364:THR:HG21	37:a:193:TYR:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2612:A:OP1	24:X:46:HIS:NE2	2.42	0.50
4:D:143:LEU:HD23	4:D:144:PRO:HD2	1.93	0.50
4:D:246:ILE:HG21	4:D:251:VAL:HA	1.93	0.50
1:A:1806:C:H2'	1:A:1830:G:C8	2.46	0.50
2:B:209:PHE:HB2	2:B:241:LEU:HB3	1.94	0.50
1:A:1535:A:H2'	1:A:1536:A:C8	2.47	0.50
1:A:419:U:H2'	1:A:420:U:O4'	2.12	0.50
1:A:2317:A:O2'	1:A:2318:U:P	2.69	0.50
1:A:2898:U:H2'	1:A:2899:U:C6	2.45	0.50
1:A:488:A:H2'	1:A:489:A:C8	2.47	0.50
1:A:1993:U:H1'	19:S:101:VAL:HG11	1.93	0.50
1:A:2258:C:OP1	19:S:96:TRP:HZ3	1.95	0.50
18:R:286:LEU:HD12	18:R:324:TYR:CG	2.46	0.50
1:A:3069:A:O2'	1:A:3070:A:OP2	2.21	0.50
1:A:3192:A:H2'	1:A:3193:A:O4'	2.11	0.50
2:B:286:ILE:HD11	2:B:296:TYR:CE1	2.46	0.50
22:V:49:MET:HE3	22:V:70:LEU:HD11	1.94	0.50
33:6:171:LYS:HA	33:6:177:TRP:CB	2.41	0.50
1:A:502:A:C8	1:A:563:U:C5	3.00	0.50
1:A:1972:G:C6	1:A:1973:C:C4	3.00	0.50
1:A:2263:U:O2'	1:A:2265:G:N7	2.39	0.50
1:A:275:A:N6	1:A:276:U:O4	2.45	0.49
1:A:346:G:C6	1:A:357:C:N3	2.80	0.49
1:A:645:U:H2'	1:A:646:C:C6	2.47	0.49
1:A:2958:U:O2	1:A:2958:U:C3'	2.60	0.49
1:A:3069:A:C8	1:A:3108:U:H1'	2.46	0.49
8:H:139:ASN:HB3	32:5:329:ARG:O	2.12	0.49
11:K:60:THR:HG23	39:c:128:PRO:HB3	1.94	0.49
1:A:3159:G:C2	1:A:3248:C:C2	3.00	0.49
4:D:200:ILE:O	4:D:201:PHE:CB	2.59	0.49
1:A:238:C:O2	1:A:238:C:C5'	2.60	0.49
1:A:365:A:N3	1:A:365:A:H2'	2.28	0.49
1:A:1318:A:N7	12:L:116:ASN:ND2	2.59	0.49
33:6:27:VAL:HG11	33:6:195:ALA:HB2	1.94	0.49
36:9:118:GLN:O	36:9:121:ILE:HG22	2.13	0.49
1:A:2648:A:O3'	5:E:19:PRO:N	2.45	0.49
1:A:2706:C:OP2	2:B:349:ARG:NH2	2.42	0.49
15:O:271:SER:O	15:O:275:ARG:HD3	2.13	0.49
1:A:3164:A:N1	1:A:3233:A:C2	2.81	0.49
18:R:165:ARG:HH22	38:b:154:ILE:HG12	1.76	0.49
29:2:41:ARG:O	29:2:44:THR:OG1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:A:C6	1:A:367:A:N6	2.81	0.49
1:A:789:A:N7	1:A:840:C:C4	2.80	0.49
1:A:2607:G:C6	1:A:2608:C:C4	3.00	0.49
1:A:2814:U:C2	1:A:2815:U:C5	3.01	0.49
13:M:61:LEU:O	13:M:62:ILE:CB	2.60	0.49
20:T:116:GLU:O	20:T:119:VAL:HG22	2.13	0.49
20:T:147:THR:HA	20:T:150:TRP:CD1	2.48	0.49
39:c:88:PRO:O	39:c:125:ARG:NH1	2.46	0.49
1:A:207:U:C2	1:A:208:A:C8	3.01	0.49
1:A:538:A:N1	1:A:556:A:C2	2.81	0.49
35:8:189:ILE:HG22	35:8:194:LEU:HD23	1.95	0.49
1:A:304:A:H1'	1:A:365:A:H2	1.78	0.49
1:A:543:A:C2	1:A:550:A:N1	2.81	0.49
15:O:294:LEU:HD21	32:5:335:VAL:CG1	2.42	0.49
26:Z:65:TRP:CZ3	26:Z:100:ALA:HB2	2.48	0.49
1:A:133:A:C6	1:A:134:U:C2	3.00	0.49
1:A:1846:G:C6	1:A:1847:C:C4	3.00	0.49
11:K:225:GLN:HG2	11:K:226:TYR:N	2.28	0.49
15:O:112:LEU:HD21	16:P:227:ILE:HG21	1.95	0.49
15:O:171:LYS:HD2	15:O:260:TYR:CZ	2.48	0.49
20:T:97:GLU:C	20:T:97:GLU:CD	2.81	0.49
34:7:104:ARG:HG3	34:7:105:ASN:N	2.26	0.49
1:A:1743:G:N1	1:A:1744:C:C4	2.81	0.48
16:P:186:THR:N	16:P:187:PRO:CD	2.76	0.48
33:6:192:HIS:CE1	33:6:193:VAL:HG23	2.48	0.48
1:A:735:A:H4'	1:A:736:A:OP1	2.11	0.48
40:d:164:TYR:HA	40:d:191:LYS:O	2.13	0.48
1:A:119:A:H2'	1:A:119:A:N3	2.28	0.48
1:A:2468:A:OP1	5:E:97:LYS:NZ	2.46	0.48
6:F:77:LYS:HA	6:F:84:ILE:HG22	1.95	0.48
18:R:155:LYS:N	18:R:156:PRO:CD	2.76	0.48
23:W:118:MET:HA	23:W:118:MET:HE2	1.95	0.48
34:7:93:ILE:HD12	34:7:128:ILE:HD11	1.95	0.48
36:9:200:ILE:O	36:9:203:ILE:HG12	2.13	0.48
1:A:708:U:O2'	1:A:730:U:H5''	2.14	0.48
1:A:2590:U:H3'	1:A:2591:A:C5'	2.43	0.48
1:A:3158:G:H2'	1:A:3159:G:O4'	2.13	0.48
23:W:137:ILE:O	23:W:137:ILE:HG23	2.13	0.48
35:8:118:LEU:HB3	35:8:168:GLY:HA2	1.95	0.48
1:A:1360:G:H2'	1:A:1361:C:H5'	1.95	0.48
1:A:1382:A:C6	1:A:1392:A:N6	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1901:U:OP1	12:L:8:LYS:NZ	2.46	0.48
1:A:3163:U:C2	1:A:3164:A:C8	3.02	0.48
10:J:114:TYR:O	26:Z:64:ARG:HD3	2.13	0.48
29:2:44:THR:O	29:2:48:VAL:HG23	2.13	0.48
31:4:121:LEU:N	31:4:121:LEU:HD23	2.28	0.48
1:A:364:U:O2'	1:A:365:A:C8	2.66	0.48
1:A:409:A:N3	1:A:409:A:H2'	2.29	0.48
1:A:2802:G:C6	1:A:2803:C:C4	3.02	0.48
8:H:19:VAL:HG13	8:H:59:VAL:HG22	1.94	0.48
1:A:448:U:O4'	1:A:448:U:O2	2.28	0.48
1:A:3122:U:O2'	1:A:3123:A:OP2	2.29	0.48
4:D:50:PRO:CD	4:D:183:ASP:HB2	2.43	0.48
5:E:154:LEU:HG	29:2:42:VAL:HG11	1.95	0.48
5:E:274:TYR:HA	5:E:277:ARG:HG2	1.95	0.48
18:R:205:LEU:HD21	18:R:211:ILE:HG22	1.95	0.48
28:1:174:PRO:O	28:1:334:ILE:O	2.31	0.48
1:A:25:A:O2'	1:A:26:A:P	2.71	0.48
1:A:27:A:O2'	1:A:28:U:P	2.72	0.48
1:A:364:U:O2'	1:A:365:A:H8	1.97	0.48
1:A:945:A:N1	1:A:1107:U:O2'	2.32	0.48
2:B:180:ILE:HD12	2:B:193:TYR:CD1	2.49	0.48
39:c:29:THR:HG22	39:c:32:ARG:HH22	1.79	0.48
1:A:615:U:O2'	1:A:616:A:OP1	2.29	0.48
1:A:915:G:OP2	21:U:11:SER:OG	2.31	0.48
1:A:1969:G:C6	1:A:1970:C:C4	3.02	0.48
6:F:24:LEU:CD1	6:F:107:ILE:HD11	2.37	0.48
36:9:103:TYR:O	36:9:104:ASN:HB2	2.13	0.48
1:A:119:A:N3	1:A:119:A:C2'	2.76	0.48
1:A:1981:U:O4	1:A:2263:U:C4	2.67	0.48
1:A:651:G:H2'	1:A:652:A:O4'	2.14	0.47
1:A:880:G:OP2	11:K:55:ARG:NH1	2.44	0.47
1:A:1555:A:H2'	1:A:1556:A:O4'	2.13	0.47
1:A:2452:U:H2'	1:A:2453:G:O4'	2.14	0.47
1:A:2707:G:C2	1:A:2708:C:C6	3.02	0.47
8:H:56:TYR:CD2	8:H:125:ARG:HG3	2.49	0.47
16:P:103:TYR:CE1	16:P:167:PRO:HB3	2.49	0.47
18:R:77:VAL:CG1	18:R:85:ILE:HG23	2.44	0.47
32:5:98:LEU:HG	32:5:227:GLY:HA2	1.96	0.47
32:5:340:VAL:HG23	32:5:362:ALA:HB1	1.95	0.47
1:A:169:A:H2'	1:A:170:U:O4'	2.14	0.47
1:A:275:A:C6	1:A:276:U:O4	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1541:U:H2'	1:A:1542:U:C6	2.49	0.47
1:A:2947:C:H5'	3:C:253:ALA:HA	1.96	0.47
3:C:63:THR:HG22	3:C:87:VAL:HG22	1.96	0.47
4:D:135:ALA:HB1	4:D:136:PRO:HD3	1.95	0.47
5:E:245:PHE:CD1	5:E:245:PHE:N	2.82	0.47
21:U:11:SER:OG	21:U:13:ILE:HG22	2.14	0.47
36:9:166:HIS:O	36:9:167:ASN:CB	2.62	0.47
1:A:274:U:O4	1:A:367:A:C2	2.62	0.47
1:A:880:G:C6	1:A:881:C:C4	3.02	0.47
1:A:1142:U:H2'	1:A:1143:A:O4'	2.15	0.47
1:A:1756:U:C2	1:A:1757:A:C8	3.02	0.47
2:B:173:ASP:OD2	2:B:176:ARG:NH1	2.44	0.47
15:O:299:ILE:HD11	31:4:128:ILE:HG23	1.97	0.47
36:9:118:GLN:HA	36:9:121:ILE:HG22	1.95	0.47
36:9:199:PHE:O	36:9:203:ILE:HG23	2.13	0.47
1:A:275:A:N1	1:A:367:A:C2	2.81	0.47
1:A:954:A:O2'	1:A:955:A:OP2	2.27	0.47
1:A:3137:A:H1'	1:A:3143:A:C2	2.50	0.47
1:A:3261:U:O2	1:A:3261:U:O4'	2.31	0.47
17:Q:195:ASN:O	30:3:91:LYS:HG2	2.14	0.47
28:1:176:ALA:HB3	28:1:334:ILE:HD12	1.95	0.47
1:A:231:A:H2'	1:A:232:C:C6	2.50	0.47
1:A:718:G:H2'	1:A:1968:U:C2	2.48	0.47
1:A:2885:G:C6	1:A:2886:C:C4	3.02	0.47
2:B:268:SER:O	2:B:271:THR:HG22	2.13	0.47
39:c:101:THR:HG23	39:c:113:ILE:HD13	1.96	0.47
1:A:832:U:H4'	11:K:70:GLN:HG3	1.97	0.47
1:A:1630:A:O2'	1:A:1891:U:H4'	2.14	0.47
6:F:60:GLY:HA3	6:F:114:VAL:HB	1.97	0.47
15:O:183:LEU:HD11	23:W:97:MET:HG3	1.97	0.47
19:S:66:PHE:CE1	19:S:79:VAL:HG23	2.50	0.47
1:A:643:U:H4'	1:A:644:A:O5'	2.13	0.47
1:A:1258:A:H2'	1:A:1259:A:O4'	2.15	0.47
1:A:2785:U:C5	1:A:2808:A:C6	3.02	0.47
1:A:2951:U:O2'	9:I:80:ASN:HA	2.15	0.47
2:B:385:ARG:HG3	2:B:386:PRO:HD2	1.96	0.47
6:F:24:LEU:HB2	6:F:84:ILE:HG13	1.95	0.47
8:H:46:VAL:HG13	15:O:299:ILE:HG23	1.96	0.47
8:H:125:ARG:CG	8:H:125:ARG:HH11	2.28	0.47
1:A:1116:A:N6	1:A:1117:G:C6	2.82	0.47
1:A:1535:A:OP1	2:B:151:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2741:G:N2	1:A:2796:G:N1	2.62	0.47
18:R:117:LEU:O	18:R:119:SER:N	2.47	0.47
1:A:328:A:H2'	1:A:329:A:H5'	1.96	0.47
1:A:716:A:H2'	1:A:717:U:O4'	2.14	0.47
1:A:1364:C:O2'	1:A:1536:A:N3	2.42	0.47
1:A:1938:A:H2'	1:A:1939:U:O4'	2.15	0.47
1:A:2954:U:H2'	1:A:2955:G:O4'	2.15	0.47
1:A:3109:U:OP1	3:C:169:ARG:NH2	2.47	0.47
1:A:3122:U:O2'	1:A:3123:A:P	2.73	0.47
19:S:122:VAL:O	19:S:125:THR:OG1	2.28	0.47
24:X:47:VAL:HA	38:b:133:ILE:HD11	1.97	0.47
29:2:68:LYS:O	29:2:71:THR:OG1	2.29	0.47
38:b:60:LEU:O	38:b:63:MET:HG3	2.15	0.47
1:A:221:A:H2'	1:A:222:A:C8	2.50	0.47
1:A:789:A:H2'	1:A:790:A:C8	2.50	0.47
18:R:196:SER:HA	18:R:199:ILE:HG12	1.96	0.47
1:A:1805:G:C6	1:A:1806:C:C4	3.03	0.46
1:A:1995:G:H2'	1:A:1996:A:O4'	2.14	0.46
1:A:3254:U:OP1	23:W:102:ASN:HB2	2.15	0.46
5:E:161:LEU:HD22	29:2:45:GLN:CB	2.45	0.46
1:A:2207:A:C5	1:A:2208:A:N7	2.83	0.46
1:A:2446:U:H4'	1:A:2447:A:OP1	2.15	0.46
2:B:183:LEU:HG	2:B:194:ILE:HG12	1.97	0.46
19:S:132:ILE:N	19:S:132:ILE:CD1	2.78	0.46
1:A:1392:A:HO2'	1:A:1393:U:P	2.39	0.46
1:A:1493:U:O2'	1:A:1494:A:OP1	2.32	0.46
1:A:1833:G:C5	1:A:1834:C:C5	3.04	0.46
1:A:2597:G:N1	1:A:2652:C:C4	2.84	0.46
1:A:2732:G:OP1	27:0:59:ARG:HB2	2.16	0.46
1:A:3029:U:C4	1:A:3030:U:C4	3.03	0.46
16:P:67:LYS:HG3	40:d:196:VAL:HG11	1.96	0.46
18:R:216:PHE:CZ	28:1:264:ARG:HD2	2.51	0.46
28:1:171:THR:HG22	28:1:172:LEU:N	2.30	0.46
33:6:30:LEU:HD12	33:6:30:LEU:O	2.14	0.46
1:A:28:U:O2'	1:A:29:A:P	2.73	0.46
1:A:308:U:C2'	1:A:309:C:O5'	2.63	0.46
1:A:1245:U:O4	1:A:1267:A:N1	2.49	0.46
1:A:1706:G:O2'	2:B:295:ARG:NH1	2.48	0.46
1:A:1808:G:C6	1:A:1809:C:C4	3.04	0.46
1:A:2317:A:C2	1:A:2318:U:C2	3.04	0.46
10:J:225:ASN:CG	10:J:225:ASN:O	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:8:169:TYR:CD2	35:8:193:ILE:HG21	2.50	0.46
1:A:914:A:C5	21:U:13:ILE:HD13	2.50	0.46
1:A:1765:A:C6	1:A:1786:A:C2	3.03	0.46
1:A:3120:A:N1	1:A:3261:U:C4	2.84	0.46
16:P:146:ASN:O	16:P:147:LEU:CB	2.63	0.46
1:A:840:C:O2	1:A:840:C:H3'	2.16	0.46
3:C:69:MET:HB2	3:C:70:PRO:CD	2.45	0.46
3:C:115:LEU:HD11	13:M:28:VAL:HG21	1.97	0.46
4:D:230:GLU:O	4:D:233:ILE:HG13	2.15	0.46
40:d:24:PRO:HB3	40:d:82:TYR:HA	1.97	0.46
1:A:28:U:O2'	1:A:29:A:OP1	2.26	0.46
1:A:1261:U:C5'	31:4:71:LEU:HD21	2.46	0.46
1:A:1312:G:C2'	1:A:1313:G:H5''	2.45	0.46
1:A:1362:C:H2'	1:A:1363:C:C6	2.51	0.46
1:A:1364:C:C2	1:A:1402:G:C2	3.03	0.46
1:A:3268:A:H2'	1:A:3269:U:H6	1.81	0.46
12:L:174:ALA:O	12:L:175:LYS:C	2.59	0.46
1:A:123:A:C2	1:A:139:U:C2	3.02	0.46
1:A:2874:G:H2'	1:A:2875:G:O4'	2.16	0.46
12:L:127:VAL:HG12	12:L:128:ASP:N	2.31	0.46
18:R:128:ARG:O	28:1:239:ASP:O	2.33	0.46
20:T:147:THR:O	20:T:151:GLN:HG2	2.16	0.46
1:A:328:A:C2'	1:A:329:A:H5'	2.45	0.46
1:A:673:A:C2	2:B:338:MET:HG2	2.51	0.46
1:A:1759:A:H2'	1:A:1760:U:O4'	2.16	0.46
2:B:294:HIS:O	2:B:382:VAL:HG23	2.16	0.46
6:F:161:LYS:HG2	6:F:169:ILE:CG2	2.46	0.46
1:A:268:C:N4	38:b:100:MET:SD	2.89	0.46
1:A:581:C:C2	1:A:700:G:N2	2.83	0.46
1:A:1274:A:C8	31:4:33:TRP:CH2	3.04	0.46
1:A:2730:G:C6	1:A:2731:C:C4	3.03	0.46
2:B:278:LYS:C	2:B:279:LEU:HD12	2.40	0.46
22:V:57:VAL:HB	29:2:133:THR:HG22	1.98	0.46
32:5:200:ALA:HB2	32:5:260:VAL:HG23	1.97	0.46
34:7:118:SER:HB2	34:7:131:LYS:HB2	1.97	0.46
1:A:1220:G:H2'	1:A:1221:G:O4'	2.16	0.45
1:A:2796:G:H2'	1:A:2797:U:OP1	2.15	0.45
1:A:2898:U:H2'	1:A:2899:U:H6	1.79	0.45
1:A:3143:A:H2'	1:A:3144:A:O4'	2.16	0.45
5:E:73:TYR:HA	5:E:77:LEU:HB2	1.97	0.45
13:M:95:LEU:HD12	13:M:109:LEU:HD13	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:129:PHE:HB3	28:1:239:ASP:O	2.16	0.45
24:X:66:LEU:O	24:X:67:ARG:C	2.58	0.45
1:A:346:G:N1	1:A:357:C:C2	2.85	0.45
1:A:416:U:H2'	1:A:417:U:C6	2.52	0.45
1:A:910:G:N3	1:A:910:G:H2'	2.32	0.45
1:A:1356:U:OP2	1:A:1358:C:O2	2.33	0.45
1:A:1360:G:N3	1:A:1361:C:O2	2.48	0.45
1:A:1392:A:N3	1:A:1392:A:H2'	2.31	0.45
1:A:1702:C:H2'	1:A:1703:U:O4'	2.15	0.45
1:A:1925:U:H2'	1:A:1926:A:C8	2.51	0.45
1:A:2607:G:C2	1:A:2608:C:C2	3.04	0.45
3:C:110:TYR:CD1	3:C:110:TYR:C	2.94	0.45
13:M:76:VAL:HG21	13:M:94:ILE:HD11	1.97	0.45
15:O:155:GLU:HG2	16:P:235:ILE:HD11	1.98	0.45
16:P:121:TYR:O	16:P:125:ILE:HG12	2.16	0.45
38:b:70:ALA:HB1	38:b:75:VAL:O	2.16	0.45
1:A:114:U:H3	1:A:118:A:N6	2.13	0.45
1:A:275:A:C2	1:A:367:A:N3	2.84	0.45
1:A:1116:A:H2'	1:A:1117:G:H5'	1.98	0.45
1:A:1245:U:H2'	1:A:1246:A:C8	2.52	0.45
1:A:2373:U:O2'	1:A:2374:A:P	2.73	0.45
1:A:2631:G:H2'	1:A:2632:A:O4'	2.16	0.45
1:A:3160:U:OP1	12:L:52:THR:HG21	2.15	0.45
6:F:26:ILE:HD11	6:F:84:ILE:HG12	1.98	0.45
19:S:137:THR:OG1	19:S:159:LEU:HD11	2.16	0.45
20:T:49:ILE:HD11	40:d:98:LEU:HB3	1.98	0.45
36:9:159:ALA:HB1	36:9:196:LEU:HD23	1.97	0.45
1:A:1111:U:H3'	1:A:1112:A:H5''	1.98	0.45
1:A:2777:U:H2'	1:A:2778:C:O4'	2.16	0.45
1:A:3281:U:C2	1:A:3282:A:C8	3.04	0.45
2:B:240:CYS:CB	2:B:304:THR:HG22	2.46	0.45
36:9:36:PRO:O	36:9:43:ARG:NH2	2.49	0.45
41:e:6:G:C2	41:e:68:C:C2	3.04	0.45
1:A:164:U:H3	16:P:82:ASN:C	2.25	0.45
1:A:2324:U:H4'	1:A:2325:A:OP1	2.17	0.45
1:A:1391:U:H2'	1:A:1392:A:H5'	1.98	0.45
1:A:1825:A:H3'	1:A:1826:U:H5''	1.99	0.45
1:A:2913:U:C4	1:A:2941:A:N1	2.85	0.45
18:R:135:THR:O	18:R:136:ASN:C	2.58	0.45
18:R:165:ARG:NH2	38:b:154:ILE:HG21	2.32	0.45
39:c:111:LYS:HD3	39:c:115:LYS:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:779:A:N1	1:A:847:U:H5	2.13	0.45
1:A:1678:C:O2'	1:A:1693:A:H1'	2.16	0.45
1:A:2586:U:H1'	1:A:2587:U:C6	2.52	0.45
1:A:2730:G:C2	1:A:2731:C:C2	3.05	0.45
2:B:270:GLY:HA2	2:B:311:ILE:HG22	1.98	0.45
1:A:261:A:C8	1:A:307:G:O6	2.70	0.45
1:A:536:A:C2	1:A:557:A:C2	3.05	0.45
1:A:1371:A:H3'	1:A:1372:A:C5'	2.47	0.45
1:A:3138:U:H2'	1:A:3139:A:H5''	1.98	0.45
2:B:381:LYS:O	2:B:382:VAL:C	2.60	0.45
5:E:137:LEU:CB	5:E:202:MET:HE1	2.47	0.45
19:S:32:ILE:HD12	19:S:32:ILE:N	2.32	0.45
31:4:65:ARG:HD2	31:4:65:ARG:C	2.42	0.45
34:7:91:THR:OG1	34:7:130:ILE:HB	2.17	0.45
35:8:181:THR:HG23	35:8:184:GLN:HB2	1.99	0.45
1:A:58:A:OP1	15:O:264:ARG:NH2	2.49	0.45
1:A:482:G:C6	1:A:483:C:C4	3.05	0.45
1:A:603:U:OP2	2:B:149:ARG:NH1	2.50	0.45
1:A:685:G:H2'	1:A:686:U:O4'	2.17	0.45
12:L:132:MET:HB3	12:L:188:LEU:HD13	1.99	0.45
16:P:186:THR:CG2	16:P:187:PRO:HD3	2.47	0.45
19:S:104:GLY:HA2	19:S:115:SER:HA	1.99	0.45
20:T:152:ILE:O	20:T:155:VAL:HG22	2.17	0.45
21:U:58:VAL:HG21	39:c:47:LEU:HD12	1.99	0.45
26:Z:92:LYS:HA	26:Z:92:LYS:HE2	1.99	0.45
1:A:355:U:H2'	1:A:356:U:O4'	2.17	0.45
1:A:2811:G:H2'	1:A:2812:G:O4'	2.17	0.45
1:A:3279:U:H2'	1:A:3280:C:H6	1.81	0.45
30:3:74:TRP:C	30:3:76:LYS:N	2.74	0.45
1:A:1750:G:C2	1:A:1751:C:C2	3.05	0.44
1:A:2872:A:C6	1:A:2873:U:O4	2.70	0.44
1:A:2915:A:H2'	1:A:2916:U:C6	2.52	0.44
2:B:194:ILE:HG22	2:B:195:ILE:N	2.32	0.44
18:R:38:SER:O	18:R:39:MET:CB	2.65	0.44
32:5:341:PHE:CD2	37:a:94:ALA:HB2	2.53	0.44
33:6:78:LYS:O	33:6:81:SER:OG	2.31	0.44
1:A:551:U:H2'	1:A:552:A:H8	1.81	0.44
1:A:840:C:H2'	1:A:841:G:H5''	1.99	0.44
1:A:2860:A:C6	1:A:2861:U:C4	3.05	0.44
2:B:240:CYS:HA	2:B:304:THR:HA	1.99	0.44
5:E:68:ARG:NH2	22:V:57:VAL:HG21	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:229:VAL:HG21	28:1:322:ILE:HD12	2.00	0.44
1:A:307:G:O2'	1:A:308:U:C5'	2.65	0.44
1:A:2951:U:O2	9:I:80:ASN:OD1	2.36	0.44
4:D:60:VAL:HG21	4:D:65:VAL:HG21	1.99	0.44
5:E:82:LEU:C	5:E:82:LEU:HD23	2.43	0.44
32:5:268:TRP:HA	32:5:279:VAL:CG2	2.47	0.44
34:7:90:ILE:HD13	34:7:129:ILE:HG23	1.99	0.44
1:A:918:U:H2'	1:A:919:A:O4'	2.18	0.44
1:A:1743:G:C6	1:A:1744:C:C4	3.05	0.44
1:A:2584:A:C2	1:A:2585:A:H1'	2.52	0.44
22:V:43:HIS:HA	33:6:60:MET:SD	2.58	0.44
1:A:1430:U:H2'	1:A:1431:U:O4'	2.18	0.44
2:B:125:VAL:HG23	2:B:154:LEU:HD11	1.99	0.44
2:B:158:ASN:O	2:B:210:ARG:NH1	2.50	0.44
5:E:30:HIS:HB2	28:1:165:ILE:HD12	2.00	0.44
8:H:125:ARG:HH11	8:H:125:ARG:HG2	1.82	0.44
19:S:110:LEU:HD23	19:S:158:VAL:HG22	1.99	0.44
21:U:13:ILE:O	21:U:13:ILE:HG23	2.17	0.44
31:4:63:VAL:HB	35:8:226:VAL:HG22	1.99	0.44
38:b:49:VAL:O	38:b:50:THR:OG1	2.29	0.44
1:A:276:U:H1'	1:A:277:U:OP1	2.17	0.44
1:A:461:U:C6	1:A:461:U:C5'	3.01	0.44
1:A:727:G:C5	1:A:728:C:C4	3.06	0.44
1:A:3268:A:H2'	1:A:3269:U:C6	2.53	0.44
20:T:73:SER:OG	20:T:74:ASN:N	2.50	0.44
28:1:117:TYR:CD1	28:1:117:TYR:C	2.96	0.44
1:A:640:C:O2	1:A:1570:A:H2'	2.17	0.44
1:A:1125:U:OP2	39:c:32:ARG:NH1	2.50	0.44
1:A:2696:A:N3	1:A:2696:A:H2'	2.33	0.44
6:F:67:VAL:HG22	6:F:110:HIS:CE1	2.52	0.44
28:1:121:PHE:CE1	29:2:67:ILE:HD11	2.53	0.44
1:A:272:G:N2	38:b:61:ARG:HB2	2.32	0.44
1:A:583:G:O2'	4:D:115:ARG:HD2	2.18	0.44
1:A:1848:C:C2	1:A:1859:G:C2	3.06	0.44
8:H:139:ASN:CB	32:5:329:ARG:O	2.66	0.44
17:Q:27:LEU:N	17:Q:28:PRO:CD	2.77	0.44
28:1:172:LEU:HD12	28:1:172:LEU:C	2.43	0.44
32:5:380:GLU:O	32:5:381:PRO:C	2.61	0.44
33:6:168:LEU:HD23	33:6:169:LEU:N	2.33	0.44
38:b:14:LEU:HD22	38:b:18:PHE:CE2	2.53	0.44
41:e:6:G:N2	41:e:68:C:C2	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:A:O2'	4:D:238:PRO:O	2.36	0.44
1:A:208:A:H2'	1:A:209:U:C6	2.53	0.44
1:A:315:A:O2'	1:A:317:U:C1'	2.65	0.44
1:A:1720:U:HO2'	2:B:135:ASN:H	1.66	0.44
1:A:1833:G:C2	1:A:1834:C:C2	3.06	0.44
1:A:2373:U:HO2'	1:A:2374:A:P	2.37	0.44
1:A:2787:C:C2	1:A:2812:G:N2	2.86	0.44
1:A:2905:A:O2'	3:C:44:HIS:O	2.35	0.44
2:B:253:HIS:O	2:B:255:VAL:HG23	2.18	0.44
1:A:136:A:H2'	1:A:137:A:C8	2.53	0.43
1:A:673:A:N3	2:B:338:MET:HG2	2.33	0.43
1:A:1366:A:O4'	1:A:1534:G:N2	2.51	0.43
1:A:2814:U:C5'	1:A:2833:A:C2	3.00	0.43
16:P:157:ILE:HD12	17:Q:5:TYR:HB3	1.99	0.43
32:5:324:VAL:HG21	32:5:339:HIS:CG	2.53	0.43
1:A:466:U:H2'	1:A:467:U:O4'	2.18	0.43
1:A:1210:A:O2'	31:4:90:ASN:ND2	2.51	0.43
1:A:1754:A:N1	1:A:1755:A:C6	2.86	0.43
1:A:2336:G:C4	28:1:62:ILE:HD13	2.53	0.43
1:A:2364:U:H2'	1:A:2365:A:C8	2.52	0.43
1:A:2584:A:H3'	1:A:2585:A:H5''	1.99	0.43
1:A:3193:A:H2'	1:A:3194:U:H4'	2.00	0.43
4:D:164:LYS:HG2	4:D:260:GLN:O	2.18	0.43
10:J:91:ARG:HD3	10:J:98:ALA:HA	1.99	0.43
38:b:34:THR:HG23	38:b:46:LYS:C	2.43	0.43
39:c:25:THR:O	39:c:29:THR:HG23	2.18	0.43
40:d:66:LEU:O	40:d:67:ARG:C	2.61	0.43
1:A:443:U:H4'	1:A:445:U:OP1	2.19	0.43
1:A:1279:A:H2'	1:A:1280:A:O4'	2.18	0.43
1:A:1631:G:N2	1:A:1671:A:O2'	2.51	0.43
1:A:1846:G:C2	1:A:1847:C:C2	3.07	0.43
6:F:26:ILE:HD11	6:F:84:ILE:HG23	1.99	0.43
28:1:113:PRO:HG3	29:2:71:THR:HG21	1.99	0.43
40:d:30:ARG:HG3	40:d:74:MET:HB2	1.99	0.43
1:A:827:U:C2	1:A:828:A:C8	3.06	0.43
1:A:1693:A:N6	1:A:2873:U:O4'	2.50	0.43
1:A:1717:A:H2'	1:A:1718:A:C8	2.52	0.43
1:A:1763:A:H2'	1:A:1990:A:H1'	2.00	0.43
1:A:2722:G:C2	1:A:2762:C:C2	3.05	0.43
7:G:44:LEU:CD2	7:G:49:LEU:HD13	2.48	0.43
10:J:164:GLY:O	10:J:165:LEU:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:46:SER:C	31:4:48:ARG:H	2.26	0.43
34:7:89:ILE:O	34:7:131:LYS:O	2.36	0.43
40:d:11:ARG:HG2	40:d:15:TRP:CE3	2.53	0.43
1:A:95:A:H2'	1:A:96:C:C6	2.54	0.43
1:A:866:G:H5'	1:A:867:A:OP2	2.18	0.43
1:A:1113:A:N3	1:A:1113:A:O5'	2.52	0.43
1:A:1698:C:H5	1:A:1736:G:H21	1.65	0.43
1:A:1769:U:C2'	1:A:1770:U:OP1	2.66	0.43
2:B:344:PRO:HB3	2:B:356:LYS:HD3	2.01	0.43
4:D:165:LEU:HD12	4:D:262:VAL:HG23	2.00	0.43
10:J:146:ARG:CZ	34:7:73:THR:HG23	2.48	0.43
35:8:247:GLN:O	35:8:251:ASP:HB2	2.18	0.43
1:A:929:G:N7	39:c:30:ARG:NH2	2.66	0.43
1:A:1786:A:H2'	1:A:1787:A:C8	2.53	0.43
1:A:1949:G:C6	1:A:1950:C:C4	3.07	0.43
1:A:3231:A:OP1	12:L:56:ARG:NH2	2.52	0.43
4:D:152:PHE:HZ	4:D:251:VAL:HG13	1.84	0.43
25:Y:95:ARG:CZ	25:Y:100:ARG:HD3	2.48	0.43
35:8:166:LYS:N	35:8:166:LYS:HD2	2.33	0.43
36:9:80:ILE:HG22	36:9:82:LEU:CD1	2.49	0.43
40:d:66:LEU:O	40:d:68:ARG:N	2.51	0.43
41:e:3:C:C2	41:e:71:G:C2	3.07	0.43
1:A:2427:U:HO2'	1:A:2428:A:P	2.41	0.43
1:A:2607:G:H2'	1:A:2608:C:O4'	2.19	0.43
5:E:64:THR:HA	33:6:52:GLN:HB3	2.00	0.43
6:F:111:ILE:O	6:F:115:THR:HG22	2.19	0.43
12:L:237:ARG:NH1	13:M:30:PRO:O	2.52	0.43
1:A:577:U:C4	1:A:579:A:C8	3.06	0.43
1:A:676:A:H4'	1:A:1686:U:H4'	2.00	0.43
1:A:1750:G:H2'	1:A:1751:C:O4'	2.19	0.43
1:A:3058:G:C6	1:A:3059:C:C4	3.06	0.43
1:A:3118:U:C4	1:A:3119:A:N7	2.87	0.43
1:A:3159:G:N1	1:A:3248:C:C4	2.87	0.43
4:D:229:ARG:O	4:D:233:ILE:HG23	2.18	0.43
28:1:247:TYR:CZ	28:1:249:LEU:HD21	2.53	0.43
1:A:1104:A:O2'	8:H:108:ALA:O	2.37	0.43
1:A:1113:A:O2'	1:A:1114:U:OP1	2.29	0.43
1:A:2292:C:H1'	1:A:2298:U:O4	2.19	0.43
1:A:2440:G:H2'	1:A:2441:U:O4'	2.19	0.43
1:A:3058:G:H2'	1:A:3059:C:O4'	2.18	0.43
2:B:94:LYS:HB2	2:B:110:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:73:ASP:O	3:C:77:GLY:N	2.52	0.43
17:Q:80:ILE:HD11	35:8:84:LEU:CD1	2.49	0.43
28:1:128:VAL:HG23	28:1:131:ILE:HB	2.00	0.43
32:5:268:TRP:HA	32:5:279:VAL:HG21	2.01	0.43
1:A:486:G:H4'	1:A:487:U:O5'	2.18	0.43
1:A:1374:U:C6	1:A:1374:U:OP1	2.72	0.43
1:A:1848:C:C2	1:A:1859:G:N2	2.87	0.43
2:B:246:ILE:HG22	2:B:250:THR:HG21	2.01	0.43
41:e:3:C:N3	41:e:71:G:C2	2.87	0.43
1:A:536:A:C2	1:A:557:A:H2	2.37	0.42
1:A:657:U:H2'	1:A:658:U:O4'	2.19	0.42
1:A:2586:U:H4'	1:A:2587:U:OP1	2.19	0.42
1:A:2651:G:H5'	5:E:19:PRO:CG	2.49	0.42
5:E:245:PHE:N	5:E:245:PHE:HD1	2.15	0.42
39:c:101:THR:HG23	39:c:113:ILE:CD1	2.49	0.42
41:e:71:G:C2	41:e:72:C:C2	3.07	0.42
1:A:142:A:H2'	1:A:143:A:O4'	2.18	0.42
1:A:294:G:H4'	1:A:328:A:C5	2.54	0.42
1:A:673:A:C2	2:B:338:MET:HE3	2.54	0.42
1:A:1284:A:O2'	1:A:1286:A:OP1	2.36	0.42
1:A:1490:A:C2	1:A:1523:A:H2	2.37	0.42
1:A:1743:G:C2	1:A:1744:C:C2	3.08	0.42
12:L:35:SER:HG	12:L:40:CYS:HG	1.64	0.42
18:R:143:GLU:HB3	28:1:361:VAL:HG11	2.01	0.42
40:d:173:ASP:OD1	40:d:173:ASP:N	2.52	0.42
1:A:121:A:H3'	1:A:122:A:H5''	2.02	0.42
1:A:1314:U:O2	1:A:1316:U:H2'	2.18	0.42
1:A:1516:U:C2	1:A:3022:G:N2	2.87	0.42
1:A:2674:U:H2'	1:A:2675:U:C6	2.53	0.42
2:B:257:ILE:CD1	2:B:265:PHE:CE2	3.03	0.42
15:O:107:LEU:HD21	15:O:161:PRO:HB3	2.01	0.42
15:O:165:ALA:HB3	15:O:265:CYS:SG	2.60	0.42
21:U:11:SER:CB	21:U:13:ILE:HG22	2.49	0.42
28:1:211:ILE:N	28:1:211:ILE:HD12	2.34	0.42
1:A:720:A:N3	1:A:720:A:H2'	2.34	0.42
1:A:951:A:O2'	1:A:952:A:O5'	2.32	0.42
1:A:1680:A:H2'	1:A:1681:C:O4'	2.19	0.42
1:A:2858:C:OP1	2:B:351:LYS:HD3	2.19	0.42
1:A:3147:U:OP2	3:C:117:LYS:HE3	2.18	0.42
2:B:197:CYS:SG	2:B:198:ASP:N	2.92	0.42
4:D:50:PRO:HG2	4:D:183:ASP:CB	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:11:ILE:HD11	9:I:74:VAL:HG21	2.01	0.42
17:Q:65:PRO:HA	17:Q:83:ILE:HG13	2.00	0.42
40:d:16:PHE:O	40:d:20:LYS:N	2.45	0.42
1:A:268:C:OP1	10:J:216:THR:HG21	2.19	0.42
1:A:1589:A:C5	1:A:1590:U:C5	3.07	0.42
1:A:1605:U:O4	12:L:8:LYS:HB3	2.19	0.42
1:A:1869:A:O2'	1:A:1872:G:N3	2.45	0.42
1:A:1946:U:H2'	1:A:1947:C:C6	2.54	0.42
1:A:3138:U:O2'	1:A:3140:C:OP2	2.32	0.42
2:B:294:HIS:HB2	2:B:383:LYS:HB2	2.02	0.42
21:U:4:TYR:O	21:U:36:TYR:HA	2.19	0.42
1:A:230:A:O4'	1:A:230:A:N3	2.51	0.42
1:A:231:A:H2'	1:A:232:C:H6	1.83	0.42
1:A:904:G:N2	1:A:912:C:C2	2.88	0.42
1:A:1706:G:O2'	1:A:1707:C:OP2	2.29	0.42
1:A:1826:U:H4'	1:A:1826:U:OP1	2.20	0.42
1:A:2418:U:H2'	1:A:2419:U:O4'	2.19	0.42
1:A:2751:G:C6	1:A:2752:C:C4	3.08	0.42
2:B:145:GLY:HA3	2:B:330:ARG:HG3	2.02	0.42
3:C:168:VAL:HB	3:C:231:ILE:HG23	2.01	0.42
6:F:161:LYS:HG2	6:F:169:ILE:HG23	2.01	0.42
13:M:46:LEU:O	13:M:49:ILE:HG13	2.19	0.42
19:S:105:LEU:HD12	19:S:118:MET:CE	2.50	0.42
1:A:587:G:C6	1:A:588:C:C4	3.07	0.42
1:A:720:A:N3	1:A:720:A:C2'	2.82	0.42
1:A:1581:U:H2'	1:A:1582:A:H5'	2.01	0.42
1:A:2669:A:H4'	1:A:2670:C:H5''	2.01	0.42
1:A:204:A:C2	1:A:205:A:C8	3.08	0.42
1:A:261:A:H4'	1:A:262:A:O5'	2.19	0.42
1:A:274:U:N3	1:A:367:A:N6	2.43	0.42
1:A:1181:U:C4	1:A:1182:A:N7	2.88	0.42
1:A:2707:G:C6	1:A:2708:C:C4	3.07	0.42
1:A:3019:U:O4	1:A:3033:A:C2	2.72	0.42
1:A:3127:U:OP1	3:C:120:ARG:HB2	2.20	0.42
2:B:125:VAL:CG2	2:B:154:LEU:HD11	2.50	0.42
4:D:74:LEU:HG	4:D:257:LEU:HD11	2.00	0.42
5:E:160:ALA:HB1	29:2:49:MET:HE1	2.01	0.42
6:F:26:ILE:HD11	6:F:84:ILE:CG2	2.50	0.42
9:I:24:VAL:HG11	9:I:27:LYS:HD2	2.01	0.42
17:Q:149:VAL:HG13	35:8:92:ILE:HD12	2.01	0.42
1:A:34:U:HO2'	1:A:35:U:P	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:A:H2'	1:A:317:U:C6	2.55	0.42
1:A:536:A:H2	1:A:557:A:C2	2.37	0.42
1:A:551:U:H2'	1:A:552:A:C8	2.55	0.42
1:A:1127:A:OP2	1:A:1169:A:O3'	2.37	0.42
1:A:1391:U:C2'	1:A:1392:A:H5'	2.50	0.42
1:A:2434:A:N3	5:E:188:GLY:HA2	2.35	0.42
1:A:3015:U:C4	1:A:3016:A:N6	2.88	0.42
1:A:3163:U:C4	1:A:3164:A:N7	2.87	0.42
4:D:75:TRP:CZ3	10:J:66:PRO:HB3	2.55	0.42
5:E:220:TYR:CZ	5:E:222:GLY:HA2	2.54	0.42
16:P:131:MET:SD	40:d:196:VAL:O	2.78	0.42
22:V:76:ASN:OD1	22:V:76:ASN:C	2.63	0.42
29:2:126:PRO:O	29:2:127:MET:CB	2.67	0.42
1:A:1360:G:H2'	1:A:1361:C:C5'	2.49	0.42
1:A:2359:U:C2'	1:A:2360:U:O5'	2.68	0.42
1:A:2802:G:C2	1:A:2803:C:C2	3.08	0.42
1:A:3162:U:C2	1:A:3243:A:N1	2.88	0.42
3:C:217:GLY:HA3	8:H:83:ARG:NH1	2.35	0.42
11:K:115:THR:HA	11:K:140:VAL:HB	2.01	0.42
12:L:27:LEU:HD21	12:L:125:GLU:HA	2.01	0.42
18:R:128:ARG:O	18:R:130:GLY:N	2.52	0.42
28:1:321:ASP:HB2	28:1:324:GLN:HB3	2.01	0.42
29:2:140:LEU:O	29:2:141:TRP:HB2	2.19	0.42
31:4:52:TRP:HH2	31:4:99:LYS:HA	1.85	0.42
33:6:83:GLN:OE1	33:6:115:LYS:N	2.48	0.42
1:A:578:G:N2	1:A:579:A:C2	2.88	0.41
1:A:1697:C:H2'	1:A:1698:C:C6	2.55	0.41
1:A:1769:U:H3'	1:A:1770:U:H5''	2.01	0.41
4:D:49:PHE:HB2	4:D:168:ILE:HG12	2.01	0.41
6:F:119:LEU:HA	6:F:170:ILE:O	2.20	0.41
10:J:144:LYS:O	10:J:145:ASN:HB2	2.19	0.41
11:K:216:LEU:HD22	11:K:216:LEU:HA	1.93	0.41
15:O:189:VAL:HG11	15:O:267:LEU:HD13	2.01	0.41
20:T:95:ILE:HB	20:T:96:PRO:HD3	2.02	0.41
28:1:334:ILE:HG13	28:1:335:GLY:N	2.35	0.41
31:4:31:CYS:SG	31:4:67:SER:HA	2.60	0.41
1:A:22:U:C4	1:A:23:U:C5	3.08	0.41
1:A:84:A:H2'	1:A:85:A:C8	2.55	0.41
1:A:162:U:C2	30:3:76:LYS:HE2	2.56	0.41
1:A:308:U:H2'	1:A:309:C:O5'	2.20	0.41
1:A:1530:U:H3	1:A:1533:G:H1	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1594:G:H2'	1:A:1595:G:O4'	2.20	0.41
1:A:1663:A:H3'	13:M:150:TYR:CD1	2.55	0.41
2:B:198:ASP:HA	2:B:309:SER:HA	2.01	0.41
40:d:36:GLN:HG3	40:d:64:PRO:HG3	2.02	0.41
40:d:79:LEU:HD13	40:d:84:GLN:HG2	2.03	0.41
1:A:350:A:H2'	1:A:351:C:C6	2.55	0.41
1:A:434:U:O3'	15:O:300:ARG:HB2	2.20	0.41
1:A:620:G:C5	2:B:320:LYS:HB2	2.56	0.41
1:A:1521:U:H2'	1:A:1522:A:C8	2.56	0.41
1:A:2427:U:O2'	1:A:2428:A:OP1	2.35	0.41
1:A:2787:C:C2	1:A:2812:G:C2	3.07	0.41
30:3:119:LEU:HA	30:3:122:ILE:HD12	2.02	0.41
36:9:118:GLN:O	36:9:121:ILE:CG2	2.69	0.41
1:A:119:A:N6	20:T:153:ARG:HH11	2.19	0.41
1:A:1344:U:C5	1:A:1555:A:H2	2.36	0.41
1:A:1564:C:C2	1:A:1572:G:N2	2.88	0.41
1:A:1735:U:OP2	2:B:334:ARG:NE	2.51	0.41
2:B:257:ILE:HD11	2:B:265:PHE:CZ	2.54	0.41
21:U:26:LEU:HD21	21:U:47:LEU:CD2	2.51	0.41
40:d:28:ILE:HB	40:d:75:CYS:HB2	2.02	0.41
1:A:1112:A:O4'	1:A:1112:A:OP1	2.38	0.41
1:A:1846:G:C6	1:A:1847:C:N3	2.88	0.41
1:A:2828:A:H2'	1:A:2829:U:O4'	2.20	0.41
15:O:306:VAL:HG11	37:a:44:TYR:CB	2.50	0.41
16:P:100:HIS:CE1	16:P:106:LYS:HD2	2.55	0.41
16:P:148:GLN:OE1	16:P:148:GLN:N	2.54	0.41
17:Q:76:SER:O	17:Q:79:ASN:HB2	2.20	0.41
17:Q:131:LEU:O	17:Q:131:LEU:HD12	2.20	0.41
18:R:261:ASN:HD21	18:R:265:GLU:HB2	1.85	0.41
1:A:874:U:H2'	1:A:875:U:C6	2.55	0.41
1:A:955:A:H2'	1:A:956:A:C8	2.55	0.41
1:A:1249:U:H2'	1:A:1250:U:C6	2.56	0.41
1:A:1493:U:O2'	1:A:1494:A:P	2.78	0.41
1:A:1768:A:H2'	1:A:1769:U:C6	2.55	0.41
1:A:1808:G:C2	1:A:1809:C:C2	3.09	0.41
1:A:3152:A:H4'	1:A:3152:A:OP1	2.20	0.41
17:Q:213:VAL:CG2	30:3:122:ILE:HD13	2.51	0.41
17:Q:252:PRO:HG2	19:S:159:LEU:HB3	2.03	0.41
20:T:127:LEU:O	20:T:131:VAL:HG13	2.19	0.41
41:e:75:C:O5'	41:e:75:C:H6	2.04	0.41
1:A:425:A:H5''	8:H:117:LYS:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1265:A:H2'	1:A:1266:U:C6	2.56	0.41
1:A:2601:A:O2'	1:A:2602:A:H8	1.99	0.41
4:D:212:GLU:OE1	35:8:109:VAL:HG13	2.21	0.41
5:E:217:ILE:HG23	5:E:220:TYR:CB	2.46	0.41
6:F:151:GLY:C	6:F:152:LEU:HD23	2.46	0.41
8:H:63:GLN:HA	8:H:101:PHE:CD1	2.55	0.41
12:L:136:HIS:O	12:L:137:THR:CB	2.69	0.41
17:Q:95:LEU:O	17:Q:96:ASP:C	2.64	0.41
26:Z:102:PRO:O	26:Z:103:ALA:C	2.63	0.41
28:1:310:ILE:O	28:1:311:ASP:C	2.64	0.41
35:8:140:THR:HG21	35:8:159:PHE:HA	2.02	0.41
40:d:207:LEU:HD13	40:d:207:LEU:HA	1.94	0.41
1:A:228:U:H2'	1:A:229:G:O4'	2.21	0.41
1:A:2001:U:H2'	1:A:2002:U:O4'	2.21	0.41
1:A:2358:A:C6	1:A:2359:U:C4	3.09	0.41
4:D:171:GLU:O	4:D:172:LYS:CB	2.69	0.41
6:F:24:LEU:HD11	6:F:104:ARG:HG2	2.02	0.41
1:A:26:A:C6	36:9:41:LEU:HD12	2.55	0.41
1:A:402:A:H2'	1:A:403:A:O4'	2.20	0.41
1:A:449:A:H2'	1:A:450:U:C6	2.56	0.41
1:A:564:A:O2'	1:A:565:A:C8	2.69	0.41
1:A:1433:A:H2'	1:A:1434:A:C8	2.56	0.41
1:A:1609:U:H2'	1:A:1610:A:C8	2.56	0.41
1:A:1959:A:N6	1:A:1960:A:C2	2.89	0.41
1:A:1963:C:H2'	1:A:1964:C:O4'	2.20	0.41
1:A:2441:U:H2'	1:A:2442:A:C8	2.55	0.41
1:A:2772:U:O2'	1:A:2773:C:OP2	2.29	0.41
2:B:155:ILE:HD11	2:B:157:PHE:CE1	2.55	0.41
2:B:378:ASN:O	2:B:381:LYS:HB2	2.21	0.41
4:D:45:THR:O	4:D:45:THR:HG23	2.21	0.41
4:D:105:LEU:HD11	4:D:119:ALA:HB2	2.02	0.41
15:O:107:LEU:HD13	15:O:221:LEU:HD13	2.03	0.41
18:R:160:LYS:O	18:R:163:GLU:HG3	2.21	0.41
35:8:157:PHE:CD1	35:8:157:PHE:C	2.98	0.41
37:a:29:THR:OG1	37:a:47:HIS:CE1	2.74	0.41
1:A:214:A:H2'	1:A:215:A:C4'	2.51	0.41
1:A:602:A:H1'	1:A:1367:A:H1'	2.03	0.41
1:A:2628:A:OP1	26:Z:74:ARG:NH1	2.54	0.41
1:A:3090:U:H2'	1:A:3092:U:OP1	2.21	0.41
17:Q:104:VAL:HG13	17:Q:105:PRO:HD2	2.02	0.41
17:Q:170:PRO:O	17:Q:184:TRP:NE1	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:28:LEU:HD13	31:4:72:LEU:HD21	2.02	0.41
32:5:70:LEU:O	32:5:70:LEU:HD23	2.21	0.41
1:A:274:U:O2	1:A:274:U:C2'	2.68	0.40
1:A:337:A:N6	1:A:338:G:C2	2.89	0.40
1:A:1808:G:N2	1:A:1809:C:C2	2.89	0.40
1:A:1849:U:H2'	1:A:1850:A:O4'	2.20	0.40
1:A:2779:A:H2'	1:A:2780:A:C8	2.56	0.40
1:A:2796:G:O2'	1:A:2797:U:P	2.80	0.40
1:A:3020:U:C2'	1:A:3021:A:O5'	2.69	0.40
5:E:180:VAL:O	5:E:183:TRP:O	2.39	0.40
8:H:15:LEU:O	8:H:55:ASP:HB3	2.22	0.40
13:M:151:ILE:O	13:M:154:THR:HG22	2.20	0.40
17:Q:100:PRO:HB2	17:Q:124:VAL:HG23	2.01	0.40
28:1:140:ARG:HG3	28:1:214:TYR:HD1	1.86	0.40
36:9:80:ILE:HG22	36:9:82:LEU:HD12	2.02	0.40
40:d:79:LEU:HD12	40:d:85:SER:CA	2.48	0.40
1:A:248:A:H2'	1:A:249:C:C6	2.56	0.40
1:A:638:U:O2'	15:O:248:LYS:HE3	2.21	0.40
1:A:1361:C:H2'	1:A:1362:C:C5	2.56	0.40
1:A:1404:A:C2'	1:A:1405:U:OP1	2.69	0.40
1:A:1609:U:H2'	1:A:1610:A:H8	1.86	0.40
1:A:1707:C:H4'	1:A:1708:A:H3'	2.04	0.40
1:A:1833:G:C4	1:A:1834:C:C6	3.09	0.40
1:A:1972:G:C2	1:A:1973:C:C2	3.09	0.40
1:A:2941:A:H2'	1:A:2942:A:H8	1.75	0.40
4:D:152:PHE:CZ	4:D:251:VAL:HG13	2.56	0.40
4:D:257:LEU:HD22	10:J:60:ILE:CG2	2.51	0.40
28:1:174:PRO:O	28:1:176:ALA:N	2.54	0.40
30:3:102:LYS:O	30:3:142:TYR:HB2	2.21	0.40
32:5:163:LEU:CD1	32:5:283:ILE:HD11	2.51	0.40
41:e:65:G:H2'	41:e:66:U:C6	2.57	0.40
1:A:326:A:H3'	1:A:326:A:N3	2.37	0.40
1:A:859:U:O2	1:A:859:U:O4'	2.37	0.40
1:A:1747:C:C4	1:A:1748:A:N7	2.90	0.40
1:A:1829:U:O2	1:A:1829:U:O4'	2.36	0.40
1:A:2379:U:O2'	1:A:2380:U:O5'	2.33	0.40
1:A:3233:A:O5'	1:A:3233:A:C8	2.73	0.40
3:C:72:PHE:CE1	3:C:79:ARG:HG3	2.56	0.40
32:5:338:VAL:HG21	32:5:359:LYS:HA	2.03	0.40
1:A:142:A:O3'	20:T:157:ASN:ND2	2.54	0.40
1:A:1361:C:C2'	1:A:1362:C:C6	3.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1388:A:N6	1:A:1715:A:C2	2.89	0.40
1:A:1549:U:OP2	40:d:201:ARG:NH2	2.54	0.40
1:A:3058:G:C2	1:A:3059:C:C2	3.09	0.40
5:E:30:HIS:CD2	28:1:166:PRO:HB3	2.56	0.40
9:I:138:ILE:HG22	13:M:121:ILE:HD11	2.02	0.40
20:T:95:ILE:HG23	20:T:155:VAL:HG12	2.03	0.40
31:4:26:ILE:HD13	31:4:98:LEU:CD2	2.51	0.40
33:6:27:VAL:CG1	33:6:195:ALA:HB2	2.51	0.40
1:A:599:A:H2'	1:A:600:C:O4'	2.21	0.40
1:A:1308:A:OP2	1:A:1597:G:O2'	2.34	0.40
1:A:1676:U:O2'	1:A:1858:G:OP1	2.35	0.40
1:A:2952:G:H4'	9:I:79:ARG:HG3	2.04	0.40
1:A:2961:A:H2'	1:A:2962:U:O4'	2.21	0.40
1:A:3069:A:H4'	1:A:3070:A:O5'	2.22	0.40
2:B:159:ARG:NE	2:B:194:ILE:HD12	2.37	0.40
18:R:262:ASN:ND2	18:R:314:LEU:HA	2.37	0.40
28:1:291:VAL:CG1	28:1:337:HIS:HB3	2.52	0.40
32:5:310:LEU:HD11	32:5:370:TRP:CG	2.56	0.40
33:6:257:LEU:HD21	33:6:265:TYR:CD2	2.57	0.40
35:8:189:ILE:HG22	35:8:194:LEU:CD2	2.50	0.40
36:9:70:ARG:HG2	36:9:75:LEU:HD12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	291/393 (74%)	272 (94%)	16 (6%)	3 (1%)	12	45
3	C	247/269 (92%)	226 (92%)	15 (6%)	6 (2%)	4	28
4	D	235/286 (82%)	211 (90%)	15 (6%)	9 (4%)	2	18
5	E	272/292 (93%)	246 (90%)	22 (8%)	4 (2%)	8	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	173/214 (81%)	163 (94%)	7 (4%)	3 (2%)	7	35
7	G	53/139 (38%)	50 (94%)	3 (6%)	0	100	100
8	H	146/163 (90%)	138 (94%)	8 (6%)	0	100	100
9	I	121/138 (88%)	110 (91%)	10 (8%)	1 (1%)	16	50
10	J	218/322 (68%)	202 (93%)	14 (6%)	2 (1%)	14	47
11	K	193/232 (83%)	182 (94%)	7 (4%)	4 (2%)	5	31
12	L	225/238 (94%)	208 (92%)	14 (6%)	3 (1%)	9	40
13	M	149/169 (88%)	138 (93%)	9 (6%)	2 (1%)	9	40
14	N	116/161 (72%)	109 (94%)	6 (5%)	1 (1%)	14	47
15	O	219/309 (71%)	199 (91%)	18 (8%)	2 (1%)	14	47
16	P	205/263 (78%)	189 (92%)	14 (7%)	2 (1%)	12	45
17	Q	269/297 (91%)	243 (90%)	22 (8%)	4 (2%)	8	37
18	R	310/371 (84%)	288 (93%)	17 (6%)	5 (2%)	7	36
19	S	142/258 (55%)	136 (96%)	6 (4%)	0	100	100
20	T	203/319 (64%)	184 (91%)	13 (6%)	6 (3%)	3	23
21	U	80/86 (93%)	77 (96%)	3 (4%)	0	100	100
22	V	62/177 (35%)	57 (92%)	5 (8%)	0	100	100
23	W	110/183 (60%)	100 (91%)	6 (6%)	4 (4%)	2	19
24	X	62/70 (89%)	55 (89%)	6 (10%)	1 (2%)	7	36
25	Y	43/105 (41%)	41 (95%)	1 (2%)	1 (2%)	5	29
26	Z	60/115 (52%)	57 (95%)	3 (5%)	0	100	100
27	0	36/93 (39%)	34 (94%)	2 (6%)	0	100	100
28	1	324/367 (88%)	293 (90%)	26 (8%)	5 (2%)	8	37
29	2	111/147 (76%)	103 (93%)	5 (4%)	3 (3%)	4	25
30	3	120/146 (82%)	103 (86%)	16 (13%)	1 (1%)	16	50
31	4	136/140 (97%)	128 (94%)	8 (6%)	0	100	100
32	5	324/390 (83%)	299 (92%)	23 (7%)	2 (1%)	21	56
33	6	195/281 (69%)	179 (92%)	12 (6%)	4 (2%)	5	31
34	7	104/146 (71%)	99 (95%)	5 (5%)	0	100	100
35	8	178/264 (67%)	168 (94%)	10 (6%)	0	100	100
36	9	185/253 (73%)	163 (88%)	14 (8%)	8 (4%)	2	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	a	174/195 (89%)	161 (92%)	7 (4%)	6 (3%)	3	20
38	b	153/157 (98%)	139 (91%)	12 (8%)	2 (1%)	9	40
39	c	116/131 (88%)	108 (93%)	5 (4%)	3 (3%)	4	26
40	d	200/226 (88%)	179 (90%)	16 (8%)	5 (2%)	4	27
All	All	6560/8505 (77%)	6037 (92%)	421 (6%)	102 (2%)	10	36

All (102) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	382	VAL
3	C	211	PRO
4	D	49	PHE
4	D	50	PRO
4	D	135	ALA
4	D	248	LYS
6	F	70	PRO
6	F	71	ASP
10	J	165	LEU
11	K	154	ASP
13	M	62	ILE
13	M	145	ARG
14	N	108	PRO
20	T	31	LYS
23	W	100	HIS
28	1	55	ILE
29	2	141	TRP
36	9	77	LYS
38	b	83	GLU
38	b	151	ASN
3	C	193	HIS
3	C	208	ASN
4	D	172	LYS
4	D	278	LYS
6	F	29	GLU
10	J	145	ASN
11	K	59	ARG
12	L	127	VAL
12	L	137	THR
15	O	185	GLY
15	O	239	GLY
16	P	177	ASP

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Mol	Chain	Res	Type
17	Q	96	ASP
18	R	129	PHE
18	R	262	ASN
20	T	20	THR
20	T	29	LEU
20	T	46	ASN
24	X	67	ARG
28	1	110	ILE
28	1	125	LEU
28	1	175	ARG
29	2	127	MET
36	9	33	HIS
36	9	104	ASN
36	9	167	ASN
37	a	79	SER
40	d	67	ARG
40	d	172	GLY
40	d	196	VAL
4	D	201	PHE
5	E	37	LYS
9	I	80	ASN
12	L	136	HIS
16	P	147	LEU
18	R	184	LEU
18	R	306	LYS
20	T	73	SER
25	Y	104	SER
29	2	118	ALA
32	5	219	MET
33	6	153	ASN
33	6	180	PRO
36	9	59	GLU
37	a	88	PRO
37	a	109	GLY
2	B	355	ASN
4	D	51	SER
5	E	21	SER
5	E	88	HIS
11	K	64	ILE
17	Q	211	ASP
17	Q	235	ARG
23	W	136	GLU

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Mol	Chain	Res	Type
39	c	124	ILE
40	d	33	GLU
40	d	68	ARG
4	D	170	GLY
17	Q	273	PRO
18	R	39	MET
20	T	25	LYS
23	W	107	CYS
23	W	137	ILE
30	3	144	GLU
36	9	36	PRO
36	9	74	GLN
39	c	117	PRO
2	B	386	PRO
3	C	197	ILE
3	C	210	ASP
5	E	35	ILE
32	5	381	PRO
33	6	154	ASP
37	a	116	PRO
28	1	98	PRO
3	C	111	GLY
11	K	224	PRO
33	6	146	ILE
37	a	28	VAL
37	a	87	MET
36	9	208	GLY
39	c	58	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	233/337 (69%)	209 (90%)	24 (10%)	7 28
3	C	209/229 (91%)	188 (90%)	21 (10%)	7 30
4	D	200/248 (81%)	174 (87%)	26 (13%)	4 20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	225/260 (86%)	199 (88%)	26 (12%)	5	24
6	F	141/190 (74%)	116 (82%)	25 (18%)	2	10
7	G	50/129 (39%)	47 (94%)	3 (6%)	17	50
8	H	126/141 (89%)	118 (94%)	8 (6%)	16	48
9	I	106/117 (91%)	102 (96%)	4 (4%)	29	62
10	J	175/274 (64%)	148 (85%)	27 (15%)	2	14
11	K	167/200 (84%)	136 (81%)	31 (19%)	1	9
12	L	202/212 (95%)	185 (92%)	17 (8%)	10	38
13	M	136/153 (89%)	124 (91%)	12 (9%)	9	35
14	N	107/147 (73%)	95 (89%)	12 (11%)	6	25
15	O	191/270 (71%)	168 (88%)	23 (12%)	5	23
16	P	183/236 (78%)	152 (83%)	31 (17%)	2	11
17	Q	219/268 (82%)	202 (92%)	17 (8%)	11	41
18	R	250/337 (74%)	218 (87%)	32 (13%)	4	20
19	S	126/231 (54%)	110 (87%)	16 (13%)	4	20
20	T	171/298 (57%)	152 (89%)	19 (11%)	6	25
21	U	73/77 (95%)	68 (93%)	5 (7%)	14	46
22	V	59/161 (37%)	58 (98%)	1 (2%)	53	75
23	W	104/167 (62%)	93 (89%)	11 (11%)	6	27
24	X	56/62 (90%)	52 (93%)	4 (7%)	13	44
25	Y	39/93 (42%)	37 (95%)	2 (5%)	21	54
26	Z	50/100 (50%)	46 (92%)	4 (8%)	11	40
27	0	36/84 (43%)	36 (100%)	0	100	100
28	1	299/341 (88%)	266 (89%)	33 (11%)	6	26
29	2	99/137 (72%)	89 (90%)	10 (10%)	7	30
30	3	102/126 (81%)	99 (97%)	3 (3%)	37	67
31	4	121/123 (98%)	107 (88%)	14 (12%)	5	24
32	5	263/345 (76%)	237 (90%)	26 (10%)	7	31
33	6	153/252 (61%)	134 (88%)	19 (12%)	4	21
34	7	94/128 (73%)	82 (87%)	12 (13%)	4	20
35	8	149/240 (62%)	134 (90%)	15 (10%)	7	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	9	140/221 (63%)	126 (90%)	14 (10%)	7	30
37	a	156/171 (91%)	138 (88%)	18 (12%)	5	24
38	b	144/146 (99%)	118 (82%)	26 (18%)	2	9
39	c	110/120 (92%)	103 (94%)	7 (6%)	16	48
40	d	185/210 (88%)	162 (88%)	23 (12%)	4	21
All	All	5649/7581 (74%)	5028 (89%)	621 (11%)	8	26

All (621) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	90	VAL
2	B	94	LYS
2	B	95	ARG
2	B	99	VAL
2	B	107	ARG
2	B	127	ARG
2	B	128	LYS
2	B	140	THR
2	B	153	ARG
2	B	159	ARG
2	B	167	VAL
2	B	169	ARG
2	B	195	ILE
2	B	205	VAL
2	B	207	GLU
2	B	210	ARG
2	B	241	LEU
2	B	246	ILE
2	B	339	ASN
2	B	351	LYS
2	B	364	GLN
2	B	376	ASN
2	B	382	VAL
2	B	383	LYS
3	C	27	VAL
3	C	61	LEU
3	C	78	GLU
3	C	79	ARG
3	C	86	GLU
3	C	89	ASN

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Mol	Chain	Res	Type
3	C	94	MET
3	C	106	CYS
3	C	122	MET
3	C	134	LYS
3	C	146	LYS
3	C	153	THR
3	C	156	LYS
3	C	164	GLN
3	C	183	ARG
3	C	193	HIS
3	C	197	ILE
3	C	218	ARG
3	C	231	ILE
3	C	239	VAL
3	C	240	ASP
4	D	56	THR
4	D	69	LEU
4	D	86	ARG
4	D	106	MET
4	D	109	LYS
4	D	115	ARG
4	D	142	GLU
4	D	143	LEU
4	D	152	PHE
4	D	182	LEU
4	D	184	LEU
4	D	186	ARG
4	D	187	LEU
4	D	204	GLU
4	D	216	LEU
4	D	219	LYS
4	D	221	LEU
4	D	222	LEU
4	D	233	ILE
4	D	247	GLN
4	D	252	GLU
4	D	254	ASN
4	D	269	LEU
4	D	274	MET
4	D	277	GLN
4	D	278	LYS
5	E	47	LEU

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Mol	Chain	Res	Type
5	E	51	LYS
5	E	94	LYS
5	E	96	LEU
5	E	120	LYS
5	E	139	SER
5	E	147	ARG
5	E	154	LEU
5	E	162	GLN
5	E	163	LEU
5	E	164	GLN
5	E	165	GLN
5	E	170	LYS
5	E	180	VAL
5	E	189	HIS
5	E	198	LYS
5	E	201	GLU
5	E	202	MET
5	E	204	GLN
5	E	209	LEU
5	E	211	GLU
5	E	214	LEU
5	E	226	GLN
5	E	259	THR
5	E	278	THR
5	E	280	LEU
6	F	33	SER
6	F	34	ILE
6	F	57	THR
6	F	64	GLU
6	F	65	LEU
6	F	69	VAL
6	F	71	ASP
6	F	74	HIS
6	F	86	VAL
6	F	92	GLU
6	F	106	LEU
6	F	115	THR
6	F	119	LEU
6	F	130	ARG
6	F	141	ASN
6	F	142	VAL
6	F	143	LYS

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Mol	Chain	Res	Type
6	F	150	GLN
6	F	152	LEU
6	F	161	LYS
6	F	171	GLU
6	F	175	LYS
6	F	176	GLN
6	F	186	ARG
6	F	194	TYR
7	G	34	LYS
7	G	45	MET
7	G	49	LEU
8	H	19	VAL
8	H	39	LEU
8	H	60	THR
8	H	68	THR
8	H	83	ARG
8	H	123	LEU
8	H	125	ARG
8	H	133	GLU
9	I	4	LEU
9	I	17	GLN
9	I	48	LYS
9	I	129	LYS
10	J	72	LYS
10	J	76	ARG
10	J	79	ARG
10	J	89	SER
10	J	103	LYS
10	J	107	GLU
10	J	114	TYR
10	J	132	GLU
10	J	133	LEU
10	J	149	LEU
10	J	153	GLU
10	J	158	ASN
10	J	159	LYS
10	J	161	ARG
10	J	165	LEU
10	J	171	LYS
10	J	185	ASN
10	J	190	LEU
10	J	225	ASN

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Mol	Chain	Res	Type
10	J	233	ARG
10	J	238	LEU
10	J	244	LYS
10	J	246	ARG
10	J	263	GLU
10	J	264	LYS
10	J	266	LYS
10	J	269	GLN
11	K	38	LYS
11	K	39	HIS
11	K	44	ARG
11	K	59	ARG
11	K	60	THR
11	K	64	ILE
11	K	69	LEU
11	K	71	PHE
11	K	76	LEU
11	K	86	SER
11	K	90	LEU
11	K	98	MET
11	K	99	ARG
11	K	102	ARG
11	K	108	HIS
11	K	109	LEU
11	K	113	LEU
11	K	114	CYS
11	K	126	THR
11	K	127	ARG
11	K	128	MET
11	K	130	LYS
11	K	156	LEU
11	K	181	LEU
11	K	184	LEU
11	K	191	SER
11	K	196	LYS
11	K	210	LYS
11	K	216	LEU
11	K	225	GLN
11	K	227	LYS
12	L	15	HIS
12	L	26	GLN
12	L	27	LEU

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Mol	Chain	Res	Type
12	L	62	ASN
12	L	68	GLU
12	L	69	LEU
12	L	70	LYS
12	L	76	GLN
12	L	79	LEU
12	L	90	LEU
12	L	93	GLU
12	L	112	GLU
12	L	163	ASN
12	L	165	LEU
12	L	188	LEU
12	L	194	LEU
12	L	207	ASN
13	M	24	LYS
13	M	39	GLN
13	M	49	ILE
13	M	50	GLU
13	M	65	LYS
13	M	102	LEU
13	M	108	LEU
13	M	109	LEU
13	M	110	LEU
13	M	125	LEU
13	M	145	ARG
13	M	155	ARG
14	N	46	THR
14	N	51	LEU
14	N	55	LEU
14	N	123	LYS
14	N	126	ARG
14	N	131	ARG
14	N	141	VAL
14	N	142	ARG
14	N	145	LYS
14	N	149	ASP
14	N	154	ARG
14	N	158	LEU
15	O	93	LEU
15	O	110	GLN
15	O	122	GLU
15	O	133	LYS

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Mol	Chain	Res	Type
15	O	135	ASP
15	O	145	GLU
15	O	159	LEU
15	O	171	LYS
15	O	184	LEU
15	O	202	LYS
15	O	205	ARG
15	O	210	LEU
15	O	223	LEU
15	O	224	LYS
15	O	235	THR
15	O	250	ARG
15	O	261	ILE
15	O	264	ARG
15	O	272	VAL
15	O	276	ARG
15	O	285	GLU
15	O	308	LYS
15	O	309	TRP
16	P	56	ILE
16	P	60	GLU
16	P	65	TRP
16	P	71	GLU
16	P	72	GLN
16	P	83	LYS
16	P	88	LYS
16	P	93	LEU
16	P	106	LYS
16	P	113	PHE
16	P	118	LEU
16	P	119	ARG
16	P	128	LEU
16	P	134	THR
16	P	136	GLN
16	P	137	LEU
16	P	141	LYS
16	P	145	MET
16	P	151	ARG
16	P	156	GLN
16	P	157	ILE
16	P	161	THR
16	P	164	MET

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Mol	Chain	Res	Type
16	P	182	TRP
16	P	190	MET
16	P	196	GLU
16	P	197	ARG
16	P	227	ILE
16	P	229	ARG
16	P	232	LYS
16	P	233	ARG
17	Q	14	ARG
17	Q	38	THR
17	Q	68	ARG
17	Q	69	VAL
17	Q	77	LYS
17	Q	79	ASN
17	Q	86	PHE
17	Q	102	LYS
17	Q	124	VAL
17	Q	127	LEU
17	Q	133	LEU
17	Q	186	LYS
17	Q	190	ILE
17	Q	196	LEU
17	Q	206	GLN
17	Q	213	VAL
17	Q	254	THR
18	R	40	LYS
18	R	46	ARG
18	R	59	THR
18	R	61	GLU
18	R	75	GLU
18	R	77	VAL
18	R	104	ARG
18	R	111	LEU
18	R	115	LEU
18	R	116	LYS
18	R	133	GLU
18	R	137	LYS
18	R	159	LEU
18	R	163	GLU
18	R	168	LYS
18	R	172	LEU
18	R	175	LYS

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Mol	Chain	Res	Type
18	R	178	LYS
18	R	182	ASP
18	R	191	ILE
18	R	193	LEU
18	R	198	LEU
18	R	205	LEU
18	R	206	LYS
18	R	239	LYS
18	R	263	LYS
18	R	266	LEU
18	R	304	LEU
18	R	314	LEU
18	R	322	ARG
18	R	362	ARG
18	R	367	PHE
19	S	23	GLN
19	S	25	ARG
19	S	32	ILE
19	S	51	GLU
19	S	52	ARG
19	S	65	ILE
19	S	73	LEU
19	S	92	THR
19	S	93	ARG
19	S	95	LYS
19	S	102	LYS
19	S	116	ILE
19	S	118	MET
19	S	124	LYS
19	S	132	ILE
19	S	154	LEU
20	T	17	THR
20	T	25	LYS
20	T	34	ILE
20	T	59	ASN
20	T	60	LEU
20	T	105	ASP
20	T	115	ARG
20	T	120	LEU
20	T	127	LEU
20	T	131	VAL
20	T	150	TRP

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Mol	Chain	Res	Type
20	T	151	GLN
20	T	155	VAL
20	T	161	LEU
20	T	171	GLN
20	T	176	ARG
20	T	182	THR
20	T	187	TYR
20	T	210	PHE
21	U	8	LEU
21	U	26	LEU
21	U	35	VAL
21	U	43	ILE
21	U	54	VAL
22	V	68	ILE
23	W	73	VAL
23	W	82	LYS
23	W	84	ARG
23	W	86	LYS
23	W	101	LEU
23	W	111	LYS
23	W	127	ILE
23	W	141	GLN
23	W	163	THR
23	W	169	LYS
23	W	178	ARG
24	X	27	ILE
24	X	33	LEU
24	X	37	VAL
24	X	45	ARG
25	Y	73	ARG
25	Y	80	LEU
26	Z	89	ARG
26	Z	95	THR
26	Z	111	LEU
26	Z	112	LEU
28	1	62	ILE
28	1	70	ILE
28	1	73	ILE
28	1	84	ARG
28	1	105	LEU
28	1	107	LYS
28	1	120	GLN

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Mol	Chain	Res	Type
28	1	123	ASN
28	1	128	VAL
28	1	138	VAL
28	1	142	LEU
28	1	144	LYS
28	1	154	LEU
28	1	155	LEU
28	1	156	MET
28	1	165	ILE
28	1	177	GLU
28	1	212	GLN
28	1	216	LEU
28	1	230	ASN
28	1	232	ASP
28	1	239	ASP
28	1	262	ASP
28	1	264	ARG
28	1	290	VAL
28	1	291	VAL
28	1	296	GLN
28	1	314	GLU
28	1	322	ILE
28	1	327	LYS
28	1	346	LYS
28	1	360	ARG
28	1	366	ARG
29	2	58	LEU
29	2	59	LEU
29	2	60	LYS
29	2	64	GLU
29	2	65	ASP
29	2	80	GLN
29	2	102	MET
29	2	105	LEU
29	2	121	LYS
29	2	133	THR
30	3	22	LYS
30	3	47	GLN
30	3	73	ASN
31	4	13	ARG
31	4	38	GLU
31	4	42	LYS

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Mol	Chain	Res	Type
31	4	47	LYS
31	4	54	GLN
31	4	59	ILE
31	4	65	ARG
31	4	91	ILE
31	4	98	LEU
31	4	100	LEU
31	4	102	LYS
31	4	121	LEU
31	4	132	LEU
31	4	136	LYS
32	5	94	LYS
32	5	99	ARG
32	5	101	LEU
32	5	104	ARG
32	5	116	LEU
32	5	117	SER
32	5	143	THR
32	5	148	LYS
32	5	187	VAL
32	5	236	LEU
32	5	237	ASN
32	5	240	ASP
32	5	244	LEU
32	5	271	THR
32	5	277	GLN
32	5	281	ARG
32	5	283	ILE
32	5	296	LYS
32	5	297	MET
32	5	310	LEU
32	5	314	GLU
32	5	320	VAL
32	5	335	VAL
32	5	368	MET
32	5	369	LYS
32	5	390	VAL
33	6	30	LEU
33	6	31	LEU
33	6	33	ARG
33	6	52	GLN
33	6	56	GLU

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Mol	Chain	Res	Type
33	6	70	LYS
33	6	80	LEU
33	6	97	ARG
33	6	103	LYS
33	6	104	HIS
33	6	106	ARG
33	6	111	LYS
33	6	113	GLU
33	6	115	LYS
33	6	169	LEU
33	6	178	LYS
33	6	198	GLU
33	6	254	PHE
33	6	266	VAL
34	7	47	LEU
34	7	51	LYS
34	7	72	ARG
34	7	87	ASN
34	7	88	LYS
34	7	111	LEU
34	7	116	LYS
34	7	117	LYS
34	7	121	VAL
34	7	143	THR
34	7	145	LYS
34	7	146	PHE
35	8	118	LEU
35	8	132	MET
35	8	148	VAL
35	8	163	LEU
35	8	166	LYS
35	8	170	LEU
35	8	179	LEU
35	8	181	THR
35	8	183	LEU
35	8	191	GLU
35	8	202	LEU
35	8	238	LYS
35	8	258	LEU
35	8	260	THR
35	8	262	ARG
36	9	41	LEU

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Mol	Chain	Res	Type
36	9	56	LEU
36	9	65	CYS
36	9	86	LEU
36	9	108	ASN
36	9	118	GLN
36	9	124	LEU
36	9	154	THR
36	9	160	CYS
36	9	163	VAL
36	9	184	HIS
36	9	204	LEU
36	9	211	LYS
36	9	217	GLN
37	a	20	GLN
37	a	28	VAL
37	a	30	THR
37	a	36	LYS
37	a	49	ASP
37	a	70	THR
37	a	100	VAL
37	a	101	LEU
37	a	114	LEU
37	a	119	ILE
37	a	132	LYS
37	a	150	SER
37	a	158	GLN
37	a	162	ILE
37	a	175	LYS
37	a	182	ARG
37	a	191	LEU
37	a	192	TRP
38	b	5	GLN
38	b	14	LEU
38	b	19	GLN
38	b	26	LYS
38	b	32	THR
38	b	35	LYS
38	b	43	LEU
38	b	46	LYS
38	b	52	ARG
38	b	57	LYS
38	b	63	MET

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Mol	Chain	Res	Type
38	b	65	ASP
38	b	71	LEU
38	b	83	GLU
38	b	99	LEU
38	b	105	LEU
38	b	114	LYS
38	b	117	GLU
38	b	119	LEU
38	b	123	GLU
38	b	126	LEU
38	b	129	VAL
38	b	132	LEU
38	b	137	LYS
38	b	143	LYS
38	b	146	GLU
39	c	28	LYS
39	c	30	ARG
39	c	45	LEU
39	c	51	VAL
39	c	70	LYS
39	c	78	LEU
39	c	101	THR
40	d	9	ARG
40	d	11	ARG
40	d	22	ILE
40	d	32	LEU
40	d	36	GLN
40	d	38	LEU
40	d	62	ARG
40	d	72	LYS
40	d	74	MET
40	d	83	LYS
40	d	94	ARG
40	d	96	ARG
40	d	101	VAL
40	d	110	LEU
40	d	137	LEU
40	d	142	LEU
40	d	173	ASP
40	d	191	LYS
40	d	194	GLN
40	d	203	GLU

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Mol	Chain	Res	Type
40	d	207	LEU
40	d	210	LEU
40	d	213	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	313	HIS
2	B	376	ASN
2	B	378	ASN
3	C	101	ASN
4	D	185	ASN
5	E	78	GLN
5	E	88	HIS
5	E	127	HIS
5	E	152	ASN
5	E	189	HIS
5	E	190	GLN
6	F	35	ASN
7	G	22	GLN
7	G	51	ASN
7	G	63	HIS
9	I	17	GLN
9	I	70	HIS
10	J	150	GLN
10	J	223	HIS
12	L	62	ASN
12	L	76	GLN
12	L	83	ASN
12	L	154	ASN
12	L	168	GLN
12	L	207	ASN
13	M	113	GLN
14	N	82	GLN
14	N	138	ASN
15	O	282	HIS
16	P	143	ASN
16	P	179	ASN
17	Q	109	GLN
18	R	173	GLN
18	R	319	HIS
19	S	84	ASN

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Mol	Chain	Res	Type
20	T	45	ASN
20	T	59	ASN
20	T	89	HIS
20	T	154	HIS
21	U	68	GLN
22	V	43	HIS
26	Z	83	ASN
27	0	90	GLN
28	1	145	GLN
28	1	253	ASN
29	2	81	GLN
29	2	88	ASN
30	3	73	ASN
30	3	97	ASN
30	3	132	GLN
31	4	60	GLN
32	5	142	ASN
32	5	379	GLN
33	6	194	HIS
34	7	110	GLN
35	8	158	GLN
40	d	84	GLN
40	d	91	ASN
40	d	147	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2682/3296 (81%)	702 (26%)	132 (4%)
41	e	18/20 (90%)	6 (33%)	0
All	All	2700/3316 (81%)	708 (26%)	132 (4%)

All (708) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	22	U
1	A	26	A
1	A	27	A
1	A	28	U
1	A	29	A
1	A	30	U

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Mol	Chain	Res	Type
1	A	31	U
1	A	32	U
1	A	34	U
1	A	35	U
1	A	38	A
1	A	41	G
1	A	43	U
1	A	45	U
1	A	48	A
1	A	49	G
1	A	68	A
1	A	69	U
1	A	70	A
1	A	85	A
1	A	93	U
1	A	94	A
1	A	106	A
1	A	112	G
1	A	115	A
1	A	116	C
1	A	117	U
1	A	118	A
1	A	119	A
1	A	120	U
1	A	122	A
1	A	134	U
1	A	135	U
1	A	139	U
1	A	149	A
1	A	150	A
1	A	151	A
1	A	152	G
1	A	153	G
1	A	155	A
1	A	161	U
1	A	162	U
1	A	163	A
1	A	164	U
1	A	165	A
1	A	204	A
1	A	209	U
1	A	215	A

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Mol	Chain	Res	Type
1	A	216	U
1	A	217	A
1	A	218	A
1	A	219	U
1	A	222	A
1	A	236	A
1	A	239	A
1	A	244	A
1	A	245	G
1	A	246	U
1	A	253	A
1	A	255	G
1	A	256	A
1	A	261	A
1	A	262	A
1	A	264	U
1	A	266	A
1	A	269	A
1	A	270	G
1	A	276	U
1	A	277	U
1	A	281	A
1	A	288	G
1	A	290	G
1	A	292	G
1	A	301	A
1	A	307	G
1	A	308	U
1	A	309	C
1	A	311	A
1	A	312	A
1	A	313	U
1	A	314	A
1	A	315	A
1	A	316	G
1	A	327	A
1	A	328	A
1	A	329	A
1	A	330	A
1	A	331	A
1	A	332	A
1	A	336	A

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Mol	Chain	Res	Type
1	A	337	A
1	A	342	A
1	A	343	U
1	A	344	A
1	A	348	U
1	A	349	A
1	A	355	U
1	A	359	A
1	A	365	A
1	A	366	A
1	A	380	G
1	A	382	A
1	A	384	A
1	A	386	U
1	A	387	A
1	A	401	A
1	A	409	A
1	A	410	A
1	A	425	A
1	A	427	G
1	A	428	C
1	A	429	A
1	A	430	A
1	A	433	A
1	A	435	G
1	A	442	U
1	A	445	U
1	A	448	U
1	A	450	U
1	A	455	A
1	A	461	U
1	A	462	A
1	A	472	U
1	A	474	A
1	A	486	G
1	A	487	U
1	A	494	U
1	A	498	A
1	A	502	A
1	A	503	A
1	A	507	A
1	A	508	U

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Mol	Chain	Res	Type
1	A	510	A
1	A	516	A
1	A	526	A
1	A	527	A
1	A	536	A
1	A	537	U
1	A	546	A
1	A	548	A
1	A	551	U
1	A	554	U
1	A	561	U
1	A	562	U
1	A	563	U
1	A	564	A
1	A	565	A
1	A	578	G
1	A	579	A
1	A	595	U
1	A	604	G
1	A	614	A
1	A	615	U
1	A	616	A
1	A	617	A
1	A	618	A
1	A	619	C
1	A	620	G
1	A	621	A
1	A	637	U
1	A	638	U
1	A	644	A
1	A	655	A
1	A	656	A
1	A	661	G
1	A	666	G
1	A	667	U
1	A	673	A
1	A	674	A
1	A	675	G
1	A	676	A
1	A	681	U
1	A	682	C
1	A	683	U

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Mol	Chain	Res	Type
1	A	684	G
1	A	696	G
1	A	703	U
1	A	706	U
1	A	707	A
1	A	710	A
1	A	718	G
1	A	719	U
1	A	720	A
1	A	733	A
1	A	734	U
1	A	736	A
1	A	737	A
1	A	747	U
1	A	755	U
1	A	767	A
1	A	776	A
1	A	777	G
1	A	778	A
1	A	781	G
1	A	782	G
1	A	783	U
1	A	789	A
1	A	790	A
1	A	797	U
1	A	798	A
1	A	803	A
1	A	833	U
1	A	835	A
1	A	840	C
1	A	841	G
1	A	843	A
1	A	845	U
1	A	854	A
1	A	855	U
1	A	856	A
1	A	857	U
1	A	858	A
1	A	866	G
1	A	867	A
1	A	871	A
1	A	872	G

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Mol	Chain	Res	Type
1	A	884	U
1	A	887	G
1	A	891	A
1	A	900	A
1	A	901	A
1	A	909	A
1	A	910	G
1	A	912	C
1	A	916	A
1	A	919	A
1	A	925	U
1	A	928	A
1	A	929	G
1	A	938	A
1	A	939	A
1	A	942	A
1	A	947	G
1	A	948	U
1	A	951	A
1	A	952	A
1	A	953	U
1	A	961	A
1	A	966	A
1	A	967	U
1	A	1058	U
1	A	1062	U
1	A	1063	A
1	A	1065	A
1	A	1075	A
1	A	1077	A
1	A	1078	U
1	A	1086	U
1	A	1087	U
1	A	1094	U
1	A	1095	A
1	A	1096	A
1	A	1097	U
1	A	1099	U
1	A	1101	C
1	A	1102	G
1	A	1105	U
1	A	1110	A

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Mol	Chain	Res	Type
1	A	1111	U
1	A	1112	A
1	A	1113	A
1	A	1114	U
1	A	1115	A
1	A	1117	G
1	A	1118	A
1	A	1119	A
1	A	1126	A
1	A	1127	A
1	A	1130	C
1	A	1161	A
1	A	1169	A
1	A	1170	U
1	A	1171	A
1	A	1182	A
1	A	1191	U
1	A	1206	A
1	A	1213	A
1	A	1242	A
1	A	1243	U
1	A	1244	A
1	A	1255	A
1	A	1256	U
1	A	1257	U
1	A	1258	A
1	A	1260	U
1	A	1267	A
1	A	1269	G
1	A	1271	A
1	A	1272	U
1	A	1273	U
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1283	G
1	A	1286	A
1	A	1287	A
1	A	1289	G
1	A	1298	A
1	A	1304	G
1	A	1305	A

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Mol	Chain	Res	Type
1	A	1306	A
1	A	1307	A
1	A	1308	A
1	A	1312	G
1	A	1313	G
1	A	1314	U
1	A	1315	A
1	A	1316	U
1	A	1317	A
1	A	1331	A
1	A	1332	A
1	A	1333	A
1	A	1337	U
1	A	1342	U
1	A	1344	U
1	A	1346	A
1	A	1349	A
1	A	1350	U
1	A	1352	A
1	A	1356	U
1	A	1357	A
1	A	1358	C
1	A	1359	G
1	A	1360	G
1	A	1361	C
1	A	1362	C
1	A	1365	U
1	A	1368	U
1	A	1371	A
1	A	1372	A
1	A	1374	U
1	A	1386	A
1	A	1387	A
1	A	1389	U
1	A	1392	A
1	A	1393	U
1	A	1396	A
1	A	1399	A
1	A	1400	U
1	A	1404	A
1	A	1405	U
1	A	1406	A

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Mol	Chain	Res	Type
1	A	1409	C
1	A	1410	U
1	A	1411	A
1	A	1412	U
1	A	1418	U
1	A	1423	A
1	A	1424	U
1	A	1477	A
1	A	1490	A
1	A	1493	U
1	A	1494	A
1	A	1500	U
1	A	1501	A
1	A	1507	U
1	A	1516	U
1	A	1523	A
1	A	1528	G
1	A	1531	C
1	A	1534	G
1	A	1537	A
1	A	1546	G
1	A	1548	A
1	A	1549	U
1	A	1560	A
1	A	1562	A
1	A	1563	C
1	A	1568	U
1	A	1569	C
1	A	1578	A
1	A	1579	A
1	A	1583	G
1	A	1598	A
1	A	1599	A
1	A	1600	U
1	A	1603	G
1	A	1604	A
1	A	1605	U
1	A	1606	A
1	A	1612	A
1	A	1616	A
1	A	1618	G
1	A	1626	G

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Mol	Chain	Res	Type
1	A	1632	A
1	A	1633	U
1	A	1634	A
1	A	1635	G
1	A	1648	U
1	A	1649	C
1	A	1653	A
1	A	1655	A
1	A	1661	A
1	A	1662	U
1	A	1663	A
1	A	1664	A
1	A	1665	G
1	A	1666	A
1	A	1671	A
1	A	1672	G
1	A	1680	A
1	A	1687	A
1	A	1689	U
1	A	1693	A
1	A	1694	A
1	A	1706	G
1	A	1707	C
1	A	1708	A
1	A	1709	G
1	A	1715	A
1	A	1716	U
1	A	1717	A
1	A	1720	U
1	A	1724	A
1	A	1727	A
1	A	1728	U
1	A	1737	A
1	A	1740	U
1	A	1743	G
1	A	1746	C
1	A	1755	A
1	A	1764	U
1	A	1767	A
1	A	1768	A
1	A	1769	U
1	A	1770	U

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Mol	Chain	Res	Type
1	A	1777	C
1	A	1778	G
1	A	1782	A
1	A	1786	A
1	A	1789	U
1	A	1790	A
1	A	1797	G
1	A	1807	A
1	A	1813	A
1	A	1814	U
1	A	1815	U
1	A	1818	G
1	A	1819	A
1	A	1820	G
1	A	1824	U
1	A	1825	A
1	A	1826	U
1	A	1829	U
1	A	1830	G
1	A	1831	U
1	A	1836	A
1	A	1837	A
1	A	1838	A
1	A	1851	U
1	A	1854	U
1	A	1855	U
1	A	1863	C
1	A	1867	U
1	A	1869	A
1	A	1870	A
1	A	1871	U
1	A	1872	G
1	A	1875	G
1	A	1882	U
1	A	1891	U
1	A	1892	G
1	A	1893	U
1	A	1897	C
1	A	1920	A
1	A	1923	C
1	A	1930	A
1	A	1931	A

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Mol	Chain	Res	Type
1	A	1933	A
1	A	1936	C
1	A	1943	C
1	A	1949	G
1	A	1951	A
1	A	1952	A
1	A	1955	C
1	A	1956	G
1	A	1959	A
1	A	1961	G
1	A	1963	C
1	A	1964	C
1	A	1969	G
1	A	1980	G
1	A	1989	U
1	A	1990	A
1	A	1991	G
1	A	1995	G
1	A	2005	U
1	A	2009	U
1	A	2084	G
1	A	2093	A
1	A	2094	A
1	A	2095	U
1	A	2251	A
1	A	2253	A
1	A	2263	U
1	A	2264	G
1	A	2276	G
1	A	2293	A
1	A	2301	C
1	A	2305	A
1	A	2306	U
1	A	2309	G
1	A	2310	U
1	A	2313	A
1	A	2314	U
1	A	2315	A
1	A	2316	A
1	A	2317	A
1	A	2318	U
1	A	2323	A

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Mol	Chain	Res	Type
1	A	2324	U
1	A	2325	A
1	A	2330	A
1	A	2332	U
1	A	2349	A
1	A	2356	A
1	A	2358	A
1	A	2360	U
1	A	2361	A
1	A	2362	U
1	A	2363	A
1	A	2369	U
1	A	2372	U
1	A	2373	U
1	A	2374	A
1	A	2379	U
1	A	2380	U
1	A	2419	U
1	A	2423	G
1	A	2424	U
1	A	2425	A
1	A	2427	U
1	A	2428	A
1	A	2430	A
1	A	2431	U
1	A	2435	A
1	A	2436	A
1	A	2438	A
1	A	2439	U
1	A	2444	A
1	A	2447	A
1	A	2453	G
1	A	2455	A
1	A	2458	G
1	A	2461	A
1	A	2462	A
1	A	2467	A
1	A	2468	A
1	A	2469	U
1	A	2470	A
1	A	2575	A
1	A	2580	A

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Mol	Chain	Res	Type
1	A	2585	A
1	A	2586	U
1	A	2587	U
1	A	2588	A
1	A	2591	A
1	A	2597	G
1	A	2599	A
1	A	2601	A
1	A	2603	C
1	A	2610	A
1	A	2612	A
1	A	2613	A
1	A	2614	U
1	A	2616	G
1	A	2618	A
1	A	2638	G
1	A	2650	G
1	A	2652	C
1	A	2656	A
1	A	2659	A
1	A	2660	A
1	A	2666	A
1	A	2670	C
1	A	2671	U
1	A	2672	G
1	A	2673	A
1	A	2674	U
1	A	2691	A
1	A	2695	A
1	A	2696	A
1	A	2700	A
1	A	2701	A
1	A	2705	A
1	A	2707	G
1	A	2711	G
1	A	2713	G
1	A	2714	A
1	A	2720	G
1	A	2725	A
1	A	2737	A
1	A	2740	A
1	A	2741	G

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Mol	Chain	Res	Type
1	A	2742	A
1	A	2744	A
1	A	2750	A
1	A	2753	U
1	A	2760	G
1	A	2766	U
1	A	2773	C
1	A	2774	G
1	A	2779	A
1	A	2784	U
1	A	2791	U
1	A	2795	U
1	A	2796	G
1	A	2797	U
1	A	2802	G
1	A	2813	U
1	A	2814	U
1	A	2815	U
1	A	2821	U
1	A	2823	C
1	A	2826	C
1	A	2829	U
1	A	2833	A
1	A	2834	A
1	A	2836	G
1	A	2840	C
1	A	2852	U
1	A	2853	A
1	A	2869	A
1	A	2870	G
1	A	2876	U
1	A	2877	U
1	A	2880	U
1	A	2881	A
1	A	2894	A
1	A	2896	U
1	A	2897	A
1	A	2898	U
1	A	2907	U
1	A	2909	A
1	A	2913	U
1	A	2928	A

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Mol	Chain	Res	Type
1	A	2930	G
1	A	2940	G
1	A	2950	A
1	A	2956	U
1	A	2957	A
1	A	2958	U
1	A	2959	C
1	A	2980	A
1	A	3016	A
1	A	3017	U
1	A	3021	A
1	A	3023	U
1	A	3024	U
1	A	3037	A
1	A	3038	U
1	A	3039	A
1	A	3043	U
1	A	3050	G
1	A	3060	U
1	A	3062	A
1	A	3069	A
1	A	3070	A
1	A	3080	A
1	A	3092	U
1	A	3093	U
1	A	3094	A
1	A	3098	A
1	A	3102	A
1	A	3103	G
1	A	3106	G
1	A	3122	U
1	A	3123	A
1	A	3124	A
1	A	3125	U
1	A	3126	C
1	A	3127	U
1	A	3134	U
1	A	3135	U
1	A	3136	U
1	A	3141	U
1	A	3148	A
1	A	3150	U

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Mol	Chain	Res	Type
1	A	3151	A
1	A	3152	A
1	A	3153	U
1	A	3155	A
1	A	3159	G
1	A	3168	A
1	A	3169	U
1	A	3171	A
1	A	3172	U
1	A	3173	U
1	A	3193	A
1	A	3194	U
1	A	3248	C
1	A	3251	A
1	A	3252	U
1	A	3253	U
1	A	3255	A
1	A	3256	U
1	A	3257	C
1	A	3264	C
1	A	3265	U
1	A	3268	A
1	A	3269	U
1	A	3274	U
41	e	2	C
41	e	6	G
41	e	68	C
41	e	71	G
41	e	74	C
41	e	76	A

All (132) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	25	A
1	A	27	A
1	A	34	U
1	A	44	U
1	A	93	U
1	A	134	U
1	A	162	U
1	A	164	U

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Mol	Chain	Res	Type
1	A	216	U
1	A	217	A
1	A	236	A
1	A	239	A
1	A	261	A
1	A	268	C
1	A	276	U
1	A	306	G
1	A	313	U
1	A	326	A
1	A	329	A
1	A	365	A
1	A	409	A
1	A	426	A
1	A	429	A
1	A	454	A
1	A	461	U
1	A	486	G
1	A	507	A
1	A	526	A
1	A	536	A
1	A	561	U
1	A	563	U
1	A	564	A
1	A	578	G
1	A	614	A
1	A	615	U
1	A	616	A
1	A	617	A
1	A	637	U
1	A	643	U
1	A	655	A
1	A	666	G
1	A	675	G
1	A	682	C
1	A	696	G
1	A	733	A
1	A	735	A
1	A	746	A
1	A	781	G
1	A	840	C
1	A	856	A

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Mol	Chain	Res	Type
1	A	909	A
1	A	951	A
1	A	1062	U
1	A	1064	A
1	A	1093	A
1	A	1113	A
1	A	1126	A
1	A	1272	U
1	A	1306	A
1	A	1312	G
1	A	1313	G
1	A	1316	U
1	A	1331	A
1	A	1349	A
1	A	1409	C
1	A	1410	U
1	A	1422	A
1	A	1489	U
1	A	1493	U
1	A	1522	A
1	A	1547	U
1	A	1560	A
1	A	1591	G
1	A	1662	U
1	A	1663	A
1	A	1664	A
1	A	1665	G
1	A	1693	A
1	A	1706	G
1	A	1707	C
1	A	1708	A
1	A	1727	A
1	A	1818	G
1	A	1829	U
1	A	1830	G
1	A	1854	U
1	A	1892	G
1	A	1990	A
1	A	2301	C
1	A	2304	A
1	A	2309	G
1	A	2314	U

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Mol	Chain	Res	Type
1	A	2316	A
1	A	2324	U
1	A	2329	A
1	A	2357	U
1	A	2359	U
1	A	2372	U
1	A	2373	U
1	A	2378	A
1	A	2426	A
1	A	2427	U
1	A	2437	U
1	A	2446	U
1	A	2467	A
1	A	2585	A
1	A	2587	U
1	A	2591	A
1	A	2612	A
1	A	2613	A
1	A	2713	G
1	A	2783	U
1	A	2796	G
1	A	2880	U
1	A	2897	A
1	A	2906	U
1	A	2956	U
1	A	3020	U
1	A	3023	U
1	A	3036	U
1	A	3068	U
1	A	3069	A
1	A	3122	U
1	A	3124	A
1	A	3125	U
1	A	3126	C
1	A	3135	U
1	A	3150	U
1	A	3171	A
1	A	3193	A
1	A	3252	U
1	A	3268	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 113 ligands modelled in this entry, 113 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	5
41	e	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2226:A	O3'	2227:U	P	17.43
1	A	2197:A	O3'	2198:U	P	17.36
1	e	6:G	O3'	63:G	P	15.82
1	A	2344:A	O3'	2345:A	P	15.67
1	A	1374:U	O3'	1375:A	P	11.56
1	A	558:A	O3'	559:U	P	8.70

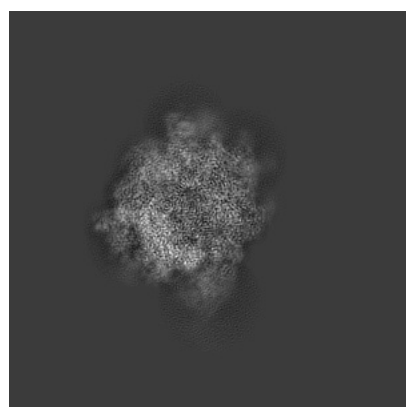
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2566. These allow visual inspection of the internal detail of the map and identification of artifacts.

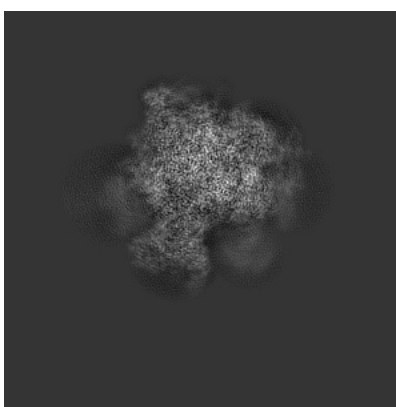
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

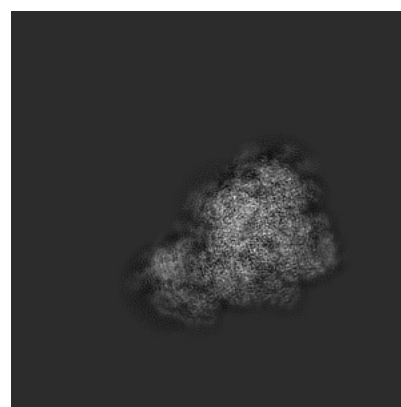
6.1.1 Primary map



X



Y

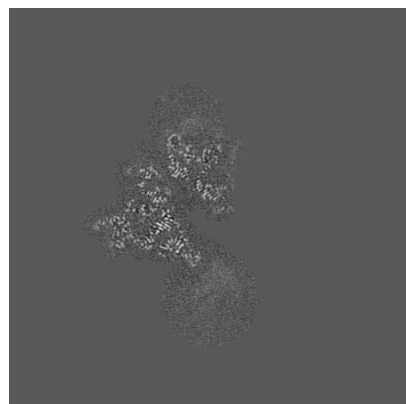


Z

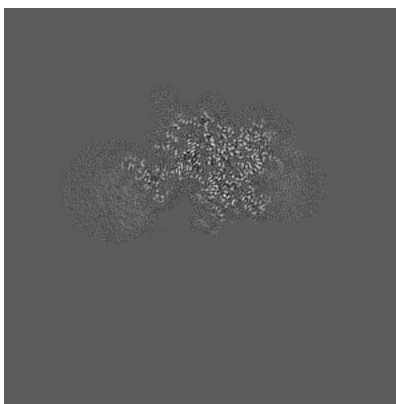
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

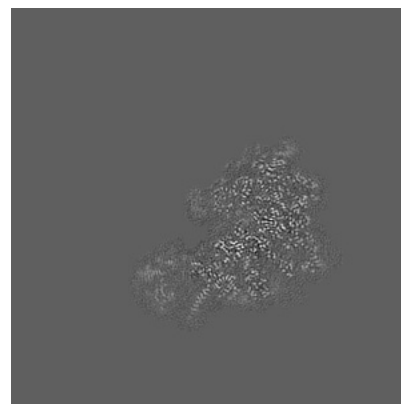
6.2.1 Primary map



X Index: 180



Y Index: 180

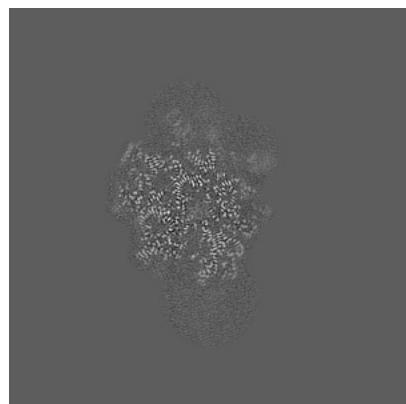


Z Index: 180

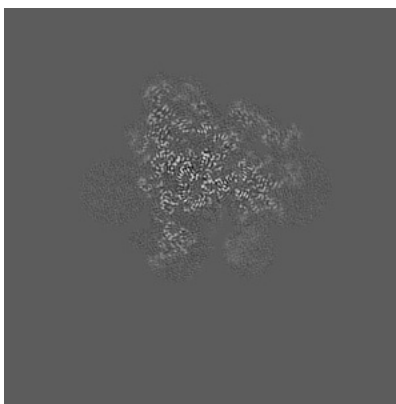
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

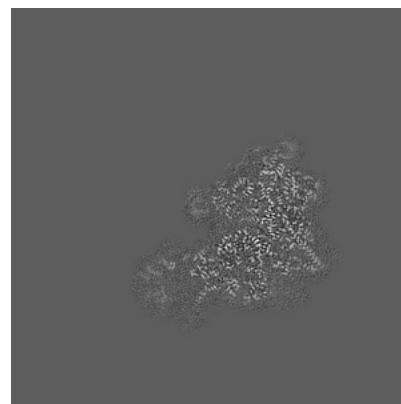
6.3.1 Primary map



X Index: 212



Y Index: 145

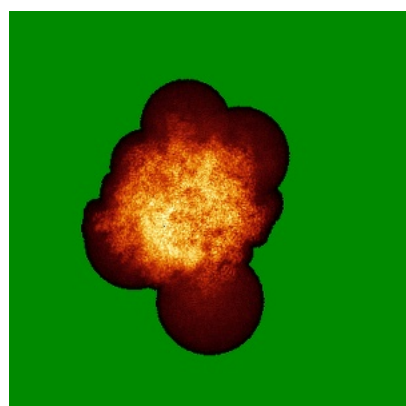


Z Index: 182

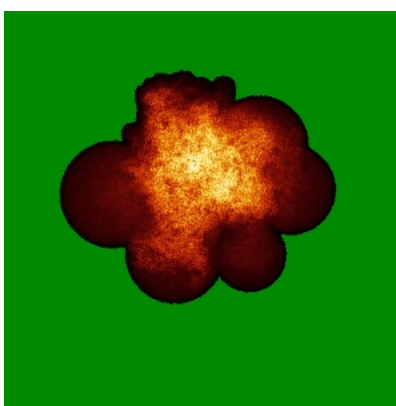
The images above show the largest variance slices of the map in three orthogonal directions.

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

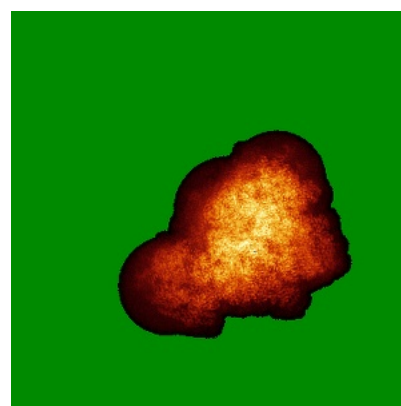
6.4.1 Primary map



X



Y



Z

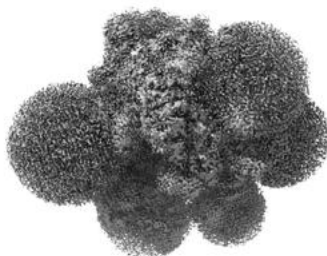
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0681. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

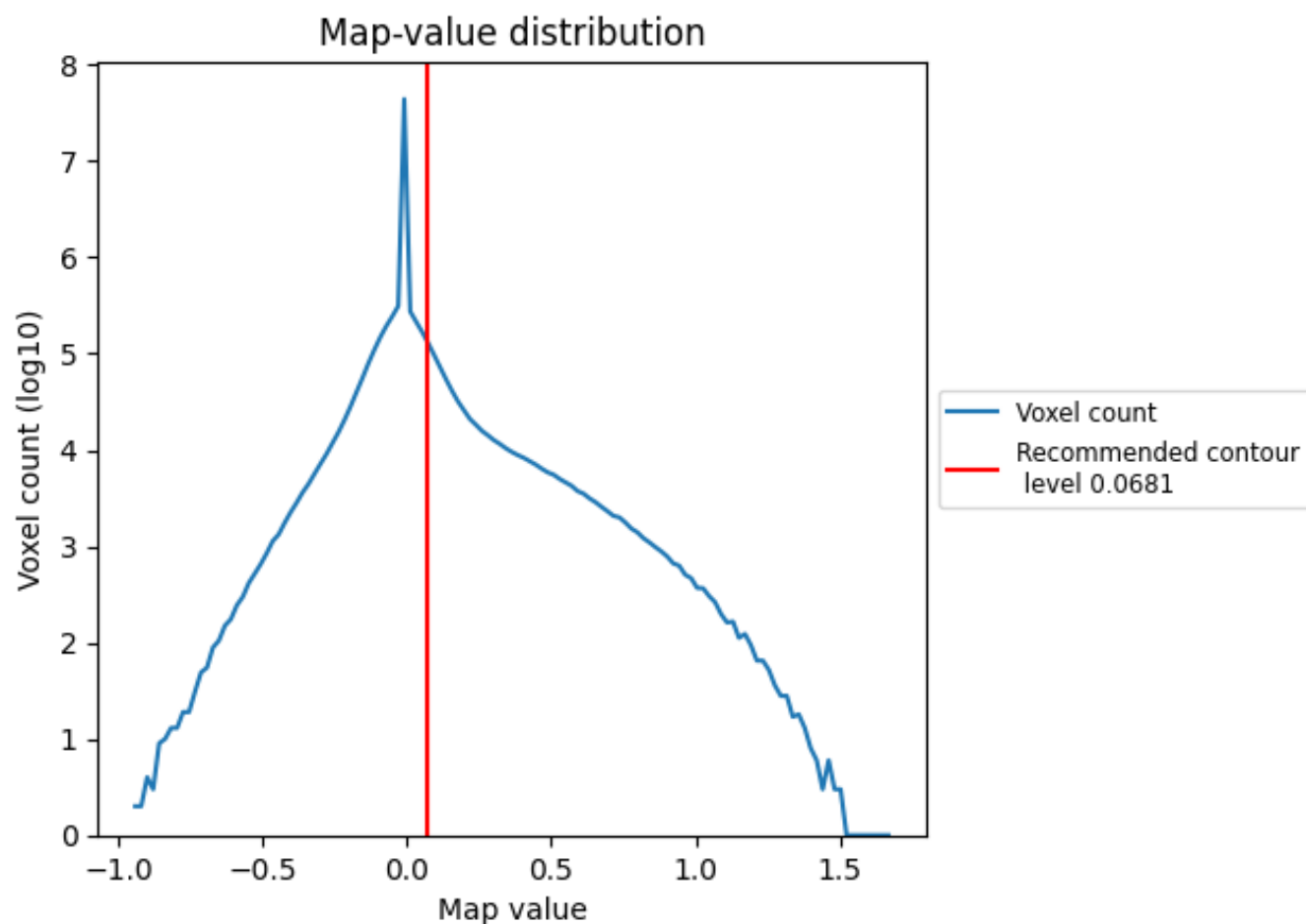
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

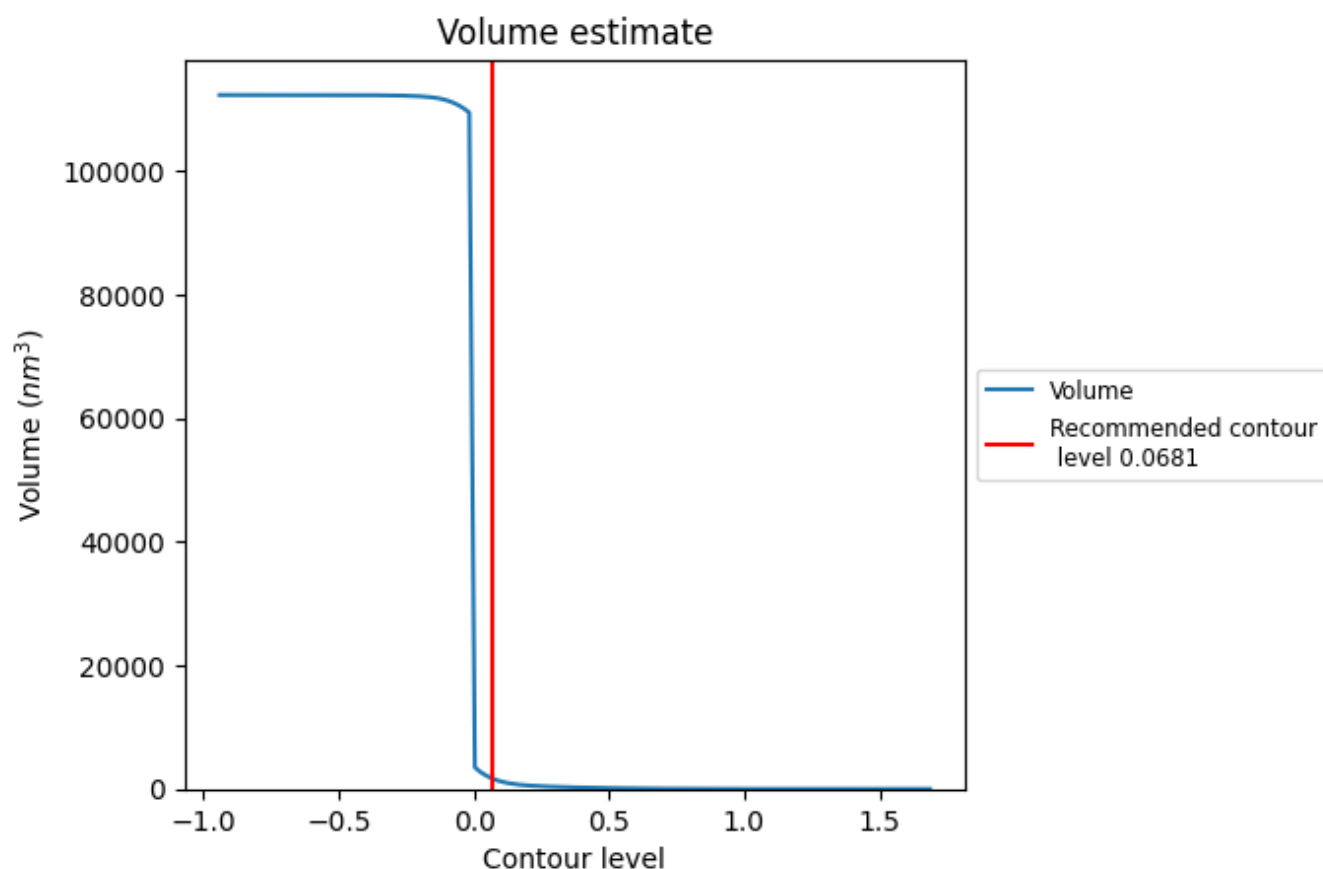
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

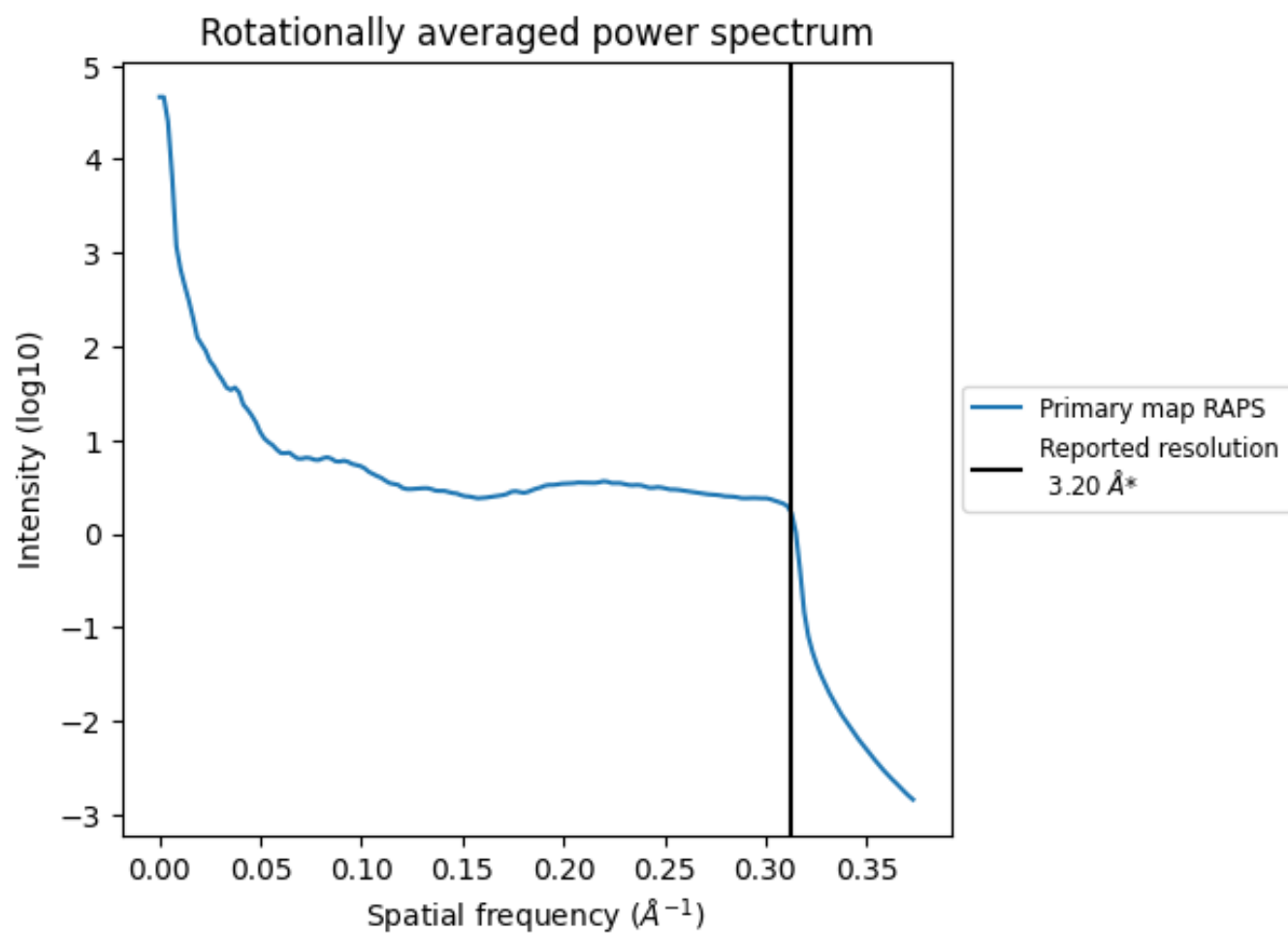
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1704 nm^3 ; this corresponds to an approximate mass of 1539 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

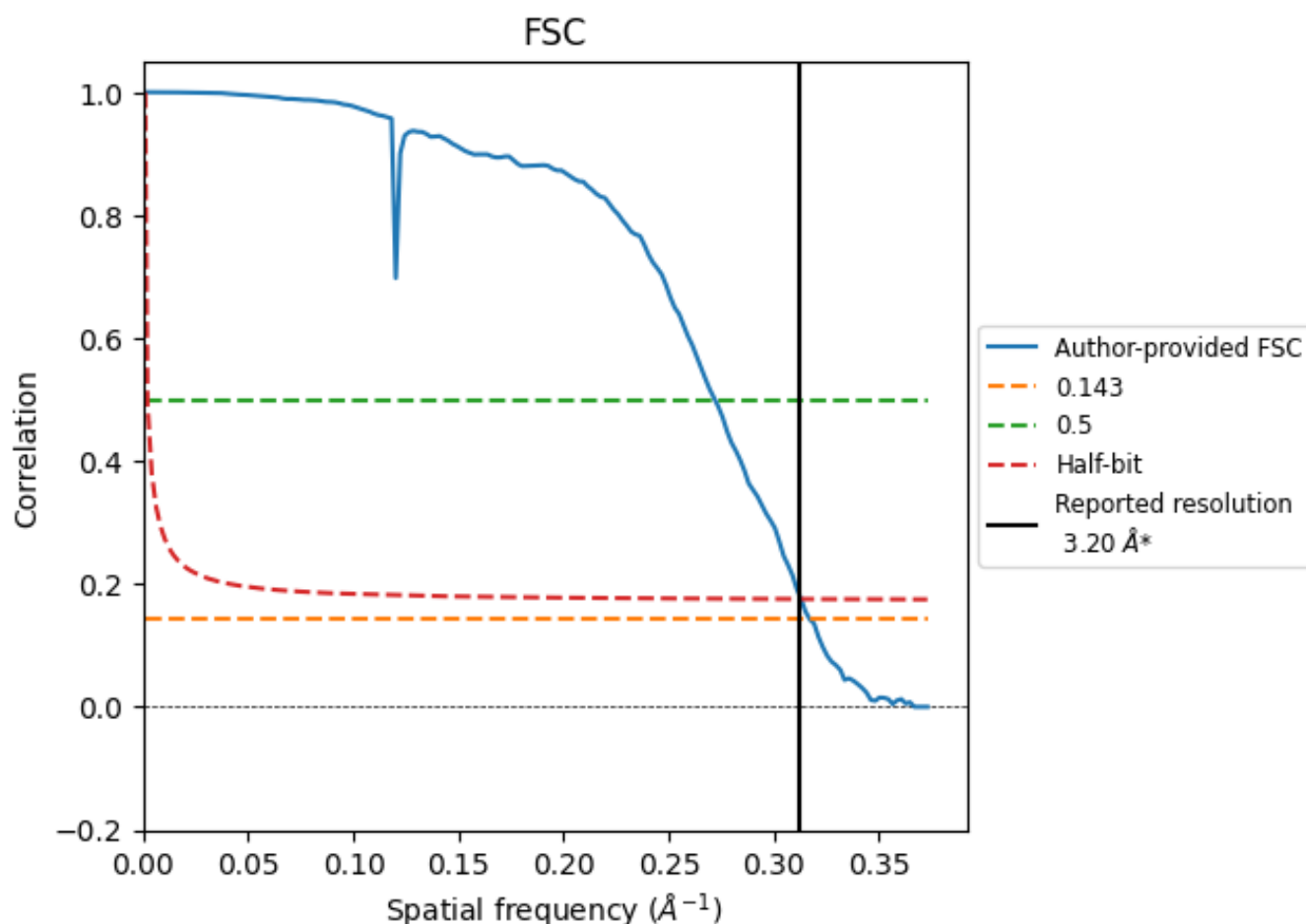


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

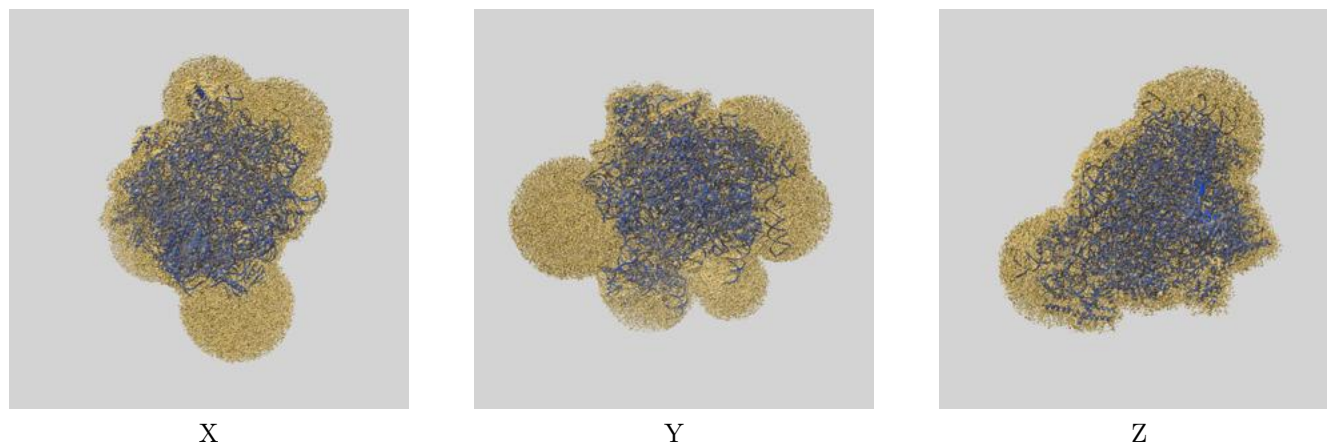
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.15	3.68	3.19
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

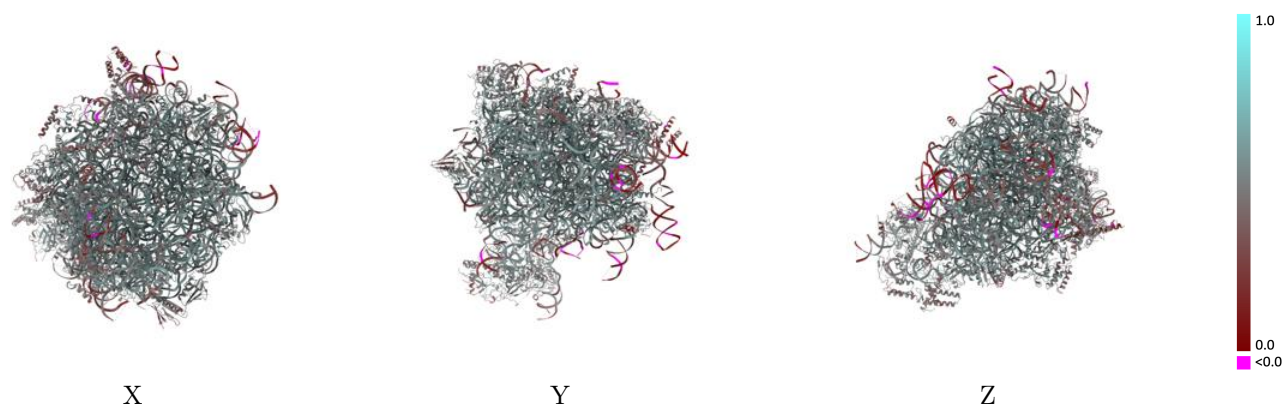
This section contains information regarding the fit between EMDB map EMD-2566 and PDB model 3J6B. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



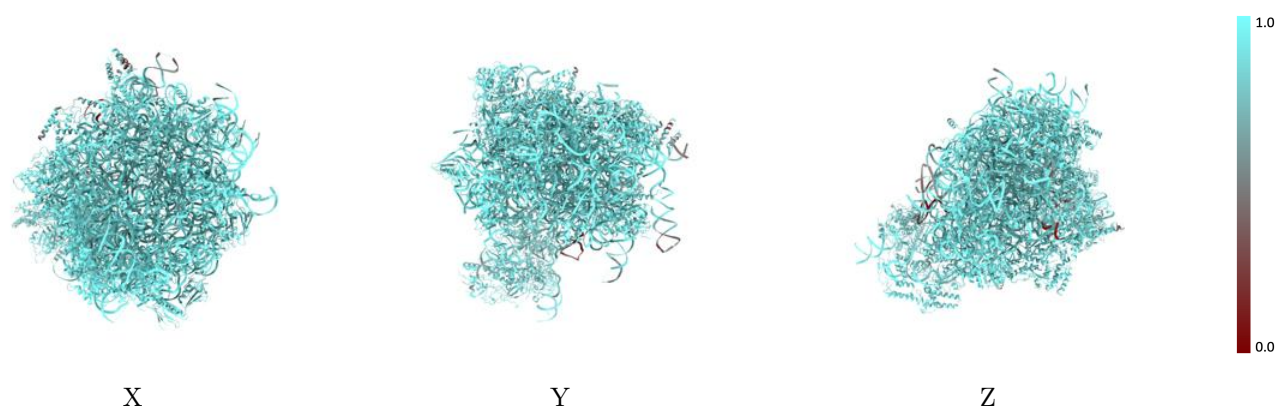
The images above show the 3D surface view of the map at the recommended contour level 0.0681 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



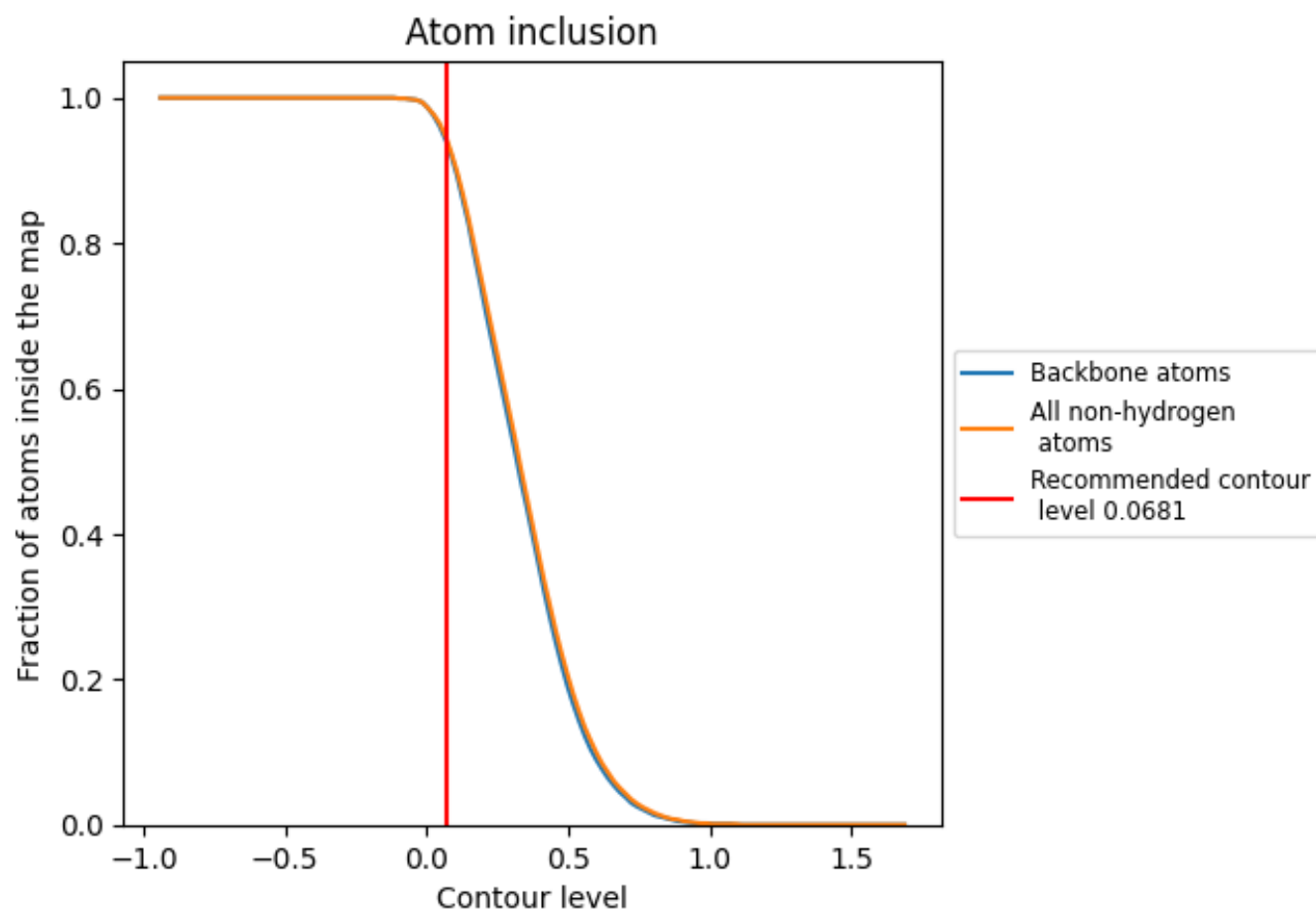
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0681).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 95% 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 (0.0681) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.5070
0	 0.9550	 0.5600
1	 0.9440	 0.5060
2	 0.9420	 0.4870
3	 0.9400	 0.5180
4	 0.9500	 0.5420
5	 0.9400	 0.5190
6	 0.9260	 0.4600
7	 0.9420	 0.5170
8	 0.8880	 0.4180
9	 0.9420	 0.4650
A	 0.9600	 0.5070
B	 0.9490	 0.5350
C	 0.9580	 0.5580
D	 0.9310	 0.5210
E	 0.9350	 0.5150
F	 0.9140	 0.4500
G	 0.9580	 0.5080
H	 0.9470	 0.5580
I	 0.9150	 0.5150
J	 0.9570	 0.5360
K	 0.9390	 0.5240
L	 0.9380	 0.5230
M	 0.9380	 0.5120
N	 0.9520	 0.5500
O	 0.9350	 0.5230
P	 0.9280	 0.5110
Q	 0.8950	 0.4610
R	 0.9300	 0.4700
S	 0.9430	 0.5270
T	 0.8780	 0.4520
U	 0.9490	 0.5350
V	 0.9330	 0.5010
W	 0.9440	 0.5330
X	 0.9260	 0.5300



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Chain	Atom inclusion	Q-score
Y	 0.9190	 0.5590
Z	 0.9610	 0.5640
a	 0.9390	 0.5060
b	 0.9180	 0.4930
c	 0.9370	 0.5390
d	 0.9390	 0.5240
e	 0.2880	 0.1130