



Full wwPDB EM Validation Report ⓘ

Jul 6, 2026 – 04:49 PM JST

PDB ID : 9VTG / pdb_00009vtg
EMDB ID : EMD-65327
Title : cryoEM structure of tobacco mosaic virus tRNA-like structure complexed with tobacco 60S
Authors : Lu, G.; Lin, J.
Deposited on : 2025-07-10
Resolution : 3.80 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.dev133
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) : 2.50

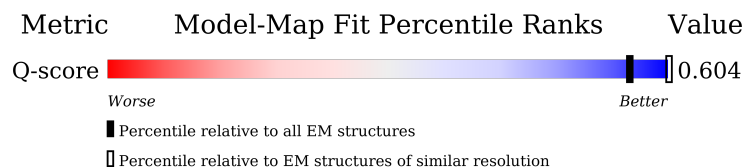
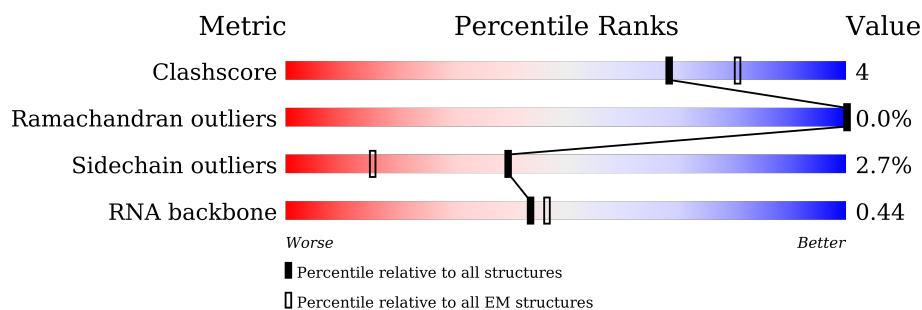
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	LA	217	
2	LB	260	
3	LC	389	

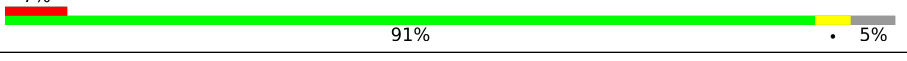
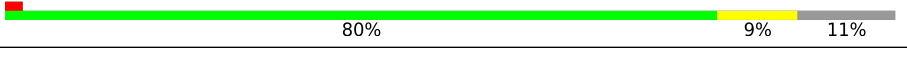
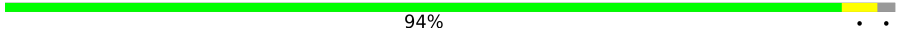
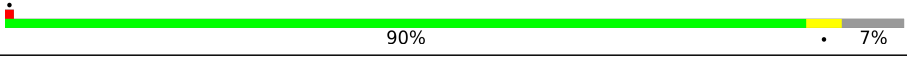
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Mol	Chain	Length	Quality of chain
4	LD	405	
5	LE	181	
6	LF	194	
7	LG	206	
8	LH	140	
9	LI	148	
10	LJ	219	
11	LK	293	
12	LL	175	
13	LM	154	
14	LN	146	
15	LO	123	
16	LP	242	
17	LQ	230	
18	LR	237	
19	LS	200	
20	LT	130	
21	LU	204	
22	LV	187	
23	LW	211	
24	LX	178	
25	LY	164	
26	LZ	108	
27	La	164	
28	Lb	135	

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Mol	Chain	Length	Quality of chain
29	Lc	143	
30	Ld	50	
31	Le	113	
32	Lf	120	
33	Lg	133	
34	Lh	112	
35	Li	120	
36	Lj	110	
37	Lk	95	
38	Ll	69	
39	Lm	51	
40	Ln	128	
41	Lp	105	
42	Lq	77	
43	10	204	
44	12	119	
45	13	163	
46	14	3390	

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 129544 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	215	Total	C	N	O	S	0	0
			1710	1092	300	307	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LA	2	SER	-	insertion	UNP A0A1S3Y379
LA	216	ILE	VAL	conflict	UNP A0A1S3Y379

- Molecule 2 is a protein called 60S ribosomal protein L8-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	245	Total	C	N	O	S	0	0
			1880	1174	381	315	10		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	386	Total	C	N	O	S	0	0
			3107	1983	577	532	15		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LC	200	SER	GLY	conflict	UNP A0A1S3ZLI9
LC	308	GLU	ASP	conflict	UNP A0A1S3ZLI9
LC	381	GLU	GLN	conflict	UNP A0A1S3ZLI9

- Molecule 4 is a protein called 60S ribosomal protein L4-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LD	398	Total	C	N	O	S	0	0
			3099	1958	583	548	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LD	27	VAL	LEU	conflict	UNP A0A1S4BWA4

- Molecule 5 is a protein called 60S ribosomal protein L11-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LE	169	Total	C	N	O	S	0	0
			1356	859	251	239	7		

- Molecule 6 is a protein called 60S ribosomal protein L9-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	191	Total	C	N	O	S	0	0
			1520	966	274	275	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LF	125	LYS	ARG	conflict	UNP A0A1S4CJ62
LF	191	VAL	ALA	conflict	UNP A0A1S4CJ62

- Molecule 7 is a protein called 60S ribosomal protein L13a-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LG	205	Total	C	N	O	S	0	0
			1644	1046	320	270	8		

- Molecule 8 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LH	131	Total	C	N	O	S	0	0
			985	623	183	170	9		

- Molecule 9 is a protein called 60s ribosomal protein l27a-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	147	Total	C	N	O	S	0	0
			1155	735	226	191	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	94	SER	ASN	conflict	UNP A0A1J6IJF4

- Molecule 10 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	209	Total	C	N	O	S	0	0
			1671	1058	329	273	11		

- Molecule 11 is a protein called 60S ribosomal protein L5-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LK	288	Total	C	N	O	S	0	0
			2342	1482	428	427	5		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LK	85	ARG	GLN	conflict	UNP A0A1S3XE16
LK	126	THR	SER	conflict	UNP A0A1S3XE16
LK	150	VAL	ILE	conflict	UNP A0A1S3XE16
LK	218	PHE	TYR	conflict	UNP A0A1S3XE16

- Molecule 12 is a protein called 60S ribosomal protein L17-1 isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	154	Total	C	N	O	S	0	0
			1236	769	245	217	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LL	46	LYS	ARG	conflict	UNP A0A1S4DQP0
LL	168	SER	PRO	conflict	UNP A0A1S4DQP0

- Molecule 13 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	117	Total	C	N	O	S	0	0
			950	609	170	169	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LM	31	PHE	LEU	conflict	UNP Q07761

- Molecule 14 is a protein called 60S ribosomal protein L26-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LN	126	Total	C	N	O	S	0	0
			1023	635	209	176	3		

- Molecule 15 is a protein called 60S ribosomal protein L35-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LO	122	Total	C	N	O	S	0	0
			997	640	191	165	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LO	100	ALA	VAL	conflict	UNP A0A1S3WY31

- Molecule 16 is a protein called 60S ribosomal protein L7-4-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LP	238	Total	C	N	O	S	0	0
			1958	1255	361	338	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LP	7	PRO	LEU	conflict	UNP A0A1U7X2X8
LP	64	ARG	GLN	conflict	UNP A0A1U7X2X8
LP	157	ASP	GLU	conflict	UNP A0A1U7X2X8

- Molecule 17 is a protein called 60S ribosomal protein L6-like isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LQ	207	Total	C	N	O	S	0	0
			1600	1040	285	272	3		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LQ	60	ILE	PHE	conflict	UNP A0A1U7WD54

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Chain	Residue	Modelled	Actual	Comment	Reference
LQ	97	LYS	ARG	conflict	UNP A0A1U7WD54
LQ	144	VAL	ILE	conflict	UNP A0A1U7WD54
LQ	148	SER	ASN	conflict	UNP A0A1U7WD54
LQ	152	PHE	ILE	conflict	UNP A0A1U7WD54
LQ	187	GLU	GLY	conflict	UNP A0A1U7WD54

- Molecule 18 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LR	233	Total	C	N	O	S	0	0
			1874	1206	343	318	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LR	108	ILE	VAL	conflict	UNP A0A1U7XNI3
LR	110	LYS	ARG	conflict	UNP A0A1U7XNI3

- Molecule 19 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	200	Total	C	N	O	S	0	0
			1608	1010	324	270	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LS	139	VAL	ALA	conflict	UNP A0A1S4CSN1
LS	163	GLU	ASP	conflict	UNP A0A1S4CSN1

- Molecule 20 is a protein called 60S ribosomal protein L14-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LT	129	Total	C	N	O	S	0	0
			1046	673	195	175	3		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LT	82	THR	ASN	conflict	UNP A0A1U7UYX7
LT	86	ASN	SER	conflict	UNP A0A1U7UYX7

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Chain	Residue	Modelled	Actual	Comment	Reference
LT	101	ALA	SER	conflict	UNP A0A1U7UYX7

- Molecule 21 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	203	Total	C	N	O	S	0	0
			1701	1072	350	276	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	186	Total	C	N	O	S	0	0
			1462	931	283	245	3		

- Molecule 23 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LW	182	Total	C	N	O	S	0	0
			1519	940	323	247	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	190	VAL	ALA	conflict	UNP A0A1S4A7M5
LW	195	SER	PRO	conflict	UNP A0A1S4A7M5
LW	197	THR	ALA	conflict	UNP A0A1S4A7M5
LW	198	PRO	SER	conflict	UNP A0A1S4A7M5

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LX	177	Total	C	N	O	S	0	0
			1505	969	277	251	8		

- Molecule 25 is a protein called 60S ribosomal protein L21-1-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	163	Total	C	N	O	S	0	0
			1306	823	255	224	4		

- Molecule 26 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LZ	98	Total	C	N	O	S	0	0
			799	510	140	147	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LZ	61	ALA	THR	conflict	UNP A0A1S4BSU3
LZ	63	ALA	THR	conflict	UNP A0A1S4BSU3

- Molecule 27 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	La	62	Total	C	N	O	S	0	0
			526	341	101	81	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lb	134	Total	C	N	O	S	0	0
			1091	704	203	182	2		

- Molecule 29 is a protein called 60S ribosomal protein L28-1-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	142	Total	C	N	O	S	0	0
			1107	700	206	199	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lc	53	TYR	ASN	conflict	UNP A0A1U7WYY1
Lc	98	ALA	THR	conflict	UNP A0A1U7WYY1

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ld	49	Total	C	N	O	S	0	0
			407	249	87	70	1		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Le	97	Total	C	N	O	S	0	0
			745	475	130	135	5		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	108	Total	C	N	O	S	0	0
			875	549	168	156	2		

- Molecule 33 is a protein called 60S ribosomal protein L32-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lg	126	Total	C	N	O	S	0	0
			1034	653	206	170	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lg	9	THR	LYS	conflict	UNP A0A1U7YAK1

- Molecule 34 is a protein called 60S ribosomal protein L35a-3-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lh	103	Total	C	N	O	S	0	0
			836	534	155	142	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lh	57	VAL	ILE	conflict	UNP A0A1S4AHL7
Lh	91	LYS	ASN	conflict	UNP A0A1S4AHL7

- Molecule 35 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	114	Total	C	N	O	S	0	0
			926	579	193	153	1		

- Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	98	Total	C	N	O	S	0	0
			784	491	162	129	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lj	45	SER	GLY	conflict	UNP A0A1U7VXX3

- Molecule 37 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lk	86	Total	C	N	O	S	0	0
			701	429	155	112	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ll	68	Total	C	N	O	S	0	0
			558	358	99	98	3		

- Molecule 39 is a protein called 60S ribosomal protein L39-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lm	50	Total	C	N	O	S	0	0
			448	286	96	64	2		

- Molecule 40 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ln	51	Total	C	N	O	S	0	0
			420	261	88	65	6		

- Molecule 41 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lp	98	Total	C	N	O	S	0	0
			785	493	157	131	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lp	17	GLY	CYS	conflict	UNP A0A1U7YPT7

- Molecule 42 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lq	76	Total	C	N	O	S	0	0
			593	377	109	102	5		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lq	8	THR	ALA	conflict	UNP A0A1U7XSD1
Lq	35	ASN	SER	conflict	UNP A0A1U7XSD1
Lq	59	TYR	ASP	conflict	UNP A0A1U7XSD1
Lq	62	ASN	LYS	conflict	UNP A0A1U7XSD1
Lq	65	VAL	ALA	conflict	UNP A0A1U7XSD1
Lq	76	ASP	ALA	conflict	UNP A0A1U7XSD1

- Molecule 43 is a RNA chain called RNA (204-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
43	10	158	Total	C	N	O	P	0	0
			3359	1500	590	1111	158		

- Molecule 44 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	12	119	Total	C	N	O	P	0	0
			2538	1133	457	829	119		

- Molecule 45 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	13	163	Total	C	N	O	P	0	0
			3478	1553	628	1134	163		

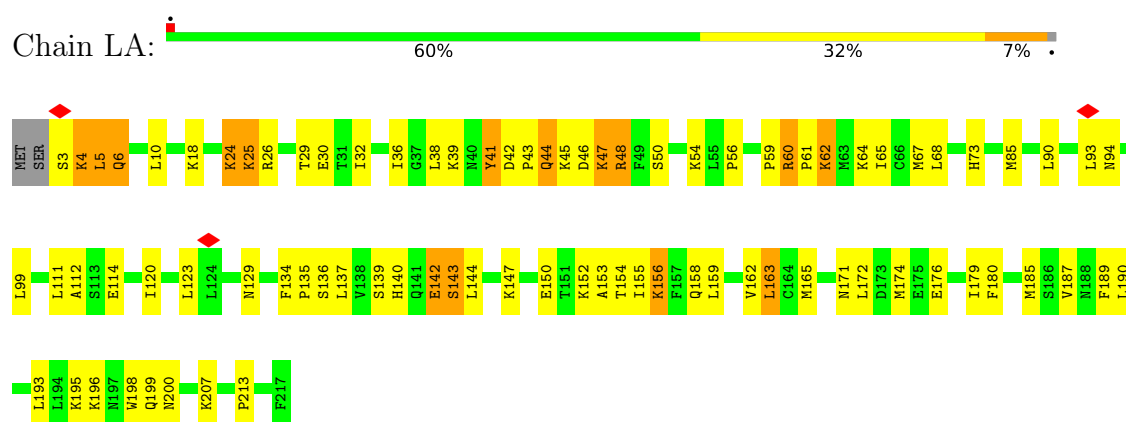
- Molecule 46 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	14	3142	Total	C	N	O	P	0	0
			67280	30009	12243	21886	3142		

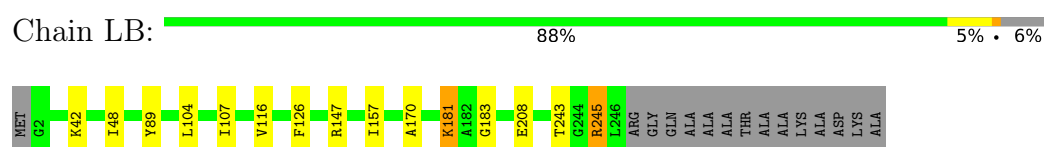
3 Residue-property plots

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.

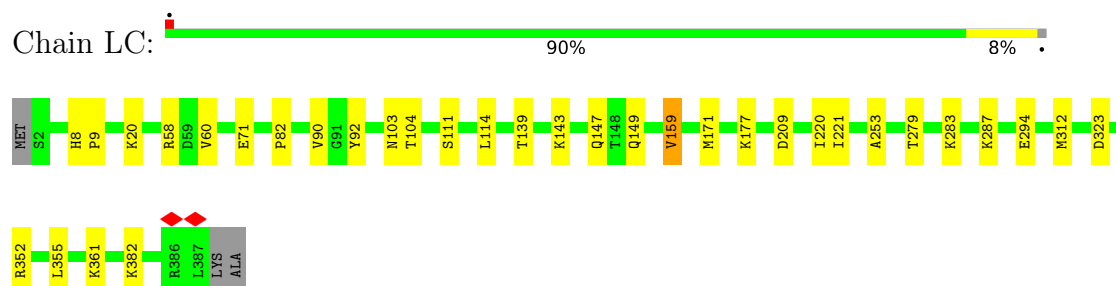
• Molecule 1: Ribosomal protein



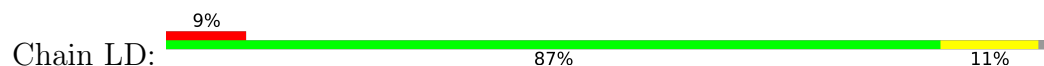
• Molecule 2: 60S ribosomal protein L8-like

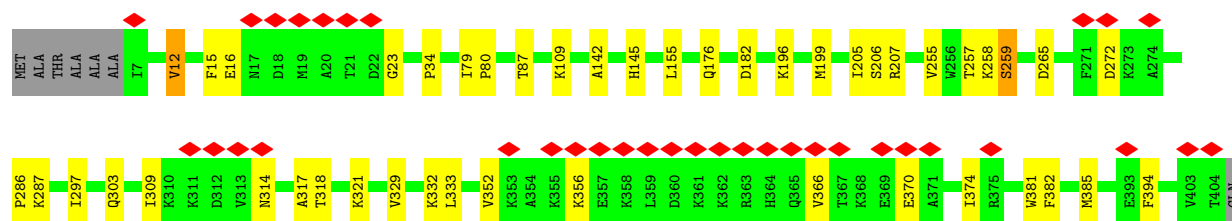


• Molecule 3: 60S ribosomal protein L3

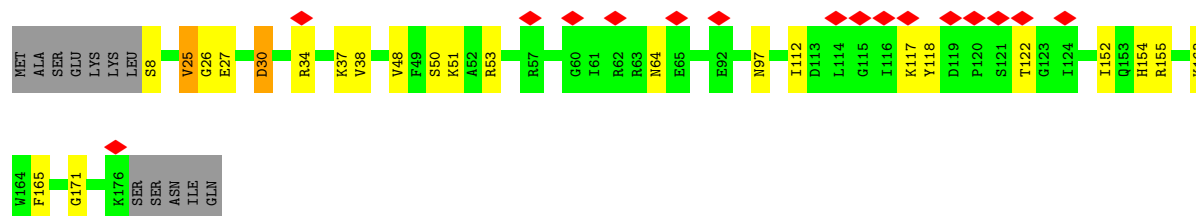
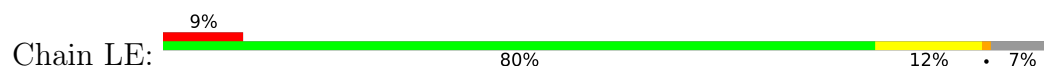


• Molecule 4: 60S ribosomal protein L4-like

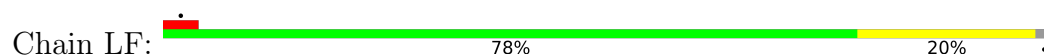




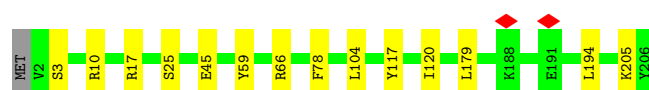
• Molecule 5: 60S ribosomal protein L11-1



• Molecule 6: 60S ribosomal protein L9-1



• Molecule 7: 60S ribosomal protein L13a-4



• Molecule 8: 60S ribosomal protein L23

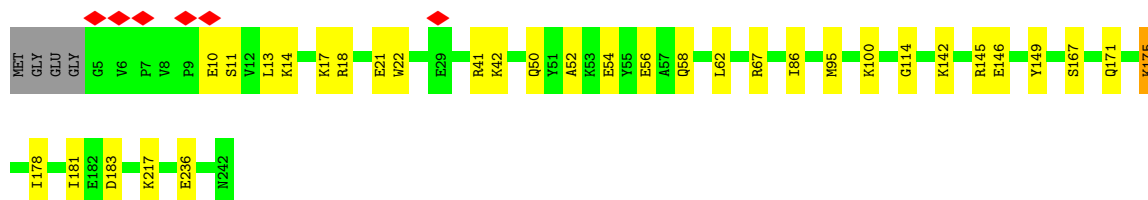
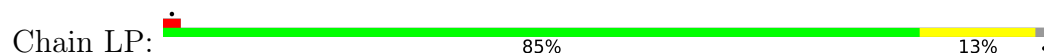


• Molecule 9: 60s ribosomal protein l27a-3

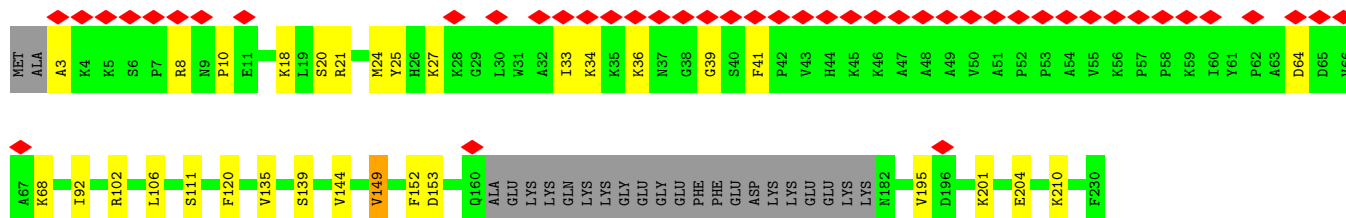
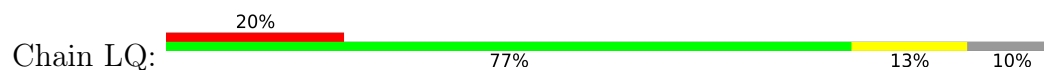




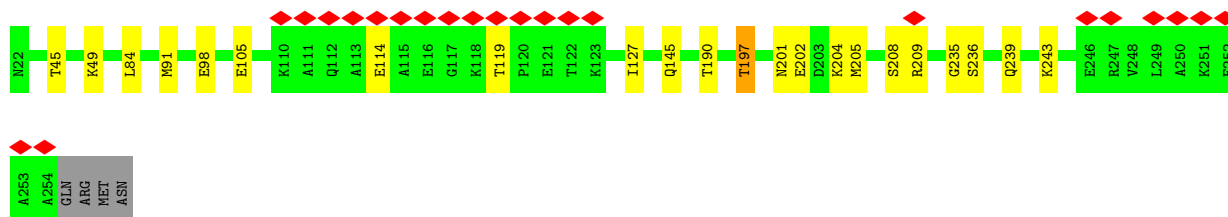
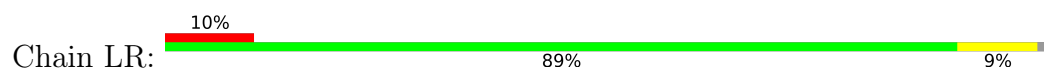
- Molecule 16: 60S ribosomal protein L7-4-like



- Molecule 17: 60S ribosomal protein L6-like isoform X1



- Molecule 18: 60S ribosomal protein L7a



- Molecule 19: 60S ribosomal protein L13

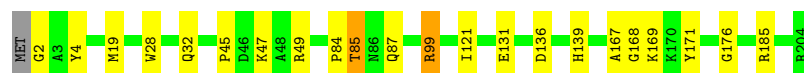


- Molecule 20: 60S ribosomal protein L14-1





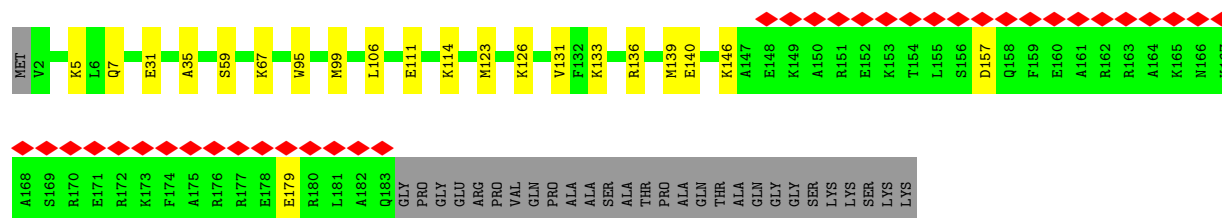
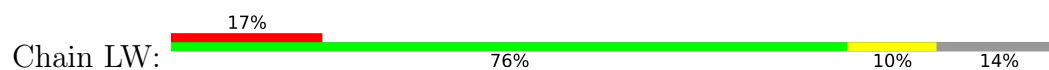
- Molecule 21: Ribosomal protein L15



- Molecule 22: 60S ribosomal protein L18-2



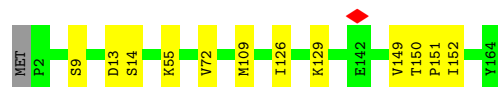
- Molecule 23: Ribosomal protein L19



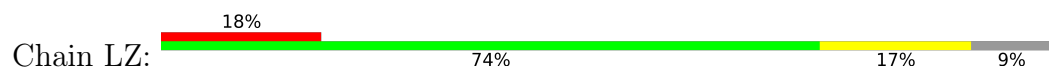
- Molecule 24: 60S ribosomal protein L18a



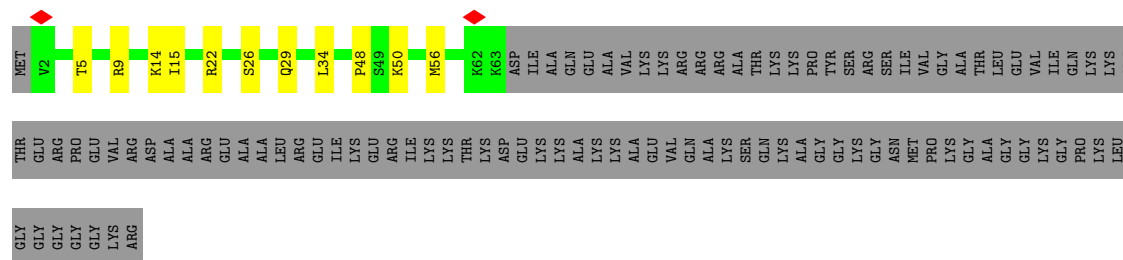
- Molecule 25: 60S ribosomal protein L21-1-like



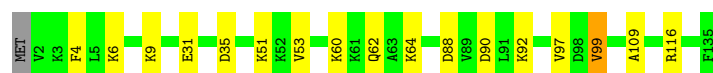
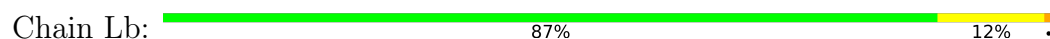
- Molecule 26: Large ribosomal subunit protein eL22



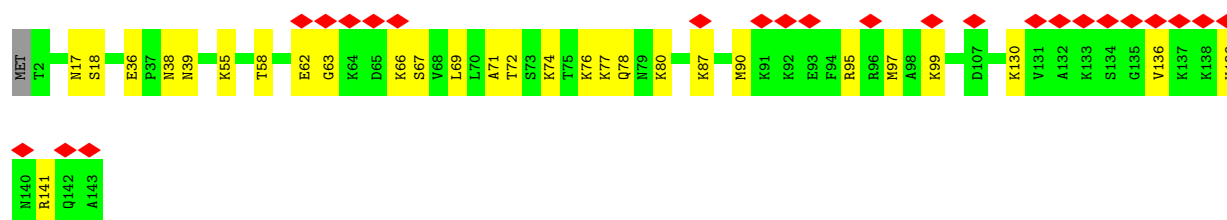
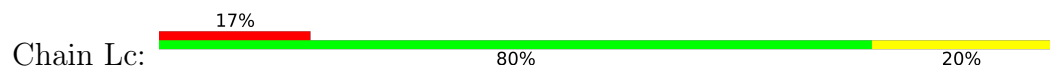
- Molecule 27: 60S ribosomal protein L24



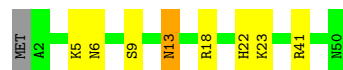
- Molecule 28: 60S ribosomal protein L27



- Molecule 29: 60S ribosomal protein L28-1-like

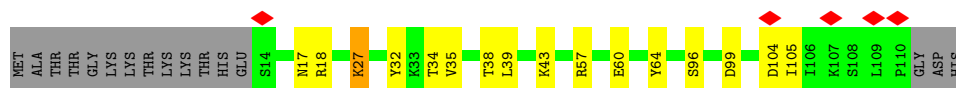


- Molecule 30: 60S ribosomal protein L29

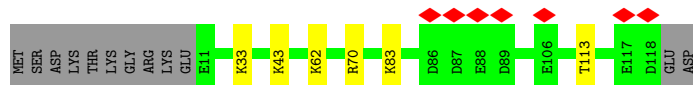
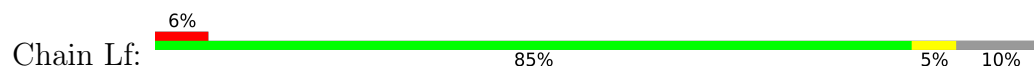


- Molecule 31: 60S ribosomal protein L30

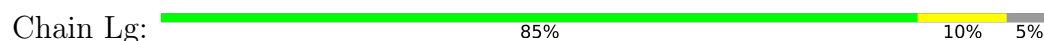




- Molecule 32: 60S ribosomal protein L31



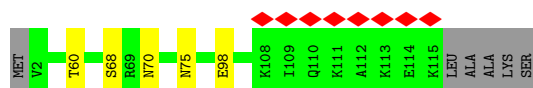
- Molecule 33: 60S ribosomal protein L32-1



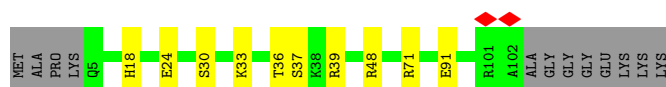
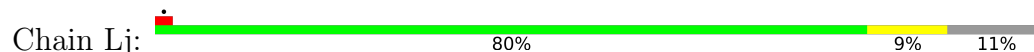
- Molecule 34: 60S ribosomal protein L35a-3-like



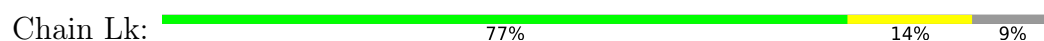
- Molecule 35: Large ribosomal subunit protein eL34



- Molecule 36: 60S ribosomal protein L36

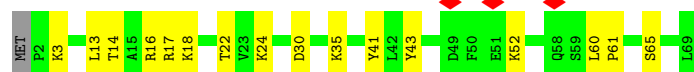


- Molecule 37: Ribosomal protein L37



- Molecule 38: 60S ribosomal protein L38

Chain Ll:



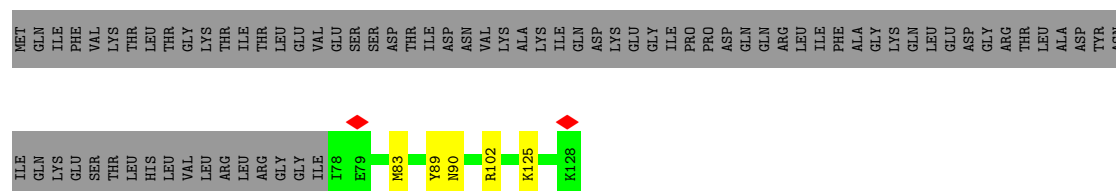
- Molecule 39: 60S ribosomal protein L39-3

Chain Lm: 94%

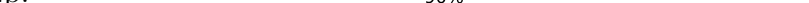


- Molecule 40: Ubiquitin-60S ribosomal protein L40

Chain Ln: 36% 4% 60%

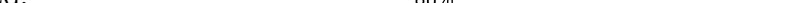


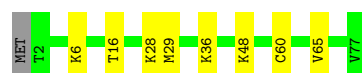
- Molecule 41: 60S ribosomal protein L44

Chain Lp:  90% . 7%

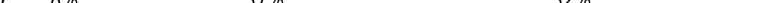


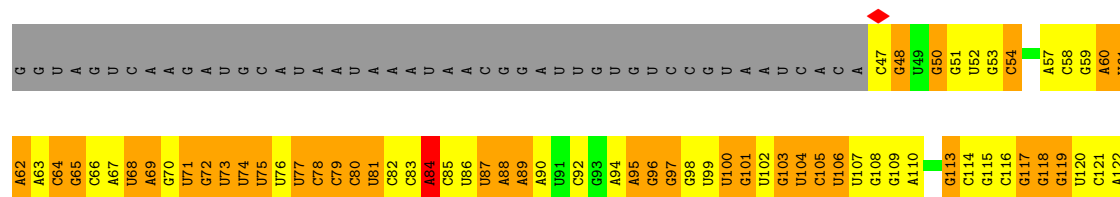
- Molecule 42: 60S ribosomal protein L37a

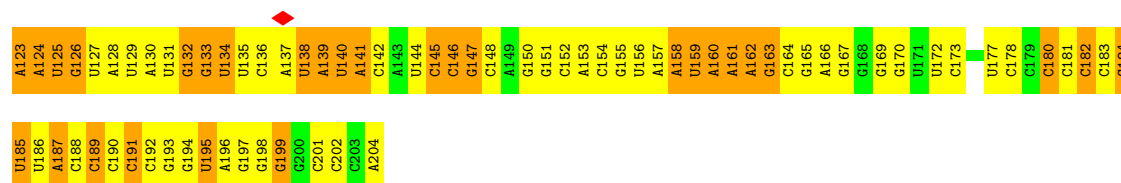
Chain Lq:  88% 10%



- Molecule 43: RNA (204-MER)

Chain 10: 





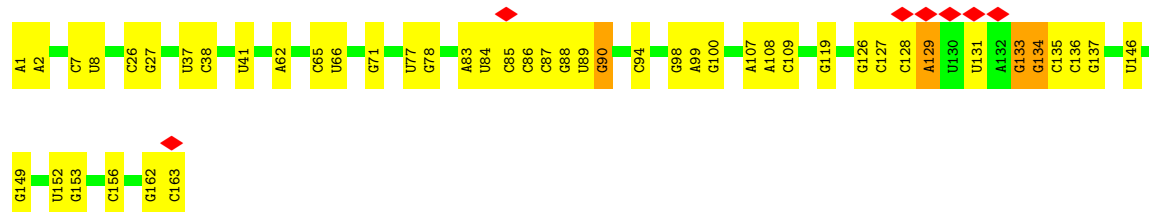
• Molecule 44: 5S rRNA

Chain 12: 85% 12% .



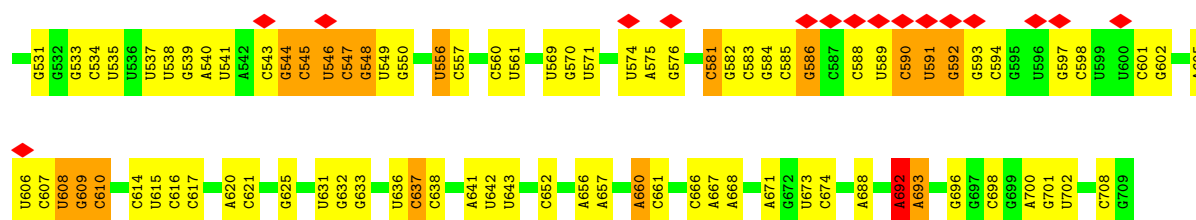
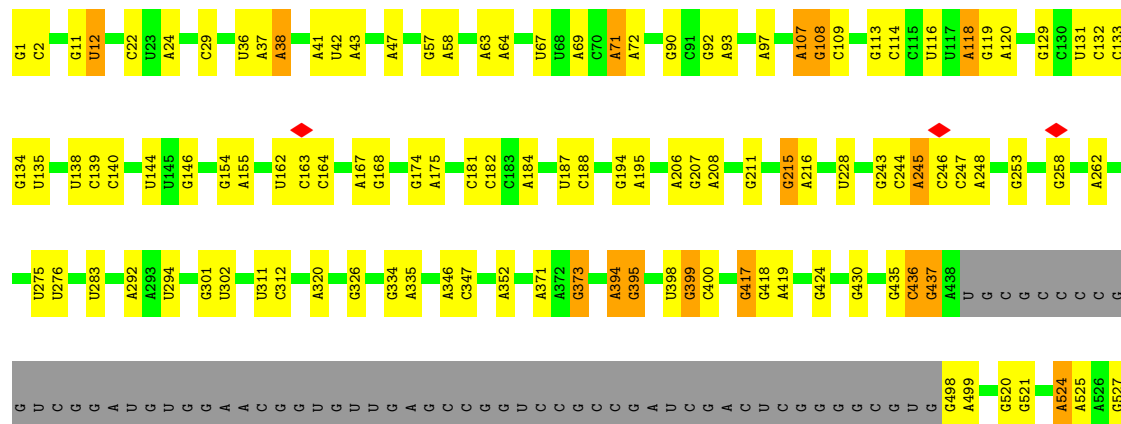
• Molecule 45: 5.8S rRNA

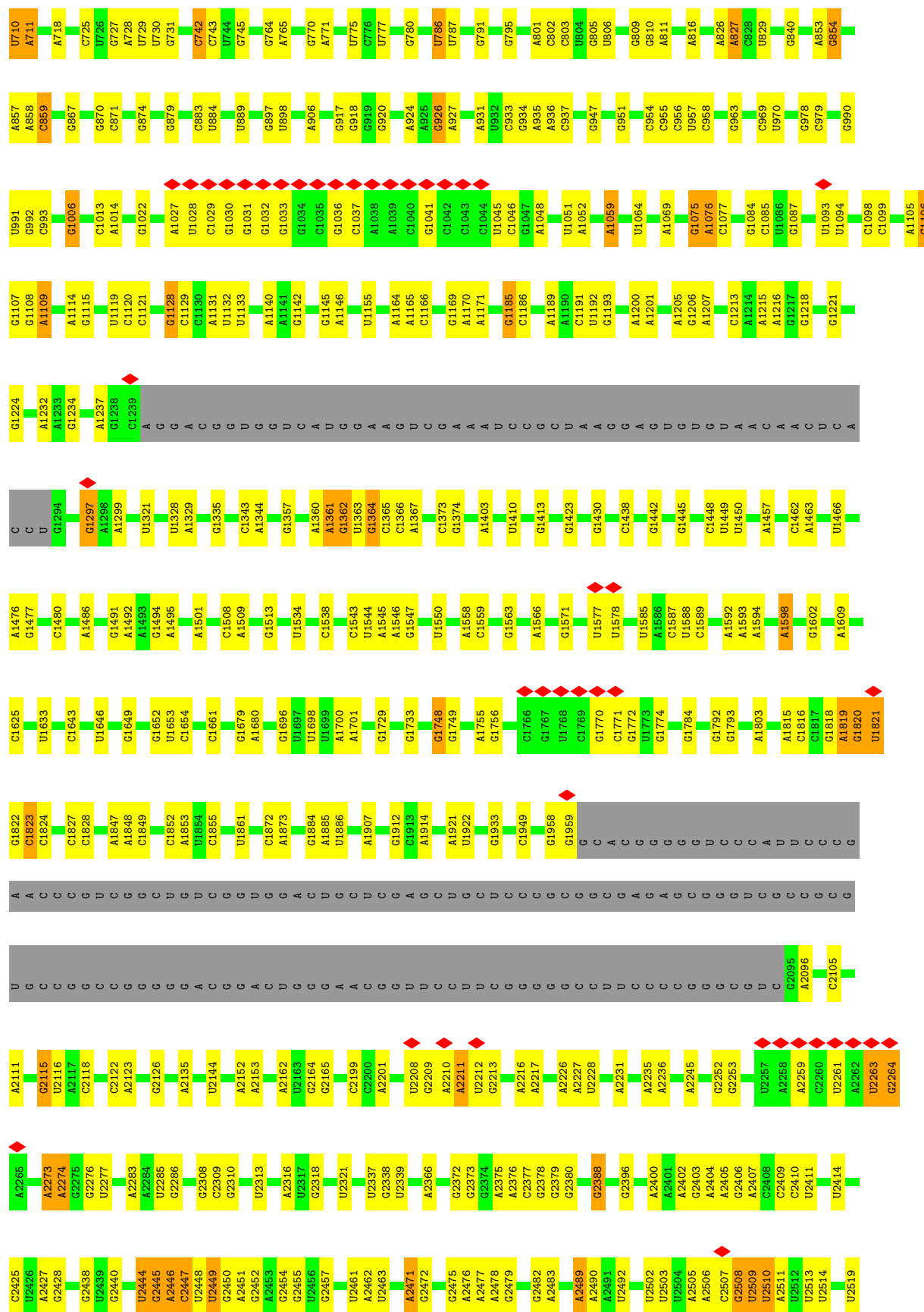
Chain 13: 71% 27% .



• Molecule 46: 25S rRNA

Chain 14: 67% 22% 7% .







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53930	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	1.904	Depositor
Minimum map value	-0.681	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	460.32, 460.32, 460.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.959, 0.959, 0.959	Depositor

5 Model quality

5.1 Standard geometry

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	LA	0.75	0/1735	1.11	2/2318 (0.1%)
2	LB	0.36	0/1924	0.53	0/2585
3	LC	0.42	0/3175	0.61	0/4253
4	LD	0.37	0/3161	0.60	0/4263
5	LE	0.30	0/1378	0.52	0/1845
6	LF	0.38	0/1539	0.55	0/2058
7	LG	0.28	0/1673	0.42	0/2241
8	LH	0.27	0/1001	0.47	0/1345
9	LI	0.43	0/1183	0.65	2/1581 (0.1%)
10	LJ	0.25	0/1707	0.39	0/2283
11	LK	0.35	0/2387	0.53	0/3201
12	LL	0.36	0/1261	0.59	0/1693
13	LM	0.27	0/965	0.45	0/1295
14	LN	0.35	0/1037	0.54	0/1385
15	LO	0.24	0/1007	0.37	0/1340
16	LP	0.32	0/1993	0.50	0/2672
17	LQ	0.19	0/1634	0.37	0/2196
18	LR	0.23	0/1907	0.36	0/2555
19	LS	0.31	0/1638	0.47	0/2198
20	LT	0.25	0/1059	0.40	0/1415
21	LU	0.32	0/1740	0.49	0/2333
22	LV	0.29	0/1487	0.45	0/1989
23	LW	0.32	0/1538	0.49	0/2031
24	LX	0.33	0/1544	0.44	0/2071
25	LY	0.29	0/1331	0.44	0/1784
26	LZ	0.21	0/810	0.45	0/1085
27	La	0.23	0/539	0.39	0/716
28	Lb	0.30	0/1110	0.43	0/1482
29	Lc	0.29	0/1122	0.49	0/1503
30	Ld	0.57	0/417	0.82	0/555
31	Le	0.27	0/757	0.42	0/1018
32	Lf	0.27	0/885	0.37	0/1184
33	Lg	0.37	0/1051	0.56	0/1407
34	Lh	0.28	0/856	0.43	0/1149

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Li	0.27	0/939	0.42	0/1251
36	Lj	0.24	0/793	0.44	0/1050
37	Lk	0.36	0/714	0.60	0/949
38	Ll	0.34	0/566	0.49	0/752
39	Lm	0.29	0/460	0.41	0/611
40	Ln	0.17	0/426	0.36	0/561
41	Lp	0.30	0/799	0.43	0/1055
42	Lq	0.40	0/603	0.55	0/802
43	10	0.67	0/3752	1.05	1/5844 (0.0%)
44	12	0.31	0/2837	0.35	0/4420
45	13	0.35	0/3889	0.41	0/6060
46	14	0.42	0/75291	0.53	3/117423 (0.0%)
All	All	0.40	0/139620	0.54	8/205807 (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	LA	0	3
2	LB	0	1
3	LC	0	2
4	LD	0	1
14	LN	0	1
16	LP	0	1
24	LX	0	1
30	Ld	0	1
All	All	0	11

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	LI	15	VAL	N-CA-CB	-6.85	102.91	110.51
9	LI	15	VAL	N-CA-C	6.83	117.53	110.36
46	14	692	A	C3'-C2'-C1'	-6.68	94.82	101.50
46	14	883	C	C2'-C3'-O3'	-6.52	103.93	113.70
46	14	926	G	C2'-C3'-O3'	-5.61	105.29	113.70
43	10	84	A	C4'-C3'-C2'	-5.55	97.05	102.60
1	LA	152	LYS	CA-C-N	-5.12	116.17	123.03
1	LA	152	LYS	C-N-CA	-5.12	116.17	123.03

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	LA	26	ARG	Sidechain
1	LA	48	ARG	Sidechain
1	LA	60	ARG	Sidechain
2	LB	245	ARG	Sidechain
3	LC	352	ARG	Sidechain
3	LC	58	ARG	Sidechain
4	LD	207	ARG	Sidechain
14	LN	59	ARG	Sidechain
16	LP	41	ARG	Sidechain
24	LX	28	ARG	Sidechain
30	Ld	18	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LA	1710	0	1812	55	0
2	LB	1880	0	1915	9	0
3	LC	3107	0	3232	18	0
4	LD	3099	0	3229	30	0
5	LE	1356	0	1394	17	0
6	LF	1520	0	1614	24	0
7	LG	1644	0	1773	8	0
8	LH	985	0	1046	6	0
9	LI	1155	0	1197	8	0
10	LJ	1671	0	1731	15	0
11	LK	2342	0	2379	20	0
12	LL	1236	0	1262	5	0
13	LM	950	0	1029	12	0
14	LN	1023	0	1105	7	0
15	LO	997	0	1136	8	0
16	LP	1958	0	2057	20	0
17	LQ	1600	0	1731	24	0
18	LR	1874	0	2030	10	0
19	LS	1608	0	1697	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	LT	1046	0	1144	12	0
21	LU	1701	0	1771	14	0
22	LV	1462	0	1581	5	0
23	LW	1519	0	1630	10	0
24	LX	1505	0	1557	11	0
25	LY	1306	0	1367	8	0
26	LZ	799	0	836	11	0
27	La	526	0	554	10	0
28	Lb	1091	0	1171	8	0
29	Lc	1107	0	1182	19	0
30	Ld	407	0	393	4	0
31	Le	745	0	783	10	0
32	Lf	875	0	934	4	0
33	Lg	1034	0	1110	8	0
34	Lh	836	0	865	4	0
35	Li	926	0	1013	3	0
36	Lj	784	0	871	6	0
37	Lk	701	0	729	10	0
38	Ll	558	0	604	9	0
39	Lm	448	0	480	1	0
40	Ln	420	0	461	5	0
41	Lp	785	0	844	2	0
42	Lq	593	0	618	6	0
43	10	3359	0	1699	98	0
44	12	2538	0	1286	6	0
45	13	3478	0	1761	17	0
46	14	67280	0	33921	282	0
All	All	129544	0	94534	802	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 4.

All (802) 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:LA:4:LYS:NZ	1:LA:198:TRP:HB3	1.76	1.00
1:LA:39:LYS:HE3	1:LA:199:GLN:O	1.70	0.92
25:LY:129:LYS:HB3	46:14:1109:A:H5'	1.51	0.91
26:LZ:39:LEU:HD23	26:LZ:69:ILE:HD12	1.54	0.86
1:LA:171:ASN:OD1	1:LA:174:MET:HG3	1.74	0.86
1:LA:36:ILE:HG21	1:LA:190:LEU:HD21	1.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:2445:G:H1	46:14:2510:U:H3	1.25	0.84
43:10:74:U:H2'	43:10:75:U:H2'	1.60	0.83
46:14:1031:G:H1	46:14:1045:U:H3	1.26	0.81
1:LA:4:LYS:HZ2	1:LA:198:TRP:HB3	1.44	0.80
46:14:498:G:H2'	46:14:499:A:H8	1.46	0.79
43:10:70:G:H1'	43:10:88:A:H62	1.46	0.79
4:LD:303:GLN:HG3	16:LP:18:ARG:HH12	1.47	0.78
4:LD:12:VAL:HG13	4:LD:23:GLY:HA2	1.66	0.78
22:LV:36:LEU:O	22:LV:40:THR:HB	1.85	0.77
17:LQ:24:MET:HE2	17:LQ:24:MET:HA	1.67	0.76
46:14:424:G:H22	46:14:643:U:H3	1.31	0.76
3:LC:92:TYR:HB2	3:LC:159:VAL:HG13	1.67	0.75
4:LD:317:ALA:HB2	46:14:1373:C:H5''	1.69	0.75
43:10:60:A:H5''	43:10:61:U:H2'	1.67	0.75
46:14:3208:C:H4'	46:14:3209:G:H5'	1.68	0.74
43:10:70:G:H2'	43:10:71:U:C6	2.22	0.74
1:LA:4:LYS:HG3	1:LA:198:TRP:CG	2.24	0.73
29:Lc:90:MET:HE2	29:Lc:97:MET:HG2	1.71	0.72
43:10:80:C:H3'	43:10:81:U:H6	1.55	0.72
43:10:71:U:H1'	43:10:89:A:H62	1.55	0.71
33:Lg:103:THR:HG22	33:Lg:126:ARG:HB3	1.73	0.70
46:14:3225:C:H2'	46:14:3226:A:H8	1.57	0.69
11:LK:93:THR:HG22	11:LK:157:ARG:NH1	2.08	0.69
3:LC:103:ASN:HD21	3:LC:149:GLN:HG2	1.57	0.69
17:LQ:68:LYS:H	17:LQ:68:LYS:HD2	1.57	0.69
1:LA:36:ILE:HD13	1:LA:190:LEU:HD22	1.75	0.69
1:LA:39:LYS:CE	1:LA:199:GLN:O	2.39	0.68
19:LS:37:ARG:NH2	46:14:696:G:OP1	2.26	0.68
23:LW:67:LYS:NZ	46:14:2105:C:OP1	2.24	0.68
23:LW:123:MET:HE2	23:LW:123:MET:HA	1.75	0.68
37:Lk:46:LYS:NZ	46:14:22:C:OP1	2.26	0.68
12:LL:57:ALA:HB3	12:LL:73:VAL:HG13	1.76	0.67
1:LA:120:ILE:HD13	1:LA:135:PRO:HG2	1.75	0.67
1:LA:114:GLU:HG2	1:LA:137:LEU:HD11	1.75	0.67
43:10:79:C:H2'	43:10:80:C:C6	2.30	0.67
13:LM:93:THR:HG22	13:LM:137:ARG:HG3	1.77	0.67
46:14:764:G:H2'	46:14:765:A:H8	1.60	0.67
27:La:5:THR:HG21	27:La:14:LYS:HG3	1.76	0.66
43:10:152:C:H2'	43:10:153:A:C8	2.29	0.66
43:10:140:U:H2'	43:10:141:A:H8	1.60	0.66
45:13:1:A:O2'	46:14:2999:A:N7	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:520:G:H2'	46:14:521:G:H8	1.60	0.65
1:LA:4:LYS:HZ1	1:LA:198:TRP:HB3	1.61	0.65
29:Lc:69:LEU:HD11	29:Lc:87:LYS:HB2	1.79	0.65
6:LF:141:GLU:N	6:LF:141:GLU:OE1	2.30	0.65
10:LJ:204:GLY:O	44:12:63:U:H3'	1.97	0.65
8:LH:96:MET:HE2	27:La:22:ARG:HD2	1.79	0.64
46:14:537:U:H3	46:14:541:U:H1'	1.61	0.64
43:10:189:C:H2'	43:10:190:C:C6	2.32	0.64
13:LM:145:LEU:O	13:LM:149:ASN:ND2	2.31	0.64
43:10:195:U:C4	43:10:196:A:H1'	2.32	0.64
26:LZ:100:ARG:HD3	26:LZ:116:PHE:HB3	1.80	0.64
41:Lp:6:LYS:HD3	41:Lp:94:GLY:HA3	1.79	0.64
16:LP:217:LYS:NZ	46:14:1169:G:OP1	2.31	0.63
46:14:2273:A:H2'	46:14:2274:A:C8	2.32	0.63
16:LP:50:GLN:NE2	16:LP:54:GLU:OE2	2.25	0.63
3:LC:82:PRO:HG2	3:LC:171:MET:HE2	1.80	0.63
15:LO:55:ALA:O	15:LO:59:THR:HG23	1.99	0.63
45:13:133:G:H2'	45:13:134:G:C8	2.34	0.63
46:14:2216:A:H2'	46:14:2217:A:C8	2.33	0.63
11:LK:89:LYS:HG2	11:LK:90:VAL:HG13	1.79	0.63
4:LD:16:GLU:H	4:LD:176:GLN:NE2	1.97	0.63
6:LF:131:MET:HB3	6:LF:135:VAL:HG13	1.78	0.63
6:LF:97:PHE:HB2	6:LF:145:ASP:HB3	1.81	0.62
18:LR:201:ASN:HA	18:LR:204:LYS:HG3	1.80	0.62
46:14:520:G:H2'	46:14:521:G:C8	2.34	0.62
18:LR:205:MET:HE1	18:LR:209:ARG:HE	1.63	0.62
46:14:1819:A:H2'	46:14:1820:G:C8	2.35	0.62
24:LX:84:GLN:HG3	24:LX:89:TYR:CE1	2.35	0.61
46:14:1206:G:H2'	46:14:1207:A:C8	2.36	0.61
13:LM:71:GLN:NE2	13:LM:114:MET:SD	2.72	0.61
46:14:2235:A:H2'	46:14:2236:A:C8	2.36	0.61
6:LF:12:ILE:HD13	6:LF:18:ILE:HG21	1.81	0.61
43:10:152:C:H2'	43:10:153:A:H8	1.65	0.61
43:10:87:U:H4'	43:10:88:A:C2	2.35	0.60
43:10:125:U:H1'	43:10:126:G:H5'	1.82	0.60
46:14:2263:U:O2'	46:14:2264:G:H8	1.85	0.60
46:14:2547:C:H2'	46:14:2548:C:C6	2.36	0.60
15:LO:3:ARG:NH2	45:13:90:G:OP2	2.32	0.60
4:LD:366:VAL:HG21	46:14:524:A:N1	2.15	0.60
46:14:583:C:H2'	46:14:584:G:C8	2.37	0.60
46:14:692:A:H61	46:14:708:C:H2'	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LI:110:VAL:HB	9:LI:129:ILE:HD12	1.83	0.60
46:14:1959:G:O4'	46:14:2096:A:N6	2.34	0.59
6:LF:95:MET:HE2	6:LF:182:ILE:HG22	1.84	0.59
7:LG:179:LEU:HD11	20:LT:129:LYS:HE2	1.84	0.59
44:12:29:C:O2'	44:12:50:A:N1	2.35	0.59
10:LJ:76:MET:HE2	10:LJ:148:ALA:HA	1.84	0.59
1:LA:85:MET:HE1	1:LA:93:LEU:HD11	1.83	0.59
17:LQ:8:ARG:HD2	17:LQ:27:LYS:HB3	1.85	0.59
46:14:955:C:H2'	46:14:956:C:C6	2.37	0.59
1:LA:5:LEU:HB3	1:LA:198:TRP:CH2	2.37	0.59
43:10:70:G:H21	43:10:89:A:H61	1.50	0.59
43:10:118:G:C4	43:10:119:G:H1'	2.38	0.59
46:14:673:U:H2'	46:14:674:C:C6	2.37	0.59
11:LK:265:ARG:NH1	11:LK:267:ASN:O	2.36	0.59
46:14:556:U:H2'	46:14:557:C:C6	2.38	0.59
15:LO:107:GLU:O	15:LO:111:GLU:HG2	2.03	0.58
46:14:3049:C:O2'	46:14:3050:A:H5'	2.03	0.58
46:14:1818:G:H2'	46:14:1819:A:O4'	2.03	0.58
43:10:160:A:H2'	43:10:161:A:C8	2.38	0.58
46:14:2444:U:H2'	46:14:2445:G:C8	2.39	0.58
2:LB:104:LEU:HA	2:LB:107:ILE:HD12	1.86	0.58
43:10:140:U:H2'	43:10:141:A:C8	2.38	0.58
46:14:2263:U:HO2'	46:14:2264:G:H8	1.50	0.58
3:LC:90:VAL:HG22	3:LC:104:THR:HG23	1.85	0.57
36:Lj:24:GLU:CD	36:Lj:24:GLU:H	2.13	0.57
46:14:498:G:H2'	46:14:499:A:C8	2.35	0.57
16:LP:67:ARG:HD3	46:14:524:A:C6	2.39	0.57
43:10:100:U:H5'	43:10:101:G:H5'	1.86	0.57
43:10:199:G:OP2	43:10:199:G:H3'	2.04	0.57
46:14:417:G:N2	46:14:2388:G:OP2	2.30	0.57
9:LI:35:ALA:HB1	46:14:38:A:H5''	1.86	0.57
1:LA:94:ASN:HA	1:LA:123:LEU:O	2.04	0.57
43:10:82:C:H1'	43:10:95:A:N1	2.19	0.57
46:14:1:G:H2'	46:14:2:C:C6	2.39	0.57
4:LD:272:ASP:OD1	4:LD:272:ASP:N	2.36	0.57
43:10:182:C:H2'	43:10:183:C:C6	2.40	0.57
4:LD:303:GLN:HG3	16:LP:18:ARG:NH1	2.20	0.56
43:10:131:U:H3'	43:10:132:G:H8	1.71	0.56
43:10:132:G:H3'	43:10:133:G:C8	2.40	0.56
1:LA:48:ARG:HA	1:LA:159:LEU:HD23	1.87	0.56
23:LW:7:GLN:NE2	23:LW:35:ALA:O	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:692:A:N6	46:14:708:C:H2'	2.21	0.56
46:14:3169:U:H5	46:14:3172:C:OP2	1.87	0.56
11:LK:93:THR:HG22	11:LK:157:ARG:HH12	1.70	0.56
17:LQ:41:PHE:HB3	46:14:609:G:N3	2.21	0.56
46:14:162:U:H3	46:14:253:G:H1	1.51	0.56
46:14:3273:C:H2'	46:14:3274:G:C8	2.41	0.56
6:LF:176:ARG:NH1	40:Ln:125:LYS:O	2.38	0.56
10:LJ:83:ASP:OD1	10:LJ:83:ASP:N	2.36	0.56
4:LD:297:ILE:O	4:LD:303:GLN:NE2	2.39	0.56
46:14:116:U:O2	46:14:119:G:H5''	2.06	0.56
21:LU:4:TYR:OH	46:14:146:G:OP2	2.23	0.56
46:14:181:C:H2'	46:14:182:C:C6	2.41	0.56
46:14:3168:C:H4'	46:14:3169:U:H5''	1.87	0.56
31:Le:32:TYR:CE1	31:Le:57:ARG:HG3	2.41	0.55
43:10:184:G:H5''	43:10:185:U:H3	1.70	0.55
21:LU:45:PRO:O	21:LU:49:ARG:HG3	2.06	0.55
16:LP:10:GLU:O	16:LP:14:LYS:HG3	2.06	0.55
46:14:625:G:O2'	46:14:3265:A:N6	2.38	0.55
5:LE:37:LYS:HB2	5:LE:37:LYS:NZ	2.20	0.55
4:LD:145:HIS:HD2	4:LD:182:ASP:OD2	1.89	0.55
11:LK:83:LEU:HD13	11:LK:88:LEU:HD23	1.88	0.55
43:10:115:G:H2'	43:10:116:C:C6	2.42	0.55
5:LE:163:LYS:NZ	5:LE:163:LYS:HB3	2.22	0.55
43:10:189:C:H2'	43:10:190:C:H6	1.70	0.55
11:LK:22:ARG:HB3	11:LK:28:THR:HG22	1.89	0.55
4:LD:329:VAL:HA	4:LD:332:LYS:HB2	1.88	0.54
23:LW:126:LYS:HG2	23:LW:131:VAL:HG21	1.90	0.54
43:10:182:C:H2'	43:10:183:C:H6	1.72	0.54
1:LA:111:LEU:HD23	1:LA:136:SER:OG	2.07	0.54
6:LF:143:VAL:HB	6:LF:146:GLU:HG3	1.89	0.54
43:10:113:G:H2'	43:10:114:C:C6	2.43	0.54
46:14:2372:G:H2'	46:14:2373:G:C8	2.42	0.54
46:14:3018:A:H2'	46:14:3019:A:C8	2.43	0.54
3:LC:177:LYS:NZ	46:14:3307:A:OP1	2.34	0.54
20:LT:71:LEU:O	20:LT:75:MET:HG3	2.08	0.54
43:10:77:U:H1'	43:10:160:A:C5	2.42	0.54
46:14:1032:G:H2'	46:14:1033:G:H8	1.71	0.54
46:14:3271:A:HO2'	46:14:3272:U:H6	1.54	0.54
37:Lk:17:THR:HG23	37:Lk:29:ILE:HD11	1.90	0.54
43:10:51:G:H1	43:10:68:U:H3	1.55	0.54
28:Lb:4:PHE:O	28:Lb:9:LYS:HD2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:10:114:C:H2'	43:10:115:G:C8	2.43	0.54
4:LD:87:THR:HG22	46:14:352:A:N1	2.23	0.54
21:LU:28:TRP:O	21:LU:32:GLN:NE2	2.40	0.54
10:LJ:212:GLY:H	11:LK:288:ASN:ND2	2.06	0.53
43:10:54:C:H42	43:10:65:G:H1	1.55	0.53
43:10:61:U:H3'	43:10:62:A:C8	2.43	0.53
43:10:80:C:H3'	43:10:81:U:C6	2.40	0.53
1:LA:4:LYS:CE	1:LA:198:TRP:HB3	2.38	0.53
3:LC:103:ASN:ND2	3:LC:149:GLN:HG2	2.23	0.53
17:LQ:34:LYS:O	17:LQ:39:GLY:N	2.30	0.53
43:10:190:C:H2'	43:10:191:C:C6	2.44	0.53
46:14:1550:U:O4	46:14:1563:G:O2'	2.27	0.53
4:LD:381:TRP:O	4:LD:385:MET:HG3	2.08	0.53
16:LP:167:SER:O	16:LP:171:GLN:HG3	2.08	0.53
43:10:47:C:H2'	43:10:48:G:C8	2.44	0.53
43:10:138:U:H2'	43:10:139:A:C8	2.44	0.53
46:14:2548:C:H2'	46:14:2549:C:C6	2.43	0.53
5:LE:51:LYS:HG2	5:LE:64:ASN:HA	1.90	0.53
46:14:1215:A:H2'	46:14:1216:A:C8	2.44	0.53
46:14:2774:A:O2'	46:14:2775:C:H5''	2.09	0.53
46:14:1819:A:C2'	46:14:1822:G:H21	2.22	0.53
13:LM:147:VAL:O	13:LM:151:ILE:HG13	2.08	0.53
43:10:104:U:H2'	43:10:105:C:C6	2.43	0.53
18:LR:114:GLU:OE2	18:LR:119:THR:OG1	2.25	0.53
46:14:2476:A:H3'	46:14:2477:A:H8	1.73	0.53
1:LA:30:GLU:HB2	1:LA:172:LEU:CD1	2.38	0.52
5:LE:112:ILE:HG21	5:LE:118:TYR:HB2	1.91	0.52
17:LQ:106:LEU:HD13	17:LQ:149:VAL:HG11	1.91	0.52
20:LT:117:ARG:HG2	20:LT:117:ARG:HH11	1.73	0.52
46:14:2379:G:H2'	46:14:2380:G:C8	2.44	0.52
11:LK:277:LYS:O	11:LK:281:ILE:HG13	2.09	0.52
23:LW:5:LYS:NZ	23:LW:5:LYS:HB3	2.23	0.52
46:14:1680:A:H2	46:14:1696:G:H22	1.56	0.52
1:LA:32:ILE:CD1	1:LA:179:ILE:HD13	2.40	0.52
10:LJ:184:TYR:HE1	10:LJ:219:VAL:HG11	1.74	0.52
11:LK:76:ALA:HB3	11:LK:109:VAL:HG22	1.91	0.52
46:14:3153:U:H5''	46:14:3285:A:H4'	1.92	0.52
2:LB:147:ARG:HG2	2:LB:157:ILE:HG12	1.91	0.52
25:LY:150:THR:HG22	25:LY:151:PRO:O	2.09	0.52
10:LJ:184:TYR:CE1	10:LJ:219:VAL:HG11	2.45	0.52
38:LI:3:LYS:HD2	38:LI:41:TYR:CD2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:10:81:U:H2'	43:10:82:C:O4'	2.09	0.52
46:14:1362:G:H2'	46:14:1364:G:C8	2.44	0.52
3:LC:71:GLU:OE2	3:LC:361:LYS:NZ	2.27	0.52
34:Lh:61:LYS:HB2	46:14:3168:C:H42	1.75	0.52
43:10:180:C:H2'	43:10:181:C:C6	2.44	0.52
46:14:764:G:H2'	46:14:765:A:C8	2.43	0.52
46:14:3307:A:HO2'	46:14:3308:A:P	2.33	0.52
21:LU:121:ILE:HG21	21:LU:131:GLU:HG3	1.92	0.52
29:Lc:76:LYS:NZ	29:Lc:77:LYS:HD2	2.25	0.52
1:LA:18:LYS:HD2	1:LA:176:GLU:HG2	1.92	0.52
37:Lk:76:THR:HG22	37:Lk:79:ARG:HB3	1.92	0.52
46:14:138:U:H2'	46:14:139:C:C6	2.44	0.52
46:14:3018:A:H2'	46:14:3019:A:H8	1.74	0.52
46:14:3225:C:H2'	46:14:3226:A:C8	2.43	0.52
14:LN:87:GLU:H	14:LN:87:GLU:CD	2.18	0.52
21:LU:2:GLY:O	36:Lj:39:ARG:NH2	2.43	0.52
27:La:5:THR:HG23	27:La:15:ILE:O	2.10	0.52
28:Lb:99:VAL:HG21	28:Lb:109:ALA:HB2	1.92	0.52
3:LC:139:THR:O	3:LC:143:LYS:NZ	2.43	0.51
11:LK:222:PHE:O	11:LK:226:ILE:HG13	2.11	0.51
46:14:1:G:H2'	46:14:2:C:H6	1.75	0.51
46:14:742:C:H2'	46:14:743:C:O4'	2.10	0.51
21:LU:99:ARG:HG2	21:LU:167:ALA:HB2	1.92	0.51
43:10:77:U:H1'	43:10:160:A:C4	2.46	0.51
4:LD:352:VAL:O	4:LD:356:LYS:N	2.36	0.51
38:Ll:30:ASP:OD1	38:Ll:30:ASP:N	2.40	0.51
43:10:72:G:H2'	43:10:73:U:O4'	2.10	0.51
46:14:2549:C:H2'	46:14:2550:C:C6	2.45	0.51
19:LS:103:ARG:NH1	46:14:72:A:H5''	2.25	0.51
29:Lc:62:GLU:HG3	29:Lc:63:GLY:H	1.75	0.51
36:Lj:30:SER:O	36:Lj:33:LYS:HG2	2.11	0.51
43:10:71:U:H1'	43:10:89:A:N6	2.22	0.51
46:14:2572:C:O2'	46:14:2573:U:O5'	2.29	0.51
46:14:3168:C:H4'	46:14:3169:U:C5'	2.40	0.51
5:LE:50:SER:OG	46:14:2684:U:O3'	2.25	0.51
17:LQ:25:TYR:HE2	46:14:608:U:H5'	1.76	0.51
20:LT:117:ARG:HG2	20:LT:117:ARG:NH1	2.26	0.51
24:LX:29:MET:HG3	24:LX:43:PHE:CD1	2.46	0.51
43:10:84:A:H2'	43:10:85:C:C6	2.46	0.51
29:Lc:139:LYS:HB3	29:Lc:141:ARG:HG3	1.92	0.50
43:10:114:C:H2'	43:10:115:G:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:2446:A:H2'	46:14:2447:C:C6	2.46	0.50
16:LP:17:LYS:NZ	16:LP:21:GLU:OE2	2.44	0.50
18:LR:145:GLN:HG3	18:LR:197:THR:O	2.12	0.50
46:14:569:U:O2'	46:14:570:G:H5'	2.11	0.50
46:14:1051:U:H2'	46:14:1052:A:C8	2.47	0.50
46:14:3166:C:H2'	46:14:3167:G:C8	2.45	0.50
4:LD:394:PHE:HE1	25:LY:152:ILE:HD12	1.76	0.50
11:LK:83:LEU:HB3	11:LK:88:LEU:HB3	1.93	0.50
24:LX:9:TYR:CE1	24:LX:65:GLU:HG3	2.46	0.50
26:LZ:100:ARG:HE	26:LZ:102:ILE:HD11	1.76	0.50
43:10:118:G:H2'	43:10:119:G:H4'	1.94	0.50
43:10:118:G:N2	43:10:145:C:N3	2.60	0.50
2:LB:183:GLY:HA2	46:14:906:A:H5''	1.93	0.50
33:Lg:106:ARG:NH2	46:14:1423:G:OP1	2.44	0.50
46:14:2263:U:O2'	46:14:2264:G:O5'	2.29	0.50
46:14:3380:C:H2'	46:14:3381:U:C6	2.46	0.50
43:10:85:C:H2'	43:10:86:U:O4'	2.12	0.50
1:LA:5:LEU:HB3	1:LA:198:TRP:HH2	1.76	0.50
24:LX:35:ASN:HB2	24:LX:38:ARG:HG3	1.93	0.50
43:10:131:U:H3'	43:10:132:G:C8	2.47	0.50
46:14:3072:A:H2'	46:14:3073:A:C8	2.46	0.50
17:LQ:204:GLU:OE2	17:LQ:210:LYS:HD2	2.12	0.50
29:Lc:74:LYS:O	29:Lc:78:GLN:NE2	2.45	0.50
43:10:180:C:H2'	43:10:181:C:H6	1.77	0.50
46:14:3006:C:H2'	46:14:3007:A:O4'	2.12	0.50
2:LB:170:ALA:CB	42:Lq:65:VAL:HG12	2.42	0.49
3:LC:220:ILE:HD12	3:LC:283:LYS:HG3	1.92	0.49
11:LK:264:LYS:HG2	11:LK:265:ARG:H	1.77	0.49
17:LQ:21:ARG:NH1	46:14:581:C:OP2	2.45	0.49
46:14:3224:U:H2'	46:14:3225:C:C6	2.48	0.49
8:LH:96:MET:HE2	27:La:22:ARG:HH11	1.77	0.49
43:10:161:A:H1'	43:10:162:A:H5'	1.95	0.49
46:14:583:C:H2'	46:14:584:G:H8	1.76	0.49
4:LD:314:ASN:OD1	46:14:1357:G:N2	2.45	0.49
6:LF:61:ASP:N	6:LF:61:ASP:OD1	2.44	0.49
16:LP:11:SER:HB2	46:14:1361:A:O2'	2.13	0.49
46:14:955:C:H2'	46:14:956:C:H6	1.78	0.49
46:14:3271:A:O2'	46:14:3272:U:H6	1.96	0.49
9:LI:2:THR:HG22	9:LI:4:ARG:HG2	1.95	0.49
18:LR:235:GLY:O	18:LR:239:GLN:HG3	2.13	0.49
29:Lc:77:LYS:HG3	29:Lc:80:LYS:HG3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Lk:77:ASN:OD1	37:Lk:77:ASN:O	2.31	0.49
46:14:1700:A:H2'	46:14:1701:A:C8	2.48	0.49
12:LL:7:GLU:HG3	12:LL:8:PRO:HD2	1.93	0.49
18:LR:205:MET:O	18:LR:208:SER:OG	2.20	0.49
42:Lq:16:THR:HG22	46:14:1933:G:C8	2.48	0.49
43:10:86:U:O2'	43:10:88:A:N1	2.39	0.49
46:14:246:C:H5'	46:14:247:C:H5'	1.95	0.49
1:LA:38:LEU:HA	1:LA:200:ASN:O	2.13	0.49
1:LA:196:LYS:HB2	1:LA:200:ASN:OD1	2.12	0.48
5:LE:117:LYS:NZ	5:LE:117:LYS:HB3	2.27	0.48
11:LK:105:LEU:O	11:LK:109:VAL:HG23	2.13	0.48
10:LJ:153:ARG:O	10:LJ:156:LYS:HB2	2.13	0.48
13:LM:80:THR:O	13:LM:80:THR:HG22	2.13	0.48
44:12:24:C:H2'	44:12:25:G:O4'	2.13	0.48
4:LD:287:LYS:NZ	22:LV:23:ASP:OD2	2.44	0.48
21:LU:19:MET:HE2	21:LU:19:MET:HA	1.94	0.48
28:Lb:60:LYS:HE2	28:Lb:64:LYS:HE2	1.95	0.48
46:14:2263:U:O2'	46:14:2264:G:C8	2.61	0.48
6:LF:118:ARG:HG2	6:LF:126:VAL:HG12	1.96	0.48
7:LG:17:ARG:HA	7:LG:45:GLU:HB2	1.96	0.48
9:LI:76:ASP:HB3	9:LI:114:GLY:HA3	1.96	0.48
26:LZ:43:LEU:O	26:LZ:47:ILE:HG13	2.13	0.48
46:14:544:G:H2'	46:14:545:C:C6	2.49	0.48
46:14:609:G:H2'	46:14:610:C:C6	2.48	0.48
1:LA:5:LEU:HD22	1:LA:187:VAL:HG11	1.95	0.48
1:LA:68:LEU:O	1:LA:112:ALA:HA	2.14	0.48
38:Ll:14:THR:O	38:Ll:17:ARG:HG2	2.13	0.48
46:14:978:G:H2'	46:14:979:C:C6	2.48	0.48
46:14:1045:U:H2'	46:14:1046:C:C6	2.49	0.48
46:14:1059:A:N3	46:14:2636:U:O2'	2.46	0.48
46:14:2471:A:N3	46:14:2472:G:H1'	2.28	0.48
4:LD:333:LEU:HD22	16:LP:181:ILE:HD12	1.94	0.48
20:LT:45:ARG:HE	24:LX:72:THR:HG22	1.79	0.48
32:Lf:113:THR:O	46:14:3377:U:O2'	2.30	0.48
46:14:1131:A:H2'	46:14:1132:U:H6	1.79	0.48
46:14:1921:A:H2'	46:14:1922:U:C6	2.49	0.48
1:LA:36:ILE:CD1	1:LA:190:LEU:HD22	2.42	0.48
16:LP:142:LYS:O	16:LP:146:GLU:HG3	2.14	0.48
26:LZ:30:GLU:HA	26:LZ:30:GLU:OE1	2.12	0.48
43:10:87:U:H1'	43:10:88:A:C5	2.49	0.48
46:14:92:G:H2'	46:14:93:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:394:A:H4'	46:14:395:G:H3'	1.96	0.48
46:14:802:C:H2'	46:14:803:C:C6	2.48	0.48
17:LQ:36:LYS:HD2	46:14:586:G:H4'	1.95	0.48
43:10:139:A:H2'	43:10:140:U:O4'	2.14	0.48
45:13:133:G:H2'	45:13:134:G:H8	1.76	0.48
10:LJ:162:ARG:HG3	10:LJ:162:ARG:HH11	1.79	0.48
25:LY:109:MET:HE2	46:14:1075:G:N7	2.29	0.48
31:Le:32:TYR:OH	31:Le:60:GLU:OE1	2.31	0.48
43:10:71:U:C2	43:10:72:G:C8	3.02	0.48
46:14:1748:G:H2'	46:14:1749:G:H8	1.78	0.48
46:14:3133:U:H2'	46:14:3134:C:C6	2.49	0.48
1:LA:68:LEU:HD22	1:LA:90:LEU:HD21	1.96	0.47
4:LD:257:THR:HG23	4:LD:259:SER:H	1.78	0.47
21:LU:168:GLY:HA2	21:LU:171:TYR:CE2	2.49	0.47
27:La:48:PRO:HB2	27:La:56:MET:HE3	1.95	0.47
1:LA:156:LYS:HE2	1:LA:158:GLN:HG3	1.95	0.47
16:LP:145:ARG:HG2	16:LP:149:TYR:CE2	2.50	0.47
21:LU:176:GLY:O	21:LU:185:ARG:NH2	2.46	0.47
25:LY:9:SER:O	25:LY:55:LYS:NZ	2.38	0.47
46:14:2750:A:H2'	46:14:2751:A:C8	2.49	0.47
46:14:3072:A:H2'	46:14:3073:A:H8	1.80	0.47
6:LF:8:GLU:HB3	6:LF:77:LEU:HD11	1.96	0.47
46:14:897:G:H2'	46:14:898:U:C6	2.49	0.47
46:14:3164:U:H2'	46:14:3165:C:C6	2.49	0.47
2:LB:42:LYS:HG3	2:LB:89:TYR:CE2	2.49	0.47
17:LQ:41:PHE:HB3	46:14:609:G:C2	2.49	0.47
23:LW:136:ARG:O	23:LW:140:GLU:HG3	2.14	0.47
42:Lq:36:LYS:HG3	42:Lq:48:LYS:HE2	1.96	0.47
43:10:83:C:H2'	43:10:84:A:C8	2.49	0.47
5:LE:26:GLY:HA3	46:14:2683:A:C2	2.50	0.47
10:LJ:164:LYS:HB2	10:LJ:164:LYS:HE2	1.64	0.47
28:Lb:51:LYS:HD3	46:14:1815:A:OP2	2.15	0.47
31:Le:104:ASP:OD1	31:Le:104:ASP:N	2.47	0.47
45:13:135:C:H2'	45:13:136:C:C6	2.49	0.47
46:14:805:G:H2'	46:14:806:U:C6	2.49	0.47
6:LF:135:VAL:HG23	6:LF:157:VAL:HG22	1.96	0.47
17:LQ:153:ASP:N	17:LQ:153:ASP:OD1	2.48	0.47
43:10:85:C:C4	43:10:86:U:C4	3.02	0.47
1:LA:56:PRO:HD3	1:LA:185:MET:SD	2.54	0.47
4:LD:142:ALA:HB1	29:Lc:17:ASN:HB2	1.97	0.47
17:LQ:10:PRO:HG2	17:LQ:18:LYS:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:10:70:G:N2	43:10:89:A:H61	2.13	0.47
46:14:1232:A:H4'	46:14:1234:G:H5''	1.96	0.47
1:LA:93:LEU:HD22	1:LA:99:LEU:HB3	1.96	0.47
13:LM:103:ASP:OD1	13:LM:103:ASP:N	2.46	0.47
16:LP:178:ILE:HG23	16:LP:183:ASP:HB3	1.96	0.47
39:Lm:36:ARG:HH22	46:14:399:G:H1'	1.80	0.47
12:LL:2:VAL:HG22	12:LL:3:LYS:H	1.80	0.47
4:LD:309:ILE:HG22	16:LP:22:TRP:CZ3	2.49	0.47
6:LF:142:LYS:HG3	6:LF:143:VAL:HG23	1.96	0.47
10:LJ:38:MET:HE3	10:LJ:41:LYS:HG2	1.97	0.47
18:LR:49:LYS:HG3	46:14:2528:A:C5	2.50	0.47
46:14:174:G:C4	46:14:175:A:C8	3.03	0.47
4:LD:382:PHE:HA	4:LD:385:MET:HG3	1.96	0.46
7:LG:10:ARG:HB3	7:LG:10:ARG:HH11	1.80	0.46
38:LI:22:THR:HG22	38:LI:65:SER:HB3	1.96	0.46
46:14:243:G:H2'	46:14:244:C:C6	2.50	0.46
1:LA:25:LYS:HB2	1:LA:25:LYS:HE2	1.57	0.46
10:LJ:162:ARG:HG3	10:LJ:162:ARG:NH1	2.30	0.46
17:LQ:152:PHE:HE2	17:LQ:195:VAL:HG21	1.80	0.46
18:LR:202:GLU:H	18:LR:202:GLU:CD	2.24	0.46
19:LS:126:PRO:HB3	19:LS:136:ASP:OD2	2.15	0.46
23:LW:139:MET:HE3	23:LW:139:MET:HB3	1.81	0.46
33:Lg:97:ILE:HG21	33:Lg:106:ARG:HG2	1.97	0.46
43:10:96:G:H3'	43:10:97:G:H8	1.80	0.46
46:14:1084:G:H2'	46:14:1085:C:C6	2.50	0.46
46:14:3002:G:H2'	46:14:3003:U:C6	2.50	0.46
1:LA:54:LYS:HA	1:LA:153:ALA:O	2.14	0.46
3:LC:382:LYS:HE3	3:LC:382:LYS:HB2	1.65	0.46
4:LD:16:GLU:H	4:LD:176:GLN:HE22	1.61	0.46
5:LE:51:LYS:O	5:LE:53:ARG:NH1	2.48	0.46
4:LD:155:LEU:HD23	4:LD:255:VAL:HG22	1.98	0.46
5:LE:152:ILE:HA	5:LE:155:ARG:HG3	1.97	0.46
7:LG:59:TYR:OH	7:LG:78:PHE:O	2.30	0.46
46:14:129:G:H1	46:14:135:U:H3	1.64	0.46
46:14:437:G:O6	46:14:633:G:H1'	2.15	0.46
46:14:1131:A:H2'	46:14:1132:U:C6	2.51	0.46
46:14:2508:G:H2'	46:14:2509:U:C6	2.50	0.46
46:14:2697:A:H3'	46:14:2698:G:N2	2.30	0.46
11:LK:81:ARG:CZ	11:LK:81:ARG:HB2	2.45	0.46
23:LW:146:LYS:HB3	23:LW:146:LYS:HE3	1.78	0.46
29:Lc:38:ASN:OD1	29:Lc:38:ASN:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:371:A:N3	46:14:373:G:H5''	2.30	0.46
46:14:652:C:H42	46:14:656:A:H2	1.62	0.46
46:14:2513:U:H2'	46:14:2514:U:C6	2.51	0.46
6:LF:74:ARG:HD2	6:LF:74:ARG:HA	1.55	0.46
46:14:2904:G:O2'	46:14:3026:A:N1	2.46	0.46
46:14:3015:U:H2'	46:14:3016:U:C6	2.50	0.46
45:13:7:C:H2'	45:13:8:U:C6	2.51	0.46
46:14:2476:A:H3'	46:14:2477:A:C8	2.50	0.46
29:Lc:136:VAL:HG21	33:Lg:114:ALA:HB1	1.98	0.46
46:14:1145:G:O2'	46:14:2645:A:N3	2.45	0.46
46:14:2964:G:H2'	46:14:2965:U:C6	2.51	0.46
11:LK:126:THR:HG22	11:LK:128:GLU:H	1.80	0.46
27:La:9:ARG:HH22	27:La:29:GLN:HE22	1.63	0.46
43:10:105:C:H2'	43:10:106:U:C6	2.51	0.46
43:10:113:G:H2'	43:10:114:C:H6	1.80	0.46
6:LF:7:SER:HB2	6:LF:61:ASP:HB3	1.98	0.45
17:LQ:3:ALA:O	46:14:590:C:N4	2.50	0.45
19:LS:26:GLN:HB3	19:LS:27:PRO:HD3	1.97	0.45
23:LW:95:TRP:CH2	23:LW:99:MET:HE3	2.52	0.45
26:LZ:24:ASP:OD1	26:LZ:24:ASP:C	2.59	0.45
44:12:37:A:H2'	44:12:38:U:C6	2.51	0.45
46:14:1543:C:H2'	46:14:1544:U:C6	2.51	0.45
46:14:2700:A:H2'	46:14:2701:G:C8	2.51	0.45
26:LZ:22:VAL:HB	26:LZ:110:VAL:HG12	1.98	0.45
35:Li:98:GLU:HA	35:Li:98:GLU:OE1	2.15	0.45
43:10:126:G:H2'	43:10:127:U:C6	2.51	0.45
46:14:3195:G:H2'	46:14:3196:C:C6	2.51	0.45
29:Lc:36:GLU:HG2	29:Lc:39:ASN:HB2	1.98	0.45
46:14:2164:G:H2'	46:14:2165:G:H8	1.81	0.45
46:14:2448:U:H2'	46:14:2449:U:O4'	2.15	0.45
2:LB:48:ILE:HG12	42:Lq:65:VAL:HG22	1.98	0.45
33:Lg:3:VAL:HG12	33:Lg:91:ARG:HH21	1.81	0.45
43:10:141:A:H3'	43:10:142:C:C6	2.52	0.45
45:13:162:G:H2'	45:13:163:C:O4'	2.16	0.45
5:LE:154:HIS:ND1	44:12:54:A:O2'	2.47	0.45
8:LH:30:ASP:OD2	8:LH:32:THR:HG23	2.17	0.45
9:LI:135:LYS:HB2	9:LI:135:LYS:HE3	1.65	0.45
13:LM:120:LYS:HD3	13:LM:137:ARG:HD3	1.97	0.45
14:LN:50:ARG:HG2	14:LN:51:LYS:H	1.82	0.45
27:La:9:ARG:HH22	27:La:29:GLN:NE2	2.14	0.45
46:14:195:A:N3	46:14:215:G:O2'	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LT:23:LYS:HB3	20:LT:23:LYS:HE3	1.69	0.45
27:La:50:LYS:HD3	46:14:2115:G:C5'	2.47	0.45
43:10:87:U:O2	43:10:88:A:N6	2.50	0.45
43:10:133:G:H5'	43:10:134:U:H5'	1.98	0.45
43:10:156:U:H2'	43:10:158:A:OP2	2.17	0.45
46:14:1120:C:H2'	46:14:1121:C:C6	2.52	0.45
46:14:1185:G:H2'	46:14:1186:C:C6	2.52	0.45
46:14:1476:A:H2'	46:14:1477:G:O4'	2.17	0.45
46:14:2216:A:H2'	46:14:2217:A:H8	1.79	0.45
46:14:2543:A:H1'	46:14:2546:G:N2	2.32	0.45
1:LA:142:GLU:O	1:LA:143:SER:C	2.59	0.45
3:LC:143:LYS:O	3:LC:147:GLN:HG2	2.16	0.45
24:LX:14:ARG:HG3	24:LX:15:ALA:O	2.17	0.45
30:Ld:6:ASN:HB2	46:14:1146:A:OP1	2.16	0.45
43:10:64:C:H2'	43:10:65:G:C8	2.52	0.45
9:LI:104:GLN:HB3	19:LS:160:PRO:HB3	1.98	0.45
26:LZ:80:ARG:HG3	26:LZ:80:ARG:HH11	1.82	0.45
30:Ld:5:LYS:HA	30:Ld:5:LYS:HD2	1.71	0.45
43:10:60:A:H4'	43:10:61:U:H5''	1.98	0.45
45:13:126:G:H2'	45:13:127:C:C6	2.52	0.45
46:14:978:G:H2'	46:14:979:C:H6	1.82	0.45
2:LB:48:ILE:HG12	42:Lq:65:VAL:CG2	2.46	0.45
5:LE:25:VAL:C	5:LE:27:GLU:H	2.24	0.45
6:LF:140:SER:HB3	6:LF:146:GLU:HB2	1.99	0.45
46:14:1958:G:H2'	46:14:2096:A:H61	1.81	0.45
5:LE:34:ARG:NE	5:LE:122:THR:O	2.46	0.45
46:14:3272:U:HO2'	46:14:3273:C:H6	1.63	0.45
1:LA:18:LYS:HD2	1:LA:176:GLU:CG	2.47	0.44
3:LC:312:MET:HE2	46:14:3321:U:H5''	1.99	0.44
32:Lf:83:LYS:HB2	32:Lf:83:LYS:HE3	1.73	0.44
46:14:692:A:H3'	46:14:693:A:C8	2.53	0.44
3:LC:8:HIS:ND1	3:LC:9:PRO:O	2.50	0.44
5:LE:8:SER:O	5:LE:8:SER:OG	2.35	0.44
6:LF:180:ASP:N	6:LF:180:ASP:OD1	2.49	0.44
7:LG:104:LEU:HD23	7:LG:104:LEU:HA	1.84	0.44
12:LL:15:CYS:SG	12:LL:103:ALA:HB2	2.57	0.44
15:LO:119:TYR:CZ	19:LS:47:ARG:HG2	2.52	0.44
25:LY:13:ASP:OD2	46:14:1006:G:H3'	2.17	0.44
27:La:15:ILE:HG12	27:La:34:LEU:HD13	1.99	0.44
28:Lb:53:VAL:HG13	28:Lb:62:GLN:HG2	1.99	0.44
46:14:641:A:H2'	46:14:642:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:771:A:N6	46:14:780:G:H1'	2.32	0.44
46:14:2638:A:H4'	46:14:2639:A:O5'	2.17	0.44
46:14:2888:C:O2'	46:14:2889:U:H5'	2.17	0.44
19:LS:78:GLU:HG3	19:LS:108:LEU:HD12	1.99	0.44
31:Le:39:LEU:HD13	31:Le:64:TYR:HB3	1.98	0.44
43:10:52:U:H2'	43:10:53:G:O4'	2.18	0.44
43:10:199:G:OP2	43:10:199:G:C3'	2.64	0.44
46:14:1449:U:H2'	46:14:1450:U:C6	2.53	0.44
46:14:1679:G:H2'	46:14:1680:A:C8	2.52	0.44
46:14:2658:U:H4'	46:14:2659:A:O4'	2.16	0.44
6:LF:190:ILE:HG22	6:LF:191:VAL:HG23	1.99	0.44
31:Le:27:LYS:HE3	31:Le:27:LYS:HB2	1.75	0.44
40:Ln:89:TYR:C	40:Ln:90:ASN:HD22	2.25	0.44
43:10:184:G:N2	43:10:196:A:H62	2.16	0.44
46:14:301:G:N3	46:14:301:G:H5'	2.31	0.44
46:14:801:A:H2'	46:14:802:C:C6	2.52	0.44
46:14:1821:U:H4'	46:14:1822:G:O4'	2.18	0.44
46:14:2576:C:H2'	46:14:2577:A:H8	1.83	0.44
1:LA:207:LYS:HB3	1:LA:213:PRO:HA	1.98	0.44
4:LD:34:PRO:HG3	4:LD:286:PRO:HD3	1.99	0.44
13:LM:143:ASP:C	13:LM:143:ASP:OD1	2.60	0.44
44:12:33:U:H2'	44:12:34:C:O4'	2.18	0.44
46:14:107:A:H4'	46:14:108:G:OP1	2.17	0.44
46:14:2614:U:H2'	46:14:2615:U:C6	2.53	0.44
31:Le:34:THR:O	31:Le:38:THR:HG23	2.17	0.44
40:Ln:83:MET:HE2	40:Ln:83:MET:HB3	1.87	0.44
43:10:95:A:H3'	43:10:96:G:H8	1.81	0.44
43:10:187:A:H2'	43:10:188:C:C6	2.53	0.44
46:14:2402:A:H2'	46:14:2403:G:O4'	2.18	0.44
17:LQ:24:MET:HA	17:LQ:24:MET:CE	2.42	0.44
21:LU:84:PRO:HA	21:LU:87:GLN:HG3	2.00	0.44
45:13:129:A:C8	45:13:133:G:N1	2.86	0.44
46:14:11:G:H5'	46:14:12:U:P	2.57	0.44
46:14:436:C:O3'	46:14:437:G:H8	2.01	0.44
46:14:1234:G:N1	46:14:1297:G:N7	2.66	0.44
46:14:2990:A:H2'	46:14:2991:C:C6	2.53	0.44
3:LC:253:ALA:HB3	46:14:2883:U:H1'	1.99	0.44
14:LN:54:GLU:HB2	14:LN:107:LYS:HB3	2.00	0.44
16:LP:52:ALA:O	16:LP:56:GLU:HG2	2.18	0.44
33:Lg:87:MET:HG3	33:Lg:116:LEU:HD22	1.99	0.44
43:10:102:U:H2'	43:10:103:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:10:191:C:H2'	43:10:192:C:O4'	2.18	0.44
45:13:136:C:H2'	45:13:137:G:C8	2.52	0.44
46:14:588:C:H2'	46:14:589:U:H2'	1.99	0.44
46:14:666:C:H2'	46:14:667:A:C8	2.52	0.44
46:14:2308:G:OP2	46:14:2308:G:N2	2.32	0.44
46:14:2890:A:N3	46:14:2890:A:H2'	2.33	0.44
17:LQ:20:SER:O	17:LQ:24:MET:HB2	2.18	0.43
20:LT:9:ILE:HD13	20:LT:64:ARG:HB3	2.00	0.43
31:Le:27:LYS:HE3	31:Le:99:ASP:HB3	1.99	0.43
35:Li:68:SER:OG	35:Li:70:ASN:OD1	2.35	0.43
36:Lj:36:THR:OG1	36:Lj:37:SER:N	2.50	0.43
38:Ll:60:LEU:HD13	38:Ll:61:PRO:HD2	1.99	0.43
46:14:2510:U:H2'	46:14:2511:A:C8	2.53	0.43
9:Li:4:ARG:NH2	46:14:1438:C:OP2	2.33	0.43
16:LP:86:ILE:O	16:LP:114:GLY:HA2	2.18	0.43
20:LT:128:LEU:HD23	20:LT:128:LEU:HA	1.88	0.43
26:LZ:67:THR:HG23	26:LZ:68:LYS:HG3	1.99	0.43
19:LS:101:ARG:HH11	19:LS:103:ARG:HE	1.65	0.43
28:Lb:31:GLU:CD	28:Lb:31:GLU:H	2.27	0.43
31:Le:17:ASN:H	31:Le:17:ASN:ND2	2.17	0.43
37:Lk:81:GLY:N	45:13:99:A:OP1	2.40	0.43
43:10:69:A:H3'	43:10:70:G:H8	1.83	0.43
46:14:2726:U:H2'	46:14:2727:U:C6	2.53	0.43
14:LN:83:ARG:HG3	14:LN:83:ARG:HH11	1.84	0.43
16:LP:95:MET:HE3	16:LP:100:LYS:HB2	2.00	0.43
21:LU:85:THR:HG23	46:14:42:U:H5''	2.01	0.43
37:Lk:45:ARG:C	37:Lk:46:LYS:HG2	2.44	0.43
43:10:78:C:H1'	43:10:159:U:C5	2.53	0.43
43:10:118:G:C2	43:10:119:G:H1'	2.53	0.43
43:10:184:G:H4'	43:10:196:A:H5'	1.99	0.43
46:14:245:A:H2'	46:14:246:C:O4'	2.18	0.43
1:LA:143:SER:O	1:LA:144:LEU:C	2.60	0.43
13:LM:69:LEU:HD23	13:LM:69:LEU:HA	1.72	0.43
21:LU:47:LYS:HE2	46:14:266:G:OP1	2.18	0.43
30:Ld:41:ARG:HD3	46:14:786:U:OP1	2.18	0.43
43:10:57:A:H1'	43:10:63:A:C2	2.52	0.43
46:14:2711:U:H2'	46:14:2712:C:C6	2.53	0.43
2:LB:181:LYS:NZ	46:14:870:G:OP2	2.52	0.43
24:LX:161:PRO:HD2	24:LX:165:LEU:HD12	2.00	0.43
43:10:51:G:N2	43:10:87:U:O4	2.38	0.43
43:10:153:A:H2'	43:10:154:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:6:GLN:HE21	1:LA:6:GLN:HB3	1.60	0.43
15:LO:18:LEU:HD12	15:LO:18:LEU:HA	1.82	0.43
17:LQ:144:VAL:HG12	17:LQ:144:VAL:O	2.18	0.43
29:Lc:58:THR:HB	29:Lc:71:ALA:HB3	2.00	0.43
38:Ll:16:ARG:HG3	38:Ll:16:ARG:NH1	2.34	0.43
45:13:86:C:H4'	45:13:88:G:N3	2.34	0.43
46:14:1819:A:HO2'	46:14:1822:G:H21	1.66	0.43
46:14:1823:C:H2'	46:14:1824:C:C6	2.53	0.43
46:14:2576:C:H2'	46:14:2577:A:C8	2.53	0.43
3:LC:82:PRO:HA	3:LC:323:ASP:OD2	2.19	0.43
37:Lk:87:ARG:HD2	45:13:71:G:OP2	2.19	0.43
46:14:637:C:H2'	46:14:638:C:H6	1.82	0.43
46:14:957:U:H2'	46:14:958:C:C6	2.54	0.43
46:14:1119:U:H2'	46:14:1120:C:C6	2.53	0.43
1:LA:38:LEU:HB2	1:LA:163:LEU:HD22	2.00	0.43
1:LA:44:GLN:CD	1:LA:44:GLN:H	2.25	0.43
10:LJ:40:LYS:HB2	10:LJ:40:LYS:HE2	1.72	0.43
13:LM:77:TYR:CD1	15:LO:36:VAL:HG21	2.52	0.43
17:LQ:34:LYS:NZ	46:14:608:U:OP1	2.51	0.43
18:LR:202:GLU:OE1	18:LR:202:GLU:N	2.47	0.43
21:LU:85:THR:HG21	46:14:43:A:P	2.59	0.43
24:LX:14:ARG:O	24:LX:59:GLN:N	2.43	0.43
28:Lb:90:ASP:O	28:Lb:116:ARG:NH1	2.52	0.43
32:Lf:62:LYS:HB2	32:Lf:62:LYS:HE3	1.57	0.43
36:Lj:18:HIS:HB3	46:14:71:A:H5'	2.00	0.43
38:Ll:60:LEU:CD1	38:Ll:61:PRO:HD2	2.49	0.43
46:14:3168:C:H4'	46:14:3169:U:O5'	2.18	0.43
46:14:3253:C:H2'	46:14:3254:C:O4'	2.19	0.43
1:LA:189:PHE:CE2	1:LA:193:LEU:HD11	2.54	0.43
4:LD:321:LYS:NZ	46:14:617:C:OP1	2.51	0.43
15:LO:105:GLU:HA	15:LO:108:LYS:HD3	2.01	0.43
20:LT:102:LEU:HD22	20:LT:106:ASP:HB2	2.00	0.43
22:LV:2:GLY:N	46:14:1171:A:OP1	2.52	0.43
46:14:2122:C:H2'	46:14:2123:A:O4'	2.18	0.43
46:14:2692:G:H2'	46:14:2692:G:N3	2.34	0.43
7:LG:117:TYR:HA	7:LG:120:ILE:HD12	2.00	0.42
13:LM:50:LEU:CD2	45:13:152:U:H4'	2.49	0.42
43:10:117:G:C4	43:10:147:G:N2	2.87	0.42
3:LC:209:ASP:OD1	3:LC:209:ASP:N	2.49	0.42
9:LI:10:LYS:HB3	9:LI:10:LYS:HE2	1.75	0.42
43:10:50:G:H1	43:10:54:C:H41	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:10:LEU:HD23	1:LA:180:PHE:CE2	2.53	0.42
4:LD:79:ILE:HG13	4:LD:80:PRO:HD2	2.01	0.42
17:LQ:33:ILE:HD13	46:14:585:C:C4	2.55	0.42
19:LS:101:ARG:NH1	19:LS:103:ARG:HH21	2.17	0.42
29:Lc:87:LYS:HB3	29:Lc:87:LYS:HE3	1.63	0.42
34:Lh:14:VAL:HG23	34:Lh:105:VAL:HB	2.00	0.42
40:Ln:90:ASN:HD22	40:Ln:90:ASN:N	2.17	0.42
43:10:115:G:H1'	43:10:163:G:N2	2.35	0.42
46:14:181:C:H2'	46:14:182:C:H6	1.84	0.42
46:14:2199:C:O2'	46:14:2273:A:N3	2.46	0.42
46:14:2210:A:O2'	46:14:2211:A:O4'	2.36	0.42
46:14:2680:G:N3	46:14:2680:G:H2'	2.33	0.42
46:14:2843:C:H2'	46:14:2844:G:O4'	2.20	0.42
5:LE:38:VAL:HG23	5:LE:122:THR:HG21	2.01	0.42
10:LJ:48:PHE:O	10:LJ:139:ARG:HA	2.20	0.42
14:LN:51:LYS:O	14:LN:69:VAL:HB	2.19	0.42
15:LO:12:LYS:NZ	15:LO:20:GLN:OE1	2.49	0.42
20:LT:61:ASP:OD1	20:LT:61:ASP:C	2.62	0.42
26:LZ:34:MET:HE3	26:LZ:34:MET:HB2	1.86	0.42
26:LZ:66:LYS:HE3	26:LZ:66:LYS:HA	2.01	0.42
29:Lc:76:LYS:HZ1	29:Lc:77:LYS:HD2	1.85	0.42
31:Le:35:VAL:HG22	31:Le:96:SER:HB2	2.01	0.42
34:Lh:63:LYS:HG3	34:Lh:68:HIS:CE1	2.54	0.42
43:10:125:U:C2	43:10:126:G:C8	3.07	0.42
46:14:2409:C:H2'	46:14:2410:C:C6	2.54	0.42
46:14:3025:U:H2'	46:14:3026:A:H8	1.83	0.42
1:LA:41:TYR:HB3	1:LA:163:LEU:HD21	2.00	0.42
41:Lp:33:ASP:OD1	46:14:2769:U:O2'	2.35	0.42
46:14:2571:G:OP2	46:14:2572:C:N4	2.53	0.42
1:LA:42:ASP:O	1:LA:43:PRO:C	2.62	0.42
14:LN:112:LYS:NZ	45:13:88:G:OP2	2.53	0.42
17:LQ:201:LYS:HE3	17:LQ:201:LYS:HA	2.01	0.42
34:Lh:64:LYS:HG3	46:14:632:G:OP1	2.20	0.42
43:10:126:G:H2'	43:10:127:U:O4'	2.19	0.42
46:14:854:G:H1	46:14:859:C:H42	1.67	0.42
46:14:1128:G:H2'	46:14:1129:C:C6	2.55	0.42
46:14:2210:A:H2'	46:14:2211:A:C5	2.54	0.42
2:LB:116:VAL:HB	2:LB:126:PHE:HB2	2.02	0.42
4:LD:374:ILE:HD13	46:14:524:A:N6	2.35	0.42
5:LE:97:ASN:N	5:LE:97:ASN:HD22	2.17	0.42
5:LE:165:PHE:CE2	5:LE:171:GLY:HA3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LS:101:ARG:HH11	19:LS:103:ARG:HH21	1.68	0.42
19:LS:157:ARG:HG2	19:LS:158:GLU:N	2.35	0.42
25:LY:126:ILE:O	46:14:1106:C:O2'	2.38	0.42
46:14:1545:A:H2'	46:14:1546:A:C8	2.55	0.42
1:LA:50:SER:HB2	1:LA:158:GLN:HG2	2.01	0.42
13:LM:53:ASP:N	13:LM:53:ASP:OD1	2.52	0.42
43:10:133:G:H4'	43:10:134:U:O4'	2.20	0.42
46:14:311:U:H2'	46:14:312:C:C6	2.54	0.42
46:14:936:A:H2'	46:14:937:C:C6	2.55	0.42
46:14:2843:C:N4	46:14:2848:A:O2'	2.53	0.42
1:LA:24:LYS:H	1:LA:24:LYS:HG2	1.67	0.42
1:LA:47:LYS:HE2	1:LA:47:LYS:HB3	1.62	0.42
16:LP:54:GLU:O	16:LP:58:GLN:HG3	2.20	0.42
35:Li:60:THR:HG21	46:14:1598:A:H5'	2.01	0.42
46:14:666:C:H2'	46:14:667:A:H8	1.84	0.42
46:14:857:A:H3'	46:14:858:A:C8	2.55	0.42
1:LA:30:GLU:HB2	1:LA:172:LEU:HD12	2.02	0.42
6:LF:92:ARG:HE	6:LF:92:ARG:HB2	1.70	0.42
6:LF:112:ASN:HB3	6:LF:137:VAL:O	2.20	0.42
17:LQ:120:PHE:CZ	46:14:3258:A:H2'	2.55	0.42
20:LT:124:GLU:OE1	20:LT:124:GLU:HA	2.19	0.42
27:La:50:LYS:HD3	46:14:2115:G:H5'	2.00	0.42
29:Lc:55:LYS:HB2	29:Lc:55:LYS:HE3	1.79	0.42
31:Le:18:ARG:HB3	31:Le:105:ILE:HG23	2.02	0.42
42:Lq:28:LYS:HB2	42:Lq:28:LYS:HE2	1.83	0.42
46:14:2152:A:H2'	46:14:2153:A:C5	2.54	0.42
46:14:2410:C:H2'	46:14:2411:U:C6	2.54	0.42
46:14:2574:U:O2'	46:14:2575:G:N7	2.44	0.42
6:LF:49:LYS:HB2	6:LF:49:LYS:HE2	1.85	0.41
28:Lb:6:LYS:HE3	28:Lb:6:LYS:HB2	1.48	0.41
37:Lk:39:TYR:CD1	37:Lk:40:PRO:HA	2.55	0.41
38:Ll:35:LYS:HA	38:Ll:43:TYR:O	2.19	0.41
46:14:786:U:H5	46:14:2740:C:N3	2.18	0.41
46:14:1237:A:N6	46:14:3118:G:C6	2.88	0.41
46:14:1733:G:H5'	46:14:1733:G:N3	2.35	0.41
46:14:1818:G:H2'	46:14:1819:A:C1'	2.50	0.41
46:14:2454:G:H2'	46:14:2455:G:C8	2.54	0.41
1:LA:61:PRO:HD2	1:LA:62:LYS:HE2	2.03	0.41
1:LA:67:MET:HE2	1:LA:73:HIS:HB3	2.02	0.41
32:Lf:70:ARG:HH11	46:14:3060:C:N4	2.18	0.41
43:10:88:A:H1'	43:10:89:A:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:10:119:G:N3	43:10:119:G:H2'	2.35	0.41
46:14:2427:A:H2'	46:14:2428:G:O4'	2.20	0.41
1:LA:36:ILE:HG21	1:LA:190:LEU:CD2	2.41	0.41
4:LD:370:GLU:O	4:LD:374:ILE:HD12	2.20	0.41
6:LF:10:MET:HE1	6:LF:81:GLU:HG3	2.01	0.41
12:LL:32:THR:HG21	12:LL:88:SER:HB3	2.02	0.41
14:LN:83:ARG:HG3	14:LN:83:ARG:NH1	2.35	0.41
19:LS:66:MET:HE3	19:LS:66:MET:H	1.85	0.41
40:Ln:102:ARG:HH21	46:14:2899:A:P	2.42	0.41
46:14:2885:U:H2'	46:14:2886:U:C6	2.55	0.41
46:14:3223:G:H2'	46:14:3224:U:C6	2.54	0.41
1:LA:47:LYS:H	1:LA:195:LYS:NZ	2.17	0.41
11:LK:116:ASP:OD1	11:LK:116:ASP:N	2.48	0.41
19:LS:168:THR:O	19:LS:172:LYS:HG3	2.20	0.41
46:14:545:C:H2'	46:14:546:U:C6	2.56	0.41
46:14:660:A:H2'	46:14:661:C:C6	2.55	0.41
46:14:2725:U:H2'	46:14:2726:U:H6	1.86	0.41
8:LH:109:LYS:HB2	8:LH:109:LYS:NZ	2.36	0.41
22:LV:23:ASP:O	22:LV:27:LYS:HG2	2.20	0.41
1:LA:165:MET:HE2	1:LA:165:MET:HB3	1.58	0.41
3:LC:221:ILE:HG12	3:LC:279:THR:HG23	2.03	0.41
11:LK:238:MET:HE2	11:LK:238:MET:HB3	1.90	0.41
22:LV:123:ASP:OD1	22:LV:124:GLN:N	2.53	0.41
29:Lc:66:LYS:H	29:Lc:66:LYS:HE2	1.85	0.41
46:14:857:A:H3'	46:14:858:A:H8	1.86	0.41
46:14:1653:U:H2'	46:14:1654:C:O4'	2.20	0.41
46:14:2226:A:H2'	46:14:2227:A:C8	2.56	0.41
10:LJ:101:LYS:HZ2	10:LJ:101:LYS:HG3	1.68	0.41
16:LP:13:LEU:HD23	16:LP:13:LEU:HA	1.88	0.41
16:LP:175:LYS:H	16:LP:175:LYS:HG2	1.61	0.41
43:10:127:U:H2'	43:10:128:A:O4'	2.21	0.41
46:14:582:G:H2'	46:14:583:C:C6	2.55	0.41
46:14:1508:C:H2'	46:14:1509:A:C8	2.56	0.41
46:14:2482:G:H3'	46:14:2483:A:H8	1.86	0.41
17:LQ:92:ILE:HG12	17:LQ:102:ARG:HG2	2.02	0.41
21:LU:136:ASP:OD2	21:LU:139:HIS:HB2	2.21	0.41
43:10:71:U:C2'	43:10:72:G:H5'	2.50	0.41
46:14:1748:G:H2'	46:14:1749:G:C8	2.55	0.41
3:LC:20:LYS:HB2	3:LC:20:LYS:HE2	1.78	0.41
6:LF:1:MET:HB3	6:LF:1:MET:HE3	1.83	0.41
6:LF:10:MET:HE3	6:LF:10:MET:HB2	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LF:121:LEU:HD23	6:LF:121:LEU:O	2.21	0.41
7:LG:10:ARG:HB3	7:LG:10:ARG:NH1	2.35	0.41
7:LG:205:LYS:HE3	7:LG:205:LYS:HB3	1.91	0.41
11:LK:11:ALA:O	11:LK:15:ARG:HG2	2.21	0.41
24:LX:25:LYS:HE2	24:LX:25:LYS:HB2	1.71	0.41
30:Ld:13:ASN:HD22	30:Ld:13:ASN:HA	1.57	0.41
43:10:132:G:H3'	43:10:133:G:H8	1.85	0.41
45:13:162:G:C6	46:14:1:G:C6	3.09	0.41
46:14:206:A:O2'	46:14:208:A:OP2	2.30	0.41
46:14:275:U:H2'	46:14:276:U:C6	2.55	0.41
46:14:2533:G:H2'	46:14:2534:A:O4'	2.21	0.41
46:14:2963:C:H2'	46:14:2964:G:C8	2.56	0.41
46:14:3189:C:H2'	46:14:3190:C:O4'	2.21	0.41
1:LA:129:ASN:OD1	1:LA:134:PHE:CD1	2.74	0.41
10:LJ:213:ARG:HA	10:LJ:213:ARG:HD2	1.87	0.41
11:LK:196:LYS:HG2	11:LK:201:GLY:HA3	2.03	0.41
17:LQ:64:ASP:CG	33:Lg:5:LEU:HD11	2.45	0.41
29:Lc:95:ARG:O	29:Lc:99:LYS:HD3	2.21	0.41
36:Lj:48:ARG:O	36:Lj:48:ARG:HD3	2.20	0.41
46:14:547:C:H2'	46:14:548:G:C8	2.56	0.41
46:14:710:U:O2'	46:14:711:A:H3'	2.21	0.41
1:LA:147:LYS:O	1:LA:150:GLU:HB3	2.21	0.40
19:LS:171:MET:H	19:LS:171:MET:HG3	1.64	0.40
23:LW:114:LYS:HE3	23:LW:114:LYS:HB2	1.71	0.40
29:Lc:130:LYS:HB2	29:Lc:130:LYS:HE2	1.86	0.40
43:10:123:A:H3'	43:10:124:A:H8	1.86	0.40
46:14:560:C:H2'	46:14:561:U:O4'	2.21	0.40
46:14:700:A:N7	46:14:702:U:O2'	2.51	0.40
46:14:2489:A:H2'	46:14:2490:A:C8	2.56	0.40
8:LH:96:MET:HG2	8:LH:97:TYR:N	2.37	0.40
11:LK:110:LEU:HD23	11:LK:110:LEU:HA	1.85	0.40
29:Lc:62:GLU:HB3	29:Lc:67:SER:HB2	2.03	0.40
46:14:36:U:H2'	46:14:37:A:O4'	2.22	0.40
4:LD:15:PHE:O	4:LD:16:GLU:C	2.63	0.40
5:LE:30:ASP:OD1	5:LE:34:ARG:NH1	2.55	0.40
20:LT:29:ASP:OD2	24:LX:74:ILE:HD12	2.21	0.40
24:LX:29:MET:HE3	25:LY:149:VAL:O	2.21	0.40
33:Lg:10:VAL:HG22	33:Lg:64:THR:HB	2.02	0.40
37:Lk:13:ASN:O	46:14:827:A:C4	2.74	0.40
37:Lk:76:THR:CG2	37:Lk:79:ARG:HB3	2.51	0.40
38:Ll:18:LYS:HB3	38:Ll:18:LYS:HE3	1.72	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:667:A:H2'	46:14:668:A:C8	2.56	0.40
46:14:1558:A:H2'	46:14:1559:C:C6	2.57	0.40
46:14:2536:G:H1	46:14:2552:C:H42	1.68	0.40
1:LA:4:LYS:HG3	1:LA:198:TRP:CB	2.52	0.40
4:LD:196:LYS:O	4:LD:199:MET:HG2	2.22	0.40
8:LH:123:LYS:HE2	8:LH:123:LYS:HB2	1.75	0.40
43:10:73:U:H2'	43:10:74:U:C6	2.57	0.40
43:10:138:U:H2'	43:10:139:A:H8	1.85	0.40
43:10:146:C:H2'	43:10:147:G:O4'	2.21	0.40
46:14:118:A:H3'	46:14:119:G:H5'	2.04	0.40
46:14:591:U:H3'	46:14:592:G:O4'	2.21	0.40
46:14:1098:C:H2'	46:14:1099:C:C6	2.57	0.40
46:14:1792:G:H2'	46:14:1793:G:C8	2.57	0.40
18:LR:243:LYS:HD2	18:LR:243:LYS:C	2.46	0.40
45:13:134:G:C6	45:13:135:C:C4	3.10	0.40
46:14:826:A:H1'	46:14:829:U:O4	2.21	0.40
46:14:1076:A:N6	46:14:1105:A:H2'	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	213/217 (98%)	190 (89%)	21 (10%)	2 (1%)	14	45
2	LB	243/260 (94%)	231 (95%)	12 (5%)	0	100	100
3	LC	384/389 (99%)	374 (97%)	10 (3%)	0	100	100
4	LD	396/405 (98%)	384 (97%)	12 (3%)	0	100	100
5	LE	167/181 (92%)	163 (98%)	4 (2%)	0	100	100
6	LF	189/194 (97%)	184 (97%)	5 (3%)	0	100	100
7	LG	203/206 (98%)	201 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	LH	129/140 (92%)	127 (98%)	2 (2%)	0	100	100
9	LI	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
10	LJ	205/219 (94%)	201 (98%)	4 (2%)	0	100	100
11	LK	286/293 (98%)	277 (97%)	9 (3%)	0	100	100
12	LL	152/175 (87%)	150 (99%)	2 (1%)	0	100	100
13	LM	115/154 (75%)	114 (99%)	1 (1%)	0	100	100
14	LN	124/146 (85%)	120 (97%)	4 (3%)	0	100	100
15	LO	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
16	LP	236/242 (98%)	229 (97%)	7 (3%)	0	100	100
17	LQ	203/230 (88%)	199 (98%)	4 (2%)	0	100	100
18	LR	231/237 (98%)	228 (99%)	3 (1%)	0	100	100
19	LS	198/200 (99%)	192 (97%)	6 (3%)	0	100	100
20	LT	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
21	LU	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
22	LV	184/187 (98%)	180 (98%)	4 (2%)	0	100	100
23	LW	180/211 (85%)	179 (99%)	1 (1%)	0	100	100
24	LX	175/178 (98%)	174 (99%)	1 (1%)	0	100	100
25	LY	161/164 (98%)	157 (98%)	4 (2%)	0	100	100
26	LZ	96/108 (89%)	94 (98%)	2 (2%)	0	100	100
27	La	60/164 (37%)	59 (98%)	1 (2%)	0	100	100
28	Lb	132/135 (98%)	130 (98%)	2 (2%)	0	100	100
29	Lc	140/143 (98%)	139 (99%)	1 (1%)	0	100	100
30	Ld	47/50 (94%)	46 (98%)	1 (2%)	0	100	100
31	Le	95/113 (84%)	93 (98%)	2 (2%)	0	100	100
32	Lf	106/120 (88%)	105 (99%)	1 (1%)	0	100	100
33	Lg	124/133 (93%)	123 (99%)	1 (1%)	0	100	100
34	Lh	101/112 (90%)	100 (99%)	1 (1%)	0	100	100
35	Li	112/120 (93%)	111 (99%)	1 (1%)	0	100	100
36	Lj	96/110 (87%)	94 (98%)	2 (2%)	0	100	100
37	Lk	84/95 (88%)	83 (99%)	1 (1%)	0	100	100
38	Ll	66/69 (96%)	66 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	Lm	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
40	Ln	49/128 (38%)	49 (100%)	0	0	100	100
41	Lp	96/105 (91%)	93 (97%)	3 (3%)	0	100	100
42	Lq	74/77 (96%)	70 (95%)	4 (5%)	0	100	100
All	All	6493/7066 (92%)	6328 (98%)	163 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	LA	59	PRO
1	LA	143	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	192/196 (98%)	168 (88%)	24 (12%)	4	21
2	LB	190/197 (96%)	186 (98%)	4 (2%)	47	64
3	LC	331/333 (99%)	324 (98%)	7 (2%)	47	64
4	LD	327/331 (99%)	319 (98%)	8 (2%)	43	62
5	LE	144/157 (92%)	141 (98%)	3 (2%)	47	64
6	LF	167/170 (98%)	161 (96%)	6 (4%)	31	54
7	LG	174/175 (99%)	170 (98%)	4 (2%)	44	63
8	LH	103/109 (94%)	100 (97%)	3 (3%)	37	58
9	LI	119/120 (99%)	117 (98%)	2 (2%)	53	67
10	LJ	173/180 (96%)	167 (96%)	6 (4%)	32	54
11	LK	244/246 (99%)	235 (96%)	9 (4%)	30	54
12	LL	133/151 (88%)	132 (99%)	1 (1%)	73	76
13	LM	106/134 (79%)	105 (99%)	1 (1%)	70	74
14	LN	115/132 (87%)	113 (98%)	2 (2%)	53	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	LO	108/109 (99%)	106 (98%)	2 (2%)	50	66
16	LP	207/209 (99%)	203 (98%)	4 (2%)	50	66
17	LQ	174/194 (90%)	170 (98%)	4 (2%)	44	63
18	LR	201/205 (98%)	192 (96%)	9 (4%)	24	48
19	LS	166/166 (100%)	165 (99%)	1 (1%)	78	79
20	LT	112/113 (99%)	109 (97%)	3 (3%)	39	59
21	LU	176/177 (99%)	173 (98%)	3 (2%)	53	67
22	LV	154/155 (99%)	151 (98%)	3 (2%)	50	66
23	LW	158/180 (88%)	151 (96%)	7 (4%)	25	49
24	LX	163/164 (99%)	159 (98%)	4 (2%)	42	61
25	LY	140/141 (99%)	138 (99%)	2 (1%)	59	70
26	LZ	89/97 (92%)	87 (98%)	2 (2%)	45	63
27	La	57/133 (43%)	56 (98%)	1 (2%)	51	67
28	Lb	115/117 (98%)	110 (96%)	5 (4%)	26	50
29	Lc	121/123 (98%)	119 (98%)	2 (2%)	53	67
30	Ld	42/43 (98%)	38 (90%)	4 (10%)	8	30
31	Le	85/98 (87%)	83 (98%)	2 (2%)	43	62
32	Lf	95/106 (90%)	93 (98%)	2 (2%)	47	64
33	Lg	114/121 (94%)	113 (99%)	1 (1%)	70	74
34	Lh	92/99 (93%)	92 (100%)	0	100	100
35	Li	100/104 (96%)	99 (99%)	1 (1%)	68	74
36	Lj	84/91 (92%)	82 (98%)	2 (2%)	43	62
37	Lk	72/77 (94%)	71 (99%)	1 (1%)	59	70
38	Ll	64/65 (98%)	61 (95%)	3 (5%)	23	48
39	Lm	47/48 (98%)	46 (98%)	1 (2%)	47	64
40	Ln	46/114 (40%)	46 (100%)	0	100	100
41	Lp	85/91 (93%)	84 (99%)	1 (1%)	63	72
42	Lq	61/62 (98%)	58 (95%)	3 (5%)	22	47
All	All	5646/6033 (94%)	5493 (97%)	153 (3%)	40	59

All (153) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	LA	3	SER
1	LA	4	LYS
1	LA	5	LEU
1	LA	6	GLN
1	LA	24	LYS
1	LA	25	LYS
1	LA	29	THR
1	LA	41	TYR
1	LA	44	GLN
1	LA	45	LYS
1	LA	46	ASP
1	LA	47	LYS
1	LA	60	ARG
1	LA	62	LYS
1	LA	64	LYS
1	LA	65	ILE
1	LA	139	SER
1	LA	140	HIS
1	LA	142	GLU
1	LA	154	THR
1	LA	155	ILE
1	LA	156	LYS
1	LA	162	VAL
1	LA	163	LEU
2	LB	181	LYS
2	LB	208	GLU
2	LB	243	THR
2	LB	245	ARG
3	LC	60	VAL
3	LC	111	SER
3	LC	114	LEU
3	LC	159	VAL
3	LC	287	LYS
3	LC	294	GLU
3	LC	355	LEU
4	LD	12	VAL
4	LD	109	LYS
4	LD	205	ILE
4	LD	206	SER
4	LD	258	LYS
4	LD	259	SER
4	LD	265	ASP
4	LD	318	THR

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Mol	Chain	Res	Type
5	LE	25	VAL
5	LE	30	ASP
5	LE	48	VAL
6	LF	14	ASP
6	LF	33	LYS
6	LF	87	VAL
6	LF	136	THR
6	LF	154	ILE
6	LF	186	GLU
7	LG	3	SER
7	LG	25	SER
7	LG	66	ARG
7	LG	194	LEU
8	LH	35	LYS
8	LH	77	MET
8	LH	84	GLN
9	LI	75	ILE
9	LI	77	ASN
10	LJ	44	ASP
10	LJ	50	VAL
10	LJ	91	VAL
10	LJ	113	THR
10	LJ	179	THR
10	LJ	186	SER
11	LK	65	VAL
11	LK	81	ARG
11	LK	120	GLN
11	LK	124	GLU
11	LK	183	SER
11	LK	184	LYS
11	LK	251	SER
11	LK	269	LYS
11	LK	274	GLU
12	LL	91	ILE
13	LM	69	LEU
14	LN	59	ARG
14	LN	87	GLU
15	LO	18	LEU
15	LO	36	VAL
16	LP	42	LYS
16	LP	62	LEU
16	LP	175	LYS

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Mol	Chain	Res	Type
16	LP	236	GLU
17	LQ	111	SER
17	LQ	135	VAL
17	LQ	139	SER
17	LQ	149	VAL
18	LR	45	THR
18	LR	84	LEU
18	LR	91	MET
18	LR	98	GLU
18	LR	105	GLU
18	LR	127	ILE
18	LR	190	THR
18	LR	197	THR
18	LR	236	SER
19	LS	105	LEU
20	LT	7	VAL
20	LT	87	SER
20	LT	88	SER
21	LU	85	THR
21	LU	99	ARG
21	LU	169	LYS
22	LV	40	THR
22	LV	79	VAL
22	LV	162	THR
23	LW	31	GLU
23	LW	59	SER
23	LW	106	LEU
23	LW	111	GLU
23	LW	133	LYS
23	LW	157	ASP
23	LW	179	GLU
24	LX	28	ARG
24	LX	41	SER
24	LX	106	GLU
24	LX	168	THR
25	LY	14	SER
25	LY	72	VAL
26	LZ	82	LEU
26	LZ	94	ASN
27	La	26	SER
28	Lb	35	ASP
28	Lb	88	ASP

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Mol	Chain	Res	Type
28	Lb	92	LYS
28	Lb	97	VAL
28	Lb	99	VAL
29	Lc	18	SER
29	Lc	72	THR
30	Ld	9	SER
30	Ld	13	ASN
30	Ld	22	HIS
30	Ld	23	LYS
31	Le	27	LYS
31	Le	43	LYS
32	Lf	33	LYS
32	Lf	43	LYS
33	Lg	111	GLU
35	Li	75	ASN
36	Lj	71	ARG
36	Lj	91	GLU
37	Lk	64	MET
38	Ll	13	LEU
38	Ll	24	LYS
38	Ll	52	LYS
39	Lm	45	ARG
41	Lp	24	LYS
42	Lq	6	LYS
42	Lq	29	MET
42	Lq	60	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (99) such sidechains are listed below:

Mol	Chain	Res	Type
1	LA	6	GLN
1	LA	35	GLN
1	LA	72	GLN
1	LA	182	ASN
1	LA	197	ASN
1	LA	199	GLN
2	LB	115	ASN
2	LB	233	GLN
3	LC	121	ASN
3	LC	273	ASN
4	LD	13	GLN
4	LD	53	GLN

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Mol	Chain	Res	Type
4	LD	145	HIS
4	LD	176	GLN
4	LD	290	ASN
4	LD	303	GLN
4	LD	334	ASN
4	LD	350	GLN
5	LE	97	ASN
5	LE	109	GLN
6	LF	101	HIS
6	LF	165	ASN
6	LF	166	GLN
7	LG	18	HIS
7	LG	36	GLN
7	LG	73	HIS
7	LG	163	ASN
7	LG	170	GLN
9	LI	25	HIS
9	LI	66	ASN
9	LI	84	GLN
9	LI	132	ASN
10	LJ	112	GLN
10	LJ	144	ASN
11	LK	63	GLN
11	LK	120	GLN
11	LK	122	ASN
11	LK	188	GLN
11	LK	228	GLN
11	LK	243	HIS
11	LK	288	ASN
12	LL	56	GLN
12	LL	79	ASN
14	LN	18	HIS
14	LN	43	ASN
14	LN	56	GLN
16	LP	46	ASN
16	LP	110	GLN
16	LP	113	ASN
16	LP	128	HIS
16	LP	171	GLN
16	LP	186	HIS
16	LP	206	GLN
17	LQ	37	ASN

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Mol	Chain	Res	Type
18	LR	57	GLN
18	LR	74	ASN
18	LR	142	ASN
18	LR	239	GLN
19	LS	60	GLN
19	LS	149	GLN
21	LU	86	ASN
21	LU	87	GLN
21	LU	144	ASN
21	LU	196	GLN
22	LV	143	ASN
22	LV	150	HIS
22	LV	161	HIS
23	LW	141	ASN
24	LX	8	GLN
24	LX	64	ASN
24	LX	107	GLN
24	LX	175	ASN
25	LY	54	HIS
25	LY	66	ASN
25	LY	112	ASN
25	LY	114	GLN
27	La	29	GLN
28	Lb	62	GLN
28	Lb	96	ASN
29	Lc	79	ASN
30	Ld	13	ASN
30	Ld	50	ASN
31	Le	17	ASN
31	Le	52	ASN
32	Lf	46	GLN
32	Lf	85	ASN
34	Lh	41	ASN
34	Lh	68	HIS
34	Lh	111	ASN
35	Li	33	GLN
35	Li	75	ASN
36	Lj	41	HIS
36	Lj	95	ASN
37	Lk	48	ASN
38	Ll	67	GLN
39	Lm	38	ASN

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Mol	Chain	Res	Type
40	Ln	90	ASN
41	Lp	27	GLN
41	Lp	83	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	10	157/204 (76%)	111 (70%)	19 (12%)
44	12	118/119 (99%)	12 (10%)	0
45	13	162/163 (99%)	33 (20%)	0
46	14	3138/3390 (92%)	569 (18%)	21 (0%)
All	All	3575/3876 (92%)	725 (20%)	40 (1%)

All (725) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	10	48	G
43	10	50	G
43	10	54	C
43	10	58	C
43	10	59	G
43	10	60	A
43	10	61	U
43	10	62	A
43	10	64	C
43	10	65	G
43	10	66	C
43	10	67	A
43	10	68	U
43	10	69	A
43	10	71	U
43	10	72	G
43	10	73	U
43	10	74	U
43	10	75	U
43	10	76	U
43	10	77	U
43	10	78	C
43	10	79	C
43	10	80	C
43	10	81	U

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Mol	Chain	Res	Type
43	10	84	A
43	10	87	U
43	10	88	A
43	10	89	A
43	10	90	A
43	10	92	C
43	10	94	A
43	10	95	A
43	10	96	G
43	10	97	G
43	10	98	G
43	10	99	U
43	10	100	U
43	10	101	G
43	10	103	G
43	10	104	U
43	10	105	C
43	10	106	U
43	10	107	U
43	10	108	G
43	10	109	G
43	10	110	A
43	10	113	G
43	10	117	G
43	10	118	G
43	10	119	G
43	10	120	U
43	10	121	C
43	10	122	A
43	10	123	A
43	10	124	A
43	10	125	U
43	10	126	G
43	10	129	U
43	10	130	A
43	10	132	G
43	10	133	G
43	10	134	U
43	10	135	U
43	10	136	C
43	10	137	A
43	10	138	U

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Mol	Chain	Res	Type
43	10	139	A
43	10	140	U
43	10	141	A
43	10	144	U
43	10	145	C
43	10	146	C
43	10	147	G
43	10	148	C
43	10	150	G
43	10	151	G
43	10	155	G
43	10	157	A
43	10	158	A
43	10	159	U
43	10	160	A
43	10	161	A
43	10	162	A
43	10	163	G
43	10	164	C
43	10	165	G
43	10	166	A
43	10	167	G
43	10	169	G
43	10	170	G
43	10	172	U
43	10	173	C
43	10	178	C
43	10	180	C
43	10	182	C
43	10	184	G
43	10	185	U
43	10	186	U
43	10	187	A
43	10	189	C
43	10	191	C
43	10	193	G
43	10	194	G
43	10	195	U
43	10	197	G
43	10	198	G
43	10	199	G
43	10	201	C

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Mol	Chain	Res	Type
43	10	202	C
43	10	204	A
44	12	2	G
44	12	10	C
44	12	13	A
44	12	25	G
44	12	33	U
44	12	38	U
44	12	53	U
44	12	54	A
44	12	64	G
44	12	89	G
44	12	110	G
44	12	117	C
45	13	2	A
45	13	26	C
45	13	27	G
45	13	37	U
45	13	38	C
45	13	41	U
45	13	62	A
45	13	65	C
45	13	66	U
45	13	77	U
45	13	78	G
45	13	83	A
45	13	84	U
45	13	85	C
45	13	87	C
45	13	89	U
45	13	90	G
45	13	94	C
45	13	98	G
45	13	100	G
45	13	107	A
45	13	108	A
45	13	109	C
45	13	119	G
45	13	128	C
45	13	129	A
45	13	131	U
45	13	133	G

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Mol	Chain	Res	Type
45	13	134	G
45	13	146	U
45	13	149	G
45	13	153	G
45	13	156	C
46	14	12	U
46	14	24	A
46	14	29	C
46	14	38	A
46	14	41	A
46	14	47	A
46	14	57	G
46	14	58	A
46	14	63	A
46	14	64	A
46	14	67	U
46	14	69	A
46	14	71	A
46	14	90	G
46	14	97	A
46	14	107	A
46	14	108	G
46	14	109	C
46	14	113	G
46	14	114	C
46	14	118	A
46	14	120	A
46	14	131	U
46	14	132	C
46	14	133	C
46	14	134	G
46	14	140	C
46	14	144	U
46	14	154	G
46	14	155	A
46	14	163	C
46	14	164	C
46	14	167	A
46	14	168	G
46	14	184	A
46	14	187	U
46	14	188	C

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Mol	Chain	Res	Type
46	14	194	G
46	14	207	G
46	14	211	G
46	14	215	G
46	14	216	A
46	14	228	U
46	14	245	A
46	14	248	A
46	14	258	G
46	14	262	A
46	14	266	G
46	14	283	U
46	14	292	A
46	14	294	U
46	14	302	U
46	14	320	A
46	14	326	G
46	14	334	G
46	14	335	A
46	14	346	A
46	14	347	C
46	14	373	G
46	14	394	A
46	14	395	G
46	14	398	U
46	14	399	G
46	14	400	C
46	14	417	G
46	14	418	G
46	14	419	A
46	14	430	G
46	14	435	G
46	14	436	C
46	14	437	G
46	14	524	A
46	14	525	A
46	14	527	G
46	14	531	G
46	14	533	G
46	14	534	C
46	14	535	U
46	14	538	U

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Mol	Chain	Res	Type
46	14	539	G
46	14	540	A
46	14	543	C
46	14	544	G
46	14	545	C
46	14	546	U
46	14	547	C
46	14	548	G
46	14	549	U
46	14	550	G
46	14	556	U
46	14	571	U
46	14	574	U
46	14	575	A
46	14	576	G
46	14	581	C
46	14	586	G
46	14	590	C
46	14	591	U
46	14	592	G
46	14	593	G
46	14	594	C
46	14	597	G
46	14	598	C
46	14	601	C
46	14	602	G
46	14	605	A
46	14	606	U
46	14	607	C
46	14	608	U
46	14	609	G
46	14	610	C
46	14	614	C
46	14	615	U
46	14	616	C
46	14	620	A
46	14	621	C
46	14	631	U
46	14	636	U
46	14	637	C
46	14	657	A
46	14	660	A

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Mol	Chain	Res	Type
46	14	671	A
46	14	688	A
46	14	692	A
46	14	693	A
46	14	698	C
46	14	701	G
46	14	710	U
46	14	711	A
46	14	718	A
46	14	725	C
46	14	727	G
46	14	728	A
46	14	729	U
46	14	730	U
46	14	731	G
46	14	742	C
46	14	745	G
46	14	770	G
46	14	775	U
46	14	777	U
46	14	786	U
46	14	787	U
46	14	791	G
46	14	795	G
46	14	809	G
46	14	810	G
46	14	811	A
46	14	816	A
46	14	827	A
46	14	840	G
46	14	853	A
46	14	854	G
46	14	859	C
46	14	867	G
46	14	871	C
46	14	874	G
46	14	879	G
46	14	884	U
46	14	889	U
46	14	917	G
46	14	918	G
46	14	920	G

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Mol	Chain	Res	Type
46	14	924	A
46	14	926	G
46	14	927	A
46	14	931	A
46	14	933	C
46	14	934	G
46	14	935	A
46	14	947	G
46	14	951	G
46	14	954	C
46	14	963	G
46	14	969	C
46	14	970	U
46	14	991	U
46	14	992	G
46	14	993	C
46	14	1006	G
46	14	1013	C
46	14	1014	A
46	14	1022	G
46	14	1028	U
46	14	1029	C
46	14	1030	G
46	14	1036	G
46	14	1037	C
46	14	1041	G
46	14	1048	A
46	14	1059	A
46	14	1064	U
46	14	1069	A
46	14	1075	G
46	14	1076	A
46	14	1077	C
46	14	1087	G
46	14	1093	U
46	14	1094	U
46	14	1106	C
46	14	1107	G
46	14	1108	G
46	14	1109	A
46	14	1114	A
46	14	1115	G

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Mol	Chain	Res	Type
46	14	1128	G
46	14	1133	U
46	14	1140	A
46	14	1142	G
46	14	1155	U
46	14	1164	A
46	14	1165	A
46	14	1166	C
46	14	1170	A
46	14	1185	G
46	14	1189	A
46	14	1191	C
46	14	1192	U
46	14	1193	G
46	14	1200	A
46	14	1201	A
46	14	1205	A
46	14	1213	C
46	14	1218	G
46	14	1221	G
46	14	1224	G
46	14	1297	G
46	14	1299	A
46	14	1321	U
46	14	1328	U
46	14	1329	A
46	14	1335	G
46	14	1343	C
46	14	1344	A
46	14	1360	A
46	14	1361	A
46	14	1362	G
46	14	1363	U
46	14	1364	G
46	14	1365	C
46	14	1366	C
46	14	1367	A
46	14	1374	G
46	14	1403	A
46	14	1410	U
46	14	1413	G
46	14	1430	G

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Mol	Chain	Res	Type
46	14	1442	G
46	14	1445	G
46	14	1448	C
46	14	1457	A
46	14	1462	C
46	14	1463	A
46	14	1466	U
46	14	1480	C
46	14	1486	A
46	14	1491	G
46	14	1492	A
46	14	1494	G
46	14	1495	A
46	14	1501	A
46	14	1513	G
46	14	1534	U
46	14	1538	C
46	14	1547	G
46	14	1566	A
46	14	1571	G
46	14	1577	U
46	14	1578	U
46	14	1585	U
46	14	1587	C
46	14	1588	U
46	14	1589	C
46	14	1592	A
46	14	1593	A
46	14	1594	A
46	14	1598	A
46	14	1602	G
46	14	1609	A
46	14	1625	C
46	14	1633	U
46	14	1643	C
46	14	1646	U
46	14	1649	G
46	14	1652	G
46	14	1661	C
46	14	1698	U
46	14	1729	G
46	14	1748	G

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Mol	Chain	Res	Type
46	14	1755	A
46	14	1756	G
46	14	1770	G
46	14	1771	C
46	14	1772	G
46	14	1774	G
46	14	1784	G
46	14	1803	A
46	14	1816	C
46	14	1819	A
46	14	1820	G
46	14	1821	U
46	14	1823	C
46	14	1827	C
46	14	1828	C
46	14	1848	A
46	14	1849	C
46	14	1852	C
46	14	1853	A
46	14	1855	C
46	14	1861	U
46	14	1872	C
46	14	1873	A
46	14	1884	G
46	14	1885	A
46	14	1886	U
46	14	1907	A
46	14	1912	G
46	14	1914	A
46	14	1949	C
46	14	2111	A
46	14	2115	G
46	14	2116	U
46	14	2118	C
46	14	2126	G
46	14	2135	A
46	14	2144	U
46	14	2162	A
46	14	2201	A
46	14	2208	U
46	14	2209	G
46	14	2211	A

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Mol	Chain	Res	Type
46	14	2212	U
46	14	2213	G
46	14	2228	U
46	14	2231	A
46	14	2245	A
46	14	2252	G
46	14	2253	G
46	14	2259	A
46	14	2261	U
46	14	2263	U
46	14	2264	G
46	14	2273	A
46	14	2274	A
46	14	2276	G
46	14	2277	U
46	14	2283	A
46	14	2285	U
46	14	2286	G
46	14	2309	C
46	14	2310	G
46	14	2313	U
46	14	2316	A
46	14	2318	G
46	14	2321	U
46	14	2337	U
46	14	2338	G
46	14	2339	U
46	14	2366	A
46	14	2375	A
46	14	2376	A
46	14	2377	C
46	14	2378	G
46	14	2388	G
46	14	2396	G
46	14	2400	A
46	14	2404	A
46	14	2405	A
46	14	2406	G
46	14	2407	A
46	14	2414	U
46	14	2425	C
46	14	2438	G

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Mol	Chain	Res	Type
46	14	2440	G
46	14	2444	U
46	14	2445	G
46	14	2446	A
46	14	2447	C
46	14	2449	U
46	14	2450	G
46	14	2451	A
46	14	2452	G
46	14	2457	G
46	14	2461	U
46	14	2462	A
46	14	2463	U
46	14	2471	A
46	14	2475	G
46	14	2478	A
46	14	2479	G
46	14	2489	A
46	14	2492	U
46	14	2502	U
46	14	2503	U
46	14	2505	A
46	14	2506	A
46	14	2507	C
46	14	2508	G
46	14	2509	U
46	14	2510	U
46	14	2519	U
46	14	2520	A
46	14	2529	A
46	14	2536	G
46	14	2538	G
46	14	2540	G
46	14	2543	A
46	14	2545	U
46	14	2546	G
46	14	2547	C
46	14	2548	C
46	14	2551	U
46	14	2552	C
46	14	2553	U
46	14	2556	U

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Mol	Chain	Res	Type
46	14	2557	U
46	14	2558	G
46	14	2559	G
46	14	2570	U
46	14	2571	G
46	14	2572	C
46	14	2573	U
46	14	2574	U
46	14	2575	G
46	14	2576	C
46	14	2588	G
46	14	2596	A
46	14	2598	A
46	14	2606	G
46	14	2609	G
46	14	2610	G
46	14	2617	G
46	14	2622	G
46	14	2629	A
46	14	2640	A
46	14	2655	U
46	14	2659	A
46	14	2677	A
46	14	2680	G
46	14	2692	G
46	14	2694	A
46	14	2699	A
46	14	2706	A
46	14	2707	A
46	14	2717	G
46	14	2722	U
46	14	2731	G
46	14	2732	U
46	14	2752	G
46	14	2756	G
46	14	2758	C
46	14	2762	A
46	14	2765	A
46	14	2776	C
46	14	2780	G
46	14	2781	G
46	14	2794	G

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Mol	Chain	Res	Type
46	14	2799	G
46	14	2802	A
46	14	2803	G
46	14	2804	A
46	14	2805	A
46	14	2813	C
46	14	2820	A
46	14	2832	U
46	14	2845	U
46	14	2848	A
46	14	2853	G
46	14	2870	C
46	14	2874	G
46	14	2875	A
46	14	2890	A
46	14	2892	C
46	14	2897	U
46	14	2902	C
46	14	2912	C
46	14	2914	A
46	14	2917	G
46	14	2926	U
46	14	2928	C
46	14	2933	A
46	14	2938	U
46	14	2939	A
46	14	2945	C
46	14	2948	G
46	14	2950	G
46	14	2951	C
46	14	2954	G
46	14	2974	A
46	14	2975	G
46	14	2983	U
46	14	2986	C
46	14	3000	G
46	14	3014	A
46	14	3030	G
46	14	3032	G
46	14	3059	U
46	14	3060	C
46	14	3061	G

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Mol	Chain	Res	Type
46	14	3073	A
46	14	3080	G
46	14	3094	C
46	14	3103	G
46	14	3118	G
46	14	3119	C
46	14	3120	C
46	14	3132	A
46	14	3133	U
46	14	3136	G
46	14	3144	A
46	14	3146	C
46	14	3154	G
46	14	3156	G
46	14	3160	G
46	14	3161	C
46	14	3166	C
46	14	3168	C
46	14	3169	U
46	14	3172	C
46	14	3173	C
46	14	3174	G
46	14	3179	G
46	14	3181	A
46	14	3185	G
46	14	3191	U
46	14	3194	G
46	14	3201	A
46	14	3203	G
46	14	3208	C
46	14	3209	G
46	14	3211	G
46	14	3212	U
46	14	3213	C
46	14	3214	G
46	14	3216	U
46	14	3219	C
46	14	3235	G
46	14	3236	A
46	14	3240	G
46	14	3254	C
46	14	3257	G

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Mol	Chain	Res	Type
46	14	3260	G
46	14	3264	A
46	14	3266	U
46	14	3267	U
46	14	3268	U
46	14	3269	C
46	14	3271	A
46	14	3272	U
46	14	3273	C
46	14	3275	A
46	14	3278	G
46	14	3279	G
46	14	3281	G
46	14	3285	A
46	14	3296	C
46	14	3299	A
46	14	3308	A
46	14	3311	C
46	14	3334	A
46	14	3337	G
46	14	3343	U
46	14	3344	U
46	14	3348	G
46	14	3361	G
46	14	3370	C
46	14	3374	U
46	14	3383	C
46	14	3390	U

All (40) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
43	10	75	U
43	10	76	U
43	10	106	U
43	10	108	G
43	10	109	G
43	10	120	U
43	10	124	A
43	10	125	U
43	10	133	G
43	10	134	U

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Mol	Chain	Res	Type
43	10	135	U
43	10	144	U
43	10	157	A
43	10	160	A
43	10	161	A
43	10	177	U
43	10	186	U
43	10	194	G
43	10	198	G
46	14	113	G
46	14	590	C
46	14	601	C
46	14	608	U
46	14	692	A
46	14	917	G
46	14	926	G
46	14	990	G
46	14	1027	A
46	14	1847	A
46	14	1848	A
46	14	1852	C
46	14	2375	A
46	14	2376	A
46	14	2544	C
46	14	2552	C
46	14	2553	U
46	14	2556	U
46	14	2731	G
46	14	2793	A
46	14	3168	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

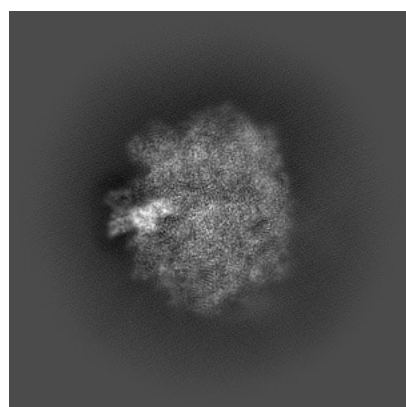
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65327. These allow visual inspection of the internal detail of the map and identification of artifacts.

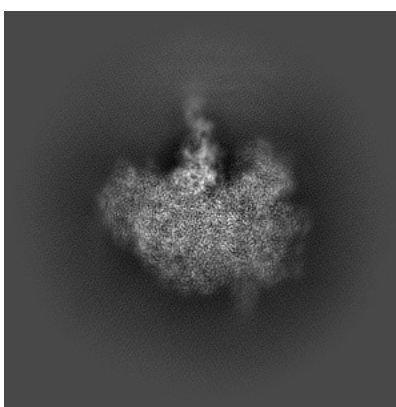
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

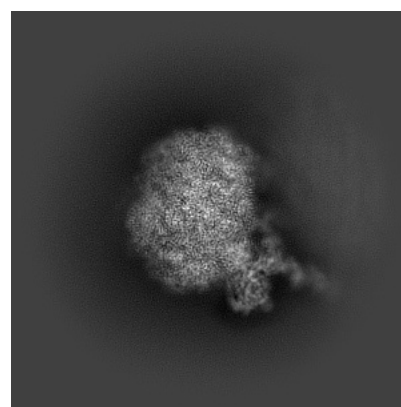
6.1.1 Primary map



X



Y

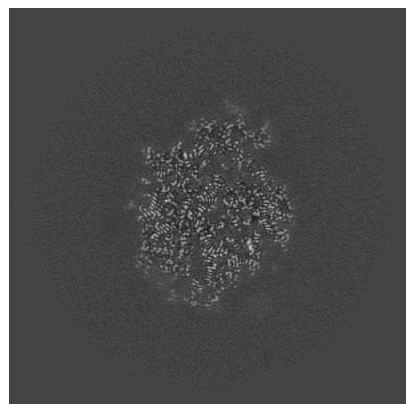


Z

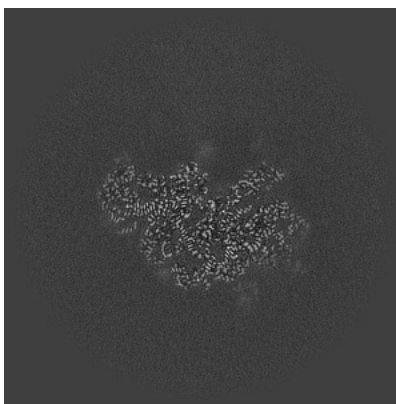
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

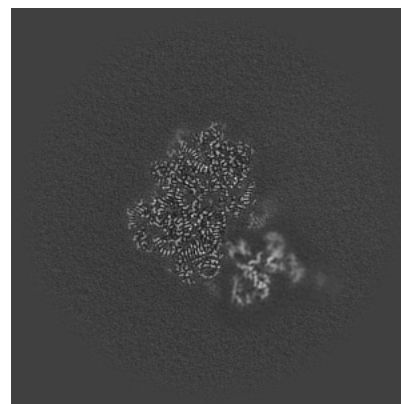
6.2.1 Primary map



X Index: 240



Y Index: 240

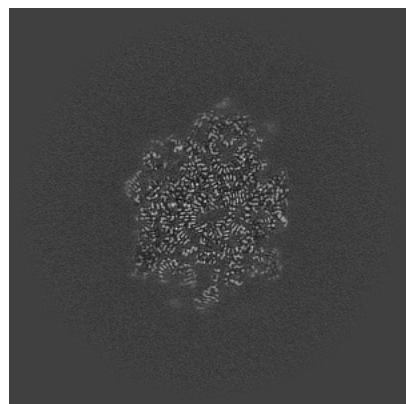


Z Index: 240

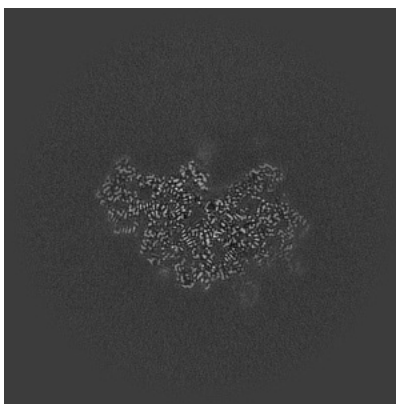
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

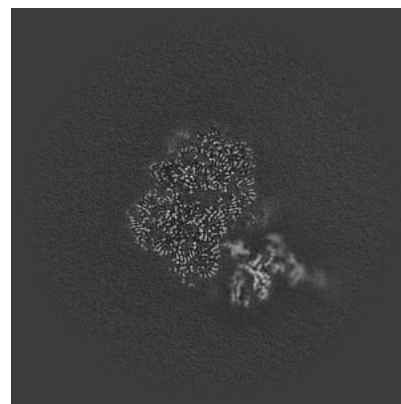
6.3.1 Primary map



X Index: 227



Y Index: 242

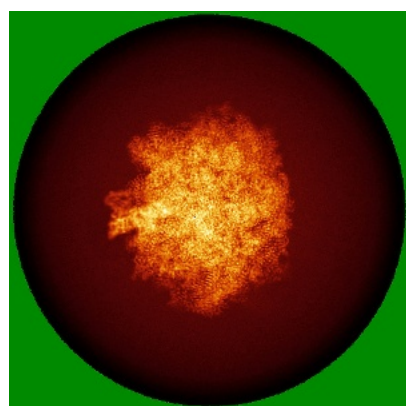


Z Index: 237

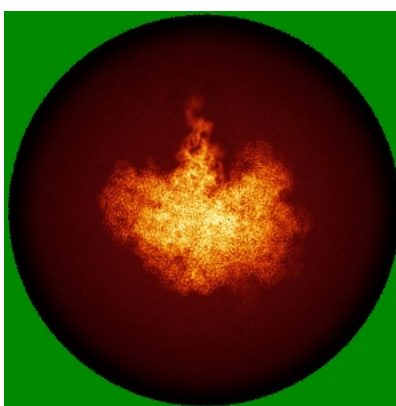
The images above show the largest variance slices of the map in three orthogonal directions.

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

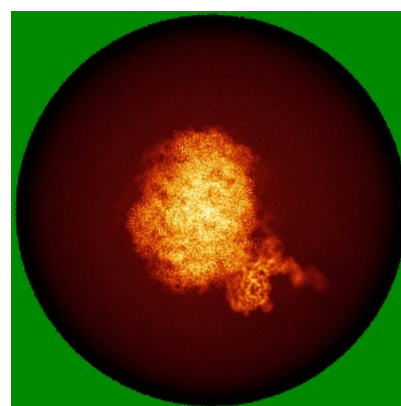
6.4.1 Primary map



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

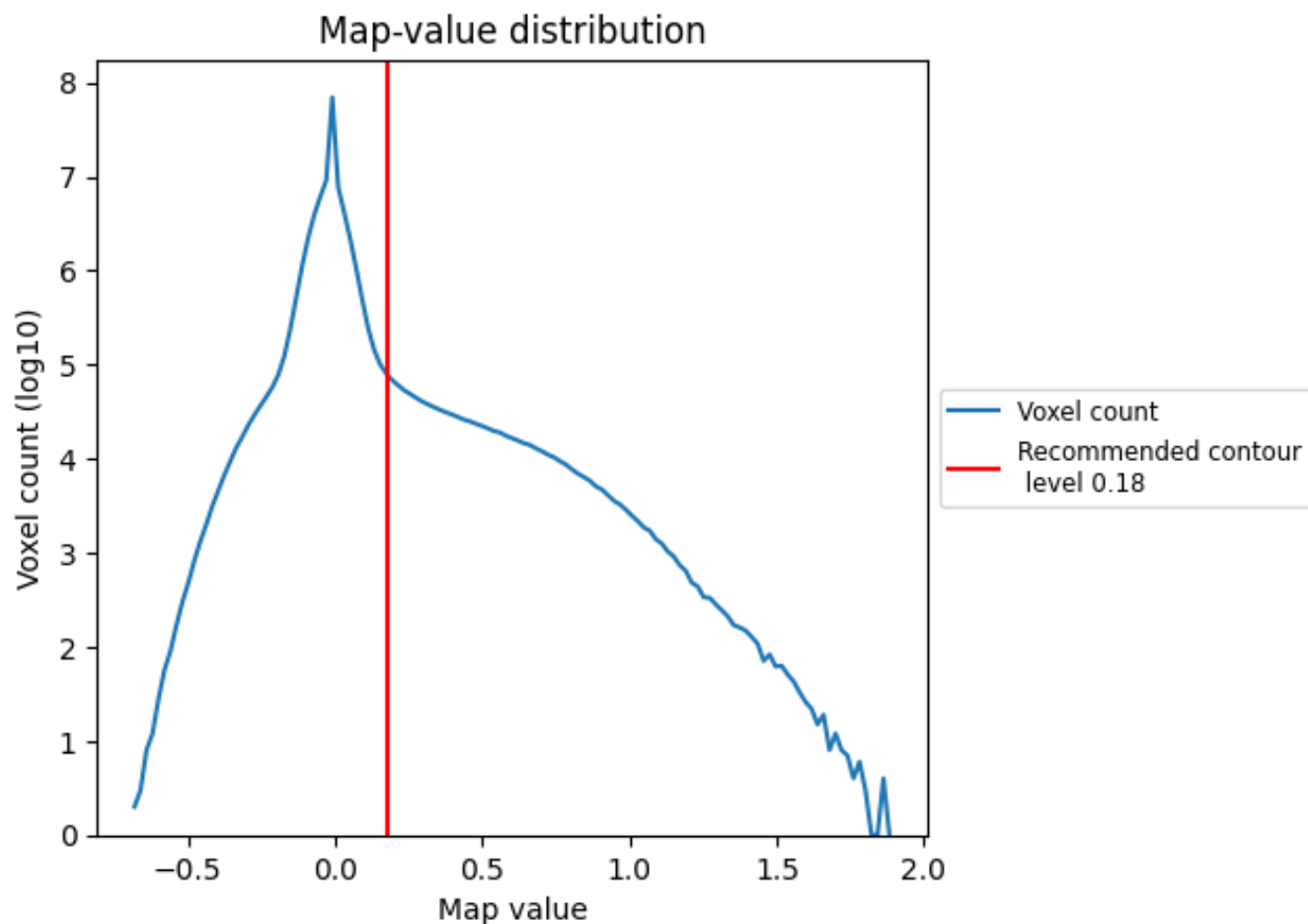
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

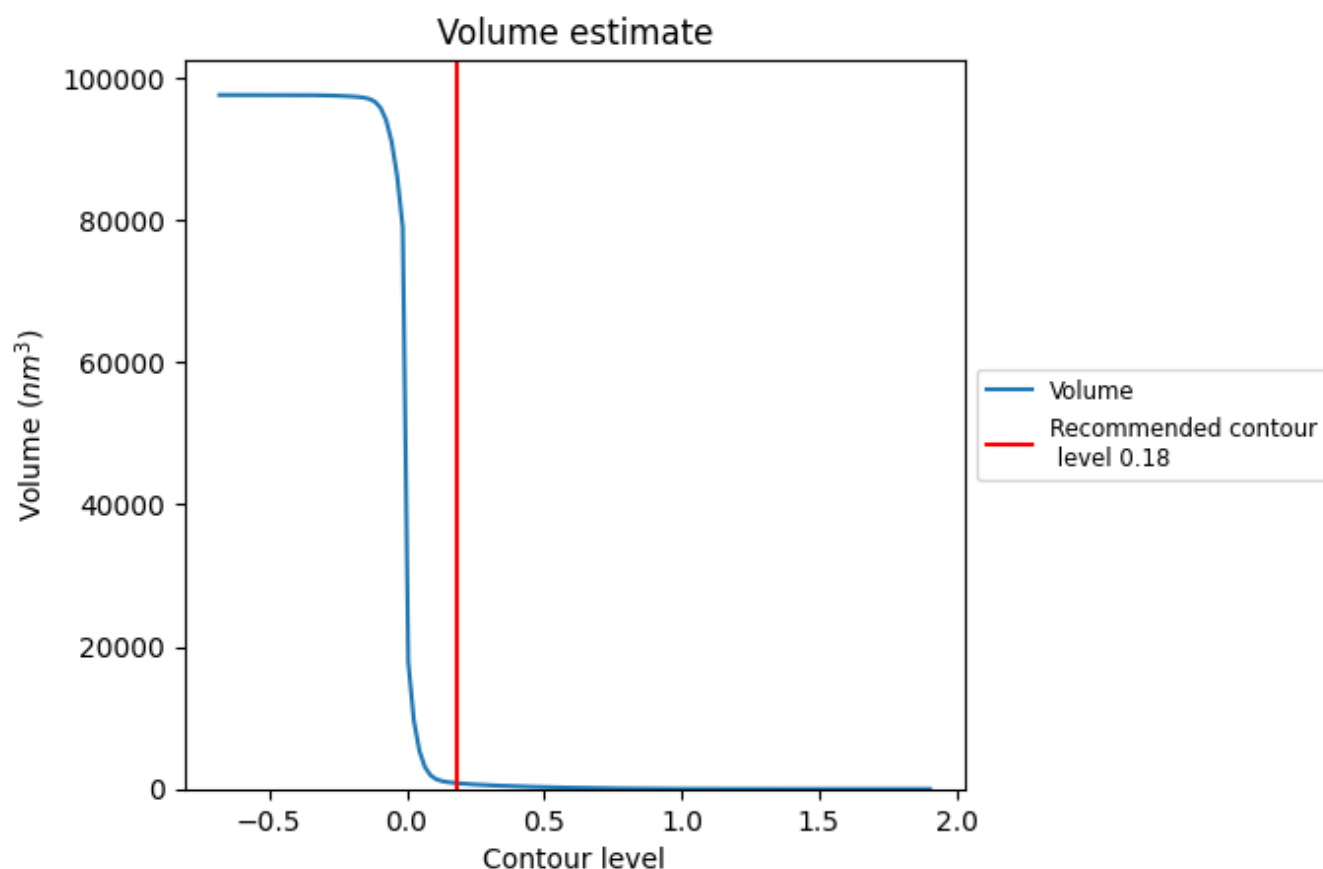
This section contains the results of statistical analysis of the map.

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.

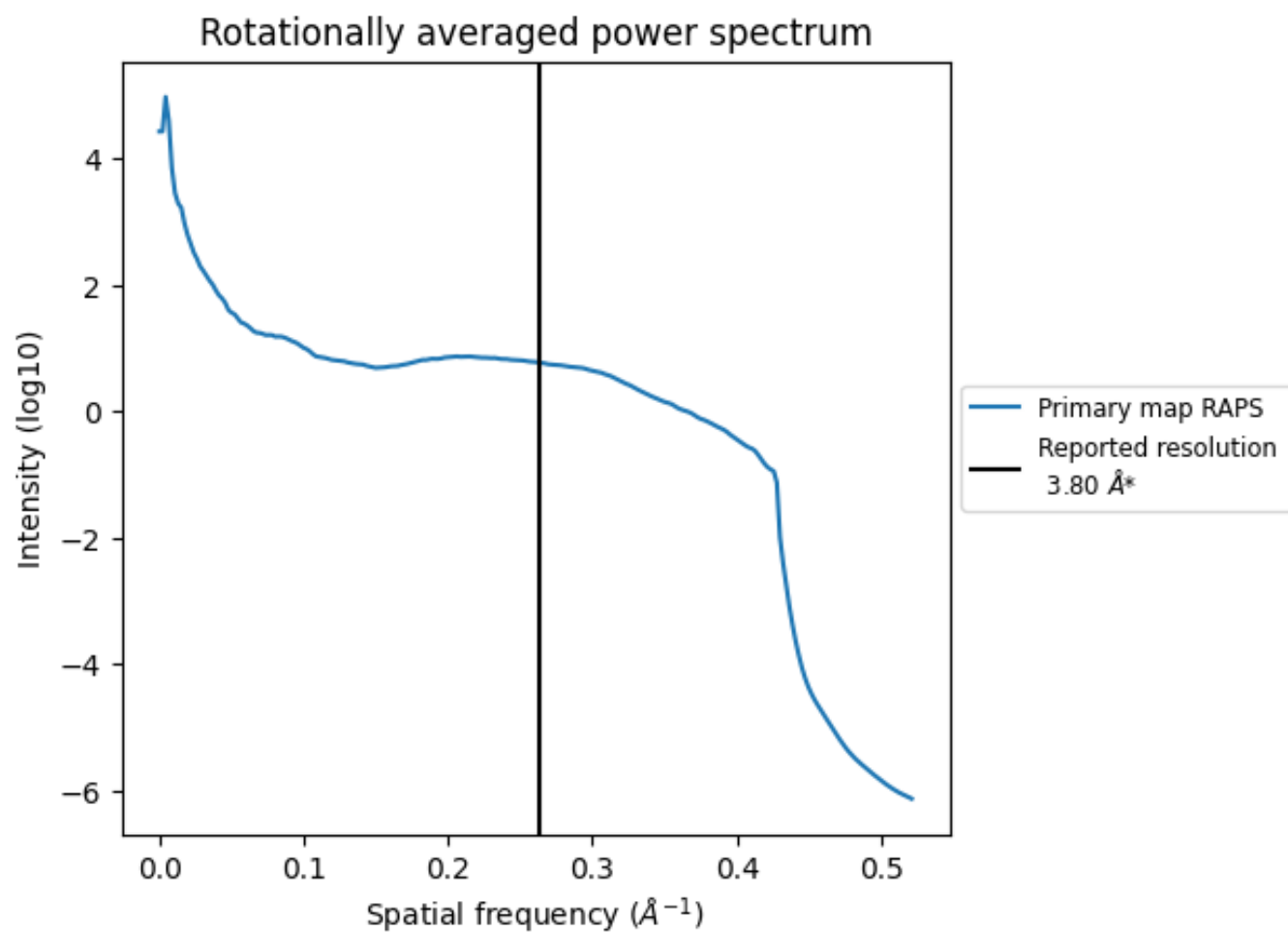
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 827 nm^3 ; this corresponds to an approximate mass of 747 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 0.263 Å⁻¹

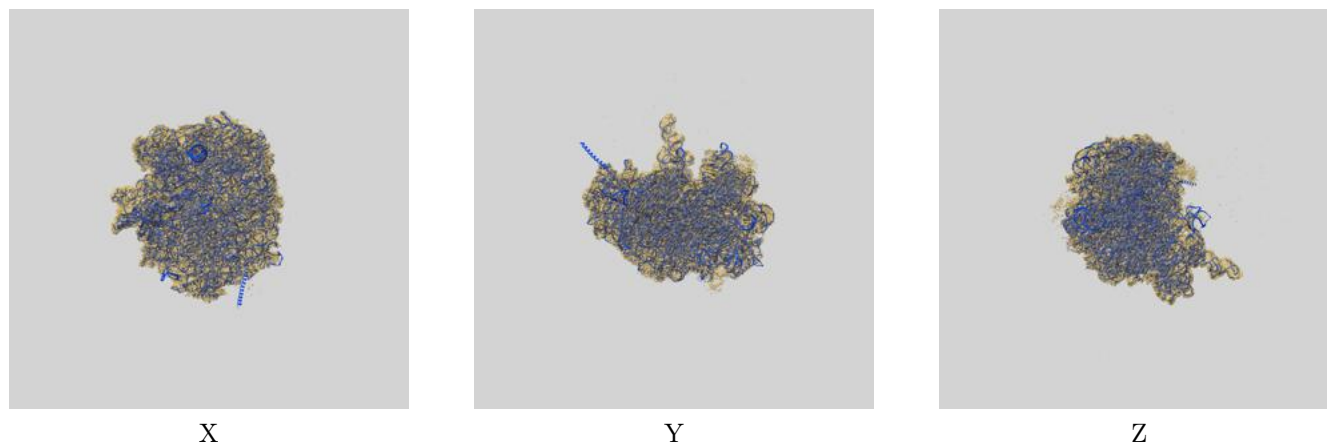
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

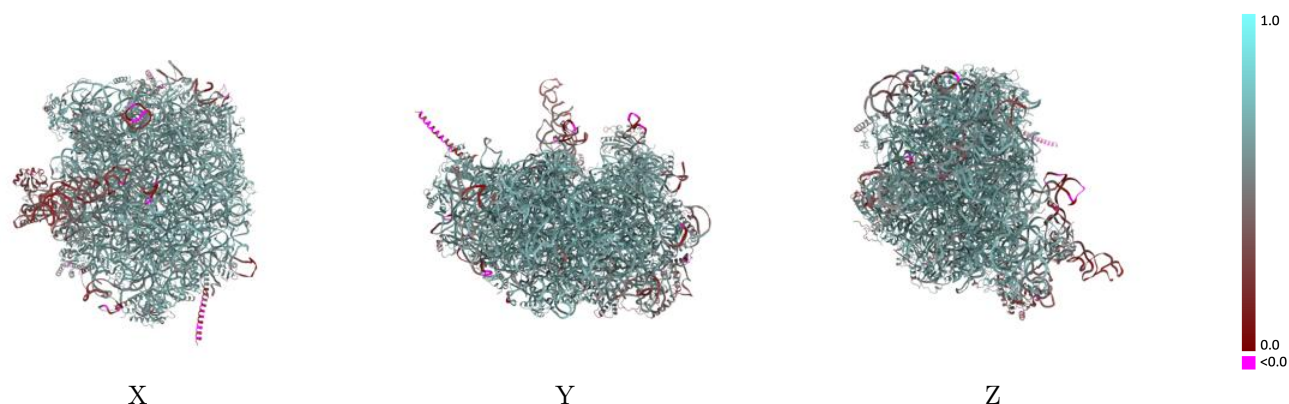
This section contains information regarding the fit between EMDB map EMD-65327 and PDB model 9VTG. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



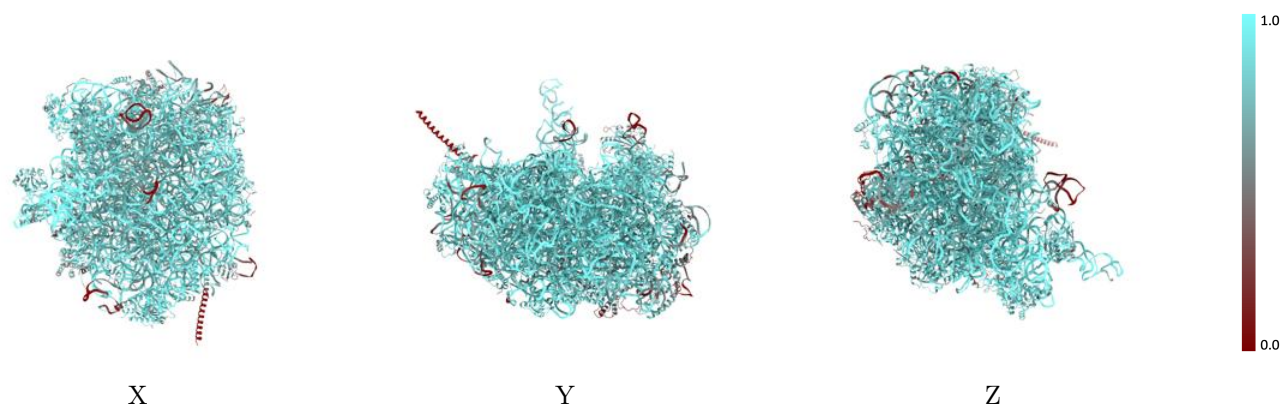
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



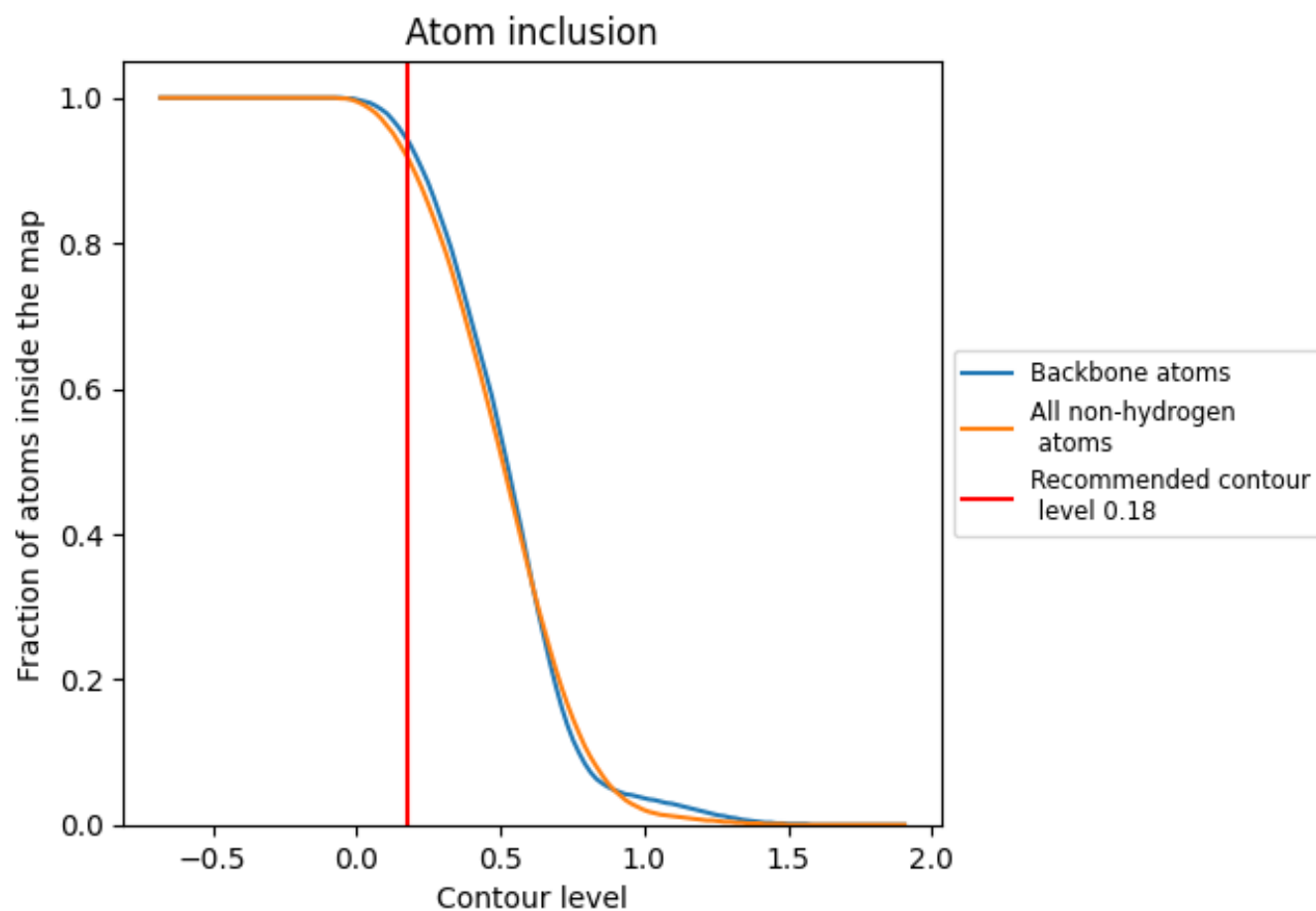
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.18).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9160	 0.6040
10	 0.9450	 0.3020
12	 0.9960	 0.6450
13	 0.9230	 0.6120
14	 0.9400	 0.6180
LA	 0.8010	 0.3190
LB	 0.9780	 0.6670
LC	 0.9500	 0.6620
LD	 0.8410	 0.5880
LE	 0.7370	 0.5300
LF	 0.8230	 0.5740
LG	 0.9330	 0.6370
LH	 0.9500	 0.6510
LI	 0.9600	 0.6560
LJ	 0.9160	 0.6310
LK	 0.8660	 0.5970
LL	 0.9500	 0.6550
LM	 0.8970	 0.6220
LN	 0.9420	 0.6370
LO	 0.8780	 0.6030
LP	 0.8810	 0.6180
LQ	 0.6650	 0.5060
LR	 0.7910	 0.5510
LS	 0.9160	 0.6280
LT	 0.8700	 0.5940
LU	 0.9860	 0.6740
LV	 0.9670	 0.6600
LW	 0.7390	 0.5160
LX	 0.9370	 0.6410
LY	 0.9230	 0.6360
LZ	 0.6290	 0.4970
La	 0.8190	 0.6190
Lb	 0.8960	 0.6080
Lc	 0.6620	 0.5600
Ld	 0.9120	 0.6300



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Chain	Atom inclusion	Q-score
Le	 0.8690	 0.5900
Lf	 0.8780	 0.6040
Lg	 0.9620	 0.6580
Lh	 0.9620	 0.6680
Li	 0.8830	 0.6110
Lj	 0.8770	 0.6020
Lk	 0.9770	 0.6690
Ll	 0.8010	 0.5610
Lm	 0.9530	 0.6600
Ln	 0.8080	 0.6160
Lp	 0.9440	 0.6590
Lq	 0.9240	 0.6470