



Full wwPDB EM Validation Report ⓘ

Mar 26, 2026 – 08:36 PM UTC

PDB ID : 5MGP / pdb_00005mgp
EMDB ID : EMD-3508
Title : Structural basis for ArfA-RF2 mediated translation termination on stop-codon lacking mRNAs
Authors : Huter, P.; Mueller, C.; Beckert, B.; Arenz, S.; Berninghausen, O.; Beckmann, R.; Wilson, N.D.
Deposited on : 2016-11-21
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

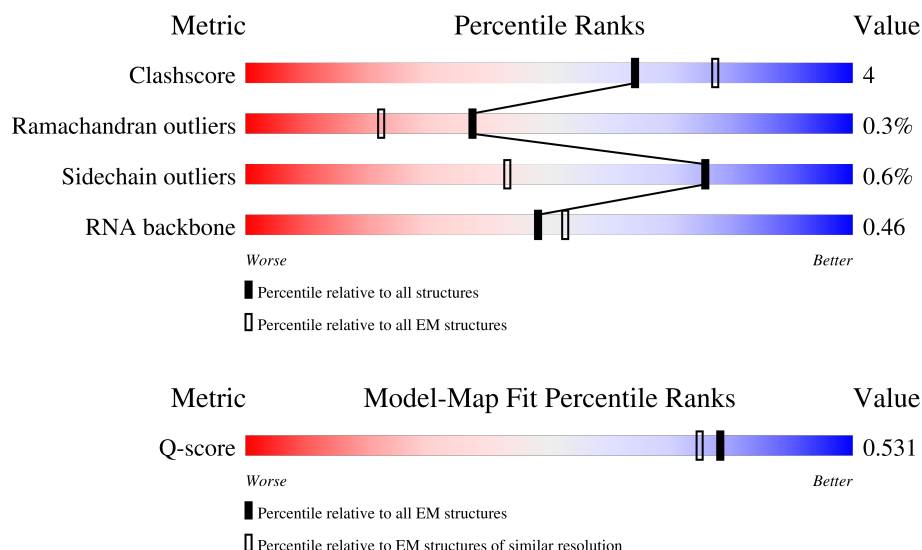
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	A	2903	9% 70% 27% .
2	B	120	6% 69% 26% 5%
3	C	271	6% 84% 16%

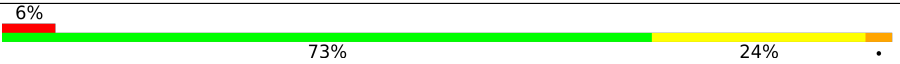
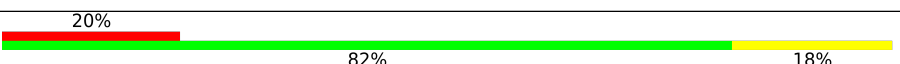
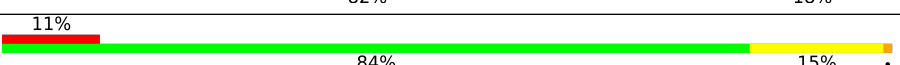
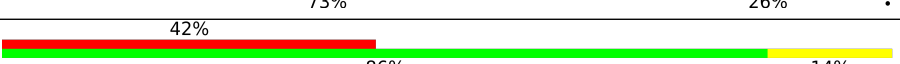
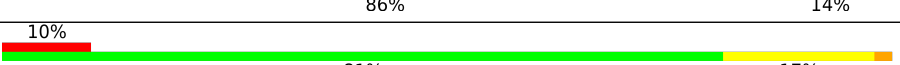
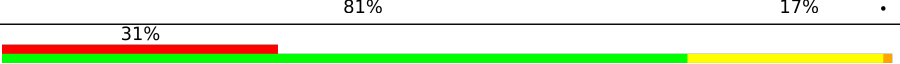
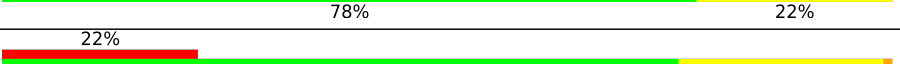
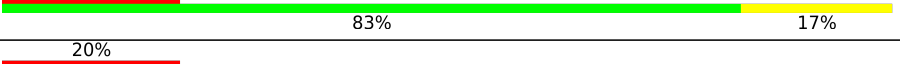
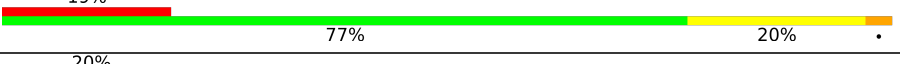
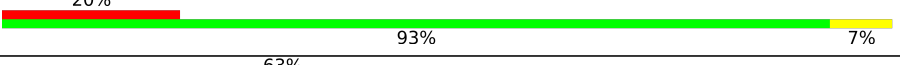
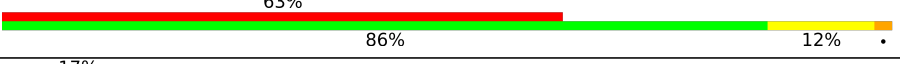
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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	201	
6	F	177	
7	G	176	
8	H	149	
9	J	142	
10	K	122	
11	L	143	
12	M	136	
13	N	120	
14	O	116	
15	P	114	
16	Q	117	
17	R	103	
18	S	110	
19	T	93	
20	U	102	
21	V	94	
22	W	75	
23	X	77	
24	Y	63	
25	Z	58	
26	0	56	
27	1	50	
28	2	46	

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Mol	Chain	Length	Quality of chain
29	3	64	
30	4	38	
31	6	66	
32	a	1539	
33	b	218	
34	c	206	
35	d	205	
36	e	157	
37	f	100	
38	g	151	
39	h	129	
40	i	127	
41	j	98	
42	k	116	
43	l	123	
44	m	114	
45	n	101	
46	o	88	
47	p	82	
48	q	80	
49	r	65	
50	s	79	
51	t	85	
52	u	65	
53	v	6	

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Mol	Chain	Length	Quality of chain
54	w	45	13% 58% 27% 13%
55	x	77	12% 74% 26%
56	z	359	59% 80% 19%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 147155 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2900	Total	C	N	O	P	0	0
			62261	27774	11460	20127	2900		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	747	C	U	conflict	GB 802133627
A	1847	G	A	conflict	GB 802133627
A	2069	A	G	conflict	GB 802133627

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	120	A	U	conflict	GB 1028480521

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

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

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 32 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1539	Total	C	N	O	P	0	0
			33016	14725	6052	10700	1539		

- Molecule 33 is a protein called 30S ribosomal protein S2.

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

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 35 is a protein called 30S ribosomal protein S4.

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

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 39 is a protein called 30S ribosomal protein S8.

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

- Molecule 40 is a protein called 30S ribosomal protein S9.

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

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 45 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP P0AG59

- Molecule 46 is a protein called 30S ribosomal protein S15.

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

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 48 is a protein called 30S ribosomal protein S17.

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

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	r	65	Total	C	N	O	0	0
			504	317	96	91		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 52 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	6	Total	C	N	O	P	0	0
			126	56	22	42	6		

- Molecule 54 is a protein called Alternative ribosome-rescue factor A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	45	Total	C	N	O	S	0	0
			369	229	76	63	1		

- Molecule 55 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	x	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		

- Molecule 56 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	359	Total	C	N	O	S	0	0
			2846	1749	500	587	10		

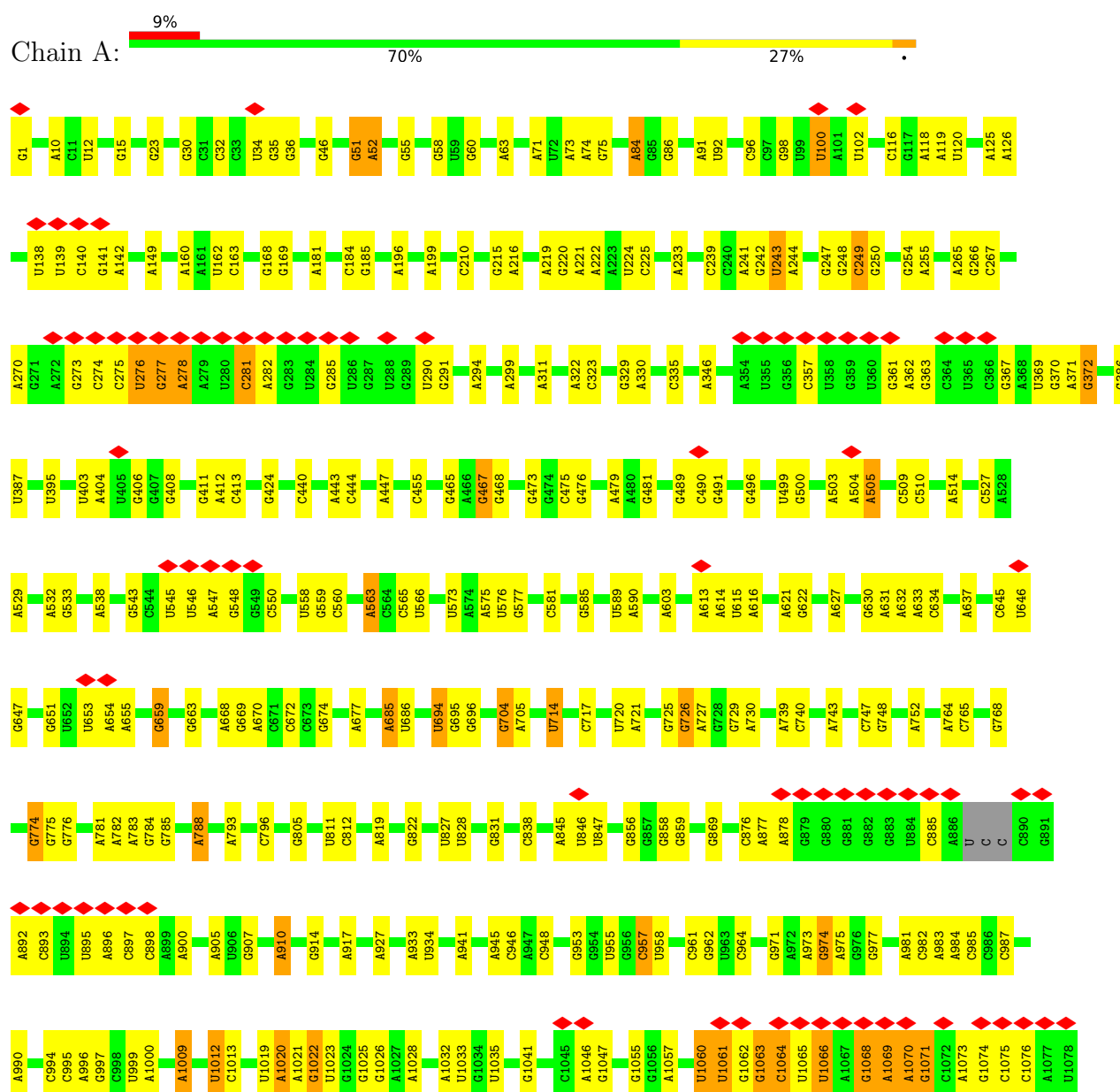
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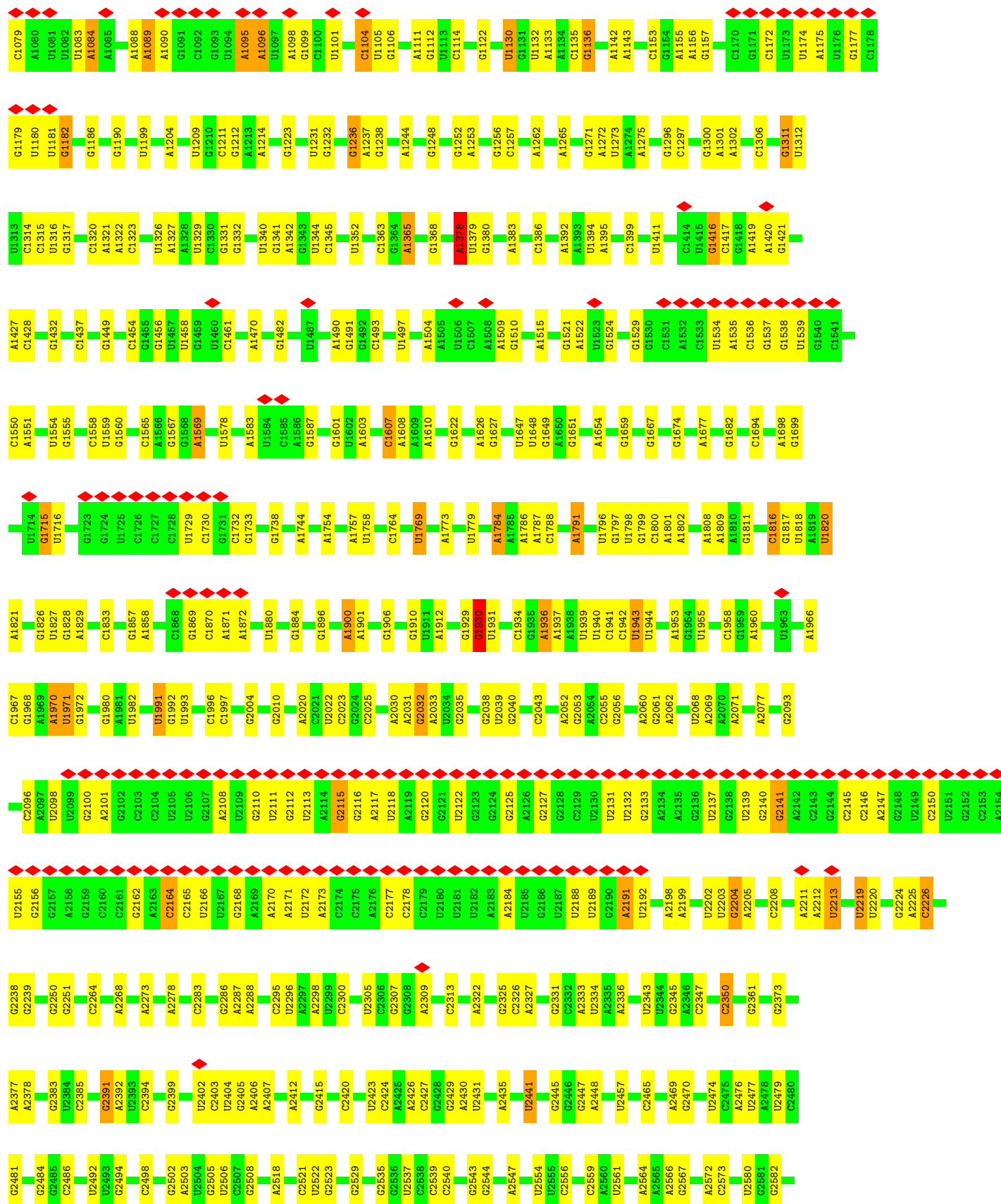
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z	251	ALA	GLY	conflict	UNP P07012

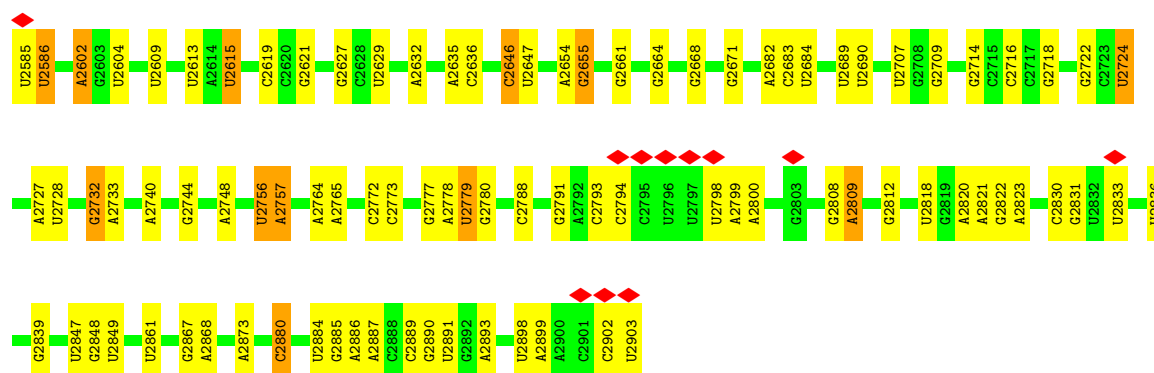
3 Residue-property plots

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

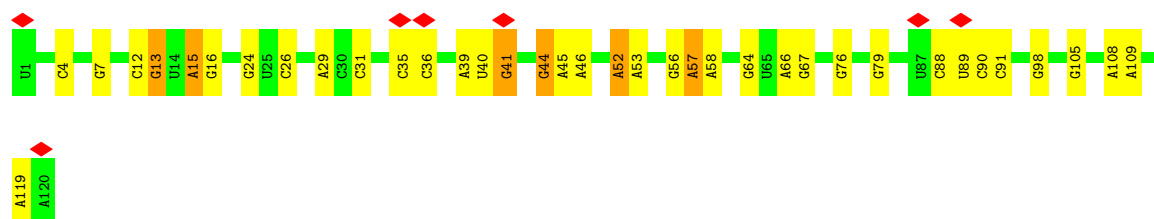
• Molecule 1: 23S ribosomal RNA



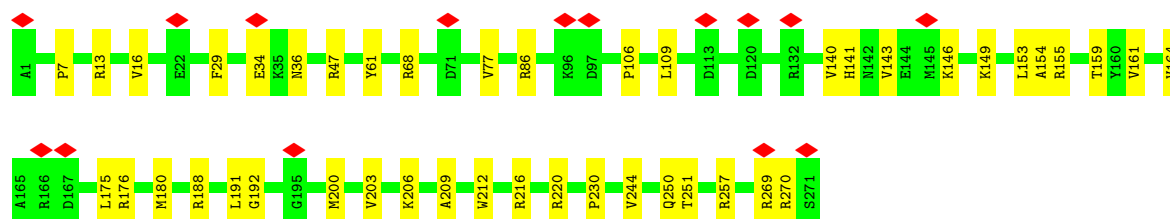
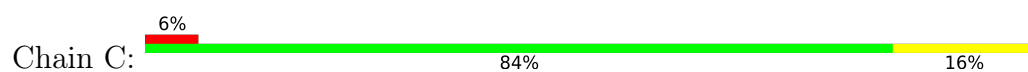




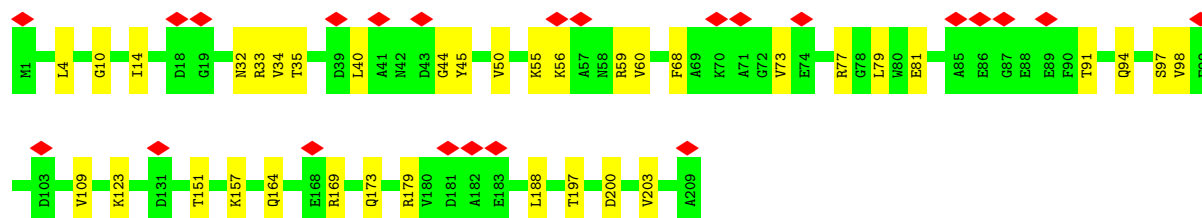
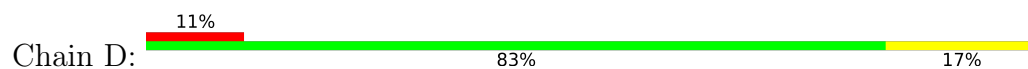
• Molecule 2: 5S ribosomal RNA



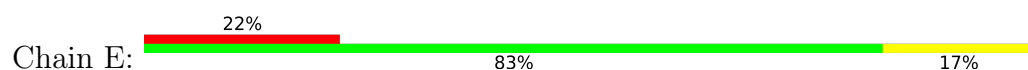
• Molecule 3: 50S ribosomal protein L2

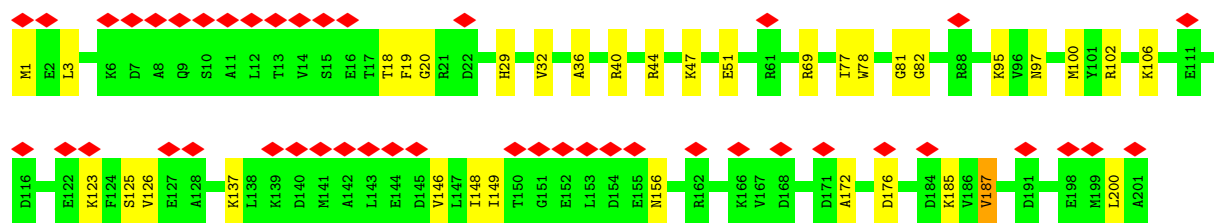


• Molecule 4: 50S ribosomal protein L3

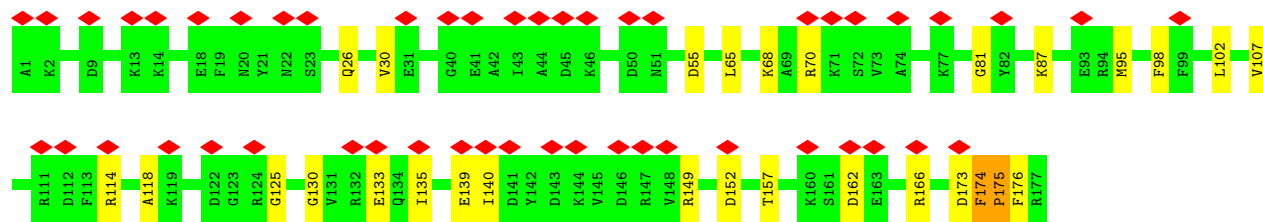
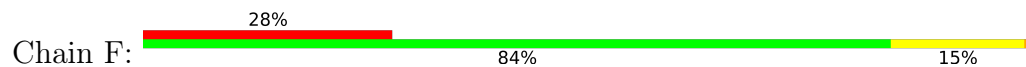


• Molecule 5: 50S ribosomal protein L4

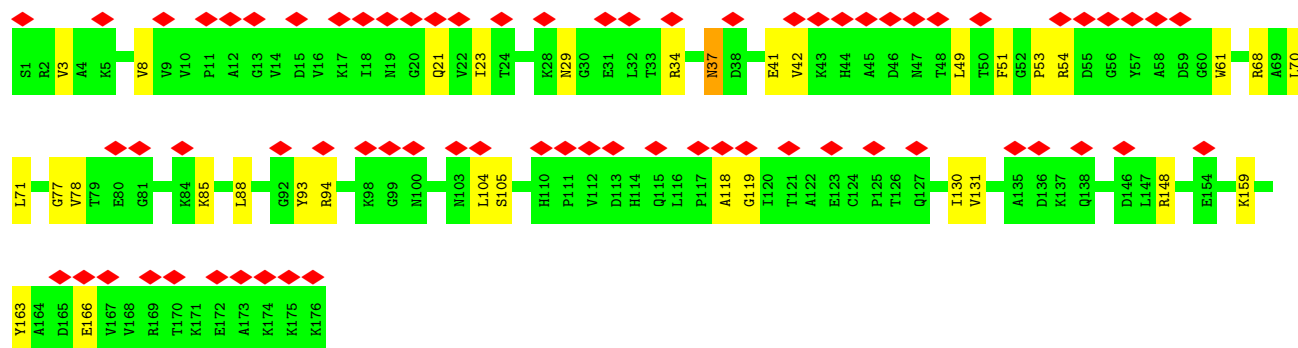
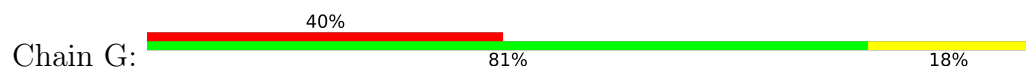




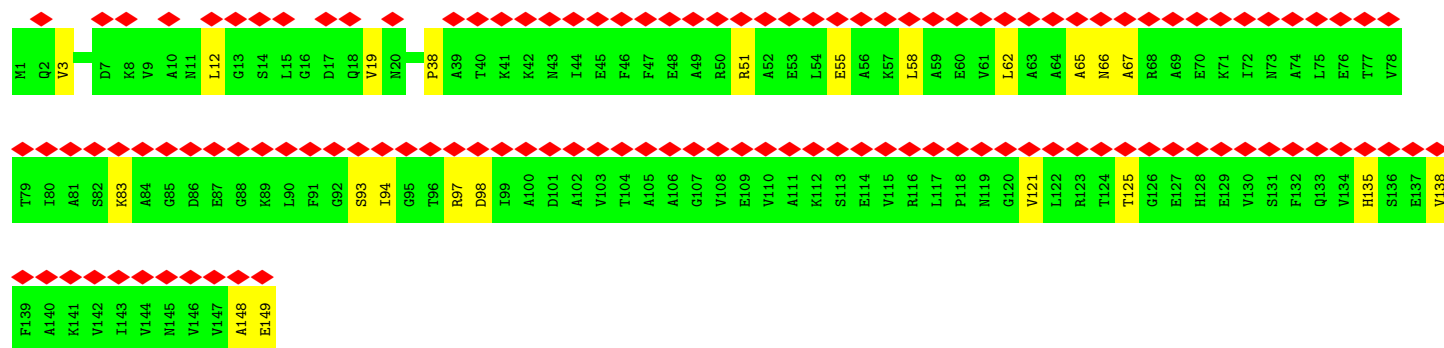
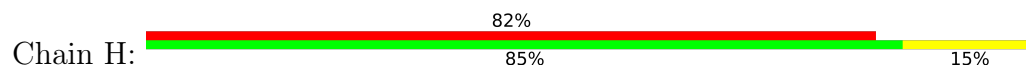
• Molecule 6: 50S ribosomal protein L5



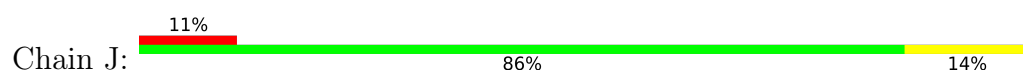
• Molecule 7: 50S ribosomal protein L6



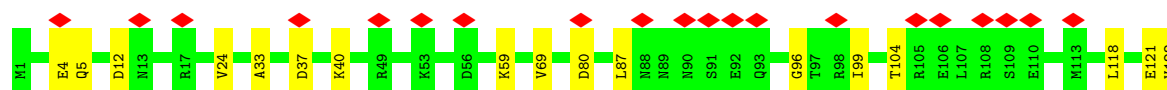
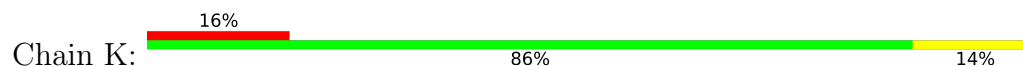
• Molecule 8: 50S ribosomal protein L9



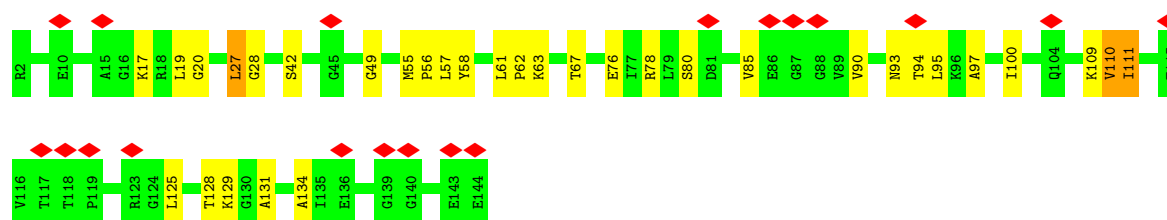
• Molecule 9: 50S ribosomal protein L13



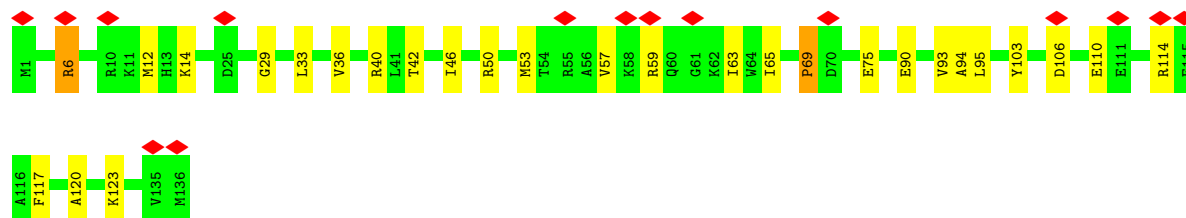
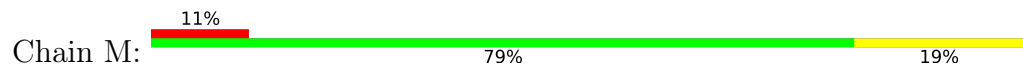
- Molecule 10: 50S ribosomal protein L14



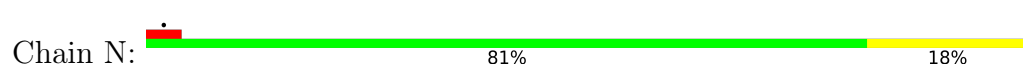
- Molecule 11: 50S ribosomal protein L15



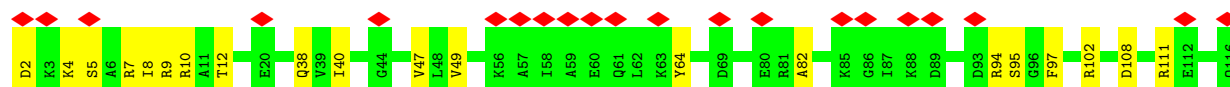
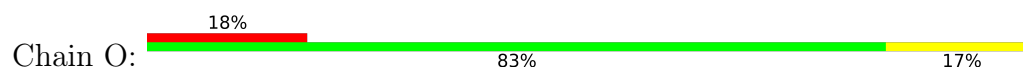
- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17



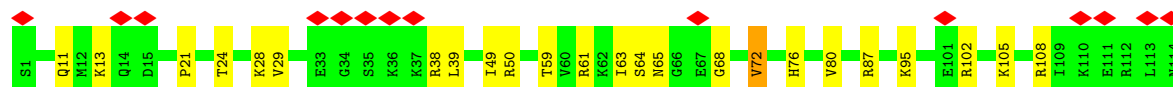
- Molecule 14: 50S ribosomal protein L18



F117

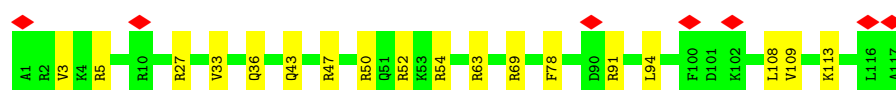
- Molecule 15: 50S ribosomal protein L19

Chain P: 

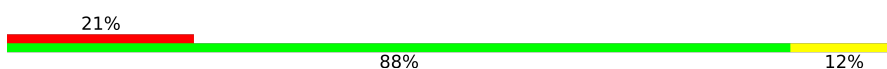


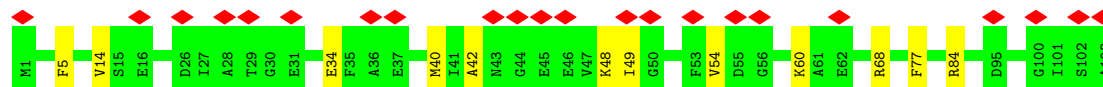
- Molecule 16: 50S ribosomal protein L20

Chain Q: 



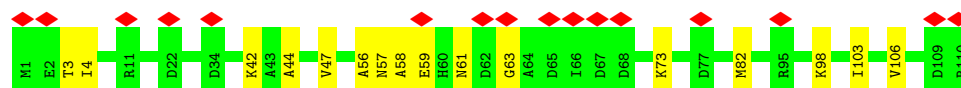
- Molecule 17: 50S ribosomal protein L21

Chain R: 



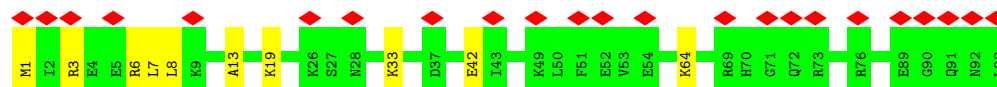
- Molecule 18: 50S ribosomal protein L22

Chain S: 



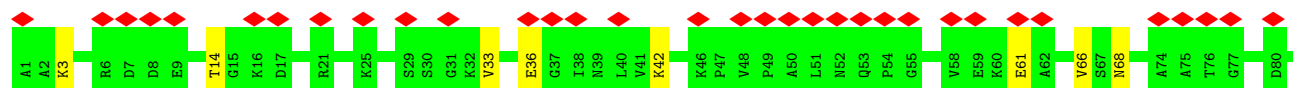
- Molecule 19: 50S ribosomal protein L23

Chain T: 



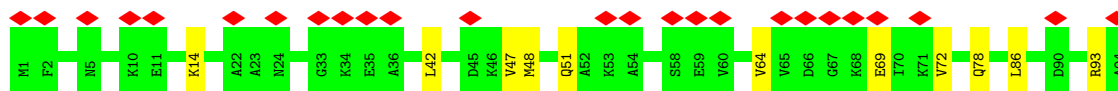
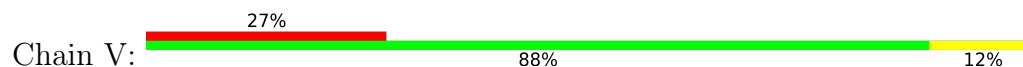
- Molecule 20: 50S ribosomal protein L24

Chain U: 





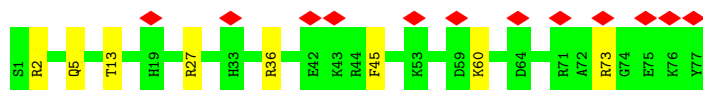
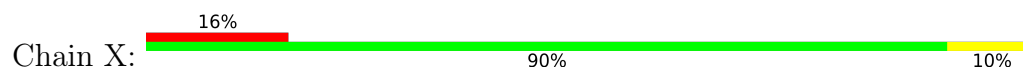
- Molecule 21: 50S ribosomal protein L25



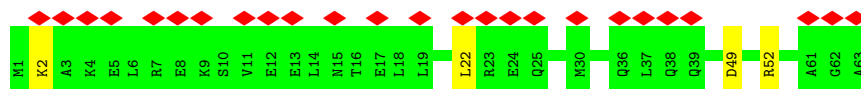
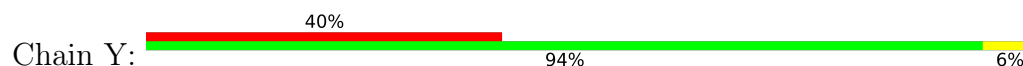
- Molecule 22: 50S ribosomal protein L27



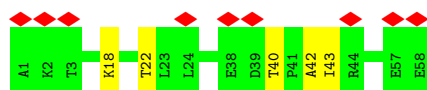
- Molecule 23: 50S ribosomal protein L28



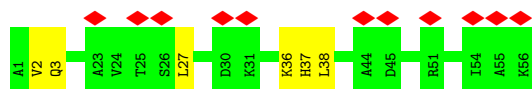
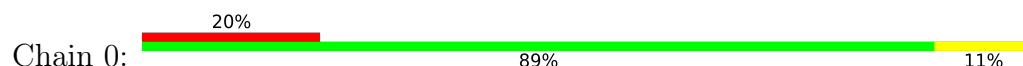
- Molecule 24: 50S ribosomal protein L29



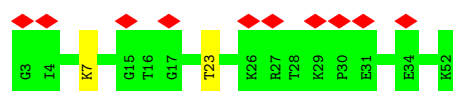
- Molecule 25: 50S ribosomal protein L30



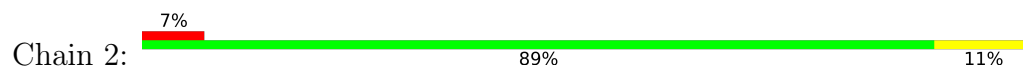
- Molecule 26: 50S ribosomal protein L32



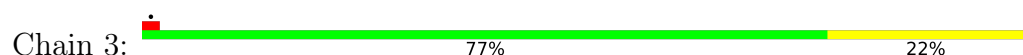
- Molecule 27: 50S ribosomal protein L33



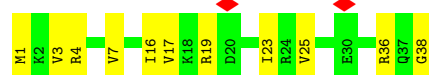
- Molecule 28: 50S ribosomal protein L34



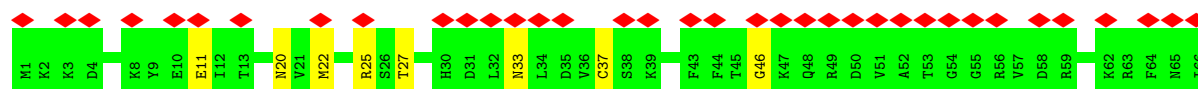
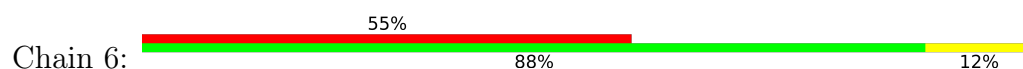
- Molecule 29: 50S ribosomal protein L35



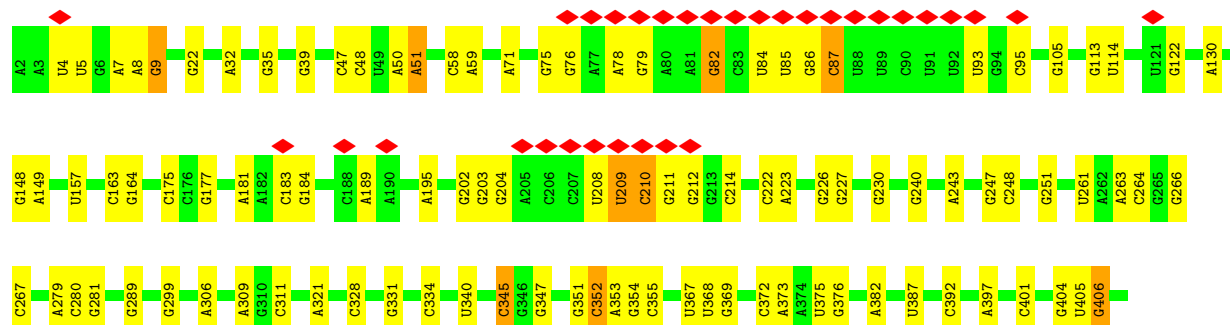
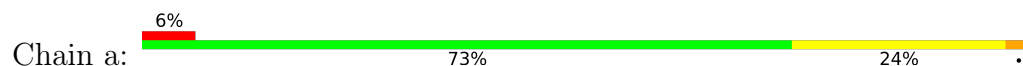
- Molecule 30: 50S ribosomal protein L36

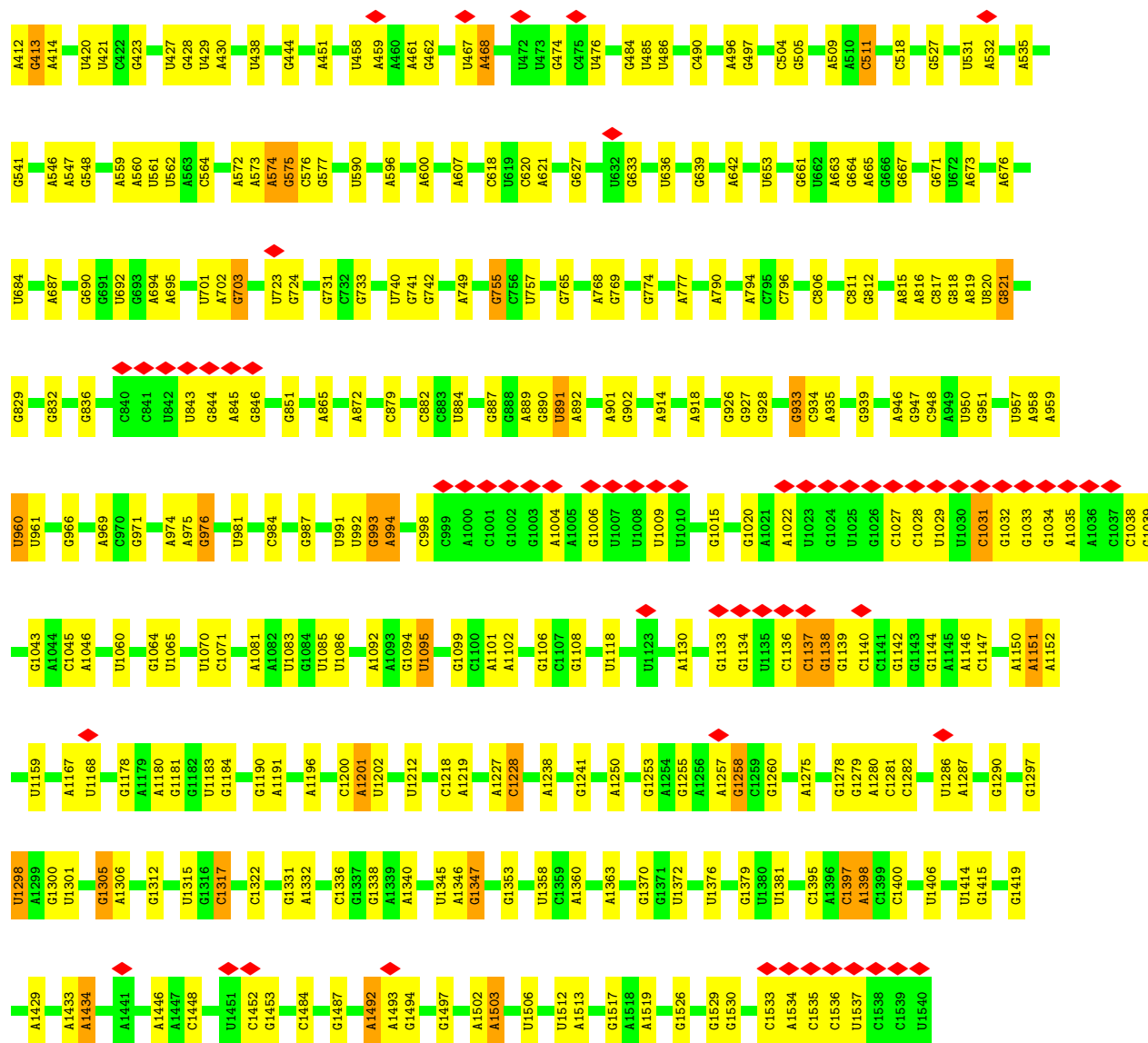


- Molecule 31: 50S ribosomal protein L31

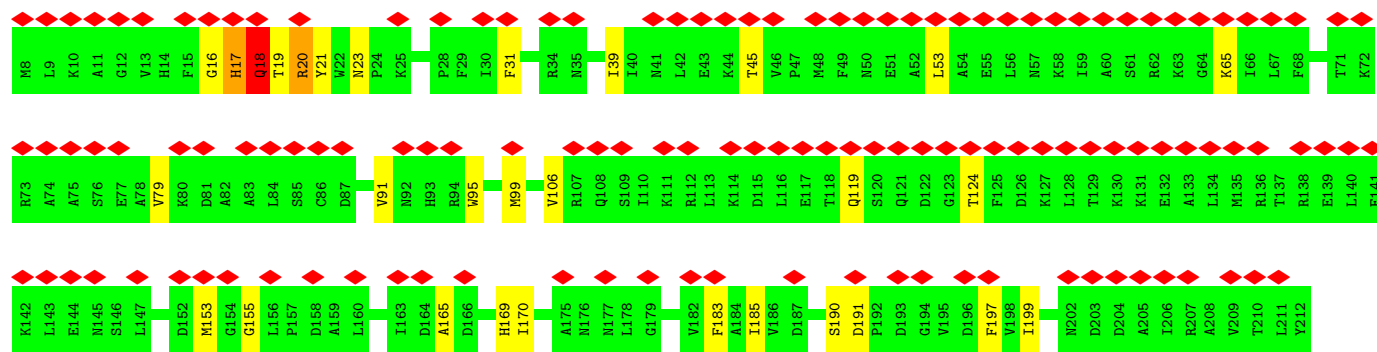
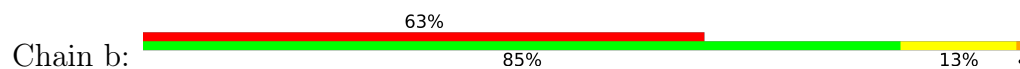


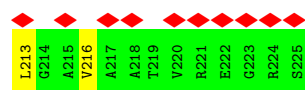
- Molecule 32: 16S ribosomal RNA



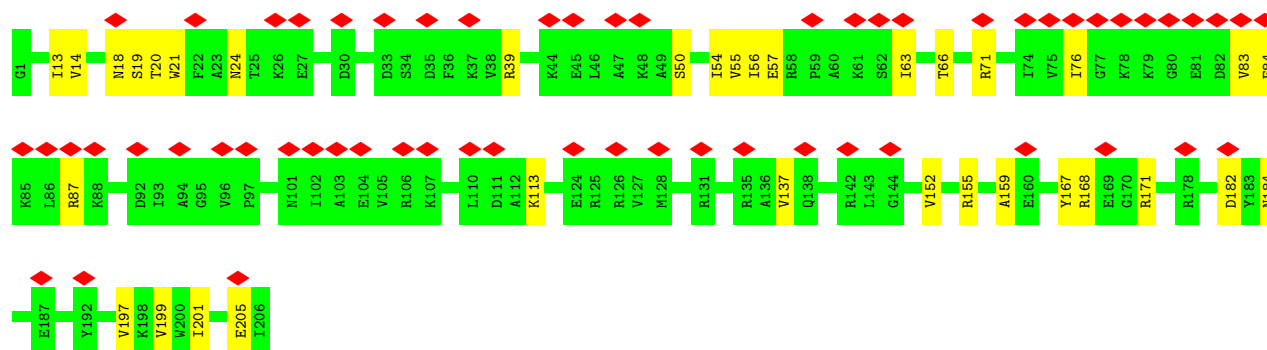
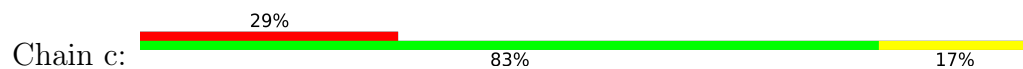


• Molecule 33: 30S ribosomal protein S2

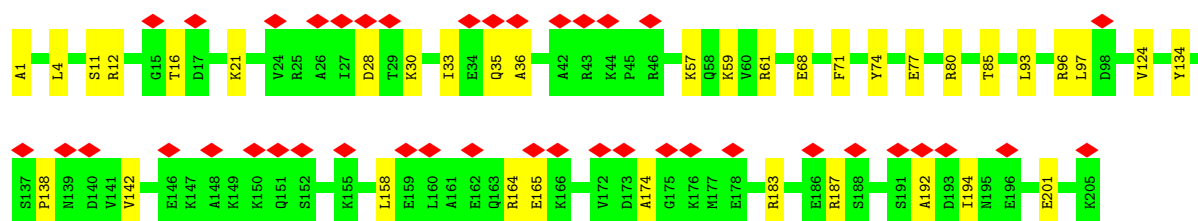
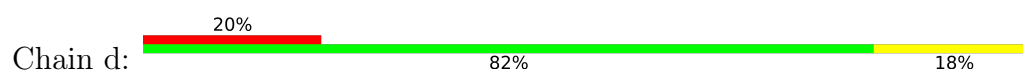




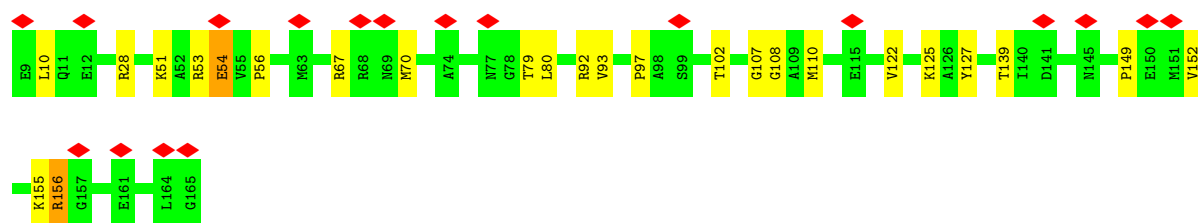
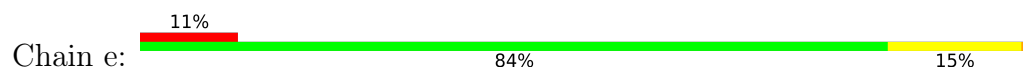
• Molecule 34: 30S ribosomal protein S3



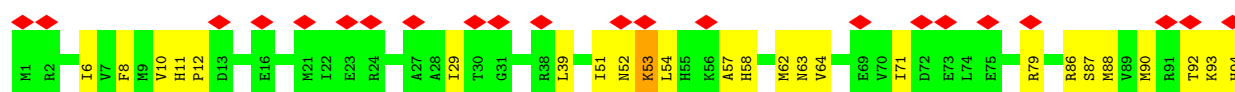
• Molecule 35: 30S ribosomal protein S4

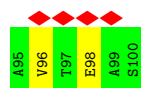


• Molecule 36: 30S ribosomal protein S5

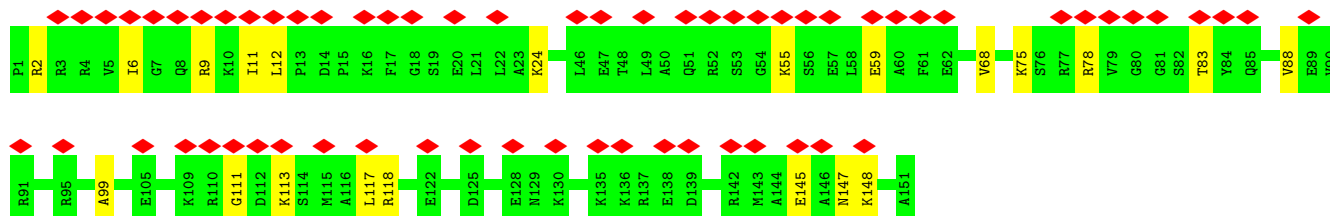
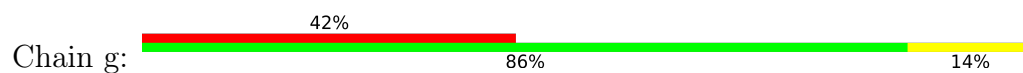


• Molecule 37: 30S ribosomal protein S6

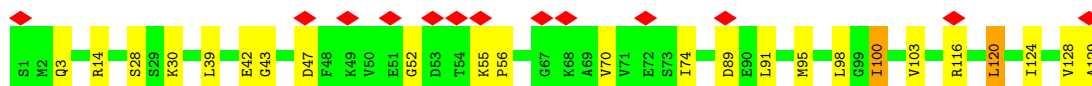
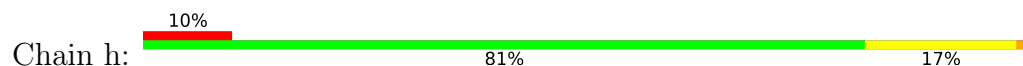




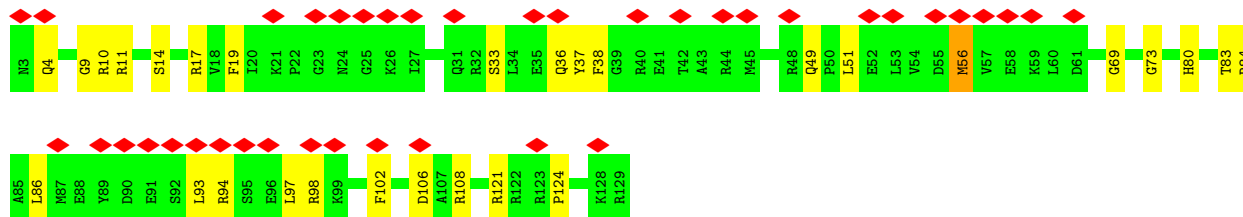
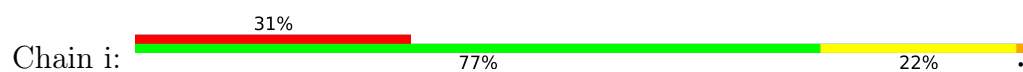
- Molecule 38: 30S ribosomal protein S7



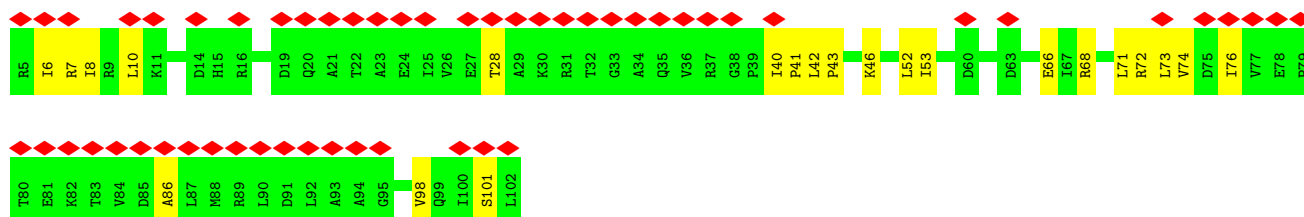
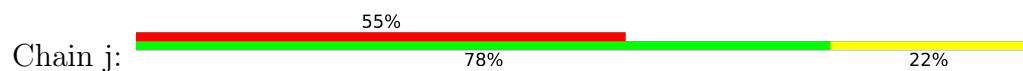
- Molecule 39: 30S ribosomal protein S8



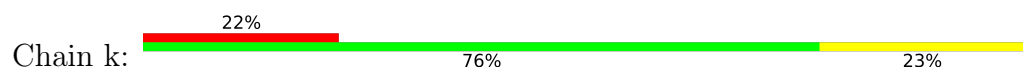
- Molecule 40: 30S ribosomal protein S9

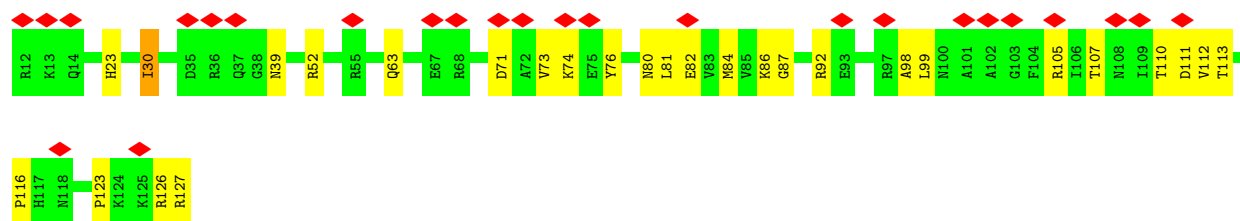


- Molecule 41: 30S ribosomal protein S10

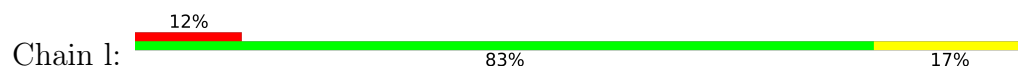


- Molecule 42: 30S ribosomal protein S11

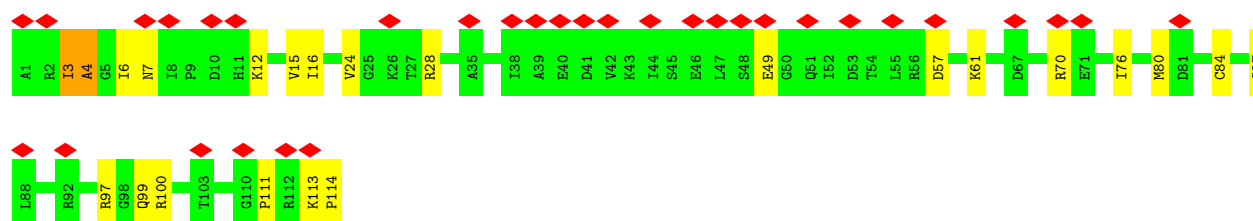
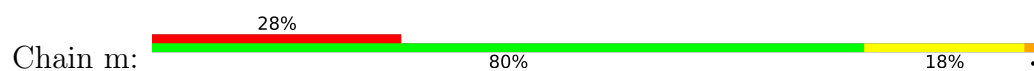




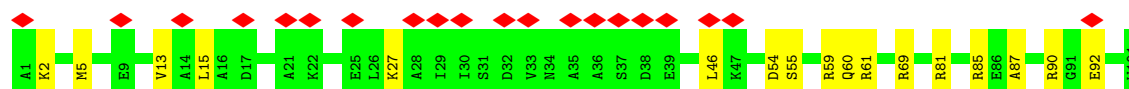
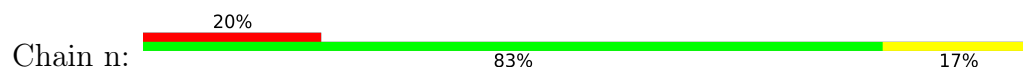
- Molecule 43: 30S ribosomal protein S12



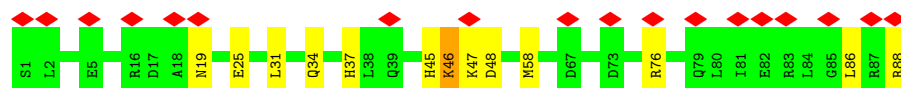
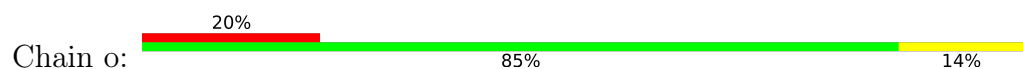
- Molecule 44: 30S ribosomal protein S13



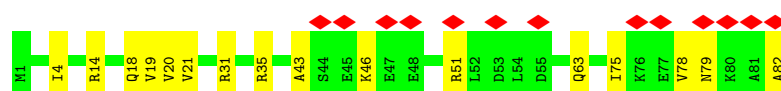
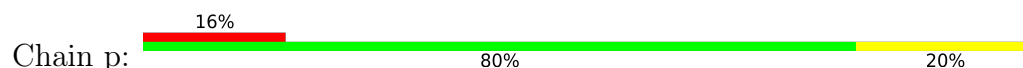
- Molecule 45: 30S ribosomal protein S14



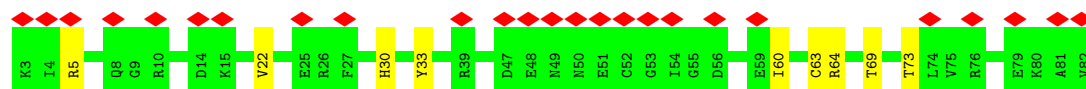
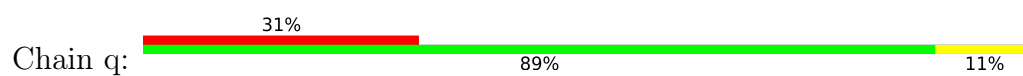
- Molecule 46: 30S ribosomal protein S15



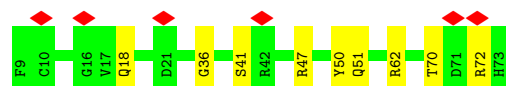
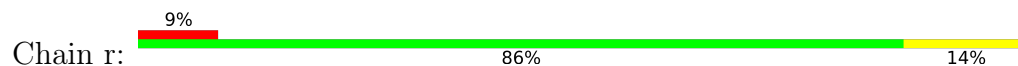
- Molecule 47: 30S ribosomal protein S16



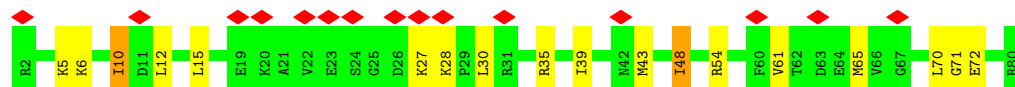
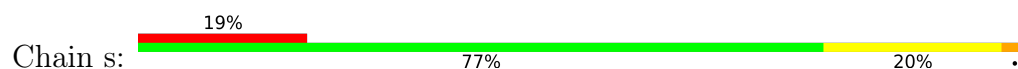
- Molecule 48: 30S ribosomal protein S17



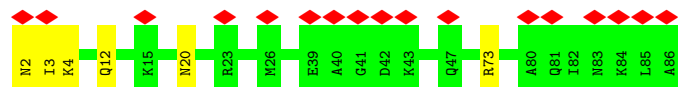
- Molecule 49: 30S ribosomal protein S18



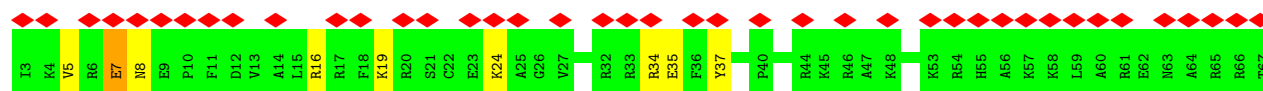
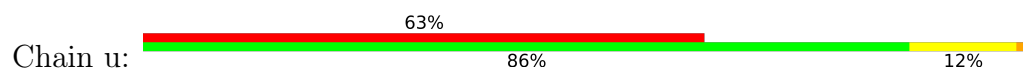
- Molecule 50: 30S ribosomal protein S19



- Molecule 51: 30S ribosomal protein S20



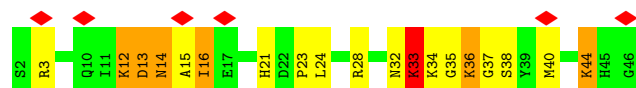
- Molecule 52: 30S ribosomal protein S21



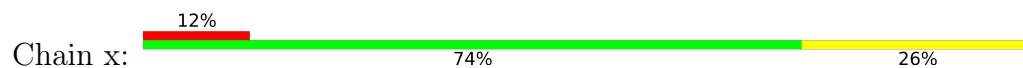
- Molecule 53: mRNA



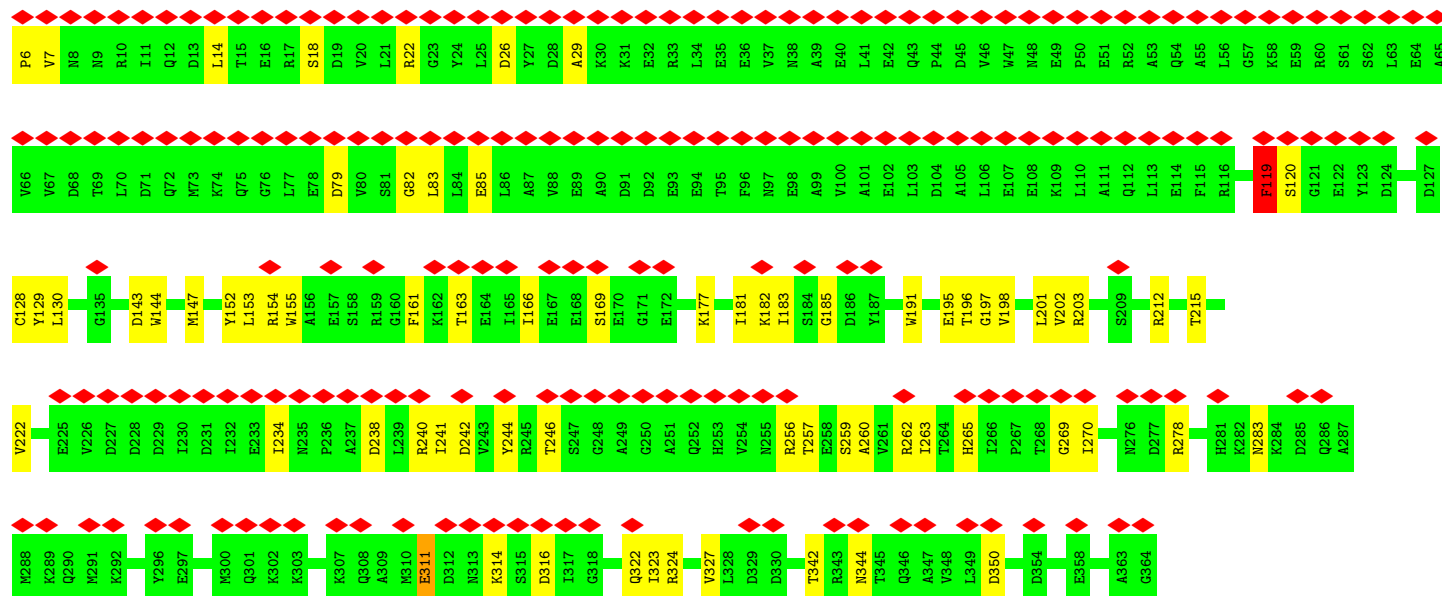
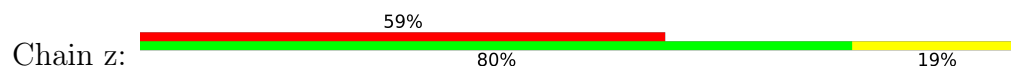
- Molecule 54: Alternative ribosome-rescue factor A



- Molecule 55: P-site tRNA



- Molecule 56: Peptide chain release factor 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	69089	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	302	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	2.041	Depositor
Minimum map value	-1.154	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.140	Depositor
Recommended contour level	0.358	Depositor
Map size (Å)	271.0, 281.84, 252.57199	wwPDB
Map dimensions	250, 260, 233	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.35	0/69733	0.40	6/108786 (0.0%)
2	B	0.31	0/2876	0.43	1/4483 (0.0%)
3	C	0.40	0/2121	0.69	2/2852 (0.1%)
4	D	0.39	0/1586	0.62	0/2134
5	E	0.33	0/1571	0.63	1/2113 (0.0%)
6	F	0.31	0/1434	0.72	0/1926
7	G	0.27	0/1343	0.57	0/1816
8	H	0.26	0/1122	0.66	0/1515
9	J	0.36	0/1152	0.60	0/1551
10	K	0.39	0/947	0.74	0/1268
11	L	0.36	0/1054	0.84	4/1403 (0.3%)
12	M	0.38	0/1093	0.73	5/1460 (0.3%)
13	N	0.39	0/973	0.75	0/1301
14	O	0.35	0/902	0.63	0/1209
15	P	0.36	0/929	0.64	0/1242
16	Q	0.41	0/960	0.63	0/1278
17	R	0.36	0/829	0.70	0/1107
18	S	0.37	0/864	0.68	0/1156
19	T	0.29	0/744	0.59	0/994
20	U	0.29	0/787	0.61	0/1051
21	V	0.30	0/766	0.60	0/1025
22	W	0.40	0/582	0.58	0/769
23	X	0.40	0/635	0.59	0/848
24	Y	0.25	0/510	0.56	0/677
25	Z	0.30	0/453	0.58	0/605
26	0	0.38	0/450	0.64	0/599
27	1	0.27	0/416	0.58	0/554
28	2	0.40	0/380	0.63	0/498
29	3	0.37	0/513	0.67	0/676
30	4	0.38	0/303	0.60	0/397
31	6	0.24	0/531	0.62	0/709
32	a	0.34	0/36967	0.39	2/57666 (0.0%)
33	b	0.29	0/1735	0.74	5/2338 (0.2%)
34	c	0.32	0/1651	0.64	0/2225

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	d	0.33	0/1665	0.72	2/2227 (0.1%)
36	e	0.38	0/1154	0.82	2/1554 (0.1%)
37	f	0.35	0/835	0.80	1/1128 (0.1%)
38	g	0.27	0/1195	0.65	0/1602
39	h	0.36	0/989	0.72	1/1326 (0.1%)
40	i	0.34	0/1034	0.74	0/1375
41	j	0.35	0/796	0.78	0/1077
42	k	0.34	0/885	0.67	0/1195
43	l	0.42	0/969	0.81	0/1300
44	m	0.34	0/892	0.77	0/1193
45	n	0.35	0/811	0.69	0/1081
46	o	0.32	0/722	0.68	0/964
47	p	0.35	0/659	0.69	0/884
48	q	0.31	0/657	0.75	1/881 (0.1%)
49	r	0.35	0/511	0.69	0/689
50	s	0.31	0/652	0.68	0/877
51	t	0.28	0/671	0.66	0/888
52	u	0.34	0/500	1.04	4/668 (0.6%)
53	v	0.27	0/139	0.29	0/214
54	w	0.43	0/375	1.05	4/494 (0.8%)
55	x	0.25	0/1839	0.40	0/2866
56	z	0.30	0/2886	0.64	2/3887 (0.1%)
All	All	0.35	0/159748	0.50	43/238601 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	E	0	1
6	F	0	1
7	G	0	1
9	J	0	1
12	M	0	1
13	N	0	1
18	S	0	1
29	3	0	1
33	b	0	1
35	d	0	1
37	f	0	3
40	i	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
43	l	0	2
44	m	0	2
49	r	0	1
52	u	0	1
54	w	0	1
56	z	0	2
All	All	0	24

There are no bond length outliers.

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	b	45	THR	CA-C-N	7.04	124.67	120.24
33	b	45	THR	C-N-CA	7.04	124.67	120.24
54	w	21	HIS	CA-C-N	6.83	130.41	120.51
54	w	21	HIS	C-N-CA	6.83	130.41	120.51
1	A	1930	G	C2'-C3'-O3'	6.78	119.67	109.50
52	u	35	GLU	CA-C-N	6.34	133.66	121.54
52	u	35	GLU	C-N-CA	6.34	133.66	121.54
56	z	119	PHE	CA-C-N	6.13	132.74	121.70
56	z	119	PHE	C-N-CA	6.13	132.74	121.70
39	h	47	ASP	N-CA-C	5.94	117.86	110.91
33	b	16	GLY	N-CA-C	5.60	126.46	113.18
54	w	40	MET	CA-C-N	5.59	132.21	121.54
54	w	40	MET	C-N-CA	5.59	132.21	121.54
48	q	69	THR	N-CA-C	-5.52	100.45	108.07
12	M	6	ARG	CA-CB-CG	5.46	125.03	114.10
5	E	81	GLY	N-CA-C	-5.41	100.36	113.18
35	d	35	GLN	CA-C-N	-5.30	115.90	122.42
35	d	35	GLN	C-N-CA	-5.30	115.90	122.42
3	C	29	PHE	CA-C-N	5.26	126.32	120.06
3	C	29	PHE	C-N-CA	5.26	126.32	120.06
33	b	18	GLN	CA-C-N	5.25	131.56	121.54
33	b	18	GLN	C-N-CA	5.25	131.56	121.54
1	A	1378	A	P-O3'-C3'	5.24	128.06	120.20
12	M	57	VAL	CA-C-N	5.15	131.38	121.54
12	M	57	VAL	C-N-CA	5.15	131.38	121.54
2	B	44	G	P-O3'-C3'	5.14	127.91	120.20
36	e	54	GLU	CA-C-N	5.14	124.44	120.33
36	e	54	GLU	C-N-CA	5.14	124.44	120.33
12	M	36	VAL	N-CA-C	-5.12	107.75	111.90
11	L	110	VAL	CA-C-N	5.10	131.15	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	L	110	VAL	C-N-CA	5.10	131.15	121.97
11	L	93	ASN	CA-C-N	5.09	131.27	121.54
11	L	93	ASN	C-N-CA	5.09	131.27	121.54
1	A	1930	G	P-O3'-C3'	5.09	127.84	120.20
52	u	7	GLU	CA-C-N	5.08	128.88	121.31
52	u	7	GLU	C-N-CA	5.08	128.88	121.31
12	M	57	VAL	N-CA-C	-5.07	108.56	113.53
37	f	54	LEU	CA-CB-CG	5.06	134.00	116.30
1	A	1236	G	P-O3'-C3'	5.04	127.76	120.20
32	a	960	U	P-O3'-C3'	5.03	127.75	120.20
1	A	1020	A	P-O3'-C3'	5.02	127.73	120.20
1	A	1022	G	P-O3'-C3'	5.01	127.72	120.20
32	a	1305	G	P-O3'-C3'	5.00	127.70	120.20

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	3	30	HIS	Peptide
5	E	82	GLY	Peptide
6	F	173	ASP	Peptide
7	G	118	ALA	Peptide
9	J	81	ILE	Peptide
12	M	59	ARG	Peptide
13	N	116	VAL	Peptide
18	S	63	GLY	Peptide
33	b	17	HIS	Peptide
35	d	21	LYS	Peptide
37	f	52	ASN	Peptide
37	f	94	HIS	Peptide
37	f	98	GLU	Peptide
40	i	124	PRO	Peptide
40	i	56	MET	Peptide
43	l	42	LYS	Peptide
43	l	75	GLU	Peptide
44	m	3	ILE	Peptide
44	m	4	ALA	Mainchain
49	r	18	GLN	Peptide
52	u	8	ASN	Peptide
54	w	44	LYS	Peptide
56	z	119	PHE	Peptide
56	z	311	GLU	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	62261	0	31314	238	0
2	B	2572	0	1302	11	0
3	C	2082	0	2157	28	0
4	D	1565	0	1616	24	0
5	E	1552	0	1619	22	0
6	F	1410	0	1447	19	0
7	G	1323	0	1374	17	0
8	H	1111	0	1148	13	0
9	J	1129	0	1162	12	0
10	K	938	0	1012	10	0
11	L	1045	0	1117	21	0
12	M	1074	0	1157	16	0
13	N	960	0	1000	16	0
14	O	892	0	923	15	0
15	P	917	0	965	15	0
16	Q	947	0	1022	18	0
17	R	816	0	839	9	0
18	S	857	0	922	10	0
19	T	738	0	807	7	0
20	U	779	0	834	6	0
21	V	753	0	780	8	0
22	W	575	0	592	4	0
23	X	625	0	655	7	0
24	Y	509	0	543	3	0
25	Z	449	0	491	3	0
26	0	444	0	461	3	0
27	1	409	0	440	2	0
28	2	377	0	418	4	0
29	3	504	0	574	12	0
30	4	302	0	343	7	0
31	6	522	0	522	6	0
32	a	33016	0	16617	129	0
33	b	1704	0	1732	16	0
34	c	1624	0	1699	17	0
35	d	1643	0	1710	23	0
36	e	1141	0	1170	20	0
37	f	817	0	808	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	g	1181	0	1240	13	0
39	h	979	0	1034	18	0
40	i	1022	0	1070	19	0
41	j	786	0	828	13	0
42	k	869	0	878	17	0
43	l	955	0	1019	11	0
44	m	883	0	944	15	0
45	n	799	0	841	12	0
46	o	714	0	737	9	0
47	p	649	0	666	12	0
48	q	648	0	691	5	0
49	r	504	0	502	4	0
50	s	637	0	665	13	0
51	t	665	0	714	6	0
52	u	495	0	486	6	0
53	v	126	0	67	0	0
54	w	369	0	381	44	0
55	x	1646	0	832	5	0
56	z	2846	0	2744	67	0
All	All	147155	0	99631	878	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (878) 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)
54:w:15:ALA:HB1	56:z:314:LYS:HB2	1.41	1.01
54:w:15:ALA:HB2	56:z:311:GLU:CD	1.92	0.94
54:w:32:ASN:OD1	56:z:212:ARG:HG2	1.67	0.92
32:a:1398:A:P	54:w:36:LYS:HE3	2.13	0.88
54:w:15:ALA:HB2	56:z:311:GLU:OE1	1.76	0.85
54:w:15:ALA:HB1	56:z:314:LYS:CB	2.08	0.82
54:w:15:ALA:HB2	56:z:311:GLU:CG	2.11	0.80
54:w:32:ASN:HD21	56:z:212:ARG:HD3	1.46	0.80
54:w:15:ALA:N	56:z:311:GLU:OE1	2.15	0.80
54:w:15:ALA:HB2	56:z:311:GLU:HB3	1.64	0.78
54:w:16:ILE:HD11	56:z:198:VAL:HG23	1.69	0.74
54:w:35:GLY:O	54:w:37:GLY:N	2.23	0.72
54:w:15:ALA:HB2	56:z:311:GLU:CB	2.20	0.71
54:w:32:ASN:CG	56:z:212:ARG:HG2	2.15	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:664:G:H22	32:a:741:G:H1	1.39	0.69
32:a:546:A:HO2'	32:a:548:G:HO2'	1.39	0.69
54:w:15:ALA:CB	56:z:311:GLU:OE1	2.40	0.68
54:w:32:ASN:HD21	56:z:212:ARG:CD	2.06	0.68
36:e:54:GLU:HG2	36:e:56:PRO:HD2	1.76	0.68
38:g:111:GLY:HA2	38:g:118:ARG:HD3	1.75	0.68
54:w:15:ALA:HB3	56:z:314:LYS:HD2	1.75	0.68
56:z:256:ARG:HG3	56:z:257:THR:HG23	1.76	0.67
32:a:684:U:H1'	42:k:39:ASN:HB2	1.76	0.67
54:w:32:ASN:HD21	56:z:212:ARG:CG	2.08	0.67
42:k:87:GLY:H	42:k:113:THR:HG22	1.58	0.67
54:w:15:ALA:CB	56:z:314:LYS:HD2	2.24	0.67
1:A:2101:A:H61	1:A:2188:U:H3	1.42	0.66
32:a:311:C:OP1	47:p:31:ARG:NH1	2.30	0.65
7:G:8:VAL:HB	7:G:49:LEU:HB2	1.79	0.65
1:A:2683:C:OP1	15:P:50:ARG:NH2	2.31	0.64
37:f:6:ILE:HD11	37:f:71:ILE:HD11	1.79	0.64
36:e:80:LEU:HD13	36:e:122:VAL:HG11	1.79	0.64
32:a:1398:A:OP1	54:w:36:LYS:HE3	1.97	0.64
50:s:27:LYS:HG2	50:s:28:LYS:HG2	1.80	0.63
1:A:1858:A:N6	1:A:1884:G:O2'	2.30	0.63
1:A:585:G:N7	16:Q:5:ARG:NH1	2.46	0.63
32:a:261:U:OP2	51:t:73:ARG:NH2	2.32	0.63
54:w:13:ASP:CG	54:w:14:ASN:H	2.06	0.63
1:A:2523:G:HO2'	1:A:2764:A:HO2'	1.43	0.62
40:i:83:THR:HG21	40:i:102:PHE:HB3	1.80	0.62
33:b:165:ALA:HB3	33:b:190:SER:HB3	1.82	0.62
36:e:93:VAL:HG11	36:e:139:THR:HG22	1.80	0.62
17:R:34:GLU:HG2	17:R:60:LYS:HG2	1.81	0.62
47:p:4:ILE:HG12	47:p:21:VAL:HG22	1.82	0.62
9:J:35:ARG:HB2	9:J:54:ILE:HD11	1.81	0.62
22:W:17:LEU:HD21	22:W:37:ARG:HH21	1.65	0.62
34:c:13:ILE:HG22	34:c:14:VAL:HG23	1.81	0.62
1:A:254:G:N7	29:3:4:LYS:NZ	2.47	0.61
54:w:15:ALA:CB	56:z:311:GLU:CD	2.70	0.61
41:j:6:ILE:HB	41:j:76:ILE:HB	1.82	0.61
43:l:32:VAL:HB	43:l:55:ARG:HB3	1.82	0.61
1:A:1223:G:OP1	17:R:68:ARG:NH2	2.33	0.61
54:w:32:ASN:ND2	56:z:212:ARG:HD3	2.14	0.61
1:A:249:C:O2	29:3:11:LYS:NZ	2.33	0.61
1:A:2682:A:H61	1:A:2728:U:H1'	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:l:67:GLY:O	43:l:98:ARG:NH1	2.34	0.61
14:O:4:LYS:HE3	14:O:8:ILE:HD11	1.83	0.61
23:X:36:ARG:HG2	23:X:45:PHE:HB3	1.82	0.61
20:U:14:THR:OG1	20:U:68:ASN:ND2	2.34	0.60
1:A:475:C:O2	1:A:479:A:N6	2.33	0.60
39:h:52:GLY:HA3	39:h:56:PRO:HA	1.83	0.60
37:f:92:THR:OG1	37:f:93:LYS:N	2.27	0.60
42:k:23:HIS:HB3	42:k:30:ILE:HG23	1.83	0.60
1:A:2098:U:H3	1:A:2191:A:H61	1.48	0.60
32:a:1106:G:O2'	34:c:168:ARG:NH1	2.35	0.60
32:a:1151:A:H1'	41:j:41:PRO:HB2	1.84	0.60
54:w:15:ALA:HB3	56:z:314:LYS:CD	2.31	0.60
6:F:114:ARG:NH2	31:6:46:GLY:O	2.35	0.60
32:a:405:U:O4	35:d:1:ALA:N	2.35	0.60
56:z:342:THR:HG22	56:z:344:ASN:H	1.67	0.60
20:U:33:VAL:HG13	20:U:66:VAL:HG22	1.84	0.59
1:A:243:U:OP1	29:3:7:ARG:NH1	2.34	0.59
32:a:1397:C:OP2	36:e:28:ARG:NH2	2.36	0.59
38:g:12:LEU:HD11	40:i:49:GLN:HE22	1.66	0.59
56:z:195:GLU:OE1	56:z:324:ARG:NH2	2.34	0.59
33:b:23:ASN:ND2	33:b:191:ASP:OD1	2.35	0.59
1:A:1817:G:OP2	3:C:155:ARG:NH2	2.35	0.59
1:A:1960:A:HO2'	32:a:1484:C:HO2'	1.48	0.59
1:A:2032:G:N2	4:D:151:THR:OG1	2.34	0.59
7:G:85:LYS:HG3	7:G:131:VAL:HG22	1.84	0.59
11:L:109:LYS:HE3	11:L:128:THR:HG22	1.85	0.59
32:a:618:C:H1'	47:p:14:ARG:HH12	1.67	0.59
1:A:910:A:H62	12:M:12:MET:HA	1.67	0.59
12:M:69:PRO:HA	12:M:94:ALA:HB2	1.85	0.59
21:V:64:VAL:HG22	21:V:69:GLU:HG2	1.83	0.59
34:c:55:VAL:HB	34:c:66:THR:HB	1.85	0.59
3:C:143:VAL:HB	3:C:153:LEU:HB2	1.83	0.59
11:L:95:LEU:HD22	11:L:100:ILE:HD11	1.85	0.59
39:h:14:ARG:NH1	39:h:74:ILE:O	2.36	0.59
54:w:16:ILE:O	54:w:16:ILE:HG13	2.03	0.59
1:A:224:U:OP2	1:A:408:G:N2	2.36	0.59
36:e:156:ARG:NH1	39:h:42:GLU:OE2	2.36	0.59
1:A:685:A:H5''	1:A:788:A:H62	1.67	0.58
10:K:121:GLU:HG2	10:K:122:VAL:HG23	1.84	0.58
56:z:259:SER:O	56:z:283:ASN:ND2	2.36	0.58
8:H:66:ASN:HD22	8:H:135:HIS:HD2	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:1298:U:OP2	38:g:113:LYS:NZ	2.36	0.58
56:z:143:ASP:OD2	56:z:203:ARG:NH2	2.36	0.58
6:F:55:ASP:OD2	6:F:149:ARG:NH2	2.35	0.58
48:q:63:CYS:SG	48:q:73:THR:OG1	2.61	0.58
1:A:781:A:OP1	3:C:216:ARG:NH2	2.37	0.58
1:A:1153:C:OP1	16:Q:91:ARG:NH2	2.36	0.58
1:A:2139:U:H2'	1:A:2140:G:H8	1.67	0.58
1:A:714:U:H5''	46:o:88:ARG:HH22	1.68	0.58
23:X:5:GLN:O	23:X:73:ARG:NH2	2.37	0.58
3:C:153:LEU:HD13	3:C:175:LEU:HD21	1.84	0.58
32:a:264:C:O3'	48:q:64:ARG:NH2	2.36	0.58
52:u:16:ARG:HB3	52:u:19:LYS:HD3	1.85	0.58
1:A:1365:A:OP1	23:X:2:ARG:NH1	2.36	0.58
26:O:37:HIS:ND1	26:O:38:LEU:O	2.36	0.58
33:b:31:PHE:O	33:b:39:ILE:N	2.37	0.58
39:h:91:LEU:O	39:h:116:ARG:NH2	2.37	0.58
41:j:40:ILE:HB	41:j:73:LEU:HB2	1.86	0.57
56:z:26:ASP:HB3	56:z:29:ALA:HB3	1.87	0.57
1:A:994:C:OP1	16:Q:52:ARG:NH2	2.37	0.57
1:A:2116:G:O6	1:A:2165:C:N4	2.37	0.57
7:G:94:ARG:HB2	7:G:105:SER:HB2	1.86	0.57
1:A:1416:G:O2'	1:A:1587:G:N2	2.37	0.57
18:S:57:ASN:OD1	18:S:61:ASN:ND2	2.37	0.57
34:c:19:SER:OG	34:c:21:TRP:NE1	2.38	0.57
54:w:32:ASN:ND2	56:z:212:ARG:HG2	2.20	0.57
55:x:18:G:O2'	55:x:57:G:N2	2.35	0.57
6:F:133:GLU:HB3	6:F:135:ILE:HG13	1.87	0.57
32:a:331:G:O2'	51:t:2:ASN:ND2	2.38	0.57
32:a:1081:A:OP2	36:e:51:LYS:NZ	2.38	0.57
1:A:1930:G:HO2'	1:A:1968:G:H1	1.52	0.57
2:B:39:A:O2'	2:B:46:A:N1	2.38	0.57
41:j:52:LEU:HB2	45:n:81:ARG:HD2	1.86	0.57
1:A:1:G:N2	1:A:2903:U:O2'	2.38	0.57
35:d:77:GLU:OE2	35:d:80:ARG:NH1	2.38	0.57
56:z:240:ARG:NH1	56:z:242:ASP:OD2	2.38	0.57
25:Z:40:THR:HG23	25:Z:42:ALA:H	1.69	0.57
56:z:128:CYS:SG	56:z:129:TYR:N	2.78	0.57
36:e:149:PRO:HA	36:e:152:VAL:HG22	1.86	0.57
1:A:1063:G:H1	1:A:1075:C:H42	1.51	0.56
6:F:68:LYS:HB3	6:F:81:GLY:HA2	1.87	0.56
32:a:1060:U:OP1	45:n:85:ARG:NH2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:z:196:THR:HG22	56:z:222:VAL:H	1.68	0.56
1:A:468:G:OP2	28:2:37:LYS:NZ	2.37	0.56
48:q:30:HIS:HD2	48:q:33:TYR:H	1.53	0.56
54:w:13:ASP:O	56:z:311:GLU:OE1	2.23	0.56
34:c:20:THR:HB	34:c:57:GLU:HG2	1.88	0.56
1:A:877:A:O2'	1:A:900:A:N6	2.37	0.56
15:P:105:LYS:O	15:P:108:ARG:NH2	2.39	0.56
52:u:19:LYS:HB3	52:u:24:LYS:HD2	1.86	0.56
54:w:15:ALA:CB	56:z:314:LYS:HB2	2.26	0.56
1:A:958:U:OP2	12:M:14:LYS:NZ	2.38	0.56
36:e:92:ARG:HB2	36:e:127:TYR:HB2	1.86	0.56
42:k:127:ARG:HB2	52:u:34:ARG:HH22	1.70	0.56
11:L:78:ARG:NH2	11:L:80:SER:OG	2.39	0.56
35:d:97:LEU:HB2	35:d:134:TYR:HB3	1.88	0.56
42:k:84:MET:SD	42:k:110:THR:OG1	2.59	0.56
11:L:128:THR:OG1	11:L:129:LYS:N	2.37	0.56
41:j:71:LEU:O	41:j:72:ARG:NH1	2.37	0.56
1:A:2296:U:OP2	14:O:9:ARG:NH2	2.38	0.56
12:M:110:GLU:OE2	12:M:114:ARG:NH1	2.39	0.56
18:S:82:MET:HB2	18:S:98:LYS:HB2	1.88	0.56
32:a:1134:G:H1	32:a:1140:C:H42	1.54	0.56
35:d:74:TYR:OH	35:d:96:ARG:NH1	2.39	0.56
56:z:197:GLY:HA3	56:z:323:ILE:HD12	1.86	0.56
44:m:3:ILE:HG12	44:m:7:ASN:HD22	1.71	0.56
1:A:1064:C:N4	1:A:1066:U:O2'	2.37	0.56
7:G:23:ILE:HD11	7:G:42:VAL:HG11	1.88	0.56
35:d:124:VAL:HA	35:d:142:VAL:HA	1.88	0.56
42:k:92:ARG:NH2	42:k:111:ASP:OD1	2.37	0.56
34:c:76:ILE:HA	34:c:83:VAL:HG23	1.88	0.55
1:A:443:A:N6	5:E:36:ALA:O	2.39	0.55
34:c:152:VAL:HG12	34:c:197:VAL:HG22	1.89	0.55
15:P:59:THR:HA	15:P:72:VAL:HA	1.88	0.55
32:a:993:G:O2'	32:a:994:A:N7	2.39	0.55
37:f:10:VAL:HB	37:f:58:HIS:HB3	1.88	0.55
1:A:714:U:OP2	46:o:88:ARG:NH2	2.40	0.55
1:A:2313:C:H5''	6:F:87:LYS:HD2	1.89	0.55
7:G:148:ARG:NH2	7:G:166:GLU:OE2	2.39	0.55
32:a:1180:A:OP2	40:i:98:ARG:NH2	2.40	0.55
32:a:1376:U:O4	38:g:9:ARG:NH1	2.38	0.55
54:w:28:ARG:HB2	56:z:215:THR:HB	1.87	0.55
8:H:94:ILE:HG23	8:H:98:ASP:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:18:GLN:NE2	33:b:21:TYR:OH	2.39	0.55
40:i:4:GLN:HE21	40:i:19:PHE:HB3	1.72	0.55
1:A:2199:A:OP1	23:X:36:ARG:NH2	2.39	0.55
1:A:2220:U:O2'	8:H:97:ARG:NH2	2.40	0.55
5:E:47:LYS:HB2	5:E:51:GLU:HB2	1.89	0.55
7:G:3:VAL:HG12	7:G:68:ARG:HD2	1.89	0.55
32:a:927:G:O2'	32:a:1503:A:N7	2.39	0.55
39:h:28:SER:HB3	39:h:56:PRO:HB2	1.88	0.54
43:l:49:ARG:NH1	43:l:88:ASP:OD2	2.40	0.54
1:A:2655:G:O2'	1:A:2664:G:N1	2.38	0.54
43:l:33:CYS:HA	43:l:54:VAL:HA	1.89	0.54
56:z:130:LEU:HB2	56:z:181:ILE:HG12	1.89	0.54
1:A:2780:G:N1	9:J:102:GLU:OE2	2.40	0.54
2:B:76:G:N3	21:V:78:GLN:NE2	2.51	0.54
32:a:957:U:O4	56:z:154:ARG:NH2	2.40	0.54
43:l:113:ARG:HB2	43:l:118:VAL:HB	1.89	0.54
1:A:948:C:O2	1:A:984:A:O2'	2.23	0.54
3:C:154:ALA:HB2	3:C:161:VAL:HG23	1.89	0.54
6:F:118:ALA:O	6:F:166:ARG:NH1	2.41	0.54
32:a:1144:G:H21	32:a:1146:A:H62	1.55	0.54
47:p:43:ALA:HB1	47:p:46:LYS:HE3	1.88	0.54
1:A:2391:G:H2'	1:A:2424:C:H41	1.73	0.54
13:N:24:MET:HE2	13:N:44:LEU:HD22	1.89	0.54
56:z:144:TRP:HE3	56:z:147:MET:HE3	1.72	0.54
6:F:114:ARG:HH11	44:m:70:ARG:HD2	1.72	0.54
37:f:12:PRO:HG3	37:f:57:ALA:HA	1.90	0.54
46:o:25:GLU:OE2	46:o:76:ARG:NH1	2.33	0.54
1:A:1817:G:OP1	3:C:86:ARG:NH2	2.41	0.54
32:a:352:C:O2	32:a:355:C:N4	2.39	0.54
56:z:241:ILE:HG12	56:z:263:ILE:HG12	1.88	0.54
1:A:244:A:H5''	11:L:67:THR:HG21	1.90	0.54
1:A:2831:G:N2	1:A:2884:U:OP2	2.38	0.54
32:a:1064:G:O2'	32:a:1190:G:N2	2.37	0.54
35:d:59:LYS:HE3	35:d:194:ILE:HG22	1.89	0.54
1:A:2521:C:O2'	1:A:2564:A:N3	2.40	0.53
4:D:77:ARG:NH2	4:D:200:ASP:OD1	2.40	0.53
32:a:891:U:H2'	32:a:892:A:H8	1.73	0.53
32:a:933:G:O6	38:g:2:ARG:NH2	2.40	0.53
32:a:974:A:OP1	45:n:69:ARG:NH2	2.39	0.53
32:a:1317:C:OP2	45:n:27:LYS:NZ	2.34	0.53
1:A:1297:C:O2'	1:A:1302:A:N1	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:123:LYS:HE3	5:E:125:SER:HB2	1.88	0.53
19:T:6:ARG:NH1	19:T:42:GLU:OE1	2.42	0.53
34:c:182:ASP:HB2	34:c:201:ILE:HB	1.90	0.53
3:C:141:HIS:ND1	3:C:192:GLY:O	2.38	0.53
22:W:33:ILE:HG22	22:W:34:VAL:HG23	1.90	0.53
41:j:8:ILE:HB	41:j:74:VAL:HB	1.90	0.53
32:a:636:U:H5'	48:q:5:ARG:HH21	1.73	0.53
5:E:1:MET:HE3	5:E:20:GLY:HA3	1.90	0.53
50:s:10:ILE:HD13	50:s:15:LEU:HB2	1.90	0.53
1:A:1651:G:OP2	13:N:40:LYS:NZ	2.41	0.53
21:V:72:VAL:HG12	21:V:93:ARG:HA	1.91	0.53
38:g:55:LYS:HB3	38:g:59:GLU:HG3	1.90	0.53
46:o:45:HIS:O	46:o:47:LYS:N	2.42	0.53
1:A:2540:C:O2'	1:A:2740:A:N3	2.41	0.53
32:a:404:G:O6	35:d:1:ALA:N	2.42	0.53
32:a:1060:U:H4'	41:j:53:ILE:HG23	1.91	0.53
9:J:36:LEU:HD22	9:J:121:LYS:HB2	1.91	0.53
32:a:1414:U:H2'	32:a:1415:G:H8	1.73	0.53
4:D:14:ILE:HA	15:P:11:GLN:HE22	1.74	0.53
5:E:149:ILE:HD11	5:E:172:ALA:HA	1.89	0.53
9:J:17:VAL:HG23	9:J:137:PRO:HB2	1.91	0.53
12:M:75:GLU:HB2	12:M:90:GLU:HG3	1.91	0.53
32:a:202:G:O2'	32:a:468:A:N3	2.41	0.53
35:d:138:PRO:HB3	35:d:183:ARG:HA	1.91	0.53
40:i:51:LEU:HB3	40:i:56:MET:HB2	1.89	0.53
1:A:1715:G:N2	1:A:1716:U:O4	2.41	0.53
1:A:2773:C:OP1	4:D:169:ARG:NH2	2.43	0.53
2:B:57:A:H4'	6:F:26:GLN:HE21	1.72	0.53
32:a:663:A:H61	32:a:742:G:H1	1.57	0.53
32:a:687:A:N6	32:a:703:G:O2'	2.42	0.52
35:d:187:ARG:HH12	35:d:192:ALA:HA	1.73	0.52
1:A:100:U:O2	20:U:90:LYS:NZ	2.39	0.52
29:3:32:LEU:HD23	29:3:35:LYS:HD2	1.90	0.52
52:u:16:ARG:HH11	52:u:19:LYS:HE2	1.73	0.52
1:A:1315:C:O2'	1:A:1392:A:N3	2.38	0.52
1:A:1601:G:OP1	19:T:64:LYS:NZ	2.37	0.52
32:a:1345:U:OP1	40:i:121:ARG:NH1	2.43	0.52
41:j:28:THR:HG22	41:j:86:ALA:HB1	1.90	0.52
45:n:15:LEU:HD23	45:n:55:SER:HB3	1.91	0.52
1:A:1779:U:OP2	1:A:1784:A:N6	2.41	0.52
14:O:94:ARG:NH2	14:O:97:PHE:O	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:816:A:OP1	32:a:1526:G:O2'	2.25	0.52
39:h:39:LEU:HD21	39:h:128:VAL:HG21	1.92	0.52
44:m:84:CYS:HB2	50:s:72:GLU:HG3	1.92	0.52
1:A:1032:A:H1'	30:4:23:ILE:HD13	1.90	0.52
4:D:179:ARG:HB3	4:D:188:LEU:HD12	1.91	0.52
15:P:29:VAL:HG22	15:P:80:VAL:HG12	1.92	0.52
41:j:46:LYS:HG2	41:j:68:ARG:HG2	1.92	0.52
19:T:13:ALA:HB3	19:T:33:LYS:HD3	1.90	0.52
32:a:1178:G:N2	32:a:1181:G:OP2	2.43	0.52
7:G:29:ASN:HB2	7:G:78:VAL:HA	1.92	0.52
41:j:7:ARG:HB3	41:j:101:SER:HB2	1.92	0.52
1:A:2602:A:N7	56:z:278:ARG:NE	2.58	0.52
37:f:51:ILE:N	37:f:53:LYS:O	2.43	0.52
1:A:499:U:H5''	20:U:42:LYS:HE3	1.91	0.52
32:a:692:U:O2'	32:a:694:A:N7	2.38	0.52
34:c:39:ARG:HG3	34:c:54:ILE:HD11	1.91	0.52
35:d:85:THR:HB	36:e:102:THR:HG21	1.91	0.52
4:D:35:THR:HG22	4:D:73:VAL:HG21	1.92	0.52
13:N:44:LEU:HD23	13:N:113:ILE:HD13	1.91	0.52
32:a:334:C:HO2'	32:a:1434:A:HO2'	1.58	0.52
32:a:749:A:O2'	46:o:19:ASN:OD1	2.28	0.52
34:c:50:SER:OG	34:c:71:ARG:NH1	2.43	0.52
32:a:76:G:H1	32:a:93:U:H3	1.58	0.51
45:n:13:VAL:HG22	45:n:60:GLN:HE22	1.74	0.51
1:A:1992:G:N2	1:A:1996:C:O2'	2.43	0.51
1:A:2205:A:H61	1:A:2219:U:H3	1.57	0.51
4:D:109:VAL:HG22	4:D:203:VAL:HG22	1.92	0.51
21:V:42:LEU:HD13	21:V:47:VAL:HG21	1.93	0.51
44:m:76:ILE:HG22	44:m:80:MET:HE2	1.91	0.51
20:U:3:LYS:O	20:U:93:ARG:NH2	2.40	0.51
32:a:676:A:H1'	42:k:116:PRO:HB3	1.92	0.51
32:a:1200:C:H5''	32:a:1201:A:H3'	1.92	0.51
32:a:1255:G:O2'	32:a:1258:G:N3	2.36	0.51
36:e:110:MET:HG3	36:e:139:THR:HG21	1.92	0.51
1:A:2508:G:H1	1:A:2580:U:H5	1.59	0.51
10:K:80:ASP:OD2	15:P:61:ARG:NH1	2.40	0.51
32:a:755:G:H21	39:h:3:GLN:HE22	1.58	0.51
33:b:19:THR:OG1	33:b:20:ARG:N	2.35	0.51
5:E:77:ILE:HG13	5:E:78:TRP:HD1	1.75	0.51
5:E:125:SER:O	5:E:137:LYS:NZ	2.41	0.51
49:r:36:GLY:O	49:r:62:ARG:NH2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:w:15:ALA:CA	56:z:311:GLU:OE1	2.58	0.51
54:w:35:GLY:O	54:w:36:LYS:C	2.52	0.51
56:z:234:ILE:HD12	56:z:238:ASP:HB2	1.92	0.51
1:A:1071:G:H1'	1:A:1089:A:H2'	1.91	0.51
1:A:1798:U:OP2	3:C:270:ARG:NH2	2.41	0.51
56:z:202:VAL:HB	56:z:327:VAL:HG12	1.93	0.51
1:A:1012:U:OP2	16:Q:69:ARG:NH1	2.39	0.51
14:O:8:ILE:O	14:O:12:THR:OG1	2.29	0.51
31:6:11:GLU:HA	31:6:25:ARG:HA	1.93	0.51
54:w:14:ASN:C	56:z:311:GLU:OE1	2.53	0.51
12:M:50:ARG:HD3	12:M:65:ILE:HD11	1.92	0.51
1:A:274:C:H42	1:A:363:G:H1	1.57	0.51
32:a:210:C:O2'	32:a:211:G:N2	2.44	0.51
1:A:1607:C:N4	1:A:1622:G:OP2	2.41	0.51
1:A:2847:U:OP1	15:P:95:LYS:NZ	2.36	0.51
7:G:93:TYR:OH	7:G:159:LYS:NZ	2.41	0.51
32:a:959:A:HO2'	32:a:984:C:HO2'	1.54	0.51
1:A:560:C:O2'	16:Q:47:ARG:NH2	2.43	0.50
1:A:1041:G:H1	1:A:1114:C:H42	1.59	0.50
1:A:1323:C:OP1	18:S:98:LYS:NZ	2.43	0.50
15:P:63:ILE:HA	15:P:68:GLY:HA2	1.92	0.50
19:T:1:MET:HE2	19:T:3:ARG:HB2	1.93	0.50
40:i:33:SER:HB3	40:i:36:GLN:HG2	1.93	0.50
1:A:910:A:N3	1:A:2264:C:O2'	2.39	0.50
1:A:2212:A:H4'	1:A:2213:U:H5	1.76	0.50
32:a:230:G:H5''	47:p:31:ARG:HH21	1.76	0.50
35:d:71:PHE:HE1	35:d:93:LEU:HD11	1.76	0.50
8:H:51:ARG:HG3	8:H:55:GLU:HB2	1.93	0.50
11:L:111:ILE:HD12	11:L:111:ILE:H	1.76	0.50
37:f:29:ILE:HD13	37:f:64:VAL:HG21	1.93	0.50
1:A:981:A:OP2	1:A:982:C:N4	2.37	0.50
1:A:1799:G:N2	1:A:1818:U:O2'	2.45	0.50
1:A:2722:G:O2'	13:N:3:HIS:O	2.29	0.50
32:a:796:C:O3'	42:k:126:ARG:NH2	2.43	0.50
39:h:103:VAL:HA	39:h:124:ILE:HA	1.93	0.50
56:z:82:GLY:HA2	56:z:85:GLU:HG2	1.93	0.50
1:A:2772:C:H5'	4:D:173:GLN:HE21	1.76	0.50
22:W:17:LEU:HD11	22:W:37:ARG:HE	1.76	0.50
32:a:690:G:O6	42:k:52:ARG:NH2	2.45	0.50
11:L:76:GLU:HB2	11:L:111:ILE:HD13	1.92	0.50
32:a:401:C:O2'	32:a:621:A:N3	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:673:A:H5''	37:f:86:ARG:HH21	1.76	0.50
38:g:11:ILE:HD13	38:g:24:LYS:HE3	1.94	0.50
54:w:15:ALA:CB	56:z:311:GLU:HB3	2.39	0.50
16:Q:109:VAL:HG12	16:Q:113:LYS:HE2	1.94	0.50
32:a:195:A:N3	32:a:222:C:O2'	2.42	0.50
32:a:590:U:OP1	39:h:30:LYS:N	2.45	0.50
1:A:51:G:H4'	1:A:52:A:H5'	1.93	0.50
1:A:1248:G:OP1	5:E:44:ARG:NH1	2.44	0.50
1:A:1826:G:O2'	1:A:1971:U:OP2	2.30	0.50
16:Q:78:PHE:HE2	16:Q:94:LEU:HD21	1.77	0.50
32:a:559:A:H4'	32:a:560:A:H3'	1.94	0.50
35:d:12:ARG:NH1	35:d:36:ALA:O	2.45	0.50
1:A:210:C:OP1	28:2:29:GLN:NE2	2.40	0.49
7:G:34:ARG:HH12	7:G:70:LEU:HD22	1.77	0.49
1:A:1155:A:H5''	16:Q:54:ARG:HH11	1.77	0.49
1:A:2141:G:H1	1:A:2150:C:H42	1.58	0.49
42:k:73:VAL:HA	42:k:76:TYR:HD2	1.77	0.49
1:A:299:A:N1	1:A:322:A:O2'	2.41	0.49
1:A:630:G:N2	1:A:633:A:OP2	2.40	0.49
1:A:1068:G:O6	1:A:1069:A:N6	2.45	0.49
1:A:1667:G:O2'	1:A:1991:U:O4	2.27	0.49
1:A:1816:C:N4	3:C:34:GLU:OE2	2.32	0.49
1:A:2115:G:OP1	1:A:2166:U:O2'	2.29	0.49
32:a:208:U:H4'	32:a:209:U:H5	1.77	0.49
33:b:31:PHE:N	33:b:39:ILE:O	2.46	0.49
1:A:2636:C:O2'	4:D:45:TYR:OH	2.27	0.49
19:T:8:LEU:HD11	24:Y:22:LEU:HD12	1.94	0.49
1:A:2880:C:O3'	13:N:90:ARG:NH2	2.46	0.49
3:C:106:PRO:HG2	3:C:109:LEU:HB2	1.95	0.49
32:a:1029:U:O2	32:a:1031:C:O2'	2.30	0.49
47:p:79:ASN:HB2	47:p:82:ALA:HB3	1.93	0.49
32:a:51:A:N7	32:a:114:U:O2'	2.43	0.49
32:a:627:G:H5'	47:p:51:ARG:HH12	1.76	0.49
47:p:18:GLN:HE22	47:p:35:ARG:HH21	1.61	0.49
54:w:35:GLY:N	54:w:38:SER:OG	2.46	0.49
1:A:1326:U:H2'	1:A:1327:A:H8	1.78	0.49
11:L:57:LEU:HD22	29:3:53:ASP:HB3	1.94	0.49
28:2:24:THR:HG23	28:2:27:GLY:H	1.77	0.49
55:x:74:C:OP2	56:z:278:ARG:NH2	2.40	0.49
2:B:7:G:O2'	14:O:38:GLN:NE2	2.45	0.49
3:C:106:PRO:HD2	3:C:109:LEU:HD22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:406:G:H5'	35:d:4:LEU:HD22	1.95	0.49
32:a:1492:A:H1'	54:w:23:PRO:HD3	1.94	0.49
5:E:176:ASP:N	5:E:176:ASP:OD1	2.44	0.49
1:A:500:G:N1	1:A:503:A:OP2	2.46	0.49
4:D:10:GLY:H	4:D:197:THR:HG23	1.78	0.49
11:L:20:GLY:HA2	11:L:28:GLY:HA2	1.94	0.49
13:N:86:ARG:NE	13:N:117:ASP:OD2	2.45	0.49
36:e:67:ARG:HA	36:e:70:MET:HE3	1.95	0.49
1:A:563:A:N3	16:Q:36:GLN:NE2	2.61	0.48
4:D:55:LYS:HD2	4:D:60:VAL:HB	1.94	0.48
30:4:7:VAL:HG22	30:4:38:GLY:HA3	1.95	0.48
47:p:75:ILE:HA	47:p:78:VAL:HG12	1.95	0.48
1:A:2830:C:OP1	4:D:56:LYS:NZ	2.41	0.48
2:B:52:A:N7	14:O:64:TYR:OH	2.33	0.48
15:P:38:ARG:NH2	32:a:345:C:OP1	2.46	0.48
33:b:91:VAL:HG11	33:b:95:TRP:HD1	1.79	0.48
33:b:79:VAL:HA	33:b:213:LEU:HD21	1.95	0.48
37:f:63:ASN:HD21	37:f:96:VAL:H	1.61	0.48
38:g:68:VAL:HG23	38:g:99:ALA:HB1	1.96	0.48
8:H:125:THR:HG21	8:H:148:ALA:HB2	1.94	0.48
10:K:69:VAL:HG21	10:K:104:THR:HG21	1.96	0.48
18:S:3:THR:HG21	18:S:58:ALA:HB2	1.96	0.48
32:a:9:G:H4'	36:e:108:GLY:H	1.78	0.48
1:A:476:G:N1	1:A:479:A:OP2	2.43	0.48
1:A:1342:A:O2'	1:A:1344:U:OP2	2.26	0.48
32:a:35:G:O2'	43:l:114:SER:O	2.24	0.48
35:d:28:ASP:O	35:d:30:LYS:NZ	2.39	0.48
38:g:113:LYS:HB2	38:g:117:LEU:HD23	1.95	0.48
1:A:704:G:H2'	1:A:726:G:H22	1.78	0.48
17:R:49:ILE:HG22	17:R:54:VAL:HA	1.94	0.48
32:a:811:C:O2'	32:a:901:A:N1	2.46	0.48
39:h:91:LEU:HB2	39:h:116:ARG:HE	1.79	0.48
1:A:647:G:N2	1:A:2350:C:O2'	2.44	0.48
1:A:729:G:OP2	3:C:206:LYS:NZ	2.37	0.48
1:A:2539:C:H5'	30:4:3:VAL:HG21	1.96	0.48
15:P:28:LYS:HG2	15:P:39:LEU:HG	1.96	0.48
7:G:163:TYR:HB2	7:G:166:GLU:HB2	1.95	0.48
18:S:73:LYS:HB2	18:S:106:VAL:HB	1.94	0.48
19:T:3:ARG:HH12	19:T:7:LEU:HD21	1.78	0.48
35:d:187:ARG:NH2	35:d:194:ILE:O	2.46	0.48
1:A:514:A:N3	1:A:581:C:O2'	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:651:G:H5'	29:3:18:LYS:HG3	1.96	0.48
1:A:2343:U:O2'	1:A:2373:G:O2'	2.26	0.48
1:A:2441:U:OP2	1:A:2586:U:O2'	2.31	0.48
1:A:1791:A:N6	1:A:1828:G:O2'	2.42	0.48
37:f:88:MET:HG3	37:f:90:MET:HE2	1.96	0.48
1:A:2457:U:H5	1:A:2494:G:H1	1.61	0.47
3:C:68:ARG:O	3:C:188:ARG:NH1	2.47	0.47
10:K:99:ILE:HD12	10:K:118:LEU:HB2	1.96	0.47
20:U:36:GLU:HA	20:U:61:GLU:HG2	1.95	0.47
32:a:1137:C:H5'	32:a:1138:G:H5'	1.96	0.47
1:A:2522:U:O2'	1:A:2647:U:OP1	2.25	0.47
32:a:203:G:H1	32:a:214:C:H42	1.61	0.47
32:a:227:G:O2'	47:p:63:GLN:NE2	2.48	0.47
32:a:958:A:N7	50:s:54:ARG:NH1	2.61	0.47
55:x:18:G:HO2'	55:x:57:G:H22	1.57	0.47
12:M:42:THR:HG22	12:M:93:VAL:HG12	1.96	0.47
32:a:263:A:OP1	51:t:73:ARG:NH1	2.47	0.47
32:a:1228:C:H5'	44:m:114:PRO:HG2	1.96	0.47
34:c:171:ARG:NH2	34:c:205:GLU:OE2	2.47	0.47
56:z:201:LEU:HD21	56:z:203:ARG:HE	1.79	0.47
1:A:538:A:H5''	9:J:7:LYS:HE3	1.96	0.47
32:a:1338:G:N3	55:x:41:A:O2'	2.45	0.47
1:A:1796:U:H2'	1:A:1797:G:H8	1.79	0.47
12:M:29:GLY:HA2	12:M:106:ASP:HB2	1.96	0.47
24:Y:49:ASP:OD1	24:Y:52:ARG:NH2	2.47	0.47
32:a:765:G:H1	32:a:812:G:HO2'	1.61	0.47
9:J:11:VAL:HG11	9:J:50:THR:HA	1.96	0.47
16:Q:43:GLN:HE21	17:R:77:PHE:HB3	1.78	0.47
32:a:1372:U:OP1	40:i:73:GLY:N	2.47	0.47
42:k:82:GLU:HG3	42:k:107:THR:HB	1.97	0.47
54:w:32:ASN:ND2	56:z:212:ARG:CG	2.74	0.47
1:A:362:A:H3'	1:A:363:G:H8	1.79	0.47
1:A:558:U:H2'	1:A:559:G:H8	1.79	0.47
1:A:1061:U:H4'	1:A:1070:A:C4	2.49	0.47
1:A:2394:C:H5''	11:L:63:LYS:HE3	1.95	0.47
1:A:2615:U:C2	26:0:3:GLN:HA	2.49	0.47
7:G:104:LEU:HD21	7:G:130:ILE:HD11	1.96	0.47
11:L:19:LEU:HA	11:L:27:LEU:HD13	1.95	0.47
14:O:40:ILE:HG12	14:O:47:VAL:HG12	1.97	0.47
15:P:21:PRO:HD3	15:P:49:ILE:HD12	1.95	0.47
26:0:27:LEU:HD23	26:0:36:LYS:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:14:LYS:HB3	29:3:22:LYS:HE2	1.97	0.47
32:a:769:G:H4'	32:a:1513:A:H4'	1.96	0.47
32:a:1083:U:O2'	32:a:1102:A:OP2	2.30	0.47
34:c:56:ILE:HG23	34:c:63:ILE:HD11	1.97	0.47
1:A:1069:A:OP1	1:A:1096:A:O2'	2.33	0.47
1:A:1509:A:H2'	1:A:1510:G:H8	1.79	0.47
3:C:209:ALA:HA	3:C:212:TRP:CE2	2.50	0.47
3:C:250:GLN:NE2	3:C:251:THR:O	2.47	0.47
16:Q:108:LEU:HA	17:R:48:LYS:HE3	1.97	0.47
27:1:7:LYS:HA	27:1:23:THR:HA	1.97	0.47
32:a:1347:G:O6	40:i:11:ARG:NH2	2.48	0.47
44:m:15:VAL:HG23	44:m:16:ILE:HD12	1.97	0.47
48:q:22:VAL:HG11	48:q:60:ILE:HD11	1.95	0.47
40:i:14:SER:HB2	40:i:69:GLY:HA3	1.97	0.47
40:i:106:ASP:OD2	40:i:108:ARG:NE	2.48	0.47
54:w:13:ASP:CG	54:w:14:ASN:N	2.73	0.47
1:A:971:G:OP1	1:A:974:G:O2'	2.28	0.47
6:F:125:GLY:O	6:F:157:THR:OG1	2.32	0.47
15:P:24:THR:HB	15:P:87:ARG:HB3	1.97	0.47
37:f:11:HIS:HA	37:f:12:PRO:HD3	1.81	0.47
47:p:20:VAL:HG23	47:p:35:ARG:HA	1.97	0.47
1:A:1136:G:O2'	1:A:2038:G:O2'	2.23	0.46
1:A:2010:G:H5''	18:S:42:LYS:HB2	1.96	0.46
5:E:126:VAL:O	5:E:156:ASN:ND2	2.47	0.46
13:N:59:SER:OG	13:N:62:ASN:OD1	2.33	0.46
33:b:153:MET:HG2	33:b:155:GLY:H	1.80	0.46
1:A:1788:C:OP1	3:C:220:ARG:NH2	2.48	0.46
35:d:61:ARG:NH1	35:d:68:GLU:OE1	2.48	0.46
38:g:75:LYS:HE3	38:g:88:VAL:HG11	1.96	0.46
5:E:29:HIS:HA	5:E:32:VAL:HG12	1.98	0.46
8:H:83:LYS:HA	8:H:149:GLU:HB3	1.97	0.46
14:O:7:ARG:NH1	14:O:95:SER:O	2.46	0.46
36:e:79:THR:OG1	36:e:97:PRO:O	2.29	0.46
36:e:155:LYS:HB3	39:h:70:VAL:HG13	1.96	0.46
39:h:95:MET:HE3	39:h:129:ALA:HB1	1.98	0.46
56:z:265:HIS:O	56:z:269:GLY:N	2.43	0.46
1:A:1340:U:OP1	19:T:19:LYS:NZ	2.38	0.46
1:A:1378:A:O2'	1:A:1380:G:OP2	2.33	0.46
1:A:2561:U:O3'	10:K:40:LYS:NZ	2.48	0.46
3:C:140:VAL:HG12	3:C:191:LEU:HD23	1.97	0.46
14:O:2:ASP:OD2	14:O:5:SER:N	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2788:C:O2'	1:A:2809:A:N3	2.48	0.46
1:A:2809:A:OP2	1:A:2890:G:N1	2.45	0.46
8:H:67:ALA:HA	8:H:138:VAL:HG11	1.97	0.46
32:a:976:G:OP2	32:a:1358:U:O2'	2.32	0.46
35:d:158:LEU:HD21	35:d:174:ALA:HB1	1.97	0.46
1:A:276:U:O2'	1:A:278:A:N6	2.47	0.46
1:A:465:G:OP1	28:2:12:ARG:NH1	2.48	0.46
1:A:764:A:O2'	1:A:781:A:N6	2.49	0.46
1:A:1068:G:N2	1:A:1095:A:O3'	2.49	0.46
1:A:1084:A:N3	1:A:1105:U:O2'	2.46	0.46
1:A:1682:G:OP2	1:A:1699:G:N2	2.42	0.46
11:L:95:LEU:HD11	11:L:125:LEU:HD21	1.98	0.46
13:N:28:LEU:HD23	13:N:48:VAL:HG11	1.98	0.46
54:w:3:ARG:NH1	56:z:316:ASP:OD2	2.43	0.46
1:A:659:G:O2'	5:E:95:LYS:O	2.28	0.46
32:a:444:G:H1	32:a:490:C:H42	1.64	0.46
33:b:119:GLN:NE2	33:b:124:THR:OG1	2.48	0.46
1:A:1900:A:H1'	1:A:1970:A:H2'	1.98	0.46
7:G:88:LEU:HD21	7:G:104:LEU:HD22	1.98	0.46
34:c:137:VAL:HG21	34:c:167:TYR:HD2	1.81	0.46
42:k:80:ASN:HB3	42:k:105:ARG:HB2	1.97	0.46
1:A:84:A:N1	1:A:98:G:O2'	2.41	0.46
1:A:1509:A:H2'	1:A:1510:G:C8	2.50	0.46
1:A:2646:C:OP2	1:A:2732:G:O2'	2.27	0.46
5:E:148:ILE:HA	5:E:187:VAL:HG13	1.98	0.46
13:N:45:ARG:HG2	13:N:95:THR:HG21	1.98	0.46
46:o:34:GLN:HB3	46:o:58:MET:HE1	1.97	0.46
1:A:1394:U:H4'	1:A:1603:A:H4'	1.98	0.46
1:A:1869:G:N2	1:A:1872:A:OP2	2.46	0.46
32:a:757:U:O2'	32:a:879:C:O2	2.33	0.46
34:c:18:ASN:ND2	45:n:90:ARG:O	2.48	0.46
1:A:1953:A:O2'	1:A:2559:C:O2	2.32	0.45
6:F:107:VAL:HG11	6:F:175:PRO:HG2	1.98	0.45
32:a:427:U:O2'	32:a:541:G:OP1	2.34	0.45
34:c:113:LYS:HB2	34:c:184:ASN:HD22	1.81	0.45
54:w:15:ALA:CB	56:z:314:LYS:CD	2.91	0.45
1:A:1754:A:O3'	15:P:102:ARG:NH2	2.49	0.45
18:S:47:VAL:HG23	18:S:103:ILE:HG21	1.96	0.45
22:W:19:VAL:HG22	22:W:34:VAL:HG22	1.98	0.45
33:b:99:MET:HA	33:b:106:VAL:HG21	1.99	0.45
38:g:145:GLU:H	38:g:148:LYS:HB2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:k:123:PRO:O	52:u:34:ARG:N	2.43	0.45
56:z:246:THR:HG22	56:z:260:ALA:HB2	1.98	0.45
1:A:1019:U:OP1	1:A:1035:U:O2'	2.25	0.45
5:E:106:LYS:HG3	5:E:200:LEU:HD23	1.97	0.45
9:J:44:TYR:O	16:Q:63:ARG:NE	2.46	0.45
12:M:53:MET:HE2	12:M:63:ILE:HG12	1.98	0.45
18:S:4:ILE:O	18:S:57:ASN:ND2	2.50	0.45
40:i:37:TYR:HD2	40:i:38:PHE:HD1	1.64	0.45
1:A:184:C:H2'	1:A:185:G:C8	2.51	0.45
1:A:2469:A:N6	1:A:2481:G:O2'	2.49	0.45
7:G:29:ASN:ND2	7:G:77:GLY:O	2.41	0.45
32:a:148:G:N2	32:a:175:C:O2	2.50	0.45
1:A:116:C:O2'	1:A:126:A:N3	2.45	0.45
4:D:97:SER:OG	4:D:98:VAL:N	2.50	0.45
8:H:62:LEU:HA	8:H:65:ALA:HB3	1.98	0.45
32:a:1315:U:O2'	32:a:1360:A:N3	2.46	0.45
43:l:53:ARG:HA	43:l:63:THR:HA	1.99	0.45
1:A:1156:A:C8	16:Q:50:ARG:HG2	2.52	0.45
1:A:1769:U:O2'	1:A:1958:C:OP1	2.34	0.45
1:A:1796:U:H2'	1:A:1797:G:C8	2.52	0.45
4:D:34:VAL:HG22	4:D:50:VAL:HG12	1.98	0.45
12:M:40:ARG:HD2	12:M:93:VAL:HG21	1.97	0.45
32:a:740:U:OP1	46:o:37:HIS:NE2	2.38	0.45
50:s:48:ILE:H	50:s:48:ILE:HG13	1.52	0.45
1:A:674:G:H1'	5:E:69:ARG:HE	1.82	0.45
1:A:2477:U:O2	30:4:4:ARG:NH2	2.50	0.45
5:E:18:THR:HA	5:E:106:LYS:HE3	1.99	0.45
8:H:3:VAL:HA	8:H:38:PRO:HA	1.99	0.45
15:P:13:LYS:HE3	15:P:76:HIS:HA	1.98	0.45
17:R:40:MET:HE3	17:R:42:ALA:HB2	1.98	0.45
32:a:701:U:OP1	32:a:702:A:O2'	2.29	0.45
32:a:1086:U:H3	32:a:1099:G:H22	1.65	0.45
41:j:10:LEU:HB3	41:j:98:VAL:HG23	1.97	0.45
42:k:81:LEU:HD11	42:k:99:LEU:HD23	1.98	0.45
1:A:974:G:H8	1:A:990:A:H62	1.64	0.45
2:B:79:G:N7	21:V:14:LYS:NZ	2.65	0.45
3:C:77:VAL:HG21	3:C:109:LEU:HD11	1.99	0.45
31:6:20:ASN:ND2	31:6:37:CYS:SG	2.83	0.45
32:a:9:G:OP2	36:e:125:LYS:NZ	2.50	0.45
46:o:31:LEU:HD22	46:o:58:MET:HB2	1.98	0.45
1:A:290:U:H2'	1:A:291:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:4:PHE:O	16:Q:63:ARG:NH2	2.39	0.45
34:c:155:ARG:NE	34:c:159:ALA:O	2.39	0.45
37:f:8:PHE:HA	37:f:87:SER:HA	1.98	0.45
1:A:964:C:O2'	1:A:2273:A:N3	2.40	0.44
6:F:174:PHE:O	6:F:176:PHE:N	2.50	0.44
13:N:24:MET:HE1	13:N:40:LYS:HB3	1.99	0.44
32:a:59:A:H5''	32:a:387:U:H5''	1.99	0.44
45:n:46:LEU:HG	50:s:12:LEU:HD21	1.99	0.44
51:t:2:ASN:OD1	51:t:3:ILE:N	2.50	0.44
5:E:97:ASN:ND2	5:E:100:MET:SD	2.90	0.44
35:d:28:ASP:OD1	35:d:28:ASP:N	2.50	0.44
50:s:30:LEU:HB2	50:s:48:ILE:HG22	1.99	0.44
1:A:2543:G:H2'	1:A:2544:G:C8	2.53	0.44
1:A:160:A:N3	1:A:2208:C:O2'	2.47	0.44
1:A:672:C:OP2	11:L:42:SER:OG	2.32	0.44
1:A:705:A:OP2	1:A:725:G:N1	2.42	0.44
9:J:56:VAL:HB	9:J:124:VAL:HG12	1.98	0.44
10:K:4:GLU:HG2	10:K:5:GLN:HG2	2.00	0.44
41:j:66:GLU:OE2	41:j:68:ARG:NE	2.50	0.44
45:n:2:LYS:O	45:n:5:MET:N	2.46	0.44
56:z:6:PRO:HB2	56:z:7:VAL:H	1.62	0.44
1:A:30:G:O2'	1:A:1214:A:N3	2.46	0.44
1:A:793:A:OP2	1:A:2071:A:O2'	2.29	0.44
5:E:102:ARG:NH1	5:E:200:LEU:O	2.49	0.44
16:Q:27:ARG:HG2	16:Q:33:VAL:HG12	2.00	0.44
32:a:420:U:O2'	32:a:423:G:O6	2.33	0.44
1:A:694:U:H3	1:A:768:G:H1	1.66	0.44
1:A:917:A:H5''	1:A:2268:A:H61	1.83	0.44
7:G:21:GLN:NE2	7:G:37:ASN:O	2.50	0.44
36:e:152:VAL:HG21	39:h:98:LEU:HB2	2.00	0.44
43:l:54:VAL:HG21	43:l:81:ILE:HD11	2.00	0.44
1:A:1231:U:H2'	1:A:1232:G:H8	1.83	0.44
4:D:33:ARG:HG3	4:D:73:VAL:HB	2.00	0.44
6:F:139:GLU:HG2	31:6:27:THR:HG23	1.99	0.44
10:K:12:ASP:HB2	10:K:96:GLY:HA3	1.99	0.44
32:a:9:G:H5'	36:e:107:GLY:HA3	2.00	0.44
32:a:671:G:H4'	37:f:79:ARG:HH22	1.82	0.44
35:d:164:ARG:HG2	35:d:165:GLU:H	1.83	0.44
50:s:5:LYS:HG3	50:s:6:LYS:HG2	2.00	0.44
50:s:35:ARG:HB3	50:s:71:GLY:HA3	2.00	0.44
1:A:2627:G:N2	1:A:2777:G:OP2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:5:PHE:HE1	17:R:14:VAL:HG11	1.83	0.44
23:X:13:THR:HG22	23:X:27:ARG:HG2	1.99	0.44
32:a:82:G:H22	32:a:87:C:H42	1.66	0.44
1:A:32:C:N4	1:A:447:A:OP2	2.50	0.43
1:A:102:U:H1'	24:Y:2:LYS:HE2	2.00	0.43
1:A:1651:G:H4'	13:N:39:PRO:HG2	1.99	0.43
1:A:1936:A:H2	1:A:1943:U:H3	1.66	0.43
11:L:49:GLY:HA3	11:L:58:TYR:HE1	1.83	0.43
11:L:94:THR:HA	11:L:97:ALA:HB3	2.00	0.43
31:6:33:ASN:ND2	44:m:49:GLU:OE2	2.50	0.43
32:a:1071:C:OP1	36:e:53:ARG:NH2	2.50	0.43
32:a:1095:U:OP1	32:a:1108:G:N2	2.41	0.43
56:z:244:TYR:HE1	56:z:262:ARG:HG3	1.82	0.43
1:A:1028:A:N3	1:A:2486:C:O2'	2.44	0.43
40:i:94:ARG:HA	40:i:97:LEU:HB3	1.99	0.43
44:m:97:ARG:HB2	44:m:99:GLN:HE22	1.83	0.43
1:A:957:C:H5'	12:M:75:GLU:HG2	2.00	0.43
1:A:1060:U:H4'	1:A:1061:U:H5'	2.00	0.43
8:H:93:SER:OG	8:H:121:VAL:O	2.34	0.43
14:O:49:VAL:HG21	14:O:82:ALA:HA	2.00	0.43
15:P:64:SER:OG	15:P:65:ASN:N	2.50	0.43
32:a:105:G:OP2	51:t:12:GLN:NE2	2.51	0.43
33:b:65:LYS:HD2	33:b:153:MET:HG3	2.00	0.43
36:e:10:LEU:HD22	36:e:67:ARG:HH12	1.82	0.43
1:A:1417:C:HO2'	1:A:1587:G:HO2'	1.64	0.43
1:A:2039:U:H2'	1:A:2040:G:C8	2.53	0.43
1:A:2724:U:OP1	4:D:123:LYS:NZ	2.47	0.43
3:C:159:THR:HG23	3:C:176:ARG:HG2	2.00	0.43
56:z:155:TRP:HH2	56:z:191:TRP:HB3	1.83	0.43
1:A:2202:U:O2'	1:A:2204:G:OP1	2.34	0.43
2:B:29:A:O2'	2:B:58:A:N1	2.43	0.43
3:C:230:PRO:HB2	3:C:244:VAL:HG21	2.00	0.43
56:z:79:ASP:O	56:z:83:LEU:N	2.50	0.43
1:A:467:G:O2'	1:A:796:C:O2'	2.34	0.43
1:A:2295:C:OP1	14:O:10:ARG:NH1	2.40	0.43
32:a:113:G:N3	32:a:353:A:O2'	2.48	0.43
32:a:1398:A:OP1	54:w:36:LYS:CE	2.66	0.43
49:r:41:SER:HB2	49:r:51:GLN:HE21	1.83	0.43
50:s:43:MET:HE1	50:s:70:LEU:HD21	1.99	0.43
1:A:1055:G:H1	1:A:1104:C:H42	1.67	0.43
2:B:15:A:H3'	2:B:16:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:7:PRO:HB3	3:C:13:ARG:HG3	2.00	0.43
3:C:16:VAL:HB	3:C:203:VAL:HG22	2.01	0.43
10:K:24:VAL:HG13	10:K:33:ALA:HB2	2.00	0.43
32:a:768:A:N3	32:a:1512:U:O2'	2.46	0.43
32:a:1038:C:H2'	32:a:1039:G:H8	1.84	0.43
55:x:23:C:H2'	55:x:24:G:C8	2.54	0.43
1:A:413:C:HO2'	1:A:1880:U:HO2'	1.58	0.43
1:A:631:A:N3	1:A:2415:G:O2'	2.42	0.43
32:a:8:A:N6	35:d:201:GLU:O	2.45	0.43
32:a:309:A:O2'	32:a:607:A:N1	2.48	0.43
33:b:183:PHE:HB3	33:b:197:PHE:HB2	2.00	0.43
44:m:57:ASP:O	44:m:61:LYS:NZ	2.52	0.43
50:s:39:ILE:HG12	50:s:70:LEU:HD23	2.00	0.43
1:A:1032:A:H2	1:A:1122:G:H22	1.67	0.43
1:A:1199:U:H1'	16:Q:3:VAL:HG22	2.00	0.43
1:A:2479:U:OP1	1:A:2537:U:O2'	2.34	0.43
14:O:108:ASP:OD1	14:O:111:ARG:NH1	2.52	0.43
56:z:152:TYR:OH	56:z:195:GLU:OE1	2.29	0.43
6:F:98:PHE:O	6:F:102:LEU:N	2.48	0.43
10:K:59:LYS:HB2	10:K:87:LEU:HB2	2.00	0.43
31:6:22:MET:HE2	31:6:22:MET:HB3	1.75	0.43
1:A:2117:A:H61	1:A:2166:U:H3	1.67	0.42
2:B:98:G:H1	21:V:14:LYS:HB2	1.84	0.42
10:K:33:ALA:HB1	10:K:37:ASP:HB2	2.01	0.42
17:R:77:PHE:HD1	17:R:84:ARG:HB3	1.84	0.42
38:g:2:ARG:HA	38:g:2:ARG:HD3	1.89	0.42
56:z:14:LEU:O	56:z:18:SER:OG	2.28	0.42
1:A:589:U:H2'	1:A:590:A:C8	2.54	0.42
1:A:2116:G:H1	1:A:2164:C:H42	1.67	0.42
32:a:1218:C:H2'	32:a:1219:A:C8	2.54	0.42
42:k:71:ASP:HA	42:k:74:LYS:HG3	2.01	0.42
44:m:84:CYS:SG	44:m:87:GLY:N	2.83	0.42
45:n:87:ALA:HB1	45:n:92:GLU:HB2	2.00	0.42
50:s:61:VAL:HA	50:s:65:MET:HE3	2.00	0.42
56:z:166:ILE:HD11	56:z:182:LYS:HB2	2.01	0.42
1:A:739:A:H1'	1:A:740:C:H5	1.84	0.42
1:A:774:G:H5''	3:C:47:ARG:HH21	1.84	0.42
1:A:1009:A:N3	1:A:1153:C:O2'	2.46	0.42
1:A:1365:A:O5'	23:X:27:ARG:NH2	2.46	0.42
25:Z:18:LYS:O	25:Z:22:THR:OG1	2.35	0.42
32:a:951:G:OP2	44:m:100:ARG:NH2	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:185:ILE:HA	33:b:199:ILE:HB	2.01	0.42
35:d:11:SER:OG	35:d:16:THR:O	2.32	0.42
42:k:86:LYS:HB2	42:k:112:VAL:HG23	2.01	0.42
1:A:270:A:N1	1:A:369:U:O2'	2.39	0.42
1:A:1470:A:N6	1:A:1521:G:O2'	2.52	0.42
1:A:1827:U:O2'	1:A:1970:A:N3	2.41	0.42
1:A:2822:G:H5''	4:D:164:GLN:HE22	1.84	0.42
3:C:36:ASN:HB2	3:C:61:TYR:HB2	2.02	0.42
9:J:32:LEU:HD22	9:J:54:ILE:HG21	2.01	0.42
11:L:62:PRO:HB2	29:3:29:ARG:HH11	1.84	0.42
11:L:85:VAL:HG21	11:L:90:VAL:HG22	2.00	0.42
32:a:600:A:H5'	39:h:120:LEU:HA	2.00	0.42
32:a:958:A:C4	50:s:54:ARG:HD3	2.54	0.42
40:i:33:SER:H	40:i:36:GLN:HE21	1.66	0.42
1:A:168:G:H2'	1:A:169:G:H8	1.85	0.42
1:A:1980:G:O2'	1:A:1982:U:OP2	2.31	0.42
4:D:40:LEU:HA	4:D:44:GLY:H	1.84	0.42
11:L:61:LEU:HD23	29:3:26:ALA:HB2	2.01	0.42
13:N:87:PHE:HD1	13:N:90:ARG:HD3	1.84	0.42
43:l:73:LEU:HD21	43:l:79:ILE:HD13	2.01	0.42
44:m:12:LYS:HD3	44:m:16:ILE:HG22	2.02	0.42
45:n:54:ASP:OD1	45:n:59:ARG:NE	2.48	0.42
49:r:70:THR:HG23	49:r:72:ARG:H	1.83	0.42
1:A:2420:C:H5''	27:1:7:LYS:HD2	2.01	0.42
2:B:41:G:H21	6:F:65:LEU:HD11	1.84	0.42
5:E:146:VAL:HG12	5:E:185:LYS:HB2	2.01	0.42
7:G:41:GLU:HA	7:G:54:ARG:HH21	1.83	0.42
21:V:51:GLN:HE22	21:V:86:LEU:HD21	1.85	0.42
29:3:15:LYS:HE2	29:3:19:GLY:HA2	2.02	0.42
32:a:574:A:O2'	32:a:882:C:O2'	2.34	0.42
1:A:277:G:H4'	1:A:278:A:C5	2.55	0.42
1:A:558:U:H2'	1:A:559:G:C8	2.54	0.42
12:M:40:ARG:HG2	12:M:95:LEU:HD23	2.02	0.42
13:N:96:ARG:HH22	13:N:116:VAL:HG13	1.85	0.42
29:3:31:ILE:O	29:3:35:LYS:NZ	2.51	0.42
32:a:458:U:H2'	32:a:459:A:C8	2.54	0.42
44:m:24:VAL:HG23	44:m:28:ARG:HB3	2.01	0.42
54:w:33:LYS:HA	54:w:34:LYS:HA	1.83	0.42
1:A:955:U:H5	1:A:962:G:H1	1.67	0.42
1:A:2220:U:H4'	8:H:97:ARG:HH21	1.84	0.42
1:A:2756:U:H1'	1:A:2757:A:H5''	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2839:G:O2'	13:N:49:GLU:OE1	2.37	0.42
8:H:55:GLU:HG2	8:H:58:LEU:HD12	2.01	0.42
1:A:527:C:N4	1:A:2779:U:OP2	2.42	0.42
1:A:1296:G:OP1	1:A:2709:G:O2'	2.26	0.42
1:A:2635:A:O2'	4:D:81:GLU:OE1	2.36	0.42
1:A:2848:G:O2'	1:A:2868:A:N6	2.53	0.42
9:J:37:ARG:NH2	9:J:110:PRO:HG3	2.35	0.42
17:R:40:MET:HG3	17:R:48:LYS:HA	2.00	0.42
30:4:1:MET:HE2	30:4:36:ARG:HB2	2.02	0.42
1:A:987:C:O2'	1:A:1000:A:N3	2.48	0.42
1:A:2224:G:H4'	1:A:2226:C:C2	2.55	0.42
1:A:2831:G:OP2	4:D:59:ARG:NH1	2.52	0.42
3:C:257:ARG:HG2	3:C:269:ARG:HH12	1.85	0.42
6:F:30:VAL:HA	6:F:157:THR:HA	2.01	0.42
9:J:99:ARG:HA	9:J:102:GLU:HB3	2.02	0.41
12:M:33:LEU:HB2	12:M:117:PHE:CD1	2.56	0.41
32:a:504:C:H2'	32:a:511:C:H5	1.85	0.41
32:a:575:G:O2'	32:a:821:G:OP2	2.34	0.41
32:a:1150:A:H4'	41:j:43:PRO:HB3	2.02	0.41
43:l:45:ASN:ND2	43:l:88:ASP:OD1	2.32	0.41
56:z:153:LEU:HG	56:z:163:THR:HG21	2.01	0.41
1:A:247:G:OP2	1:A:249:C:N4	2.53	0.41
1:A:1550:C:H2'	1:A:1551:A:C8	2.55	0.41
1:A:2405:G:O2'	1:A:2412:A:N6	2.53	0.41
4:D:68:PHE:HE1	4:D:79:LEU:HD21	1.84	0.41
12:M:53:MET:HE1	12:M:103:TYR:HB3	2.01	0.41
32:a:667:G:O2'	46:o:48:ASP:OD1	2.32	0.41
1:A:58:G:O2'	1:A:73:A:N1	2.52	0.41
1:A:243:U:OP2	1:A:254:G:N1	2.44	0.41
1:A:576:U:H2'	1:A:577:G:C8	2.55	0.41
1:A:633:A:O2'	1:A:2404:U:OP1	2.36	0.41
32:a:535:A:H62	54:w:44:LYS:HG3	1.86	0.41
32:a:950:U:H2'	32:a:951:G:C8	2.55	0.41
32:a:981:U:H4'	45:n:61:ARG:HG2	2.02	0.41
32:a:1118:U:OP1	40:i:10:ARG:NH1	2.39	0.41
39:h:89:ASP:OD1	39:h:89:ASP:N	2.53	0.41
40:i:80:HIS:CE1	40:i:84:ARG:HD2	2.55	0.41
1:A:1820:U:C2	3:C:200:MET:HB2	2.55	0.41
6:F:95:MET:HE3	6:F:95:MET:HB2	1.89	0.41
8:H:12:LEU:HB2	8:H:19:VAL:HG11	2.01	0.41
18:S:56:ALA:HA	18:S:59:GLU:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:z:128:CYS:HB3	56:z:183:ILE:HG23	2.03	0.41
1:A:372:G:C4	23:X:60:LYS:HD2	2.55	0.41
1:A:444:C:OP1	5:E:40:ARG:NH2	2.54	0.41
1:A:720:U:H2'	1:A:721:A:C8	2.55	0.41
12:M:53:MET:HB2	12:M:120:ALA:HB2	2.03	0.41
29:3:31:ILE:H	29:3:31:ILE:HG13	1.71	0.41
32:a:946:A:H2'	32:a:947:G:C8	2.55	0.41
32:a:1147:C:O2	40:i:17:ARG:NH2	2.54	0.41
1:A:281:C:H2'	1:A:282:A:H8	1.85	0.41
1:A:704:G:H1'	1:A:727:A:H61	1.85	0.41
16:Q:78:PHE:HE1	16:Q:109:VAL:HA	1.85	0.41
33:b:53:LEU:HD21	33:b:216:VAL:HG22	2.03	0.41
56:z:119:PHE:H	56:z:120:SER:HB2	1.86	0.41
1:A:2377:A:H2'	1:A:2378:A:C8	2.55	0.41
4:D:4:LEU:HD23	4:D:32:ASN:HD22	1.85	0.41
11:L:55:MET:HA	11:L:56:PRO:HD3	1.96	0.41
25:Z:40:THR:HG22	25:Z:43:ILE:HG12	2.03	0.41
56:z:169:SER:O	56:z:177:LYS:N	2.46	0.41
1:A:475:C:O2'	1:A:505:A:N3	2.54	0.41
1:A:1130:U:N3	1:A:2025:C:OP1	2.38	0.41
1:A:2619:C:H5''	4:D:157:LYS:HA	2.03	0.41
6:F:125:GLY:HA2	6:F:162:ASP:HA	2.03	0.41
6:F:130:GLY:HA2	6:F:152:ASP:HA	2.02	0.41
32:a:1015:G:N2	32:a:1218:C:O2	2.49	0.41
36:e:156:ARG:HA	39:h:43:GLY:HA3	2.01	0.41
56:z:161:PHE:HD1	56:z:185:GLY:HA3	1.86	0.41
1:A:663:G:H5''	11:L:17:LYS:HD3	2.02	0.41
1:A:743:A:O2'	1:A:1659:G:OP1	2.31	0.41
1:A:1939:U:OP1	1:A:2604:U:O2'	2.36	0.41
5:E:3:LEU:HD21	5:E:19:PHE:HE2	1.85	0.41
5:E:69:ARG:HH11	5:E:69:ARG:HD3	1.73	0.41
7:G:51:PHE:HZ	7:G:71:LEU:HD22	1.85	0.41
13:N:22:ARG:HG3	13:N:70:THR:HA	2.03	0.41
13:N:98:LEU:O	13:N:112:TYR:N	2.49	0.41
21:V:48:MET:SD	21:V:51:GLN:NE2	2.94	0.41
33:b:169:HIS:CE1	33:b:170:ILE:HG23	2.55	0.41
37:f:88:MET:HE3	37:f:88:MET:HB2	1.81	0.41
40:i:86:LEU:HB3	40:i:93:LEU:HD13	2.03	0.41
51:t:4:LYS:HD3	51:t:4:LYS:HA	1.91	0.41
52:u:5:VAL:HG22	52:u:7:GLU:HG2	2.03	0.41
56:z:18:SER:HB3	56:z:22:ARG:HH12	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1311:G:H21	1:A:1603:A:H62	1.69	0.41
1:A:1316:U:H2'	1:A:1317:G:C8	2.56	0.41
32:a:653:U:H1'	39:h:55:LYS:HE3	2.03	0.41
42:k:63:GLN:HG3	42:k:98:ALA:HB2	2.03	0.41
56:z:154:ARG:NH1	56:z:350:ASP:OD1	2.54	0.41
1:A:2298:A:OP1	6:F:70:ARG:NH2	2.54	0.40
1:A:2484:G:O2'	12:M:123:LYS:O	2.35	0.40
18:S:44:ALA:HA	18:S:47:VAL:HG12	2.04	0.40
32:a:865:A:N3	32:a:918:A:O2'	2.47	0.40
34:c:84:GLU:HG2	34:c:87:ARG:HH12	1.85	0.40
35:d:12:ARG:HG2	35:d:33:ILE:HD12	2.03	0.40
40:i:9:GLY:HA2	40:i:80:HIS:ND1	2.36	0.40
43:l:23:LEU:HD22	43:l:58:ASN:HD22	1.85	0.40
44:m:111:PRO:HB2	44:m:113:LYS:HG3	2.03	0.40
1:A:694:U:H5'	1:A:1569:A:C5	2.56	0.40
1:A:1181:U:H2'	1:A:1182:G:C8	2.56	0.40
2:B:13:G:N2	2:B:16:G:N3	2.68	0.40
3:C:146:LYS:HB2	3:C:149:LYS:HB2	2.04	0.40
14:O:10:ARG:HH21	14:O:10:ARG:HD2	1.76	0.40
30:4:17:VAL:HG12	30:4:19:ARG:HG3	2.03	0.40
49:r:47:ARG:HB2	49:r:50:TYR:HD2	1.85	0.40
1:A:977:G:H5'	16:Q:54:ARG:HH12	1.86	0.40
14:O:102:ARG:HH21	14:O:102:ARG:HD2	1.74	0.40
32:a:222:C:H2'	32:a:223:A:C8	2.57	0.40
32:a:998:C:H42	32:a:1043:G:H1	1.70	0.40
32:a:1414:U:H2'	32:a:1415:G:C8	2.56	0.40
44:m:6:ILE:HG13	44:m:7:ASN:H	1.85	0.40
47:p:18:GLN:NE2	47:p:35:ARG:HE	2.19	0.40
54:w:15:ALA:CB	56:z:314:LYS:CB	2.91	0.40
1:A:1316:U:H2'	1:A:1317:G:H8	1.87	0.40
3:C:164:VAL:HG21	3:C:180:MET:HE1	2.03	0.40
4:D:91:THR:HG22	4:D:94:GLN:HB2	2.03	0.40
7:G:53:PRO:HG3	7:G:61:TRP:CE2	2.57	0.40
11:L:131:ALA:HA	11:L:134:ALA:HB3	2.03	0.40
32:a:413:G:O2'	32:a:428:G:N2	2.54	0.40
38:g:78:ARG:HE	38:g:83:THR:HG1	1.68	0.40
54:w:24:LEU:O	54:w:28:ARG:NH1	2.39	0.40
1:A:1363:C:O2'	1:A:1809:A:N3	2.50	0.40
14:O:5:SER:HA	14:O:8:ILE:HD12	2.03	0.40
30:4:16:ILE:HD13	30:4:25:VAL:HG22	2.02	0.40
32:a:928:G:O2'	32:a:1533:C:OP1	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:d:57:LYS:NZ	35:d:68:GLU:OE1	2.55	0.40
37:f:39:LEU:HD23	37:f:62:MET:HA	2.03	0.40
39:h:42:GLU:HG2	39:h:100:ILE:HG12	2.04	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	
3	C	269/271 (99%)	252 (94%)	17 (6%)	0	100	100
4	D	207/209 (99%)	194 (94%)	13 (6%)	0	100	100
5	E	199/201 (99%)	186 (94%)	13 (6%)	0	100	100
6	F	175/177 (99%)	160 (91%)	13 (7%)	2 (1%)	11	39
7	G	174/176 (99%)	161 (92%)	12 (7%)	1 (1%)	21	52
8	H	147/149 (99%)	131 (89%)	16 (11%)	0	100	100
9	J	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
10	K	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
11	L	141/143 (99%)	123 (87%)	17 (12%)	1 (1%)	18	49
12	M	134/136 (98%)	127 (95%)	6 (4%)	1 (1%)	18	49
13	N	118/120 (98%)	106 (90%)	12 (10%)	0	100	100
14	O	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
15	P	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
16	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
17	R	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
18	S	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
19	T	91/93 (98%)	87 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	U	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
21	V	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
22	W	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
23	X	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
24	Y	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
25	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
26	0	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
27	1	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
28	2	44/46 (96%)	44 (100%)	0	0	100	100
29	3	62/64 (97%)	52 (84%)	9 (14%)	1 (2%)	7	30
30	4	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
31	6	64/66 (97%)	57 (89%)	7 (11%)	0	100	100
33	b	216/218 (99%)	189 (88%)	24 (11%)	3 (1%)	9	34
34	c	204/206 (99%)	195 (96%)	9 (4%)	0	100	100
35	d	203/205 (99%)	179 (88%)	24 (12%)	0	100	100
36	e	155/157 (99%)	129 (83%)	26 (17%)	0	100	100
37	f	98/100 (98%)	83 (85%)	14 (14%)	1 (1%)	12	41
38	g	149/151 (99%)	137 (92%)	12 (8%)	0	100	100
39	h	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
40	i	125/127 (98%)	103 (82%)	22 (18%)	0	100	100
41	j	96/98 (98%)	83 (86%)	12 (12%)	1 (1%)	12	41
42	k	114/116 (98%)	93 (82%)	21 (18%)	0	100	100
43	l	121/123 (98%)	97 (80%)	24 (20%)	0	100	100
44	m	112/114 (98%)	99 (88%)	12 (11%)	1 (1%)	14	44
45	n	99/101 (98%)	89 (90%)	10 (10%)	0	100	100
46	o	86/88 (98%)	78 (91%)	7 (8%)	1 (1%)	10	37
47	p	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
48	q	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
49	r	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
50	s	77/79 (98%)	74 (96%)	3 (4%)	0	100	100
51	t	83/85 (98%)	80 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	u	63/65 (97%)	41 (65%)	21 (33%)	1 (2%)	7	30
54	w	43/45 (96%)	28 (65%)	11 (26%)	4 (9%)	0	3
56	z	357/359 (99%)	334 (94%)	22 (6%)	1 (0%)	36	67
All	All	5979/6081 (98%)	5420 (91%)	540 (9%)	19 (0%)	37	67

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	b	18	GLN
44	m	4	ALA
46	o	46	LYS
54	w	13	ASP
54	w	33	LYS
54	w	36	LYS
29	3	31	ILE
52	u	37	TYR
6	F	175	PRO
7	G	119	GLY
56	z	322	GLN
33	b	17	HIS
37	f	53	LYS
6	F	174	PHE
33	b	20	ARG
54	w	12	LYS
12	M	69	PRO
11	L	111	ILE
41	j	42	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	216/216 (100%)	216 (100%)	0	100	100
4	D	164/164 (100%)	164 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	165/165 (100%)	164 (99%)	1 (1%)	78	83
6	F	148/148 (100%)	147 (99%)	1 (1%)	76	82
7	G	137/137 (100%)	136 (99%)	1 (1%)	76	82
8	H	114/114 (100%)	114 (100%)	0	100	100
9	J	116/116 (100%)	115 (99%)	1 (1%)	70	80
10	K	103/103 (100%)	103 (100%)	0	100	100
11	L	102/102 (100%)	100 (98%)	2 (2%)	48	72
12	M	109/109 (100%)	107 (98%)	2 (2%)	51	73
13	N	100/100 (100%)	100 (100%)	0	100	100
14	O	86/86 (100%)	86 (100%)	0	100	100
15	P	99/99 (100%)	98 (99%)	1 (1%)	68	79
16	Q	89/89 (100%)	89 (100%)	0	100	100
17	R	84/84 (100%)	84 (100%)	0	100	100
18	S	93/93 (100%)	93 (100%)	0	100	100
19	T	80/80 (100%)	80 (100%)	0	100	100
20	U	83/83 (100%)	83 (100%)	0	100	100
21	V	78/78 (100%)	78 (100%)	0	100	100
22	W	57/57 (100%)	57 (100%)	0	100	100
23	X	67/67 (100%)	67 (100%)	0	100	100
24	Y	55/55 (100%)	55 (100%)	0	100	100
25	Z	48/48 (100%)	48 (100%)	0	100	100
26	0	47/47 (100%)	46 (98%)	1 (2%)	47	71
27	1	45/45 (100%)	45 (100%)	0	100	100
28	2	38/38 (100%)	38 (100%)	0	100	100
29	3	51/51 (100%)	51 (100%)	0	100	100
30	4	34/34 (100%)	34 (100%)	0	100	100
31	6	59/59 (100%)	59 (100%)	0	100	100
33	b	180/180 (100%)	180 (100%)	0	100	100
34	c	170/170 (100%)	168 (99%)	2 (1%)	63	78
35	d	172/172 (100%)	172 (100%)	0	100	100
36	e	114/119 (96%)	113 (99%)	1 (1%)	70	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	f	87/87 (100%)	87 (100%)	0	100	100
38	g	124/124 (100%)	122 (98%)	2 (2%)	55	75
39	h	104/104 (100%)	102 (98%)	2 (2%)	50	73
40	i	105/105 (100%)	105 (100%)	0	100	100
41	j	86/86 (100%)	86 (100%)	0	100	100
42	k	89/89 (100%)	88 (99%)	1 (1%)	65	78
43	l	103/103 (100%)	103 (100%)	0	100	100
44	m	92/92 (100%)	92 (100%)	0	100	100
45	n	79/83 (95%)	79 (100%)	0	100	100
46	o	76/76 (100%)	74 (97%)	2 (3%)	40	68
47	p	65/65 (100%)	64 (98%)	1 (2%)	57	75
48	q	74/74 (100%)	74 (100%)	0	100	100
49	r	48/56 (86%)	48 (100%)	0	100	100
50	s	70/70 (100%)	68 (97%)	2 (3%)	37	66
51	t	65/65 (100%)	64 (98%)	1 (2%)	57	75
52	u	44/55 (80%)	44 (100%)	0	100	100
54	w	38/38 (100%)	34 (90%)	4 (10%)	6	26
56	z	305/305 (100%)	304 (100%)	1 (0%)	86	87
All	All	4957/4985 (99%)	4928 (99%)	29 (1%)	76	83

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	187	VAL
6	F	140	ILE
7	G	37	ASN
9	J	57	LEU
11	L	27	LEU
11	L	110	VAL
12	M	6	ARG
12	M	46	ILE
15	P	72	VAL
26	O	2	VAL
34	c	24	ASN
34	c	199	VAL
36	e	156	ARG

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Mol	Chain	Res	Type
38	g	6	ILE
38	g	147	ASN
39	h	100	ILE
39	h	120	LEU
42	k	30	ILE
46	o	46	LYS
46	o	86	LEU
47	p	19	VAL
50	s	10	ILE
50	s	48	ILE
51	t	20	ASN
54	w	12	LYS
54	w	14	ASN
54	w	16	ILE
54	w	33	LYS
56	z	270	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (80) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	42	ASN
4	D	164	GLN
4	D	173	GLN
5	E	136	GLN
5	E	156	ASN
7	G	37	ASN
7	G	138	GLN
8	H	66	ASN
9	J	40	HIS
9	J	58	ASN
11	L	104	GLN
14	O	38	GLN
14	O	98	GLN
15	P	2	ASN
15	P	11	GLN
16	Q	43	GLN
16	Q	51	GLN
17	R	6	GLN
17	R	12	HIS
17	R	18	GLN
17	R	43	ASN
18	S	7	HIS

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Mol	Chain	Res	Type
18	S	9	HIS
19	T	15	HIS
20	U	68	ASN
22	W	8	ASN
22	W	53	HIS
25	Z	8	GLN
25	Z	19	HIS
31	6	20	ASN
33	b	18	GLN
33	b	23	ASN
33	b	38	HIS
33	b	57	ASN
33	b	119	GLN
34	c	24	ASN
34	c	138	GLN
35	d	35	GLN
36	e	120	HIS
36	e	145	ASN
37	f	37	HIS
37	f	55	HIS
37	f	58	HIS
37	f	63	ASN
38	g	147	ASN
39	h	3	GLN
39	h	37	ASN
39	h	75	GLN
40	i	3	ASN
40	i	4	GLN
40	i	30	ASN
40	i	49	GLN
41	j	58	ASN
42	k	21	HIS
42	k	118	ASN
43	l	76	HIS
44	m	7	ASN
44	m	13	HIS
45	n	60	GLN
47	p	9	HIS
47	p	18	GLN
47	p	63	GLN
47	p	79	ASN
48	q	30	HIS

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Mol	Chain	Res	Type
48	q	44	HIS
49	r	51	GLN
50	s	13	HIS
51	t	2	ASN
51	t	47	GLN
51	t	60	GLN
54	w	5	GLN
54	w	14	ASN
54	w	21	HIS
54	w	32	ASN
56	z	8	ASN
56	z	48	ASN
56	z	252	GLN
56	z	276	ASN
56	z	280	GLN
56	z	308	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2898/2903 (99%)	588 (20%)	29 (1%)
2	B	119/120 (99%)	27 (22%)	2 (1%)
32	a	1538/1539 (99%)	272 (17%)	0
53	v	5/6 (83%)	0	0
55	x	76/77 (98%)	14 (18%)	0
All	All	4636/4645 (99%)	901 (19%)	31 (0%)

All (901) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	12	U
1	A	15	G
1	A	23	G
1	A	34	U
1	A	35	G
1	A	36	G
1	A	46	G
1	A	51	G
1	A	52	A
1	A	55	G

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Mol	Chain	Res	Type
1	A	60	G
1	A	63	A
1	A	71	A
1	A	74	A
1	A	75	G
1	A	84	A
1	A	92	U
1	A	96	C
1	A	100	U
1	A	118	A
1	A	119	A
1	A	120	U
1	A	125	A
1	A	138	U
1	A	139	U
1	A	140	C
1	A	141	G
1	A	142	A
1	A	149	A
1	A	162	U
1	A	163	C
1	A	181	A
1	A	196	A
1	A	199	A
1	A	215	G
1	A	216	A
1	A	219	A
1	A	220	G
1	A	221	A
1	A	222	A
1	A	225	C
1	A	233	A
1	A	239	C
1	A	241	A
1	A	242	G
1	A	243	U
1	A	248	G
1	A	249	C
1	A	250	G
1	A	255	A
1	A	265	A
1	A	266	G

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Mol	Chain	Res	Type
1	A	267	C
1	A	273	G
1	A	275	C
1	A	276	U
1	A	277	G
1	A	278	A
1	A	281	C
1	A	285	G
1	A	294	A
1	A	311	A
1	A	323	C
1	A	329	G
1	A	330	A
1	A	335	C
1	A	346	A
1	A	357	C
1	A	361	G
1	A	367	G
1	A	370	G
1	A	371	A
1	A	372	G
1	A	386	G
1	A	387	U
1	A	395	U
1	A	403	U
1	A	404	A
1	A	406	G
1	A	411	G
1	A	412	A
1	A	424	G
1	A	440	C
1	A	455	C
1	A	467	G
1	A	473	G
1	A	481	G
1	A	489	G
1	A	490	C
1	A	491	G
1	A	496	G
1	A	504	A
1	A	505	A
1	A	509	C

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Mol	Chain	Res	Type
1	A	510	C
1	A	529	A
1	A	532	A
1	A	533	G
1	A	543	G
1	A	545	U
1	A	547	A
1	A	548	G
1	A	550	C
1	A	563	A
1	A	565	C
1	A	566	U
1	A	573	U
1	A	575	A
1	A	603	A
1	A	613	A
1	A	614	A
1	A	615	U
1	A	616	A
1	A	621	A
1	A	622	G
1	A	627	A
1	A	632	A
1	A	634	C
1	A	637	A
1	A	645	C
1	A	646	U
1	A	653	U
1	A	654	A
1	A	655	A
1	A	659	G
1	A	668	A
1	A	669	G
1	A	670	A
1	A	677	A
1	A	685	A
1	A	686	U
1	A	694	U
1	A	695	G
1	A	696	G
1	A	704	G
1	A	714	U

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Mol	Chain	Res	Type
1	A	717	C
1	A	726	G
1	A	730	A
1	A	747	C
1	A	748	G
1	A	752	A
1	A	765	C
1	A	775	G
1	A	776	G
1	A	782	A
1	A	783	A
1	A	784	G
1	A	785	G
1	A	788	A
1	A	805	G
1	A	811	U
1	A	812	C
1	A	819	A
1	A	822	G
1	A	827	U
1	A	828	U
1	A	831	G
1	A	838	C
1	A	845	A
1	A	846	U
1	A	847	U
1	A	856	G
1	A	858	G
1	A	859	G
1	A	869	G
1	A	876	C
1	A	878	A
1	A	885	C
1	A	892	A
1	A	893	C
1	A	895	U
1	A	896	A
1	A	897	C
1	A	898	C
1	A	905	A
1	A	907	G
1	A	910	A

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Mol	Chain	Res	Type
1	A	914	G
1	A	927	A
1	A	933	A
1	A	934	U
1	A	941	A
1	A	945	A
1	A	946	C
1	A	953	G
1	A	957	C
1	A	961	C
1	A	973	A
1	A	974	G
1	A	975	A
1	A	983	A
1	A	985	C
1	A	995	C
1	A	996	A
1	A	997	G
1	A	999	U
1	A	1009	A
1	A	1012	U
1	A	1013	C
1	A	1021	A
1	A	1022	G
1	A	1023	U
1	A	1025	G
1	A	1026	G
1	A	1033	U
1	A	1046	A
1	A	1047	G
1	A	1057	A
1	A	1060	U
1	A	1061	U
1	A	1062	G
1	A	1063	G
1	A	1064	C
1	A	1065	U
1	A	1066	U
1	A	1068	G
1	A	1069	A
1	A	1070	A
1	A	1071	G

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Mol	Chain	Res	Type
1	A	1073	A
1	A	1074	G
1	A	1076	C
1	A	1079	C
1	A	1083	U
1	A	1084	A
1	A	1088	A
1	A	1089	A
1	A	1090	A
1	A	1095	A
1	A	1096	A
1	A	1098	A
1	A	1099	G
1	A	1101	U
1	A	1104	C
1	A	1106	G
1	A	1111	A
1	A	1112	G
1	A	1130	U
1	A	1132	U
1	A	1133	A
1	A	1135	C
1	A	1136	G
1	A	1142	A
1	A	1143	A
1	A	1157	G
1	A	1172	C
1	A	1174	U
1	A	1175	A
1	A	1177	G
1	A	1179	G
1	A	1180	U
1	A	1186	G
1	A	1204	A
1	A	1209	U
1	A	1211	C
1	A	1212	G
1	A	1236	G
1	A	1237	A
1	A	1238	G
1	A	1244	A
1	A	1252	G

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Mol	Chain	Res	Type
1	A	1253	A
1	A	1256	G
1	A	1257	C
1	A	1262	A
1	A	1265	A
1	A	1271	G
1	A	1272	A
1	A	1273	U
1	A	1275	A
1	A	1300	G
1	A	1301	A
1	A	1306	C
1	A	1311	G
1	A	1312	U
1	A	1314	C
1	A	1320	C
1	A	1321	A
1	A	1322	A
1	A	1329	U
1	A	1332	G
1	A	1341	G
1	A	1345	C
1	A	1352	U
1	A	1365	A
1	A	1368	G
1	A	1378	A
1	A	1379	U
1	A	1383	A
1	A	1386	C
1	A	1395	A
1	A	1411	U
1	A	1416	G
1	A	1419	A
1	A	1420	A
1	A	1421	G
1	A	1427	A
1	A	1428	C
1	A	1437	C
1	A	1449	G
1	A	1454	C
1	A	1456	G
1	A	1458	U

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Mol	Chain	Res	Type
1	A	1461	C
1	A	1482	G
1	A	1490	A
1	A	1491	G
1	A	1493	C
1	A	1497	U
1	A	1504	A
1	A	1515	A
1	A	1522	A
1	A	1524	G
1	A	1529	G
1	A	1534	U
1	A	1535	A
1	A	1536	C
1	A	1537	G
1	A	1538	G
1	A	1539	U
1	A	1554	U
1	A	1555	G
1	A	1558	C
1	A	1559	U
1	A	1560	G
1	A	1565	C
1	A	1567	G
1	A	1569	A
1	A	1578	U
1	A	1583	A
1	A	1607	C
1	A	1608	A
1	A	1610	A
1	A	1627	G
1	A	1647	U
1	A	1648	U
1	A	1649	G
1	A	1654	A
1	A	1674	G
1	A	1677	A
1	A	1694	C
1	A	1698	A
1	A	1715	G
1	A	1729	U
1	A	1730	C

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Mol	Chain	Res	Type
1	A	1732	C
1	A	1733	G
1	A	1738	G
1	A	1744	A
1	A	1757	A
1	A	1758	U
1	A	1764	C
1	A	1769	U
1	A	1773	A
1	A	1784	A
1	A	1786	A
1	A	1787	A
1	A	1791	A
1	A	1800	C
1	A	1801	A
1	A	1802	A
1	A	1808	A
1	A	1811	G
1	A	1816	C
1	A	1820	U
1	A	1821	A
1	A	1829	A
1	A	1833	C
1	A	1857	G
1	A	1870	C
1	A	1871	A
1	A	1896	G
1	A	1900	A
1	A	1901	A
1	A	1906	G
1	A	1910	G
1	A	1912	A
1	A	1929	G
1	A	1930	G
1	A	1931	U
1	A	1934	C
1	A	1936	A
1	A	1937	A
1	A	1940	U
1	A	1941	C
1	A	1942	C
1	A	1943	U

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Mol	Chain	Res	Type
1	A	1944	U
1	A	1955	U
1	A	1966	A
1	A	1967	C
1	A	1970	A
1	A	1971	U
1	A	1972	G
1	A	1991	U
1	A	1993	U
1	A	1997	C
1	A	2004	G
1	A	2020	A
1	A	2022	U
1	A	2023	C
1	A	2030	A
1	A	2031	A
1	A	2032	G
1	A	2033	A
1	A	2035	G
1	A	2043	C
1	A	2052	A
1	A	2053	G
1	A	2055	C
1	A	2056	G
1	A	2060	A
1	A	2061	G
1	A	2062	A
1	A	2068	U
1	A	2069	A
1	A	2077	A
1	A	2093	G
1	A	2096	C
1	A	2100	G
1	A	2108	A
1	A	2110	G
1	A	2111	U
1	A	2112	G
1	A	2113	U
1	A	2115	G
1	A	2118	U
1	A	2120	G
1	A	2122	U

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Mol	Chain	Res	Type
1	A	2125	G
1	A	2127	G
1	A	2131	U
1	A	2132	U
1	A	2133	G
1	A	2137	U
1	A	2141	G
1	A	2145	C
1	A	2146	C
1	A	2147	A
1	A	2155	U
1	A	2156	G
1	A	2162	G
1	A	2164	C
1	A	2168	G
1	A	2170	A
1	A	2171	A
1	A	2172	U
1	A	2173	A
1	A	2177	C
1	A	2178	C
1	A	2184	A
1	A	2189	U
1	A	2191	A
1	A	2192	U
1	A	2198	A
1	A	2203	U
1	A	2204	G
1	A	2211	A
1	A	2213	U
1	A	2219	U
1	A	2225	A
1	A	2226	C
1	A	2238	G
1	A	2239	G
1	A	2250	G
1	A	2251	G
1	A	2278	A
1	A	2283	C
1	A	2287	A
1	A	2288	A
1	A	2300	C

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Mol	Chain	Res	Type
1	A	2305	U
1	A	2307	G
1	A	2309	A
1	A	2322	A
1	A	2325	G
1	A	2327	A
1	A	2331	G
1	A	2333	A
1	A	2334	U
1	A	2336	A
1	A	2345	G
1	A	2347	C
1	A	2350	C
1	A	2361	G
1	A	2383	G
1	A	2385	C
1	A	2391	G
1	A	2392	A
1	A	2399	G
1	A	2402	U
1	A	2403	C
1	A	2406	A
1	A	2407	A
1	A	2423	U
1	A	2426	A
1	A	2427	C
1	A	2429	G
1	A	2430	A
1	A	2431	U
1	A	2435	A
1	A	2441	U
1	A	2445	G
1	A	2447	G
1	A	2448	A
1	A	2465	C
1	A	2470	G
1	A	2474	U
1	A	2476	A
1	A	2492	U
1	A	2498	C
1	A	2502	G
1	A	2503	A

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Mol	Chain	Res	Type
1	A	2505	G
1	A	2506	U
1	A	2518	A
1	A	2529	G
1	A	2535	G
1	A	2547	A
1	A	2554	U
1	A	2556	C
1	A	2566	A
1	A	2567	G
1	A	2572	A
1	A	2573	C
1	A	2582	G
1	A	2585	U
1	A	2586	U
1	A	2602	A
1	A	2609	U
1	A	2613	U
1	A	2615	U
1	A	2621	G
1	A	2629	U
1	A	2632	A
1	A	2646	C
1	A	2654	A
1	A	2655	G
1	A	2661	G
1	A	2668	G
1	A	2671	G
1	A	2684	U
1	A	2689	U
1	A	2690	U
1	A	2707	U
1	A	2714	G
1	A	2716	C
1	A	2718	G
1	A	2724	U
1	A	2727	A
1	A	2732	G
1	A	2733	A
1	A	2744	G
1	A	2748	A
1	A	2757	A

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Mol	Chain	Res	Type
1	A	2765	A
1	A	2778	A
1	A	2779	U
1	A	2791	G
1	A	2793	C
1	A	2794	C
1	A	2799	A
1	A	2800	A
1	A	2808	G
1	A	2809	A
1	A	2812	G
1	A	2818	U
1	A	2820	A
1	A	2821	A
1	A	2823	A
1	A	2833	U
1	A	2836	U
1	A	2849	U
1	A	2861	U
1	A	2867	G
1	A	2873	A
1	A	2880	C
1	A	2885	G
1	A	2886	A
1	A	2887	A
1	A	2889	C
1	A	2891	U
1	A	2893	A
1	A	2898	U
1	A	2899	A
1	A	2902	C
2	B	4	C
2	B	12	C
2	B	13	G
2	B	15	A
2	B	24	G
2	B	26	C
2	B	31	C
2	B	35	C
2	B	36	C
2	B	40	U
2	B	41	G

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Mol	Chain	Res	Type
2	B	44	G
2	B	45	A
2	B	53	A
2	B	56	G
2	B	57	A
2	B	64	G
2	B	66	A
2	B	67	G
2	B	88	C
2	B	89	U
2	B	90	C
2	B	91	C
2	B	105	G
2	B	108	A
2	B	109	A
2	B	119	A
32	a	4	U
32	a	5	U
32	a	7	A
32	a	9	G
32	a	22	G
32	a	32	A
32	a	39	G
32	a	47	C
32	a	48	C
32	a	50	A
32	a	51	A
32	a	58	C
32	a	71	A
32	a	75	G
32	a	78	A
32	a	79	G
32	a	82	G
32	a	84	U
32	a	85	U
32	a	86	G
32	a	87	C
32	a	95	C
32	a	122	G
32	a	130	A
32	a	149	A
32	a	157	U

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Mol	Chain	Res	Type
32	a	163	C
32	a	164	G
32	a	177	G
32	a	181	A
32	a	183	C
32	a	184	G
32	a	189	A
32	a	204	G
32	a	209	U
32	a	210	C
32	a	212	G
32	a	226	G
32	a	240	G
32	a	243	A
32	a	247	G
32	a	248	C
32	a	251	G
32	a	266	G
32	a	267	C
32	a	279	A
32	a	280	C
32	a	281	G
32	a	289	G
32	a	299	G
32	a	306	A
32	a	321	A
32	a	328	C
32	a	340	U
32	a	345	C
32	a	347	G
32	a	351	G
32	a	352	C
32	a	354	G
32	a	367	U
32	a	368	U
32	a	369	G
32	a	372	C
32	a	373	A
32	a	375	U
32	a	376	G
32	a	382	A
32	a	392	C

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Mol	Chain	Res	Type
32	a	397	A
32	a	406	G
32	a	412	A
32	a	413	G
32	a	414	A
32	a	421	U
32	a	429	U
32	a	430	A
32	a	438	U
32	a	451	A
32	a	461	A
32	a	462	G
32	a	467	U
32	a	468	A
32	a	474	G
32	a	476	U
32	a	484	G
32	a	485	U
32	a	486	U
32	a	496	A
32	a	497	G
32	a	505	G
32	a	509	A
32	a	511	C
32	a	518	C
32	a	527	G
32	a	531	U
32	a	532	A
32	a	547	A
32	a	561	U
32	a	562	U
32	a	564	C
32	a	572	A
32	a	573	A
32	a	574	A
32	a	575	G
32	a	576	C
32	a	577	G
32	a	596	A
32	a	620	C
32	a	633	G
32	a	639	G

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Mol	Chain	Res	Type
32	a	642	A
32	a	661	G
32	a	665	A
32	a	695	A
32	a	703	G
32	a	723	U
32	a	724	G
32	a	731	G
32	a	733	G
32	a	755	G
32	a	774	G
32	a	777	A
32	a	790	A
32	a	794	A
32	a	806	C
32	a	815	A
32	a	817	C
32	a	818	G
32	a	819	A
32	a	820	U
32	a	821	G
32	a	829	G
32	a	832	G
32	a	836	G
32	a	843	U
32	a	844	G
32	a	845	A
32	a	846	G
32	a	851	G
32	a	872	A
32	a	884	U
32	a	887	G
32	a	889	A
32	a	890	G
32	a	891	U
32	a	902	G
32	a	914	A
32	a	926	G
32	a	933	G
32	a	934	C
32	a	935	A
32	a	939	G

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Mol	Chain	Res	Type
32	a	948	C
32	a	960	U
32	a	961	U
32	a	966	G
32	a	969	A
32	a	971	G
32	a	975	A
32	a	976	G
32	a	987	G
32	a	991	U
32	a	992	U
32	a	993	G
32	a	994	A
32	a	1004	A
32	a	1006	G
32	a	1009	U
32	a	1020	G
32	a	1022	A
32	a	1027	C
32	a	1028	C
32	a	1031	C
32	a	1032	G
32	a	1033	G
32	a	1034	G
32	a	1035	A
32	a	1045	C
32	a	1046	A
32	a	1065	U
32	a	1070	U
32	a	1085	U
32	a	1092	A
32	a	1094	G
32	a	1095	U
32	a	1101	A
32	a	1130	A
32	a	1133	G
32	a	1136	C
32	a	1137	C
32	a	1138	G
32	a	1139	G
32	a	1142	G
32	a	1151	A

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Mol	Chain	Res	Type
32	a	1152	A
32	a	1159	U
32	a	1167	A
32	a	1168	U
32	a	1183	U
32	a	1184	G
32	a	1191	A
32	a	1196	A
32	a	1201	A
32	a	1202	U
32	a	1212	U
32	a	1227	A
32	a	1228	C
32	a	1238	A
32	a	1241	G
32	a	1250	A
32	a	1253	G
32	a	1257	A
32	a	1258	G
32	a	1260	G
32	a	1275	A
32	a	1278	G
32	a	1279	G
32	a	1280	A
32	a	1281	C
32	a	1282	C
32	a	1286	U
32	a	1287	A
32	a	1290	G
32	a	1297	G
32	a	1298	U
32	a	1300	G
32	a	1301	U
32	a	1305	G
32	a	1306	A
32	a	1312	G
32	a	1317	C
32	a	1322	C
32	a	1331	G
32	a	1332	A
32	a	1336	C
32	a	1340	A

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Mol	Chain	Res	Type
32	a	1346	A
32	a	1347	G
32	a	1353	G
32	a	1363	A
32	a	1370	G
32	a	1379	G
32	a	1381	U
32	a	1395	C
32	a	1397	C
32	a	1398	A
32	a	1400	C
32	a	1406	U
32	a	1419	G
32	a	1429	A
32	a	1433	A
32	a	1434	A
32	a	1446	A
32	a	1448	C
32	a	1452	C
32	a	1453	G
32	a	1487	G
32	a	1492	A
32	a	1493	A
32	a	1494	G
32	a	1497	G
32	a	1502	A
32	a	1503	A
32	a	1506	U
32	a	1517	G
32	a	1519	A
32	a	1529	G
32	a	1530	G
32	a	1534	A
32	a	1535	C
32	a	1536	C
32	a	1537	U
55	x	3	G
55	x	4	U
55	x	5	G
55	x	6	A
55	x	8	U
55	x	17	C

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Mol	Chain	Res	Type
55	x	19	G
55	x	20	U
55	x	21	A
55	x	47	U
55	x	59	A
55	x	65	U
55	x	66	A
55	x	76	A

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	51	G
1	A	86	G
1	A	91	A
1	A	242	G
1	A	546	U
1	A	774	G
1	A	784	G
1	A	858	G
1	A	1020	A
1	A	1022	G
1	A	1111	A
1	A	1182	G
1	A	1190	G
1	A	1236	G
1	A	1300	G
1	A	1331	G
1	A	1378	A
1	A	1399	C
1	A	1432	G
1	A	1490	A
1	A	1626	A
1	A	1930	G
1	A	1940	U
1	A	2286	G
1	A	2326	C
1	A	2391	G
1	A	2756	U
1	A	2798	U
1	A	2808	G
2	B	44	G

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Mol	Chain	Res	Type
2	B	52	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

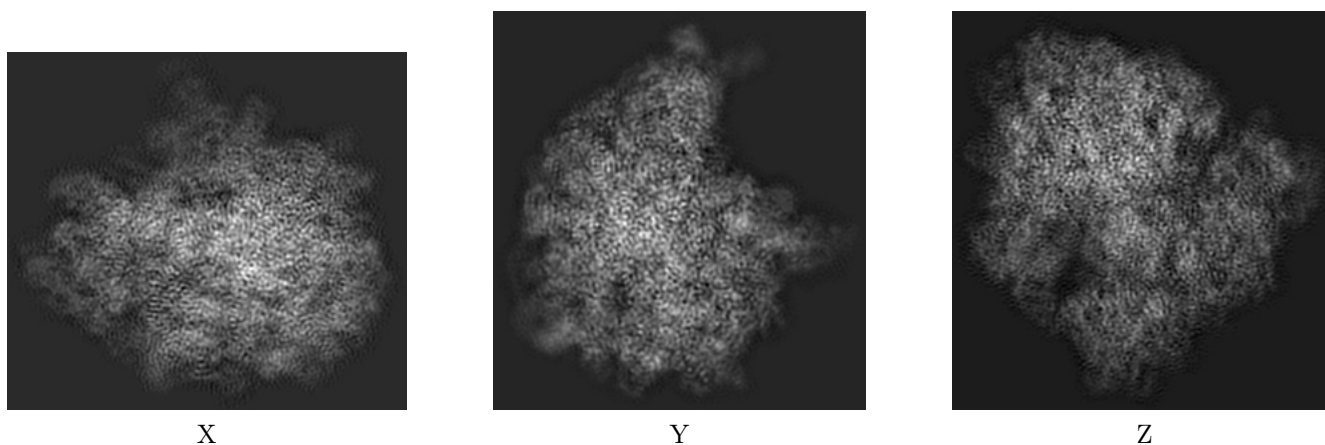
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3508. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

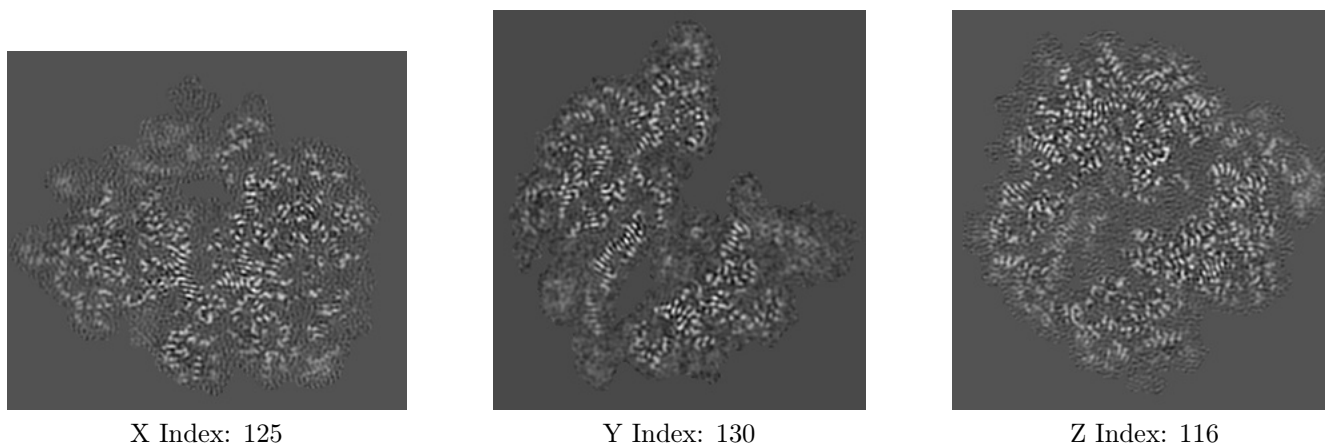
6.1.1 Primary map



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

6.2 Central slices [i](#)

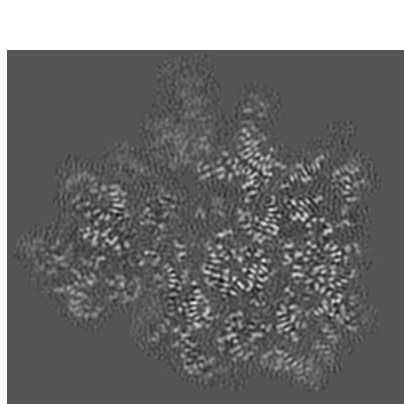
6.2.1 Primary map



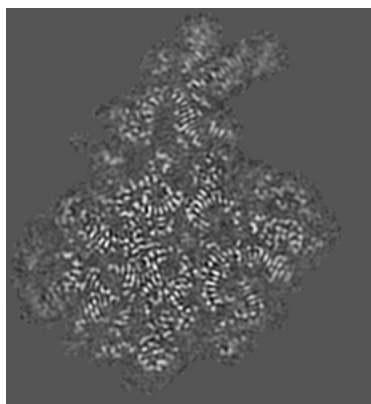
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

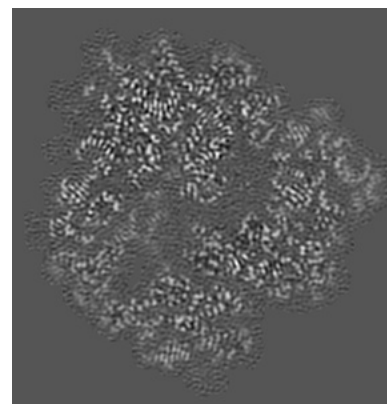
6.3.1 Primary map



X Index: 115



Y Index: 153

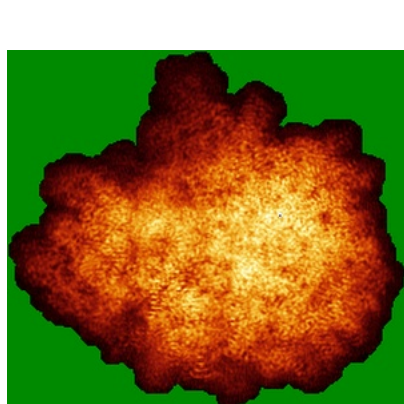


Z Index: 114

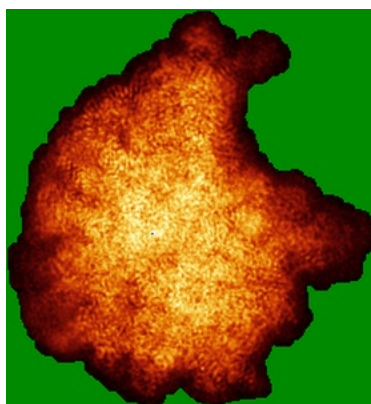
The images above show the largest variance slices of the map in three orthogonal directions.

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

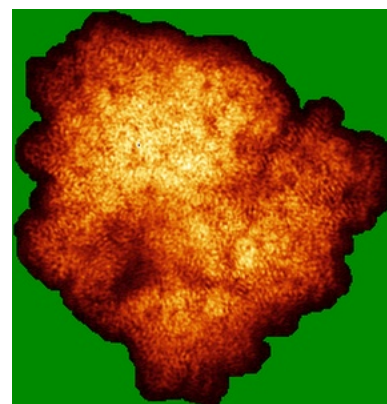
6.4.1 Primary map



X



Y

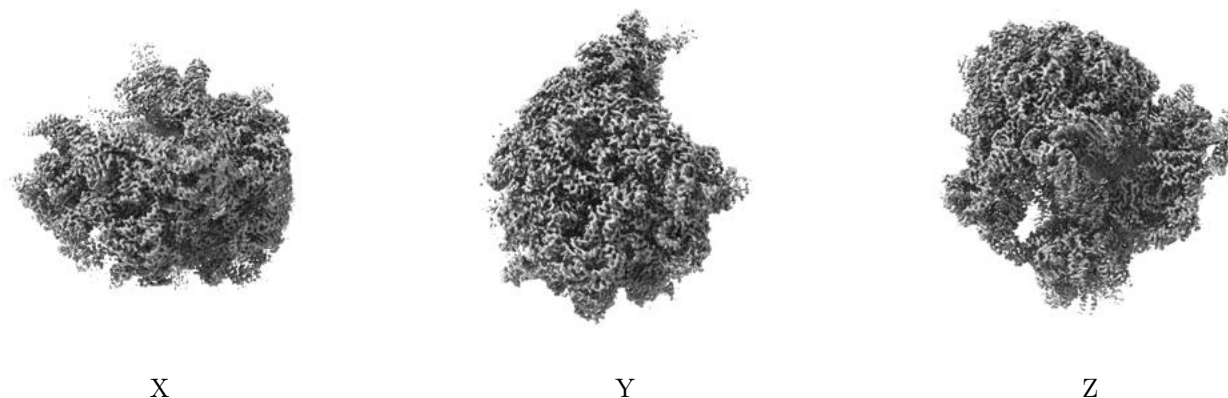


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.358. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

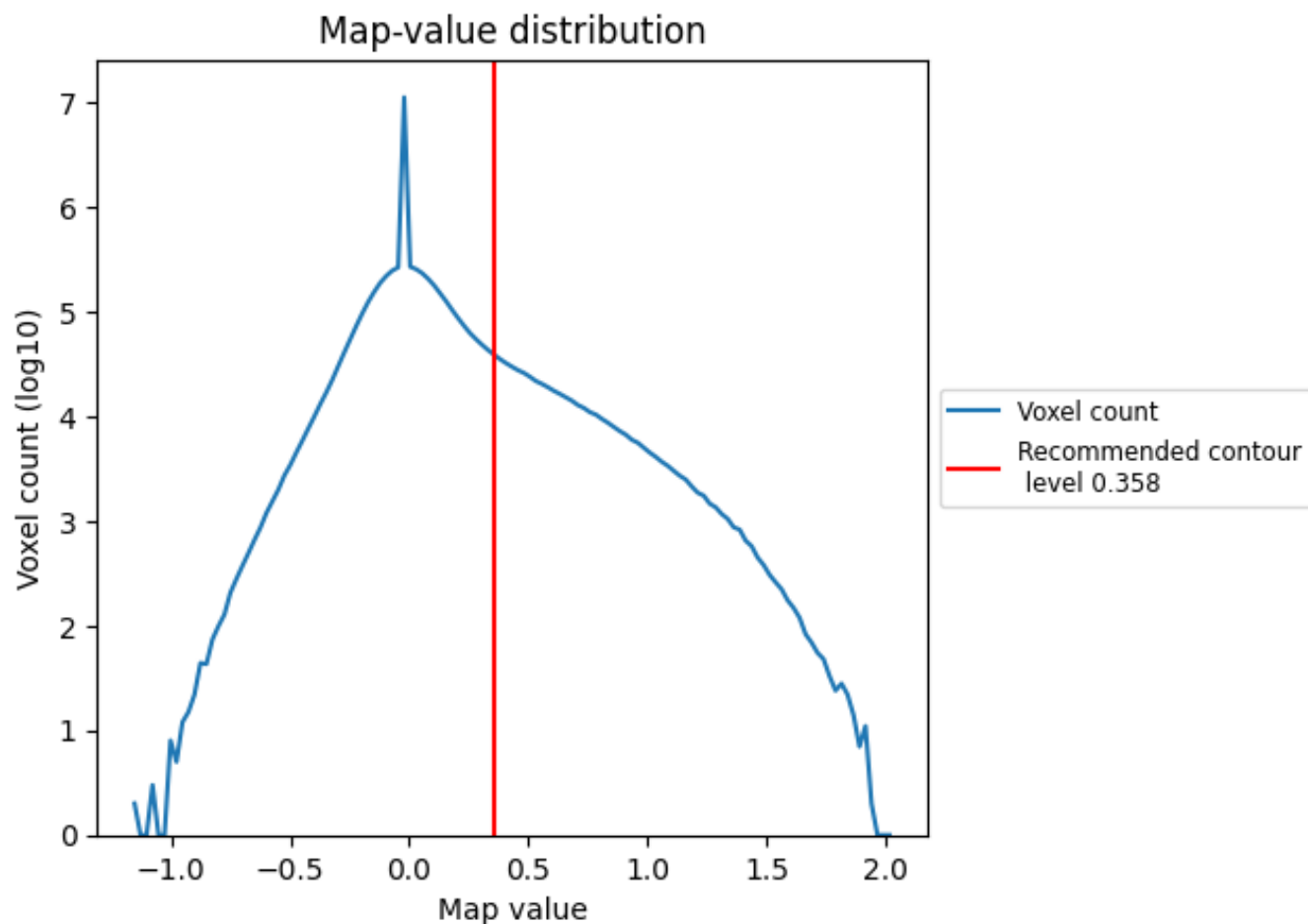
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

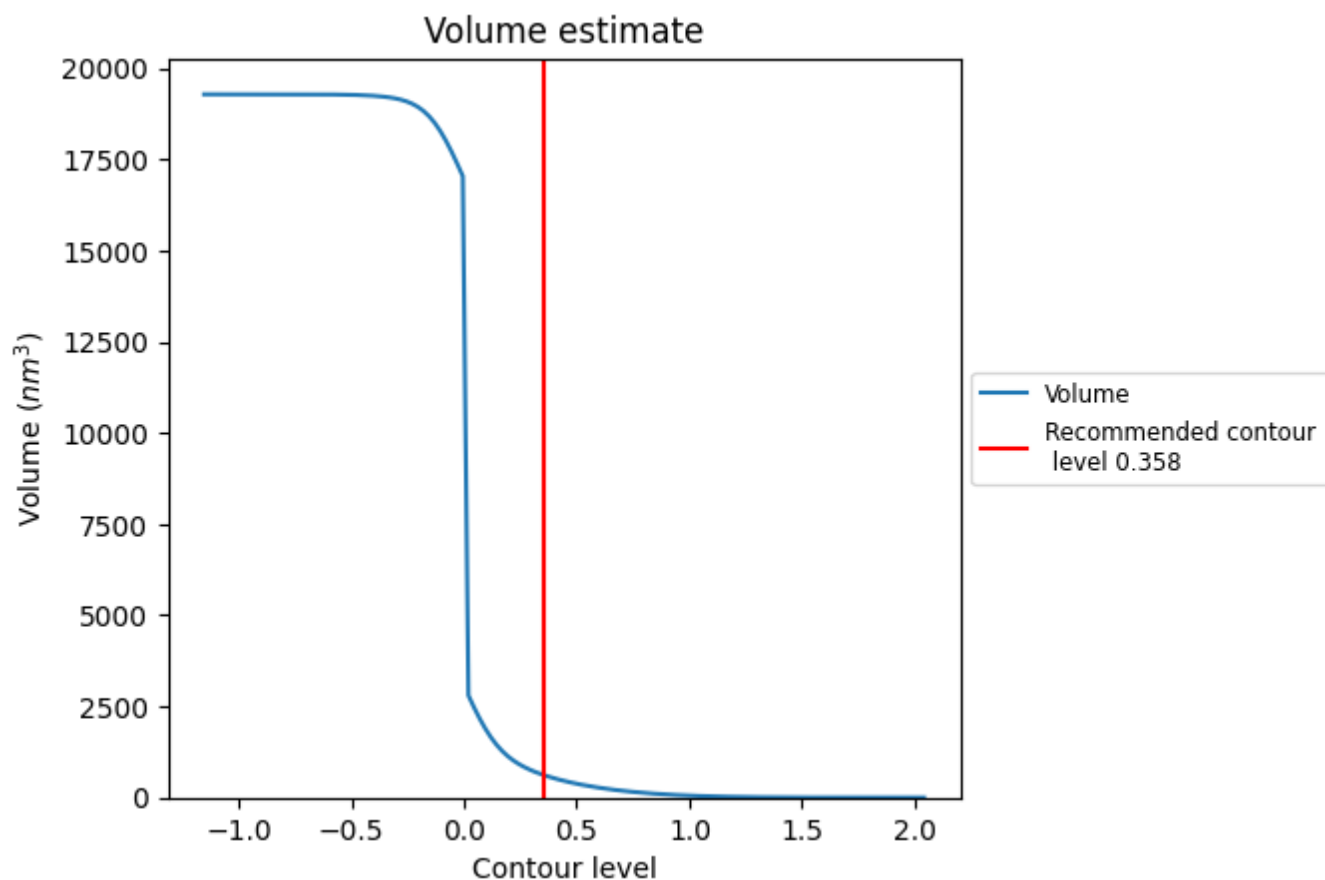
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 609 nm³; this corresponds to an approximate mass of 550 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

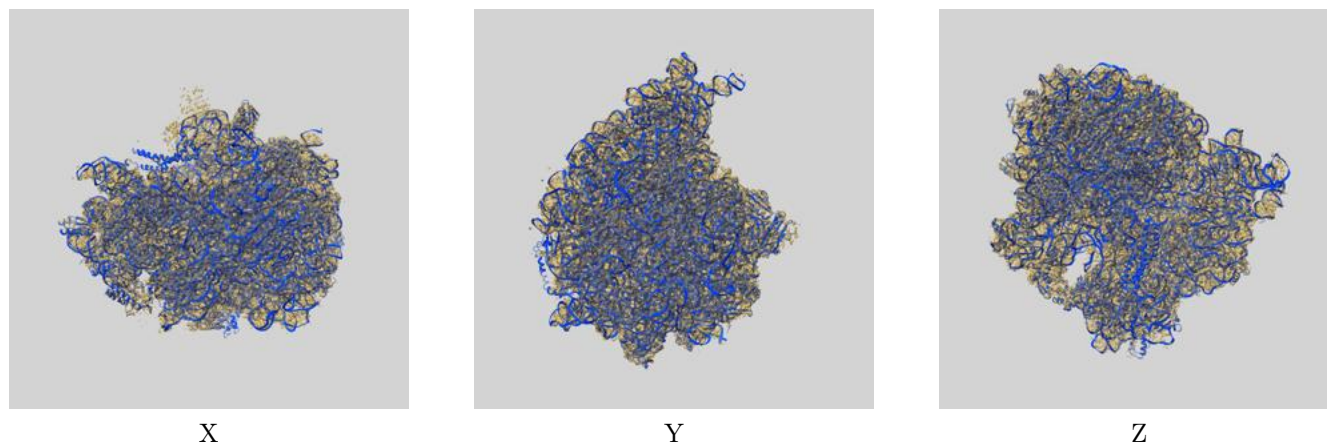
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

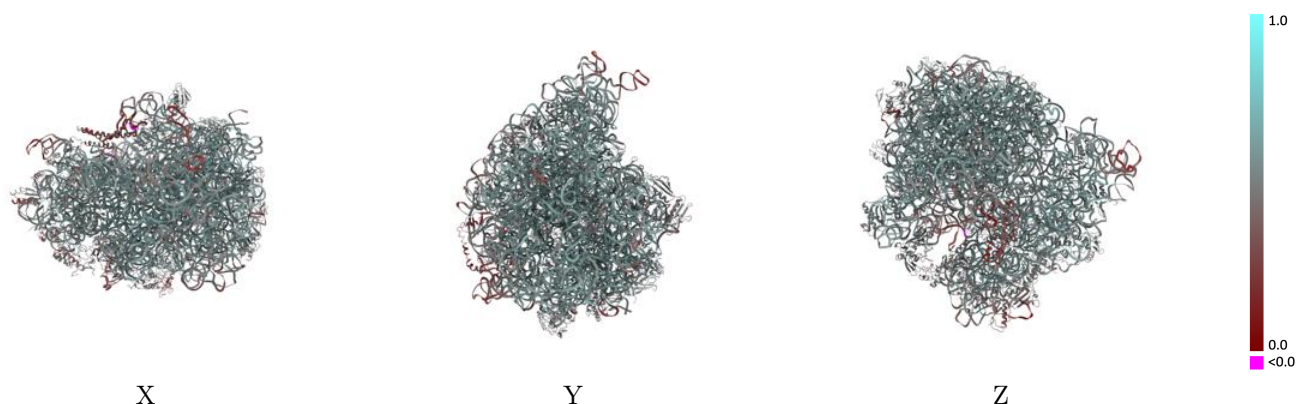
This section contains information regarding the fit between EMDB map EMD-3508 and PDB model 5MGP. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



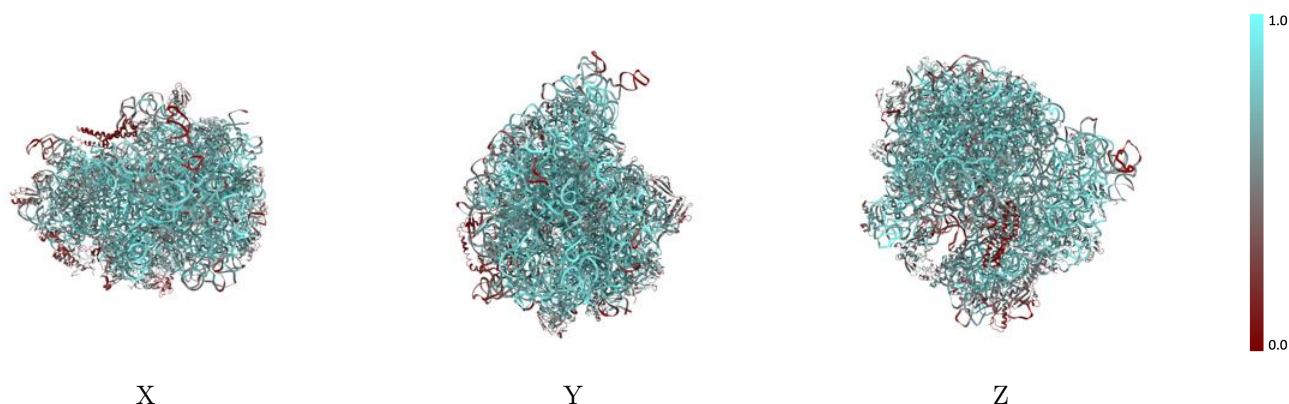
The images above show the 3D surface view of the map at the recommended contour level 0.358 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



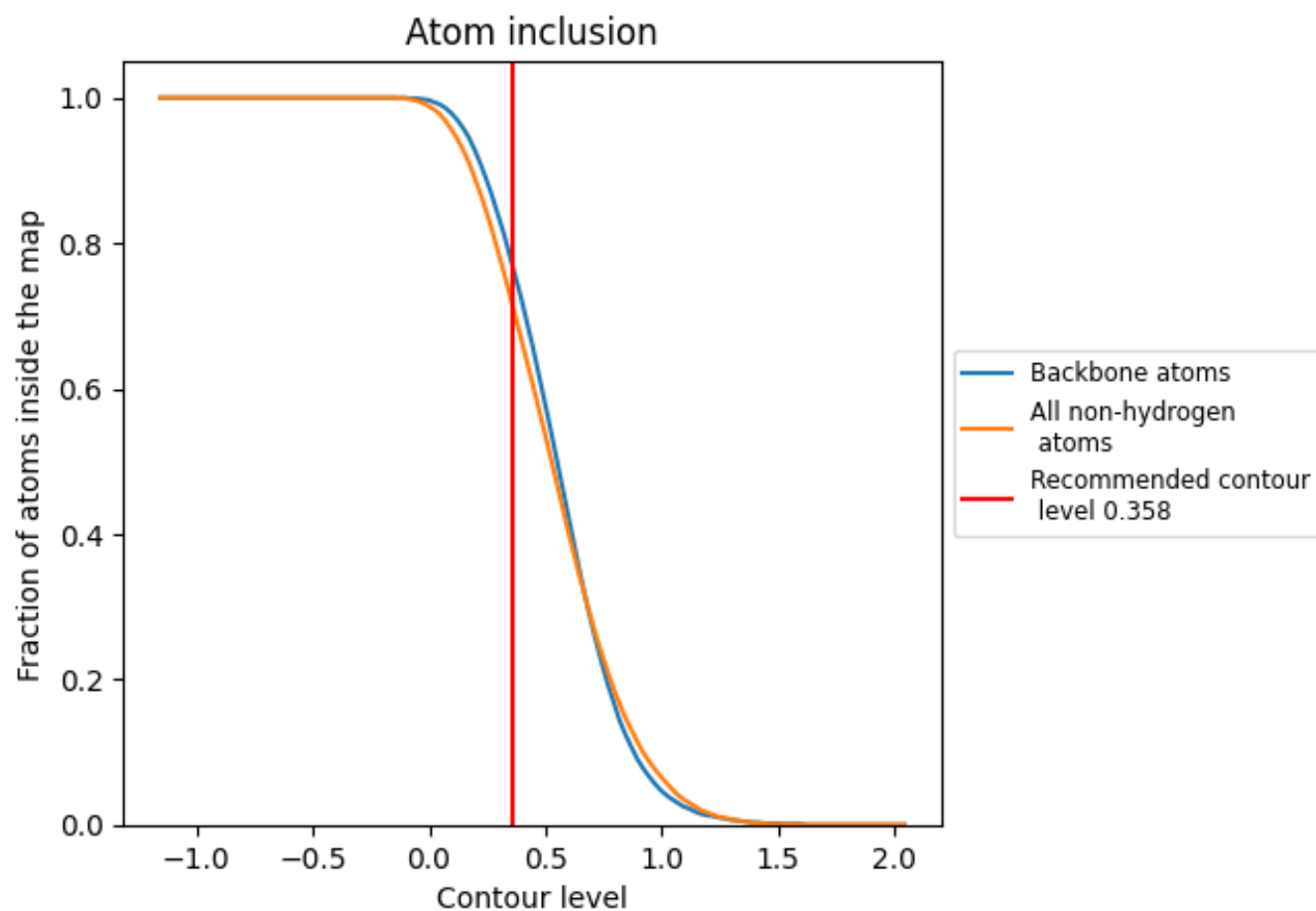
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.358).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 72% 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 (0.358) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7150	 0.5310
0	 0.6420	 0.5390
1	 0.5510	 0.5310
2	 0.7210	 0.5640
3	 0.7130	 0.5670
4	 0.6880	 0.5430
6	 0.3720	 0.4110
A	 0.7900	 0.5480
B	 0.7790	 0.5420
C	 0.6980	 0.5560
D	 0.6620	 0.5450
E	 0.5740	 0.5150
F	 0.5310	 0.4770
G	 0.4400	 0.4730
H	 0.1750	 0.3350
J	 0.6640	 0.5410
K	 0.6370	 0.5320
L	 0.6150	 0.5250
M	 0.6570	 0.5420
N	 0.6970	 0.5530
O	 0.6040	 0.5090
P	 0.6330	 0.5360
Q	 0.7100	 0.5500
R	 0.5960	 0.5060
S	 0.6120	 0.5150
T	 0.5180	 0.5070
U	 0.4350	 0.4680
V	 0.5620	 0.4960
W	 0.7080	 0.5560
X	 0.6360	 0.5240
Y	 0.4550	 0.4760
Z	 0.6000	 0.5250
a	 0.7950	 0.5530
b	 0.3330	 0.4240
c	 0.5350	 0.4950



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Chain	Atom inclusion	Q-score
d	 0.5600	 0.4950
e	 0.6350	 0.5190
f	 0.5300	 0.4540
g	 0.4630	 0.4560
h	 0.6300	 0.5200
i	 0.5220	 0.4570
j	 0.3810	 0.4280
k	 0.6050	 0.5060
l	 0.6810	 0.5260
m	 0.5490	 0.4840
n	 0.5960	 0.5020
o	 0.6070	 0.5100
p	 0.6330	 0.5030
q	 0.5250	 0.4760
r	 0.6930	 0.5240
s	 0.5770	 0.4690
t	 0.5430	 0.4970
u	 0.3420	 0.3600
v	 0.6820	 0.5590
w	 0.6270	 0.4960
x	 0.6600	 0.5210
z	 0.3520	 0.4040