



Full wwPDB EM Validation Report ⓘ

Jul 6, 2026 – 04:50 PM JST

PDB ID : 9VTJ / pdb_00009vtj
EMDB ID : EMD-65330
Title : cryoEM structure of tobacco mosaic virus tRNA-like structure complexed with tobacco 60S and cycloheximide (CHX)
Authors : Lu, G.; Lin, J.
Deposited on : 2025-07-10
Resolution : 2.50 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

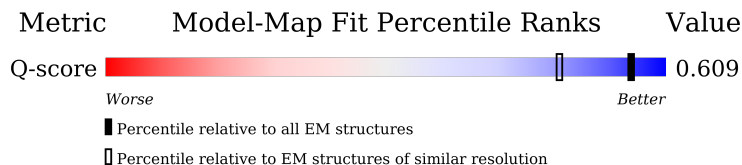
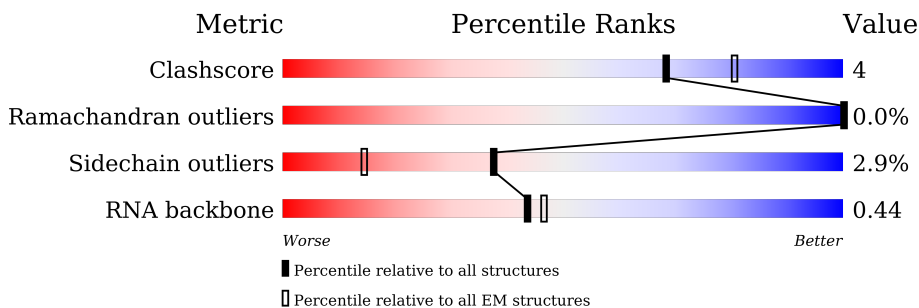
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.50 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.



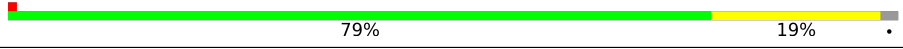
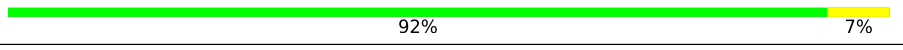
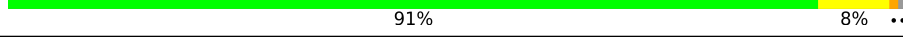
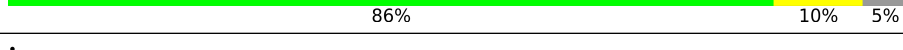
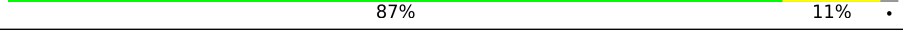
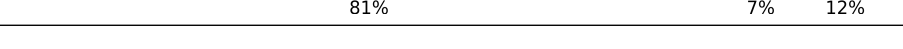
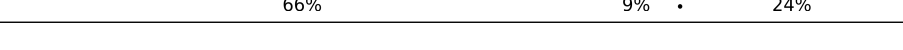
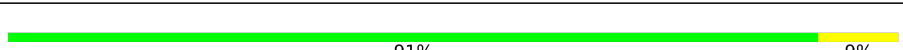
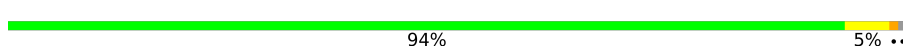
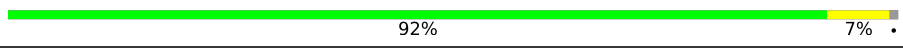
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7115 (2.00 - 3.00)

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	69% 56% 35% 9% .
2	LB	260	88% 5% . 6%
3	LC	389	91% 8% .

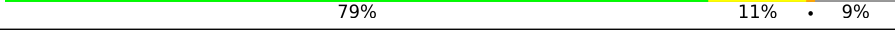
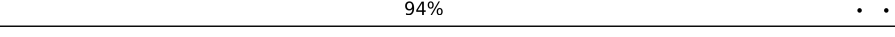
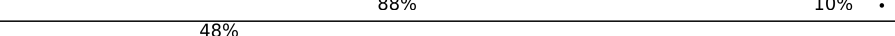
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Mol	Chain	Length	Quality of chain
4	LD	405	
5	LE	181	
6	LF	194	
7	LG	206	
8	LH	140	
9	LI	148	
10	LJ	219	
11	LK	293	
12	LL	175	
13	LM	154	
14	LN	146	
15	LO	123	
16	LP	242	
17	LQ	230	
18	LR	237	
19	LS	200	
20	LT	130	
21	LU	204	
22	LV	187	
23	LW	211	
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 129498 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
			1706	1089	299	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	156	Total	C	N	O	P	0	0
			3317	1481	582	1098	156		

- 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		

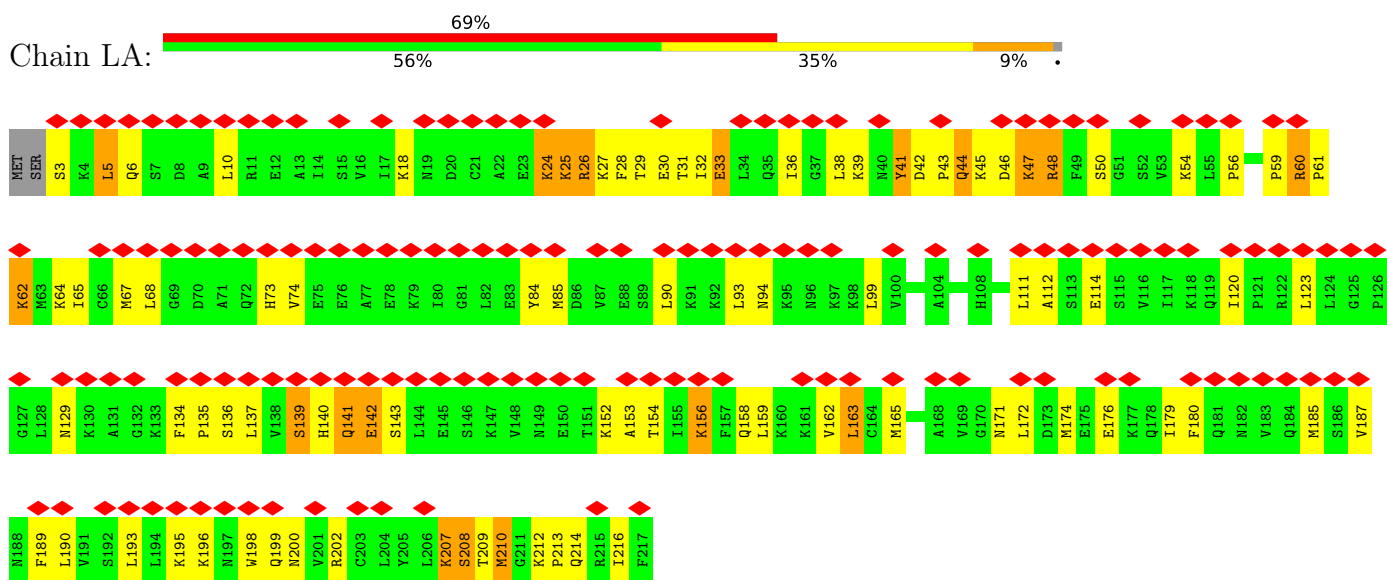
- Molecule 46 is a RNA chain called 25S rRNA.

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

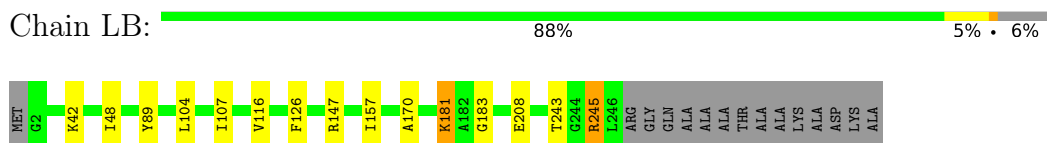
3 Residue-property plots

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.

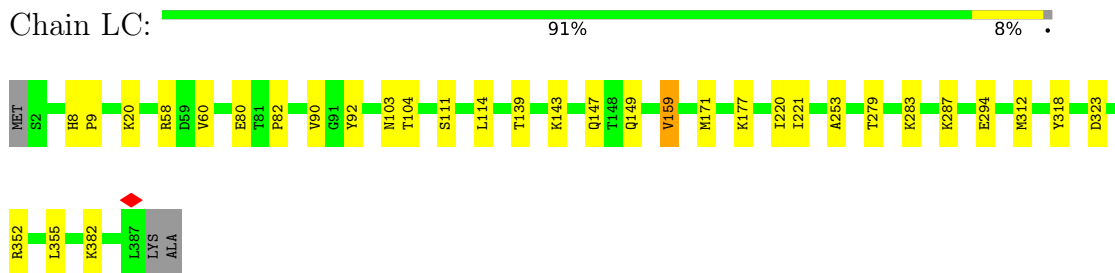
• Molecule 1: Ribosomal protein



• Molecule 2: 60S ribosomal protein L8-like

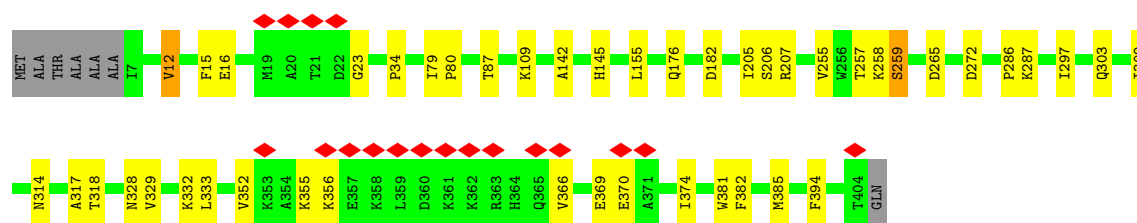


• Molecule 3: 60S ribosomal protein L3



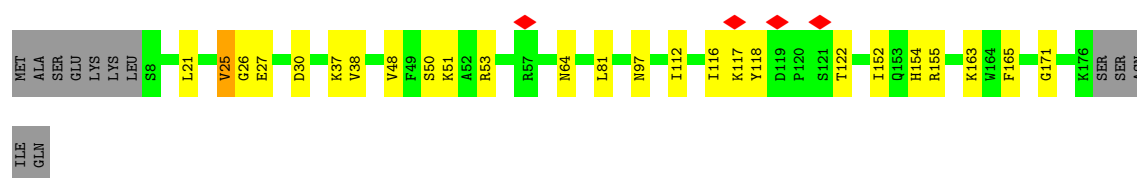
• Molecule 4: 60S ribosomal protein L4-like

Chain LD:  87% 11% .



- Molecule 5: 60S ribosomal protein L11-1

Chain LE:  80% 13% 7%



- Molecule 6: 60S ribosomal protein L9-1

Chain LF:  79% 19% .



- Molecule 7: 60S ribosomal protein L13a-4

Chain LG:  92% 7%



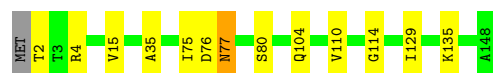
- Molecule 8: 60S ribosomal protein L23

Chain LH:  89% 5% 6%



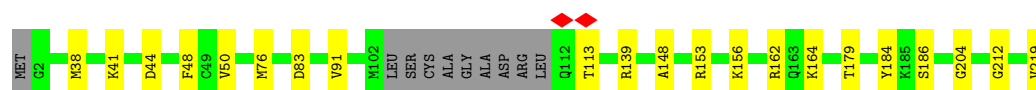
- Molecule 9: 60s ribosomal protein l27a-3

Chain LI:  91% 8% .



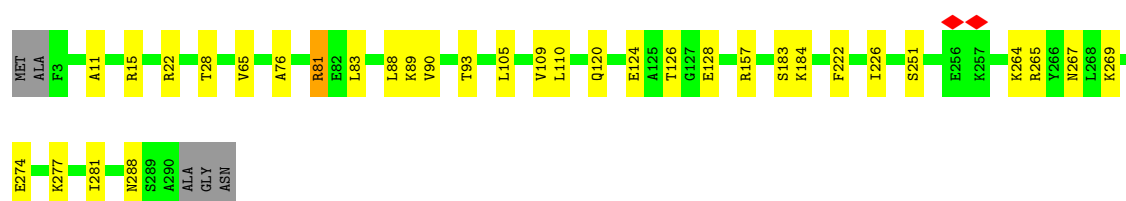
- Molecule 10: 60S ribosomal protein L10

Chain LJ:  86% 10% 5%



- Molecule 11: 60S ribosomal protein L5-like

Chain LK:  87% 11% 2%



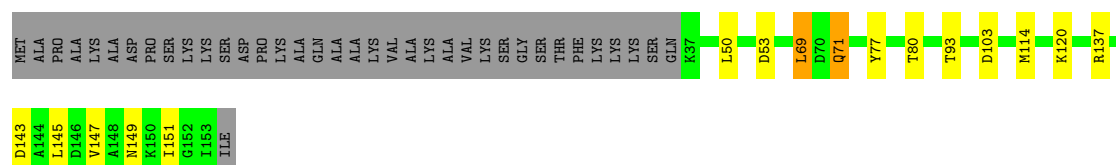
- Molecule 12: 60S ribosomal protein L17-1 isoform X2

Chain LL:  81% 7% 12%



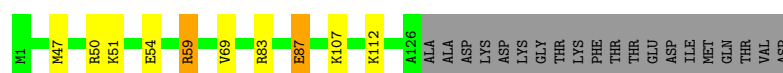
- Molecule 13: Large ribosomal subunit protein uL23

Chain LM:  66% 9% 24%

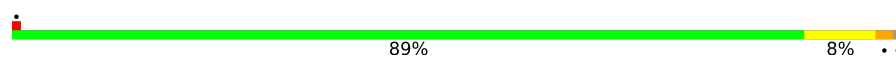


- Molecule 14: 60S ribosomal protein L26-1

Chain LN:  79% 5% 14%



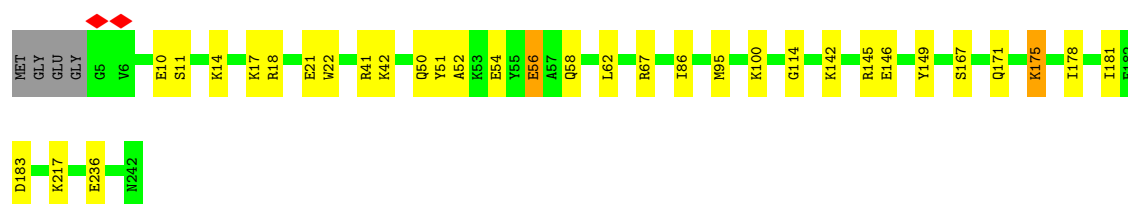
- Molecule 15: 60S ribosomal protein L35-like

Chain LO:  89% 8% 3%



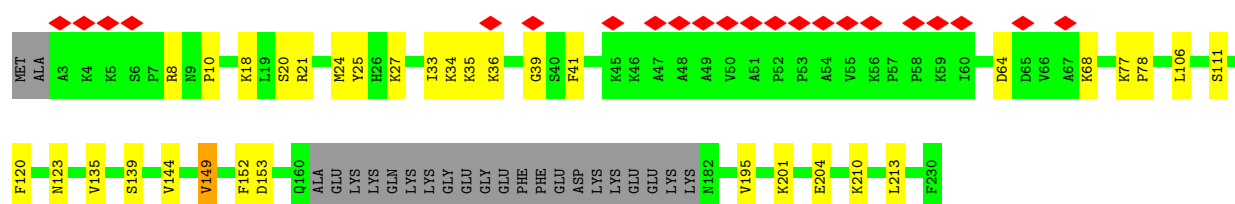
- Molecule 16: 60S ribosomal protein L7-4-like

Chain LP:  85% 13% ..



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

Chain LQ:  10% 76% 14% 10%



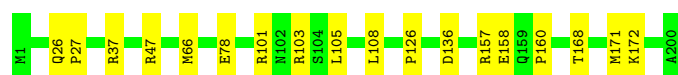
- Molecule 18: 60S ribosomal protein L7a

Chain LR:  5% 89% 9%



- Molecule 19: 60S ribosomal protein L13

Chain LS:  91% 9%



- Molecule 20: 60S ribosomal protein L14-1

Chain LT:  86% 12% ..



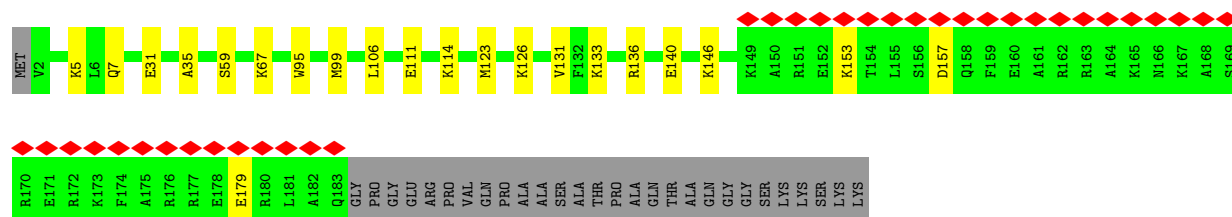
- Molecule 21: Ribosomal protein L15

Chain LU:  89% 9%



- Molecule 22: 60S ribosomal protein L18-2

Chain LW:



Chain LX: 88% 11%



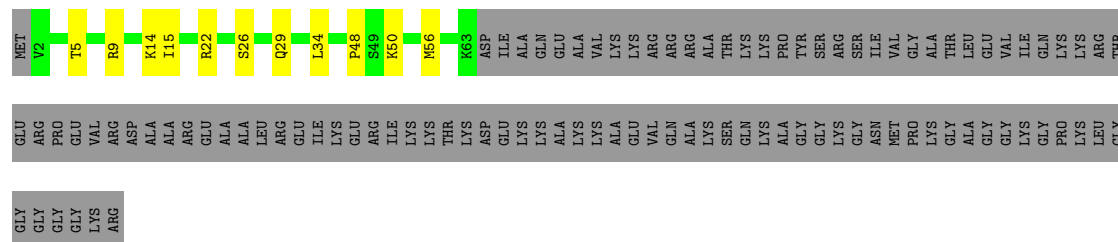
Chain LY: 92% 7%



Chain LZ: 73% 18% 9%

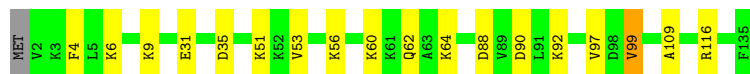


Chain La: 31% 7% 62%



- Molecule 28: 60S ribosomal protein L27

Chain Lb:  86% 13% ..



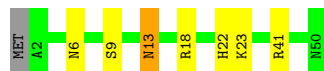
- Molecule 29: 60S ribosomal protein L28-1-like

Chain Lc:  7% 81% 18% .



- Molecule 30: 60S ribosomal protein L29

Chain Ld:  84% 12% ..



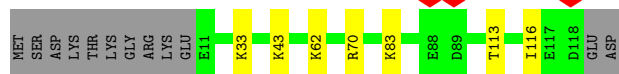
- Molecule 31: 60S ribosomal protein L30

Chain Le:  72% 13% 14%



- Molecule 32: 60S ribosomal protein L31

Chain Lf:  84% 6% 10%



- Molecule 33: 60S ribosomal protein L32-1

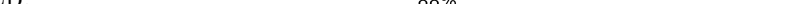
Chain Lg:  85% 10% 5%



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

Chain Lh:  87% 5% 8%



- Chain Lp:  88% 5% • 7%



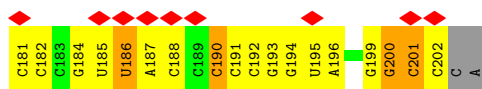
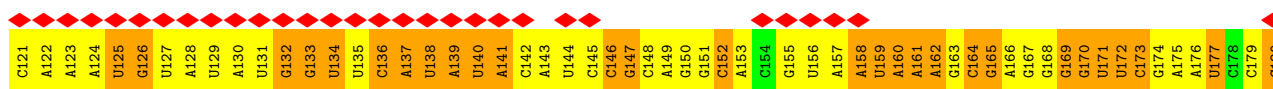
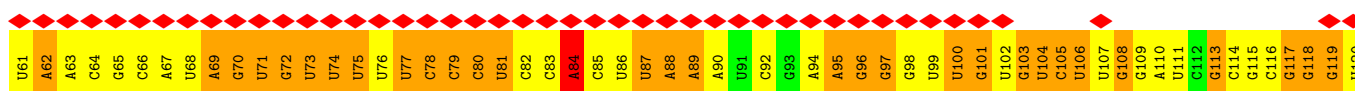
- Molecule 42: 60S ribosomal protein L37a

Chain Lq: 88% 10%



- Molecule 43: RNA (204-MER)

Chain 10: 7% 48% 37% 32% 24%



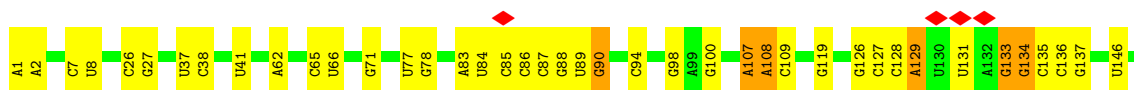
- Molecule 44: 5S rRNA

Chain 12: 85% 12%



- Molecule 45: 5.8S rRNA

Chain 13: 71% 25%



- Molecule 46: 25S rRNA

Chain 14: 67% 23% 7%

G1	C2	G134	U135	U275	U276	G	G	A526	G527	U606	C607	C708	A858	G992	A1109	A1232	C1480	U1633	C1828
G11	U12	U138	C139	U139	U140	U	U	G531	G532	U608	G609	G709	C859	C993	A1114	A1233	A1486	C1643	A1847
C22	U23	C140	U144	A232	A293	U	U	G533	G534	G610	C614	A718	G870	G1006	G1115	G1234	A1492	U1646	C1849
U24	A24	U145	U146	A294	U294	U	U	U535	U536	U615	U616	C725	C871	C1013	U1119	A1237	A1493	G1649	C1852
C29				U337	U338	U	U	U537	U538	C617	U620	U726	G874	A1022	G1128	A1238	A1494	U1652	C1853
U36	A37	G154	A155	G301	U302	A	A	U539	U540	C621	U621	U727	G879	G1027	C1129	A1239	A1495	U1653	C1855
A39		A162	U163	U311	C312	C	C	U541	U542	G625	U625	U728	U889	U1028	G1130	A1239	A1501	C1654	U1861
U42	U43	C163	C164	U312	C312	G	G	C543	C544	U631	U632	U729	U889	U1029	C1131	G1238	C1508	U1661	C1872
U47		U167	G168	U326	U326	U	U	U545	U546	G632	U632	U730	U889	U1030	U1132	G1239	A1509	G1679	A1884
G57	A58	A174	A175	G334	A335	A	A	C547	C548	G633	U633	U731	U889	U1031	U1133	G1240	U1543	A1680	G1885
A63	A64	C181	C182	A346	A347	C	C	U549	U550	U636	U637	U732	U889	U1032	G1140	A1241	C1544	U1686	U1907
U67	U68	C183	C184	A352	A352	G	G	U551	U552	U642	U643	U733	U889	U1033	A1141	A1242	U1545	U1697	G1912
U69	A69	U187	C188	A371	A372	C	C	C560	C561	U643	U644	U734	U889	U1034	U1142	A1243	U1546	U1698	C1913
C70	A71	G194	A195	A372	G373	G	G	U569	U570	U645	U646	U735	U889	U1035	G1145	A1244	U1547	U1699	A1914
A72		A196	A197	A373	G374	C	C	U571	U572	U647	U648	U736	U889	U1036	A1146	A1245	U1548	U1700	A1921
G90	G91	A206	G207	A394	G395	G	G	U573	U574	U649	U650	U737	U889	U1037	U1147	A1246	U1549	U1701	U1922
G92	A93	A208	A209	G396	G397	C	C	U575	U576	U651	U652	U738	U889	U1038	A1148	A1247	U1550	U1702	G1933
A97		G211	G212	U398	G398	U	U	C562	C563	U653	U654	U739	U889	U1039	U1149	A1248	U1551	U1703	C1949
A107	G108	U228	G243	U399	G399	C	C	U565	U566	U655	U656	U740	U889	U1040	U1150	A1249	U1552	U1704	G1958
C109		G244	C245	U400	C400	G	G	U567	U568	U657	U658	U741	U889	U1041	U1151	A1250	U1553	U1705	G1959
G113	C114	G245	A246	C436	G437	U	U	C564	C565	U659	U660	U742	U889	U1042	U1152	A1251	U1554	U1706	C
C115	U116	C247	A248	U437	G438	G	G	U569	U570	U661	U662	U743	U889	U1043	U1153	A1252	U1555	U1707	C
U117	A118	G253	G254	U438	G439	C	C	U571	U572	U663	U664	U744	U889	U1044	U1154	A1253	U1556	U1708	C
G129	C130	G258	A262	U439	G440	C	C	U573	U574	U665	U666	U745	U889	U1045	U1155	A1254	U1557	U1709	C
U131	C132	G266	A263	U440	G441	C	C	U575	U576	U667	U668	U746	U889	U1046	U1156	A1255	U1558	U1710	C
C133				U441	G442	C	C	U577	U578	U669	U670	U747	U889	U1047	U1157	A1256	U1559	U1711	C
				U442	G443	C	C	U579	U580	U671	U672	U748	U889	U1048	U1158	A1257	U1560	U1712	C
				U443	G444	C	C	U581	U582	U673	U674	U749	U889	U1049	U1159	A1258	U1561	U1713	C
				U444	G445	C	C	U583	U584	U675	U676	U750	U889	U1050	U1160	A1259	U1562	U1714	C
				U445	G446	C	C	U585	U586	U677	U678	U751	U889	U1051	U1161	A1260	U1563	U1715	C
				U446	G447	C	C	U587	U588	U679	U680	U752	U889	U1052	U1162	A1261	U1564	U1716	C
				U447	G448	C	C	U589	U590	U681	U682	U753	U889	U1053	U1163	A1262	U1565	U1717	C
				U448	G449	C	C	U591	U592	U683	U684	U754	U889	U1054	U1164	A1263	U1566	U1718	C
				U449	G450	C	C	U593	U594	U685	U686	U755	U889	U1055	U1165	A1264	U1567	U1719	C
				U450	G451	C	C	U595	U596	U687	U688	U756	U889	U1056	U1166	A1265	U1568	U1720	C
				U451	G452	C	C	U597	U598	U689	U690	U757	U889	U1057	U1167	A1266	U1569	U1721	C
				U452	G453	C	C	U599	U600	U691	U692	U758	U889	U1058	U1168	A1267	U1570	U1722	C
				U453	G454	C	C	U601	U602	U693	U694	U759	U889	U1059	U1169	A1268	U1571	U1723	C
				U454	G455	C	C	U603	U604	U695	U696	U760	U889	U1060	U1170	A1269	U1572	U1724	C
				U455	G456	C	C	U605	U606	U697	U698	U761	U889	U1061	U1171	A1270	U1573	U1725	C
				U456	G457	C	C	U607	U608	U699	U700	U762	U889	U1062	U1172	A1271	U1574	U1726	C
				U457	G458	C	C	U609	U610	U701	U702	U763	U889	U1063	U1173	A1272	U1575	U1727	C
				U458	G459	C	C	U611	U612	U703	U704	U764	U889	U1064	U1174	A1273	U1576	U1728	C
				U459	G460	C	C	U613	U614	U705	U706	U765	U889	U1065	U1175	A1274	U1577	U1729	C
				U460	G461	C	C	U615	U616	U707	U708	U766	U889	U1066	U1176	A1275	U1578	U1730	C
				U461	G462	C	C	U617	U618	U709	U710	U767	U889	U1067	U1177	A1276	U1579	U1731	C
				U462	G463	C	C	U619	U620	U711	U712	U768	U889	U1068	U1178	A1277	U1580	U1732	C
				U463	G464	C	C	U621	U622	U713	U714	U769	U889	U1069	U1179	A1278	U1581	U1733	C
				U464	G465	C	C	U623	U624	U715	U716	U770	U889	U1070	U1180	A1279	U1582	U1734	C
				U465	G466	C	C	U625	U626	U717	U718	U771	U889	U1071	U1181	A1280	U1583	U1735	C
				U466	G467	C	C	U627	U628	U719	U720	U772	U889	U1072	U1182	A1281	U1584	U1736	C
				U467	G468	C	C	U629	U630	U721	U722	U773	U889	U1073	U1183	A1282	U1585	U1737	C
				U468	G469	C	C	U631	U632	U723	U724	U774	U889	U1074	U1184	A1283	U1586	U1738	C
				U469	G470	C	C	U633	U634	U725	U726	U775	U889	U1075	U1185	A1284	U1587	U1739	C
				U470	G471	C	C	U635	U636	U727	U728	U776	U889	U1076	U1186	A1285	U1588	U1740	C
				U471	G472	C	C	U637	U638	U729	U730	U777	U889	U1077	U1187	A1286	U1589	U1741	C
				U472	G473	C	C	U639	U640	U731	U732	U778	U889	U1078	U1188	A1287	U1590	U1742	C
				U473	G474	C	C	U641	U642	U733	U734	U779	U889	U1079	U1189	A1288	U1591	U1743	C
				U474	G475	C	C	U643	U644	U735	U736	U780	U889	U1080	U1190	A1289	U1592	U1744	C
				U475	G476	C	C	U645	U646	U737	U738	U781	U889	U1081	U1191	A1290	U1593	U1745	C
				U476	G477	C	C	U647	U648	U739	U740	U782	U889	U1082	U1192	A1291	U1594	U1746	C
				U477	G478	C	C	U649	U650	U741	U742	U783	U889	U1083	U1193	A1292	U1595	U1747	C
				U478	G479	C	C	U651	U652	U743	U744	U784	U889	U1084	U1194	A1293	U1596	U1748	C
				U479	G480	C	C	U653	U654	U745	U746	U785	U889	U1085	U1195	A1294	U1597	U1749	C
				U480	G481	C	C	U655	U656	U747	U748	U786	U889	U1086	U1196	A1295	U1598	U1750	C
				U481	G482	C	C	U657	U658	U749	U750	U787	U889	U1087	U1197	A1296	U1599	U1751	C
				U482	G483	C	C	U659	U660	U751	U752	U788	U889	U1088	U1198	A1297	U1600	U1752	C
				U483	G484	C	C	U661	U662	U753	U754	U789	U889	U1089	U1199	A1298	U1601	U1753	C
				U484	G485	C	C	U663	U664	U755	U756	U790	U889	U1090	U1200	A1299	U1602	U1754	C
				U485	G486	C	C	U665	U666	U757	U758	U791	U889	U1091	U1201	A1300	U1603	U1755	C
				U486	G487	C	C	U667	U668	U759	U760	U792	U889	U1092	U1202	A1301	U1604	U1756	C
				U487	G488	C	C	U669	U670	U761	U762	U793	U889	U1093	U1203	A1302	U1605	U1757	C
				U488	G489	C	C	U671	U672	U763	U764	U794	U889	U1094	U1204	A1303	U1606	U1758	C
				U489	G490	C	C	U673	U674	U765	U766	U795	U889	U1095	U1205	A1304	U1607	U1759	C
				U490	G491	C	C	U675	U676	U767	U768	U796	U889	U1096	U1206	A1305	U1608	U1760	C
				U491	G492	C	C	U677	U678	U769	U770	U797	U889	U1097	U1207	A1306	U1609	U1761	C
				U492	G493	C	C	U679	U680	U771	U772	U79							

A3285	C3190	G3030	A2903	G2622	U2514	A2443	C2118	G
C3296	U3191	A3031	G2904	A2629	U2515	U2444	C2122	U
A3299	U3192	G3032	C2912	U2636	U2519	G2445	C2123	C
A3307	U3193	C3049	A2913	U2637	A2520	A2446	U2285	G
A3308	G3194	A3050	A2914	A2638	A2529	G2447	G2286	G
C3311	G3195	U3059	G2917	A2639	A2538	U2448	G2126	U
U3321	C3060	C3061	U2926	A2640	A2539	U2449	A2135	G
A3334	A3072	A3073	U2927	A2645	G2536	A2451	U2144	U
G3337	G3080	G3073	C2928	U2655	G2537	G2452	U2152	G
U3343	C3208	G3209	A2933	U2658	G2538	G2453	A2153	G
U3344	U3210	G3211	U2938	A2659	G2539	G2454	U2162	U
G3345	U3212	G3213	A2939	A2677	G2541	G2455	A2163	G
U3346	G3214	G3103	C2945	G2680	G2542	U2456	G2165	C
U3347	U3215	G3118	G2948	A2683	A2543	A2457	C2199	C
G3348	U3216	C3119	A2949	U2684	U2544	G2458	C2200	U
G3361	C3219	A3132	C2951	G2682	U2545	U2460	A2201	C
C3370	G3223	U3183	G2954	U2683	C2550	U2461	U2208	A
U3374	U3224	C3134	C2963	A2694	U2551	G2472	G2209	G
U3377	A3226	G3136	U2964	A2697	C2552	C2473	A2211	C
C3380	G3235	A3144	U2965	U2556	U2553	G2474	G2213	U
U3381	A3236	G3145	A2974	U2557	U2546	G2475	A2216	C
C3382	G3240	C3146	G2975	U2558	C2547	A2476	A2217	C
C3383	C3253	U3153	U2983	A2706	C2548	A2477	A2226	C
U3390	C3254	G3156	C2986	A2707	C2549	U2478	A2227	G
G3257	G3257	G3160	A2990	U2711	U2570	G2482	U2228	G
A3258	A3259	C3161	C2991	C2712	G2571	A2483	A2231	C
G3260	G3260	U3164	A2999	G2717	C2572	A2489	A2235	G
A3264	A3264	C3165	G3000	U2722	U2573	A2490	A2236	A
A3265	A3265	C3166	U3001	U2725	G2574	G2491	A2245	G
U3266	U3266	G3167	G3002	U2726	G2575	U2492	G2252	C
U3267	U3267	C3168	U3003	U2727	C2576	G2496	G2253	G
U3268	U3268	U3169	C3006	G2731	A2577	C2497	A2258	G
C3269	C3269	C3172	A3007	U2732	G2588	U2498	A2259	U
C3270	C3270	C3173	U3014	C2740	A2596	A2499	C2260	C
A3271	A3271	G3174	U3015	A2750	C2597	C2500	A2096	C
U3272	U3272	C3179	U3016	A2751	A2598	U2502	U2261	C
G3274	G3274	A3180	C3017	G2752	G2606	U2503	A2262	G
A3275	A3275	A3181	A3018	G2756	G2609	A2504	U2263	G
G3278	G3278	G3185	U3025	G2757	G2610	A2505	U2264	C
C3279	C3279	C3189	A3026	G2758	U2614	A2506	A2111	U
G3281	G3281	G3189	U3027		U2615	G2508	G2273	G
					U2616	U2509	A2273	C
					U2617	U2510	A2274	C
					G2617	A2511	G2275	C
						U2512	A2117	G
						U2513		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	269862	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	1.817	Depositor
Minimum map value	-0.607	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.1	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	0.77	0/1731	1.13	2/2314 (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	0.31	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	3/1581 (0.2%)
10	LJ	0.25	0/1707	0.39	0/2283
11	LK	0.35	0/2387	0.53	0/3201
12	LL	0.38	0/1261	0.63	0/1693
13	LM	0.27	0/965	0.45	0/1295
14	LN	0.35	0/1037	0.55	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	0.24	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	0.38	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	0.45	0/1050
37	Lk	0.37	0/714	0.60	0/949
38	Ll	0.34	0/566	0.49	0/752
39	Lm	0.29	0/460	0.42	0/611
40	Ln	0.17	0/426	0.36	0/561
41	Lp	0.41	0/799	0.54	0/1055
42	Lq	0.40	0/603	0.55	0/802
43	10	0.70	0/3705	1.03	2/5771 (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	4/117423 (0.0%)
All	All	0.40	0/139569	0.54	11/205730 (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
12	LL	0	1
14	LN	0	1
16	LP	0	1
24	LX	0	1
30	Ld	0	1
All	All	0	12

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	LI	15	VAL	N-CA-CB	-6.83	102.93	110.51
9	LI	15	VAL	N-CA-C	6.81	117.51	110.36
46	14	883	C	C2'-C3'-O3'	-6.54	103.89	113.70
43	10	134	U	O3'-P-O5'	-5.96	95.06	104.00
46	14	692	A	C3'-C2'-C1'	-5.86	95.64	101.50
46	14	3168	C	C2'-C3'-O3'	5.62	117.93	109.50
43	10	84	A	C4'-C3'-C2'	-5.56	97.04	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	14	2557	U	O3'-P-O5'	5.22	111.83	104.00
1	LA	152	LYS	CA-C-N	-5.11	116.18	123.03
1	LA	152	LYS	C-N-CA	-5.11	116.18	123.03
9	LI	15	VAL	CA-C-O	-5.03	116.04	121.27

There are no chirality outliers.

All (12) 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
12	LL	6	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	1706	0	1801	62	0
2	LB	1880	0	1915	9	0
3	LC	3107	0	3232	17	0
4	LD	3099	0	3229	31	0
5	LE	1356	0	1394	18	0
6	LF	1520	0	1614	22	0
7	LG	1644	0	1773	9	0
8	LH	985	0	1046	4	0
9	LI	1155	0	1197	8	0
10	LJ	1671	0	1731	12	0
11	LK	2342	0	2379	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	LL	1236	0	1262	5	0
13	LM	950	0	1029	13	0
14	LN	1023	0	1105	8	0
15	LO	997	0	1136	8	0
16	LP	1958	0	2057	21	0
17	LQ	1600	0	1731	25	0
18	LR	1874	0	2030	11	0
19	LS	1608	0	1697	14	0
20	LT	1046	0	1144	12	0
21	LU	1701	0	1771	14	0
22	LV	1462	0	1581	7	0
23	LW	1519	0	1630	10	0
24	LX	1505	0	1557	12	0
25	LY	1306	0	1367	8	0
26	LZ	799	0	836	12	0
27	La	526	0	554	10	0
28	Lb	1091	0	1171	9	0
29	Lc	1107	0	1182	17	0
30	Ld	407	0	393	3	0
31	Le	745	0	783	10	0
32	Lf	875	0	934	5	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	9	0
37	Lk	701	0	729	8	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	4	0
42	Lq	593	0	618	6	0
43	10	3317	0	1677	94	0
44	12	2538	0	1286	6	0
45	13	3478	0	1761	15	0
46	14	67280	0	33921	299	0
All	All	129498	0	94501	813	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 (813) 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)
25:LY:129:LYS:HB3	46:14:1109:A:H5'	1.51	0.91
1:LA:39:LYS:HE3	1:LA:199:GLN:O	1.70	0.90
1:LA:171:ASN:OD1	1:LA:174:MET:HG3	1.74	0.88
26:LZ:39:LEU:HD23	26:LZ:69:ILE:HD12	1.54	0.87
1:LA:36:ILE:HG21	1:LA:190:LEU:HD21	1.58	0.83
43:10:74:U:H2'	43:10:75:U:H2'	1.60	0.83
43:10:70:G:H1'	43:10:88:A:H62	1.43	0.82
46:14:1031:G:H1	46:14:1045:U:H3	1.25	0.82
46:14:498:G:H2'	46:14:499:A:H8	1.46	0.80
4:LD:303:GLN:HG3	16:LP:18:ARG:HH12	1.48	0.79
46:14:424:G:H22	46:14:643:U:H3	1.31	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
3:LC:92:TYR:HB2	3:LC:159:VAL:HG13	1.67	0.76
17:LQ:24:MET:HE2	17:LQ:24:MET:HA	1.67	0.76
46:14:3208:C:H4'	46:14:3209:G:H5'	1.68	0.75
4:LD:317:ALA:HB2	46:14:1373:C:H5''	1.69	0.73
1:LA:39:LYS:CE	1:LA:199:GLN:O	2.39	0.71
43:10:71:U:H1'	43:10:89:A:H62	1.55	0.71
43:10:80:C:H3'	43:10:81:U:H6	1.55	0.71
23:LW:67:LYS:NZ	46:14:2105:C:OP1	2.24	0.70
29:Lc:90:MET:HE2	29:Lc:97:MET:HG2	1.71	0.70
1:LA:28:PHE:CD1	46:14:2472:G:H4'	2.27	0.70
46:14:3225:C:H2'	46:14:3226:A:H8	1.57	0.69
33:Lg:103:THR:HG22	33:Lg:126:ARG:HB3	1.73	0.69
1:LA:114:GLU:HG2	1:LA:137:LEU:HD11	1.74	0.69
17:LQ:68:LYS:H	17:LQ:68:LYS:HD2	1.57	0.69
1:LA:120:ILE:HD13	1:LA:135:PRO:HG2	1.75	0.69
11:LK:93:THR:HG22	11:LK:157:ARG:NH1	2.08	0.68
3:LC:103:ASN:HD21	3:LC:149:GLN:HG2	1.58	0.68
23:LW:123:MET:HE2	23:LW:123:MET:HA	1.75	0.68
19:LS:37:ARG:NH2	46:14:696:G:OP1	2.26	0.68
1:LA:36:ILE:HD13	1:LA:190:LEU:HD22	1.75	0.67
37:Lk:46:LYS:NZ	46:14:22:C:OP1	2.26	0.67
46:14:764:G:H2'	46:14:765:A:H8	1.60	0.67
16:LP:50:GLN:NE2	16:LP:54:GLU:OE2	2.25	0.67
43:10:70:G:H2'	43:10:71:U:C6	2.28	0.67
43:10:79:C:H2'	43:10:80:C:C6	2.30	0.67
43:10:140:U:H2'	43:10:141:A:H8	1.60	0.67
13:LM:93:THR:HG22	13:LM:137:ARG:HG3	1.77	0.67
46:14:520:G:H2'	46:14:521:G:H8	1.60	0.66
6:LF:131:MET:HB3	6:LF:135:VAL:HG13	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Lp:6:LYS:HD3	41:Lp:94:GLY:HA3	1.78	0.65
43:10:152:C:H2'	43:10:153:A:C8	2.31	0.65
10:LJ:204:GLY:O	44:12:63:U:H3'	1.97	0.65
12:LL:57:ALA:HB3	12:LL:73:VAL:HG13	1.76	0.65
46:14:2273:A:H2'	46:14:2274:A:C8	2.32	0.65
27:La:5:THR:HG21	27:La:14:LYS:HG3	1.76	0.65
8:LH:96:MET:HE2	27:La:22:ARG:HD2	1.79	0.64
3:LC:82:PRO:HG2	3:LC:171:MET:HE2	1.80	0.64
46:14:588:C:H2'	46:14:589:U:H2'	1.79	0.64
11:LK:89:LYS:HG2	11:LK:90:VAL:HG13	1.79	0.64
26:LZ:100:ARG:HD3	26:LZ:116:PHE:HB3	1.80	0.64
13:LM:145:LEU:O	13:LM:149:ASN:ND2	2.31	0.63
46:14:520:G:H2'	46:14:521:G:C8	2.34	0.63
6:LF:141:GLU:N	6:LF:141:GLU:OE1	2.30	0.63
45:13:133:G:H2'	45:13:134:G:C8	2.34	0.63
46:14:537:U:H3	46:14:541:U:H1'	1.61	0.63
46:14:2216:A:H2'	46:14:2217:A:C8	2.33	0.63
15:LO:55:ALA:O	15:LO:59:THR:HG23	1.99	0.63
18:LR:205:MET:HE1	18:LR:209:ARG:HE	1.63	0.63
43:10:108:G:N2	43:10:174:G:H2'	2.13	0.63
45:13:1:A:O2'	46:14:2999:A:N7	2.29	0.63
1:LA:202:ARG:NH1	46:14:2499:A:OP1	2.25	0.62
6:LF:12:ILE:HD13	6:LF:18:ILE:HG21	1.81	0.62
13:LM:71:GLN:NE2	13:LM:114:MET:SD	2.72	0.62
29:Lc:69:LEU:HD11	29:Lc:87:LYS:HB2	1.79	0.62
16:LP:217:LYS:NZ	46:14:1169:G:OP1	2.31	0.62
18:LR:201:ASN:HA	18:LR:204:LYS:HG3	1.80	0.62
6:LF:97:PHE:HB2	6:LF:145:ASP:HB3	1.81	0.62
4:LD:16:GLU:H	4:LD:176:GLN:NE2	1.97	0.62
24:LX:84:GLN:HG3	24:LX:89:TYR:CE1	2.35	0.62
4:LD:366:VAL:HG21	46:14:524:A:N1	2.15	0.61
9:LI:110:VAL:HB	9:LI:129:ILE:HD12	1.83	0.61
15:LO:3:ARG:NH2	45:13:90:G:OP2	2.32	0.61
43:10:160:A:H2'	43:10:161:A:C8	2.35	0.61
46:14:1819:A:H2'	46:14:1820:G:C8	2.35	0.61
43:10:87:U:H4'	43:10:88:A:C2	2.35	0.61
46:14:2547:C:H2'	46:14:2548:C:C6	2.36	0.61
46:14:417:G:N2	46:14:2388:G:OP2	2.30	0.60
46:14:1206:G:H2'	46:14:1207:A:C8	2.36	0.60
46:14:2454:G:H2'	46:14:2455:G:C8	2.35	0.60
46:14:1959:G:O4'	46:14:2096:A:N6	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:85:MET:HE1	1:LA:93:LEU:HD11	1.84	0.60
46:14:2235:A:H2'	46:14:2236:A:C8	2.36	0.60
1:LA:27:LYS:N	46:14:2473:C:OP1	2.34	0.60
7:LG:179:LEU:HD11	20:LT:129:LYS:HE2	1.84	0.60
46:14:583:C:H2'	46:14:584:G:C8	2.37	0.59
43:10:64:C:H2'	43:10:65:G:C8	2.37	0.59
46:14:2510:U:H2'	46:14:2511:A:C8	2.38	0.59
1:LA:5:LEU:HB3	1:LA:198:TRP:CH2	2.37	0.59
10:LJ:76:MET:HE2	10:LJ:148:ALA:HA	1.84	0.59
11:LK:265:ARG:NH1	11:LK:267:ASN:O	2.36	0.59
46:14:673:U:H2'	46:14:674:C:C6	2.37	0.59
3:LC:90:VAL:HG22	3:LC:104:THR:HG23	1.85	0.59
43:10:140:U:H2'	43:10:141:A:C8	2.38	0.59
15:LO:107:GLU:O	15:LO:111:GLU:HG2	2.03	0.58
46:14:955:C:H2'	46:14:956:C:C6	2.37	0.58
46:14:3049:C:O2'	46:14:3050:A:H5'	2.03	0.58
16:LP:67:ARG:HD3	46:14:524:A:C6	2.39	0.58
46:14:1:G:H2'	46:14:2:C:C6	2.39	0.58
46:14:2263:U:O2'	46:14:2264:G:H8	1.85	0.58
6:LF:95:MET:HE2	6:LF:182:ILE:HG22	1.84	0.58
46:14:162:U:H3	46:14:253:G:H1	1.51	0.58
43:10:173:C:H2'	43:10:174:G:C8	2.38	0.58
10:LJ:83:ASP:OD1	10:LJ:83:ASP:N	2.36	0.58
46:14:692:A:H61	46:14:708:C:H2'	1.69	0.58
46:14:556:U:H2'	46:14:557:C:C6	2.38	0.58
43:10:118:G:C4	43:10:119:G:H1'	2.38	0.57
2:LB:104:LEU:HA	2:LB:107:ILE:HD12	1.86	0.57
9:LI:35:ALA:HB1	46:14:38:A:H5''	1.86	0.57
43:10:82:C:H1'	43:10:95:A:N1	2.19	0.57
17:LQ:8:ARG:HD2	17:LQ:27:LYS:HB3	1.85	0.57
23:LW:7:GLN:NE2	23:LW:35:ALA:O	2.31	0.57
1:LA:48:ARG:HA	1:LA:159:LEU:HD23	1.87	0.57
21:LU:4:TYR:OH	46:14:146:G:OP2	2.23	0.57
44:12:29:C:O2'	44:12:50:A:N1	2.35	0.57
46:14:1818:G:H2'	46:14:1819:A:O4'	2.03	0.57
1:LA:94:ASN:HA	1:LA:123:LEU:O	2.04	0.57
36:Lj:24:GLU:CD	36:Lj:24:GLU:H	2.13	0.56
11:LK:93:THR:HG22	11:LK:157:ARG:HH12	1.70	0.56
6:LF:176:ARG:NH1	40:Ln:125:LYS:O	2.38	0.56
4:LD:303:GLN:HG3	16:LP:18:ARG:NH1	2.20	0.56
5:LE:37:LYS:HB2	5:LE:37:LYS:NZ	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:2450:G:H3'	46:14:2451:A:H8	1.70	0.56
46:14:2502:U:H2'	46:14:2503:U:C6	2.40	0.56
18:LR:205:MET:O	18:LR:208:SER:OG	2.20	0.56
43:10:100:U:H5'	43:10:101:G:H5'	1.86	0.56
46:14:2508:G:H2'	46:14:2509:U:C6	2.41	0.56
43:10:132:G:H3'	43:10:133:G:C8	2.40	0.56
16:LP:10:GLU:O	16:LP:14:LYS:HG3	2.06	0.56
43:10:70:G:H21	43:10:89:A:H61	1.54	0.56
46:14:3273:C:H2'	46:14:3274:G:C8	2.41	0.56
46:14:181:C:H2'	46:14:182:C:C6	2.41	0.56
11:LK:83:LEU:HD13	11:LK:88:LEU:HD23	1.88	0.55
43:10:131:U:H3'	43:10:132:G:H8	1.71	0.55
43:10:164:C:H2'	43:10:165:G:C8	2.41	0.55
46:14:3271:A:HO2'	46:14:3272:U:H6	1.54	0.55
17:LQ:41:PHE:HB3	46:14:609:G:N3	2.21	0.55
4:LD:297:ILE:O	4:LD:303:GLN:NE2	2.39	0.55
17:LQ:34:LYS:O	17:LQ:39:GLY:N	2.30	0.55
43:10:180:C:H2'	43:10:181:C:C6	2.41	0.55
43:10:77:U:H1'	43:10:160:A:C4	2.41	0.55
46:14:116:U:O2	46:14:119:G:H5''	2.06	0.55
46:14:625:G:O2'	46:14:3265:A:N6	2.38	0.55
31:Le:32:TYR:CE1	31:Le:57:ARG:HG3	2.42	0.55
46:14:498:G:H2'	46:14:499:A:C8	2.35	0.55
46:14:2372:G:H2'	46:14:2373:G:C8	2.42	0.55
46:14:2498:U:H2'	46:14:2499:A:C8	2.42	0.55
21:LU:28:TRP:O	21:LU:32:GLN:NE2	2.40	0.54
16:LP:167:SER:O	16:LP:171:GLN:HG3	2.08	0.54
21:LU:45:PRO:O	21:LU:49:ARG:HG3	2.06	0.54
43:10:115:G:H2'	43:10:116:C:C6	2.42	0.54
46:14:1032:G:H2'	46:14:1033:G:H8	1.71	0.54
46:14:2500:C:H2'	46:14:2501:U:C6	2.42	0.54
20:LT:71:LEU:O	20:LT:75:MET:HG3	2.08	0.54
4:LD:145:HIS:HD2	4:LD:182:ASP:OD2	1.89	0.54
4:LD:329:VAL:HA	4:LD:332:LYS:HB2	1.88	0.54
13:LM:147:VAL:O	13:LM:151:ILE:HG13	2.08	0.54
23:LW:5:LYS:NZ	23:LW:5:LYS:HB3	2.23	0.54
46:14:2476:A:H3'	46:14:2477:A:H8	1.73	0.54
43:10:114:C:H2'	43:10:115:G:C8	2.43	0.54
1:LA:111:LEU:HD23	1:LA:136:SER:OG	2.07	0.54
5:LE:163:LYS:NZ	5:LE:163:LYS:HB3	2.22	0.54
43:10:193:G:H1'	43:10:196:A:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:692:A:N6	46:14:708:C:H2'	2.23	0.54
3:LC:177:LYS:NZ	46:14:3307:A:OP1	2.34	0.54
4:LD:87:THR:HG22	46:14:352:A:N1	2.23	0.54
37:Lk:17:THR:HG23	37:Lk:29:ILE:HD11	1.90	0.54
43:10:69:A:H3'	43:10:70:G:H8	1.73	0.54
43:10:104:U:H2'	43:10:105:C:C6	2.43	0.54
46:14:1680:A:H2	46:14:1696:G:H22	1.56	0.54
6:LF:143:VAL:HB	6:LF:146:GLU:HG3	1.89	0.54
28:Lb:4:PHE:O	28:Lb:9:LYS:HD2	2.08	0.54
43:10:80:C:H3'	43:10:81:U:C6	2.40	0.54
46:14:2263:U:O2'	46:14:2264:G:C8	2.61	0.54
46:14:2263:U:HO2'	46:14:2264:G:H8	1.48	0.54
3:LC:80:GLU:OE1	3:LC:318:TYR:OH	2.26	0.53
43:10:71:U:H1'	43:10:89:A:N6	2.22	0.53
43:10:113:G:H2'	43:10:114:C:C6	2.43	0.53
1:LA:26:ARG:HD2	46:14:2473:C:H5''	1.90	0.53
43:10:125:U:H1'	43:10:126:G:H5'	1.90	0.53
46:14:3018:A:H2'	46:14:3019:A:C8	2.43	0.53
4:LD:352:VAL:O	4:LD:356:LYS:N	2.36	0.53
4:LD:381:TRP:O	4:LD:385:MET:HG3	2.08	0.53
5:LE:112:ILE:HG21	5:LE:118:TYR:HB2	1.91	0.53
43:10:138:U:H2'	43:10:139:A:C8	2.44	0.53
38:Ll:3:LYS:HD2	38:Ll:41:TYR:CD2	2.44	0.53
1:LA:30:GLU:HB2	1:LA:172:LEU:CD1	2.38	0.53
5:LE:51:LYS:HG2	5:LE:64:ASN:HA	1.89	0.53
18:LR:114:GLU:OE2	18:LR:119:THR:OG1	2.25	0.53
46:14:1550:U:O4	46:14:1563:G:O2'	2.27	0.53
46:14:3272:U:HO2'	46:14:3273:C:H6	1.54	0.53
2:LB:147:ARG:HG2	2:LB:157:ILE:HG12	1.91	0.53
46:14:2548:C:H2'	46:14:2549:C:C6	2.43	0.53
1:LA:33:GLU:CD	1:LA:207:LYS:HD3	2.33	0.53
11:LK:22:ARG:HB3	11:LK:28:THR:HG22	1.89	0.53
43:10:81:U:H2'	43:10:82:C:O4'	2.08	0.53
46:14:1215:A:H2'	46:14:1216:A:C8	2.44	0.53
10:LJ:212:GLY:H	11:LK:288:ASN:ND2	2.06	0.52
43:10:52:U:H2'	43:10:53:G:C8	2.44	0.52
3:LC:139:THR:O	3:LC:143:LYS:NZ	2.43	0.52
20:LT:117:ARG:HG2	20:LT:117:ARG:HH11	1.73	0.52
43:10:86:U:O2'	43:10:88:A:N1	2.39	0.52
46:14:1362:G:H2'	46:14:1364:G:C8	2.44	0.52
46:14:2774:A:O2'	46:14:2775:C:H5''	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LN:87:GLU:H	14:LN:87:GLU:CD	2.18	0.52
23:LW:126:LYS:HG2	23:LW:131:VAL:HG21	1.90	0.52
46:14:3307:A:O2'	46:14:3308:A:OP1	2.26	0.52
41:Lp:26:THR:HG22	43:10:186:U:C2	2.45	0.52
46:14:138:U:H2'	46:14:139:C:C6	2.44	0.52
25:LY:150:THR:HG22	25:LY:151:PRO:O	2.09	0.52
46:14:1819:A:C2'	46:14:1822:G:H21	2.22	0.52
46:14:3166:C:H2'	46:14:3167:G:C8	2.45	0.52
11:LK:76:ALA:HB3	11:LK:109:VAL:HG22	1.91	0.52
38:Ll:30:ASP:OD1	38:Ll:30:ASP:N	2.40	0.52
46:14:3018:A:H2'	46:14:3019:A:H8	1.75	0.52
1:LA:32:ILE:CD1	1:LA:179:ILE:HD13	2.40	0.52
3:LC:103:ASN:ND2	3:LC:149:GLN:HG2	2.23	0.52
17:LQ:106:LEU:HD13	17:LQ:149:VAL:HG11	1.91	0.52
46:14:2549:C:H2'	46:14:2550:C:C6	2.45	0.52
1:LA:18:LYS:HD2	1:LA:176:GLU:HG2	1.92	0.52
11:LK:277:LYS:O	11:LK:281:ILE:HG13	2.09	0.52
46:14:1:G:H2'	46:14:2:C:H6	1.75	0.52
46:14:2379:G:H2'	46:14:2380:G:C8	2.44	0.51
4:LD:394:PHE:HE1	25:LY:152:ILE:HD12	1.76	0.51
10:LJ:184:TYR:CE1	10:LJ:219:VAL:HG11	2.45	0.51
19:LS:103:ARG:NH1	46:14:72:A:H5''	2.25	0.51
10:LJ:184:TYR:HE1	10:LJ:219:VAL:HG11	1.74	0.51
21:LU:2:GLY:O	36:Lj:39:ARG:NH2	2.43	0.51
46:14:2444:U:H2'	46:14:2445:G:C8	2.45	0.51
21:LU:99:ARG:HG2	21:LU:167:ALA:HB2	1.92	0.51
24:LX:9:TYR:CE1	24:LX:65:GLU:HG3	2.46	0.51
43:10:72:G:H2'	43:10:73:U:O4'	2.10	0.51
43:10:126:G:H2'	43:10:127:U:C6	2.46	0.51
46:14:3169:U:H5	46:14:3172:C:OP2	1.93	0.51
46:14:742:C:H2'	46:14:743:C:O4'	2.10	0.51
36:Lj:30:SER:O	36:Lj:33:LYS:HG2	2.11	0.51
37:Lk:76:THR:HG22	37:Lk:79:ARG:HB3	1.92	0.51
46:14:764:G:H2'	46:14:765:A:C8	2.43	0.51
46:14:2458:U:H2'	46:14:2459:A:C8	2.46	0.51
46:14:3072:A:H2'	46:14:3073:A:C8	2.46	0.51
2:LB:183:GLY:HA2	46:14:906:A:H5''	1.93	0.51
43:10:53:G:H2'	43:10:54:C:C6	2.46	0.51
3:LC:220:ILE:HD12	3:LC:283:LYS:HG3	1.92	0.51
11:LK:83:LEU:HB3	11:LK:88:LEU:HB3	1.93	0.51
16:LP:51:TYR:OH	16:LP:183:ASP:OD1	2.22	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LT:117:ARG:HG2	20:LT:117:ARG:NH1	2.26	0.51
27:La:5:THR:HG23	27:La:15:ILE:O	2.10	0.51
29:Lc:62:GLU:HG3	29:Lc:63:GLY:H	1.75	0.51
29:Lc:139:LYS:HB3	29:Lc:141:ARG:HG3	1.92	0.51
24:LX:35:ASN:HB2	24:LX:38:ARG:HG3	1.93	0.51
46:14:569:U:O2'	46:14:570:G:H5'	2.11	0.51
17:LQ:204:GLU:OE2	17:LQ:210:LYS:HD2	2.12	0.50
21:LU:121:ILE:HG21	21:LU:131:GLU:HG3	1.92	0.50
29:Lc:76:LYS:NZ	29:Lc:77:LYS:HD2	2.25	0.50
46:14:3153:U:H5''	46:14:3285:A:H4'	1.92	0.50
16:LP:17:LYS:NZ	16:LP:21:GLU:OE2	2.44	0.50
32:Lf:113:THR:O	46:14:3377:U:O2'	2.30	0.50
11:LK:222:PHE:O	11:LK:226:ILE:HG13	2.11	0.50
18:LR:145:GLN:HG3	18:LR:197:THR:O	2.12	0.50
46:14:3380:C:H2'	46:14:3381:U:C6	2.46	0.50
24:LX:29:MET:HG3	24:LX:43:PHE:CD1	2.47	0.50
43:10:169:G:H3'	43:10:170:G:H8	1.76	0.50
25:LY:9:SER:O	25:LY:55:LYS:NZ	2.38	0.50
33:Lg:106:ARG:NH2	46:14:1423:G:OP1	2.44	0.50
46:14:3006:C:H2'	46:14:3007:A:O4'	2.12	0.50
43:10:118:G:H2'	43:10:119:G:H4'	1.94	0.50
26:LZ:30:GLU:HA	26:LZ:30:GLU:OE1	2.12	0.50
43:10:173:C:H1'	46:14:2489:A:H1'	1.93	0.50
46:14:2263:U:O2'	46:14:2264:G:O5'	2.29	0.50
28:Lb:99:VAL:HG21	28:Lb:109:ALA:HB2	1.92	0.50
46:14:1051:U:H2'	46:14:1052:A:C8	2.47	0.50
2:LB:170:ALA:CB	42:Lq:65:VAL:HG12	2.42	0.50
29:Lc:77:LYS:HG3	29:Lc:80:LYS:HG3	1.93	0.50
45:13:133:G:H2'	45:13:134:G:H8	1.76	0.50
26:LZ:100:ARG:HE	26:LZ:102:ILE:HD11	1.77	0.49
29:Lc:74:LYS:O	29:Lc:78:GLN:NE2	2.45	0.49
43:10:85:C:H2'	43:10:86:U:O4'	2.12	0.49
11:LK:264:LYS:HG2	11:LK:265:ARG:H	1.77	0.49
43:10:84:A:H2'	43:10:85:C:C6	2.46	0.49
43:10:114:C:H2'	43:10:115:G:H8	1.77	0.49
46:14:2572:C:O2'	46:14:2573:U:O5'	2.29	0.49
1:LA:5:LEU:HB3	1:LA:198:TRP:HH2	1.76	0.49
1:LA:196:LYS:HB2	1:LA:200:ASN:OD1	2.12	0.49
5:LE:117:LYS:NZ	5:LE:117:LYS:HB3	2.27	0.49
4:LD:314:ASN:OD1	46:14:1357:G:N2	2.45	0.49
21:LU:19:MET:HE2	21:LU:19:MET:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:10:131:U:H3'	43:10:132:G:C8	2.47	0.49
46:14:3271:A:O2'	46:14:3272:U:H6	1.96	0.49
17:LQ:25:TYR:HE2	46:14:608:U:H5'	1.76	0.49
43:10:51:G:N2	43:10:87:U:O4	2.46	0.49
17:LQ:21:ARG:NH1	46:14:581:C:OP2	2.45	0.49
43:10:50:G:O2'	43:10:51:G:H3'	2.12	0.49
46:14:92:G:H2'	46:14:93:A:C8	2.48	0.49
46:14:978:G:H2'	46:14:979:C:C6	2.48	0.49
4:LD:287:LYS:NZ	22:LV:23:ASP:OD2	2.44	0.49
4:LD:328:ASN:ND2	46:14:617:C:O4'	2.39	0.49
46:14:246:C:H5'	46:14:247:C:H5'	1.95	0.49
11:LK:105:LEU:O	11:LK:109:VAL:HG23	2.13	0.49
28:Lb:60:LYS:HE2	28:Lb:64:LYS:HE2	1.95	0.49
1:LA:38:LEU:HA	1:LA:200:ASN:O	2.13	0.49
27:La:48:PRO:HB2	27:La:56:MET:HE3	1.95	0.49
37:Lk:77:ASN:OD1	37:Lk:77:ASN:O	2.31	0.49
42:Lq:16:THR:HG22	46:14:1933:G:C8	2.48	0.49
46:14:1700:A:H2'	46:14:1701:A:C8	2.48	0.49
4:LD:333:LEU:HD22	16:LP:181:ILE:HD12	1.94	0.48
31:Le:32:TYR:OH	31:Le:60:GLU:OE1	2.31	0.48
43:10:200:G:H3'	43:10:201:C:C6	2.48	0.48
46:14:1748:G:H2'	46:14:1749:G:H8	1.78	0.48
46:14:2308:G:OP2	46:14:2308:G:N2	2.32	0.48
21:LU:176:GLY:O	21:LU:185:ARG:NH2	2.46	0.48
1:LA:68:LEU:O	1:LA:112:ALA:HA	2.14	0.48
4:LD:257:THR:HG23	4:LD:259:SER:H	1.78	0.48
6:LF:142:LYS:HG3	6:LF:143:VAL:HG23	1.96	0.48
16:LP:178:ILE:HG23	16:LP:183:ASP:HB3	1.96	0.48
16:LP:11:SER:HB2	46:14:1361:A:O2'	2.12	0.48
21:LU:168:GLY:HA2	21:LU:171:TYR:CE2	2.49	0.48
26:LZ:43:LEU:O	26:LZ:47:ILE:HG13	2.13	0.48
44:12:24:C:H2'	44:12:25:G:O4'	2.13	0.48
6:LF:8:GLU:HB3	6:LF:77:LEU:HD11	1.95	0.48
8:LH:96:MET:HE2	27:La:22:ARG:HH11	1.77	0.48
20:LT:45:ARG:HE	24:LX:72:THR:HG22	1.79	0.48
43:10:139:A:H2'	43:10:140:U:O4'	2.14	0.48
46:14:802:C:H2'	46:14:803:C:C6	2.48	0.48
1:LA:208:SER:O	1:LA:209:THR:C	2.56	0.48
6:LF:61:ASP:N	6:LF:61:ASP:OD1	2.44	0.48
10:LJ:153:ARG:O	10:LJ:156:LYS:HB2	2.13	0.48
46:14:544:G:H2'	46:14:545:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:609:G:H2'	46:14:610:C:C6	2.48	0.48
46:14:1921:A:H2'	46:14:1922:U:C6	2.49	0.48
46:14:3224:U:H2'	46:14:3225:C:C6	2.48	0.48
7:LG:59:TYR:OH	7:LG:78:PHE:O	2.30	0.48
13:LM:80:THR:O	13:LM:80:THR:HG22	2.13	0.48
18:LR:235:GLY:O	18:LR:239:GLN:HG3	2.13	0.48
43:10:87:U:H1'	43:10:88:A:C5	2.49	0.48
46:14:2471:A:N3	46:14:2472:G:H1'	2.28	0.48
46:14:3225:C:H2'	46:14:3226:A:C8	2.43	0.48
38:LI:14:THR:O	38:LI:17:ARG:HG2	2.13	0.48
46:14:2750:A:H2'	46:14:2751:A:C8	2.49	0.48
1:LA:142:GLU:H	1:LA:142:GLU:HG3	1.62	0.48
1:LA:209:THR:HG22	1:LA:210:MET:HG2	1.96	0.48
4:LD:309:ILE:HG22	16:LP:22:TRP:CZ3	2.49	0.48
18:LR:202:GLU:OE1	18:LR:202:GLU:N	2.47	0.48
43:10:83:C:H2'	43:10:84:A:C8	2.49	0.48
46:14:652:C:H42	46:14:656:A:H2	1.62	0.48
46:14:805:G:H2'	46:14:806:U:C6	2.49	0.48
46:14:897:G:H2'	46:14:898:U:C6	2.49	0.48
7:LG:17:ARG:HA	7:LG:45:GLU:HB2	1.96	0.47
9:LI:2:THR:HG22	9:LI:4:ARG:HG2	1.95	0.47
9:LI:76:ASP:HB3	9:LI:114:GLY:HA3	1.95	0.47
46:14:1059:A:N3	46:14:2636:U:O2'	2.46	0.47
46:14:2216:A:H2'	46:14:2217:A:H8	1.79	0.47
1:LA:156:LYS:HE2	1:LA:158:GLN:HG3	1.95	0.47
6:LF:135:VAL:HG23	6:LF:157:VAL:HG22	1.96	0.47
43:10:85:C:C4	43:10:86:U:C4	3.02	0.47
46:14:1045:U:H2'	46:14:1046:C:C6	2.49	0.47
2:LB:42:LYS:HG3	2:LB:89:TYR:CE2	2.49	0.47
6:LF:118:ARG:HG2	6:LF:126:VAL:HG12	1.96	0.47
24:LX:25:LYS:HE2	24:LX:25:LYS:HB2	1.71	0.47
38:LI:22:THR:HG22	38:LI:65:SER:HB3	1.96	0.47
46:14:394:A:H4'	46:14:395:G:H3'	1.96	0.47
46:14:2498:U:H2'	46:14:2499:A:H8	1.79	0.47
1:LA:5:LEU:HD22	1:LA:187:VAL:HG11	1.95	0.47
37:Lk:64:MET:HE3	37:Lk:64:MET:HB3	1.72	0.47
46:14:955:C:H2'	46:14:956:C:H6	1.78	0.47
1:LA:56:PRO:HD3	1:LA:185:MET:SD	2.54	0.47
10:LJ:162:ARG:HG3	10:LJ:162:ARG:HH11	1.79	0.47
10:LJ:162:ARG:HG3	10:LJ:162:ARG:NH1	2.30	0.47
23:LW:136:ARG:O	23:LW:140:GLU:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:437:G:O6	46:14:633:G:H1'	2.15	0.47
25:LY:109:MET:HE2	46:14:1075:G:N7	2.29	0.47
43:10:173:C:C1'	46:14:2489:A:H1'	2.45	0.47
1:LA:93:LEU:HD22	1:LA:99:LEU:HB3	1.96	0.47
4:LD:382:PHE:HA	4:LD:385:MET:HG3	1.97	0.47
7:LG:10:ARG:HB3	7:LG:10:ARG:HH11	1.80	0.47
16:LP:145:ARG:HG2	16:LP:149:TYR:CE2	2.49	0.47
17:LQ:10:PRO:HG2	17:LQ:18:LYS:HD2	1.96	0.47
27:La:9:ARG:HH22	27:La:29:GLN:HE22	1.62	0.47
28:Lb:51:LYS:HD3	46:14:1815:A:OP2	2.15	0.47
39:Lm:36:ARG:HH22	46:14:399:G:H1'	1.80	0.47
42:Lq:36:LYS:HG3	42:Lq:48:LYS:HE2	1.96	0.47
46:14:1084:G:H2'	46:14:1085:C:C6	2.50	0.47
46:14:2476:A:H3'	46:14:2477:A:C8	2.50	0.47
13:LM:120:LYS:HD3	13:LM:137:ARG:HD3	1.96	0.47
46:14:2904:G:O2'	46:14:3026:A:N1	2.46	0.47
18:LR:49:LYS:HG3	46:14:2528:A:C5	2.50	0.47
46:14:1232:A:H4'	46:14:1234:G:H5''	1.96	0.47
5:LE:152:ILE:HA	5:LE:155:ARG:HG3	1.97	0.47
11:LK:126:THR:HG22	11:LK:128:GLU:H	1.80	0.47
17:LQ:36:LYS:HD2	46:14:586:G:H4'	1.96	0.47
17:LQ:41:PHE:HB3	46:14:609:G:C2	2.49	0.47
19:LS:26:GLN:HB3	19:LS:27:PRO:HD3	1.97	0.47
43:10:71:U:C2	43:10:72:G:C8	3.02	0.47
45:13:135:C:H2'	45:13:136:C:C6	2.49	0.47
46:14:1131:A:H2'	46:14:1132:U:H6	1.79	0.47
46:14:2450:G:H3'	46:14:2451:A:C8	2.49	0.47
1:LA:54:LYS:HA	1:LA:153:ALA:O	2.14	0.46
1:LA:68:LEU:HD22	1:LA:90:LEU:HD21	1.97	0.46
5:LE:26:GLY:HA3	46:14:2683:A:C2	2.50	0.46
35:Li:98:GLU:HA	35:Li:98:GLU:OE1	2.15	0.46
46:14:2164:G:H2'	46:14:2165:G:H8	1.81	0.46
46:14:2455:G:H22	46:14:2499:A:H2	1.62	0.46
46:14:3133:U:H2'	46:14:3134:C:C6	2.49	0.46
6:LF:1:MET:HE3	6:LF:1:MET:HB3	1.83	0.46
12:LL:2:VAL:HG22	12:LL:3:LYS:H	1.80	0.46
19:LS:126:PRO:HB3	19:LS:136:ASP:OD2	2.15	0.46
46:14:2574:U:O2'	46:14:2575:G:N7	2.44	0.46
46:14:3015:U:H2'	46:14:3016:U:C6	2.50	0.46
46:14:3164:U:H2'	46:14:3165:C:C6	2.49	0.46
1:LA:27:LYS:HG3	46:14:2473:C:OP2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LD:155:LEU:HD23	4:LD:255:VAL:HG22	1.98	0.46
5:LE:51:LYS:O	5:LE:53:ARG:NH1	2.48	0.46
6:LF:74:ARG:HA	6:LF:74:ARG:HD2	1.55	0.46
16:LP:142:LYS:O	16:LP:146:GLU:HG3	2.14	0.46
31:Le:104:ASP:OD1	31:Le:104:ASP:N	2.47	0.46
45:13:162:G:H2'	45:13:163:C:O4'	2.16	0.46
46:14:243:G:H2'	46:14:244:C:C6	2.50	0.46
10:LJ:38:MET:HE3	10:LJ:41:LYS:HG2	1.97	0.46
22:LV:21:SER:OG	46:14:684:U:OP1	2.28	0.46
46:14:371:A:N3	46:14:373:G:H5''	2.30	0.46
46:14:3002:G:H2'	46:14:3003:U:C6	2.50	0.46
17:LQ:152:PHE:HE2	17:LQ:195:VAL:HG21	1.80	0.46
45:13:7:C:H2'	45:13:8:U:C6	2.51	0.46
10:LJ:164:LYS:HB2	10:LJ:164:LYS:HE2	1.64	0.46
11:LK:81:ARG:HB2	11:LK:81:ARG:CZ	2.45	0.46
29:Lc:36:GLU:HG2	29:Lc:39:ASN:HB2	1.98	0.46
33:Lg:97:ILE:HG21	33:Lg:106:ARG:HG2	1.98	0.46
43:10:113:G:H2'	43:10:114:C:H6	1.80	0.46
46:14:2700:A:H2'	46:14:2701:G:C8	2.51	0.46
2:LB:48:ILE:HG12	42:Lq:65:VAL:HG22	1.98	0.46
4:LD:142:ALA:HB1	29:Lc:17:ASN:HB2	1.97	0.46
5:LE:25:VAL:C	5:LE:27:GLU:H	2.24	0.46
6:LF:180:ASP:OD1	6:LF:180:ASP:N	2.49	0.46
43:10:59:G:H4'	43:10:62:A:H5'	1.98	0.46
46:14:174:G:C4	46:14:175:A:C8	3.04	0.46
3:LC:143:LYS:O	3:LC:147:GLN:HG2	2.16	0.46
28:Lb:6:LYS:HE3	28:Lb:6:LYS:HB2	1.48	0.46
46:14:129:G:H1	46:14:135:U:H3	1.64	0.46
46:14:195:A:N3	46:14:215:G:O2'	2.49	0.46
46:14:1543:C:H2'	46:14:1544:U:C6	2.51	0.46
46:14:2448:U:H2'	46:14:2449:U:C6	2.51	0.46
1:LA:36:ILE:CD1	1:LA:190:LEU:HD22	2.42	0.46
23:LW:146:LYS:HB3	23:LW:146:LYS:HE3	1.78	0.46
26:LZ:24:ASP:OD1	26:LZ:24:ASP:C	2.59	0.46
29:Lc:55:LYS:HB2	29:Lc:55:LYS:HE3	1.79	0.46
46:14:583:C:H2'	46:14:584:G:H8	1.76	0.46
46:14:1131:A:H2'	46:14:1132:U:C6	2.51	0.46
15:LO:119:TYR:CZ	19:LS:47:ARG:HG2	2.52	0.45
19:LS:101:ARG:HH11	19:LS:103:ARG:HE	1.65	0.45
43:10:96:G:H3'	43:10:97:G:H8	1.80	0.45
43:10:132:G:H3'	43:10:133:G:H8	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LB:48:ILE:HG12	42:Lq:65:VAL:CG2	2.46	0.45
7:LG:104:LEU:HD23	7:LG:104:LEU:HA	1.84	0.45
26:LZ:80:ARG:HG3	26:LZ:80:ARG:HH11	1.82	0.45
43:10:87:U:O2	43:10:88:A:N6	2.50	0.45
43:10:170:G:H2'	43:10:170:G:N3	2.32	0.45
46:14:301:G:N3	46:14:301:G:H5'	2.31	0.45
46:14:3072:A:H2'	46:14:3073:A:H8	1.79	0.45
8:LH:30:ASP:OD2	8:LH:32:THR:HG23	2.17	0.45
46:14:2697:A:H3'	46:14:2698:G:N2	2.30	0.45
46:14:2888:C:O2'	46:14:2889:U:H5'	2.17	0.45
6:LF:7:SER:HB2	6:LF:61:ASP:HB3	1.98	0.45
24:LX:14:ARG:HG3	24:LX:15:ALA:O	2.17	0.45
38:Ll:60:LEU:HD13	38:Ll:61:PRO:HD2	1.99	0.45
43:10:141:A:H3'	43:10:142:C:C6	2.52	0.45
44:12:37:A:H2'	44:12:38:U:C6	2.51	0.45
45:13:126:G:H2'	45:13:127:C:C6	2.52	0.45
12:LL:15:CYS:SG	12:LL:103:ALA:HB2	2.57	0.45
14:LN:50:ARG:HG2	14:LN:51:LYS:H	1.82	0.45
26:LZ:22:VAL:HB	26:LZ:110:VAL:HG12	1.98	0.45
33:Lg:87:MET:HG3	33:Lg:116:LEU:HD22	1.99	0.45
34:Lh:61:LYS:HB2	46:14:3168:C:H42	1.80	0.45
36:Lj:38:LYS:HE2	36:Lj:38:LYS:HB2	1.76	0.45
43:10:108:G:H4'	43:10:177:U:O2	2.17	0.45
43:10:190:C:H2'	43:10:191:C:C6	2.51	0.45
46:14:2658:U:H4'	46:14:2659:A:O4'	2.16	0.45
6:LF:190:ILE:HG22	6:LF:191:VAL:HG23	1.99	0.45
27:La:15:ILE:HG12	27:La:34:LEU:HD13	1.99	0.45
31:Le:39:LEU:HD13	31:Le:64:TYR:HB3	1.98	0.45
43:10:70:G:O2'	43:10:88:A:N7	2.47	0.45
43:10:105:C:H2'	43:10:106:U:C6	2.51	0.45
46:14:107:A:H4'	46:14:108:G:OP1	2.17	0.45
46:14:2543:A:H1'	46:14:2546:G:N2	2.32	0.45
23:LW:95:TRP:CH2	23:LW:99:MET:HE3	2.52	0.45
25:LY:13:ASP:OD2	46:14:1006:G:H3'	2.17	0.45
27:La:9:ARG:HH22	27:La:29:GLN:NE2	2.14	0.45
30:Ld:6:ASN:HB2	46:14:1146:A:OP1	2.16	0.45
40:Ln:89:TYR:C	40:Ln:90:ASN:HD22	2.25	0.45
1:LA:139:SER:OG	1:LA:141:GLN:HG2	2.16	0.45
4:LD:34:PRO:HG3	4:LD:286:PRO:HD3	1.99	0.45
9:LI:104:GLN:HB3	19:LS:160:PRO:HB3	1.98	0.45
17:LQ:35:LYS:HE3	17:LQ:35:LYS:HB3	1.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:2638:A:H4'	46:14:2639:A:O5'	2.17	0.45
46:14:3195:G:H2'	46:14:3196:C:C6	2.51	0.45
27:La:50:LYS:HD3	46:14:2115:G:C5'	2.47	0.45
43:10:156:U:H2'	43:10:158:A:OP2	2.17	0.45
1:LA:26:ARG:HA	46:14:2473:C:OP1	2.17	0.45
3:LC:253:ALA:HB3	46:14:2883:U:H1'	1.99	0.45
15:LO:18:LEU:HD12	15:LO:18:LEU:HA	1.82	0.45
46:14:801:A:H2'	46:14:802:C:C6	2.53	0.45
1:LA:18:LYS:HD2	1:LA:176:GLU:CG	2.47	0.44
28:Lb:53:VAL:HG13	28:Lb:62:GLN:HG2	1.99	0.44
46:14:206:A:O2'	46:14:208:A:OP2	2.30	0.44
46:14:771:A:N6	46:14:780:G:H1'	2.32	0.44
46:14:1120:C:H2'	46:14:1121:C:C6	2.52	0.44
6:LF:140:SER:HB3	6:LF:146:GLU:HB2	1.99	0.44
13:LM:77:TYR:CD1	15:LO:36:VAL:HG21	2.52	0.44
19:LS:78:GLU:HG3	19:LS:108:LEU:HD12	1.99	0.44
31:Le:27:LYS:HE3	31:Le:99:ASP:HB3	1.99	0.44
32:Lf:83:LYS:HB2	32:Lf:83:LYS:HE3	1.73	0.44
41:Lp:6:LYS:HE2	41:Lp:6:LYS:HB2	1.84	0.44
46:14:637:C:H2'	46:14:638:C:H6	1.82	0.44
46:14:666:C:H2'	46:14:667:A:C8	2.52	0.44
46:14:1185:G:H2'	46:14:1186:C:C6	2.52	0.44
46:14:2503:U:H2'	46:14:2504:U:C6	2.52	0.44
46:14:2726:U:H2'	46:14:2727:U:C6	2.53	0.44
17:LQ:153:ASP:N	17:LQ:153:ASP:OD1	2.48	0.44
20:LT:9:ILE:HD13	20:LT:64:ARG:HB3	2.00	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
46:14:2576:C:H2'	46:14:2577:A:C8	2.53	0.44
4:LD:16:GLU:H	4:LD:176:GLN:HE22	1.61	0.44
6:LF:49:LYS:HE2	6:LF:49:LYS:HB2	1.85	0.44
29:Lc:136:VAL:HG21	33:Lg:114:ALA:HB1	1.98	0.44
34:Lh:14:VAL:HG23	34:Lh:105:VAL:HB	2.00	0.44
43:10:118:G:C2	43:10:119:G:H1'	2.52	0.44
43:10:180:C:H2'	43:10:181:C:H6	1.81	0.44
46:14:1958:G:H2'	46:14:2096:A:H61	1.81	0.44
46:14:2990:A:H2'	46:14:2991:C:C6	2.53	0.44
13:LM:143:ASP:C	13:LM:143:ASP:OD1	2.60	0.44
14:LN:54:GLU:HB2	14:LN:107:LYS:HB3	2.00	0.44
20:LT:128:LEU:HD23	20:LT:128:LEU:HA	1.88	0.44
46:14:1449:U:H2'	46:14:1450:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:1476:A:H2'	46:14:1477:G:O4'	2.17	0.44
1:LA:26:ARG:CA	46:14:2473:C:OP1	2.66	0.44
5:LE:50:SER:OG	46:14:2684:U:O3'	2.25	0.44
16:LP:86:ILE:O	16:LP:114:GLY:HA2	2.18	0.44
32:Lf:62:LYS:HB2	32:Lf:62:LYS:HE3	1.57	0.44
45:13:136:C:H2'	45:13:137:G:C8	2.52	0.44
46:14:245:A:H2'	46:14:246:C:O4'	2.18	0.44
26:LZ:67:THR:HG23	26:LZ:68:LYS:HG3	1.99	0.44
31:Le:34:THR:O	31:Le:38:THR:HG23	2.18	0.44
44:12:33:U:H2'	44:12:34:C:O4'	2.18	0.44
36:Lj:36:THR:OG1	36:Lj:37:SER:N	2.50	0.44
46:14:710:U:O2'	46:14:711:A:H3'	2.18	0.44
1:LA:44:GLN:CD	1:LA:44:GLN:H	2.25	0.44
24:LX:14:ARG:O	24:LX:59:GLN:N	2.43	0.44
1:LA:41:TYR:HB3	1:LA:163:LEU:HD21	2.00	0.43
3:LC:20:LYS:HB2	3:LC:20:LYS:HE2	1.78	0.43
16:LP:95:MET:HE3	16:LP:100:LYS:HB2	2.00	0.43
46:14:641:A:H2'	46:14:642:U:C6	2.53	0.43
1:LA:10:LEU:HD23	1:LA:180:PHE:CE2	2.53	0.43
3:LC:382:LYS:HB2	3:LC:382:LYS:HE3	1.65	0.43
14:LN:83:ARG:HG3	14:LN:83:ARG:HH11	1.84	0.43
29:Lc:87:LYS:HB3	29:Lc:87:LYS:HE3	1.63	0.43
31:Le:17:ASN:H	31:Le:17:ASN:ND2	2.17	0.43
46:14:11:G:H5'	46:14:12:U:P	2.57	0.43
46:14:978:G:H2'	46:14:979:C:H6	1.82	0.43
46:14:2122:C:H2'	46:14:2123:A:O4'	2.18	0.43
46:14:2680:G:N3	46:14:2680:G:H2'	2.33	0.43
46:14:2964:G:H2'	46:14:2965:U:C6	2.51	0.43
3:LC:8:HIS:ND1	3:LC:9:PRO:O	2.50	0.43
4:LD:355:LYS:HZ2	46:14:518:G:P	2.41	0.43
16:LP:52:ALA:O	16:LP:56:GLU:HG2	2.18	0.43
17:LQ:144:VAL:HG12	17:LQ:144:VAL:O	2.18	0.43
33:Lg:3:VAL:HG12	33:Lg:91:ARG:HH21	1.81	0.43
43:10:161:A:H4'	43:10:162:A:OP1	2.19	0.43
46:14:1234:G:N1	46:14:1297:G:N7	2.66	0.43
46:14:1821:U:H4'	46:14:1822:G:O4'	2.18	0.43
46:14:2512:U:H2'	46:14:2513:U:C6	2.53	0.43
6:LF:10:MET:HE3	6:LF:10:MET:HB2	1.83	0.43
7:LG:117:TYR:HA	7:LG:120:ILE:HD12	2.00	0.43
46:14:311:U:H2'	46:14:312:C:C6	2.54	0.43
46:14:3025:U:H2'	46:14:3026:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:31:THR:OG1	46:14:2470:G:OP1	2.31	0.43
1:LA:38:LEU:HB2	1:LA:163:LEU:HD22	2.00	0.43
1:LA:207:LYS:HB2	1:LA:207:LYS:HE2	1.65	0.43
19:LS:101:ARG:NH1	19:LS:103:ARG:HH21	2.17	0.43
20:LT:102:LEU:HD22	20:LT:106:ASP:HB2	2.00	0.43
24:LX:161:PRO:HD2	24:LX:165:LEU:HD12	2.00	0.43
46:14:1119:U:H2'	46:14:1120:C:C6	2.53	0.43
46:14:1679:G:H2'	46:14:1680:A:C8	2.52	0.43
1:LA:163:LEU:HD23	1:LA:163:LEU:HA	1.72	0.43
3:LC:312:MET:HE2	46:14:3321:U:H5'	2.00	0.43
14:LN:51:LYS:O	14:LN:69:VAL:HB	2.19	0.43
17:LQ:201:LYS:HE3	17:LQ:201:LYS:HA	2.01	0.43
20:LT:61:ASP:OD1	20:LT:61:ASP:C	2.62	0.43
30:Ld:41:ARG:HD3	46:14:786:U:OP1	2.18	0.43
45:13:129:A:C8	45:13:133:G:N1	2.86	0.43
46:14:436:C:O3'	46:14:437:G:H8	2.01	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:H8	1.83	0.43
21:LU:84:PRO:HA	21:LU:87:GLN:HG3	2.00	0.43
28:Lb:90:ASP:O	28:Lb:116:ARG:NH1	2.52	0.43
37:Lk:87:ARG:HD2	45:13:71:G:OP2	2.19	0.43
45:13:86:C:H4'	45:13:88:G:N3	2.34	0.43
46:14:666:C:H2'	46:14:667:A:H8	1.84	0.43
46:14:2711:U:H2'	46:14:2712:C:C6	2.53	0.43
1:LA:33:GLU:OE2	1:LA:207:LYS:HD3	2.19	0.43
1:LA:42:ASP:O	1:LA:43:PRO:C	2.62	0.43
18:LR:202:GLU:H	18:LR:202:GLU:CD	2.24	0.43
43:10:67:A:H2'	43:10:68:U:O4'	2.18	0.43
46:14:2409:C:H2'	46:14:2410:C:C6	2.54	0.43
14:LN:47:MET:HE3	14:LN:47:MET:HB3	1.82	0.43
17:LQ:34:LYS:NZ	46:14:608:U:OP1	2.52	0.43
21:LU:47:LYS:HE2	46:14:266:G:OP1	2.18	0.43
29:Lc:58:THR:HB	29:Lc:71:ALA:HB3	2.00	0.43
40:Ln:102:ARG:HH21	46:14:2899:A:P	2.42	0.43
46:14:2199:C:O2'	46:14:2273:A:N3	2.46	0.43
46:14:2402:A:H2'	46:14:2403:G:O4'	2.18	0.43
1:LA:189:PHE:CE2	1:LA:193:LEU:HD11	2.54	0.43
3:LC:82:PRO:HA	3:LC:323:ASP:OD2	2.19	0.43
18:LR:30:LYS:NZ	46:14:2563:C:OP1	2.49	0.43
22:LV:2:GLY:N	46:14:1171:A:OP1	2.52	0.43
26:LZ:66:LYS:HE3	26:LZ:66:LYS:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:14:2692:G:H2'	46:14:2692:G:N3	2.34	0.43
46:14:3253:C:H2'	46:14:3254:C:O4'	2.19	0.43
13:LM:50:LEU:CD2	45:13:152:U:H4'	2.49	0.42
13:LM:103:ASP:OD1	13:LM:103:ASP:N	2.46	0.42
21:LU:46:ASP:OD1	21:LU:46:ASP:N	2.47	0.42
28:Lb:31:GLU:CD	28:Lb:31:GLU:H	2.27	0.42
37:Lk:39:TYR:CD1	37:Lk:40:PRO:HA	2.54	0.42
38:Ll:35:LYS:HA	38:Ll:43:TYR:O	2.19	0.42
43:10:102:U:H2'	43:10:103:G:C8	2.53	0.42
43:10:172:U:H3	43:10:174:G:H3'	1.84	0.42
43:10:179:C:H2'	43:10:180:C:C6	2.53	0.42
43:10:200:G:H3'	43:10:201:C:H6	1.84	0.42
46:14:957:U:H2'	46:14:958:C:C6	2.54	0.42
46:14:2210:A:H2'	46:14:2211:A:C5	2.54	0.42
46:14:2458:U:H3	46:14:2490:A:H61	1.67	0.42
46:14:2843:C:N4	46:14:2848:A:O2'	2.53	0.42
1:LA:47:LYS:H	1:LA:195:LYS:NZ	2.17	0.42
9:LI:77:ASN:O	9:LI:80:SER:OG	2.29	0.42
9:LI:135:LYS:HB2	9:LI:135:LYS:HE3	1.65	0.42
21:LU:85:THR:HG21	46:14:43:A:P	2.59	0.42
27:La:50:LYS:HD3	46:14:2115:G:H5'	2.00	0.42
36:Lj:18:HIS:HB3	46:14:71:A:H5'	2.00	0.42
37:Lk:45:ARG:C	37:Lk:46:LYS:HG2	2.44	0.42
43:10:117:G:C4	43:10:147:G:N2	2.87	0.42
43:10:192:C:H2'	43:10:193:G:H8	1.84	0.42
46:14:2499:A:H2'	46:14:2500:C:O4'	2.18	0.42
1:LA:24:LYS:H	1:LA:24:LYS:HG2	1.67	0.42
2:LB:181:LYS:NZ	46:14:870:G:OP2	2.52	0.42
16:LP:175:LYS:H	16:LP:175:LYS:HG2	1.61	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
46:14:3223:G:H2'	46:14:3224:U:C6	2.54	0.42
1:LA:47:LYS:HB3	1:LA:47:LYS:HE2	1.62	0.42
20:LT:124:GLU:OE1	20:LT:124:GLU:HA	2.19	0.42
28:Lb:56:LYS:HB3	28:Lb:56:LYS:HE3	1.83	0.42
29:Lc:66:LYS:H	29:Lc:66:LYS:HE2	1.85	0.42
34:Lh:64:LYS:HG3	46:14:632:G:OP1	2.20	0.42
38:Ll:60:LEU:CD1	38:Ll:61:PRO:HD2	2.49	0.42
43:10:125:U:H4'	43:10:126:G:OP1	2.18	0.42
46:14:2614:U:H2'	46:14:2615:U:C6	2.53	0.42
17:LQ:20:SER:O	17:LQ:24:MET:HB2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lh:63:LYS:HG3	34:Lh:68:HIS:CE1	2.54	0.42
43:10:78:C:H1'	43:10:159:U:C5	2.53	0.42
46:14:275:U:H2'	46:14:276:U:C6	2.55	0.42
46:14:857:A:H3'	46:14:858:A:C8	2.55	0.42
46:14:2210:A:O2'	46:14:2211:A:O4'	2.36	0.42
46:14:2536:G:H1	46:14:2552:C:H42	1.68	0.42
4:LD:374:ILE:HD13	46:14:524:A:N6	2.35	0.42
5:LE:37:LYS:HB2	5:LE:37:LYS:HZ3	1.84	0.42
5:LE:38:VAL:HG23	5:LE:122:THR:HG21	2.01	0.42
11:LK:288:ASN:HD22	11:LK:288:ASN:HA	1.60	0.42
13:LM:53:ASP:N	13:LM:53:ASP:OD1	2.52	0.42
14:LN:112:LYS:NZ	45:13:88:G:OP2	2.53	0.42
16:LP:56:GLU:HG2	16:LP:56:GLU:H	1.68	0.42
17:LQ:120:PHE:CZ	46:14:3258:A:H2'	2.55	0.42
22:LV:98:LYS:HE3	22:LV:98:LYS:HB2	1.63	0.42
35:Li:68:SER:OG	35:Li:70:ASN:OD1	2.35	0.42
43:10:70:G:H1	43:10:85:C:H42	1.68	0.42
46:14:854:G:H1	46:14:859:C:H42	1.67	0.42
46:14:2571:G:OP2	46:14:2572:C:N4	2.53	0.42
1:LA:50:SER:HB2	1:LA:158:GLN:HG2	2.01	0.42
4:LD:272:ASP:OD1	4:LD:272:ASP:N	2.37	0.42
12:LL:42:ASP:OD1	12:LL:42:ASP:N	2.45	0.42
19:LS:66:MET:HE3	19:LS:66:MET:H	1.85	0.42
19:LS:101:ARG:HH11	19:LS:103:ARG:HH21	1.68	0.42
22:LV:123:ASP:OD1	22:LV:124:GLN:N	2.53	0.42
38:Li:16:ARG:NH1	38:Li:16:ARG:HG3	2.34	0.42
43:10:170:G:H3'	43:10:171:U:H6	1.85	0.42
46:14:660:A:H2'	46:14:661:C:C6	2.55	0.42
46:14:1539:G:O2'	46:14:1593:A:N3	2.49	0.42
1:LA:30:GLU:HB2	1:LA:172:LEU:HD12	2.02	0.42
7:LG:10:ARG:HB3	7:LG:10:ARG:NH1	2.35	0.42
22:LV:23:ASP:O	22:LV:27:LYS:HG2	2.20	0.42
23:LW:153:LYS:HB3	23:LW:153:LYS:HE3	1.85	0.42
33:Lg:10:VAL:HG22	33:Lg:64:THR:HB	2.02	0.42
43:10:66:C:H2'	43:10:67:A:O4'	2.20	0.42
46:14:582:G:H2'	46:14:583:C:C6	2.55	0.42
46:14:2890:A:N3	46:14:2890:A:H2'	2.33	0.42
17:LQ:33:ILE:HD13	46:14:585:C:C4	2.55	0.42
35:Li:60:THR:HG21	46:14:1598:A:H5'	2.01	0.42
46:14:1733:G:N3	46:14:1733:G:H5'	2.35	0.42
1:LA:61:PRO:HD2	1:LA:62:LYS:HE2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LU:85:THR:HG23	46:14:42:U:H5''	2.01	0.41
25:LY:126:ILE:O	46:14:1106:C:O2'	2.38	0.41
32:Lf:70:ARG:HH11	46:14:3060:C:N4	2.18	0.41
46:14:1237:A:N6	46:14:3118:G:C6	2.88	0.41
46:14:1545:A:H2'	46:14:1546:A:C8	2.55	0.41
46:14:2427:A:H2'	46:14:2428:G:O4'	2.20	0.41
5:LE:81:LEU:HD23	5:LE:81:LEU:HA	1.86	0.41
5:LE:97:ASN:N	5:LE:97:ASN:HD22	2.17	0.41
15:LO:105:GLU:HA	15:LO:108:LYS:HD3	2.01	0.41
1:LA:25:LYS:HB2	1:LA:25:LYS:HE2	1.57	0.41
4:LD:369:GLU:OE1	4:LD:369:GLU:N	2.34	0.41
36:Lj:48:ARG:O	36:Lj:48:ARG:HD3	2.20	0.41
46:14:667:A:H2'	46:14:668:A:C8	2.56	0.41
46:14:936:A:H2'	46:14:937:C:C6	2.55	0.41
46:14:1653:U:H2'	46:14:1654:C:O4'	2.20	0.41
46:14:2885:U:H2'	46:14:2886:U:C6	2.55	0.41
5:LE:21:LEU:HD11	5:LE:81:LEU:HD13	2.02	0.41
17:LQ:24:MET:HA	17:LQ:24:MET:CE	2.42	0.41
17:LQ:64:ASP:CG	33:Lg:5:LEU:HD11	2.45	0.41
19:LS:157:ARG:HG2	19:LS:158:GLU:N	2.35	0.41
19:LS:168:THR:O	19:LS:172:LYS:HG3	2.20	0.41
24:LX:29:MET:HG3	24:LX:43:PHE:HD1	1.84	0.41
30:Ld:13:ASN:HD22	30:Ld:13:ASN:HA	1.57	0.41
31:Le:27:LYS:HE3	31:Le:27:LYS:HB2	1.76	0.41
36:Lj:36:THR:HG23	36:Lj:41:HIS:CE1	2.56	0.41
46:14:700:A:N7	46:14:702:U:O2'	2.51	0.41
46:14:1508:C:H2'	46:14:1509:A:C8	2.56	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
41:Lp:35:LEU:HD12	41:Lp:35:LEU:HA	1.94	0.41
46:14:545:C:H2'	46:14:546:U:C6	2.56	0.41
46:14:2164:G:H2'	46:14:2165:G:C8	2.56	0.41
46:14:2725:U:H2'	46:14:2726:U:H6	1.86	0.41
46:14:2963:C:H2'	46:14:2964:G:C8	2.56	0.41
46:14:3168:C:H4'	46:14:3169:U:O5'	2.19	0.41
2:LB:116:VAL:HB	2:LB:126:PHE:HB2	2.02	0.41
4:LD:79:ILE:HG13	4:LD:80:PRO:HD2	2.01	0.41
17:LQ:123:ASN:ND2	17:LQ:213:LEU:O	2.48	0.41
43:10:71:U:C2'	43:10:72:G:H5'	2.50	0.41
43:10:138:U:H2'	43:10:139:A:H8	1.85	0.41
5:LE:154:HIS:ND1	44:12:54:A:O2'	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LF:10:MET:HE1	6:LF:81:GLU:HG3	2.01	0.41
19:LS:171:MET:H	19:LS:171:MET:HG3	1.64	0.41
31:Le:35:VAL:HG22	31:Le:96:SER:HB2	2.01	0.41
38:Ll:55:LYS:HB2	38:Ll:55:LYS:NZ	2.35	0.41
43:10:146:C:H2'	43:10:147:G:O4'	2.21	0.41
46:14:1128:G:H2'	46:14:1129:C:C6	2.55	0.41
46:14:1748:G:H2'	46:14:1749:G:C8	2.55	0.41
46:14:2482:G:H3'	46:14:2483:A:H8	1.86	0.41
10:LJ:48:PHE:O	10:LJ:139:ARG:HA	2.20	0.41
40:Ln:90:ASN:HD22	40:Ln:90:ASN:N	2.17	0.41
43:10:88:A:H1'	43:10:89:A:C8	2.55	0.41
43:10:127:U:H2'	43:10:128:A:O4'	2.21	0.41
43:10:164:C:H2'	43:10:165:G:H8	1.84	0.41
1:LA:129:ASN:OD1	1:LA:134:PHE:CD1	2.74	0.41
6:LF:112:ASN:HB3	6:LF:137:VAL:O	2.20	0.41
9:LI:4:ARG:NH2	46:14:1438:C:OP2	2.33	0.41
11:LK:110:LEU:HD23	11:LK:110:LEU:HA	1.85	0.41
12:LL:32:THR:HG21	12:LL:88:SER:HB3	2.02	0.41
16:LP:54:GLU:O	16:LP:58:GLN:HG3	2.20	0.41
20:LT:7:VAL:HG12	20:LT:55:LEU:HD11	2.03	0.41
46:14:547:C:H2'	46:14:548:G:C8	2.56	0.41
46:14:2460:G:H2'	46:14:2462:A:N7	2.35	0.41
46:14:3189:C:H2'	46:14:3190:C:O4'	2.21	0.41
1:LA:67:MET:HE2	1:LA:73:HIS:HB3	2.02	0.41
13:LM:145:LEU:HD12	13:LM:145:LEU:HA	1.87	0.41
29:Lc:76:LYS:C	29:Lc:76:LYS:HZ1	2.29	0.41
46:14:1145:G:O2'	46:14:2645:A:N3	2.45	0.41
46:14:2765:A:H2'	46:14:2766:U:H6	1.86	0.41
1:LA:165:MET:HB3	1:LA:165:MET:HE2	1.58	0.40
1:LA:213:PRO:HG3	46:14:2496:A:O3'	2.21	0.40
5:LE:165:PHE:CE2	5:LE:171:GLY:HA3	2.55	0.40
8:LH:109:LYS:HB2	8:LH:109:LYS:NZ	2.36	0.40
11:LK:11:ALA:O	11:LK:15:ARG:HG2	2.21	0.40
29:Lc:95:ARG:O	29:Lc:99:LYS:HD3	2.21	0.40
43:10:151:G:H4'	46:14:2456:U:C2	2.55	0.40
46:14:2489:A:H2'	46:14:2490:A:C8	2.56	0.40
7:LG:182:LEU:HD23	7:LG:182:LEU:HA	1.91	0.40
13:LM:69:LEU:HA	13:LM:69:LEU:HD23	1.72	0.40
15:LO:12:LYS:NZ	15:LO:20:GLN:OE1	2.49	0.40
18:LR:24:LEU:HD12	18:LR:24:LEU:HA	1.82	0.40
24:LX:29:MET:HE3	25:LY:149:VAL:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lj:47:ILE:HD13	36:Lj:47:ILE:HA	1.92	0.40
46:14:556:U:H2'	46:14:557:C:H6	1.84	0.40
46:14:560:C:H2'	46:14:561:U:O4'	2.21	0.40
46:14:1076:A:N6	46:14:1105:A:H2'	2.36	0.40
46:14:1098:C:H2'	46:14:1099:C:C6	2.57	0.40
3:LC:221:ILE:HG12	3:LC:279:THR:HG23	2.03	0.40
5:LE:116:ILE:HD13	5:LE:116:ILE:HA	1.92	0.40
23:LW:114:LYS:HE3	23:LW:114:LYS:HB2	1.71	0.40
26:LZ:66:LYS:HD3	26:LZ:66:LYS:O	2.22	0.40
43:10:119:G:N3	43:10:119:G:H2'	2.35	0.40
46:14:786:U:H5	46:14:2740:C:N3	2.18	0.40
46:14:1818:G:H2'	46:14:1819:A:C1'	2.50	0.40
46:14:2226:A:H2'	46:14:2227:A:C8	2.56	0.40
46:14:2843:C:H2'	46:14:2844:G:O4'	2.20	0.40
4:LD:15:PHE:O	4:LD:16:GLU:C	2.63	0.40
24:LX:83:TYR:CE1	24:LX:90:HIS:HB2	2.57	0.40
29:Lc:62:GLU:HB3	29:Lc:67:SER:HB2	2.04	0.40
31:Le:18:ARG:HB3	31:Le:105:ILE:HG23	2.02	0.40
32:Lf:116:ILE:HD13	32:Lf:116:ILE:HA	1.95	0.40
42:Lq:28:LYS:HB2	42:Lq:28:LYS:HE2	1.83	0.40
43:10:136:C:H2'	43:10:137:A:C8	2.57	0.40
46:14:36:U:H2'	46:14:37:A:O4'	2.21	0.40
46:14:2549:C:H2'	46:14:2550:C:H6	1.86	0.40
46:14:2841:A:H2'	46:14:2842:G:O4'	2.22	0.40
1:LA:74:VAL:HG13	1:LA:84:TYR:CE1	2.57	0.40
7:LG:170:GLN:HE22	46:14:3179:G:H21	1.69	0.40
14:LN:83:ARG:HG3	14:LN:83:ARG:NH1	2.35	0.40
17:LQ:77:LYS:HB3	17:LQ:78:PRO:HD2	2.04	0.40
20:LT:83:LYS:O	20:LT:87:SER:OG	2.39	0.40
26:LZ:20:THR:HA	26:LZ:71:VAL:O	2.22	0.40
43:10:73:U:H2'	43:10:74:U:C6	2.57	0.40
45:13:107:A:H5'	45:13:108:A:H8	1.87	0.40
46:14:1558:A:H2'	46:14:1559:C:C6	2.57	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%)	189 (89%)	23 (11%)	1 (0%)	24	43
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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%)	6327 (97%)	165 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	LA	59	PRO

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	191/196 (97%)	160 (84%)	31 (16%)	2	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	LB	190/197 (96%)	186 (98%)	4 (2%)	47	74
3	LC	331/333 (99%)	324 (98%)	7 (2%)	47	74
4	LD	327/331 (99%)	319 (98%)	8 (2%)	43	70
5	LE	144/157 (92%)	141 (98%)	3 (2%)	47	74
6	LF	167/170 (98%)	161 (96%)	6 (4%)	31	58
7	LG	174/175 (99%)	170 (98%)	4 (2%)	44	72
8	LH	103/109 (94%)	100 (97%)	3 (3%)	37	65
9	LI	119/120 (99%)	117 (98%)	2 (2%)	53	78
10	LJ	173/180 (96%)	167 (96%)	6 (4%)	32	58
11	LK	244/246 (99%)	235 (96%)	9 (4%)	30	57
12	LL	133/151 (88%)	130 (98%)	3 (2%)	44	72
13	LM	106/134 (79%)	104 (98%)	2 (2%)	50	76
14	LN	115/132 (87%)	113 (98%)	2 (2%)	53	78
15	LO	108/109 (99%)	106 (98%)	2 (2%)	50	76
16	LP	207/209 (99%)	202 (98%)	5 (2%)	43	70
17	LQ	174/194 (90%)	170 (98%)	4 (2%)	44	72
18	LR	201/205 (98%)	193 (96%)	8 (4%)	28	54
19	LS	166/166 (100%)	165 (99%)	1 (1%)	78	91
20	LT	112/113 (99%)	109 (97%)	3 (3%)	39	67
21	LU	176/177 (99%)	173 (98%)	3 (2%)	53	78
22	LV	154/155 (99%)	151 (98%)	3 (2%)	50	76
23	LW	158/180 (88%)	151 (96%)	7 (4%)	25	50
24	LX	163/164 (99%)	159 (98%)	4 (2%)	42	69
25	LY	140/141 (99%)	138 (99%)	2 (1%)	59	81
26	LZ	89/97 (92%)	87 (98%)	2 (2%)	45	73
27	La	57/133 (43%)	56 (98%)	1 (2%)	51	77
28	Lb	115/117 (98%)	110 (96%)	5 (4%)	26	51
29	Lc	121/123 (98%)	119 (98%)	2 (2%)	53	78
30	Ld	42/43 (98%)	38 (90%)	4 (10%)	8	17
31	Le	85/98 (87%)	83 (98%)	2 (2%)	43	70
32	Lf	95/106 (90%)	93 (98%)	2 (2%)	47	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Lg	114/121 (94%)	113 (99%)	1 (1%)	70	87
34	Lh	92/99 (93%)	92 (100%)	0	100	100
35	Li	100/104 (96%)	99 (99%)	1 (1%)	68	86
36	Lj	84/91 (92%)	82 (98%)	2 (2%)	43	70
37	Lk	72/77 (94%)	71 (99%)	1 (1%)	59	81
38	Ll	64/65 (98%)	62 (97%)	2 (3%)	35	62
39	Lm	47/48 (98%)	46 (98%)	1 (2%)	47	74
40	Ln	46/114 (40%)	46 (100%)	0	100	100
41	Lp	85/91 (93%)	82 (96%)	3 (4%)	32	58
42	Lq	61/62 (98%)	58 (95%)	3 (5%)	22	45
All	All	5645/6033 (94%)	5481 (97%)	164 (3%)	38	65

All (164) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	LA	3	SER
1	LA	5	LEU
1	LA	6	GLN
1	LA	24	LYS
1	LA	25	LYS
1	LA	29	THR
1	LA	33	GLU
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	141	GLN
1	LA	142	GLU
1	LA	143	SER
1	LA	154	THR
1	LA	156	LYS

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Mol	Chain	Res	Type
1	LA	162	VAL
1	LA	163	LEU
1	LA	207	LYS
1	LA	208	SER
1	LA	210	MET
1	LA	212	LYS
1	LA	214	GLN
1	LA	216	ILE
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
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

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Mol	Chain	Res	Type
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	5	SER
12	LL	7	GLU
12	LL	91	ILE
13	LM	69	LEU
13	LM	71	GLN
14	LN	59	ARG
14	LN	87	GLU
15	LO	18	LEU
15	LO	36	VAL
16	LP	42	LYS
16	LP	56	GLU
16	LP	62	LEU
16	LP	175	LYS
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	98	GLU
18	LR	105	GLU
18	LR	127	ILE
18	LR	190	THR

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
39	Lm	45	ARG
41	Lp	24	LYS
41	Lp	29	LYS
41	Lp	35	LEU
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 (94) such sidechains are listed below:

Mol	Chain	Res	Type
1	LA	6	GLN
1	LA	35	GLN
1	LA	182	ASN
1	LA	197	ASN
1	LA	199	GLN
1	LA	214	GLN
2	LB	115	ASN
2	LB	233	GLN
3	LC	121	ASN
3	LC	167	GLN
3	LC	273	ASN
4	LD	13	GLN
4	LD	145	HIS
4	LD	176	GLN
4	LD	303	GLN
4	LD	334	ASN
5	LE	97	ASN
5	LE	109	GLN
6	LF	101	HIS
6	LF	165	ASN
6	LF	166	GLN
7	LG	36	GLN
7	LG	73	HIS

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Mol	Chain	Res	Type
7	LG	163	ASN
7	LG	170	GLN
7	LG	197	GLN
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
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
23	LW	141	ASN
24	LX	8	GLN

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Mol	Chain	Res	Type
24	LX	64	ASN
24	LX	107	GLN
24	LX	175	ASN
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	16	ASN
31	Le	17	ASN
31	Le	52	ASN
32	Lf	46	GLN
32	Lf	85	ASN
34	Lh	41	ASN
34	Lh	111	ASN
35	Li	75	ASN
36	Lj	41	HIS
36	Lj	95	ASN
37	Lk	48	ASN
37	Lk	77	ASN
38	Ll	67	GLN
39	Lm	38	ASN
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	155/204 (75%)	113 (72%)	15 (9%)
44	12	118/119 (99%)	12 (10%)	0
45	13	162/163 (99%)	33 (20%)	0
46	14	3138/3390 (92%)	572 (18%)	21 (0%)
All	All	3573/3876 (92%)	730 (20%)	36 (1%)

All (730) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	10	49	U
43	10	50	G
43	10	51	G
43	10	52	U
43	10	53	G
43	10	55	G
43	10	60	A
43	10	61	U
43	10	62	A
43	10	63	A
43	10	69	A
43	10	70	G
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
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

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Mol	Chain	Res	Type
43	10	109	G
43	10	110	A
43	10	111	U
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
43	10	139	A
43	10	140	U
43	10	141	A
43	10	143	A
43	10	144	U
43	10	145	C
43	10	146	C
43	10	147	G
43	10	148	C
43	10	149	A
43	10	150	G
43	10	152	C
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

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Mol	Chain	Res	Type
43	10	163	G
43	10	164	C
43	10	165	G
43	10	166	A
43	10	167	G
43	10	168	G
43	10	169	G
43	10	170	G
43	10	171	U
43	10	172	U
43	10	173	C
43	10	175	A
43	10	176	A
43	10	177	U
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	188	C
43	10	190	C
43	10	194	G
43	10	195	U
43	10	199	G
43	10	200	G
43	10	201	C
43	10	202	C
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
46	14	2443	A
46	14	2445	G
46	14	2446	A
46	14	2449	U
46	14	2451	A
46	14	2452	G
46	14	2454	G
46	14	2455	G
46	14	2456	U
46	14	2457	G
46	14	2458	U
46	14	2461	U
46	14	2463	U
46	14	2464	A
46	14	2471	A
46	14	2475	G
46	14	2478	A

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Mol	Chain	Res	Type
46	14	2479	G
46	14	2489	A
46	14	2492	U
46	14	2499	A
46	14	2501	U
46	14	2503	U
46	14	2505	A
46	14	2506	A
46	14	2507	C
46	14	2508	G
46	14	2512	U
46	14	2514	U
46	14	2515	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
46	14	2557	U
46	14	2558	G
46	14	2559	G
46	14	2563	C
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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 (36) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
43	10	75	U
43	10	76	U
43	10	106	U
43	10	120	U
43	10	124	A
43	10	125	U
43	10	133	G
43	10	134	U
43	10	135	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
46	14	113	G
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

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Mol	Chain	Res	Type
46	14	1847	A
46	14	1848	A
46	14	1852	C
46	14	2375	A
46	14	2376	A
46	14	2455	G
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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

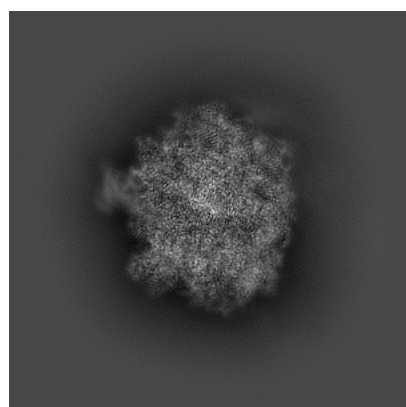
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65330. These allow visual inspection of the internal detail of the map and identification of artifacts.

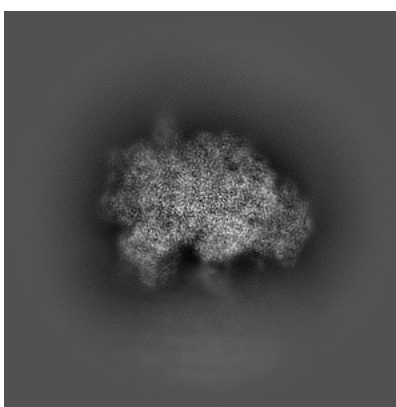
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

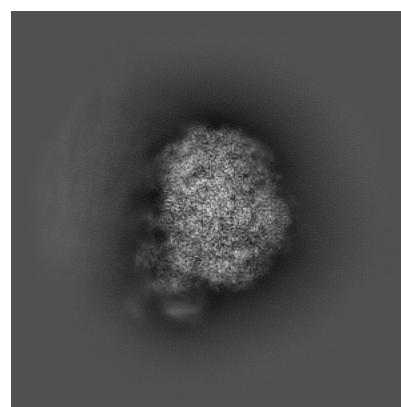
6.1.1 Primary map



X



Y

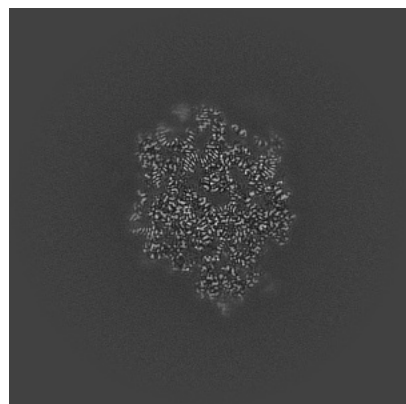


Z

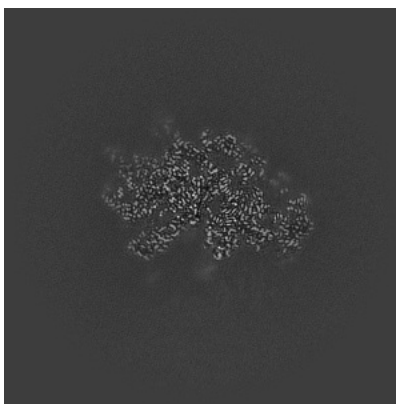
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

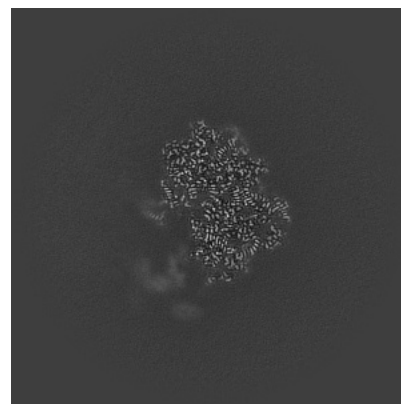
6.2.1 Primary map



X Index: 240



Y Index: 240

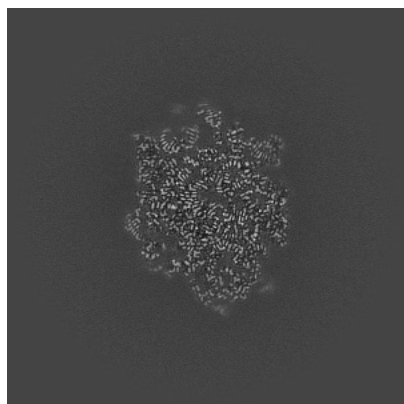


Z Index: 240

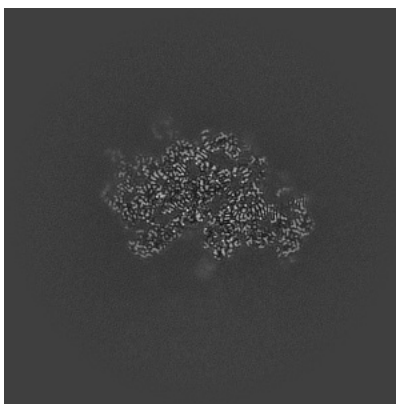
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

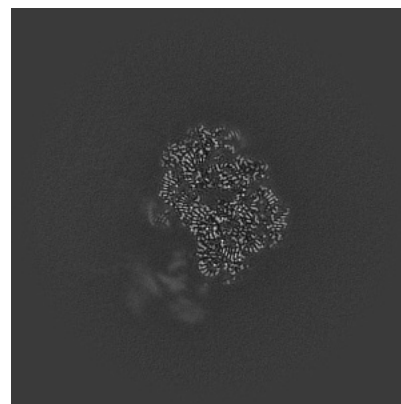
6.3.1 Primary map



X Index: 246



Y Index: 242

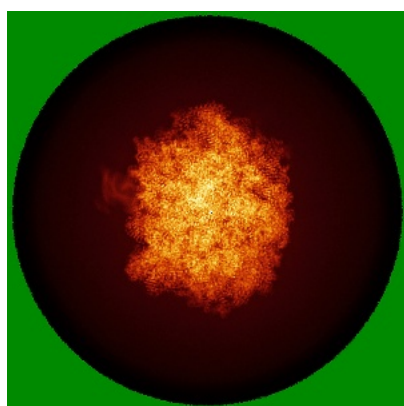


Z Index: 247

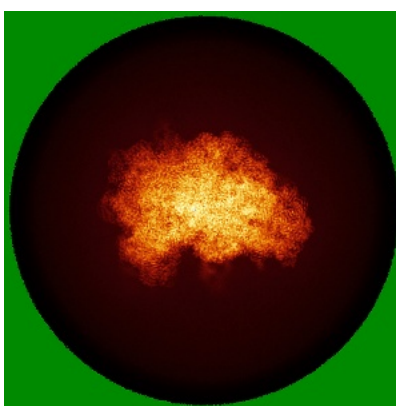
The images above show the largest variance slices of the map in three orthogonal directions.

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

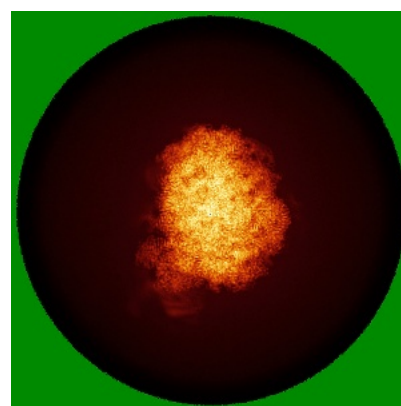
6.4.1 Primary map



X



Y

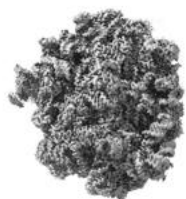


Z

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

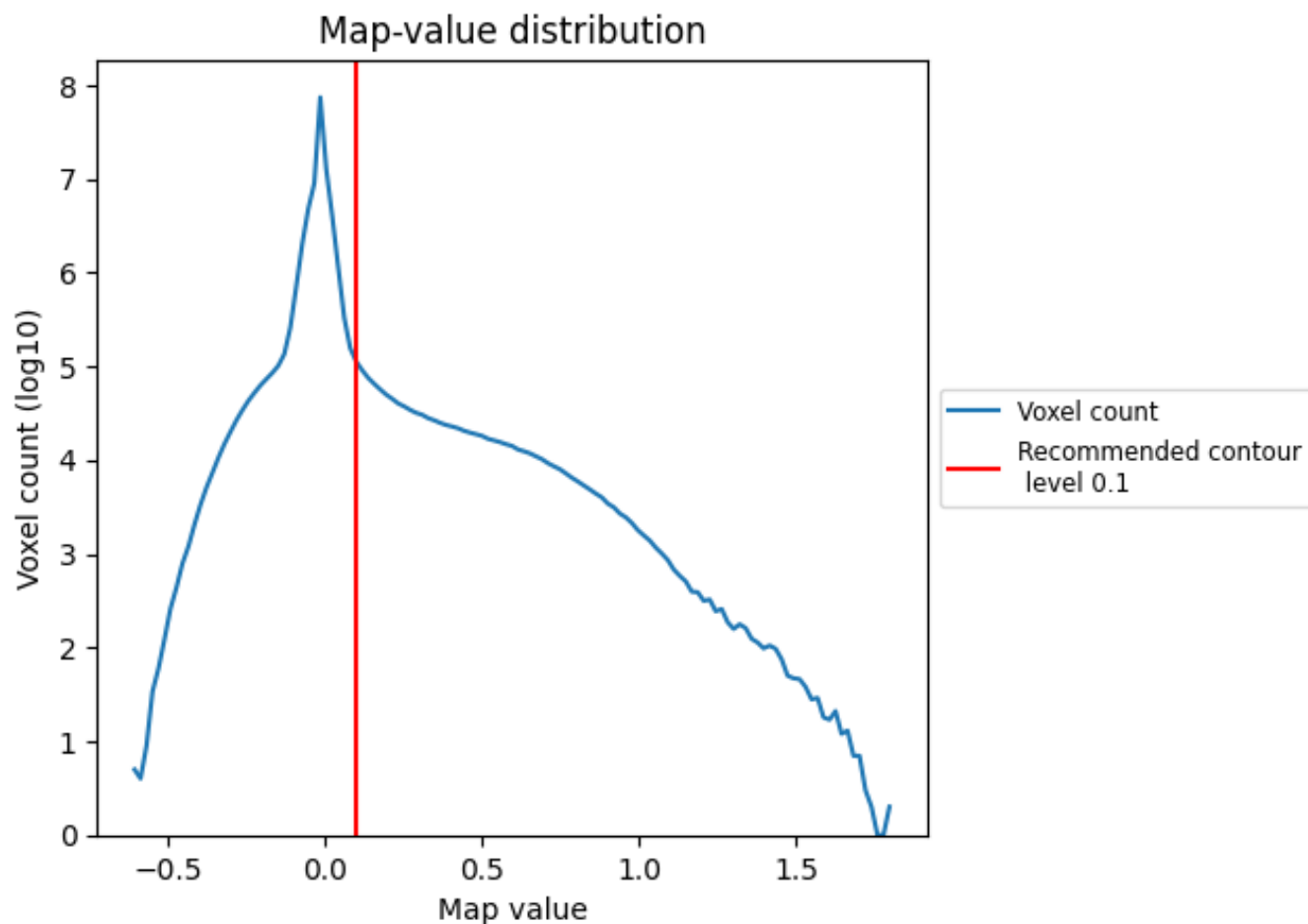
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

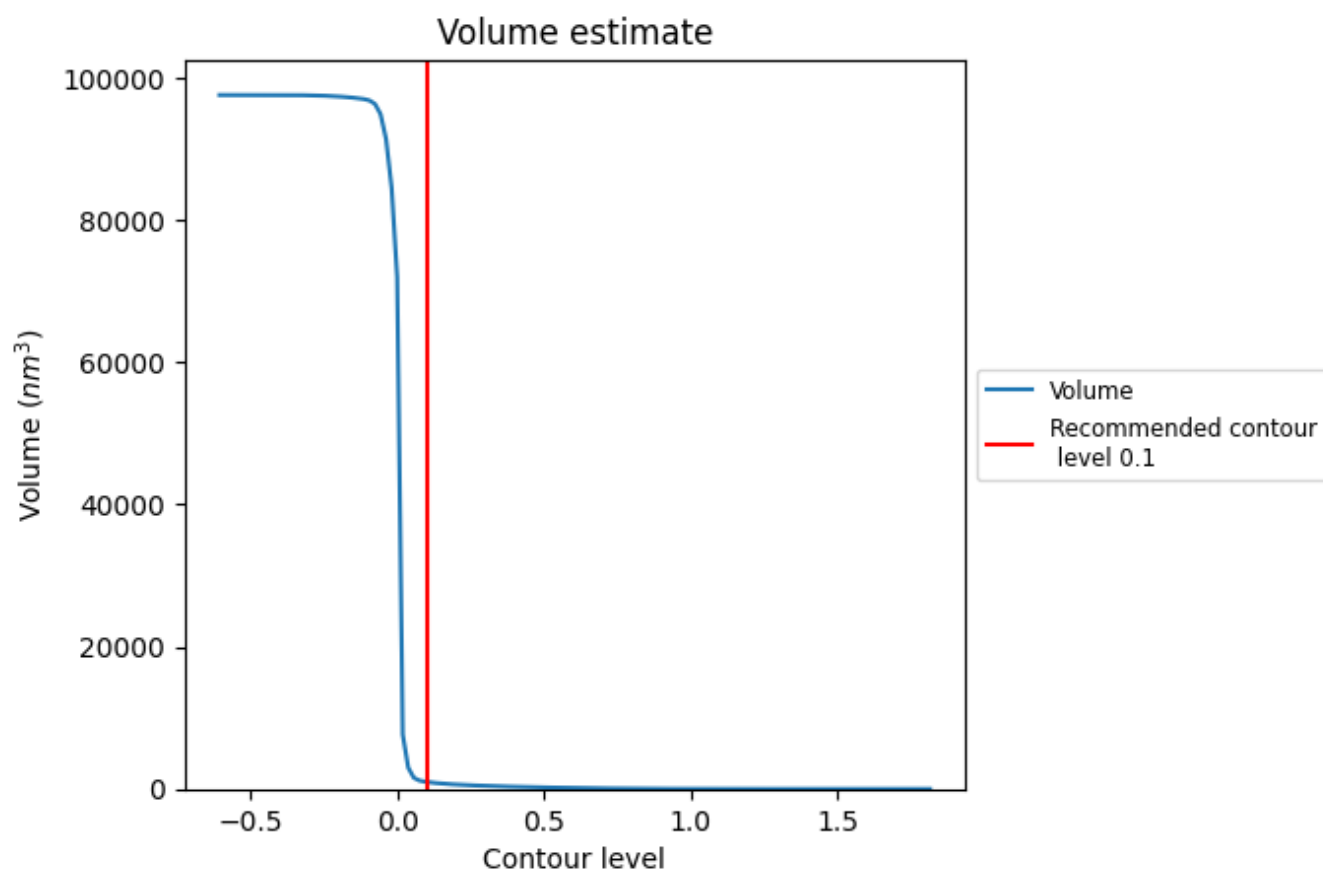
This section contains the results of statistical analysis of the map.

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.

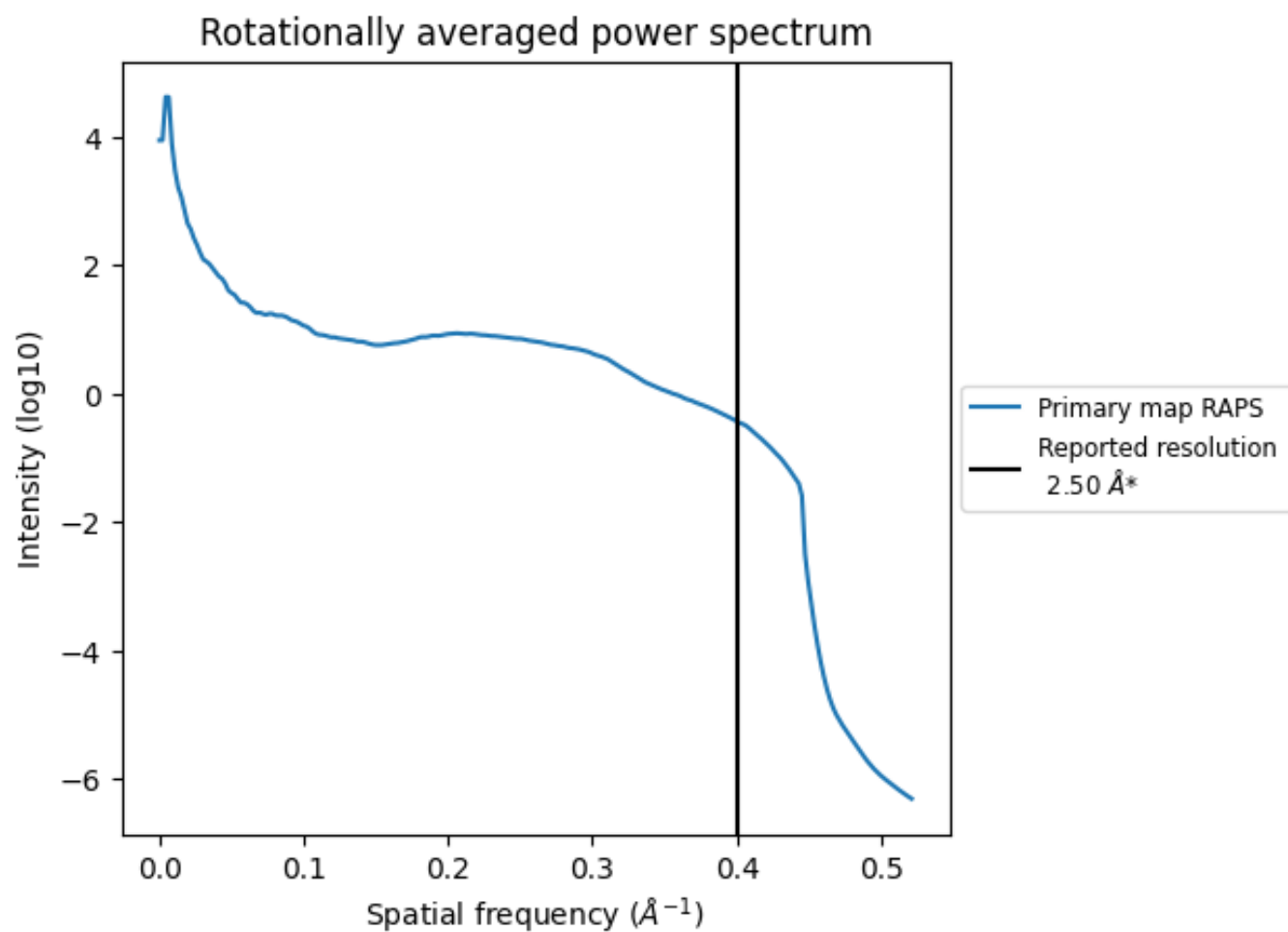
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 986 nm^3 ; this corresponds to an approximate mass of 891 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 0.400 Å⁻¹

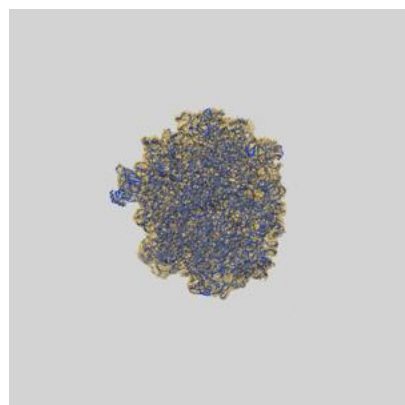
8 Fourier-Shell correlation ⓘ

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

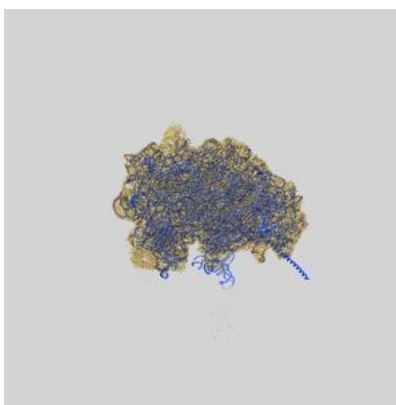
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65330 and PDB model 9VTJ. Per-residue inclusion information can be found in section 3 on page 15.

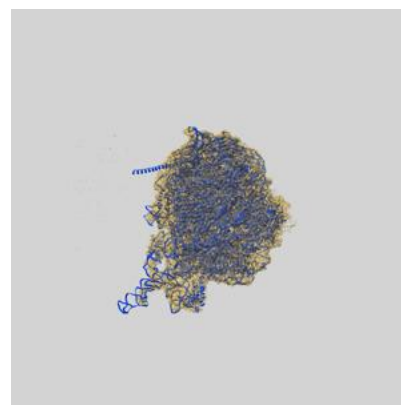
9.1 Map-model overlay [i](#)



X



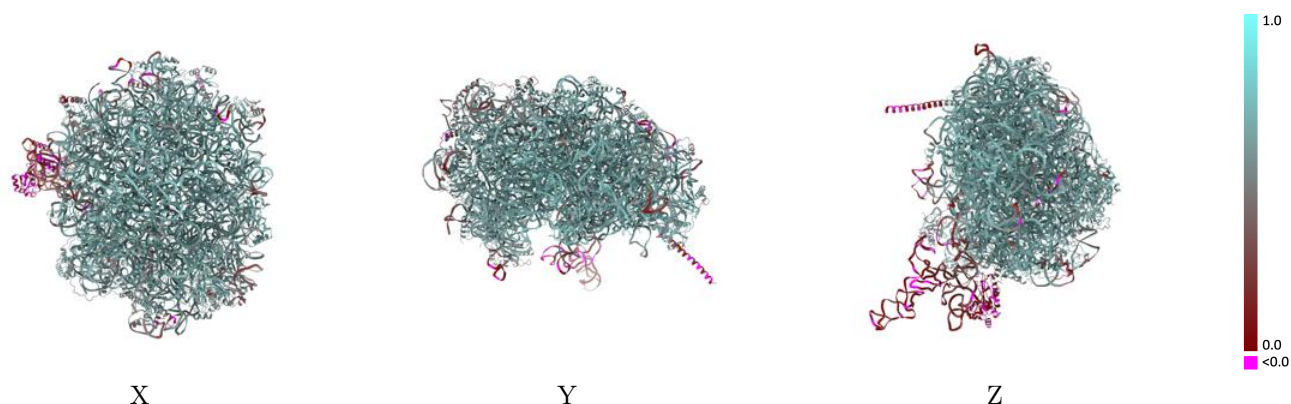
Y



Z

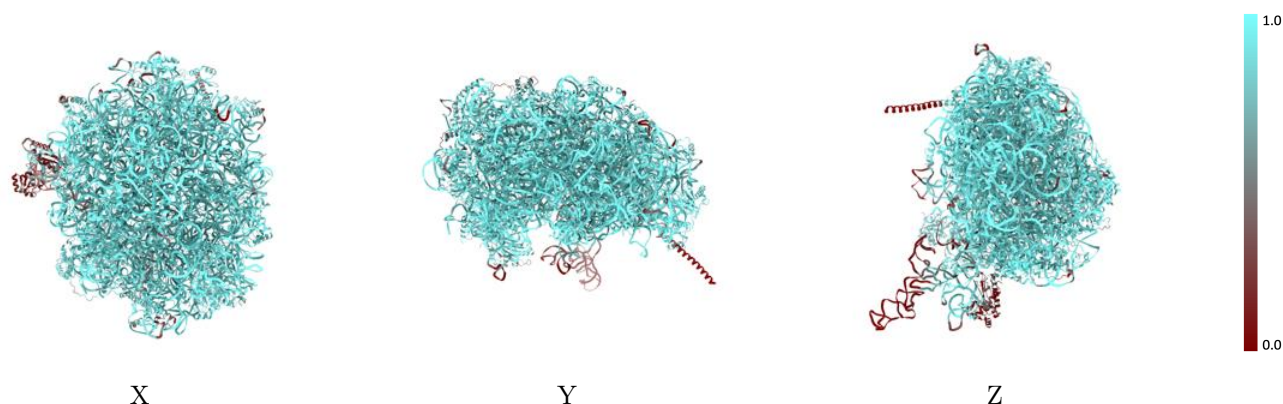
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



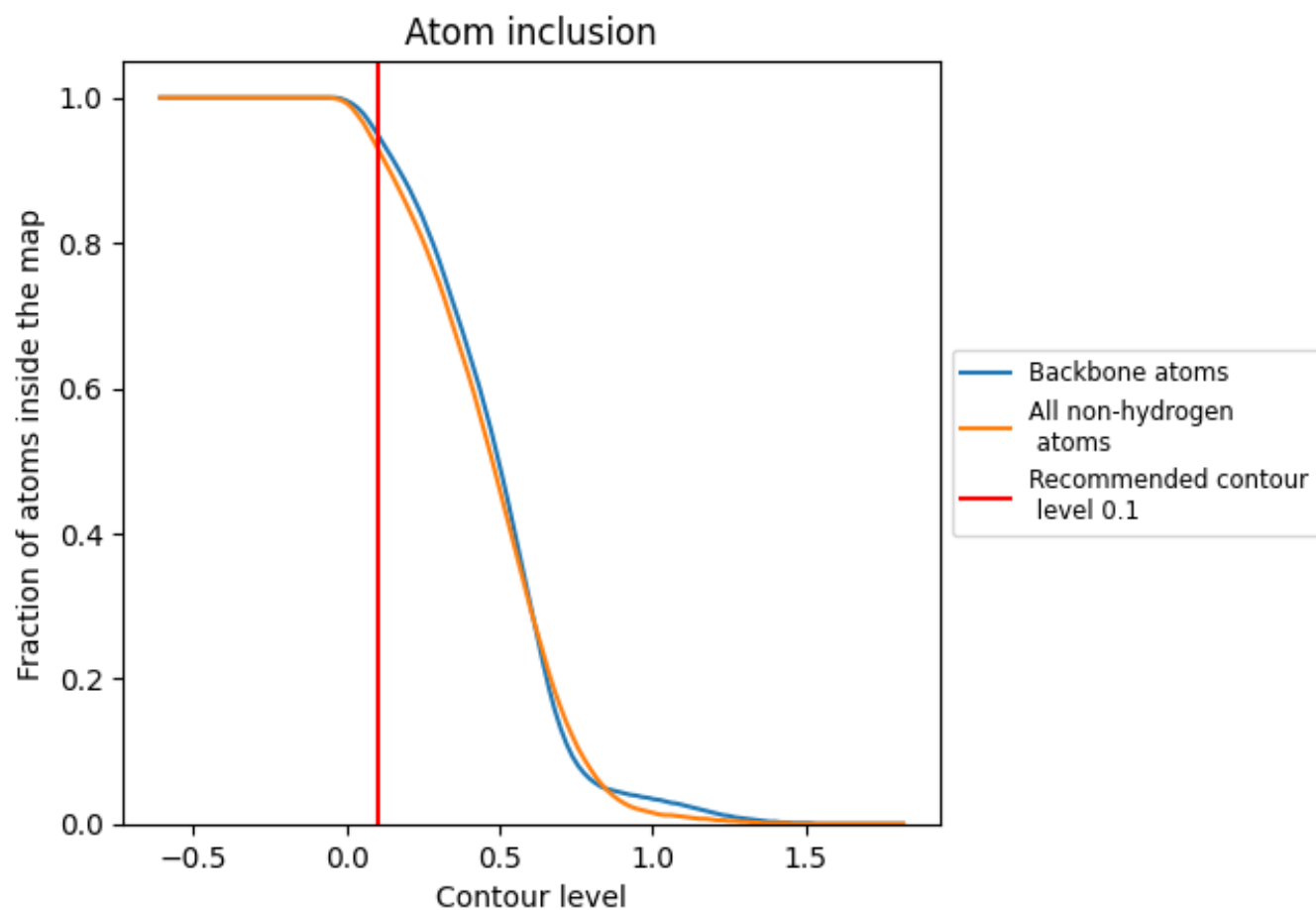
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9320	 0.6090
10	 0.3370	 0.1250
12	 0.9990	 0.6510
13	 0.9610	 0.6270
14	 0.9700	 0.6280
LA	 0.2910	 0.0720
LB	 0.9930	 0.6860
LC	 0.9750	 0.6780
LD	 0.9070	 0.5960
LE	 0.8670	 0.5500
LF	 0.9190	 0.5920
LG	 0.9680	 0.6560
LH	 0.9790	 0.6680
LI	 0.9760	 0.6630
LJ	 0.9620	 0.6440
LK	 0.9280	 0.6100
LL	 0.9700	 0.6660
LM	 0.9500	 0.6470
LN	 0.9680	 0.6480
LO	 0.9360	 0.6210
LP	 0.9290	 0.6260
LQ	 0.8060	 0.5270
LR	 0.8900	 0.5820
LS	 0.9600	 0.6430
LT	 0.9440	 0.6190
LU	 0.9960	 0.6870
LV	 0.9860	 0.6670
LW	 0.7810	 0.5430
LX	 0.9700	 0.6510
LY	 0.9630	 0.6510
LZ	 0.8360	 0.5400
La	 0.9350	 0.6500
Lb	 0.9640	 0.6430
Lc	 0.8360	 0.5920
Ld	 0.9320	 0.6260



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Chain	Atom inclusion	Q-score
Le	 0.9320	 0.6210
Lf	 0.9170	 0.6270
Lg	 0.9780	 0.6610
Lh	 0.9830	 0.6710
Li	 0.9340	 0.6350
Lj	 0.9510	 0.6220
Lk	 0.9960	 0.6850
Ll	 0.8850	 0.5840
Lm	 0.9860	 0.6760
Ln	 0.9290	 0.6370
Lp	 0.9730	 0.6680
Lq	 0.9590	 0.6630