



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 02:14 AM UTC

PDB ID : 7QGR / pdb_00007qgr
EMDB ID : EMD-13958
Title : Structure of the SmrB-bound E. coli disome - collided 70S ribosome
Authors : Kratzat, H.; Buschauer, R.; Berninghausen, O.; Beckmann, R.
Deposited on : 2021-12-09
Resolution : 5.70 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

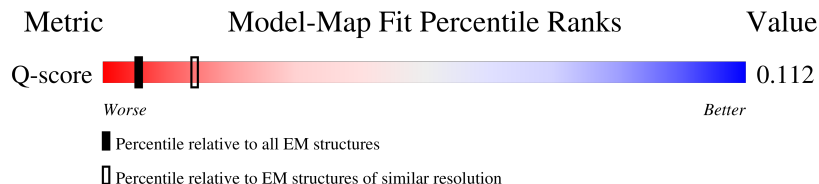
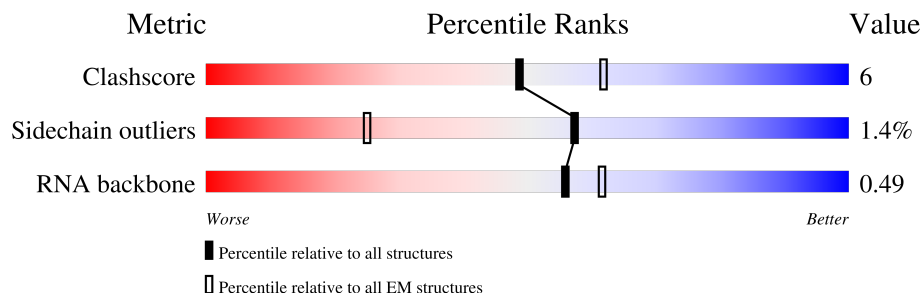
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.70 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	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	503 (5.20 - 6.20)

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	O	120	
2	P	273	
3	Q	209	
4	R	201	

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Mol	Chain	Length	Quality of chain
5	S	179	85% 84% 15% .
6	T	177	87% 87% 12% .
7	V	142	93% 78% 20% ..
8	W	142	49% 80% 19% .
9	X	123	80% 73% 24% ..
10	Y	144	65% 77% 18% . .
11	Z	136	60% 82% 16% .
12	a	127	59% 66% 28% . 6%
13	b	117	72% 83% 15% ..
14	c	115	76% 80% 17% ...
15	d	118	51% 80% 15% . . .
16	e	103	73% 73% 26% .
17	f	110	71% 87% 12% .
18	g	100	70% 84% 9% 7%
19	h	104	56% 77% 20% ..
20	i	94	45% 85% 15%
21	j	85	18% 68% 16% . . 12%
22	k	78	59% 69% 29% .
23	l	63	70% 81% 17% .
24	m	59	46% 90% 8% .
25	n	57	42% 70% 25% . .
26	o	55	69% 65% 24% . 9%
27	p	46	57% 59% 35% 7%
28	q	65	46% 80% 15% . .
29	r	55	49% 51% 11% 7% 31%

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Mol	Chain	Length	Quality of chain
30	N	2903	
31	L	70	
32	C	223	
33	U	149	
34	M	75	
35	x	692	
36	0	1539	
37	1	239	
38	2	218	
39	3	206	
40	4	162	
41	5	131	
42	6	152	
43	7	130	
44	8	130	
45	9	103	
46	A	129	
47	B	124	
48	D	118	
49	E	101	
50	F	89	
51	G	82	
52	H	84	
53	I	75	
54	J	92	

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Mol	Chain	Length	Quality of chain
55	K	87	44%76%20%••
56	s	71	42%54%15%•28%
57	t	557	26%25%•74%
58	u	73	34%66%27%7%
59	v	182	74%67%24%5%•

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 149850 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 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	O	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 2 is a protein called 50S ribosomal protein L2.

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

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Q	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 4 is a protein called 50S ribosomal protein L4.

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

- Molecule 5 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	177	Total	C	N	O	S	0	0
			1397	891	249	251	6		

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	T	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 7 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	V	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	W	142	Total	C	N	O	S	0	0
			1128	714	212	198	4		

- Molecule 9 is a protein called 50S ribosomal protein L14.

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

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Y	143	Total	C	N	O	S	0	0
			1044	649	206	188	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Z	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 12 is a protein called 50S ribosomal protein L17.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	123	ALA	GLU	conflict	UNP A0A829CNM8

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	b	116	Total	C	N	O	0	0
			891	552	178	161		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	c	114	Total	C	N	O	S	0	0
			915	573	179	162	1		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	d	117	Total	C	N	O	0	0
			946	604	192	150		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	e	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 17 is a protein called 50S ribosomal protein L22.

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

- Molecule 18 is a protein called 50S ribosomal protein L23.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	98	SER	GLY	conflict	UNP A0A829CFV1

- Molecule 19 is a protein called 50S ribosomal protein L24.

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

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	i	94	Total	C	N	O	S	
			752	479	137	133	3	0

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	j	75	Total	C	N	O	S	
			568	353	113	101	1	0

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	k	77	Total	C	N	O	S	
			624	388	129	105	2	0

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	l	63	Total	C	N	O	S	
			508	313	99	94	2	0

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	m	58	Total	C	N	O	S	
			448	281	87	78	2	0

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	n	56	Total	C	N	O	S	
			443	269	94	79	1	0

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	o	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	p	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	q	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	r	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 30 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N	2897	Total	C	N	O	P	1	0
			62215	27754	11448	20115	2898		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L	54	Total	C	N	O	S	0	0
			415	256	75	78	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	68	SER	GLY	conflict	UNP A0A1X3HZV8

- Molecule 32 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	C	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	M	75	Total	C	N	O	P	0	0
			1594	711	281	527	75		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	x	44	Total	C	N	O	P	0	0
			928	416	160	308	44		

- Molecule 36 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	0	1539	Total	C	N	O	P	0	0
			33015	14725	6052	10699	1539		

- Molecule 37 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1	218	Total	C	N	O	S	0	0
			1699	1078	303	311	7		

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 39 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	3	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 40 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	4	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	4	MET	ILE	conflict	UNP A0A377C6M5

- Molecule 41 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	101	SER	PRO	conflict	UNP P02358

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	6	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 43 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	7	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 44 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	8	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	3	ASP	GLU	conflict	UNP A0A1Z3UZ18

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	9	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 46 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	ALA	PRO	conflict	UNP A0A829AF87

- Molecule 47 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 48 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	D	114	Total	C	N	O	S	0	0
			877	543	175	156	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	VAL	MET	conflict	UNP A0A7U9IV78

- Molecule 49 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	E	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	40	ALA	GLU	conflict	UNP A0A090BZT4

- Molecule 50 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	F	88	Total	C	N	O	S	0	0
			709	437	143	128	1		

- Molecule 51 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	G	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 52 is a protein called 30S ribosomal protein S17.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	2	ALA	THR	conflict	UNP A0A829A8C6

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	I	55	Total	C	N	O	0	0
			455	288	86	81		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	15	THR	ALA	conflict	UNP A0A376I7P4
I	58	ALA	CYS	conflict	UNP A0A376I7P4

- Molecule 54 is a protein called 30S ribosomal protein S19.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	82	TYR	GLY	conflict	UNP S1EA57
J	83	TYR	HIS	conflict	UNP S1EA57

- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	K	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	1	LEU	MET	conflict	UNP P0A7U7

- Molecule 56 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	s	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 57 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	t	143	Total	C	N	O		0	0
			704	418	143	143			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	241	VAL	ILE	conflict	UNP A0A829CYC5

- Molecule 58 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	u	73	Total	C	N	O	P	0	0
			1561	695	279	514	73		

- Molecule 59 is a protein called UPF0115 protein YfcN.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	v	175	Total	C	N	O	S	0	0
			1256	796	226	229	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	99	ALA	ASP	conflict	UNP Q6KCY1
v	101	ALA	HIS	conflict	UNP Q6KCY1

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	u	2	Total	Mg	0
			2	2	

- Molecule 61 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
61	u	1	Total	K	0
			1	1	

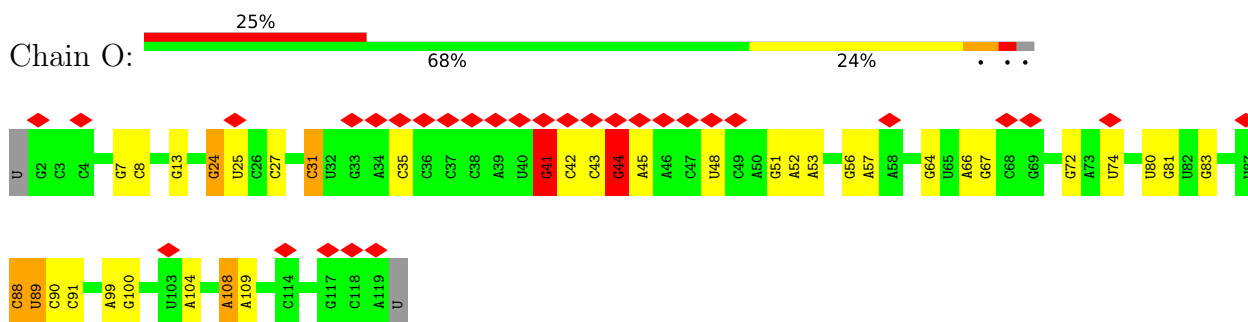
- Molecule 62 is water.

Mol	Chain	Residues	Atoms		AltConf
62	u	9	Total	O	0
			9	9	

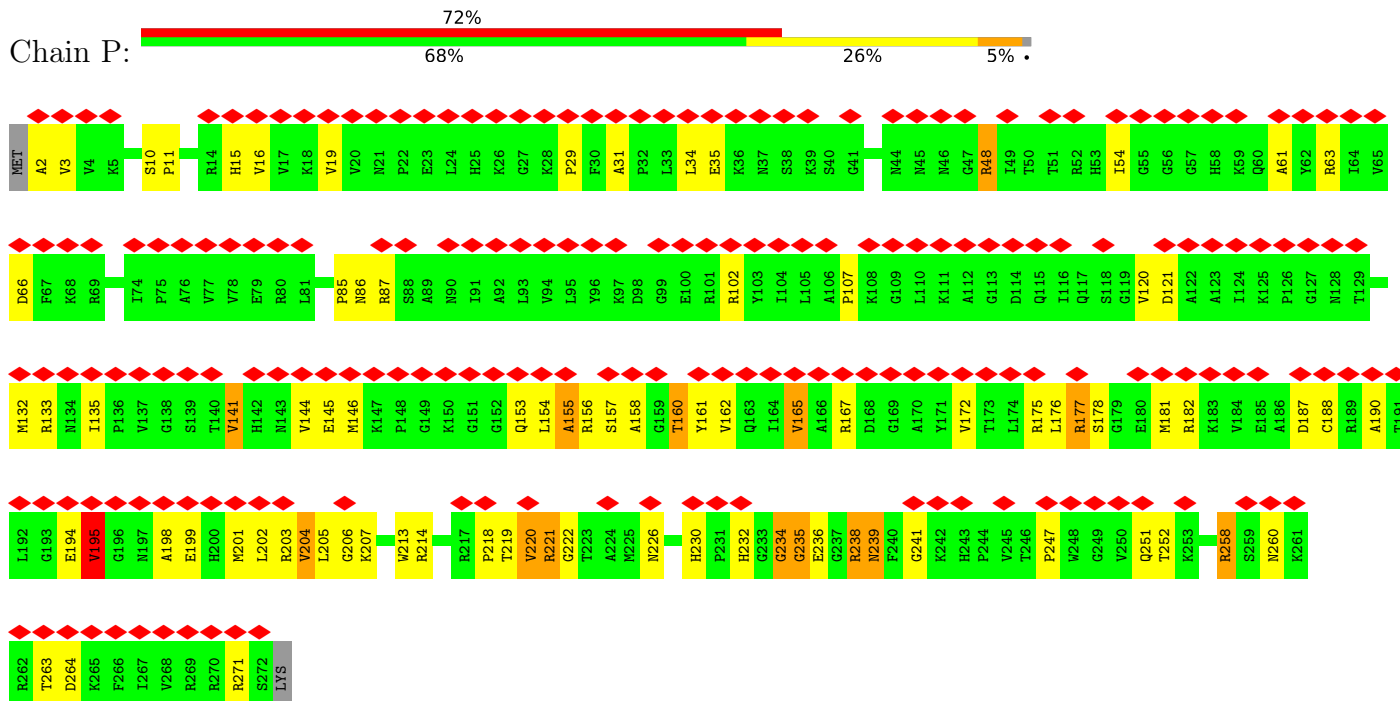
3 Residue-property plots

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.

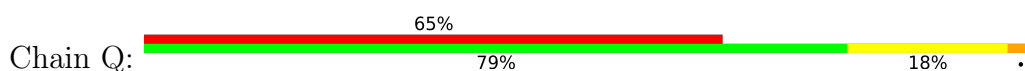
• Molecule 1: 5S rRNA

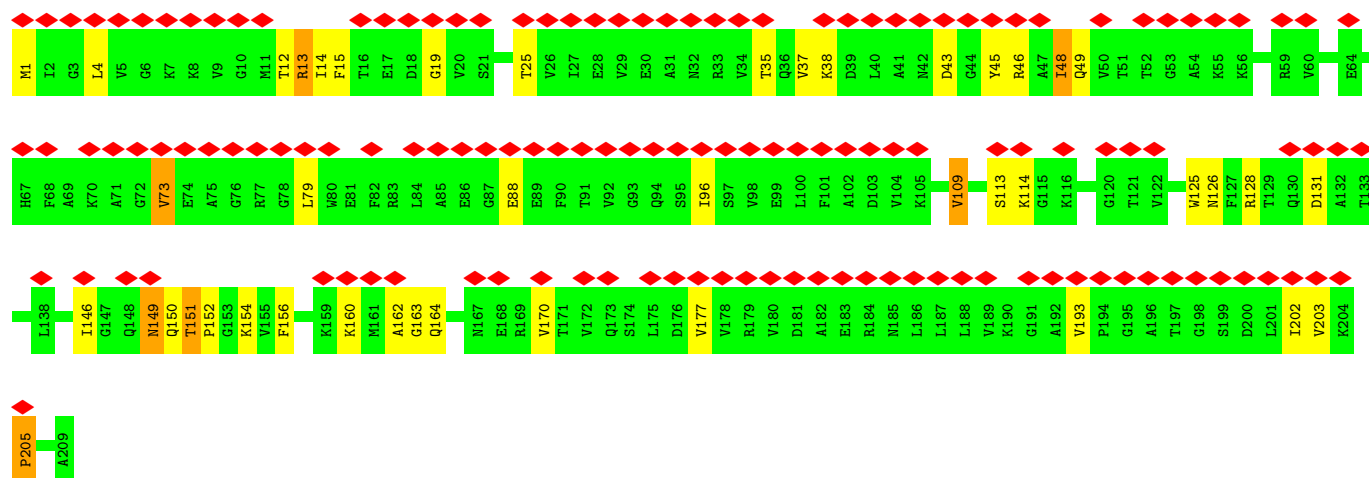


• Molecule 2: 50S ribosomal protein L2

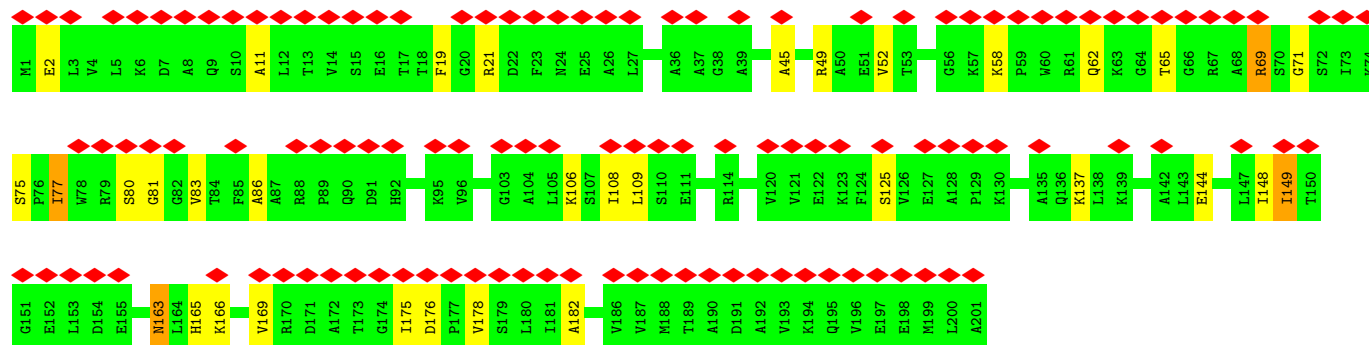
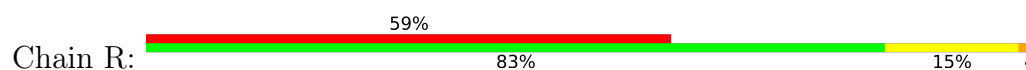


• Molecule 3: 50S ribosomal protein L3

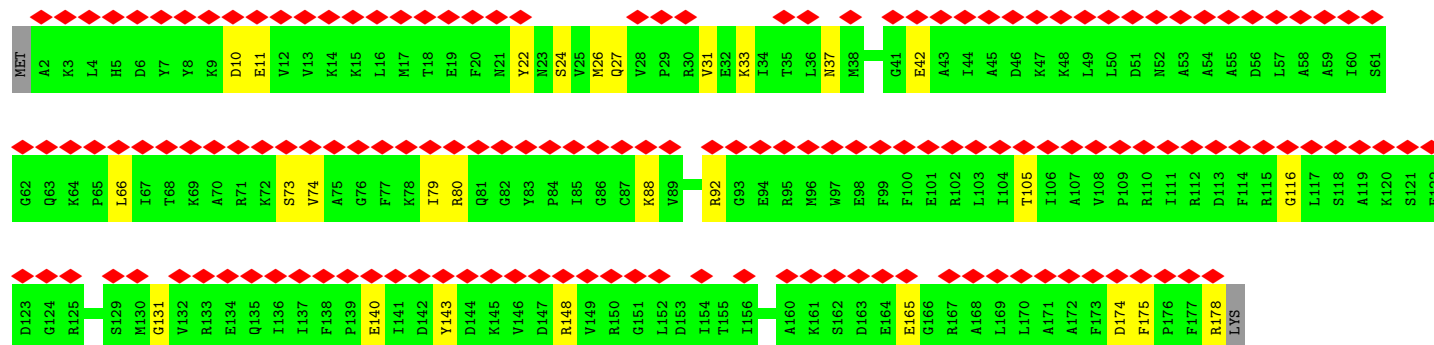
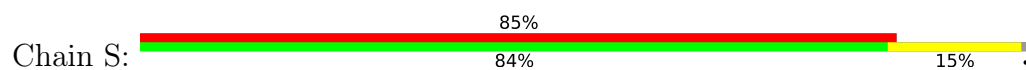




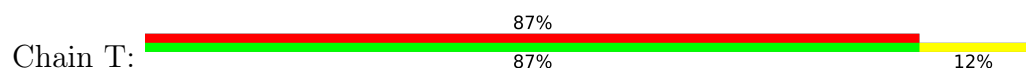
• Molecule 4: 50S ribosomal protein L4

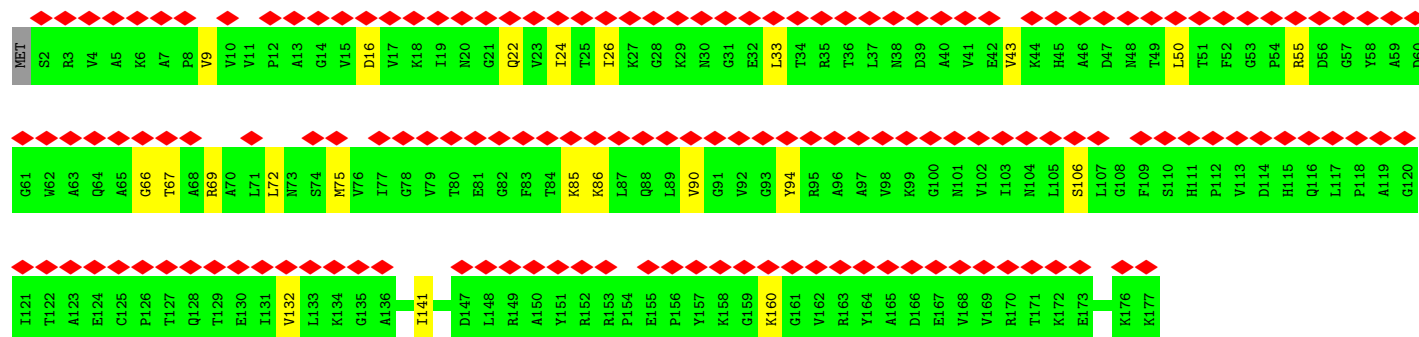


• Molecule 5: 50S ribosomal protein L5

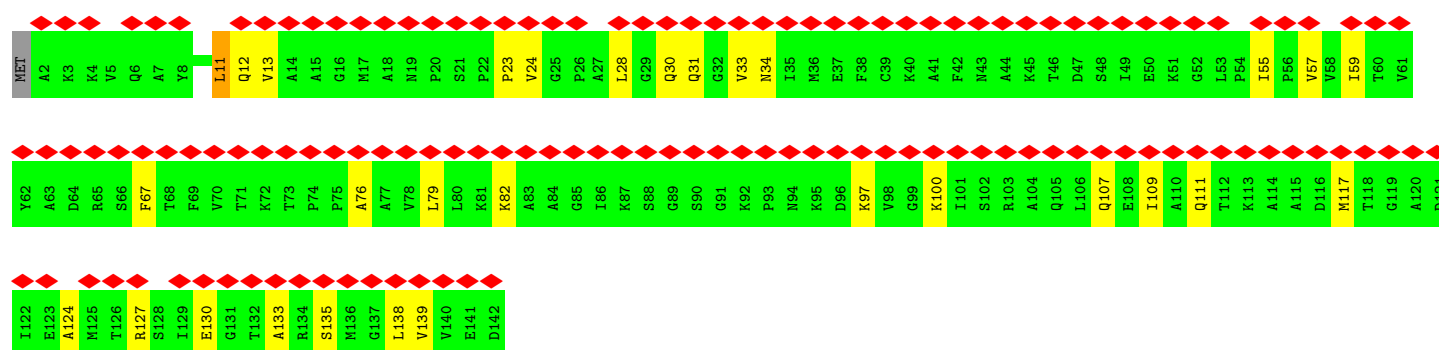
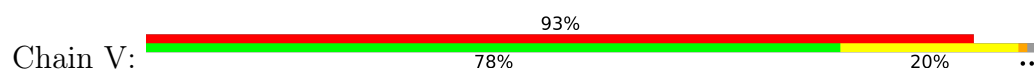


• Molecule 6: 50S ribosomal protein L6

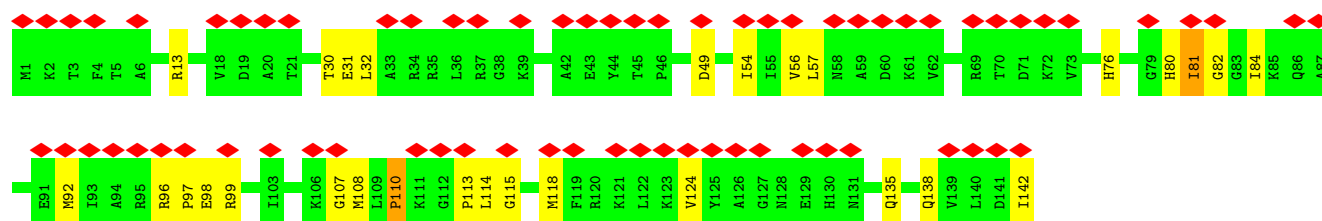
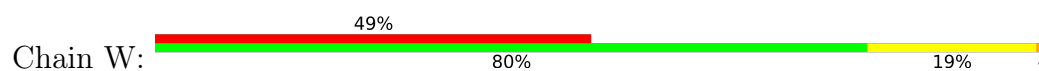




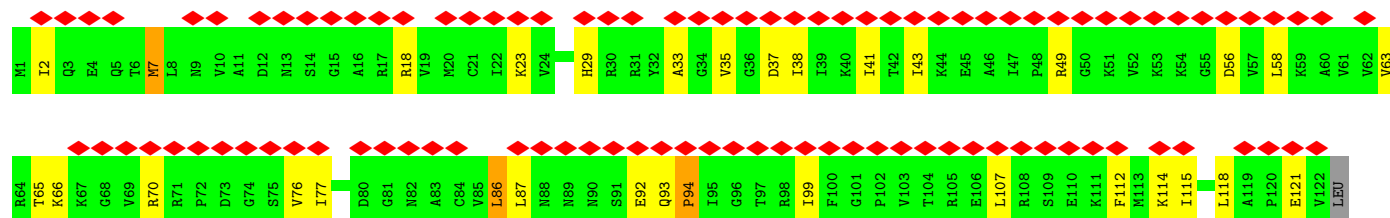
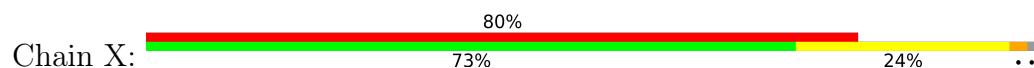
• Molecule 7: 50S ribosomal protein L11



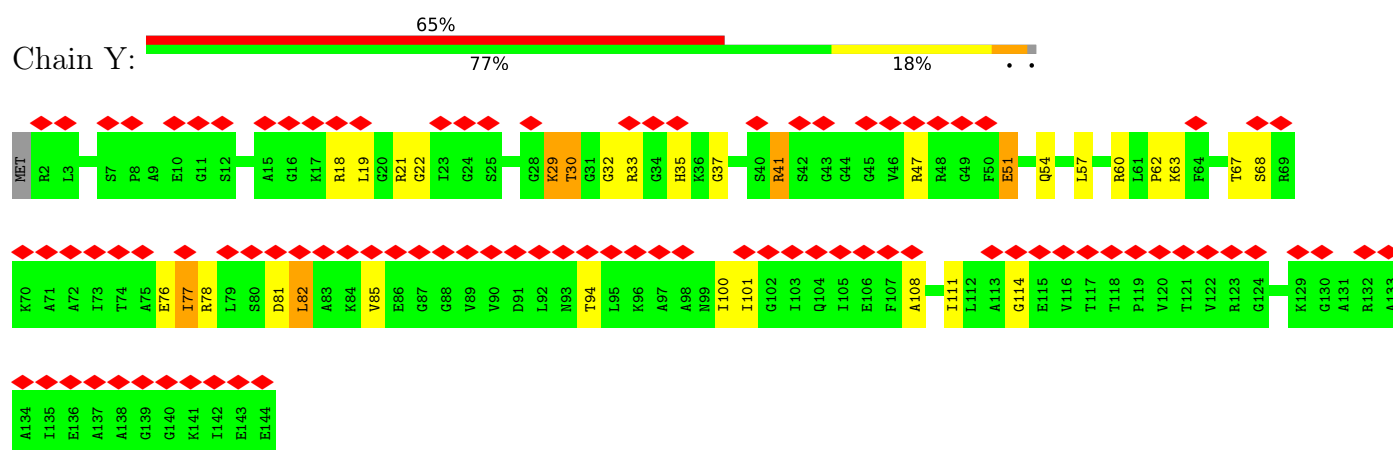
• Molecule 8: 50S ribosomal protein L13



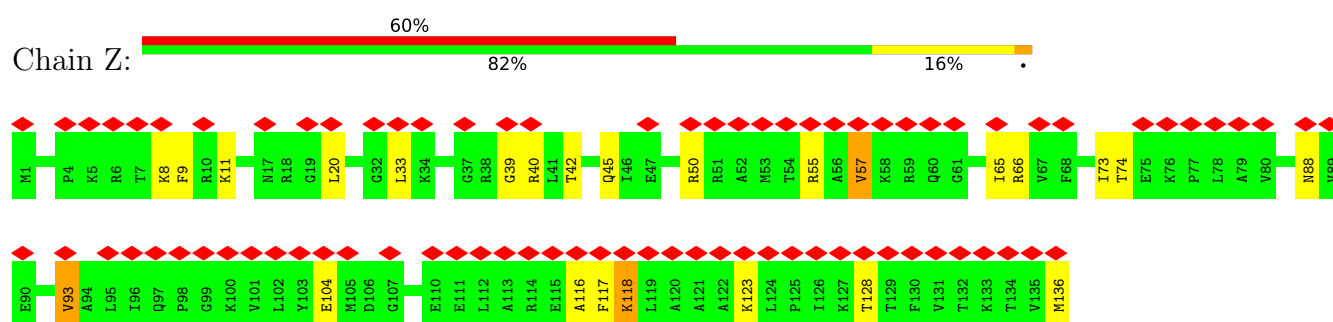
• Molecule 9: 50S ribosomal protein L14



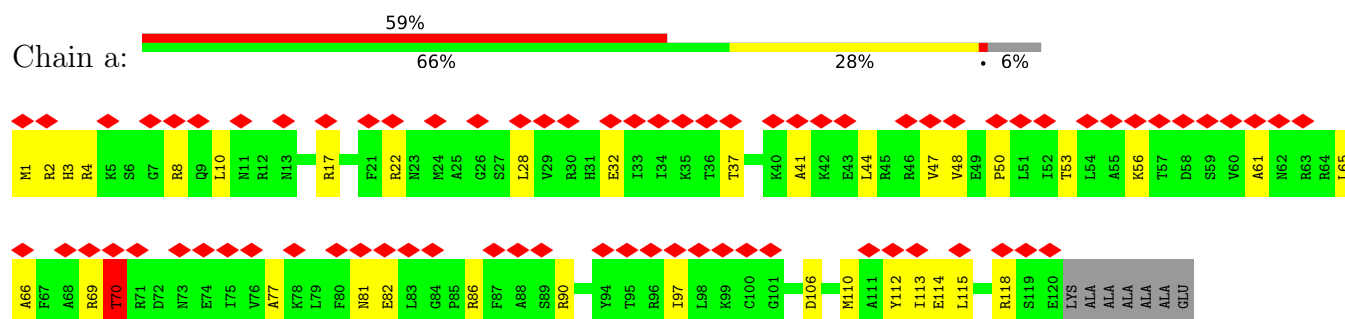
• Molecule 10: 50S ribosomal protein L15



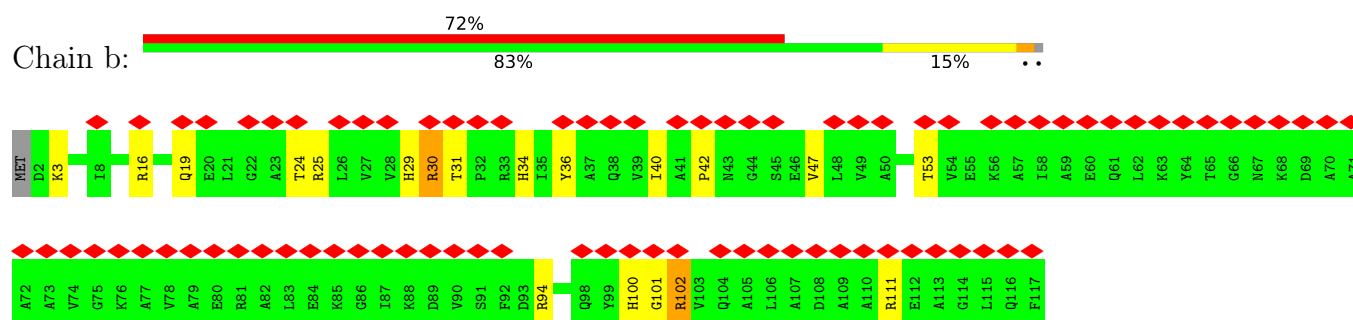
• Molecule 11: 50S ribosomal protein L16



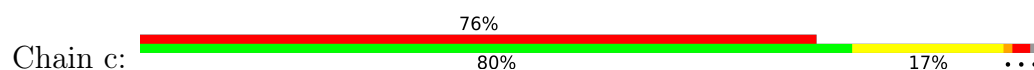
• Molecule 12: 50S ribosomal protein L17

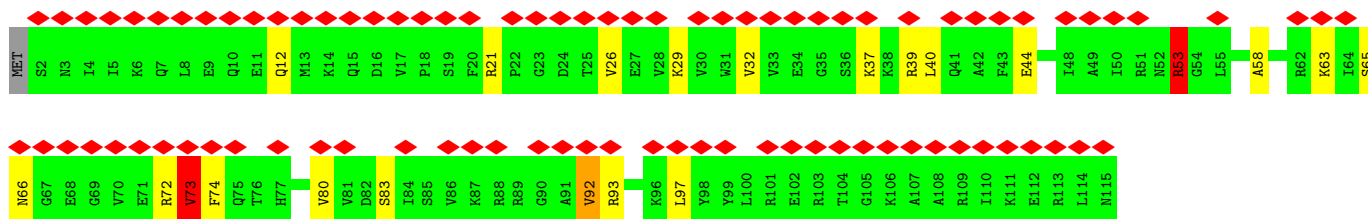


• Molecule 13: 50S ribosomal protein L18

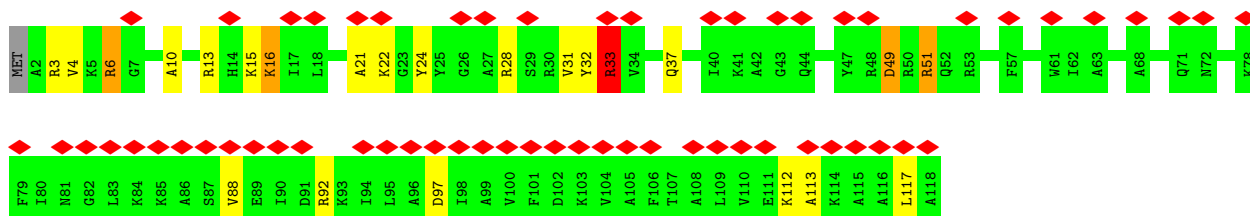
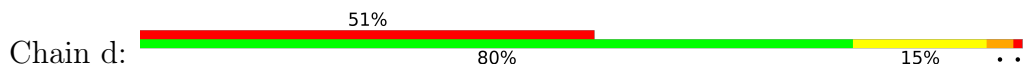


• Molecule 14: 50S ribosomal protein L19

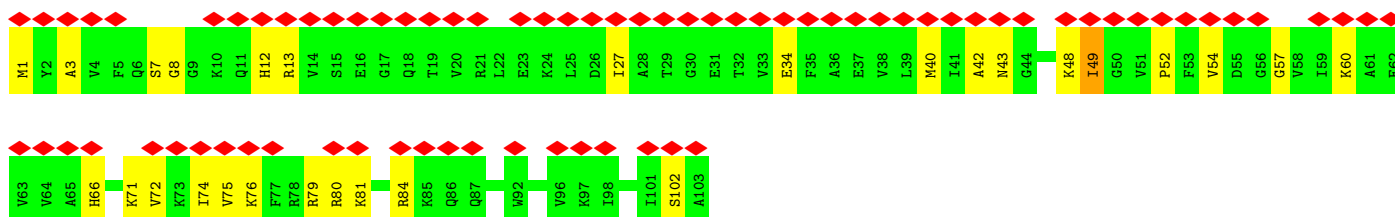




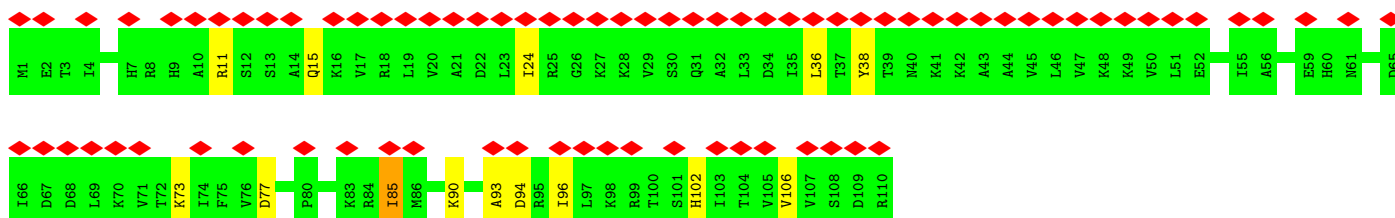
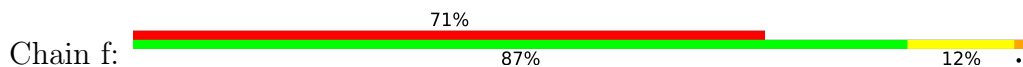
• Molecule 15: 50S ribosomal protein L20



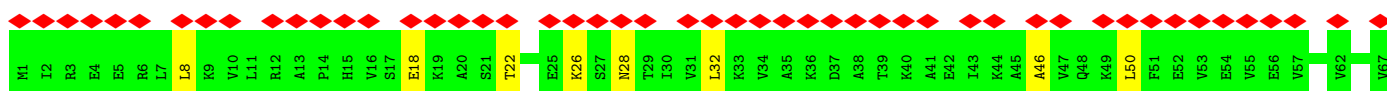
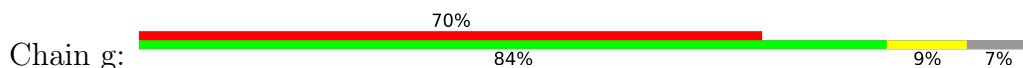
• Molecule 16: 50S ribosomal protein L21

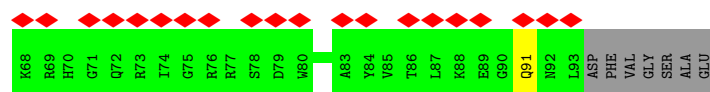


• Molecule 17: 50S ribosomal protein L22

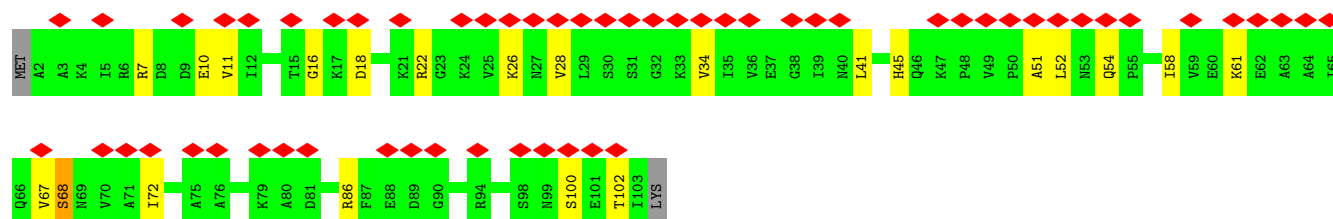
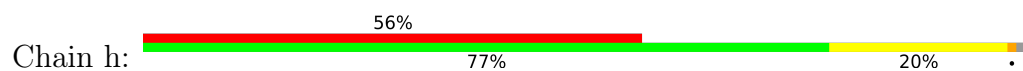


• Molecule 18: 50S ribosomal protein L23

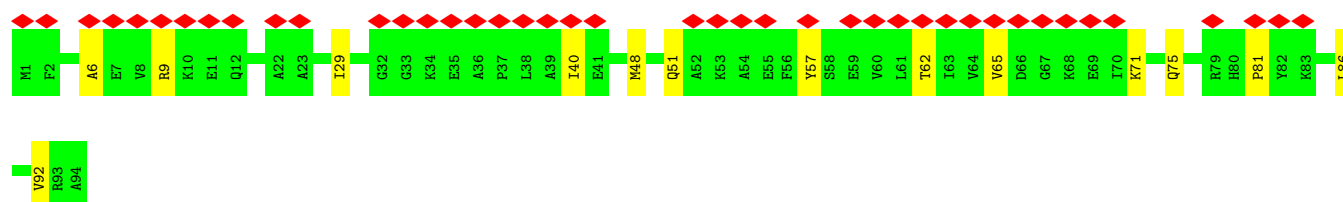
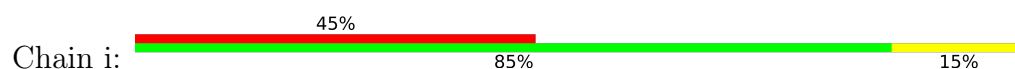




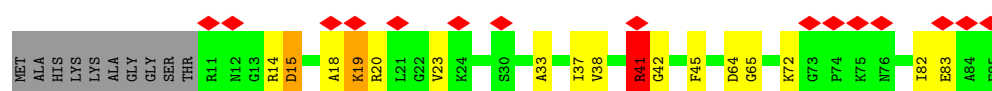
- Molecule 19: 50S ribosomal protein L24



- Molecule 20: 50S ribosomal protein L25



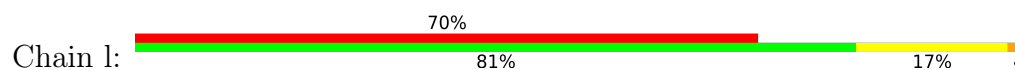
- Molecule 21: 50S ribosomal protein L27

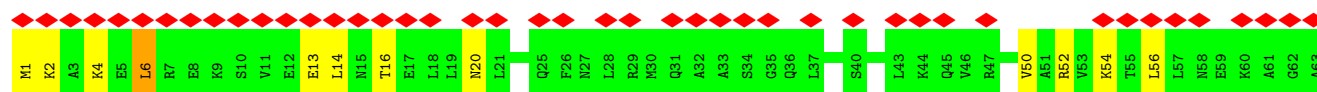


- Molecule 22: 50S ribosomal protein L28

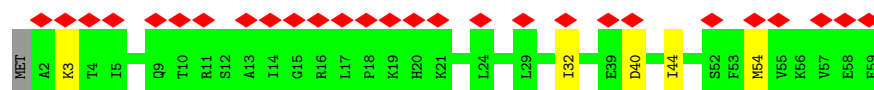
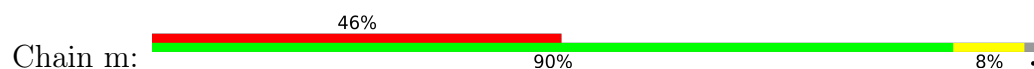


- Molecule 23: 50S ribosomal protein L29

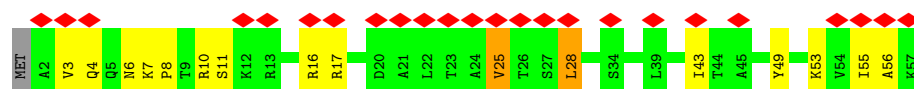
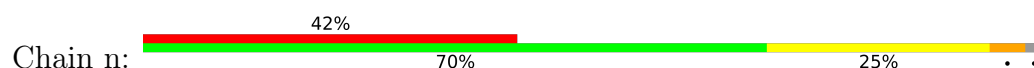




- Molecule 24: 50S ribosomal protein L30



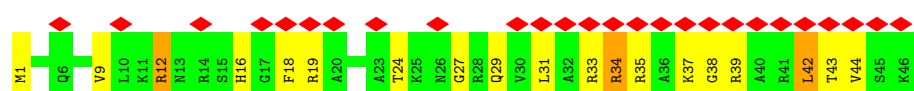
- Molecule 25: 50S ribosomal protein L32



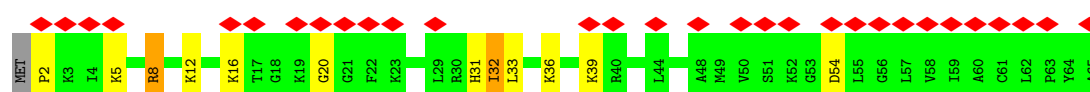
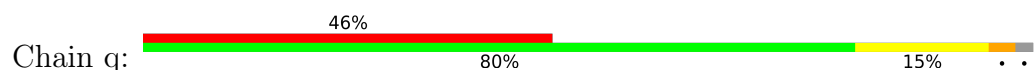
- Molecule 26: 50S ribosomal protein L33



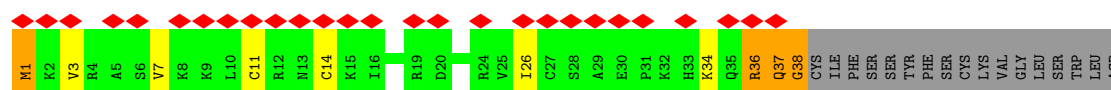
- Molecule 27: 50S ribosomal protein L34



- Molecule 28: 50S ribosomal protein L35

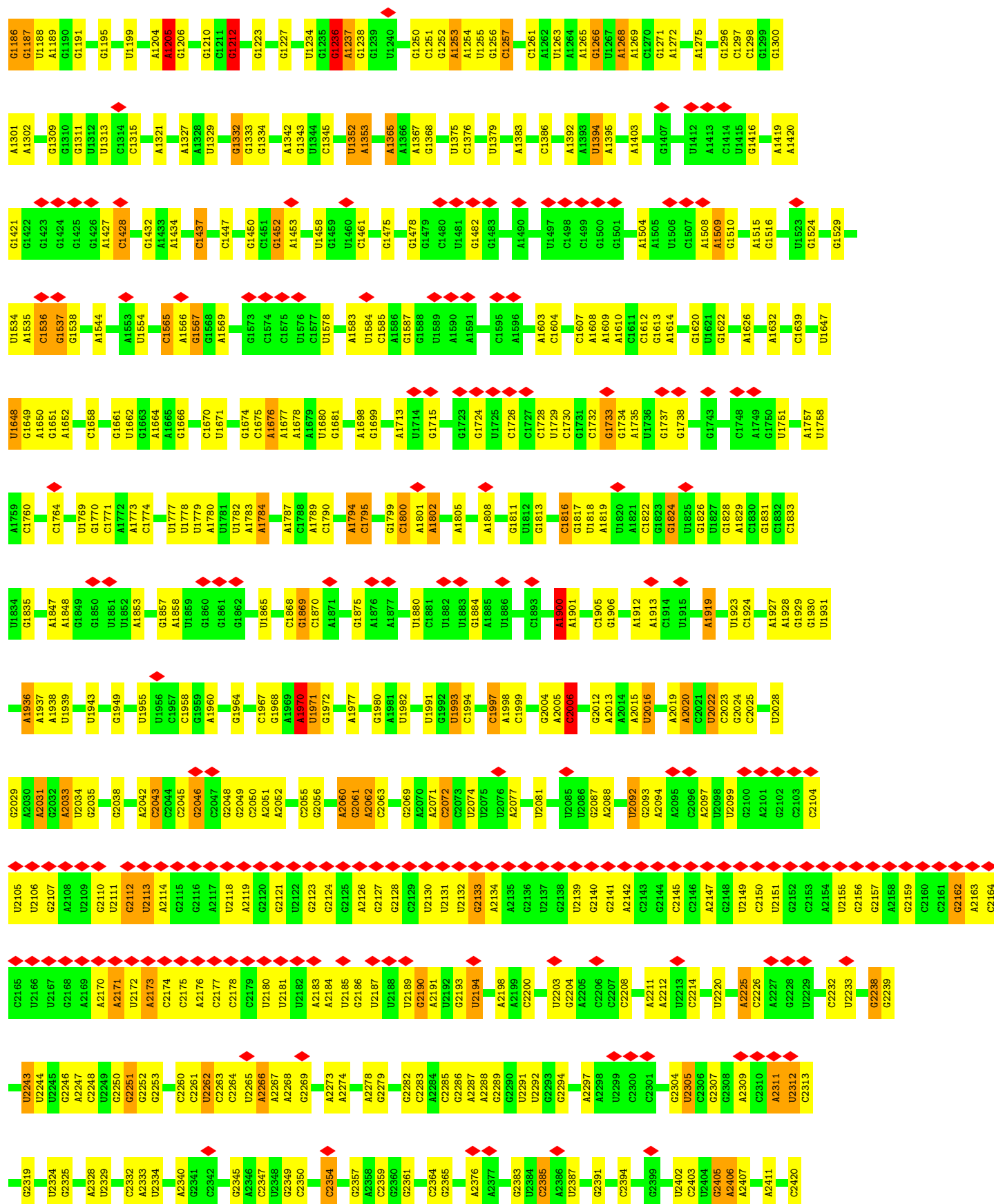


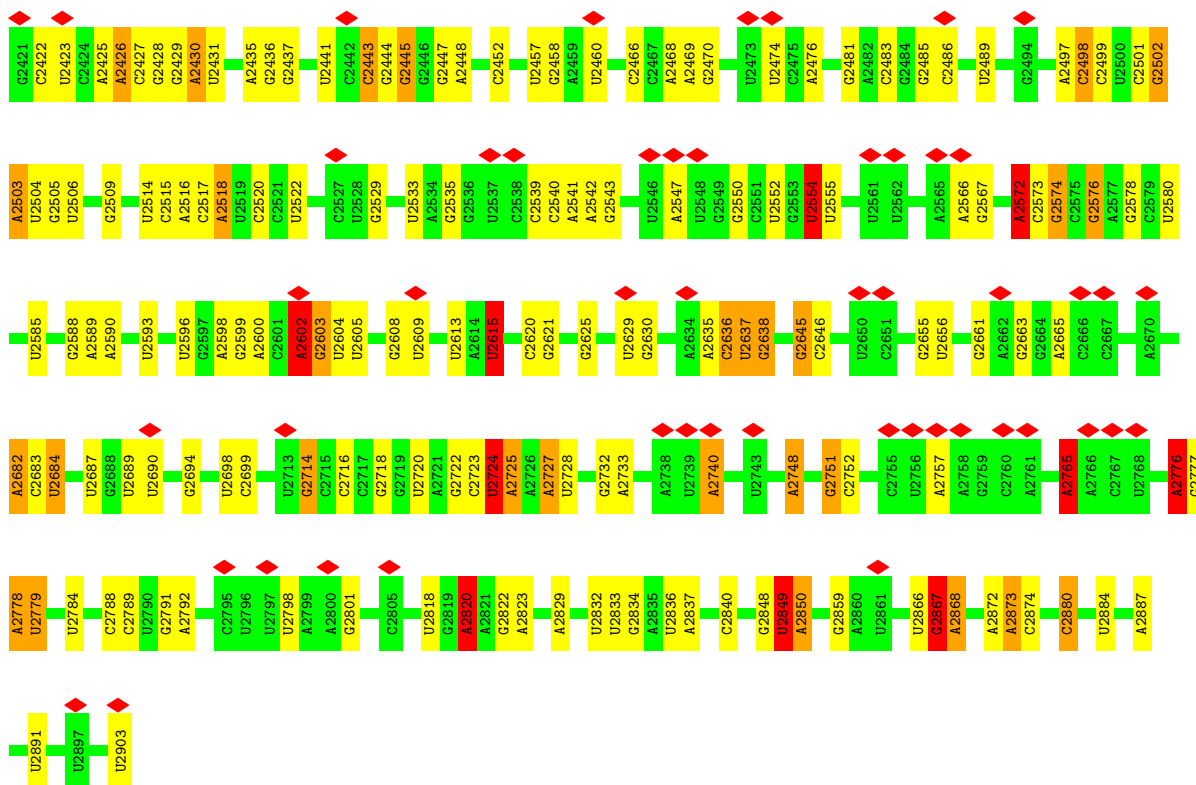
- Molecule 29: 50S ribosomal protein L36



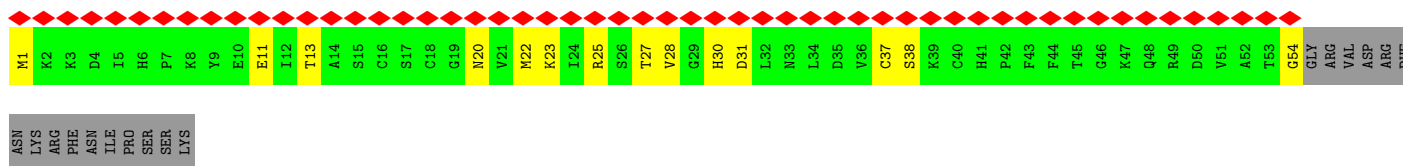
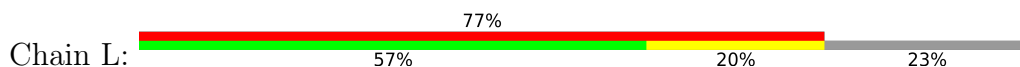
- Molecule 30: 23S rRNA



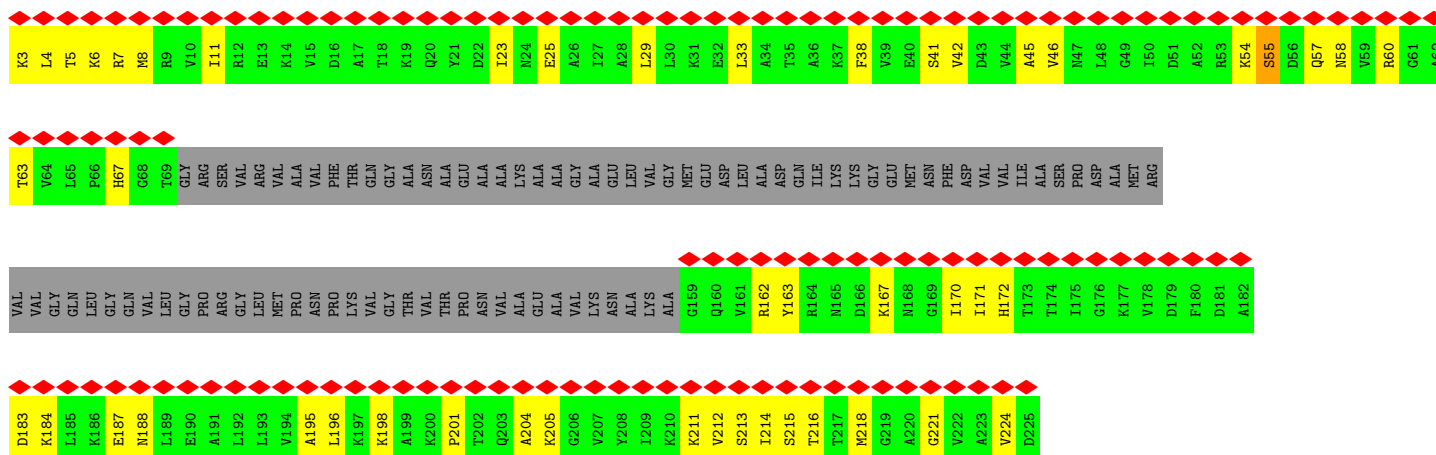




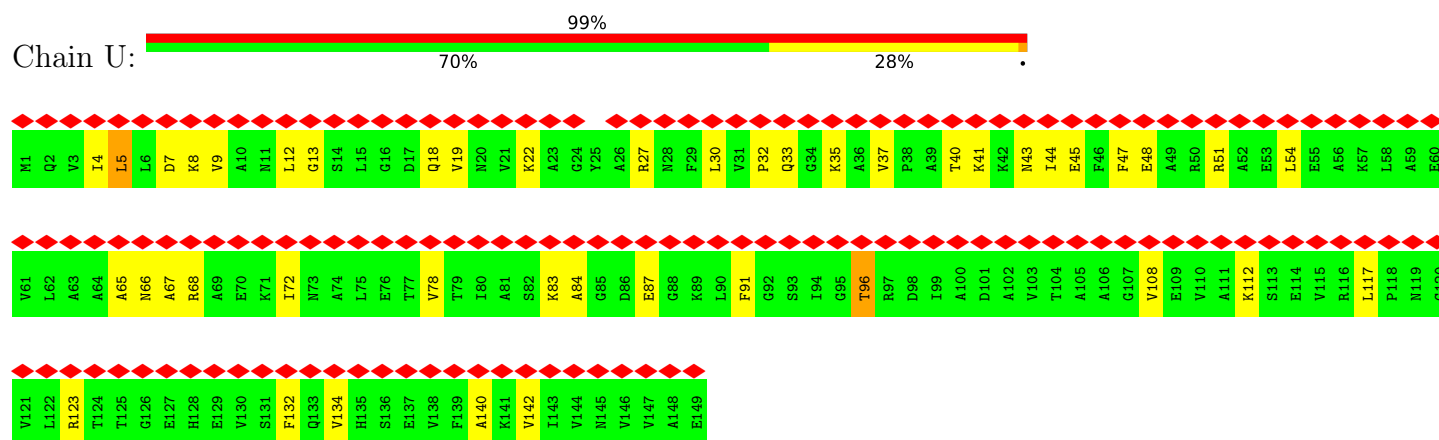
- Molecule 31: 50S ribosomal protein L31



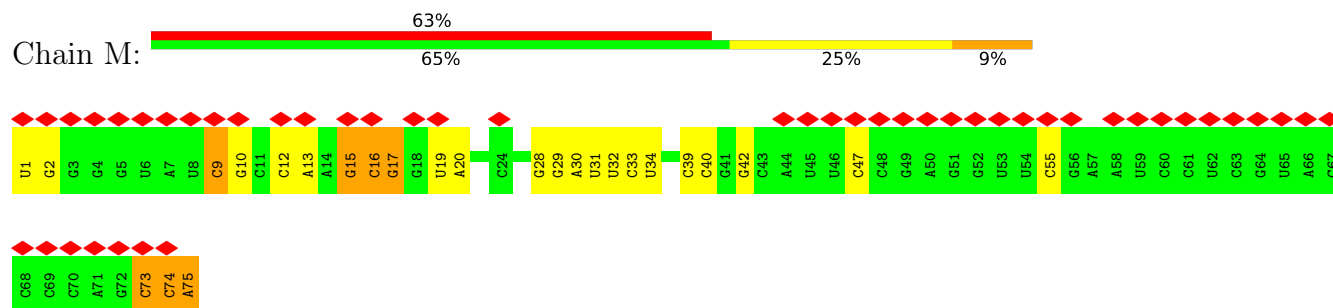
- Molecule 32: 50S ribosomal protein L1



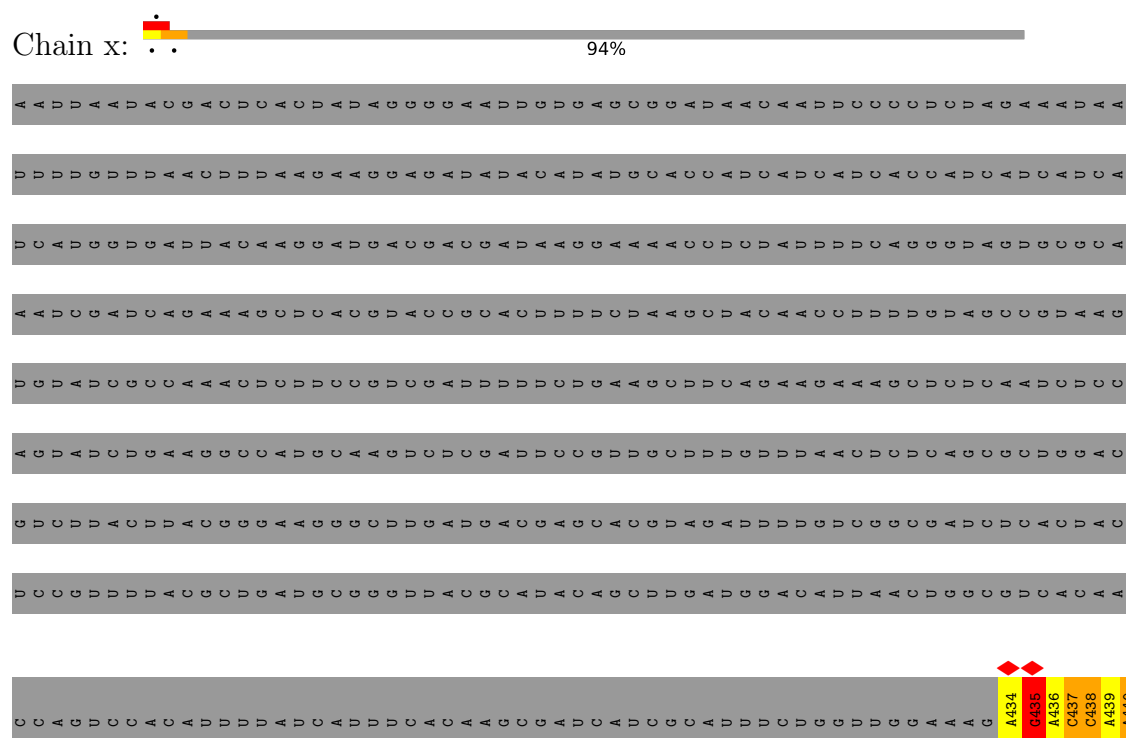
- Molecule 33: 50S ribosomal protein L9



- Molecule 34: P-site tRNA

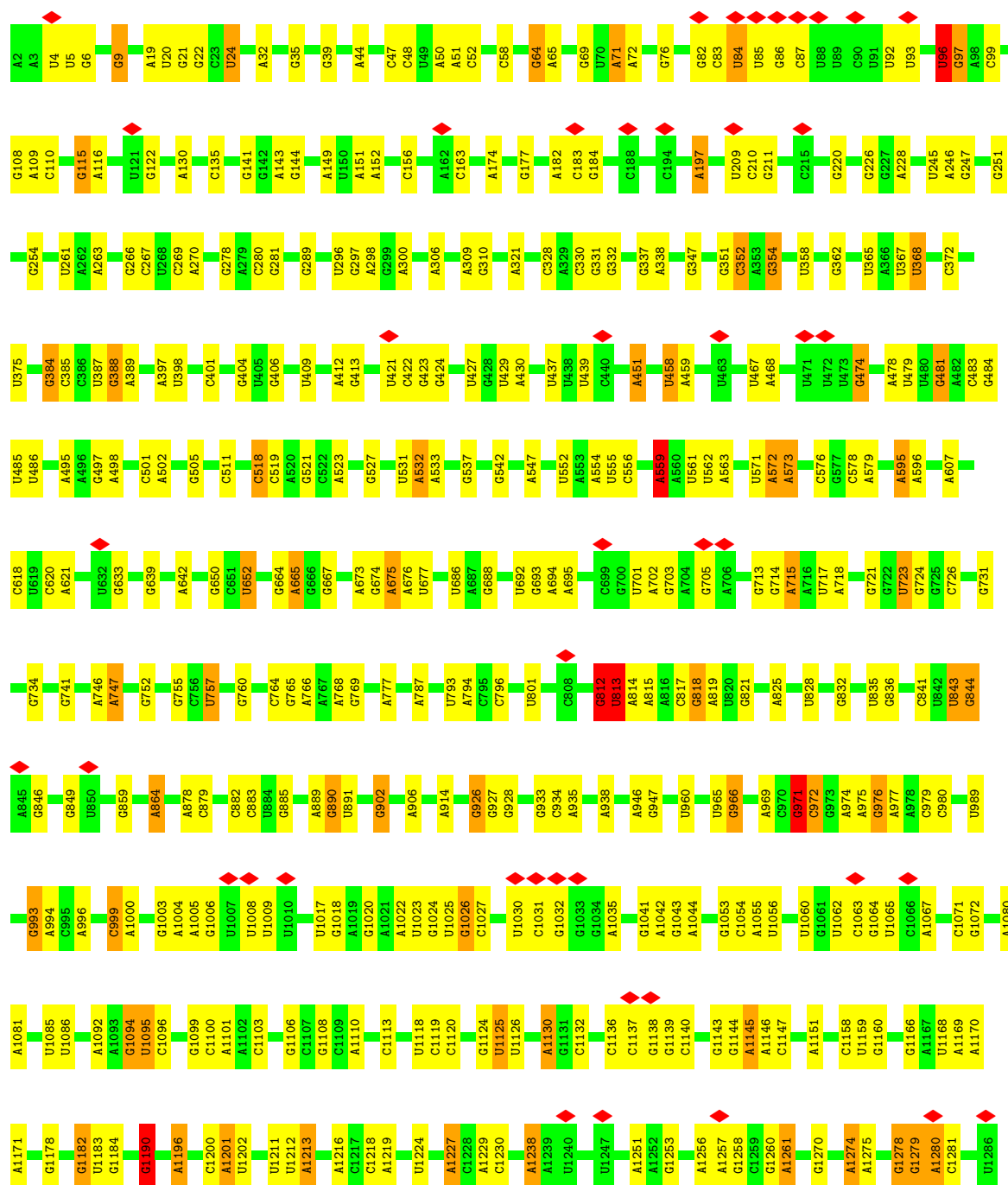


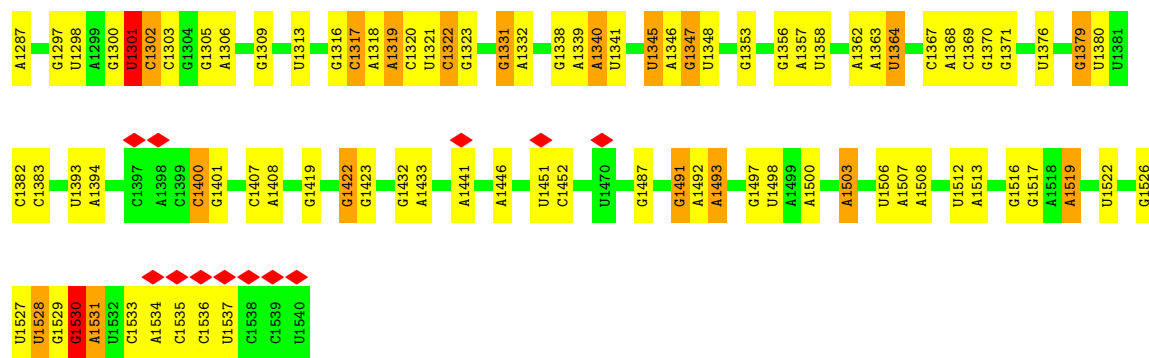
- Molecule 35: mRNA



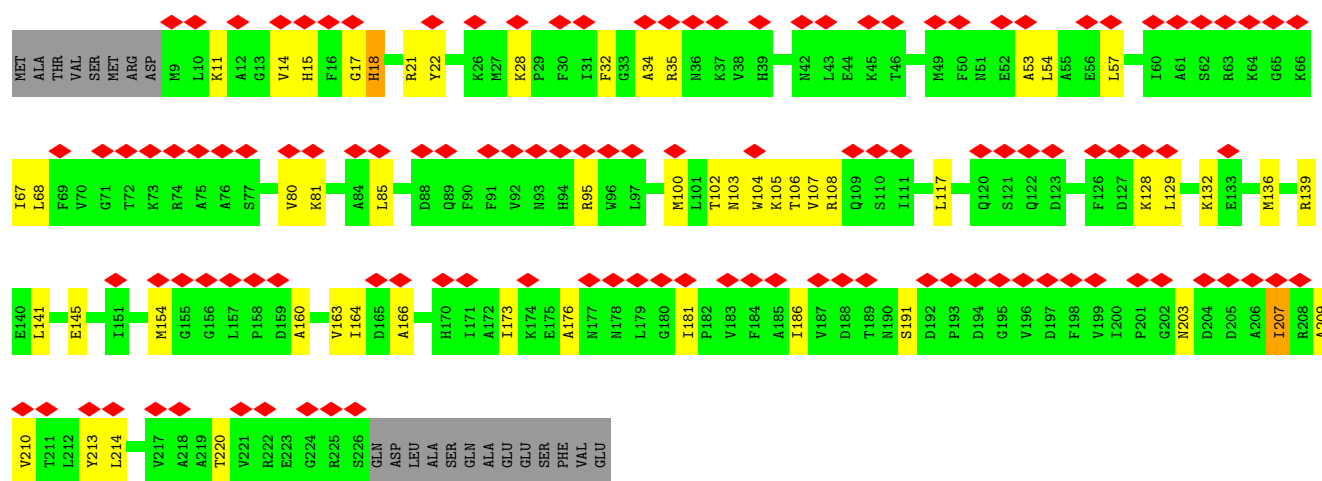
- Molecule 36: 16S rRNA

Chain 0:  68% 26% 5%

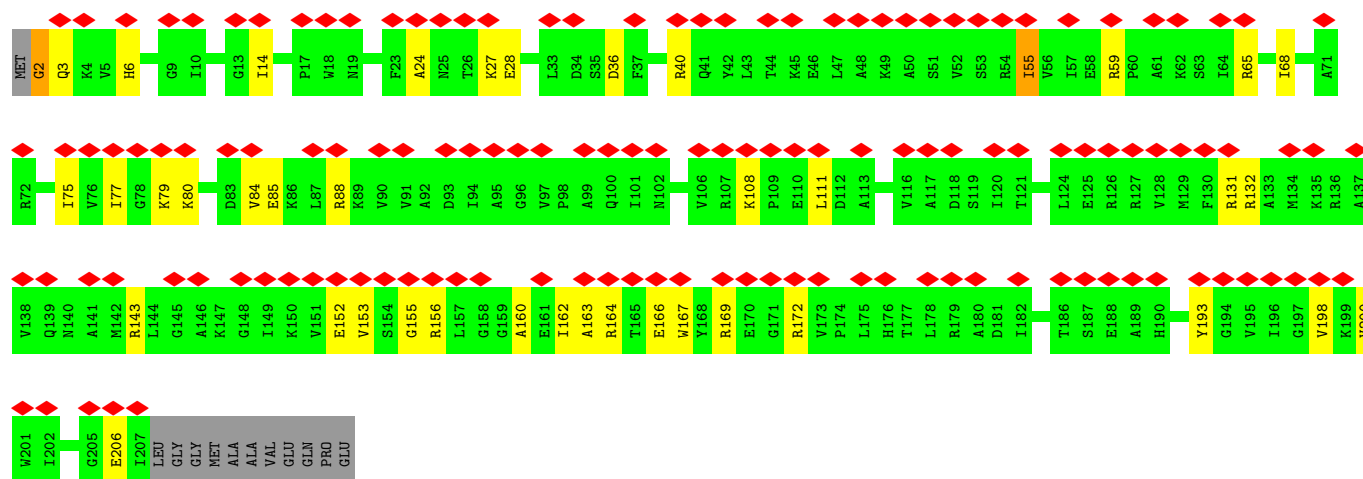
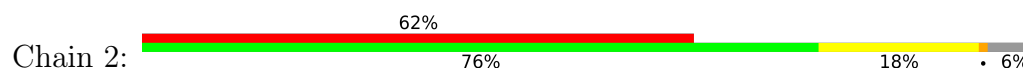




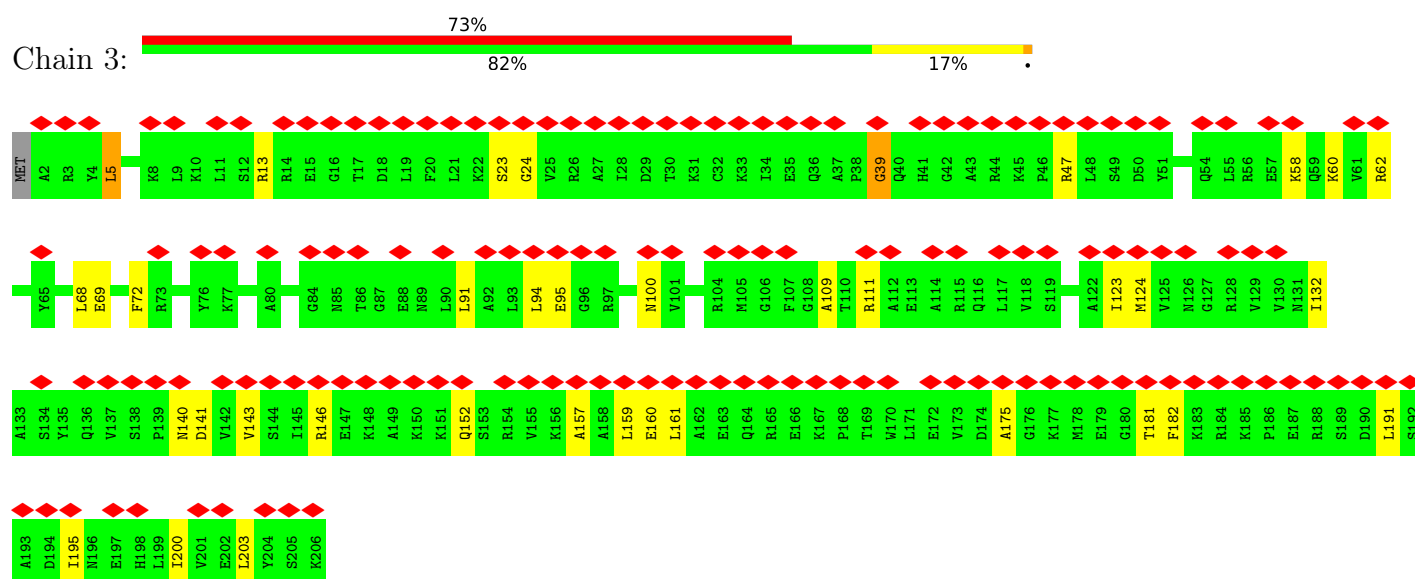
• Molecule 37: 30S ribosomal protein S2



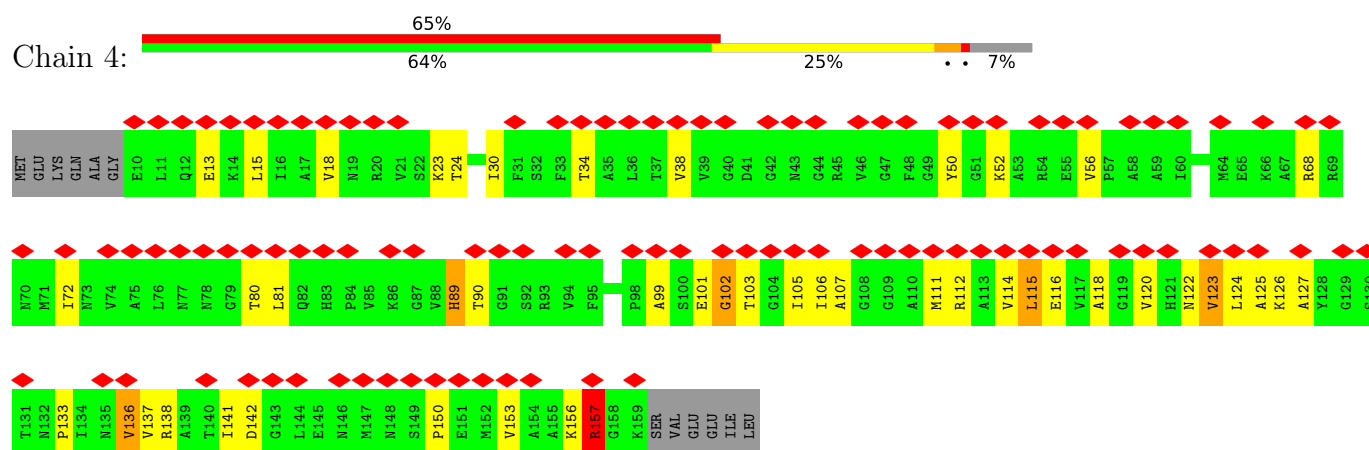
• Molecule 38: 30S ribosomal protein S3



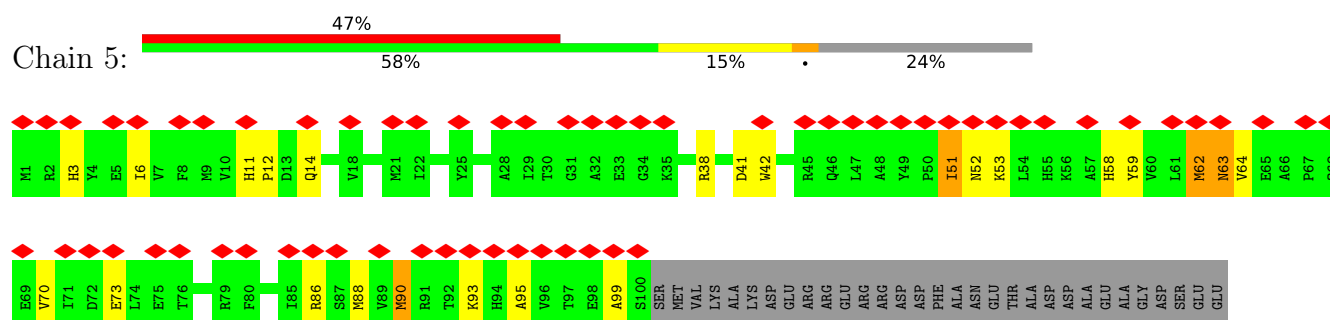
• Molecule 39: 30S ribosomal protein S4



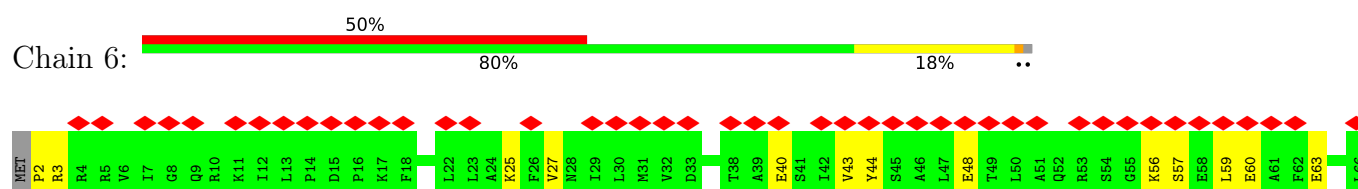
• Molecule 40: 30S ribosomal protein S5

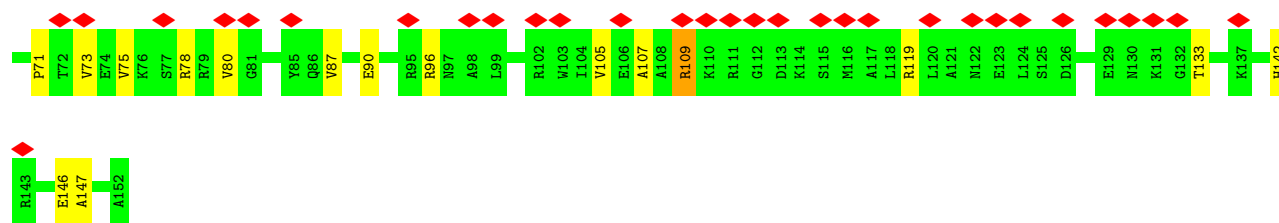


• Molecule 41: 30S ribosomal protein S6, non-modified isoform

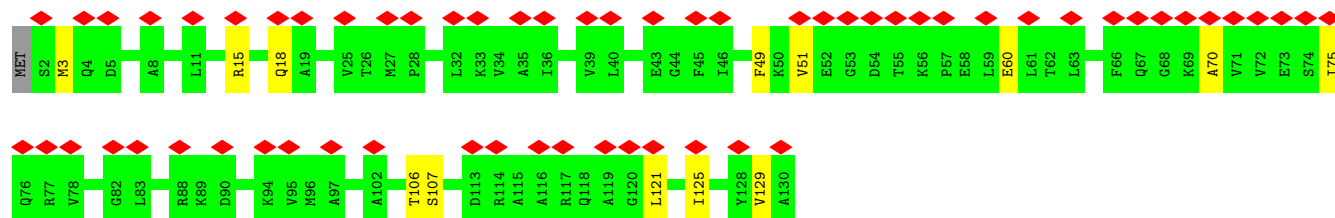
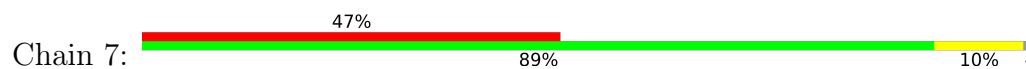


• Molecule 42: 30S ribosomal protein S7

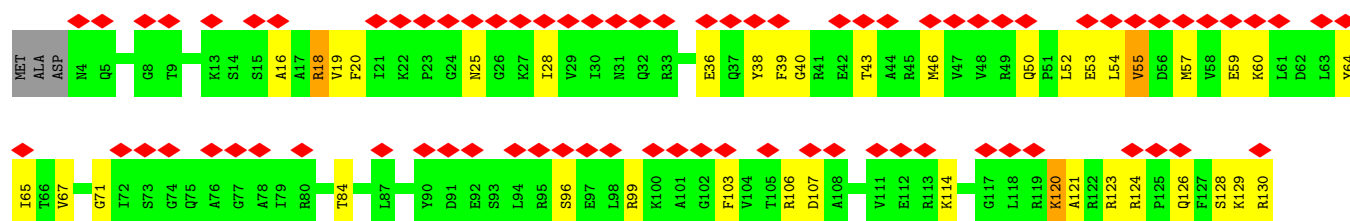




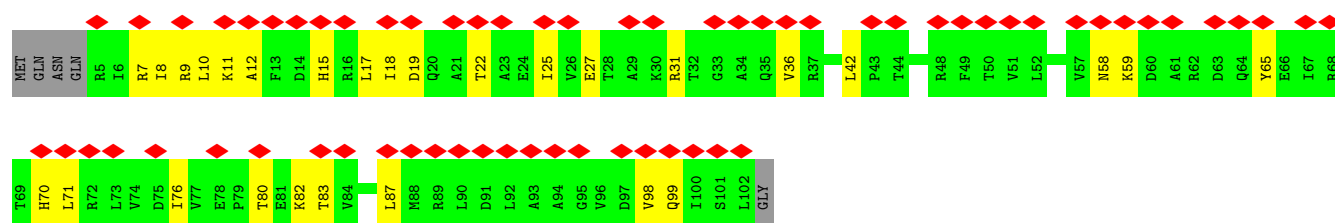
- Molecule 43: 30S ribosomal protein S8



- Molecule 44: 30S ribosomal protein S9

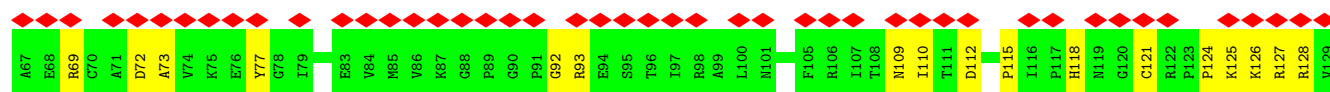


- Molecule 45: 30S ribosomal protein S10

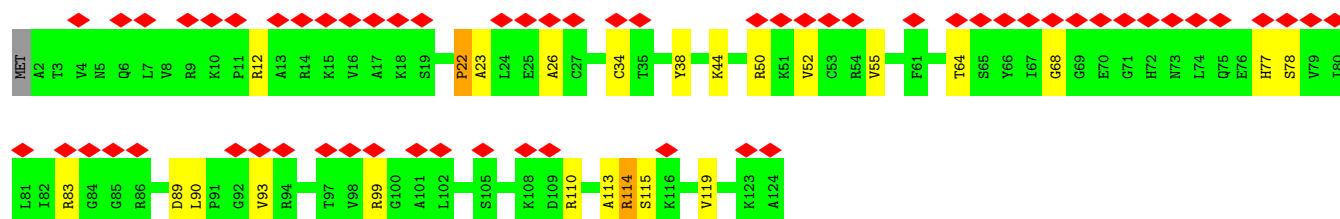
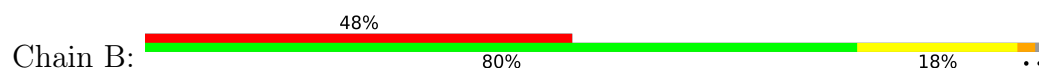


- Molecule 46: 30S ribosomal protein S11

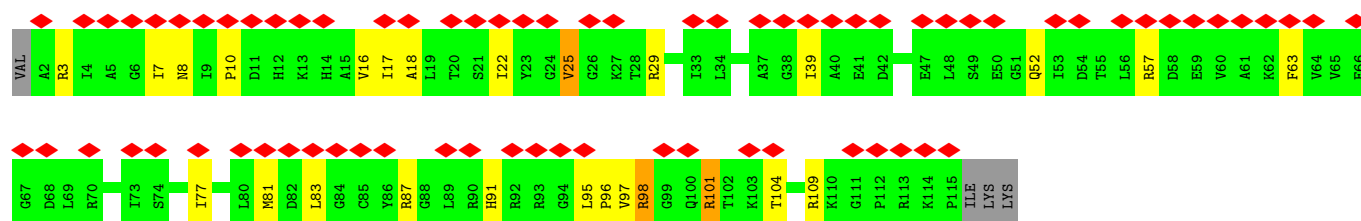
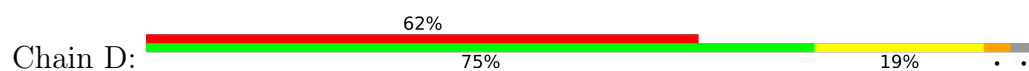




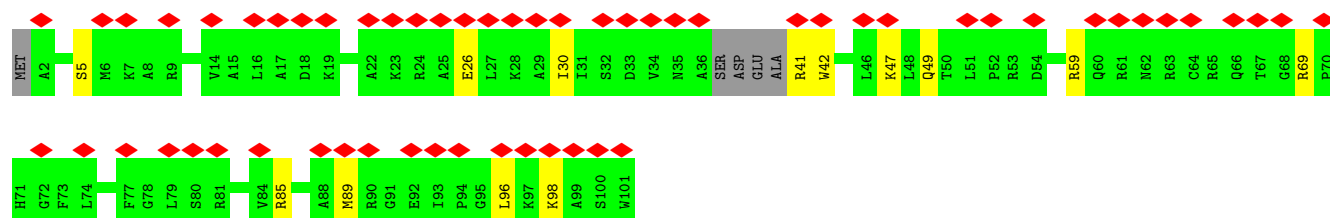
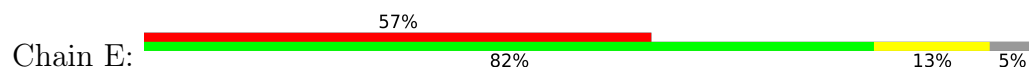
• Molecule 47: 30S ribosomal protein S12



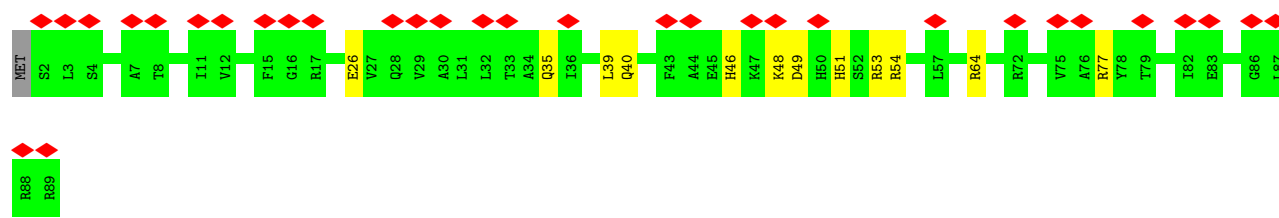
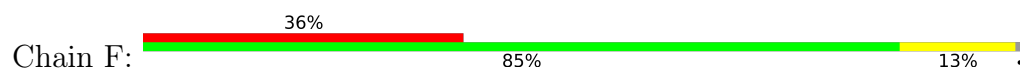
• Molecule 48: 30S ribosomal protein S13



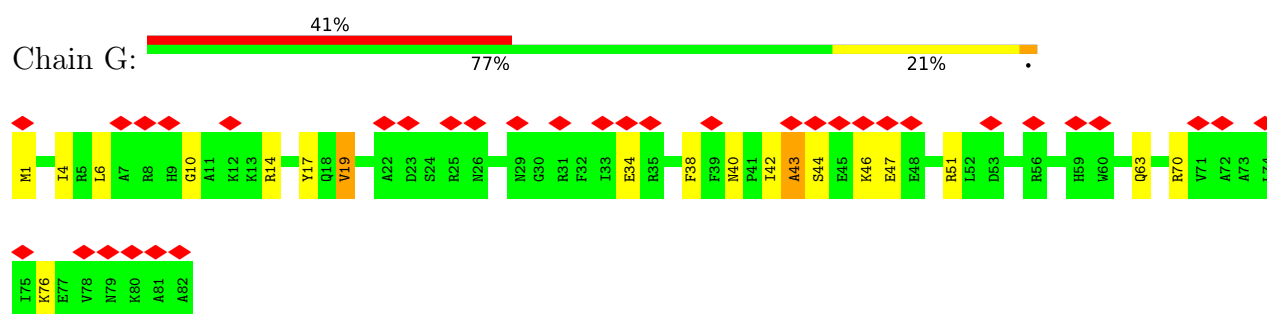
• Molecule 49: 30S ribosomal protein S14



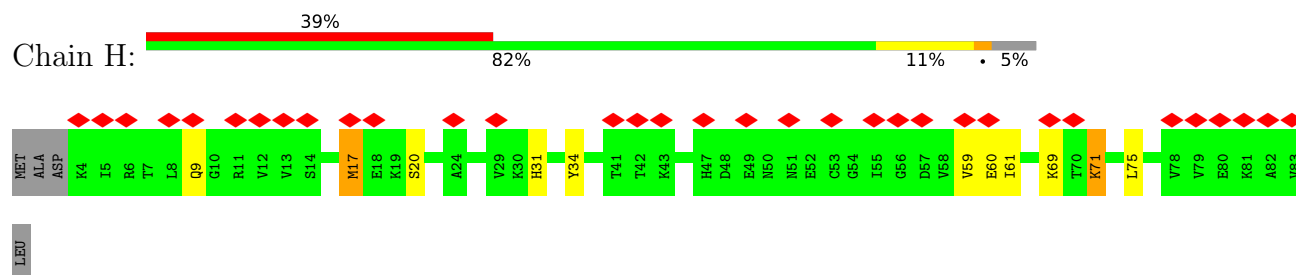
• Molecule 50: 30S ribosomal protein S15



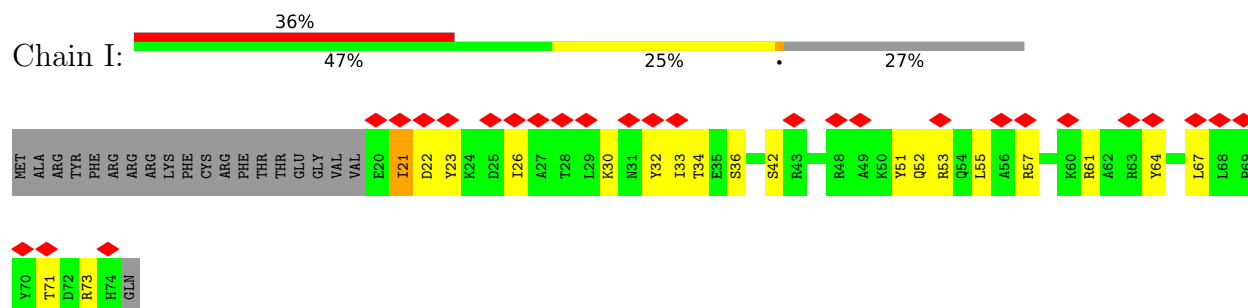
• Molecule 51: 30S ribosomal protein S16



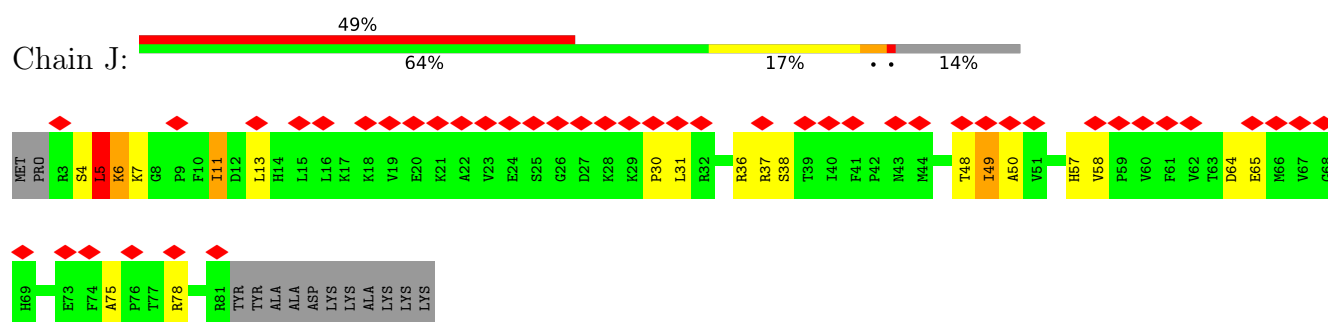
- Molecule 52: 30S ribosomal protein S17



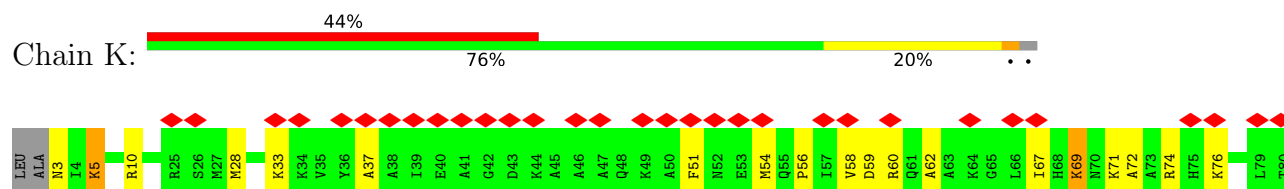
- Molecule 53: 30S ribosomal protein S18

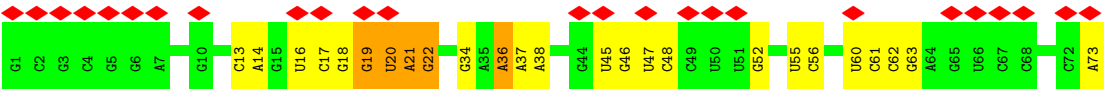


- Molecule 54: 30S ribosomal protein S19

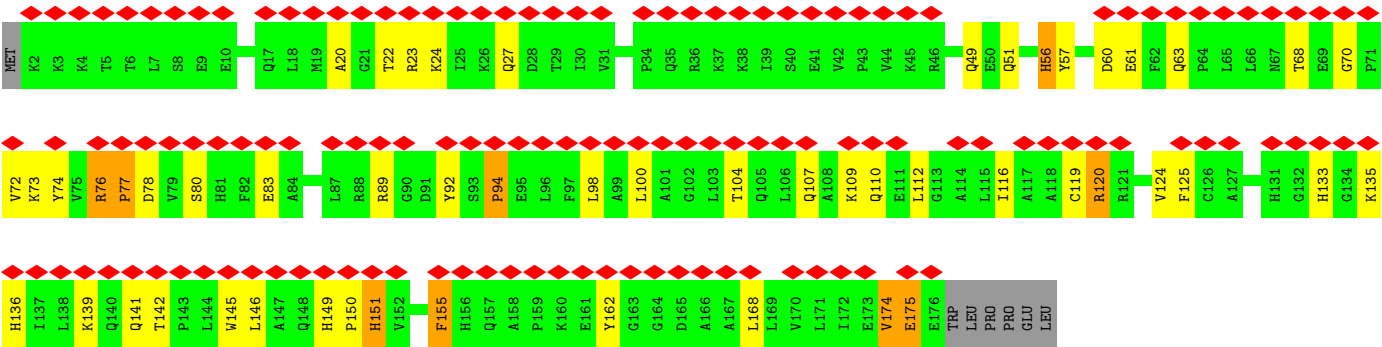


- Molecule 55: 30S ribosomal protein S20





• Molecule 59: UPF0115 protein YfcN



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32412	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.070	Depositor
Minimum map value	-0.867	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.081	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	847.19995, 847.19995, 847.19995	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.412, 1.412, 1.412	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	O	0.65	1/2828 (0.0%)	0.83	7/4410 (0.2%)
2	P	1.72	39/2121 (1.8%)	1.42	17/2852 (0.6%)
3	Q	1.54	14/1585 (0.9%)	1.29	10/2134 (0.5%)
4	R	1.21	8/1571 (0.5%)	1.09	5/2113 (0.2%)
5	S	0.84	0/1420	0.90	0/1907
6	T	0.83	0/1342	0.87	0/1816
7	V	0.77	0/1045	0.74	0/1410
8	W	1.42	10/1151 (0.9%)	1.10	0/1551
9	X	1.53	9/947 (1.0%)	1.27	4/1268 (0.3%)
10	Y	1.65	14/1053 (1.3%)	1.44	7/1403 (0.5%)
11	Z	1.42	4/1092 (0.4%)	1.20	2/1460 (0.1%)
12	a	1.65	10/973 (1.0%)	1.35	5/1301 (0.4%)
13	b	1.05	2/901 (0.2%)	1.04	5/1209 (0.4%)
14	c	1.38	4/927 (0.4%)	1.21	4/1240 (0.3%)
15	d	1.57	7/959 (0.7%)	1.32	7/1278 (0.5%)
16	e	1.40	6/828 (0.7%)	1.21	1/1107 (0.1%)
17	f	1.33	2/864 (0.2%)	1.14	1/1156 (0.1%)
18	g	1.22	0/744	1.11	0/994
19	h	1.01	1/787 (0.1%)	1.06	0/1051
20	i	0.96	0/765	0.90	0/1025
21	j	1.50	5/575 (0.9%)	1.37	6/762 (0.8%)
22	k	1.35	1/634 (0.2%)	1.16	2/848 (0.2%)
23	l	0.89	0/509	1.00	1/677 (0.1%)
24	m	1.18	0/452	1.14	1/605 (0.2%)
25	n	1.48	2/449 (0.4%)	1.40	6/599 (1.0%)
26	o	1.45	5/416 (1.2%)	1.02	0/554
27	p	1.73	5/379 (1.3%)	1.61	5/498 (1.0%)
28	q	1.50	0/512	1.35	2/676 (0.3%)
29	r	1.42	3/302 (1.0%)	1.34	3/397 (0.8%)
30	N	0.95	274/69681 (0.4%)	0.95	167/108706 (0.2%)
31	L	0.76	0/422	0.85	0/565
32	C	0.32	0/1034	0.81	1/1387 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	U	0.32	0/1122	0.96	4/1515 (0.3%)
34	M	0.51	0/1779	0.77	3/2768 (0.1%)
35	x	0.81	5/1035 (0.5%)	1.08	11/1608 (0.7%)
36	0	0.76	27/36966 (0.1%)	0.85	49/57666 (0.1%)
37	1	1.01	1/1729 (0.1%)	0.98	2/2330 (0.1%)
38	2	1.08	4/1651 (0.2%)	0.97	3/2225 (0.1%)
39	3	0.97	2/1664 (0.1%)	1.03	2/2227 (0.1%)
40	4	1.52	6/1118 (0.5%)	1.35	7/1504 (0.5%)
41	5	1.16	5/835 (0.6%)	1.14	3/1128 (0.3%)
42	6	0.83	0/1195	0.86	1/1602 (0.1%)
43	7	1.15	1/988 (0.1%)	1.05	0/1326
44	8	1.09	1/1033 (0.1%)	1.13	2/1375 (0.1%)
45	9	0.94	1/796 (0.1%)	1.02	2/1077 (0.2%)
46	A	1.11	0/892	1.12	4/1205 (0.3%)
47	B	1.38	5/968 (0.5%)	1.24	3/1300 (0.2%)
48	D	1.09	1/886 (0.1%)	1.07	0/1186
49	E	1.10	0/784	1.14	0/1043
50	F	1.20	2/717 (0.3%)	1.03	1/959 (0.1%)
51	G	1.18	3/658 (0.5%)	1.19	5/884 (0.6%)
52	H	1.08	1/657 (0.2%)	1.06	1/881 (0.1%)
53	I	1.20	0/462	1.15	1/621 (0.2%)
54	J	1.01	1/652 (0.2%)	0.99	1/877 (0.1%)
55	K	1.19	2/670 (0.3%)	1.20	2/888 (0.2%)
56	s	1.32	5/430 (1.2%)	1.22	1/570 (0.2%)
57	t	0.58	0/702	0.91	0/973
58	u	0.51	0/1744	0.72	0/2716
59	v	1.01	16/1282 (1.2%)	1.05	7/1746 (0.4%)
All	All	0.99	515/162683 (0.3%)	0.97	384/243159 (0.2%)

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
2	P	0	3
3	Q	0	1
5	S	0	2
7	V	0	1
10	Y	0	2
11	Z	0	2
19	h	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	q	0	1
30	N	0	6
36	0	0	5
37	1	0	2
38	2	0	2
40	4	0	5
41	5	0	2
44	8	0	4
46	A	0	1
47	B	0	2
52	H	0	2
54	J	0	1
55	K	0	1
56	s	0	1
59	v	0	3
All	All	0	50

All (515) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	N	2502	G	P-OP2	14.08	1.77	1.49
30	N	1156	A	P-OP2	12.95	1.74	1.49
30	N	1333	G	P-OP2	10.92	1.70	1.49
30	N	783	A	P-OP2	10.80	1.70	1.49
40	4	127	ALA	C-O	-10.50	1.11	1.23
30	N	945	A	P-OP2	10.49	1.70	1.49
2	P	221	ARG	CA-C	-10.41	1.38	1.53
30	N	1639	C	P-OP1	10.26	1.69	1.49
10	Y	51	GLU	C-O	10.19	1.37	1.23
30	N	1664	A	P-OP2	10.07	1.69	1.49
30	N	945	A	P-OP1	10.06	1.69	1.49
2	P	219	THR	C-O	10.00	1.35	1.24
30	N	1670	C	P-OP1	9.78	1.68	1.49
47	B	23	ALA	N-CA	9.73	1.58	1.46
30	N	2074	U	P-OP1	9.70	1.68	1.49
2	P	213	TRP	CD2-CE2	9.67	1.57	1.41
12	a	2	ARG	C-O	-9.67	1.11	1.24
41	5	63	ASN	C-O	-9.39	1.09	1.23
30	N	2588	G	P-OP1	9.34	1.67	1.49
30	N	2005	A	P-OP1	9.11	1.67	1.49
30	N	450	G	P-OP2	9.07	1.67	1.49
30	N	827	U	P-OP1	8.98	1.67	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	o	50	LYS	C-O	-8.81	1.14	1.24
30	N	943	A	P-OP2	8.79	1.66	1.49
55	K	5	LYS	C-O	-8.78	1.17	1.24
30	N	828	U	O3'-P	-8.67	1.48	1.61
30	N	2349	G	O3'-P	-8.61	1.48	1.61
30	N	2025	C	P-OP2	8.57	1.66	1.49
30	N	800	A	P-OP1	8.52	1.66	1.49
30	N	2445	G	O3'-P	-8.52	1.48	1.61
36	0	578	C	P-OP1	8.52	1.66	1.49
30	N	567	U	P-OP1	8.50	1.66	1.49
2	P	213	TRP	CA-C	-8.47	1.39	1.52
30	N	963	U	O3'-P	-8.37	1.48	1.61
3	Q	162	ALA	CA-C	-8.32	1.41	1.52
59	v	120	ARG	C-N	-8.30	1.22	1.33
2	P	48	ARG	C-O	-8.27	1.13	1.23
30	N	1604	C	P-OP1	8.27	1.65	1.49
29	r	38	GLY	N-CA	8.25	1.58	1.45
30	N	2615	U	P-OP1	8.25	1.65	1.49
30	N	1777	U	O3'-P	-8.22	1.48	1.61
30	N	1774	C	P-OP1	8.21	1.65	1.49
30	N	2589	A	O3'-P	-8.21	1.48	1.61
36	0	21	G	P-OP1	8.20	1.65	1.49
39	3	39	GLY	N-CA	8.20	1.52	1.45
36	0	757	U	O3'-P	-8.14	1.49	1.61
30	N	2502	G	O5'-C5'	-8.12	1.30	1.42
30	N	2060	A	O3'-P	-8.10	1.49	1.61
4	R	80	SER	C-O	-8.08	1.12	1.23
10	Y	22	GLY	C-O	-8.04	1.11	1.23
59	v	151	HIS	C-N	-7.99	1.24	1.33
2	P	238	ARG	C-O	7.93	1.33	1.24
30	N	782	A	O3'-P	-7.93	1.49	1.61
30	N	1828	G	P-OP2	7.91	1.64	1.49
30	N	963	U	P-OP1	7.89	1.64	1.49
2	P	204	VAL	CA-C	-7.89	1.42	1.52
30	N	692	C	O3'-P	-7.85	1.49	1.61
30	N	576	U	P-OP1	7.83	1.64	1.49
10	Y	62	PRO	C-O	7.82	1.33	1.23
30	N	1968	G	O3'-P	-7.81	1.49	1.61
30	N	787	C	O3'-P	-7.81	1.49	1.61
30	N	1009	A	O3'-P	-7.80	1.49	1.61
2	P	230	HIS	CA-C	-7.79	1.43	1.52
30	N	825	A	O3'-P	-7.77	1.49	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	4	30	ILE	C-O	-7.76	1.16	1.24
30	N	2687	U	O3'-P	-7.75	1.49	1.61
36	0	20	U	O3'-P	-7.75	1.49	1.61
10	Y	18	ARG	CZ-NH1	7.72	1.43	1.32
30	N	1269	A	P-OP2	7.71	1.64	1.49
59	v	89	ARG	C-N	7.70	1.43	1.33
30	N	948	C	P-OP1	7.70	1.64	1.49
30	N	585	G	O3'-P	-7.68	1.49	1.61
30	N	1257	C	O3'-P	-7.52	1.49	1.61
30	N	2019	A	O3'-P	-7.47	1.50	1.61
2	P	11	PRO	N-CA	7.41	1.56	1.47
30	N	2543	G	P-OP1	7.40	1.63	1.49
30	N	2588	G	P-OP2	7.40	1.63	1.49
30	N	116	C	O3'-P	-7.40	1.50	1.61
30	N	445	C	O3'-P	-7.39	1.50	1.61
30	N	809	G	O3'-P	-7.38	1.50	1.61
30	N	2025	C	O3'-P	-7.38	1.50	1.61
30	N	554	U	O3'-P	-7.37	1.50	1.61
27	p	38	GLY	CA-C	-7.36	1.41	1.51
14	c	93	ARG	CD-NE	-7.35	1.35	1.46
30	N	2576	G	P-OP1	7.34	1.63	1.49
30	N	984	A	O3'-P	-7.33	1.50	1.61
30	N	2593	U	O3'-P	-7.33	1.50	1.61
30	N	2550	G	O3'-P	-7.32	1.50	1.61
8	W	97	PRO	C-O	7.29	1.33	1.24
30	N	120	U	P-OP1	7.28	1.63	1.49
30	N	2714	G	P-OP2	7.26	1.63	1.49
36	0	667	G	O3'-P	-7.24	1.50	1.61
30	N	2050	C	O3'-P	-7.22	1.50	1.61
30	N	1664	A	P-OP1	7.21	1.63	1.49
30	N	2588	G	O3'-P	-7.17	1.50	1.61
36	0	882	C	O3'-P	-7.17	1.50	1.61
30	N	1152	C	O3'-P	-7.17	1.50	1.61
2	P	213	TRP	CZ3-CH2	7.16	1.58	1.40
30	N	1375	U	O3'-P	-7.14	1.50	1.61
10	Y	19	LEU	C-O	7.13	1.32	1.23
30	N	2873	A	C6-N1	-7.12	1.21	1.35
13	b	30	ARG	CZ-NH1	7.12	1.42	1.32
41	5	63	ASN	N-CA	7.10	1.55	1.46
9	X	86	LEU	C-O	-7.09	1.15	1.24
59	v	155	PHE	C-N	-7.07	1.24	1.33
21	j	14	ARG	C-O	-7.07	1.15	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	N	673	C	O3'-P	-7.03	1.50	1.61
30	N	2503	A	P-OP2	7.03	1.63	1.49
30	N	397	U	O3'-P	-7.03	1.50	1.61
4	R	77	ILE	CB-CG1	-7.00	1.39	1.53
12	a	47	VAL	C-O	-6.96	1.15	1.23
30	N	859	G	O3'-P	6.95	1.71	1.61
30	N	826	U	P-OP1	6.95	1.62	1.49
30	N	2498	C	P-OP2	6.95	1.62	1.49
59	v	73	LYS	C-N	-6.94	1.24	1.33
30	N	453	A	P-OP1	6.93	1.62	1.49
30	N	1780	A	P-OP1	6.92	1.62	1.49
25	n	11	SER	N-CA	-6.91	1.38	1.46
30	N	2022	U	P-OP1	6.91	1.62	1.49
30	N	2635	A	O3'-P	-6.91	1.50	1.61
30	N	1774	C	O3'-P	-6.88	1.50	1.61
3	Q	125	TRP	CA-C	-6.87	1.44	1.52
47	B	22	PRO	CA-C	6.87	1.62	1.52
30	N	1019	U	O3'-P	-6.86	1.50	1.61
30	N	2052	A	O3'-P	-6.85	1.50	1.61
2	P	222	GLY	C-O	-6.83	1.14	1.23
30	N	2698	U	O3'-P	-6.83	1.50	1.61
52	H	71	LYS	C-O	-6.80	1.15	1.24
30	N	1612	C	O3'-P	-6.79	1.50	1.61
30	N	1658	C	P-OP1	6.79	1.62	1.49
30	N	200	U	O3'-P	-6.78	1.50	1.61
2	P	221	ARG	C-O	-6.78	1.15	1.23
35	x	435	G	C1'-N9	-6.77	1.36	1.47
2	P	86	ASN	C-O	-6.77	1.15	1.24
59	v	57	TYR	C-N	-6.73	1.24	1.33
30	N	1994	C	O3'-P	-6.72	1.51	1.61
30	N	2466	C	O3'-P	-6.72	1.51	1.61
59	v	56	HIS	C-N	-6.71	1.23	1.33
2	P	15	HIS	C-O	-6.70	1.14	1.24
19	h	68	SER	CB-OG	6.70	1.55	1.42
30	N	1658	C	O3'-P	-6.70	1.51	1.61
36	0	1500	A	O3'-P	-6.69	1.51	1.61
12	a	66	ALA	CA-C	-6.67	1.43	1.52
15	d	49	ASP	CA-C	-6.66	1.43	1.52
8	W	81	ILE	C-O	6.63	1.31	1.24
30	N	641	U	O3'-P	-6.63	1.51	1.61
30	N	2006	C	P-OP1	6.63	1.62	1.49
30	N	1751	U	O3'-P	-6.63	1.51	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	d	49	ASP	C-O	6.62	1.32	1.24
30	N	192	C	P-OP1	6.62	1.62	1.49
30	N	2062	A	P-OP2	6.62	1.62	1.49
30	N	1782	U	P-OP1	6.61	1.62	1.49
30	N	1900	A	O3'-P	6.60	1.71	1.61
14	c	21	ARG	C-O	-6.59	1.18	1.24
30	N	955	U	O3'-P	-6.58	1.51	1.61
30	N	1831	G	O3'-P	-6.55	1.51	1.61
30	N	2035	G	O5'-C5'	-6.55	1.33	1.42
30	N	2765	A	C6-N1	-6.55	1.22	1.35
30	N	1993	U	O5'-C5'	-6.54	1.32	1.42
36	0	812	G	O3'-P	6.54	1.71	1.61
2	P	221	ARG	CB-CG	-6.52	1.32	1.52
11	Z	39	GLY	C-O	-6.52	1.15	1.23
12	a	2	ARG	C-N	-6.52	1.24	1.33
30	N	2740	A	O3'-P	-6.51	1.51	1.61
30	N	1268	A	P-OP1	6.51	1.61	1.49
25	n	10	ARG	CA-C	6.50	1.61	1.52
30	N	810	U	P-OP1	6.49	1.61	1.49
30	N	2518	A	P-OP2	6.49	1.61	1.49
30	N	1254	A	O3'-P	-6.47	1.51	1.61
9	X	66	LYS	CA-C	-6.46	1.44	1.52
30	N	1353	A	O3'-P	-6.46	1.51	1.61
9	X	7	MET	N-CA	6.45	1.54	1.46
2	P	213	TRP	CB-CG	-6.45	1.30	1.50
30	N	2605	U	O3'-P	-6.43	1.51	1.61
16	e	79	ARG	C-O	6.40	1.31	1.23
12	a	1	MET	C-O	6.40	1.36	1.23
30	N	1813	G	O3'-P	-6.38	1.51	1.61
30	N	2543	G	O5'-C5'	-6.38	1.32	1.42
2	P	234	GLY	C-O	-6.37	1.15	1.23
2	P	204	VAL	N-CA	-6.36	1.39	1.46
30	N	2489	U	O3'-P	-6.36	1.51	1.61
30	N	1970	A	P-OP2	6.36	1.61	1.49
30	N	2031	A	P-OP1	-6.35	1.36	1.49
30	N	2264	C	O3'-P	-6.35	1.51	1.61
30	N	1828	G	P-OP1	6.34	1.61	1.49
30	N	1678	A	P-OP2	6.33	1.61	1.49
2	P	271	ARG	CZ-NH1	6.32	1.41	1.32
30	N	2437	G	O3'-P	-6.32	1.51	1.61
30	N	975	A	P-OP2	6.30	1.61	1.49
14	c	53	ARG	N-CA	-6.29	1.36	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	N	839	U	O3'-P	-6.29	1.51	1.61
30	N	2265	U	O3'-P	-6.28	1.51	1.61
44	8	121	ALA	C-O	-6.28	1.16	1.24
3	Q	126	ASN	CA-C	-6.28	1.45	1.53
30	N	2590	A	O3'-P	-6.27	1.51	1.61
47	B	114	ARG	C-O	-6.25	1.16	1.24
2	P	220	VAL	CA-CB	-6.23	1.46	1.54
36	0	24	U	N3-C4	-6.23	1.25	1.38
35	x	469	U	C1'-N1	6.22	1.56	1.47
36	0	726	C	O3'-P	-6.21	1.51	1.61
10	Y	41	ARG	CA-C	-6.21	1.45	1.52
10	Y	62	PRO	CA-CB	-6.21	1.45	1.53
3	Q	163	GLY	N-CA	6.20	1.52	1.45
30	N	733	G	O3'-P	-6.20	1.51	1.61
30	N	1794	A	O3'-P	-6.19	1.51	1.61
26	o	10	LYS	C-O	-6.19	1.16	1.24
30	N	832	U	O3'-P	-6.18	1.51	1.61
30	N	192	C	O3'-P	-6.17	1.51	1.61
30	N	515	A	O3'-P	-6.17	1.51	1.61
30	N	1189	A	O3'-P	-6.16	1.51	1.61
8	W	138	GLN	C-O	-6.16	1.16	1.23
30	N	2447	G	O3'-P	-6.16	1.51	1.61
12	a	112	TYR	CA-C	-6.15	1.45	1.52
27	p	39	ARG	NE-CZ	6.15	1.39	1.33
22	k	22	LEU	C-O	-6.14	1.15	1.23
30	N	572	A	P-OP1	6.14	1.61	1.49
30	N	372	G	O3'-P	6.14	1.70	1.61
8	W	107	GLY	C-O	-6.13	1.17	1.24
29	r	37	GLN	CA-C	-6.13	1.44	1.52
15	d	10	ALA	C-O	6.10	1.31	1.24
30	N	2822	G	O3'-P	-6.09	1.52	1.61
30	N	1778	U	O3'-P	-6.09	1.52	1.61
30	N	997	G	O3'-P	-6.08	1.52	1.61
41	5	51	ILE	C-O	-6.07	1.17	1.24
40	4	24	THR	CA-C	-6.07	1.47	1.53
30	N	2572	A	O3'-P	-6.06	1.52	1.61
30	N	1790	C	O3'-P	-6.06	1.52	1.61
2	P	10	SER	CA-CB	6.04	1.62	1.53
30	N	1771	C	O3'-P	-6.03	1.52	1.61
38	2	3	GLN	N-CA	-6.03	1.39	1.46
10	Y	37	GLY	C-O	-6.02	1.16	1.23
40	4	24	THR	C-O	-6.02	1.14	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	N	2620	C	O3'-P	-6.02	1.52	1.61
30	N	254	G	O3'-P	-6.02	1.52	1.61
30	N	569	U	O3'-P	-6.01	1.52	1.61
4	R	75	SER	CA-C	-6.00	1.46	1.53
30	N	818	G	P-OP2	6.00	1.60	1.49
30	N	821	A	O3'-P	-5.99	1.52	1.61
30	N	2867	G	O3'-P	5.99	1.70	1.61
30	N	464	U	O3'-P	-5.99	1.52	1.61
56	s	34	ARG	CZ-NH1	5.98	1.41	1.32
30	N	671	C	P-OP2	5.97	1.60	1.49
30	N	2406	A	P-OP1	5.97	1.60	1.49
56	s	37	PHE	N-CA	5.97	1.53	1.46
30	N	676	A	O3'-P	-5.96	1.52	1.61
8	W	84	ILE	CA-C	-5.95	1.46	1.53
8	W	98	GLU	N-CA	-5.95	1.39	1.46
2	P	214	ARG	CZ-NH1	5.93	1.41	1.32
30	N	2081	U	O3'-P	-5.93	1.52	1.61
36	0	1367	C	O3'-P	-5.93	1.52	1.61
10	Y	29	LYS	C-O	5.92	1.31	1.24
10	Y	51	GLU	N-CA	-5.92	1.39	1.46
30	N	566	U	O3'-P	-5.92	1.52	1.61
30	N	2061	G	C2'-O2'	5.92	1.51	1.42
30	N	2444	G	O3'-P	-5.92	1.52	1.61
30	N	2637	U	O3'-P	-5.92	1.52	1.61
30	N	2499	C	P-OP2	5.91	1.60	1.49
30	N	2625	G	O3'-P	-5.91	1.52	1.61
30	N	2247	A	O3'-P	-5.91	1.52	1.61
30	N	2025	C	O5'-C5'	-5.90	1.33	1.42
30	N	2072	C	O5'-C5'	-5.90	1.33	1.42
30	N	2385	C	P-OP1	5.89	1.60	1.49
36	0	1393	U	O3'-P	-5.89	1.52	1.61
47	B	23	ALA	C-O	-5.89	1.16	1.24
51	G	4	ILE	C-O	-5.89	1.17	1.23
2	P	158	ALA	CA-C	-5.88	1.45	1.52
30	N	2837	A	O3'-P	-5.86	1.52	1.61
30	N	730	A	P-OP2	5.86	1.60	1.49
35	x	439	A	C1'-N9	-5.86	1.39	1.48
2	P	235	GLY	C-N	-5.85	1.25	1.33
2	P	258	ARG	NE-CZ	-5.85	1.26	1.33
36	0	980	C	P-OP1	5.85	1.60	1.49
35	x	474	U	C1'-N1	5.85	1.56	1.47
30	N	1822	C	O3'-P	-5.84	1.52	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	204	VAL	C-N	-5.83	1.25	1.33
29	r	36	ARG	CD-NE	-5.83	1.38	1.46
30	N	198	C	O3'-P	-5.83	1.52	1.61
30	N	2072	C	O3'-P	-5.83	1.52	1.61
30	N	1824	G	P-OP2	5.82	1.60	1.49
2	P	235	GLY	CA-C	-5.82	1.43	1.51
4	R	62	GLN	N-CA	5.82	1.53	1.46
26	o	48	ILE	C-O	-5.82	1.17	1.24
45	9	58	ASN	CA-C	-5.81	1.45	1.52
30	N	2359	C	O3'-P	-5.80	1.52	1.61
30	N	2232	C	O3'-P	-5.80	1.52	1.61
40	4	50	TYR	C-O	5.80	1.31	1.24
38	2	2	GLY	N-CA	5.80	1.54	1.45
15	d	51	ARG	CA-CB	-5.80	1.44	1.53
30	N	538	A	O3'-P	-5.79	1.52	1.61
26	o	23	THR	C-O	-5.79	1.19	1.24
2	P	160	THR	C-O	-5.78	1.16	1.24
30	N	2598	A	O3'-P	-5.78	1.52	1.61
30	N	2062	A	O5'-C5'	-5.77	1.34	1.42
36	0	387	U	O3'-P	-5.77	1.52	1.61
59	v	107	GLN	C-N	-5.77	1.26	1.33
30	N	2542	A	O3'-P	-5.76	1.52	1.61
12	a	106	ASP	N-CA	-5.76	1.40	1.46
36	0	22	G	O3'-P	-5.76	1.52	1.61
54	J	6	LYS	N-CA	5.75	1.53	1.46
51	G	10	GLY	N-CA	5.75	1.51	1.45
30	N	2268	A	P-OP1	5.74	1.60	1.49
30	N	2602	A	O3'-P	5.74	1.69	1.61
30	N	783	A	C4'-O4'	5.73	1.54	1.45
30	N	966	G	O3'-P	-5.73	1.52	1.61
30	N	2457	U	O3'-P	-5.73	1.52	1.61
8	W	30	THR	CB-CG2	-5.72	1.33	1.52
30	N	126	A	O3'-P	-5.72	1.52	1.61
9	X	23	LYS	CA-C	-5.72	1.45	1.52
30	N	2572	A	P-OP1	-5.71	1.37	1.49
30	N	2013	A	O3'-P	-5.71	1.52	1.61
30	N	1261	C	O3'-P	-5.71	1.52	1.61
30	N	940	G	O3'-P	-5.71	1.52	1.61
30	N	2684	U	O3'-P	-5.70	1.52	1.61
59	v	124	VAL	C-N	-5.69	1.25	1.33
30	N	1298	C	O3'-P	-5.69	1.52	1.61
36	0	505	G	O3'-P	-5.69	1.52	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Q	164	GLN	C-O	5.69	1.30	1.24
30	N	29	U	O3'-P	-5.69	1.52	1.61
36	0	814	A	P-OP2	5.69	1.60	1.49
9	X	65	THR	C-O	-5.68	1.16	1.23
30	N	1805	A	O3'-P	-5.68	1.52	1.61
41	5	99	ALA	CA-C	5.68	1.56	1.52
4	R	81	GLY	C-N	-5.67	1.25	1.33
12	a	17	ARG	C-O	5.67	1.30	1.24
30	N	1795	C	O3'-P	-5.67	1.52	1.61
30	N	1681	G	O3'-P	-5.66	1.52	1.61
30	N	796	C	O3'-P	-5.66	1.52	1.61
30	N	1662	U	P-OP2	5.66	1.60	1.49
30	N	2016	U	O3'-P	-5.66	1.52	1.61
27	p	34	ARG	CG-CD	-5.65	1.35	1.52
50	F	51	HIS	C-O	5.65	1.30	1.24
30	N	578	G	P-OP2	5.63	1.60	1.49
30	N	571	U	O3'-P	-5.63	1.52	1.61
30	N	25	U	O3'-P	-5.63	1.52	1.61
30	N	2499	C	P-OP1	5.62	1.60	1.49
11	Z	93	VAL	CA-CB	5.61	1.63	1.54
50	F	49	ASP	C-O	5.61	1.31	1.23
21	j	42	GLY	N-CA	5.61	1.55	1.45
1	O	83	G	O3'-P	-5.61	1.52	1.61
30	N	773	U	O3'-P	-5.57	1.52	1.61
9	X	41	ILE	C-O	-5.57	1.17	1.23
30	N	761	A	P-OP1	5.57	1.60	1.49
8	W	80	HIS	CA-C	-5.56	1.45	1.53
30	N	2072	C	P-OP1	5.56	1.60	1.49
30	N	2049	G	O3'-P	-5.56	1.52	1.61
30	N	680	C	O3'-P	-5.55	1.52	1.61
2	P	205	LEU	N-CA	5.54	1.53	1.46
30	N	1009	A	P-OP2	5.54	1.60	1.49
36	0	764	C	O3'-P	-5.54	1.52	1.61
3	Q	162	ALA	C-O	-5.54	1.17	1.23
11	Z	11	LYS	C-O	-5.54	1.17	1.24
30	N	393	C	P-OP1	5.53	1.60	1.49
59	v	76	ARG	C-N	5.53	1.40	1.33
59	v	119	CYS	C-N	-5.53	1.26	1.33
16	e	75	VAL	C-O	-5.52	1.18	1.24
30	N	1010	A	P-OP2	5.52	1.59	1.49
30	N	2248	C	P-OP2	5.52	1.59	1.49
30	N	2332	C	O3'-P	-5.52	1.52	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	5	62	MET	C-N	-5.51	1.27	1.33
59	v	77	PRO	N-CD	5.51	1.55	1.47
30	N	2829	A	O3'-P	-5.51	1.52	1.61
8	W	110	PRO	CA-C	-5.51	1.45	1.52
59	v	94	PRO	N-CD	5.51	1.55	1.47
30	N	1949	G	O3'-P	-5.50	1.52	1.61
39	3	123	ILE	C-O	-5.49	1.18	1.24
47	B	113	ALA	CA-C	-5.49	1.46	1.53
3	Q	126	ASN	N-CA	5.48	1.54	1.46
30	N	2436	G	O3'-P	-5.47	1.52	1.61
30	N	688	U	O3'-P	-5.47	1.52	1.61
3	Q	109	VAL	C-O	-5.46	1.18	1.24
30	N	784	G	O3'-P	5.46	1.69	1.61
9	X	114	LYS	C-O	-5.46	1.17	1.24
16	e	72	VAL	C-O	-5.46	1.18	1.24
36	0	765	G	O3'-P	-5.46	1.52	1.61
2	P	239	ASN	CA-C	5.45	1.60	1.52
38	2	166	GLU	C-O	-5.45	1.17	1.24
30	N	1671	U	P-OP2	5.45	1.59	1.49
15	d	32	TYR	C-N	-5.44	1.25	1.33
27	p	34	ARG	C-O	-5.43	1.17	1.24
30	N	2051	A	O3'-P	5.43	1.69	1.61
59	v	104	THR	C-N	-5.42	1.26	1.33
30	N	2516	A	O3'-P	-5.42	1.53	1.61
30	N	1186	G	P-OP2	5.42	1.59	1.49
10	Y	35	HIS	CA-C	-5.42	1.46	1.53
16	e	12	HIS	C-O	5.41	1.30	1.23
2	P	198	ALA	C-O	5.40	1.30	1.24
30	N	2243	U	P-OP1	5.40	1.59	1.49
3	Q	126	ASN	C-O	-5.38	1.16	1.23
56	s	40	LYS	CA-C	5.38	1.59	1.52
30	N	1255	U	O5'-C5'	-5.37	1.34	1.42
30	N	239	C	O3'-P	-5.36	1.53	1.61
2	P	155	ALA	CA-C	-5.36	1.47	1.53
30	N	503	A	C6-N1	-5.35	1.24	1.35
30	N	419	U	O3'-P	-5.35	1.53	1.61
30	N	1394	U	O3'-P	-5.35	1.53	1.61
21	j	15	ASP	N-CA	-5.35	1.39	1.45
30	N	2554	U	P-OP2	-5.34	1.38	1.49
30	N	1026	G	P-OP2	-5.34	1.38	1.49
30	N	1327	A	P-OP2	5.33	1.59	1.49
30	N	923	G	O3'-P	-5.32	1.53	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	N	2048	G	O3'-P	-5.32	1.53	1.61
4	R	81	GLY	N-CA	-5.32	1.37	1.45
21	j	72	LYS	C-O	5.31	1.30	1.23
30	N	1782	U	O3'-P	-5.31	1.53	1.61
10	Y	101	ILE	N-CA	-5.31	1.40	1.46
30	N	120	U	P-OP2	5.31	1.59	1.49
30	N	117	G	O3'-P	-5.30	1.53	1.61
30	N	1234	U	O3'-P	-5.30	1.53	1.61
8	W	76	HIS	C-O	-5.30	1.17	1.23
30	N	2260	C	O3'-P	-5.30	1.53	1.61
2	P	156	ARG	CD-NE	-5.30	1.38	1.46
3	Q	149	ASN	CA-CB	-5.30	1.44	1.53
30	N	2694	G	O3'-P	-5.29	1.53	1.61
2	P	54	ILE	N-CA	5.29	1.52	1.46
30	N	2045	C	O3'-P	-5.29	1.53	1.61
35	x	472	U	C1'-N1	5.29	1.56	1.48
30	N	698	C	O3'-P	-5.28	1.53	1.61
30	N	2452	C	O3'-P	-5.28	1.53	1.61
30	N	411	G	P-OP1	5.28	1.59	1.49
30	N	1977	A	O3'-P	-5.28	1.53	1.61
30	N	2285	C	O3'-P	-5.28	1.53	1.61
30	N	1432	G	O3'-P	-5.27	1.53	1.61
27	p	42	LEU	N-CA	-5.27	1.41	1.46
4	R	45	ALA	N-CA	-5.26	1.40	1.46
30	N	1960	A	O3'-P	-5.26	1.53	1.61
9	X	35	VAL	C-O	5.25	1.29	1.24
15	d	49	ASP	CB-CG	5.25	1.65	1.52
30	N	2074	U	O3'-P	-5.25	1.53	1.61
36	0	572	A	P-OP1	5.25	1.59	1.49
2	P	195	VAL	CB-CG1	-5.24	1.35	1.52
10	Y	62	PRO	N-CA	-5.24	1.41	1.46
15	d	21	ALA	C-O	-5.22	1.16	1.23
2	P	239	ASN	N-CA	-5.22	1.39	1.46
3	Q	12	THR	CA-CB	5.22	1.61	1.54
30	N	946	C	P-OP2	5.22	1.59	1.49
30	N	2732	G	C3'-O3'	5.22	1.50	1.42
30	N	1342	A	P-OP2	5.22	1.59	1.49
14	c	92	VAL	CA-C	-5.22	1.46	1.52
16	e	54	VAL	C-O	5.22	1.29	1.24
17	f	96	ILE	N-CA	-5.22	1.39	1.46
16	e	43	ASN	CA-C	5.21	1.56	1.52
26	o	21	TYR	CE2-CZ	-5.21	1.25	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	N	2028	U	O3'-P	-5.21	1.53	1.61
12	a	8	ARG	NE-CZ	-5.21	1.27	1.33
30	N	1649	G	O3'-P	-5.21	1.53	1.61
30	N	2426	A	O3'-P	-5.21	1.53	1.61
30	N	2723	C	O3'-P	-5.21	1.53	1.61
30	N	2682	A	P-OP2	5.20	1.59	1.49
30	N	2727	A	O3'-P	-5.20	1.53	1.61
2	P	195	VAL	C-O	-5.20	1.17	1.24
30	N	2289	G	O3'-P	-5.20	1.53	1.61
30	N	2699	C	O3'-P	-5.20	1.53	1.61
30	N	1680	U	O3'-P	-5.19	1.53	1.61
30	N	1191	G	O3'-P	-5.18	1.53	1.61
30	N	1677	A	O3'-P	-5.18	1.53	1.61
36	0	1182	G	O3'-P	5.18	1.69	1.61
37	1	18	HIS	C-O	-5.18	1.20	1.24
56	s	35	ARG	CA-C	-5.18	1.46	1.52
30	N	1141	U	N3-C4	-5.17	1.28	1.38
30	N	1153	C	P-OP2	5.17	1.59	1.49
38	2	152	GLU	CA-C	-5.17	1.47	1.53
3	Q	150	GLN	N-CA	5.17	1.52	1.46
30	N	1968	G	P-OP1	5.17	1.59	1.49
3	Q	170	VAL	CA-C	-5.17	1.46	1.52
36	0	19	A	O3'-P	-5.17	1.53	1.61
30	N	960	A	O3'-P	-5.16	1.53	1.61
56	s	34	ARG	CA-C	5.16	1.59	1.52
4	R	52	VAL	C-O	-5.15	1.18	1.24
30	N	193	U	O3'-P	-5.15	1.53	1.61
30	N	2262	U	O3'-P	-5.14	1.53	1.61
2	P	213	TRP	CD1-NE1	5.13	1.48	1.37
51	G	34	GLU	CA-C	-5.13	1.46	1.52
30	N	1652	A	O3'-P	-5.12	1.53	1.61
36	0	559	A	N1-C2	5.12	1.44	1.34
30	N	234	U	N3-C4	-5.12	1.28	1.38
30	N	1334	G	O3'-P	-5.12	1.53	1.61
59	v	61	GLU	C-N	-5.12	1.25	1.33
2	P	175	ARG	CA-C	-5.12	1.46	1.52
36	0	1110	A	P-OP2	5.11	1.59	1.49
55	K	10	ARG	CD-NE	-5.11	1.39	1.46
30	N	1648	U	P-OP2	5.11	1.59	1.49
48	D	101	ARG	CZ-NH1	5.11	1.40	1.32
30	N	1296	G	O3'-P	-5.11	1.53	1.61
30	N	694	U	O3'-P	-5.11	1.53	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	f	85	ILE	C-O	-5.10	1.18	1.24
30	N	1650	A	O3'-P	-5.10	1.53	1.61
30	N	2503	A	P-OP1	5.10	1.59	1.49
30	N	1186	G	O3'-P	-5.10	1.53	1.61
40	4	50	TYR	CA-C	-5.09	1.46	1.52
30	N	632	A	O3'-P	-5.09	1.53	1.61
43	7	106	THR	CA-C	-5.09	1.46	1.53
21	j	45	PHE	CA-CB	-5.08	1.45	1.53
30	N	1004	U	O3'-P	-5.08	1.53	1.61
30	N	963	U	P-OP2	5.08	1.59	1.49
30	N	2502	G	O3'-P	-5.08	1.53	1.61
10	Y	63	LYS	N-CA	-5.07	1.39	1.46
30	N	1142	A	O3'-P	5.07	1.68	1.61
30	N	745	G	O3'-P	-5.07	1.53	1.61
12	a	10	LEU	CA-C	-5.06	1.46	1.53
30	N	727	A	P-OP1	5.06	1.59	1.49
30	N	208	C	O3'-P	-5.06	1.53	1.61
30	N	1367	A	O3'-P	-5.05	1.53	1.61
30	N	408	G	O3'-P	-5.05	1.53	1.61
36	0	715	A	O3'-P	-5.04	1.53	1.61
30	N	7	G	O3'-P	-5.04	1.53	1.61
30	N	1006	C	O3'-P	-5.04	1.53	1.61
30	N	1187	G	P-OP2	5.04	1.59	1.49
13	b	102	ARG	CZ-NH2	5.03	1.40	1.33
36	0	787	A	O3'-P	-5.03	1.53	1.61
30	N	1676	A	P-OP2	5.03	1.58	1.49
36	0	368	U	N3-C4	-5.02	1.28	1.38
9	X	37	ASP	C-O	-5.01	1.17	1.23
3	Q	131	ASP	C-O	-5.01	1.17	1.23
59	v	49	GLN	C-N	-5.00	1.27	1.33
11	Z	73	ILE	C-O	-5.00	1.18	1.24

All (384) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	M	73	C	O3'-P-O5'	18.16	131.24	104.00
3	Q	151	THR	CA-C-N	12.68	134.18	119.47
3	Q	151	THR	C-N-CA	12.68	134.18	119.47
30	N	1936	A	C4'-C3'-O3'	-11.07	96.39	113.00
30	N	2725	A	C3'-C2'-O2'	-10.59	94.82	110.70
59	v	175	GLU	O-C-N	-10.24	108.97	122.59
30	N	242	G	C4'-C3'-O3'	10.00	124.40	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	x	439	A	C1'-C2'-O2'	-9.79	93.71	108.40
35	x	466	C	C1'-C2'-O2'	-9.78	93.73	108.40
30	N	774	G	C1'-C2'-O2'	-9.41	94.29	108.40
55	K	10	ARG	CB-CG-CD	-9.41	89.66	111.30
30	N	2251	G	C3'-C2'-O2'	9.30	124.65	110.70
30	N	774	G	C4'-C3'-O3'	-9.27	99.09	113.00
36	0	561	U	C4'-C3'-O3'	-9.24	99.15	113.00
30	N	995	C	C4'-C3'-O3'	-8.79	96.21	109.40
30	N	2776	A	C2'-C3'-O3'	8.73	122.59	109.50
30	N	670	A	C2'-C3'-O3'	8.66	122.49	109.50
2	P	204	VAL	N-CA-C	8.60	120.35	112.43
30	N	2732	G	C4'-C3'-O3'	-8.48	100.28	113.00
36	0	1528	U	C1'-C2'-O2'	-8.42	99.16	111.80
30	N	1937	A	C4'-C3'-O3'	-8.40	100.39	113.00
30	N	2060	A	O3'-P-O5'	8.27	116.41	104.00
36	0	1347	G	C4'-C3'-O3'	8.24	121.76	109.40
30	N	1136	G	P-O5'-C5'	-8.24	108.54	120.90
30	N	784	G	C2'-C3'-O3'	8.19	125.98	113.70
59	v	174	VAL	O-C-N	-8.11	114.42	123.18
30	N	1236	G	C4'-C3'-O3'	-8.08	100.88	113.00
36	0	717	U	C4'-C3'-O3'	-8.07	100.89	113.00
30	N	2324	U	C4'-C3'-O3'	-7.99	101.01	113.00
36	0	1345	U	C4'-C3'-O3'	7.97	121.35	109.40
2	P	221	ARG	CG-CD-NE	-7.94	94.52	112.00
30	N	746	U	C4'-C3'-O3'	-7.89	101.16	113.00
2	P	232	HIS	O-C-N	-7.88	113.82	123.04
30	N	1141	U	C2'-C3'-O3'	7.83	121.24	109.50
9	X	94	PRO	N-CA-C	7.73	122.85	110.40
30	N	2266	A	C4'-C3'-O3'	-7.59	98.01	109.40
1	O	44	G	C4'-C3'-O3'	-7.58	101.63	113.00
41	5	90	MET	CA-C-N	7.56	135.98	121.54
41	5	90	MET	C-N-CA	7.56	135.98	121.54
30	N	2406	A	C2'-C3'-O3'	-7.53	102.41	113.70
36	0	115	G	C2'-C3'-O3'	7.47	120.70	109.50
33	U	30	LEU	N-CA-C	7.46	119.11	110.97
9	X	35	VAL	O-C-N	7.42	129.88	121.94
28	q	8	ARG	CD-NE-CZ	-7.40	114.04	124.40
30	N	1142	A	C2'-C3'-O3'	7.39	120.59	109.50
36	0	518	C	C4'-C3'-O3'	7.37	120.45	109.40
4	R	81	GLY	O-C-N	-7.32	113.18	122.70
54	J	5	LEU	CB-CG-CD2	7.29	132.56	110.70
36	0	1278	G	C4'-C3'-O3'	-7.28	102.08	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	b	101	GLY	O-C-N	7.24	125.91	121.85
4	R	81	GLY	CA-C-N	-7.22	107.26	121.41
4	R	81	GLY	C-N-CA	-7.22	107.26	121.41
35	x	469	U	C1'-C2'-O2'	-7.22	100.97	111.80
30	N	2543	G	P-O5'-C5'	-7.21	110.08	120.90
35	x	442	G	C1'-C2'-O2'	-7.21	100.99	111.80
30	N	2497	A	C5'-C4'-C3'	-7.18	104.42	115.20
36	0	752	G	C4'-C3'-O3'	-7.12	102.31	113.00
30	N	2225	A	C2'-C3'-O3'	7.05	120.07	109.50
36	0	878	A	C3'-C2'-O2'	7.04	121.26	110.70
2	P	239	ASN	N-CA-C	7.03	125.78	110.80
30	N	33	C	C4'-C3'-O3'	-7.02	102.47	113.00
30	N	2732	G	C1'-C2'-O2'	-7.02	97.87	108.40
36	0	1362	A	C4'-C3'-O3'	-7.02	102.47	113.00
30	N	227	A	C4'-C3'-O3'	-7.00	102.50	113.00
27	p	39	ARG	NE-CZ-NH2	-6.98	112.92	119.20
46	A	126	LYS	N-CA-C	6.97	120.66	109.79
40	4	111	MET	CG-SD-CE	-6.96	85.59	100.90
21	j	14	ARG	CG-CD-NE	-6.95	96.71	112.00
30	N	1648	U	P-O5'-C5'	-6.95	110.48	120.90
30	N	1993	U	C3'-C2'-O2'	-6.94	100.29	110.70
36	0	1279	G	N9-C1'-C2'	6.90	122.36	112.00
3	Q	13	ARG	NE-CZ-NH2	6.90	125.41	119.20
2	P	157	SER	N-CA-C	-6.89	100.59	110.59
30	N	1865	U	C4'-C3'-O3'	-6.85	102.72	113.00
30	N	1666	G	C3'-C2'-O2'	6.84	120.96	110.70
34	M	73	C	OP1-P-O3'	-6.84	87.49	108.00
27	p	39	ARG	NE-CZ-NH1	6.83	128.33	121.50
15	d	6	ARG	NE-CZ-NH2	6.81	125.33	119.20
15	d	22	LYS	N-CA-C	-6.80	100.42	110.48
30	N	989	G	C4'-C3'-O3'	-6.78	102.84	113.00
30	N	995	C	C2'-C3'-O3'	6.75	119.63	109.50
36	0	1190	G	C1'-C2'-O2'	-6.75	101.68	111.80
30	N	974	G	N9-C1'-C2'	6.73	124.09	114.00
30	N	2061	G	C4'-C3'-O3'	-6.73	102.91	113.00
4	R	65	THR	O-C-N	-6.72	114.54	122.81
2	P	241	GLY	N-CA-C	6.72	124.62	114.61
30	N	2238	G	C2'-C3'-O3'	6.71	119.56	109.50
42	6	109	ARG	CG-CD-NE	-6.70	97.25	112.00
27	p	34	ARG	NE-CZ-NH1	-6.70	114.80	121.50
30	N	2832	U	C4'-C3'-O3'	-6.68	102.98	113.00
30	N	1313	U	N1-C1'-C2'	6.68	122.02	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	c	93	ARG	CG-CD-NE	-6.64	97.40	112.00
36	0	1190	G	C4'-C3'-O3'	-6.59	99.52	109.40
30	N	1666	G	O4'-C4'-C3'	-6.57	97.44	104.00
1	O	108	A	C2'-C3'-O3'	-6.55	103.87	113.70
30	N	2509	G	C3'-C2'-O2'	6.55	120.52	110.70
30	N	421	C	C2'-C3'-O3'	6.54	119.32	109.50
44	8	18	ARG	CB-CG-CD	-6.54	96.25	111.30
36	0	388	G	C2'-C3'-O3'	6.54	119.31	109.50
30	N	2071	A	C3'-C2'-O2'	6.53	120.50	110.70
35	x	475	G	C2'-C3'-O3'	6.53	119.30	109.50
13	b	102	ARG	NE-CZ-NH2	6.53	125.07	119.20
36	0	665	A	C2'-C3'-O3'	-6.52	103.92	113.70
36	0	1145	A	C4'-C3'-O3'	-6.50	103.25	113.00
55	K	69	LYS	N-CA-C	6.47	124.58	110.80
36	0	1301	U	N1-C1'-C2'	6.46	121.69	112.00
10	Y	30	THR	N-CA-CB	6.45	121.39	110.49
30	N	1452	G	C4'-C3'-O3'	-6.44	103.34	113.00
36	0	1151	A	C4'-C3'-O3'	-6.43	103.36	113.00
10	Y	47	ARG	NE-CZ-NH2	6.39	124.95	119.20
10	Y	68	SER	N-CA-C	6.39	118.33	111.36
36	0	1491	G	C2'-C3'-O3'	-6.39	104.12	113.70
36	0	818	G	C4'-C3'-O3'	-6.39	103.42	113.00
30	N	1212	G	C4'-C3'-O3'	-6.37	103.44	113.00
2	P	11	PRO	CB-CA-C	-6.34	103.28	111.39
14	c	73	VAL	N-CA-CB	6.34	117.63	110.72
40	4	127	ALA	N-CA-C	6.33	119.55	110.24
30	N	2443	C	O4'-C4'-C3'	-6.32	97.68	104.00
25	n	25	VAL	CA-C-N	6.32	133.07	121.70
25	n	25	VAL	C-N-CA	6.32	133.07	121.70
53	I	57	ARG	CA-CB-CG	6.30	126.71	114.10
30	N	404	A	C4'-C3'-O3'	6.27	118.81	109.40
38	2	167	TRP	N-CA-C	6.26	119.74	110.48
51	G	43	ALA	CA-C-N	6.26	133.50	121.54
51	G	43	ALA	C-N-CA	6.26	133.50	121.54
22	k	57	ARG	NE-CZ-NH2	6.25	124.83	119.20
36	0	1213	A	C4'-C3'-O3'	-6.25	103.62	113.00
1	O	44	G	N9-C1'-C2'	6.24	121.36	112.00
21	j	41	ARG	CD-NE-CZ	6.23	133.12	124.40
30	N	2364	C	O4'-C4'-C3'	-6.23	97.77	104.00
30	N	859	G	C1'-C2'-O2'	-6.21	102.48	111.80
30	N	2728	U	C2'-C3'-O3'	-6.21	104.39	113.70
33	U	67	ALA	N-CA-C	-6.20	105.20	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	N	2501	C	C4'-C3'-O3'	-6.15	103.77	113.00
30	N	446	G	C2'-C3'-O3'	6.13	118.70	109.50
36	0	1201	A	C2'-C3'-O3'	6.12	118.68	109.50
30	N	2728	U	C4'-C3'-O3'	-6.10	103.85	113.00
21	j	41	ARG	CB-CG-CD	6.10	125.32	111.30
36	0	818	G	N9-C1'-C2'	6.09	121.14	112.00
35	x	440	A	C1'-C2'-O2'	-6.08	99.28	108.40
35	x	467	A	C1'-C2'-O2'	-6.07	99.29	108.40
30	N	1352	U	O4'-C1'-C2'	-6.06	101.54	107.60
47	B	44	LYS	N-CA-C	6.05	120.46	112.35
27	p	12	ARG	CA-CB-CG	6.04	126.18	114.10
10	Y	78	ARG	NE-CZ-NH2	6.04	124.64	119.20
2	P	221	ARG	N-CA-CB	6.03	120.11	110.46
40	4	138	ARG	N-CA-CB	6.03	120.68	110.49
47	B	22	PRO	O-C-N	-6.03	114.50	122.64
30	N	2725	A	C1'-C2'-O2'	-6.01	99.38	108.40
46	A	124	PRO	CA-C-N	6.01	128.94	120.28
46	A	124	PRO	C-N-CA	6.01	128.94	120.28
51	G	44	SER	N-CA-C	-6.01	98.00	110.80
30	N	827	U	C2'-C3'-O3'	-6.00	104.70	113.70
30	N	2319	G	C4'-C3'-O3'	-6.00	104.00	113.00
12	a	70	THR	N-CA-C	5.98	123.54	110.80
36	0	64	G	C2'-C3'-O3'	-5.98	104.73	113.70
30	N	2246	G	O4'-C4'-C3'	-5.96	98.04	104.00
30	N	2034	U	C4'-C3'-O3'	-5.95	104.07	113.00
30	N	1567	G	C1'-C2'-O2'	-5.95	102.88	111.80
29	r	36	ARG	NE-CZ-NH1	-5.92	115.58	121.50
21	j	19	LYS	N-CA-C	5.92	120.50	113.16
24	m	32	ILE	N-CA-CB	5.92	116.98	110.53
12	a	69	ARG	NE-CZ-NH2	5.92	124.52	119.20
30	N	974	G	C4'-C3'-O3'	-5.91	100.54	109.40
30	N	1626	A	C2'-C3'-O3'	-5.88	104.88	113.70
30	N	2035	G	C4'-C3'-O3'	-5.88	100.58	109.40
30	N	2543	G	C5'-C4'-C3'	-5.88	107.18	116.00
30	N	1254	A	C4'-C3'-O3'	-5.87	104.19	113.00
30	N	782	A	C4'-C3'-O3'	-5.86	100.61	109.40
30	N	2518	A	C1'-C2'-O2'	-5.86	103.01	111.80
30	N	871	U	P-O5'-C5'	-5.86	112.11	120.90
21	j	41	ARG	N-CA-C	5.86	120.72	112.93
30	N	820	A	O4'-C4'-C3'	-5.85	98.15	104.00
30	N	2468	A	C4'-C3'-O3'	-5.85	104.22	113.00
3	Q	113	SER	N-CA-C	5.82	117.57	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	N	301	G	C4'-C3'-O3'	-5.82	104.27	113.00
2	P	258	ARG	NE-CZ-NH1	-5.82	115.69	121.50
3	Q	151	THR	O-C-N	-5.81	114.92	121.43
25	n	25	VAL	N-CA-C	5.81	116.46	110.82
36	0	330	C	P-O5'-C5'	-5.80	112.20	120.90
30	N	140	C	N1-C1'-C2'	5.79	120.68	112.00
2	P	177	ARG	CG-CD-NE	-5.77	99.30	112.00
2	P	238	ARG	N-CA-C	5.77	123.09	110.80
40	4	38	VAL	CG1-CB-CG2	-5.77	98.11	110.80
30	N	974	G	C2'-C3'-O3'	5.77	118.15	109.50
30	N	782	A	C2'-C3'-O3'	5.76	118.14	109.50
30	N	2873	A	P-O5'-C5'	-5.76	112.27	120.90
30	N	2447	G	P-O3'-C3'	5.74	128.81	120.20
15	d	33	ARG	CB-CG-CD	-5.74	98.10	111.30
30	N	1970	A	C2'-C3'-O3'	5.74	118.11	109.50
30	N	512	G	P-O3'-C3'	5.72	128.79	120.20
16	e	79	ARG	CD-NE-CZ	-5.72	116.39	124.40
30	N	2543	G	O5'-C5'-C4'	5.72	120.08	111.50
2	P	31	ALA	CA-C-N	-5.72	115.00	120.83
2	P	31	ALA	C-N-CA	-5.72	115.00	120.83
30	N	2049	G	C3'-C2'-O2'	5.71	119.26	110.70
15	d	13	ARG	NE-CZ-NH2	5.70	124.33	119.20
30	N	2035	G	C1'-C2'-O2'	-5.70	103.25	111.80
30	N	2267	A	N9-C1'-C2'	5.70	120.54	112.00
2	P	156	ARG	CB-CG-CD	-5.69	98.22	111.30
30	N	555	G	C4'-C3'-O3'	-5.68	104.47	113.00
13	b	100	HIS	CA-C-N	-5.67	115.44	123.95
13	b	100	HIS	C-N-CA	-5.67	115.44	123.95
13	b	102	ARG	NE-CZ-NH1	-5.67	115.83	121.50
36	0	971	G	C2'-C3'-O3'	-5.66	105.21	113.70
25	n	7	LYS	CD-CE-NZ	5.65	129.98	111.90
30	N	2776	A	C8-N9-C1'	-5.65	110.75	127.70
36	0	96	U	C2'-C3'-O3'	5.65	122.17	113.70
44	8	126	GLN	CA-C-O	-5.64	114.84	121.16
1	O	88	C	C4'-C3'-O3'	-5.64	104.54	113.00
14	c	53	ARG	CB-CG-CD	-5.64	98.33	111.30
30	N	301	G	N9-C1'-C2'	5.64	120.46	112.00
40	4	24	THR	N-CA-C	5.63	117.50	110.91
36	0	1280	A	C4'-C3'-O3'	-5.62	104.57	113.00
38	2	3	GLN	N-CA-C	5.62	122.08	113.19
38	2	6	HIS	N-CA-C	-5.62	102.56	109.65
30	N	1900	A	P-O3'-C3'	5.60	128.60	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	N	2776	A	C4'-N9-C1'	5.60	143.10	126.30
30	N	1661	G	C3'-C2'-O2'	5.60	119.10	110.70
1	O	24	G	C2'-C3'-O3'	-5.60	105.31	113.70
36	0	1432	G	C4'-C3'-O3'	-5.60	104.61	113.00
36	0	1196	A	C4'-C3'-O3'	-5.59	104.61	113.00
12	a	69	ARG	CG-CD-NE	5.59	124.29	112.00
33	U	5	LEU	N-CA-C	5.59	118.79	110.52
30	N	2019	A	C3'-C2'-O2'	5.59	119.08	110.70
30	N	1261	C	O4'-C4'-C3'	-5.58	98.42	104.00
30	N	2034	U	O3'-P-O5'	-5.58	95.63	104.00
25	n	55	ILE	N-CA-C	5.58	120.94	109.34
30	N	1205	A	C4'-C3'-O3'	5.57	117.76	109.40
30	N	2517	C	O3'-P-O5'	-5.55	95.68	104.00
28	q	8	ARG	CG-CD-NE	5.55	124.20	112.00
30	N	727	A	N9-C1'-C2'	5.55	120.32	112.00
30	N	752	A	N9-C1'-C2'	5.54	122.31	114.00
59	v	68	THR	CA-C-N	-5.54	115.40	122.77
59	v	68	THR	C-N-CA	-5.54	115.40	122.77
30	N	1565	C	C5'-C4'-C3'	-5.54	106.89	115.20
30	N	784	G	P-O3'-C3'	5.54	128.51	120.20
30	N	1565	C	C2'-C3'-O3'	5.54	117.81	109.50
36	0	686	U	C4'-C3'-O3'	-5.54	104.70	113.00
36	0	665	A	C3'-C2'-O2'	5.53	119.00	110.70
30	N	2751	G	C2'-C3'-O3'	-5.52	105.42	113.70
30	N	2645	G	C5'-C4'-C3'	-5.51	106.93	115.20
37	1	17	GLY	CA-C-O	-5.50	117.83	122.29
41	5	63	ASN	N-CA-C	5.50	117.34	110.91
30	N	372	G	C1'-C2'-O2'	-5.49	103.57	111.80
30	N	2645	G	P-O5'-C5'	-5.49	112.67	120.90
30	N	2724	U	C2'-C3'-O3'	-5.49	105.47	113.70
30	N	645	C	N1-C1'-C2'	5.48	120.22	112.00
30	N	1428	C	C2'-C3'-O3'	-5.48	105.48	113.70
14	c	21	ARG	NE-CZ-NH1	-5.47	116.03	121.50
59	v	174	VAL	CA-C-N	5.47	131.98	121.54
59	v	174	VAL	C-N-CA	5.47	131.98	121.54
3	Q	160	LYS	CG-CD-CE	5.46	123.87	111.30
30	N	947	A	C3'-C2'-O2'	-5.46	102.51	110.70
36	0	1125	U	N1-C1'-C2'	5.46	120.19	112.00
30	N	1012	U	C2'-C3'-O3'	-5.45	105.53	113.70
36	0	813	U	C4'-C3'-O3'	-5.44	104.84	113.00
30	N	962	G	C3'-C2'-O2'	5.43	118.85	110.70
30	N	983	A	C5'-C4'-O4'	-5.42	101.67	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	n	7	LYS	CG-CD-CE	-5.41	98.86	111.30
30	N	923	G	C3'-C2'-O2'	5.41	118.81	110.70
40	4	157	ARG	NE-CZ-NH1	-5.41	116.09	121.50
52	H	71	LYS	N-CA-C	5.40	122.30	110.80
29	r	1	MET	CB-CG-SD	-5.39	96.52	112.70
36	0	563	A	N9-C1'-C2'	5.39	120.08	112.00
30	N	2820	A	C4'-C3'-O3'	-5.39	104.92	113.00
30	N	2038	G	C3'-C2'-O2'	5.39	118.78	110.70
30	N	51	G	C4'-C3'-O3'	-5.38	104.93	113.00
30	N	1819	A	C1'-C2'-O2'	-5.37	103.75	111.80
30	N	1937	A	N9-C1'-C2'	5.37	120.05	112.00
35	x	469	U	O4'-C1'-C2'	-5.37	100.43	105.80
35	x	442	G	O4'-C1'-C2'	-5.36	100.44	105.80
36	0	1211	U	C2'-C3'-O3'	-5.36	105.67	113.70
21	j	41	ARG	NH1-CZ-NH2	-5.34	112.36	119.30
30	N	783	A	O4'-C1'-C2'	-5.34	102.26	107.60
36	0	5	U	C2'-C3'-O3'	-5.34	105.69	113.70
30	N	2497	A	C2'-C3'-O3'	5.34	117.51	109.50
30	N	2552	U	C3'-C2'-O2'	5.34	118.71	110.70
30	N	2645	G	C2'-C3'-O3'	5.34	117.51	109.50
30	N	1620	G	C3'-C2'-O2'	5.33	118.70	110.70
10	Y	29	LYS	CD-CE-NZ	-5.32	94.87	111.90
36	0	388	G	O3'-P-O5'	-5.32	96.02	104.00
30	N	2354	C	C5'-C4'-C3'	-5.32	108.03	116.00
10	Y	18	ARG	NE-CZ-NH2	-5.31	114.42	119.20
45	9	42	LEU	CA-C-N	5.29	126.46	119.84
45	9	42	LEU	C-N-CA	5.29	126.46	119.84
30	N	1977	A	C2'-C3'-O3'	-5.29	105.77	113.70
30	N	1770	G	C3'-C2'-O2'	5.29	118.63	110.70
11	Z	118	LYS	CB-CG-CD	-5.28	99.15	111.30
36	0	1094	G	C4'-C3'-O3'	-5.28	105.09	113.00
30	N	1650	A	C3'-C2'-O2'	5.27	118.61	110.70
22	k	28	ARG	NE-CZ-NH2	-5.27	114.45	119.20
27	p	12	ARG	CB-CG-CD	-5.27	99.17	111.30
30	N	2498	C	C3'-C2'-O2'	5.26	118.59	110.70
30	N	669	G	N9-C1'-C2'	5.26	119.89	112.00
3	Q	114	LYS	CA-CB-CG	5.26	124.61	114.10
30	N	1236	G	P-O3'-C3'	5.26	128.09	120.20
30	N	2092	U	P-O5'-C5'	-5.26	113.02	120.90
30	N	2849	U	P-O5'-C5'	5.24	128.77	120.90
50	F	64	ARG	CG-CD-NE	-5.24	100.46	112.00
30	N	2474	U	N1-C1'-C2'	5.24	119.86	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	N	785	G	P-O5'-C5'	-5.24	113.05	120.90
30	N	2394	C	O4'-C4'-C3'	-5.23	98.77	104.00
4	R	49	ARG	NE-CZ-NH1	-5.23	116.27	121.50
30	N	310	A	C1'-C2'-O2'	-5.23	100.56	108.40
30	N	2502	G	C3'-C2'-O2'	-5.23	102.86	110.70
35	x	439	A	C3'-C2'-O2'	-5.23	102.86	110.70
35	x	466	C	C3'-C2'-O2'	-5.23	102.86	110.70
39	3	5	LEU	CB-CA-C	-5.23	104.48	112.11
30	N	2497	A	C4'-C3'-O3'	-5.22	101.57	109.40
9	X	29	HIS	CB-CA-C	-5.21	103.47	111.66
30	N	2867	G	C4'-C3'-O3'	5.21	117.22	109.40
30	N	2430	A	C3'-C2'-O2'	5.20	118.50	110.70
30	N	1343	G	N9-C1'-C2'	5.20	119.80	112.00
30	N	2638	G	C4'-C3'-O3'	-5.20	105.20	113.00
2	P	226	ASN	CA-C-N	-5.20	114.31	119.56
2	P	226	ASN	C-N-CA	-5.20	114.31	119.56
30	N	421	C	C4'-C3'-O3'	5.20	117.19	109.40
36	0	652	U	C2'-C3'-O3'	-5.20	105.91	113.70
36	0	1303	C	N1-C1'-C2'	5.19	119.78	112.00
30	N	2596	U	C2'-C3'-O3'	-5.19	105.92	113.70
30	N	278	A	N9-C1'-C2'	5.18	119.78	112.00
30	N	2311	A	P-O3'-C3'	5.18	127.97	120.20
30	N	2580	U	N1-C1'-C2'	5.18	119.77	112.00
30	N	372	G	C2'-C3'-O3'	5.18	117.27	109.50
36	0	812	G	C1'-C2'-O2'	-5.18	100.63	108.40
3	Q	12	THR	N-CA-C	-5.17	101.52	108.19
12	a	69	ARG	N-CA-C	-5.17	103.21	110.50
36	0	1530	G	C4'-C3'-O3'	-5.17	105.25	113.00
1	O	41	G	C4'-C3'-O3'	-5.16	105.25	113.00
2	P	156	ARG	CG-CD-NE	5.16	123.36	112.00
30	N	27	G	C5'-C4'-O4'	-5.16	102.07	109.80
30	N	2621	G	C3'-C2'-O2'	5.15	118.43	110.70
32	C	55	SER	N-CA-C	5.15	116.90	111.28
30	N	2049	G	O4'-C4'-C3'	-5.15	98.85	104.00
56	s	33	ARG	CA-CB-CG	5.14	124.39	114.10
33	U	96	THR	N-CA-C	-5.14	106.86	113.23
30	N	1676	A	C3'-C2'-O2'	5.13	118.40	110.70
30	N	2035	G	C2'-C3'-O3'	5.13	117.20	109.50
3	Q	128	ARG	CA-C-N	5.13	128.00	120.71
3	Q	128	ARG	C-N-CA	5.13	128.00	120.71
17	f	11	ARG	N-CA-CB	5.13	117.97	110.58
15	d	3	ARG	NE-CZ-NH1	-5.13	116.37	121.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	N	2019	A	C2'-C3'-O3'	-5.13	106.01	113.70
1	O	100	G	C3'-C2'-O2'	5.12	118.39	110.70
30	N	1180	U	N1-C1'-C2'	5.12	119.68	112.00
47	B	12	ARG	NE-CZ-NH1	-5.11	116.39	121.50
30	N	481	G	C2'-C3'-O3'	-5.11	106.04	113.70
30	N	1998	A	O4'-C4'-C3'	-5.11	98.89	104.00
30	N	2238	G	C4'-C3'-O3'	-5.11	101.74	109.40
9	X	35	VAL	CA-C-O	-5.10	115.27	121.18
30	N	2062	A	O4'-C4'-C3'	-5.10	101.00	106.10
29	r	36	ARG	CG-CD-NE	-5.10	100.78	112.00
51	G	42	ILE	CA-C-N	5.10	131.28	121.54
51	G	42	ILE	C-N-CA	5.10	131.28	121.54
30	N	1997	C	O4'-C4'-C3'	-5.10	98.90	104.00
10	Y	41	ARG	CA-CB-CG	-5.09	103.92	114.10
30	N	1928	A	C3'-C2'-O2'	5.09	118.34	110.70
30	N	2732	G	C3'-C2'-O2'	-5.08	103.08	110.70
30	N	566	U	C2'-C3'-O3'	-5.08	106.08	113.70
30	N	2502	G	P-O5'-C5'	5.08	128.52	120.90
34	M	9	C	C2'-C3'-O3'	-5.07	106.09	113.70
30	N	123	G	C3'-C2'-O2'	5.07	118.31	110.70
30	N	1131	G	O3'-P-O5'	-5.07	96.40	104.00
39	3	23	SER	O-C-N	5.06	127.98	122.11
15	d	32	TYR	CA-C-O	5.06	125.82	120.10
30	N	820	A	O4'-C1'-C2'	-5.05	102.55	107.60
36	0	971	G	P-O5'-C5'	-5.05	113.32	120.90
30	N	1253	A	C2'-C3'-O3'	5.05	117.08	109.50
59	v	70	GLY	O-C-N	5.05	126.82	121.77
30	N	2049	G	C2'-C3'-O3'	-5.05	106.13	113.70
36	0	812	G	P-O3'-C3'	5.04	127.76	120.20
37	1	103	ASN	N-CA-CB	5.04	119.93	110.56
23	l	52	ARG	NE-CZ-NH1	-5.03	116.47	121.50
40	4	30	ILE	CB-CA-C	5.03	117.67	110.33
11	Z	8	LYS	CB-CG-CD	-5.03	99.74	111.30
12	a	1	MET	CB-CG-SD	-5.03	97.63	112.70
15	d	32	TYR	N-CA-C	5.03	117.49	111.71
36	0	532	A	C2'-C3'-O3'	-5.02	106.17	113.70
30	N	995	C	C1'-C2'-O2'	-5.02	104.27	111.80
36	0	595	A	C4'-C3'-O3'	5.02	116.93	109.40
30	N	750	A	C2'-C3'-O3'	-5.01	106.19	113.70
46	A	121	CYS	N-CA-C	5.01	117.16	110.35
36	0	801	U	C2'-C3'-O3'	-5.01	106.19	113.70

There are no chirality outliers.

All (50) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	0	24	U	Sidechain
36	0	368	U	Sidechain
36	0	559	A	Sidechain
36	0	571	U	Sidechain
36	0	864	A	Sidechain
37	1	102	THR	Peptide
37	1	14	VAL	Peptide
38	2	79	LYS	Peptide
38	2	80	LYS	Peptide
40	4	102	GLY	Peptide
40	4	136	VAL	Peptide
40	4	137	VAL	Peptide
40	4	142	ASP	Peptide
40	4	89	HIS	Peptide
41	5	52	ASN	Peptide
41	5	93	LYS	Peptide
44	8	128	SER	Peptide
44	8	53	GLU	Peptide
44	8	54	LEU	Peptide
44	8	55	VAL	Peptide
46	A	125	LYS	Peptide
47	B	22	PRO	Peptide
47	B	77	HIS	Peptide
52	H	17	MET	Peptide
52	H	69	LYS	Peptide
54	J	37	ARG	Peptide
55	K	3	ASN	Peptide
30	N	1802	A	Sidechain
30	N	2522	U	Sidechain
30	N	2765	A	Sidechain
30	N	586	A	Sidechain
30	N	850	U	Sidechain
30	N	927	A	Sidechain
2	P	195	VAL	Peptide
2	P	234	GLY	Peptide
2	P	238	ARG	Peptide
3	Q	151	THR	Peptide
5	S	174	ASP	Peptide
5	S	175	PHE	Peptide
7	V	11	LEU	Peptide
10	Y	114	GLY	Peptide
10	Y	82	LEU	Peptide

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Mol	Chain	Res	Type	Group
11	Z	57	VAL	Mainchain,Peptide
19	h	52	LEU	Peptide
28	q	31	HIS	Peptide
56	s	34	ARG	Peptide
59	v	174	VAL	Mainchain
59	v	175	GLU	Mainchain
59	v	22	THR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O	2529	0	1281	16	0
2	P	2082	0	2154	59	0
3	Q	1564	0	1616	23	0
4	R	1552	0	1619	19	0
5	S	1397	0	1433	27	0
6	T	1322	0	1371	13	0
7	V	1031	0	1085	21	0
8	W	1128	0	1162	16	0
9	X	938	0	1012	20	0
10	Y	1044	0	1117	17	0
11	Z	1073	0	1157	17	0
12	a	960	0	1000	15	0
13	b	891	0	923	11	0
14	c	915	0	958	14	0
15	d	946	0	1019	21	0
16	e	815	0	839	17	0
17	f	857	0	922	9	0
18	g	738	0	807	5	0
19	h	779	0	831	11	0
20	i	752	0	780	10	0
21	j	568	0	581	11	0
22	k	624	0	652	14	0
23	l	508	0	543	8	0
24	m	448	0	488	3	0
25	n	443	0	458	13	0
26	o	409	0	440	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	p	376	0	418	18	0
28	q	503	0	572	12	0
29	r	301	0	341	7	0
30	N	62215	0	31274	417	0
31	L	415	0	415	11	0
32	C	1027	0	1091	41	0
33	U	1111	0	1148	53	0
34	M	1594	0	809	108	0
35	x	928	0	468	98	0
36	0	33015	0	16607	257	0
37	1	1699	0	1722	65	0
38	2	1624	0	1696	50	0
39	3	1642	0	1704	30	0
40	4	1105	0	1148	24	0
41	5	817	0	808	16	0
42	6	1181	0	1238	18	0
43	7	978	0	1031	6	0
44	8	1021	0	1070	36	0
45	9	786	0	828	20	0
46	A	876	0	887	20	0
47	B	954	0	1016	16	0
48	D	877	0	930	20	0
49	E	773	0	824	11	0
50	F	709	0	728	14	0
51	G	648	0	666	11	0
52	H	648	0	691	6	0
53	I	455	0	478	13	0
54	J	637	0	665	11	0
55	K	664	0	714	14	0
56	s	425	0	449	12	0
57	t	704	0	328	3	0
58	u	1561	0	785	61	0
59	v	1256	0	1123	65	0
60	u	2	0	0	0	0
61	u	1	0	0	0	0
62	u	9	0	0	0	0
All	All	149850	0	100920	1414	0

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

All (1414) 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)
35:x:448:U:C6	38:2:162:ILE:HD11	1.46	1.49
30:N:306:U:H3	30:N:310:A:N6	1.15	1.40
35:x:451:G:N3	39:3:47:ARG:HD3	1.35	1.40
2:P:133:ARG:CD	33:U:123:ARG:NH1	1.86	1.38
36:0:1238:A:N6	36:0:1301:U:H3	1.22	1.37
35:x:448:U:C5	38:2:162:ILE:HD11	1.60	1.35
36:0:1160:G:OP1	37:1:132:LYS:NZ	1.60	1.34
2:P:133:ARG:HD3	33:U:123:ARG:NH1	1.41	1.32
37:1:32:PHE:HE2	59:v:23:ARG:O	0.98	1.32
34:M:31:U:H5'	36:0:1340:A:O2'	1.29	1.31
36:0:1493:A:N1	58:u:37:A:O2'	1.66	1.28
30:N:2251:G:O6	34:M:75:A:N1	1.63	1.28
37:1:32:PHE:CE2	59:v:23:ARG:O	1.86	1.28
35:x:442:G:O6	58:u:38:A:H1'	1.20	1.26
22:k:60:ASP:OD2	33:U:27:ARG:NH2	1.68	1.26
37:1:32:PHE:CE2	59:v:24:LYS:HA	1.72	1.25
34:M:33:C:OP2	44:8:130:ARG:HG3	1.36	1.24
30:N:2253:G:H1	34:M:73:C:N4	1.33	1.23
30:N:882:G:C4'	58:u:19:G:H22	1.47	1.22
36:0:1493:A:C2	58:u:37:A:O2'	1.80	1.21
37:1:105:LYS:CG	59:v:56:HIS:CE1	2.23	1.21
30:N:882:G:C4'	58:u:19:G:N2	1.94	1.21
30:N:499:U:H3	30:N:503:A:N6	1.39	1.20
34:M:29:G:OP1	36:0:1229:A:O2'	1.60	1.17
34:M:40:C:O2	36:0:1338:G:N2	1.79	1.16
37:1:105:LYS:HG3	59:v:56:HIS:ND1	1.61	1.15
30:N:1924:C:H4'	34:M:13:A:C4'	1.76	1.15
37:1:105:LYS:HG2	59:v:56:HIS:CE1	1.81	1.12
2:P:133:ARG:HD2	33:U:123:ARG:HH11	0.96	1.12
30:N:1924:C:C4'	34:M:13:A:H4'	1.78	1.12
30:N:1924:C:H4'	34:M:13:A:H4'	1.11	1.11
36:0:1103:C:O2'	37:1:106:THR:CG2	1.99	1.11
35:x:448:U:C5	38:2:162:ILE:CD1	2.34	1.10
36:0:1103:C:O2'	37:1:106:THR:HG21	1.52	1.09
30:N:2253:G:N1	34:M:73:C:N4	1.99	1.09
35:x:442:G:O6	58:u:38:A:C1'	2.02	1.08
38:2:143:ARG:O	59:v:63:GLN:NE2	1.85	1.08
35:x:442:G:C6	58:u:38:A:H1'	1.88	1.07
37:1:105:LYS:HG3	59:v:56:HIS:CG	1.66	1.07
30:N:882:G:O4'	58:u:56:C:N3	1.88	1.06
35:x:448:U:C6	38:2:162:ILE:CD1	2.37	1.06
30:N:715:A:C6	50:F:53:ARG:NH1	2.23	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1:105:LYS:HG2	59:v:56:HIS:NE2	1.67	1.05
30:N:306:U:N3	30:N:310:A:N6	1.86	1.04
37:1:105:LYS:CG	59:v:56:HIS:NE2	2.02	1.04
35:x:451:G:N3	39:3:47:ARG:CD	2.19	1.04
37:1:105:LYS:HG3	59:v:56:HIS:CE1	1.90	1.04
30:N:1924:C:H4'	34:M:13:A:C5'	1.87	1.03
30:N:1923:U:H4'	34:M:12:C:H1'	1.41	1.03
34:M:34:U:OP2	44:8:129:LYS:NZ	1.90	1.03
30:N:882:G:O2'	58:u:56:C:O2	1.76	1.02
30:N:882:G:H4'	58:u:19:G:N2	1.24	1.01
37:1:35:ARG:HE	59:v:20:ALA:N	1.59	1.00
35:x:442:G:N2	58:u:37:A:H1'	1.76	1.00
30:N:1924:C:C5'	34:M:13:A:H4'	1.91	1.00
34:M:32:U:C5	44:8:129:LYS:NZ	2.29	0.99
35:x:455:C:H5	59:v:135:LYS:N	1.58	0.99
35:x:455:C:H41	59:v:135:LYS:CB	1.75	0.99
34:M:30:A:H1'	36:0:1339:A:C2	1.97	0.99
35:x:451:G:C2	39:3:47:ARG:HD3	1.98	0.98
2:P:133:ARG:CD	33:U:123:ARG:HH11	1.60	0.97
35:x:450:C:H42	38:2:164:ARG:NH1	1.63	0.97
59:v:76:ARG:NH1	59:v:150:PRO:O	1.98	0.97
34:M:30:A:C1'	36:0:1339:A:C2	2.47	0.97
34:M:33:C:OP2	44:8:130:ARG:CG	2.15	0.94
34:M:15:G:H5''	34:M:15:G:C8	2.02	0.94
34:M:15:G:H5''	34:M:15:G:H8	1.30	0.94
30:N:2251:G:C6	34:M:75:A:N1	2.35	0.93
30:N:897:C:H5'	58:u:56:C:C5'	1.93	0.93
35:x:449:A:H62	38:2:164:ARG:HD3	1.34	0.93
34:M:40:C:O2'	36:0:1338:G:H1'	1.69	0.91
34:M:29:G:OP1	36:0:1229:A:O3'	1.87	0.91
36:0:1493:A:C2	58:u:37:A:H1'	2.04	0.91
34:M:28:G:O3'	36:0:1229:A:H4'	1.71	0.91
35:x:455:C:H5	59:v:135:LYS:H	1.02	0.91
35:x:442:G:H22	58:u:37:A:H1'	1.29	0.90
36:0:1060:U:C5	38:2:2:GLY:HA3	2.07	0.90
2:P:187:ASP:OD1	33:U:123:ARG:NH2	2.06	0.89
35:x:448:U:H5	38:2:162:ILE:CD1	1.82	0.88
35:x:448:U:H6	38:2:162:ILE:HD11	1.11	0.88
35:x:455:C:N4	59:v:135:LYS:CB	2.37	0.87
34:M:30:A:O4'	36:0:1339:A:C2	2.28	0.87
9:X:49:ARG:HH22	36:0:1423:G:P	1.97	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:N:2304:G:H22	30:N:2312:U:H3	1.23	0.87
2:P:121:ASP:CG	33:U:91:PHE:CE1	2.53	0.87
30:N:882:G:C1'	58:u:56:C:C2	2.59	0.86
30:N:715:A:C1'	50:F:40:GLN:HE22	1.90	0.85
34:M:29:G:OP1	36:O:1229:A:C3'	2.24	0.85
30:N:2251:G:N1	34:M:75:A:C2	2.45	0.84
37:1:32:PHE:CZ	59:v:24:LYS:HA	2.11	0.84
30:N:2177:C:O3'	32:C:211:LYS:HE2	1.75	0.84
34:M:40:C:H4'	36:O:1338:G:O2'	1.77	0.84
36:O:1103:C:O2'	37:1:106:THR:HG22	1.77	0.84
5:S:80:ARG:HD3	34:M:55:C:N1	1.87	0.84
35:x:440:A:OP1	36:O:1498:U:O2'	1.96	0.83
2:P:35:GLU:OE2	30:N:1816:C:N4	2.10	0.83
35:x:438:C:H2'	36:O:926:G:N2	1.94	0.83
36:O:1054:C:C4	58:u:34:G:C8	2.67	0.83
2:P:121:ASP:CG	33:U:91:PHE:HE1	1.87	0.83
2:P:133:ARG:HD3	33:U:123:ARG:HH12	1.38	0.83
35:x:442:G:H22	58:u:37:A:C1'	1.80	0.83
36:O:1493:A:N1	58:u:37:A:C2'	2.42	0.82
46:A:109:ASN:OD1	56:s:7:ARG:HG2	1.80	0.82
34:M:31:U:H5''	36:O:1341:U:H5'	1.62	0.82
2:P:133:ARG:HD2	33:U:123:ARG:NH1	1.64	0.82
45:9:83:THR:O	45:9:87:LEU:HB2	1.79	0.81
30:N:499:U:N3	30:N:503:A:N6	2.11	0.81
34:M:15:G:H5'	34:M:16:C:OP2	1.81	0.80
34:M:29:G:OP1	36:O:1229:A:C2'	2.29	0.80
30:N:882:G:O4'	58:u:56:C:C2	2.34	0.80
34:M:31:U:C5'	36:O:1340:A:O2'	2.21	0.80
36:O:1493:A:H2	58:u:37:A:H1'	1.47	0.80
59:v:77:PRO:O	59:v:78:ASP:HB2	1.79	0.79
36:O:1493:A:C2	58:u:37:A:C2'	2.66	0.79
36:O:1493:A:N1	58:u:37:A:C1'	2.46	0.79
36:O:1100:C:OP2	37:1:95:ARG:HD3	1.81	0.79
30:N:2251:G:C6	34:M:75:A:C2	2.71	0.79
30:N:284:U:H3	30:N:356:G:H1	1.31	0.79
34:M:34:U:OP1	44:8:129:LYS:HD3	1.83	0.78
59:v:74:TYR:HB3	59:v:155:PHE:CZ	2.19	0.78
37:1:105:LYS:CG	59:v:56:HIS:CG	2.39	0.78
35:x:449:A:H62	38:2:164:ARG:CD	1.95	0.78
59:v:83:GLU:OE2	59:v:92:TYR:OH	1.98	0.78
12:a:53:THR:HG21	30:N:2840:C:H5''	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:D:101:ARG:NH1	48:D:104:THR:OG1	2.16	0.78
5:S:143:TYR:CB	48:D:7:ILE:HG22	2.13	0.78
30:N:882:G:H1'	58:u:56:C:C2	2.19	0.78
29:r:3:VAL:HG21	30:N:2539:C:H5'	1.67	0.77
33:U:40:THR:HB	33:U:43:ASN:HD22	1.50	0.77
36:0:1238:A:N7	36:0:1301:U:O4	2.18	0.77
36:0:1279:G:OP1	45:9:9:ARG:NH2	2.18	0.77
9:X:49:ARG:NH2	36:0:1423:G:OP1	2.18	0.76
9:X:49:ARG:NH2	36:0:1422:G:O3'	2.19	0.76
5:S:80:ARG:CD	34:M:55:C:C6	2.68	0.76
35:x:442:G:N2	36:0:1493:A:H2	1.84	0.76
36:0:1100:C:OP2	37:1:95:ARG:CD	2.33	0.76
34:M:16:C:H3'	34:M:17:G:H5'	1.68	0.76
30:N:306:U:C2	30:N:310:A:N6	2.54	0.76
35:x:443:C:O2	58:u:36:A:H2	1.69	0.75
2:P:121:ASP:OD1	33:U:91:PHE:HE1	1.69	0.75
2:P:221:ARG:NH1	30:N:1789:A:OP2	2.20	0.75
40:4:101:GLU:OE2	40:4:103:THR:OG1	2.05	0.75
34:M:29:G:P	36:0:1229:A:H4'	2.26	0.75
37:1:35:ARG:NE	59:v:20:ALA:N	2.35	0.75
32:C:3:LYS:HG3	32:C:4:LEU:H	1.50	0.75
3:Q:14:ILE:HA	14:c:12:GLN:HE22	1.52	0.74
36:0:673:A:O3'	41:5:86:ARG:NH2	2.20	0.74
35:x:448:U:H6	38:2:162:ILE:CD1	1.85	0.74
36:0:1493:A:C2	58:u:37:A:C1'	2.70	0.74
54:J:6:LYS:HG3	54:J:7:LYS:HG2	1.70	0.74
59:v:60:ASP:OD1	59:v:109:LYS:NZ	2.20	0.74
2:P:121:ASP:OD2	33:U:91:PHE:CE1	2.39	0.74
48:D:87:ARG:O	48:D:91:HIS:HB2	1.87	0.74
30:N:2112:G:H2'	30:N:2113:U:H5'	1.69	0.74
30:N:1093:G:N2	30:N:1098:A:H62	1.85	0.73
30:N:2253:G:H1	34:M:73:C:H42	1.14	0.73
54:J:30:PRO:HA	54:J:48:THR:O	1.88	0.73
30:N:1924:C:C5'	34:M:13:A:C4'	2.67	0.73
30:N:882:G:C3'	58:u:19:G:N2	2.52	0.73
30:N:896:A:C4	58:u:56:C:H5''	2.23	0.73
30:N:1924:C:H5''	34:M:13:A:H4'	1.68	0.73
36:0:1493:A:C6	58:u:37:A:O2'	2.40	0.73
45:9:65:TYR:HB3	49:E:96:LEU:HD11	1.69	0.73
34:M:34:U:P	44:8:129:LYS:NZ	2.61	0.73
35:x:449:A:N6	38:2:164:ARG:HD3	2.02	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:N:1093:G:H21	30:N:1098:A:N6	1.87	0.73
37:1:34:ALA:HB3	59:v:23:ARG:HA	1.71	0.73
30:N:882:G:C4'	58:u:56:C:N3	2.51	0.72
36:0:1527:U:OP2	56:s:39:GLU:OE1	2.07	0.72
36:0:664:G:H22	36:0:741:G:H1	1.37	0.72
30:N:2251:G:N1	34:M:75:A:H2	1.85	0.72
37:1:18:HIS:CB	57:t:43:LYS:CB	2.68	0.72
5:S:80:ARG:HD2	34:M:55:C:C6	2.25	0.72
36:0:404:G:O2'	36:0:498:A:N1	2.23	0.72
12:a:77:ALA:O	12:a:81:ASN:HB2	1.90	0.71
49:E:47:LYS:HB3	54:J:13:LEU:HD12	1.72	0.71
36:0:1081:A:OP2	40:4:52:LYS:NZ	2.23	0.71
59:v:74:TYR:HB3	59:v:155:PHE:CE2	2.25	0.71
40:4:81:LEU:HD13	40:4:123:VAL:HG11	1.72	0.71
2:P:258:ARG:NH1	2:P:264:ASP:OD1	2.23	0.71
36:0:1147:C:O2	44:8:18:ARG:NH2	2.22	0.71
30:N:2093:G:H5'	33:U:22:LYS:HD3	1.71	0.71
37:1:35:ARG:HE	59:v:20:ALA:H	1.34	0.71
30:N:715:A:C5	50:F:53:ARG:NH1	2.59	0.70
28:q:8:ARG:NH2	30:N:243:U:OP1	2.24	0.70
35:x:435:G:N2	36:0:693:G:OP2	2.25	0.70
34:M:34:U:P	44:8:129:LYS:HZ3	2.13	0.70
37:1:34:ALA:CB	59:v:23:ARG:HA	2.22	0.70
4:R:163:ASN:ND2	30:N:323:C:H2'	2.07	0.70
36:0:1238:A:N6	36:0:1301:U:N3	2.01	0.70
5:S:37:ASN:ND2	30:N:2312:U:O2	2.24	0.69
34:M:16:C:C3'	34:M:17:G:H5'	2.20	0.69
30:N:1919:A:H1'	36:0:1407:C:O2'	1.92	0.69
35:x:442:G:N2	58:u:37:A:C1'	2.46	0.69
35:x:448:U:H5	38:2:162:ILE:HD13	1.57	0.69
36:0:1309:G:OP2	48:D:98:ARG:NH1	2.25	0.69
17:f:15:GLN:HE22	30:N:1266:G:H5''	1.56	0.69
36:0:501:C:OP1	47:B:114:ARG:NH2	2.26	0.69
30:N:2637:U:N3	30:N:2776:A:N6	2.40	0.69
59:v:60:ASP:CG	59:v:109:LYS:HZ1	2.01	0.69
30:N:2128:G:H21	30:N:2173:A:H1'	1.57	0.69
35:x:450:C:N4	38:2:164:ARG:NH1	2.39	0.68
5:S:143:TYR:CB	48:D:7:ILE:CG2	2.72	0.68
22:k:60:ASP:OD2	33:U:27:ARG:CZ	2.41	0.68
44:8:84:THR:HG21	44:8:103:PHE:HB3	1.75	0.68
1:O:48:U:OP1	13:b:30:ARG:NH2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:45:TYR:HH	30:N:2636:C:HO2'	1.41	0.68
35:x:450:C:H42	38:2:164:ARG:HH11	1.38	0.68
36:0:1054:C:N4	58:u:34:G:N7	2.41	0.68
30:N:613:A:N7	30:N:616:A:N1	2.41	0.68
48:D:29:ARG:HH21	48:D:63:PHE:HB2	1.59	0.68
5:S:80:ARG:HD3	34:M:55:C:C6	2.28	0.67
2:P:87:ARG:NH2	30:N:1817:G:OP1	2.26	0.67
34:M:29:G:P	36:0:1229:A:O3'	2.52	0.67
36:0:1493:A:H61	58:u:37:A:H4'	1.58	0.67
34:M:30:A:O4'	36:0:1339:A:N1	2.27	0.67
30:N:2134:A:N6	30:N:2157:G:H4'	2.09	0.67
30:N:962:G:H21	30:N:2250:G:H1	1.41	0.67
2:P:133:ARG:CD	33:U:123:ARG:CZ	2.71	0.67
36:0:1064:G:N2	36:0:1190:G:O2'	2.28	0.67
37:1:209:ALA:O	37:1:213:TYR:HB2	1.94	0.67
36:0:427:U:OP1	39:3:13:ARG:NH2	2.28	0.67
6:T:67:THR:HG21	30:N:2757:A:N1	2.11	0.66
8:W:113:PRO:HD2	30:N:558:U:OP1	1.94	0.66
18:g:46:ALA:O	18:g:50:LEU:HB2	1.94	0.66
30:N:2156:G:H2'	30:N:2157:G:H5'	1.78	0.66
49:E:26:GLU:HG2	49:E:30:ILE:HD12	1.77	0.66
30:N:882:G:C1'	58:u:56:C:O2	2.42	0.66
30:N:2107:G:OP1	32:C:3:LYS:HE3	1.94	0.66
59:v:77:PRO:O	59:v:78:ASP:CB	2.43	0.66
30:N:499:U:C2	30:N:503:A:N6	2.63	0.66
30:N:2253:G:N1	34:M:73:C:C4	2.47	0.66
30:N:1912:A:N1	36:0:1408:A:H4'	2.11	0.66
46:A:24:HIS:HB3	46:A:31:ILE:HG23	1.78	0.66
58:u:21:A:H4'	58:u:22:G:OP1	1.96	0.65
30:N:715:A:C1'	50:F:40:GLN:NE2	2.60	0.65
30:N:2177:C:H4'	32:C:211:LYS:HZ1	1.60	0.65
36:0:554:A:H5'	47:B:26:ALA:HB1	1.78	0.65
22:k:39:TRP:CD1	33:U:32:PRO:HA	2.32	0.65
35:x:455:C:H41	59:v:135:LYS:CA	2.08	0.65
36:0:974:A:OP1	49:E:69:ARG:NH2	2.30	0.65
35:x:443:C:C2	58:u:36:A:H2	2.15	0.65
37:1:32:PHE:CE2	59:v:24:LYS:CA	2.65	0.65
30:N:1019:U:H3	30:N:1142:A:N6	1.95	0.65
34:M:74:C:H2'	34:M:75:A:H1'	1.78	0.65
27:p:37:LYS:HE2	30:N:469:G:O6	1.97	0.65
30:N:140:C:OP1	30:N:141:G:N2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1:32:PHE:HE2	59:v:23:ARG:C	1.99	0.65
2:P:29:PRO:HG2	2:P:34:LEU:HD11	1.78	0.65
28:q:8:ARG:NH2	30:N:243:U:P	2.69	0.65
35:x:449:A:N7	38:2:164:ARG:HD3	2.12	0.65
33:U:87:GLU:OE2	41:5:14:GLN:NE2	2.30	0.64
34:M:28:G:O3'	36:0:1229:A:C4'	2.43	0.64
43:7:75:ILE:HD13	43:7:129:VAL:HG22	1.79	0.64
9:X:2:ILE:HB	9:X:33:ALA:HB3	1.80	0.64
30:N:2405:G:O2'	30:N:2411:A:N6	2.30	0.64
34:M:33:C:P	44:8:130:ARG:HG3	2.36	0.64
36:0:437:U:OP1	39:3:152:GLN:NE2	2.30	0.64
36:0:1060:U:OP1	49:E:85:ARG:NH2	2.30	0.64
43:7:15:ARG:NH1	43:7:75:ILE:O	2.30	0.64
30:N:1311:G:H21	30:N:1603:A:H62	1.45	0.64
37:1:28:LYS:NZ	59:v:27:GLN:CB	2.61	0.64
30:N:2121:G:H4'	32:C:167:LYS:HD3	1.79	0.64
30:N:2178:C:P	32:C:211:LYS:HE2	2.37	0.64
33:U:84:ALA:HA	33:U:91:PHE:H	1.62	0.64
44:8:46:MET:HE2	44:8:50:GLN:HE21	1.63	0.64
5:S:88:LYS:HD3	30:N:2313:C:H5''	1.80	0.64
30:N:2141:G:H2'	30:N:2142:A:H8	1.63	0.64
36:0:1054:C:N4	58:u:34:G:C8	2.66	0.64
36:0:1086:U:H3	36:0:1099:G:H22	1.46	0.64
44:8:123:ARG:NH1	44:8:124:ARG:O	2.31	0.64
3:Q:38:LYS:O	3:Q:46:ARG:HA	1.97	0.63
15:d:6:ARG:NH1	30:N:585:G:N7	2.46	0.63
34:M:34:U:OP1	44:8:129:LYS:CD	2.45	0.63
35:x:435:G:H21	36:0:693:G:P	2.21	0.63
30:N:896:A:C4	58:u:56:C:C5'	2.79	0.63
36:0:458:U:H3	36:0:474:G:H1	1.44	0.63
59:v:74:TYR:CB	59:v:155:PHE:CZ	2.81	0.63
2:P:121:ASP:CG	33:U:91:PHE:CD1	2.75	0.63
30:N:2637:U:H3	30:N:2776:A:N6	1.96	0.63
1:O:31:C:H4'	5:S:26:MET:HE1	1.79	0.63
35:x:441:U:C4	36:0:1400:C:H5'	2.32	0.63
35:x:455:C:C5	59:v:135:LYS:N	2.44	0.63
54:J:11:ILE:HG22	54:J:38:SER:HB3	1.81	0.63
6:T:86:LYS:HG3	6:T:132:VAL:HG22	1.81	0.63
11:Z:55:ARG:NH2	30:N:2469:A:O2'	2.32	0.63
27:p:44:VAL:HG13	27:p:44:VAL:O	1.99	0.63
9:X:49:ARG:NH2	36:0:1423:G:P	2.71	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:N:1066:U:O2'	30:N:1074:G:N2	2.32	0.63
34:M:33:C:OP2	44:8:130:ARG:CD	2.47	0.63
42:6:147:ALA:O	46:A:56:ARG:NH2	2.32	0.63
30:N:882:G:O3'	58:u:19:G:N2	2.31	0.63
3:Q:49:GLN:HE21	3:Q:79:LEU:HB3	1.64	0.62
9:X:92:GLU:O	9:X:93:GLN:HB2	1.98	0.62
30:N:1105:U:H2'	30:N:1106:G:H8	1.64	0.62
36:0:1527:U:OP2	56:s:39:GLU:CD	2.42	0.62
44:8:25:ASN:HA	44:8:59:GLU:HG3	1.81	0.62
36:0:972:C:OP2	45:9:59:LYS:HD3	1.98	0.62
52:H:9:GLN:HG2	52:H:60:GLU:HG2	1.81	0.62
35:x:450:C:C2	38:2:131:ARG:NH2	2.68	0.62
36:0:1160:G:P	37:1:132:LYS:NZ	2.71	0.62
13:b:16:ARG:NH2	13:b:19:GLN:OE1	2.33	0.62
22:k:12:PRO:HB3	22:k:30:LEU:HD23	1.82	0.62
28:q:12:LYS:NZ	30:N:249:C:O2	2.33	0.61
30:N:475:C:O2	30:N:479:A:N6	2.33	0.61
30:N:693:A:O2'	30:N:1353:A:N3	2.33	0.61
36:0:812:G:OP1	36:0:902:G:N2	2.34	0.61
22:k:16:ASN:HA	22:k:25:THR:O	2.01	0.61
20:i:51:GLN:HE22	20:i:86:LEU:HD21	1.65	0.61
35:x:442:G:O6	58:u:38:A:N9	2.33	0.61
34:M:40:C:O2'	36:0:1338:G:O2'	2.19	0.61
35:x:442:G:O6	58:u:38:A:C4	2.53	0.61
59:v:133:HIS:HA	59:v:139:LYS:HD2	1.81	0.61
11:Z:20:LEU:HD13	20:i:81:PRO:HG2	1.81	0.61
35:x:456:A:OP2	59:v:133:HIS:O	2.18	0.61
56:s:4:ILE:O	56:s:20:LYS:NZ	2.33	0.61
30:N:882:G:C2'	58:u:56:C:O2	2.49	0.61
30:N:2251:G:O6	34:M:75:A:C6	2.50	0.61
1:O:24:G:O2'	1:O:27:C:N4	2.34	0.61
33:U:9:VAL:HB	33:U:13:GLY:HA3	1.83	0.61
44:8:52:LEU:HB3	44:8:57:MET:HB3	1.81	0.61
30:N:1315:C:O2'	30:N:1392:A:N3	2.30	0.60
30:N:2849:U:O2'	30:N:2866:U:O2	2.15	0.60
34:M:30:A:H1'	36:0:1339:A:N3	2.16	0.60
36:0:933:G:N7	42:6:3:ARG:NH1	2.49	0.60
30:N:613:A:H62	30:N:616:A:H61	1.50	0.60
35:x:452:U:C2	38:2:132:ARG:NH2	2.69	0.60
30:N:1779:U:H5	30:N:1784:A:N7	1.99	0.60
3:Q:156:PHE:CE1	8:W:81:ILE:HD12	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:f:15:GLN:NE2	30:N:1266:G:H5''	2.16	0.60
45:9:19:ASP:HA	45:9:22:THR:HG22	1.83	0.60
33:U:7:ASP:HB3	33:U:9:VAL:HG23	1.83	0.60
7:V:135:SER:OG	30:N:1062:G:N3	2.34	0.60
31:L:20:ASN:ND2	31:L:37:CYS:SG	2.73	0.60
36:0:1055:A:H1'	38:2:156:ARG:HH21	1.66	0.60
27:p:9:VAL:HG23	30:N:1309:G:OP1	2.01	0.59
2:P:121:ASP:OD1	33:U:91:PHE:CE1	2.53	0.59
21:j:18:ALA:O	21:j:20:ARG:NH1	2.35	0.59
34:M:29:G:H5''	36:0:1230:C:C5'	2.31	0.59
46:A:112:ASP:HB3	56:s:20:LYS:HE2	1.84	0.59
30:N:1212:G:O2'	30:N:1237:A:N6	2.36	0.59
35:x:441:U:C2	36:0:1400:C:H4'	2.37	0.59
35:x:451:G:OP2	40:4:56:VAL:HG11	2.02	0.59
30:N:2127:G:H4'	32:C:38:PHE:CD1	2.36	0.59
36:0:693:G:OP1	46:A:127:ARG:NH2	2.36	0.59
18:g:28:ASN:OD1	18:g:91:GLN:NE2	2.31	0.59
34:M:30:A:O2'	36:0:1340:A:H1'	2.02	0.59
34:M:40:C:O2'	36:0:1338:G:C1'	2.46	0.59
59:v:60:ASP:CG	59:v:109:LYS:NZ	2.60	0.59
41:5:38:ARG:HG2	41:5:63:ASN:HB2	1.85	0.59
53:I:26:ILE:O	53:I:30:LYS:HB2	2.03	0.59
38:2:40:ARG:NH1	38:2:55:ILE:O	2.36	0.59
11:Z:66:ARG:NH1	11:Z:104:GLU:OE2	2.36	0.59
30:N:1019:U:N3	30:N:1142:A:N6	2.50	0.59
30:N:1068:G:N1	30:N:1073:A:N6	2.50	0.59
36:0:1526:G:H3'	56:s:39:GLU:OE1	2.03	0.59
50:F:46:HIS:O	50:F:48:LYS:N	2.36	0.59
2:P:133:ARG:HD3	33:U:123:ARG:CZ	2.28	0.58
33:U:72:ILE:HB	33:U:108:VAL:HG12	1.84	0.58
47:B:50:ARG:NH1	47:B:89:ASP:OD2	2.35	0.58
28:q:32:ILE:O	28:q:36:LYS:NZ	2.36	0.58
30:N:2506[A]:U:OP2	30:N:2576:G:N1	2.33	0.58
39:3:60:LYS:HE3	39:3:195:ILE:HG22	1.84	0.58
15:d:88:VAL:HA	16:e:49:ILE:HD12	1.85	0.58
30:N:1019:U:C4	30:N:1142:A:N6	2.72	0.58
33:U:96:THR:HG23	33:U:112:LYS:HE2	1.85	0.58
34:M:29:G:N3	36:0:1339:A:H2	2.01	0.58
36:0:1238:A:N6	36:0:1301:U:C2	2.68	0.58
37:1:141:LEU:O	37:1:145:GLU:HB2	2.03	0.58
15:d:92:ARG:HG2	30:N:997:G:OP1	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:x:442:G:C6	58:u:38:A:C1'	2.72	0.58
36:0:769:G:H4'	36:0:1513:A:H4'	1.84	0.58
7:V:31:GLN:NE2	30:N:1097:U:O4	2.34	0.58
8:W:32:LEU:HD22	8:W:54:ILE:HG21	1.85	0.58
30:N:1726:C:N4	30:N:1735:A:N6	2.51	0.58
36:0:946:A:H2'	36:0:947:G:C8	2.38	0.58
46:A:93:ARG:HH12	56:s:25:LYS:HD3	1.68	0.58
21:j:15:ASP:OD1	30:N:2263:C:N4	2.35	0.58
28:q:16:LYS:HE2	28:q:20:GLY:HA2	1.84	0.58
30:N:2850:A:N7	30:N:2868:A:O2'	2.35	0.58
35:x:450:C:H42	38:2:164:ARG:HH12	1.49	0.58
36:0:890:G:O2'	36:0:906:A:N6	2.36	0.58
45:9:27:GLU:O	45:9:31:ARG:HB2	2.04	0.58
30:N:1924:C:C4'	34:M:13:A:C5'	2.73	0.58
36:0:1316:G:H22	36:0:1319:A:H5''	1.69	0.58
37:1:81:LYS:O	37:1:85:LEU:HB2	2.04	0.58
30:N:2128:G:H4'	32:C:218:MET:HE1	1.85	0.58
2:P:236:GLU:HG2	30:N:2600:A:N7	2.18	0.57
22:k:10:LYS:NZ	30:N:396:G:OP2	2.37	0.57
36:0:675:A:H1'	46:A:118:HIS:CD2	2.38	0.57
36:0:1261:A:N6	36:0:1274:A:O2'	2.35	0.57
47:B:68:GLY:O	47:B:99:ARG:NH1	2.36	0.57
54:J:31:LEU:HB2	54:J:49:ILE:HG22	1.84	0.57
1:O:43:C:O2	5:S:92:ARG:NH2	2.36	0.57
9:X:70:ARG:NH1	30:N:2684:U:O4'	2.37	0.57
36:0:1302:C:C5	48:D:17:ILE:HD13	2.38	0.57
30:N:481:G:O2'	30:N:506:G:N2	2.37	0.57
30:N:1093:G:N2	30:N:1098:A:N6	2.48	0.57
35:x:437:C:H6	35:x:437:C:O5'	1.87	0.57
36:0:1224:U:O2'	36:0:1322:C:OP1	2.21	0.57
48:D:83:LEU:HD21	54:J:65:GLU:HG2	1.85	0.57
2:P:121:ASP:OD2	33:U:91:PHE:CD1	2.57	0.57
7:V:34:ASN:H	7:V:67:PHE:HE2	1.52	0.57
3:Q:46:ARG:NH2	3:Q:88:GLU:O	2.36	0.57
32:C:54:LYS:HD2	32:C:57:GLN:HG3	1.85	0.57
32:C:213:SER:C	32:C:214:ILE:HD12	2.29	0.57
36:0:927:G:O2'	36:0:1503:A:N7	2.35	0.57
6:T:24:ILE:HD11	6:T:43:VAL:HG11	1.87	0.57
21:j:23:VAL:HG22	21:j:38:VAL:HG22	1.87	0.57
30:N:1924:C:H4'	34:M:13:A:H5'	1.83	0.57
36:0:579:A:O2'	50:F:54:ARG:NH1	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:42:C:C5	5:S:66:LEU:HD22	2.40	0.57
22:k:6:GLN:O	22:k:74:ARG:NH1	2.37	0.57
28:q:5:LYS:HE2	30:N:254:G:N7	2.19	0.57
35:x:451:G:C4	39:3:47:ARG:NE	2.71	0.57
37:1:35:ARG:HG2	59:v:20:ALA:O	2.03	0.57
39:3:91:LEU:HD13	39:3:191:LEU:HD11	1.86	0.57
4:R:69:ARG:HG3	30:N:674:G:O2'	2.05	0.57
10:Y:111:ILE:HD12	10:Y:111:ILE:H	1.70	0.57
11:Z:50:ARG:HD3	11:Z:65:ILE:HD11	1.87	0.57
30:N:370:G:O2'	30:N:424:G:OP1	2.22	0.56
30:N:715:A:H1'	50:F:40:GLN:NE2	2.20	0.56
30:N:805:G:N2	30:N:829:A:OP1	2.38	0.56
35:x:437:C:O5'	35:x:437:C:C6	2.57	0.56
36:0:1368:A:OP2	44:8:114:LYS:HD3	2.05	0.56
38:2:36:ASP:OD1	38:2:59:ARG:NH2	2.34	0.56
2:P:144:VAL:HB	2:P:154:LEU:HB2	1.86	0.56
30:N:2176:A:H5''	32:C:221:GLY:N	2.20	0.56
35:x:451:G:C4	39:3:47:ARG:CD	2.87	0.56
44:8:36:GLU:HA	44:8:40:GLY:HA3	1.87	0.56
7:V:97:LYS:HD2	7:V:139:VAL:HG21	1.87	0.56
8:W:135:GLN:NE2	30:N:6:A:N3	2.53	0.56
30:N:1980:G:O2'	30:N:1982:U:OP2	2.22	0.56
32:C:201:PRO:HB2	32:C:204:ALA:HB2	1.86	0.56
34:M:30:A:C4'	36:0:1339:A:N1	2.68	0.56
36:0:1493:A:N1	58:u:37:A:H1'	2.13	0.56
31:L:54:GLY:C	54:J:64:ASP:OD2	2.48	0.56
22:k:45:ARG:HH21	22:k:47:VAL:HG22	1.71	0.56
36:0:796:C:O3'	46:A:127:ARG:NH1	2.38	0.56
46:A:93:ARG:NH2	46:A:112:ASP:OD1	2.39	0.56
35:x:473:C:H5''	35:x:474:U:C6	2.41	0.56
38:2:156:ARG:HD3	38:2:193:TYR:HB3	1.86	0.56
32:C:63:THR:HG22	32:C:163:TYR:HE1	1.69	0.56
36:0:451:A:H61	36:0:481:G:H5'	1.70	0.56
22:k:72:ARG:NH2	22:k:78:TYR:OH	2.33	0.56
27:p:34:ARG:HD3	30:N:467:G:OP2	2.05	0.56
36:0:409:U:OP1	39:3:24:GLY:HA3	2.06	0.56
20:i:62:THR:HG22	20:i:71:LYS:HG2	1.86	0.56
30:N:1724:G:O6	30:N:1737:G:C2	2.59	0.56
34:M:39:C:O2'	36:0:1339:A:H4'	2.06	0.56
40:4:13:GLU:OE1	40:4:68:ARG:NH2	2.39	0.56
45:9:10:LEU:HG	45:9:98:VAL:HG12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:235:GLY:O	2:P:239:ASN:ND2	2.39	0.56
32:C:54:LYS:HD2	32:C:57:GLN:HE21	1.70	0.56
59:v:92:TYR:HD1	59:v:125:PHE:HE2	1.54	0.56
10:Y:76:GLU:OE2	30:N:627:A:O2'	2.23	0.55
30:N:715:A:C4'	50:F:40:GLN:HE22	2.18	0.55
30:N:1726:C:H42	30:N:1735:A:N6	2.04	0.55
42:6:40:GLU:OE2	44:8:43:THR:HG23	2.06	0.55
30:N:2163:A:H2'	30:N:2164:C:H5'	1.88	0.55
2:P:133:ARG:HE	33:U:123:ARG:HD3	1.70	0.55
30:N:837:C:N3	30:N:941:A:N6	2.54	0.55
5:S:140:GLU:OE2	31:L:27:THR:HG23	2.07	0.55
4:R:149:ILE:HD12	4:R:175:ILE:HG21	1.88	0.55
8:W:13:ARG:NH1	8:W:49:ASP:O	2.39	0.55
30:N:1924:C:C4'	34:M:13:A:C4'	2.58	0.55
36:0:979:C:O2	49:E:59:ARG:NH1	2.35	0.55
2:P:2:ALA:N	2:P:199:GLU:OE1	2.39	0.55
3:Q:13:ARG:NH1	30:N:2683:C:H4'	2.22	0.55
30:N:897:C:H1'	58:u:56:C:H5	1.71	0.55
30:N:1332:G:N7	30:N:1609:A:O2'	2.37	0.55
35:x:438:C:H2'	35:x:438:C:O2	2.07	0.55
36:0:246:A:N1	36:0:278:G:O2'	2.35	0.55
30:N:2156:G:C2'	30:N:2157:G:H5'	2.36	0.55
36:0:673:A:H2'	36:0:674:G:C8	2.42	0.55
36:0:993:G:O2'	36:0:994:A:N7	2.40	0.55
46:A:30:THR:HG21	46:A:92:GLY:HA3	1.89	0.55
16:e:49:ILE:HB	16:e:52:PRO:HA	1.89	0.55
27:p:31:LEU:HD22	27:p:42:LEU:HD23	1.88	0.55
30:N:897:C:H1'	58:u:56:C:C5	2.41	0.55
34:M:16:C:O2	34:M:16:C:H5''	2.07	0.55
30:N:2848:G:O2'	30:N:2867:G:N2	2.36	0.54
33:U:132:PHE:HB2	33:U:140:ALA:HB3	1.87	0.54
4:R:176:ASP:OD1	4:R:176:ASP:N	2.40	0.54
30:N:1450:G:N2	30:N:1452:G:O6	2.41	0.54
1:O:72:G:H21	1:O:104:A:H62	1.55	0.54
25:n:43:ILE:HG22	25:n:49:TYR:HB2	1.88	0.54
34:M:29:G:OP1	36:0:1229:A:H4'	2.07	0.54
35:x:441:U:N3	36:0:1400:C:C4'	2.71	0.54
6:T:33:LEU:HD22	6:T:75:MET:HG2	1.89	0.54
11:Z:74:THR:HA	11:Z:88:ASN:O	2.07	0.54
29:r:36:ARG:HD2	29:r:37:GLN:HB2	1.89	0.54
30:N:413:C:HO2'	30:N:1880:U:HO2'	1.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:0:1166:G:N1	36:0:1169:A:OP2	2.40	0.54
2:P:204:VAL:O	2:P:206:GLY:N	2.40	0.54
9:X:43:ILE:HD12	9:X:56:ASP:HB2	1.90	0.54
15:d:37:GLN:HE21	30:N:1252:G:H1	1.55	0.54
35:x:448:U:C6	38:2:162:ILE:CG1	2.91	0.54
25:n:53:LYS:HE2	25:n:56:ALA:HB2	1.89	0.54
30:N:897:C:H5'	58:u:56:C:H5'	1.86	0.54
41:5:11:HIS:HD2	41:5:12:PRO:HD2	1.73	0.54
4:R:178:VAL:O	4:R:182:ALA:HB2	2.07	0.54
8:W:56:VAL:HB	8:W:124:VAL:HG12	1.88	0.54
33:U:33:GLN:HB3	33:U:35:LYS:HE2	1.89	0.54
34:M:15:G:C8	34:M:15:G:C5'	2.86	0.54
35:x:440:A:OP1	36:0:1498:U:C2'	2.56	0.54
35:x:450:C:N3	38:2:131:ARG:NH2	2.56	0.54
48:D:77:ILE:HG22	48:D:81:MET:HE2	1.90	0.54
12:a:53:THR:HA	12:a:56:LYS:HD3	1.88	0.54
16:e:1:MET:HA	16:e:42:ALA:O	2.08	0.54
30:N:987:C:O2'	30:N:1000:A:N3	2.36	0.54
36:0:768:A:N3	36:0:1512:U:O2'	2.40	0.54
32:C:67:HIS:HB2	32:C:188:ASN:HD21	1.71	0.54
41:5:41:ASP:OD1	41:5:58:HIS:NE2	2.41	0.54
45:9:8:ILE:HA	45:9:99:GLN:O	2.08	0.54
25:n:17:ARG:NE	30:N:1266:G:OP2	2.40	0.54
30:N:306:U:O4	30:N:310:A:N7	2.41	0.54
34:M:29:G:OP1	36:0:1229:A:C4'	2.55	0.54
9:X:77:ILE:HG12	14:c:72:ARG:HD2	1.90	0.53
27:p:29:GLN:NE2	30:N:210:C:OP1	2.40	0.53
49:E:41:ARG:NH1	49:E:42:TRP:O	2.41	0.53
59:v:120:ARG:NH1	59:v:151:HIS:NE2	2.56	0.53
7:V:100:LYS:HA	7:V:139:VAL:O	2.08	0.53
30:N:1536:C:O2	30:N:1537:G:N2	2.40	0.53
34:M:33:C:H4'	36:0:966:G:N3	2.22	0.53
36:0:676:A:H5''	46:A:115:PRO:HB3	1.90	0.53
7:V:12:GLN:HE21	7:V:55:ILE:H	1.57	0.53
30:N:2162:G:H2'	30:N:2163:A:H8	1.73	0.53
30:N:1924:C:C4'	34:M:13:A:O5'	2.56	0.53
37:1:32:PHE:CE2	59:v:23:ARG:C	2.80	0.53
37:1:117:LEU:HB3	37:1:141:LEU:HD11	1.89	0.53
15:d:88:VAL:HG22	16:e:49:ILE:O	2.09	0.53
30:N:28:A:N6	30:N:512:G:H1'	2.23	0.53
48:D:39:ILE:HD12	48:D:52:GLN:HE21	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:f:73:LYS:HB2	17:f:106:VAL:HB	1.90	0.53
30:N:2177:C:O3'	32:C:211:LYS:CE	2.53	0.53
34:M:74:C:H2'	34:M:75:A:C1'	2.38	0.53
54:J:36:ARG:NH2	54:J:75:ALA:O	2.42	0.53
35:x:438:C:H2'	36:0:926:G:C2	2.44	0.53
37:1:67:ILE:HD12	37:1:160:ALA:HB3	1.91	0.53
37:1:80:VAL:HG12	37:1:214:LEU:HD21	1.91	0.53
10:Y:21:ARG:HA	30:N:811:U:H2'	1.90	0.53
36:0:76:G:H1	36:0:93:U:H3	1.56	0.53
40:4:99:ALA:O	40:4:102:GLY:N	2.39	0.53
12:a:114:GLU:OE1	12:a:118:ARG:NH2	2.42	0.53
33:U:7:ASP:OD2	33:U:35:LYS:HD2	2.09	0.53
33:U:40:THR:HB	33:U:43:ASN:ND2	2.22	0.53
36:0:263:A:OP2	55:K:74:ARG:NH1	2.42	0.53
55:K:28:MET:HE1	55:K:67:ILE:HG12	1.91	0.53
4:R:163:ASN:HD21	30:N:323:C:H2'	1.74	0.52
12:a:22:ARG:HG3	12:a:70:THR:HA	1.91	0.52
16:e:74:ILE:HD13	30:N:992:C:H4'	1.90	0.52
30:N:51:G:O2'	30:N:118:A:N6	2.42	0.52
35:x:450:C:N4	38:2:164:ARG:HH11	2.02	0.52
36:0:1003:G:H21	36:0:1005:A:H5'	1.73	0.52
36:0:1006:G:O6	36:0:1023:U:O2	2.27	0.52
19:h:86:ARG:NH1	19:h:100:SER:OG	2.42	0.52
30:N:1070:A:H2'	30:N:1097:U:H4'	1.92	0.52
36:0:502:A:OP1	47:B:115:SER:HB3	2.09	0.52
37:1:68:LEU:HD12	37:1:154:MET:HE1	1.92	0.52
44:8:19:VAL:HA	44:8:65:ILE:HG22	1.92	0.52
7:V:76:ALA:HA	7:V:79:LEU:HB3	1.91	0.52
30:N:1726:C:N4	30:N:1735:A:H61	2.06	0.52
30:N:1939:U:OP1	30:N:2604:U:O2'	2.27	0.52
55:K:59:ASP:OD1	55:K:76:LYS:NZ	2.33	0.52
2:P:48:ARG:HD3	30:N:773:U:O2'	2.09	0.52
10:Y:76:GLU:HG3	10:Y:111:ILE:HD13	1.91	0.52
18:g:8:LEU:HD23	18:g:50:LEU:HD21	1.91	0.52
30:N:877:A:O2'	30:N:900:A:N6	2.43	0.52
34:M:29:G:N3	36:0:1339:A:C2	2.77	0.52
35:x:473:C:OP2	35:x:474:U:H5	1.93	0.52
59:v:72:VAL:HG11	59:v:168:LEU:HD21	1.92	0.52
29:r:3:VAL:HG12	29:r:36:ARG:HE	1.73	0.52
35:x:453:C:H41	38:2:132:ARG:HE	1.56	0.52
36:0:1527:U:OP2	56:s:39:GLU:OE2	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:B:34:CYS:SG	47:B:78:SER:OG	2.67	0.52
52:H:17:MET:HG3	52:H:20:SER:HB3	1.92	0.52
1:O:89:U:H6	30:N:958:U:H2'	1.74	0.52
2:P:133:ARG:NE	33:U:123:ARG:HD3	2.24	0.52
36:O:1522:U:OP1	46:A:128:ARG:NH1	2.40	0.52
4:R:2:GLU:HB3	4:R:11:ALA:HB1	1.92	0.52
4:R:19:PHE:HE1	4:R:109:LEU:HD13	1.75	0.52
12:a:41:ALA:HB1	12:a:97:ILE:HD12	1.92	0.52
19:h:86:ARG:NH2	19:h:102:THR:OG1	2.42	0.52
35:x:445:A:H2'	35:x:446:U:H4'	1.91	0.52
35:x:450:C:O2	38:2:131:ARG:NH1	2.39	0.52
45:9:80:THR:HG22	45:9:82:LYS:H	1.74	0.52
58:u:20:U:O2'	58:u:21:A:P	2.67	0.52
2:P:3:VAL:HG12	2:P:19:VAL:HG22	1.92	0.52
15:d:49:ASP:OD2	30:N:534:U:O2'	2.21	0.52
18:g:18:GLU:OE2	30:N:1392:A:N6	2.43	0.52
30:N:299:A:N3	30:N:319:G:O2'	2.37	0.52
30:N:372:G:HO2'	30:N:400:G:H1	1.56	0.52
2:P:160:THR:HG23	2:P:177:ARG:HG2	1.91	0.51
16:e:57:GLY:HA2	16:e:102:SER:O	2.10	0.51
35:x:441:U:C2	36:O:1400:C:C4'	2.93	0.51
35:x:451:G:C2	39:3:47:ARG:CD	2.82	0.51
35:x:465:U:H2'	35:x:465:U:O2	2.09	0.51
37:1:28:LYS:HZ3	59:v:27:GLN:CB	2.21	0.51
14:c:37:LYS:HD2	14:c:39:ARG:HH11	1.75	0.51
30:N:612:G:N2	30:N:614:A:O2'	2.44	0.51
30:N:882:G:H4'	58:u:19:G:H22	0.53	0.51
34:M:28:G:N2	36:O:1338:G:H22	2.07	0.51
53:I:42:SER:HB3	53:I:52:GLN:HE21	1.75	0.51
5:S:116:GLY:HA3	5:S:178:ARG:HB3	1.91	0.51
21:j:41:ARG:HH11	30:N:2387:U:H1'	1.74	0.51
30:N:270:A:N1	30:N:369:U:O2'	2.38	0.51
30:N:639:U:H2'	30:N:640:C:C6	2.45	0.51
34:M:30:A:C2'	36:O:1340:A:HO2'	2.22	0.51
9:X:99:ILE:HD12	9:X:118:LEU:HB2	1.93	0.51
27:p:12:ARG:NH1	30:N:465:G:OP1	2.42	0.51
28:q:39:LYS:NZ	30:N:2365:G:N7	2.51	0.51
36:O:552:U:H5'	47:B:83:ARG:HH11	1.76	0.51
40:4:153:VAL:HG12	40:4:156:LYS:HZ1	1.76	0.51
42:6:109:ARG:O	42:6:119:ARG:NH2	2.44	0.51
13:b:31:THR:O	13:b:102:ARG:NH1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1:54:LEU:HG	37:1:220:THR:HG21	1.92	0.51
38:2:156:ARG:NH1	38:2:160:ALA:O	2.43	0.51
53:I:32:TYR:HB3	53:I:55:LEU:HD21	1.93	0.51
9:X:77:ILE:HG12	14:c:72:ARG:CD	2.41	0.51
23:l:6:LEU:HD13	23:l:56:LEU:HD22	1.93	0.51
25:n:4:GLN:HA	30:N:2615:U:C2	2.45	0.51
30:N:2602:A:OP1	34:M:75:A:OP2	2.29	0.51
36:0:401:C:O2'	36:0:621:A:N3	2.39	0.51
59:v:112:LEU:HD11	59:v:142:THR:HG23	1.91	0.51
6:T:24:ILE:HG21	6:T:72:LEU:HD21	1.91	0.51
21:j:19:LYS:NZ	30:N:2261:C:OP1	2.33	0.51
30:N:27:G:HO2'	30:N:28:A:H8	1.56	0.51
57:t:91:ARG:HA	57:t:94:ALA:HB3	1.93	0.51
4:R:144:GLU:HG2	4:R:166:LYS:HD2	1.92	0.51
9:X:76:VAL:HG12	14:c:73:VAL:HG22	1.92	0.51
34:M:28:G:H22	36:0:1338:G:N2	2.09	0.51
34:M:33:C:C4'	36:0:966:G:N3	2.74	0.51
42:6:57:SER:HB3	42:6:60:GLU:HG2	1.93	0.51
52:H:59:VAL:HG21	52:H:75:LEU:HD22	1.93	0.51
19:h:51:ALA:O	19:h:54:GLN:NE2	2.44	0.51
30:N:1534:U:O2'	30:N:1537:G:O6	2.29	0.51
36:0:976:G:OP2	36:0:1358:U:O2'	2.29	0.51
30:N:2114:A:N3	30:N:2114:A:H2'	2.25	0.51
30:N:2638:G:O2'	30:N:2778:A:N6	2.44	0.51
34:M:16:C:H4'	34:M:17:G:OP2	2.10	0.51
36:0:1493:A:N1	58:u:37:A:HO2'	1.41	0.51
23:l:54:LYS:HE3	30:N:72:U:OP2	2.11	0.50
28:q:8:ARG:NH2	30:N:243:U:OP2	2.44	0.50
46:A:35:THR:OG1	46:A:36:ASP:N	2.44	0.50
30:N:527:C:N4	30:N:2779:U:OP2	2.44	0.50
30:N:948:C:O2	30:N:984:A:O2'	2.28	0.50
30:N:1936:A:H2	30:N:1943:U:H3	1.56	0.50
34:M:16:C:O2	34:M:16:C:H2'	2.11	0.50
38:2:77:ILE:HA	38:2:84:VAL:HG23	1.92	0.50
41:5:90:MET:SD	53:I:61:ARG:NH1	2.83	0.50
7:V:117:MET:HA	30:N:1058:U:O2'	2.11	0.50
11:Z:45:GLN:NE2	30:N:2485:G:OP1	2.34	0.50
19:h:34:VAL:HG13	19:h:67:VAL:HG22	1.93	0.50
30:N:2105:U:H2'	30:N:2106:U:O4'	2.12	0.50
38:2:55:ILE:HG22	38:2:68:ILE:HG12	1.92	0.50
40:4:99:ALA:HB2	40:4:124:LEU:HG	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:V:55:ILE:HG22	7:V:57:VAL:HB	1.94	0.50
30:N:882:G:H1'	58:u:56:C:O2	2.11	0.50
32:C:183:ASP:O	32:C:187:GLU:HG2	2.12	0.50
46:A:72:ASP:O	46:A:73:ALA:HB3	2.11	0.50
32:C:23:ILE:HG12	32:C:224:VAL:HB	1.93	0.50
45:9:11:LYS:HA	45:9:70:HIS:O	2.12	0.50
48:D:3:ARG:O	48:D:57:ARG:NH1	2.38	0.50
51:G:6:LEU:HG	51:G:17:TYR:HB3	1.93	0.50
30:N:2185:U:H2'	30:N:2186:G:C8	2.47	0.50
30:N:2533:U:OP1	30:N:2665:A:O2'	2.29	0.50
34:M:30:A:P	36:0:1230:C:H5''	2.52	0.50
35:x:455:C:N4	59:v:135:LYS:O	2.44	0.50
36:0:843:U:OP1	36:0:844:G:N2	2.43	0.50
38:2:172:ARG:NH2	38:2:206:GLU:OE2	2.44	0.50
46:A:110:ILE:HG22	56:s:17:ARG:NH1	2.27	0.50
2:P:220:VAL:HG21	30:N:782:A:N7	2.26	0.50
7:V:124:ALA:HB1	30:N:1081:U:H4'	1.93	0.50
16:e:27:ILE:O	16:e:66:HIS:NE2	2.42	0.50
16:e:76:LYS:O	16:e:84:ARG:HA	2.11	0.50
28:q:8:ARG:HH21	30:N:243:U:P	2.33	0.50
4:R:21:ARG:HD3	4:R:106:LYS:HB3	1.93	0.50
31:L:37:CYS:SG	31:L:38:SER:N	2.85	0.50
33:U:83:LYS:HG3	33:U:91:PHE:HB3	1.92	0.50
37:1:28:LYS:HZ2	59:v:27:GLN:CB	2.24	0.50
45:9:15:HIS:HA	45:9:18:ILE:HG22	1.93	0.50
30:N:2177:C:H4'	32:C:211:LYS:NZ	2.26	0.50
34:M:28:G:N2	36:0:1338:G:N2	2.59	0.50
48:D:10:PRO:HB2	48:D:18:ALA:HB1	1.94	0.50
50:F:46:HIS:C	50:F:48:LYS:H	2.17	0.49
30:N:2113:U:H2'	30:N:2114:A:H8	1.77	0.49
16:e:7:SER:OG	16:e:8:GLY:N	2.45	0.49
19:h:11:VAL:HG12	19:h:72:ILE:HG22	1.93	0.49
39:3:58:LYS:NZ	39:3:69:GLU:OE1	2.44	0.49
23:l:2:LYS:HD3	30:N:77:G:OP1	2.13	0.49
30:N:2540:C:O2'	30:N:2740:A:N3	2.42	0.49
35:x:442:G:O6	58:u:37:A:C6	2.63	0.49
45:9:27:GLU:O	45:9:31:ARG:CB	2.60	0.49
8:W:108:MET:HE2	30:N:1138:G:N3	2.27	0.49
24:m:3:LYS:HE2	24:m:40:ASP:HB3	1.93	0.49
35:x:443:C:N3	58:u:36:A:C2	2.80	0.49
37:1:108:ARG:NH2	59:v:150:PRO:HG3	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:R:83:VAL:HB	4:R:86:ALA:HB2	1.95	0.49
7:V:127:ARG:HA	7:V:130:GLU:HB2	1.94	0.49
12:a:32:GLU:HG2	12:a:115:LEU:HD12	1.94	0.49
27:p:1:MET:SD	30:N:752:A:H3'	2.53	0.49
30:N:1047:G:O2'	30:N:1111:A:N6	2.46	0.49
36:0:1493:A:N6	58:u:37:A:H4'	2.24	0.49
55:K:54:MET:HE3	55:K:58:VAL:HG21	1.94	0.49
35:x:441:U:H2'	36:0:1401:G:P	2.52	0.49
36:0:362:G:N1	36:0:365:U:OP2	2.43	0.49
2:P:165:VAL:HG21	2:P:181:MET:HE1	1.93	0.49
11:Z:33:LEU:HD13	11:Z:117:PHE:HB3	1.95	0.49
30:N:2128:G:N2	30:N:2173:A:H1'	2.27	0.49
37:1:141:LEU:O	37:1:145:GLU:CB	2.61	0.49
42:6:142:HIS:O	42:6:146:GLU:HB2	2.13	0.49
55:K:69:LYS:O	55:K:72:ALA:HB3	2.12	0.49
10:Y:67:THR:HG21	30:N:244:A:H5''	1.95	0.49
15:d:4:VAL:HG22	30:N:1199:U:H1'	1.95	0.49
20:i:6:ALA:HB1	20:i:40:ILE:HG23	1.95	0.49
25:n:3:VAL:HG23	30:N:2015:A:C6	2.47	0.49
35:x:449:A:C5	38:2:164:ARG:HD3	2.47	0.49
36:0:1103:C:C2'	37:1:106:THR:HG21	2.39	0.49
37:1:176:ALA:HB1	37:1:181:ILE:HB	1.94	0.49
39:3:141:ASP:O	39:3:181:THR:HA	2.12	0.49
2:P:207:LYS:HB2	30:N:729:G:C6	2.48	0.49
6:T:67:THR:HG22	30:N:2748:A:H1'	1.95	0.49
10:Y:51:GLU:OE1	10:Y:60:ARG:NH1	2.46	0.49
19:h:7:ARG:NH2	19:h:26:LYS:O	2.45	0.49
30:N:1868:C:N4	30:N:1869:G:O6	2.46	0.49
32:C:212:VAL:HG23	32:C:224:VAL:HG23	1.95	0.49
34:M:33:C:OP2	44:8:130:ARG:NE	2.46	0.49
36:0:812:G:HO2'	36:0:813:U:H6	1.61	0.49
44:8:55:VAL:O	44:8:60:LYS:NZ	2.43	0.49
2:P:66:ASP:OD2	2:P:102:ARG:NH1	2.46	0.48
16:e:71:LYS:NZ	30:N:1223:G:N7	2.61	0.48
26:o:35:GLU:HA	26:o:49:TYR:O	2.13	0.48
30:N:715:A:C4'	50:F:40:GLN:NE2	2.76	0.48
30:N:2150:C:H2'	30:N:2151:U:O4'	2.13	0.48
32:C:25:GLU:O	32:C:29:LEU:HG	2.13	0.48
36:0:812:G:O2'	36:0:813:U:H6	1.96	0.48
59:v:94:PRO:HD2	59:v:162:TYR:CZ	2.47	0.48
13:b:40:ILE:HG12	13:b:47:VAL:HG12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:N:1297:C:O2'	30:N:1302:A:N1	2.39	0.48
30:N:1853:A:N3	30:N:2233:U:O2'	2.43	0.48
36:0:835:U:OP1	53:I:53:ARG:NH2	2.32	0.48
52:H:31:HIS:HD2	52:H:34:TYR:H	1.59	0.48
2:P:235:GLY:O	30:N:2599:G:N7	2.47	0.48
30:N:698:C:O2'	30:N:734:A:N6	2.44	0.48
30:N:1266:G:O2'	30:N:2012:G:O6	2.22	0.48
30:N:1724:G:C6	30:N:1737:G:N2	2.81	0.48
30:N:2106:U:H2'	30:N:2107:G:C8	2.48	0.48
34:M:16:C:H3'	34:M:17:G:C5'	2.40	0.48
36:0:705:G:H21	46:A:31:ILE:HD11	1.79	0.48
44:8:120:LYS:HG2	44:8:123:ARG:HB3	1.94	0.48
30:N:160:A:N3	30:N:2208:C:O2'	2.44	0.48
30:N:2149:U:H2'	30:N:2150:C:O4'	2.13	0.48
33:U:51:ARG:HG3	33:U:51:ARG:HH11	1.79	0.48
35:x:449:A:H62	38:2:164:ARG:CG	2.25	0.48
35:x:465:U:P	35:x:465:U:H3'	2.54	0.48
36:0:642:A:C5	43:7:107:SER:HA	2.49	0.48
36:0:757:U:O2'	36:0:879:C:O2	2.31	0.48
48:D:8:ASN:HD22	48:D:22:ILE:HG13	1.78	0.48
57:t:32:ASP:O	57:t:33:LYS:C	2.56	0.48
30:N:897:C:O2'	58:u:55:U:O3'	2.30	0.48
34:M:1:U:H2'	34:M:2:G:H8	1.78	0.48
10:Y:57:LEU:HD22	28:q:54:ASP:HB3	1.96	0.48
15:d:51:ARG:HG2	30:N:1156:A:C8	2.49	0.48
30:N:1028:A:N3	30:N:2486:C:O2'	2.42	0.48
36:0:542:G:H5'	39:3:39:GLY:HA3	1.94	0.48
36:0:972:C:P	45:9:59:LYS:HD3	2.53	0.48
12:a:61:ALA:O	12:a:65:LEU:HB2	2.13	0.48
37:1:108:ARG:HH21	59:v:150:PRO:HG3	1.78	0.48
30:N:1475:G:H1'	30:N:1732:C:H41	1.79	0.48
32:C:171:ILE:HD13	32:C:196:LEU:HD11	1.96	0.48
33:U:68:ARG:C	33:U:68:ARG:HD2	2.38	0.48
47:B:64:THR:HG23	47:B:93:VAL:HG12	1.95	0.48
51:G:46:LYS:HG3	51:G:47:GLU:H	1.79	0.48
11:Z:57:VAL:HG13	11:Z:116:ALA:HB2	1.96	0.48
30:N:1070:A:N7	30:N:1096:A:O2'	2.36	0.48
35:x:434:A:O5'	36:0:1536:C:N4	2.42	0.48
37:1:81:LYS:O	37:1:85:LEU:CB	2.62	0.48
4:R:58:LYS:HG3	4:R:71:GLY:HA2	1.94	0.48
19:h:45:HIS:HB3	19:h:58:ILE:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:N:33:C:O2	30:N:447:A:N6	2.47	0.48
30:N:1783:A:H5'	30:N:2608:G:H4'	1.95	0.48
34:M:40:C:O2'	36:O:1338:G:C2'	2.61	0.48
35:x:455:C:H41	59:v:135:LYS:C	2.20	0.48
10:Y:111:ILE:HD11	30:N:636:G:C6	2.49	0.47
14:c:26:VAL:O	14:c:44:GLU:HA	2.14	0.47
27:p:19:ARG:HG2	30:N:126:A:O5'	2.14	0.47
30:N:2139:U:H2'	30:N:2140:G:C8	2.49	0.47
35:x:449:A:N6	38:2:164:ARG:CD	2.69	0.47
37:1:34:ALA:CB	59:v:23:ARG:CA	2.92	0.47
38:2:143:ARG:NH2	59:v:136:HIS:CB	2.77	0.47
41:5:88:MET:HE3	53:I:64:TYR:CD2	2.49	0.47
53:I:34:THR:HG23	53:I:36:SER:H	1.79	0.47
1:O:74:U:O2	20:i:29:ILE:HD13	2.13	0.47
30:N:306:U:H3	30:N:310:A:H62	0.61	0.47
30:N:500:G:N1	30:N:503:A:OP2	2.42	0.47
30:N:910:A:H2'	30:N:911:A:C8	2.50	0.47
33:U:5:LEU:HD12	33:U:5:LEU:N	2.29	0.47
35:x:438:C:P	35:x:438:C:H3'	2.54	0.47
36:O:618:C:O2'	51:G:14:ARG:NH2	2.47	0.47
44:8:28:ILE:HD11	44:8:57:MET:HE1	1.95	0.47
56:s:37:PHE:HB3	56:s:39:GLU:H	1.79	0.47
2:P:132:MET:HG2	2:P:135:ILE:HD12	1.96	0.47
3:Q:35:THR:HG22	3:Q:73:VAL:HG11	1.96	0.47
36:O:1103:C:HO2'	37:1:106:THR:HG21	1.74	0.47
37:1:207:ILE:HA	37:1:210:VAL:HG22	1.95	0.47
39:3:95:GLU:HA	39:3:100:ASN:ND2	2.29	0.47
7:V:33:VAL:HG13	7:V:59:ILE:HG21	1.97	0.47
8:W:114:LEU:HG	8:W:118:MET:HE3	1.96	0.47
12:a:82:GLU:OE2	12:a:86:ARG:NH2	2.47	0.47
17:f:90:LYS:NZ	30:N:746:U:O2'	2.47	0.47
21:j:65:GLY:HA3	21:j:83:GLU:O	2.15	0.47
30:N:355:U:H2'	30:N:356:G:H8	1.78	0.47
30:N:503:A:H4'	30:N:504:A:H5'	1.96	0.47
30:N:528:A:C2	30:N:2042:A:H2'	2.49	0.47
35:x:473:C:H5''	35:x:474:U:H6	1.79	0.47
49:E:89:MET:HE1	49:E:98:LYS:HD3	1.95	0.47
7:V:107:GLN:O	7:V:111:GLN:HB2	2.15	0.47
21:j:41:ARG:NH1	30:N:2262:U:OP1	2.47	0.47
31:L:13:THR:HA	31:L:23:LYS:HA	1.97	0.47
32:C:163:TYR:CD2	32:C:171:ILE:HD11	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:0:261:U:OP2	55:K:74:ARG:NH2	2.47	0.47
45:9:83:THR:O	45:9:87:LEU:CB	2.58	0.47
46:A:16:VAL:HG12	46:A:77:TYR:HB3	1.96	0.47
5:S:42:GLU:OE1	5:S:148:ARG:NH1	2.48	0.47
11:Z:136:MET:HE3	20:i:57:TYR:HB3	1.96	0.47
27:p:1:MET:HE2	27:p:1:MET:HB3	1.83	0.47
27:p:18:PHE:HA	27:p:43:THR:HG21	1.95	0.47
30:N:1187:G:N2	30:N:1188:U:O4	2.47	0.47
30:N:1724:G:O6	30:N:1737:G:N2	2.47	0.47
30:N:2243:U:H2'	30:N:2244:U:C6	2.50	0.47
37:1:136:MET:SD	37:1:139:ARG:NH2	2.87	0.47
1:O:44:G:OP2	31:L:1:MET:N	2.40	0.47
8:W:31:GLU:HG2	8:W:142:ILE:HG12	1.97	0.47
30:N:1509:A:H2'	30:N:1510:G:C8	2.50	0.47
30:N:2189:U:H2'	30:N:2190:G:C8	2.49	0.47
32:C:55:SER:O	32:C:58:ASN:ND2	2.48	0.47
32:C:163:TYR:HD2	32:C:171:ILE:HD11	1.79	0.47
34:M:28:G:O3'	36:0:1229:A:C5'	2.62	0.47
35:x:435:G:N2	36:0:693:G:P	2.88	0.47
36:0:1130:A:H61	36:0:1144:G:H1'	1.79	0.47
36:0:1302:C:C6	48:D:17:ILE:HD13	2.50	0.47
59:v:51:GLN:HE21	59:v:110:GLN:HB3	1.78	0.47
59:v:80:SER:OG	59:v:83:GLU:HG2	2.13	0.47
11:Z:42:THR:HG22	11:Z:93:VAL:HG12	1.97	0.47
27:p:12:ARG:CZ	27:p:44:VAL:HG21	2.45	0.47
29:r:11:CYS:SG	29:r:14:CYS:N	2.88	0.47
30:N:548:G:H5''	30:N:549:G:H5'	1.97	0.47
30:N:2776:A:O5'	30:N:2776:A:H8	1.97	0.47
37:1:35:ARG:NE	59:v:20:ALA:H	2.04	0.47
7:V:30:GLN:OE1	30:N:1095:A:N6	2.48	0.47
10:Y:81:ASP:HB2	10:Y:100:ILE:HD11	1.96	0.47
15:d:37:GLN:HE21	30:N:1252:G:H22	1.62	0.47
30:N:1999:C:O3'	30:N:2722:G:N2	2.48	0.47
44:8:38:TYR:HD2	44:8:39:PHE:HD1	1.61	0.47
45:9:10:LEU:O	45:9:71:LEU:HA	2.15	0.47
46:A:23:ILE:HG22	46:A:32:VAL:HG13	1.96	0.47
53:I:51:TYR:O	53:I:55:LEU:HB2	2.15	0.47
2:P:251:GLN:NE2	2:P:252:THR:O	2.48	0.47
8:W:81:ILE:O	30:N:1131:G:OP1	2.32	0.47
18:g:22:THR:O	18:g:26:LYS:HB3	2.15	0.47
30:N:2126:A:H2'	30:N:2162:G:C2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:N:2176:A:H2'	30:N:2177:C:C6	2.49	0.47
30:N:2252:G:N2	34:M:74:C:C2	2.83	0.47
34:M:28:G:H4'	36:0:1229:A:C5'	2.45	0.47
36:0:1006:G:O6	36:0:1023:U:C2	2.67	0.47
59:v:116:ILE:HG21	59:v:149:HIS:CE1	2.50	0.47
36:0:1006:G:C6	36:0:1023:U:O2	2.68	0.46
5:S:74:VAL:HG22	5:S:79:ILE:HD11	1.97	0.46
10:Y:41:ARG:NH1	30:N:807:U:OP2	2.48	0.46
35:x:461:A:H2'	35:x:462:U:C6	2.51	0.46
36:0:928:G:O2'	36:0:1533:C:OP1	2.34	0.46
36:0:1103:C:HO2'	37:1:106:THR:CG2	2.18	0.46
40:4:122:ASN:N	40:4:122:ASN:OD1	2.42	0.46
2:P:155:ALA:HB2	2:P:162:VAL:HG23	1.97	0.46
14:c:29:LYS:HD3	14:c:40:LEU:HD21	1.97	0.46
28:q:5:LYS:CE	30:N:254:G:N7	2.79	0.46
30:N:1847:A:O2'	30:N:1848:A:H8	1.98	0.46
34:M:40:C:C4'	36:0:1338:G:O2'	2.58	0.46
35:x:449:A:C6	38:2:164:ARG:HD3	2.51	0.46
40:4:89:HIS:CD2	40:4:90:THR:H	2.33	0.46
54:J:50:ALA:HB1	54:J:57:HIS:HB3	1.98	0.46
2:P:120:VAL:HG11	33:U:91:PHE:O	2.14	0.46
25:n:6:ASN:ND2	30:N:2020:A:H62	2.12	0.46
30:N:1447:C:O2'	30:N:1544:A:N3	2.39	0.46
30:N:1900:A:H1'	30:N:1970:A:H2'	1.97	0.46
30:N:2183:A:H2'	30:N:2184:A:C8	2.51	0.46
36:0:254:G:O3'	52:H:71:LYS:NZ	2.47	0.46
36:0:1113:C:H4'	38:2:14:ILE:HD12	1.97	0.46
36:0:1227:A:OP2	48:D:95:LEU:HD21	2.15	0.46
40:4:105:ILE:HD11	40:4:115:LEU:HD23	1.96	0.46
40:4:133:PRO:HA	40:4:136:VAL:HG12	1.98	0.46
30:N:857:G:N2	30:N:2269:G:O4'	2.49	0.46
30:N:2177:C:O2'	32:C:170:ILE:HG12	2.15	0.46
32:C:163:TYR:HB2	32:C:171:ILE:HD11	1.97	0.46
33:U:41:LYS:HD3	33:U:44:ILE:HD12	1.98	0.46
34:M:28:G:O3'	36:0:1229:A:H5''	2.16	0.46
34:M:28:G:H4'	36:0:1229:A:H5''	1.98	0.46
34:M:29:G:N2	36:0:1339:A:C2	2.84	0.46
36:0:674:G:P	41:5:86:ARG:HH22	2.38	0.46
36:0:677:U:H3	36:0:713:G:H22	1.62	0.46
36:0:999:C:N3	36:0:1042:A:N6	2.63	0.46
35:x:464:G:O5'	35:x:464:G:H8	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:8:129:LYS:HB2	44:8:129:LYS:HE3	1.71	0.46
59:v:98:LEU:HD21	59:v:100:LEU:HD21	1.98	0.46
2:P:167:ARG:HG2	2:P:172:VAL:HG12	1.96	0.46
11:Z:55:ARG:NH2	30:N:2469:A:O3'	2.49	0.46
14:c:92:VAL:HG21	14:c:97:LEU:HD21	1.98	0.46
19:h:41:LEU:HA	19:h:61:LYS:O	2.15	0.46
30:N:897:C:H5'	58:u:56:C:H5''	1.92	0.46
39:3:58:LYS:HD3	39:3:203:LEU:HD23	1.98	0.46
15:d:16:LYS:NZ	30:N:1227:G:OP2	2.48	0.46
25:n:16:ARG:NE	30:N:1266:G:OP1	2.37	0.46
30:N:284:U:O4	30:N:356:G:O6	2.33	0.46
30:N:1733:G:H2'	30:N:1734:G:C8	2.51	0.46
30:N:2273:A:H2'	30:N:2274:A:C8	2.51	0.46
35:x:451:G:N3	39:3:47:ARG:NE	2.64	0.46
37:1:104:TRP:O	37:1:108:ARG:N	2.46	0.46
39:3:140:ASN:N	39:3:182:PHE:O	2.49	0.46
41:5:62:MET:HG2	41:5:64:VAL:HG23	1.97	0.46
59:v:51:GLN:NE2	59:v:110:GLN:HB3	2.31	0.46
4:R:77:ILE:HD13	4:R:77:ILE:HG21	1.24	0.46
11:Z:9:PHE:HZ	30:N:911:A:H2'	1.80	0.46
30:N:1077:A:N6	30:N:1089:A:OP1	2.46	0.46
36:0:309:A:H2'	36:0:310:G:H8	1.81	0.46
59:v:149:HIS:HE1	59:v:151:HIS:CD2	2.34	0.46
3:Q:45:TYR:OH	30:N:2636:C:O2'	2.07	0.46
16:e:34:GLU:HG2	16:e:60:LYS:HG2	1.98	0.46
30:N:2104:C:H2'	30:N:2105:U:C6	2.51	0.46
30:N:2180:U:H2'	30:N:2181:U:O4'	2.16	0.46
30:N:2186:G:H2'	30:N:2187:U:O4'	2.16	0.46
36:0:1126:U:OP1	45:9:7:ARG:NH2	2.49	0.46
2:P:182:ARG:NH1	30:N:1800:C:OP2	2.49	0.45
5:S:24:SER:HB3	5:S:27:GLN:HB2	1.97	0.45
12:a:44:LEU:HD23	12:a:113:ILE:HD13	1.98	0.45
25:n:25:VAL:HG21	25:n:28:LEU:HD23	1.97	0.45
34:M:32:U:C6	44:8:129:LYS:NZ	2.75	0.45
35:x:464:G:O5'	35:x:464:G:C8	2.69	0.45
36:0:352:C:O2'	36:0:354:G:OP1	2.32	0.45
36:0:523:A:N1	47:B:89:ASP:HB2	2.31	0.45
45:9:12:ALA:HB3	45:9:18:ILE:HB	1.99	0.45
1:O:7:G:H5'	13:b:29:HIS:CE1	2.52	0.45
20:i:48:MET:SD	20:i:51:GLN:NE2	2.89	0.45
30:N:1064:C:N4	30:N:1070:A:OP2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:N:1794:A:H2'	30:N:1795:C:C6	2.52	0.45
35:x:449:A:N7	38:2:164:ARG:NH1	2.64	0.45
36:0:1106:G:O2'	38:2:169:ARG:NH1	2.49	0.45
36:0:1218:C:H2'	36:0:1219:A:C8	2.51	0.45
59:v:92:TYR:CD1	59:v:125:PHE:HE2	2.34	0.45
5:S:80:ARG:HA	34:M:55:C:H4'	1.97	0.45
7:V:79:LEU:HD21	7:V:109:ILE:HG21	1.99	0.45
15:d:37:GLN:NE2	30:N:1252:G:H22	2.14	0.45
27:p:33:ARG:NH2	30:N:467:G:OP1	2.46	0.45
33:U:4:ILE:HG22	33:U:37:VAL:O	2.16	0.45
36:0:1380:U:O2	36:0:1382:C:N4	2.49	0.45
38:2:108:LYS:HD3	38:2:111:LEU:HD12	1.96	0.45
47:B:38:TYR:HB2	47:B:52:VAL:O	2.15	0.45
2:P:19:VAL:HG23	2:P:203:ARG:HB3	1.99	0.45
22:k:37:ARG:HG2	22:k:46:PHE:HB3	1.99	0.45
36:0:481:G:O2'	36:0:483:C:N4	2.50	0.45
36:0:1379:G:O6	42:6:2:PRO:HB2	2.17	0.45
37:1:53:ALA:O	37:1:57:LEU:CB	2.65	0.45
38:2:65:ARG:O	38:2:65:ARG:HG3	2.16	0.45
5:S:140:GLU:CD	31:L:27:THR:HG23	2.41	0.45
8:W:82:GLY:HA2	30:N:1131:G:OP1	2.17	0.45
11:Z:9:PHE:CZ	30:N:911:A:H2'	2.52	0.45
17:f:38:TYR:CD2	25:n:28:LEU:HD22	2.50	0.45
32:C:184:LYS:O	32:C:188:ASN:ND2	2.50	0.45
36:0:1160:G:OP1	37:1:132:LYS:CE	2.58	0.45
37:1:100:MET:HA	37:1:107:VAL:HG21	1.99	0.45
37:1:163:VAL:HG21	37:1:173:ILE:HD11	1.98	0.45
46:A:49:GLY:O	46:A:69:ARG:NH1	2.50	0.45
7:V:11:LEU:HD23	30:N:1097:U:O2	2.16	0.45
36:0:766:A:OP2	36:0:812:G:N2	2.49	0.45
37:1:53:ALA:O	37:1:57:LEU:HB2	2.16	0.45
38:2:155:GLY:HA2	38:2:163:ALA:HB1	1.98	0.45
3:Q:149:ASN:HD22	30:N:2572:A:H2'	1.81	0.45
14:c:63:LYS:HE3	14:c:65:SER:HB2	1.99	0.45
30:N:219:A:N3	30:N:234:U:O2'	2.40	0.45
30:N:1078:U:O2'	30:N:1088:A:OP1	2.34	0.45
30:N:2514:U:H2'	30:N:2515:C:C6	2.51	0.45
2:P:260:ASN:ND2	2:P:263:THR:OG1	2.48	0.45
10:Y:54:GLN:HE21	30:N:2428:G:N2	2.14	0.45
10:Y:100:ILE:HG21	10:Y:100:ILE:HD13	1.75	0.45
16:e:3:ALA:HA	16:e:40:MET:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:N:45:G:H5''	30:N:46:G:H5'	1.97	0.45
36:O:971:G:O6	36:O:1364:U:O2'	2.35	0.45
40:4:18:VAL:HA	40:4:34:THR:O	2.16	0.45
40:4:80:THR:OG1	40:4:81:LEU:N	2.50	0.45
44:8:106:ARG:NH1	44:8:107:ASP:O	2.50	0.45
51:G:38:PHE:CE1	51:G:51:ARG:HG2	2.52	0.45
2:P:145:GLU:HB2	2:P:188:CYS:HB3	1.98	0.45
25:n:4:GLN:NE2	30:N:2016:U:O2	2.49	0.45
29:r:1:MET:HE2	29:r:34:LYS:HD3	1.98	0.45
30:N:499:U:O4	30:N:503:A:N7	2.50	0.45
30:N:749:A:N1	30:N:753:A:O2'	2.43	0.45
30:N:897:C:O2'	58:u:55:U:H4'	2.17	0.45
30:N:2123:G:H2'	30:N:2124:G:C8	2.52	0.45
34:M:39:C:H1'	36:O:1339:A:O2'	2.17	0.45
36:O:552:U:H5'	47:B:83:ARG:NH1	2.32	0.45
3:Q:37:VAL:HG22	3:Q:48:ILE:HG22	2.00	0.44
3:Q:146:ILE:HD13	3:Q:146:ILE:HG21	1.62	0.44
10:Y:82:LEU:HA	10:Y:85:VAL:HG13	1.99	0.44
11:Z:123:LYS:HE3	30:N:2483:C:N3	2.31	0.44
12:a:3:HIS:O	12:a:4:ARG:HB2	2.17	0.44
14:c:29:LYS:HB2	14:c:83:SER:HB2	1.98	0.44
15:d:97:ASP:OD2	16:e:13:ARG:NE	2.47	0.44
30:N:514:A:N3	30:N:581:C:O2'	2.44	0.44
30:N:1176:U:H2'	30:N:1177:G:C8	2.51	0.44
33:U:18:GLN:HE22	33:U:44:ILE:HD13	1.83	0.44
36:O:1356:G:H2'	36:O:1357:A:C8	2.51	0.44
44:8:16:ALA:O	44:8:67:VAL:HA	2.17	0.44
30:N:613:A:N7	30:N:616:A:C6	2.85	0.44
30:N:1311:G:N2	30:N:1603:A:H62	2.14	0.44
33:U:12:LEU:HD22	33:U:19:VAL:HG11	1.99	0.44
35:x:441:U:N3	36:O:1400:C:O4'	2.50	0.44
39:3:62:ARG:HH21	39:3:68:LEU:HA	1.82	0.44
39:3:100:ASN:OD1	39:3:111:ARG:NH1	2.51	0.44
41:5:70:VAL:HA	41:5:73:GLU:HG2	1.99	0.44
53:I:71:THR:HG23	53:I:73:ARG:H	1.82	0.44
3:Q:4:LEU:HD21	3:Q:96:ILE:HG22	1.99	0.44
4:R:148:ILE:HB	4:R:169:VAL:HG22	1.98	0.44
24:m:54:MET:HB2	24:m:54:MET:HE3	1.75	0.44
26:o:40:ASP:O	26:o:44:ARG:N	2.50	0.44
30:N:1437:C:O2'	30:N:1516:G:O2'	2.35	0.44
32:C:45:ALA:HA	32:C:172:HIS:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:0:1096:C:O2	36:0:1170:A:O2'	2.34	0.44
36:0:1317:C:H4'	49:E:49:GLN:HE21	1.83	0.44
2:P:141:VAL:HG13	2:P:190:ALA:HB1	1.99	0.44
3:Q:13:ARG:HD2	3:Q:15:PHE:CZ	2.53	0.44
9:X:99:ILE:HD13	9:X:115:ILE:HG23	1.99	0.44
11:Z:40:ARG:HD3	11:Z:93:VAL:HG21	2.00	0.44
30:N:537:G:O2'	30:N:556:A:N6	2.50	0.44
30:N:2130:U:H5'	30:N:2159:G:N2	2.33	0.44
30:N:2141:G:H2'	30:N:2142:A:C8	2.48	0.44
35:x:442:G:O6	58:u:38:A:N3	2.51	0.44
51:G:6:LEU:HD12	51:G:19:VAL:HB	1.99	0.44
3:Q:43:ASP:OD1	30:N:2784:U:H4'	2.17	0.44
5:S:131:GLY:HA3	30:N:2305:U:H5''	1.98	0.44
13:b:29:HIS:HB3	13:b:36:TYR:HB2	2.00	0.44
15:d:113:ALA:O	15:d:117:LEU:HB2	2.18	0.44
17:f:77:ASP:HB2	17:f:102:HIS:HB2	2.00	0.44
23:l:1:MET:HG2	23:l:4:LYS:HD3	2.00	0.44
23:l:13:GLU:HA	23:l:16:THR:HG22	1.99	0.44
27:p:35:ARG:HG3	27:p:42:LEU:HD21	1.98	0.44
30:N:33:C:N4	30:N:446:G:O2'	2.46	0.44
30:N:1072:C:H42	30:N:1098:A:N6	2.15	0.44
15:d:88:VAL:HA	16:e:49:ILE:CD1	2.47	0.44
27:p:16:HIS:ND1	30:N:684:G:OP1	2.48	0.44
32:C:5:THR:OG1	32:C:6:LYS:N	2.49	0.44
37:1:166:ALA:HB3	37:1:191:SER:HB3	2.00	0.44
40:4:107:ALA:HA	40:4:125:ALA:HB3	1.99	0.44
55:K:67:ILE:HG13	55:K:71:LYS:HD3	2.00	0.44
4:R:108:ILE:HG21	4:R:108:ILE:HD13	1.72	0.44
15:d:31:VAL:HG13	30:N:580:U:O3'	2.17	0.44
25:n:16:ARG:HA	30:N:2046:G:H5'	1.99	0.44
30:N:675:A:N3	30:N:2443:C:O2'	2.47	0.44
36:0:296:U:O2'	36:0:556:C:O2	2.33	0.44
42:6:56:LYS:HE3	42:6:60:GLU:HG3	1.99	0.44
2:P:85:PRO:HG3	30:N:1567:G:H2'	2.00	0.44
7:V:133:ALA:O	7:V:138:LEU:N	2.51	0.44
30:N:569:U:H5''	30:N:821:A:C2	2.52	0.44
30:N:881:G:N2	30:N:895:U:O2	2.49	0.44
30:N:2506[A]:U:OP2	30:N:2576:G:N2	2.47	0.44
35:x:442:G:N2	36:0:1493:A:C2	2.74	0.44
36:0:1060:U:P	49:E:85:ARG:HH22	2.41	0.44
36:0:1067:A:N1	36:0:1108:G:O2'	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:0:1080:A:OP1	40:4:52:LYS:HD2	2.18	0.44
36:0:1178:G:C5	44:8:99:ARG:NH2	2.86	0.44
3:Q:1:MET:HG2	3:Q:205:PRO:HG2	2.00	0.44
3:Q:19:GLY:HA3	14:c:80:VAL:HG23	2.00	0.44
4:R:165:HIS:CD2	30:N:1205:A:C6	3.05	0.44
8:W:113:PRO:HD2	30:N:558:U:P	2.58	0.44
21:j:33:ALA:N	21:j:64:ASP:OD1	2.51	0.44
23:l:20:ASN:HB3	23:l:50:VAL:HG22	2.00	0.44
32:C:42:VAL:HG12	32:C:216:THR:HG22	2.00	0.44
36:0:1062:U:H2'	36:0:1063:C:C6	2.52	0.44
36:0:1507:A:H2'	36:0:1508:A:C8	2.53	0.44
42:6:73:VAL:HG12	42:6:90:GLU:HA	2.00	0.44
6:T:66:GLY:O	6:T:69:ARG:HB3	2.17	0.43
22:k:17:ASN:HB2	22:k:25:THR:HB	1.99	0.43
30:N:221:A:N1	30:N:265:A:O2'	2.51	0.43
36:0:714:G:H2'	36:0:715:A:C8	2.53	0.43
36:0:1270:G:O2'	36:0:1313:U:O2'	2.31	0.43
40:4:106:ILE:HG21	40:4:106:ILE:HD13	1.74	0.43
46:A:31:ILE:HD13	46:A:31:ILE:HG21	1.70	0.43
47:B:114:ARG:HG2	47:B:119:VAL:HB	1.99	0.43
59:v:149:HIS:HE1	59:v:151:HIS:HD2	1.66	0.43
2:P:201:MET:HG3	2:P:202:LEU:HD12	2.01	0.43
7:V:24:VAL:HG12	30:N:1070:A:H61	1.83	0.43
12:a:90:ARG:HD2	30:N:2880:C:O2'	2.18	0.43
36:0:723:U:C5'	56:s:49:LYS:HE2	2.48	0.43
7:V:11:LEU:HD11	7:V:28:LEU:HB3	1.99	0.43
30:N:1826:G:O2'	30:N:1971:U:OP2	2.35	0.43
33:U:66:ASN:ND2	33:U:134:VAL:O	2.51	0.43
10:Y:77:ILE:CD1	10:Y:108:ALA:HB1	2.48	0.43
30:N:476:G:N1	30:N:479:A:OP2	2.46	0.43
30:N:2170:A:H2'	30:N:2171:A:O4'	2.19	0.43
5:S:22:TYR:OH	5:S:165:GLU:OE2	2.34	0.43
36:0:825:A:H4'	43:7:3:MET:HE2	1.99	0.43
36:0:938:A:N3	36:0:1376:U:O2'	2.40	0.43
40:4:114:VAL:O	40:4:118:ALA:HB2	2.18	0.43
48:D:16:VAL:HG23	48:D:17:ILE:HG13	2.00	0.43
11:Z:118:LYS:HE3	11:Z:118:LYS:HB3	1.84	0.43
29:r:7:VAL:HG22	29:r:38:GLY:HA3	1.99	0.43
30:N:715:A:N1	50:F:53:ARG:NH1	2.59	0.43
30:N:2006:C:O2'	30:N:2823:A:N3	2.48	0.43
36:0:9:G:OP2	40:4:126:LYS:HD2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:0:620:C:C2	39:3:132:ILE:HD13	2.53	0.43
42:6:59:LEU:O	42:6:63:GLU:HB2	2.18	0.43
42:6:107:ALA:HB1	42:6:133:THR:HB	2.00	0.43
3:Q:109:VAL:HG22	3:Q:203:VAL:HG22	2.00	0.43
4:R:165:HIS:CD2	30:N:1205:A:C5	3.06	0.43
6:T:85:LYS:HG2	6:T:141:ILE:HD12	1.99	0.43
9:X:63:VAL:HG12	9:X:107:LEU:HD21	2.00	0.43
25:n:8:PRO:HD2	30:N:1263:U:O2'	2.19	0.43
26:o:21:TYR:HE2	26:o:38:LYS:HB3	1.83	0.43
30:N:2291:U:H2'	30:N:2292:U:C6	2.54	0.43
36:0:35:G:O2'	47:B:115:SER:O	2.31	0.43
36:0:71:A:N1	36:0:99:C:O2'	2.47	0.43
36:0:269:C:H2'	36:0:270:A:C8	2.54	0.43
55:K:51:PHE:HA	55:K:54:MET:HG2	2.01	0.43
58:u:20:U:HO2'	58:u:21:A:P	2.41	0.43
2:P:61:ALA:O	2:P:63:ARG:NH2	2.52	0.43
9:X:70:ARG:NH2	30:N:2683:C:O2	2.52	0.43
21:j:37:ILE:HG22	21:j:38:VAL:HG23	2.01	0.43
30:N:1875:G:O3'	32:C:205:LYS:HE3	2.13	0.43
30:N:1924:C:O4'	34:M:13:A:O5'	2.37	0.43
36:0:228:A:H5'	51:G:63:GLN:NE2	2.34	0.43
36:0:1321:U:O2'	54:J:78:ARG:NH1	2.51	0.43
39:3:95:GLU:HG3	39:3:191:LEU:HD22	2.00	0.43
41:5:51:ILE:HG21	41:5:51:ILE:HD13	1.64	0.43
41:5:51:ILE:N	41:5:53:LYS:O	2.52	0.43
5:S:37:ASN:ND2	30:N:2313:C:O4'	2.52	0.43
10:Y:29:LYS:O	10:Y:30:THR:OG1	2.31	0.43
16:e:80:ARG:NH2	30:N:572:A:OP2	2.47	0.43
20:i:75:GLN:HB2	20:i:92:VAL:HG23	2.01	0.43
25:n:43:ILE:HG21	25:n:43:ILE:HD13	1.78	0.43
31:L:11:GLU:HA	31:L:25:ARG:HA	2.01	0.43
35:x:437:C:H2'	35:x:437:C:O2	2.18	0.43
35:x:443:C:C2	58:u:36:A:C2	3.02	0.43
36:0:1064:G:O2'	36:0:1190:G:N2	2.51	0.43
36:0:1119:C:H2'	36:0:1120:C:H6	1.84	0.43
36:0:1143:G:H2'	36:0:1144:G:H8	1.83	0.43
36:0:1530:G:H2'	36:0:1531:A:C8	2.54	0.43
39:3:159:LEU:HD13	39:3:175:ALA:HB1	2.01	0.43
53:I:33:ILE:HG21	53:I:33:ILE:HD13	1.68	0.43
5:S:105:THR:HG21	31:L:22:MET:SD	2.59	0.43
6:T:9:VAL:HB	6:T:50:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:a:3:HIS:CD2	30:N:2820:A:H4'	2.54	0.43
12:a:37:THR:HG22	12:a:110:MET:HE1	2.00	0.43
14:c:53:ARG:NH2	30:N:2720:U:OP1	2.51	0.43
30:N:828:U:H2'	30:N:829:A:C8	2.53	0.43
30:N:1044:C:O2'	30:N:1111:A:N1	2.48	0.43
30:N:2174:C:O2'	30:N:2175:C:H5'	2.19	0.43
36:0:713:G:H2'	36:0:714:G:C8	2.54	0.43
36:0:1026:G:C6	36:0:1035:A:C6	3.06	0.43
42:6:105:VAL:O	42:6:109:ARG:HG2	2.19	0.43
43:7:49:PHE:HA	43:7:60:GLU:O	2.19	0.43
48:D:29:ARG:NH2	48:D:63:PHE:HB2	2.32	0.43
3:Q:154:LYS:HE2	30:N:2024:G:O3'	2.19	0.42
7:V:79:LEU:O	7:V:82:LYS:NZ	2.52	0.42
10:Y:30:THR:O	10:Y:32:GLY:N	2.52	0.42
15:d:15:LYS:HE2	15:d:15:LYS:HB2	1.80	0.42
30:N:81:G:HO2'	30:N:295:G:HO2'	1.60	0.42
32:C:7:ARG:O	32:C:11:ILE:HG12	2.19	0.42
34:M:30:A:O2'	36:0:1340:A:C1'	2.67	0.42
36:0:96:U:H2'	36:0:97:G:C8	2.54	0.42
36:0:197:A:N1	36:0:220:G:O2'	2.45	0.42
36:0:555:U:H2'	36:0:556:C:C6	2.55	0.42
50:F:35:GLN:HE21	50:F:39:LEU:HD13	1.84	0.42
59:v:141:GLN:HB3	59:v:145:TRP:CZ2	2.54	0.42
3:Q:152:PRO:HG2	3:Q:156:PHE:CZ	2.54	0.42
10:Y:33:ARG:NH1	30:N:587:C:O2	2.46	0.42
15:d:37:GLN:NE2	30:N:1252:G:H1	2.17	0.42
33:U:47:PHE:HA	33:U:51:ARG:HB2	2.00	0.42
36:0:71:A:H61	36:0:99:C:H1'	1.83	0.42
37:1:15:HIS:HB2	37:1:203:ASN:HD22	1.84	0.42
37:1:186:ILE:HB	37:1:213:TYR:CZ	2.54	0.42
38:2:27:LYS:HE3	38:2:27:LYS:HB3	1.88	0.42
39:3:109:ALA:HA	39:3:161:LEU:HD11	2.00	0.42
40:4:157:ARG:HH11	40:4:157:ARG:HD3	1.64	0.42
47:B:50:ARG:HG3	47:B:90:LEU:HD11	2.01	0.42
6:T:16:ASP:O	6:T:26:ILE:HA	2.19	0.42
15:d:112:LYS:HG3	16:e:48:LYS:HE2	2.01	0.42
26:o:9:ILE:HG22	26:o:53:LYS:HB2	2.00	0.42
30:N:84:A:N1	30:N:98:G:O2'	2.46	0.42
30:N:285:G:O6	30:N:355:U:O2	2.36	0.42
30:N:2177:C:H5''	32:C:211:LYS:HZ3	1.84	0.42
36:0:537:G:H5''	47:B:110:ARG:HH12	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:4:72:ILE:HG21	40:4:72:ILE:HD13	1.83	0.42
42:6:71:PRO:O	42:6:96:ARG:NH1	2.51	0.42
12:a:28:LEU:HD23	12:a:48:VAL:HG21	2.01	0.42
17:f:93:ALA:HB2	30:N:1614:A:C2	2.55	0.42
22:k:31:PRO:HG2	22:k:33:LEU:HD13	2.01	0.42
30:N:1769:U:O2'	30:N:1958:C:OP1	2.36	0.42
34:M:34:U:P	44:8:129:LYS:CE	3.08	0.42
36:0:1118:U:H2'	36:0:1119:C:C6	2.55	0.42
40:4:112:ARG:O	40:4:116:GLU:HB2	2.19	0.42
43:7:18:GLN:NE2	43:7:70:ALA:HB1	2.35	0.42
51:G:70:ARG:HD2	51:G:70:ARG:HA	1.62	0.42
6:T:94:TYR:HA	6:T:106:SER:O	2.19	0.42
30:N:320:A:H4'	30:N:322:A:C8	2.54	0.42
30:N:1075:C:H2'	30:N:1076:C:C6	2.54	0.42
30:N:1236:G:HO2'	30:N:1237:A:P	2.42	0.42
30:N:2458:G:O2'	30:N:2460:U:O4	2.34	0.42
32:C:46:VAL:HG13	32:C:212:VAL:HG12	2.01	0.42
32:C:211:LYS:HE3	32:C:211:LYS:HB3	1.83	0.42
34:M:33:C:H5'	36:0:966:G:N2	2.35	0.42
36:0:746:A:H2'	36:0:747:A:C8	2.55	0.42
37:1:21:ARG:HG3	37:1:22:TYR:CD2	2.55	0.42
37:1:128:LYS:HG3	37:1:129:LEU:HG	2.01	0.42
2:P:247:PRO:HD3	30:N:1824:G:O3'	2.20	0.42
3:Q:25:THR:HG21	3:Q:193:VAL:HG22	2.00	0.42
30:N:503:A:O2'	30:N:506:G:OP2	2.28	0.42
30:N:700:G:O2'	30:N:1632:A:N3	2.48	0.42
30:N:2602:A:H4'	30:N:2603:G:H5'	2.01	0.42
31:L:30:HIS:ND1	31:L:31:ASP:O	2.52	0.42
34:M:30:A:HO2'	36:0:1340:A:H1'	1.81	0.42
35:x:440:A:H5''	36:0:1498:U:C4	2.55	0.42
36:0:228:A:C4'	51:G:63:GLN:HE21	2.32	0.42
36:0:1100:C:OP2	37:1:95:ARG:HD2	2.14	0.42
36:0:1380:U:C5	42:6:3:ARG:HA	2.54	0.42
37:1:164:ILE:HD11	37:1:210:VAL:HB	2.02	0.42
39:3:157:ALA:O	39:3:160:GLU:HB3	2.19	0.42
48:D:96:PRO:HA	48:D:109:ARG:HG2	2.01	0.42
2:P:146:MET:HE1	30:N:1800:C:C5'	2.50	0.42
5:S:140:GLU:HA	31:L:28:VAL:HG22	2.01	0.42
9:X:121:GLU:HG3	14:c:66:ASN:HD21	1.85	0.42
27:p:19:ARG:NH2	30:N:125:A:OP2	2.53	0.42
30:N:499:U:H3	30:N:503:A:H62	0.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:N:1058:U:H2'	30:N:1059:G:C8	2.55	0.42
35:x:448:U:H6	38:2:162:ILE:CG1	2.29	0.42
38:2:153:VAL:HG12	38:2:198:VAL:HG22	2.01	0.42
2:P:161:TYR:HB3	2:P:194:GLU:HB3	2.01	0.42
9:X:38:ILE:HD11	9:X:112:PHE:HZ	1.84	0.42
14:c:58:ALA:HA	14:c:74:PHE:O	2.20	0.42
16:e:81:LYS:HD2	30:N:973:A:OP2	2.20	0.42
30:N:1437:C:HO2'	30:N:1516:G:HO2'	1.67	0.42
35:x:473:C:H5''	35:x:474:U:C5	2.55	0.42
36:0:135:C:O2	51:G:1:MET:HB2	2.20	0.42
36:0:1081:A:H5'	40:4:23:LYS:HG3	2.01	0.42
42:6:78:ARG:HB3	42:6:80:VAL:HG23	2.01	0.42
53:I:21:ILE:HD12	53:I:22:ASP:HB2	2.01	0.42
55:K:62:ALA:HA	55:K:67:ILE:HG22	2.02	0.42
9:X:7:MET:HB3	9:X:18:ARG:HD2	2.02	0.42
22:k:37:ARG:HG3	22:k:48:THR:HB	2.02	0.42
30:N:373:U:H2'	30:N:374:A:H8	1.84	0.42
30:N:932:U:O2'	30:N:934:U:O4	2.36	0.42
30:N:1173:U:H3'	30:N:1174:U:H4'	2.02	0.42
30:N:1212:G:H2'	30:N:1236:G:H22	1.85	0.42
30:N:1394:U:H4'	30:N:1603:A:H4'	2.02	0.42
33:U:45:GLU:HA	33:U:48:GLU:HG2	2.00	0.42
33:U:51:ARG:HG3	33:U:51:ARG:NH1	2.35	0.42
35:x:443:C:O2	58:u:36:A:C2	2.61	0.42
36:0:1041:G:H2'	36:0:1042:A:C8	2.54	0.42
42:6:27:VAL:HG12	42:6:43:VAL:HG21	2.02	0.42
45:9:22:THR:HA	45:9:25:ILE:HG22	2.02	0.42
1:O:89:U:H1'	30:N:958:U:H2'	2.02	0.42
3:Q:149:ASN:ND2	30:N:2572:A:H2'	2.35	0.42
6:T:22:GLN:HE22	6:T:55:ARG:HH21	1.66	0.42
36:0:573:A:N3	36:0:883:C:O2'	2.47	0.42
36:0:1216:A:H5''	49:E:5:SER:HB2	2.02	0.42
53:I:26:ILE:HG21	53:I:67:LEU:HB3	2.01	0.42
15:d:24:TYR:CD1	30:N:533:G:H5'	2.55	0.41
17:f:85:ILE:HA	17:f:94:ASP:O	2.19	0.41
30:N:1912:A:N1	36:0:1408:A:C4'	2.81	0.41
30:N:2155:U:H2'	30:N:2156:G:H5'	2.01	0.41
30:N:2469:A:N6	30:N:2481:G:O2'	2.50	0.41
41:5:6:ILE:HB	41:5:62:MET:HB3	2.02	0.41
54:J:4:SER:HB3	54:J:5:LEU:HD12	2.00	0.41
55:K:33:LYS:O	55:K:37:ALA:HB3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:V:13:VAL:HG21	7:V:23:PRO:HG2	2.02	0.41
9:X:77:ILE:HD13	9:X:77:ILE:HG21	1.75	0.41
13:b:94:ARG:HH12	30:N:2294:G:P	2.43	0.41
23:l:56:LEU:HD23	23:l:56:LEU:HA	1.86	0.41
29:r:3:VAL:HG12	29:r:36:ARG:HB3	2.02	0.41
30:N:372:G:H1'	30:N:373:U:H5	1.85	0.41
30:N:2029:G:N1	30:N:2033:A:OP2	2.34	0.41
30:N:2554:U:H2'	30:N:2555:U:C6	2.55	0.41
34:M:40:C:HO2'	36:O:1338:G:H1'	1.76	0.41
36:O:254:G:H5''	52:H:71:LYS:HE3	2.02	0.41
36:O:1371:G:O3'	44:8:71:GLY:HA3	2.21	0.41
39:3:95:GLU:HA	39:3:100:ASN:HD22	1.84	0.41
47:B:34:CYS:HA	47:B:55:VAL:HA	2.01	0.41
2:P:16:VAL:HG22	2:P:206:GLY:HA3	2.02	0.41
2:P:236:GLU:HB3	30:N:2599:G:N7	2.35	0.41
35:x:441:U:C2	36:O:1400:C:O4'	2.72	0.41
36:O:331:G:H2'	55:K:5:LYS:NZ	2.35	0.41
36:O:1071:C:H2'	36:O:1072:G:H8	1.85	0.41
13:b:34:HIS:ND1	13:b:53:THR:OG1	2.44	0.41
19:h:16:GLY:C	19:h:18:ASP:H	2.28	0.41
21:j:41:ARG:HH12	30:N:2262:U:H5''	1.84	0.41
21:j:82:ILE:HG21	21:j:82:ILE:HD13	1.88	0.41
30:N:2175:C:OP1	32:C:8:MET:HG2	2.20	0.41
30:N:2788:C:H2'	30:N:2789:C:C6	2.56	0.41
30:N:2866:U:H4'	30:N:2867:G:H5'	2.02	0.41
33:U:65:ALA:O	33:U:68:ARG:HB3	2.20	0.41
35:x:451:G:N3	39:3:47:ARG:NH1	2.68	0.41
36:O:1118:U:H2'	36:O:1119:C:H6	1.85	0.41
39:3:200:ILE:HD13	39:3:200:ILE:HG21	1.76	0.41
41:5:3:HIS:CE1	41:5:95:ALA:HB2	2.56	0.41
55:K:33:LYS:O	55:K:37:ALA:CB	2.68	0.41
55:K:56:PRO:O	55:K:60:ARG:HB2	2.20	0.41
2:P:146:MET:HE1	30:N:1800:C:H5'	2.02	0.41
30:N:493:G:H2'	30:N:494:G:O4'	2.21	0.41
30:N:526:A:O2'	30:N:2043:C:O2	2.34	0.41
30:N:2724:U:H2'	30:N:2725:A:C8	2.56	0.41
32:C:195:ALA:O	32:C:198:LYS:HB2	2.20	0.41
33:U:12:LEU:HD12	33:U:13:GLY:N	2.36	0.41
33:U:78:VAL:HG23	33:U:142:VAL:HG11	2.01	0.41
36:O:297:G:N2	36:O:300:A:OP2	2.48	0.41
1:O:72:G:N2	1:O:104:A:H62	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:156:PHE:CD1	8:W:81:ILE:HD12	2.55	0.41
5:S:33:LYS:HD3	5:S:92:ARG:NH1	2.35	0.41
28:q:33:LEU:HB2	30:N:2420:C:OP2	2.19	0.41
30:N:927:A:H2'	30:N:928:A:C8	2.56	0.41
30:N:2124:G:O2'	32:C:41:SER:HB3	2.20	0.41
30:N:2572:A:OP1	30:N:2574:G:H4'	2.20	0.41
33:U:54:LEU:HD23	33:U:54:LEU:C	2.45	0.41
34:M:1:U:H2'	34:M:2:G:C8	2.54	0.41
8:W:96:ARG:HH21	8:W:99:ARG:HG2	1.84	0.41
8:W:110:PRO:O	8:W:115:GLY:HA3	2.20	0.41
15:d:33:ARG:HG2	30:N:1252:G:N3	2.35	0.41
19:h:10:GLU:OE2	19:h:22:ARG:NH2	2.48	0.41
27:p:34:ARG:HD3	27:p:34:ARG:HH11	1.53	0.41
30:N:1509:A:H2'	30:N:1510:G:H8	1.84	0.41
30:N:2176:A:H4'	32:C:215:SER:CB	2.50	0.41
30:N:2193:G:H2'	30:N:2194:U:C6	2.56	0.41
36:0:723:U:H5''	56:s:49:LYS:HE2	2.01	0.41
39:3:72:PHE:HE1	39:3:94:LEU:HD11	1.84	0.41
41:5:42:TRP:HB2	41:5:59:TYR:HB2	2.01	0.41
44:8:96:SER:O	44:8:99:ARG:HB3	2.21	0.41
2:P:153:GLN:O	30:N:1818:U:O2'	2.31	0.41
2:P:178:SER:HB2	30:N:1799:G:N7	2.36	0.41
33:U:8:LYS:O	33:U:9:VAL:O	2.38	0.41
36:0:337:G:H2'	36:0:338:A:C8	2.56	0.41
36:0:692:U:O2'	36:0:694:A:N7	2.50	0.41
36:0:1251:A:N3	36:0:1369:C:O2'	2.51	0.41
45:9:36:VAL:HG22	45:9:76:ILE:HG12	2.03	0.41
48:D:87:ARG:HG3	48:D:97:VAL:HG13	2.03	0.41
59:v:112:LEU:HD22	59:v:146:LEU:HD21	2.02	0.41
1:O:8:C:O3'	13:b:25:ARG:NH1	2.54	0.41
4:R:69:ARG:NH2	30:N:2445:G:OP1	2.47	0.41
11:Z:136:MET:SD	20:i:75:GLN:O	2.78	0.41
22:k:3:ARG:HD3	30:N:1365:A:OP1	2.21	0.41
27:p:24:THR:HG23	27:p:27:GLY:H	1.86	0.41
30:N:307:G:N1	30:N:310:A:OP2	2.50	0.41
30:N:2087:G:H2'	30:N:2088:A:H8	1.86	0.41
30:N:2602:A:C6	34:M:75:A:H5''	2.56	0.41
36:0:151:A:H3'	36:0:152:A:H8	1.86	0.41
36:0:384:G:H2'	36:0:385:C:C6	2.56	0.41
36:0:1306:A:N6	36:0:1331:G:H1'	2.35	0.41
42:6:44:TYR:O	42:6:48:GLU:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:6:75:VAL:HA	42:6:87:VAL:O	2.21	0.41
51:G:40:ASN:HB3	51:G:43:ALA:HB2	2.03	0.41
1:O:41:G:H21	30:N:2340:A:H5'	1.86	0.41
5:S:73:SER:OG	34:M:55:C:H4'	2.21	0.41
26:o:5:ILE:HG21	26:o:28:ARG:HH12	1.86	0.41
30:N:1912:A:C6	36:O:1408:A:H4'	2.56	0.41
33:U:96:THR:HB	33:U:117:LEU:HD21	2.03	0.41
36:O:109:A:H5'	36:O:110:C:C5	2.56	0.41
36:O:501:C:H2'	36:O:502:A:C8	2.56	0.41
48:D:25:VAL:HG23	48:D:29:ARG:HB3	2.03	0.41
1:O:42:C:C6	5:S:66:LEU:HB2	2.56	0.40
2:P:154:LEU:HD13	2:P:176:LEU:HD21	2.03	0.40
5:S:10:ASP:OD1	5:S:11:GLU:N	2.54	0.40
9:X:87:LEU:HD23	9:X:94:PRO:HB3	2.03	0.40
30:N:629:G:N3	30:N:639:U:O2'	2.52	0.40
30:N:1019:U:H3	30:N:1142:A:H61	1.61	0.40
30:N:2328:A:H2'	30:N:2329:U:C6	2.55	0.40
36:O:82:G:N2	36:O:84:U:O4	2.55	0.40
38:2:55:ILE:HD13	38:2:55:ILE:HG21	1.65	0.40
39:3:124:MET:HE3	39:3:146:ARG:HG2	2.03	0.40
4:R:125:SER:O	4:R:137:LYS:NZ	2.54	0.40
30:N:632:A:H2'	30:N:633:A:C8	2.56	0.40
30:N:1074:G:H2'	30:N:1075:C:C6	2.57	0.40
30:N:1858:A:H61	30:N:1884:G:H1'	1.86	0.40
32:C:60:ARG:HE	32:C:162:ARG:HH11	1.68	0.40
36:O:1095:U:P	36:O:1108:G:H1	2.45	0.40
40:4:150:PRO:HA	40:4:153:VAL:HG22	2.03	0.40
44:8:129:LYS:HG3	44:8:130:ARG:H	1.86	0.40
51:G:76:LYS:HE3	51:G:76:LYS:HB3	1.87	0.40
58:u:21:A:HO2'	58:u:22:G:C5'	2.34	0.40
13:b:111:ARG:NH1	30:N:2376:A:N3	2.69	0.40
23:l:14:LEU:HD23	23:l:14:LEU:HA	1.94	0.40
30:N:214:G:N2	30:N:216:A:N3	2.68	0.40
30:N:373:U:H2'	30:N:374:A:C8	2.56	0.40
35:x:465:U:O2	35:x:465:U:C2'	2.69	0.40
36:O:1516:G:N2	36:O:1519:A:OP2	2.48	0.40
2:P:107:PRO:HA	2:P:195:VAL:HA	2.03	0.40
6:T:90:VAL:O	6:T:160:LYS:HA	2.21	0.40
13:b:24:THR:HG22	13:b:42:PRO:HD3	2.03	0.40
17:f:24:ILE:HD13	17:f:36:LEU:HD11	2.02	0.40
19:h:11:VAL:HA	19:h:72:ILE:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:i:9:ARG:HH11	20:i:9:ARG:HD3	1.75	0.40
30:N:657:U:H2'	30:N:658:U:C6	2.56	0.40
30:N:715:A:N6	50:F:53:ARG:NH1	2.66	0.40
30:N:2220:U:H5''	33:U:112:LYS:HE3	2.04	0.40
30:N:2541:A:HO2'	30:N:2765:A:H2	1.68	0.40
34:M:34:U:OP2	44:8:129:LYS:CE	2.64	0.40
38:2:85:GLU:HA	38:2:88:ARG:HG2	2.03	0.40
44:8:20:PHE:HB2	44:8:64:TYR:O	2.21	0.40
45:9:25:ILE:HD12	45:9:25:ILE:HA	2.00	0.40
50:F:26:GLU:OE2	50:F:77:ARG:NE	2.53	0.40
1:O:80:U:H2'	1:O:81:G:H8	1.87	0.40
8:W:92:MET:HE3	8:W:92:MET:HB3	1.92	0.40
15:d:28:ARG:NH1	30:N:532:A:H3'	2.36	0.40
24:m:44:ILE:HD13	24:m:44:ILE:HA	1.96	0.40
30:N:1182:G:H2'	30:N:1183:U:O4'	2.22	0.40
30:N:2131:U:O5'	30:N:2133:G:H4'	2.21	0.40
38:2:24:ALA:HB1	38:2:28:GLU:HG2	2.02	0.40
41:5:90:MET:HE1	53:I:23:TYR:CE1	2.56	0.40
55:K:28:MET:HE3	55:K:58:VAL:HG22	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	216/218 (99%)	213 (99%)	3 (1%)	59	71
3	Q	164/164 (100%)	159 (97%)	5 (3%)	36	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	R	165/165 (100%)	162 (98%)	3 (2%)	51	67
5	S	145/150 (97%)	144 (99%)	1 (1%)	76	80
6	T	137/138 (99%)	137 (100%)	0	100	100
7	V	109/110 (99%)	109 (100%)	0	100	100
8	W	116/116 (100%)	115 (99%)	1 (1%)	70	77
9	X	103/104 (99%)	101 (98%)	2 (2%)	50	66
10	Y	102/103 (99%)	100 (98%)	2 (2%)	48	66
11	Z	109/109 (100%)	108 (99%)	1 (1%)	70	77
12	a	100/102 (98%)	98 (98%)	2 (2%)	48	66
13	b	86/87 (99%)	85 (99%)	1 (1%)	63	74
14	c	98/100 (98%)	95 (97%)	3 (3%)	35	56
15	d	89/90 (99%)	87 (98%)	2 (2%)	45	64
16	e	84/84 (100%)	83 (99%)	1 (1%)	63	74
17	f	93/93 (100%)	93 (100%)	0	100	100
18	g	80/85 (94%)	79 (99%)	1 (1%)	61	73
19	h	83/85 (98%)	81 (98%)	2 (2%)	43	63
20	i	78/78 (100%)	77 (99%)	1 (1%)	61	73
21	j	56/63 (89%)	55 (98%)	1 (2%)	51	67
22	k	67/68 (98%)	67 (100%)	0	100	100
23	l	55/55 (100%)	54 (98%)	1 (2%)	51	67
24	m	48/49 (98%)	48 (100%)	0	100	100
25	n	47/48 (98%)	46 (98%)	1 (2%)	47	65
26	o	45/49 (92%)	45 (100%)	0	100	100
27	p	38/38 (100%)	38 (100%)	0	100	100
28	q	51/52 (98%)	49 (96%)	2 (4%)	28	49
29	r	34/50 (68%)	33 (97%)	1 (3%)	37	57
31	L	48/63 (76%)	48 (100%)	0	100	100
32	C	110/174 (63%)	109 (99%)	1 (1%)	70	77
33	U	114/114 (100%)	114 (100%)	0	100	100
37	1	179/198 (90%)	177 (99%)	2 (1%)	65	75
38	2	170/178 (96%)	167 (98%)	3 (2%)	51	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	3	172/173 (99%)	170 (99%)	2 (1%)	63	74
40	4	113/123 (92%)	107 (95%)	6 (5%)	20	41
41	5	87/112 (78%)	87 (100%)	0	100	100
42	6	124/125 (99%)	123 (99%)	1 (1%)	73	79
43	7	104/105 (99%)	101 (97%)	3 (3%)	37	57
44	8	105/107 (98%)	104 (99%)	1 (1%)	68	77
45	9	86/90 (96%)	85 (99%)	1 (1%)	63	74
46	A	90/98 (92%)	89 (99%)	1 (1%)	65	75
47	B	103/104 (99%)	103 (100%)	0	100	100
48	D	91/96 (95%)	89 (98%)	2 (2%)	45	64
49	E	79/83 (95%)	79 (100%)	0	100	100
50	F	75/77 (97%)	75 (100%)	0	100	100
51	G	65/65 (100%)	64 (98%)	1 (2%)	57	71
52	H	74/77 (96%)	73 (99%)	1 (1%)	59	71
53	I	48/66 (73%)	47 (98%)	1 (2%)	47	65
54	J	70/80 (88%)	66 (94%)	4 (6%)	18	40
55	K	65/66 (98%)	65 (100%)	0	100	100
56	s	44/61 (72%)	43 (98%)	1 (2%)	44	63
59	v	108/156 (69%)	108 (100%)	0	100	100
All	All	4922/5244 (94%)	4854 (99%)	68 (1%)	57	71

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	P	141	VAL
2	P	165	VAL
2	P	218	PRO
3	Q	48	ILE
3	Q	73	VAL
3	Q	177	VAL
3	Q	202	ILE
3	Q	205	PRO
4	R	69	ARG
4	R	149	ILE
4	R	163	ASN

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Mol	Chain	Res	Type
5	S	31	VAL
8	W	57	LEU
9	X	58	LEU
9	X	86	LEU
10	Y	77	ILE
10	Y	94	THR
11	Z	128	THR
12	a	50	PRO
12	a	70	THR
13	b	3	LYS
14	c	32	VAL
14	c	53	ARG
14	c	73	VAL
15	d	16	LYS
15	d	33	ARG
16	e	49	ILE
18	g	32	LEU
19	h	28	VAL
19	h	68	SER
20	i	65	VAL
21	j	41	ARG
23	l	6	LEU
25	n	28	LEU
28	q	2	PRO
28	q	32	ILE
29	r	26	ILE
32	C	33	LEU
37	1	11	LYS
37	1	207	ILE
38	2	55	ILE
38	2	75	ILE
38	2	200	VAL
39	3	5	LEU
39	3	143	VAL
40	4	15	LEU
40	4	115	LEU
40	4	120	VAL
40	4	123	VAL
40	4	141	ILE
40	4	157	ARG
42	6	25	LYS
43	7	51	VAL

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Mol	Chain	Res	Type
43	7	121	LEU
43	7	125	ILE
44	8	120	LYS
45	9	17	LEU
46	A	31	ILE
48	D	25	VAL
48	D	98	ARG
51	G	19	VAL
52	H	61	ILE
53	I	21	ILE
54	J	5	LEU
54	J	11	ILE
54	J	49	ILE
54	J	58	VAL
56	s	29	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (77) such sidechains are listed below:

Mol	Chain	Res	Type
2	P	53	HIS
2	P	86	ASN
2	P	239	ASN
2	P	260	ASN
3	Q	32	ASN
3	Q	49	GLN
3	Q	149	ASN
3	Q	150	GLN
3	Q	173	GLN
4	R	136	GLN
4	R	163	ASN
4	R	165	HIS
6	T	22	GLN
6	T	73	ASN
6	T	143	GLN
7	V	12	GLN
8	W	40	HIS
8	W	86	GLN
12	a	3	HIS
12	a	73	ASN
14	c	12	GLN
14	c	15	GLN
14	c	52	ASN

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Mol	Chain	Res	Type
15	d	37	GLN
15	d	44	GLN
16	e	12	HIS
17	f	15	GLN
20	i	51	GLN
22	k	36	HIS
25	n	6	ASN
25	n	19	HIS
25	n	38	HIS
25	n	42	HIS
26	o	19	HIS
31	L	20	ASN
32	C	57	GLN
32	C	67	HIS
32	C	172	HIS
32	C	188	ASN
33	U	2	GLN
33	U	18	GLN
33	U	28	ASN
33	U	43	ASN
37	1	177	ASN
37	1	203	ASN
38	2	8	ASN
38	2	123	GLN
38	2	190	HIS
40	4	73	ASN
40	4	89	HIS
40	4	121	HIS
41	5	11	HIS
41	5	14	GLN
41	5	55	HIS
42	6	28	ASN
42	6	148	ASN
44	8	32	GLN
44	8	50	GLN
44	8	81	HIS
45	9	56	HIS
45	9	58	ASN
46	A	118	HIS
48	D	8	ASN
49	E	49	GLN
49	E	66	GLN

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Mol	Chain	Res	Type
50	F	35	GLN
50	F	37	ASN
51	G	63	GLN
52	H	31	HIS
53	I	52	GLN
53	I	54	GLN
54	J	56	GLN
55	K	20	HIS
55	K	48	GLN
59	v	51	GLN
59	v	56	HIS
59	v	151	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	O	117/120 (97%)	21 (17%)	1 (0%)
30	N	2894/2903 (99%)	522 (18%)	34 (1%)
34	M	74/75 (98%)	11 (14%)	0
35	x	43/692 (6%)	34 (79%)	0
36	0	1538/1539 (99%)	282 (18%)	21 (1%)
58	u	72/73 (98%)	20 (27%)	0
All	All	4738/5402 (87%)	890 (18%)	56 (1%)

All (890) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	O	13	G
1	O	25	U
1	O	31	C
1	O	35	C
1	O	41	G
1	O	44	G
1	O	45	A
1	O	51	G
1	O	53	A
1	O	56	G
1	O	57	A
1	O	64	G
1	O	66	A
1	O	67	G

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Mol	Chain	Res	Type
1	O	88	C
1	O	89	U
1	O	90	C
1	O	91	C
1	O	99	A
1	O	108	A
1	O	109	A
30	N	10	A
30	N	23	G
30	N	28	A
30	N	35	G
30	N	36	G
30	N	42	A
30	N	46	G
30	N	51	G
30	N	55	G
30	N	60	G
30	N	61	C
30	N	63	A
30	N	71	A
30	N	74	A
30	N	75	G
30	N	84	A
30	N	96	C
30	N	101	A
30	N	102	U
30	N	103	A
30	N	118	A
30	N	119	A
30	N	120	U
30	N	125	A
30	N	138	U
30	N	139	U
30	N	140	C
30	N	141	G
30	N	142	A
30	N	162	U
30	N	163	C
30	N	165	A
30	N	166	U
30	N	188	G
30	N	196	A

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Mol	Chain	Res	Type
30	N	199	A
30	N	201	C
30	N	215	G
30	N	216	A
30	N	221	A
30	N	222	A
30	N	223	A
30	N	224	U
30	N	228	C
30	N	241	A
30	N	242	G
30	N	243	U
30	N	248	G
30	N	255	A
30	N	265	A
30	N	266	G
30	N	267	C
30	N	271	G
30	N	272	A
30	N	276	U
30	N	278	A
30	N	281	C
30	N	284	U
30	N	294	A
30	N	301	G
30	N	311	A
30	N	323	C
30	N	329	G
30	N	330	A
30	N	332	A
30	N	346	A
30	N	361	G
30	N	362	A
30	N	371	A
30	N	372	G
30	N	373	U
30	N	386	G
30	N	396	G
30	N	399	U
30	N	403	U
30	N	404	A
30	N	405	U

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Mol	Chain	Res	Type
30	N	406	G
30	N	411	G
30	N	412	A
30	N	421	C
30	N	422	A
30	N	424	G
30	N	435	C
30	N	447	A
30	N	455	C
30	N	456	C
30	N	457	A
30	N	467	G
30	N	471	A
30	N	473	G
30	N	481	G
30	N	491	G
30	N	501	A
30	N	504	A
30	N	505	A
30	N	509	C
30	N	513	A
30	N	529	A
30	N	531	C
30	N	532	A
30	N	543	G
30	N	544	C
30	N	546	U
30	N	548	G
30	N	549	G
30	N	550	C
30	N	556	A
30	N	563	A
30	N	573	U
30	N	575	A
30	N	578	G
30	N	586	A
30	N	603	A
30	N	613	A
30	N	614	A
30	N	616	A
30	N	622	G
30	N	627	A

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Mol	Chain	Res	Type
30	N	637	A
30	N	645	C
30	N	646	U
30	N	647	G
30	N	648	G
30	N	654	A
30	N	655	A
30	N	669	G
30	N	670	A
30	N	671	C
30	N	677	A
30	N	686	U
30	N	695	G
30	N	696	G
30	N	717	C
30	N	729	G
30	N	730	A
30	N	738	G
30	N	747	U
30	N	764	A
30	N	765	C
30	N	775	G
30	N	776	G
30	N	782	A
30	N	783	A
30	N	784	G
30	N	785	G
30	N	792	A
30	N	800	A
30	N	805	G
30	N	806	C
30	N	812	C
30	N	819	A
30	N	827	U
30	N	828	U
30	N	829	A
30	N	845	A
30	N	846	U
30	N	858	G
30	N	860	U
30	N	866	A
30	N	869	G

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Mol	Chain	Res	Type
30	N	878	A
30	N	885	C
30	N	896	A
30	N	897	C
30	N	907	G
30	N	910	A
30	N	914	G
30	N	919	U
30	N	932	U
30	N	941	A
30	N	945	A
30	N	946	C
30	N	953	G
30	N	961	C
30	N	973	A
30	N	974	G
30	N	983	A
30	N	985	C
30	N	989	G
30	N	995	C
30	N	996	A
30	N	997	G
30	N	1004	U
30	N	1012	U
30	N	1013	C
30	N	1020	A
30	N	1021	A
30	N	1022	G
30	N	1023	U
30	N	1025	G
30	N	1026	G
30	N	1033	U
30	N	1046	A
30	N	1047	G
30	N	1057	A
30	N	1060	U
30	N	1062	G
30	N	1064	C
30	N	1066	U
30	N	1067	A
30	N	1068	G
30	N	1070	A

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Mol	Chain	Res	Type
30	N	1077	A
30	N	1082	U
30	N	1083	U
30	N	1088	A
30	N	1089	A
30	N	1090	A
30	N	1094	U
30	N	1096	A
30	N	1097	U
30	N	1100	C
30	N	1104	C
30	N	1110	G
30	N	1111	A
30	N	1112	G
30	N	1119	U
30	N	1122	G
30	N	1130	U
30	N	1132	U
30	N	1133	A
30	N	1135	C
30	N	1136	G
30	N	1141	U
30	N	1142	A
30	N	1143	A
30	N	1155	A
30	N	1168	G
30	N	1171	G
30	N	1173	U
30	N	1174	U
30	N	1175	A
30	N	1180	U
30	N	1186	G
30	N	1195	G
30	N	1204	A
30	N	1205	A
30	N	1206	G
30	N	1210	G
30	N	1212	G
30	N	1237	A
30	N	1238	G
30	N	1250	G
30	N	1251	C

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Mol	Chain	Res	Type
30	N	1253	A
30	N	1256	G
30	N	1257	C
30	N	1265	A
30	N	1266	G
30	N	1268	A
30	N	1271	G
30	N	1272	A
30	N	1275	A
30	N	1300	G
30	N	1301	A
30	N	1321	A
30	N	1329	U
30	N	1332	G
30	N	1345	C
30	N	1352	U
30	N	1365	A
30	N	1368	G
30	N	1376	C
30	N	1379	U
30	N	1383	A
30	N	1386	C
30	N	1395	A
30	N	1403	A
30	N	1416	G
30	N	1419	A
30	N	1420	A
30	N	1421	G
30	N	1427	A
30	N	1428	C
30	N	1434	A
30	N	1437	C
30	N	1453	A
30	N	1458	U
30	N	1461	C
30	N	1478	G
30	N	1482	G
30	N	1504	A
30	N	1508	A
30	N	1509	A
30	N	1515	A
30	N	1524	G

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Mol	Chain	Res	Type
30	N	1529	G
30	N	1535	A
30	N	1536	C
30	N	1537	G
30	N	1538	G
30	N	1554	U
30	N	1565	C
30	N	1566	A
30	N	1569	A
30	N	1578	U
30	N	1583	A
30	N	1584	U
30	N	1585	C
30	N	1587	G
30	N	1607	C
30	N	1608	A
30	N	1610	A
30	N	1613	G
30	N	1622	G
30	N	1647	U
30	N	1648	U
30	N	1651	G
30	N	1674	G
30	N	1675	C
30	N	1676	A
30	N	1698	A
30	N	1699	G
30	N	1713	A
30	N	1715	G
30	N	1728	C
30	N	1729	U
30	N	1730	C
30	N	1733	G
30	N	1738	G
30	N	1757	A
30	N	1758	U
30	N	1760	C
30	N	1764	C
30	N	1773	A
30	N	1784	A
30	N	1787	A
30	N	1800	C

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Mol	Chain	Res	Type
30	N	1801	A
30	N	1802	A
30	N	1808	A
30	N	1811	G
30	N	1816	C
30	N	1829	A
30	N	1833	C
30	N	1835	G
30	N	1857	G
30	N	1869	G
30	N	1870	C
30	N	1900	A
30	N	1901	A
30	N	1905	C
30	N	1906	G
30	N	1913	A
30	N	1919	A
30	N	1927	A
30	N	1929	G
30	N	1930	G
30	N	1931	U
30	N	1938	A
30	N	1955	U
30	N	1964	G
30	N	1967	C
30	N	1970	A
30	N	1971	U
30	N	1972	G
30	N	1991	U
30	N	1993	U
30	N	1997	C
30	N	2004	G
30	N	2006	C
30	N	2020	A
30	N	2022	U
30	N	2023	C
30	N	2031	A
30	N	2033	A
30	N	2043	C
30	N	2046	G
30	N	2055	C
30	N	2056	G

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Mol	Chain	Res	Type
30	N	2060	A
30	N	2061	G
30	N	2062	A
30	N	2063	C
30	N	2069	G
30	N	2072	C
30	N	2077	A
30	N	2092	U
30	N	2094	A
30	N	2097	A
30	N	2099	U
30	N	2110	G
30	N	2111	U
30	N	2112	G
30	N	2113	U
30	N	2118	U
30	N	2119	A
30	N	2132	U
30	N	2133	G
30	N	2145	C
30	N	2147	A
30	N	2162	G
30	N	2171	A
30	N	2172	U
30	N	2173	A
30	N	2190	G
30	N	2191	A
30	N	2194	U
30	N	2198	A
30	N	2200	C
30	N	2203	U
30	N	2204	G
30	N	2211	A
30	N	2212	A
30	N	2214	C
30	N	2225	A
30	N	2226	C
30	N	2238	G
30	N	2239	G
30	N	2266	A
30	N	2278	A
30	N	2279	G

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Mol	Chain	Res	Type
30	N	2283	C
30	N	2286	G
30	N	2287	A
30	N	2288	A
30	N	2297	A
30	N	2305	U
30	N	2307	G
30	N	2309	A
30	N	2312	U
30	N	2325	G
30	N	2333	A
30	N	2334	U
30	N	2345	G
30	N	2347	C
30	N	2350	C
30	N	2354	C
30	N	2357	G
30	N	2361	G
30	N	2383	G
30	N	2385	C
30	N	2391	G
30	N	2402	U
30	N	2403	C
30	N	2406	A
30	N	2407	A
30	N	2422	C
30	N	2423	U
30	N	2425	A
30	N	2426	A
30	N	2427	C
30	N	2429	G
30	N	2430	A
30	N	2431	U
30	N	2435	A
30	N	2441	U
30	N	2448	A
30	N	2470	G
30	N	2476	A
30	N	2498	C
30	N	2502	G
30	N	2503	A
30	N	2504	U

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Mol	Chain	Res	Type
30	N	2505	G
30	N	2518	A
30	N	2520	C
30	N	2529	G
30	N	2535	G
30	N	2547	A
30	N	2554	U
30	N	2566	A
30	N	2567	G
30	N	2572	A
30	N	2573	C
30	N	2574	G
30	N	2578	G
30	N	2585	U
30	N	2602	A
30	N	2603	G
30	N	2609	U
30	N	2613	U
30	N	2615	U
30	N	2629	U
30	N	2630	G
30	N	2636	C
30	N	2645	G
30	N	2646	C
30	N	2655	G
30	N	2656	U
30	N	2661	G
30	N	2663	G
30	N	2682	A
30	N	2689	U
30	N	2690	U
30	N	2714	G
30	N	2716	C
30	N	2718	G
30	N	2724	U
30	N	2727	A
30	N	2733	A
30	N	2748	A
30	N	2751	G
30	N	2752	C
30	N	2765	A
30	N	2776	A

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Mol	Chain	Res	Type
30	N	2777	G
30	N	2778	A
30	N	2779	U
30	N	2791	G
30	N	2792	A
30	N	2798	U
30	N	2801	G
30	N	2818	U
30	N	2820	A
30	N	2833	U
30	N	2834	G
30	N	2836	U
30	N	2849	U
30	N	2850	A
30	N	2859	G
30	N	2867	G
30	N	2868	A
30	N	2872	A
30	N	2873	A
30	N	2874	C
30	N	2880	C
30	N	2884	U
30	N	2887	A
30	N	2891	U
30	N	2903	U
34	M	9	C
34	M	10	G
34	M	15	G
34	M	16	C
34	M	17	G
34	M	19	U
34	M	20	A
34	M	42	G
34	M	47	C
34	M	74	C
34	M	75	A
35	x	435	G
35	x	436	A
35	x	437	C
35	x	438	C
35	x	442	G
35	x	443	C

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Mol	Chain	Res	Type
35	x	444	C
35	x	445	A
35	x	446	U
35	x	448	U
35	x	449	A
35	x	450	C
35	x	451	G
35	x	452	U
35	x	453	C
35	x	455	C
35	x	457	C
35	x	458	U
35	x	459	C
35	x	460	A
35	x	461	A
35	x	462	U
35	x	463	A
35	x	464	G
35	x	465	U
35	x	469	U
35	x	470	U
35	x	471	U
35	x	472	U
35	x	473	C
35	x	474	U
35	x	475	G
35	x	476	C
35	x	477	A
36	0	4	U
36	0	6	G
36	0	9	G
36	0	32	A
36	0	39	G
36	0	44	A
36	0	47	C
36	0	48	C
36	0	50	A
36	0	51	A
36	0	52	C
36	0	58	C
36	0	65	A
36	0	69	G

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Mol	Chain	Res	Type
36	0	71	A
36	0	72	A
36	0	83	C
36	0	84	U
36	0	85	U
36	0	86	G
36	0	87	C
36	0	92	U
36	0	97	G
36	0	108	G
36	0	115	G
36	0	116	A
36	0	122	G
36	0	130	A
36	0	141	G
36	0	143	A
36	0	144	G
36	0	149	A
36	0	156	C
36	0	163	C
36	0	174	A
36	0	177	G
36	0	182	A
36	0	183	C
36	0	184	G
36	0	197	A
36	0	209	U
36	0	210	C
36	0	211	G
36	0	226	G
36	0	245	U
36	0	247	G
36	0	251	G
36	0	266	G
36	0	267	C
36	0	280	C
36	0	281	G
36	0	289	G
36	0	298	A
36	0	306	A
36	0	321	A
36	0	328	C

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Mol	Chain	Res	Type
36	0	332	G
36	0	347	G
36	0	351	G
36	0	352	C
36	0	354	G
36	0	358	U
36	0	367	U
36	0	372	C
36	0	375	U
36	0	384	G
36	0	388	G
36	0	389	A
36	0	397	A
36	0	398	U
36	0	406	G
36	0	412	A
36	0	413	G
36	0	421	U
36	0	422	C
36	0	423	G
36	0	424	G
36	0	429	U
36	0	430	A
36	0	439	U
36	0	451	A
36	0	458	U
36	0	459	A
36	0	467	U
36	0	468	A
36	0	474	G
36	0	478	A
36	0	479	U
36	0	481	G
36	0	484	G
36	0	485	U
36	0	486	U
36	0	495	A
36	0	497	G
36	0	511	C
36	0	518	C
36	0	519	C
36	0	521	G

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Mol	Chain	Res	Type
36	0	527	G
36	0	531	U
36	0	532	A
36	0	533	A
36	0	547	A
36	0	559	A
36	0	562	U
36	0	572	A
36	0	573	A
36	0	576	C
36	0	595	A
36	0	596	A
36	0	607	A
36	0	633	G
36	0	639	G
36	0	650	G
36	0	652	U
36	0	665	A
36	0	675	A
36	0	688	G
36	0	695	A
36	0	701	U
36	0	702	A
36	0	703	G
36	0	718	A
36	0	721	G
36	0	723	U
36	0	724	G
36	0	731	G
36	0	734	G
36	0	747	A
36	0	755	G
36	0	760	G
36	0	777	A
36	0	793	U
36	0	794	A
36	0	813	U
36	0	815	A
36	0	817	C
36	0	818	G
36	0	819	A
36	0	821	G

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Mol	Chain	Res	Type
36	0	828	U
36	0	832	G
36	0	836	G
36	0	841	C
36	0	843	U
36	0	844	G
36	0	846	G
36	0	849	G
36	0	859	G
36	0	864	A
36	0	885	G
36	0	889	A
36	0	890	G
36	0	891	U
36	0	902	G
36	0	914	A
36	0	926	G
36	0	934	C
36	0	935	A
36	0	960	U
36	0	965	U
36	0	966	G
36	0	969	A
36	0	971	G
36	0	972	C
36	0	975	A
36	0	976	G
36	0	977	A
36	0	989	U
36	0	993	G
36	0	996	A
36	0	999	C
36	0	1000	A
36	0	1004	A
36	0	1008	U
36	0	1009	U
36	0	1017	U
36	0	1018	G
36	0	1020	G
36	0	1022	A
36	0	1024	G
36	0	1025	U

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Mol	Chain	Res	Type
36	0	1026	G
36	0	1027	C
36	0	1030	U
36	0	1031	C
36	0	1032	G
36	0	1043	G
36	0	1044	A
36	0	1053	G
36	0	1056	U
36	0	1065	U
36	0	1085	U
36	0	1092	A
36	0	1094	G
36	0	1095	U
36	0	1101	A
36	0	1125	U
36	0	1130	A
36	0	1132	C
36	0	1136	C
36	0	1137	C
36	0	1138	G
36	0	1139	G
36	0	1140	C
36	0	1146	A
36	0	1158	C
36	0	1159	U
36	0	1168	U
36	0	1171	A
36	0	1182	G
36	0	1183	U
36	0	1184	G
36	0	1190	G
36	0	1196	A
36	0	1200	C
36	0	1201	A
36	0	1202	U
36	0	1212	U
36	0	1213	A
36	0	1227	A
36	0	1238	A
36	0	1253	G
36	0	1256	A

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Mol	Chain	Res	Type
36	0	1257	A
36	0	1258	G
36	0	1260	G
36	0	1261	A
36	0	1274	A
36	0	1275	A
36	0	1278	G
36	0	1280	A
36	0	1281	C
36	0	1287	A
36	0	1297	G
36	0	1298	U
36	0	1300	G
36	0	1301	U
36	0	1302	C
36	0	1305	G
36	0	1317	C
36	0	1318	A
36	0	1319	A
36	0	1320	C
36	0	1322	C
36	0	1323	G
36	0	1331	G
36	0	1332	A
36	0	1340	A
36	0	1346	A
36	0	1347	G
36	0	1348	U
36	0	1353	G
36	0	1363	A
36	0	1364	U
36	0	1370	G
36	0	1379	G
36	0	1383	C
36	0	1394	A
36	0	1400	C
36	0	1419	G
36	0	1422	G
36	0	1433	A
36	0	1441	A
36	0	1446	A
36	0	1451	U

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Mol	Chain	Res	Type
36	0	1452	C
36	0	1487	G
36	0	1491	G
36	0	1492	A
36	0	1493	A
36	0	1497	G
36	0	1503	A
36	0	1506	U
36	0	1517	G
36	0	1519	A
36	0	1529	G
36	0	1530	G
36	0	1531	A
36	0	1534	A
36	0	1535	C
36	0	1537	U
58	u	13	C
58	u	14	A
58	u	16	U
58	u	17	C
58	u	18	G
58	u	19	G
58	u	20	U
58	u	21	A
58	u	22	G
58	u	36	A
58	u	45	U
58	u	46	G
58	u	47	U
58	u	48	C
58	u	52	G
58	u	60	U
58	u	61	C
58	u	62	C
58	u	63	G
58	u	73	A

All (56) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	O	52	A
30	N	60	G

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Mol	Chain	Res	Type
30	N	227	A
30	N	242	G
30	N	249	C
30	N	372	G
30	N	404	A
30	N	421	C
30	N	446	G
30	N	456	C
30	N	474	G
30	N	503	A
30	N	512	G
30	N	555	G
30	N	670	A
30	N	774	G
30	N	784	G
30	N	859	G
30	N	995	C
30	N	1020	A
30	N	1134	A
30	N	1141	U
30	N	1142	A
30	N	1236	G
30	N	1900	A
30	N	2062	A
30	N	2225	A
30	N	2282	G
30	N	2286	G
30	N	2311	A
30	N	2405	G
30	N	2655	G
30	N	2776	A
30	N	2867	G
30	N	2873	A
36	0	64	G
36	0	85	U
36	0	96	U
36	0	115	G
36	0	388	G
36	0	429	U
36	0	518	C
36	0	595	A
36	0	812	G

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Mol	Chain	Res	Type
36	0	890	G
36	0	965	U
36	0	1124	G
36	0	1145	A
36	0	1182	G
36	0	1190	G
36	0	1201	A
36	0	1300	G
36	0	1345	U
36	0	1347	G
36	0	1491	G
36	0	1528	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

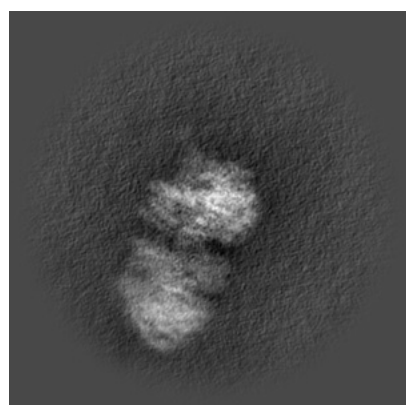
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13958. These allow visual inspection of the internal detail of the map and identification of artifacts.

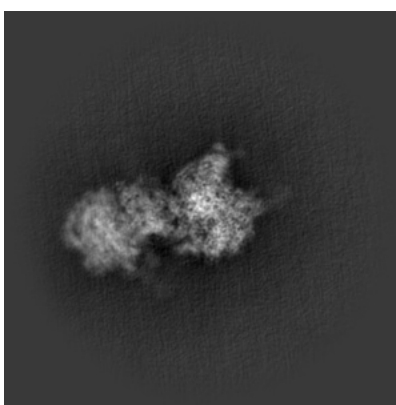
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

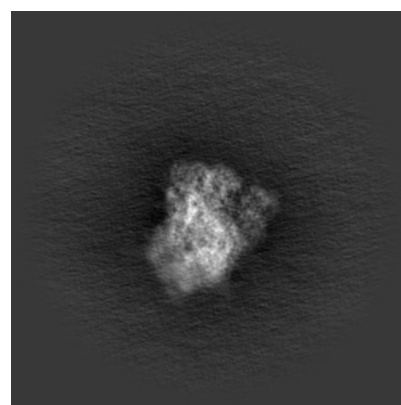
6.1.1 Primary map



X



Y

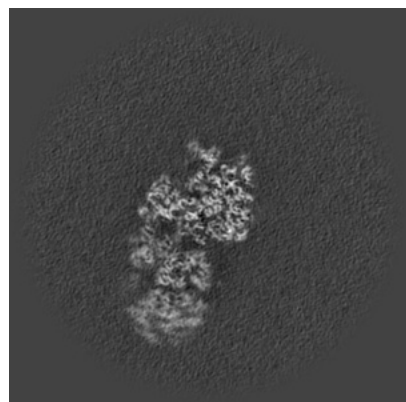


Z

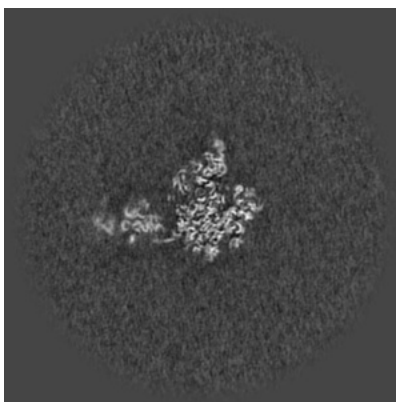
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

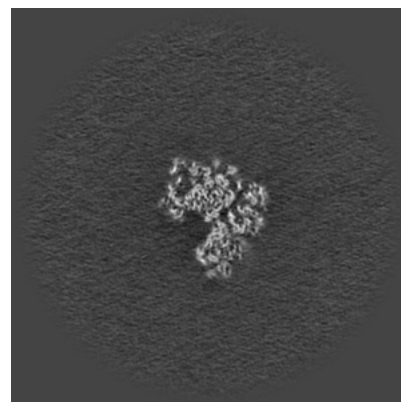
6.2.1 Primary map



X Index: 300



Y Index: 300

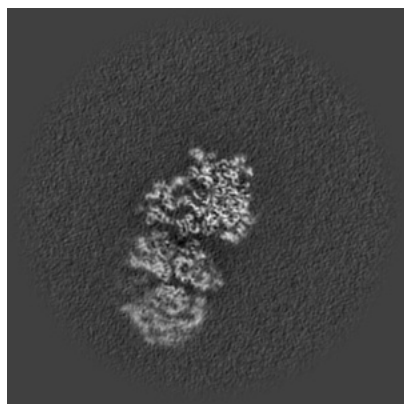


Z Index: 300

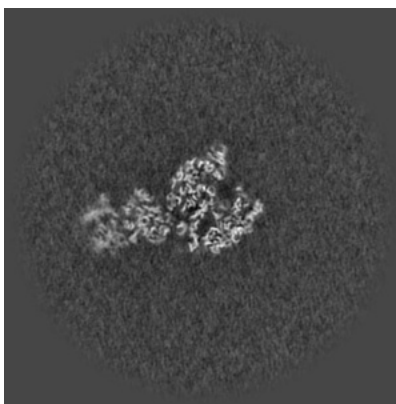
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

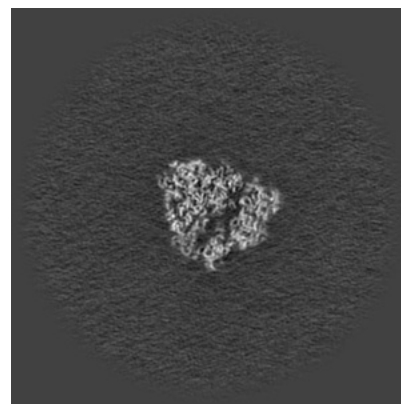
6.3.1 Primary map



X Index: 293



Y Index: 289

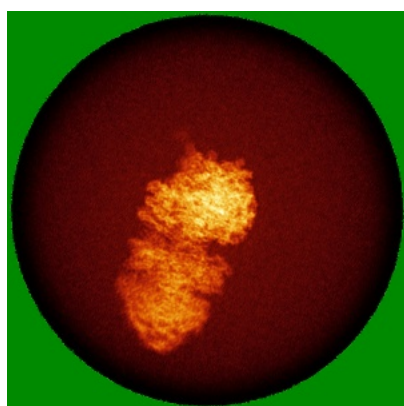


Z Index: 321

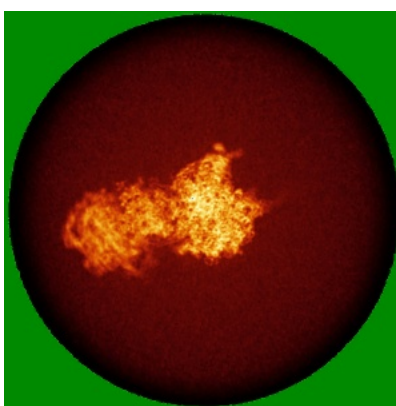
The images above show the largest variance slices of the map in three orthogonal directions.

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

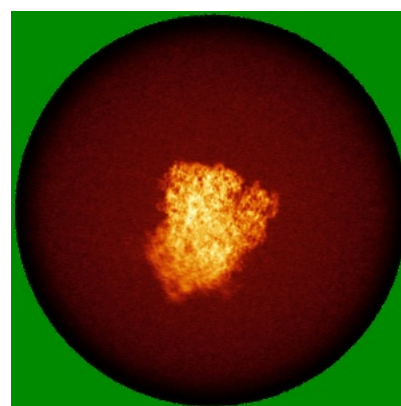
6.4.1 Primary map



X



Y

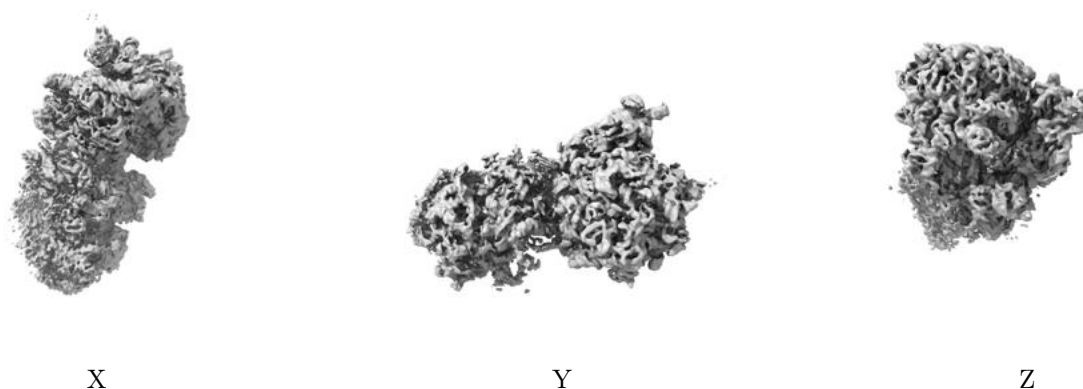


Z

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

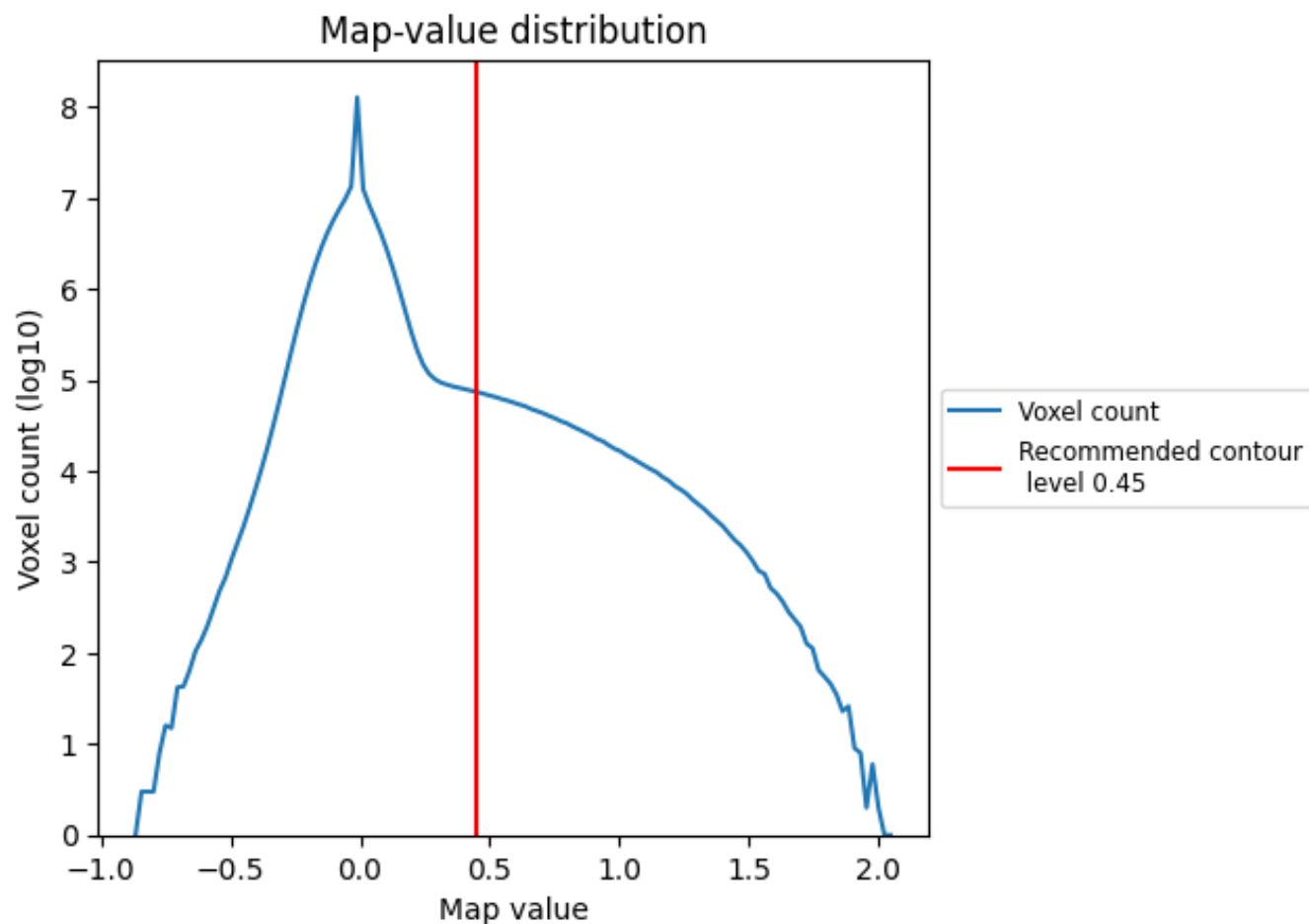
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

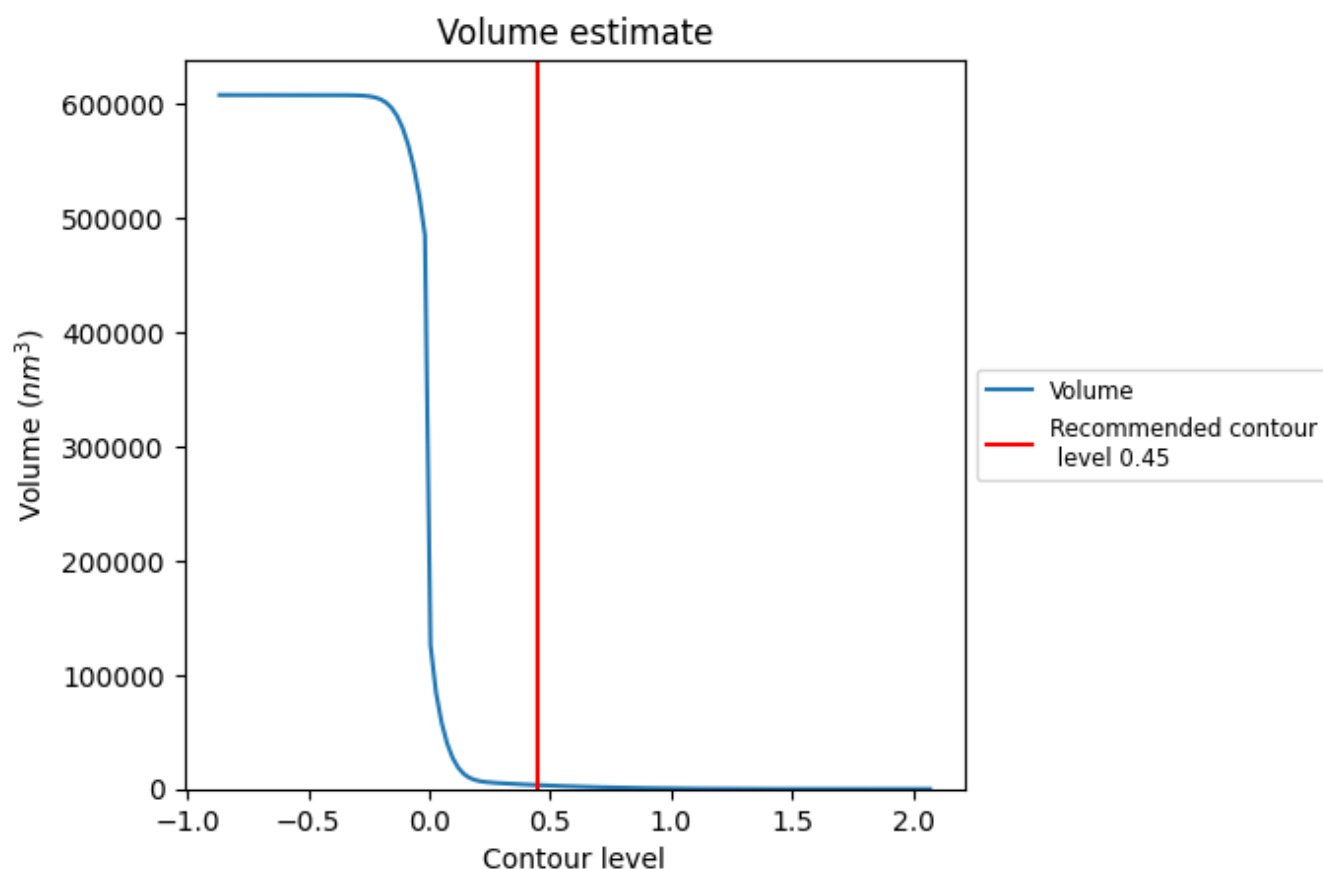
This section contains the results of statistical analysis of the map.

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.

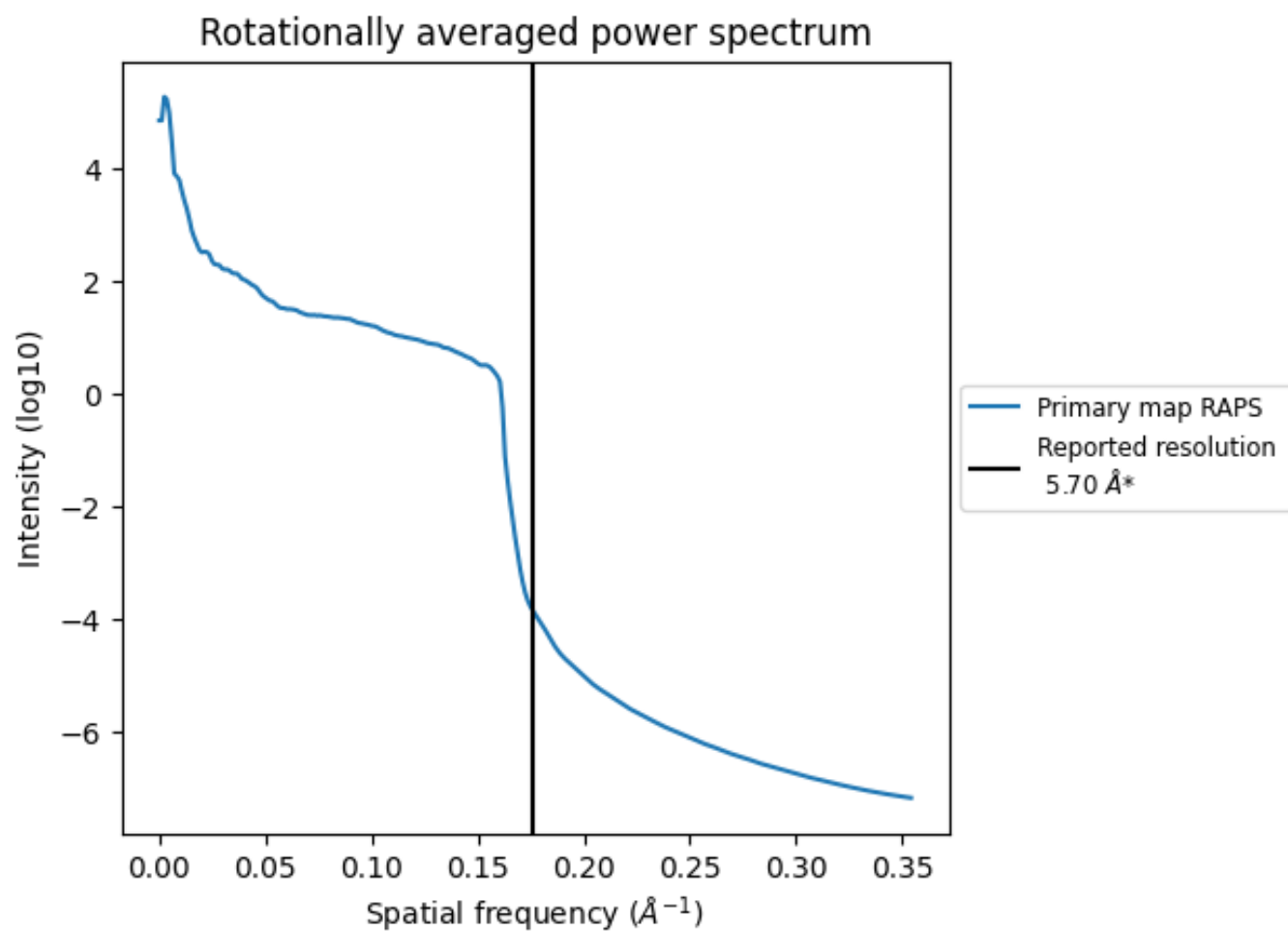
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3383 nm^3 ; this corresponds to an approximate mass of 3056 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.175 Å⁻¹

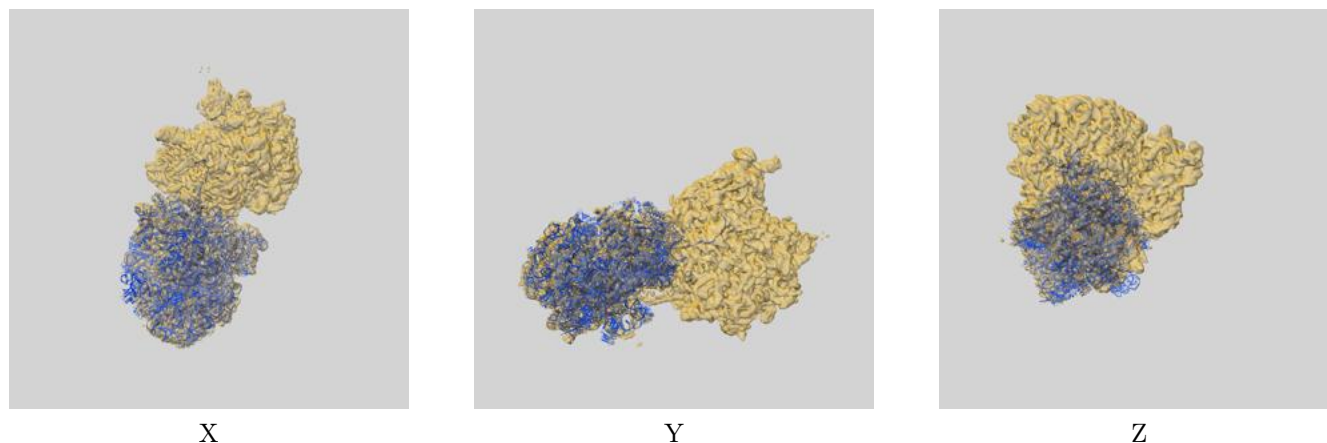
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13958 and PDB model 7QGR. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.45 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](#)

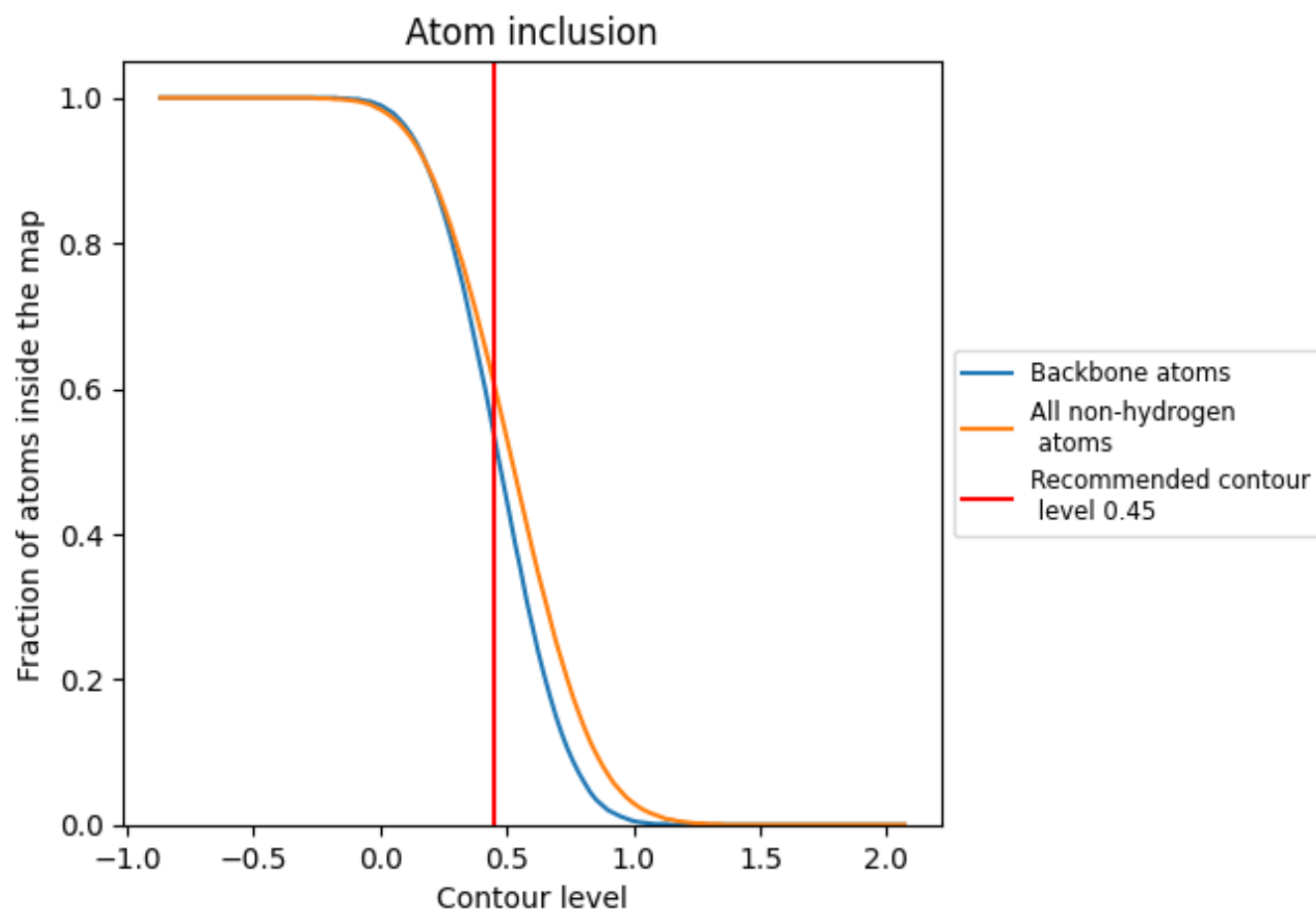


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 53% of all backbone atoms, 61% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6060	 0.1120
0	 0.8330	 0.1680
1	 0.3620	 0.1410
2	 0.2970	 0.1100
3	 0.2500	 0.0970
4	 0.2750	 0.1150
5	 0.3430	 0.0910
6	 0.3930	 0.0880
7	 0.4510	 0.0910
8	 0.3530	 0.0620
9	 0.3170	 0.0750
A	 0.2630	 0.0770
B	 0.4250	 0.1380
C	 0.0010	 0.0310
D	 0.3240	 0.0920
E	 0.3620	 0.0880
F	 0.5200	 0.1100
G	 0.4790	 0.1000
H	 0.4510	 0.0900
I	 0.3920	 0.0760
J	 0.3610	 0.0700
K	 0.4750	 0.1070
L	 0.0050	 0.0850
M	 0.3450	 0.1300
N	 0.7260	 0.1120
O	 0.6460	 0.0810
P	 0.2350	 0.0630
Q	 0.2930	 0.0460
R	 0.3730	 0.0600
S	 0.1120	 0.0550
T	 0.1350	 0.0410
U	 0.0090	 -0.0030
V	 0.0680	 0.0050
W	 0.4510	 0.0470
X	 0.1770	 0.0770



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Chain	Atom inclusion	Q-score
Y	 0.3190	 -0.0160
Z	 0.3300	 0.0750
a	 0.3730	 0.1000
b	 0.2510	 0.0340
c	 0.1850	 0.0390
d	 0.3980	 0.0380
e	 0.2400	 0.0540
f	 0.2510	 0.0750
g	 0.2580	 0.0730
h	 0.3640	 0.0510
i	 0.4480	 0.0630
j	 0.6900	 0.0690
k	 0.4020	 0.0460
l	 0.2760	 0.0520
m	 0.4500	 0.0680
n	 0.5130	 0.1020
o	 0.2020	 0.0300
p	 0.3930	 0.0730
q	 0.4710	 0.0590
r	 0.2650	 0.0610
s	 0.3620	 0.1080
t	 0.0070	 0.0240
u	 0.4900	 0.1310
v	 0.1890	 0.1340
x	 0.5100	 0.1920