Full wwPDB EM Validation Report ⓘ

Jun 9, 2025 – 07:20 PM JST

PDB ID	:	8ZEJ / pdb_00008zej
EMDB ID	:	EMD-60034
Title	:	Structure of E.coli ribosome in complex with an engineered arrest peptide
Authors	:	Sriramoju, M.K.; Ko, T.P.; Draczkowski, P.; Hsu, S.T.D.
Deposited on	:	2024-05-06
Resolution	:	2.69 Å(reported)
Based on initial model	:	3JBU

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:

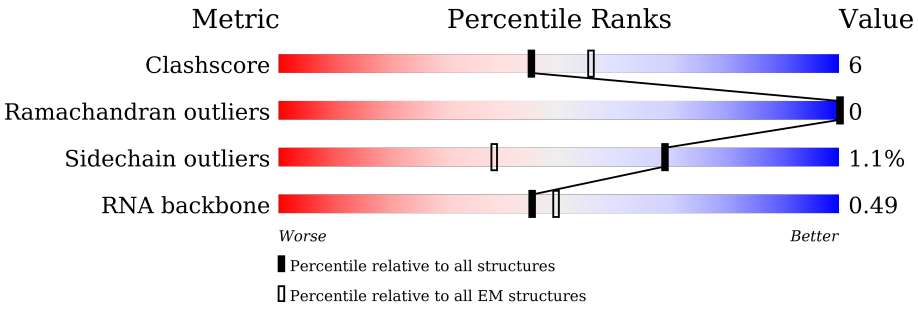
EMDB validation analysis	:	0.0.1.dev118
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 2.69 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	78	83% 15%
2	1	63	86% 11%
3	2	59	85% 14%
4	4	57	77% 21%
5	5	55	73% 22% 5%
6	6	46	93% 7%
7	7	65	88% 11%

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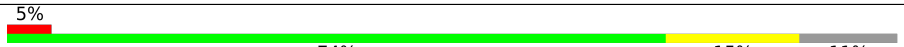
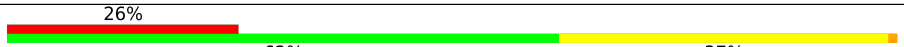
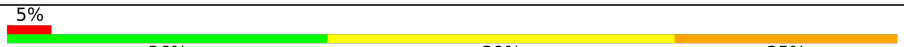
Mol	Chain	Length	Quality of chain
8	8	38	
9	A	1533	
10	B	241	
11	C	233	
12	D	206	
13	E	167	
14	F	135	
15	G	179	
16	H	130	
17	I	130	
18	J	103	
19	K	129	
20	L	124	
21	M	118	
22	N	101	
23	O	89	
24	P	82	
25	Q	84	
26	R	75	
27	S	92	
28	T	87	
29	U	71	
30	X	76	
31	Y	77	
31	Z	77	

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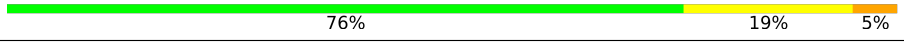
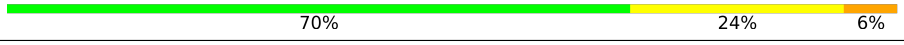
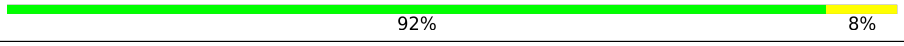
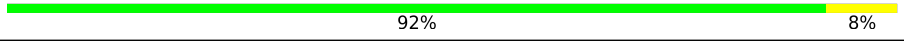
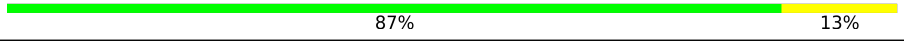
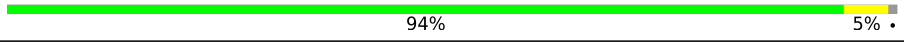
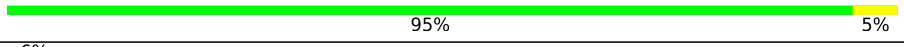
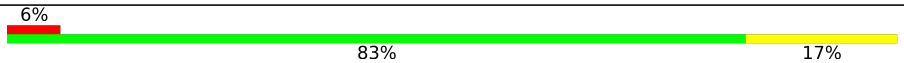
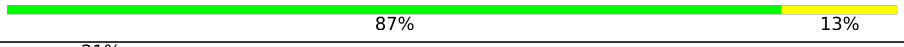
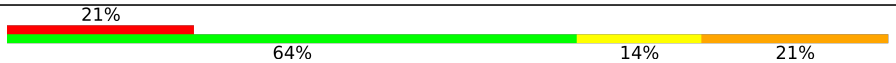
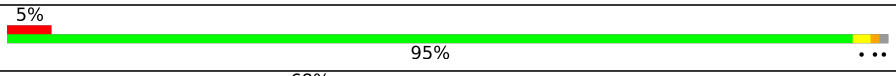
Mol	Chain	Length	Quality of chain
32	a	120	
33	b	2904	
34	c	273	
35	d	209	
36	e	201	
37	f	179	
38	g	177	
39	h	149	
40	k	142	
41	l	123	
42	m	144	
43	n	136	
44	o	127	
45	p	117	
46	q	115	
47	r	118	
48	s	103	
49	t	110	
50	u	100	
51	v	104	
52	w	94	
53	x	14	
54	y	85	
55	z	28	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	PRO	Z	163	-	-	X	-

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 147438 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	5	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 9 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		

- Molecule 10 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 11 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	207	Total	C	N	O	S	0	0
			1632	1034	306	289	3		

- Molecule 12 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 13 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 14 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 15 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 16 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 17 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 18 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	100	Total	C	N	O	S	0	0
			803	502	154	146	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	122	Total	C	N	O	S	0	0
			949	587	195	163	4		

- Molecule 21 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 22 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 23 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 24 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 25 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 26 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 27 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 28 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 29 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	64	Total	C	N	O	S	0	0
			529	329	110	89	1		

- Molecule 30 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	76	Total	C	N	O	P	0	0
			1621	722	287	536	76		

- Molecule 31 is a RNA chain called P-site tRNA (Chain Y), A-site tRNA-PRO (Chain Z).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		
31	Z	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		

- Molecule 32 is a RNA chain called 5S rRNA.

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

- Molecule 33 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	2902	Total	C	N	O	P	0	0
			62297	27791	11462	20142	2902		

- Molecule 34 is a protein called 50S ribosomal protein L2.

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

- Molecule 35 is a protein called 50S ribosomal protein L3.

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

- Molecule 36 is a protein called 50S ribosomal protein L4.

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

- Molecule 37 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	178	Total	C	N	O	S	0	0
			1419	905	251	257	6		

- Molecule 38 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 39 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	149	Total	C	N	O	S	0	0
			1108	699	197	211	1		

- Molecule 40 is a protein called 50S ribosomal protein L13.

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

- Molecule 41 is a protein called 50S ribosomal protein L14.

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

- Molecule 42 is a protein called 50S ribosomal protein L15.

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

- Molecule 43 is a protein called 50S ribosomal protein L16.

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

- Molecule 44 is a protein called 50S ribosomal protein L17.

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

- Molecule 45 is a protein called 50S ribosomal protein L18.

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

- Molecule 46 is a protein called 50S ribosomal protein L19.

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

- Molecule 47 is a protein called 50S ribosomal protein L20.

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

- Molecule 48 is a protein called 50S ribosomal protein L21.

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

- Molecule 49 is a protein called 50S ribosomal protein L22.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	100	Total	C	N	O	S	0	0
			786	496	146	142	2		

- Molecule 51 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	v	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 52 is a protein called 50S ribosomal protein L25.

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

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	14	Total	C	N	O	P	0	0
			299	133	55	97	14		

- Molecule 54 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

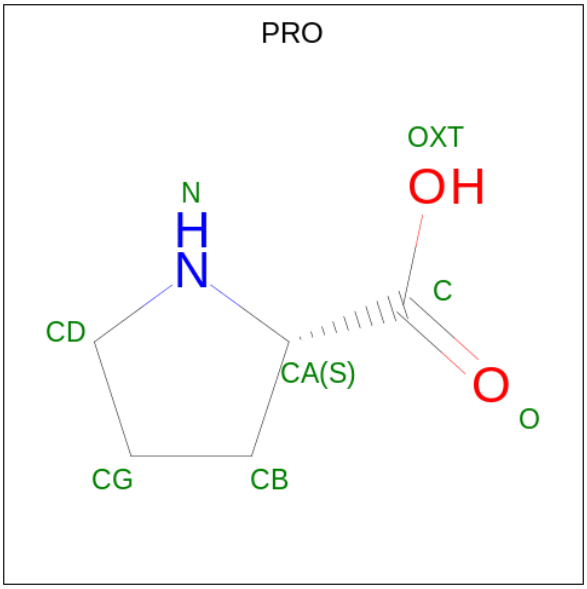
- Molecule 55 is a protein called eRAP.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	z	26	Total	C	N	O	8	0
			298	204	52	42		

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
56	8	1	Total Zn 1 1	0

- Molecule 57 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$).



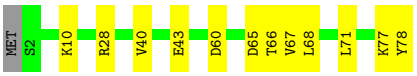
Mol	Chain	Residues	Atoms	AltConf
57	Z	1	Total C N O 7 5 1 1	0

3 Residue-property plots (i)

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

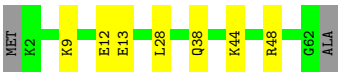
• Molecule 1: 50S ribosomal protein L28

Chain 0:



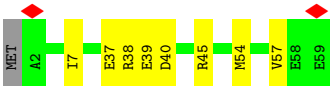
• Molecule 2: 50S ribosomal protein L29

Chain 1:



• Molecule 3: 50S ribosomal protein L30

Chain 2:

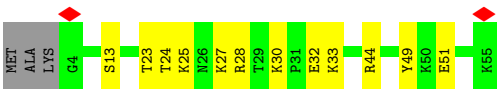


• Molecule 4: 50S ribosomal protein L32

Chain 4:

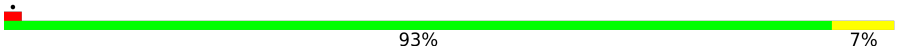
• Molecule 5: 50S ribosomal protein L33

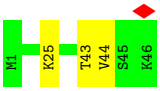
Chain 5:



• Molecule 6: 50S ribosomal protein L34

Chain 6:





• Molecule 7: 50S ribosomal protein L35

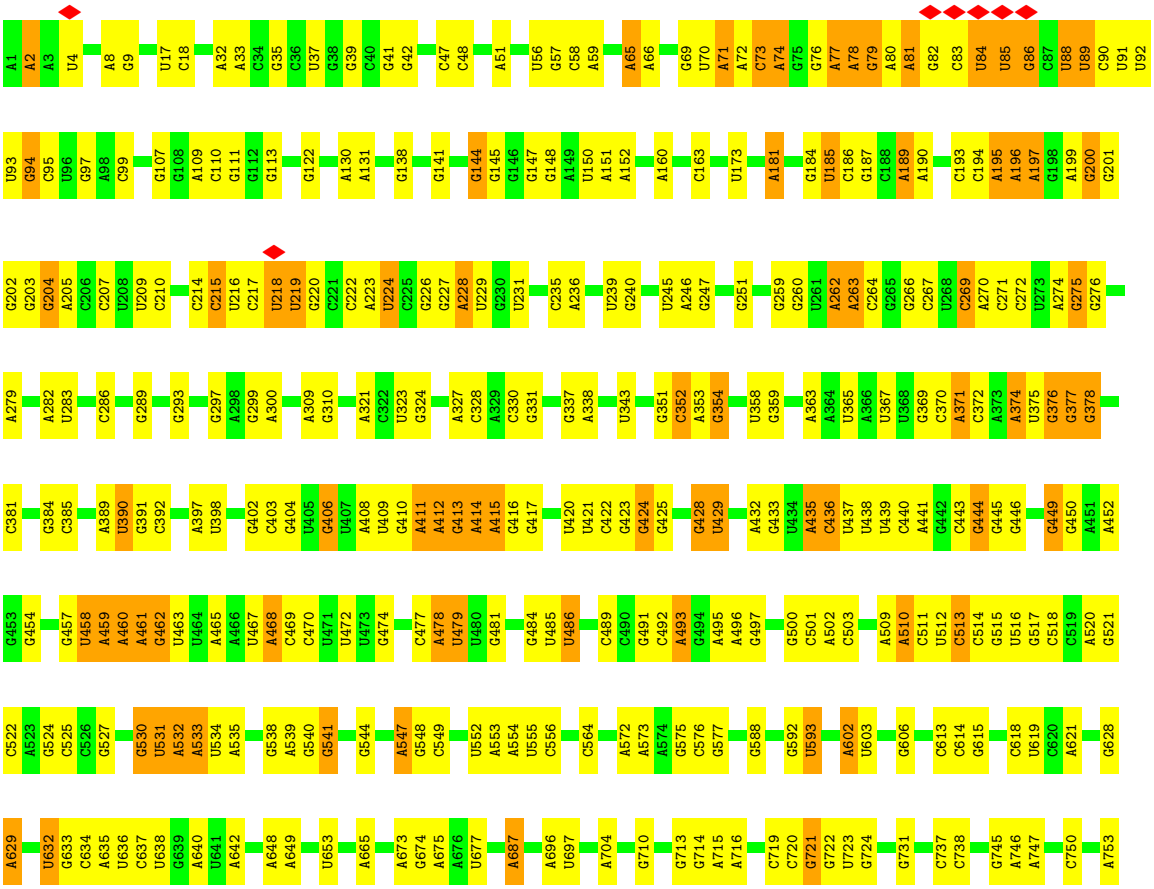
Chain 7:

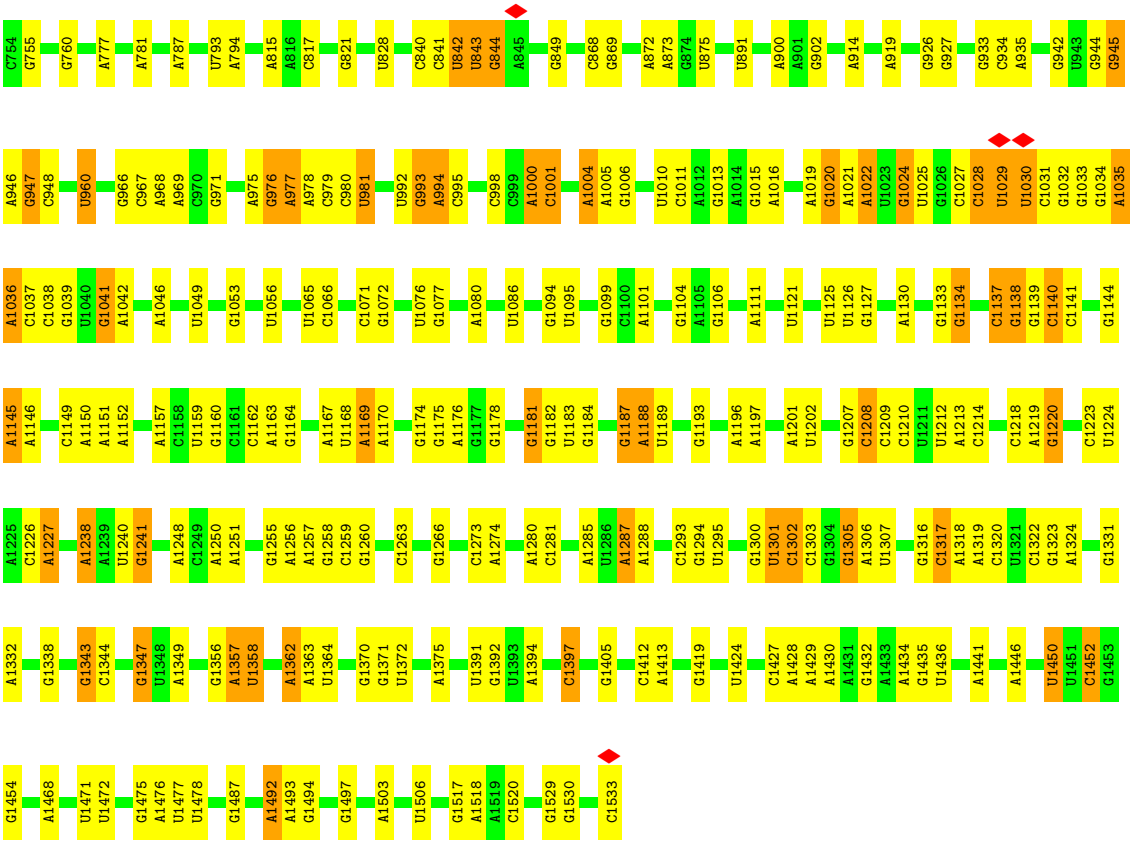
• Molecule 8: 50S ribosomal protein L36

Chain 8:

• Molecule 9: 16S rRNA

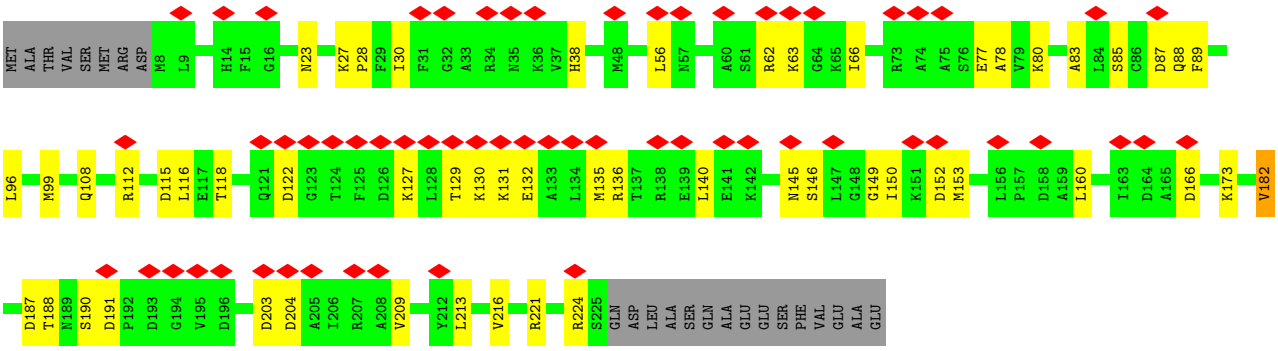
Chain A:





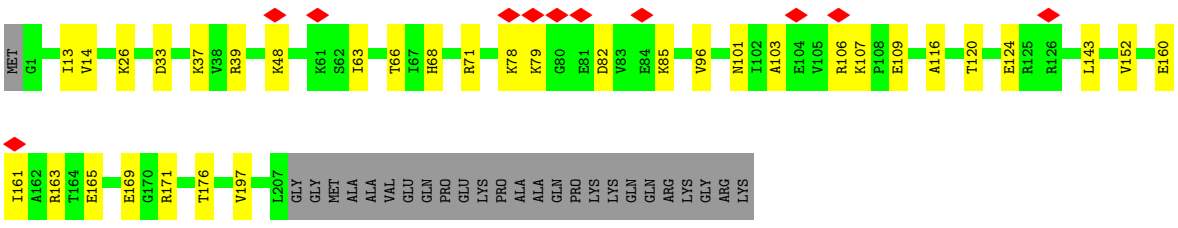
- Molecule 10: 30S ribosomal protein S2

Chain B:



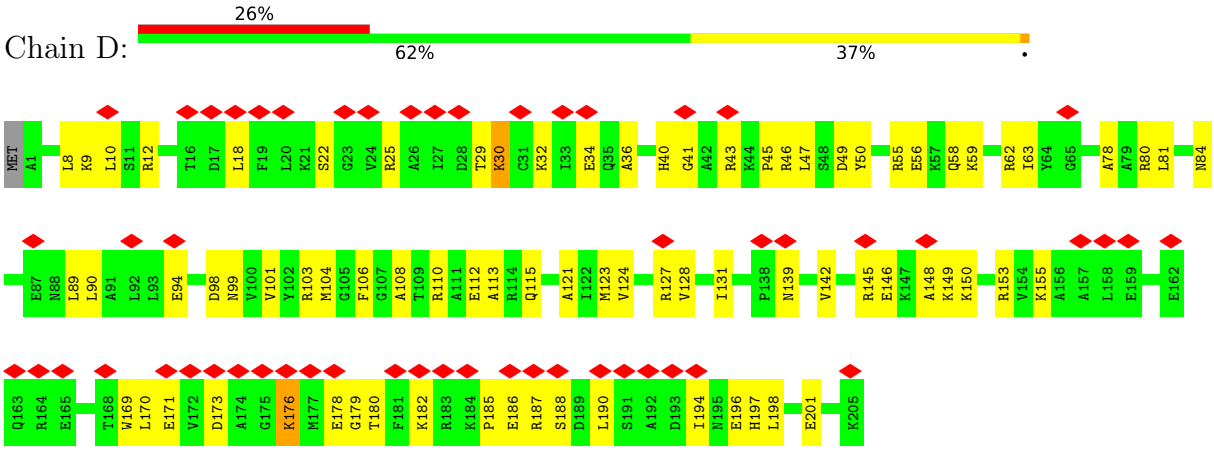
- Molecule 11: 30S ribosomal protein S3

Chain C:



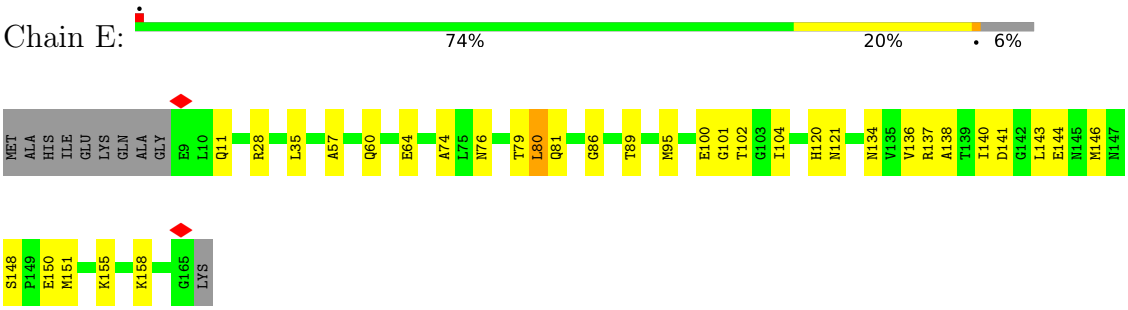
• Molecule 12: 30S ribosomal protein S4

Chain D:



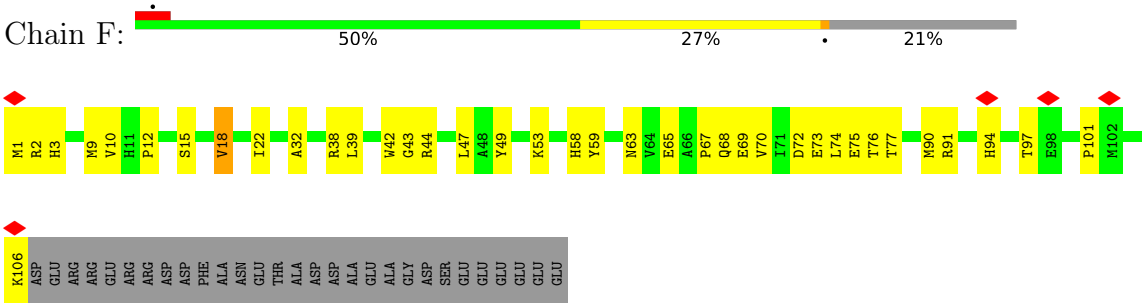
• Molecule 13: 30S ribosomal protein S5

Chain E:



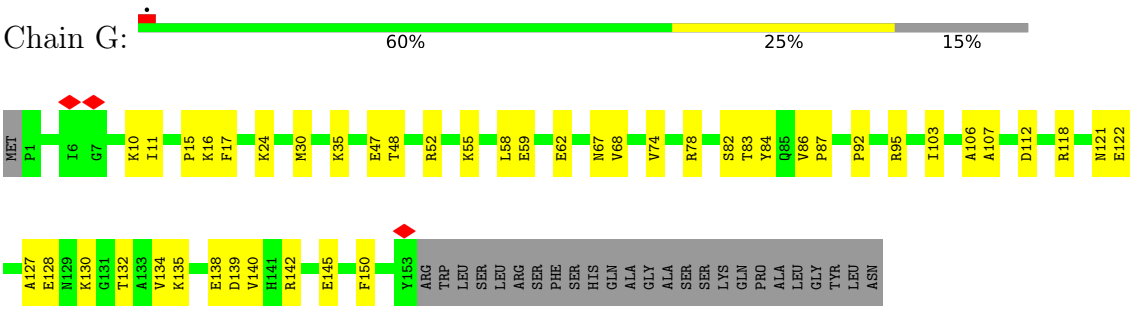
• Molecule 14: 30S ribosomal protein S6, fully modified isoform

Chain F:



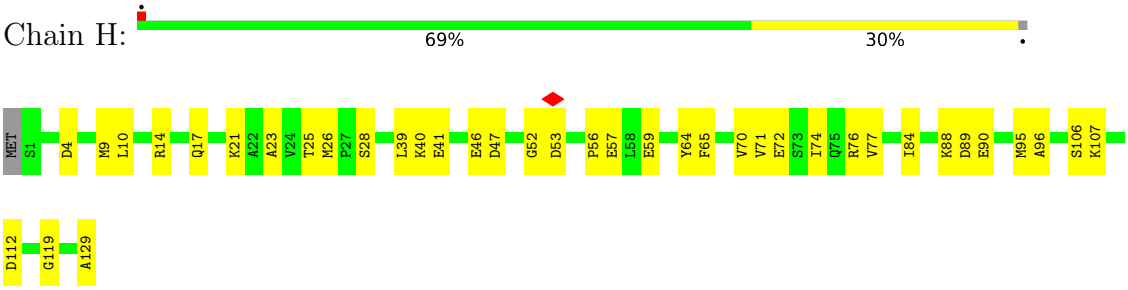
• Molecule 15: 30S ribosomal protein S7

Chain G:



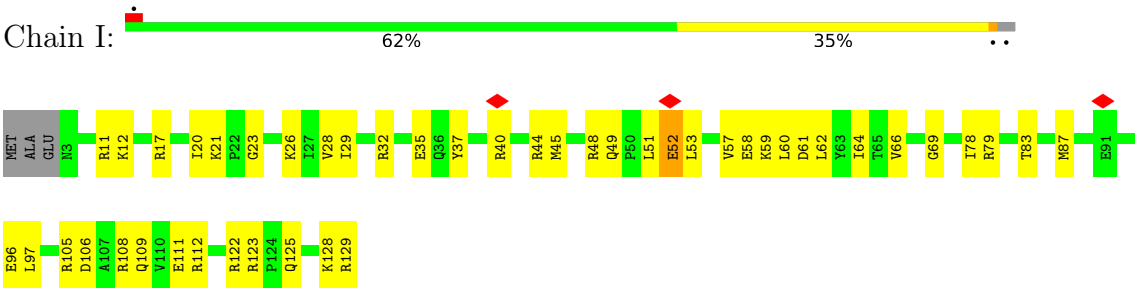
• Molecule 16: 30S ribosomal protein S8

Chain H:



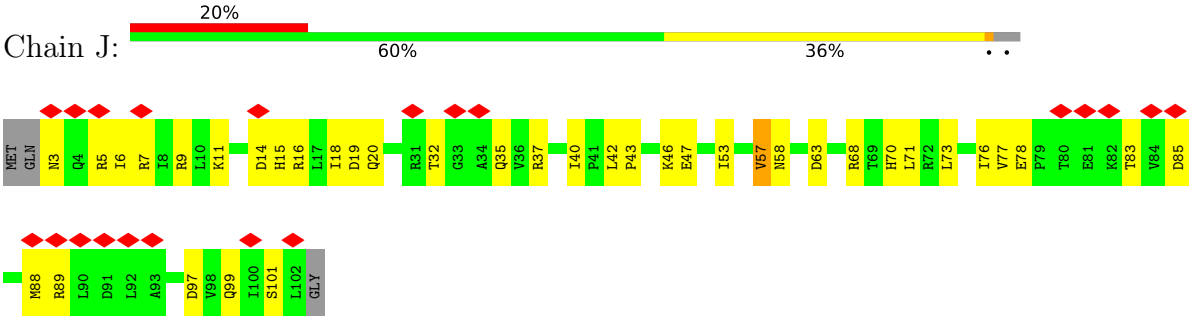
• Molecule 17: 30S ribosomal protein S9

Chain I:



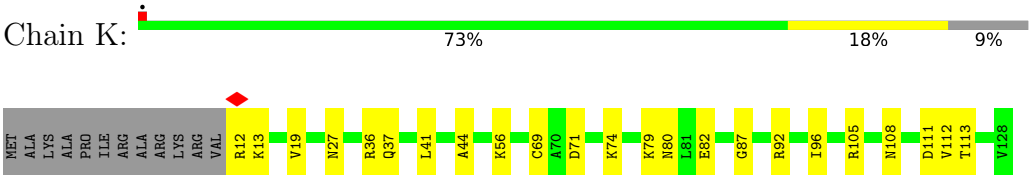
• Molecule 18: 30S ribosomal protein S10

Chain J:



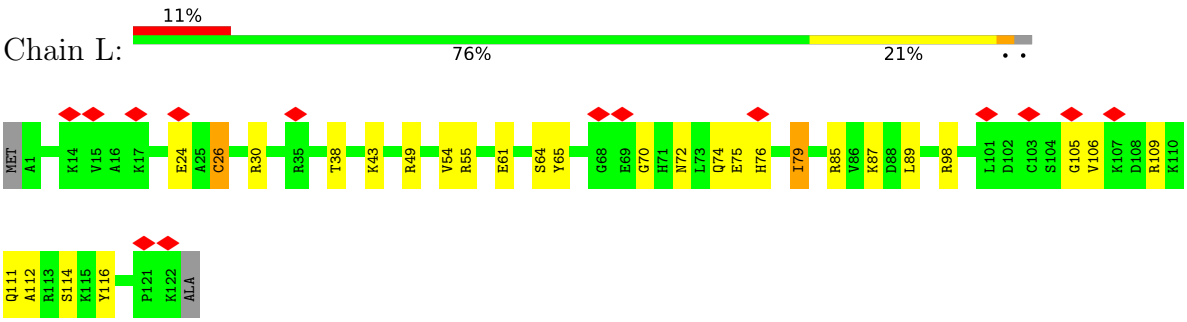
• Molecule 19: Small ribosomal subunit protein uS11

Chain K:



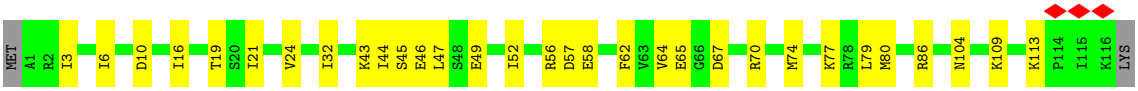
• Molecule 20: Small ribosomal subunit protein uS12

Chain L:



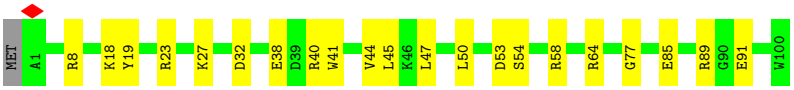
• Molecule 21: 30S ribosomal protein S13

Chain M:



• Molecule 22: 30S ribosomal protein S14

Chain N:

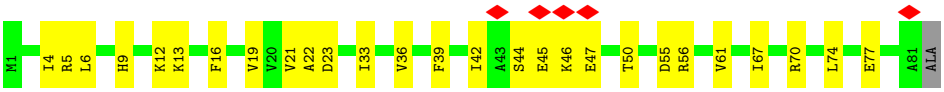


• Molecule 23: 30S ribosomal protein S15

Chain O:

• Molecule 24: 30S ribosomal protein S16

Chain P:

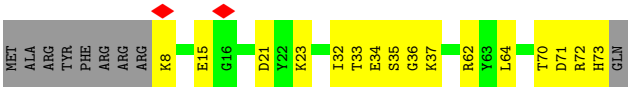


• Molecule 25: 30S ribosomal protein S17

Chain Q:

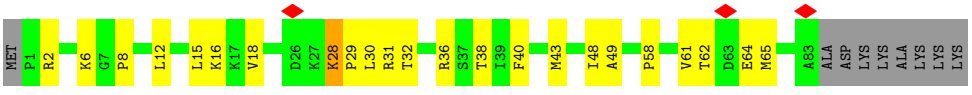
• Molecule 26: 30S ribosomal protein S18

Chain R:



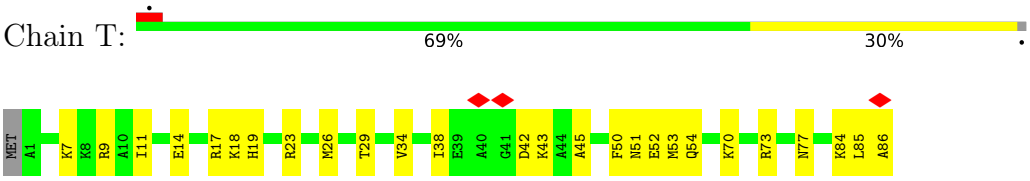
• Molecule 27: 30S ribosomal protein S19

Chain S:



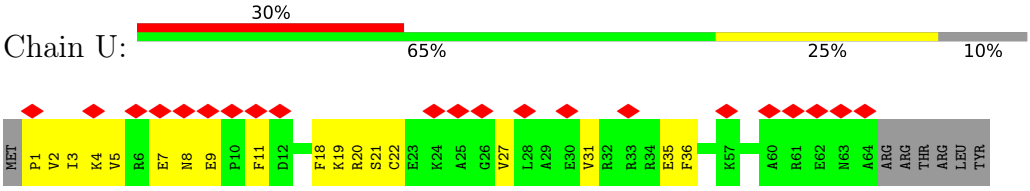
• Molecule 28: 30S ribosomal protein S20

Chain T:



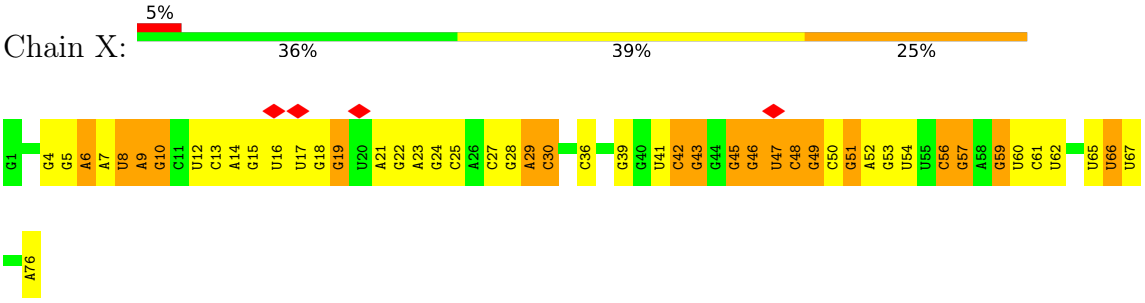
• Molecule 29: 30S ribosomal protein S21

Chain U:



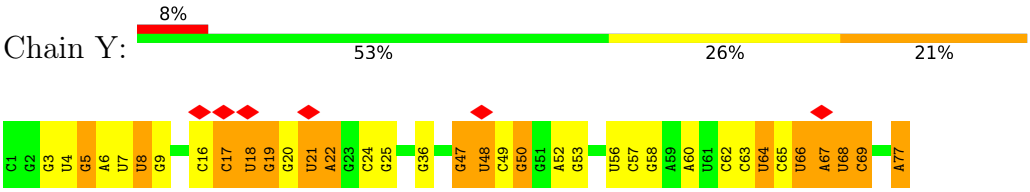
• Molecule 30: E-site tRNA

Chain X:



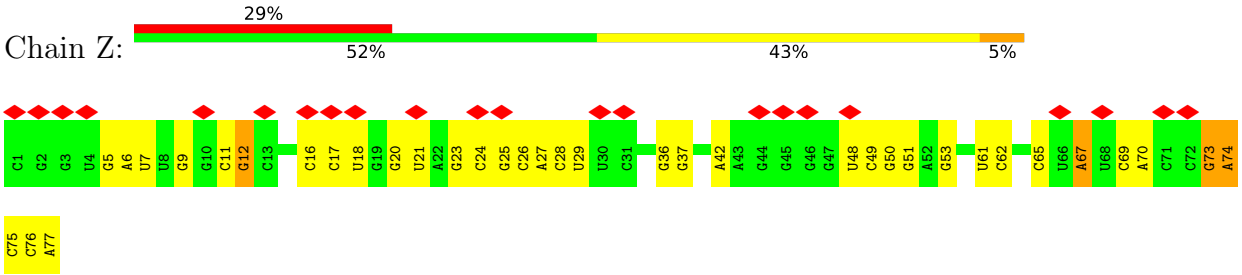
• Molecule 31: P-site tRNA (Chain Y), A-site tRNA-PRO (Chain Z)

Chain Y:



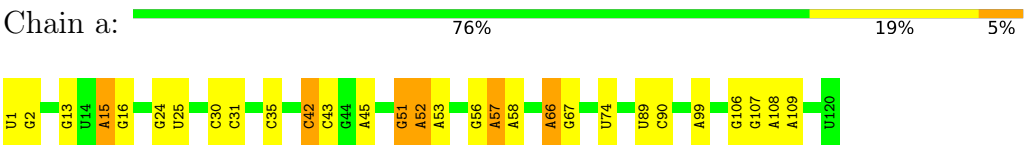
• Molecule 31: P-site tRNA (Chain Y), A-site tRNA-PRO (Chain Z)

Chain Z:



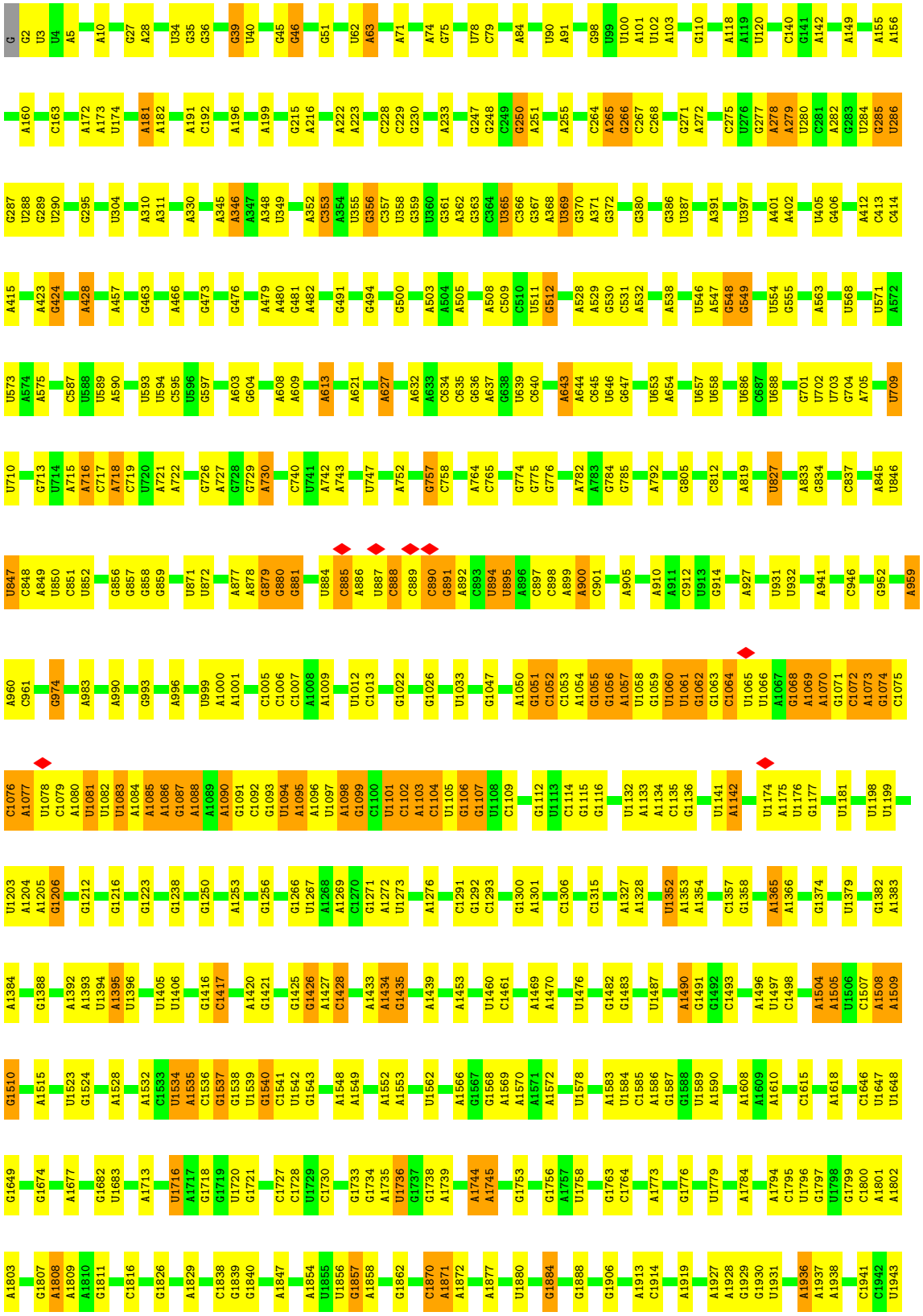
• Molecule 32: 5S rRNA

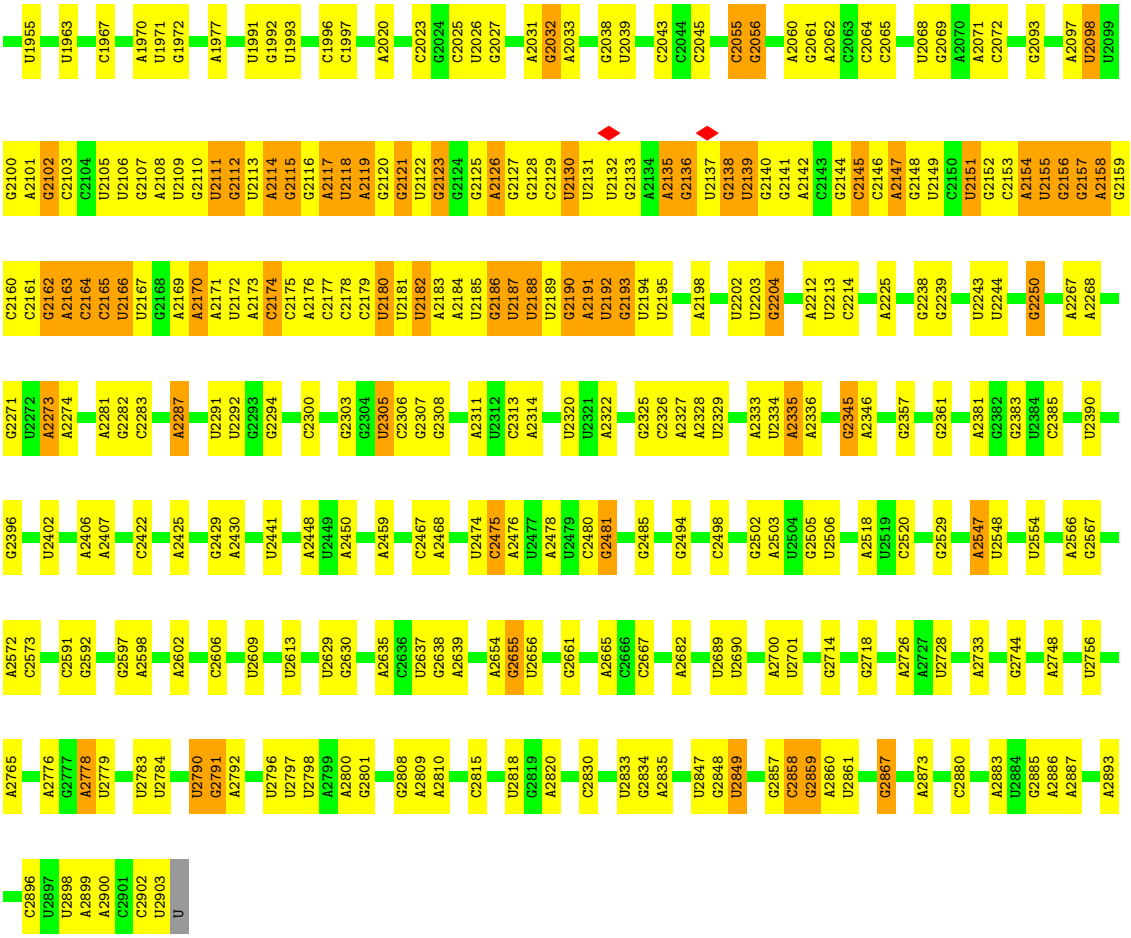
Chain a:



• Molecule 33: 23S rRNA

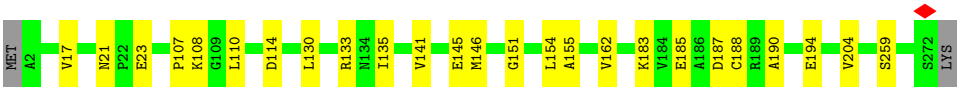
Chain b:





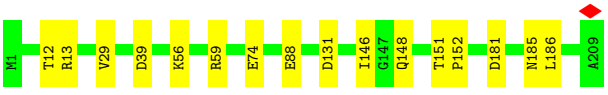
• Molecule 34: 50S ribosomal protein L2

Chain c:



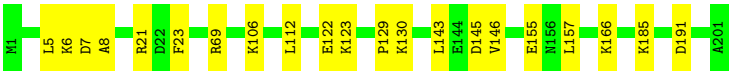
• Molecule 35: 50S ribosomal protein L3

Chain d:



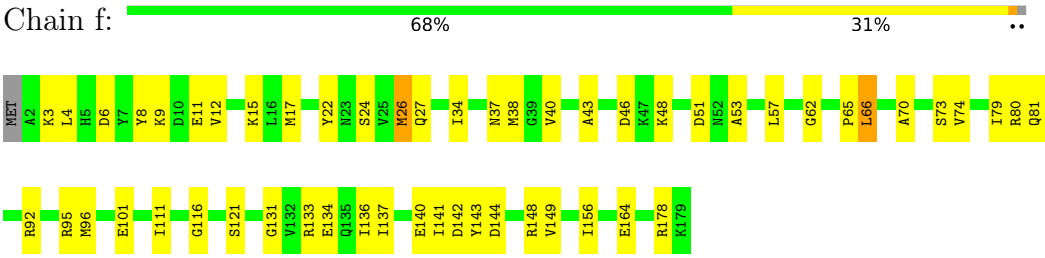
• Molecule 36: 50S ribosomal protein L4

Chain e:



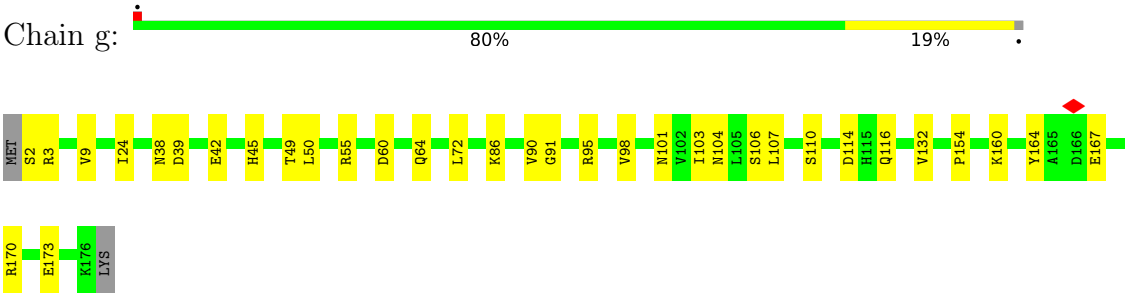
• Molecule 37: 50S ribosomal protein L5

Chain f:



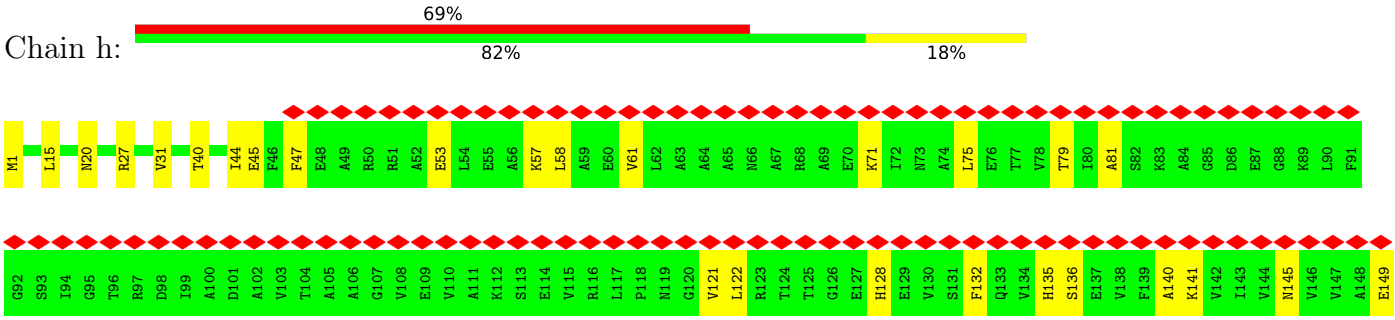
• Molecule 38: 50S ribosomal protein L6

Chain g:



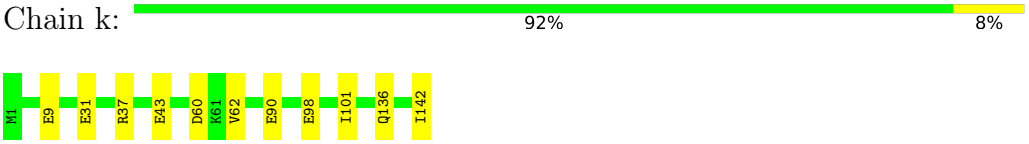
• Molecule 39: 50S ribosomal protein L9

Chain h:



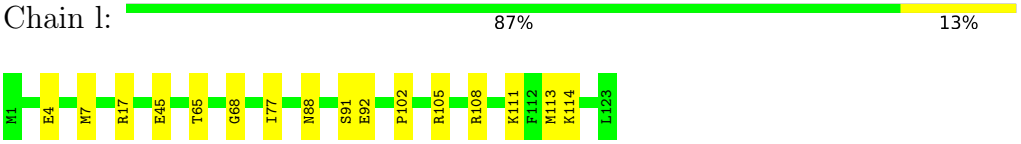
• Molecule 40: 50S ribosomal protein L13

Chain k:



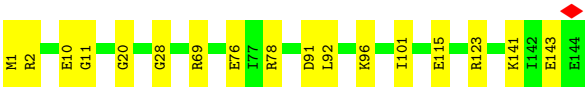
• Molecule 41: 50S ribosomal protein L14

Chain l:



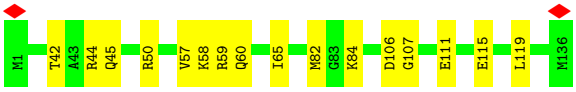
• Molecule 42: 50S ribosomal protein L15

Chain m:



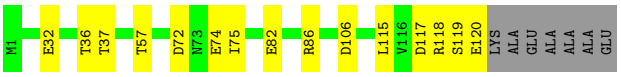
• Molecule 43: 50S ribosomal protein L16

Chain n:



• Molecule 44: 50S ribosomal protein L17

Chain o:

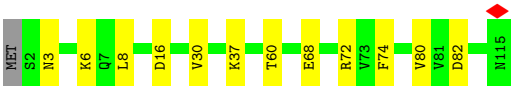


• Molecule 45: 50S ribosomal protein L18

Chain p:

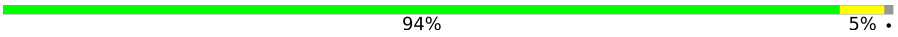
• Molecule 46: 50S ribosomal protein L19

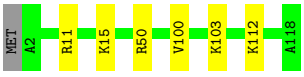
Chain q:



• Molecule 47: 50S ribosomal protein L20

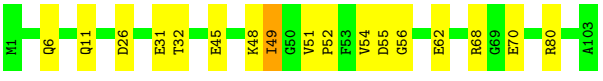
Chain r:





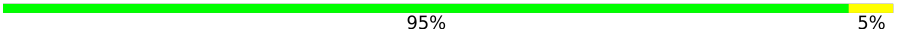
• Molecule 48: 50S ribosomal protein L21

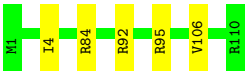
Chain s:



• Molecule 49: 50S ribosomal protein L22

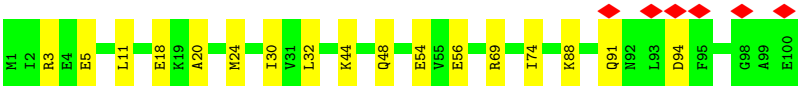
Chain t:





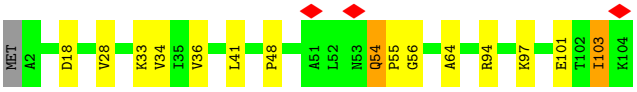
• Molecule 50: 50S ribosomal protein L23

Chain u:



• Molecule 51: 50S ribosomal protein L24

Chain v:

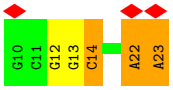


• Molecule 52: 50S ribosomal protein L25

Chain w:

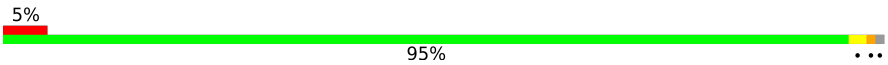
• Molecule 53: mRNA

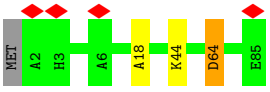
Chain x:



• Molecule 54: 50S ribosomal protein L27

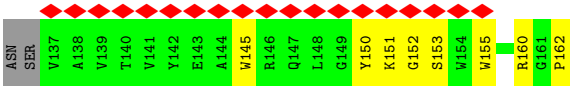
Chain y:





• Molecule 55: eRAP

Chain z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	152000	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 ($e^-/Å^2$)	38	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.638	Depositor
Minimum map value	-0.680	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.062	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	682.0, 682.0, 682.0	wwPDB
Map dimensions	620, 620, 620	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	0	0.34	0/635	0.29	0/848
2	1	0.28	0/496	0.30	0/660
3	2	0.32	0/453	0.30	0/605
4	4	0.34	0/450	0.36	0/599
5	5	0.27	0/433	0.30	0/576
6	6	0.37	0/380	0.43	0/498
7	7	0.36	0/513	0.35	0/676
8	8	0.35	0/303	0.30	0/397
9	A	0.25	0/36834	0.28	0/57462
10	B	0.22	0/1735	0.34	0/2338
11	C	0.20	0/1659	0.30	0/2236
12	D	0.15	0/1665	0.33	0/2227
13	E	0.24	0/1169	0.36	0/1573
14	F	0.57	1/881 (0.1%)	0.43	0/1189
15	G	0.18	0/1219	0.29	0/1635
16	H	0.26	0/989	0.31	0/1326
17	I	0.20	0/1034	0.36	0/1375
18	J	0.20	0/813	0.43	0/1100
19	K	0.23	0/893	0.30	0/1205
20	L	0.19	0/963	0.34	0/1293
21	M	0.18	0/909	0.30	0/1215
22	N	0.20	0/817	0.31	0/1088
23	O	0.23	0/722	0.32	0/964
24	P	0.21	0/653	0.29	0/877
25	Q	0.21	0/657	0.31	0/881
26	R	0.24	0/553	0.31	0/742
27	S	0.17	0/680	0.34	0/915
28	T	0.22	0/676	0.33	0/895
29	U	0.16	0/536	0.29	0/711
30	X	0.16	0/1810	0.27	0/2820
31	Y	0.21	0/1839	0.33	0/2866
31	Z	0.16	0/1839	0.27	0/2866

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	a	0.29	0/2872	0.28	0/4478
33	b	0.37	0/69773	0.32	0/108851
34	c	0.35	0/2121	0.33	0/2852
35	d	0.34	0/1586	0.34	0/2134
36	e	0.32	0/1571	0.28	0/2113
37	f	0.23	0/1443	0.32	0/1937
38	g	0.22	0/1333	0.29	0/1805
39	h	0.53	1/1119 (0.1%)	0.32	0/1512
40	k	0.41	1/1152 (0.1%)	0.30	0/1551
41	l	0.32	0/955	0.38	0/1279
42	m	0.34	0/1062	0.35	0/1413
43	n	0.27	0/1093	0.32	0/1460
44	o	0.36	0/973	0.38	0/1301
45	p	0.27	0/902	0.31	0/1209
46	q	0.32	0/929	0.29	0/1242
47	r	0.39	0/960	0.34	0/1278
48	s	0.34	0/829	0.35	0/1107
49	t	0.35	0/864	0.35	0/1156
50	u	0.32	0/793	0.35	0/1060
51	v	0.61	1/796 (0.1%)	0.38	0/1062
52	w	0.26	0/766	0.31	0/1025
53	x	0.20	0/333	0.27	0/517
54	y	0.33	0/642	0.29	0/848
55	z	0.17	0/316	0.33	0/435
All	All	0.32	4/160391 (0.0%)	0.31	0/240283

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	h	31	VAL	CA-CB	16.57	1.63	1.54
14	F	18	VAL	CA-CB	14.55	1.62	1.54
51	v	54	GLN	C-O	13.48	1.30	1.23
40	k	136	GLN	C-O	-5.93	1.21	1.23

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	625	0	652	8	0
2	1	495	0	526	5	0
3	2	449	0	488	7	0
4	4	444	0	458	11	0
5	5	426	0	464	11	0
6	6	377	0	418	2	0
7	7	504	0	572	5	0
8	8	302	0	340	3	0
9	A	32895	0	16553	335	0
10	B	1704	0	1732	42	0
11	C	1632	0	1710	24	0
12	D	1643	0	1710	65	0
13	E	1156	0	1199	27	0
14	F	862	0	864	24	0
15	G	1203	0	1256	27	0
16	H	979	0	1034	29	0
17	I	1022	0	1070	42	0
18	J	803	0	842	34	0
19	K	877	0	887	18	0
20	L	949	0	1014	23	0
21	M	900	0	968	20	0
22	N	805	0	847	14	0
23	O	714	0	737	10	0
24	P	643	0	661	16	0
25	Q	648	0	691	16	0
26	R	544	0	565	12	0
27	S	663	0	690	15	0
28	T	670	0	722	18	0
29	U	529	0	565	10	0
30	X	1621	0	820	33	0
31	Y	1646	0	832	27	0
31	Z	1646	0	832	19	0
32	a	2569	0	1301	11	0
33	b	62297	0	31333	373	0
34	c	2082	0	2154	17	0
35	d	1565	0	1616	11	0
36	e	1552	0	1619	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	f	1419	0	1457	36	0
38	g	1313	0	1358	20	0
39	h	1108	0	1148	14	0
40	k	1129	0	1162	8	0
41	l	946	0	1023	13	0
42	m	1053	0	1129	12	0
43	n	1074	0	1157	10	0
44	o	960	0	1000	10	0
45	p	892	0	923	16	0
46	q	917	0	962	11	0
47	r	947	0	1019	5	0
48	s	816	0	839	14	0
49	t	857	0	922	3	0
50	u	786	0	846	11	0
51	v	788	0	844	9	0
52	w	753	0	780	8	0
53	x	299	0	154	3	0
54	y	634	0	653	2	0
55	z	298	0	273	9	0
56	8	1	0	0	0	0
57	Z	7	0	7	5	0
All	All	147438	0	98398	1453	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (1453) 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)
10:B:150:ILE:HD11	10:B:153:MET:SD	1.77	1.25
10:B:150:ILE:CD1	10:B:153:MET:SD	2.28	1.22
31:Z:77:A:O3'	57:Z:163:PRO:C	1.90	1.14
31:Y:77:A:O3'	55:z:162:PRO:C	1.90	1.14
31:Z:77:A:O3'	57:Z:163:PRO:O	1.76	1.03
33:b:1352:U:HO2'	33:b:1570:A:H8	1.06	0.93
12:D:139:ASN:H	12:D:182:LYS:HA	1.34	0.93
31:Z:77:A:HO3'	57:Z:163:PRO:C	1.77	0.86
3:2:7:ILE:CD1	3:2:57:VAL:HG22	2.08	0.83
9:A:110:C:H3'	9:A:111:G:H21	1.44	0.82
10:B:150:ILE:CG1	10:B:153:MET:SD	2.70	0.80
1:0:68:LEU:HD23	1:0:71:LEU:HD12	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:2114:A:N6	33:b:2119:A:N7	2.30	0.79
33:b:713:G:H21	33:b:718:A:H2	1.30	0.79
30:X:15:G:N2	30:X:48:C:H42	1.80	0.78
33:b:2189:U:H2'	33:b:2190:G:H8	1.48	0.78
13:E:86:GLY:HA3	13:E:141:ASP:HB3	1.65	0.77
30:X:15:G:H22	30:X:48:C:H42	1.32	0.77
33:b:886:A:N1	33:b:892:A:N6	2.32	0.76
9:A:445:G:H22	9:A:489:C:H42	1.34	0.75
12:D:186:GLU:HG2	12:D:188:SER:H	1.51	0.75
9:A:673:A:H2'	9:A:674:G:C8	2.21	0.75
12:D:36:ALA:HB3	12:D:41:GLY:HA2	1.69	0.74
33:b:1056:G:O2'	33:b:1086:A:O2'	2.05	0.74
51:v:94:ARG:HB2	51:v:103:ILE:HG13	1.69	0.74
3:2:7:ILE:HD13	3:2:57:VAL:HG22	1.68	0.74
33:b:1060:U:H4'	33:b:1061:U:H5'	1.70	0.74
10:B:150:ILE:HG13	10:B:153:MET:SD	2.28	0.73
34:c:146:MET:HE3	34:c:154:LEU:HD21	1.70	0.72
9:A:510:A:OP1	12:D:46:ARG:NH1	2.22	0.72
31:Y:50:G:N2	31:Y:67:A:N7	2.38	0.72
33:b:1080:A:H3'	33:b:1081:U:H4'	1.72	0.72
9:A:1397:C:OP2	13:E:28:ARG:NH2	2.23	0.71
33:b:1439:A:H62	33:b:1552:A:H8	1.37	0.71
48:s:49:ILE:HG21	48:s:54:VAL:HA	1.72	0.71
11:C:13:ILE:HG22	11:C:14:VAL:HG13	1.72	0.71
23:O:88:ARG:NE	33:b:713:G:OP2	2.24	0.71
33:b:1532:A:N6	33:b:1540:G:O6	2.23	0.71
30:X:15:G:H22	30:X:48:C:N4	1.89	0.70
9:A:263:A:OP2	28:T:73:ARG:NH1	2.25	0.70
9:A:477:C:N3	9:A:478:A:N6	2.36	0.70
33:b:1428:C:H42	33:b:1570:A:H2	1.40	0.70
20:L:85:ARG:HH12	20:L:87:LYS:HZ2	1.41	0.69
30:X:19:G:N3	30:X:57:G:N2	2.40	0.69
9:A:76:G:H22	9:A:92:U:H3	1.41	0.69
33:b:1509:A:O2'	33:b:1510:G:O4'	2.09	0.69
9:A:41:G:H2'	9:A:42:G:H8	1.57	0.69
10:B:150:ILE:HD12	10:B:153:MET:SD	2.30	0.69
18:J:9:ARG:HB2	18:J:99:GLN:HE22	1.56	0.69
33:b:1854:A:H62	33:b:1888:G:H8	1.40	0.69
9:A:509:A:OP2	12:D:46:ARG:NH2	2.26	0.69
9:A:371:A:N1	9:A:389:A:N6	2.40	0.68
9:A:71:A:N6	9:A:99:C:O2'	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:K:80:ASN:OD1	19:K:105:ARG:NH1	2.26	0.68
9:A:107:G:N7	28:T:9:ARG:NH2	2.41	0.68
33:b:1106:G:H2'	33:b:1107:G:C8	2.29	0.68
41:l:77:ILE:HG13	46:q:72:ARG:HG3	1.75	0.68
9:A:967:C:H5"	17:I:128:LYS:HD3	1.73	0.68
9:A:501:C:H2'	9:A:502:A:H8	1.58	0.68
31:Y:66:U:O2	31:Y:67:A:N6	2.27	0.67
27:S:31:ARG:NH1	27:S:32:THR:O	2.28	0.67
9:A:710:G:OP1	14:F:53:LYS:NZ	2.27	0.67
30:X:12:U:H3	30:X:23:A:H61	1.40	0.67
4:4:55:ILE:HD13	44:o:118:ARG:HH12	1.59	0.67
9:A:1126:U:OP1	18:J:5:ARG:NH1	2.28	0.67
15:G:30:MET:HE2	15:G:35:LYS:HG3	1.76	0.67
9:A:437:U:OP1	12:D:150:LYS:NZ	2.28	0.67
16:H:77:VAL:HG12	16:H:84:ILE:HD11	1.77	0.67
37:f:11:GLU:O	37:f:15:LYS:NZ	2.28	0.66
16:H:52:GLY:HA2	16:H:56:PRO:HA	1.75	0.66
9:A:1021:A:H2'	9:A:1022:A:C8	2.30	0.66
35:d:56:LYS:HD2	35:d:59:ARG:HG3	1.76	0.66
21:M:65:GLU:HG2	21:M:67:ASP:H	1.60	0.66
33:b:1060:U:H3	33:b:1088:A:H8	1.42	0.65
33:b:2174:C:H2'	33:b:2175:C:C6	2.31	0.65
30:X:19:G:C6	33:b:2112:G:H1'	2.31	0.65
33:b:2136:G:N7	33:b:2153:C:N4	2.44	0.65
9:A:406:G:O2'	12:D:115:GLN:NE2	2.30	0.65
9:A:478:A:H2'	9:A:479:U:H4'	1.77	0.65
16:H:10:LEU:HG	16:H:74:ILE:HD11	1.79	0.65
33:b:1058:U:H5'	33:b:1060:U:H5"	1.79	0.65
16:H:95:MET:HE3	16:H:129:ALA:HB1	1.77	0.65
17:I:45:MET:SD	17:I:45:MET:N	2.68	0.65
17:I:23:GLY:O	17:I:60:LEU:N	2.29	0.65
36:e:146:VAL:HG12	36:e:185:LYS:HB2	1.77	0.65
9:A:187:G:N2	9:A:190:A:OP2	2.30	0.65
30:X:46:G:O2'	30:X:47:U:O4'	2.14	0.65
9:A:552:U:H2'	9:A:553:A:H8	1.62	0.64
9:A:376:G:C6	9:A:390:U:N3	2.64	0.64
33:b:1858:A:N6	33:b:1884:G:O2'	2.30	0.64
40:k:90:GLU:OE1	40:k:90:GLU:N	2.28	0.64
9:A:628:G:H2'	9:A:629:A:C8	2.32	0.64
33:b:884:U:O4	33:b:886:A:N6	2.29	0.64
31:Y:52:A:N6	31:Y:64:U:O4	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:2135:A:N6	33:b:2158:A:H4'	2.13	0.64
33:b:1057:A:N6	33:b:1087:G:O2'	2.22	0.64
43:n:58:LYS:O	43:n:60:GLN:NE2	2.31	0.64
50:u:54:GLU:N	50:u:54:GLU:OE1	2.30	0.64
5:5:30:LYS:NZ	33:b:2287:A:OP1	2.31	0.64
9:A:477:C:H2'	9:A:478:A:C8	2.33	0.64
11:C:78:LYS:HD2	11:C:79:LYS:HG2	1.78	0.64
38:g:86:LYS:HG2	38:g:132:VAL:HG22	1.79	0.64
30:X:14:A:H3'	30:X:15:G:H8	1.62	0.64
33:b:740:C:H5	33:b:758:C:H1'	1.63	0.64
33:b:2127:G:O2'	33:b:2128:G:O4'	2.13	0.63
12:D:149:LYS:O	12:D:155:LYS:NZ	2.31	0.63
23:O:73:ASP:OD2	23:O:76:ARG:NE	2.29	0.63
9:A:384:G:H2'	9:A:385:C:C6	2.34	0.63
9:A:544:G:OP1	12:D:58:GLN:NE2	2.31	0.63
13:E:102:THR:O	13:E:121:ASN:ND2	2.31	0.63
11:C:68:HIS:HA	11:C:103:ALA:HB3	1.80	0.63
30:X:49:G:H1	30:X:65:U:H3	1.45	0.63
33:b:1936:A:H2	33:b:1943:U:H5	1.45	0.63
9:A:412:A:N6	9:A:414:A:O3'	2.32	0.63
33:b:878:A:H3'	33:b:879:G:H8	1.62	0.63
7:7:35:LYS:NZ	33:b:2390:U:OP2	2.29	0.63
9:A:977:A:N6	9:A:1224:U:OP1	2.31	0.63
15:G:10:LYS:NZ	15:G:11:ILE:O	2.32	0.63
9:A:1150:A:H4'	18:J:43:PRO:HG3	1.79	0.63
12:D:169:TRP:CE2	12:D:185:PRO:HB3	2.34	0.63
24:P:5:ARG:NH2	24:P:23:ASP:O	2.32	0.63
41:l:113:MET:SD	41:l:113:MET:N	2.72	0.63
9:A:1071:C:H2'	9:A:1072:G:H8	1.63	0.62
38:g:104:ASN:ND2	38:g:114:ASP:OD1	2.32	0.62
22:N:45:LEU:HD12	27:S:12:LEU:HB3	1.81	0.62
9:A:363:A:N6	20:L:26:CYS:SG	2.73	0.62
33:b:1057:A:H62	33:b:1087:G:HO2'	1.48	0.62
41:l:4:GLU:N	41:l:4:GLU:OE1	2.31	0.62
18:J:57:VAL:HG12	18:J:58:ASN:H	1.63	0.62
24:P:12:LYS:HG2	24:P:13:LYS:HG2	1.80	0.62
24:P:39:PHE:HD1	24:P:50:THR:HB	1.64	0.62
9:A:376:G:O6	9:A:390:U:C4	2.53	0.62
9:A:1029:U:O2'	9:A:1032:G:N2	2.32	0.62
9:A:1432:G:O2'	9:A:1468:A:N6	2.33	0.62
33:b:636:G:N1	42:m:76:GLU:OE2	2.19	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:65:A:N7	9:A:200:G:O2'	2.30	0.62
9:A:714:G:H2'	9:A:715:A:C8	2.35	0.62
20:L:106:VAL:HG21	20:L:116:TYR:HD2	1.65	0.62
33:b:1064:C:N4	33:b:1072:C:OP1	2.32	0.62
9:A:516:U:O2	9:A:533:A:N7	2.33	0.62
9:A:840:C:N4	9:A:842:U:O2	2.33	0.62
18:J:40:ILE:HB	18:J:73:LEU:HB3	1.82	0.62
48:s:49:ILE:HD13	48:s:52:PRO:HA	1.82	0.62
20:L:54:VAL:HG21	20:L:79:ILE:HD11	1.81	0.62
9:A:501:C:H2'	9:A:502:A:C8	2.35	0.61
13:E:11:GLN:OE1	13:E:11:GLN:N	2.32	0.61
40:k:43:GLU:OE1	40:k:43:GLU:N	2.34	0.61
41:l:17:ARG:HB2	41:l:45:GLU:HG3	1.81	0.61
9:A:1357:A:O2'	9:A:1358:U:OP1	2.18	0.61
37:f:134:GLU:N	37:f:134:GLU:OE1	2.33	0.61
9:A:35:G:N3	20:L:114:SER:OG	2.33	0.61
9:A:640:A:O2'	16:H:107:LYS:NZ	2.33	0.61
10:B:78:ALA:HB1	10:B:213:LEU:HD21	1.82	0.61
18:J:46:LYS:HG2	18:J:68:ARG:HG2	1.82	0.61
12:D:10:LEU:HD23	12:D:62:ARG:HD2	1.83	0.61
12:D:194:ILE:HG22	12:D:197:HIS:HE1	1.65	0.61
31:Y:9:G:OP1	31:Y:47:G:N2	2.33	0.61
9:A:460:A:N7	9:A:474:G:N2	2.49	0.61
9:A:512:U:OP1	12:D:43:ARG:NH1	2.33	0.61
12:D:190:LEU:HD11	12:D:194:ILE:HG13	1.82	0.61
18:J:11:LYS:HG3	18:J:97:ASP:HB3	1.83	0.61
23:O:25:GLU:OE2	23:O:76:ARG:NH1	2.34	0.61
9:A:1013:G:N1	9:A:1016:A:OP2	2.33	0.61
9:A:746:A:H2'	9:A:747:A:C8	2.35	0.61
33:b:1870:C:O2'	33:b:1871:A:O4'	2.18	0.61
13:E:64:GLU:OE1	13:E:64:GLU:N	2.33	0.61
14:F:22:ILE:HD13	14:F:39:LEU:HD21	1.83	0.60
22:N:32:ASP:O	22:N:40:ARG:NH2	2.34	0.60
13:E:76:ASN:N	13:E:79:THR:O	2.33	0.60
33:b:1507:C:H2'	33:b:1508:A:N3	2.16	0.60
33:b:2126:A:N6	33:b:2162:G:O4'	2.33	0.60
14:F:38:ARG:HD2	14:F:97:THR:O	2.01	0.60
33:b:877:A:O2'	33:b:900:A:N6	2.33	0.60
9:A:1130:A:OP1	17:I:17:ARG:NH2	2.34	0.60
17:I:87:MET:HE3	17:I:97:LEU:HD12	1.82	0.60
18:J:47:GLU:N	18:J:47:GLU:OE1	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Y:77:A:C3’	55:z:162:PRO:O	2.49	0.60
31:Y:77:A:H3’	55:z:162:PRO:O	2.01	0.60
33:b:247:G:N2	33:b:250:G:O2’	2.35	0.60
37:f:6:ASP:HA	37:f:9:LYS:HG2	1.83	0.60
30:X:36:C:H5	53:x:12:G:H1	1.49	0.60
33:b:2790:U:H2’	33:b:2893:A:N7	2.16	0.60
1:0:67:VAL:O	1:0:71:LEU:HG	2.01	0.60
4:4:38:HIS:ND1	4:4:39:LEU:O	2.33	0.60
9:A:946:A:H2’	9:A:947:G:H8	1.67	0.60
10:B:127:LYS:HG2	10:B:129:THR:H	1.67	0.60
9:A:41:G:H2’	9:A:42:G:C8	2.36	0.60
33:b:2147:A:H2’	33:b:2148:G:O4’	2.02	0.60
33:b:2164:C:H4’	33:b:2165:C:H5’	1.84	0.60
11:C:82:ASP:HA	11:C:85:LYS:HD2	1.83	0.60
13:E:155:LYS:HG2	16:H:65:PHE:CD2	2.37	0.60
28:T:43:LYS:HB3	28:T:86:ALA:HA	1.84	0.60
33:b:1453:A:N6	44:o:74:GLU:OE2	2.22	0.60
37:f:24:SER:HB2	37:f:27:GLN:HB2	1.83	0.60
9:A:1152:A:H4’	18:J:15:HIS:NE2	2.17	0.59
22:N:53:ASP:OD1	22:N:58:ARG:NH1	2.33	0.59
25:Q:17:GLU:CD	25:Q:17:GLU:H	2.10	0.59
38:g:98:VAL:HG12	38:g:103:ILE:HG12	1.83	0.59
48:s:26:ASP:OD1	48:s:26:ASP:N	2.35	0.59
1:0:10:LYS:NZ	33:b:397:U:OP2	2.29	0.59
17:I:129:ARG:NH2	31:Y:36:G:OP2	2.35	0.59
9:A:202:G:O2’	9:A:468:A:OP1	2.20	0.59
15:G:128:GLU:O	15:G:130:LYS:NZ	2.35	0.59
5:5:27:LYS:HB2	5:5:28:ARG:HH12	1.66	0.59
12:D:108:ALA:HB3	12:D:112:GLU:HG3	1.84	0.59
17:I:11:ARG:HG3	17:I:12:LYS:H	1.67	0.59
9:A:1287:A:H2’	9:A:1288:A:C8	2.38	0.59
12:D:40:HIS:CG	12:D:43:ARG:HE	2.21	0.59
10:B:116:LEU:HD23	10:B:140:LEU:HB2	1.84	0.59
21:M:24:VAL:HG23	21:M:64:VAL:HG11	1.85	0.59
33:b:2118:U:O2	33:b:2145:C:N4	2.35	0.59
33:b:2188:U:H2’	33:b:2189:U:C2	2.38	0.59
38:g:2:SER:OG	38:g:3:ARG:N	2.35	0.59
43:n:50:ARG:HG3	43:n:65:ILE:HD11	1.84	0.59
9:A:1077:G:N2	9:A:1080:A:OP2	2.31	0.59
10:B:150:ILE:O	10:B:153:MET:HG2	2.03	0.59
33:b:1315:C:O2’	33:b:1392:A:H8	1.86	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:35:G:O2'	20:L:114:SER:O	2.21	0.59
13:E:35:LEU:HD21	13:E:136:VAL:HG21	1.85	0.59
33:b:993:G:OP1	47:r:50:ARG:NH1	2.36	0.59
33:b:1753:G:N2	33:b:1756:G:OP2	2.30	0.59
43:n:57:VAL:O	43:n:59:ARG:N	2.36	0.59
9:A:443:C:H2'	9:A:444:G:C8	2.38	0.58
17:I:29:ILE:HG12	17:I:64:ILE:HB	1.85	0.58
29:U:5:VAL:HG13	29:U:9:GLU:HB2	1.85	0.58
44:o:119:SER:OG	44:o:120:GLU:OE1	2.18	0.58
7:7:14:PHE:O	7:7:15:LYS:HG3	2.02	0.58
20:L:70:GLY:HA3	20:L:98:ARG:HH22	1.68	0.58
52:w:51:GLN:OE1	52:w:57:TYR:OH	2.20	0.58
33:b:1103:A:H2'	33:b:1104:C:H5'	1.84	0.58
33:b:1509:A:O2'	33:b:1510:G:O5'	2.18	0.58
43:n:106:ASP:OD1	43:n:107:GLY:N	2.36	0.58
9:A:628:G:H2'	9:A:629:A:H8	1.68	0.58
24:P:4:ILE:HG12	24:P:21:VAL:HG22	1.86	0.58
29:U:3:ILE:HD13	29:U:18:PHE:HD1	1.68	0.58
33:b:2335:A:H5'	45:p:13:ARG:NH2	2.19	0.58
9:A:459:A:H62	9:A:474:G:N2	2.02	0.58
9:A:946:A:H2'	9:A:947:G:C8	2.39	0.58
33:b:284:U:H3	33:b:356:G:H1	1.51	0.58
38:g:60:ASP:OD1	38:g:60:ASP:N	2.36	0.58
9:A:262:A:O2'	9:A:263:A:OP1	2.20	0.58
9:A:375:U:H4'	24:P:6:LEU:HD11	1.86	0.58
33:b:1115:G:H2'	33:b:1116:G:H8	1.67	0.58
10:B:66:ILE:N	10:B:88:GLN:OE1	2.37	0.58
14:F:42:TRP:HB2	14:F:59:TYR:HB2	1.86	0.58
31:Y:77:A:C3'	55:z:162:PRO:C	2.76	0.58
33:b:2135:A:H62	33:b:2158:A:H4'	1.69	0.58
1:0:60:ASP:OD2	39:h:27:ARG:NH1	2.37	0.58
10:B:87:ASP:HB2	10:B:224:ARG:NH1	2.19	0.58
9:A:449:G:H2'	9:A:450:G:C8	2.38	0.57
16:H:112:ASP:OD1	16:H:112:ASP:N	2.37	0.57
19:K:82:GLU:N	19:K:82:GLU:OE1	2.37	0.57
30:X:50:C:H2'	30:X:51:G:H5'	1.87	0.57
33:b:2790:U:H2'	33:b:2893:A:C8	2.38	0.57
9:A:713:G:H2'	9:A:714:G:C8	2.39	0.57
24:P:19:VAL:HG23	24:P:36:VAL:HG23	1.85	0.57
25:Q:30:HIS:HB2	25:Q:37:ILE:HD11	1.86	0.57
9:A:337:G:H2'	9:A:338:A:C8	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1035:A:H5”	9:A:1036:A:C8	2.40	0.57
11:C:152:VAL:HG12	11:C:197:VAL:HG22	1.86	0.57
13:E:80:LEU:HG	13:E:81:GLN:H	1.70	0.57
20:L:74:GLN:HG3	20:L:75:GLU:H	1.69	0.57
33:b:1417:C:HO2’	33:b:1587:G:HO2’	1.51	0.57
33:b:2202:U:O2’	33:b:2204:G:OP1	2.20	0.57
33:b:2250:G:OP1	43:n:84:LYS:NZ	2.38	0.57
9:A:531:U:H4’	9:A:532:A:H5’	1.87	0.57
9:A:673:A:H2’	9:A:674:G:H8	1.67	0.57
21:M:49:GLU:OE1	21:M:49:GLU:N	2.36	0.57
9:A:417:G:N2	9:A:541:G:OP1	2.38	0.57
9:A:1151:A:H5’	18:J:43:PRO:HA	1.87	0.57
27:S:62:THR:OG1	27:S:64:GLU:OE2	2.23	0.57
33:b:2858:C:O2’	33:b:2859:G:O5’	2.22	0.57
28:T:14:GLU:HA	28:T:17:ARG:HG2	1.87	0.57
28:T:70:LYS:HA	28:T:73:ARG:HE	1.69	0.57
10:B:166:ASP:OD2	10:B:190:SER:OG	2.22	0.57
38:g:38:ASN:ND2	38:g:64:GLN:OE1	2.33	0.57
9:A:449:G:O6	9:A:486:U:O4	2.23	0.57
9:A:1041:G:H2’	9:A:1042:A:C8	2.40	0.57
35:d:74:GLU:OE1	35:d:74:GLU:N	2.32	0.57
35:d:39:ASP:N	35:d:39:ASP:OD1	2.37	0.56
10:B:30:ILE:HD11	10:B:38:HIS:HB3	1.85	0.56
33:b:414:C:H2’	33:b:415:A:C8	2.40	0.56
11:C:160:GLU:HG2	11:C:161:ILE:H	1.71	0.56
15:G:86:VAL:HG12	15:G:150:PHE:HB2	1.86	0.56
18:J:78:GLU:O	18:J:78:GLU:HG2	2.05	0.56
20:L:106:VAL:HB	20:L:116:TYR:HB3	1.86	0.56
26:R:15:GLU:N	26:R:15:GLU:OE1	2.32	0.56
33:b:345:A:H1’	33:b:346:A:H2	1.71	0.56
33:b:2185:U:H2’	33:b:2186:G:H8	1.70	0.56
9:A:193:C:H2’	9:A:194:C:C6	2.39	0.56
9:A:634:C:H2’	9:A:635:A:H8	1.70	0.56
27:S:18:VAL:HG21	27:S:43:MET:HG3	1.88	0.56
33:b:1802:A:H2’	33:b:1803:A:C8	2.40	0.56
33:b:2109:U:N3	33:b:2110:G:O6	2.38	0.56
33:b:463:G:N2	33:b:466:A:OP2	2.33	0.56
33:b:2126:A:N3	33:b:2127:G:N1	2.54	0.56
9:A:403:C:H2’	9:A:404:G:H8	1.70	0.56
10:B:152:ASP:OD1	10:B:152:ASP:N	2.36	0.56
33:b:2187:U:H2’	33:b:2188:U:C4	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:337:G:H2'	9:A:338:A:H8	1.70	0.56
9:A:370:C:H2'	9:A:371:A:C8	2.41	0.56
9:A:500:G:H2'	9:A:501:C:C6	2.40	0.56
27:S:8:PRO:HB3	27:S:38:THR:HG21	1.88	0.56
36:e:122:GLU:OE1	36:e:122:GLU:N	2.31	0.56
17:I:35:GLU:OE1	17:I:35:GLU:N	2.34	0.56
33:b:1936:A:H2	33:b:1943:U:C5	2.24	0.56
9:A:201:G:H3'	9:A:202:G:C8	2.40	0.56
11:C:109:GLU:HB2	11:C:143:LEU:HD22	1.88	0.56
17:I:20:ILE:HD11	17:I:60:LEU:HD12	1.86	0.56
31:Y:21:U:O4	31:Y:60:A:N6	2.39	0.56
9:A:184:G:H4'	9:A:224:U:H4'	1.87	0.55
33:b:2130:U:H5'	33:b:2131:U:H5"	1.88	0.55
37:f:65:PRO:HB3	37:f:89:VAL:HG23	1.88	0.55
52:w:11:GLU:N	52:w:11:GLU:OE1	2.39	0.55
33:b:2151:U:N3	33:b:2152:G:O6	2.39	0.55
42:m:123:ARG:NE	42:m:143:GLU:OE2	2.38	0.55
9:A:462:G:N2	9:A:470:C:O2	2.40	0.55
9:A:1412:C:H2'	9:A:1413:A:C8	2.41	0.55
42:m:141:LYS:HZ3	42:m:143:GLU:HG2	1.71	0.55
33:b:1862:G:H1	33:b:1880:U:H5	1.55	0.55
33:b:2783:U:H2'	33:b:2784:U:C6	2.41	0.55
46:q:16:ASP:OD1	46:q:16:ASP:N	2.38	0.55
9:A:1000:A:H2'	9:A:1001:C:C6	2.42	0.55
33:b:28:A:N6	33:b:512:G:O2'	2.39	0.55
37:f:142:ASP:OD1	37:f:144:ASP:N	2.40	0.55
4:4:54:VAL:HG12	4:4:55:ILE:H	1.72	0.55
9:A:411:A:OP1	12:D:25:ARG:NH2	2.39	0.55
10:B:127:LYS:HZ3	10:B:129:THR:HB	1.72	0.55
34:c:185:GLU:HG3	34:c:187:ASP:H	1.71	0.55
40:k:62:VAL:HG21	40:k:101:ILE:HD11	1.87	0.55
9:A:458:U:O2	9:A:459:A:N6	2.40	0.55
11:C:106:ARG:HB3	11:C:107:LYS:HD2	1.89	0.55
14:F:18:VAL:HG11	14:F:58:HIS:CE1	2.42	0.55
16:H:17:GLN:HG3	16:H:71:VAL:HG22	1.89	0.55
19:K:112:VAL:HG12	26:R:72:ARG:HE	1.72	0.55
33:b:2135:A:H2'	33:b:2156:G:N2	2.21	0.55
33:b:2783:U:H2'	33:b:2784:U:H6	1.72	0.55
19:K:36:ARG:NH1	19:K:82:GLU:OE2	2.40	0.55
33:b:546:U:H2'	33:b:547:A:C2	2.42	0.55
13:E:144:GLU:OE1	13:E:144:GLU:N	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:E:148:SER:OG	13:E:150:GLU:OE2	2.25	0.55
16:H:46:GLU:OE1	16:H:46:GLU:N	2.40	0.55
33:b:878:A:C2	33:b:879:G:H1'	2.42	0.55
46:q:72:ARG:HD2	46:q:74:PHE:CZ	2.42	0.55
48:s:6:GLN:HB3	48:s:11:GLN:HG2	1.87	0.55
9:A:445:G:H2'	9:A:446:G:C8	2.42	0.54
9:A:1028:C:N4	9:A:1029:U:O2	2.40	0.54
22:N:38:GLU:OE1	22:N:38:GLU:N	2.33	0.54
32:a:1:U:H2'	32:a:2:G:H8	1.72	0.54
39:h:79:THR:HA	39:h:145:ASN:HB2	1.88	0.54
9:A:219:U:H2'	9:A:220:G:H8	1.72	0.54
19:K:19:VAL:HG13	19:K:82:GLU:HG2	1.89	0.54
28:T:73:ARG:O	28:T:77:ASN:ND2	2.26	0.54
33:b:2133:G:N7	33:b:2154:A:H5"	2.21	0.54
33:b:2177:C:H2'	33:b:2178:C:C6	2.41	0.54
38:g:173:GLU:N	38:g:173:GLU:OE1	2.41	0.54
9:A:389:A:N3	9:A:390:U:H5"	2.22	0.54
9:A:1032:G:O2'	9:A:1033:G:O4'	2.21	0.54
33:b:1483:G:O6	33:b:1505:A:N1	2.40	0.54
33:b:2335:A:P	45:p:13:ARG:HH12	2.30	0.54
34:c:21:ASN:ND2	34:c:23:GLU:OE2	2.39	0.54
38:g:9:VAL:HG12	38:g:50:LEU:HB2	1.88	0.54
52:w:35:GLU:N	52:w:35:GLU:OE1	2.40	0.54
17:I:44:ARG:O	17:I:48:ARG:HG2	2.07	0.54
33:b:845:A:H62	33:b:932:U:H3	1.56	0.54
33:b:2032:G:N2	35:d:151:THR:OG1	2.40	0.54
33:b:2178:C:H2'	33:b:2179:C:C6	2.42	0.54
52:w:32:GLY:O	52:w:93:ARG:NH1	2.41	0.54
9:A:92:U:H2'	9:A:93:U:C2	2.42	0.54
9:A:993:G:O2'	9:A:994:A:N7	2.41	0.54
32:a:51:G:O2'	32:a:52:A:OP1	2.26	0.54
33:b:1713:A:H61	33:b:1745:A:N6	2.05	0.54
11:C:163:ARG:NH1	11:C:165:GLU:OE2	2.41	0.54
33:b:2305:U:H4'	37:f:133:ARG:HH12	1.73	0.54
51:v:101:GLU:N	51:v:101:GLU:OE1	2.41	0.54
9:A:979:C:O2	22:N:58:ARG:NE	2.40	0.54
18:J:88:MET:SD	18:J:88:MET:N	2.81	0.54
33:b:2191:A:H2'	33:b:2192:U:C6	2.43	0.54
33:b:2192:U:H2'	33:b:2193:G:H8	1.73	0.54
34:c:17:VAL:HB	34:c:204:VAL:HG22	1.90	0.54
35:d:88:GLU:N	35:d:88:GLU:OE1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:s:31:GLU:N	48:s:31:GLU:OE1	2.37	0.54
9:A:358:U:H2'	9:A:359:G:H8	1.72	0.54
9:A:1347:G:H5"	17:I:108:ARG:HB3	1.90	0.54
21:M:57:ASP:OD1	21:M:58:GLU:N	2.40	0.54
27:S:43:MET:N	27:S:43:MET:SD	2.81	0.54
28:T:42:ASP:OD1	28:T:45:ALA:N	2.33	0.54
50:u:94:ASP:OD1	50:u:94:ASP:N	2.41	0.54
9:A:1149:C:H2'	9:A:1150:A:C8	2.43	0.54
9:A:1492:A:H5"	20:L:43:LYS:HD3	1.90	0.54
33:b:1141:U:H4'	33:b:1142:A:O4'	2.08	0.54
33:b:1538:G:H2'	33:b:1539:U:C6	2.42	0.54
51:v:28:VAL:HG12	51:v:34:VAL:HG12	1.90	0.54
10:B:96:LEU:H	10:B:99:MET:HE3	1.72	0.54
3:2:7:ILE:HD12	3:2:57:VAL:HG22	1.89	0.53
8:8:32:LYS:HE2	33:b:2478:A:H5'	1.91	0.53
15:G:112:ASP:O	15:G:118:ARG:NE	2.41	0.53
26:R:36:GLY:O	26:R:62:ARG:NH2	2.40	0.53
39:h:132:PHE:HB2	39:h:140:ALA:HB3	1.90	0.53
20:L:75:GLU:O	20:L:76:HIS:ND1	2.39	0.53
30:X:42:C:N4	30:X:43:G:O6	2.42	0.53
31:Z:73:G:H2'	31:Z:74:A:C8	2.44	0.53
33:b:880:G:H2'	33:b:881:G:C8	2.44	0.53
52:w:77:VAL:HG12	52:w:89:ILE:HD13	1.90	0.53
9:A:677:U:H3	9:A:713:G:H22	1.55	0.53
9:A:1306:A:N6	9:A:1331:G:O2'	2.42	0.53
23:O:6:ALA:O	23:O:10:ILE:HG12	2.07	0.53
38:g:42:GLU:HB3	38:g:55:ARG:HE	1.74	0.53
1:0:65:ASP:OD1	1:0:66:THR:N	2.41	0.53
9:A:185:U:H2'	9:A:186:C:C6	2.43	0.53
9:A:1187:G:O2'	9:A:1188:A:OP1	2.23	0.53
18:J:7:ARG:N	18:J:7:ARG:HE	2.06	0.53
30:X:28:G:N1	30:X:29:A:N3	2.57	0.53
32:a:1:U:H2'	32:a:2:G:C8	2.44	0.53
33:b:1095:A:OP2	33:b:1098:A:N6	2.42	0.53
33:b:1779:U:H5	33:b:1784:A:N7	2.07	0.53
3:2:37:GLU:O	3:2:38:ARG:NH1	2.41	0.53
13:E:81:GLN:NE2	16:H:96:ALA:O	2.41	0.53
26:R:34:GLU:OE1	26:R:34:GLU:N	2.36	0.53
33:b:1053:C:H3'	33:b:1054:A:H2	1.74	0.53
36:e:7:ASP:OD1	36:e:7:ASP:N	2.41	0.53
9:A:438:U:O2'	9:A:493:A:N6	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:221:ARG:HA	10:B:224:ARG:HE	1.74	0.53
12:D:78:ALA:HA	12:D:81:LEU:HD12	1.90	0.53
17:I:105:ARG:NH1	17:I:106:ASP:O	2.33	0.53
33:b:887:U:O2	33:b:891:G:N2	2.38	0.53
33:b:952:G:H21	33:b:2267:A:H2	1.55	0.53
9:A:1305:G:N2	9:A:1332:A:OP2	2.42	0.53
10:B:160:LEU:HB2	10:B:182:VAL:HG12	1.90	0.53
30:X:29:A:H2	30:X:42:C:C4	2.27	0.53
33:b:848:C:H2'	33:b:849:A:H8	1.73	0.53
45:p:43:ASN:ND2	45:p:46:GLU:OE1	2.39	0.53
14:F:67:PRO:HB2	14:F:69:GLU:OE1	2.08	0.53
23:O:5:GLU:OE1	23:O:5:GLU:N	2.37	0.53
31:Y:9:G:OP2	31:Y:47:G:H1'	2.08	0.53
33:b:1068:G:H2'	33:b:1070:A:H62	1.72	0.53
9:A:197:A:N1	9:A:220:G:O2'	2.42	0.53
13:E:100:GLU:OE1	13:E:101:GLY:N	2.42	0.53
16:H:90:GLU:N	16:H:90:GLU:OE1	2.42	0.53
33:b:310:A:O2'	33:b:311:A:H2'	2.09	0.53
33:b:848:C:H2'	33:b:849:A:C8	2.44	0.53
33:b:2306:C:OP2	33:b:2307:G:O2'	2.18	0.53
9:A:374:A:O2'	9:A:375:U:O4'	2.23	0.53
9:A:1356:G:H2'	9:A:1357:A:C8	2.44	0.53
24:P:55:ASP:OD1	24:P:56:ARG:N	2.42	0.53
25:Q:4:ILE:HD12	25:Q:61:ARG:HH11	1.74	0.53
17:I:32:ARG:HH21	17:I:37:TYR:HA	1.74	0.52
18:J:3:ASN:N	18:J:78:GLU:HA	2.24	0.52
33:b:2112:G:H5'	33:b:2113:U:C5	2.44	0.52
33:b:2345:G:O2'	33:b:2381:A:N3	2.39	0.52
10:B:77:GLU:HA	10:B:80:LYS:HG2	1.91	0.52
10:B:112:ARG:HH22	10:B:116:LEU:HD13	1.74	0.52
33:b:894:U:O2'	33:b:895:U:O4'	2.24	0.52
1:0:40:VAL:HG12	1:0:43:GLU:H	1.74	0.52
9:A:745:G:H2'	9:A:746:A:H8	1.74	0.52
21:M:62:PHE:HB3	21:M:64:VAL:HG23	1.90	0.52
30:X:30:C:H42	30:X:39:G:H1	1.57	0.52
33:b:1106:G:H2'	33:b:1107:G:H8	1.75	0.52
21:M:70:ARG:O	21:M:74:MET:HG3	2.10	0.52
33:b:1076:C:H2'	33:b:1088:A:H61	1.75	0.52
9:A:269:C:H2'	9:A:270:A:H8	1.75	0.52
9:A:449:G:H1	9:A:486:U:H3	1.58	0.52
9:A:948:C:H5"	21:M:104:ASN:HD21	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1111:A:N1	11:C:176:THR:HG22	2.24	0.52
17:I:58:GLU:HB2	17:I:59:LYS:HD3	1.92	0.52
17:I:83:THR:HG23	17:I:97:LEU:HD13	1.90	0.52
33:b:286:U:H2'	33:b:287:G:C8	2.45	0.52
33:b:370:G:O2'	33:b:424:G:OP1	2.25	0.52
9:A:269:C:H2'	9:A:270:A:C8	2.45	0.52
9:A:410:G:H1'	9:A:433:G:H22	1.73	0.52
9:A:1175:G:H2'	9:A:1176:A:H8	1.74	0.52
42:m:10:GLU:OE1	42:m:10:GLU:N	2.30	0.52
3:2:39:GLU:N	3:2:39:GLU:OE1	2.38	0.52
29:U:1:PRO:HG2	29:U:22:CYS:HA	1.91	0.52
33:b:597:G:O2'	42:m:11:GLY:O	2.28	0.52
33:b:1871:A:H2'	33:b:1872:A:C8	2.45	0.52
33:b:2180:U:H2'	33:b:2181:U:C6	2.45	0.52
33:b:2189:U:H2'	33:b:2190:G:C8	2.37	0.52
9:A:436:C:H2'	9:A:437:U:C6	2.44	0.52
17:I:57:VAL:HA	17:I:60:LEU:HD23	1.91	0.52
18:J:32:THR:HG21	18:J:83:THR:HA	1.92	0.52
20:L:74:GLN:NE2	20:L:75:GLU:OE2	2.43	0.52
33:b:856:G:H2'	33:b:857:G:C8	2.45	0.52
33:b:1086:A:H1'	33:b:1104:C:C4	2.45	0.52
8:8:2:LYS:NZ	33:b:2478:A:OP2	2.43	0.52
9:A:363:A:OP2	20:L:30:ARG:NE	2.42	0.52
9:A:413:G:N7	12:D:30:LYS:HD3	2.24	0.52
12:D:99:ASN:OD1	12:D:110:ARG:NH2	2.43	0.52
33:b:511:U:O2'	33:b:512:G:OP1	2.24	0.52
33:b:2114:A:C6	33:b:2115:G:H1'	2.45	0.52
33:b:2859:G:H2'	33:b:2860:A:C8	2.45	0.52
12:D:84:ASN:HB2	13:E:101:GLY:HA3	1.90	0.52
31:Y:24:C:H2'	31:Y:25:G:C8	2.45	0.52
33:b:2097:A:H2'	33:b:2098:U:C6	2.45	0.52
33:b:2830:C:H5'	35:d:56:LYS:HE3	1.92	0.52
38:g:90:VAL:HG12	38:g:91:GLY:H	1.74	0.52
30:X:18:G:H4'	30:X:59:G:H1	1.75	0.51
33:b:45:G:H5'	33:b:46:G:OP1	2.10	0.51
33:b:705:A:N6	33:b:726:G:H1'	2.24	0.51
9:A:274:A:N3	9:A:275:G:H1'	2.25	0.51
9:A:1015:G:H2'	9:A:1016:A:C8	2.45	0.51
33:b:1936:A:C2	33:b:1943:U:H5	2.25	0.51
50:u:18:GLU:CD	50:u:18:GLU:H	2.19	0.51
9:A:81:A:O2'	9:A:82:G:O4'	2.21	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:151:A:H3'	9:A:152:A:H8	1.75	0.51
15:G:68:VAL:HG21	15:G:103:ILE:HD11	1.91	0.51
31:Z:77:A:C3'	57:Z:163:PRO:O	2.58	0.51
38:g:101:ASN:ND2	38:g:116:GLN:OE1	2.43	0.51
9:A:502:A:H2'	9:A:503:C:C6	2.45	0.51
30:X:6:A:H62	30:X:66:U:H3	1.58	0.51
11:C:33:ASP:O	11:C:37:LYS:HG2	2.11	0.51
18:J:6:ILE:HB	18:J:76:ILE:HG23	1.93	0.51
22:N:23:ARG:NH1	22:N:54:SER:OG	2.44	0.51
37:f:70:ALA:HB3	37:f:82:GLY:H	1.76	0.51
37:f:111:ILE:HG12	37:f:137:ILE:HD13	1.92	0.51
41:l:65:THR:HG23	41:l:68:GLY:H	1.75	0.51
9:A:89:U:H2'	9:A:90:C:C6	2.45	0.51
9:A:445:G:N2	9:A:489:C:H42	2.05	0.51
14:F:68:GLN:OE1	14:F:68:GLN:N	2.43	0.51
24:P:45:GLU:OE1	24:P:46:LYS:NZ	2.39	0.51
37:f:148:ARG:NH1	37:f:149:VAL:H	2.08	0.51
48:s:49:ILE:HB	48:s:51:VAL:O	2.11	0.51
28:T:34:VAL:O	28:T:38:ILE:HD12	2.10	0.51
33:b:2136:G:O2'	33:b:2137:U:O4'	2.20	0.51
41:l:102:PRO:HD2	46:q:68:GLU:OE2	2.10	0.51
12:D:18:LEU:H	12:D:18:LEU:HD23	1.75	0.51
19:K:79:LYS:HD3	19:K:80:ASN:HD22	1.76	0.51
31:Z:5:G:H2'	31:Z:6:A:H8	1.74	0.51
33:b:2243:U:H2'	33:b:2244:U:C6	2.46	0.51
33:b:2335:A:OP1	45:p:13:ARG:NH1	2.43	0.51
33:b:2847:U:H2'	33:b:2848:G:O4'	2.10	0.51
34:c:155:ALA:HB2	34:c:162:VAL:HG23	1.92	0.51
38:g:42:GLU:HB3	38:g:55:ARG:NE	2.26	0.51
9:A:324:G:N1	9:A:327:A:OP2	2.44	0.51
18:J:42:LEU:HD23	18:J:71:LEU:HB3	1.92	0.51
9:A:309:A:H2'	9:A:310:G:H8	1.76	0.51
9:A:425:G:O3'	12:D:32:LYS:NZ	2.44	0.51
9:A:944:G:N1	9:A:1338:G:OP2	2.40	0.51
33:b:1203:U:OP2	33:b:1204:A:O2'	2.23	0.51
33:b:2328:A:H2'	33:b:2329:U:C6	2.46	0.51
34:c:108:LYS:HB2	34:c:194:GLU:HB2	1.92	0.51
37:f:136:ILE:HA	37:f:141:ILE:HD11	1.93	0.51
9:A:376:G:C6	9:A:390:U:C4	2.99	0.50
9:A:602:A:H2'	9:A:603:U:C6	2.46	0.50
9:A:1133:G:H2'	9:A:1134:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:92:PRO:HA	15:G:95:ARG:HD3	1.93	0.50
27:S:61:VAL:HA	27:S:65:MET:HE2	1.91	0.50
33:b:849:A:H2'	33:b:850:U:C6	2.46	0.50
33:b:1537:G:H2'	33:b:1538:G:C4	2.45	0.50
12:D:187:ARG:NH2	12:D:196:GLU:OE2	2.42	0.50
14:F:1:MET:HE3	14:F:2:ARG:N	2.25	0.50
33:b:1469:A:H2'	33:b:1470:A:C8	2.45	0.50
41:l:92:GLU:OE1	41:l:92:GLU:N	2.45	0.50
9:A:613:C:H2'	9:A:614:C:C6	2.47	0.50
15:G:107:ALA:HA	15:G:122:GLU:CD	2.37	0.50
33:b:627:A:OP1	42:m:78:ARG:NH1	2.43	0.50
33:b:2637:U:H2'	33:b:2638:G:O4'	2.11	0.50
12:D:12:ARG:HA	12:D:34:GLU:HG2	1.92	0.50
17:I:59:LYS:O	17:I:60:LEU:HD13	2.11	0.50
24:P:61:VAL:HG22	24:P:67:ILE:HD11	1.93	0.50
2:1:9:LYS:HB3	2:1:13:GLU:HG3	1.94	0.50
9:A:1021:A:H2'	9:A:1022:A:H8	1.75	0.50
9:A:1056:U:OP1	11:C:161:ILE:HA	2.11	0.50
10:B:132:GLU:OE1	10:B:132:GLU:N	2.45	0.50
33:b:287:G:H2'	33:b:288:U:C6	2.47	0.50
33:b:2848:G:O2'	33:b:2849:U:O5'	2.23	0.50
16:H:72:GLU:N	16:H:72:GLU:OE1	2.44	0.50
33:b:1744:A:H3'	33:b:1745:A:H5"	1.92	0.50
33:b:2100:G:H2'	33:b:2101:A:C8	2.47	0.50
24:P:44:SER:HB2	24:P:47:GLU:OE1	2.12	0.50
33:b:356:G:H2'	33:b:357:C:H6	1.76	0.50
33:b:1353:A:H2'	33:b:1354:A:C8	2.47	0.50
9:A:219:U:H2'	9:A:220:G:C8	2.46	0.50
32:a:66:A:OP2	32:a:108:A:N6	2.45	0.50
33:b:358:U:H2'	33:b:359:G:H8	1.76	0.50
9:A:276:G:H5'	25:Q:16:MET:CE	2.42	0.49
9:A:415:A:H3'	9:A:416:G:H8	1.76	0.49
9:A:1227:A:O3'	21:M:113:LYS:NZ	2.45	0.49
9:A:1424:U:H3	9:A:1476:A:H62	1.58	0.49
11:C:66:THR:HG22	11:C:101:ASN:HB2	1.94	0.49
11:C:82:ASP:N	11:C:82:ASP:OD1	2.44	0.49
12:D:56:GLU:HG2	12:D:198:LEU:HD22	1.92	0.49
15:G:74:VAL:HA	15:G:87:PRO:HA	1.94	0.49
33:b:1216:G:OP1	47:r:11:ARG:NH1	2.45	0.49
33:b:1585:C:H2'	33:b:1586:A:O4'	2.12	0.49
33:b:2155:U:H2'	33:b:2156:G:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:s:32:THR:HA	48:s:62:GLU:HA	1.93	0.49
9:A:410:G:H2'	9:A:429:U:C5	2.48	0.49
33:b:284:U:O2	33:b:356:G:N2	2.41	0.49
33:b:2667:C:N3	38:g:110:SER:OG	2.42	0.49
36:e:143:LEU:HD13	36:e:146:VAL:HG11	1.93	0.49
9:A:674:G:H2'	9:A:675:A:H8	1.76	0.49
9:A:981:U:OP2	22:N:8:ARG:NH2	2.46	0.49
9:A:1207:G:H3'	9:A:1208:C:H6	1.77	0.49
13:E:104:ILE:HD11	13:E:120:HIS:HA	1.95	0.49
20:L:109:ARG:HH22	20:L:112:ALA:HB3	1.77	0.49
57:Z:163:PRO:HG2	55:z:160:ARG:HG2	1.94	0.49
33:b:1064:C:O2'	33:b:1069:A:N7	2.43	0.49
41:l:105:ARG:HG3	41:l:108:ARG:HH12	1.77	0.49
51:v:33:LYS:HB3	51:v:64:ALA:HB1	1.94	0.49
9:A:113:G:N3	9:A:353:A:O2'	2.39	0.49
9:A:276:G:H5'	25:Q:16:MET:HE1	1.93	0.49
9:A:462:G:H2'	9:A:463:U:C6	2.47	0.49
9:A:1301:U:O2'	9:A:1302:C:H5'	2.12	0.49
22:N:85:GLU:OE1	22:N:89:ARG:NH2	2.45	0.49
31:Y:77:A:O3'	55:z:162:PRO:O	2.23	0.49
33:b:1062:G:O2'	33:b:1063:G:O4'	2.12	0.49
34:c:107:PRO:HD2	34:c:110:LEU:HD22	1.94	0.49
38:g:95:ARG:HH21	38:g:106:SER:HB3	1.77	0.49
10:B:108:GLN:OE1	10:B:108:GLN:N	2.44	0.49
17:I:96:GLU:N	17:I:96:GLU:OE1	2.45	0.49
21:M:3:ILE:HG13	21:M:56:ARG:HD2	1.94	0.49
33:b:368:A:O2'	33:b:369:U:OP1	2.26	0.49
33:b:715:A:O2'	33:b:716:A:O4'	2.31	0.49
33:b:2121:G:H2'	33:b:2122:U:C6	2.48	0.49
35:d:181:ASP:HB3	35:d:186:LEU:HB2	1.93	0.49
42:m:115:GLU:N	42:m:115:GLU:OE1	2.45	0.49
14:F:12:PRO:O	14:F:44:ARG:NH2	2.45	0.49
16:H:40:LYS:NZ	16:H:47:ASP:HA	2.28	0.49
19:K:92:ARG:NH2	19:K:111:ASP:OD2	2.34	0.49
5:5:33:LYS:CE	5:5:51:GLU:OE1	2.61	0.49
9:A:147:G:H2'	9:A:148:G:C8	2.47	0.49
33:b:2186:G:N3	33:b:2186:G:H2'	2.27	0.49
2:1:12:GLU:OE1	2:1:12:GLU:N	2.38	0.49
9:A:376:G:H4'	24:P:5:ARG:HH11	1.78	0.49
9:A:1226:C:O2'	21:M:109:LYS:NZ	2.45	0.49
17:I:40:ARG:HD2	17:I:44:ARG:CZ	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:L:72:ASN:OD1	20:L:72:ASN:N	2.46	0.49
27:S:49:ALA:HA	27:S:58:PRO:HA	1.93	0.49
33:b:191:A:H2'	33:b:192:C:C6	2.47	0.49
33:b:286:U:H2'	33:b:287:G:H8	1.77	0.49
33:b:2135:A:H5"	33:b:2136:G:C5	2.47	0.49
33:b:2655:G:N2	33:b:2665:A:OP2	2.45	0.49
37:f:73:SER:OG	37:f:81:GLN:N	2.46	0.49
9:A:1035:A:H5"	9:A:1036:A:H8	1.77	0.49
12:D:104:MET:HG2	12:D:170:LEU:HD21	1.95	0.49
14:F:72:ASP:OD1	14:F:72:ASP:N	2.46	0.49
30:X:53:G:H2'	30:X:54:U:H6	1.78	0.49
54:y:64:ASP:OD1	54:y:64:ASP:N	2.46	0.49
9:A:592:G:H2'	9:A:593:U:C6	2.48	0.49
33:b:1796:U:H2'	33:b:1797:G:H8	1.77	0.49
37:f:164:GLU:OE1	37:f:164:GLU:N	2.42	0.49
5:5:44:ARG:HD3	33:b:643:A:C6	2.48	0.48
9:A:84:U:H2'	9:A:86:G:H21	1.78	0.48
9:A:199:A:H61	9:A:217:C:H42	1.61	0.48
9:A:1037:C:H2'	9:A:1038:C:C6	2.48	0.48
12:D:94:GLU:HA	12:D:99:ASN:HD22	1.77	0.48
16:H:28:SER:HB2	16:H:56:PRO:HB2	1.94	0.48
20:L:55:ARG:NE	20:L:61:GLU:OE1	2.45	0.48
33:b:2112:G:H5'	33:b:2113:U:H5	1.78	0.48
9:A:618:C:N4	9:A:621:A:OP2	2.43	0.48
9:A:1162:C:H2'	9:A:1163:A:H8	1.78	0.48
18:J:7:ARG:HB2	18:J:101:SER:OG	2.13	0.48
18:J:35:GLN:N	18:J:78:GLU:OE2	2.45	0.48
33:b:1838:C:H4'	33:b:1839:G:H5'	1.94	0.48
33:b:2133:G:H1'	33:b:2157:G:H22	1.77	0.48
33:b:2638:G:HO2'	33:b:2639:A:H8	1.58	0.48
52:w:48:MET:O	52:w:51:GLN:HG3	2.13	0.48
9:A:753:A:OP1	23:O:72:LYS:NZ	2.46	0.48
9:A:1178:G:N2	9:A:1181:G:OP2	2.43	0.48
33:b:2055:C:O2'	33:b:2056:G:OP2	2.22	0.48
33:b:2114:A:N6	33:b:2117:A:H62	2.11	0.48
33:b:2138:G:N1	33:b:2153:C:N3	2.61	0.48
33:b:2635:A:N1	33:b:2783:U:H5	2.10	0.48
37:f:17:MET:HE1	37:f:22:TYR:HB2	1.95	0.48
13:E:138:ALA:HA	13:E:141:ASP:HB2	1.96	0.48
12:D:123:MET:HE1	12:D:128:VAL:HG22	1.96	0.48
27:S:40:PHE:HB2	27:S:43:MET:HE1	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:476:G:N1	33:b:479:A:OP2	2.44	0.48
33:b:2480:C:H2'	33:b:2481:G:O4'	2.13	0.48
7:7:62:LEU:HB3	7:7:65:ALA:HB3	1.96	0.48
9:A:85:U:O4'	9:A:86:G:N2	2.46	0.48
9:A:428:G:H5"	12:D:9:LYS:NZ	2.28	0.48
9:A:1086:U:H3	9:A:1099:G:H22	1.61	0.48
9:A:1144:G:N2	9:A:1146:A:H62	2.11	0.48
17:I:21:LYS:O	17:I:61:ASP:N	2.46	0.48
33:b:890:C:H2'	33:b:891:G:H4'	1.95	0.48
33:b:2809:A:H2'	33:b:2810:A:C8	2.49	0.48
34:c:145:GLU:HB2	34:c:188:CYS:HB3	1.96	0.48
5:5:27:LYS:HB2	5:5:28:ARG:NH1	2.28	0.48
16:H:53:ASP:OD1	16:H:53:ASP:N	2.46	0.48
33:b:886:A:O4'	33:b:890:C:N4	2.46	0.48
9:A:2:A:H1'	9:A:613:C:O2'	2.13	0.48
9:A:70:U:O2'	9:A:94:G:N2	2.46	0.48
9:A:203:G:N2	9:A:204:G:O6	2.46	0.48
10:B:62:ARG:HH12	10:B:63:LYS:NZ	2.12	0.48
13:E:79:THR:OG1	13:E:80:LEU:N	2.46	0.48
17:I:62:LEU:O	17:I:64:ILE:HG12	2.13	0.48
31:Y:8:U:O2'	31:Y:22:A:N1	2.44	0.48
33:b:1434:A:H8	33:b:1435:G:N7	2.11	0.48
45:p:115:LEU:HB3	45:p:117:PHE:CD2	2.49	0.48
46:q:68:GLU:N	46:q:68:GLU:OE1	2.47	0.48
9:A:978:A:O2'	9:A:1322:C:H5	1.96	0.48
12:D:187:ARG:HH12	12:D:190:LEU:HB2	1.79	0.48
13:E:74:ALA:O	13:E:80:LEU:HD13	2.14	0.48
13:E:151:MET:O	13:E:155:LYS:HG3	2.14	0.48
28:T:51:ASN:OD1	28:T:51:ASN:N	2.46	0.48
33:b:1425:G:H2'	33:b:1426:G:C8	2.48	0.48
40:k:31:GLU:HG2	40:k:142:ILE:HG22	1.96	0.48
9:A:458:U:O2	9:A:474:G:N2	2.46	0.48
9:A:1151:A:O2'	9:A:1152:A:H5"	2.14	0.48
12:D:30:LYS:HE2	12:D:30:LYS:O	2.14	0.48
16:H:89:ASP:OD1	16:H:89:ASP:N	2.35	0.48
21:M:45:SER:OG	21:M:46:GLU:OE1	2.32	0.48
25:Q:14:ASP:OD1	25:Q:14:ASP:N	2.45	0.48
29:U:4:LYS:HD3	29:U:5:VAL:N	2.28	0.48
33:b:1425:G:O2'	33:b:1426:G:OP1	2.31	0.48
33:b:1734:G:H2'	33:b:1735:A:H8	1.79	0.48
6:6:43:THR:OG1	6:6:44:VAL:N	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:195:A:O2'	9:A:196:A:O5'	2.24	0.47
9:A:222:C:H2'	9:A:223:A:H8	1.79	0.47
9:A:524:G:H2'	9:A:525:C:C6	2.49	0.47
11:C:169:GLU:OE1	11:C:169:GLU:N	2.47	0.47
15:G:142:ARG:NH2	30:X:41:U:O5'	2.44	0.47
16:H:9:MET:HG3	16:H:26:MET:SD	2.54	0.47
31:Z:69:C:H2'	31:Z:70:A:H8	1.79	0.47
33:b:265:A:N6	33:b:428:A:C8	2.82	0.47
33:b:890:C:C4	33:b:891:G:H1'	2.49	0.47
33:b:1062:G:H22	33:b:1088:A:N6	2.11	0.47
33:b:1064:C:N3	33:b:1073:A:H5'	2.29	0.47
37:f:8:TYR:HA	37:f:12:VAL:HB	1.96	0.47
37:f:62:GLY:HA3	37:f:95:ARG:HH21	1.79	0.47
9:A:409:U:OP1	12:D:22:SER:OG	2.30	0.47
9:A:1218:C:H2'	9:A:1219:A:H8	1.79	0.47
14:F:15:SER:HB2	14:F:44:ARG:HH12	1.80	0.47
15:G:82:SER:HB3	15:G:84:TYR:CZ	2.49	0.47
28:T:19:HIS:CD2	28:T:23:ARG:HD3	2.50	0.47
28:T:52:GLU:OE1	28:T:52:GLU:N	2.43	0.47
33:b:286:U:N3	33:b:355:U:O2	2.47	0.47
38:g:170:ARG:H	38:g:170:ARG:HD2	1.80	0.47
9:A:17:U:H2'	9:A:18:C:C6	2.49	0.47
9:A:478:A:C5	9:A:479:U:H1'	2.49	0.47
9:A:530:G:N7	31:Z:36:G:O2'	2.45	0.47
12:D:187:ARG:O	12:D:187:ARG:NH1	2.45	0.47
31:Y:22:A:N6	31:Y:47:G:H2'	2.29	0.47
33:b:27:G:H22	33:b:512:G:H2'	1.79	0.47
33:b:2064:C:H2'	33:b:2065:C:C6	2.50	0.47
4:4:15:MET:HE3	33:b:2045:C:H5"	1.96	0.47
9:A:1405:G:HO2'	9:A:1518:A:HO2'	1.61	0.47
24:P:9:HIS:N	24:P:16:PHE:O	2.46	0.47
31:Y:77:A:O3'	55:z:162:PRO:CA	2.60	0.47
31:Z:28:C:H2'	31:Z:29:U:H6	1.79	0.47
9:A:520:A:H2	9:A:533:A:H61	1.61	0.47
9:A:634:C:H2'	9:A:635:A:C8	2.49	0.47
9:A:737:C:H2'	9:A:738:C:H6	1.79	0.47
17:I:111:GLU:N	17:I:111:GLU:OE1	2.47	0.47
23:O:11:VAL:HG21	23:O:21:THR:HG22	1.97	0.47
33:b:608:A:H2'	33:b:609:A:C8	2.50	0.47
33:b:960:A:H61	43:n:82:MET:HE2	1.78	0.47
33:b:1050:A:N3	33:b:1050:A:H2'	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:1064:C:H41	33:b:1072:C:P	2.38	0.47
33:b:2115:G:O2'	33:b:2166:U:O2	2.32	0.47
33:b:2291:U:H2'	33:b:2292:U:C6	2.50	0.47
55:z:151[B]:LYS:HG2	55:z:152[B]:GLY:H	1.78	0.47
9:A:410:G:H2'	9:A:429:U:C4	2.49	0.47
9:A:1218:C:H2'	9:A:1219:A:C8	2.50	0.47
33:b:1583:A:O2'	33:b:1585:C:N4	2.47	0.47
33:b:1870:C:H2'	33:b:1871:A:C8	2.49	0.47
9:A:376:G:N2	9:A:377:G:C5	2.83	0.47
17:I:53:LEU:H	17:I:53:LEU:HD23	1.79	0.47
18:J:42:LEU:HD12	18:J:42:LEU:HA	1.74	0.47
19:K:44:ALA:HB3	19:K:69:CYS:HB2	1.96	0.47
26:R:64:LEU:HD23	26:R:64:LEU:HA	1.74	0.47
27:S:15:LEU:HA	27:S:18:VAL:HG12	1.97	0.47
30:X:51:G:C4	30:X:52:A:C8	3.03	0.47
31:Y:5:G:H1	31:Y:68:U:H3	1.63	0.47
33:b:368:A:HO2'	33:b:369:U:P	2.37	0.47
33:b:500:G:N1	33:b:503:A:OP2	2.47	0.47
33:b:2133:G:C1'	33:b:2157:G:H22	2.28	0.47
33:b:2327:A:H2'	33:b:2328:A:C8	2.50	0.47
36:e:157:LEU:HD23	36:e:157:LEU:HA	1.74	0.47
37:f:4:LEU:HG	37:f:101:GLU:HG2	1.97	0.47
9:A:478:A:C2'	9:A:479:U:H4'	2.42	0.47
9:A:1318:A:H1'	27:S:36:ARG:HH11	1.80	0.47
10:B:203:ASP:OD1	10:B:203:ASP:N	2.47	0.47
12:D:146:GLU:CD	12:D:146:GLU:H	2.22	0.47
20:L:98:ARG:NH2	20:L:105:GLY:O	2.42	0.47
30:X:48:C:N4	30:X:59:G:O4'	2.47	0.47
33:b:703:U:H2'	33:b:704:G:O4'	2.15	0.47
33:b:885:C:O2'	33:b:886:A:N7	2.47	0.47
33:b:2155:U:H2'	33:b:2156:G:C2	2.50	0.47
33:b:2155:U:H5"	33:b:2156:G:OP1	2.14	0.47
34:c:141:VAL:CG1	34:c:190:ALA:HB1	2.45	0.47
43:n:42:THR:HG22	43:n:44:ARG:H	1.80	0.47
44:o:32:GLU:HG2	44:o:115:LEU:HD12	1.97	0.47
9:A:410:G:H1'	9:A:433:G:N2	2.30	0.47
9:A:432:A:H2'	9:A:433:G:O4'	2.14	0.47
9:A:1020:G:O6	9:A:1021:A:N6	2.48	0.47
9:A:1137:C:H1'	9:A:1138:G:N1	2.30	0.47
12:D:40:HIS:CE1	12:D:43:ARG:HH21	2.33	0.47
14:F:18:VAL:HG21	14:F:58:HIS:CD2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:J:42:LEU:HB3	18:J:71:LEU:HB2	1.96	0.47
33:b:634:C:H2'	33:b:635:C:C6	2.50	0.47
33:b:1534:U:H1'	33:b:1535:A:H2'	1.96	0.47
33:b:1856:U:H2'	33:b:1857:G:O4'	2.15	0.47
33:b:2334:U:O3'	45:p:13:ARG:NH1	2.48	0.47
37:f:116:GLY:HA3	37:f:178:ARG:HB2	1.97	0.47
39:h:53:GLU:O	39:h:57:LYS:HG2	2.15	0.47
50:u:11:LEU:HD22	50:u:32:LEU:HD23	1.97	0.47
9:A:1169:A:H3'	9:A:1170:A:H8	1.80	0.47
17:I:122:ARG:NH1	17:I:123:ARG:O	2.48	0.47
31:Z:61:U:H5"	31:Z:62:C:H5	1.80	0.47
33:b:845:A:C2	33:b:847:U:H1'	2.50	0.47
33:b:1720:U:H2'	33:b:1721:G:O4'	2.15	0.47
48:s:45:GLU:OE1	48:s:45:GLU:N	2.48	0.47
9:A:462:G:H1	9:A:469:C:H41	1.62	0.46
9:A:868:C:H2'	9:A:869:G:O4'	2.14	0.46
9:A:1004:A:H5'	9:A:1025:U:H1'	1.98	0.46
19:K:37:GLN:OE1	19:K:37:GLN:N	2.47	0.46
33:b:2123:G:O6	33:b:2176:A:N6	2.47	0.46
33:b:2139:U:H2'	33:b:2152:G:C6	2.50	0.46
9:A:203:G:O6	9:A:215:C:N4	2.48	0.46
9:A:1450:U:H3'	9:A:1452:C:N4	2.31	0.46
12:D:25:ARG:HD2	12:D:29:THR:HG22	1.97	0.46
16:H:40:LYS:HZ1	16:H:47:ASP:HA	1.80	0.46
33:b:1352:U:O2'	33:b:1570:A:H8	1.83	0.46
45:p:83:LEU:HD23	45:p:115:LEU:HD12	1.96	0.46
9:A:77:A:H2'	9:A:78:A:H4'	1.97	0.46
17:I:51:LEU:HD13	17:I:57:VAL:HB	1.96	0.46
33:b:887:U:H4'	33:b:888:C:H5'	1.97	0.46
33:b:1071:G:N1	33:b:1091:G:OP2	2.48	0.46
9:A:185:U:H2'	9:A:186:C:H6	1.80	0.46
9:A:613:C:P	12:D:80:ARG:HH21	2.39	0.46
12:D:101:VAL:HG13	12:D:113:ALA:HB1	1.97	0.46
17:I:49:GLN:HA	17:I:52:GLU:OE2	2.16	0.46
20:L:24:GLU:N	20:L:24:GLU:OE1	2.48	0.46
31:Z:76:C:H2'	31:Z:77:A:C8	2.50	0.46
33:b:285:G:H8	33:b:285:G:OP2	1.99	0.46
33:b:2305:U:H5"	37:f:131:GLY:HA3	1.96	0.46
49:t:4:ILE:HG13	49:t:106:VAL:HG22	1.97	0.46
50:u:69:ARG:HH21	50:u:74:ILE:HD11	1.80	0.46
9:A:1140:C:H2'	9:A:1141:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:K:96:ILE:HG22	29:U:11:PHE:HZ	1.81	0.46
33:b:358:U:H2'	33:b:359:G:C8	2.51	0.46
33:b:548:G:H5"	33:b:549:G:OP2	2.16	0.46
33:b:1051:G:C2	33:b:1052:C:N4	2.83	0.46
9:A:613:C:H2'	9:A:614:C:H6	1.81	0.46
9:A:637:C:H2'	9:A:638:U:C6	2.51	0.46
13:E:57:ALA:O	13:E:60:GLN:HG3	2.16	0.46
21:M:49:GLU:HA	21:M:52:ILE:HB	1.98	0.46
30:X:8:U:H1'	30:X:48:C:O2	2.15	0.46
33:b:2114:A:H61	33:b:2117:A:H62	1.63	0.46
33:b:2335:A:OP1	45:p:13:ARG:NH2	2.46	0.46
33:b:2857:G:H5'	33:b:2858:C:OP2	2.16	0.46
12:D:176:LYS:H	12:D:176:LYS:HD2	1.80	0.46
14:F:73:GLU:HA	14:F:76:THR:HB	1.98	0.46
21:M:10:ASP:HA	21:M:44:ILE:HB	1.97	0.46
25:Q:67:SER:HB3	25:Q:70:LYS:HB2	1.98	0.46
31:Z:48:U:H4'	31:Z:49:C:H5'	1.98	0.46
33:b:79:C:O2'	33:b:346:A:H8	1.98	0.46
33:b:974:G:H8	33:b:990:A:H62	1.64	0.46
33:b:1528:A:N6	33:b:1543:G:O2'	2.49	0.46
33:b:2071:A:H2'	33:b:2072:C:C6	2.51	0.46
36:e:5:LEU:HD22	36:e:8:ALA:HB3	1.97	0.46
45:p:69:ASP:OD1	45:p:69:ASP:N	2.47	0.46
9:A:449:G:O6	9:A:486:U:C4	2.69	0.46
10:B:116:LEU:HD11	10:B:136:ARG:HD3	1.98	0.46
15:G:15:PRO:HB2	17:I:45:MET:HE2	1.97	0.46
27:S:28:LYS:HD2	27:S:29:PRO:HD2	1.98	0.46
31:Z:7:U:H5	31:Z:67:A:N1	2.14	0.46
9:A:461:A:H2'	9:A:462:G:C8	2.51	0.46
9:A:967:C:H2'	9:A:968:A:C2	2.51	0.46
15:G:78:ARG:HB2	15:G:83:THR:HA	1.97	0.46
18:J:7:ARG:HE	18:J:7:ARG:H	1.63	0.46
25:Q:60:ILE:HG22	25:Q:74:LEU:HA	1.98	0.46
33:b:90:U:H2'	33:b:91:A:C2	2.50	0.46
33:b:2182:U:H2'	33:b:2183:A:N3	2.30	0.46
33:b:2790:U:H5"	33:b:2791:G:OP1	2.16	0.46
34:c:145:GLU:HG2	34:c:151:GLY:C	2.41	0.46
42:m:96:LYS:HG3	42:m:101:ILE:HD11	1.98	0.46
50:u:44:LYS:O	50:u:48:GLN:HG2	2.16	0.46
7:7:14:PHE:O	7:7:15:LYS:CG	2.64	0.46
9:A:235:C:H2'	9:A:236:A:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:539:A:H2'	9:A:540:G:C8	2.51	0.46
12:D:171:GLU:HB2	12:D:180:THR:HG22	1.97	0.46
26:R:33:THR:HG22	26:R:37:LYS:H	1.80	0.46
29:U:19:LYS:HE2	29:U:20:ARG:HH21	1.80	0.46
30:X:30:C:N4	30:X:39:G:H1	2.13	0.46
33:b:742:A:H2'	33:b:743:A:C8	2.51	0.46
33:b:2122:U:H2'	33:b:2123:G:C8	2.51	0.46
11:C:26:LYS:HE2	11:C:26:LYS:HB2	1.84	0.45
18:J:77:VAL:HG13	18:J:78:GLU:OE1	2.16	0.45
33:b:2193:G:H2'	33:b:2194:U:C6	2.52	0.45
38:g:45:HIS:ND1	38:g:49:THR:O	2.43	0.45
45:p:35:ILE:HG22	45:p:53:THR:HG23	1.98	0.45
45:p:115:LEU:HB3	45:p:117:PHE:HD2	1.81	0.45
9:A:462:G:H2'	9:A:463:U:H6	1.81	0.45
33:b:593:U:H2'	33:b:594:U:C6	2.51	0.45
33:b:639:U:H2'	33:b:640:C:C6	2.50	0.45
33:b:2591:C:H2'	33:b:2592:G:C8	2.51	0.45
33:b:2682:A:H61	33:b:2728:U:H1'	1.82	0.45
40:k:98:GLU:H	40:k:98:GLU:CD	2.24	0.45
4:4:40:ARG:HE	33:b:2815:C:H1'	1.80	0.45
34:c:259:SER:O	34:c:259:SER:OG	2.34	0.45
36:e:145:ASP:N	36:e:145:ASP:OD1	2.49	0.45
4:4:32:LYS:HG3	4:4:33:THR:HG23	1.98	0.45
9:A:424:G:H2'	9:A:425:G:C8	2.52	0.45
27:S:15:LEU:HD23	27:S:16:LYS:HD2	1.98	0.45
33:b:1589:U:H2'	33:b:1590:A:H8	1.82	0.45
33:b:1649:G:O2'	44:o:106:ASP:OD2	2.30	0.45
37:f:80:ARG:HB2	37:f:83:TYR:CZ	2.52	0.45
9:A:37:U:O2'	9:A:547:A:N1	2.44	0.45
9:A:1071:C:H2'	9:A:1072:G:C8	2.46	0.45
9:A:1144:G:O6	9:A:1145:A:N6	2.50	0.45
17:I:109:GLN:N	17:I:109:GLN:OE1	2.49	0.45
33:b:827:U:O2'	33:b:2068:U:C2	2.70	0.45
7:7:55:LEU:HD12	7:7:59:ILE:HD11	1.99	0.45
9:A:377:G:HO2'	9:A:378:G:H8	1.65	0.45
10:B:145:ASN:OD1	10:B:146:SER:N	2.50	0.45
12:D:59:LYS:O	12:D:63:ILE:HG23	2.16	0.45
14:F:2:ARG:HD3	14:F:91:ARG:NE	2.32	0.45
40:k:9:GLU:OE1	40:k:9:GLU:N	2.32	0.45
51:v:18:ASP:OD1	51:v:18:ASP:N	2.49	0.45
4:4:40:ARG:NH2	33:b:2815:C:O4'	2.27	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:8:A:N6	12:D:201:GLU:O	2.49	0.45
9:A:323:U:H2'	9:A:324:G:O4'	2.17	0.45
9:A:1250:A:H2'	9:A:1251:A:C8	2.51	0.45
9:A:1250:A:H4'	17:I:69:GLY:H	1.80	0.45
12:D:45:PRO:HB2	12:D:47:LEU:HG	1.98	0.45
19:K:27:ASN:O	19:K:56:LYS:HE3	2.17	0.45
24:P:22:ALA:HA	24:P:33:ILE:HD12	1.98	0.45
28:T:14:GLU:O	28:T:18:LYS:HG2	2.17	0.45
33:b:2192:U:H2'	33:b:2193:G:C8	2.51	0.45
36:e:191:ASP:OD1	36:e:191:ASP:N	2.48	0.45
45:p:77:ALA:O	45:p:80:GLU:HG3	2.17	0.45
46:q:30:VAL:HG13	46:q:80:VAL:HG12	1.99	0.45
9:A:297:G:N2	9:A:300:A:OP2	2.44	0.45
9:A:721:G:H4'	9:A:722:G:O4'	2.17	0.45
9:A:875:U:O2'	16:H:14:ARG:NH1	2.49	0.45
9:A:1030:U:OP2	9:A:1031:C:N4	2.49	0.45
14:F:38:ARG:HB2	14:F:63:ASN:HB2	1.98	0.45
16:H:23:ALA:HB1	16:H:59:GLU:OE2	2.17	0.45
28:T:84:LYS:HG3	28:T:85:LEU:HG	1.99	0.45
33:b:1794:A:H2'	33:b:1795:C:C6	2.52	0.45
33:b:2135:A:H3'	33:b:2136:G:C4	2.52	0.45
33:b:2294:G:P	45:p:94:ARG:HH22	2.40	0.45
9:A:1106:G:H5"	11:C:171:ARG:HG2	1.98	0.45
10:B:83:ALA:C	10:B:85:SER:H	2.25	0.45
18:J:9:ARG:HB2	18:J:99:GLN:NE2	2.29	0.45
28:T:50:PHE:O	28:T:53:MET:HG3	2.17	0.45
33:b:1394:U:H2'	33:b:1395:A:O4'	2.17	0.45
4:4:54:VAL:HG12	4:4:55:ILE:N	2.32	0.45
5:5:33:LYS:HE2	5:5:51:GLU:OE1	2.17	0.45
9:A:1125:U:H5"	18:J:37:ARG:NH2	2.32	0.45
10:B:115:ASP:O	10:B:118:THR:OG1	2.31	0.45
10:B:122:ASP:N	10:B:122:ASP:OD1	2.50	0.45
35:d:148:GLN:HB2	35:d:152:PRO:HG3	1.98	0.45
9:A:259:G:C4	9:A:260:G:C8	3.05	0.44
12:D:101:VAL:HG22	12:D:106:PHE:HB2	1.99	0.44
12:D:186:GLU:HG2	12:D:188:SER:N	2.27	0.44
28:T:26:MET:O	28:T:29:THR:OG1	2.32	0.44
31:Z:5:G:H2'	31:Z:6:A:C8	2.52	0.44
32:a:31:C:O2'	32:a:53:A:N1	2.42	0.44
33:b:1738:G:O2'	33:b:1739:A:H8	2.00	0.44
33:b:2111:U:OP2	33:b:2118:U:O2'	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:2273:A:H2'	33:b:2274:A:C8	2.52	0.44
47:r:100:VAL:O	47:r:103:LYS:NZ	2.50	0.44
9:A:445:G:H2'	9:A:446:G:H8	1.79	0.44
12:D:49:ASP:OD1	12:D:50:TYR:N	2.49	0.44
33:b:2173:A:H2'	33:b:2174:C:C6	2.52	0.44
33:b:2181:U:H2'	33:b:2182:U:C6	2.52	0.44
49:t:84:ARG:O	49:t:95:ARG:HD3	2.17	0.44
9:A:553:A:H2'	9:A:554:A:H8	1.82	0.44
9:A:1477:U:H2'	9:A:1478:U:C6	2.52	0.44
33:b:571:U:H3'	48:s:80:ARG:NH2	2.33	0.44
38:g:164:TYR:HB2	38:g:167:GLU:HG2	1.99	0.44
46:q:8:LEU:HD23	46:q:8:LEU:HA	1.83	0.44
50:u:54:GLU:OE2	50:u:91:GLN:NE2	2.31	0.44
2:1:28:LEU:HD23	2:1:28:LEU:HA	1.81	0.44
5:5:25:LYS:NZ	5:5:32:GLU:O	2.29	0.44
9:A:81:A:N6	9:A:88:U:O4	2.51	0.44
9:A:435:A:H2'	9:A:436:C:C6	2.51	0.44
17:I:66:VAL:HB	17:I:78:ILE:HD11	2.00	0.44
41:l:108:ARG:HG3	41:l:113:MET:HE1	1.98	0.44
9:A:424:G:H2'	9:A:425:G:H8	1.83	0.44
13:E:89:THR:OG1	13:E:134:ASN:ND2	2.51	0.44
18:J:11:LYS:HA	18:J:70:HIS:O	2.17	0.44
33:b:547:A:H3'	33:b:548:G:C8	2.53	0.44
33:b:1057:A:N6	33:b:1088:A:OP2	2.51	0.44
33:b:1087:G:N7	33:b:1102:C:N4	2.65	0.44
33:b:1198:U:H2'	33:b:1199:U:C6	2.51	0.44
33:b:2038:G:H2'	33:b:2039:U:O4'	2.17	0.44
40:k:60:ASP:OD1	40:k:60:ASP:N	2.37	0.44
2:1:38:GLN:OE1	2:1:38:GLN:N	2.42	0.44
9:A:246:A:C2	9:A:282:A:C5	3.05	0.44
12:D:196:GLU:OE1	12:D:196:GLU:N	2.39	0.44
14:F:9:MET:HA	14:F:58:HIS:O	2.17	0.44
15:G:16:LYS:HG3	15:G:17:PHE:CD2	2.53	0.44
17:I:32:ARG:NH2	17:I:37:TYR:HA	2.33	0.44
17:I:129:ARG:HH21	31:Y:36:G:P	2.40	0.44
19:K:79:LYS:HD2	19:K:80:ASN:N	2.33	0.44
19:K:113:THR:OG1	29:U:27:VAL:HG11	2.17	0.44
26:R:33:THR:OG1	26:R:34:GLU:OE1	2.32	0.44
30:X:15:G:N2	30:X:48:C:N4	2.55	0.44
31:Z:51:G:H1	31:Z:65:C:N4	2.15	0.44
33:b:1083:U:C2	33:b:1085:A:H5"	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:h:71:LYS:O	39:h:75:LEU:HG	2.18	0.44
39:h:135:HIS:CG	39:h:136:SER:H	2.35	0.44
46:q:6:LYS:HE3	46:q:6:LYS:HB3	1.81	0.44
9:A:384:G:H2'	9:A:385:C:H6	1.83	0.44
9:A:1181:G:O2'	9:A:1182:G:N7	2.47	0.44
32:a:57:A:C4	37:f:26:MET:HE1	2.53	0.44
33:b:959:A:H2'	33:b:960:A:C8	2.52	0.44
33:b:1727:C:H2'	33:b:1728:C:C6	2.52	0.44
45:p:60:GLU:H	45:p:60:GLU:CD	2.24	0.44
51:v:54:GLN:N	51:v:55:PRO:HD3	2.33	0.44
11:C:48:LYS:HD3	11:C:48:LYS:HA	1.82	0.44
25:Q:18:LYS:O	25:Q:46:HIS:ND1	2.43	0.44
30:X:39:G:N3	30:X:39:G:H2'	2.33	0.44
41:l:7:MET:HE3	41:l:7:MET:HB3	1.80	0.44
44:o:36:THR:HG22	44:o:37:THR:H	1.82	0.44
9:A:199:A:H2'	9:A:200:G:C8	2.52	0.44
9:A:235:C:H2'	9:A:236:A:C8	2.52	0.44
15:G:55:LYS:HB3	15:G:59:GLU:HB2	1.98	0.44
17:I:26:LYS:O	17:I:62:LEU:HB2	2.18	0.44
30:X:27:C:H2'	30:X:28:G:C8	2.52	0.44
33:b:1054:A:N7	33:b:1055:G:N1	2.65	0.44
33:b:1453:A:H62	44:o:74:GLU:CD	2.20	0.44
39:h:81:ALA:HB2	39:h:149:GLU:HG3	2.00	0.44
4:4:9:THR:HG21	33:b:2020:A:H5'	2.00	0.43
9:A:275:G:H4'	25:Q:15:LYS:NZ	2.33	0.43
9:A:942:G:N2	17:I:125:GLN:OE1	2.50	0.43
9:A:1005:A:N7	9:A:1006:G:H1'	2.32	0.43
16:H:25:THR:HG23	16:H:57:GLU:OE2	2.18	0.43
21:M:80:MET:HE2	21:M:80:MET:HB2	1.88	0.43
26:R:70:THR:H	26:R:73:HIS:CE1	2.35	0.43
31:Y:47:G:H4'	31:Y:48:U:C5	2.53	0.43
31:Z:11:C:H2'	31:Z:12:G:C8	2.53	0.43
33:b:181:A:H2'	33:b:182:A:C8	2.53	0.43
33:b:715:A:O2'	33:b:716:A:O5'	2.36	0.43
33:b:2159:G:H2'	33:b:2160:C:H6	1.83	0.43
33:b:2474:U:H5"	33:b:2475:C:H5	1.83	0.43
48:s:49:ILE:HD12	48:s:49:ILE:O	2.18	0.43
9:A:512:U:H2'	9:A:513:C:C6	2.54	0.43
9:A:674:G:H2'	9:A:675:A:C8	2.53	0.43
11:C:109:GLU:OE1	11:C:109:GLU:N	2.48	0.43
17:I:49:GLN:OE1	17:I:79:ARG:NH1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:59:LYS:HE2	17:I:59:LYS:HB2	1.77	0.43
33:b:1417:C:O2'	33:b:1587:G:O2'	2.27	0.43
33:b:2119:A:C2	33:b:2169:A:H2'	2.53	0.43
50:u:3:ARG:HG2	50:u:5:GLU:H	1.83	0.43
5:5:23:THR:OG1	5:5:24:THR:N	2.50	0.43
9:A:403:C:H2'	9:A:404:G:C8	2.53	0.43
9:A:1219:A:H2'	9:A:1220:G:C8	2.53	0.43
13:E:143:LEU:HD23	13:E:143:LEU:HA	1.81	0.43
14:F:74:LEU:O	14:F:77:THR:OG1	2.30	0.43
30:X:9:A:H61	30:X:22:G:H2'	1.83	0.43
33:b:589:U:H2'	33:b:590:A:C8	2.52	0.43
33:b:1115:G:H2'	33:b:1116:G:C8	2.50	0.43
33:b:2102:G:N1	33:b:2187:U:O2	2.50	0.43
33:b:2166:U:H2'	33:b:2167:U:C6	2.53	0.43
43:n:119:LEU:HD12	43:n:119:LEU:HA	1.85	0.43
9:A:408:A:C6	9:A:409:U:C4	3.06	0.43
9:A:592:G:H2'	9:A:593:U:H6	1.82	0.43
9:A:750:C:O2'	23:O:20:ASP:O	2.32	0.43
9:A:967:C:OP2	9:A:968:A:O2'	2.20	0.43
9:A:1391:U:H2'	9:A:1392:G:C8	2.54	0.43
10:B:131:LYS:O	10:B:135:MET:HG3	2.17	0.43
31:Y:17:C:H5"	31:Y:18:U:H2'	1.99	0.43
33:b:287:G:H2'	33:b:288:U:H6	1.83	0.43
35:d:146:ILE:HD13	35:d:146:ILE:HA	1.82	0.43
42:m:2:ARG:HD3	42:m:2:ARG:HA	1.83	0.43
50:u:24:MET:HE3	50:u:30:ILE:HG22	2.01	0.43
9:A:193:C:O4'	28:T:54:GLN:NE2	2.51	0.43
9:A:264:C:O2'	25:Q:65:PRO:O	2.36	0.43
9:A:1375:A:OP1	15:G:24:LYS:NZ	2.38	0.43
13:E:95:MET:HE3	13:E:95:MET:HB2	1.83	0.43
23:O:79:GLN:HE22	23:O:83:ARG:HD2	1.83	0.43
25:Q:80:LYS:NZ	25:Q:81:ALA:O	2.51	0.43
31:Z:24:C:H2'	31:Z:25:G:C8	2.53	0.43
33:b:78:U:H2'	33:b:79:C:C6	2.53	0.43
33:b:1114:C:H2'	33:b:1115:G:C8	2.54	0.43
33:b:1490:A:H5"	33:b:1491:G:OP2	2.19	0.43
33:b:1796:U:H2'	33:b:1797:G:C8	2.53	0.43
36:e:21:ARG:HD3	36:e:106:LYS:HB3	2.01	0.43
39:h:1:MET:N	39:h:20:ASN:OD1	2.42	0.43
9:A:715:A:H2'	9:A:716:A:C8	2.54	0.43
12:D:145:ARG:O	12:D:149:LYS:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:47:GLU:HG3	15:G:48:THR:N	2.34	0.43
31:Y:18:U:O2'	31:Y:19:G:O5'	2.30	0.43
33:b:2:G:H2'	33:b:3:U:C6	2.54	0.43
33:b:277:G:H5"	33:b:278:A:H5'	1.99	0.43
38:g:38:ASN:OD1	38:g:39:ASP:N	2.52	0.43
42:m:20:GLY:HA2	42:m:28:GLY:HA2	2.01	0.43
9:A:522:C:H5	20:L:49:ARG:HH22	1.65	0.43
9:A:1294:G:H2'	9:A:1295:U:C6	2.54	0.43
12:D:196:GLU:H	12:D:196:GLU:CD	2.23	0.43
17:I:112:ARG:HE	17:I:112:ARG:HB3	1.48	0.43
18:J:14:ASP:OD1	18:J:15:HIS:N	2.52	0.43
18:J:15:HIS:NE2	18:J:19:ASP:OD2	2.52	0.43
18:J:53:ILE:HG23	18:J:63:ASP:OD1	2.18	0.43
25:Q:76:ARG:HE	25:Q:78:VAL:HG12	1.82	0.43
31:Y:56:U:O2'	31:Y:58:G:N7	2.48	0.43
33:b:39:G:H2'	33:b:40:U:O2	2.19	0.43
33:b:2159:G:H2'	33:b:2160:C:C6	2.54	0.43
33:b:2281:A:O2'	33:b:2282:G:H5'	2.17	0.43
34:c:183:LYS:HB3	34:c:183:LYS:HE2	1.87	0.43
9:A:459:A:H62	9:A:474:G:H21	1.65	0.43
9:A:462:G:H1	9:A:469:C:N4	2.15	0.43
15:G:106:ALA:HB1	15:G:132:THR:HG23	1.99	0.43
33:b:2188:U:H2'	33:b:2189:U:N1	2.33	0.43
37:f:51:ASP:OD1	37:f:51:ASP:N	2.50	0.43
43:n:111:GLU:O	43:n:115:GLU:HG2	2.18	0.43
47:r:112:LYS:HE3	47:r:112:LYS:HB2	1.82	0.43
52:w:34:LYS:HB2	52:w:34:LYS:HE2	1.74	0.43
55:z:153[A]:SER:HB3	55:z:155[A]:TRP:HE1	1.82	0.43
9:A:202:G:H2'	9:A:203:G:H5'	2.00	0.43
9:A:217:C:H4'	9:A:218:U:C5	2.53	0.43
9:A:262:A:H2'	9:A:263:A:C8	2.53	0.43
9:A:271:C:H2'	9:A:272:C:H6	1.83	0.43
9:A:555:U:H2'	9:A:556:C:C6	2.54	0.43
9:A:1010:U:H2'	9:A:1011:C:C6	2.54	0.43
10:B:209:VAL:O	10:B:213:LEU:HG	2.18	0.43
14:F:43:GLY:HA2	14:F:58:HIS:CD2	2.53	0.43
21:M:10:ASP:O	21:M:43:LYS:HB3	2.19	0.43
31:Z:26:C:C2	31:Z:27:A:C8	3.07	0.43
33:b:718:A:H5"	33:b:719:C:C5	2.53	0.43
33:b:740:C:N4	33:b:757:G:H1	2.17	0.43
37:f:74:VAL:H	37:f:79:ILE:HG13	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:g:24:ILE:HD13	38:g:72:LEU:HD11	2.00	0.43
42:m:91:ASP:OD1	42:m:92:LEU:N	2.52	0.43
9:A:189:A:H8	9:A:189:A:OP2	2.02	0.43
9:A:648:A:H2'	9:A:649:A:C8	2.54	0.43
10:B:62:ARG:HH12	10:B:63:LYS:HZ3	1.66	0.43
11:C:63:ILE:HG22	11:C:96:VAL:HG23	2.01	0.43
22:N:64:ARG:HG2	22:N:77:GLY:O	2.19	0.43
33:b:1062:G:H2'	33:b:1063:G:C8	2.53	0.43
34:c:145:GLU:OE2	34:c:151:GLY:N	2.48	0.43
37:f:38:MET:SD	37:f:53:ALA:HB1	2.58	0.43
48:s:48:LYS:HE2	48:s:48:LYS:HB3	1.74	0.43
50:u:20:ALA:O	50:u:24:MET:HG3	2.19	0.43
9:A:389:A:C2	9:A:390:U:H2'	2.54	0.42
9:A:553:A:H2'	9:A:554:A:C8	2.54	0.42
9:A:1027:C:C2	9:A:1035:A:C6	3.07	0.42
9:A:1273:C:H2'	9:A:1274:A:O4'	2.19	0.42
9:A:1371:G:H2'	9:A:1372:U:C6	2.53	0.42
32:a:42:C:C5	37:f:66:LEU:HD23	2.54	0.42
33:b:833:A:H2'	33:b:834:G:C8	2.54	0.42
33:b:974:G:H2'	33:b:974:G:N3	2.34	0.42
33:b:1077:A:H1'	33:b:1088:A:C6	2.54	0.42
33:b:2271:G:OP1	54:y:18:ALA:HB1	2.19	0.42
34:c:23:GLU:N	34:c:23:GLU:OE1	2.52	0.42
37:f:140:GLU:OE1	37:f:140:GLU:N	2.51	0.42
48:s:55:ASP:OD1	48:s:56:GLY:N	2.52	0.42
6:6:25:LYS:HB2	6:6:25:LYS:HE3	1.65	0.42
9:A:1125:U:C2	9:A:1127:G:C8	3.07	0.42
9:A:1343:G:H2'	9:A:1344:C:C6	2.54	0.42
12:D:55:ARG:HA	12:D:55:ARG:NE	2.34	0.42
14:F:10:VAL:HB	14:F:58:HIS:HB3	2.01	0.42
18:J:15:HIS:O	18:J:18:ILE:HG22	2.18	0.42
27:S:2:ARG:HH21	27:S:6:LYS:HE2	1.83	0.42
28:T:34:VAL:HG21	28:T:53:MET:HG2	2.01	0.42
31:Y:5:G:N2	31:Y:69:C:C2	2.87	0.42
31:Y:19:G:H1	31:Y:56:U:H1'	1.83	0.42
33:b:1504:A:H2'	33:b:1504:A:N3	2.34	0.42
33:b:2187:U:OP2	33:b:2187:U:H3'	2.18	0.42
33:b:2485:G:OP1	43:n:45:GLN:NE2	2.45	0.42
36:e:129:PRO:O	36:e:130:LYS:HD2	2.19	0.42
9:A:222:C:H2'	9:A:223:A:C8	2.55	0.42
9:A:262:A:O2'	9:A:263:A:P	2.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:539:A:H2'	9:A:540:G:H8	1.85	0.42
12:D:176:LYS:HB3	12:D:176:LYS:HE3	1.86	0.42
16:H:4:ASP:OD2	16:H:76:ARG:NH2	2.49	0.42
32:a:13:G:O2'	32:a:15:A:OP2	2.30	0.42
32:a:106:G:H2'	32:a:107:G:O4'	2.19	0.42
33:b:1205:A:O2'	33:b:1206:G:OP1	2.34	0.42
41:l:92:GLU:HG2	41:l:111:LYS:NZ	2.35	0.42
9:A:195:A:H2'	9:A:196:A:C8	2.54	0.42
9:A:203:G:N2	9:A:465:A:H61	2.18	0.42
9:A:263:A:H2'	9:A:264:C:C5	2.54	0.42
16:H:88:LYS:HG3	16:H:119:GLY:C	2.44	0.42
29:U:7:GLU:HB3	29:U:8:ASN:H	1.69	0.42
33:b:2467:C:H2'	33:b:2468:A:O4'	2.19	0.42
33:b:2808:G:HO2'	33:b:2809:A:H8	1.64	0.42
37:f:3:LYS:HG2	37:f:101:GLU:OE2	2.19	0.42
5:5:28:ARG:HA	5:5:28:ARG:NE	2.34	0.42
9:A:56:U:H2'	9:A:57:G:C8	2.55	0.42
9:A:227:G:H2'	9:A:228:A:C8	2.54	0.42
9:A:229:U:O2'	24:P:23:ASP:OD2	2.27	0.42
26:R:21:ASP:OD1	26:R:23:LYS:N	2.35	0.42
30:X:49:G:H2'	30:X:50:C:O4'	2.19	0.42
33:b:721:A:H2'	33:b:722:A:C8	2.54	0.42
33:b:880:G:H1'	33:b:898:C:O2	2.19	0.42
33:b:1735:A:H2'	33:b:1736:U:C6	2.54	0.42
33:b:2126:A:H61	33:b:2162:G:C4'	2.32	0.42
33:b:2848:G:HO2'	33:b:2849:U:P	2.40	0.42
37:f:57:LEU:HD23	37:f:57:LEU:HA	1.89	0.42
38:g:154:PRO:HA	38:g:160:LYS:O	2.19	0.42
45:p:7:ARG:NH2	45:p:95:SER:O	2.47	0.42
3:2:40:ASP:OD2	3:2:45:ARG:NH2	2.48	0.42
13:E:137:ARG:O	13:E:141:ASP:N	2.46	0.42
17:I:21:LYS:HB3	17:I:61:ASP:HB2	2.00	0.42
21:M:47:LEU:HD12	21:M:47:LEU:HA	1.93	0.42
24:P:70:ARG:HD2	24:P:70:ARG:HA	1.82	0.42
33:b:191:A:H2'	33:b:192:C:H6	1.84	0.42
34:c:133:ARG:NH2	34:c:187:ASP:OD1	2.51	0.42
36:e:155:GLU:OE1	36:e:155:GLU:N	2.42	0.42
51:v:48:PRO:HG3	51:v:56:GLY:HA3	2.01	0.42
1:0:77:LYS:HD3	1:0:78:TYR:N	2.35	0.42
9:A:69:G:H2'	9:A:70:U:C6	2.54	0.42
9:A:1126:U:P	18:J:5:ARG:HH12	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Q:17:GLU:OE1	25:Q:17:GLU:N	2.41	0.42
36:e:5:LEU:HD23	36:e:6:LYS:N	2.35	0.42
49:t:92:ARG:HE	49:t:92:ARG:HB3	1.68	0.42
9:A:411:A:N6	9:A:429:U:O5'	2.52	0.42
9:A:458:U:H3	9:A:474:G:H22	1.67	0.42
15:G:52:ARG:HH22	15:G:121:ASN:HA	1.84	0.42
16:H:21:LYS:O	16:H:64:TYR:OH	2.29	0.42
16:H:70:VAL:HG23	16:H:71:VAL:HG13	2.01	0.42
19:K:12:ARG:HB3	19:K:13:LYS:NZ	2.35	0.42
22:N:47:LEU:HD12	22:N:50:LEU:HD12	2.02	0.42
28:T:7:LYS:O	28:T:11:ILE:HG13	2.20	0.42
32:a:51:G:H5'	45:p:64:TYR:CD2	2.55	0.42
33:b:181:A:H2'	33:b:182:A:H8	1.84	0.42
33:b:1000:A:H2'	33:b:1001:A:C8	2.55	0.42
33:b:1090:A:C2	33:b:1101:U:C2	3.08	0.42
33:b:1542:U:H2'	33:b:1543:G:O4'	2.20	0.42
46:q:82:ASP:N	46:q:82:ASP:OD1	2.52	0.42
9:A:514:C:C2	9:A:515:G:C8	3.08	0.42
9:A:976:G:N2	9:A:1362:A:O2'	2.53	0.42
10:B:130:LYS:HD3	10:B:130:LYS:HA	1.83	0.42
33:b:709:U:H2'	33:b:710:U:C6	2.55	0.42
33:b:1062:G:N1	33:b:1088:A:C5	2.88	0.42
33:b:2547:A:H2'	33:b:2548:U:C6	2.55	0.42
33:b:2638:G:H1'	33:b:2778:A:H61	1.84	0.42
33:b:2849:U:N3	33:b:2867:G:O4'	2.53	0.42
36:e:23:PHE:CE1	42:m:1:MET:HE3	2.54	0.42
44:o:106:ASP:OD1	44:o:106:ASP:N	2.50	0.42
9:A:642:A:C5	16:H:106:SER:HA	2.55	0.42
9:A:1187:G:HO2'	9:A:1188:A:P	2.42	0.42
9:A:1317:C:OP2	22:N:27:LYS:NZ	2.46	0.42
15:G:134:VAL:HB	15:G:135:LYS:NZ	2.35	0.42
17:I:51:LEU:HD23	17:I:51:LEU:HA	1.87	0.42
31:Z:11:C:H2'	31:Z:12:G:H8	1.85	0.42
33:b:1069:A:OP2	33:b:1095:A:N6	2.53	0.42
36:e:123:LYS:HE2	36:e:123:LYS:HB2	1.94	0.42
44:o:72:ASP:HB3	44:o:75:ILE:HD12	2.01	0.42
53:x:22:A:O2'	53:x:23:A:H5'	2.20	0.42
9:A:636:U:H2'	9:A:637:C:C6	2.55	0.41
9:A:1427:C:H2'	9:A:1428:A:C8	2.55	0.41
10:B:221:ARG:HA	10:B:224:ARG:HH21	1.85	0.41
16:H:26:MET:N	16:H:57:GLU:OE2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Q:30:HIS:CE1	25:Q:32:ILE:HB	2.55	0.41
30:X:10:G:OP1	30:X:45:G:O2'	2.26	0.41
33:b:1074:G:H8	33:b:1074:G:OP1	2.01	0.41
37:f:40:VAL:HG11	37:f:43:ALA:HB2	2.01	0.41
39:h:57:LYS:HA	39:h:57:LYS:HD3	1.88	0.41
2:1:44:LYS:O	2:1:48:ARG:HG2	2.20	0.41
9:A:436:C:H2'	9:A:437:U:H6	1.82	0.41
11:C:39:ARG:NH1	22:N:91:GLU:OE1	2.53	0.41
14:F:32:ALA:HB1	14:F:70:VAL:HG21	2.01	0.41
15:G:84:TYR:O	15:G:86:VAL:HG13	2.20	0.41
17:I:11:ARG:HG3	17:I:12:LYS:HG3	2.01	0.41
20:L:64:SER:OG	20:L:65:TYR:N	2.52	0.41
21:M:32:ILE:HD11	21:M:62:PHE:HE2	1.85	0.41
30:X:56:C:O2	33:b:2112:G:N2	2.53	0.41
33:b:172:A:H2'	33:b:173:A:C8	2.55	0.41
33:b:1051:G:H4'	33:b:1052:C:OP1	2.20	0.41
33:b:1713:A:C4	33:b:1716:U:H1'	2.55	0.41
35:d:12:THR:OG1	35:d:13:ARG:N	2.51	0.41
35:d:29:VAL:O	35:d:185:ASN:HB3	2.21	0.41
37:f:46:ASP:OD1	37:f:48:LYS:HE2	2.20	0.41
9:A:262:A:HO2'	9:A:263:A:P	2.40	0.41
9:A:696:A:H2'	9:A:697:U:H6	1.86	0.41
9:A:1024:G:H2'	9:A:1025:U:C6	2.55	0.41
9:A:1323:G:H2'	9:A:1324:A:C8	2.53	0.41
9:A:1412:C:H2'	9:A:1413:A:H8	1.83	0.41
10:B:89:PHE:HB3	10:B:149:GLY:O	2.19	0.41
14:F:47:LEU:HD13	14:F:49:TYR:O	2.19	0.41
18:J:14:ASP:OD1	18:J:16:ARG:N	2.52	0.41
19:K:82:GLU:HB2	19:K:108:ASN:HB2	2.01	0.41
19:K:87:GLY:H	19:K:113:THR:HG22	1.85	0.41
26:R:35:SER:HA	26:R:71:ASP:HB3	2.03	0.41
31:Y:19:G:HO2'	31:Y:58:G:N2	2.18	0.41
33:b:352:A:H2'	33:b:353:C:C6	2.55	0.41
33:b:547:A:H2'	33:b:548:G:H5'	2.02	0.41
33:b:2313:C:H2'	33:b:2314:A:H8	1.84	0.41
37:f:34:ILE:HG12	37:f:156:ILE:HG13	2.02	0.41
41:l:114:LYS:HB2	41:l:114:LYS:HE2	1.84	0.41
52:w:55:GLU:OE1	52:w:55:GLU:N	2.30	0.41
9:A:402:G:O2'	12:D:131:ILE:HD11	2.20	0.41
9:A:440:C:C2	9:A:441:A:C8	3.08	0.41
9:A:538:G:OP1	20:L:109:ARG:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:538:G:P	20:L:111:GLN:HE22	2.43	0.41
9:A:1238:A:H2	9:A:1241:G:N3	2.19	0.41
13:E:140:ILE:H	13:E:140:ILE:HG13	1.63	0.41
15:G:139:ASP:OD1	15:G:140:VAL:N	2.54	0.41
27:S:30:LEU:HB2	27:S:48:ILE:HD13	2.03	0.41
32:a:45:A:O4'	37:f:92:ARG:NH1	2.54	0.41
33:b:1007:C:OP1	40:k:37:ARG:NH1	2.53	0.41
33:b:1548:A:H2'	33:b:1549:A:C8	2.56	0.41
33:b:1808:A:H3'	33:b:1809:A:C8	2.55	0.41
36:e:145:ASP:HB3	36:e:166:LYS:HB3	2.02	0.41
37:f:96:MET:HE3	37:f:96:MET:HB2	1.78	0.41
39:h:40:THR:O	39:h:44:ILE:HG13	2.21	0.41
47:r:15:LYS:HE3	47:r:15:LYS:HB3	1.90	0.41
1:0:28:ARG:NH2	33:b:1365:A:H5"	2.34	0.41
3:2:54:MET:HE3	3:2:54:MET:HB2	1.89	0.41
9:A:144:G:H2'	9:A:145:G:O4'	2.20	0.41
9:A:843:U:H5"	9:A:844:G:C5	2.55	0.41
33:b:1292:G:H2'	33:b:1293:C:C6	2.55	0.41
33:b:1794:A:H2'	33:b:1795:C:H6	1.85	0.41
33:b:2111:U:H4'	33:b:2119:A:H5'	2.02	0.41
46:q:3:ASN:HA	46:q:6:LYS:HE3	2.02	0.41
9:A:275:G:H4'	25:Q:15:LYS:HZ3	1.86	0.41
9:A:500:G:H2'	9:A:501:C:H6	1.86	0.41
9:A:687:A:C2	9:A:704:A:C5	3.09	0.41
9:A:1152:A:H4'	18:J:15:HIS:HE2	1.85	0.41
12:D:36:ALA:HB3	12:D:41:GLY:CA	2.46	0.41
21:M:16:ILE:O	21:M:19:THR:OG1	2.31	0.41
31:Y:24:C:H2'	31:Y:25:G:H8	1.83	0.41
33:b:288:U:H2'	33:b:289:G:C8	2.55	0.41
33:b:401:A:H2'	33:b:402:A:C8	2.55	0.41
33:b:827:U:O2'	33:b:2068:U:N3	2.52	0.41
33:b:1682:G:H2'	33:b:1683:U:C6	2.56	0.41
33:b:2141:G:H2'	33:b:2142:A:C8	2.54	0.41
34:c:130:LEU:HB2	34:c:135:ILE:HD11	2.01	0.41
48:s:70:GLU:OE1	48:s:70:GLU:N	2.50	0.41
53:x:13:G:H2'	53:x:14:C:C6	2.56	0.41
5:5:44:ARG:NH1	33:b:643:A:N7	2.69	0.41
9:A:299:G:H2'	9:A:300:A:C8	2.56	0.41
9:A:1076:U:OP1	10:B:173:LYS:NZ	2.53	0.41
29:U:3:ILE:HD11	29:U:21:SER:OG	2.21	0.41
31:Y:52:A:O2'	31:Y:53:G:H5"	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:554:U:H2'	33:b:555:G:O4'	2.20	0.41
33:b:1063:G:N7	33:b:1070:A:H5'	2.36	0.41
33:b:1086:A:H8	33:b:1104:C:N4	2.18	0.41
33:b:2117:A:H61	33:b:2170:A:N6	2.18	0.41
33:b:2597:G:H2'	33:b:2598:A:C8	2.55	0.41
33:b:2898:U:H2'	33:b:2899:A:H8	1.86	0.41
39:h:15:LEU:HD12	39:h:47:PHE:HZ	1.85	0.41
39:h:58:LEU:O	39:h:61:VAL:HG12	2.20	0.41
51:v:41:LEU:HD22	51:v:41:LEU:H	1.85	0.41
9:A:352:C:O2'	9:A:354:G:OP1	2.26	0.41
9:A:960:U:O2'	9:A:1223:C:H4'	2.21	0.41
10:B:116:LEU:HD23	10:B:140:LEU:HD12	2.01	0.41
11:C:78:LYS:HB3	11:C:78:LYS:HE3	1.89	0.41
12:D:98:ASP:OD1	12:D:98:ASP:N	2.54	0.41
15:G:67:ASN:HD22	15:G:127:ALA:HA	1.85	0.41
15:G:134:VAL:O	15:G:138:GLU:HG2	2.21	0.41
15:G:142:ARG:O	15:G:145:GLU:HG3	2.21	0.41
18:J:85:ASP:OD2	18:J:89:ARG:NH1	2.51	0.41
22:N:18:LYS:HD3	22:N:19:TYR:CZ	2.56	0.41
33:b:265:A:O2'	33:b:266:G:O5'	2.37	0.41
33:b:365:U:H2'	33:b:366:C:C6	2.56	0.41
33:b:613:A:H3'	33:b:613:A:N3	2.35	0.41
33:b:2025:C:H2'	33:b:2026:U:C6	2.56	0.41
46:q:37:LYS:H	46:q:37:LYS:HD3	1.85	0.41
9:A:57:G:H2'	9:A:58:C:H6	1.86	0.41
9:A:78:A:H3'	9:A:79:G:H5"	2.02	0.41
9:A:89:U:H2'	9:A:90:C:C5	2.56	0.41
9:A:186:C:N4	9:A:187:G:C6	2.89	0.41
9:A:358:U:H2'	9:A:359:G:C8	2.54	0.41
9:A:435:A:N3	12:D:153:ARG:NH2	2.68	0.41
9:A:606:G:N2	9:A:632:U:OP1	2.49	0.41
9:A:737:C:H2'	9:A:738:C:C6	2.56	0.41
9:A:1357:A:O2'	9:A:1358:U:P	2.79	0.41
12:D:99:ASN:O	12:D:103:ARG:HG2	2.20	0.41
12:D:104:MET:SD	12:D:179:GLY:HA3	2.61	0.41
12:D:121:ALA:HB1	12:D:148:ALA:HB2	2.03	0.41
12:D:176:LYS:HG2	12:D:178:GLU:HB2	2.03	0.41
14:F:90:MET:HE2	14:F:90:MET:HB3	2.00	0.41
19:K:71:ASP:O	19:K:74:LYS:NZ	2.53	0.41
26:R:8:LYS:HE2	26:R:8:LYS:HB2	1.84	0.41
30:X:19:G:N1	33:b:2112:G:H1'	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:657:U:H2'	33:b:658:U:C6	2.56	0.41
33:b:729:G:H5'	33:b:730:A:H5"	2.02	0.41
33:b:1062:G:O6	33:b:1088:A:H2'	2.21	0.41
33:b:1071:G:H22	33:b:1091:G:P	2.44	0.41
33:b:1094:U:O4	33:b:1099:G:C6	2.74	0.41
33:b:1223:G:OP1	48:s:68:ARG:NH1	2.54	0.41
33:b:1357:C:H2'	33:b:1358:G:O4'	2.19	0.41
33:b:1405:U:H2'	33:b:1406:U:C6	2.56	0.41
33:b:2118:U:O2'	33:b:2145:C:N3	2.54	0.41
33:b:2194:U:H2'	33:b:2195:U:H6	1.85	0.41
33:b:2303:G:O2'	37:f:121:SER:O	2.37	0.41
37:f:142:ASP:OD1	37:f:143:TYR:N	2.54	0.41
44:o:86:ARG:NE	44:o:117:ASP:OD2	2.51	0.41
9:A:978:A:C5	9:A:1319:A:C2	3.09	0.41
9:A:1010:U:H2'	9:A:1011:C:H6	1.85	0.41
9:A:1163:A:H2'	9:A:1164:G:H8	1.85	0.41
15:G:78:ARG:HB2	15:G:82:SER:O	2.20	0.41
24:P:44:SER:HB2	24:P:47:GLU:HB2	2.03	0.41
33:b:155:A:H2'	33:b:156:A:C8	2.55	0.41
33:b:871:U:H2'	33:b:872:U:C6	2.56	0.41
33:b:1057:A:C2	33:b:1081:U:C2	3.09	0.41
33:b:1069:A:H5"	33:b:1070:A:N7	2.36	0.41
9:A:181:A:N6	9:A:195:A:OP2	2.54	0.40
10:B:204:ASP:OD1	10:B:204:ASP:N	2.38	0.40
11:C:116:ALA:O	11:C:120:THR:HG23	2.21	0.40
11:C:120:THR:O	11:C:124:GLU:HG2	2.21	0.40
21:M:6:ILE:HD11	21:M:21:ILE:HD13	2.02	0.40
29:U:35:GLU:HG2	29:U:36:PHE:CG	2.56	0.40
30:X:52:A:H2'	30:X:53:G:H8	1.86	0.40
33:b:279:A:H2'	33:b:280:U:O4'	2.21	0.40
33:b:288:U:H2'	33:b:289:G:H8	1.86	0.40
33:b:1327:A:H2'	33:b:1328:A:O4'	2.22	0.40
33:b:2100:G:C6	33:b:2190:G:C6	3.09	0.40
9:A:59:A:H3'	9:A:331:G:H22	1.86	0.40
9:A:462:G:H22	9:A:469:C:N4	2.20	0.40
9:A:619:U:H4'	12:D:127:ARG:NH2	2.36	0.40
9:A:636:U:H2'	9:A:637:C:H6	1.85	0.40
9:A:945:G:C2	9:A:946:A:C8	3.09	0.40
10:B:23:ASN:ND2	10:B:191:ASP:HB3	2.36	0.40
10:B:27:LYS:N	10:B:28:PRO:HD2	2.36	0.40
10:B:187:ASP:OD1	10:B:188:THR:N	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:F:38:ARG:HH21	14:F:101:PRO:HD3	1.86	0.40
21:M:79:LEU:HD11	21:M:86:ARG:HH21	1.86	0.40
22:N:41:TRP:O	22:N:44:VAL:HG12	2.20	0.40
23:O:79:GLN:HA	23:O:82:GLU:OE1	2.20	0.40
33:b:511:U:HO2'	33:b:512:G:P	2.43	0.40
33:b:2097:A:H2'	33:b:2098:U:H6	1.85	0.40
33:b:2161:C:OP1	33:b:2163:A:N6	2.55	0.40
39:h:122:LEU:HD22	39:h:128:HIS:CD2	2.56	0.40
50:u:56:GLU:HG3	50:u:88:LYS:HE2	2.03	0.40
9:A:84:U:O2'	9:A:86:G:H5"	2.21	0.40
9:A:1028:C:C4	9:A:1029:U:H1'	2.56	0.40
12:D:173:ASP:OD2	12:D:176:LYS:HD2	2.21	0.40
14:F:3:HIS:ND1	14:F:65:GLU:OE1	2.54	0.40
33:b:63:A:N6	33:b:91:A:H62	2.19	0.40
33:b:2110:G:O2'	33:b:2120:G:OP2	2.32	0.40
33:b:2700:A:H2'	33:b:2701:U:C6	2.56	0.40
37:f:37:ASN:OD1	37:f:38:MET:N	2.54	0.40
39:h:45:GLU:H	39:h:45:GLU:HG3	1.73	0.40
4:4:57:LYS:HB2	4:4:57:LYS:HE3	1.85	0.40
5:5:13:SER:HB3	5:5:49:TYR:CZ	2.56	0.40
9:A:73:C:H2'	9:A:74:A:C8	2.56	0.40
9:A:429:U:OP1	12:D:8:LEU:HD23	2.21	0.40
10:B:56:LEU:HD13	10:B:216:VAL:HG13	2.03	0.40
15:G:58:LEU:O	15:G:62:GLU:HG2	2.22	0.40
16:H:39:LEU:HD12	16:H:39:LEU:HA	1.88	0.40
20:L:87:LYS:C	20:L:89:LEU:H	2.28	0.40
26:R:32:ILE:HD12	26:R:33:THR:O	2.21	0.40
33:b:858:G:N3	33:b:2268:A:H2'	2.36	0.40
33:b:2187:U:H5"	33:b:2188:U:OP1	2.22	0.40
4:4:25:VAL:O	4:4:26:THR:OG1	2.36	0.40
8:8:19:ARG:NE	33:b:2756:U:OP2	2.45	0.40
9:A:1219:A:H2'	9:A:1220:G:H8	1.87	0.40
9:A:1435:G:H2'	9:A:1436:U:C6	2.57	0.40
12:D:104:MET:HE2	12:D:170:LEU:HD11	2.04	0.40
12:D:124:VAL:HG22	12:D:142:VAL:HG22	2.03	0.40
13:E:120:HIS:O	13:E:121:ASN:ND2	2.55	0.40
13:E:158:LYS:NZ	16:H:41:GLU:O	2.40	0.40
17:I:87:MET:HE2	17:I:87:MET:HA	2.03	0.40
19:K:79:LYS:CD	19:K:80:ASN:HD22	2.33	0.40
30:X:7:A:O2'	30:X:49:G:O4'	2.27	0.40
33:b:289:G:H2'	33:b:290:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:851:C:H2'	33:b:852:U:H6	1.87	0.40
33:b:2305:U:H2'	33:b:2306:C:C6	2.56	0.40
34:c:114:ASP:OD1	34:c:114:ASP:N	2.54	0.40
36:e:112:LEU:HD23	36:e:112:LEU:HA	1.89	0.40
41:l:88:ASN:OD1	41:l:91:SER:N	2.53	0.40
51:v:97:LYS:HD3	51:v:97:LYS:HA	1.74	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
2	1	59/63 (94%)	56 (95%)	3 (5%)	0	100	100
3	2	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
4	4	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
5	5	50/55 (91%)	46 (92%)	4 (8%)	0	100	100
6	6	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
7	7	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
8	8	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
10	B	216/241 (90%)	197 (91%)	19 (9%)	0	100	100
11	C	205/233 (88%)	191 (93%)	14 (7%)	0	100	100
12	D	203/206 (98%)	179 (88%)	24 (12%)	0	100	100
13	E	155/167 (93%)	136 (88%)	19 (12%)	0	100	100
14	F	104/135 (77%)	94 (90%)	10 (10%)	0	100	100
15	G	151/179 (84%)	143 (95%)	8 (5%)	0	100	100
16	H	127/130 (98%)	120 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	I	125/130 (96%)	109 (87%)	16 (13%)	0	100	100
18	J	98/103 (95%)	87 (89%)	11 (11%)	0	100	100
19	K	115/129 (89%)	105 (91%)	10 (9%)	0	100	100
20	L	120/124 (97%)	101 (84%)	19 (16%)	0	100	100
21	M	114/118 (97%)	103 (90%)	11 (10%)	0	100	100
22	N	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
23	O	86/89 (97%)	78 (91%)	8 (9%)	0	100	100
24	P	79/82 (96%)	70 (89%)	9 (11%)	0	100	100
25	Q	78/84 (93%)	73 (94%)	5 (6%)	0	100	100
26	R	64/75 (85%)	58 (91%)	6 (9%)	0	100	100
27	S	81/92 (88%)	75 (93%)	6 (7%)	0	100	100
28	T	84/87 (97%)	84 (100%)	0	0	100	100
29	U	62/71 (87%)	57 (92%)	5 (8%)	0	100	100
34	c	269/273 (98%)	253 (94%)	16 (6%)	0	100	100
35	d	207/209 (99%)	194 (94%)	13 (6%)	0	100	100
36	e	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
37	f	176/179 (98%)	165 (94%)	11 (6%)	0	100	100
38	g	173/177 (98%)	159 (92%)	14 (8%)	0	100	100
39	h	147/149 (99%)	141 (96%)	6 (4%)	0	100	100
40	k	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
41	l	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
42	m	142/144 (99%)	131 (92%)	11 (8%)	0	100	100
43	n	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
44	o	118/127 (93%)	112 (95%)	6 (5%)	0	100	100
45	p	114/117 (97%)	106 (93%)	8 (7%)	0	100	100
46	q	112/115 (97%)	109 (97%)	3 (3%)	0	100	100
47	r	115/118 (98%)	115 (100%)	0	0	100	100
48	s	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
49	t	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
50	u	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
51	v	101/104 (97%)	91 (90%)	10 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	w	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
54	y	82/85 (96%)	80 (98%)	2 (2%)	0	100	100
55	z	32/28 (114%)	29 (91%)	3 (9%)	0	100	100
All	All	5582/5871 (95%)	5197 (93%)	385 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	67/68 (98%)	67 (100%)	0	100	100
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	48/49 (98%)	48 (100%)	0	100	100
4	4	47/48 (98%)	47 (100%)	0	100	100
5	5	47/49 (96%)	47 (100%)	0	100	100
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/34 (100%)	34 (100%)	0	100	100
10	B	180/199 (90%)	179 (99%)	1 (1%)	84	94
11	C	171/190 (90%)	170 (99%)	1 (1%)	84	94
12	D	172/173 (99%)	168 (98%)	4 (2%)	45	74
13	E	119/126 (94%)	117 (98%)	2 (2%)	56	81
14	F	92/116 (79%)	89 (97%)	3 (3%)	33	62
15	G	126/147 (86%)	126 (100%)	0	100	100
16	H	104/105 (99%)	104 (100%)	0	100	100
17	I	105/107 (98%)	103 (98%)	2 (2%)	52	79
18	J	88/90 (98%)	86 (98%)	2 (2%)	45	74
19	K	90/99 (91%)	89 (99%)	1 (1%)	70	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
20	L	103/104 (99%)	100 (97%)	3 (3%)	37 67
21	M	94/96 (98%)	93 (99%)	1 (1%)	70 87
22	N	83/84 (99%)	83 (100%)	0	100 100
23	O	76/77 (99%)	74 (97%)	2 (3%)	41 70
24	P	65/65 (100%)	62 (95%)	3 (5%)	23 49
25	Q	74/78 (95%)	72 (97%)	2 (3%)	40 69
26	R	57/65 (88%)	57 (100%)	0	100 100
27	S	72/79 (91%)	71 (99%)	1 (1%)	62 84
28	T	65/66 (98%)	65 (100%)	0	100 100
29	U	54/61 (88%)	52 (96%)	2 (4%)	29 58
34	c	216/218 (99%)	216 (100%)	0	100 100
35	d	164/164 (100%)	163 (99%)	1 (1%)	84 94
36	e	165/165 (100%)	164 (99%)	1 (1%)	84 94
37	f	149/150 (99%)	147 (99%)	2 (1%)	65 85
38	g	136/138 (99%)	135 (99%)	1 (1%)	81 93
39	h	113/114 (99%)	111 (98%)	2 (2%)	54 80
40	k	116/116 (100%)	116 (100%)	0	100 100
41	l	104/104 (100%)	104 (100%)	0	100 100
42	m	103/103 (100%)	102 (99%)	1 (1%)	73 89
43	n	109/109 (100%)	109 (100%)	0	100 100
44	o	100/103 (97%)	98 (98%)	2 (2%)	50 78
45	p	86/87 (99%)	84 (98%)	2 (2%)	45 74
46	q	99/100 (99%)	98 (99%)	1 (1%)	73 89
47	r	89/90 (99%)	89 (100%)	0	100 100
48	s	84/84 (100%)	83 (99%)	1 (1%)	67 86
49	t	93/93 (100%)	93 (100%)	0	100 100
50	u	84/84 (100%)	84 (100%)	0	100 100
51	v	84/85 (99%)	82 (98%)	2 (2%)	44 73
52	w	78/78 (100%)	77 (99%)	1 (1%)	65 85
54	y	62/63 (98%)	60 (97%)	2 (3%)	34 63
55	z	26/23 (113%)	23 (88%)	3 (12%)	4 11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4636/4791 (97%)	4584 (99%)	52 (1%)	69 87

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	B	182	VAL
11	C	71	ARG
12	D	30	LYS
12	D	89	LEU
12	D	90	LEU
12	D	176	LYS
13	E	80	LEU
13	E	146	MET
14	F	75	GLU
14	F	94	HIS
14	F	106	LYS
17	I	28	VAL
17	I	52	GLU
18	J	20	GLN
18	J	57	VAL
19	K	41	LEU
20	L	26	CYS
20	L	38	THR
20	L	79	ILE
21	M	77	LYS
23	O	46	LYS
23	O	82	GLU
24	P	42	ILE
24	P	74	LEU
24	P	77	GLU
25	Q	15	LYS
25	Q	21	VAL
27	S	28	LYS
29	U	2	VAL
29	U	31	VAL
35	d	131	ASP
36	e	69	ARG
37	f	26	MET
37	f	66	LEU
38	g	107	LEU
39	h	121	VAL
39	h	141	LYS

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Mol	Chain	Res	Type
42	m	69	ARG
44	o	57	THR
44	o	82	GLU
45	p	13	ARG
45	p	83	LEU
46	q	60	THR
48	s	49	ILE
51	v	36	VAL
51	v	103	ILE
52	w	63	ILE
54	y	44	LYS
54	y	64	ASP
55	z	145	TRP
55	z	150[A]	TYR
55	z	150[B]	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
2	1	20	ASN
3	2	34	HIS
10	B	176	ASN
11	C	101	ASN
12	D	163	GLN
12	D	195	ASN
13	E	134	ASN
14	F	58	HIS
14	F	63	ASN
15	G	85	GLN
16	H	3	GLN
20	L	71	HIS
20	L	74	GLN
21	M	104	ASN
23	O	34	GLN
23	O	50	HIS
24	P	79	ASN
28	T	19	HIS
28	T	47	GLN
28	T	60	GLN
28	T	69	ASN
34	c	25	HIS
34	c	117	GLN

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Mol	Chain	Res	Type
34	c	260	ASN
35	d	49	GLN
35	d	136	ASN
35	d	140	HIS
36	e	92	HIS
36	e	115	GLN
36	e	195	GLN
40	k	58	ASN
40	k	76	HIS
41	l	82	ASN
42	m	54	GLN
47	r	14	HIS
47	r	44	GLN
48	s	89	HIS
49	t	31	GLN
50	u	70	HIS
51	v	46	GLN
52	w	44	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	X	75/76 (98%)	32 (42%)	1 (1%)
31	Y	76/77 (98%)	26 (34%)	3 (3%)
31	Z	76/77 (98%)	15 (19%)	2 (2%)
32	a	119/120 (99%)	20 (16%)	0
33	b	2901/2904 (99%)	562 (19%)	0
53	x	13/14 (92%)	3 (23%)	0
9	A	1532/1533 (99%)	336 (21%)	10 (0%)
All	All	4792/4801 (99%)	994 (20%)	16 (0%)

All (994) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	2	A
9	A	4	U
9	A	9	G
9	A	32	A
9	A	33	A
9	A	39	G
9	A	47	C

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Mol	Chain	Res	Type
9	A	48	C
9	A	51	A
9	A	65	A
9	A	66	A
9	A	71	A
9	A	72	A
9	A	73	C
9	A	74	A
9	A	77	A
9	A	78	A
9	A	79	G
9	A	80	A
9	A	81	A
9	A	83	C
9	A	84	U
9	A	85	U
9	A	86	G
9	A	88	U
9	A	89	U
9	A	91	U
9	A	94	G
9	A	95	C
9	A	97	G
9	A	109	A
9	A	122	G
9	A	130	A
9	A	131	A
9	A	138	G
9	A	141	G
9	A	144	G
9	A	150	U
9	A	160	A
9	A	163	C
9	A	173	U
9	A	181	A
9	A	185	U
9	A	189	A
9	A	196	A
9	A	197	A
9	A	200	G
9	A	204	G
9	A	205	A

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Mol	Chain	Res	Type
9	A	207	C
9	A	209	U
9	A	210	C
9	A	214	C
9	A	215	C
9	A	216	U
9	A	218	U
9	A	219	U
9	A	224	U
9	A	226	G
9	A	228	A
9	A	231	U
9	A	239	U
9	A	240	G
9	A	245	U
9	A	247	G
9	A	251	G
9	A	262	A
9	A	263	A
9	A	266	G
9	A	267	C
9	A	269	C
9	A	275	G
9	A	279	A
9	A	283	U
9	A	286	C
9	A	289	G
9	A	293	G
9	A	321	A
9	A	328	C
9	A	330	C
9	A	343	U
9	A	351	G
9	A	352	C
9	A	354	G
9	A	365	U
9	A	367	U
9	A	369	G
9	A	371	A
9	A	372	C
9	A	374	A
9	A	376	G

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Mol	Chain	Res	Type
9	A	377	G
9	A	378	G
9	A	381	C
9	A	390	U
9	A	391	G
9	A	392	C
9	A	397	A
9	A	398	U
9	A	406	G
9	A	411	A
9	A	412	A
9	A	413	G
9	A	414	A
9	A	415	A
9	A	420	U
9	A	421	U
9	A	422	C
9	A	423	G
9	A	424	G
9	A	428	G
9	A	429	U
9	A	435	A
9	A	436	C
9	A	439	U
9	A	444	G
9	A	449	G
9	A	452	A
9	A	454	G
9	A	457	G
9	A	458	U
9	A	459	A
9	A	460	A
9	A	461	A
9	A	462	G
9	A	467	U
9	A	468	A
9	A	472	U
9	A	478	A
9	A	479	U
9	A	481	G
9	A	484	G
9	A	485	U

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Mol	Chain	Res	Type
9	A	486	U
9	A	491	G
9	A	492	C
9	A	493	A
9	A	495	A
9	A	496	A
9	A	497	G
9	A	510	A
9	A	511	C
9	A	513	C
9	A	517	G
9	A	518	C
9	A	521	G
9	A	527	G
9	A	530	G
9	A	531	U
9	A	532	A
9	A	533	A
9	A	534	U
9	A	535	A
9	A	541	G
9	A	547	A
9	A	548	G
9	A	549	C
9	A	564	C
9	A	572	A
9	A	573	A
9	A	575	G
9	A	576	C
9	A	577	G
9	A	588	G
9	A	593	U
9	A	602	A
9	A	615	G
9	A	629	A
9	A	632	U
9	A	633	G
9	A	653	U
9	A	665	A
9	A	687	A
9	A	720	C
9	A	721	G

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Mol	Chain	Res	Type
9	A	723	U
9	A	724	G
9	A	731	G
9	A	755	G
9	A	760	G
9	A	777	A
9	A	781	A
9	A	787	A
9	A	793	U
9	A	794	A
9	A	815	A
9	A	817	C
9	A	821	G
9	A	828	U
9	A	841	C
9	A	842	U
9	A	843	U
9	A	844	G
9	A	849	G
9	A	872	A
9	A	873	A
9	A	891	U
9	A	900	A
9	A	902	G
9	A	914	A
9	A	919	A
9	A	926	G
9	A	927	G
9	A	933	G
9	A	934	C
9	A	935	A
9	A	945	G
9	A	947	G
9	A	960	U
9	A	966	G
9	A	969	A
9	A	971	G
9	A	975	A
9	A	976	G
9	A	977	A
9	A	980	C
9	A	981	U

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Mol	Chain	Res	Type
9	A	992	U
9	A	993	G
9	A	994	A
9	A	995	C
9	A	998	C
9	A	1000	A
9	A	1001	C
9	A	1004	A
9	A	1019	A
9	A	1020	G
9	A	1022	A
9	A	1024	G
9	A	1028	C
9	A	1029	U
9	A	1030	U
9	A	1034	G
9	A	1035	A
9	A	1036	A
9	A	1039	G
9	A	1041	G
9	A	1046	A
9	A	1049	U
9	A	1053	G
9	A	1065	U
9	A	1066	C
9	A	1094	G
9	A	1095	U
9	A	1101	A
9	A	1104	G
9	A	1121	U
9	A	1134	G
9	A	1137	C
9	A	1138	G
9	A	1139	G
9	A	1140	C
9	A	1145	A
9	A	1157	A
9	A	1159	U
9	A	1160	G
9	A	1167	A
9	A	1168	U
9	A	1169	A

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Mol	Chain	Res	Type
9	A	1174	G
9	A	1181	G
9	A	1183	U
9	A	1184	G
9	A	1188	A
9	A	1189	U
9	A	1193	G
9	A	1196	A
9	A	1197	A
9	A	1201	A
9	A	1202	U
9	A	1208	C
9	A	1209	C
9	A	1210	C
9	A	1212	U
9	A	1213	A
9	A	1214	C
9	A	1220	G
9	A	1227	A
9	A	1238	A
9	A	1240	U
9	A	1241	G
9	A	1248	A
9	A	1256	A
9	A	1257	A
9	A	1258	G
9	A	1259	C
9	A	1260	G
9	A	1263	C
9	A	1266	G
9	A	1280	A
9	A	1281	C
9	A	1285	A
9	A	1287	A
9	A	1293	C
9	A	1300	G
9	A	1301	U
9	A	1302	C
9	A	1303	C
9	A	1305	G
9	A	1307	U
9	A	1316	G

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Mol	Chain	Res	Type
9	A	1317	C
9	A	1320	C
9	A	1343	G
9	A	1347	G
9	A	1349	A
9	A	1358	U
9	A	1362	A
9	A	1363	A
9	A	1364	U
9	A	1370	G
9	A	1394	A
9	A	1397	C
9	A	1419	G
9	A	1429	A
9	A	1430	A
9	A	1434	A
9	A	1441	A
9	A	1446	A
9	A	1450	U
9	A	1452	C
9	A	1454	G
9	A	1471	U
9	A	1472	U
9	A	1475	G
9	A	1487	G
9	A	1492	A
9	A	1494	G
9	A	1497	G
9	A	1503	A
9	A	1506	U
9	A	1517	G
9	A	1520	C
9	A	1529	G
9	A	1530	G
9	A	1533	C
30	X	4	G
30	X	5	G
30	X	6	A
30	X	8	U
30	X	9	A
30	X	10	G
30	X	13	C

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Mol	Chain	Res	Type
30	X	16	U
30	X	17	U
30	X	19	G
30	X	21	A
30	X	24	G
30	X	25	C
30	X	29	A
30	X	30	C
30	X	42	C
30	X	43	G
30	X	45	G
30	X	46	G
30	X	47	U
30	X	48	C
30	X	49	G
30	X	51	G
30	X	56	C
30	X	57	G
30	X	59	G
30	X	60	U
30	X	61	C
30	X	62	U
30	X	66	U
30	X	67	U
30	X	76	A
31	Y	3	G
31	Y	4	U
31	Y	5	G
31	Y	6	A
31	Y	7	U
31	Y	8	U
31	Y	16	C
31	Y	17	C
31	Y	18	U
31	Y	19	G
31	Y	20	G
31	Y	21	U
31	Y	22	A
31	Y	47	G
31	Y	48	U
31	Y	49	C
31	Y	50	G

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Mol	Chain	Res	Type
31	Y	57	C
31	Y	62	C
31	Y	63	C
31	Y	64	U
31	Y	65	C
31	Y	67	A
31	Y	68	U
31	Y	69	C
31	Y	77	A
31	Z	9	G
31	Z	12	G
31	Z	16	C
31	Z	17	C
31	Z	18	U
31	Z	20	G
31	Z	21	U
31	Z	23	G
31	Z	37	G
31	Z	42	A
31	Z	50	G
31	Z	53	G
31	Z	67	A
31	Z	74	A
31	Z	75	C
32	a	15	A
32	a	16	G
32	a	24	G
32	a	25	U
32	a	30	C
32	a	35	C
32	a	42	C
32	a	43	C
32	a	51	G
32	a	52	A
32	a	56	G
32	a	57	A
32	a	58	A
32	a	66	A
32	a	67	G
32	a	74	U
32	a	89	U
32	a	90	C

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Mol	Chain	Res	Type
32	a	99	A
32	a	109	A
33	b	5	A
33	b	10	A
33	b	34	U
33	b	35	G
33	b	36	G
33	b	39	G
33	b	46	G
33	b	51	G
33	b	62	U
33	b	63	A
33	b	71	A
33	b	74	A
33	b	75	G
33	b	84	A
33	b	98	G
33	b	100	U
33	b	101	A
33	b	102	U
33	b	103	A
33	b	110	G
33	b	118	A
33	b	120	U
33	b	140	C
33	b	142	A
33	b	149	A
33	b	160	A
33	b	163	C
33	b	174	U
33	b	181	A
33	b	196	A
33	b	199	A
33	b	215	G
33	b	216	A
33	b	222	A
33	b	223	A
33	b	228	C
33	b	229	C
33	b	230	G
33	b	233	A
33	b	248	G

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Mol	Chain	Res	Type
33	b	250	G
33	b	251	A
33	b	255	A
33	b	264	C
33	b	265	A
33	b	266	G
33	b	267	C
33	b	268	C
33	b	271	G
33	b	272	A
33	b	275	C
33	b	278	A
33	b	279	A
33	b	282	A
33	b	285	G
33	b	286	U
33	b	295	G
33	b	304	U
33	b	330	A
33	b	346	A
33	b	348	A
33	b	349	U
33	b	353	C
33	b	356	G
33	b	361	G
33	b	362	A
33	b	363	G
33	b	365	U
33	b	367	G
33	b	369	U
33	b	371	A
33	b	372	G
33	b	380	G
33	b	386	G
33	b	387	U
33	b	391	A
33	b	405	U
33	b	406	G
33	b	412	A
33	b	413	C
33	b	423	A
33	b	424	G

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Mol	Chain	Res	Type
33	b	428	A
33	b	457	A
33	b	473	G
33	b	480	A
33	b	481	G
33	b	482	A
33	b	491	G
33	b	494	G
33	b	505	A
33	b	508	A
33	b	509	C
33	b	512	G
33	b	528	A
33	b	529	A
33	b	530	G
33	b	531	C
33	b	532	A
33	b	538	A
33	b	548	G
33	b	549	G
33	b	563	A
33	b	568	U
33	b	573	U
33	b	575	A
33	b	587	C
33	b	595	C
33	b	603	A
33	b	604	G
33	b	613	A
33	b	621	A
33	b	627	A
33	b	632	A
33	b	637	A
33	b	643	A
33	b	644	A
33	b	645	C
33	b	646	U
33	b	647	G
33	b	653	U
33	b	654	A
33	b	686	U
33	b	688	U

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Mol	Chain	Res	Type
33	b	701	G
33	b	702	U
33	b	709	U
33	b	716	A
33	b	717	C
33	b	718	A
33	b	727	A
33	b	730	A
33	b	747	U
33	b	752	A
33	b	757	G
33	b	764	A
33	b	765	C
33	b	774	G
33	b	775	G
33	b	776	G
33	b	782	A
33	b	784	G
33	b	785	G
33	b	792	A
33	b	805	G
33	b	812	C
33	b	819	A
33	b	827	U
33	b	837	C
33	b	846	U
33	b	847	U
33	b	859	G
33	b	879	G
33	b	880	G
33	b	881	G
33	b	885	C
33	b	888	C
33	b	889	C
33	b	890	C
33	b	891	G
33	b	894	U
33	b	895	U
33	b	897	C
33	b	899	A
33	b	900	A
33	b	901	C

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Mol	Chain	Res	Type
33	b	905	A
33	b	910	A
33	b	912	C
33	b	914	G
33	b	927	A
33	b	931	U
33	b	941	A
33	b	946	C
33	b	959	A
33	b	961	C
33	b	974	G
33	b	983	A
33	b	996	A
33	b	999	U
33	b	1005	C
33	b	1006	C
33	b	1009	A
33	b	1012	U
33	b	1013	C
33	b	1022	G
33	b	1026	G
33	b	1033	U
33	b	1047	G
33	b	1051	G
33	b	1052	C
33	b	1055	G
33	b	1056	G
33	b	1057	A
33	b	1059	G
33	b	1060	U
33	b	1061	U
33	b	1062	G
33	b	1064	C
33	b	1065	U
33	b	1066	U
33	b	1068	G
33	b	1069	A
33	b	1070	A
33	b	1072	C
33	b	1073	A
33	b	1074	G
33	b	1075	C

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Mol	Chain	Res	Type
33	b	1076	C
33	b	1077	A
33	b	1078	U
33	b	1079	C
33	b	1081	U
33	b	1082	U
33	b	1083	U
33	b	1084	A
33	b	1085	A
33	b	1086	A
33	b	1087	G
33	b	1088	A
33	b	1090	A
33	b	1092	C
33	b	1093	G
33	b	1094	U
33	b	1095	A
33	b	1096	A
33	b	1097	U
33	b	1098	A
33	b	1099	G
33	b	1101	U
33	b	1102	C
33	b	1103	A
33	b	1104	C
33	b	1105	U
33	b	1106	G
33	b	1107	G
33	b	1109	C
33	b	1112	G
33	b	1132	U
33	b	1133	A
33	b	1134	A
33	b	1135	C
33	b	1136	G
33	b	1142	A
33	b	1174	U
33	b	1175	A
33	b	1176	U
33	b	1177	G
33	b	1181	U
33	b	1206	G

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Mol	Chain	Res	Type
33	b	1212	G
33	b	1238	G
33	b	1250	G
33	b	1253	A
33	b	1256	G
33	b	1266	G
33	b	1267	U
33	b	1269	A
33	b	1271	G
33	b	1272	A
33	b	1273	U
33	b	1276	A
33	b	1291	C
33	b	1300	G
33	b	1301	A
33	b	1306	C
33	b	1352	U
33	b	1365	A
33	b	1366	A
33	b	1374	G
33	b	1379	U
33	b	1382	G
33	b	1383	A
33	b	1384	A
33	b	1388	G
33	b	1393	A
33	b	1395	A
33	b	1396	U
33	b	1416	G
33	b	1417	C
33	b	1420	A
33	b	1421	G
33	b	1426	G
33	b	1427	A
33	b	1428	C
33	b	1433	A
33	b	1434	A
33	b	1435	G
33	b	1460	U
33	b	1461	C
33	b	1476	U
33	b	1482	G

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Mol	Chain	Res	Type
33	b	1487	U
33	b	1490	A
33	b	1493	C
33	b	1496	A
33	b	1497	U
33	b	1498	C
33	b	1504	A
33	b	1505	A
33	b	1508	A
33	b	1509	A
33	b	1510	G
33	b	1515	A
33	b	1523	U
33	b	1524	G
33	b	1534	U
33	b	1535	A
33	b	1536	C
33	b	1537	G
33	b	1540	G
33	b	1541	C
33	b	1553	A
33	b	1562	U
33	b	1566	A
33	b	1568	G
33	b	1569	A
33	b	1572	A
33	b	1578	U
33	b	1584	U
33	b	1608	A
33	b	1610	A
33	b	1615	C
33	b	1618	A
33	b	1646	C
33	b	1647	U
33	b	1648	U
33	b	1674	G
33	b	1677	A
33	b	1716	U
33	b	1718	G
33	b	1730	C
33	b	1733	G
33	b	1736	U

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Mol	Chain	Res	Type
33	b	1744	A
33	b	1745	A
33	b	1758	U
33	b	1763	G
33	b	1764	C
33	b	1773	A
33	b	1776	G
33	b	1799	G
33	b	1800	C
33	b	1801	A
33	b	1807	G
33	b	1808	A
33	b	1811	G
33	b	1816	C
33	b	1826	G
33	b	1829	A
33	b	1840	G
33	b	1847	A
33	b	1857	G
33	b	1870	C
33	b	1871	A
33	b	1877	A
33	b	1884	G
33	b	1906	G
33	b	1913	A
33	b	1914	C
33	b	1919	A
33	b	1927	A
33	b	1928	A
33	b	1929	G
33	b	1930	G
33	b	1931	U
33	b	1936	A
33	b	1937	A
33	b	1938	A
33	b	1941	C
33	b	1955	U
33	b	1963	U
33	b	1967	C
33	b	1970	A
33	b	1971	U
33	b	1972	G

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Mol	Chain	Res	Type
33	b	1977	A
33	b	1991	U
33	b	1992	G
33	b	1993	U
33	b	1996	C
33	b	1997	C
33	b	2023	C
33	b	2027	G
33	b	2031	A
33	b	2032	G
33	b	2033	A
33	b	2043	C
33	b	2055	C
33	b	2056	G
33	b	2060	A
33	b	2061	G
33	b	2062	A
33	b	2069	G
33	b	2093	G
33	b	2098	U
33	b	2102	G
33	b	2103	C
33	b	2105	U
33	b	2106	U
33	b	2107	G
33	b	2108	A
33	b	2111	U
33	b	2112	G
33	b	2114	A
33	b	2115	G
33	b	2116	G
33	b	2117	A
33	b	2118	U
33	b	2119	A
33	b	2121	G
33	b	2123	G
33	b	2125	G
33	b	2126	A
33	b	2129	C
33	b	2130	U
33	b	2132	U
33	b	2135	A

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Mol	Chain	Res	Type
33	b	2136	G
33	b	2138	G
33	b	2139	U
33	b	2140	G
33	b	2144	G
33	b	2145	C
33	b	2146	C
33	b	2147	A
33	b	2149	U
33	b	2151	U
33	b	2154	A
33	b	2155	U
33	b	2156	G
33	b	2157	G
33	b	2158	A
33	b	2162	G
33	b	2163	A
33	b	2164	C
33	b	2165	C
33	b	2166	U
33	b	2170	A
33	b	2171	A
33	b	2172	U
33	b	2174	C
33	b	2180	U
33	b	2182	U
33	b	2184	A
33	b	2186	G
33	b	2187	U
33	b	2188	U
33	b	2190	G
33	b	2191	A
33	b	2192	U
33	b	2193	G
33	b	2198	A
33	b	2203	U
33	b	2204	G
33	b	2212	A
33	b	2213	U
33	b	2214	C
33	b	2225	A
33	b	2238	G

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Mol	Chain	Res	Type
33	b	2239	G
33	b	2250	G
33	b	2273	A
33	b	2283	C
33	b	2287	A
33	b	2300	C
33	b	2305	U
33	b	2308	G
33	b	2311	A
33	b	2320	U
33	b	2322	A
33	b	2325	G
33	b	2326	C
33	b	2333	A
33	b	2335	A
33	b	2336	A
33	b	2345	G
33	b	2346	A
33	b	2357	G
33	b	2361	G
33	b	2383	G
33	b	2385	C
33	b	2396	G
33	b	2402	U
33	b	2406	A
33	b	2407	A
33	b	2422	C
33	b	2425	A
33	b	2429	G
33	b	2430	A
33	b	2441	U
33	b	2448	A
33	b	2450	A
33	b	2459	A
33	b	2475	C
33	b	2476	A
33	b	2481	G
33	b	2494	G
33	b	2498	C
33	b	2502	G
33	b	2503	A
33	b	2505	G

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Mol	Chain	Res	Type
33	b	2506	U
33	b	2518	A
33	b	2520	C
33	b	2529	G
33	b	2547	A
33	b	2554	U
33	b	2566	A
33	b	2567	G
33	b	2572	A
33	b	2573	C
33	b	2602	A
33	b	2606	C
33	b	2609	U
33	b	2613	U
33	b	2629	U
33	b	2630	G
33	b	2654	A
33	b	2655	G
33	b	2656	U
33	b	2661	G
33	b	2689	U
33	b	2690	U
33	b	2714	G
33	b	2718	G
33	b	2726	A
33	b	2733	A
33	b	2744	G
33	b	2748	A
33	b	2765	A
33	b	2776	A
33	b	2778	A
33	b	2779	U
33	b	2790	U
33	b	2791	G
33	b	2792	A
33	b	2796	U
33	b	2797	U
33	b	2798	U
33	b	2800	A
33	b	2801	G
33	b	2818	U
33	b	2820	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
33	b	2833	U
33	b	2834	G
33	b	2835	A
33	b	2849	U
33	b	2858	C
33	b	2859	G
33	b	2861	U
33	b	2867	G
33	b	2873	A
33	b	2880	C
33	b	2883	A
33	b	2885	G
33	b	2886	A
33	b	2887	A
33	b	2896	C
33	b	2900	A
33	b	2902	C
33	b	2903	U
53	x	14	C
53	x	22	A
53	x	23	A

All (16) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	66	A
9	A	195	A
9	A	262	A
9	A	719	C
9	A	1065	U
9	A	1187	G
9	A	1201	A
9	A	1255	G
9	A	1357	A
9	A	1493	A
30	X	56	C
31	Y	6	A
31	Y	16	C
31	Y	66	U
31	Z	20	G
31	Z	73	G

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
57	PRO	Z	163	-	5,7,8	0.71	0	7,8,10	1.49	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	PRO	Z	163	-	-	0/0/9/11	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	Z	163	PRO	O-C-CA	-2.86	117.28	124.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	Z	163	PRO	5	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

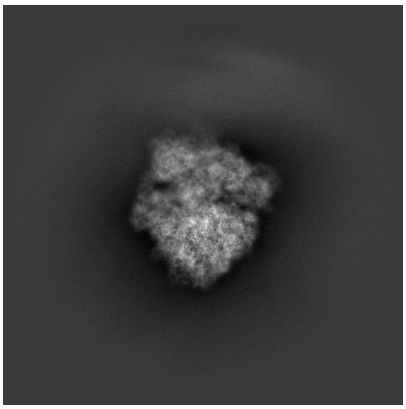
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-60034. These allow visual inspection of the internal detail of the map and identification of artifacts.

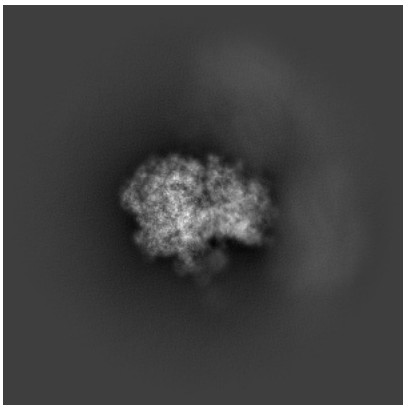
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

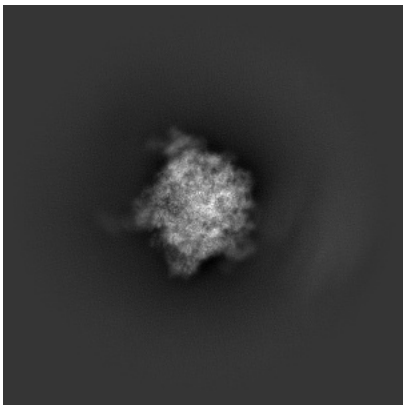
6.1.1 Primary map



X

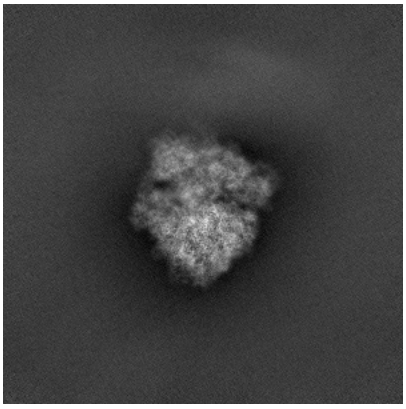


Y

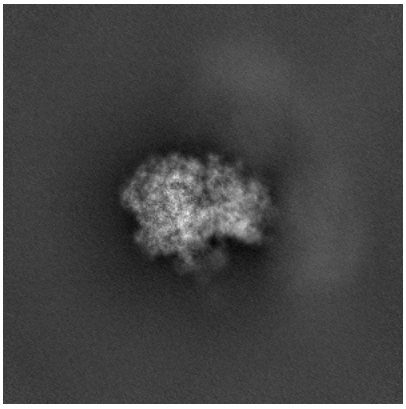


Z

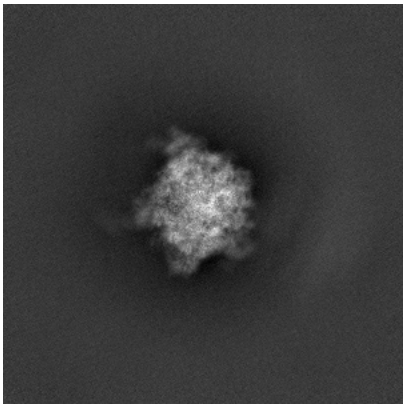
6.1.2 Raw map



X



Y

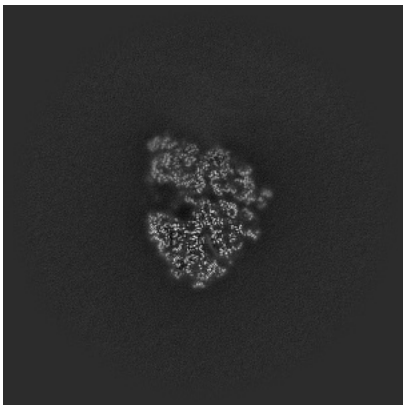


Z

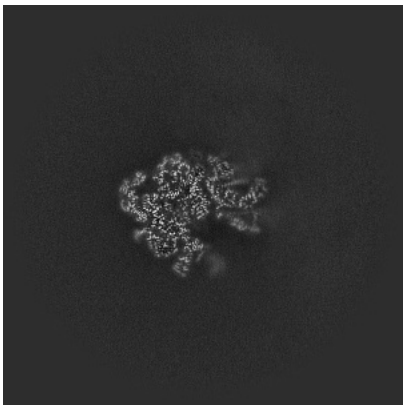
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

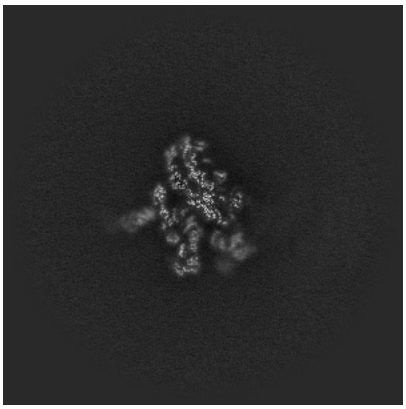
6.2.1 Primary map



X Index: 310

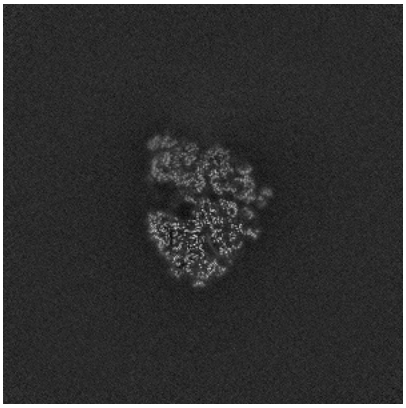


Y Index: 310

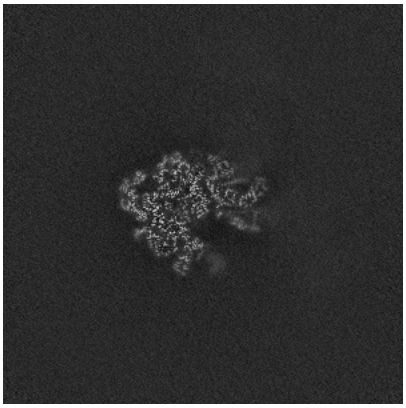


Z Index: 310

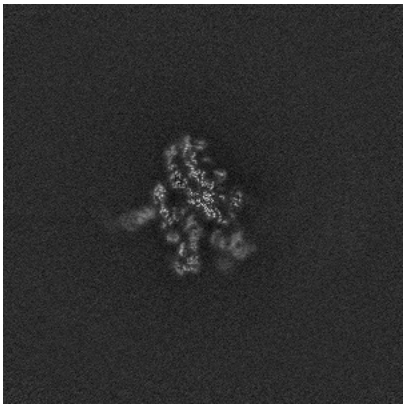
6.2.2 Raw map



X Index: 310



Y Index: 310

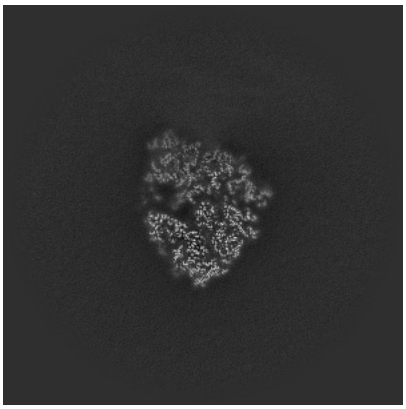


Z Index: 310

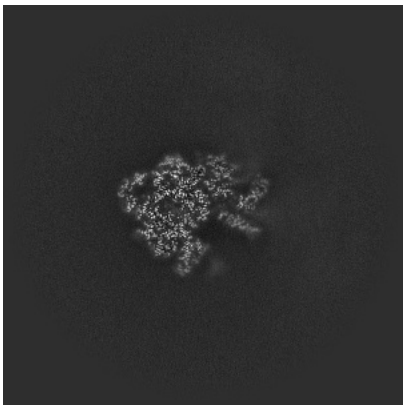
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

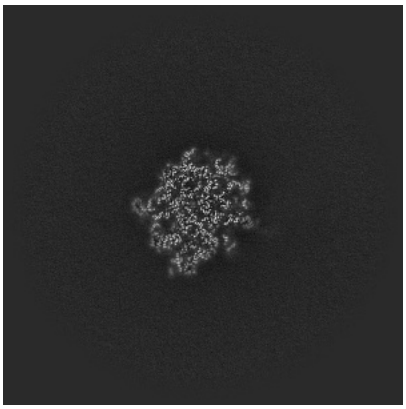
6.3.1 Primary map



X Index: 306

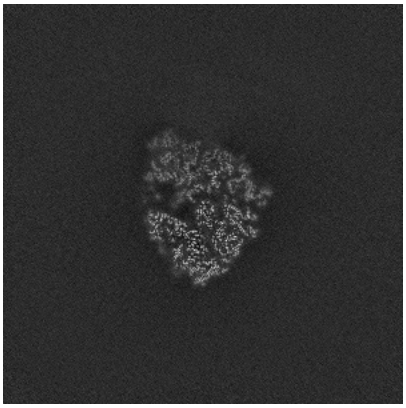


Y Index: 314

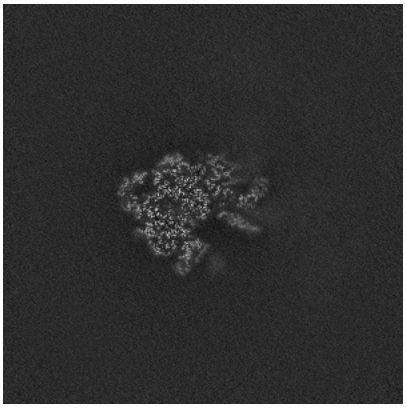


Z Index: 278

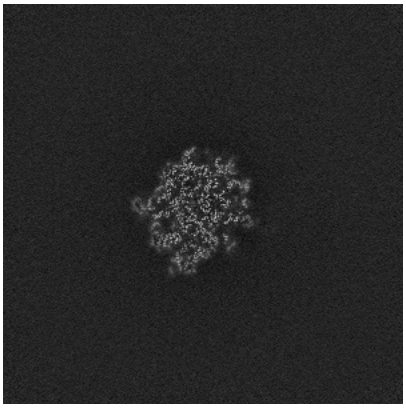
6.3.2 Raw map



X Index: 306



Y Index: 313

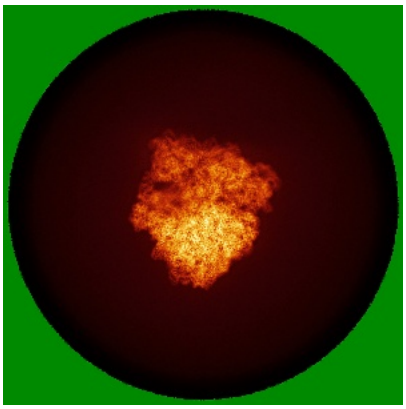


Z Index: 278

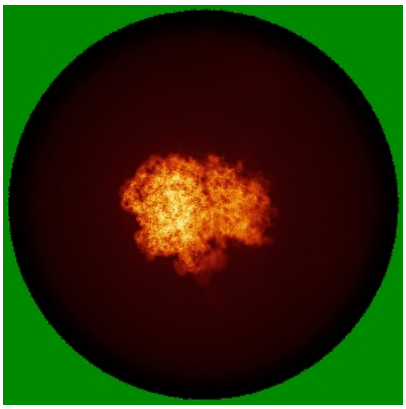
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

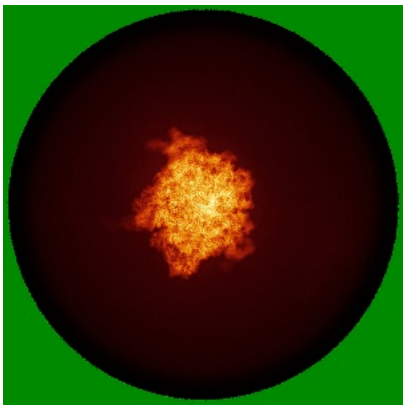
6.4.1 Primary map



X

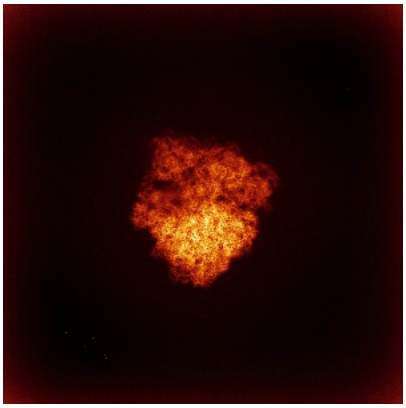


Y

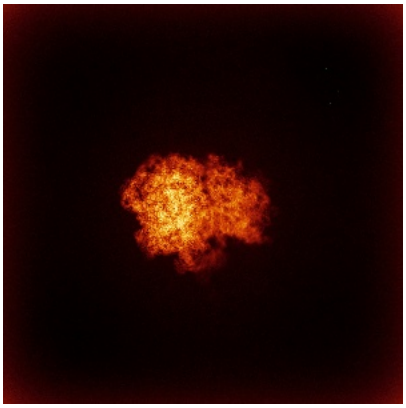


Z

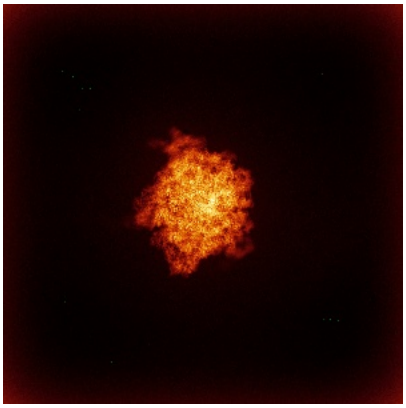
6.4.2 Raw map



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.

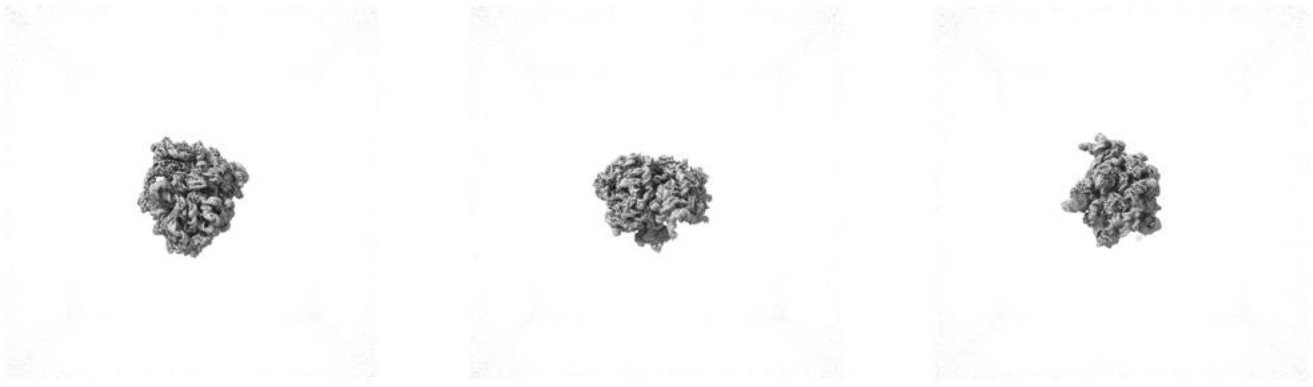
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

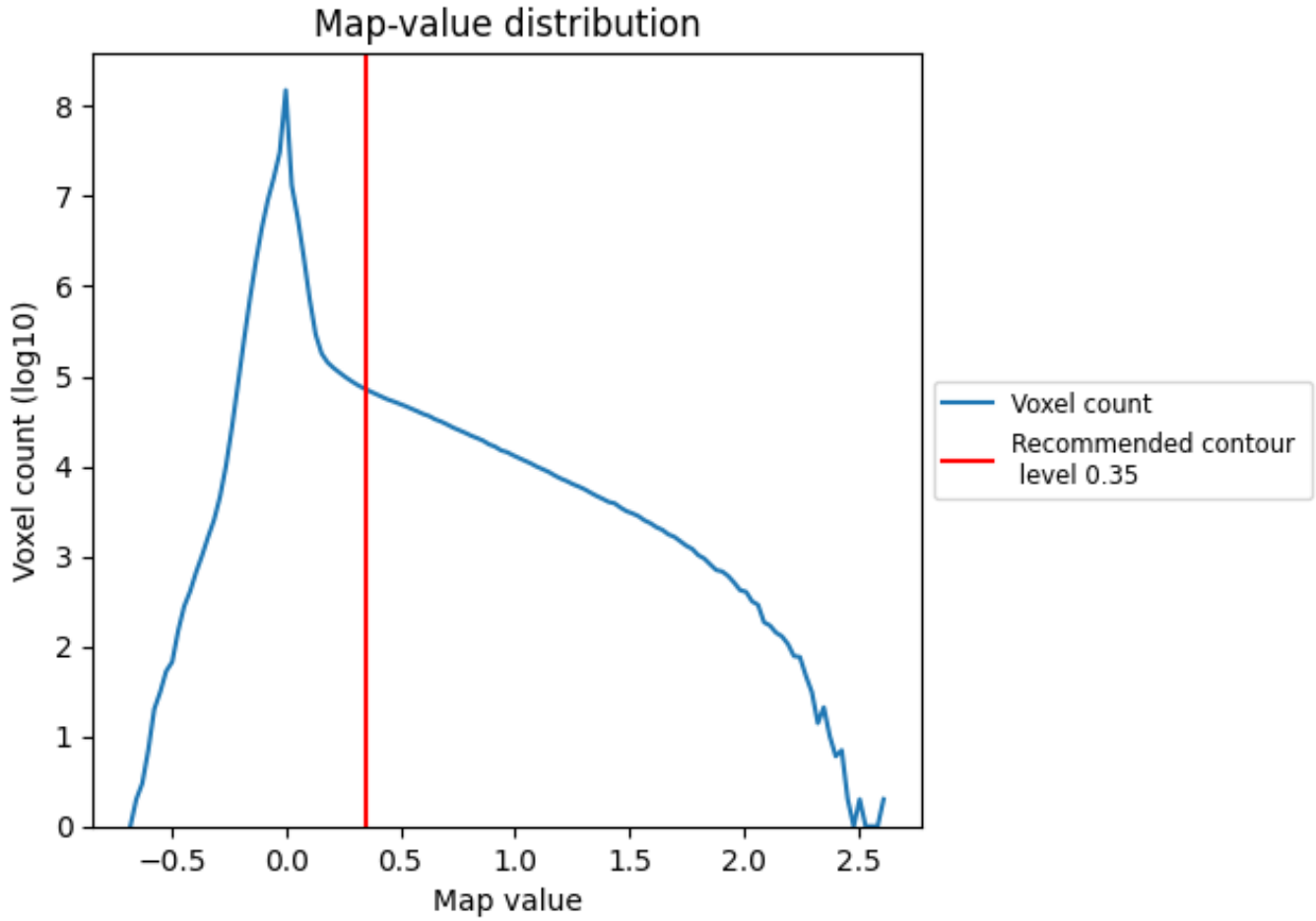
6.6 Mask visualisation (i)

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

7 Map analysis

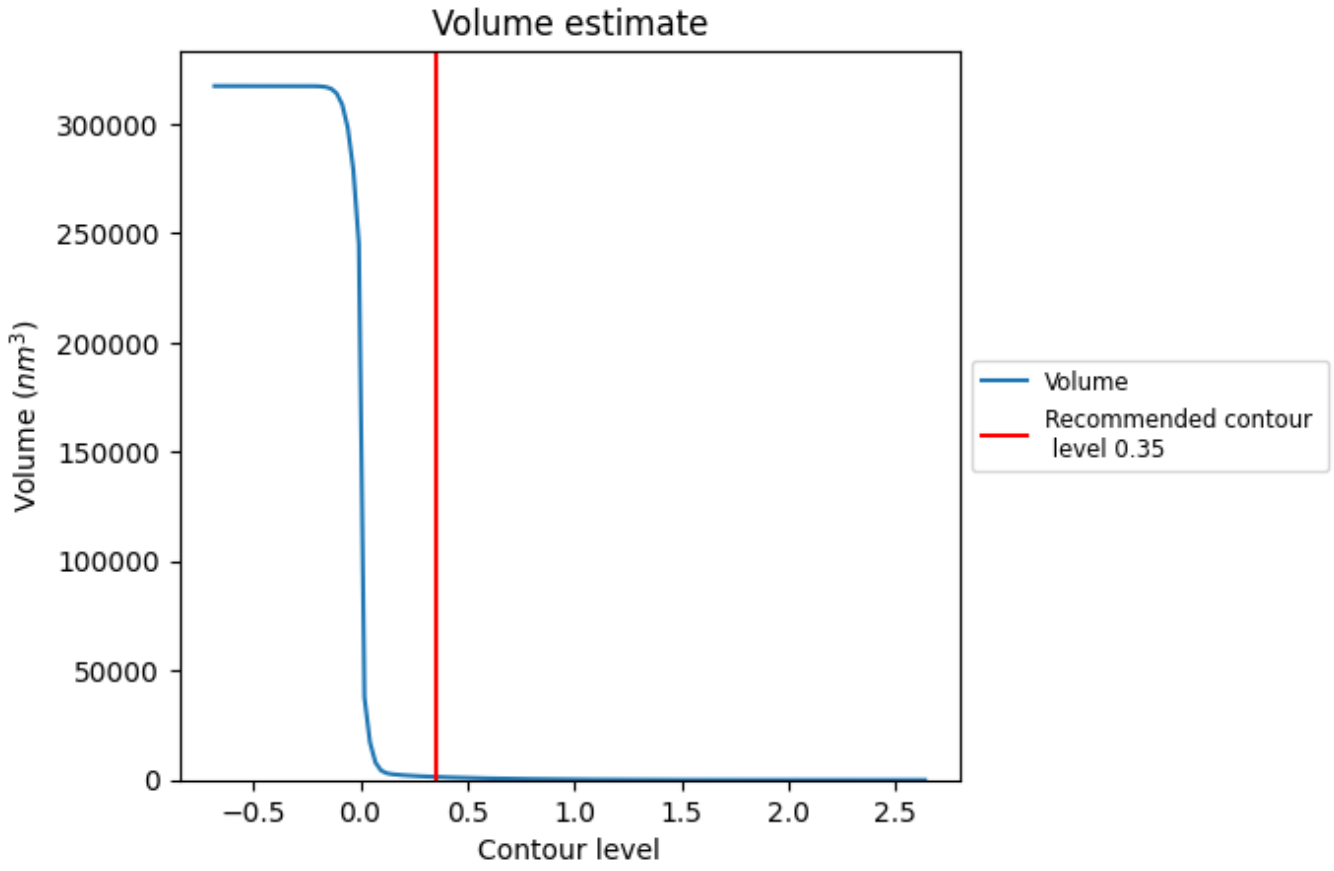
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

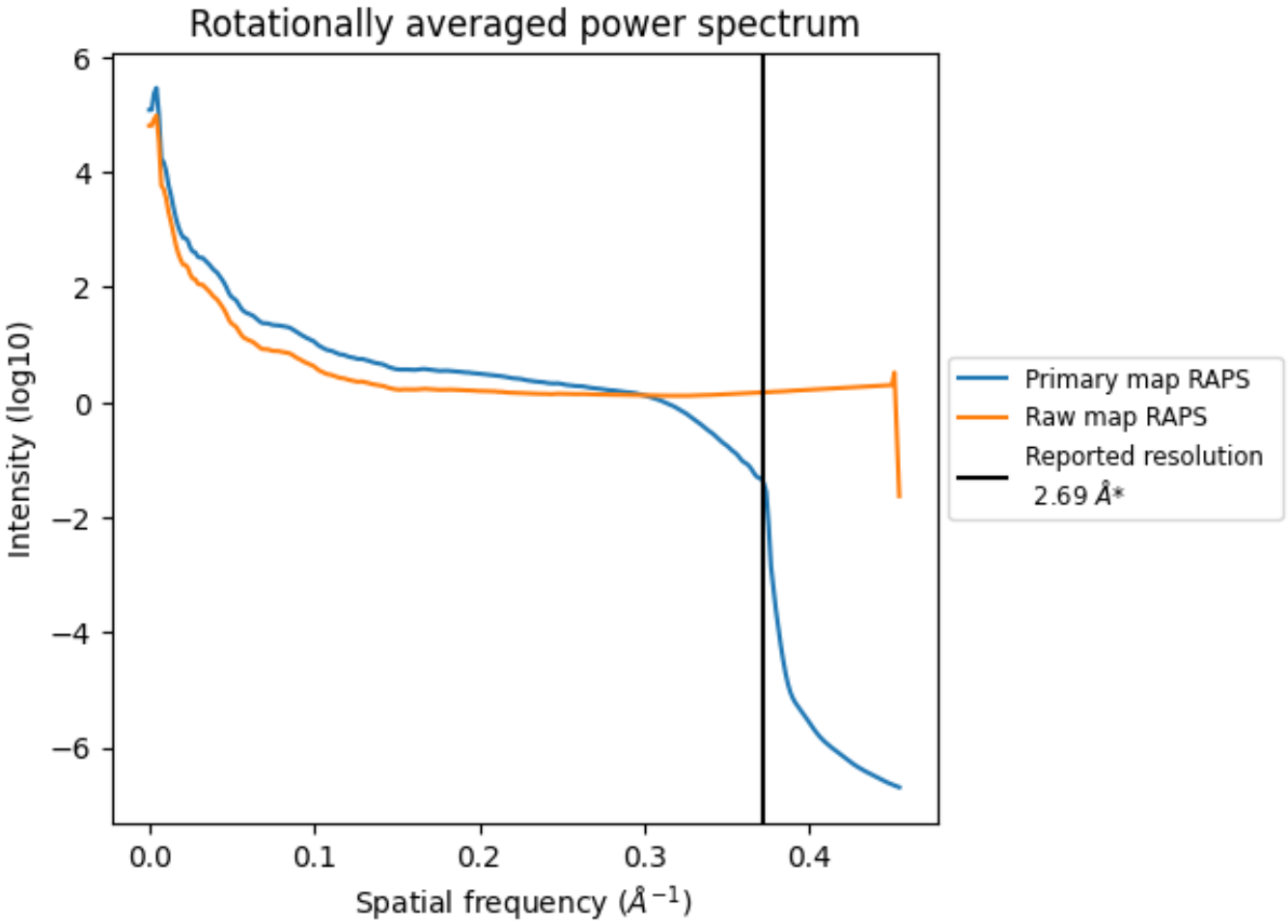
7.2 Volume estimate



The volume at the recommended contour level is 1417 nm^3; this corresponds to an approximate mass of 1280 kDa.

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

7.3 Rotationally averaged power spectrum (i)

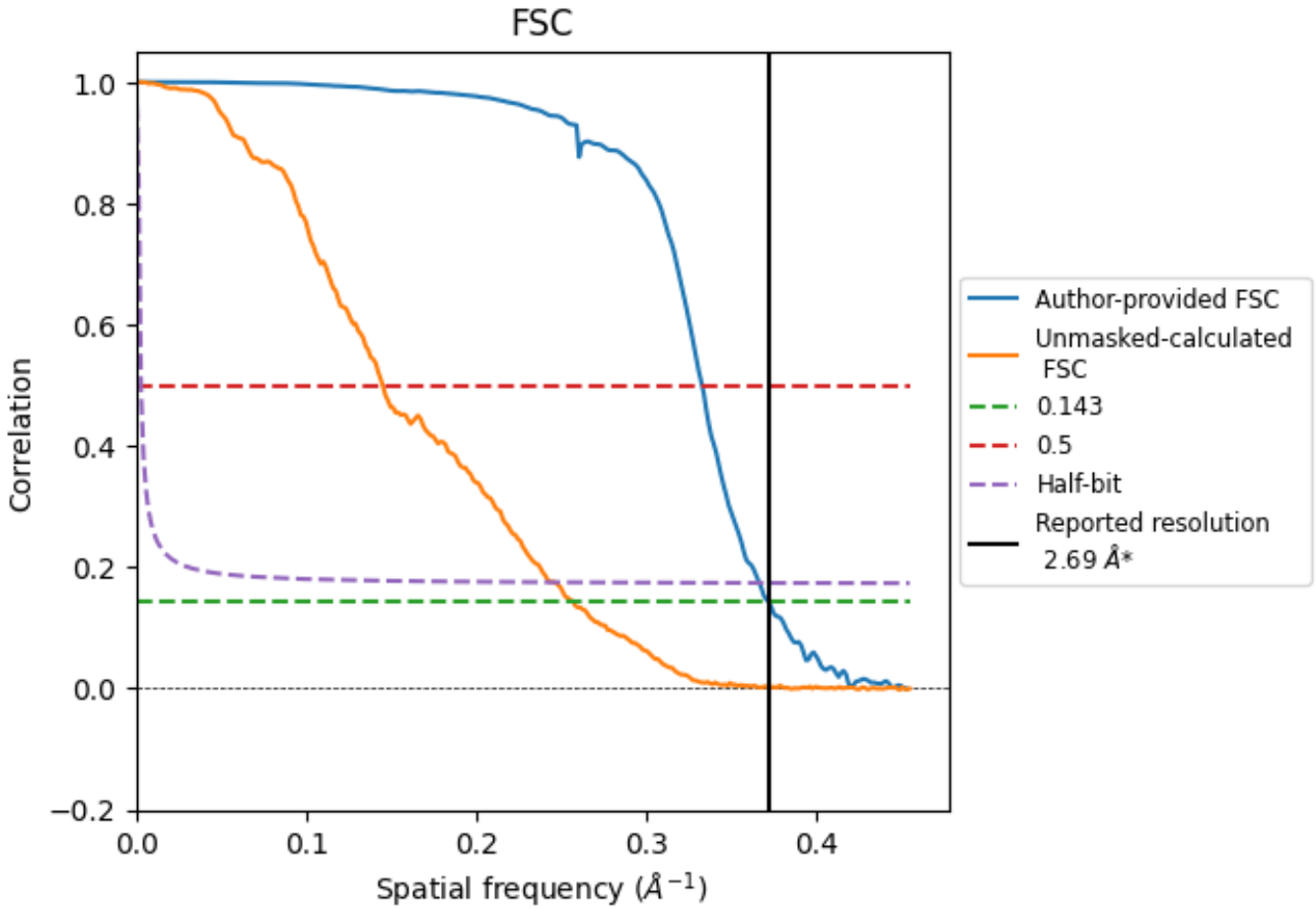


*Reported resolution corresponds to spatial frequency of 0.372 Å^{-1}

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.372 Å^{-1}

8.2 Resolution estimates (i)

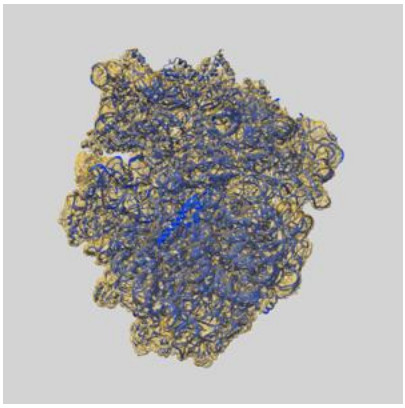
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.69	-	-
Author-provided FSC curve	2.69	3.01	2.73
Unmasked-calculated*	3.89	6.91	4.07

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.89 differs from the reported value 2.69 by more than 10 %

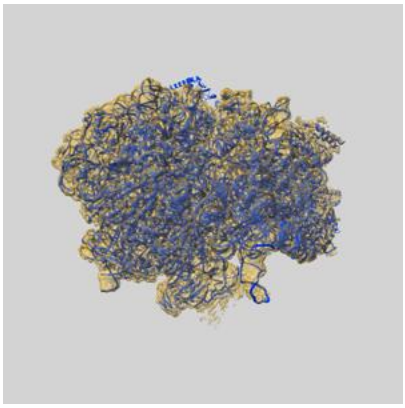
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-60034 and PDB model 8ZEJ. Per-residue inclusion information can be found in section 3 on page 15.

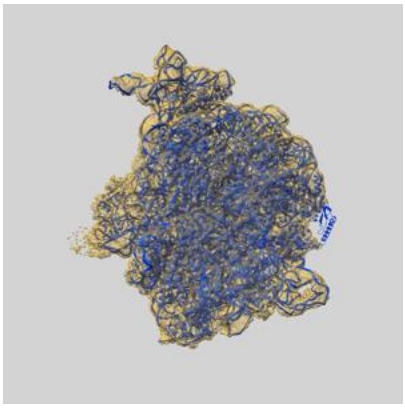
9.1 Map-model overlay



X



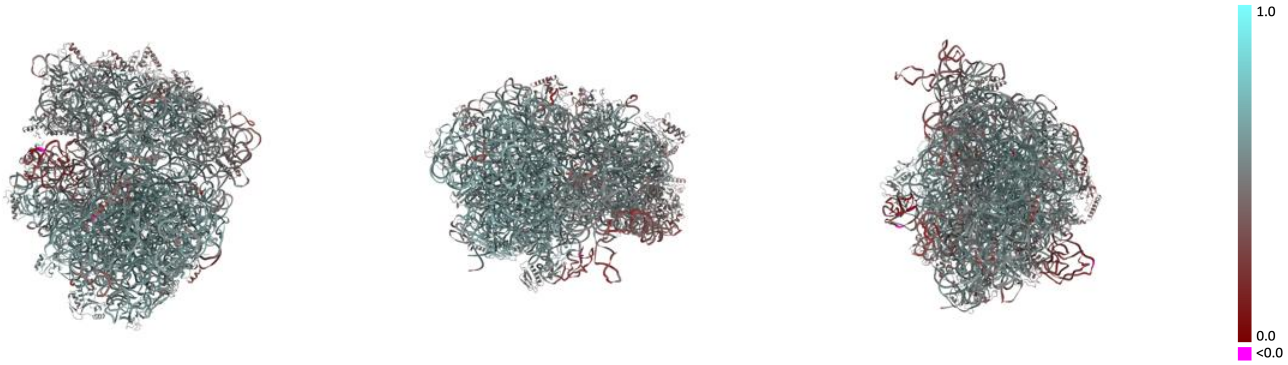
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.35 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.

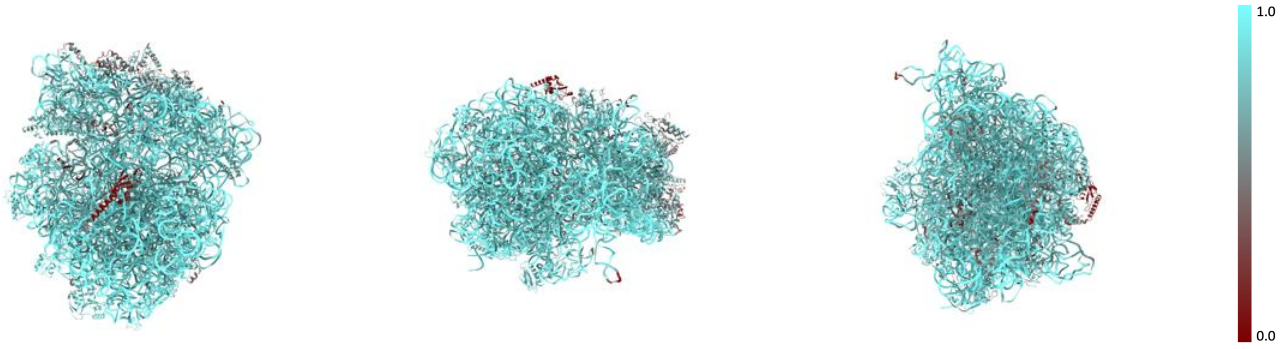
9.2 Q-score mapped to coordinate model



X Y Z

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

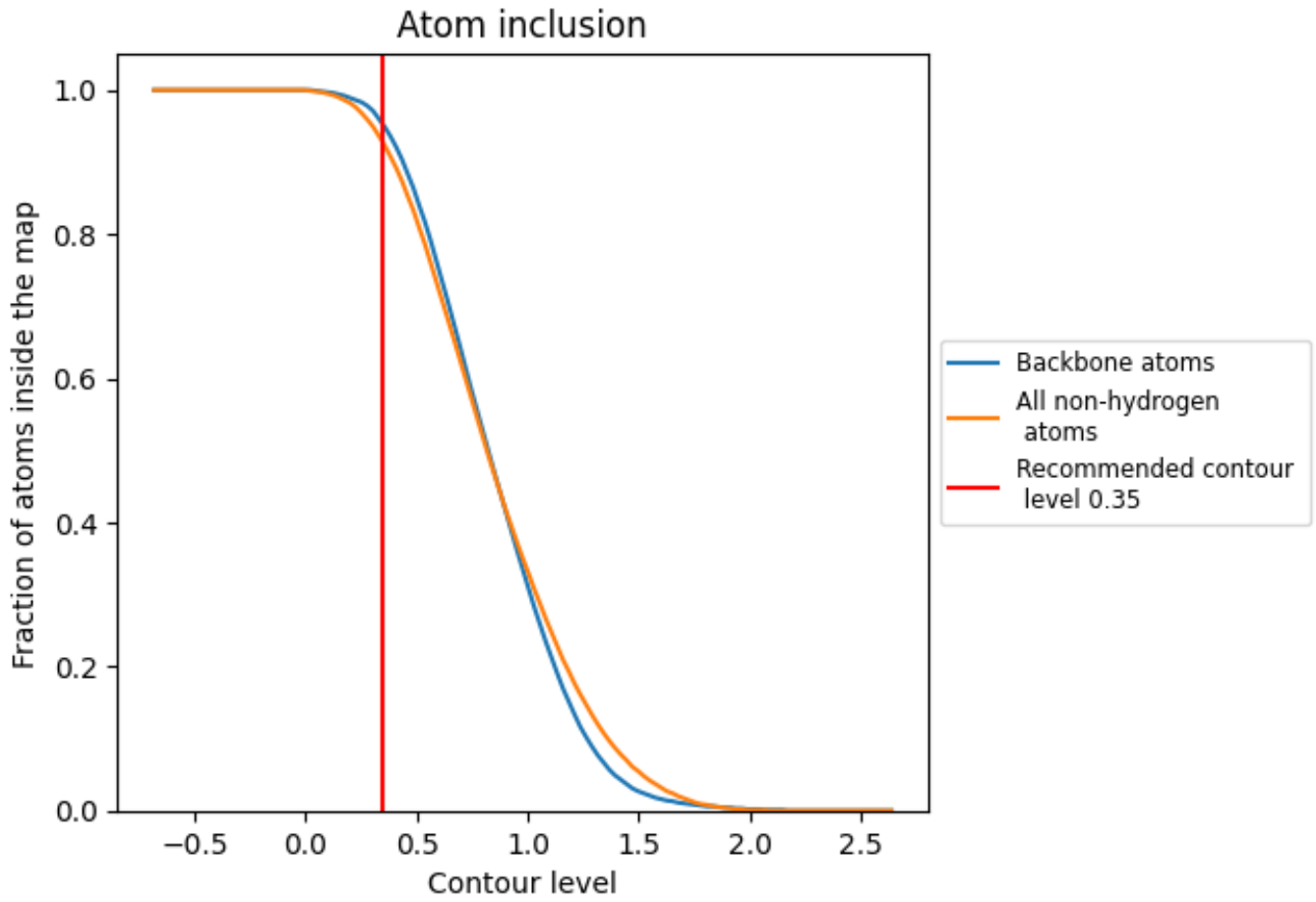
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.35).

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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9270	0.5400
0	0.9380	0.5710
1	0.9300	0.5200
2	0.9110	0.5630
4	0.9110	0.5720
5	0.7920	0.5470
6	0.9490	0.6100
7	0.9490	0.6070
8	0.9450	0.5900
A	0.9720	0.5170
B	0.5120	0.4410
C	0.7230	0.5060
D	0.5990	0.4090
E	0.8140	0.5190
F	0.7860	0.4690
G	0.7440	0.4750
H	0.8770	0.5230
I	0.8390	0.4900
J	0.6440	0.4380
K	0.8420	0.5250
L	0.6800	0.4540
M	0.8090	0.4820
N	0.8330	0.5110
O	0.8840	0.5170
P	0.8310	0.4720
Q	0.8350	0.4860
R	0.8360	0.5170
S	0.7970	0.4910
T	0.8350	0.4540
U	0.5220	0.4550
X	0.8040	0.3890
Y	0.8680	0.4840
Z	0.6020	0.5100
a	0.9900	0.5530
b	0.9850	0.5700

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	0.9390	0.5970
d	0.9490	0.5890
e	0.9240	0.5690
f	0.8650	0.4920
g	0.8930	0.5020
h	0.2480	0.3910
k	0.9460	0.5850
l	0.9120	0.5770
m	0.9460	0.5770
n	0.8770	0.5810
o	0.9630	0.5980
p	0.9320	0.5260
q	0.9090	0.5780
r	0.9680	0.5970
s	0.9490	0.5670
t	0.9280	0.5750
u	0.8660	0.5310
v	0.9210	0.5410
w	0.9090	0.5420
x	0.7190	0.4930
y	0.8920	0.5910
z	0.2870	0.4340