



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 05:39 PM UTC

PDB ID : 5GAE / pdb_00005gae
EMDB ID : EMD-8001
Title : RNC in complex with a translocating SecYEG
Authors : Jomaa, A.; Boehringer, D.; Leibundgut, M.; Ban, N.
Deposited on : 2015-11-25
Resolution : 3.33 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:

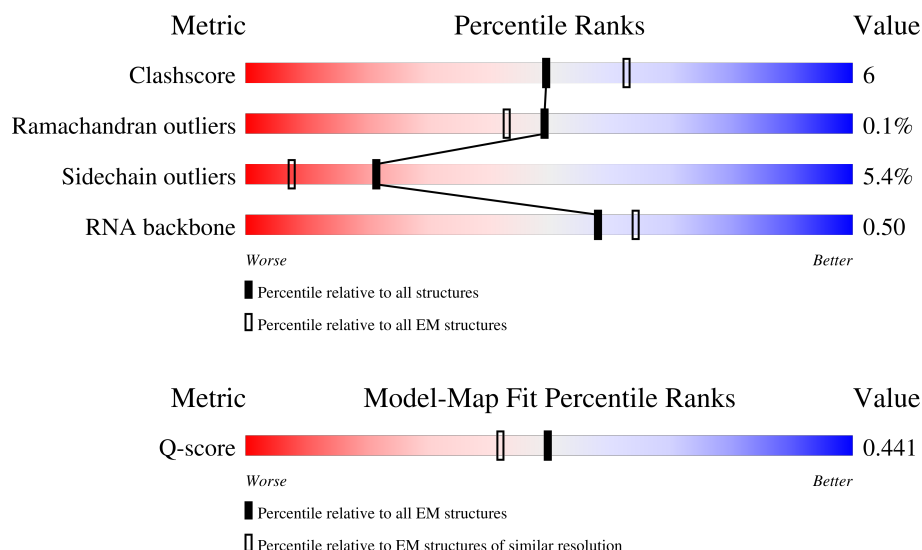
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.33 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.



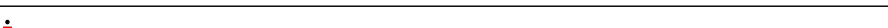
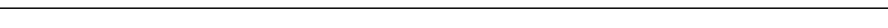
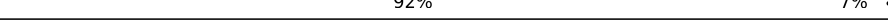
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14484 (2.83 - 3.83)

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	2903	 67% 27% 5%
2	B	120	 66% 29% 5%
3	C	273	 79% 19%

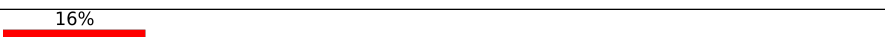
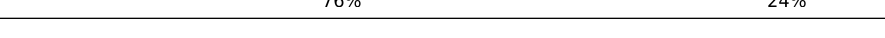
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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	201	
6	F	179	
7	G	177	
8	H	149	
9	I	165	
10	J	142	
11	K	142	
12	L	123	
13	M	144	
14	N	136	
15	O	127	
16	P	117	
17	Q	115	
18	R	118	
19	S	103	
20	T	110	
21	U	100	
22	V	104	
23	W	94	
24	X	85	
25	Y	78	
26	Z	63	
27	a	59	
28	b	57	

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Mol	Chain	Length	Quality of chain
29	c	55	
30	d	46	
31	e	65	
32	f	38	
33	g	443	
34	h	127	
35	i	25	
36	x	3	

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 95192 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2884	Total	C	N	O	P	0	0
			61923	27622	11400	20017	2884		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 3 is a protein called 50S ribosomal protein L2.

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

- Molecule 4 is a protein called 50S ribosomal protein L3.

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

- Molecule 5 is a protein called 50S ribosomal protein L4.

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

- Molecule 6 is a protein called 50S ribosomal protein L5.

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

- Molecule 7 is a protein called 50S ribosomal protein L6.

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

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	125	Total	C	N	O	S	0	0
			946	599	169	175	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	85	VAL	SER	conflict	UNP P0A7J3
I	86	THR	MET	conflict	UNP P0A7J3

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	70	Total	C	N	O	S	0	0
			502	309	92	98	3		

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	125	Total	C	N	O	S	0	0
			993	613	202	173	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	95	Total	C	N	O	S	0	0
			756	479	141	135	1		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	76	Total	C	N	O	S	0	0
			580	359	117	103	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

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

- Molecule 28 is a protein called 50S ribosomal protein L32.

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

- Molecule 29 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	51	Total	C	N	O	S	0	0
			414	266	76	72			

- Molecule 30 is a protein called 50S ribosomal protein L34.

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

- Molecule 31 is a protein called 50S ribosomal protein L35.

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

- Molecule 32 is a protein called 50S ribosomal protein L36.

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

- Molecule 33 is a protein called Protein translocase subunit SecY.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	399	Total	C	N	O	S	0	0
			3099	2056	508	520	15		

- Molecule 34 is a protein called Protein translocase subunit SecE.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	59	Total	C	N	O	S	0	0
			459	298	82	78	1		

- Molecule 35 is a protein called SecG.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	i	25	Total	C	N	O	0	0
			150	100	25	25		

- Molecule 36 is a RNA chain called tRNA CCA end (5'-R(P*CP*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
36	x	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	A	313	Total	Mg	0
			313	313	
37	B	8	Total	Mg	0
			8	8	
37	R	1	Total	Mg	0
			1	1	
37	b	1	Total	Mg	0
			1	1	

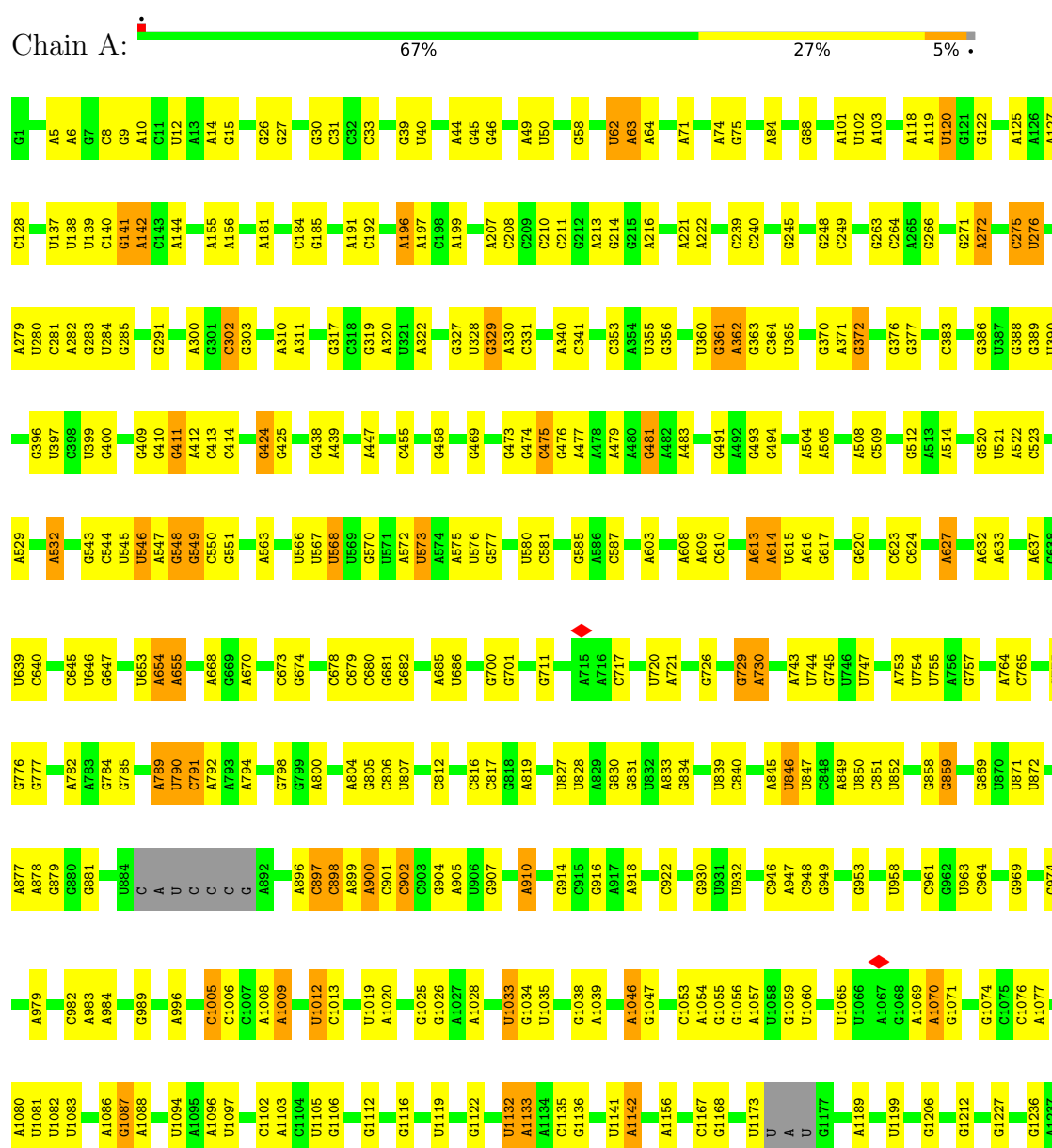
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	f	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

• Molecule 1: 23S rRNA





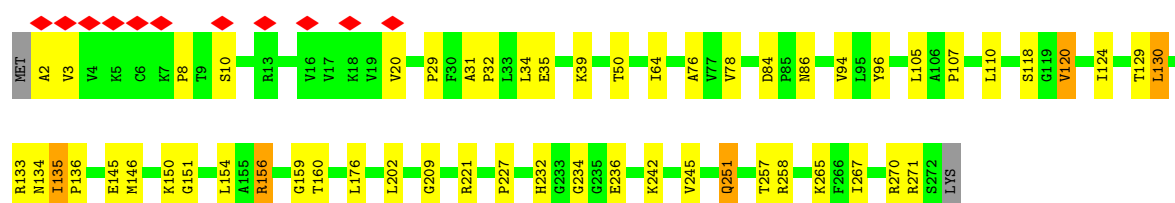
- Molecule 2: 5S rRNA

Chain B: 



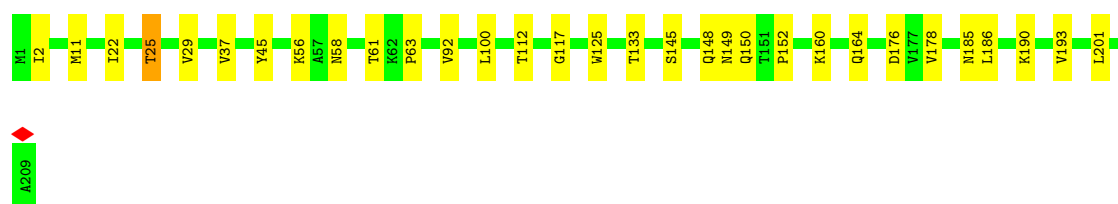
- Molecule 3: 50S ribosomal protein L2

Chain C: 



- Molecule 4: 50S ribosomal protein L3

Chain D: 



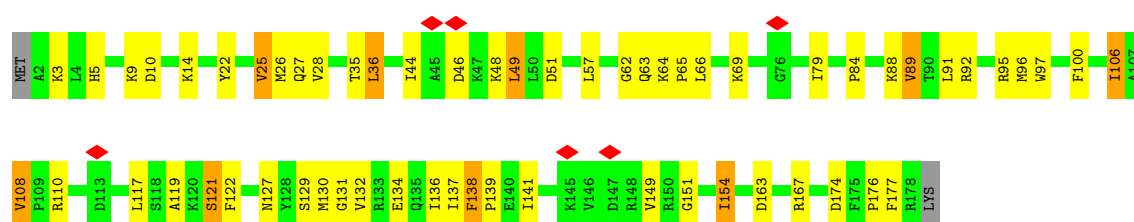
- Molecule 5: 50S ribosomal protein L4

Chain E: 



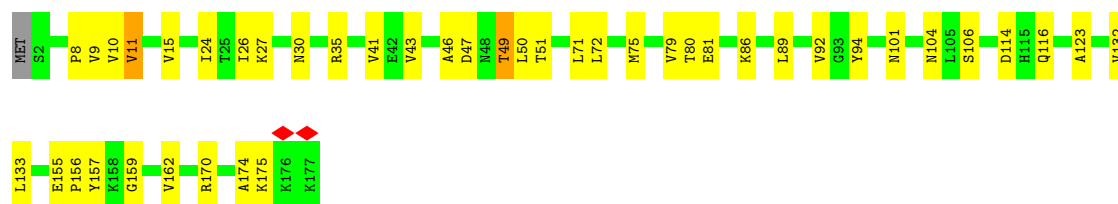
- Molecule 6: 50S ribosomal protein L5

Chain F: 



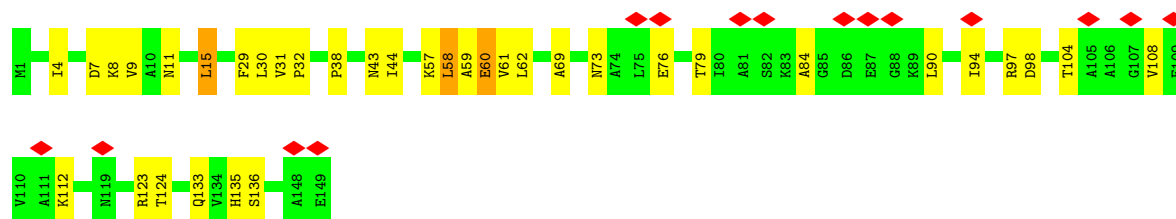
- Molecule 7: 50S ribosomal protein L6

Chain G:  75% 23% ..



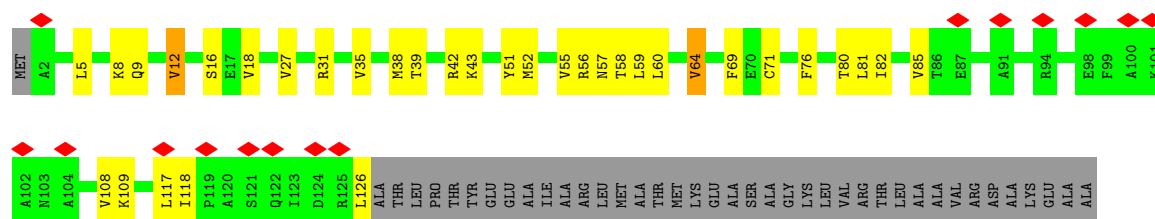
• Molecule 8: 50S ribosomal protein L9

Chain H:  10% 76% 22% .



• Molecule 9: 50S ribosomal protein L10

Chain I:  9% 55% 19% . 24%





- Molecule 12: 50S ribosomal protein L14

Chain L: 88% 11%



- Molecule 13: 50S ribosomal protein L15

Chain M: 81% 19%



- Molecule 14: 50S ribosomal protein L16

Chain N: 82% 18%



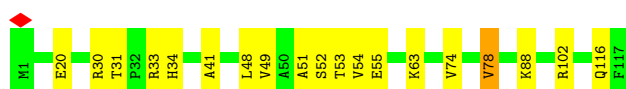
- Molecule 15: 50S ribosomal protein L17

Chain O: 86% 11%



- Molecule 16: 50S ribosomal protein L18

Chain P: 84% 15%



- Molecule 17: 50S ribosomal protein L19

Chain Q: 78% 20%



- Molecule 18: 50S ribosomal protein L20

Chain R: 82% 16%



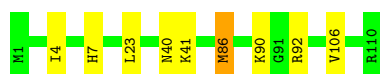
- Molecule 19: 50S ribosomal protein L21

Chain S: 83% 16% .



- Molecule 20: 50S ribosomal protein L22

Chain T: 92% 7% .



- Molecule 21: 50S ribosomal protein L23

Chain U: 78% 15% . 5%



- Molecule 22: 50S ribosomal protein L24

Chain V: 80% 18% .



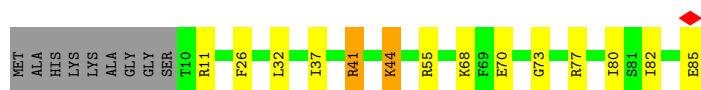
- Molecule 23: 50S ribosomal protein L25

Chain W: 81% 17% .



- Molecule 24: 50S ribosomal protein L27

Chain X: 73% 14% . 11%

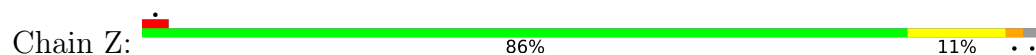


- Molecule 25: 50S ribosomal protein L28

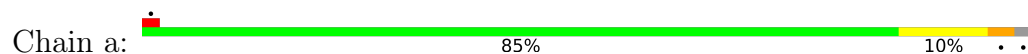
Chain Y: 82% 15% ..



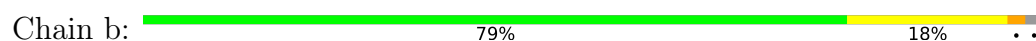
- Molecule 26: 50S ribosomal protein L29



- Molecule 27: 50S ribosomal protein L30



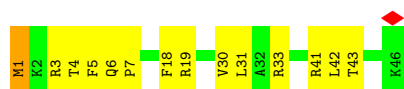
- Molecule 28: 50S ribosomal protein L32



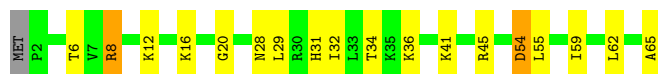
- Molecule 29: 50S ribosomal protein L33



- Molecule 30: 50S ribosomal protein L34



- Molecule 31: 50S ribosomal protein L35



- Molecule 32: 50S ribosomal protein L36





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	216907	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	101083	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.380	Depositor
Minimum map value	-0.139	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	443.2, 443.2, 443.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.385, 1.385, 1.385	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.27	0/69352	0.39	0/108188
2	B	0.23	0/2872	0.37	0/4478
3	C	0.46	0/2121	0.90	3/2852 (0.1%)
4	D	0.50	0/1586	0.85	0/2134
5	E	0.45	0/1571	0.80	0/2113
6	F	0.48	0/1434	0.88	2/1926 (0.1%)
7	G	0.40	0/1343	0.83	1/1816 (0.1%)
8	H	0.47	0/1121	0.79	0/1515
9	I	0.68	0/958	0.87	0/1292
10	J	0.73	0/504	0.95	1/673 (0.1%)
11	K	0.47	0/1152	0.88	4/1551 (0.3%)
12	L	0.47	0/955	0.87	0/1279
13	M	0.45	0/1062	0.84	0/1413
14	N	0.47	0/1093	0.85	5/1460 (0.3%)
15	O	0.49	0/1006	0.85	0/1345
16	P	0.38	0/910	0.79	0/1219
17	Q	0.46	0/929	0.91	2/1242 (0.2%)
18	R	0.58	0/960	0.84	0/1278
19	S	0.45	0/829	0.85	1/1107 (0.1%)
20	T	0.50	0/864	0.93	0/1156
21	U	0.45	0/763	0.81	0/1021
22	V	0.38	0/787	0.79	0/1051
23	W	0.38	0/766	0.81	0/1025
24	X	0.50	0/587	0.90	3/776 (0.4%)
25	Y	0.48	0/635	0.83	0/848
26	Z	0.34	0/502	0.69	0/667
27	a	0.44	0/453	0.78	0/605
28	b	0.47	0/450	0.79	0/599
29	c	0.38	0/421	0.90	2/561 (0.4%)
30	d	0.51	0/380	0.82	0/498
31	e	0.47	0/513	0.85	0/676
32	f	0.40	0/303	0.86	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.66	0/3169	0.94	5/4299 (0.1%)
34	h	0.71	0/465	0.85	0/633
36	x	0.19	0/68	0.34	0/103
All	All	0.36	0/102884	0.55	29/153796 (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
3	C	0	1
33	g	0	1
All	All	0	2

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	g	200	PRO	N-CA-C	8.66	121.26	110.70
24	X	44	LYS	N-CA-C	-7.26	104.42	113.28
29	c	40	ASP	CA-C-N	7.15	127.31	119.87
29	c	40	ASP	C-N-CA	7.15	127.31	119.87
11	K	96	ARG	CA-C-N	6.91	127.20	119.32
11	K	96	ARG	C-N-CA	6.91	127.20	119.32
11	K	7	LYS	CA-C-N	6.88	127.17	119.32
11	K	7	LYS	C-N-CA	6.88	127.17	119.32
17	Q	21	ARG	CA-C-N	-6.79	112.99	119.85
17	Q	21	ARG	C-N-CA	-6.79	112.99	119.85
6	F	138	PHE	CA-C-N	6.48	126.71	119.32
6	F	138	PHE	C-N-CA	6.48	126.71	119.32
14	N	71	LYS	CA-C-N	6.31	126.81	119.99
14	N	71	LYS	C-N-CA	6.31	126.81	119.99
3	C	130	LEU	N-CA-C	6.30	113.80	108.13
3	C	135	ILE	CA-C-N	6.24	126.19	119.76
3	C	135	ILE	C-N-CA	6.24	126.19	119.76
33	g	39	ILE	N-CA-C	6.19	114.01	107.76
24	X	73	GLY	CA-C-N	5.91	125.45	119.19
24	X	73	GLY	C-N-CA	5.91	125.45	119.19
10	J	116	ASP	N-CA-C	5.74	120.40	113.17
33	g	296	GLY	N-CA-C	-5.55	108.05	115.32
33	g	76	SER	N-CA-C	5.50	117.61	109.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	39	GLY	N-CA-C	5.47	117.56	110.45
7	G	47	ASP	CB-CA-C	-5.20	110.60	116.63
14	N	124	LEU	CA-C-N	5.17	124.78	119.56
14	N	124	LEU	C-N-CA	5.17	124.78	119.56
19	S	100	GLY	N-CA-C	5.14	117.98	110.38
33	g	199	LEU	N-CA-C	5.09	119.18	112.35

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	232	HIS	Peptide
33	g	74	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	61923	0	31144	456	0
2	B	2569	0	1301	26	0
3	C	2082	0	2154	35	0
4	D	1565	0	1616	19	0
5	E	1552	0	1619	17	0
6	F	1410	0	1444	37	0
7	G	1323	0	1371	24	0
8	H	1110	0	1148	21	0
9	I	946	0	978	21	0
10	J	502	0	540	18	0
11	K	1129	0	1162	14	0
12	L	946	0	1023	10	0
13	M	1053	0	1129	16	0
14	N	1074	0	1157	12	0
15	O	993	0	1034	8	0
16	P	900	0	935	11	0
17	Q	917	0	962	13	0
18	R	947	0	1019	12	0
19	S	816	0	839	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	T	857	0	922	6	0
21	U	756	0	817	10	0
22	V	779	0	831	11	0
23	W	753	0	780	11	0
24	X	580	0	594	9	0
25	Y	625	0	652	6	0
26	Z	501	0	531	5	0
27	a	449	0	488	5	0
28	b	444	0	458	9	0
29	c	414	0	442	6	0
30	d	377	0	418	12	0
31	e	504	0	572	13	0
32	f	302	0	341	6	0
33	g	3099	0	3246	114	0
34	h	459	0	503	14	0
35	i	150	0	153	5	0
36	x	62	0	34	0	0
37	A	313	0	0	0	0
37	B	8	0	0	0	0
37	R	1	0	0	0	0
37	b	1	0	0	0	0
38	f	1	0	0	0	0
All	All	95192	0	64357	890	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 (890) 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)
6:F:106:ILE:HD12	6:F:139:PRO:HG2	1.54	0.85
1:A:1852:U:O2	1:A:1890:A:N6	2.09	0.85
1:A:1865:U:O2	1:A:1876:A:N6	2.11	0.83
3:C:154:LEU:HD13	3:C:176:LEU:HD21	1.63	0.81
13:M:56:PRO:HG2	13:M:59:ARG:HG3	1.62	0.80
1:A:1453:A:N6	1:A:2702:G:O6	2.14	0.80
33:g:318:VAL:HG11	33:g:386:LEU:HD13	1.65	0.79
2:B:69:G:O6	2:B:107:G:N2	2.13	0.78
1:A:1869:G:N2	1:A:1871:A:O2'	2.17	0.78
1:A:2119:A:N6	1:A:2167:U:O2	2.16	0.78
1:A:2107:G:H1	1:A:2182:U:H3	1.30	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2303:G:O2'	6:F:121:SER:O	2.02	0.77
1:A:2209:G:H1	1:A:2215:C:H42	1.32	0.76
33:g:53:LEU:HD13	33:g:74:ARG:HA	1.66	0.76
1:A:2530:A:O2'	1:A:2534:A:N6	2.19	0.75
1:A:2728:U:HO2'	1:A:2729:G:H8	1.33	0.74
14:N:66:ARG:NH1	14:N:104:GLU:OE1	2.21	0.74
7:G:86:LYS:HG2	7:G:132:VAL:HG22	1.68	0.74
33:g:281:SER:HA	33:g:284:ILE:HD12	1.70	0.74
6:F:119:ALA:O	6:F:167:ARG:NH1	2.20	0.73
33:g:175:GLY:HA3	33:g:190:ILE:HD11	1.70	0.73
1:A:1077:A:H4'	10:J:94:ASN:HB2	1.70	0.73
1:A:585:G:N7	18:R:6:ARG:NH1	2.37	0.73
1:A:1818:U:OP2	3:C:156:ARG:NH1	2.21	0.72
33:g:26:VAL:HG22	33:g:178:ILE:HG23	1.71	0.72
9:I:12:VAL:HG23	9:I:59:LEU:HG	1.71	0.72
1:A:1866:A:N6	1:A:1875:G:O2'	2.23	0.72
33:g:136:ALA:HB1	33:g:157:TYR:HA	1.72	0.72
33:g:104:GLU:HA	33:g:107:LYS:HE2	1.71	0.71
1:A:1716:U:H2'	1:A:1717:A:H8	1.56	0.70
1:A:1939:U:OP1	1:A:2604:U:O2'	2.09	0.70
1:A:543:G:H1	1:A:550:C:H42	1.37	0.70
3:C:29:PRO:HG2	3:C:34:LEU:HD11	1.73	0.69
2:B:54:G:H21	6:F:26:MET:HE3	1.55	0.69
33:g:45:ASP:HB3	33:g:49:LEU:HG	1.75	0.69
9:I:57:ASN:ND2	9:I:76:PHE:O	2.26	0.68
33:g:242:ARG:NH2	33:g:369:VAL:O	2.24	0.68
2:B:43:C:O2	6:F:92:ARG:NH2	2.27	0.68
1:A:1105:U:H2'	1:A:1106:G:H8	1.59	0.68
1:A:1800:C:H3'	3:C:146:MET:HE1	1.76	0.68
1:A:1059:G:OP1	10:J:72:LYS:NZ	2.27	0.68
1:A:284:U:H3	1:A:356:G:H1	1.42	0.67
1:A:2128:G:H1	1:A:2160:C:H42	1.41	0.67
14:N:77:PRO:HG2	14:N:80:VAL:HG21	1.76	0.67
33:g:283:ILE:HG13	33:g:328:PHE:CZ	2.30	0.67
1:A:1094:U:H1'	1:A:1097:U:H5	1.59	0.67
1:A:1479:G:HO2'	1:A:1560:G:HO2'	1.29	0.67
1:A:2107:G:N2	1:A:2182:U:O2	2.27	0.67
12:L:7:MET:HE1	12:L:44:LYS:HG3	1.76	0.67
6:F:65:PRO:HA	6:F:89:VAL:HG23	1.76	0.66
33:g:284:ILE:HD11	33:g:321:TYR:HE1	1.61	0.66
22:V:72:ILE:HG21	22:V:83:VAL:HG23	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2097:A:H61	1:A:2192:U:H3	1.42	0.66
23:W:20:LEU:HD22	23:W:25:LYS:HB2	1.78	0.66
1:A:2788:C:O2'	1:A:2809:A:N3	2.30	0.65
33:g:321:TYR:OH	33:g:385:CYS:SG	2.53	0.65
1:A:1076:C:H1'	10:J:93:PRO:HD2	1.78	0.65
33:g:108:GLU:HB3	33:g:112:GLY:HA3	1.79	0.65
23:W:4:ILE:HG12	23:W:50:MET:HE1	1.76	0.65
24:X:37:ILE:HG21	24:X:80:ILE:HG21	1.79	0.65
1:A:281:C:H2'	1:A:282:A:C8	2.32	0.65
3:C:245:VAL:HG12	3:C:251:GLN:HA	1.78	0.65
1:A:2305:U:H5''	6:F:131:GLY:HA3	1.79	0.65
2:B:13:G:H21	2:B:69:G:H21	1.45	0.64
11:K:131:ASN:OD1	11:K:131:ASN:N	2.30	0.64
5:E:21:ARG:HD3	5:E:106:LYS:HB3	1.77	0.64
33:g:310:LEU:HD21	33:g:320:LEU:HD23	1.79	0.64
6:F:134:GLU:HB3	6:F:136:ILE:HG12	1.79	0.64
1:A:1327:A:N6	1:A:1647:U:O2	2.31	0.64
1:A:2162:G:H5''	1:A:2171:A:H2'	1.79	0.64
1:A:2205:A:H61	1:A:2219:U:H3	1.46	0.64
33:g:41:ILE:HG23	33:g:160:ALA:HA	1.79	0.64
1:A:249:C:O2	31:e:12:LYS:NZ	2.32	0.63
15:O:28:LEU:HD23	15:O:48:VAL:HG21	1.80	0.63
1:A:1848:A:H3'	1:A:1849:G:H8	1.64	0.63
1:A:2116:G:O6	1:A:2171:A:N6	2.31	0.63
1:A:2830:C:H5''	4:D:56:LYS:HE3	1.80	0.63
25:Y:72:ARG:HG3	25:Y:78:TYR:HE2	1.63	0.63
9:I:27:VAL:HG13	9:I:80:THR:HG23	1.81	0.63
1:A:2163:A:OP1	1:A:2170:A:O2'	2.16	0.62
1:A:2683:C:O2	12:L:70:ARG:NH2	2.31	0.62
13:M:81:ASP:HB3	13:M:100:ILE:HD13	1.80	0.62
1:A:568:U:O4	19:S:81:LYS:NZ	2.32	0.62
1:A:2530:A:HO2'	1:A:2534:A:H61	1.46	0.62
13:M:78:ARG:HG2	13:M:113:ALA:HB3	1.80	0.62
17:Q:27:GLU:HG3	17:Q:44:GLU:HB2	1.81	0.62
1:A:1248:G:OP1	5:E:44:ARG:NH2	2.33	0.62
1:A:1849:G:H2'	1:A:1850:G:C8	2.34	0.62
1:A:1105:U:H2'	1:A:1106:G:C8	2.35	0.62
33:g:86:ILE:HD11	33:g:187:ILE:HG21	1.81	0.62
2:B:49:C:H2'	2:B:50:A:H8	1.65	0.62
9:I:64:VAL:HG22	9:I:69:PHE:HB3	1.81	0.62
33:g:66:MET:HE2	33:g:195:ILE:HG23	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:C:H2'	1:A:303:G:H8	1.64	0.61
1:A:1801:A:OP2	3:C:150:LYS:NZ	2.25	0.61
8:H:97:ARG:HB2	8:H:112:LYS:HD2	1.81	0.61
33:g:219:VAL:HG11	33:g:397:VAL:HG21	1.82	0.61
1:A:614:A:O2'	1:A:616:A:N7	2.33	0.61
1:A:1846:G:H1	1:A:1894:C:H42	1.48	0.61
10:J:113:LYS:O	10:J:117:MET:N	2.34	0.61
1:A:871:U:H2'	1:A:872:U:C6	2.35	0.61
1:A:1849:G:H2'	1:A:1850:G:H8	1.66	0.61
33:g:73:SER:HB3	33:g:74:ARG:HE	1.64	0.61
1:A:2127:G:O2'	1:A:2128:G:O4'	2.18	0.61
1:A:1722:A:N6	1:A:1738:G:H1'	2.16	0.61
1:A:371:A:O2'	25:Y:61:LYS:NZ	2.34	0.60
10:J:73:THR:OG1	10:J:113:LYS:NZ	2.34	0.60
11:K:140:LEU:HD11	11:K:142:ILE:HD13	1.83	0.60
33:g:243:ARG:HB3	33:g:264:HIS:HB3	1.81	0.60
1:A:2483:C:N3	14:N:123:LYS:NZ	2.46	0.60
1:A:989:G:OP2	27:a:12:SER:OG	2.17	0.60
1:A:2209:G:H1	1:A:2215:C:N4	2.00	0.60
1:A:2602:A:H2'	1:A:2602:A:N3	2.16	0.60
33:g:242:ARG:HH11	33:g:267:LEU:HD12	1.66	0.60
7:G:35:ARG:HD3	7:G:71:LEU:HD13	1.82	0.60
1:A:627:A:OP1	13:M:78:ARG:NH1	2.25	0.60
2:B:24:G:H4'	2:B:25:U:H5	1.66	0.60
33:g:279:PHE:O	33:g:283:ILE:HG12	2.02	0.60
1:A:2158:A:H4'	1:A:2159:G:O5'	2.02	0.60
1:A:1053:C:O2'	9:I:31:ARG:NH1	2.35	0.59
17:Q:106:LYS:HA	17:Q:109:ARG:HD3	1.84	0.59
10:J:81:LYS:HG3	10:J:136:MET:HE1	1.85	0.59
18:R:62:ILE:HG23	18:R:76:TYR:CE1	2.38	0.59
7:G:46:ALA:O	7:G:49:THR:OG1	2.16	0.59
32:f:30:GLU:HG3	32:f:32:LYS:HB2	1.85	0.59
33:g:22:ARG:NH1	33:g:182:GLY:O	2.36	0.59
33:g:242:ARG:CZ	33:g:369:VAL:HG13	2.33	0.59
6:F:63:GLN:HE21	6:F:89:VAL:HG13	1.68	0.59
1:A:1819:A:H5''	3:C:160:THR:HG21	1.85	0.58
1:A:2115:G:N7	1:A:2117:A:O2'	2.32	0.58
33:g:191:ILE:HD13	33:g:278:ILE:HG21	1.85	0.58
1:A:2116:G:N7	1:A:2165:C:N4	2.49	0.58
21:U:33:LYS:HG3	21:U:80:TRP:CE3	2.38	0.58
29:c:39:PHE:HB2	29:c:46:HIS:CE1	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:g:42:PRO:HD2	33:g:45:ASP:HB2	1.85	0.58
6:F:134:GLU:HG2	6:F:149:VAL:HB	1.85	0.58
7:G:89:LEU:HG	7:G:162:VAL:HG22	1.86	0.58
33:g:132:SER:HB2	33:g:161:VAL:HA	1.85	0.58
1:A:729:G:H5''	1:A:730:A:H5''	1.86	0.58
2:B:5:U:OP1	2:B:61:G:O2'	2.21	0.58
23:W:2:PHE:HB3	23:W:50:MET:HE3	1.86	0.58
26:Z:2:LYS:NZ	26:Z:49:ASP:OD1	2.36	0.58
1:A:849:A:H2'	1:A:850:U:C6	2.38	0.58
1:A:191:A:H2'	1:A:192:C:C6	2.39	0.58
1:A:1447:C:H2'	1:A:1448:G:C8	2.39	0.58
33:g:80:LEU:HD11	33:g:293:TRP:HH2	1.67	0.58
1:A:1227:G:OP2	18:R:16:LYS:NZ	2.33	0.57
1:A:1462:C:HO2'	1:A:2702:G:HO2'	1.47	0.57
1:A:1799:G:OP1	3:C:258:ARG:NH1	2.32	0.57
1:A:2117:A:H61	1:A:2171:A:H61	1.50	0.57
22:V:36:VAL:HB	22:V:39:ILE:HB	1.86	0.57
30:d:3:ARG:HA	30:d:3:ARG:HH21	1.69	0.57
1:A:125:A:OP2	30:d:19:ARG:NH2	2.36	0.57
1:A:1570:A:H2'	1:A:1571:A:C8	2.39	0.57
34:h:70:ALA:O	34:h:74:GLU:HG3	2.04	0.57
33:g:82:ILE:HG12	33:g:187:ILE:HD12	1.86	0.57
1:A:476:G:N1	1:A:479:A:OP2	2.37	0.57
1:A:1028:A:N3	1:A:2486:C:O2'	2.36	0.57
1:A:1447:C:H2'	1:A:1448:G:H8	1.70	0.57
1:A:2529:G:H5'	7:G:175:LYS:HB2	1.85	0.57
16:P:31:THR:HG22	16:P:33:ARG:H	1.69	0.57
22:V:18:ASP:OD2	22:V:40:ASN:N	2.28	0.57
33:g:131:GLN:O	33:g:135:ILE:HG13	2.04	0.57
2:B:1:U:H2'	2:B:2:G:H8	1.69	0.57
3:C:107:PRO:HD2	3:C:110:LEU:HD22	1.87	0.57
2:B:1:U:H2'	2:B:2:G:C8	2.40	0.57
11:K:117:ALA:HA	11:K:120:ARG:HH21	1.70	0.57
1:A:2333:A:P	24:X:77:ARG:HH22	2.28	0.56
10:J:86:ILE:HD13	10:J:138:LEU:HD21	1.86	0.56
33:g:380:TYR:O	33:g:384:ILE:HG12	2.05	0.56
33:g:154:PHE:HA	33:g:157:TYR:HB3	1.86	0.56
1:A:682:G:O6	1:A:794:A:N6	2.39	0.56
1:A:743:A:O2'	1:A:1659:G:OP1	2.23	0.56
1:A:1645:G:H5''	1:A:1646:C:H5'	1.86	0.56
1:A:1141:U:H4'	1:A:1142:A:O4'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:g:269:VAL:HA	33:g:373:LEU:HG	1.88	0.56
1:A:2636:C:O2'	4:D:45:TYR:OH	2.23	0.56
1:A:1019:U:OP1	1:A:1035:U:O2'	2.19	0.56
1:A:2314:A:OP1	6:F:88:LYS:NZ	2.32	0.56
33:g:139:LEU:HB3	33:g:140:PRO:HD3	1.88	0.56
1:A:33:C:O2	1:A:447:A:N6	2.39	0.56
1:A:2127:G:O2'	1:A:2128:G:O5'	2.24	0.56
1:A:2584:U:H3'	1:A:2585:U:H5''	1.88	0.56
1:A:2780:G:N1	11:K:102:GLU:OE2	2.35	0.56
33:g:77:ILE:O	33:g:164:LEU:HA	2.06	0.56
5:E:61:ARG:NH2	5:E:63:LYS:O	2.39	0.55
8:H:7:ASP:OD1	8:H:8:LYS:N	2.38	0.55
1:A:1008:A:H2	1:A:1009:A:H62	1.54	0.55
1:A:2530:A:H61	7:G:156:PRO:HG3	1.71	0.55
11:K:114:LEU:HG	11:K:118:MET:HE3	1.88	0.55
33:g:37:SER:O	33:g:76:SER:HB2	2.06	0.55
10:J:106:LEU:HB3	10:J:126:THR:HG23	1.88	0.55
8:H:38:PRO:O	8:H:43:ASN:ND2	2.38	0.55
1:A:608:A:H2'	1:A:609:A:C8	2.41	0.55
34:h:62:THR:HG22	34:h:66:LYS:HE3	1.88	0.55
1:A:458:G:O2'	1:A:469:G:O6	2.22	0.55
1:A:2418:A:OP1	31:e:45:ARG:NH1	2.40	0.55
29:c:43:VAL:HG23	29:c:45:GLN:HB2	1.88	0.55
1:A:673:C:OP1	5:E:49:ARG:NH2	2.38	0.55
14:N:30:SER:H	14:N:106:ASP:HB3	1.70	0.55
21:U:9:LYS:HA	26:Z:29:ARG:HH22	1.72	0.55
1:A:620:G:O6	5:E:98:LYS:NZ	2.40	0.54
1:A:2845:U:H5''	17:Q:52:ASN:O	2.06	0.54
1:A:833:A:H2'	1:A:834:G:C8	2.41	0.54
1:A:904:G:H2'	1:A:905:A:H8	1.72	0.54
1:A:62:U:O2'	1:A:63:A:OP1	2.20	0.54
1:A:1054:A:H2'	1:A:1055:G:C8	2.42	0.54
23:W:75:GLN:HB2	23:W:92:VAL:HG12	1.90	0.54
1:A:543:G:H1	1:A:550:C:N4	2.05	0.54
15:O:2:ARG:HH11	15:O:2:ARG:HB3	1.73	0.54
16:P:51:ALA:HB3	16:P:78:VAL:HG13	1.88	0.54
21:U:67:VAL:HG22	21:U:76:ARG:HD2	1.90	0.54
33:g:129:ILE:HG12	33:g:165:VAL:HG21	1.90	0.54
1:A:2419:U:H5''	29:c:22:THR:HG21	1.90	0.54
3:C:133:ARG:HD2	8:H:123:ARG:NH1	2.23	0.54
30:d:3:ARG:O	30:d:6:GLN:NE2	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:62:GLY:O	6:F:95:ARG:NH1	2.40	0.54
4:D:186:LEU:HD21	17:Q:4:ILE:HG21	1.90	0.54
9:I:27:VAL:HG22	9:I:82:ILE:HG22	1.90	0.54
31:e:62:LEU:HB3	31:e:65:ALA:HB2	1.90	0.54
1:A:355:U:H2'	1:A:356:G:C8	2.43	0.54
1:A:859:G:O2'	1:A:916:G:O6	2.24	0.53
11:K:125:TYR:OH	11:K:132:HIS:NE2	2.35	0.53
1:A:1536:C:H4'	1:A:1537:G:H5''	1.90	0.53
10:J:83:ALA:HB2	10:J:109:ILE:HD11	1.89	0.53
22:V:81:ASP:OD1	22:V:82:ARG:N	2.36	0.53
1:A:1070:A:N7	1:A:1096:A:O2'	2.35	0.53
6:F:110:ARG:HH11	6:F:137:ILE:C	2.17	0.53
6:F:91:LEU:HD22	6:F:95:ARG:HB3	1.91	0.53
11:K:110:PRO:O	11:K:115:GLY:HA3	2.09	0.53
1:A:609:A:H2'	1:A:610:C:O4'	2.08	0.53
21:U:30:ILE:HG21	21:U:93:LEU:HD21	1.91	0.53
6:F:36:LEU:HD22	6:F:154:ILE:HD13	1.89	0.53
10:J:100:LYS:HB2	10:J:141:GLU:HB2	1.91	0.53
1:A:790:U:H5'	1:A:791:C:OP2	2.09	0.53
9:I:8:LYS:HD3	9:I:56:ARG:NH1	2.23	0.53
1:A:2333:A:OP2	24:X:77:ARG:NH2	2.39	0.53
30:d:18:PHE:HA	30:d:43:THR:HG21	1.91	0.53
1:A:397:U:OP2	25:Y:10:LYS:NZ	2.39	0.53
1:A:711:G:H1	1:A:720:U:H3	1.56	0.53
1:A:1490:A:H8	1:A:1491:G:N7	2.07	0.52
1:A:2479:U:H2'	1:A:2480:C:O4'	2.10	0.52
14:N:41:LEU:HG	14:N:96:ILE:HG13	1.90	0.52
25:Y:32:ASN:O	25:Y:52:SER:HA	2.09	0.52
1:A:271:G:O2'	1:A:272:A:O5'	2.25	0.52
1:A:2472:G:H2'	1:A:2475:C:H42	1.74	0.52
14:N:50:ARG:HD3	14:N:65:ILE:HD11	1.90	0.52
25:Y:71:LEU:HD12	25:Y:74:ARG:HH22	1.72	0.52
1:A:1965:C:H5''	1:A:1966:A:H2'	1.91	0.52
1:A:851:C:H2'	1:A:852:U:C6	2.45	0.52
33:g:90:ILE:O	33:g:94:LEU:HG	2.09	0.52
1:A:1590:A:H2'	1:A:1591:A:C8	2.45	0.52
1:A:1730:C:H1'	1:A:1731:G:C2	2.45	0.52
2:B:49:C:H2'	2:B:50:A:C8	2.44	0.52
1:A:1716:U:H2'	1:A:1717:A:C8	2.42	0.52
1:A:2117:A:N6	1:A:2171:A:H61	2.08	0.52
1:A:2303:G:O2'	6:F:129:SER:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:54:VAL:HG23	28:b:55:ILE:HG12	1.91	0.52
1:A:1532:A:H61	1:A:1539:U:H3	1.58	0.52
6:F:106:ILE:O	6:F:110:ARG:HG3	2.09	0.52
33:g:76:SER:OG	33:g:77:ILE:N	2.42	0.52
33:g:90:ILE:HG21	33:g:283:ILE:HD11	1.92	0.52
34:h:75:ALA:O	34:h:79:VAL:HG23	2.10	0.52
1:A:613:A:H1'	1:A:614:A:H5'	1.90	0.51
28:b:55:ILE:HG22	28:b:57:LYS:HB2	1.91	0.51
33:g:232:PHE:HE1	34:h:90:THR:HA	1.74	0.51
1:A:1394:U:H4'	1:A:1603:A:H4'	1.93	0.51
1:A:898:C:H2'	1:A:899:A:H8	1.76	0.51
33:g:274:VAL:HA	33:g:411:VAL:HG11	1.91	0.51
1:A:1597:A:H5''	1:A:1598:A:H5'	1.93	0.51
1:A:1604:C:O2'	1:A:1610:A:N1	2.42	0.51
4:D:176:ASP:HB2	4:D:190:LYS:HB3	1.92	0.51
20:T:4:ILE:HG12	20:T:106:VAL:HG22	1.93	0.51
1:A:2020:A:H5'	28:b:9:THR:HG22	1.92	0.51
1:A:2055:C:H2'	1:A:2504:U:H4'	1.92	0.51
1:A:2547:A:H4'	12:L:29:HIS:CD2	2.45	0.51
2:B:48:U:H2'	2:B:49:C:C6	2.46	0.51
1:A:1450:G:C6	1:A:1451:C:N4	2.79	0.51
5:E:149:ILE:HA	5:E:170:ARG:O	2.11	0.51
33:g:28:GLY:O	33:g:32:VAL:HG23	2.10	0.51
1:A:851:C:H2'	1:A:852:U:H6	1.76	0.51
33:g:175:GLY:CA	33:g:190:ILE:HD11	2.41	0.51
23:W:26:PHE:HE1	23:W:89:ILE:HG13	1.77	0.50
33:g:242:ARG:NH2	33:g:373:LEU:HB2	2.26	0.50
1:A:680:C:H2'	1:A:681:G:C8	2.46	0.50
1:A:388:G:H2'	1:A:390:U:C5	2.47	0.50
1:A:566:U:H5''	13:M:29:LYS:HE3	1.94	0.50
1:A:1866:A:C2	1:A:1867:G:H1'	2.47	0.50
1:A:2095:A:H5''	8:H:11:ASN:HD22	1.76	0.50
2:B:66:A:H61	2:B:107:G:H2'	1.77	0.50
5:E:175:ILE:HD12	5:E:180:LEU:HD11	1.92	0.50
7:G:157:TYR:HE1	7:G:174:ALA:HA	1.75	0.50
33:g:83:MET:SD	33:g:282:SER:OG	2.66	0.50
33:g:331:PHE:O	33:g:335:LEU:HG	2.12	0.50
1:A:1494:A:O2'	1:A:1495:A:OP1	2.27	0.50
1:A:1695:G:H8	3:C:8:PRO:HB2	1.76	0.50
7:G:11:VAL:HG23	7:G:15:VAL:HB	1.93	0.50
1:A:322:A:OP2	5:E:163:ASN:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1255:U:H3'	5:E:68:ALA:HB2	1.93	0.50
1:A:2230:G:H2'	1:A:2231:U:C6	2.46	0.50
7:G:80:THR:OG1	7:G:81:GLU:N	2.44	0.50
9:I:71:CYS:HB3	9:I:117:LEU:HD23	1.92	0.50
1:A:948:C:H2'	1:A:949:G:H8	1.76	0.50
1:A:2233:U:H2'	1:A:2234:G:C8	2.46	0.50
1:A:2859:G:H2'	1:A:2860:A:C8	2.45	0.50
4:D:148:GLN:OE1	4:D:148:GLN:N	2.44	0.50
12:L:63:VAL:HG23	12:L:64:ARG:HG3	1.92	0.50
21:U:33:LYS:HG3	21:U:80:TRP:HE3	1.75	0.50
33:g:105:ILE:HB	33:g:116:ILE:HD11	1.93	0.50
33:g:192:PHE:CZ	33:g:274:VAL:HG13	2.46	0.50
6:F:5:HIS:CE1	6:F:9:LYS:HE3	2.46	0.50
7:G:24:ILE:HD11	7:G:43:VAL:HG11	1.93	0.50
1:A:1923:U:H2'	1:A:1924:C:C6	2.47	0.50
7:G:9:VAL:HB	7:G:50:LEU:HB2	1.94	0.50
17:Q:31:TRP:NE1	17:Q:82:ASP:OD1	2.43	0.50
18:R:49:ASP:HA	18:R:52:GLN:HB2	1.91	0.50
33:g:408:ILE:O	33:g:412:VAL:HG23	2.11	0.50
1:A:2172:U:H4'	1:A:2173:A:H5'	1.94	0.50
22:V:47:LYS:HD2	33:g:256:ARG:CZ	2.42	0.50
6:F:46:ASP:HB3	6:F:49:LEU:HD22	1.93	0.49
8:H:15:LEU:HD21	8:H:58:LEU:HG	1.93	0.49
1:A:623:C:H2'	1:A:624:C:C6	2.47	0.49
7:G:8:PRO:HB3	7:G:51:THR:HG22	1.93	0.49
30:d:31:LEU:HD22	30:d:42:LEU:HD13	1.92	0.49
1:A:1540:G:H2'	1:A:1541:C:C6	2.48	0.49
2:B:13:G:N2	2:B:69:G:H21	2.09	0.49
1:A:1757:A:O2'	1:A:1758:U:OP1	2.25	0.49
4:D:149:ASN:OD1	4:D:150:GLN:N	2.41	0.49
33:g:392:ARG:HH11	33:g:402:GLY:HA2	1.77	0.49
1:A:207:A:H2'	1:A:208:C:O4'	2.12	0.49
1:A:897:C:H2'	1:A:898:C:O4'	2.13	0.49
1:A:2020:A:H5'	28:b:9:THR:CG2	2.42	0.49
33:g:231:THR:HG23	33:g:410:VAL:HG13	1.94	0.49
33:g:121:ARG:HG3	33:g:172:MET:SD	2.53	0.49
35:i:46:UNK:O	35:i:50:UNK:N	2.45	0.49
1:A:282:A:H2'	1:A:283:G:C8	2.47	0.49
5:E:61:ARG:HH22	5:E:64:GLY:HA3	1.78	0.49
33:g:181:ARG:HH22	35:i:33:UNK:HG1	1.78	0.49
33:g:291:ALA:HA	33:g:303:LEU:HD13	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:G:C6	1:A:27:G:N1	2.81	0.49
1:A:1056:G:H5''	1:A:1057:A:H5'	1.94	0.49
1:A:2040:G:H2'	1:A:2041:U:O4'	2.13	0.49
1:A:2420:C:OP1	31:e:34:THR:OG1	2.22	0.49
7:G:101:ASN:ND2	7:G:116:GLN:OE1	2.46	0.49
33:g:288:ALA:O	33:g:292:SER:HB3	2.12	0.49
1:A:2256:G:H4'	24:X:11:ARG:HH11	1.77	0.49
14:N:33:LEU:HD11	14:N:128:THR:HB	1.94	0.49
1:A:1344:U:O2'	1:A:1345:C:OP1	2.29	0.49
32:f:30:GLU:O	32:f:33:HIS:HB2	2.13	0.49
1:A:570:G:H2'	1:A:2030:A:N7	2.27	0.48
4:D:61:THR:HB	4:D:63:PRO:HD2	1.94	0.48
33:g:65:ASN:HB2	33:g:73:SER:HB2	1.95	0.48
1:A:1808:A:H3'	1:A:1809:A:C8	2.48	0.48
1:A:2291:U:H2'	1:A:2292:U:C6	2.48	0.48
2:B:78:A:H2'	2:B:79:G:O4'	2.13	0.48
3:C:145:GLU:HG2	3:C:151:GLY:C	2.37	0.48
1:A:483:A:O4'	22:V:45:HIS:HB3	2.14	0.48
1:A:1452:G:H2'	1:A:1453:A:C6	2.48	0.48
1:A:1507:C:H2'	1:A:1508:A:O4'	2.13	0.48
8:H:57:LYS:O	8:H:61:VAL:HG23	2.13	0.48
33:g:242:ARG:CZ	33:g:373:LEU:HB2	2.43	0.48
4:D:25:THR:HG21	4:D:193:VAL:HG22	1.95	0.48
8:H:57:LYS:HA	8:H:60:GLU:HG2	1.94	0.48
1:A:522:A:H2'	1:A:523:C:C6	2.49	0.48
1:A:520:G:H2'	1:A:521:U:C6	2.49	0.48
1:A:2223:G:O3'	3:C:265:LYS:NZ	2.41	0.48
7:G:155:GLU:OE2	7:G:159:GLY:N	2.47	0.48
9:I:5:LEU:HA	9:I:8:LYS:HE3	1.95	0.48
35:i:32:UNK:HA	35:i:35:UNK:HG3	1.96	0.48
1:A:1038:G:H2'	1:A:1039:A:C8	2.49	0.48
1:A:1386:C:H2'	1:A:1387:A:C8	2.49	0.48
1:A:1433:A:O2'	1:A:1434:A:H5'	2.13	0.48
1:A:1533:C:H3'	1:A:1534:U:H5''	1.95	0.48
1:A:2292:U:H2'	1:A:2293:G:H8	1.78	0.48
34:h:78:GLU:O	34:h:82:VAL:HG23	2.13	0.48
1:A:979:A:H2'	1:A:982:C:H42	1.79	0.48
1:A:1421:G:H21	1:A:1495:A:H2	1.60	0.48
1:A:1847:A:H2'	1:A:1848:A:O4'	2.14	0.48
6:F:22:TYR:HB3	6:F:27:GLN:HB2	1.96	0.48
16:P:34:HIS:ND1	16:P:53:THR:OG1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1797:G:HO2'	3:C:257:THR:HG1	1.59	0.48
1:A:2327:A:H2'	1:A:2328:A:C8	2.49	0.48
3:C:78:VAL:HG21	3:C:110:LEU:HD21	1.94	0.48
9:I:118:ILE:HD12	9:I:126:LEU:HD11	1.96	0.48
16:P:41:ALA:HB2	16:P:48:LEU:HD21	1.96	0.48
33:g:242:ARG:NH1	33:g:267:LEU:HD12	2.29	0.48
1:A:411:G:OP2	1:A:2406:A:O2'	2.30	0.48
1:A:670:A:H3'	13:M:43:GLY:HA2	1.96	0.48
1:A:2584:U:H3'	1:A:2585:U:C5'	2.44	0.48
4:D:29:VAL:O	4:D:185:ASN:HB3	2.13	0.48
9:I:38:MET:O	9:I:42:ARG:HG2	2.13	0.48
33:g:193:ALA:HA	33:g:196:VAL:HB	1.96	0.48
1:A:1366:A:H2'	1:A:1367:A:O4'	2.14	0.47
1:A:2438:U:O2'	1:A:2440:C:OP1	2.32	0.47
2:B:104:A:H2'	2:B:105:G:O4'	2.14	0.47
3:C:267:ILE:HD13	3:C:270:ARG:HH11	1.79	0.47
15:O:2:ARG:HB3	15:O:2:ARG:NH1	2.29	0.47
1:A:1005:C:H2'	1:A:1006:C:H6	1.79	0.47
1:A:1033:U:N3	1:A:1034:G:N7	2.62	0.47
1:A:1490:A:H1'	1:A:1491:G:C8	2.49	0.47
7:G:170:ARG:NH2	32:f:29:ALA:O	2.46	0.47
32:f:15:LYS:HE2	32:f:15:LYS:HB3	1.59	0.47
33:g:242:ARG:HH21	34:h:78:GLU:CD	2.21	0.47
1:A:5:A:H2'	1:A:6:A:C8	2.50	0.47
1:A:300:A:OP2	22:V:82:ARG:NH1	2.47	0.47
1:A:545:U:H2'	1:A:546:U:O3'	2.14	0.47
1:A:1342:A:O2'	1:A:1344:U:OP2	2.25	0.47
1:A:2014:A:H2'	1:A:2015:A:C8	2.49	0.47
1:A:2822:G:H2'	1:A:2823:A:H5''	1.97	0.47
11:K:36:LEU:O	11:K:51:GLY:HA3	2.14	0.47
20:T:90:LYS:HD2	20:T:92:ARG:HH22	1.80	0.47
22:V:14:LEU:HD11	22:V:71:ALA:HB2	1.96	0.47
33:g:315:PRO:O	33:g:319:LEU:HG	2.14	0.47
1:A:370:G:O2'	1:A:424:G:OP1	2.31	0.47
1:A:1848:A:H3'	1:A:1849:G:C8	2.48	0.47
1:A:1996:C:H5	12:L:32:TYR:HH	1.62	0.47
1:A:2639:A:H2'	1:A:2640:G:O4'	2.14	0.47
7:G:24:ILE:HG13	7:G:72:LEU:HD21	1.97	0.47
33:g:196:VAL:HG13	34:h:108:LEU:HD11	1.96	0.47
33:g:213:GLY:HA2	33:g:217:PHE:CZ	2.50	0.47
1:A:1340:U:OP2	21:U:82:LYS:NZ	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1993:U:H4'	4:D:133:THR:OG1	2.14	0.47
2:B:11:C:N4	2:B:109:A:H61	2.13	0.47
33:g:310:LEU:HD22	33:g:317:TYR:HD1	1.79	0.47
35:i:35:UNK:HA	35:i:38:UNK:HG3	1.97	0.47
1:A:904:G:H2'	1:A:905:A:C8	2.50	0.47
1:A:580:U:H2'	1:A:581:C:H6	1.80	0.47
1:A:1476:U:H2'	1:A:1477:A:C8	2.50	0.47
1:A:1579:A:H2'	1:A:1580:A:C8	2.50	0.47
1:A:2328:A:H2'	1:A:2329:U:C6	2.50	0.47
1:A:2684:U:H4'	12:L:76:VAL:HG21	1.95	0.47
21:U:95:PHE:HD1	34:h:80:ARG:HG3	1.79	0.47
22:V:81:ASP:OD2	22:V:96:PHE:HB3	2.15	0.47
33:g:400:TYR:O	33:g:405:SER:HB2	2.15	0.47
1:A:44:A:H2'	1:A:45:G:O4'	2.15	0.47
1:A:2130:U:O2'	1:A:2133:G:O2'	2.32	0.47
22:V:47:LYS:HD2	33:g:256:ARG:NH1	2.29	0.47
33:g:368:LYS:O	33:g:372:ARG:HG3	2.15	0.47
1:A:1944:U:O4	1:A:2557:G:N2	2.46	0.47
33:g:406:LEU:O	33:g:410:VAL:HG23	2.15	0.47
1:A:674:G:H5''	5:E:71:GLY:H	1.79	0.47
1:A:846:U:O2'	1:A:847:U:OP2	2.28	0.47
1:A:1132:U:H3'	1:A:1133:A:H5''	1.95	0.47
13:M:85:VAL:HG21	13:M:90:VAL:HG22	1.97	0.47
33:g:309:TYR:CE1	33:g:316:LEU:HB3	2.50	0.47
1:A:1039:A:H61	1:A:1116:G:H1	1.63	0.46
4:D:37:VAL:HG23	4:D:92:VAL:HG23	1.97	0.46
31:e:16:LYS:HE3	31:e:20:GLY:HA2	1.97	0.46
1:A:213:A:O2'	1:A:214:G:H5'	2.15	0.46
1:A:947:A:H2'	1:A:948:C:C6	2.51	0.46
1:A:948:C:H1'	1:A:984:A:C8	2.50	0.46
1:A:1425:G:N1	1:A:1426:G:C2	2.84	0.46
1:A:2345:G:N3	1:A:2381:A:H2'	2.30	0.46
7:G:170:ARG:HH22	32:f:29:ALA:HA	1.80	0.46
30:d:3:ARG:HA	30:d:3:ARG:NH2	2.29	0.46
1:A:1906:G:H1'	1:A:1929:G:C5	2.50	0.46
6:F:122:PHE:HB3	6:F:163:ASP:CG	2.40	0.46
21:U:4:GLU:HG3	21:U:49:LYS:HE2	1.97	0.46
28:b:36:GLU:OE2	28:b:46:ASP:HB2	2.15	0.46
1:A:2567:G:H2'	1:A:2568:U:C6	2.50	0.46
2:B:66:A:N6	2:B:107:G:H2'	2.31	0.46
1:A:587:C:C2	13:M:19:LEU:HD12	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2512:C:H1'	4:D:145:SER:O	2.16	0.46
1:A:2514:U:H2'	1:A:2515:C:C6	2.50	0.46
1:A:2547:A:H2'	1:A:2548:U:C6	2.51	0.46
1:A:2599:G:N7	3:C:236:GLU:HB2	2.31	0.46
6:F:96:MET:O	6:F:100:PHE:HB2	2.15	0.46
17:Q:32:VAL:HG11	17:Q:41:GLN:HE21	1.79	0.46
1:A:580:U:H2'	1:A:581:C:C6	2.50	0.46
1:A:789:A:C4	30:d:3:ARG:NH1	2.83	0.46
1:A:1483:G:H1	1:A:1506:U:H3	1.63	0.46
1:A:1582:C:O2'	1:A:1585:C:N3	2.40	0.46
1:A:1827:U:OP2	3:C:221:ARG:HD2	2.15	0.46
8:H:84:ALA:HA	8:H:90:LEU:HA	1.98	0.46
12:L:113:MET:O	12:L:116:ILE:HG13	2.16	0.46
33:g:26:VAL:CG2	33:g:183:ILE:H	2.29	0.46
33:g:210:ALA:HA	33:g:217:PHE:HE2	1.80	0.46
33:g:237:VAL:HG12	33:g:269:VAL:HG21	1.97	0.46
1:A:322:A:H5'	1:A:340:A:H1'	1.98	0.46
1:A:1012:U:OP2	18:R:70:ARG:NH1	2.46	0.46
1:A:1054:A:H2'	1:A:1055:G:H8	1.79	0.46
1:A:1791:A:N6	1:A:1828:G:O2'	2.44	0.46
1:A:2209:G:N2	1:A:2215:C:N3	2.54	0.46
3:C:76:ALA:HB2	3:C:96:TYR:CD2	2.51	0.46
23:W:35:GLU:OE1	23:W:35:GLU:N	2.45	0.46
1:A:144:A:H1'	21:U:3:ARG:NH2	2.30	0.46
1:A:355:U:H2'	1:A:356:G:H8	1.81	0.46
6:F:44:ILE:HG21	6:F:79:ILE:HG22	1.97	0.46
34:h:84:TRP:HB3	34:h:85:PRO:HD2	1.98	0.46
35:i:46:UNK:O	35:i:50:UNK:HB2	2.16	0.46
1:A:958:U:H2'	2:B:89:U:C2	2.51	0.46
1:A:1020:A:C2	1:A:1141:U:C2	3.04	0.46
1:A:2684:U:C4	1:A:2685:G:N7	2.84	0.46
8:H:104:THR:HA	8:H:108:VAL:O	2.15	0.46
21:U:34:VAL:HG21	21:U:43:ILE:HD11	1.98	0.46
1:A:613:A:O2'	1:A:614:A:N3	2.44	0.46
1:A:1469:A:H2'	1:A:1470:A:C8	2.51	0.46
1:A:1906:G:N2	1:A:1925:C:O2	2.48	0.46
1:A:2785:C:H2'	1:A:2786:U:H6	1.80	0.46
17:Q:32:VAL:HG23	17:Q:34:GLU:HG3	1.97	0.46
1:A:1989:G:H2'	1:A:1990:C:O4'	2.16	0.45
1:A:2099:U:H2'	1:A:2100:G:H8	1.81	0.45
1:A:2520:C:H2'	1:A:2521:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:58:VAL:HB	19:S:102:SER:HB2	1.98	0.45
34:h:114:ILE:HG23	34:h:117:ARG:NH2	2.31	0.45
1:A:807:U:OP2	13:M:41:ARG:NH1	2.50	0.45
1:A:1715:G:O2'	1:A:1743:G:O6	2.24	0.45
1:A:2100:G:H1	1:A:2189:U:H3	1.63	0.45
1:A:2339:C:H2'	1:A:2340:A:H8	1.81	0.45
1:A:567:U:H2'	1:A:568:U:O4'	2.15	0.45
1:A:617:G:OP1	5:E:102:ARG:NH2	2.50	0.45
1:A:2506:U:C5	1:A:2576:G:C4	3.04	0.45
1:A:2700:A:H2'	1:A:2701:U:C6	2.51	0.45
2:B:64:G:C6	2:B:65:U:C4	3.04	0.45
33:g:239:ARG:HA	33:g:239:ARG:HD3	1.57	0.45
1:A:127:A:H5''	1:A:128:C:O4'	2.15	0.45
1:A:1483:G:H5'	1:A:1510:G:H21	1.81	0.45
8:H:135:HIS:CG	8:H:136:SER:H	2.35	0.45
11:K:117:ALA:HA	11:K:120:ARG:NH2	2.32	0.45
23:W:20:LEU:HD23	23:W:20:LEU:HA	1.78	0.45
31:e:31:HIS:CD2	31:e:32:ILE:HG13	2.52	0.45
33:g:385:CYS:SG	33:g:407:LEU:HD12	2.57	0.45
1:A:282:A:H2'	1:A:283:G:H8	1.82	0.45
1:A:438:G:H2'	1:A:439:A:C8	2.51	0.45
1:A:2529:G:H4'	7:G:175:LYS:HG3	1.97	0.45
3:C:107:PRO:HG2	3:C:110:LEU:HB2	1.99	0.45
14:N:20:LEU:HD13	23:W:81:PRO:HG2	1.99	0.45
16:P:74:VAL:O	16:P:78:VAL:HG22	2.15	0.45
33:g:67:PHE:CD2	33:g:83:MET:HE2	2.51	0.45
1:A:654:A:HO2'	1:A:655:A:H8	1.65	0.45
10:J:74:PRO:HG2	10:J:79:LEU:HD21	1.97	0.45
33:g:78:PHE:HB2	33:g:81:GLY:HA2	1.98	0.45
33:g:83:MET:HE3	33:g:285:LEU:HD12	1.99	0.45
33:g:186:GLY:O	33:g:190:ILE:HG13	2.17	0.45
33:g:309:TYR:HD2	33:g:310:LEU:HD23	1.81	0.45
1:A:8:C:H2'	1:A:9:G:O4'	2.17	0.45
1:A:275:C:H2'	1:A:276:U:H4'	1.99	0.45
1:A:1468:U:H2'	1:A:1522:A:N6	2.31	0.45
1:A:2720:U:OP1	17:Q:53:ARG:NH2	2.50	0.45
1:A:2752:C:H2'	1:A:2753:A:O4'	2.17	0.45
1:A:2236:U:H2'	1:A:2237:G:O4'	2.16	0.45
1:A:2784:U:H2'	1:A:2785:C:H6	1.81	0.45
33:g:242:ARG:NH1	33:g:369:VAL:HG13	2.32	0.45
33:g:291:ALA:HB1	33:g:303:LEU:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2267:A:H5''	1:A:2268:A:H5'	1.98	0.45
2:B:51:G:OP1	16:P:63:LYS:NZ	2.41	0.45
6:F:5:HIS:HB2	6:F:97:TRP:CD1	2.51	0.45
8:H:4:ILE:HD11	8:H:44:ILE:HG12	1.99	0.45
1:A:210:C:H2'	1:A:211:C:C6	2.52	0.44
1:A:2784:U:H2'	1:A:2785:C:C6	2.53	0.44
1:A:2785:C:H2'	1:A:2786:U:C6	2.52	0.44
4:D:201:LEU:HD23	4:D:201:LEU:HA	1.84	0.44
10:J:110:ALA:O	10:J:114:ALA:HB2	2.17	0.44
18:R:95:LEU:HD23	18:R:95:LEU:HA	1.86	0.44
25:Y:13:VAL:HG22	25:Y:29:PHE:HB2	1.99	0.44
33:g:285:LEU:O	33:g:289:THR:HG23	2.16	0.44
1:A:184:C:H2'	1:A:185:G:H8	1.82	0.44
1:A:372:G:O2'	1:A:400:G:O6	2.35	0.44
1:A:473:G:C2'	1:A:474:G:H5'	2.48	0.44
1:A:632:A:H2'	1:A:633:A:C8	2.52	0.44
1:A:1476:U:H2'	1:A:1477:A:H8	1.82	0.44
1:A:1490:A:C8	1:A:1491:G:N7	2.85	0.44
1:A:2224:G:H4'	1:A:2226:C:C2	2.52	0.44
1:A:184:C:H2'	1:A:185:G:C8	2.52	0.44
1:A:753:A:OP1	30:d:1:MET:HG2	2.18	0.44
1:A:2489:U:C4	1:A:2490:G:C6	3.05	0.44
5:E:148:ILE:HD13	5:E:187:VAL:HB	1.99	0.44
6:F:69:LYS:HE3	6:F:84:PRO:HG3	1.99	0.44
13:M:27:LEU:HD23	13:M:27:LEU:HA	1.73	0.44
13:M:57:LEU:HD22	31:e:54:ASP:HB3	1.99	0.44
24:X:85:GLU:H	24:X:85:GLU:HG2	1.66	0.44
30:d:30:VAL:HG22	30:d:33:ARG:NH1	2.32	0.44
33:g:187:ILE:O	33:g:191:ILE:HD12	2.18	0.44
33:g:332:TYR:O	33:g:336:VAL:HG23	2.18	0.44
1:A:245:G:O6	31:e:8:ARG:HD3	2.17	0.44
1:A:548:G:H5'	1:A:549:G:OP1	2.18	0.44
23:W:72:VAL:HB	23:W:91:PHE:HB3	2.00	0.44
34:h:92:HIS:O	34:h:96:ILE:HG12	2.17	0.44
1:A:613:A:O2'	1:A:614:A:O5'	2.35	0.44
1:A:700:G:H2'	1:A:701:G:O4'	2.16	0.44
1:A:1421:G:C2	1:A:1422:G:C8	3.06	0.44
1:A:1695:G:H1'	3:C:8:PRO:O	2.18	0.44
1:A:1754:A:O3'	17:Q:103:ARG:NH2	2.49	0.44
1:A:2135:A:H5'	1:A:2136:G:OP2	2.18	0.44
3:C:31:ALA:HB3	3:C:32:PRO:HD3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:60:ASP:HB3	11:K:97:PRO:HB3	2.00	0.44
33:g:85:TYR:HA	33:g:124:THR:OG1	2.18	0.44
1:A:1039:A:N1	1:A:1116:G:N2	2.63	0.44
3:C:2:ALA:N	3:C:20:VAL:O	2.51	0.44
4:D:148:GLN:HB2	4:D:152:PRO:HD2	2.00	0.44
1:A:280:U:O4	1:A:361:G:N2	2.51	0.44
1:A:819:A:C4	1:A:1189:A:C2	3.05	0.44
1:A:1056:G:H4'	1:A:1086:A:C8	2.53	0.44
1:A:1820:U:C4	3:C:159:GLY:HA3	2.52	0.44
1:A:2556:C:H2'	1:A:2557:G:O4'	2.17	0.44
7:G:26:ILE:HG22	7:G:79:VAL:HG21	1.99	0.44
10:J:76:ALA:HB3	10:J:132:THR:HG21	2.00	0.44
19:S:24:LYS:HE2	19:S:24:LYS:HB3	1.86	0.44
1:A:654:A:O2'	1:A:655:A:H8	2.01	0.44
1:A:1813:G:H1'	3:C:50:THR:OG1	2.18	0.44
1:A:1826:G:O2'	1:A:1971:U:OP2	2.35	0.44
4:D:186:LEU:HD23	4:D:186:LEU:HA	1.72	0.44
1:A:310:A:H5''	22:V:15:THR:HG23	2.00	0.44
1:A:639:U:H2'	1:A:640:C:C6	2.53	0.44
1:A:1848:A:N6	1:A:1893:C:H42	2.16	0.44
1:A:2123:G:H2'	1:A:2124:G:H8	1.83	0.44
1:A:2615:U:C2	28:b:4:GLN:HA	2.53	0.44
2:B:67:G:O6	2:B:108:A:H2	2.01	0.44
5:E:168:ASP:OD1	5:E:169:VAL:N	2.51	0.44
1:A:1678:A:H2'	1:A:1679:A:O4'	2.18	0.43
1:A:1853:A:OP2	1:A:1888:G:N1	2.51	0.43
1:A:2128:G:H1	1:A:2160:C:N4	2.14	0.43
3:C:105:LEU:HD23	3:C:105:LEU:HA	1.86	0.43
20:T:40:ASN:O	20:T:41:LYS:HG2	2.18	0.43
29:c:17:THR:HG21	29:c:42:VAL:HB	2.00	0.43
1:A:413:C:H2'	1:A:414:C:C6	2.53	0.43
1:A:576:U:H2'	1:A:577:G:C8	2.53	0.43
1:A:2208:C:H2'	1:A:2209:G:C8	2.53	0.43
1:A:2530:A:HO2'	1:A:2534:A:N6	2.06	0.43
1:A:2795:C:H2'	1:A:2796:U:C6	2.54	0.43
14:N:36:VAL:HG13	23:W:82:TYR:CD2	2.53	0.43
17:Q:43:PHE:CE2	17:Q:63:LYS:HE2	2.53	0.43
33:g:256:ARG:HG3	33:g:257:VAL:H	1.83	0.43
1:A:969:G:O3'	27:a:15:GLY:HA2	2.17	0.43
1:A:1454:C:C2	1:A:1455:G:N7	2.86	0.43
1:A:1751:U:H2'	1:A:1752:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2314:A:H5'	6:F:35:THR:HG21	1.99	0.43
9:I:18:VAL:HG11	9:I:51:TYR:CD2	2.53	0.43
31:e:55:LEU:O	31:e:59:ILE:HG13	2.18	0.43
1:A:27:G:C4	1:A:512:G:N2	2.87	0.43
1:A:1081:U:H4'	10:J:124:ALA:HB1	2.01	0.43
1:A:2364:C:OP1	24:X:55:ARG:HD3	2.19	0.43
6:F:5:HIS:HB2	6:F:97:TRP:CG	2.53	0.43
6:F:64:LYS:HA	6:F:65:PRO:HD3	1.84	0.43
26:Z:22:LEU:HD23	26:Z:22:LEU:HA	1.86	0.43
1:A:39:G:H2'	1:A:40:U:C6	2.54	0.43
1:A:376:G:C2	1:A:377:G:C8	3.06	0.43
17:Q:91:ALA:HB2	17:Q:113:ARG:HA	2.00	0.43
18:R:83:LEU:HD23	18:R:83:LEU:HA	1.84	0.43
1:A:1056:G:H4'	1:A:1086:A:H8	1.84	0.43
1:A:2813:A:H2'	1:A:2814:A:O4'	2.18	0.43
2:B:66:A:O4'	2:B:108:A:N6	2.51	0.43
3:C:135:ILE:HA	3:C:136:PRO:HD3	1.82	0.43
29:c:9:ILE:HD13	29:c:25:LYS:HB2	2.00	0.43
31:e:28:ASN:O	31:e:36:LYS:NZ	2.50	0.43
1:A:141:G:H8	1:A:141:G:H3'	1.83	0.43
1:A:580:U:O3'	18:R:31:VAL:HG13	2.19	0.43
1:A:2680:U:O2'	1:A:2681:C:H5'	2.19	0.43
3:C:120:VAL:HG12	3:C:134:ASN:HD21	1.83	0.43
4:D:125:TRP:CE3	4:D:160:LYS:HD3	2.54	0.43
19:S:41:ILE:HD13	19:S:103:ALA:HA	2.01	0.43
1:A:1476:U:H4'	1:A:1732:C:O2'	2.19	0.43
15:O:24:MET:HB3	15:O:44:LEU:HD13	2.01	0.43
15:O:72:ASP:OD1	15:O:73:ASN:N	2.51	0.43
33:g:54:GLU:C	33:g:55:GLN:HG3	2.44	0.43
33:g:405:SER:O	33:g:408:ILE:HG13	2.19	0.43
1:A:340:A:O2'	5:E:162:ARG:NH1	2.52	0.43
1:A:1361:G:H2'	1:A:1362:C:C6	2.53	0.43
1:A:2316:G:H2'	1:A:2317:A:C8	2.53	0.43
8:H:62:LEU:HD23	8:H:135:HIS:CD2	2.53	0.43
9:I:52:MET:HE3	9:I:52:MET:HB3	1.65	0.43
16:P:88:LYS:HB2	16:P:88:LYS:HE3	1.74	0.43
1:A:280:U:H2'	1:A:281:C:O4'	2.18	0.43
1:A:281:C:H2'	1:A:282:A:H8	1.82	0.43
1:A:1317:G:H2'	1:A:1318:U:O4'	2.19	0.43
1:A:1584:U:H2'	1:A:1584:U:O2	2.19	0.43
2:B:106:G:H2'	2:B:107:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:744:U:H2'	1:A:745:G:O4'	2.19	0.42
1:A:764:A:H5'	3:C:209:GLY:HA2	2.01	0.42
1:A:1046:A:C6	9:I:9:GLN:HG2	2.54	0.42
1:A:1422:G:O2'	1:A:1492:G:N3	2.50	0.42
1:A:2349:G:OP1	31:e:45:ARG:NH2	2.53	0.42
1:A:2422:C:H2'	1:A:2423:U:O4'	2.19	0.42
1:A:2570:G:H2'	1:A:2571:U:O4'	2.19	0.42
7:G:123:ALA:HB2	7:G:133:LEU:HD23	2.01	0.42
27:a:36:VAL:HG13	27:a:38:ARG:NH1	2.34	0.42
1:A:1053:C:O2	9:I:31:ARG:NH2	2.52	0.42
1:A:1268:A:C2	1:A:2013:A:C4	3.07	0.42
1:A:1325:U:N3	20:T:86:MET:HE1	2.34	0.42
1:A:2289:G:C6	1:A:2290:G:N7	2.88	0.42
1:A:2373:G:H2'	1:A:2374:C:C6	2.54	0.42
3:C:118:SER:HB3	3:C:129:THR:HB	2.01	0.42
10:J:82:LYS:HE3	10:J:82:LYS:HB2	1.85	0.42
33:g:67:PHE:CE2	33:g:195:ILE:HD11	2.54	0.42
1:A:120:U:H5''	1:A:122:G:OP2	2.19	0.42
1:A:475:C:C4	1:A:481:G:O6	2.73	0.42
1:A:514:A:N3	1:A:581:C:O2'	2.42	0.42
1:A:1642:G:H2'	1:A:1643:G:O4'	2.19	0.42
1:A:1794:A:H2'	1:A:1795:C:C6	2.54	0.42
1:A:2102:G:N2	1:A:2187:U:O2	2.51	0.42
1:A:2121:G:H1	1:A:2177:C:H42	1.67	0.42
1:A:2282:G:C2	1:A:2425:A:C5	3.07	0.42
28:b:29:SER:OG	28:b:40:ARG:NH1	2.53	0.42
1:A:340:A:H2'	1:A:341:C:O4'	2.19	0.42
1:A:1515:A:H3'	1:A:1516:G:H8	1.83	0.42
3:C:35:GLU:HG3	3:C:64:ILE:HD11	2.01	0.42
10:J:110:ALA:HA	10:J:113:LYS:HB2	2.01	0.42
11:K:18:VAL:HG11	11:K:28:LEU:HD11	2.00	0.42
33:g:99:HIS:HA	33:g:100:PRO:HD3	1.88	0.42
1:A:910:A:N1	1:A:2277:G:H1'	2.34	0.42
1:A:1065:U:H1'	1:A:1074:G:N2	2.35	0.42
1:A:1250:G:H5''	18:R:6:ARG:HD3	2.01	0.42
1:A:2461:A:H1'	1:A:2492:U:N3	2.34	0.42
1:A:2469:A:N6	1:A:2481:G:H1'	2.34	0.42
2:B:28:C:OP1	16:P:31:THR:HG21	2.20	0.42
8:H:69:ALA:O	8:H:73:ASN:HB2	2.19	0.42
11:K:96:ARG:HA	11:K:97:PRO:HD2	1.76	0.42
13:M:50:PHE:CE2	13:M:52:GLY:HA2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:23:ARG:O	26:Z:27:ASN:ND2	2.52	0.42
1:A:364:C:H2'	1:A:365:U:C6	2.55	0.42
1:A:409:G:C2	1:A:410:G:C4	3.08	0.42
1:A:1440:U:H2'	1:A:1441:G:C8	2.55	0.42
1:A:1797:G:C5	1:A:1798:U:C5	3.07	0.42
1:A:2848:G:O2'	1:A:2867:G:N2	2.32	0.42
33:g:231:THR:HG21	34:h:97:VAL:HG11	2.00	0.42
1:A:984:A:N3	1:A:984:A:H2'	2.35	0.42
1:A:1980:G:O2'	1:A:1982:U:OP2	2.37	0.42
1:A:2144:G:N2	1:A:2146:C:O4'	2.53	0.42
1:A:2484:G:OP1	14:N:44:ARG:NH2	2.52	0.42
4:D:2:ILE:HG13	4:D:100:LEU:HD21	2.02	0.42
17:Q:4:ILE:HD12	17:Q:4:ILE:H	1.85	0.42
19:S:4:VAL:HA	19:S:12:HIS:O	2.19	0.42
30:d:5:PHE:CZ	30:d:7:PRO:HB3	2.54	0.42
31:e:29:LEU:HD12	31:e:29:LEU:HA	1.60	0.42
33:g:192:PHE:CE1	33:g:274:VAL:HG13	2.55	0.42
1:A:327:G:H2'	1:A:328:U:O4'	2.20	0.42
7:G:26:ILE:HD12	7:G:75:MET:HB3	2.02	0.42
33:g:29:ALA:O	33:g:174:LEU:HD21	2.19	0.42
1:A:197:A:N6	1:A:2430:A:O2'	2.51	0.42
1:A:963:U:H2'	1:A:964:C:C6	2.55	0.42
1:A:1069:A:H5''	1:A:1070:A:C8	2.55	0.42
1:A:1087:G:N2	1:A:1102:C:O2	2.44	0.42
1:A:1395:A:C6	1:A:1398:C:C2	3.08	0.42
1:A:1877:A:C6	1:A:1878:G:C5	3.08	0.42
1:A:2502:G:H5''	1:A:2503:A:H5''	2.02	0.42
7:G:71:LEU:HD23	7:G:71:LEU:HA	1.90	0.42
15:O:20:MET:HE2	15:O:20:MET:HB3	1.86	0.42
33:g:289:THR:HB	33:g:293:TRP:CZ3	2.55	0.42
1:A:1411:U:H3	1:A:1591:A:H61	1.67	0.42
1:A:2108:A:N1	1:A:2181:U:N3	2.68	0.42
7:G:104:ASN:ND2	7:G:114:ASP:OD1	2.52	0.42
8:H:133:GLN:HG3	8:H:135:HIS:O	2.20	0.42
11:K:60:ASP:OD1	11:K:60:ASP:N	2.48	0.42
16:P:31:THR:O	16:P:102:ARG:NH1	2.47	0.42
26:Z:28:LEU:HD23	26:Z:28:LEU:HA	1.75	0.42
27:a:24:LEU:HD23	27:a:24:LEU:HA	1.73	0.42
30:d:31:LEU:HD23	30:d:31:LEU:HA	1.86	0.42
33:g:207:ILE:O	33:g:211:ARG:NE	2.52	0.42
1:A:2260:C:H2'	1:A:2261:C:H6	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2350:C:H2'	1:A:2351:G:O4'	2.20	0.41
1:A:2865:U:C4	1:A:2866:U:C4	3.08	0.41
6:F:25:VAL:O	6:F:28:VAL:HG12	2.20	0.41
9:I:109:LYS:H	9:I:109:LYS:HG3	1.60	0.41
29:c:40:ASP:HA	29:c:41:PRO:HD2	1.86	0.41
1:A:804:A:H2'	1:A:806:C:C4	2.55	0.41
1:A:839:U:H2'	1:A:840:C:C6	2.55	0.41
1:A:1681:G:N3	1:A:1762:A:H2'	2.35	0.41
1:A:2419:U:OP1	31:e:41:LYS:NZ	2.47	0.41
6:F:108:VAL:HG11	6:F:176:PRO:HG2	2.02	0.41
9:I:60:LEU:O	9:I:64:VAL:HB	2.20	0.41
14:N:33:LEU:HD12	14:N:129:THR:O	2.20	0.41
24:X:68:LYS:NZ	24:X:70:GLU:HB3	2.35	0.41
33:g:71:ALA:CB	33:g:76:SER:HB3	2.50	0.41
33:g:231:THR:O	33:g:235:VAL:HG23	2.20	0.41
1:A:918:A:H5''	2:B:97:C:O2'	2.21	0.41
1:A:1082:U:O2'	9:I:39:THR:OG1	2.37	0.41
1:A:1243:C:H1'	13:M:4:ASN:O	2.20	0.41
1:A:1510:G:H2'	1:A:1511:G:C8	2.55	0.41
1:A:2339:C:H2'	1:A:2340:A:C8	2.54	0.41
18:R:78:LYS:O	18:R:117:LEU:HD11	2.20	0.41
23:W:21:ARG:HA	23:W:25:LYS:O	2.21	0.41
33:g:125:LEU:HD11	33:g:169:MET:HB2	2.02	0.41
33:g:302:TRP:O	33:g:305:THR:HB	2.19	0.41
34:h:87:ARG:HA	34:h:90:THR:HB	2.01	0.41
1:A:572:A:H5''	1:A:573:U:OP2	2.20	0.41
1:A:1289:C:H2'	1:A:1290:C:C6	2.55	0.41
1:A:1289:C:H2'	1:A:1290:C:H6	1.85	0.41
1:A:2834:G:H2'	1:A:2879:A:H61	1.84	0.41
3:C:84:ASP:OD1	3:C:86:ASN:ND2	2.42	0.41
19:S:14:VAL:HA	19:S:18:GLN:NE2	2.35	0.41
1:A:30:G:H2'	1:A:31:C:C6	2.55	0.41
1:A:141:G:H2'	1:A:142:A:O4'	2.19	0.41
1:A:362:A:H3'	1:A:363:G:C8	2.55	0.41
1:A:678:C:H2'	1:A:679:C:C6	2.56	0.41
1:A:1490:A:H1'	1:A:1491:G:N7	2.35	0.41
1:A:2189:U:H2'	1:A:2190:G:O4'	2.20	0.41
20:T:23:LEU:HD22	28:b:24:ALA:HB2	2.02	0.41
33:g:72:LEU:HD12	33:g:72:LEU:HA	1.82	0.41
1:A:49:A:H4'	1:A:50:U:H5''	2.03	0.41
1:A:1038:G:H2'	1:A:1039:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2820:A:H4'	15:O:3:HIS:CD2	2.56	0.41
24:X:41:ARG:HG2	24:X:41:ARG:HH11	1.84	0.41
28:b:40:ARG:HG3	28:b:40:ARG:HH11	1.85	0.41
33:g:25:PHE:CZ	33:g:177:GLN:HB3	2.56	0.41
33:g:30:LEU:HA	33:g:33:PHE:HB3	2.03	0.41
33:g:80:LEU:HD21	33:g:293:TRP:CZ2	2.55	0.41
1:A:1086:A:H4'	1:A:1103:A:C2	2.56	0.41
1:A:1688:U:O2'	1:A:1700:A:N7	2.50	0.41
2:B:48:U:P	16:P:30:ARG:HH22	2.44	0.41
8:H:31:VAL:HB	8:H:32:PRO:HD3	2.02	0.41
9:I:39:THR:HG22	9:I:43:LYS:HE3	2.03	0.41
34:h:80:ARG:HA	34:h:80:ARG:HD3	1.80	0.41
1:A:141:G:H3'	1:A:141:G:C8	2.56	0.41
1:A:239:C:H2'	1:A:240:C:O4'	2.21	0.41
1:A:319:G:H2'	1:A:320:A:O4'	2.21	0.41
1:A:729:G:H5''	1:A:730:A:C5'	2.50	0.41
1:A:900:A:C2	1:A:902:C:C5	3.09	0.41
1:A:922:C:H1'	24:X:26:PHE:CD1	2.55	0.41
1:A:1199:U:H1'	18:R:4:VAL:HG22	2.03	0.41
3:C:227:PRO:HG3	3:C:234:GLY:H	1.86	0.41
7:G:94:TYR:HA	7:G:106:SER:O	2.20	0.41
10:J:103:ARG:HA	10:J:106:LEU:HD12	2.03	0.41
33:g:242:ARG:NH1	33:g:373:LEU:HD22	2.36	0.41
33:g:407:LEU:HD23	33:g:407:LEU:HA	1.85	0.41
1:A:39:G:H2'	1:A:40:U:H6	1.86	0.41
1:A:155:A:H2'	1:A:156:A:C8	2.56	0.41
1:A:196:A:OP2	13:M:47:ARG:NH1	2.48	0.41
1:A:532:A:N3	1:A:532:A:H2'	2.35	0.41
1:A:789:A:C5	30:d:3:ARG:NH1	2.88	0.41
1:A:816:C:H2'	1:A:817:C:H6	1.85	0.41
1:A:1025:G:H8	1:A:1025:G:OP1	2.04	0.41
1:A:1080:A:H4'	10:J:127:ARG:HB3	2.02	0.41
1:A:1532:A:N6	1:A:1539:U:H3	2.19	0.41
1:A:2038:G:H2'	1:A:2039:U:O4'	2.21	0.41
4:D:117:GLY:O	4:D:164:GLN:HA	2.21	0.41
6:F:48:LYS:HA	6:F:51:ASP:OD2	2.21	0.41
6:F:117:LEU:O	6:F:177:PHE:HA	2.21	0.41
6:F:130:MET:HE3	6:F:130:MET:HB2	1.98	0.41
6:F:136:ILE:HG22	6:F:141:ILE:HG21	2.02	0.41
8:H:94:ILE:HG23	8:H:98:ASP:HB2	2.02	0.41
9:I:52:MET:HE3	9:I:81:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:26:GLY:O	11:K:30:THR:HG23	2.21	0.41
14:N:66:ARG:HB2	14:N:101:VAL:O	2.21	0.41
16:P:52:SER:OG	16:P:54:VAL:HG22	2.21	0.41
33:g:280:ALA:O	33:g:284:ILE:HG13	2.21	0.41
33:g:404:THR:O	33:g:408:ILE:HG23	2.20	0.41
1:A:1046:A:N6	9:I:9:GLN:HG2	2.35	0.41
1:A:1799:G:C4	3:C:176:LEU:HD13	2.56	0.41
1:A:2305:U:C2	6:F:151:GLY:HA3	2.55	0.41
1:A:2627:G:O2'	1:A:2781:A:N1	2.41	0.41
32:f:18:LYS:HB2	32:f:23:ILE:HD13	2.02	0.41
1:A:1005:C:H2'	1:A:1006:C:C6	2.56	0.40
1:A:1034:G:N2	1:A:1122:G:H1'	2.36	0.40
1:A:1515:A:H3'	1:A:1516:G:C8	2.56	0.40
1:A:1587:G:H2'	1:A:1588:G:H8	1.84	0.40
1:A:1924:C:H2'	1:A:1925:C:O4'	2.22	0.40
1:A:2082:A:H2'	1:A:2083:G:O4'	2.21	0.40
1:A:2774:C:H2'	1:A:2775:G:O4'	2.21	0.40
8:H:29:PHE:HD2	8:H:30:LEU:HD23	1.86	0.40
33:g:157:TYR:O	33:g:161:VAL:HG23	2.20	0.40
33:g:248:TYR:CE2	33:g:351:ALA:HB2	2.56	0.40
1:A:388:G:N7	1:A:390:U:H2'	2.35	0.40
1:A:720:U:H2'	1:A:721:A:C8	2.56	0.40
1:A:1746:A:H2'	1:A:1747:U:C6	2.56	0.40
1:A:2141:G:H2'	1:A:2142:A:C8	2.56	0.40
1:A:2472:G:H1'	1:A:2478:A:H61	1.86	0.40
17:Q:88:ARG:NH2	17:Q:112:GLU:HB2	2.36	0.40
27:a:4:THR:HG21	27:a:37:GLU:HB3	2.03	0.40
33:g:237:VAL:CG1	33:g:269:VAL:HG21	2.52	0.40
1:A:532:A:H5'	18:R:28:ARG:NH2	2.36	0.40
1:A:1268:A:H2'	1:A:1269:A:O4'	2.21	0.40
1:A:2056:G:N3	1:A:2056:G:H2'	2.37	0.40
5:E:150:THR:OG1	5:E:151:GLY:N	2.54	0.40
8:H:59:ALA:HA	8:H:62:LEU:HD12	2.03	0.40
12:L:17:ARG:HA	12:L:17:ARG:HD3	1.72	0.40
33:g:284:ILE:HD11	33:g:321:TYR:CE1	2.47	0.40
1:A:62:U:HO2'	1:A:63:A:P	2.41	0.40
1:A:329:G:O4'	1:A:477:A:H1'	2.20	0.40
1:A:493:G:O2'	20:T:7:HIS:HA	2.20	0.40
1:A:754:U:H2'	1:A:755:U:C6	2.56	0.40
1:A:830:G:H4'	1:A:831:G:OP2	2.21	0.40
1:A:1076:C:H2'	1:A:1077:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1827:U:H2'	1:A:1828:G:O4'	2.21	0.40
4:D:11:MET:HG2	4:D:25:THR:HG23	2.02	0.40
8:H:76:GLU:H	8:H:76:GLU:HG3	1.70	0.40
8:H:135:HIS:CG	8:H:136:SER:N	2.90	0.40
12:L:66:LYS:HB3	12:L:66:LYS:HE2	1.92	0.40
13:M:141:LYS:NZ	13:M:143:GLU:HB3	2.36	0.40
15:O:49:GLU:HB2	15:O:50:PRO:HD3	2.04	0.40
33:g:86:ILE:HG21	33:g:279:PHE:HA	2.04	0.40
1:A:263:G:H2'	1:A:264:C:O4'	2.22	0.40
1:A:360:U:O4	1:A:361:G:N1	2.55	0.40
1:A:1498:C:O4'	1:A:1577:C:H5'	2.22	0.40
1:A:2684:U:O4'	12:L:70:ARG:NH1	2.55	0.40
1:A:2700:A:H2'	1:A:2701:U:H6	1.87	0.40
3:C:176:LEU:HD23	3:C:176:LEU:HA	1.88	0.40
5:E:128:ALA:O	5:E:130:LYS:N	2.51	0.40
6:F:136:ILE:HA	6:F:141:ILE:HG21	2.04	0.40
6:F:138:PHE:HA	6:F:139:PRO:HD3	1.85	0.40
13:M:91:ASP:H	13:M:94:THR:HB	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	269/273 (98%)	264 (98%)	5 (2%)	0	100	100
4	D	207/209 (99%)	203 (98%)	4 (2%)	0	100	100
5	E	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
6	F	175/179 (98%)	170 (97%)	5 (3%)	0	100	100
7	G	174/177 (98%)	170 (98%)	4 (2%)	0	100	100
8	H	147/149 (99%)	137 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	123/165 (74%)	114 (93%)	8 (6%)	1 (1%)	16	46
10	J	68/142 (48%)	64 (94%)	4 (6%)	0	100	100
11	K	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
12	L	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
13	M	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
14	N	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
15	O	123/127 (97%)	120 (98%)	3 (2%)	0	100	100
16	P	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
17	Q	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
18	R	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
19	S	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
20	T	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
21	U	93/100 (93%)	89 (96%)	4 (4%)	0	100	100
22	V	100/104 (96%)	98 (98%)	2 (2%)	0	100	100
23	W	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
24	X	74/85 (87%)	72 (97%)	2 (3%)	0	100	100
25	Y	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
26	Z	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
27	a	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
28	b	54/57 (95%)	54 (100%)	0	0	100	100
29	c	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
30	d	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
31	e	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
32	f	36/38 (95%)	36 (100%)	0	0	100	100
33	g	393/443 (89%)	370 (94%)	22 (6%)	1 (0%)	36	65
34	h	57/127 (45%)	55 (96%)	2 (4%)	0	100	100
All	All	3818/4144 (92%)	3700 (97%)	116 (3%)	2 (0%)	49	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	g	135	ILE
9	I	108	VAL

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	
3	C	216/218 (99%)	204 (94%)	12 (6%)	19	47
4	D	164/164 (100%)	159 (97%)	5 (3%)	36	61
5	E	165/165 (100%)	162 (98%)	3 (2%)	51	69
6	F	148/150 (99%)	132 (89%)	16 (11%)	6	24
7	G	137/138 (99%)	130 (95%)	7 (5%)	21	50
8	H	114/114 (100%)	108 (95%)	6 (5%)	20	49
9	I	95/123 (77%)	88 (93%)	7 (7%)	13	39
10	J	52/110 (47%)	50 (96%)	2 (4%)	29	57
11	K	116/116 (100%)	111 (96%)	5 (4%)	26	54
12	L	104/104 (100%)	100 (96%)	4 (4%)	29	57
13	M	103/103 (100%)	98 (95%)	5 (5%)	22	51
14	N	109/109 (100%)	106 (97%)	3 (3%)	38	62
15	O	102/103 (99%)	95 (93%)	7 (7%)	14	42
16	P	87/87 (100%)	82 (94%)	5 (6%)	18	47
17	Q	99/100 (99%)	94 (95%)	5 (5%)	21	50
18	R	89/90 (99%)	82 (92%)	7 (8%)	11	37
19	S	84/84 (100%)	77 (92%)	7 (8%)	10	35
20	T	93/93 (100%)	92 (99%)	1 (1%)	65	75
21	U	82/84 (98%)	77 (94%)	5 (6%)	17	46
22	V	83/85 (98%)	78 (94%)	5 (6%)	17	46
23	W	78/78 (100%)	73 (94%)	5 (6%)	16	44
24	X	57/63 (90%)	53 (93%)	4 (7%)	14	41
25	Y	67/68 (98%)	63 (94%)	4 (6%)	17	46
26	Z	54/55 (98%)	52 (96%)	2 (4%)	30	57
27	a	48/49 (98%)	45 (94%)	3 (6%)	16	45
28	b	47/48 (98%)	45 (96%)	2 (4%)	26	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	c	45/49 (92%)	39 (87%)	6 (13%)	4	17
30	d	38/38 (100%)	35 (92%)	3 (8%)	11	37
31	e	51/52 (98%)	48 (94%)	3 (6%)	18	47
32	f	34/34 (100%)	31 (91%)	3 (9%)	9	33
33	g	327/359 (91%)	312 (95%)	15 (5%)	24	53
34	h	49/99 (50%)	48 (98%)	1 (2%)	48	67
All	All	3137/3332 (94%)	2969 (95%)	168 (5%)	21	49

All (168) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	3	VAL
3	C	10	SER
3	C	39	LYS
3	C	94	VAL
3	C	120	VAL
3	C	124	ILE
3	C	130	LEU
3	C	156	ARG
3	C	202	LEU
3	C	242	LYS
3	C	251	GLN
3	C	271	ARG
4	D	22	ILE
4	D	25	THR
4	D	58	ASN
4	D	112	THR
4	D	178	VAL
5	E	33	VAL
5	E	126	VAL
5	E	169	VAL
6	F	3	LYS
6	F	10	ASP
6	F	14	LYS
6	F	25	VAL
6	F	36	LEU
6	F	49	LEU
6	F	57	LEU
6	F	66	LEU
6	F	89	VAL

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Mol	Chain	Res	Type
6	F	106	ILE
6	F	108	VAL
6	F	121	SER
6	F	127	ASN
6	F	132	VAL
6	F	154	ILE
6	F	174	ASP
7	G	10	VAL
7	G	11	VAL
7	G	27	LYS
7	G	30	ASN
7	G	41	VAL
7	G	49	THR
7	G	92	VAL
8	H	9	VAL
8	H	15	LEU
8	H	58	LEU
8	H	60	GLU
8	H	79	THR
8	H	124	THR
9	I	12	VAL
9	I	16	SER
9	I	35	VAL
9	I	55	VAL
9	I	58	THR
9	I	64	VAL
9	I	85	VAL
10	J	98	VAL
10	J	113	LYS
11	K	17	VAL
11	K	90	GLU
11	K	105	VAL
11	K	131	ASN
11	K	142	ILE
12	L	29	HIS
12	L	49	ARG
12	L	58	LEU
12	L	86	LEU
13	M	46	VAL
13	M	86	GLU
13	M	89	VAL
13	M	92	LEU

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Mol	Chain	Res	Type
13	M	116	VAL
14	N	12	MET
14	N	78	LEU
14	N	132	THR
15	O	2	ARG
15	O	48	VAL
15	O	69	ARG
15	O	75	ILE
15	O	79	LEU
15	O	96	ARG
15	O	114	GLU
16	P	20	GLU
16	P	49	VAL
16	P	55	GLU
16	P	78	VAL
16	P	116	GLN
17	Q	5	ILE
17	Q	21	ARG
17	Q	26	VAL
17	Q	68	GLU
17	Q	92	VAL
18	R	9	ILE
18	R	17	ILE
18	R	28	ARG
18	R	40	ILE
18	R	51	ARG
18	R	77	SER
18	R	80	ILE
19	S	18	GLN
19	S	25	LEU
19	S	38	VAL
19	S	45	GLU
19	S	51	VAL
19	S	87	GLN
19	S	96	VAL
20	T	86	MET
21	U	10	VAL
21	U	34	VAL
21	U	63	VAL
21	U	72	GLN
21	U	93	LEU
22	V	28	VAL

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Mol	Chain	Res	Type
22	V	43	LYS
22	V	52	LEU
22	V	68	SER
22	V	101	GLU
23	W	11	GLU
23	W	25	LYS
23	W	61	LEU
23	W	77	VAL
23	W	92	VAL
24	X	32	LEU
24	X	41	ARG
24	X	44	LYS
24	X	82	ILE
25	Y	2	SER
25	Y	4	VAL
25	Y	13	VAL
25	Y	44	LYS
26	Z	2	LYS
26	Z	59	GLU
27	a	10	THR
27	a	24	LEU
27	a	36	VAL
28	b	28	LEU
28	b	57	LYS
29	c	5	ILE
29	c	6	ARG
29	c	9	ILE
29	c	22	THR
29	c	37	LYS
29	c	46	HIS
30	d	1	MET
30	d	4	THR
30	d	41	ARG
31	e	6	THR
31	e	8	ARG
31	e	54	ASP
32	f	7	VAL
32	f	17	VAL
32	f	36	ARG
33	g	32	VAL
33	g	44	ILE
33	g	45	ASP

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Mol	Chain	Res	Type
33	g	73	SER
33	g	74	ARG
33	g	78	PHE
33	g	179	THR
33	g	183	ILE
33	g	196	VAL
33	g	211	ARG
33	g	290	ILE
33	g	357	ARG
33	g	369	VAL
33	g	404	THR
33	g	420	VAL
34	h	94	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	58	HIS
3	C	117	GLN
3	C	134	ASN
3	C	142	HIS
4	D	42	ASN
4	D	58	ASN
4	D	130	GLN
4	D	136	ASN
4	D	150	GLN
4	D	185	ASN
6	F	27	GLN
6	F	37	ASN
6	F	52	ASN
6	F	63	GLN
6	F	81	GLN
7	G	88	GLN
7	G	101	ASN
7	G	116	GLN
7	G	139	GLN
8	H	11	ASN
8	H	33	GLN
11	K	136	GLN
12	L	3	GLN
12	L	9	ASN
12	L	29	HIS

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Mol	Chain	Res	Type
14	N	3	GLN
14	N	13	HIS
15	O	3	HIS
15	O	31	HIS
17	Q	41	GLN
17	Q	56	HIS
17	Q	66	ASN
18	R	44	GLN
19	S	12	HIS
20	T	7	HIS
22	V	54	GLN
23	W	24	ASN
24	X	46	HIS
26	Z	20	ASN
26	Z	27	ASN
26	Z	41	HIS
26	Z	45	GLN
27	a	9	GLN
27	a	20	HIS
28	b	6	ASN
28	b	19	HIS
28	b	42	HIS
30	d	26	ASN
33	g	185	ASN
33	g	252	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2880/2903 (99%)	438 (15%)	14 (0%)
2	B	119/120 (99%)	17 (14%)	1 (0%)
36	x	2/3 (66%)	1 (50%)	0
All	All	3001/3026 (99%)	456 (15%)	15 (0%)

All (456) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	12	U
1	A	14	A
1	A	15	G

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Mol	Chain	Res	Type
1	A	46	G
1	A	58	G
1	A	62	U
1	A	63	A
1	A	64	A
1	A	71	A
1	A	74	A
1	A	75	G
1	A	84	A
1	A	88	G
1	A	101	A
1	A	102	U
1	A	103	A
1	A	118	A
1	A	119	A
1	A	120	U
1	A	137	U
1	A	138	U
1	A	139	U
1	A	140	C
1	A	141	G
1	A	142	A
1	A	181	A
1	A	196	A
1	A	199	A
1	A	216	A
1	A	221	A
1	A	222	A
1	A	248	G
1	A	266	G
1	A	272	A
1	A	275	C
1	A	276	U
1	A	279	A
1	A	285	G
1	A	291	G
1	A	302	C
1	A	311	A
1	A	317	G
1	A	329	G
1	A	330	A
1	A	331	C

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Mol	Chain	Res	Type
1	A	353	C
1	A	361	G
1	A	362	A
1	A	372	G
1	A	383	C
1	A	386	G
1	A	389	G
1	A	396	G
1	A	399	U
1	A	411	G
1	A	412	A
1	A	424	G
1	A	425	G
1	A	455	C
1	A	475	C
1	A	481	G
1	A	491	G
1	A	494	G
1	A	504	A
1	A	505	A
1	A	508	A
1	A	509	C
1	A	529	A
1	A	532	A
1	A	544	C
1	A	546	U
1	A	547	A
1	A	548	G
1	A	549	G
1	A	551	G
1	A	563	A
1	A	568	U
1	A	573	U
1	A	575	A
1	A	603	A
1	A	613	A
1	A	614	A
1	A	615	U
1	A	627	A
1	A	637	A
1	A	646	U
1	A	647	G

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Mol	Chain	Res	Type
1	A	653	U
1	A	654	A
1	A	655	A
1	A	668	A
1	A	685	A
1	A	686	U
1	A	717	C
1	A	726	G
1	A	729	G
1	A	730	A
1	A	747	U
1	A	757	G
1	A	765	C
1	A	775	G
1	A	776	G
1	A	777	G
1	A	782	A
1	A	784	G
1	A	785	G
1	A	789	A
1	A	790	U
1	A	791	C
1	A	792	A
1	A	798	G
1	A	800	A
1	A	805	G
1	A	812	C
1	A	827	U
1	A	828	U
1	A	845	A
1	A	846	U
1	A	858	G
1	A	859	G
1	A	869	G
1	A	877	A
1	A	878	A
1	A	879	G
1	A	881	G
1	A	896	A
1	A	897	C
1	A	898	C
1	A	901	C

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Mol	Chain	Res	Type
1	A	902	C
1	A	907	G
1	A	910	A
1	A	914	G
1	A	930	G
1	A	932	U
1	A	946	C
1	A	953	G
1	A	961	C
1	A	974	G
1	A	983	A
1	A	996	A
1	A	1005	C
1	A	1009	A
1	A	1012	U
1	A	1013	C
1	A	1026	G
1	A	1033	U
1	A	1046	A
1	A	1047	G
1	A	1060	U
1	A	1070	A
1	A	1071	G
1	A	1083	U
1	A	1087	G
1	A	1088	A
1	A	1112	G
1	A	1119	U
1	A	1132	U
1	A	1133	A
1	A	1135	C
1	A	1136	G
1	A	1142	A
1	A	1156	A
1	A	1167	C
1	A	1168	G
1	A	1173	U
1	A	1206	G
1	A	1212	G
1	A	1236	G
1	A	1238	G
1	A	1250	G

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Mol	Chain	Res	Type
1	A	1253	A
1	A	1256	G
1	A	1268	A
1	A	1271	G
1	A	1272	A
1	A	1273	U
1	A	1300	G
1	A	1301	A
1	A	1310	G
1	A	1321	A
1	A	1329	U
1	A	1338	G
1	A	1345	C
1	A	1352	U
1	A	1365	A
1	A	1379	U
1	A	1383	A
1	A	1386	C
1	A	1395	A
1	A	1416	G
1	A	1417	C
1	A	1420	A
1	A	1424	G
1	A	1428	C
1	A	1433	A
1	A	1434	A
1	A	1435	G
1	A	1451	C
1	A	1452	G
1	A	1454	C
1	A	1455	G
1	A	1482	G
1	A	1489	C
1	A	1490	A
1	A	1491	G
1	A	1493	C
1	A	1494	A
1	A	1495	A
1	A	1497	U
1	A	1498	C
1	A	1509	A
1	A	1510	G

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Mol	Chain	Res	Type
1	A	1515	A
1	A	1523	U
1	A	1532	A
1	A	1533	C
1	A	1534	U
1	A	1535	A
1	A	1536	C
1	A	1554	U
1	A	1566	A
1	A	1569	A
1	A	1578	U
1	A	1581	G
1	A	1583	A
1	A	1585	C
1	A	1607	C
1	A	1608	A
1	A	1647	U
1	A	1648	U
1	A	1649	G
1	A	1654	A
1	A	1674	G
1	A	1698	A
1	A	1715	G
1	A	1729	U
1	A	1730	C
1	A	1732	C
1	A	1738	G
1	A	1744	A
1	A	1758	U
1	A	1764	C
1	A	1773	A
1	A	1782	U
1	A	1791	A
1	A	1800	C
1	A	1808	A
1	A	1816	C
1	A	1829	A
1	A	1839	G
1	A	1847	A
1	A	1849	G
1	A	1866	A
1	A	1870	C

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Mol	Chain	Res	Type
1	A	1871	A
1	A	1872	A
1	A	1876	A
1	A	1906	G
1	A	1907	G
1	A	1929	G
1	A	1930	G
1	A	1936	A
1	A	1938	A
1	A	1955	U
1	A	1963	U
1	A	1964	G
1	A	1966	A
1	A	1967	C
1	A	1970	A
1	A	1971	U
1	A	1972	G
1	A	1991	U
1	A	1993	U
1	A	1997	C
1	A	2023	C
1	A	2030	A
1	A	2031	A
1	A	2033	A
1	A	2041	U
1	A	2043	C
1	A	2049	G
1	A	2055	C
1	A	2056	G
1	A	2060	A
1	A	2061	G
1	A	2062	A
1	A	2069	G
1	A	2070	A
1	A	2085	U
1	A	2093	G
1	A	2097	A
1	A	2105	U
1	A	2111	U
1	A	2112	G
1	A	2113	U
1	A	2115	G

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Mol	Chain	Res	Type
1	A	2116	G
1	A	2117	A
1	A	2118	U
1	A	2119	A
1	A	2123	G
1	A	2126	A
1	A	2128	G
1	A	2130	U
1	A	2131	U
1	A	2132	U
1	A	2133	G
1	A	2134	A
1	A	2137	U
1	A	2145	C
1	A	2146	C
1	A	2147	A
1	A	2148	G
1	A	2149	U
1	A	2157	G
1	A	2159	G
1	A	2160	C
1	A	2161	C
1	A	2163	A
1	A	2164	C
1	A	2165	C
1	A	2167	U
1	A	2168	G
1	A	2169	A
1	A	2170	A
1	A	2171	A
1	A	2172	U
1	A	2173	A
1	A	2177	C
1	A	2178	C
1	A	2179	C
1	A	2181	U
1	A	2185	U
1	A	2187	U
1	A	2188	U
1	A	2190	G
1	A	2195	U
1	A	2198	A

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Mol	Chain	Res	Type
1	A	2203	U
1	A	2204	G
1	A	2211	A
1	A	2221	G
1	A	2225	A
1	A	2229	U
1	A	2238	G
1	A	2239	G
1	A	2268	A
1	A	2280	G
1	A	2283	C
1	A	2287	A
1	A	2305	U
1	A	2308	G
1	A	2312	U
1	A	2322	A
1	A	2325	G
1	A	2327	A
1	A	2333	A
1	A	2336	A
1	A	2345	G
1	A	2347	C
1	A	2350	C
1	A	2383	G
1	A	2385	C
1	A	2402	U
1	A	2406	A
1	A	2421	G
1	A	2422	C
1	A	2425	A
1	A	2429	G
1	A	2430	A
1	A	2431	U
1	A	2432	A
1	A	2434	A
1	A	2435	A
1	A	2441	U
1	A	2448	A
1	A	2476	A
1	A	2478	A
1	A	2480	C
1	A	2481	G

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Mol	Chain	Res	Type
1	A	2491	U
1	A	2494	G
1	A	2502	G
1	A	2504	U
1	A	2505	G
1	A	2507	C
1	A	2518	A
1	A	2520	C
1	A	2525	G
1	A	2529	G
1	A	2535	G
1	A	2566	A
1	A	2567	G
1	A	2578	G
1	A	2585	U
1	A	2586	U
1	A	2602	A
1	A	2603	G
1	A	2609	U
1	A	2613	U
1	A	2615	U
1	A	2623	G
1	A	2629	U
1	A	2630	G
1	A	2646	C
1	A	2663	G
1	A	2689	U
1	A	2690	U
1	A	2714	G
1	A	2726	A
1	A	2732	G
1	A	2733	A
1	A	2744	G
1	A	2748	A
1	A	2757	A
1	A	2778	A
1	A	2791	G
1	A	2792	A
1	A	2798	U
1	A	2818	U
1	A	2820	A
1	A	2821	A

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Mol	Chain	Res	Type
1	A	2823	A
1	A	2825	G
1	A	2835	A
1	A	2861	U
1	A	2867	G
1	A	2868	A
1	A	2873	A
1	A	2879	A
1	A	2880	C
1	A	2883	A
1	A	2884	U
1	A	2885	G
1	A	2887	A
1	A	2891	U
2	B	10	G
2	B	12	C
2	B	13	G
2	B	14	U
2	B	24	G
2	B	25	U
2	B	30	C
2	B	35	C
2	B	44	G
2	B	56	G
2	B	58	A
2	B	67	G
2	B	84	G
2	B	88	C
2	B	89	U
2	B	90	C
2	B	109	A
36	x	76	A

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	62	U
1	A	613	A
1	A	645	C
1	A	784	G
1	A	900	A
1	A	901	C

Continued on next page...

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Mol	Chain	Res	Type
1	A	1344	U
1	A	1454	C
1	A	1494	A
1	A	1757	A
1	A	2127	G
1	A	2158	A
1	A	2601	C
1	A	2756	U
2	B	13	G

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 324 ligands modelled in this entry, 324 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
33	g	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	g	398:PRO	C	399:PHE	N	5.57
1	A	2789:C	O3'	2790:U	P	3.00

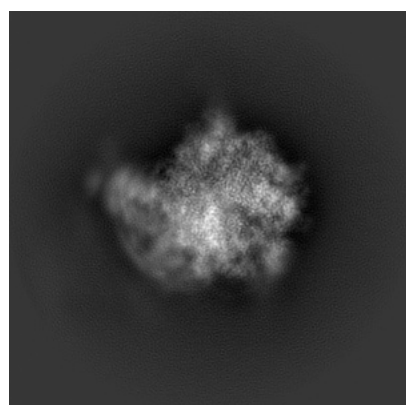
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8001. These allow visual inspection of the internal detail of the map and identification of artifacts.

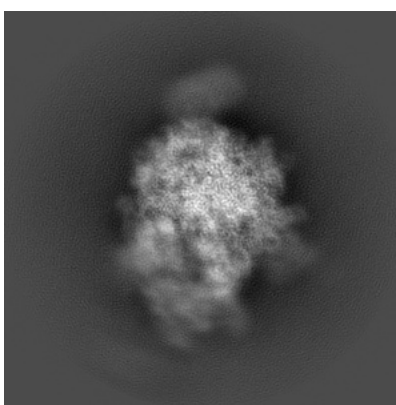
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

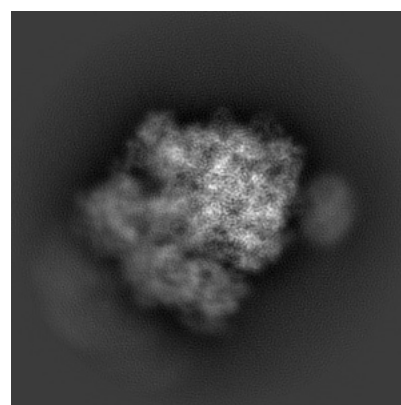
6.1.1 Primary map



X



Y

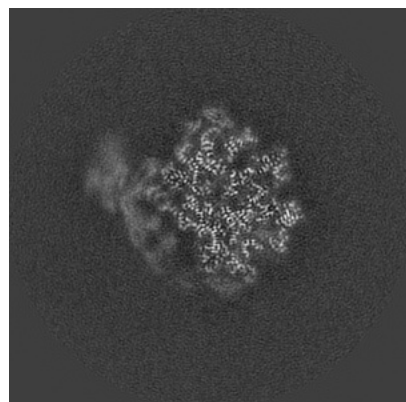


Z

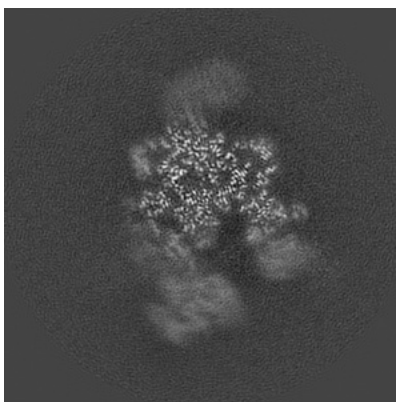
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

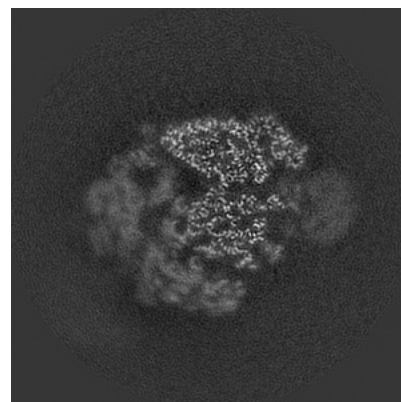
6.2.1 Primary map



X Index: 160



Y Index: 160

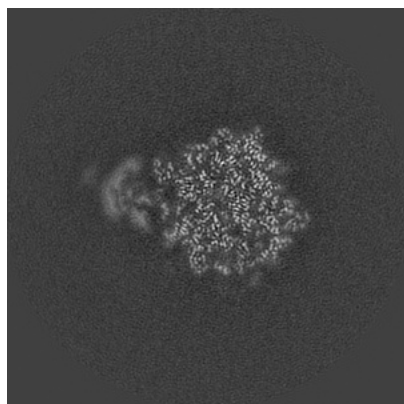


Z Index: 160

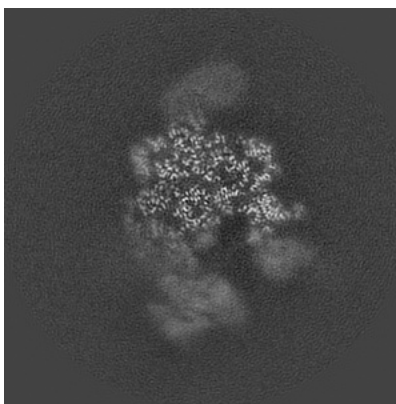
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

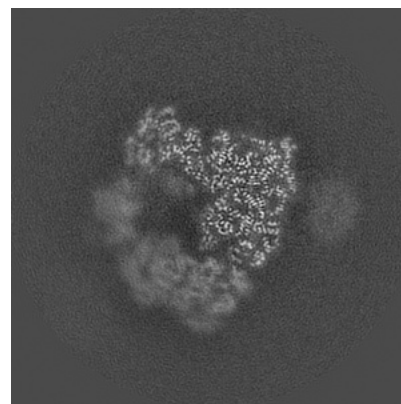
6.3.1 Primary map



X Index: 173



Y Index: 158

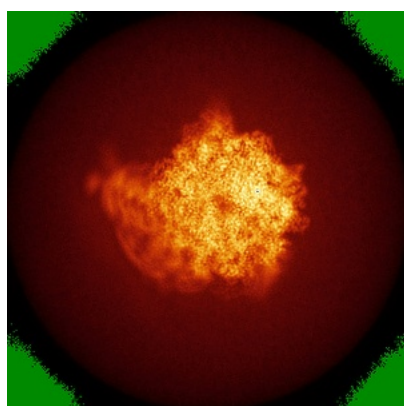


Z Index: 175

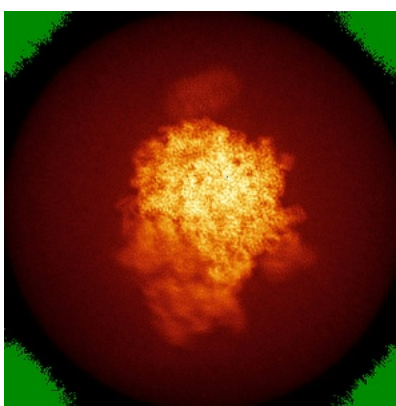
The images above show the largest variance slices of the map in three orthogonal directions.

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

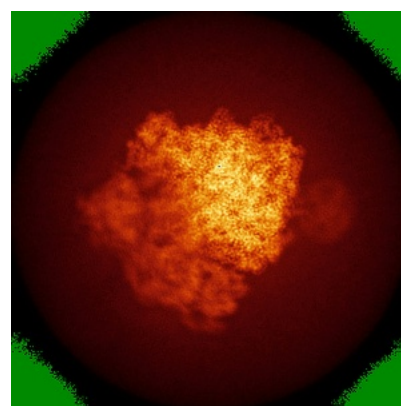
6.4.1 Primary map



X



Y

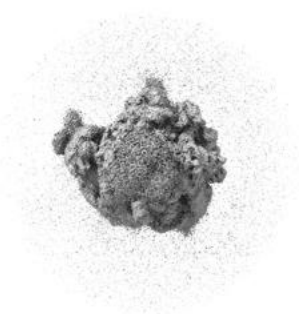


Z

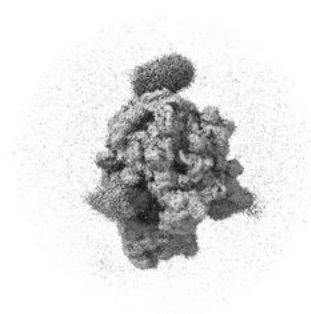
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

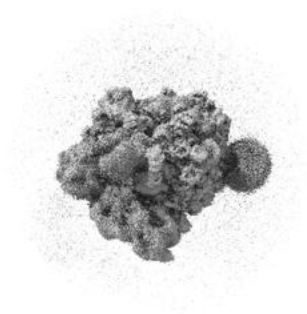
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

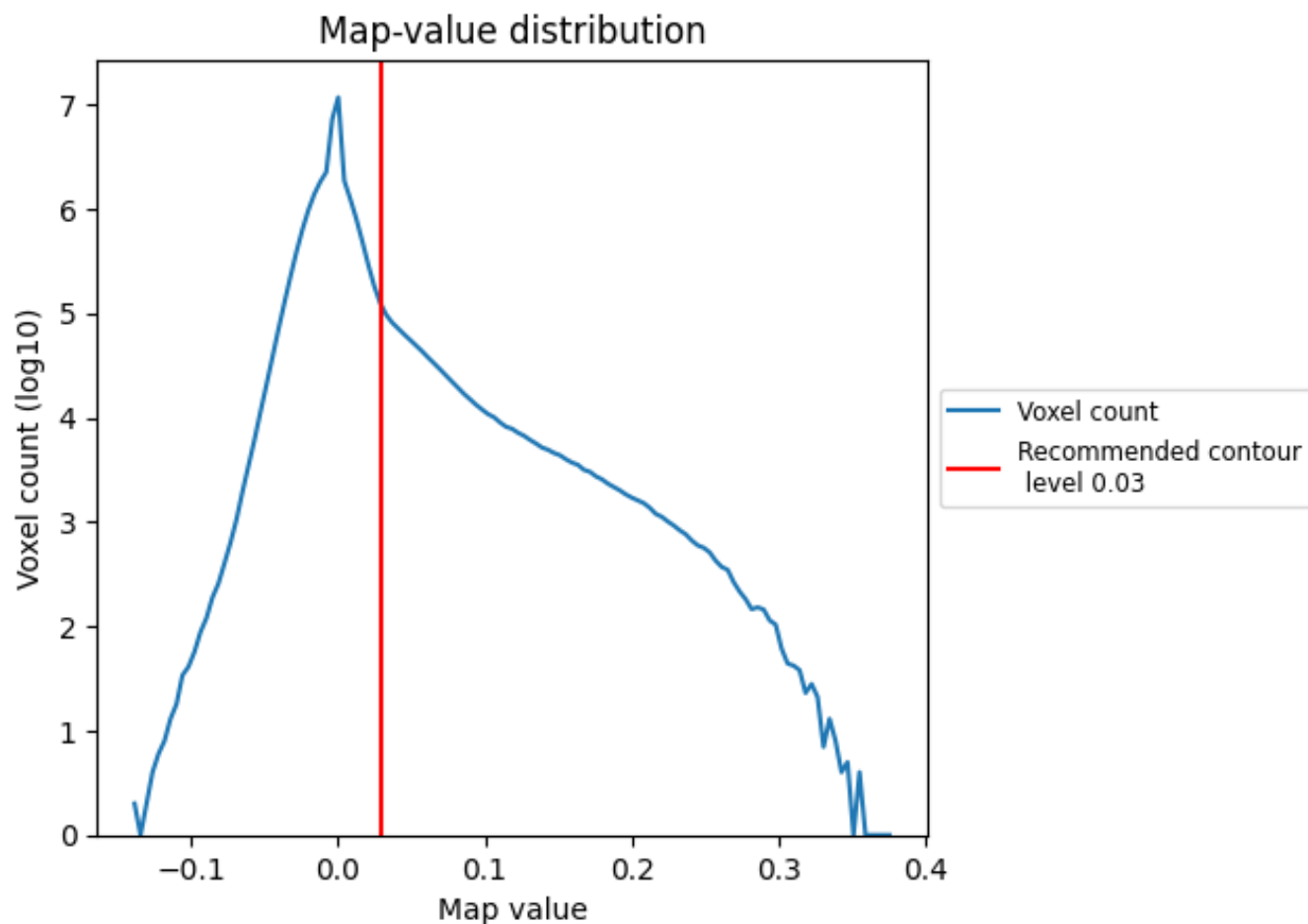
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

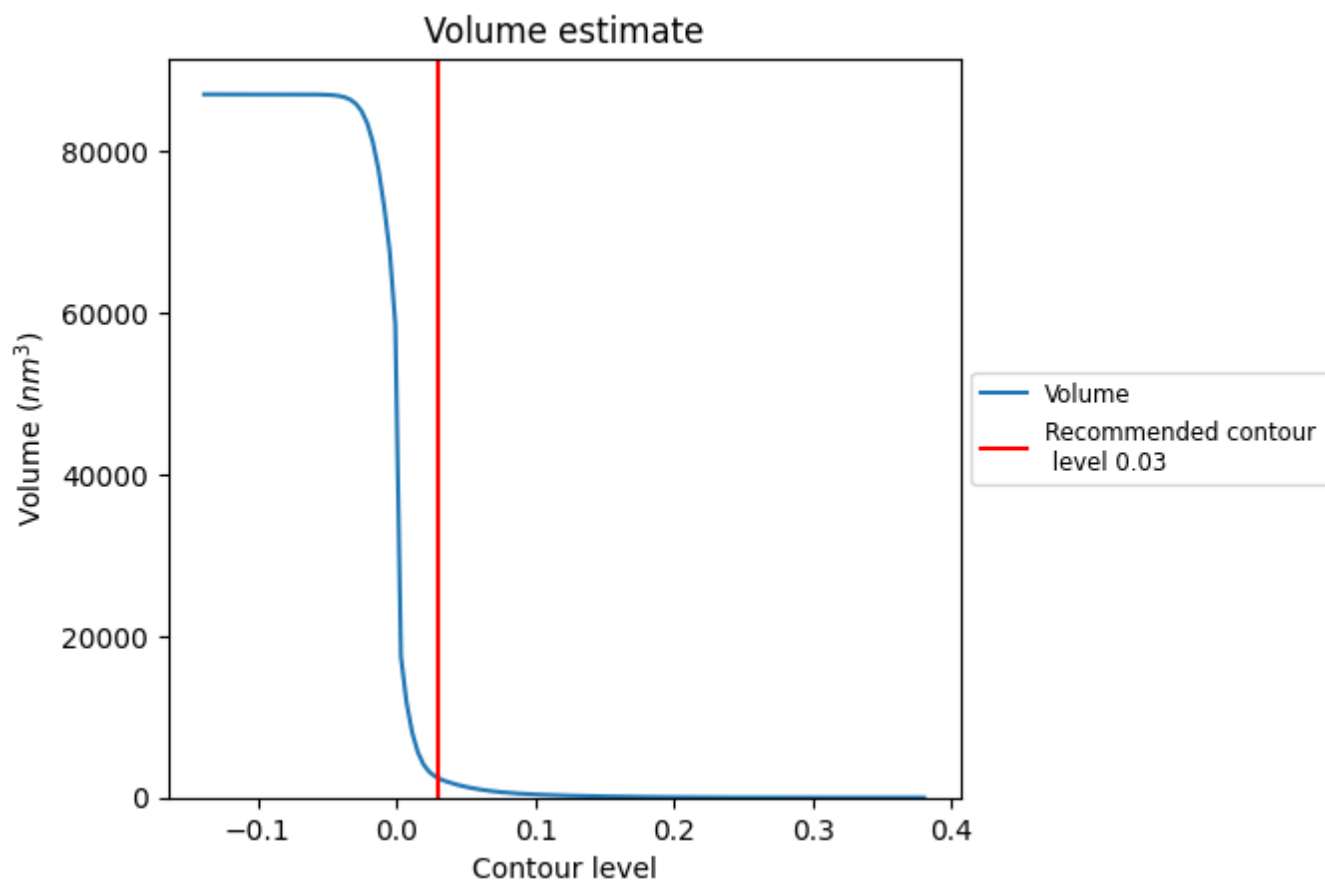
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

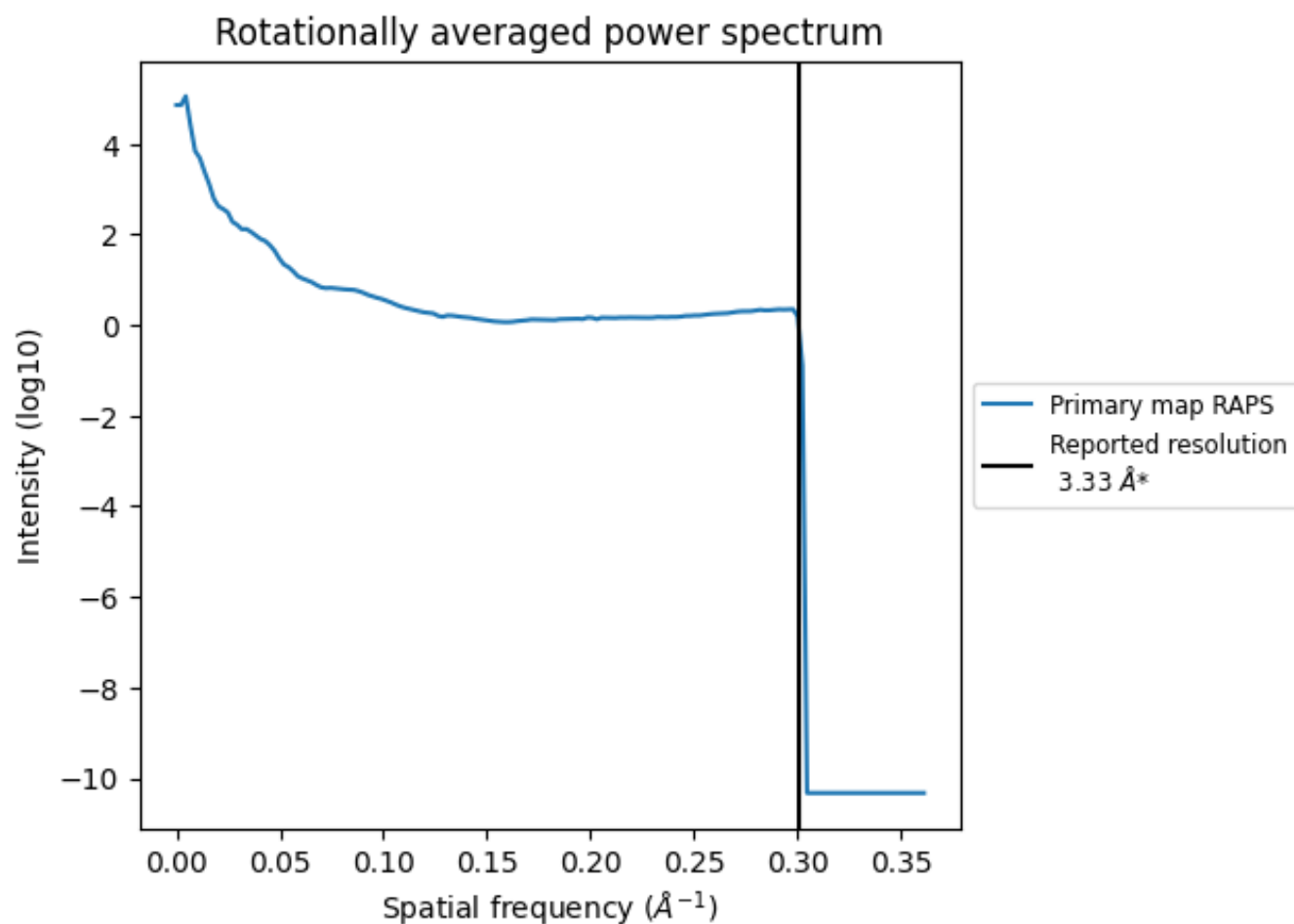
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2415 nm³; this corresponds to an approximate mass of 2182 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 0.300 Å⁻¹

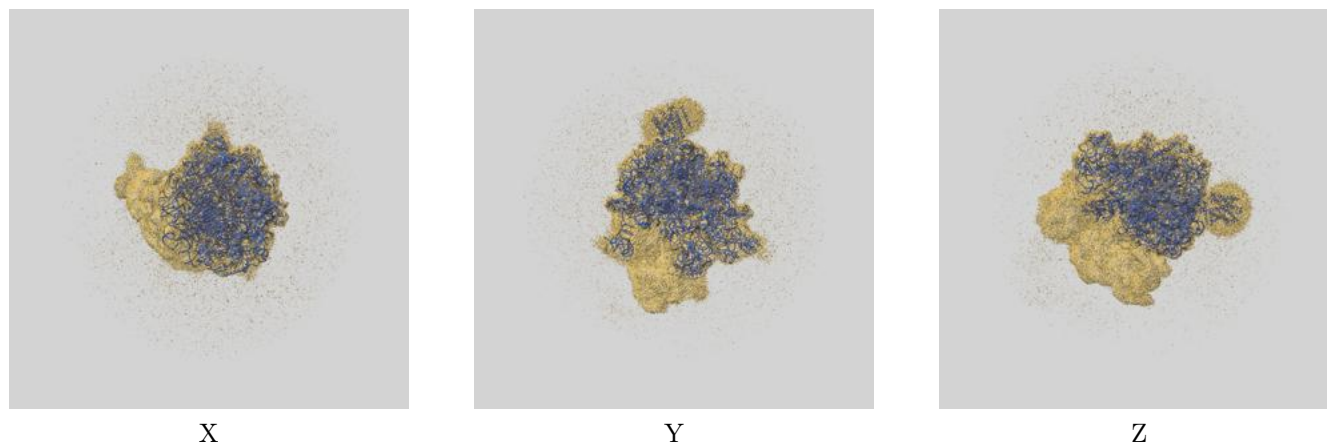
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

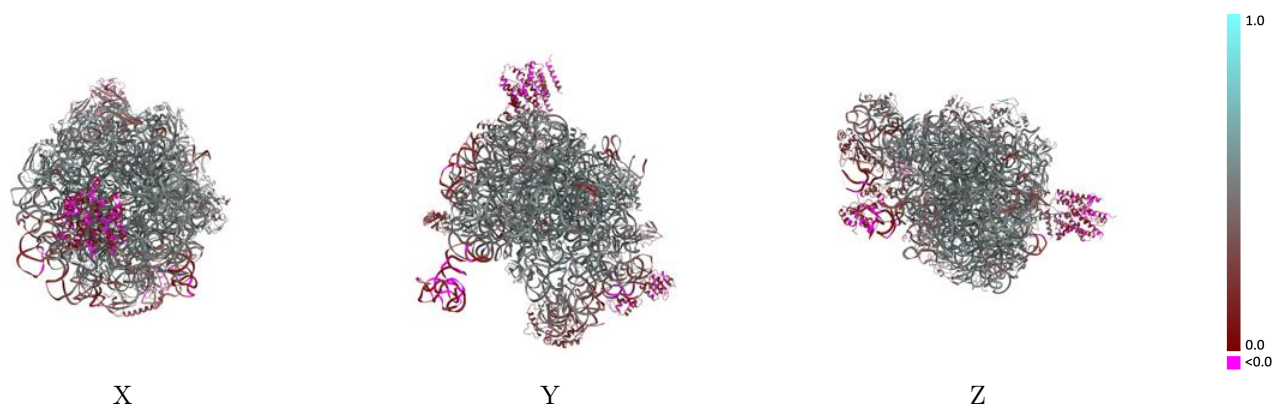
This section contains information regarding the fit between EMDB map EMD-8001 and PDB model 5GAE. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



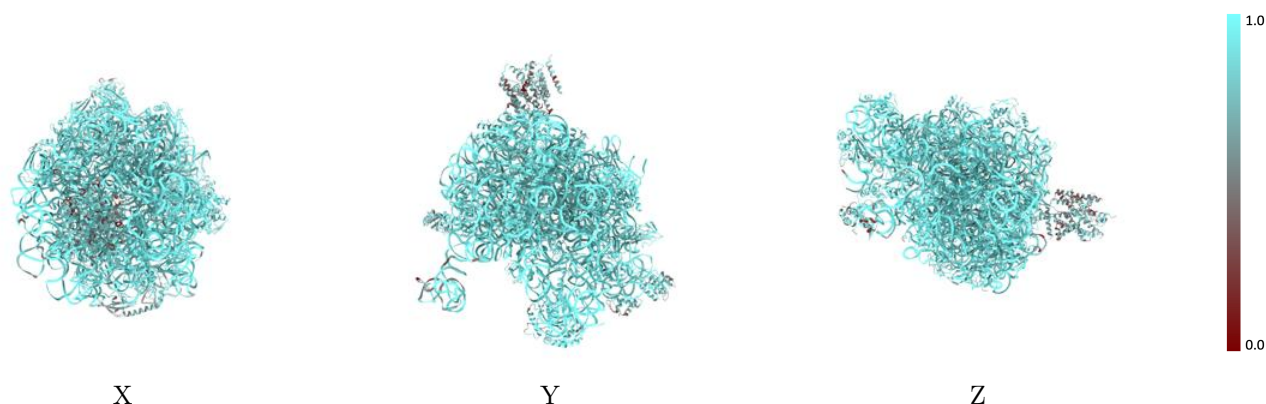
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



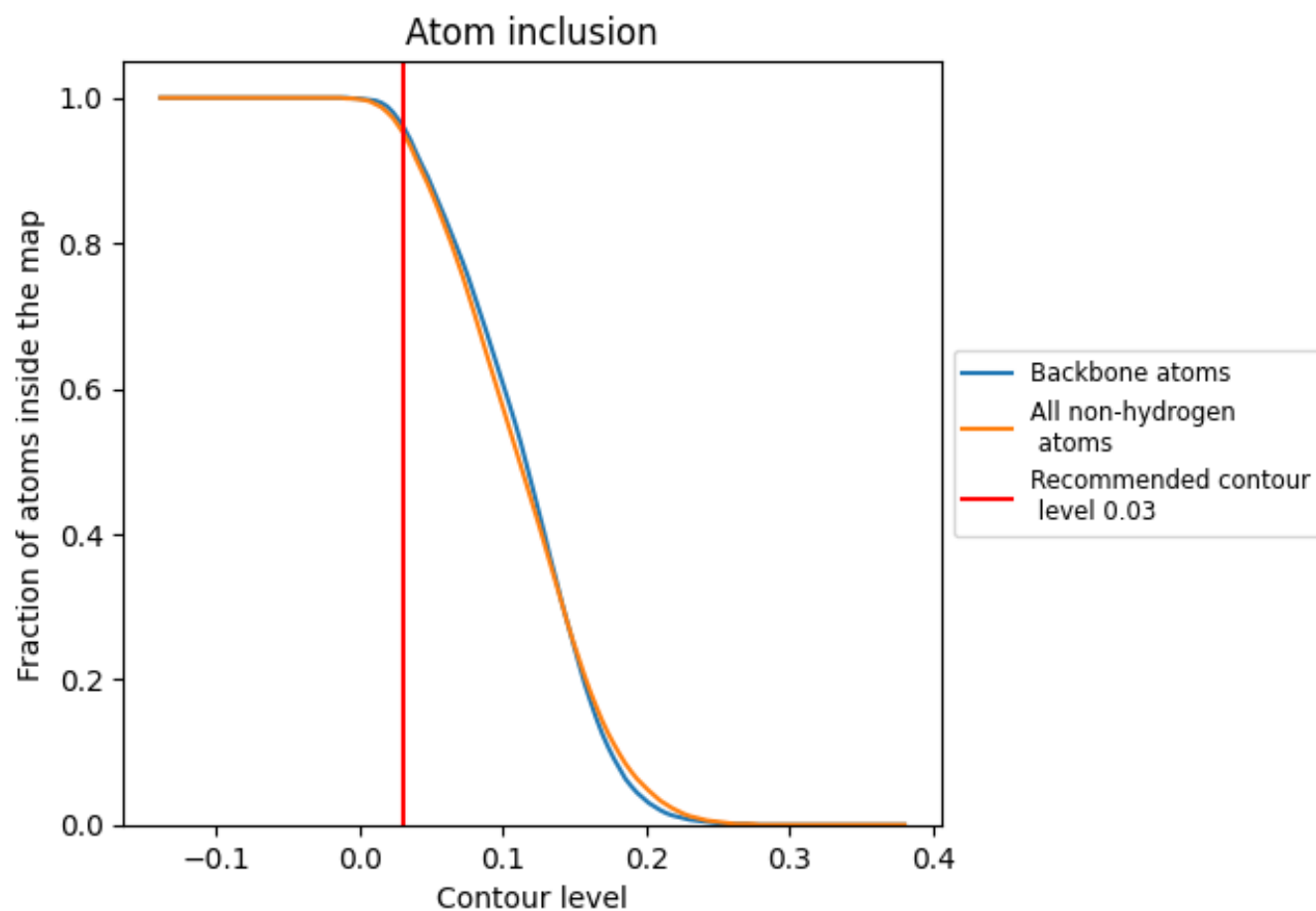
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9530	 0.4410
A	 0.9810	 0.4600
B	 0.9940	 0.4040
C	 0.9090	 0.4990
D	 0.9580	 0.5180
E	 0.9520	 0.4890
F	 0.8910	 0.2540
G	 0.9240	 0.3740
H	 0.7260	 0.2930
I	 0.7720	 0.1130
J	 0.7000	 0.0730
K	 0.9690	 0.5150
L	 0.9210	 0.5120
M	 0.9540	 0.4920
N	 0.9620	 0.5080
O	 0.9560	 0.5100
P	 0.9530	 0.4340
Q	 0.9210	 0.4870
R	 0.9820	 0.5330
S	 0.9400	 0.4950
T	 0.9450	 0.5050
U	 0.9180	 0.4730
V	 0.9350	 0.4520
W	 0.9490	 0.4780
X	 0.9420	 0.5130
Y	 0.9580	 0.4760
Z	 0.9160	 0.4240
a	 0.9470	 0.5010
b	 0.9460	 0.5030
c	 0.9090	 0.4690
d	 0.9660	 0.5390
e	 0.9720	 0.5340
f	 0.9760	 0.4850
g	 0.6790	 0.1190
h	 0.5550	 0.0700



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Chain	Atom inclusion	Q-score
i	 0.6000	 0.0380
x	 0.9680	 0.4800