



Full wwPDB EM Validation Report ⓘ

Mar 26, 2026 – 01:34 PM UTC

PDB ID : 5O2R / pdb_00005o2r
EMDB ID : EMD-3730
Title : Cryo-EM structure of the proline-rich antimicrobial peptide Api137 bound to the terminating ribosome
Authors : Graf, M.; Berninghausen, O.; Beckmann, R.; Wilson, D.N.
Deposited on : 2017-05-22
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

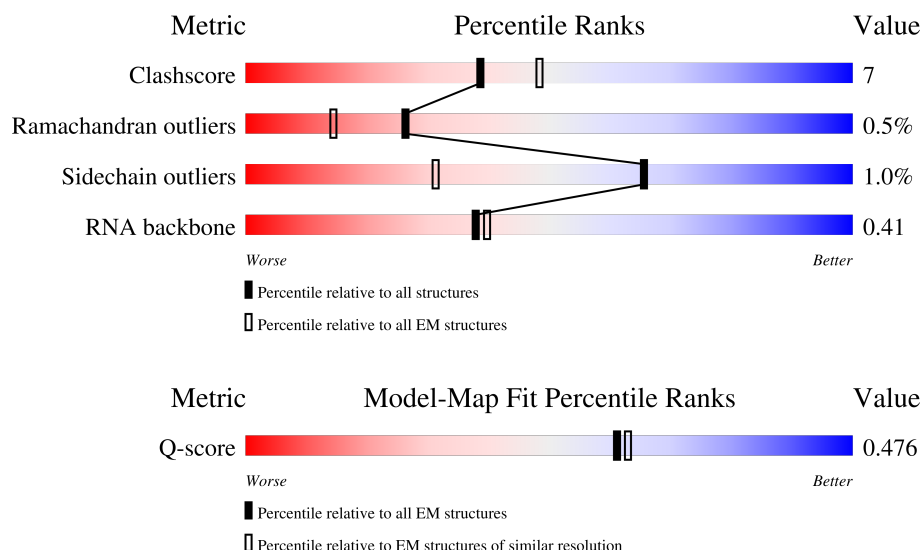
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	A	2903	
2	B	120	
3	C	271	

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	201	
6	F	177	
7	G	176	
8	H	149	
9	I	141	
10	J	142	
11	K	122	
12	L	143	
13	M	136	
14	N	120	
15	O	116	
16	P	114	
17	Q	117	
18	R	103	
19	S	110	
20	T	93	
21	U	102	
22	V	94	
23	W	75	
24	X	77	
25	Y	63	
26	Z	58	
27	0	56	
28	1	50	

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Mol	Chain	Length	Quality of chain
29	2	46	
30	3	64	
31	4	38	
32	5	131	
33	6	66	
34	7	7	
35	a	1539	
36	b	218	
37	c	206	
38	d	205	
39	e	157	
40	f	100	
41	g	151	
42	h	129	
43	i	127	
44	j	98	
45	k	116	
46	l	123	
47	m	114	
48	n	101	
49	o	88	
50	p	82	
51	q	80	
52	r	65	
53	s	79	

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Mol	Chain	Length	Quality of chain
54	t	85	35% 73% 27%
55	u	65	69% 78% 17% 5%
56	v	242	34% 71% 26% ••
57	x	77	10% 49% 38% 12% •
58	z	14	43% 64% 21% 14%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 147985 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2900	Total	C	N	O	P	0	0
			62262	27774	11460	20128	2900		

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	120	A	U	conflict	GB 1150448909

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

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

- Molecule 11 is a protein called 50S ribosomal protein L14.

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

- Molecule 12 is a protein called 50S ribosomal protein L15.

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

- Molecule 13 is a protein called 50S ribosomal protein L16.

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

- Molecule 14 is a protein called 50S ribosomal protein L17.

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

- Molecule 15 is a protein called 50S ribosomal protein L18.

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

- Molecule 16 is a protein called 50S ribosomal protein L19.

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

- Molecule 17 is a protein called 50S ribosomal protein L20.

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

- Molecule 18 is a protein called 50S ribosomal protein L21.

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

- Molecule 19 is a protein called 50S ribosomal protein L22.

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

- Molecule 20 is a protein called 50S ribosomal protein L23.

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

- Molecule 21 is a protein called 50S ribosomal protein L24.

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

- Molecule 22 is a protein called 50S ribosomal protein L25.

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

- Molecule 23 is a protein called 50S ribosomal protein L27.

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

- Molecule 24 is a protein called 50S ribosomal protein L28.

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

- Molecule 25 is a protein called 50S ribosomal protein L29.

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

- Molecule 26 is a protein called 50S ribosomal protein L30.

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

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 34 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	7	7	Total	C	N	O	P	0	0
			149	67	27	48	7		

- Molecule 35 is a RNA chain called 16S ribosomal RNA.

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

- Molecule 36 is a protein called 30S ribosomal protein S2.

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

- Molecule 37 is a protein called 30S ribosomal protein S3.

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

- Molecule 38 is a protein called 30S ribosomal protein S4.

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

- Molecule 39 is a protein called 30S ribosomal protein S5.

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

- Molecule 40 is a protein called 30S ribosomal protein S6.

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

- Molecule 41 is a protein called 30S ribosomal protein S7.

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

- Molecule 42 is a protein called 30S ribosomal protein S8.

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

- Molecule 43 is a protein called 30S ribosomal protein S9.

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

- Molecule 44 is a protein called 30S ribosomal protein S10.

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

- Molecule 45 is a protein called 30S ribosomal protein S11.

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

- Molecule 46 is a protein called 30S ribosomal protein S12.

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

- Molecule 47 is a protein called 30S ribosomal protein S13.

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

- Molecule 48 is a protein called 30S ribosomal protein S14.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 49 is a protein called 30S ribosomal protein S15.

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

- Molecule 50 is a protein called 30S ribosomal protein S16.

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

- Molecule 51 is a protein called 30S ribosomal protein S17.

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

- Molecule 52 is a protein called 30S ribosomal protein S18.

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

- Molecule 53 is a protein called 30S ribosomal protein S19.

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

- Molecule 54 is a protein called 30S ribosomal protein S20.

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

- Molecule 55 is a protein called 30S ribosomal protein S21.

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

- Molecule 56 is a protein called Peptide chain release factor RF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	v	242	Total	C	N	O	S	0	0
			1880	1151	359	362	8		

- Molecule 57 is a RNA chain called P-site Ile-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	77	Total	C	N	O	P	0	0
			1647	734	296	540	77		

- Molecule 58 is a protein called Apidaecin.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	z	14	Total	C	N	O	0	0
			120	80	25	15		

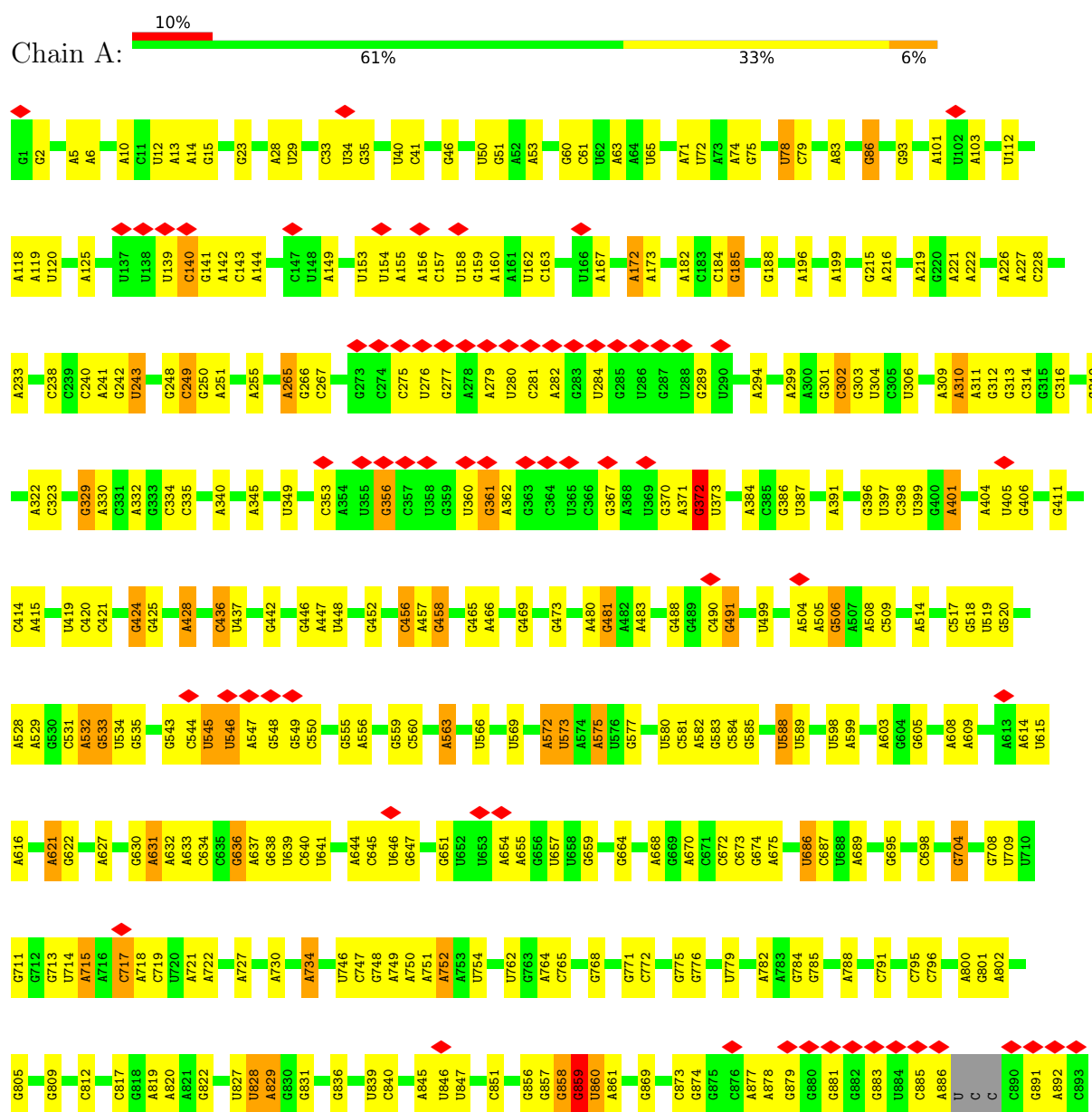
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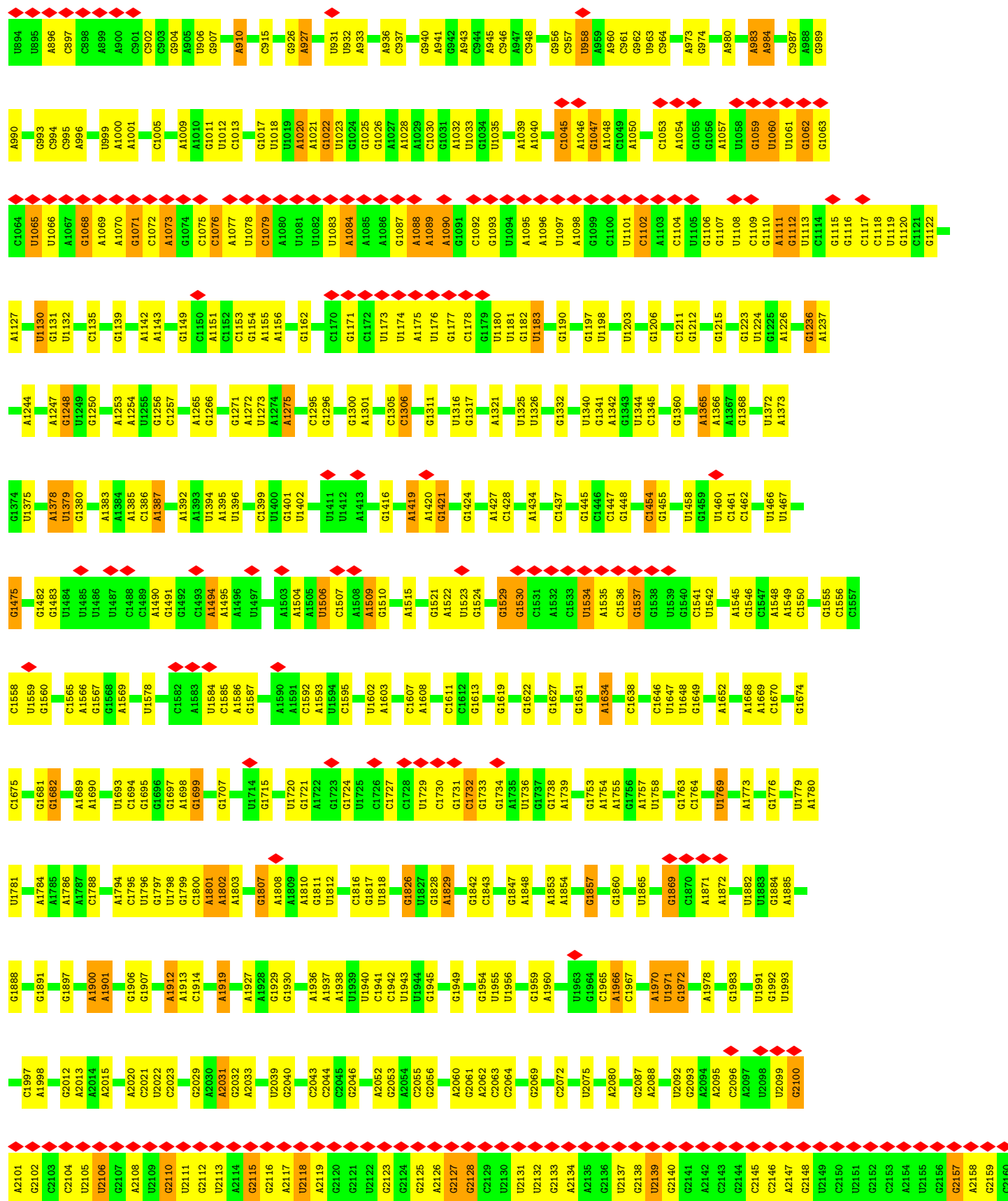
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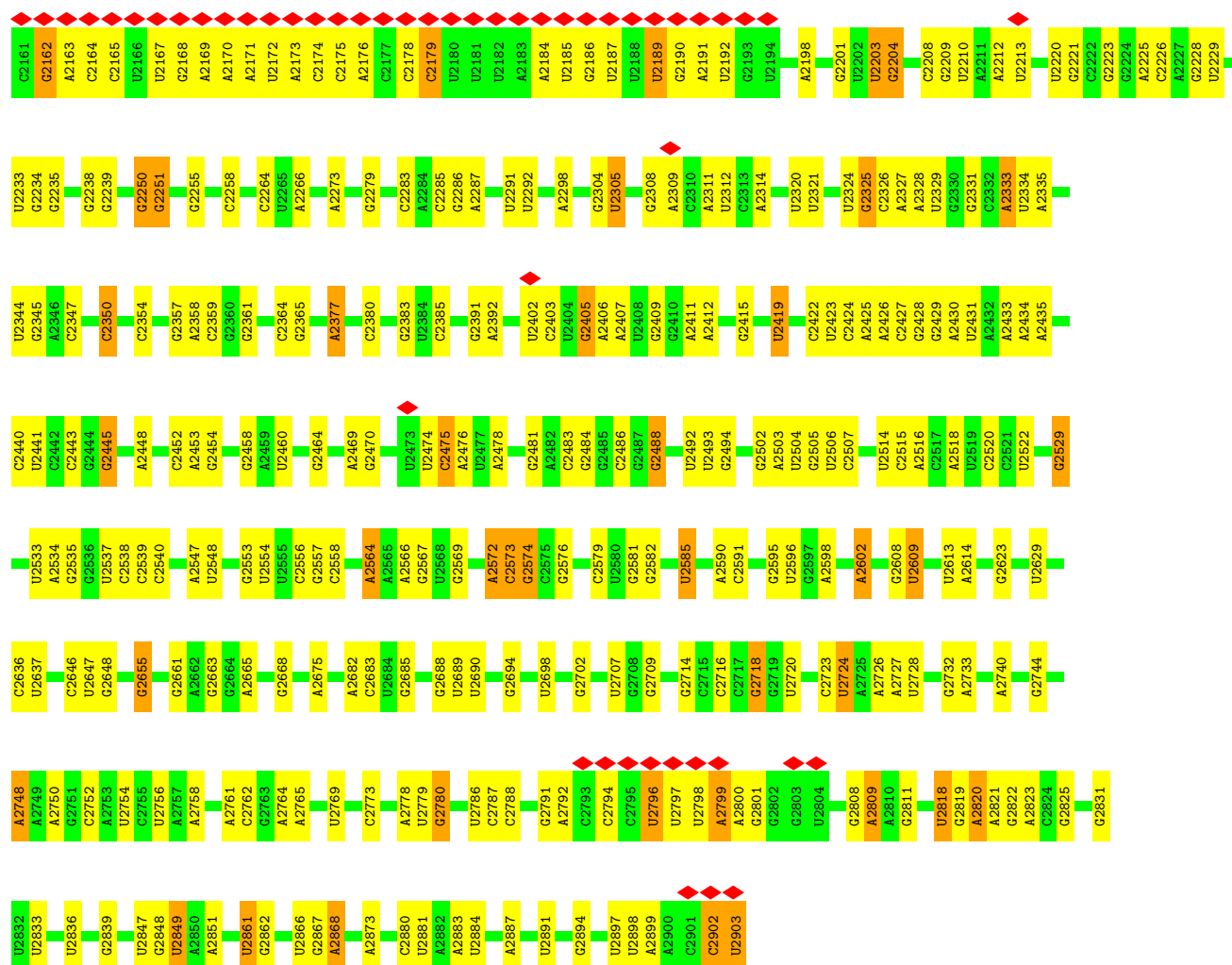
3 Residue-property plots

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

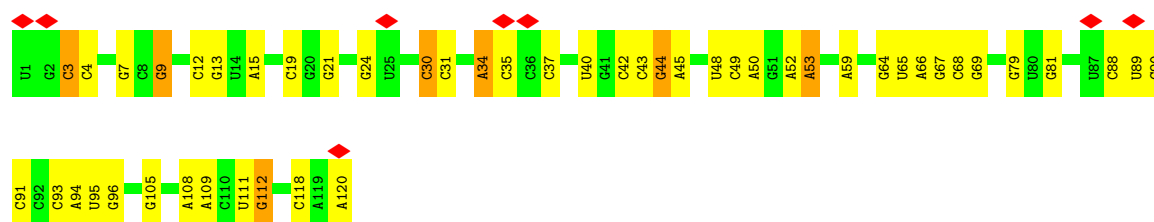
• Molecule 1: 23S ribosomal RNA



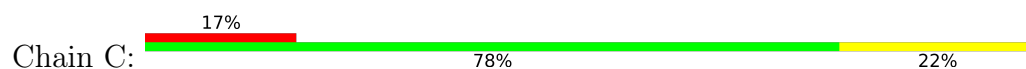


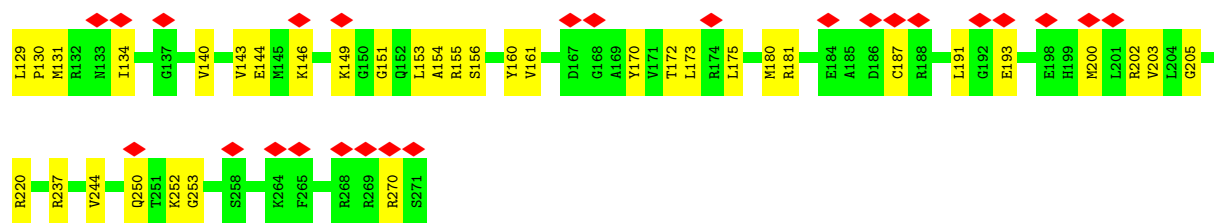


• Molecule 2: 5S ribosomal RNA

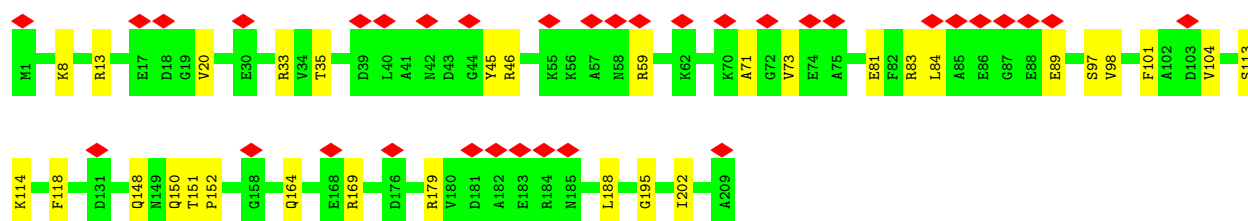
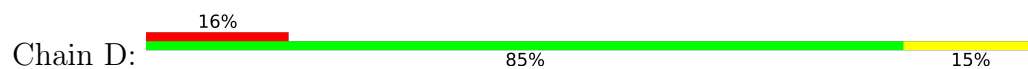


• Molecule 3: 50S ribosomal protein L2

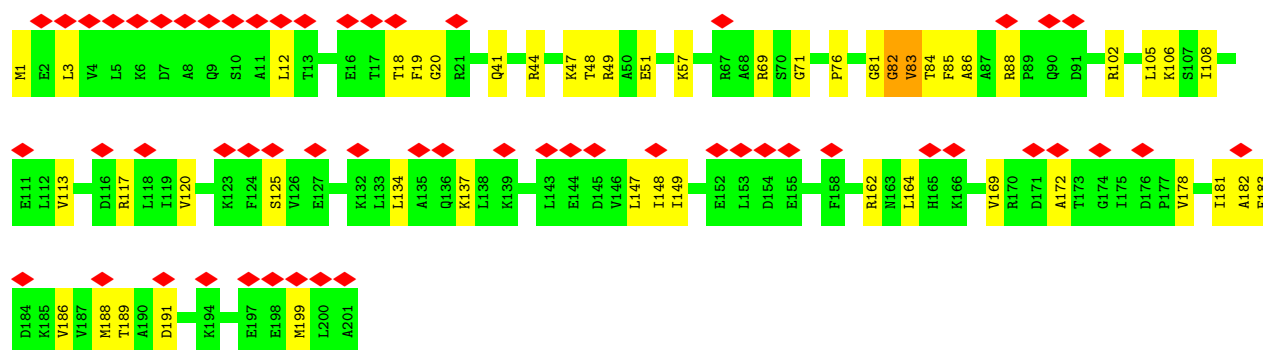
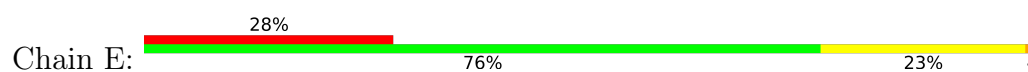




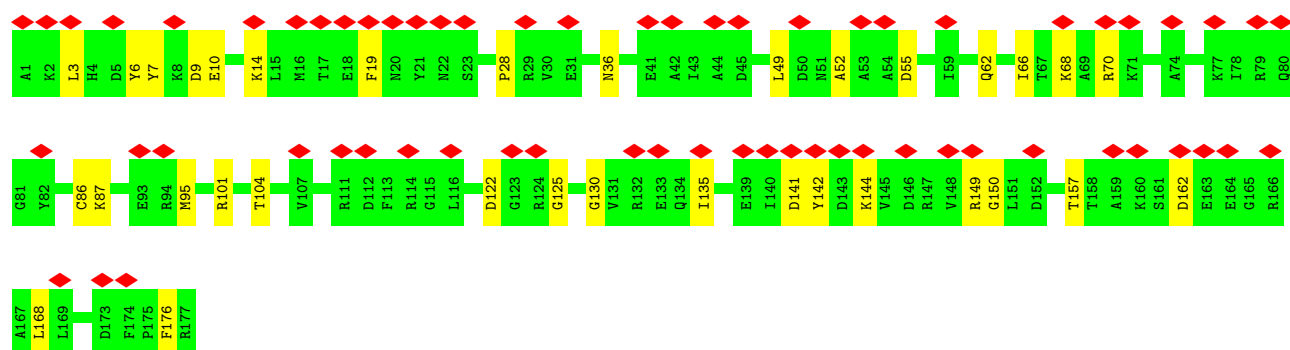
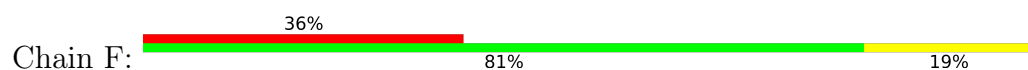
• Molecule 4: 50S ribosomal protein L3



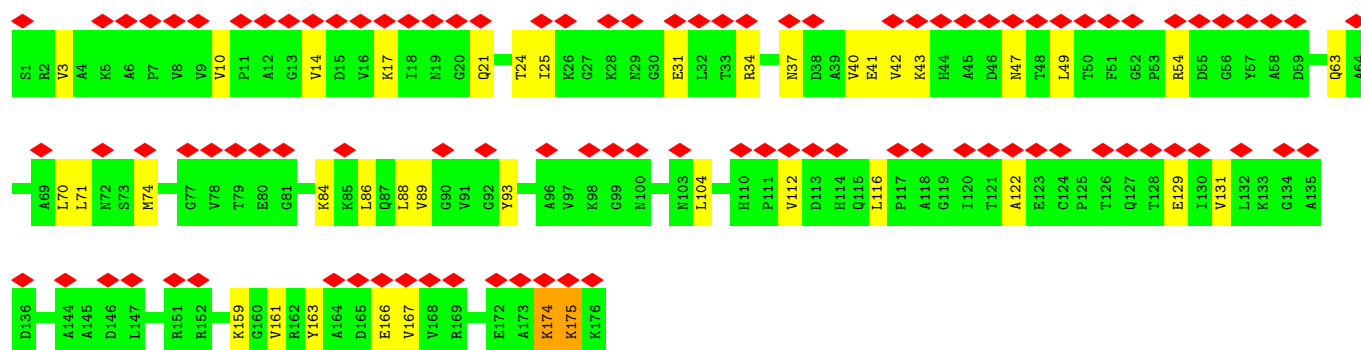
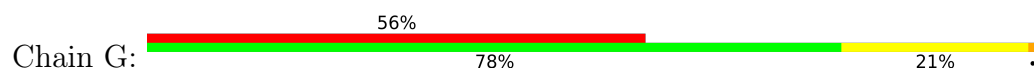
• Molecule 5: 50S ribosomal protein L4



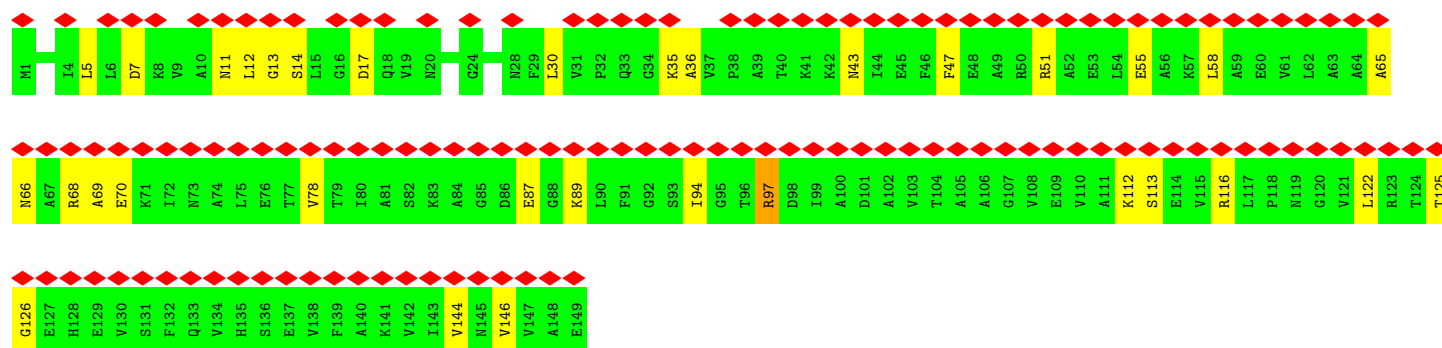
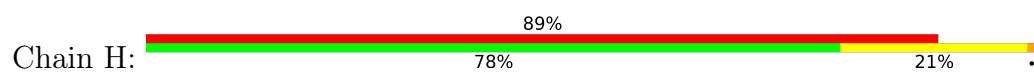
• Molecule 6: 50S ribosomal protein L5



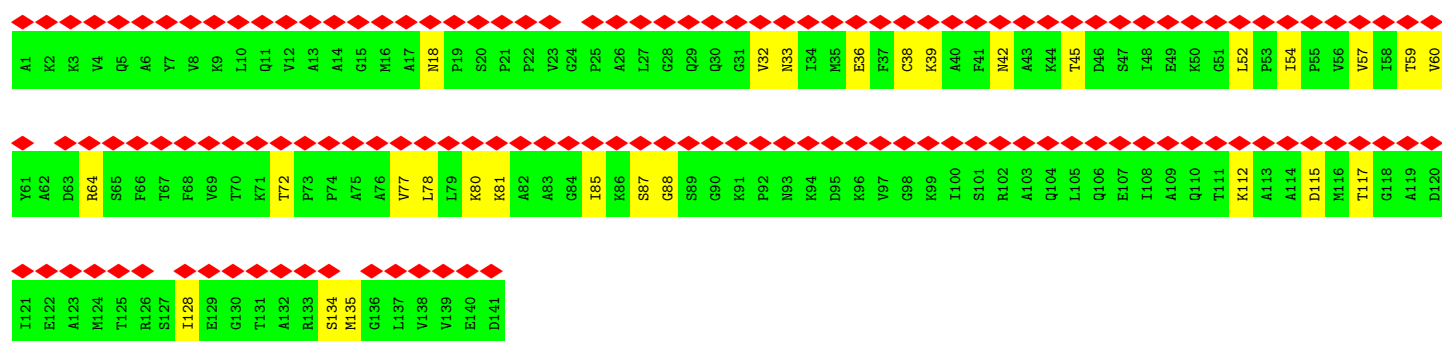
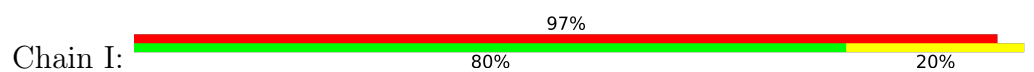
• Molecule 7: 50S ribosomal protein L6



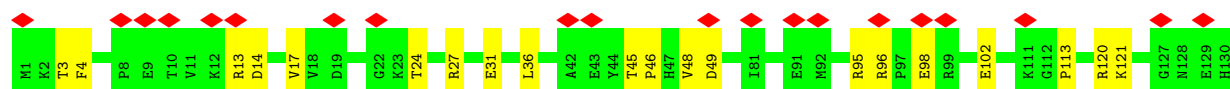
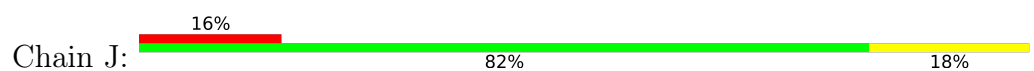
• Molecule 8: 50S ribosomal protein L9

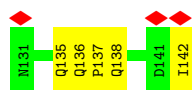


• Molecule 9: 50S ribosomal protein L11

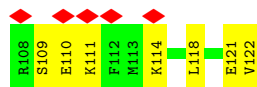
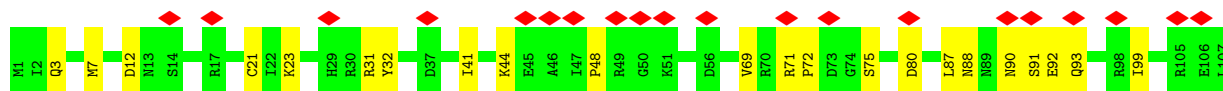
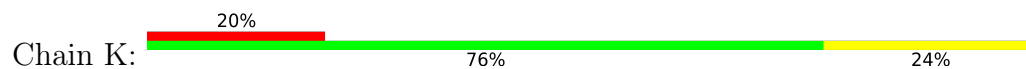


• Molecule 10: 50S ribosomal protein L13

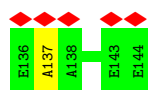
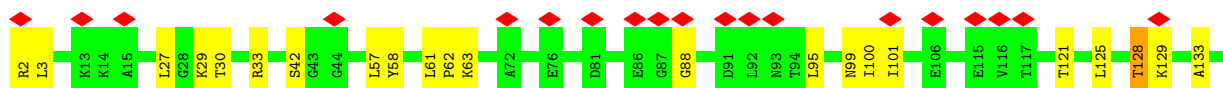
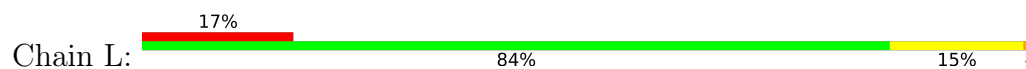




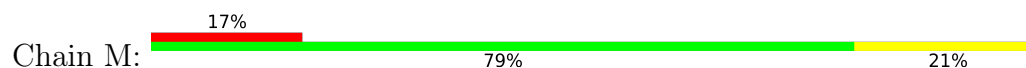
- Molecule 11: 50S ribosomal protein L14



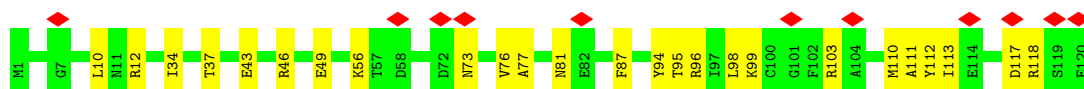
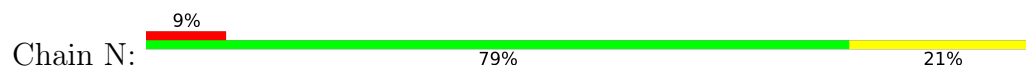
- Molecule 12: 50S ribosomal protein L15



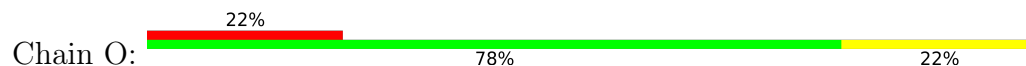
- Molecule 13: 50S ribosomal protein L16

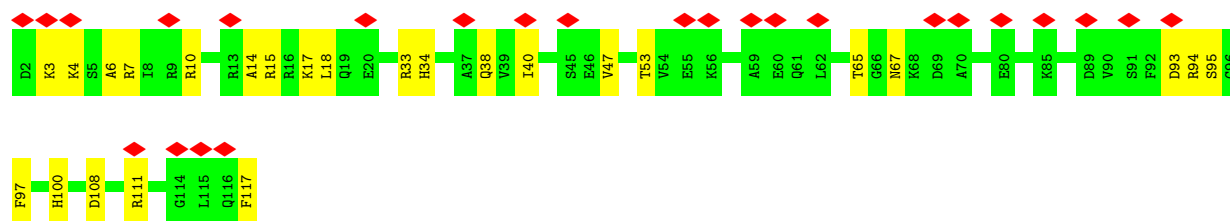


- Molecule 14: 50S ribosomal protein L17

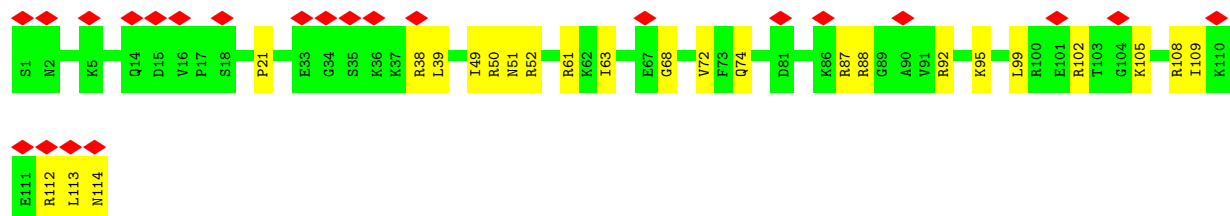
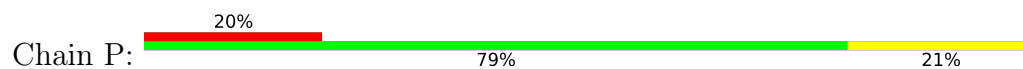


- Molecule 15: 50S ribosomal protein L18

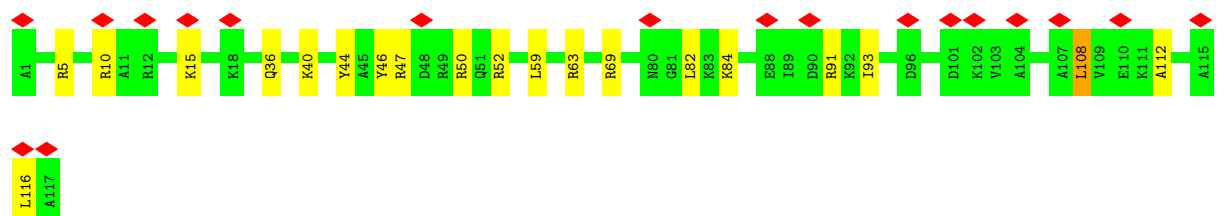
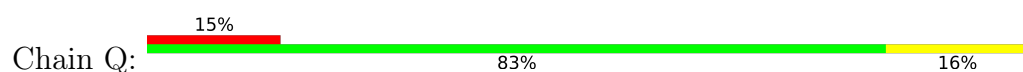




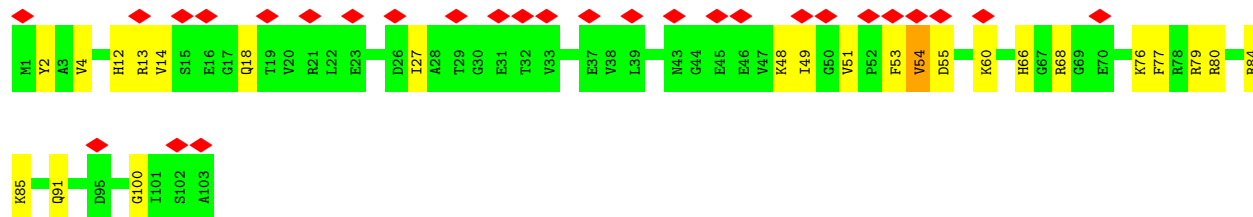
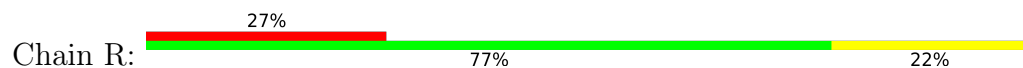
- Molecule 16: 50S ribosomal protein L19



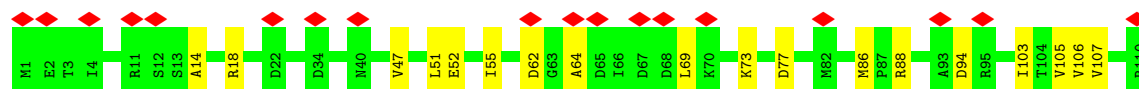
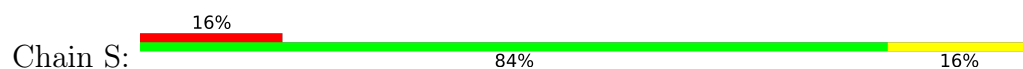
- Molecule 17: 50S ribosomal protein L20



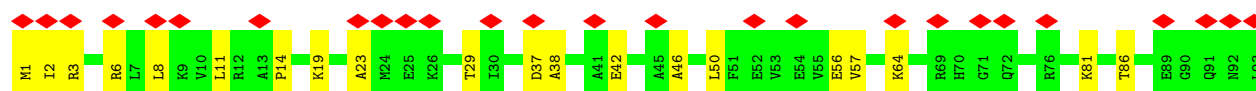
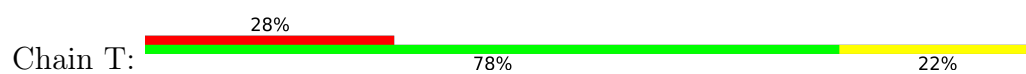
- Molecule 18: 50S ribosomal protein L21



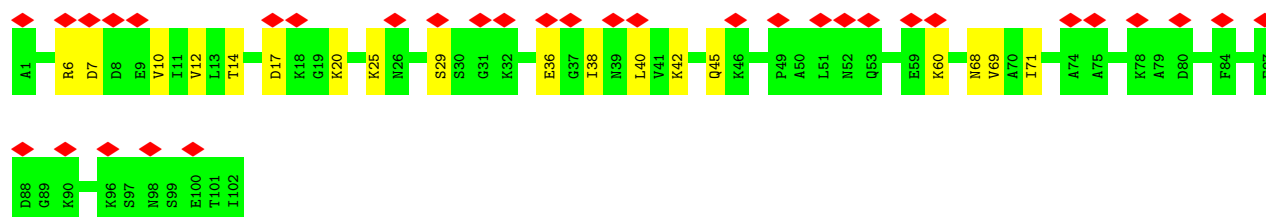
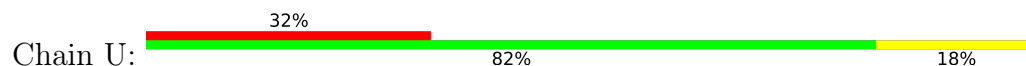
- Molecule 19: 50S ribosomal protein L22



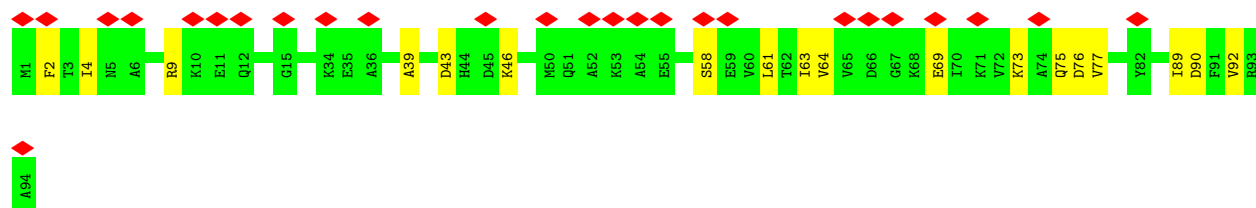
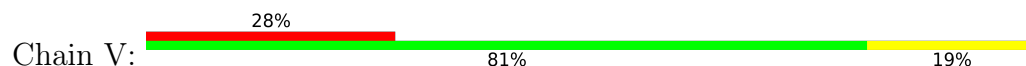
- Molecule 20: 50S ribosomal protein L23



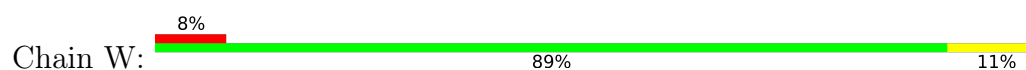
• Molecule 21: 50S ribosomal protein L24



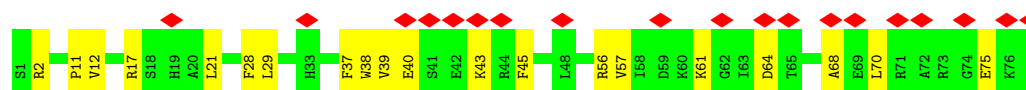
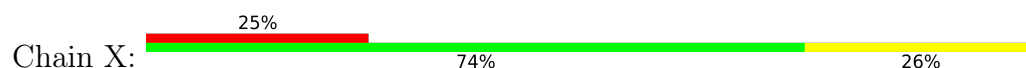
• Molecule 22: 50S ribosomal protein L25



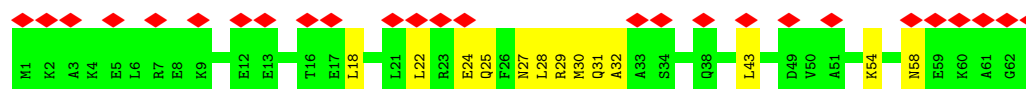
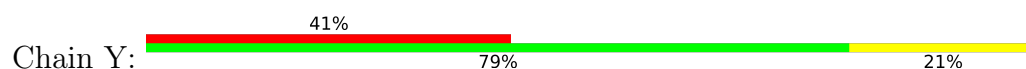
• Molecule 23: 50S ribosomal protein L27



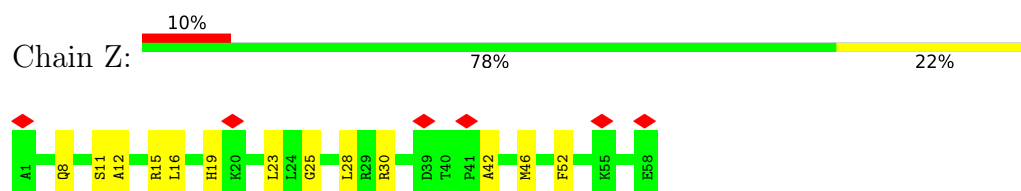
• Molecule 24: 50S ribosomal protein L28



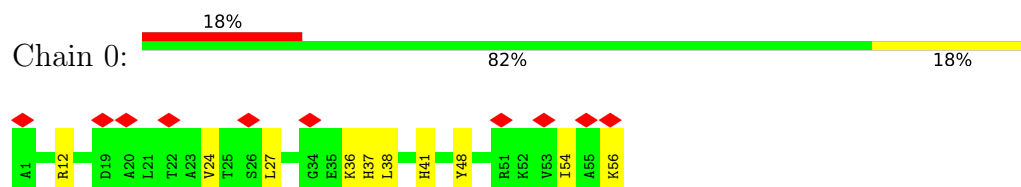
• Molecule 25: 50S ribosomal protein L29



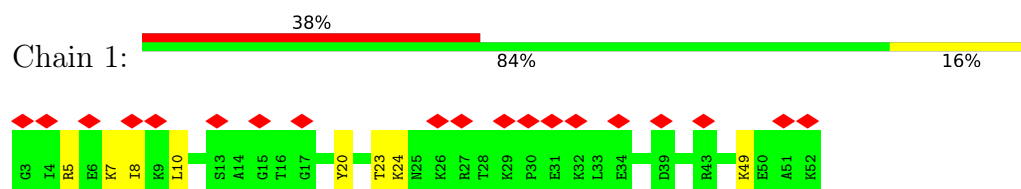
• Molecule 26: 50S ribosomal protein L30



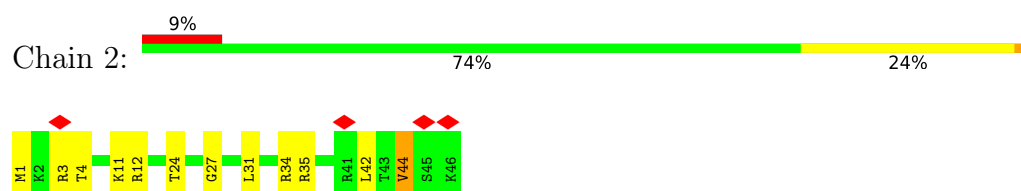
• Molecule 27: 50S ribosomal protein L32



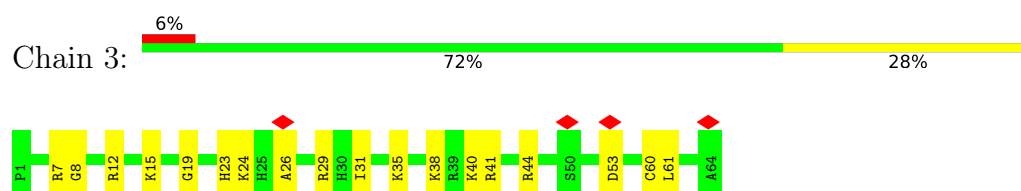
• Molecule 28: 50S ribosomal protein L33



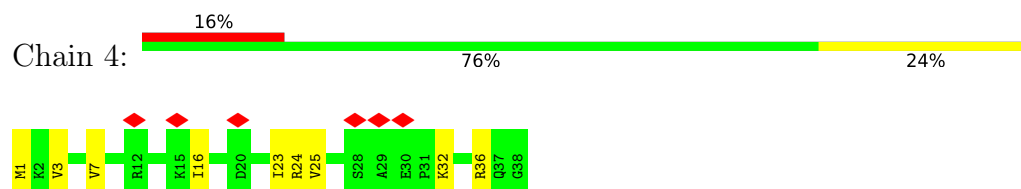
• Molecule 29: 50S ribosomal protein L34



• Molecule 30: 50S ribosomal protein L35



• Molecule 31: 50S ribosomal protein L36

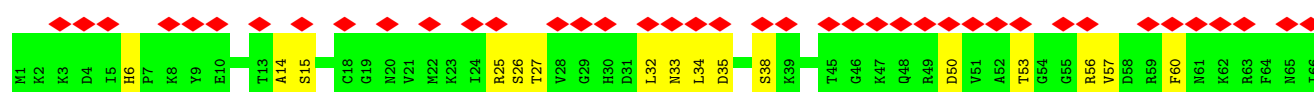
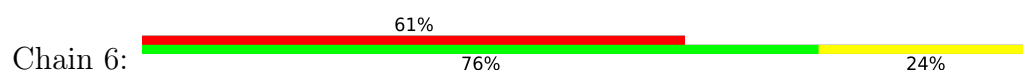


• Molecule 32: 50S ribosomal protein L10





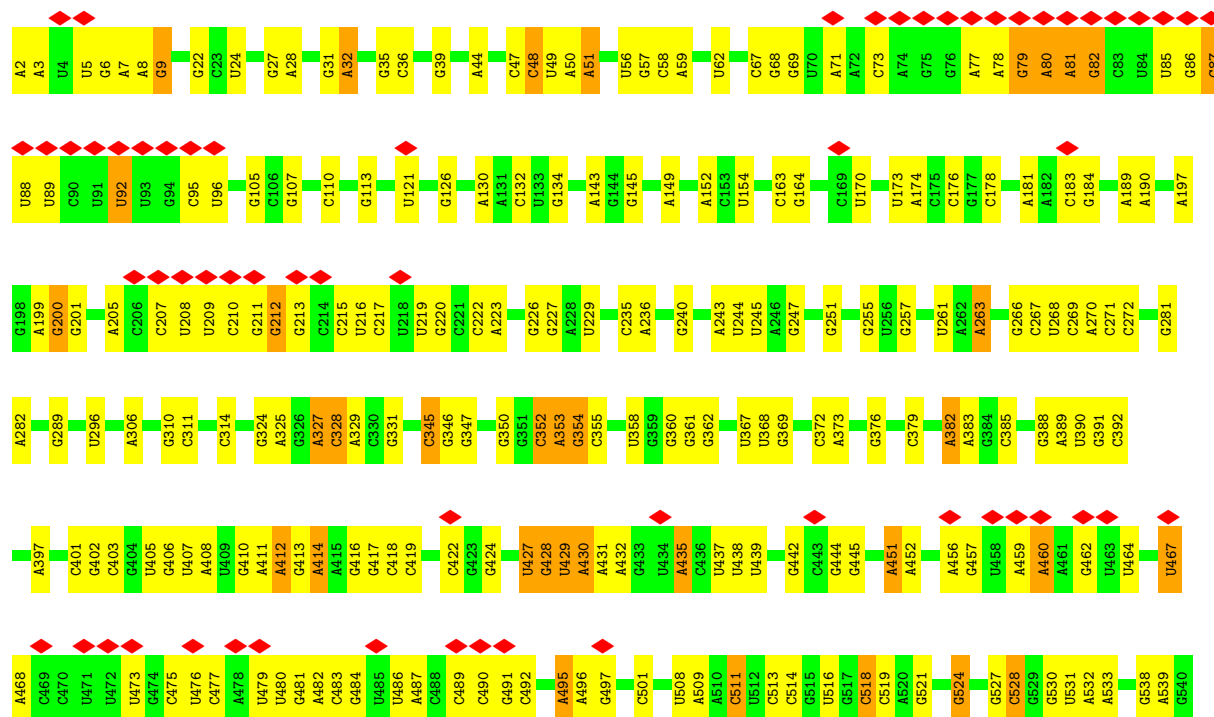
• Molecule 33: 50S ribosomal protein L31

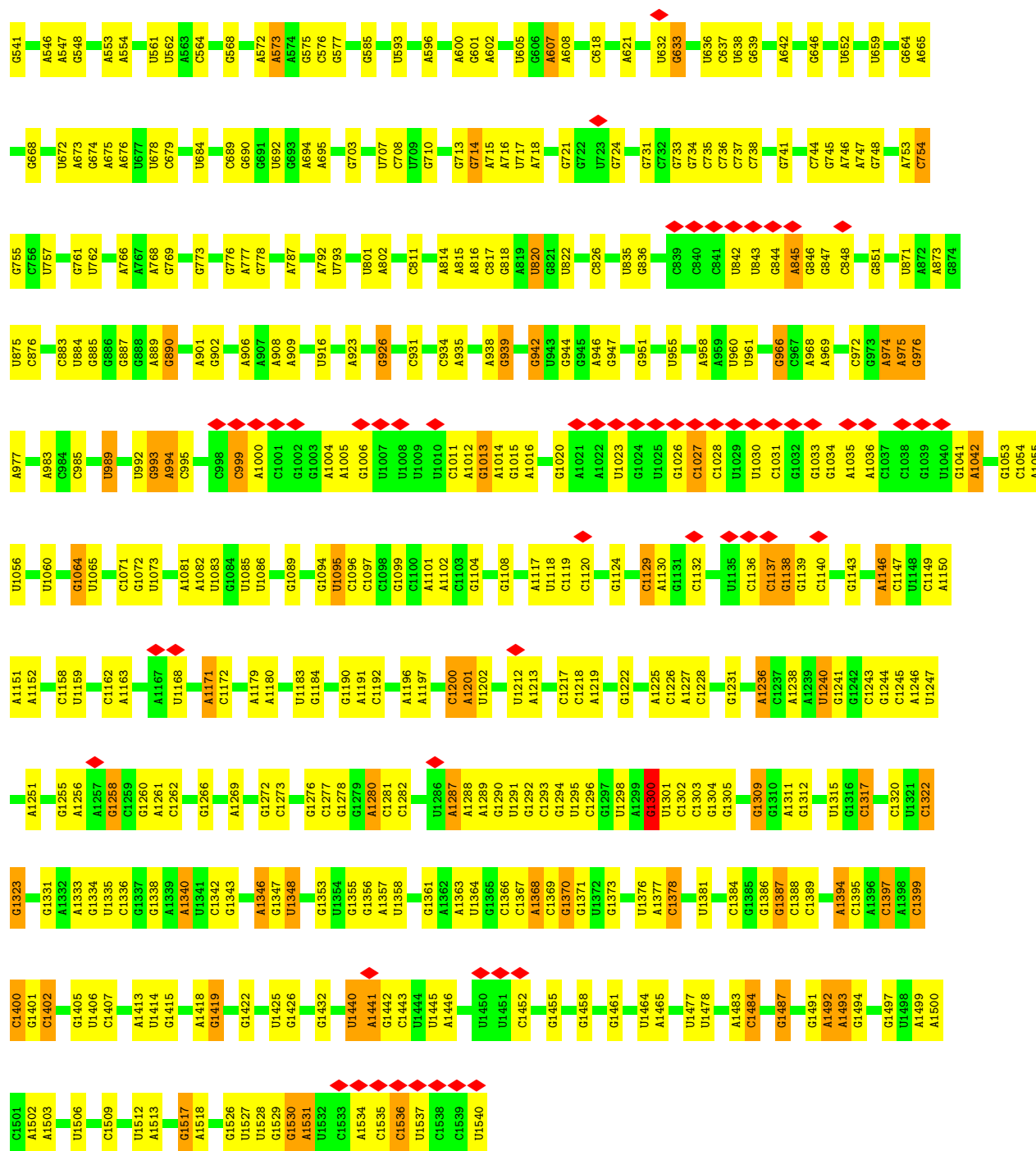


• Molecule 34: mRNA

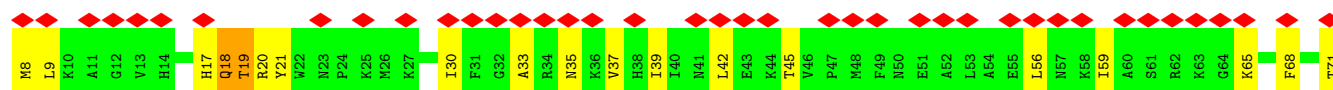
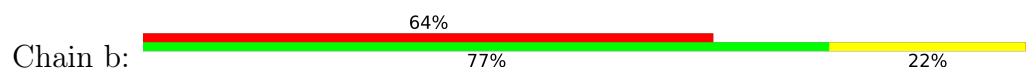


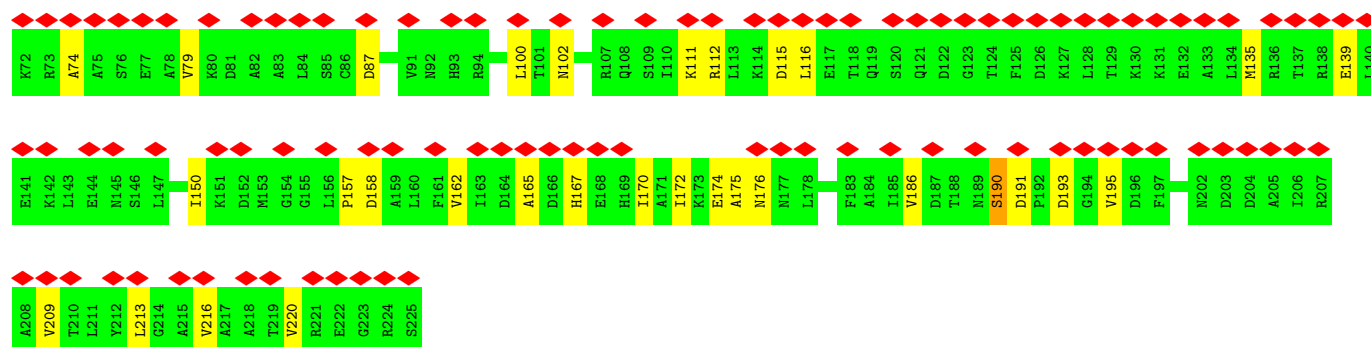
• Molecule 35: 16S ribosomal RNA



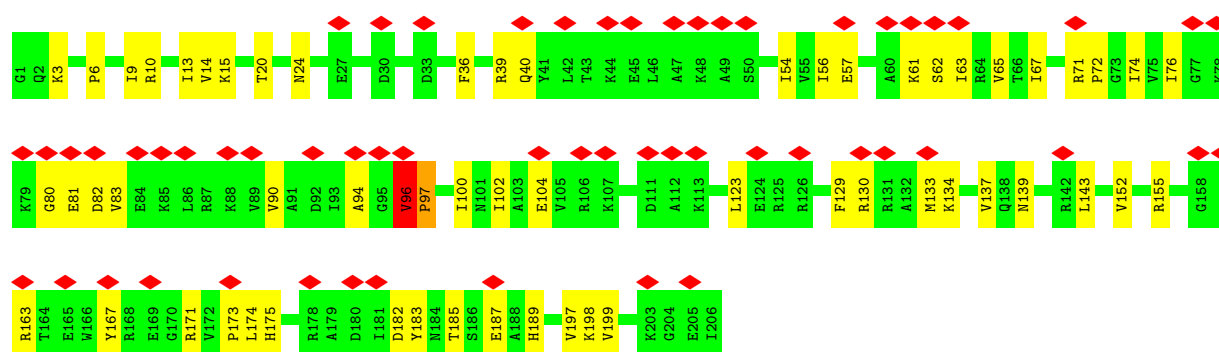
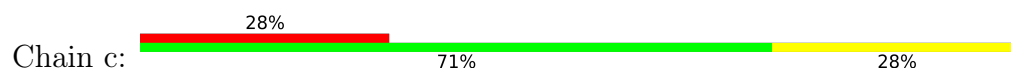


• Molecule 36: 30S ribosomal protein S2

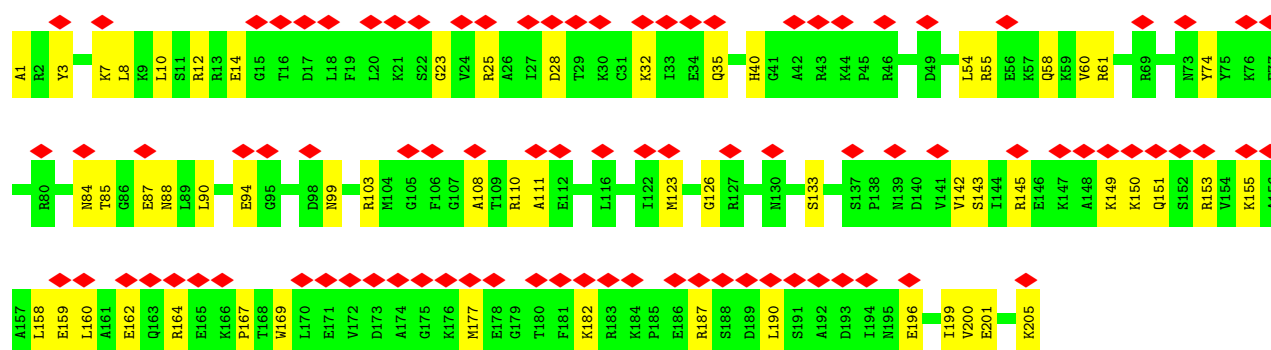
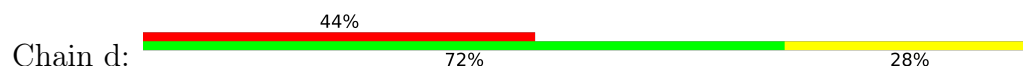




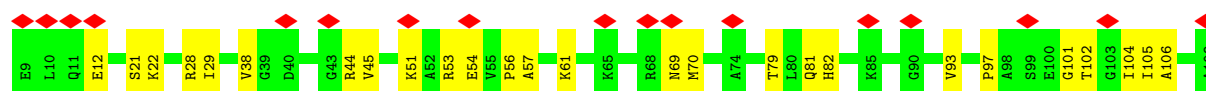
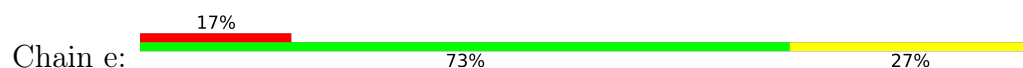
• Molecule 37: 30S ribosomal protein S3

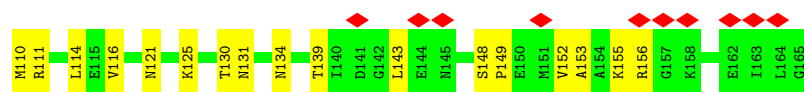


• Molecule 38: 30S ribosomal protein S4

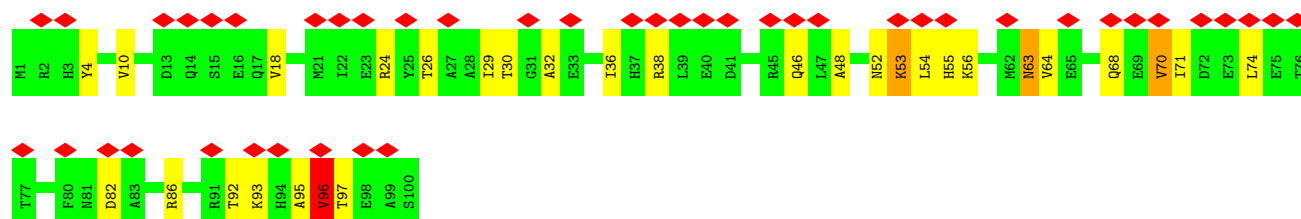
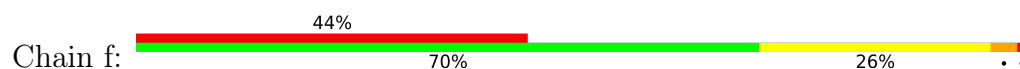


• Molecule 39: 30S ribosomal protein S5

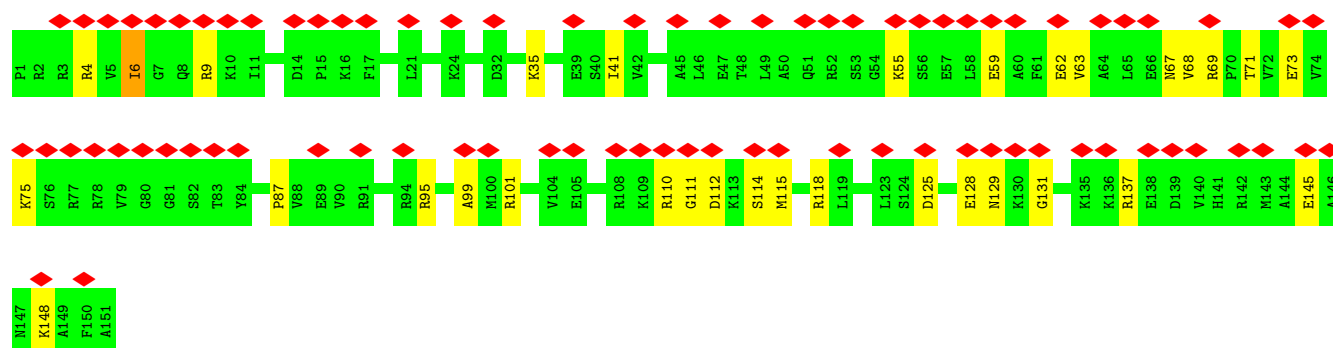
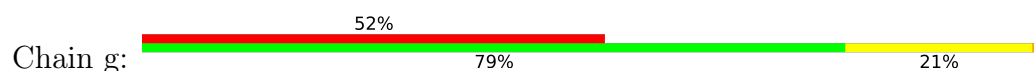




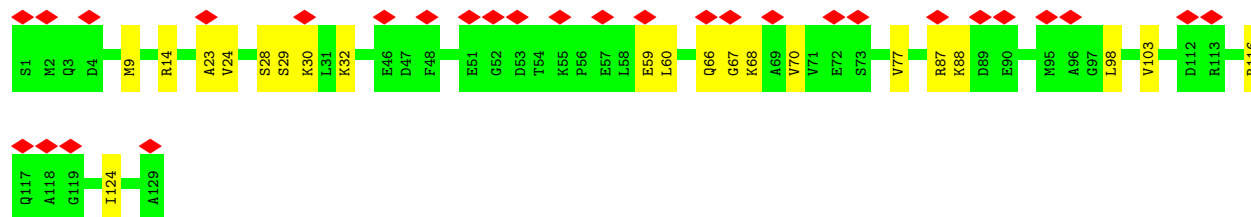
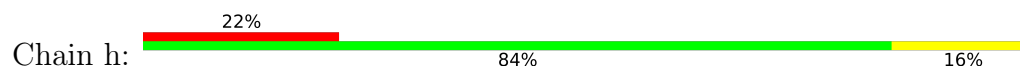
- Molecule 40: 30S ribosomal protein S6



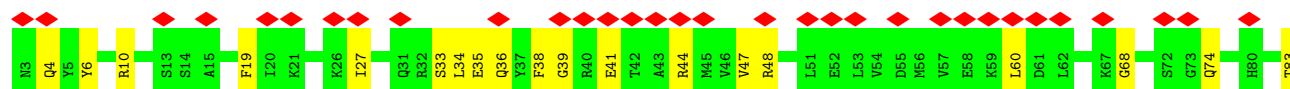
- Molecule 41: 30S ribosomal protein S7

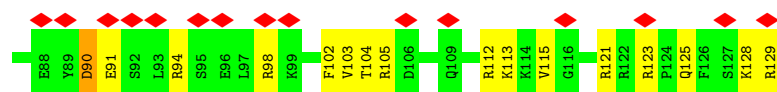


- Molecule 42: 30S ribosomal protein S8

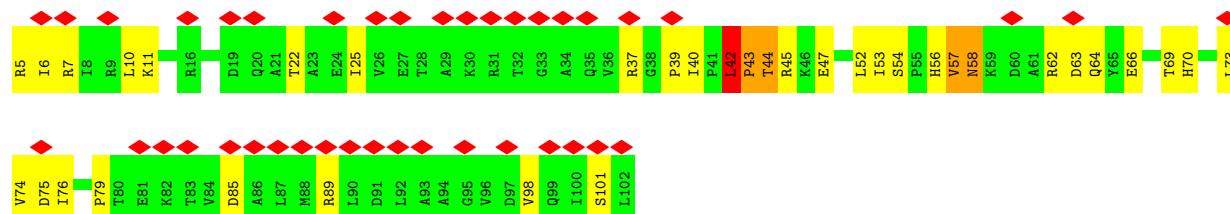
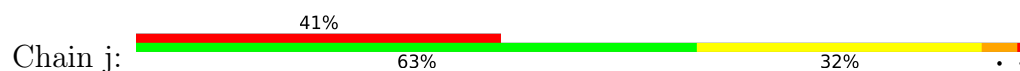


- Molecule 43: 30S ribosomal protein S9

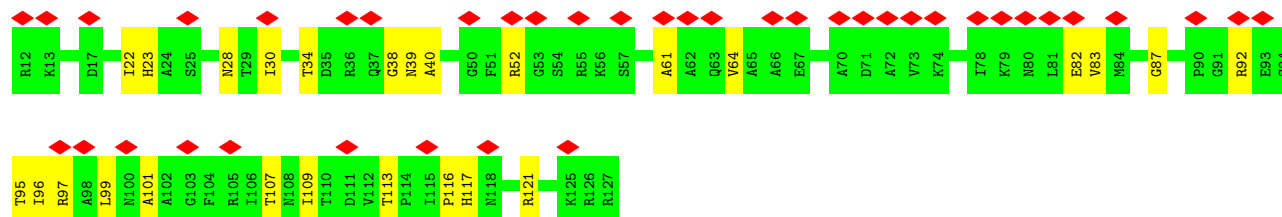
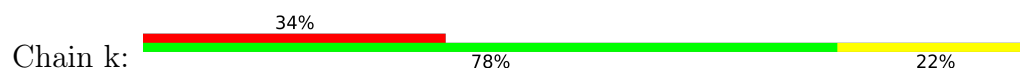




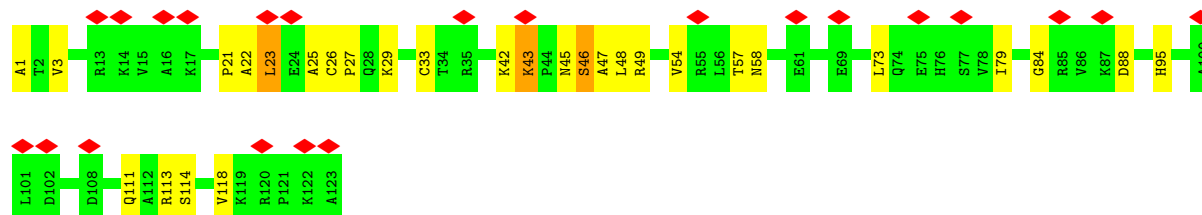
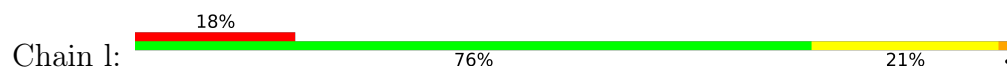
• Molecule 44: 30S ribosomal protein S10



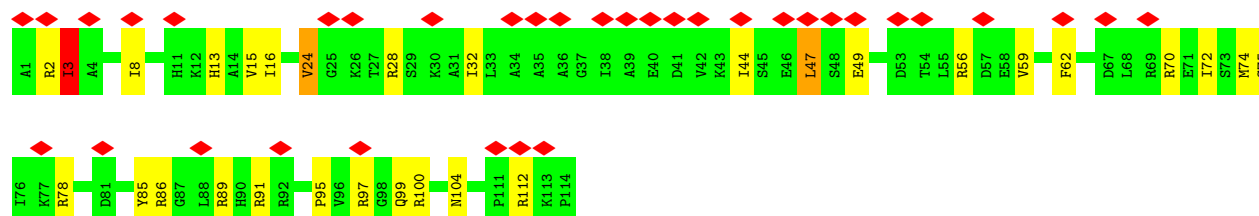
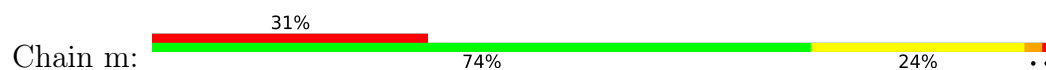
• Molecule 45: 30S ribosomal protein S11



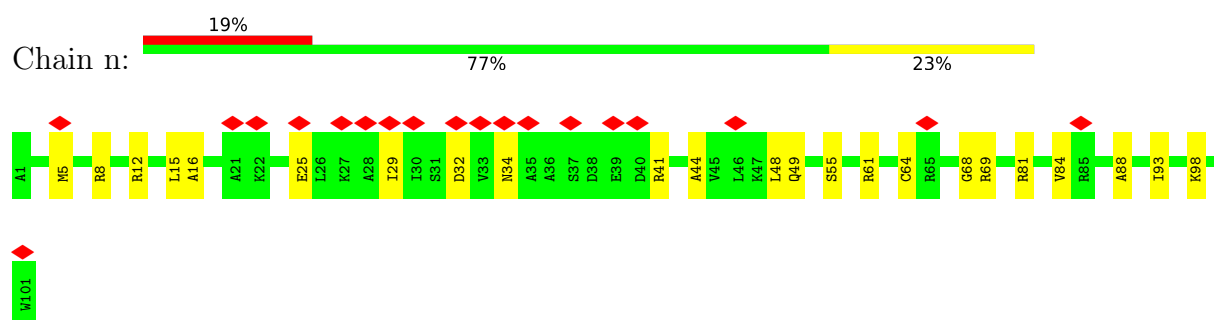
• Molecule 46: 30S ribosomal protein S12



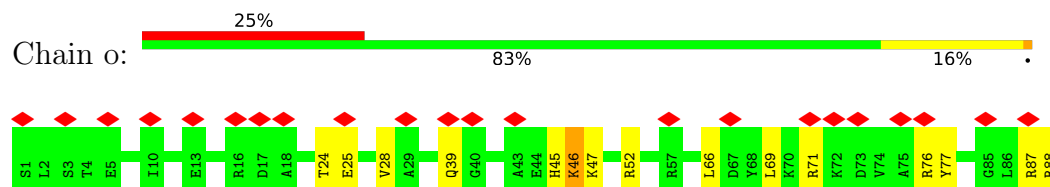
• Molecule 47: 30S ribosomal protein S13



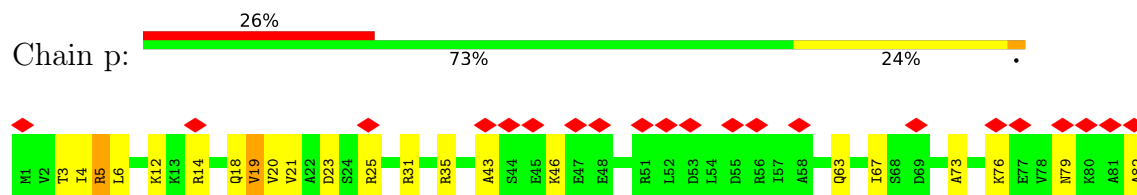
• Molecule 48: 30S ribosomal protein S14



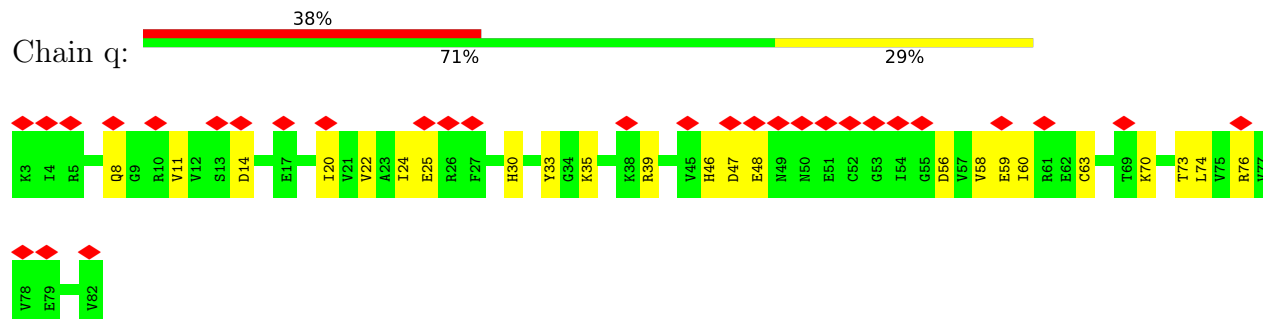
- Molecule 49: 30S ribosomal protein S15



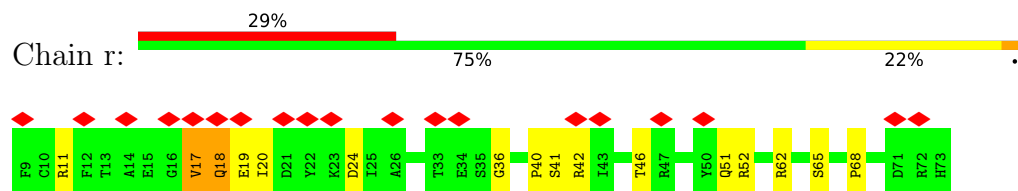
- Molecule 50: 30S ribosomal protein S16



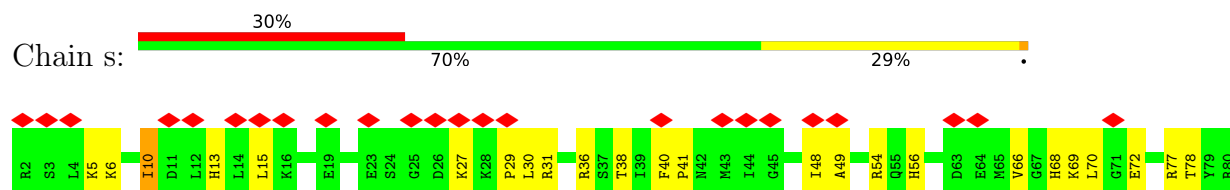
- Molecule 51: 30S ribosomal protein S17



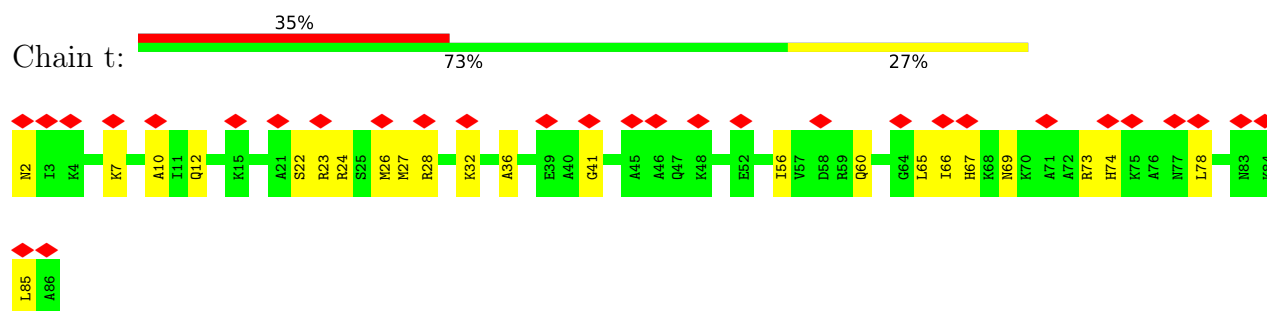
- Molecule 52: 30S ribosomal protein S18



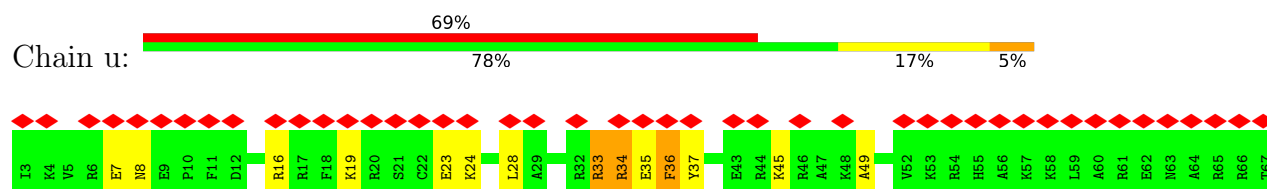
- Molecule 53: 30S ribosomal protein S19



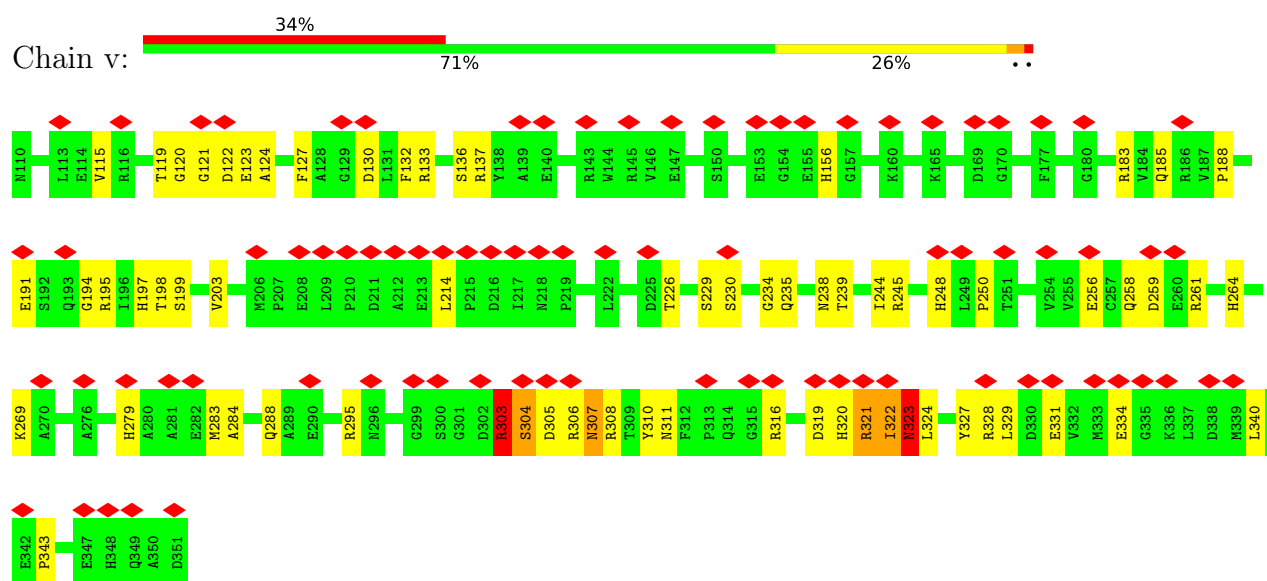
- Molecule 54: 30S ribosomal protein S20



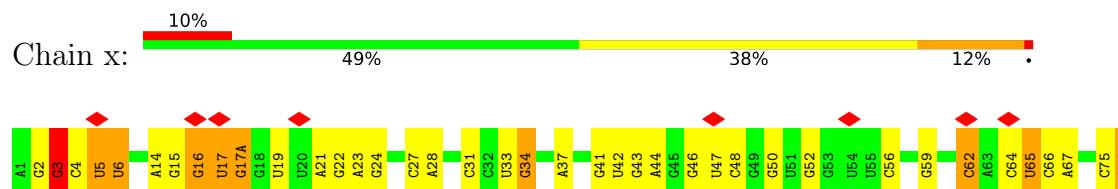
- Molecule 55: 30S ribosomal protein S21



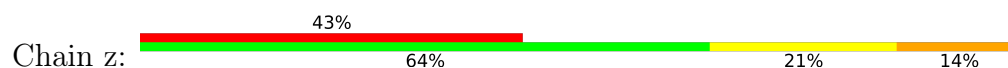
- Molecule 56: Peptide chain release factor RF1

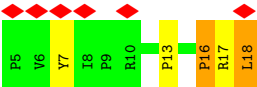


- Molecule 57: P-site Ile-tRNA



- Molecule 58: Apidaecin





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	36826	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 ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	2.131	Depositor
Minimum map value	-1.467	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.084	Depositor
Recommended contour level	0.407	Depositor
Map size (Å)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.60	0/69734	0.57	7/108788 (0.0%)
2	B	0.49	0/2876	0.62	1/4483 (0.0%)
3	C	0.61	0/2121	0.79	0/2852
4	D	0.61	0/1586	0.75	0/2134
5	E	0.58	1/1571 (0.1%)	0.78	2/2113 (0.1%)
6	F	0.47	0/1434	0.87	3/1926 (0.2%)
7	G	0.43	0/1343	0.77	1/1816 (0.1%)
8	H	0.32	0/1122	0.76	1/1515 (0.1%)
9	I	0.33	0/1046	0.75	0/1410
10	J	0.53	0/1152	0.70	0/1551
11	K	0.59	0/947	0.93	5/1268 (0.4%)
12	L	0.60	0/1054	0.90	2/1403 (0.1%)
13	M	0.60	0/1093	0.77	0/1460
14	N	0.59	0/973	0.86	0/1301
15	O	0.51	0/902	0.77	0/1209
16	P	0.55	0/929	0.74	0/1242
17	Q	0.65	0/960	0.73	0/1278
18	R	0.55	0/829	0.86	2/1107 (0.2%)
19	S	0.58	0/864	0.75	0/1156
20	T	0.51	0/744	0.78	1/994 (0.1%)
21	U	0.45	0/787	0.90	2/1051 (0.2%)
22	V	0.50	0/766	0.70	0/1025
23	W	0.63	0/582	0.75	0/769
24	X	0.51	0/635	0.74	0/848
25	Y	0.40	0/510	0.70	0/677
26	Z	0.55	0/453	0.71	0/605
27	0	0.56	0/450	0.73	0/599
28	1	0.49	0/416	0.70	0/554
29	2	0.64	0/380	0.83	0/498
30	3	0.65	0/513	0.82	0/676
31	4	0.65	0/303	0.74	0/397
32	5	0.41	0/1001	0.99	3/1350 (0.2%)
33	6	0.36	0/531	0.76	0/709
34	7	0.57	0/166	0.56	0/256

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	a	0.56	0/36967	0.56	2/57666 (0.0%)
36	b	0.43	0/1735	0.94	7/2338 (0.3%)
37	c	0.51	0/1651	0.93	3/2225 (0.1%)
38	d	0.49	0/1665	0.89	0/2227
39	e	0.57	0/1154	0.89	0/1554
40	f	0.48	0/835	1.01	6/1128 (0.5%)
41	g	0.44	0/1195	0.83	2/1602 (0.1%)
42	h	0.52	0/989	0.93	5/1326 (0.4%)
43	i	0.51	0/1034	0.87	2/1375 (0.1%)
44	j	0.56	0/796	1.02	3/1077 (0.3%)
45	k	0.50	0/885	0.86	1/1195 (0.1%)
46	l	0.57	0/969	1.00	6/1300 (0.5%)
47	m	0.52	0/892	0.86	1/1193 (0.1%)
48	n	0.50	0/811	0.75	0/1081
49	o	0.48	0/722	0.79	0/964
50	p	0.53	0/659	0.76	0/884
51	q	0.53	0/657	0.86	0/881
52	r	0.54	0/511	0.84	0/689
53	s	0.48	0/652	0.79	0/877
54	t	0.48	0/671	0.81	3/888 (0.3%)
55	u	0.45	0/500	1.18	5/668 (0.7%)
56	v	0.52	0/1910	0.89	6/2573 (0.2%)
57	x	0.49	0/1841	0.59	3/2869 (0.1%)
58	z	0.81	1/127 (0.8%)	1.03	0/175
All	All	0.56	2/160601 (0.0%)	0.66	85/239775 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
56	v	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	85	PHE	CA-CB	-5.70	1.38	1.53
58	z	13	PRO	CA-C	5.23	1.54	1.51

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	c	81	GLU	N-CA-C	18.12	131.11	111.36
8	H	97	ARG	N-CA-C	12.55	124.96	111.28
55	u	34	ARG	N-CA-C	11.39	124.24	110.91
7	G	174	LYS	N-CA-C	10.30	122.09	111.07
46	l	43	LYS	N-CA-C	9.60	126.79	113.16
44	j	42	LEU	C-N-CD	-9.53	85.92	125.00
37	c	96	VAL	C-N-CD	-9.49	86.08	125.00
40	f	95	ALA	N-CA-C	9.29	124.07	110.59
44	j	57	VAL	N-CA-C	9.20	120.99	108.84
46	l	22	ALA	N-CA-C	-8.79	94.98	108.96
36	b	45	THR	CA-C-N	8.49	127.12	120.33
36	b	45	THR	C-N-CA	8.49	127.12	120.33
21	U	45	GLN	CA-C-N	8.42	131.95	120.67
21	U	45	GLN	C-N-CA	8.42	131.95	120.67
42	h	68	LYS	CA-C-N	8.28	132.50	120.82
42	h	68	LYS	C-N-CA	8.28	132.50	120.82
36	b	17	HIS	N-CA-C	7.56	119.17	108.74
47	m	3	ILE	N-CA-C	7.53	119.29	109.58
11	K	90	ASN	CA-C-N	7.29	132.48	121.40
11	K	90	ASN	C-N-CA	7.29	132.48	121.40
56	v	304	SER	N-CA-C	-7.20	99.65	110.24
11	K	110	GLU	N-CA-C	7.16	121.40	112.24
36	b	190	SER	CA-C-N	7.07	131.09	121.20
36	b	190	SER	C-N-CA	7.07	131.09	121.20
35	a	1300	G	C2'-C3'-O3'	7.02	120.02	109.50
45	k	38	GLY	N-CA-C	6.93	124.44	114.67
56	v	327	TYR	CA-C-N	-6.85	114.29	122.44
56	v	327	TYR	C-N-CA	-6.85	114.29	122.44
11	K	90	ASN	O-C-N	6.80	130.01	121.64
11	K	109	SER	N-CA-C	6.65	119.46	108.49
12	L	29	LYS	CA-C-N	6.62	134.19	121.54
12	L	29	LYS	C-N-CA	6.62	134.19	121.54
42	h	66	GLN	CA-C-N	6.25	133.66	121.41
42	h	66	GLN	C-N-CA	6.25	133.66	121.41
5	E	82	GLY	N-CA-C	6.25	120.86	111.42
40	f	52	ASN	N-CA-C	6.24	120.00	111.39
42	h	66	GLN	O-C-N	6.21	128.74	122.03
40	f	96	VAL	N-CA-C	6.16	122.14	109.34
43	i	90	ASP	CA-C-N	6.12	130.49	120.63
43	i	90	ASP	C-N-CA	6.12	130.49	120.63
5	E	81	GLY	N-CA-C	-6.01	98.94	113.18
36	b	74	ALA	N-CA-C	-5.91	105.98	113.43
56	v	319	ASP	N-CA-C	-5.84	99.77	109.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	l	46	SER	N-CA-C	5.81	117.70	110.91
18	R	80	ARG	N-CA-CB	-5.69	107.68	114.17
6	F	176	PHE	N-CA-C	5.66	118.10	111.02
55	u	8	ASN	CA-C-N	5.66	130.50	121.62
55	u	8	ASN	C-N-CA	5.66	130.50	121.62
55	u	23	GLU	CA-C-N	5.64	132.31	121.54
55	u	23	GLU	C-N-CA	5.64	132.31	121.54
2	B	3	C	P-O3'-C3'	5.57	128.55	120.20
37	c	96	VAL	N-CA-C	5.52	120.80	108.88
46	l	43	LYS	CA-C-N	-5.45	114.73	120.94
46	l	43	LYS	C-N-CA	-5.45	114.73	120.94
18	R	53	PHE	O-C-N	5.43	129.96	123.33
57	x	3	G	P-O3'-C3'	5.42	128.33	120.20
1	A	859	G	P-O3'-C3'	5.38	128.28	120.20
20	T	38	ALA	N-CA-C	5.38	117.74	111.02
54	t	69	ASN	N-CA-C	-5.36	106.42	113.12
44	j	58	ASN	N-CA-C	-5.33	99.46	110.80
1	A	1236	G	N9-C1'-C2'	5.29	119.94	112.00
41	g	128	GLU	CA-C-N	5.27	131.61	121.54
41	g	128	GLU	C-N-CA	5.27	131.61	121.54
57	x	2	G	P-O3'-C3'	5.24	128.06	120.20
6	F	19	PHE	CA-C-N	5.21	129.81	122.46
6	F	19	PHE	C-N-CA	5.21	129.81	122.46
36	b	150	ILE	N-CA-C	-5.20	107.28	111.91
46	l	23	LEU	N-CA-C	5.20	117.89	110.24
32	5	78	GLY	N-CA-C	5.19	122.92	112.34
1	A	1022	G	P-O3'-C3'	5.18	127.96	120.20
40	f	95	ALA	CA-C-N	5.16	131.25	121.97
40	f	95	ALA	C-N-CA	5.16	131.25	121.97
54	t	67	HIS	CA-C-N	5.15	130.64	122.61
54	t	67	HIS	C-N-CA	5.15	130.64	122.61
32	5	50	VAL	CA-C-N	5.14	127.89	120.38
32	5	50	VAL	C-N-CA	5.14	127.89	120.38
1	A	1130	U	P-O3'-C3'	5.14	127.91	120.20
1	A	372	G	P-O3'-C3'	5.14	127.90	120.20
57	x	3	G	C4'-C3'-O3'	5.13	117.09	109.40
56	v	303	ARG	CA-C-N	-5.11	113.74	121.05
56	v	303	ARG	C-N-CA	-5.11	113.74	121.05
1	A	858	G	P-O3'-C3'	5.10	127.85	120.20
40	f	63	ASN	N-CA-C	5.08	117.37	111.02
35	a	1300	G	P-O3'-C3'	5.08	127.81	120.20
1	A	1020	A	P-O3'-C3'	5.07	127.80	120.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
56	v	303	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	62262	0	31312	491	0
2	B	2572	0	1302	17	0
3	C	2082	0	2157	44	0
4	D	1565	0	1616	22	0
5	E	1552	0	1619	37	0
6	F	1410	0	1447	27	0
7	G	1323	0	1374	23	0
8	H	1111	0	1148	25	0
9	I	1032	0	1088	14	0
10	J	1129	0	1162	20	0
11	K	938	0	1012	18	0
12	L	1045	0	1117	17	0
13	M	1074	0	1157	24	0
14	N	960	0	1000	16	0
15	O	892	0	923	18	0
16	P	917	0	965	36	0
17	Q	947	0	1022	18	0
18	R	816	0	839	20	0
19	S	857	0	922	12	0
20	T	738	0	807	13	0
21	U	779	0	834	13	0
22	V	753	0	780	10	0
23	W	575	0	592	5	0
24	X	625	0	655	11	0
25	Y	509	0	543	14	0
26	Z	449	0	491	8	0
27	0	444	0	461	6	0
28	1	409	0	440	5	0
29	2	377	0	418	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	3	504	0	574	13	0
31	4	302	0	343	6	0
32	5	988	0	1025	30	0
33	6	522	0	522	44	0
34	7	149	0	76	19	0
35	a	33016	0	16617	353	0
36	b	1704	0	1732	33	0
37	c	1624	0	1699	53	0
38	d	1643	0	1710	42	0
39	e	1141	0	1170	33	0
40	f	817	0	808	27	0
41	g	1181	0	1240	21	0
42	h	979	0	1034	12	0
43	i	1022	0	1070	28	0
44	j	786	0	828	37	0
45	k	869	0	878	16	0
46	l	955	0	1018	36	0
47	m	883	0	944	56	0
48	n	799	0	841	16	0
49	o	714	0	737	18	0
50	p	649	0	666	16	0
51	q	648	0	691	18	0
52	r	504	0	502	10	0
53	s	637	0	665	30	0
54	t	665	0	714	16	0
55	u	495	0	486	23	0
56	v	1880	0	1841	89	0
57	x	1647	0	831	30	0
58	z	120	0	128	10	0
All	All	147985	0	100593	1710	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 7.

All (1710) 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)
55:u:34:ARG:HG2	55:u:36:PHE:CZ	1.25	1.63
55:u:34:ARG:CG	55:u:36:PHE:CZ	1.82	1.57
33:6:53:THR:CG2	47:m:74:MET:HE1	1.43	1.47
16:P:113:LEU:HD21	35:a:1441:A:C2	1.48	1.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:6:53:THR:HG21	47:m:74:MET:CE	1.50	1.42
55:u:34:ARG:HG2	55:u:36:PHE:CE2	1.56	1.39
33:6:50:ASP:OD1	47:m:70:ARG:HD2	1.19	1.37
16:P:113:LEU:CD2	35:a:1441:A:C2	2.11	1.33
8:H:89:LYS:HE2	40:f:82:ASP:OD2	1.28	1.30
35:a:710:G:OP1	40:f:53:LYS:NZ	1.68	1.26
16:P:113:LEU:CD2	35:a:1441:A:N1	1.99	1.25
16:P:113:LEU:HD22	35:a:1441:A:N1	1.51	1.25
37:c:96:VAL:CG1	37:c:97:PRO:HD3	1.65	1.24
8:H:89:LYS:CE	40:f:82:ASP:OD2	1.87	1.21
47:m:3:ILE:HD12	47:m:59:VAL:HG21	1.23	1.19
33:6:50:ASP:OD1	47:m:70:ARG:CD	1.90	1.18
37:c:96:VAL:CB	37:c:97:PRO:HD3	1.64	1.18
37:c:96:VAL:HG12	37:c:97:PRO:HD3	1.23	1.17
1:A:2312:U:O2	6:F:36:ASN:ND2	1.78	1.16
1:A:280:U:H2'	1:A:281:C:H6	1.11	1.14
47:m:3:ILE:CD1	47:m:59:VAL:HG21	1.77	1.13
37:c:96:VAL:CB	37:c:97:PRO:CD	2.25	1.12
37:c:96:VAL:HB	37:c:97:PRO:CD	1.79	1.12
55:u:34:ARG:CG	55:u:36:PHE:CE2	2.19	1.10
47:m:3:ILE:HD12	47:m:59:VAL:CG2	1.81	1.10
35:a:1150:A:O2'	44:j:42:LEU:O	1.68	1.08
16:P:105:LYS:HG2	35:a:1432:G:O5'	1.52	1.07
35:a:554:A:H5'	46:l:25:ALA:HB1	1.36	1.06
55:u:34:ARG:HG3	55:u:36:PHE:CZ	1.84	1.06
56:v:306:ARG:O	56:v:307:ASN:HB2	1.51	1.05
1:A:2557:G:H4'	56:v:245:ARG:HH12	1.21	1.05
37:c:96:VAL:HB	37:c:97:PRO:HD2	1.32	1.05
6:F:142:TYR:CE2	47:m:8:ILE:HD13	1.92	1.04
33:6:35:ASP:OD1	47:m:56:ARG:CZ	2.00	1.04
1:A:2557:G:H4'	56:v:245:ARG:NH1	1.72	1.03
1:A:2557:G:C4'	56:v:245:ARG:HH12	1.71	1.03
35:a:972:C:O2'	44:j:57:VAL:HG23	1.56	1.02
1:A:306:U:H3	1:A:310:A:N6	1.57	1.02
1:A:2553:G:O6	56:v:230:SER:OG	1.78	1.01
1:A:280:U:H2'	1:A:281:C:C6	1.96	1.01
33:6:53:THR:CG2	47:m:74:MET:CE	2.23	1.01
34:7:28:U:O4	56:v:122:ASP:HB3	1.58	1.01
56:v:137:ARG:CZ	56:v:334:GLU:HB2	1.91	1.00
55:u:34:ARG:HG2	55:u:36:PHE:HZ	1.19	0.96
6:F:142:TYR:CD2	47:m:8:ILE:HD13	2.01	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:l:23:LEU:CD2	46:l:58:ASN:HD22	1.79	0.95
37:c:62:SER:HA	37:c:97:PRO:HG2	1.47	0.94
1:A:306:U:H3	1:A:310:A:H62	0.99	0.94
57:x:56:C:O2	57:x:56:C:H2'	1.65	0.94
46:l:23:LEU:HD22	46:l:58:ASN:HD22	1.29	0.94
35:a:1247:U:H3	35:a:1290:G:H1	1.13	0.94
11:K:88:ASN:HB3	11:K:91:SER:O	1.70	0.92
16:P:105:LYS:CG	35:a:1432:G:O5'	2.17	0.92
55:u:34:ARG:CD	55:u:36:PHE:CZ	2.53	0.91
56:v:321:ARG:NE	56:v:321:ARG:HA	1.85	0.91
1:A:714:U:C5	49:o:88:ARG:HD2	2.05	0.91
1:A:1724:G:H1	1:A:1736:U:H3	0.99	0.91
1:A:2492:U:H4'	1:A:2573:C:N4	1.85	0.90
1:A:2062:A:N1	58:z:16:PRO:O	2.05	0.89
36:b:18:GLN:O	36:b:19:THR:HB	1.74	0.88
1:A:715:A:H2	49:o:39:GLN:HE22	1.15	0.88
1:A:2452:C:H4'	56:v:239:THR:HG21	1.55	0.87
55:u:33:ARG:HH11	55:u:33:ARG:HG3	1.36	0.87
1:A:714:U:H5	49:o:88:ARG:HD2	1.40	0.87
34:7:27:C:N4	57:x:34:G:O6	2.07	0.86
55:u:34:ARG:CG	55:u:36:PHE:CE1	2.58	0.86
35:a:1440:U:H3	35:a:1461:G:H1	1.22	0.86
1:A:572:A:H61	1:A:2029:G:H21	1.25	0.85
46:l:23:LEU:HD22	46:l:58:ASN:ND2	1.91	0.84
13:M:78:LEU:CD2	56:v:264:HIS:CD2	2.60	0.84
6:F:10:GLU:O	6:F:14:LYS:HB2	1.78	0.84
40:f:38:ARG:CZ	40:f:97:THR:O	2.25	0.84
55:u:34:ARG:HH11	55:u:36:PHE:HZ	1.26	0.84
1:A:715:A:C2	49:o:39:GLN:NE2	2.45	0.83
32:5:79:PRO:O	32:5:80:THR:O	1.96	0.83
1:A:886:A:O2'	47:m:91:ARG:NH1	2.11	0.83
56:v:183:ARG:NE	56:v:305:ASP:OD1	2.10	0.83
33:6:35:ASP:OD1	47:m:56:ARG:NH1	2.12	0.83
56:v:321:ARG:HA	56:v:321:ARG:HE	1.42	0.82
56:v:320:HIS:O	56:v:323:ASN:ND2	2.13	0.82
1:A:713:G:H3'	49:o:88:ARG:HH21	1.42	0.82
16:P:108:ARG:NH1	35:a:1464:U:P	2.52	0.82
34:7:27:C:N4	35:a:1400:C:H5'	1.94	0.82
16:P:113:LEU:HD21	35:a:1441:A:N1	1.80	0.82
1:A:1108:U:H2'	1:A:1109:C:C6	2.16	0.81
56:v:214:LEU:HG	56:v:279:HIS:CE1	2.15	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:6:53:THR:CB	47:m:74:MET:HE1	2.10	0.81
55:u:34:ARG:HG3	55:u:36:PHE:CE1	2.17	0.80
25:Y:54:LYS:O	25:Y:58:ASN:HB2	1.81	0.79
16:P:113:LEU:HD21	35:a:1441:A:H2	0.92	0.78
46:l:23:LEU:CD2	46:l:58:ASN:ND2	2.47	0.78
56:v:322:ILE:O	56:v:324:LEU:N	2.17	0.77
11:K:48:PRO:HG3	35:a:1422:G:H5'	1.67	0.77
46:l:23:LEU:HB3	46:l:58:ASN:HD21	1.49	0.77
3:C:173:LEU:O	3:C:180:MET:HA	1.85	0.77
56:v:305:ASP:HB3	56:v:320:HIS:NE2	2.00	0.77
35:a:593:U:H3	35:a:646:G:H1	1.30	0.77
1:A:2304:G:H22	1:A:2312:U:H3	1.33	0.76
56:v:119:THR:HG21	56:v:303:ARG:NH2	1.99	0.76
37:c:96:VAL:HG12	37:c:97:PRO:CD	2.11	0.75
1:A:672:C:H4'	5:E:84:THR:HG21	1.69	0.75
37:c:62:SER:HA	37:c:97:PRO:CG	2.17	0.75
35:a:554:A:H5'	46:l:25:ALA:CB	2.15	0.75
1:A:715:A:N3	49:o:39:GLN:NE2	2.34	0.75
44:j:42:LEU:HD23	44:j:43:PRO:HD2	1.68	0.75
57:x:56:C:O2	57:x:56:C:C2'	2.35	0.75
1:A:2507:C:H4'	56:v:238:ASN:O	1.86	0.74
33:6:57:VAL:HG13	53:s:41:PRO:HB3	1.69	0.74
34:7:28:U:C4	56:v:122:ASP:HB3	2.22	0.74
44:j:47:GLU:O	44:j:66:GLU:HA	1.87	0.74
35:a:1086:U:H3	35:a:1099:G:H22	1.36	0.74
37:c:96:VAL:CG1	37:c:97:PRO:CD	2.58	0.74
1:A:6:A:N3	10:J:135:GLN:NE2	2.36	0.73
1:A:301:G:N2	1:A:316:C:O2	2.15	0.73
35:a:847:G:H2'	35:a:848:C:H6	1.54	0.73
33:6:60:PHE:HZ	53:s:40:PHE:CE1	2.06	0.73
47:m:3:ILE:HD11	47:m:59:VAL:HG11	1.71	0.73
56:v:214:LEU:HB2	56:v:279:HIS:CD2	2.23	0.73
16:P:108:ARG:HH11	35:a:1464:U:P	2.11	0.72
37:c:139:ASN:O	37:c:143:LEU:HB2	1.89	0.72
1:A:886:A:O2'	47:m:91:ARG:NH2	2.22	0.72
55:u:34:ARG:HG3	55:u:36:PHE:CE2	2.09	0.72
1:A:1914:C:C6	56:v:295:ARG:NE	2.48	0.72
5:E:83:VAL:HG12	5:E:86:ALA:HB2	1.70	0.72
32:5:81:LEU:C	32:5:81:LEU:HD23	2.16	0.71
13:M:78:LEU:HD22	56:v:264:HIS:CD2	2.24	0.71
16:P:108:ARG:NH1	35:a:1464:U:OP1	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:25:ILE:O	7:G:31:GLU:HA	1.91	0.71
10:J:98:GLU:O	10:J:102:GLU:HB2	1.90	0.71
18:R:54:VAL:HG12	18:R:55:ASP:N	2.06	0.71
1:A:2492:U:H4'	1:A:2573:C:H41	1.53	0.70
36:b:18:GLN:O	36:b:19:THR:CB	2.39	0.70
35:a:847:G:H2'	35:a:848:C:C6	2.26	0.70
36:b:111:LYS:O	36:b:115:ASP:HB2	1.91	0.70
56:v:284:ALA:O	56:v:288:GLN:HB2	1.90	0.70
57:x:52:G:H1	57:x:62:C:H42	1.40	0.70
40:f:38:ARG:HD3	40:f:97:THR:H	1.57	0.70
35:a:553:A:O2'	46:l:25:ALA:O	2.10	0.69
46:l:48:LEU:HD11	56:v:304:SER:HB3	1.73	0.69
33:6:50:ASP:CG	47:m:70:ARG:CD	2.65	0.69
1:A:112:U:H5'	25:Y:58:ASN:HD21	1.57	0.69
1:A:2255:G:O2'	57:x:3:G:H5''	1.92	0.69
55:u:33:ARG:HG3	55:u:33:ARG:NH1	2.04	0.69
1:A:1071:G:N2	1:A:1090:A:N7	2.40	0.69
10:J:95:ARG:HG2	10:J:96:ARG:HG2	1.75	0.69
18:R:4:VAL:HA	18:R:12:HIS:O	1.91	0.69
41:g:73:GLU:O	41:g:87:PRO:HA	1.92	0.69
33:6:56:ARG:NH2	47:m:78:ARG:NH1	2.41	0.69
1:A:2106:U:H1'	1:A:2184:A:H61	1.58	0.68
1:A:2682:A:H61	1:A:2728:U:H1'	1.57	0.68
1:A:279:A:H61	1:A:361:G:H1'	1.58	0.68
5:E:83:VAL:CG1	5:E:86:ALA:HB2	2.24	0.68
35:a:407:U:O2	38:d:153:ARG:NH1	2.26	0.68
40:f:70:VAL:O	40:f:74:LEU:HB2	1.94	0.68
56:v:323:ASN:HD22	56:v:323:ASN:N	1.90	0.68
34:7:25:A:OP2	35:a:926:G:N1	2.26	0.68
39:e:156:ARG:NH1	42:h:98:LEU:O	2.27	0.68
56:v:306:ARG:O	56:v:307:ASN:CB	2.31	0.68
1:A:572:A:H61	1:A:2029:G:N2	1.91	0.68
40:f:29:ILE:HG21	40:f:64:VAL:HG21	1.76	0.67
13:M:41:LEU:O	13:M:93:VAL:HA	1.94	0.67
5:E:76:PRO:HA	5:E:82:GLY:HA2	1.74	0.67
33:6:60:PHE:CZ	53:s:40:PHE:CD1	2.83	0.67
47:m:3:ILE:CD1	47:m:59:VAL:CG2	2.56	0.67
24:X:37:PHE:O	24:X:45:PHE:HA	1.94	0.67
57:x:65:U:O2	57:x:65:U:H2'	1.93	0.67
8:H:89:LYS:NZ	40:f:82:ASP:OD2	2.26	0.67
27:0:54:ILE:HG13	27:0:56:LYS:HB3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:456:A:H61	35:a:476:U:H3	1.42	0.67
48:n:44:ALA:O	48:n:48:LEU:HB2	1.95	0.67
1:A:796:C:OP1	5:E:57:LYS:NZ	2.28	0.67
35:a:958:A:N7	53:s:54:ARG:NH1	2.43	0.67
39:e:57:ALA:O	39:e:61:LYS:HB2	1.94	0.66
1:A:563:A:N3	17:Q:36:GLN:NE2	2.43	0.66
42:h:23:ALA:HA	42:h:60:LEU:O	1.94	0.66
47:m:3:ILE:HD12	47:m:59:VAL:HG22	1.76	0.66
1:A:2475:C:H42	1:A:2529:G:H22	1.43	0.66
6:F:104:THR:HA	33:6:38:SER:HB3	1.76	0.66
19:S:73:LYS:HB3	19:S:106:VAL:HB	1.77	0.66
36:b:172:ILE:O	36:b:176:ASN:HB2	1.95	0.66
7:G:163:TYR:HB2	7:G:166:GLU:HB2	1.78	0.66
55:u:34:ARG:NH1	55:u:36:PHE:HZ	1.92	0.66
58:z:16:PRO:O	58:z:17:ARG:HB2	1.95	0.66
3:C:74:PRO:HB3	3:C:114:GLN:HE21	1.61	0.66
34:7:30:G:H3'	56:v:195:ARG:HE	1.60	0.66
41:g:59:GLU:HA	41:g:62:GLU:HB3	1.77	0.66
1:A:2305:U:H5''	6:F:130:GLY:HA3	1.78	0.66
53:s:5:LYS:HG3	53:s:6:LYS:HG2	1.77	0.66
35:a:1305:G:N2	35:a:1331:G:O2'	2.28	0.66
1:A:1960:A:HO2'	35:a:1484:C:HO2'	1.42	0.65
10:J:31:GLU:HG2	10:J:142:ILE:HG12	1.77	0.65
39:e:54:GLU:HG2	39:e:56:PRO:HD2	1.78	0.65
16:P:105:LYS:HG2	35:a:1432:G:C5'	2.26	0.65
56:v:323:ASN:HD22	56:v:323:ASN:H	1.43	0.65
1:A:2514:U:H2'	1:A:2515:C:C6	2.30	0.65
1:A:1401:G:H2'	1:A:1402:U:C6	2.30	0.65
1:A:517:C:OP1	27:0:12:ARG:NH2	2.30	0.65
38:d:84:ASN:ND2	38:d:87:GLU:OE1	2.30	0.65
38:d:155:LYS:O	38:d:158:LEU:HB3	1.96	0.65
41:g:69:ARG:HG2	41:g:95:ARG:HG2	1.77	0.65
1:A:1721:G:O2'	1:A:1739:A:N6	2.30	0.65
22:V:75:GLN:HB2	22:V:92:VAL:HG23	1.79	0.65
1:A:2556:C:H2'	56:v:245:ARG:HH22	1.61	0.64
35:a:1055:A:N3	37:c:155:ARG:NH1	2.46	0.64
32:5:56:ARG:NH1	32:5:81:LEU:HD11	2.13	0.64
35:a:946:A:O2'	35:a:1333:A:N3	2.29	0.64
35:a:1236:A:H4'	35:a:1304:G:H4'	1.79	0.64
43:i:94:ARG:HH21	43:i:98:ARG:HD2	1.61	0.64
47:m:70:ARG:O	47:m:74:MET:HB2	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:14:THR:OG1	21:U:68:ASN:ND2	2.31	0.64
35:a:1343:G:H4'	43:i:123:ARG:HB2	1.78	0.64
36:b:18:GLN:HA	36:b:18:GLN:HE21	1.63	0.64
13:M:78:LEU:HD21	56:v:264:HIS:CD2	2.32	0.64
35:a:51:A:H61	35:a:314:C:H1'	1.63	0.64
35:a:437:U:OP1	38:d:151:GLN:NE2	2.31	0.64
56:v:214:LEU:HG	56:v:279:HIS:NE2	2.11	0.64
51:q:63:CYS:SG	51:q:73:THR:OG1	2.55	0.64
53:s:30:LEU:HB2	53:s:48:ILE:HG22	1.80	0.64
35:a:1280:A:H5'	44:j:42:LEU:CD2	2.28	0.64
56:v:261:ARG:NH2	57:x:75:C:OP2	2.30	0.64
48:n:5:MET:SD	48:n:8:ARG:NH1	2.70	0.64
1:A:886:A:O2'	47:m:91:ARG:CZ	2.46	0.64
1:A:1107:G:H2'	1:A:1108:U:C6	2.33	0.64
35:a:761:G:H2'	35:a:762:U:H6	1.63	0.64
37:c:63:ILE:HG22	37:c:97:PRO:O	1.98	0.63
1:A:2469:A:O2'	13:M:55:ARG:NH2	2.31	0.63
33:6:57:VAL:HG13	53:s:41:PRO:CB	2.27	0.63
35:a:951:G:OP2	47:m:100:ARG:NH2	2.30	0.63
54:t:74:HIS:O	54:t:78:LEU:HB3	1.97	0.63
55:u:34:ARG:HD2	55:u:36:PHE:CE1	2.33	0.63
56:v:137:ARG:NH2	56:v:334:GLU:HB2	2.14	0.63
1:A:2321:U:O2	1:A:2321:U:C2'	2.44	0.63
37:c:61:LYS:O	37:c:96:VAL:HB	1.97	0.63
57:x:16:G:O4'	57:x:59:G:N2	2.32	0.63
35:a:672:U:H3	35:a:734:G:H1	1.45	0.63
53:s:68:HIS:HB3	53:s:72:GLU:HG3	1.80	0.63
11:K:121:GLU:HG2	11:K:122:VAL:HG23	1.80	0.63
13:M:78:LEU:HD21	56:v:264:HIS:NE2	2.13	0.63
12:L:95:LEU:HD22	12:L:100:ILE:HD11	1.80	0.62
35:a:269:C:H2'	35:a:270:A:H8	1.62	0.62
46:l:23:LEU:CB	46:l:58:ASN:HD21	2.11	0.62
1:A:1779:U:H5''	1:A:1780:A:H5''	1.81	0.62
1:A:2095:A:OP1	8:H:11:ASN:ND2	2.32	0.62
35:a:636:U:H2'	35:a:637:C:H6	1.64	0.62
35:a:1222:G:H5''	53:s:77:ARG:HH11	1.64	0.62
56:v:303:ARG:O	56:v:304:SER:C	2.39	0.62
1:A:2557:G:O2'	56:v:245:ARG:NH1	2.32	0.62
13:M:66:ARG:NH1	13:M:104:GLU:OE2	2.30	0.62
30:3:41:ARG:HG2	30:3:44:ARG:HH12	1.64	0.62
55:u:34:ARG:HD2	55:u:36:PHE:CZ	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:6:53:THR:HG21	47:m:74:MET:HE1	0.66	0.62
35:a:974:A:H4'	35:a:975:A:H3'	1.81	0.62
37:c:10:ARG:NH2	37:c:174:LEU:O	2.32	0.62
38:d:23:GLY:HA2	38:d:108:ALA:HB1	1.80	0.62
35:a:955:U:OP1	56:v:133:ARG:NH1	2.31	0.62
1:A:2492:U:C4'	1:A:2573:C:N4	2.62	0.62
15:O:94:ARG:NH2	15:O:97:PHE:O	2.32	0.62
1:A:1030:C:OP2	13:M:127:LYS:NZ	2.32	0.62
35:a:269:C:H2'	35:a:270:A:C8	2.35	0.62
51:q:8:GLN:NE2	51:q:59:GLU:OE2	2.33	0.62
1:A:2492:U:C5'	1:A:2573:C:N4	2.63	0.62
5:E:83:VAL:HG12	5:E:83:VAL:O	1.99	0.62
37:c:20:THR:HB	37:c:57:GLU:HG2	1.82	0.62
35:a:673:A:H2'	35:a:674:G:C8	2.35	0.62
1:A:313:G:H2'	1:A:314:C:C6	2.35	0.61
42:h:9:MET:HB2	42:h:32:LYS:HE3	1.82	0.61
3:C:200:MET:HE3	35:a:773:G:H4'	1.81	0.61
38:d:201:GLU:OE1	39:e:111:ARG:NH2	2.34	0.61
12:L:62:PRO:HB2	30:3:29:ARG:HH11	1.65	0.61
14:N:10:LEU:O	14:N:12:ARG:NH2	2.33	0.61
35:a:35:G:N3	46:l:114:SER:OG	2.30	0.61
35:a:77:A:H61	35:a:92:U:H3	1.48	0.61
35:a:459:A:H2'	35:a:460:A:H8	1.65	0.61
1:A:1462:C:HO2'	1:A:2702:G:HO2'	1.47	0.61
33:6:50:ASP:OD1	47:m:70:ARG:HD3	1.95	0.61
1:A:1065:U:O4	1:A:1073:A:N6	2.33	0.61
10:J:17:VAL:HG23	10:J:137:PRO:HB2	1.83	0.61
44:j:85:ASP:O	44:j:89:ARG:NH1	2.33	0.61
49:o:77:TYR:OH	49:o:87:ARG:NH2	2.34	0.61
1:A:33:C:N4	1:A:446:G:O2'	2.33	0.61
1:A:2321:U:O2	1:A:2321:U:H2'	2.00	0.61
5:E:18:THR:HA	5:E:106:LYS:HE3	1.81	0.61
18:R:27:ILE:O	18:R:66:HIS:NE2	2.29	0.61
47:m:3:ILE:HD11	47:m:59:VAL:HG21	1.76	0.61
12:L:57:LEU:HD22	30:3:53:ASP:HB3	1.83	0.61
35:a:754:C:OP1	49:o:71:ARG:NH2	2.34	0.61
35:a:761:G:H2'	35:a:762:U:C6	2.35	0.61
44:j:7:ARG:HB3	44:j:101:SER:HB2	1.81	0.61
35:a:126:G:OP1	35:a:605:U:O2'	2.19	0.61
50:p:4:ILE:HG12	50:p:21:VAL:HG22	1.83	0.61
3:C:151:GLY:O	3:C:155:ARG:NH1	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:63:ILE:HA	16:P:68:GLY:HA2	1.83	0.60
40:f:54:LEU:CD2	40:f:55:HIS:O	2.49	0.60
35:a:481:G:O2'	35:a:483:C:N4	2.34	0.60
35:a:690:G:O6	45:k:52:ARG:NH2	2.33	0.60
1:A:572:A:N6	1:A:2029:G:H21	1.96	0.60
1:A:2683:C:OP1	16:P:50:ARG:NH2	2.33	0.60
15:O:14:ALA:O	15:O:18:LEU:HB2	2.01	0.60
33:6:50:ASP:CG	47:m:70:ARG:HD3	2.25	0.60
1:A:1365:A:OP1	24:X:2:ARG:NH1	2.33	0.60
6:F:142:TYR:CD2	47:m:8:ILE:CD1	2.81	0.60
21:U:6:ARG:NH2	21:U:25:LYS:O	2.34	0.60
34:7:25:A:OP2	35:a:926:G:N2	2.33	0.60
35:a:890:G:O2'	35:a:906:A:N6	2.34	0.60
46:l:47:ALA:HB3	46:l:49:ARG:HE	1.66	0.60
1:A:621:A:OP2	12:L:99:ASN:ND2	2.34	0.60
1:A:2572:A:N6	4:D:150:GLN:OE1	2.34	0.60
20:T:46:ALA:O	20:T:50:LEU:HB2	2.00	0.60
1:A:243:U:OP1	30:3:7:ARG:NH1	2.35	0.60
41:g:68:VAL:HG23	41:g:99:ALA:HB1	1.82	0.60
44:j:22:THR:HG21	44:j:39:PRO:HB3	1.84	0.60
49:o:46:LYS:O	49:o:52:ARG:NH2	2.35	0.60
1:A:2469:A:N6	1:A:2481:G:O2'	2.35	0.60
1:A:2514:U:H2'	1:A:2515:C:H6	1.65	0.60
15:O:7:ARG:NH1	15:O:95:SER:O	2.34	0.60
36:b:18:GLN:HA	36:b:18:GLN:NE2	2.16	0.60
56:v:284:ALA:O	56:v:288:GLN:CB	2.50	0.60
6:F:49:LEU:HA	6:F:52:ALA:HB3	1.83	0.60
1:A:1843:C:O2'	3:C:253:GLY:O	2.17	0.60
32:5:81:LEU:HD23	32:5:82:ILE:N	2.17	0.60
1:A:1060:U:H3	1:A:1088:A:H8	1.47	0.60
35:a:263:A:OP1	54:t:73:ARG:NH1	2.35	0.60
35:a:1272:G:H2'	35:a:1273:C:C6	2.37	0.60
41:g:145:GLU:H	41:g:148:LYS:HB2	1.66	0.60
54:t:41:GLY:HA2	54:t:85:LEU:HD21	1.83	0.60
5:E:47:LYS:HB2	5:E:51:GLU:HB2	1.84	0.59
12:L:100:ILE:HG13	12:L:101:ILE:HG23	1.84	0.59
26:Z:15:ARG:HE	26:Z:52:PHE:HE2	1.50	0.59
33:6:57:VAL:CG1	53:s:41:PRO:HB3	2.31	0.59
56:v:234:GLY:HA3	57:x:76:A:H5'	1.84	0.59
1:A:1394:U:H4'	1:A:1603:A:H4'	1.84	0.59
1:A:2032:G:N2	4:D:151:THR:OG1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:d:155:LYS:HD3	38:d:158:LEU:HD13	1.84	0.59
38:d:187:ARG:O	38:d:187:ARG:NH1	2.32	0.59
1:A:1112:G:H2'	1:A:1113:U:C6	2.37	0.59
5:E:149:ILE:HG23	5:E:188:MET:HG2	1.84	0.59
22:V:64:VAL:HG22	22:V:69:GLU:HG2	1.84	0.59
35:a:993:G:H2'	35:a:995:C:H41	1.67	0.59
1:A:1048:A:OP2	1:A:1110:G:N2	2.36	0.59
38:d:94:GLU:HA	38:d:99:ASN:HD22	1.67	0.59
46:l:23:LEU:HD23	46:l:58:ASN:HD22	1.67	0.59
1:A:2115:G:N2	1:A:2118:U:OP2	2.36	0.59
5:E:1:MET:HE3	5:E:20:GLY:HA3	1.85	0.59
5:E:148:ILE:HB	5:E:169:VAL:HG22	1.83	0.59
1:A:2788:C:O2'	1:A:2809:A:N3	2.33	0.59
32:5:26:VAL:HG22	32:5:115:GLY:H	1.68	0.59
35:a:1082:A:OP1	39:e:22:LYS:NZ	2.36	0.59
1:A:788:A:OP1	1:A:791:C:N4	2.31	0.59
1:A:1826:G:O2'	1:A:1971:U:OP2	2.21	0.59
1:A:2515:C:O2	1:A:2516:A:C8	2.56	0.59
35:a:1137:C:O2'	35:a:1138:G:N2	2.36	0.59
36:b:209:VAL:O	36:b:213:LEU:CB	2.50	0.59
47:m:3:ILE:CD1	47:m:59:VAL:HG11	2.33	0.59
1:A:1011:G:OP2	17:Q:69:ARG:NH1	2.36	0.59
38:d:99:ASN:OD1	38:d:110:ARG:NH1	2.36	0.59
49:o:25:GLU:OE2	49:o:76:ARG:NH1	2.35	0.59
1:A:1340:U:OP1	20:T:19:LYS:NZ	2.35	0.59
13:M:40:ARG:HD2	13:M:93:VAL:HG21	1.85	0.59
38:d:87:GLU:HG3	38:d:187:ARG:HB2	1.84	0.59
40:f:54:LEU:HD23	40:f:55:HIS:O	2.02	0.59
56:v:328:ARG:HB3	56:v:331:GLU:HB2	1.84	0.59
1:A:563:A:OP2	18:R:79:ARG:NH2	2.36	0.58
1:A:2492:U:H5''	1:A:2573:C:C5	2.38	0.58
38:d:58:GLN:OE1	38:d:61:ARG:NH1	2.36	0.58
1:A:13:A:O2'	1:A:15:G:N7	2.32	0.58
1:A:1779:U:OP2	1:A:1784:A:N6	2.37	0.58
11:K:48:PRO:CG	35:a:1422:G:H5'	2.33	0.58
14:N:103:ARG:HB2	14:N:110:MET:HE3	1.85	0.58
37:c:62:SER:CA	37:c:97:PRO:HG2	2.27	0.58
42:h:29:SER:OG	42:h:30:LYS:N	2.36	0.58
54:t:7:LYS:O	54:t:10:ALA:HB3	2.03	0.58
1:A:280:U:C2	1:A:281:C:C5	2.91	0.58
1:A:1454:C:N4	14:N:73:ASN:OD1	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:14:PRO:HD3	25:Y:30:MET:HG3	1.85	0.58
22:V:2:PHE:HB3	22:V:61:LEU:HG	1.84	0.58
33:6:50:ASP:OD2	47:m:70:ARG:HD3	2.02	0.58
35:a:684:U:H1'	45:k:39:ASN:HB2	1.83	0.58
41:g:71:THR:HG23	41:g:95:ARG:HH12	1.67	0.58
35:a:227:G:O2'	50:p:63:GLN:NE2	2.34	0.58
37:c:90:VAL:O	37:c:94:ALA:HB2	2.04	0.58
56:v:322:ILE:O	56:v:322:ILE:HD12	2.04	0.58
1:A:2062:A:C2	58:z:16:PRO:O	2.56	0.58
7:G:41:GLU:OE2	7:G:43:LYS:NZ	2.36	0.58
56:v:214:LEU:CB	56:v:279:HIS:CD2	2.86	0.58
1:A:544:C:H3'	1:A:545:U:C6	2.38	0.58
8:H:14:SER:OG	8:H:17:ASP:OD2	2.22	0.58
33:6:56:ARG:HH22	53:s:68:HIS:HE1	1.52	0.58
33:6:60:PHE:HZ	53:s:40:PHE:CD1	2.20	0.58
44:j:52:LEU:HB2	48:n:81:ARG:HD2	1.86	0.58
1:A:1607:C:N4	1:A:1622:G:OP2	2.36	0.58
1:A:2585:U:O2'	58:z:18:LEU:HD13	2.04	0.58
25:Y:25:GLN:O	25:Y:29:ARG:HB2	2.03	0.58
35:a:9:G:OP2	39:e:125:LYS:NZ	2.36	0.58
1:A:1796:U:H2'	1:A:1797:G:H8	1.69	0.58
38:d:84:ASN:O	38:d:88:ASN:ND2	2.37	0.58
45:k:83:VAL:HB	45:k:109:ILE:HG12	1.84	0.58
16:P:51:ASN:O	16:P:52:ARG:NH1	2.35	0.57
35:a:28:A:O2'	35:a:296:U:OP1	2.22	0.57
1:A:249:C:O2'	12:L:63:LYS:NZ	2.32	0.57
1:A:465:G:OP1	29:2:12:ARG:NH1	2.36	0.57
1:A:2655:G:N2	1:A:2665:A:OP2	2.37	0.57
35:a:972:C:C2'	44:j:57:VAL:HG23	2.32	0.57
35:a:1200:C:H5''	35:a:1201:A:H3'	1.86	0.57
1:A:458:G:O2'	1:A:469:G:N1	2.37	0.57
1:A:1248:G:OP1	5:E:44:ARG:NH1	2.37	0.57
9:I:38:CYS:SG	9:I:39:LYS:NZ	2.74	0.57
10:J:4:PHE:HB3	17:Q:63:ARG:HH12	1.69	0.57
30:3:31:ILE:O	30:3:35:LYS:NZ	2.33	0.57
33:6:14:ALA:HA	33:6:32:LEU:HB3	1.86	0.57
35:a:437:U:O2	35:a:495:A:N7	2.37	0.57
35:a:1081:A:OP2	39:e:51:LYS:NZ	2.37	0.57
1:A:2849:U:OP1	16:P:92:ARG:NH2	2.37	0.57
19:S:62:ASP:N	19:S:62:ASP:OD1	2.36	0.57
44:j:10:LEU:HB3	44:j:98:VAL:HG23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:t:23:ARG:HH21	54:t:60:GLN:HE22	1.52	0.57
33:6:35:ASP:H	47:m:2:ARG:HH22	1.51	0.57
35:a:993:G:O2'	35:a:994:A:N7	2.37	0.57
38:d:85:THR:HB	39:e:102:THR:HG21	1.87	0.57
42:h:28:SER:OG	42:h:29:SER:N	2.36	0.57
50:p:73:ALA:HA	50:p:76:LYS:HB2	1.86	0.57
1:A:1162:G:H21	18:R:91:GLN:HE22	1.52	0.57
1:A:2522:U:O2'	1:A:2647:U:OP1	2.21	0.57
16:P:113:LEU:CD2	35:a:1441:A:H2	1.75	0.57
35:a:401:C:O2'	35:a:621:A:N3	2.34	0.57
35:a:501:C:OP1	46:l:113:ARG:NH2	2.38	0.57
35:a:1073:U:OP2	39:e:61:LYS:NZ	2.36	0.57
35:a:1266:G:N2	35:a:1269:A:OP2	2.33	0.57
1:A:1998:A:HO2'	1:A:2724:U:HO2'	1.52	0.57
1:A:2557:G:C4'	56:v:245:ARG:NH1	2.45	0.57
35:a:8:A:N6	38:d:201:GLU:O	2.37	0.57
1:A:1084:A:OP2	32:5:53:ARG:NH1	2.36	0.57
1:A:1682:G:OP2	1:A:1699:G:N2	2.36	0.57
4:D:20:VAL:HG23	11:K:72:PRO:HB2	1.87	0.57
35:a:1071:C:OP1	39:e:53:ARG:NH2	2.37	0.57
56:v:229:SER:HA	56:v:258:GLN:HE21	1.70	0.57
35:a:427:U:OP1	38:d:12:ARG:NH2	2.37	0.57
44:j:11:LYS:HA	44:j:70:HIS:O	2.05	0.57
46:l:23:LEU:HB3	46:l:58:ASN:ND2	2.18	0.57
1:A:72:U:O4	25:Y:58:ASN:ND2	2.37	0.56
1:A:1035:U:H3	1:A:1120:G:H1	1.53	0.56
1:A:1733:G:H2'	1:A:1734:G:C8	2.39	0.56
1:A:2539:C:H5'	31:4:3:VAL:HG21	1.87	0.56
35:a:511:C:O2'	38:d:40:HIS:NE2	2.37	0.56
54:t:74:HIS:O	54:t:78:LEU:CB	2.53	0.56
1:A:1869:G:N2	1:A:1872:A:OP2	2.38	0.56
1:A:2581:G:N2	1:A:2581:G:OP2	2.37	0.56
45:k:87:GLY:H	45:k:113:THR:HG22	1.69	0.56
55:u:34:ARG:CD	55:u:36:PHE:CE1	2.88	0.56
1:A:686:U:O2'	29:2:4:THR:O	2.23	0.56
1:A:771:G:OP2	29:2:11:LYS:NZ	2.36	0.56
1:A:1378:A:O2'	1:A:1380:G:OP2	2.24	0.56
3:C:143:VAL:HB	3:C:153:LEU:HB2	1.86	0.56
8:H:43:ASN:O	8:H:47:PHE:HB2	2.06	0.56
43:i:83:THR:HG21	43:i:102:PHE:HB3	1.86	0.56
46:l:23:LEU:CB	46:l:58:ASN:ND2	2.68	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:A:H4'	20:T:2:ILE:HD11	1.88	0.56
1:A:1949:G:O2'	35:a:1419:G:O2'	2.23	0.56
43:i:129:ARG:NH2	57:x:34:G:OP2	2.39	0.56
49:o:45:HIS:O	49:o:47:LYS:N	2.37	0.56
6:F:66:ILE:O	6:F:68:LYS:NZ	2.38	0.56
35:a:110:C:O2'	50:p:25:ARG:O	2.23	0.56
36:b:165:ALA:HB3	36:b:190:SER:HB3	1.88	0.56
52:r:19:GLU:O	52:r:20:ILE:C	2.46	0.56
35:a:744:C:H2'	35:a:745:G:H8	1.70	0.56
35:a:1366:C:HO2'	44:j:62:ARG:NH2	2.03	0.56
41:g:67:ASN:O	41:g:137:ARG:NE	2.37	0.56
1:A:2576:G:O2'	1:A:2579:C:OP2	2.23	0.56
13:M:50:ARG:HD3	13:M:65:ILE:HD11	1.88	0.56
20:T:6:ARG:NH1	20:T:42:GLU:OE1	2.39	0.56
25:Y:24:GLU:H	25:Y:27:ASN:HD22	1.54	0.56
38:d:155:LYS:NZ	38:d:177:MET:SD	2.79	0.56
4:D:113:SER:OG	4:D:114:LYS:N	2.39	0.56
58:z:16:PRO:O	58:z:17:ARG:CB	2.54	0.56
1:A:279:A:N1	1:A:361:G:O2'	2.36	0.56
2:B:43:C:OP1	33:6:6:HIS:NE2	2.37	0.56
21:U:17:ASP:HB3	21:U:20:LYS:HB2	1.88	0.56
35:a:939:G:OP1	41:g:101:ARG:NH1	2.39	0.56
35:a:1095:U:OP1	35:a:1108:G:N2	2.32	0.56
42:h:24:VAL:O	42:h:59:GLU:HA	2.05	0.56
1:A:340:A:O2'	5:E:162:ARG:NH1	2.39	0.56
1:A:704:G:O2'	1:A:727:A:N6	2.38	0.56
1:A:2063:C:O4'	58:z:18:LEU:HD23	2.06	0.56
8:H:126:GLY:H	8:H:146:VAL:HB	1.70	0.56
19:S:88:ARG:NH2	19:S:94:ASP:OD2	2.38	0.56
35:a:1378:C:O2	41:g:75:LYS:NZ	2.37	0.56
56:v:311:ASN:HB3	56:v:316:ARG:HG3	1.86	0.56
1:A:714:U:H5	49:o:88:ARG:CD	2.14	0.55
1:A:2204:G:H4'	3:C:149:LYS:HD3	1.88	0.55
4:D:46:ARG:NH2	4:D:89:GLU:OE1	2.39	0.55
35:a:1300:G:O2'	35:a:1303:C:N4	2.38	0.55
36:b:209:VAL:O	36:b:213:LEU:HB3	2.06	0.55
37:c:13:ILE:HG22	37:c:14:VAL:HG23	1.87	0.55
57:x:64:C:C4	57:x:65:U:C5	2.94	0.55
7:G:89:VAL:O	7:G:159:LYS:HA	2.05	0.55
13:M:53:MET:HB2	13:M:120:ALA:HB2	1.86	0.55
51:q:30:HIS:HD2	51:q:33:TYR:H	1.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1153:C:OP1	17:Q:91:ARG:NH2	2.39	0.55
15:O:6:ALA:O	15:O:10:ARG:HB2	2.06	0.55
37:c:9:ILE:HG23	37:c:10:ARG:HG3	1.86	0.55
56:v:321:ARG:O	56:v:322:ILE:HG13	2.06	0.55
1:A:1059:G:H1	1:A:1079:C:H42	1.54	0.55
7:G:93:TYR:OH	7:G:159:LYS:NZ	2.39	0.55
19:S:52:GLU:HA	19:S:55:ILE:HD12	1.89	0.55
32:5:42:ARG:O	32:5:46:ARG:HB2	2.05	0.55
35:a:1394:A:N1	35:a:1500:A:O2'	2.38	0.55
39:e:44:ARG:NH1	39:e:70:MET:SD	2.80	0.55
56:v:137:ARG:NH2	56:v:334:GLU:CB	2.70	0.55
1:A:910:A:N3	1:A:2264:C:O2'	2.37	0.55
1:A:1724:G:O6	1:A:1736:U:O4	2.24	0.55
1:A:2636:C:O2'	4:D:45:TYR:OH	2.25	0.55
35:a:222:C:H2'	35:a:223:A:H8	1.71	0.55
36:b:191:ASP:HB3	36:b:193:ASP:HB3	1.89	0.55
38:d:32:LYS:HB3	38:d:35:GLN:HB2	1.86	0.55
9:I:78:LEU:O	9:I:81:LYS:NZ	2.30	0.55
18:R:49:ILE:HG22	18:R:54:VAL:H	1.71	0.55
35:a:1129:C:O2'	35:a:1146:A:N6	2.40	0.55
40:f:38:ARG:NE	40:f:97:THR:O	2.40	0.55
51:q:46:HIS:HB2	51:q:70:LYS:HE3	1.87	0.55
56:v:322:ILE:HD13	56:v:343:PRO:HB2	1.89	0.55
35:a:490:C:OP1	38:d:145:ARG:NH2	2.40	0.55
35:a:694:A:N1	35:a:787:A:O2'	2.40	0.55
35:a:1255:G:O2'	35:a:1258:G:N3	2.36	0.55
1:A:1296:G:OP1	1:A:2709:G:O2'	2.22	0.55
1:A:2099:U:O2	1:A:2191:A:N6	2.39	0.55
1:A:2602:A:C8	56:v:261:ARG:NE	2.73	0.55
1:A:2780:G:OP2	10:J:120:ARG:NE	2.40	0.55
1:A:2780:G:N1	10:J:102:GLU:OE2	2.40	0.55
8:H:55:GLU:HA	8:H:58:LEU:HD12	1.87	0.55
33:6:35:ASP:H	47:m:2:ARG:NH2	2.05	0.55
35:a:674:G:H2'	35:a:675:A:H8	1.70	0.55
39:e:79:THR:OG1	39:e:97:PRO:O	2.24	0.55
47:m:15:VAL:HG23	47:m:16:ILE:HD12	1.89	0.55
52:r:17:VAL:O	52:r:18:GLN:CB	2.54	0.55
1:A:715:A:H2	49:o:39:GLN:NE2	1.93	0.55
1:A:1009:A:N3	1:A:1153:C:O2'	2.38	0.55
9:I:72:THR:HB	9:I:115:ASP:HB2	1.89	0.55
16:P:113:LEU:CD1	35:a:1441:A:C2	2.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:734:G:C4	35:a:735:C:C5	2.94	0.55
39:e:45:VAL:HG12	39:e:116:VAL:HG23	1.89	0.55
51:q:24:ILE:HD11	51:q:60:ILE:HD12	1.89	0.55
1:A:2365:G:N7	30:3:38:LYS:NZ	2.50	0.55
11:K:92:GLU:O	11:K:93:GLN:C	2.49	0.55
21:U:25:LYS:HE2	21:U:36:GLU:HB3	1.89	0.55
37:c:129:PHE:O	37:c:133:MET:CB	2.55	0.55
1:A:636:G:HO2'	1:A:638:G:HO2'	1.50	0.54
1:A:1638:C:O2	1:A:2698:U:O2'	2.25	0.54
32:5:103:ASN:HA	32:5:107:GLU:HB3	1.88	0.54
40:f:36:ILE:HA	40:f:64:VAL:HG23	1.89	0.54
1:A:546:U:O2	1:A:548:G:N1	2.39	0.54
6:F:125:GLY:O	6:F:157:THR:OG1	2.22	0.54
29:2:31:LEU:O	29:2:35:ARG:NH1	2.41	0.54
35:a:944:G:N1	35:a:1338:G:OP2	2.34	0.54
39:e:149:PRO:HA	39:e:152:VAL:HG22	1.89	0.54
1:A:1959:G:N3	35:a:1483:A:H2	2.04	0.54
1:A:2134:A:O2'	1:A:2159:G:N3	2.40	0.54
29:2:12:ARG:HE	29:2:44:VAL:HG21	1.72	0.54
35:a:412:A:H62	35:a:431:A:H61	1.55	0.54
35:a:875:U:O2'	42:h:14:ARG:NH1	2.40	0.54
40:f:38:ARG:HB2	40:f:63:ASN:HB3	1.90	0.54
46:l:113:ARG:HB2	46:l:118:VAL:HB	1.88	0.54
35:a:736:C:H2'	35:a:737:C:H6	1.72	0.54
1:A:1039:A:H61	1:A:1116:G:H1	1.54	0.54
1:A:2380:C:H5'	15:O:17:LYS:HZ1	1.73	0.54
1:A:2405:G:O2'	1:A:2412:A:N6	2.40	0.54
21:U:10:VAL:HG12	21:U:71:ILE:HG22	1.90	0.54
44:j:45:ARG:HB3	44:j:69:THR:HB	1.88	0.54
52:r:36:GLY:O	52:r:62:ARG:NH2	2.40	0.54
1:A:2769:U:H5'	10:J:95:ARG:HH22	1.73	0.54
33:6:56:ARG:NH2	47:m:78:ARG:CZ	2.71	0.54
35:a:946:A:H2'	35:a:947:G:C8	2.43	0.54
51:q:47:ASP:N	51:q:47:ASP:OD1	2.39	0.54
1:A:306:U:N3	1:A:310:A:N6	2.40	0.54
3:C:244:VAL:HG12	3:C:250:GLN:HA	1.89	0.54
35:a:1405:G:H21	35:a:1518:A:H8	1.56	0.54
36:b:18:GLN:HE21	36:b:18:GLN:CA	2.20	0.54
50:p:43:ALA:HA	50:p:46:LYS:HE3	1.89	0.54
1:A:546:U:O2	1:A:548:G:C6	2.61	0.54
1:A:820:A:H4'	1:A:836:G:H22	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:34:A:C2	2:B:44:G:C6	2.96	0.54
28:1:10:LEU:HA	28:1:49:LYS:O	2.07	0.54
35:a:768:A:N3	35:a:1512:U:O2'	2.41	0.54
35:a:842:U:O2'	35:a:845:A:OP1	2.21	0.54
37:c:65:VAL:HB	37:c:100:ILE:HG22	1.89	0.54
38:d:14:GLU:OE2	38:d:55:ARG:NH1	2.40	0.54
1:A:572:A:OP2	18:R:79:ARG:NH1	2.40	0.54
45:k:22:ILE:HG21	45:k:95:THR:HG21	1.88	0.54
4:D:35:THR:HG22	4:D:73:VAL:HG21	1.90	0.54
35:a:62:U:O2'	35:a:379:C:O2	2.26	0.54
35:a:352:C:O2	35:a:355:C:N4	2.40	0.54
39:e:106:ALA:HB1	39:e:110:MET:HE3	1.89	0.54
1:A:159:G:O2'	1:A:167:A:N6	2.40	0.53
1:A:2831:G:OP2	4:D:59:ARG:NH1	2.37	0.53
9:I:33:ASN:HB2	9:I:64:ARG:HH22	1.73	0.53
33:6:34:LEU:HA	47:m:2:ARG:HH21	1.72	0.53
35:a:816:A:OP1	35:a:1526:G:O2'	2.26	0.53
35:a:1340:A:O2'	57:x:31:C:O2'	2.25	0.53
47:m:95:PRO:HB2	47:m:99:GLN:HE21	1.73	0.53
1:A:577:G:O2'	1:A:1254:A:OP1	2.26	0.53
1:A:1032:A:H1'	31:4:23:ILE:HD13	1.90	0.53
1:A:1900:A:H1'	1:A:1970:A:H2'	1.89	0.53
18:R:54:VAL:HG12	18:R:55:ASP:H	1.73	0.53
30:3:8:GLY:O	30:3:12:ARG:NH2	2.39	0.53
33:6:53:THR:CG2	47:m:74:MET:HE3	2.32	0.53
37:c:61:LYS:O	37:c:97:PRO:CD	2.56	0.53
41:g:41:ILE:HD13	41:g:115:MET:HB3	1.91	0.53
42:h:88:LYS:HE2	42:h:116:ARG:HA	1.90	0.53
53:s:29:PRO:O	53:s:31:ARG:NH1	2.41	0.53
1:A:714:U:N3	1:A:717:C:OP2	2.38	0.53
1:A:2475:C:H42	1:A:2529:G:N2	2.06	0.53
14:N:96:ARG:O	14:N:113:ILE:HA	2.09	0.53
23:W:33:ILE:HG22	23:W:34:VAL:HG23	1.90	0.53
51:q:56:ASP:N	51:q:56:ASP:OD1	2.40	0.53
57:x:17:U:H3'	57:x:17(A):G:H2'	1.90	0.53
3:C:70:LYS:O	3:C:117:SER:OG	2.26	0.53
8:H:66:ASN:O	8:H:70:GLU:CB	2.57	0.53
35:a:664:G:H22	35:a:741:G:H1	1.55	0.53
35:a:974:A:OP1	48:n:69:ARG:NH2	2.41	0.53
35:a:1366:C:HO2'	44:j:62:ARG:HH22	1.57	0.53
37:c:90:VAL:O	37:c:94:ALA:CB	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:10:GLU:O	6:F:14:LYS:CB	2.55	0.53
16:P:105:LYS:HG2	35:a:1432:G:P	2.48	0.53
35:a:972:C:O2'	44:j:57:VAL:CG2	2.44	0.53
41:g:55:LYS:HD3	41:g:59:GLU:HG3	1.90	0.53
51:q:11:VAL:HG22	51:q:22:VAL:HG22	1.90	0.53
1:A:86:G:OP2	21:U:29:SER:OG	2.23	0.53
1:A:265:A:O2'	1:A:428:A:N6	2.42	0.53
1:A:1901:A:H4'	3:C:252:LYS:HD3	1.91	0.53
2:B:30:C:OP1	15:O:3:LYS:NZ	2.39	0.53
28:1:10:LEU:HB2	28:1:20:TYR:O	2.08	0.53
32:5:57:ASN:HB2	32:5:62:ARG:HD3	1.90	0.53
44:j:7:ARG:NE	44:j:75:ASP:OD1	2.41	0.53
1:A:370:G:O2'	1:A:424:G:OP1	2.26	0.53
1:A:647:G:N2	1:A:2350:C:O2'	2.36	0.53
1:A:768:G:N2	1:A:1379:U:O2'	2.40	0.53
1:A:2204:G:OP2	3:C:146:LYS:NZ	2.35	0.53
1:A:2537:U:H2'	1:A:2538:C:H6	1.74	0.53
16:P:105:LYS:HG3	35:a:1432:G:O5'	2.04	0.53
35:a:568:G:O6	46:l:1:ALA:N	2.42	0.53
56:v:226:THR:HG22	56:v:244:ILE:HG12	1.91	0.53
1:A:714:U:C5	49:o:88:ARG:CD	2.86	0.53
1:A:861:A:N3	2:B:79:G:O2'	2.40	0.53
11:K:21:CYS:HA	11:K:41:ILE:HG22	1.91	0.53
21:U:6:ARG:NH2	21:U:7:ASP:OD1	2.41	0.53
24:X:11:PRO:HB3	24:X:29:LEU:HD23	1.91	0.53
36:b:65:LYS:HB2	36:b:157:PRO:HA	1.91	0.53
56:v:123:GLU:HG3	56:v:188:PRO:HB3	1.90	0.53
1:A:33:C:O2	1:A:447:A:N6	2.42	0.53
30:3:23:HIS:ND1	30:3:24:LYS:O	2.33	0.53
35:a:673:A:H4'	40:f:86:ARG:HE	1.74	0.53
37:c:152:VAL:HG12	37:c:197:VAL:HG22	1.90	0.53
42:h:103:VAL:HA	42:h:124:ILE:HA	1.90	0.53
13:M:33:LEU:HD13	13:M:117:PHE:HB3	1.91	0.53
35:a:1118:U:OP1	43:i:10:ARG:NH1	2.39	0.53
35:a:1370:G:C2	35:a:1371:G:C8	2.96	0.53
37:c:15:LYS:NZ	37:c:182:ASP:OD1	2.36	0.53
1:A:546:U:OP2	1:A:546:U:H6	1.92	0.52
1:A:1681:G:N2	1:A:1763:G:OP2	2.39	0.52
1:A:2116:G:O6	1:A:2165:C:N4	2.37	0.52
35:a:229:U:O2'	50:p:23:ASP:OD1	2.26	0.52
35:a:1280:A:C5'	44:j:42:LEU:CD2	2.87	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:1373:G:H5''	41:g:35:LYS:HD2	1.90	0.52
37:c:54:ILE:HG22	37:c:67:ILE:HA	1.91	0.52
43:i:38:PHE:HB2	43:i:41:GLU:HB2	1.91	0.52
1:A:1386:C:H2'	1:A:1387:A:H8	1.74	0.52
1:A:2285:C:OP2	28:1:5:ARG:NH1	2.42	0.52
33:6:60:PHE:CD2	53:s:41:PRO:HD3	2.44	0.52
35:a:659:U:H3	35:a:747:A:H61	1.57	0.52
35:a:835:U:OP1	52:r:52:ARG:NH2	2.38	0.52
37:c:61:LYS:HB3	37:c:96:VAL:HG21	1.90	0.52
43:i:4:GLN:HE21	43:i:19:PHE:HB3	1.74	0.52
1:A:948:C:O2	1:A:984:A:O2'	2.24	0.52
1:A:993:G:H1'	18:R:91:GLN:HE21	1.75	0.52
6:F:101:ARG:NH2	33:6:25:ARG:O	2.42	0.52
18:R:60:LYS:HE2	18:R:100:GLY:HA3	1.92	0.52
33:6:57:VAL:HG13	53:s:41:PRO:CG	2.38	0.52
43:i:33:SER:HB3	43:i:36:GLN:HG2	1.91	0.52
5:E:117:ARG:NH2	5:E:183:PHE:O	2.41	0.52
16:P:113:LEU:HD22	35:a:1441:A:C2	2.05	0.52
35:a:1340:A:HO2'	57:x:31:C:HO2'	1.57	0.52
48:n:84:VAL:O	48:n:88:ALA:HB2	2.08	0.52
1:A:1223:G:OP1	18:R:68:ARG:NH2	2.43	0.52
1:A:1796:U:H2'	1:A:1797:G:C8	2.45	0.52
1:A:1818:U:H5'	3:C:156:SER:HB2	1.92	0.52
5:E:125:SER:O	5:E:137:LYS:NZ	2.43	0.52
10:J:46:PRO:HD3	17:Q:59:LEU:HD13	1.91	0.52
35:a:311:C:OP1	50:p:31:ARG:NH1	2.42	0.52
35:a:407:U:H5''	38:d:111:ALA:HB1	1.91	0.52
35:a:1064:G:O2'	35:a:1190:G:N2	2.36	0.52
35:a:1317:C:O2	53:s:36:ARG:NH2	2.32	0.52
53:s:54:ARG:HH22	53:s:78:THR:HG21	1.74	0.52
56:v:198:THR:O	56:v:303:ARG:NH1	2.40	0.52
57:x:65:U:O2	57:x:65:U:C2'	2.54	0.52
4:D:13:ARG:NH1	16:P:74:GLN:OE1	2.35	0.52
16:P:108:ARG:NH1	35:a:1464:U:OP2	2.42	0.52
22:V:77:VAL:HG23	22:V:89:ILE:HG12	1.91	0.52
35:a:459:A:H2'	35:a:460:A:C8	2.44	0.52
1:A:2064:C:O2'	1:A:2251:G:N2	2.36	0.52
1:A:2139:U:H2'	1:A:2140:G:H8	1.74	0.52
12:L:133:ALA:O	12:L:137:ALA:CB	2.58	0.52
35:a:1179:A:OP2	43:i:98:ARG:NH1	2.42	0.52
37:c:129:PHE:O	37:c:133:MET:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1084:A:H4'	32:5:55:VAL:HG12	1.92	0.52
38:d:123:MET:HB2	38:d:145:ARG:HG3	1.92	0.52
1:A:1891:G:HO2'	1:A:2235:G:HO2'	1.54	0.52
5:E:149:ILE:HD11	5:E:172:ALA:HA	1.90	0.52
18:R:54:VAL:CG1	18:R:55:ASP:H	2.20	0.52
35:a:490:C:H2'	35:a:491:G:H8	1.75	0.52
1:A:1419:A:H61	1:A:1494:A:H61	1.56	0.52
1:A:1529:G:O6	1:A:1542:U:O2	2.26	0.52
16:P:38:ARG:NH2	16:P:39:LEU:O	2.43	0.52
16:P:87:ARG:HH12	16:P:109:ILE:HD11	1.74	0.52
35:a:324:G:N1	35:a:327:A:OP2	2.43	0.52
40:f:4:TYR:O	40:f:63:ASN:HA	2.10	0.52
44:j:25:ILE:HD13	44:j:74:VAL:HG21	1.92	0.52
1:A:2773:C:OP1	4:D:169:ARG:NE	2.42	0.51
12:L:133:ALA:O	12:L:137:ALA:HB2	2.09	0.51
1:A:61:C:H5''	25:Y:43:LEU:HD22	1.93	0.51
1:A:397:U:H2'	1:A:398:C:C6	2.45	0.51
10:J:13:ARG:NH1	10:J:49:ASP:O	2.38	0.51
35:a:1060:U:H4'	44:j:53:ILE:HG23	1.92	0.51
1:A:65:U:O2'	1:A:456:C:O2	2.20	0.51
6:F:55:ASP:OD2	6:F:149:ARG:NE	2.43	0.51
6:F:162:ASP:OD1	6:F:162:ASP:N	2.42	0.51
35:a:585:G:O2'	51:q:35:LYS:NZ	2.43	0.51
35:a:1491:G:H5''	35:a:1492:A:OP2	2.10	0.51
37:c:61:LYS:O	37:c:96:VAL:CG1	2.59	0.51
1:A:2031:A:O2'	1:A:2454:G:N2	2.40	0.51
1:A:2556:C:H2'	56:v:245:ARG:NH2	2.26	0.51
7:G:174:LYS:O	7:G:175:LYS:HB2	2.11	0.51
1:A:2478:A:H5'	31:4:32:LYS:HE3	1.93	0.51
5:E:3:LEU:HD13	5:E:120:VAL:HG21	1.93	0.51
14:N:43:GLU:OE2	14:N:46:ARG:NH2	2.41	0.51
32:5:51:TYR:HE2	32:5:89:PRO:HD3	1.75	0.51
35:a:692:U:O2'	35:a:694:A:N7	2.38	0.51
47:m:28:ARG:HH21	47:m:62:PHE:HB2	1.75	0.51
55:u:35:GLU:O	55:u:37:TYR:N	2.38	0.51
1:A:466:A:N1	1:A:795:C:O2'	2.39	0.51
11:K:3:GLN:HB3	11:K:32:TYR:HB3	1.92	0.51
15:O:40:ILE:HG12	15:O:47:VAL:HG12	1.91	0.51
35:a:389:A:H3'	35:a:390:U:H6	1.76	0.51
53:s:36:ARG:O	53:s:69:LYS:NZ	2.38	0.51
1:A:545:U:OP2	1:A:545:U:H6	1.94	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1788:C:OP1	3:C:220:ARG:NH2	2.42	0.51
1:A:2087:G:H2'	1:A:2088:A:H8	1.75	0.51
38:d:159:GLU:O	38:d:162:GLU:HB2	2.11	0.51
41:g:110:ARG:NH1	41:g:112:ASP:OD2	2.44	0.51
56:v:323:ASN:ND2	56:v:323:ASN:H	2.06	0.51
1:A:569:U:O2'	1:A:983:A:N1	2.38	0.51
1:A:1475:G:O2'	1:A:1732:C:N4	2.44	0.51
1:A:1619:G:O2'	29:2:1:MET:N	2.44	0.51
11:K:87:LEU:HD13	11:K:92:GLU:HB3	1.92	0.51
24:X:70:LEU:HD22	24:X:75:GLU:HB2	1.92	0.51
30:3:31:ILE:O	30:3:31:ILE:HG22	2.11	0.51
35:a:636:U:H2'	35:a:637:C:C6	2.43	0.51
35:a:1397:C:OP2	39:e:28:ARG:NH2	2.38	0.51
39:e:22:LYS:HB3	39:e:29:ILE:HG23	1.93	0.51
46:l:43:LYS:O	46:l:43:LYS:HG2	2.10	0.51
1:A:994:C:OP1	17:Q:52:ARG:NH2	2.43	0.51
1:A:1548:A:H2'	1:A:1549:A:C8	2.46	0.51
1:A:1860:G:H1	1:A:1882:U:H3	1.57	0.51
14:N:49:GLU:OE2	14:N:94:TYR:N	2.41	0.51
33:6:60:PHE:CE2	53:s:41:PRO:HD3	2.46	0.51
36:b:35:ASN:HB3	36:b:37:VAL:HG12	1.93	0.51
1:A:155:A:H2'	1:A:156:A:C8	2.45	0.51
1:A:1445:G:O6	1:A:1466:U:O2	2.29	0.51
1:A:2364:C:OP1	23:W:51:ARG:NH1	2.40	0.50
7:G:21:GLN:NE2	7:G:37:ASN:O	2.44	0.50
35:a:539:A:OP2	46:l:111:GLN:NE2	2.41	0.50
36:b:112:ARG:O	36:b:116:LEU:HB2	2.11	0.50
41:g:63:VAL:O	41:g:67:ASN:ND2	2.44	0.50
55:u:35:GLU:C	55:u:37:TYR:H	2.17	0.50
1:A:1801:A:N6	1:A:2201:G:O2'	2.41	0.50
1:A:2515:C:C2	1:A:2516:A:C8	2.99	0.50
1:A:2685:G:H1	1:A:2724:U:H3	1.57	0.50
4:D:45:TYR:OH	4:D:81:GLU:OE2	2.28	0.50
35:a:1071:C:H2'	35:a:1072:G:H8	1.75	0.50
37:c:130:ARG:O	37:c:134:LYS:HB2	2.10	0.50
41:g:111:GLY:HA2	41:g:118:ARG:HD3	1.92	0.50
1:A:2540:C:O2'	1:A:2740:A:N3	2.36	0.50
1:A:2758:A:H1'	7:G:63:GLN:HE22	1.76	0.50
1:A:2848:G:O2'	1:A:2868:A:N6	2.45	0.50
2:B:81:G:O6	2:B:95:U:O2	2.30	0.50
7:G:17:LYS:HB3	7:G:24:THR:HB	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:36:LEU:HD22	10:J:121:LYS:HB2	1.92	0.50
16:P:113:LEU:HD11	35:a:1441:A:C2	2.46	0.50
35:a:938:A:N3	35:a:1376:U:O2'	2.34	0.50
36:b:18:GLN:C	36:b:19:THR:HG22	2.36	0.50
38:d:74:TYR:HH	38:d:133:SER:HG	1.52	0.50
18:R:14:VAL:HG23	18:R:18:GLN:HE21	1.76	0.50
20:T:1:MET:HG3	20:T:3:ARG:H	1.76	0.50
24:X:17:ARG:HH11	24:X:21:LEU:HD22	1.77	0.50
37:c:39:ARG:HA	37:c:54:ILE:HD11	1.93	0.50
1:A:2475:C:N4	1:A:2529:G:H22	2.10	0.50
34:7:27:C:C4	35:a:1400:C:H5'	2.46	0.50
35:a:1477:U:H2'	35:a:1478:U:C6	2.47	0.50
36:b:56:LEU:HD13	36:b:216:VAL:HG13	1.94	0.50
1:A:2537:U:H2'	1:A:2538:C:C6	2.47	0.50
28:1:8:ILE:HD13	28:1:24:LYS:HB2	1.92	0.50
35:a:909:A:N3	35:a:1413:A:O2'	2.39	0.50
57:x:27:C:H2'	57:x:28:A:H8	1.76	0.50
1:A:851:C:O2'	26:Z:42:ALA:O	2.30	0.50
1:A:2258:C:O2'	1:A:2427:C:OP2	2.29	0.50
7:G:86:LEU:O	7:G:129:GLU:HA	2.12	0.50
12:L:61:LEU:HD23	30:3:26:ALA:HB2	1.92	0.50
34:7:27:C:OP2	35:a:1402:C:N4	2.38	0.50
35:a:513:C:H2'	35:a:514:C:H6	1.77	0.50
51:q:63:CYS:HG	51:q:73:THR:HG1	1.45	0.50
1:A:29:U:O2	1:A:1215:G:O2'	2.30	0.50
1:A:281:C:O2	1:A:281:C:H2'	2.11	0.50
1:A:436:C:C2	1:A:437:U:C5	3.00	0.50
1:A:1919:A:O3'	35:a:1517:G:H1'	2.12	0.50
22:V:43:ASP:OD2	22:V:46:LYS:N	2.41	0.50
1:A:886:A:HO2'	47:m:91:ARG:HH22	1.60	0.50
1:A:1108:U:H2'	1:A:1109:C:H6	1.69	0.50
9:I:87:SER:OG	9:I:88:GLY:N	2.40	0.50
35:a:373:A:O2'	35:a:451:A:N7	2.45	0.50
35:a:435:A:H2	38:d:153:ARG:HH11	1.60	0.50
35:a:1118:U:H1'	35:a:1179:A:C5	2.47	0.50
37:c:61:LYS:O	37:c:96:VAL:CB	2.59	0.50
46:l:3:VAL:HG23	51:q:33:TYR:HB3	1.94	0.50
56:v:323:ASN:ND2	56:v:323:ASN:N	2.60	0.50
1:A:1724:G:N2	1:A:1736:U:O2	2.34	0.49
1:A:2515:C:C2	1:A:2516:A:N7	2.79	0.49
1:A:2548:U:O2	11:K:23:LYS:NZ	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2839:G:O2'	14:N:49:GLU:OE1	2.30	0.49
32:5:56:ARG:HH11	32:5:81:LEU:HD11	1.76	0.49
35:a:261:U:OP2	54:t:73:ARG:NH2	2.40	0.49
35:a:1367:C:H5''	43:i:115:VAL:HG23	1.94	0.49
1:A:1223:G:N2	1:A:1226:A:OP2	2.41	0.49
1:A:2899:A:H5'	10:J:136:GLN:HE22	1.77	0.49
35:a:200:G:H2'	35:a:201:G:H8	1.77	0.49
35:a:1147:C:HO2'	43:i:6:TYR:HH	1.57	0.49
35:a:1440:U:O4	35:a:1461:G:O6	2.30	0.49
37:c:187:GLU:HG3	37:c:189:HIS:CE1	2.47	0.49
1:A:2564:A:OP1	1:A:2648:G:O2'	2.29	0.49
2:B:37:C:O2	15:O:100:HIS:NE2	2.46	0.49
5:E:83:VAL:CG1	5:E:86:ALA:CB	2.91	0.49
33:6:56:ARG:HH21	47:m:78:ARG:NH1	2.09	0.49
35:a:1295:U:H2'	35:a:1296:C:C6	2.46	0.49
37:c:185:THR:HG23	37:c:198:LYS:HB3	1.94	0.49
56:v:288:GLN:OE1	56:v:288:GLN:HA	2.11	0.49
1:A:1028:A:N3	1:A:2486:C:O2'	2.39	0.49
1:A:2822:G:H5''	4:D:164:GLN:HE22	1.78	0.49
22:V:9:ARG:HD3	22:V:39:ALA:HB1	1.95	0.49
35:a:1366:C:O2'	44:j:62:ARG:NH2	2.36	0.49
52:r:41:SER:HB3	52:r:51:GLN:HG2	1.94	0.49
1:A:910:A:H62	13:M:12:MET:HA	1.77	0.49
1:A:2515:C:H2'	1:A:2516:A:H8	1.76	0.49
1:A:2572:A:H5''	1:A:2574:G:H4'	1.95	0.49
3:C:106:PRO:HG2	3:C:109:LEU:HB2	1.95	0.49
17:Q:108:LEU:HA	18:R:48:LYS:HE3	1.93	0.49
31:4:1:MET:HE2	31:4:36:ARG:HB2	1.94	0.49
35:a:51:A:N1	35:a:314:C:O2'	2.46	0.49
35:a:769:G:H4'	35:a:1513:A:H4'	1.95	0.49
35:a:1013:G:N2	35:a:1016:A:OP2	2.39	0.49
44:j:7:ARG:O	44:j:101:SER:N	2.44	0.49
1:A:140:C:H42	1:A:1595:C:H4'	1.77	0.49
1:A:1798:U:OP2	3:C:270:ARG:NH2	2.41	0.49
1:A:2688:G:N1	1:A:2720:U:OP2	2.35	0.49
1:A:2796:U:O2	1:A:2799:A:C2	2.64	0.49
3:C:144:GLU:HB2	3:C:187:CYS:HB3	1.94	0.49
5:E:3:LEU:HB2	5:E:12:LEU:HB3	1.93	0.49
8:H:87:GLU:OE2	40:f:24:ARG:CD	2.60	0.49
39:e:12:GLU:HA	39:e:38:VAL:HG12	1.93	0.49
1:A:1936:A:H2	1:A:1943:U:H3	1.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:1493:A:O2'	56:v:121:GLY:N	2.43	0.49
1:A:304:U:H3	1:A:313:G:H1	1.61	0.49
28:1:7:LYS:HA	28:1:23:THR:HA	1.95	0.49
34:7:27:C:C4	57:x:34:G:O6	2.65	0.49
35:a:113:G:N3	35:a:353:A:O2'	2.44	0.49
35:a:1368:A:OP1	43:i:112:ARG:NH2	2.46	0.49
37:c:56:ILE:HD12	37:c:63:ILE:HD11	1.94	0.49
52:r:65:SER:O	52:r:65:SER:OG	2.30	0.49
32:5:15:VAL:HG22	32:5:66:GLY:HA3	1.94	0.49
1:A:2220:U:H2'	1:A:2221:G:H8	1.78	0.49
11:K:114:LYS:HE3	11:K:118:LEU:HD11	1.95	0.49
33:6:33:ASN:HD21	47:m:49:GLU:CD	2.21	0.49
35:a:56:U:H2'	35:a:57:G:H8	1.78	0.49
35:a:942:G:H21	43:i:125:GLN:HE22	1.60	0.49
43:i:27:ILE:HG21	43:i:34:LEU:HD22	1.94	0.49
1:A:2483:C:N3	13:M:123:LYS:NZ	2.61	0.48
8:H:113:SER:O	8:H:116:ARG:NH1	2.42	0.48
26:Z:11:SER:OG	26:Z:12:ALA:N	2.46	0.48
1:A:672:C:OP2	12:L:42:SER:OG	2.29	0.48
7:G:25:ILE:HD12	7:G:74:MET:HE2	1.93	0.48
20:T:56:GLU:N	20:T:86:THR:O	2.45	0.48
22:V:58:SER:O	22:V:73:LYS:NZ	2.35	0.48
32:5:42:ARG:O	32:5:46:ARG:CB	2.61	0.48
33:6:15:SER:O	33:6:34:LEU:N	2.45	0.48
48:n:15:LEU:HD23	48:n:55:SER:HB3	1.95	0.48
1:A:532:A:N7	1:A:2021:C:O2'	2.44	0.48
1:A:1032:A:H2	1:A:1122:G:H22	1.61	0.48
19:S:47:VAL:HG23	19:S:103:ILE:HG21	1.95	0.48
33:6:33:ASN:OD1	47:m:49:GLU:OE2	2.31	0.48
35:a:1251:A:N3	35:a:1369:C:O2'	2.43	0.48
44:j:42:LEU:CB	44:j:43:PRO:CD	2.87	0.48
36:b:8:MET:N	36:b:42:LEU:O	2.46	0.48
1:A:820:A:N3	1:A:943:A:O2'	2.45	0.48
1:A:2298:A:OP1	6:F:70:ARG:NH2	2.45	0.48
3:C:15:VAL:HG22	3:C:205:GLY:HA3	1.94	0.48
3:C:77:VAL:HG21	3:C:109:LEU:HD11	1.95	0.48
14:N:73:ASN:HA	14:N:76:VAL:HG12	1.96	0.48
20:T:57:VAL:O	20:T:86:THR:OG1	2.30	0.48
5:E:147:LEU:HB3	5:E:186:VAL:HG13	1.96	0.48
35:a:736:C:H2'	35:a:737:C:C6	2.47	0.48
35:a:811:C:O2'	35:a:901:A:N1	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:v:214:LEU:CG	56:v:279:HIS:NE2	2.77	0.48
1:A:514:A:N3	1:A:581:C:O2'	2.37	0.48
1:A:1807:G:N2	1:A:1810:A:OP2	2.44	0.48
1:A:1912:A:C2	35:a:1407:C:O2	2.67	0.48
1:A:2557:G:C2'	56:v:245:ARG:HH12	2.27	0.48
8:H:125:THR:HG23	8:H:146:VAL:HG12	1.96	0.48
11:K:7:MET:HE1	11:K:44:LYS:HE2	1.96	0.48
32:5:81:LEU:C	32:5:81:LEU:CD2	2.86	0.48
35:a:1322:C:OP1	53:s:77:ARG:NH2	2.46	0.48
37:c:61:LYS:O	37:c:97:PRO:HD2	2.14	0.48
43:i:44:ARG:HG2	43:i:48:ARG:HH22	1.79	0.48
47:m:70:ARG:O	47:m:74:MET:CB	2.62	0.48
1:A:309:A:N3	1:A:329:G:O2'	2.43	0.48
1:A:2469:A:H4'	13:M:55:ARG:HD3	1.96	0.48
1:A:2492:U:H5''	1:A:2573:C:C4	2.49	0.48
3:C:18:VAL:HB	3:C:202:ARG:HH21	1.78	0.48
5:E:178:VAL:O	5:E:182:ALA:CB	2.62	0.48
6:F:28:PRO:HB2	6:F:168:LEU:HD22	1.95	0.48
12:L:128:THR:OG1	12:L:129:LYS:N	2.45	0.48
19:S:77:ASP:OD1	19:S:77:ASP:N	2.46	0.48
21:U:40:LEU:HA	21:U:60:LYS:O	2.14	0.48
25:Y:27:ASN:O	25:Y:31:GLN:CB	2.61	0.48
34:7:27:C:N3	57:x:34:G:O6	2.47	0.48
35:a:951:G:C6	35:a:1231:G:C6	3.01	0.48
39:e:101:GLY:H	39:e:121:ASN:HB2	1.79	0.48
1:A:534:U:O2	1:A:559:G:O6	2.32	0.48
1:A:1865:U:OP1	1:A:2409:G:N2	2.46	0.48
8:H:30:LEU:HB3	8:H:36:ALA:HB3	1.96	0.48
17:Q:84:LYS:HZ2	17:Q:116:LEU:HA	1.79	0.48
21:U:17:ASP:HB2	21:U:38:ILE:HG23	1.95	0.48
35:a:1006:G:O6	35:a:1023:U:O2	2.31	0.48
35:a:1041:G:H2'	35:a:1042:A:C8	2.49	0.48
35:a:1054:C:H41	56:v:195:ARG:HA	1.79	0.48
40:f:26:THR:O	40:f:30:THR:OG1	2.24	0.48
1:A:238:C:O2'	1:A:608:A:N3	2.40	0.48
1:A:251:A:OP1	12:L:58:TYR:OH	2.26	0.48
1:A:299:A:N3	1:A:319:G:O2'	2.39	0.48
1:A:1530:G:N2	1:A:1541:C:O2	2.34	0.48
1:A:2255:G:O2'	57:x:3:G:C5'	2.62	0.48
3:C:119:VAL:HG12	3:C:130:PRO:HG2	1.96	0.48
3:C:200:MET:HE1	35:a:773:G:O2'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:94:ILE:HB	8:H:122:LEU:HB2	1.95	0.48
15:O:108:ASP:OD1	15:O:111:ARG:NH1	2.45	0.48
21:U:14:THR:HG1	21:U:68:ASN:ND2	2.11	0.48
22:V:4:ILE:HB	22:V:63:ILE:HG12	1.96	0.48
35:a:216:U:H2'	35:a:217:C:C6	2.49	0.48
35:a:1536:C:H5'	35:a:1537:U:H5	1.79	0.48
36:b:170:ILE:O	36:b:174:GLU:HB3	2.14	0.48
36:b:209:VAL:O	36:b:213:LEU:HB2	2.13	0.48
38:d:60:VAL:HG21	38:d:199:ILE:HD11	1.94	0.48
1:A:839:U:H2'	1:A:840:C:C6	2.48	0.47
1:A:1266:G:O2'	1:A:2012:G:O6	2.27	0.47
1:A:2324:U:H5''	1:A:2325:G:H5''	1.96	0.47
6:F:9:ASP:OD1	6:F:9:ASP:N	2.43	0.47
9:I:32:VAL:HG21	9:I:60:VAL:HG21	1.96	0.47
35:a:362:G:OP1	46:l:57:THR:OG1	2.32	0.47
45:k:82:GLU:HG3	45:k:107:THR:HB	1.95	0.47
46:l:84:GLY:O	46:l:95:HIS:ND1	2.41	0.47
1:A:280:U:C2	1:A:281:C:C6	3.02	0.47
1:A:2101:A:H2'	1:A:2102:G:H8	1.78	0.47
16:P:105:LYS:CG	35:a:1432:G:P	3.03	0.47
34:7:27:C:N3	57:x:34:G:C6	2.82	0.47
35:a:528:C:H41	46:l:45:ASN:HD22	1.62	0.47
35:a:1346:A:OP1	43:i:121:ARG:NH1	2.37	0.47
1:A:1117:C:H2'	1:A:1118:C:H6	1.79	0.47
1:A:2786:U:H2'	1:A:2787:C:C6	2.49	0.47
13:M:61:GLY:HA2	13:M:107:GLY:HA3	1.95	0.47
35:a:255:G:OP1	51:q:70:LYS:NZ	2.38	0.47
39:e:57:ALA:O	39:e:61:LYS:CB	2.63	0.47
44:j:52:LEU:HD23	44:j:62:ARG:HG2	1.94	0.47
4:D:148:GLN:HB2	4:D:152:PRO:HG2	1.96	0.47
24:X:57:VAL:O	24:X:61:LYS:N	2.43	0.47
32:5:20:LYS:O	32:5:88:HIS:ND1	2.39	0.47
35:a:714:G:H2'	35:a:715:A:C8	2.48	0.47
36:b:18:GLN:NE2	36:b:21:TYR:OH	2.48	0.47
38:d:123:MET:O	38:d:143:SER:OG	2.31	0.47
40:f:54:LEU:HD23	40:f:55:HIS:N	2.29	0.47
1:A:1106:G:H2'	1:A:1107:G:H8	1.79	0.47
1:A:1203:U:H5'	12:L:3:LEU:HD23	1.96	0.47
1:A:2101:A:H2'	1:A:2102:G:C8	2.50	0.47
1:A:566:U:O2'	1:A:809:G:OP2	2.29	0.47
1:A:2897:U:H2'	1:A:2898:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:12:ASP:HA	11:K:99:ILE:HA	1.97	0.47
17:Q:46:TYR:OH	17:Q:50:ARG:NH2	2.47	0.47
32:5:94:ARG:HD3	32:5:131:THR:HA	1.96	0.47
35:a:24:U:O2'	35:a:524:G:O2'	2.32	0.47
35:a:407:U:H2'	35:a:408:A:H8	1.79	0.47
35:a:1083:U:O2'	35:a:1102:A:OP2	2.26	0.47
35:a:1149:C:H2'	35:a:1150:A:H8	1.78	0.47
39:e:155:LYS:HB3	42:h:70:VAL:HG13	1.97	0.47
56:v:322:ILE:O	56:v:323:ASN:C	2.58	0.47
1:A:372:G:N2	1:A:401:A:OP2	2.43	0.47
1:A:519:U:H2'	1:A:520:G:H8	1.80	0.47
1:A:631:A:N3	1:A:2415:G:O2'	2.41	0.47
1:A:639:U:H2'	1:A:640:C:C6	2.50	0.47
1:A:1754:A:N1	1:A:2716:C:O2'	2.44	0.47
1:A:1769:U:H3	1:A:1983:G:H1	1.63	0.47
8:H:66:ASN:O	8:H:70:GLU:HB2	2.15	0.47
9:I:134:SER:OG	9:I:135:MET:SD	2.67	0.47
13:M:35:ALA:HA	13:M:128:THR:HG22	1.96	0.47
16:P:38:ARG:NE	35:a:345:C:OP1	2.47	0.47
25:Y:27:ASN:O	25:Y:31:GLN:HB3	2.14	0.47
37:c:6:PRO:HD2	37:c:183:TYR:CD2	2.49	0.47
38:d:123:MET:HE2	38:d:126:GLY:HA2	1.97	0.47
43:i:34:LEU:HD11	43:i:47:VAL:HG21	1.96	0.47
43:i:98:ARG:HG2	43:i:103:VAL:HG21	1.95	0.47
1:A:1483:G:O6	1:A:1506:U:O2	2.31	0.47
3:C:106:PRO:HD2	3:C:109:LEU:HD22	1.96	0.47
15:O:33:ARG:HG2	15:O:34:HIS:CD2	2.50	0.47
48:n:84:VAL:O	48:n:88:ALA:CB	2.63	0.47
53:s:27:LYS:HD3	53:s:30:LEU:HG	1.97	0.47
56:v:115:VAL:HG22	56:v:203:VAL:HG22	1.95	0.47
1:A:1070:A:N7	1:A:1096:A:O2'	2.41	0.47
1:A:1602:U:OP2	20:T:64:LYS:NZ	2.47	0.47
26:Z:8:GLN:HB2	26:Z:28:LEU:HD13	1.96	0.47
32:5:24:SER:HB2	32:5:116:GLU:H	1.80	0.47
35:a:1464:U:H2'	35:a:1465:A:C8	2.49	0.47
44:j:42:LEU:CD2	44:j:43:PRO:HD2	2.39	0.47
52:r:11:ARG:HA	52:r:46:THR:H	1.80	0.47
55:u:45:LYS:O	55:u:49:ALA:HB2	2.15	0.47
1:A:281:C:H2'	1:A:282:A:H8	1.79	0.47
3:C:38:LYS:NZ	3:C:55:GLY:O	2.37	0.47
14:N:37:THR:HG22	14:N:110:MET:HE1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:69:LEU:HG	19:S:107:VAL:HG22	1.96	0.47
33:6:56:ARG:NH2	47:m:78:ARG:HH12	2.13	0.47
35:a:1192:C:OP2	37:c:3:LYS:NZ	2.39	0.47
36:b:33:ALA:HB2	36:b:39:ILE:HD11	1.96	0.47
37:c:72:PRO:HG3	37:c:104:GLU:HB3	1.97	0.47
40:f:46:GLN:HA	40:f:56:LYS:HG2	1.96	0.47
46:l:33:CYS:HA	46:l:54:VAL:HA	1.96	0.47
56:v:183:ARG:HH12	56:v:185:GLN:NE2	2.13	0.47
1:A:419:U:H2'	1:A:420:C:C6	2.50	0.46
3:C:77:VAL:HG21	3:C:109:LEU:HD21	1.97	0.46
10:J:45:THR:HB	10:J:48:VAL:HB	1.97	0.46
14:N:99:LYS:HB3	27:0:41:HIS:CD2	2.50	0.46
15:O:93:ASP:OD2	15:O:95:SER:OG	2.25	0.46
24:X:39:VAL:O	24:X:43:LYS:N	2.48	0.46
38:d:25:ARG:HE	38:d:28:ASP:HB3	1.79	0.46
1:A:1047:G:P	32:5:62:ARG:HH21	2.38	0.46
1:A:2075:U:O2'	1:A:2596:U:N3	2.44	0.46
3:C:57:HIS:ND1	3:C:58:LYS:O	2.44	0.46
13:M:78:LEU:CD2	56:v:264:HIS:NE2	2.77	0.46
33:6:26:SER:OG	33:6:27:THR:N	2.47	0.46
34:7:30:G:OP1	46:l:43:LYS:CE	2.64	0.46
35:a:189:A:H2'	35:a:190:A:H8	1.80	0.46
35:a:999:C:H2'	35:a:1000:A:H8	1.80	0.46
37:c:76:ILE:HA	37:c:83:VAL:HG23	1.97	0.46
52:r:24:ASP:N	52:r:24:ASP:OD1	2.45	0.46
52:r:40:PRO:HB2	52:r:42:ARG:HG3	1.96	0.46
1:A:630:G:O2'	1:A:632:A:N6	2.38	0.46
1:A:1943:U:H5''	56:v:256:GLU:OE2	2.16	0.46
1:A:2718:G:O2'	1:A:2847:U:OP1	2.29	0.46
4:D:179:ARG:HB3	4:D:188:LEU:HD12	1.98	0.46
35:a:444:G:H2'	35:a:445:G:H8	1.80	0.46
35:a:554:A:C5'	46:l:25:ALA:HB1	2.26	0.46
35:a:1280:A:O4'	44:j:43:PRO:HG2	2.15	0.46
41:g:4:ARG:HB3	41:g:6:ILE:HG23	1.97	0.46
41:g:6:ILE:H	41:g:6:ILE:HG13	1.42	0.46
44:j:5:ARG:HG2	44:j:79:PRO:HD3	1.97	0.46
56:v:119:THR:HG21	56:v:303:ARG:HH21	1.75	0.46
3:C:153:LEU:HD13	3:C:175:LEU:HD21	1.97	0.46
7:G:104:LEU:HB2	7:G:112:VAL:HB	1.97	0.46
9:I:33:ASN:HB3	9:I:36:GLU:HG2	1.97	0.46
34:7:29:A:C8	56:v:197:HIS:NE2	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:1527:U:H2'	35:a:1528:U:C6	2.51	0.46
37:c:130:ARG:O	37:c:134:LYS:CB	2.64	0.46
44:j:53:ILE:HD12	44:j:63:ASP:HB2	1.98	0.46
45:k:23:HIS:HB3	45:k:30:ILE:HG23	1.97	0.46
49:o:24:THR:HB	49:o:69:LEU:HD13	1.97	0.46
2:B:111:U:H2'	2:B:112:G:C8	2.51	0.46
5:E:102:ARG:NH1	5:E:199:MET:O	2.43	0.46
16:P:38:ARG:CD	35:a:345:C:OP1	2.64	0.46
20:T:37:ASP:O	20:T:81:LYS:NZ	2.41	0.46
35:a:212:G:H2'	35:a:213:G:H8	1.80	0.46
35:a:243:A:H4'	35:a:244:U:H3'	1.98	0.46
1:A:442:G:O4'	5:E:41:GLN:NE2	2.49	0.46
1:A:1509:A:H2'	1:A:1510:G:H8	1.81	0.46
1:A:1509:A:H2'	1:A:1510:G:C8	2.51	0.46
1:A:2723:C:OP1	4:D:114:LYS:NZ	2.38	0.46
5:E:83:VAL:CG1	5:E:86:ALA:HA	2.46	0.46
8:H:7:ASP:HB2	8:H:35:LYS:HD2	1.98	0.46
11:K:71:ARG:HB2	11:K:75:SER:HB2	1.96	0.46
12:L:88:GLY:O	12:L:121:THR:N	2.48	0.46
18:R:76:LYS:HD2	18:R:85:LYS:HE2	1.97	0.46
35:a:618:C:N4	35:a:621:A:OP2	2.48	0.46
35:a:776:G:N2	35:a:802:A:OP2	2.36	0.46
1:A:2492:U:H5''	1:A:2573:C:N4	2.31	0.46
1:A:2861:U:H2'	1:A:2862:G:H8	1.80	0.46
1:A:2881:U:O2'	14:N:95:THR:O	2.26	0.46
5:E:105:LEU:HD23	5:E:108:ILE:HD11	1.97	0.46
29:2:24:THR:HG23	29:2:27:GLY:H	1.79	0.46
33:6:53:THR:CB	47:m:74:MET:CE	2.82	0.46
35:a:410:G:H21	35:a:432:A:H62	1.63	0.46
35:a:600:A:H2'	35:a:601:G:H8	1.81	0.46
35:a:1124:G:H5''	44:j:37:ARG:HG3	1.98	0.46
1:A:926:G:H2'	1:A:927:A:C8	2.50	0.46
1:A:2110:G:H22	1:A:2179:C:H42	1.64	0.46
6:F:3:LEU:HA	6:F:6:TYR:HB3	1.98	0.46
8:H:65:ALA:O	8:H:69:ALA:HB3	2.16	0.46
9:I:117:THR:HA	32:5:42:ARG:HH21	1.81	0.46
14:N:77:ALA:O	14:N:81:ASN:ND2	2.43	0.46
32:5:24:SER:OG	32:5:86:MET:SD	2.74	0.46
40:f:92:THR:OG1	40:f:93:LYS:N	2.38	0.46
1:A:6:A:H1'	10:J:135:GLN:HE22	1.81	0.46
1:A:828:U:H2'	1:A:829:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1495:A:N3	1:A:1578:U:O2'	2.41	0.46
1:A:2099:U:H2'	1:A:2100:G:C8	2.50	0.46
35:a:1276:G:H2'	35:a:1277:C:C6	2.51	0.46
54:t:24:ARG:HD3	54:t:65:LEU:HD11	1.97	0.46
56:v:124:ALA:HB2	56:v:199:SER:HB3	1.97	0.46
56:v:279:HIS:O	56:v:283:MET:HG2	2.16	0.46
1:A:399:U:H5''	24:X:56:ARG:HH12	1.81	0.46
1:A:2032:G:O6	1:A:2453:A:O2'	2.32	0.46
1:A:2377:A:O2'	15:O:117:PHE:O	2.32	0.46
8:H:87:GLU:OE2	40:f:24:ARG:HD3	2.16	0.46
33:6:56:ARG:HH12	53:s:68:HIS:CE1	2.33	0.46
35:a:1414:U:O2	35:a:1487:G:N2	2.48	0.46
44:j:40:ILE:HB	44:j:73:LEU:HB2	1.96	0.46
56:v:248:HIS:CE1	56:v:250:PRO:HD2	2.51	0.46
1:A:528:A:H5''	10:J:113:PRO:HG3	1.98	0.45
1:A:2902:C:H3'	1:A:2903:U:C5	2.51	0.45
6:F:7:TYR:OH	6:F:28:PRO:O	2.32	0.45
35:a:235:C:H2'	35:a:236:A:C8	2.51	0.45
50:p:20:VAL:HG23	50:p:35:ARG:HA	1.98	0.45
1:A:641:U:O4	1:A:647:G:O6	2.34	0.45
1:A:1115:G:H2'	1:A:1116:G:H8	1.81	0.45
1:A:1342:A:O2'	1:A:1344:U:OP2	2.28	0.45
1:A:1754:A:O3'	16:P:102:ARG:NH2	2.50	0.45
1:A:2474:U:H5''	1:A:2475:C:H5	1.81	0.45
16:P:88:ARG:NH1	16:P:114:ASN:OD1	2.50	0.45
27:0:37:HIS:ND1	27:0:38:LEU:O	2.49	0.45
33:6:50:ASP:CG	47:m:70:ARG:HD2	2.18	0.45
35:a:354:G:O2'	35:a:389:A:OP1	2.30	0.45
1:A:2492:U:C4'	1:A:2573:C:H41	2.24	0.45
11:K:92:GLU:OE1	11:K:92:GLU:HA	2.16	0.45
35:a:618:C:H1'	50:p:14:ARG:HH12	1.81	0.45
35:a:815:A:N7	35:a:1509:C:O2'	2.40	0.45
35:a:958:A:N3	35:a:985:C:O2'	2.44	0.45
36:b:56:LEU:HB3	36:b:220:VAL:HG22	1.98	0.45
36:b:100:LEU:HD13	36:b:175:ALA:HB2	1.97	0.45
44:j:42:LEU:CB	44:j:43:PRO:HD2	2.47	0.45
51:q:47:ASP:HB3	51:q:74:LEU:HB2	1.97	0.45
57:x:23:A:H2'	57:x:24:G:C8	2.52	0.45
1:A:1076:C:H2'	1:A:1077:A:C8	2.51	0.45
1:A:1668:A:N3	1:A:1670:C:N4	2.64	0.45
1:A:1755:A:N6	1:A:2694:G:O2'	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2233:U:H2'	1:A:2234:G:C8	2.51	0.45
3:C:131:MET:HE1	3:C:143:VAL:HG13	1.98	0.45
3:C:153:LEU:HD11	3:C:181:ARG:HH21	1.81	0.45
6:F:135:ILE:HG21	6:F:142:TYR:HD1	1.81	0.45
35:a:429:U:H5'	38:d:8:LEU:HD23	1.99	0.45
35:a:1243:C:H2'	35:a:1244:G:H8	1.82	0.45
1:A:1017:G:H2'	1:A:1018:U:H6	1.81	0.45
1:A:1802:A:H2'	1:A:1803:A:C8	2.52	0.45
36:b:68:PHE:HB3	36:b:79:VAL:HG13	1.99	0.45
39:e:81:GLN:HB2	39:e:82:HIS:HD2	1.80	0.45
51:q:46:HIS:NE2	51:q:48:GLU:OE2	2.37	0.45
1:A:718:A:H3'	1:A:719:C:H6	1.82	0.45
1:A:1062:G:H2'	1:A:1063:G:C4	2.52	0.45
1:A:1087:G:N2	1:A:1089:A:N1	2.65	0.45
1:A:1372:U:H2'	1:A:1373:A:H8	1.81	0.45
1:A:2126:A:H2'	1:A:2162:G:H21	1.81	0.45
1:A:2484:G:OP1	13:M:44:ARG:NH2	2.38	0.45
2:B:64:G:H2'	2:B:65:U:C6	2.52	0.45
3:C:23:LEU:HD23	3:C:80:LEU:HB3	1.99	0.45
24:X:64:ASP:O	24:X:68:ALA:HB2	2.16	0.45
35:a:1376:U:O4	41:g:9:ARG:NH1	2.31	0.45
46:l:42:LYS:HG2	46:l:88:ASP:O	2.17	0.45
53:s:5:LYS:HE3	53:s:6:LYS:HE3	1.99	0.45
1:A:436:C:N3	1:A:437:U:C5	2.85	0.45
1:A:698:C:O2'	1:A:734:A:N6	2.41	0.45
1:A:1549:A:H2'	1:A:1550:C:C6	2.51	0.45
1:A:2419:U:OP1	30:3:40:LYS:NZ	2.50	0.45
1:A:2595:G:N2	1:A:2598:A:OP2	2.37	0.45
30:3:60:CYS:SG	30:3:61:LEU:N	2.90	0.45
35:a:633:G:OP1	42:h:87:ARG:NH2	2.45	0.45
35:a:938:A:H2	35:a:1376:U:O2	2.00	0.45
35:a:1011:C:H2'	35:a:1012:A:C8	2.52	0.45
37:c:61:LYS:O	37:c:96:VAL:HG11	2.17	0.45
56:v:191:GLU:HG3	56:v:194:GLY:H	1.81	0.45
1:A:302:C:H2'	1:A:303:G:H8	1.82	0.45
1:A:585:G:N7	17:Q:5:ARG:NH1	2.64	0.45
1:A:605:G:N3	1:A:657:U:O2'	2.50	0.45
3:C:160:TYR:HB3	3:C:193:GLU:HG2	1.99	0.45
8:H:47:PHE:HA	8:H:51:ARG:HB2	1.99	0.45
15:O:7:ARG:HH12	15:O:95:SER:HB3	1.81	0.45
46:l:26:CYS:SG	46:l:29:LYS:HD3	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:o:46:LYS:HE3	49:o:46:LYS:HB2	1.78	0.45
57:x:5:U:O2'	57:x:6:U:O5'	2.34	0.45
1:A:1087:G:H22	1:A:1102:C:H42	1.63	0.45
1:A:2291:U:H2'	1:A:2292:U:C6	2.52	0.45
1:A:2291:U:OP1	1:A:2380:C:O2'	2.27	0.45
1:A:2492:U:C5'	1:A:2573:C:C4	3.00	0.45
26:Z:23:LEU:HD22	26:Z:28:LEU:HD12	1.98	0.45
35:a:271:C:H2'	35:a:272:C:H6	1.82	0.45
43:i:129:ARG:NH1	57:x:33:U:OP2	2.39	0.45
54:t:27:MET:HE1	54:t:66:ILE:HD11	1.98	0.45
1:A:839:U:H2'	1:A:840:C:H6	1.80	0.45
1:A:987:C:O2'	1:A:1000:A:N3	2.43	0.45
1:A:1112:G:H2'	1:A:1113:U:H6	1.81	0.45
1:A:1965:C:H5''	1:A:1966:A:H2'	1.97	0.45
1:A:2637:U:OP1	4:D:83:ARG:NH2	2.50	0.45
3:C:154:ALA:HB2	3:C:161:VAL:HG23	1.99	0.45
7:G:10:VAL:O	7:G:47:ASN:ND2	2.50	0.45
21:U:12:VAL:HG22	21:U:69:VAL:HG12	1.98	0.45
38:d:103:ARG:HD2	38:d:167:PRO:HG2	1.98	0.45
1:A:675:A:N3	1:A:2443:C:O2'	2.49	0.44
6:F:66:ILE:HG22	6:F:86:CYS:HB3	1.99	0.44
23:W:14:ALA:O	23:W:16:ARG:NH1	2.47	0.44
35:a:672:U:H2'	35:a:673:A:C8	2.53	0.44
35:a:1117:A:H4'	43:i:105:ARG:HD2	2.00	0.44
55:u:34:ARG:CD	55:u:36:PHE:HZ	2.19	0.44
1:A:674:G:H5''	5:E:71:GLY:N	2.32	0.44
1:A:713:G:O2'	1:A:718:A:N6	2.50	0.44
1:A:906:U:O2'	13:M:66:ARG:NH2	2.50	0.44
1:A:1817:G:OP1	3:C:61:TYR:OH	2.31	0.44
21:U:10:VAL:HA	21:U:71:ILE:HA	1.99	0.44
34:7:25:A:OP2	35:a:926:G:C2	2.70	0.44
35:a:674:G:H2'	35:a:675:A:C8	2.52	0.44
38:d:3:TYR:CZ	38:d:10:LEU:HD21	2.52	0.44
40:f:68:GLN:HA	40:f:71:ILE:HG22	1.98	0.44
43:i:90:ASP:OD1	43:i:90:ASP:N	2.46	0.44
48:n:25:GLU:HB2	48:n:29:ILE:HD12	1.99	0.44
53:s:10:ILE:HD13	53:s:15:LEU:HD22	1.98	0.44
1:A:2458:G:O2'	1:A:2460:U:O4	2.32	0.44
1:A:2820:A:OP2	1:A:2821:A:N6	2.37	0.44
2:B:40:U:O2'	2:B:43:C:OP2	2.31	0.44
5:E:83:VAL:CG1	5:E:86:ALA:CA	2.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:79:G:C2	35:a:80:A:H1'	2.53	0.44
35:a:528:C:H41	46:l:45:ASN:ND2	2.16	0.44
35:a:1015:G:H2'	35:a:1016:A:C8	2.52	0.44
35:a:1245:C:H2'	35:a:1246:A:H8	1.81	0.44
37:c:123:LEU:HD23	37:c:123:LEU:HA	1.80	0.44
42:h:77:VAL:HG11	42:h:124:ILE:HD11	1.99	0.44
56:v:235:GLN:NE2	58:z:17:ARG:O	2.50	0.44
1:A:1794:A:H2'	1:A:1795:C:C6	2.52	0.44
8:H:87:GLU:OE2	40:f:24:ARG:HD2	2.17	0.44
35:a:553:A:O2'	46:l:25:ALA:C	2.61	0.44
35:a:1376:U:H2'	35:a:1377:A:C8	2.53	0.44
44:j:54:SER:OG	44:j:56:HIS:O	2.28	0.44
56:v:127:PHE:O	56:v:130:ASP:N	2.51	0.44
1:A:962:G:H2'	1:A:963:U:C6	2.52	0.44
1:A:1613:G:H4'	29:2:3:ARG:HD3	1.99	0.44
1:A:2190:G:H2'	1:A:2191:A:H8	1.82	0.44
31:4:16:ILE:HA	31:4:24:ARG:O	2.18	0.44
32:5:45:GLY:HA2	32:5:49:GLY:HA2	1.99	0.44
35:a:518:C:O2'	35:a:530:G:N2	2.51	0.44
35:a:668:G:H21	49:o:45:HIS:CE1	2.36	0.44
56:v:132:PHE:O	56:v:136:SER:HB2	2.17	0.44
1:A:817:C:O2'	1:A:839:U:OP1	2.35	0.44
1:A:2452:C:H4'	56:v:239:THR:CG2	2.39	0.44
6:F:122:ASP:OD1	6:F:122:ASP:N	2.44	0.44
36:b:186:VAL:HB	36:b:190:SER:HB2	1.98	0.44
1:A:751:A:C2	58:z:7:TYR:CE1	3.06	0.44
19:S:14:ALA:O	19:S:18:ARG:HB2	2.17	0.44
35:a:67:C:H2'	35:a:68:G:C8	2.52	0.44
35:a:189:A:H2'	35:a:190:A:C8	2.53	0.44
35:a:1014:A:H5''	53:s:13:HIS:HB2	1.99	0.44
36:b:65:LYS:O	36:b:158:ASP:N	2.49	0.44
40:f:48:ALA:HB1	52:r:68:PRO:HG3	2.00	0.44
48:n:34:ASN:N	48:n:34:ASN:OD1	2.50	0.44
1:A:534:U:H2'	1:A:535:G:C8	2.52	0.44
1:A:546:U:OP2	1:A:546:U:C6	2.70	0.44
35:a:538:G:H2'	35:a:539:A:H8	1.83	0.44
35:a:923:A:O2'	35:a:1399:C:OP2	2.27	0.44
35:a:1073:U:O2	36:b:102:ASN:ND2	2.50	0.44
56:v:191:GLU:OE1	56:v:197:HIS:CE1	2.71	0.44
56:v:322:ILE:CD1	56:v:343:PRO:HB2	2.47	0.44
1:A:172:A:H2'	1:A:173:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1183:U:H5''	26:Z:30:ARG:HH12	1.83	0.44
1:A:2515:C:N3	1:A:2516:A:N7	2.65	0.44
35:a:607:A:H2'	35:a:608:A:C8	2.52	0.44
35:a:1309:G:OP1	47:m:86:ARG:NH2	2.51	0.44
1:A:1753:G:H5''	16:P:92:ARG:HD3	2.00	0.43
1:A:1829:A:N3	3:C:14:HIS:NE2	2.62	0.43
1:A:1998:A:O2'	1:A:2724:U:O2'	2.26	0.43
1:A:2590:A:H5''	3:C:237:ARG:HE	1.83	0.43
1:A:2883:A:OP1	27:O:48:TYR:OH	2.36	0.43
4:D:46:ARG:HH21	4:D:84:LEU:HD13	1.82	0.43
9:I:112:LYS:HE3	9:I:128:ILE:HG21	2.00	0.43
10:J:3:THR:OG1	10:J:4:PHE:N	2.51	0.43
35:a:145:G:N2	35:a:178:C:N3	2.65	0.43
35:a:908:A:H2'	35:a:909:A:C8	2.52	0.43
37:c:71:ARG:HH11	37:c:74:ILE:HD12	1.83	0.43
51:q:22:VAL:HG11	51:q:60:ILE:HD11	2.00	0.43
1:A:279:A:H2'	1:A:280:U:C6	2.53	0.43
1:A:936:A:H2'	1:A:937:C:C6	2.53	0.43
1:A:1419:A:N6	1:A:1421:G:N3	2.66	0.43
1:A:1799:G:N2	1:A:1818:U:O2'	2.51	0.43
1:A:1857:G:O2'	1:A:1885:A:N6	2.51	0.43
1:A:2818:U:H2'	1:A:2819:G:C8	2.53	0.43
8:H:66:ASN:O	8:H:70:GLU:HB3	2.19	0.43
14:N:56:LYS:NZ	14:N:87:PHE:O	2.38	0.43
29:2:34:ARG:HB2	29:2:42:LEU:HD12	1.98	0.43
35:a:1530:G:H2'	35:a:1531:A:C8	2.53	0.43
41:g:125:ASP:HB3	41:g:131:GLY:HA3	2.00	0.43
47:m:97:ARG:HB2	47:m:99:GLN:HE22	1.84	0.43
53:s:49:ALA:HB1	53:s:56:HIS:HB3	2.00	0.43
1:A:153:U:H2'	1:A:154:U:C6	2.54	0.43
1:A:284:U:H3	1:A:356:G:H1	1.65	0.43
1:A:1385:A:O2'	1:A:1396:U:O2	2.35	0.43
1:A:1972:G:OP2	3:C:237:ARG:NH1	2.52	0.43
5:E:83:VAL:HG12	5:E:86:ALA:CB	2.45	0.43
35:a:1346:A:H1'	35:a:1348:U:C6	2.54	0.43
37:c:76:ILE:O	37:c:82:ASP:N	2.36	0.43
39:e:81:GLN:HG3	39:e:148:SER:HA	1.99	0.43
44:j:44:THR:O	44:j:44:THR:HG22	2.17	0.43
1:A:752:A:H62	1:A:2609:U:H3	1.67	0.43
1:A:1000:A:OP2	1:A:1154:G:N1	2.31	0.43
1:A:2493:U:O2	56:v:264:HIS:CE1	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2557:G:H4'	56:v:245:ARG:CZ	2.45	0.43
35:a:32:A:O2'	35:a:48:C:N4	2.51	0.43
35:a:1296:C:H5'	47:m:13:HIS:CD2	2.53	0.43
39:e:104:ILE:HD11	39:e:114:LEU:HD23	2.00	0.43
1:A:962:G:H21	1:A:2250:G:H1	1.66	0.43
1:A:1316:U:H2'	1:A:1317:G:H8	1.83	0.43
1:A:1689:A:H2'	1:A:1690:A:C8	2.53	0.43
3:C:77:VAL:HG13	3:C:91:ALA:HB1	2.01	0.43
5:E:178:VAL:O	5:E:182:ALA:HB3	2.18	0.43
7:G:37:ASN:HB3	7:G:40:VAL:HG23	2.01	0.43
34:7:29:A:N7	56:v:197:HIS:CE1	2.86	0.43
35:a:81:A:H2'	35:a:82:G:C8	2.54	0.43
35:a:636:U:C2	35:a:637:C:C5	3.06	0.43
35:a:818:G:O2'	35:a:820:U:OP2	2.32	0.43
35:a:976:G:OP2	35:a:1358:U:O2'	2.37	0.43
35:a:1119:C:H2'	35:a:1120:C:H6	1.84	0.43
38:d:90:LEU:HD11	38:d:196:GLU:HB3	2.00	0.43
57:x:43:G:H2'	57:x:44:A:C8	2.53	0.43
1:A:481:G:O2'	1:A:506:G:N2	2.51	0.43
1:A:708:G:H2'	1:A:709:U:C6	2.54	0.43
1:A:1521:G:H3'	1:A:1522:A:H2'	2.01	0.43
1:A:2233:U:H2'	1:A:2234:G:H8	1.84	0.43
1:A:2328:A:H2'	1:A:2329:U:C6	2.53	0.43
12:L:95:LEU:HD11	12:L:125:LEU:HD21	2.01	0.43
16:P:88:ARG:HB3	16:P:112:ARG:HD3	2.00	0.43
35:a:382:A:H2'	35:a:383:A:C8	2.53	0.43
35:a:734:G:N3	35:a:735:C:C6	2.86	0.43
35:a:757:U:OP1	35:a:822:U:O2'	2.35	0.43
35:a:1492:A:H62	46:l:46:SER:CB	2.31	0.43
37:c:139:ASN:O	37:c:143:LEU:CB	2.61	0.43
38:d:169:TRP:HA	38:d:182:LYS:HD2	2.01	0.43
48:n:12:ARG:O	48:n:16:ALA:HB2	2.19	0.43
53:s:38:THR:HA	53:s:69:LYS:HA	2.01	0.43
57:x:27:C:H2'	57:x:28:A:C8	2.53	0.43
1:A:1275:A:N1	1:A:1295:C:O2'	2.47	0.43
1:A:2087:G:H2'	1:A:2088:A:C8	2.53	0.43
5:E:189:THR:HG22	5:E:191:ASP:H	1.84	0.43
7:G:116:LEU:HD11	7:G:122:ALA:HB2	2.00	0.43
9:I:42:ASN:HA	9:I:45:THR:HB	2.01	0.43
10:J:98:GLU:O	10:J:102:GLU:CB	2.61	0.43
13:M:34:LYS:HE3	13:M:131:VAL:HG11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:1171:A:H2'	35:a:1172:C:C6	2.54	0.43
35:a:1240:U:OP2	41:g:114:SER:OG	2.29	0.43
47:m:44:ILE:HD13	47:m:47:LEU:HD13	2.00	0.43
48:n:12:ARG:O	48:n:16:ALA:CB	2.67	0.43
48:n:64:CYS:HB3	48:n:68:GLY:H	1.83	0.43
57:x:66:C:H2'	57:x:67:A:C8	2.53	0.43
1:A:1068:G:H21	1:A:1096:A:H5'	1.83	0.43
1:A:1954:G:O2'	1:A:1956:U:O4	2.28	0.43
7:G:14:VAL:HG13	7:G:25:ILE:HG23	2.01	0.43
7:G:49:LEU:HD13	7:G:71:LEU:HD23	2.01	0.43
8:H:65:ALA:HA	8:H:68:ARG:HB2	2.01	0.43
14:N:98:LEU:O	14:N:111:ALA:HA	2.19	0.43
22:V:75:GLN:HG3	22:V:76:ASP:HB2	2.01	0.43
35:a:67:C:H2'	35:a:68:G:H8	1.84	0.43
35:a:745:G:H2'	35:a:746:A:C8	2.54	0.43
36:b:19:THR:OG1	36:b:20:ARG:N	2.46	0.43
37:c:137:VAL:HG21	37:c:167:TYR:HD2	1.83	0.43
1:A:1156:A:C8	17:Q:50:ARG:HG2	2.54	0.43
1:A:1386:C:H2'	1:A:1387:A:C8	2.52	0.43
1:A:2223:G:OP1	3:C:170:TYR:OH	2.34	0.43
1:A:2305:U:N3	6:F:150:GLY:O	2.52	0.43
1:A:2431:U:O2'	1:A:2433:A:N7	2.38	0.43
10:J:14:ASP:OD2	10:J:138:GLN:NE2	2.45	0.43
12:L:30:THR:O	12:L:33:ARG:HG2	2.18	0.43
15:O:4:LYS:HE3	15:O:7:ARG:HH21	1.84	0.43
24:X:12:VAL:O	24:X:28:PHE:HB2	2.19	0.43
35:a:176:C:H5''	54:t:23:ARG:HH12	1.84	0.43
35:a:1016:A:O2'	35:a:1217:C:O2'	2.31	0.43
45:k:96:ILE:HA	45:k:99:LEU:HD13	2.00	0.43
50:p:3:THR:HG23	50:p:5:ARG:HD2	2.00	0.43
1:A:499:U:H5''	21:U:42:LYS:HD2	2.01	0.43
1:A:580:U:H2'	1:A:581:C:C6	2.54	0.43
1:A:632:A:H2'	1:A:633:A:C8	2.54	0.43
1:A:1127:A:N7	1:A:2488:G:O2'	2.44	0.43
1:A:2748:A:H5'	7:G:3:VAL:HG21	2.00	0.43
2:B:9:G:OP2	15:O:15:ARG:NH1	2.52	0.43
20:T:23:ALA:HB1	20:T:29:THR:HB	2.01	0.43
24:X:38:TRP:NE1	24:X:40:GLU:OE1	2.51	0.43
32:5:26:VAL:H	32:5:115:GLY:HA2	1.84	0.43
35:a:152:A:N6	35:a:170:U:C2	2.87	0.43
35:a:457:G:H22	35:a:475:C:H42	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:1414:U:H2'	35:a:1415:G:H8	1.84	0.43
1:A:1117:C:C2	1:A:1118:C:C5	3.08	0.42
1:A:2185:U:H2'	1:A:2186:G:H8	1.83	0.42
1:A:2533:U:OP1	1:A:2665:A:O2'	2.28	0.42
25:Y:54:LYS:O	25:Y:58:ASN:CB	2.59	0.42
32:5:18:VAL:HG22	32:5:86:MET:HE2	2.00	0.42
35:a:1287:A:H2'	35:a:1288:A:C8	2.54	0.42
35:a:1355:G:H2'	35:a:1356:G:H8	1.84	0.42
45:k:61:ALA:HA	45:k:64:VAL:HG12	2.01	0.42
1:A:488:G:H22	1:A:491:G:H5''	1.83	0.42
1:A:664:G:O2'	1:A:940:G:OP1	2.29	0.42
1:A:2102:G:H1	1:A:2187:U:H3	1.67	0.42
1:A:2405:G:O2'	1:A:2411:A:N6	2.53	0.42
14:N:34:ILE:O	14:N:112:TYR:HA	2.19	0.42
35:a:328:C:H4'	35:a:329:A:H5'	2.01	0.42
35:a:966:G:H21	43:i:128:LYS:HD2	1.83	0.42
35:a:1536:C:H5'	35:a:1537:U:C5	2.54	0.42
36:b:71:THR:HB	36:b:167:HIS:HE1	1.83	0.42
39:e:131:ASN:HD22	39:e:134:ASN:ND2	2.17	0.42
50:p:18:GLN:HE22	50:p:35:ARG:HE	1.67	0.42
51:q:14:ASP:HA	51:q:20:ILE:HG13	2.00	0.42
56:v:308:ARG:NH1	56:v:310:TYR:OH	2.51	0.42
1:A:673:C:OP1	5:E:49:ARG:NH2	2.49	0.42
1:A:2013:A:H2	19:S:88:ARG:HH12	1.67	0.42
1:A:2208:C:H2'	1:A:2209:G:C8	2.54	0.42
1:A:2220:U:H2'	1:A:2221:G:C8	2.54	0.42
18:R:49:ILE:HB	18:R:51:VAL:O	2.19	0.42
35:a:1108:G:H5'	37:c:175:HIS:ND1	2.35	0.42
35:a:1387:G:H2'	35:a:1388:C:H6	1.84	0.42
1:A:40:U:H2'	1:A:41:C:C6	2.55	0.42
1:A:1801:A:H5''	1:A:2203:U:H2'	2.00	0.42
2:B:93:C:N3	2:B:94:A:N7	2.67	0.42
2:B:111:U:H2'	2:B:112:G:H8	1.84	0.42
5:E:181:ILE:HG23	12:L:2:ARG:HB2	2.02	0.42
32:5:68:PRO:HA	32:5:72:LEU:HG	2.01	0.42
35:a:513:C:H2'	35:a:514:C:C6	2.55	0.42
35:a:674:G:H21	45:k:117:HIS:HB2	1.84	0.42
1:A:240:C:H3'	1:A:241:A:H2'	2.01	0.42
1:A:573:U:O2'	1:A:575:A:OP1	2.37	0.42
1:A:721:A:H2'	1:A:722:A:C8	2.55	0.42
1:A:1853:A:H2'	1:A:1854:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2754:U:O2'	1:A:2756:U:OP2	2.36	0.42
2:B:31:C:H1'	2:B:53:A:H61	1.84	0.42
2:B:37:C:N3	2:B:48:U:O2'	2.40	0.42
11:K:80:ASP:OD2	16:P:61:ARG:NH2	2.51	0.42
27:O:27:LEU:HD23	27:O:36:LYS:HB3	2.01	0.42
35:a:2:A:N6	35:a:3:A:N1	2.67	0.42
35:a:105:G:OP2	54:t:12:GLN:NE2	2.52	0.42
35:a:1356:G:H2'	35:a:1357:A:C8	2.54	0.42
36:b:56:LEU:HD23	36:b:59:ILE:HD11	2.01	0.42
1:A:160:A:N3	1:A:2208:C:O2'	2.50	0.42
1:A:956:G:N2	1:A:960:A:OP2	2.50	0.42
1:A:1197:G:H2'	1:A:1198:U:H6	1.85	0.42
1:A:2100:G:O2'	1:A:2101:A:O4'	2.35	0.42
1:A:2311:A:O2'	1:A:2312:U:C6	2.67	0.42
1:A:2333:A:OP1	23:W:73:ARG:NH1	2.38	0.42
1:A:2718:G:H4'	16:P:95:LYS:HB2	2.00	0.42
2:B:95:U:H2'	2:B:96:G:C8	2.55	0.42
3:C:134:ILE:HD13	3:C:140:VAL:HG11	1.99	0.42
35:a:44:A:OP1	50:p:12:LYS:N	2.48	0.42
35:a:143:A:H2	35:a:220:G:H1	1.67	0.42
35:a:1292:G:H2'	35:a:1293:C:C6	2.54	0.42
45:k:92:ARG:HE	55:u:24:LYS:NZ	2.17	0.42
45:k:97:ARG:O	45:k:101:ALA:N	2.52	0.42
1:A:156:A:H2'	1:A:157:C:O4'	2.19	0.42
1:A:859:G:H1'	1:A:860:U:H5	1.85	0.42
1:A:1534:U:O2'	1:A:1537:G:N1	2.52	0.42
1:A:1733:G:H2'	1:A:1734:G:H8	1.84	0.42
1:A:2075:U:HO2'	1:A:2596:U:H3	1.66	0.42
1:A:2507:C:C4'	56:v:238:ASN:O	2.63	0.42
7:G:88:LEU:HG	7:G:161:VAL:HG22	2.00	0.42
15:O:67:ASN:N	15:O:67:ASN:OD1	2.52	0.42
35:a:235:C:H2'	35:a:236:A:H8	1.85	0.42
35:a:430:A:OP2	38:d:7:LYS:HD3	2.19	0.42
35:a:778:G:H21	45:k:121:ARG:HD3	1.84	0.42
35:a:1492:A:N6	46:l:46:SER:HB3	2.35	0.42
43:i:68:GLY:O	43:i:74:GLN:NE2	2.37	0.42
45:k:34:THR:HA	45:k:40:ALA:HA	2.02	0.42
1:A:2039:U:H2'	1:A:2040:G:C8	2.55	0.42
3:C:140:VAL:HG12	3:C:191:LEU:HD23	2.00	0.42
8:H:97:ARG:HE	8:H:112:LYS:HD2	1.85	0.42
19:S:86:MET:HB3	19:S:94:ASP:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5:17:GLU:HB3	32:5:88:HIS:HE1	1.83	0.42
33:6:57:VAL:HG22	53:s:66:VAL:HG21	2.02	0.42
35:a:416:G:H2'	35:a:417:G:H8	1.85	0.42
35:a:737:C:C2	35:a:738:C:C5	3.07	0.42
36:b:135:MET:O	36:b:139:GLU:HB2	2.19	0.42
39:e:149:PRO:O	39:e:153:ALA:N	2.46	0.42
1:A:281:C:O2	1:A:281:C:C2'	2.66	0.42
1:A:332:A:O2'	1:A:334:C:OP2	2.34	0.42
4:D:101:PHE:HD1	4:D:104:VAL:HG21	1.85	0.42
35:a:270:A:H2'	35:a:271:C:C6	2.55	0.42
35:a:637:C:H2'	35:a:638:U:H6	1.85	0.42
35:a:707:U:H2'	35:a:708:C:C6	2.55	0.42
35:a:1095:U:P	35:a:1108:G:H1	2.43	0.42
35:a:1317:C:O2'	48:n:49:GLN:OE1	2.37	0.42
35:a:1338:G:N3	57:x:41:G:O2'	2.53	0.42
39:e:93:VAL:HG11	39:e:139:THR:HG22	2.01	0.42
1:A:582:A:H2'	1:A:583:G:H8	1.85	0.42
1:A:1106:G:H2'	1:A:1107:G:C8	2.55	0.42
1:A:2127:G:H2'	1:A:2128:G:C8	2.54	0.42
8:H:78:VAL:HB	8:H:144:VAL:HG22	2.01	0.42
19:S:51:LEU:HD13	19:S:105:VAL:HG11	2.02	0.42
35:a:107:G:OP1	35:a:325:A:N6	2.53	0.42
35:a:418:C:H2'	35:a:419:C:C6	2.55	0.42
35:a:1492:A:H62	46:l:46:SER:HB2	1.85	0.42
38:d:54:LEU:HD12	38:d:54:LEU:HA	1.88	0.42
54:t:26:MET:HE1	54:t:56:ILE:HD11	2.01	0.42
1:A:184:C:H2'	1:A:185:G:C8	2.55	0.41
1:A:1462:C:O2'	1:A:2702:G:O2'	2.25	0.41
7:G:41:GLU:HB2	7:G:54:ARG:HB2	2.01	0.41
17:Q:82:LEU:HD23	17:Q:82:LEU:HA	1.68	0.41
17:Q:112:ALA:O	17:Q:116:LEU:CB	2.67	0.41
34:7:27:C:N4	35:a:1400:C:C5'	2.76	0.41
35:a:390:U:H2'	35:a:391:G:C8	2.55	0.41
35:a:744:C:H2'	35:a:745:G:C8	2.54	0.41
35:a:1027:C:N4	35:a:1035:A:N1	2.56	0.41
35:a:1071:C:H2'	35:a:1072:G:C8	2.54	0.41
35:a:1425:U:H2'	35:a:1426:G:H8	1.84	0.41
1:A:580:U:H2'	1:A:581:C:H6	1.85	0.41
1:A:598:U:H2'	1:A:599:A:H8	1.84	0.41
1:A:689:A:N3	1:A:779:U:O2'	2.46	0.41
1:A:958:U:OP1	13:M:40:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:964:C:O2'	1:A:2273:A:N3	2.43	0.41
1:A:1306:C:N4	1:A:1607:C:OP2	2.53	0.41
1:A:2162:G:H2'	1:A:2163:A:H8	1.85	0.41
1:A:2484:G:O2'	13:M:123:LYS:O	2.36	0.41
1:A:2557:G:H2'	1:A:2558:C:C6	2.55	0.41
7:G:70:LEU:HD23	7:G:70:LEU:HA	1.90	0.41
22:V:76:ASP:HB3	22:V:90:ASP:HB2	2.01	0.41
35:a:407:U:H2'	35:a:408:A:C8	2.55	0.41
35:a:1015:G:H2'	35:a:1016:A:H8	1.85	0.41
37:c:129:PHE:O	37:c:133:MET:HB3	2.20	0.41
39:e:110:MET:HG3	39:e:139:THR:HG21	2.02	0.41
47:m:72:ILE:O	47:m:75:SER:OG	2.36	0.41
47:m:86:ARG:HH11	47:m:86:ARG:HD3	1.71	0.41
56:v:259:ASP:OD2	56:v:269:LYS:HD3	2.20	0.41
1:A:936:A:H2'	1:A:937:C:H6	1.85	0.41
1:A:2157:G:O2'	1:A:2158:A:O4'	2.30	0.41
1:A:2314:A:OP1	6:F:87:LYS:NZ	2.48	0.41
1:A:2675:A:H5''	11:K:31:ARG:HH11	1.86	0.41
35:a:85:U:O4'	35:a:87:C:N4	2.53	0.41
35:a:464:U:N3	35:a:467:U:OP2	2.53	0.41
35:a:593:U:O4	35:a:646:G:O6	2.38	0.41
35:a:676:A:H1'	45:k:116:PRO:HB3	2.02	0.41
35:a:801:U:H2'	35:a:802:A:H8	1.86	0.41
35:a:1180:A:H5'	43:i:104:THR:HG23	2.02	0.41
37:c:171:ARG:HG2	37:c:173:PRO:HD3	2.02	0.41
44:j:63:ASP:OD1	48:n:98:LYS:NZ	2.53	0.41
50:p:6:LEU:HD23	50:p:19:VAL:HB	2.02	0.41
1:A:1445:G:O6	1:A:1466:U:C2	2.74	0.41
1:A:1720:U:H2'	1:A:1721:G:O4'	2.20	0.41
1:A:1847:G:O2'	1:A:1848:A:H8	2.04	0.41
1:A:2585:U:O2'	58:z:18:LEU:CD1	2.67	0.41
6:F:62:GLN:HB2	33:6:6:HIS:CE1	2.54	0.41
15:O:53:THR:HB	15:O:65:THR:HB	2.01	0.41
35:a:389:A:H3'	35:a:390:U:C6	2.55	0.41
35:a:402:G:C6	35:a:403:C:C4	3.09	0.41
35:a:1218:C:H2'	35:a:1219:A:C8	2.56	0.41
39:e:21:SER:OG	39:e:22:LYS:N	2.54	0.41
39:e:143:LEU:HD23	39:e:143:LEU:HA	1.94	0.41
43:i:35:GLU:HA	43:i:39:GLY:HA3	2.03	0.41
50:p:79:ASN:H	50:p:82:ALA:HB3	1.85	0.41
51:q:59:GLU:HG3	51:q:76:ARG:CZ	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:t:32:LYS:O	54:t:36:ALA:N	2.50	0.41
1:A:78:U:H2'	1:A:79:C:C6	2.54	0.41
1:A:414:C:H2'	1:A:415:A:C8	2.54	0.41
7:G:34:ARG:HE	7:G:70:LEU:HD13	1.85	0.41
9:I:52:LEU:HD23	9:I:54:ILE:HD11	2.01	0.41
9:I:77:VAL:HA	9:I:80:LYS:HE2	2.01	0.41
17:Q:93:ILE:HD12	18:R:13:ARG:HB2	2.01	0.41
25:Y:28:LEU:O	25:Y:32:ALA:HB2	2.19	0.41
26:Z:25:GLY:HA3	26:Z:46:MET:HE1	2.03	0.41
30:3:15:LYS:HD2	30:3:19:GLY:HA2	2.01	0.41
35:a:601:G:H2'	35:a:602:A:C8	2.55	0.41
35:a:678:U:H2'	35:a:679:C:H6	1.86	0.41
35:a:689:C:OP1	45:k:28:ASN:ND2	2.49	0.41
35:a:946:A:H2'	35:a:947:G:H8	1.82	0.41
39:e:104:ILE:HD12	39:e:104:ILE:HA	1.92	0.41
55:u:16:ARG:HH21	55:u:19:LYS:HE2	1.85	0.41
1:A:1000:A:H2'	1:A:1001:A:C8	2.56	0.41
1:A:1162:G:N2	18:R:91:GLN:HE22	2.17	0.41
1:A:2623:G:H4'	1:A:2825:G:C8	2.56	0.41
3:C:172:THR:HG22	3:C:180:MET:HE3	2.03	0.41
4:D:8:LYS:NZ	4:D:195:GLY:O	2.43	0.41
10:J:24:THR:HB	10:J:27:ARG:HB2	2.01	0.41
18:R:2:TYR:HA	18:R:14:VAL:O	2.20	0.41
23:W:7:ARG:O	23:W:10:ARG:NH1	2.54	0.41
32:5:58:THR:HG21	32:5:82:ILE:H	1.85	0.41
35:a:331:G:O3'	54:t:2:ASN:ND2	2.53	0.41
35:a:546:A:O2'	35:a:548:G:O2'	2.33	0.41
35:a:946:A:OP1	47:m:112:ARG:NH1	2.53	0.41
43:i:39:GLY:HA2	43:i:44:ARG:HB2	2.02	0.41
1:A:2557:G:HO2'	56:v:245:ARG:NH1	2.17	0.41
1:A:2902:C:H3'	1:A:2903:U:C6	2.56	0.41
16:P:21:PRO:HD3	16:P:49:ILE:HD12	2.02	0.41
20:T:8:LEU:HD11	25:Y:22:LEU:HD12	2.02	0.41
31:4:7:VAL:HB	31:4:25:VAL:HG23	2.02	0.41
32:5:43:LYS:HD2	32:5:95:LEU:HD22	2.03	0.41
35:a:310:G:H5''	50:p:31:ARG:HB2	2.02	0.41
35:a:490:C:H2'	35:a:491:G:C8	2.54	0.41
35:a:600:A:H2'	35:a:601:G:C8	2.54	0.41
36:b:9:LEU:HB2	36:b:42:LEU:HD13	2.02	0.41
49:o:28:VAL:HG11	49:o:66:LEU:HD21	2.03	0.41
54:t:24:ARG:HG2	54:t:28:ARG:HH21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:560:C:O2'	17:Q:47:ARG:NH2	2.54	0.41
1:A:588:U:H2'	1:A:589:U:C6	2.56	0.41
1:A:1447:C:H2'	1:A:1448:G:C8	2.56	0.41
1:A:2189:U:H2'	1:A:2190:G:C8	2.55	0.41
3:C:146:LYS:HB2	3:C:149:LYS:HB2	2.03	0.41
4:D:71:ALA:HB3	4:D:73:VAL:HG22	2.03	0.41
5:E:83:VAL:HG11	5:E:86:ALA:HB2	2.02	0.41
35:a:8:A:C6	38:d:205:LYS:HD2	2.56	0.41
35:a:1458:G:O2'	54:t:22:SER:OG	2.32	0.41
37:c:36:PHE:O	37:c:40:GLN:HG3	2.20	0.41
37:c:54:ILE:HD13	37:c:54:ILE:HG21	1.88	0.41
44:j:6:ILE:HB	44:j:76:ILE:HB	2.03	0.41
46:l:26:CYS:HA	46:l:27:PRO:HD3	1.92	0.41
46:l:73:LEU:HD21	46:l:79:ILE:HG21	2.03	0.41
53:s:70:LEU:HD23	53:s:70:LEU:HA	1.82	0.41
1:A:184:C:H2'	1:A:185:G:H8	1.84	0.41
1:A:519:U:H2'	1:A:520:G:C8	2.55	0.41
1:A:873:C:H2'	1:A:874:G:H8	1.86	0.41
1:A:1017:G:H2'	1:A:1018:U:C6	2.56	0.41
1:A:1631:G:N2	1:A:1634:A:OP2	2.45	0.41
1:A:1960:A:O2'	35:a:1484:C:O2'	2.18	0.41
1:A:2062:A:H2	58:z:18:LEU:HG	1.85	0.41
1:A:2116:G:H1	1:A:2171:A:H61	1.68	0.41
1:A:2255:G:H4'	57:x:3:G:C5'	2.50	0.41
1:A:2445:G:P	5:E:69:ARG:HH22	2.44	0.41
1:A:2590:A:H2'	1:A:2591:C:H6	1.85	0.41
5:E:134:LEU:HD23	5:E:164:LEU:HD22	2.03	0.41
7:G:84:LYS:O	7:G:131:VAL:HA	2.21	0.41
20:T:11:LEU:O	25:Y:29:ARG:NH1	2.39	0.41
26:Z:16:LEU:HB2	26:Z:19:HIS:HD2	1.86	0.41
35:a:35:G:H2'	35:a:36:C:C6	2.56	0.41
35:a:208:U:O2'	35:a:211:G:N1	2.54	0.41
35:a:427:U:O2'	35:a:541:G:OP1	2.37	0.41
35:a:618:C:O2'	50:p:14:ARG:NH1	2.54	0.41
35:a:637:C:C2	35:a:638:U:C6	3.09	0.41
35:a:716:A:C5	35:a:717:U:C5	3.09	0.41
35:a:1096:C:H2'	35:a:1097:C:C6	2.56	0.41
35:a:1162:C:H2'	35:a:1163:A:C8	2.55	0.41
35:a:1323:G:H1'	35:a:1361:G:H21	1.86	0.41
39:e:110:MET:HE2	39:e:110:MET:HB3	1.92	0.41
48:n:61:ARG:HA	48:n:61:ARG:HD2	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:q:25:GLU:HA	51:q:39:ARG:O	2.21	0.41
56:v:137:ARG:CZ	56:v:334:GLU:CB	2.81	0.41
1:A:83:A:O2'	1:A:103:A:N6	2.53	0.41
1:A:1697:G:H4'	1:A:1978:A:H5''	2.02	0.41
1:A:2106:U:H1'	1:A:2184:A:N6	2.30	0.41
4:D:97:SER:OG	4:D:98:VAL:N	2.53	0.41
6:F:95:MET:HE2	6:F:95:MET:HB2	1.86	0.41
25:Y:18:LEU:HG	25:Y:22:LEU:HD13	2.03	0.41
32:5:26:VAL:HG23	32:5:111:ALA:HB3	2.03	0.41
34:7:27:C:C4	35:a:1400:C:C5'	3.04	0.41
35:a:989:U:H1'	35:a:1016:A:H2	1.86	0.41
38:d:200:VAL:HG11	39:e:102:THR:HG22	2.03	0.41
40:f:10:VAL:HG21	40:f:18:VAL:HG22	2.02	0.41
40:f:53:LYS:HA	40:f:53:LYS:HE3	2.03	0.41
44:j:42:LEU:HB3	44:j:43:PRO:CD	2.50	0.41
2:B:49:C:H2'	2:B:50:A:H8	1.86	0.40
5:E:48:THR:HG23	5:E:88:ARG:HH12	1.87	0.40
13:M:42:THR:N	13:M:45:GLN:OE1	2.37	0.40
17:Q:40:LYS:HD2	17:Q:44:TYR:CZ	2.55	0.40
18:R:77:PHE:CD1	18:R:84:ARG:HB3	2.57	0.40
32:5:29:ASP:HB2	32:5:56:ARG:HH22	1.87	0.40
35:a:1342:C:H2'	35:a:1343:G:C8	2.55	0.40
35:a:1388:C:H2'	35:a:1389:C:H6	1.86	0.40
40:f:32:ALA:HB2	40:f:70:VAL:HG21	2.03	0.40
43:i:44:ARG:HG2	43:i:48:ARG:NH2	2.36	0.40
47:m:24:VAL:HG23	47:m:28:ARG:HB3	2.03	0.40
56:v:120:GLY:O	56:v:124:ALA:HB3	2.21	0.40
1:A:962:G:H2'	1:A:963:U:H6	1.85	0.40
1:A:1045:C:O4'	1:A:1111:A:N6	2.54	0.40
1:A:1226:A:H5''	17:Q:15:LYS:NZ	2.36	0.40
2:B:7:G:O2'	15:O:38:GLN:NE2	2.54	0.40
5:E:19:PHE:CE2	5:E:113:VAL:HG21	2.56	0.40
35:a:405:U:O4	38:d:1:ALA:N	2.54	0.40
35:a:939:G:H5'	41:g:101:ARG:NH1	2.36	0.40
35:a:1367:C:P	43:i:113:LYS:HZ1	2.45	0.40
35:a:1368:A:OP1	44:j:64:GLN:NE2	2.48	0.40
36:b:71:THR:HB	36:b:167:HIS:CE1	2.57	0.40
47:m:28:ARG:O	47:m:32:ILE:HG12	2.21	0.40
47:m:85:TYR:O	47:m:89:ARG:HG2	2.21	0.40
48:n:32:ASP:O	48:n:41:ARG:NH2	2.51	0.40
56:v:322:ILE:O	56:v:322:ILE:CG1	2.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:360:U:O4	1:A:361:G:N2	2.54	0.40
1:A:2127:G:H2'	1:A:2128:G:H8	1.87	0.40
1:A:2255:G:H4'	57:x:3:G:H5'	2.03	0.40
9:I:57:VAL:HG12	9:I:59:THR:H	1.86	0.40
35:a:360:G:H2'	35:a:361:G:C8	2.56	0.40
56:v:133:ARG:O	56:v:137:ARG:HG3	2.21	0.40
1:A:532:A:H4'	1:A:533:G:C8	2.56	0.40
1:A:2823:A:OP1	4:D:118:PHE:HB2	2.21	0.40
3:C:1:ALA:N	3:C:19:VAL:O	2.55	0.40
3:C:16:VAL:HB	3:C:203:VAL:HG22	2.03	0.40
6:F:141:ASP:HB3	6:F:144:LYS:H	1.86	0.40
11:K:12:ASP:HB3	11:K:99:ILE:HG12	2.04	0.40
14:N:117:ASP:HB3	14:N:118:ARG:H	1.64	0.40
19:S:69:LEU:HD12	19:S:69:LEU:HA	1.91	0.40
34:7:25:A:C6	57:x:37:A:C2	3.10	0.40
35:a:573:A:N3	35:a:883:C:O2'	2.45	0.40
35:a:958:A:C5	53:s:54:ARG:HD3	2.56	0.40
38:d:149:LYS:HG2	38:d:150:LYS:HG2	2.03	0.40
56:v:122:ASP:OD2	56:v:156:HIS:ND1	2.54	0.40
1:A:5:A:H2'	1:A:6:A:C8	2.57	0.40
1:A:583:G:OP1	17:Q:10:ARG:NH1	2.55	0.40
3:C:69:ASN:OD1	3:C:69:ASN:N	2.54	0.40
8:H:5:LEU:HD22	8:H:13:GLY:HA3	2.04	0.40
35:a:414:A:OP2	35:a:428:G:N2	2.42	0.40
38:d:160:LEU:O	38:d:164:ARG:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	C	269/271 (99%)	242 (90%)	27 (10%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	207/209 (99%)	182 (88%)	25 (12%)	0	100	100
5	E	199/201 (99%)	182 (92%)	16 (8%)	1 (0%)	24	54
6	F	175/177 (99%)	159 (91%)	16 (9%)	0	100	100
7	G	174/176 (99%)	159 (91%)	14 (8%)	1 (1%)	21	50
8	H	147/149 (99%)	127 (86%)	20 (14%)	0	100	100
9	I	139/141 (99%)	114 (82%)	25 (18%)	0	100	100
10	J	140/142 (99%)	129 (92%)	11 (8%)	0	100	100
11	K	120/122 (98%)	103 (86%)	16 (13%)	1 (1%)	16	44
12	L	141/143 (99%)	117 (83%)	23 (16%)	1 (1%)	18	47
13	M	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	8	30
14	N	118/120 (98%)	105 (89%)	13 (11%)	0	100	100
15	O	114/116 (98%)	104 (91%)	10 (9%)	0	100	100
16	P	112/114 (98%)	102 (91%)	10 (9%)	0	100	100
17	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
18	R	101/103 (98%)	87 (86%)	13 (13%)	1 (1%)	12	40
19	S	108/110 (98%)	101 (94%)	6 (6%)	1 (1%)	14	42
20	T	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
21	U	100/102 (98%)	84 (84%)	16 (16%)	0	100	100
22	V	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
23	W	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
24	X	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
25	Y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
26	Z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
27	0	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
28	1	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
29	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
30	3	62/64 (97%)	54 (87%)	8 (13%)	0	100	100
31	4	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
32	5	129/131 (98%)	101 (78%)	27 (21%)	1 (1%)	16	44
33	6	64/66 (97%)	53 (83%)	11 (17%)	0	100	100
36	b	216/218 (99%)	177 (82%)	37 (17%)	2 (1%)	14	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	c	204/206 (99%)	183 (90%)	18 (9%)	3 (2%)	8	30
38	d	203/205 (99%)	180 (89%)	23 (11%)	0	100	100
39	e	155/157 (99%)	136 (88%)	19 (12%)	0	100	100
40	f	98/100 (98%)	82 (84%)	15 (15%)	1 (1%)	12	40
41	g	149/151 (99%)	134 (90%)	14 (9%)	1 (1%)	18	47
42	h	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	16	44
43	i	125/127 (98%)	105 (84%)	19 (15%)	1 (1%)	16	44
44	j	96/98 (98%)	79 (82%)	15 (16%)	2 (2%)	5	24
45	k	114/116 (98%)	91 (80%)	23 (20%)	0	100	100
46	l	121/123 (98%)	94 (78%)	26 (22%)	1 (1%)	16	44
47	m	112/114 (98%)	98 (88%)	13 (12%)	1 (1%)	14	42
48	n	99/101 (98%)	88 (89%)	11 (11%)	0	100	100
49	o	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	35
50	p	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
51	q	78/80 (98%)	62 (80%)	16 (20%)	0	100	100
52	r	63/65 (97%)	50 (79%)	11 (18%)	2 (3%)	3	17
53	s	77/79 (98%)	69 (90%)	8 (10%)	0	100	100
54	t	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
55	u	63/65 (97%)	43 (68%)	17 (27%)	3 (5%)	2	11
56	v	240/242 (99%)	213 (89%)	24 (10%)	3 (1%)	9	33
58	z	12/14 (86%)	10 (83%)	1 (8%)	1 (8%)	0	4
All	All	6099/6205 (98%)	5361 (88%)	706 (12%)	32 (0%)	26	54

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	G	175	LYS
18	R	54	VAL
32	5	80	THR
36	b	19	THR
37	c	96	VAL
37	c	97	PRO
49	o	46	LYS
55	u	36	PHE
56	v	323	ASN

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Mol	Chain	Res	Type
12	L	128	THR
36	b	18	GLN
40	f	96	VAL
44	j	42	LEU
58	z	16	PRO
11	K	111	LYS
52	r	17	VAL
52	r	18	GLN
55	u	33	ARG
56	v	329	LEU
42	h	67	GLY
44	j	43	PRO
56	v	307	ASN
13	M	70	ASP
19	S	64	ALA
41	g	129	ASN
47	m	104	ASN
43	i	91	GLU
55	u	7	GLU
37	c	80	GLY
5	E	83	VAL
13	M	69	PRO
46	l	21	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	216/216 (100%)	215 (100%)	1 (0%)	81	81
4	D	164/164 (100%)	162 (99%)	2 (1%)	63	72
5	E	165/165 (100%)	165 (100%)	0	100	100
6	F	148/148 (100%)	148 (100%)	0	100	100
7	G	137/137 (100%)	135 (98%)	2 (2%)	57	69
8	H	114/114 (100%)	113 (99%)	1 (1%)	70	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	109/109 (100%)	107 (98%)	2 (2%)	51	67
10	J	116/116 (100%)	116 (100%)	0	100	100
11	K	103/103 (100%)	102 (99%)	1 (1%)	68	75
12	L	102/102 (100%)	101 (99%)	1 (1%)	68	75
13	M	109/109 (100%)	108 (99%)	1 (1%)	70	76
14	N	100/100 (100%)	100 (100%)	0	100	100
15	O	86/86 (100%)	86 (100%)	0	100	100
16	P	99/99 (100%)	97 (98%)	2 (2%)	48	65
17	Q	89/89 (100%)	88 (99%)	1 (1%)	65	74
18	R	84/84 (100%)	84 (100%)	0	100	100
19	S	93/93 (100%)	93 (100%)	0	100	100
20	T	80/80 (100%)	80 (100%)	0	100	100
21	U	83/83 (100%)	83 (100%)	0	100	100
22	V	78/78 (100%)	78 (100%)	0	100	100
23	W	57/57 (100%)	57 (100%)	0	100	100
24	X	67/67 (100%)	67 (100%)	0	100	100
25	Y	55/55 (100%)	55 (100%)	0	100	100
26	Z	48/48 (100%)	48 (100%)	0	100	100
27	0	47/47 (100%)	46 (98%)	1 (2%)	47	64
28	1	45/45 (100%)	45 (100%)	0	100	100
29	2	38/38 (100%)	37 (97%)	1 (3%)	40	61
30	3	51/51 (100%)	51 (100%)	0	100	100
31	4	34/34 (100%)	34 (100%)	0	100	100
32	5	100/100 (100%)	100 (100%)	0	100	100
33	6	59/59 (100%)	59 (100%)	0	100	100
36	b	180/180 (100%)	176 (98%)	4 (2%)	45	63
37	c	170/170 (100%)	166 (98%)	4 (2%)	43	62
38	d	172/172 (100%)	170 (99%)	2 (1%)	63	72
39	e	114/119 (96%)	111 (97%)	3 (3%)	40	61
40	f	87/87 (100%)	84 (97%)	3 (3%)	32	57
41	g	124/124 (100%)	123 (99%)	1 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	h	104/104 (100%)	104 (100%)	0	100	100
43	i	105/105 (100%)	104 (99%)	1 (1%)	68	75
44	j	86/86 (100%)	83 (96%)	3 (4%)	32	56
45	k	89/89 (100%)	89 (100%)	0	100	100
46	l	103/103 (100%)	103 (100%)	0	100	100
47	m	92/92 (100%)	89 (97%)	3 (3%)	33	57
48	n	79/83 (95%)	78 (99%)	1 (1%)	61	71
49	o	76/76 (100%)	76 (100%)	0	100	100
50	p	65/65 (100%)	62 (95%)	3 (5%)	24	50
51	q	74/74 (100%)	73 (99%)	1 (1%)	59	70
52	r	48/56 (86%)	48 (100%)	0	100	100
53	s	70/70 (100%)	69 (99%)	1 (1%)	59	70
54	t	65/65 (100%)	65 (100%)	0	100	100
55	u	44/55 (80%)	43 (98%)	1 (2%)	44	63
56	v	195/195 (100%)	191 (98%)	4 (2%)	47	64
58	z	14/14 (100%)	13 (93%)	1 (7%)	13	39
All	All	5032/5060 (99%)	4980 (99%)	52 (1%)	65	75

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

Mol	Chain	Res	Type
3	C	129	LEU
4	D	33	ARG
4	D	202	ILE
7	G	42	VAL
7	G	167	VAL
8	H	12	LEU
9	I	18	ASN
9	I	85	ILE
11	K	69	VAL
12	L	27	LEU
13	M	6	ARG
16	P	72	VAL
16	P	99	LEU
17	Q	108	LEU
27	O	24	VAL

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Mol	Chain	Res	Type
29	2	44	VAL
36	b	30	ILE
36	b	87	ASP
36	b	162	VAL
36	b	195	VAL
37	c	24	ASN
37	c	102	ILE
37	c	163	ARG
37	c	199	VAL
38	d	142	VAL
38	d	190	LEU
39	e	69	ASN
39	e	105	ILE
39	e	130	THR
40	f	53	LYS
40	f	70	VAL
40	f	96	VAL
41	g	6	ILE
43	i	60	LEU
44	j	42	LEU
44	j	44	THR
44	j	58	ASN
47	m	3	ILE
47	m	24	VAL
47	m	47	LEU
48	n	93	ILE
50	p	5	ARG
50	p	19	VAL
50	p	67	ILE
51	q	58	VAL
53	s	10	ILE
55	u	28	LEU
56	v	321	ARG
56	v	322	ILE
56	v	323	ASN
56	v	340	LEU
58	z	18	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (92) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	36	ASN

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Mol	Chain	Res	Type
3	C	114	GLN
3	C	199	HIS
3	C	242	HIS
4	D	164	GLN
5	E	62	GLN
5	E	90	GLN
5	E	92	HIS
5	E	136	GLN
7	G	44	HIS
7	G	47	ASN
7	G	63	GLN
7	G	115	GLN
7	G	138	GLN
8	H	28	ASN
8	H	66	ASN
10	J	47	HIS
10	J	135	GLN
10	J	136	GLN
13	M	13	HIS
15	O	38	GLN
16	P	55	HIS
17	Q	70	GLN
17	Q	71	ASN
18	R	6	GLN
18	R	18	GLN
18	R	43	ASN
18	R	89	HIS
18	R	91	GLN
19	S	7	HIS
19	S	57	ASN
20	T	48	GLN
21	U	68	ASN
23	W	8	ASN
25	Y	27	ASN
25	Y	58	ASN
26	Z	19	HIS
27	0	18	HIS
27	0	41	HIS
28	1	44	GLN
30	3	42	HIS
31	4	35	GLN
32	5	6	GLN

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Mol	Chain	Res	Type
33	6	30	HIS
33	6	33	ASN
33	6	41	HIS
36	b	18	GLN
36	b	23	ASN
36	b	35	ASN
36	b	119	GLN
36	b	121	GLN
37	c	24	ASN
37	c	189	HIS
38	d	135	GLN
38	d	151	GLN
39	e	69	ASN
39	e	82	HIS
39	e	96	GLN
39	e	134	ASN
40	f	11	HIS
40	f	55	HIS
40	f	63	ASN
41	g	67	ASN
41	g	121	ASN
41	g	147	ASN
42	h	3	GLN
43	i	4	GLN
43	i	30	ASN
43	i	36	GLN
43	i	125	GLN
44	j	56	HIS
45	k	118	ASN
46	l	28	GLN
46	l	45	ASN
46	l	58	ASN
47	m	7	ASN
47	m	99	GLN
48	n	43	ASN
48	n	60	GLN
50	p	40	ASN
50	p	63	GLN
51	q	30	HIS
52	r	51	GLN
53	s	68	HIS
54	t	47	GLN

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Mol	Chain	Res	Type
54	t	60	GLN
54	t	69	ASN
56	v	185	GLN
56	v	258	GLN
56	v	264	HIS
56	v	323	ASN
58	z	15	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2898/2903 (99%)	681 (23%)	27 (0%)
2	B	119/120 (99%)	30 (25%)	5 (4%)
34	7	6/7 (85%)	4 (66%)	0
35	a	1538/1539 (99%)	345 (22%)	0
57	x	76/77 (98%)	21 (27%)	0
All	All	4637/4646 (99%)	1081 (23%)	32 (0%)

All (1081) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	G
1	A	10	A
1	A	12	U
1	A	14	A
1	A	23	G
1	A	28	A
1	A	34	U
1	A	35	G
1	A	46	G
1	A	50	U
1	A	51	G
1	A	53	A
1	A	60	G
1	A	63	A
1	A	71	A
1	A	74	A
1	A	75	G
1	A	78	U
1	A	86	G
1	A	93	G

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Mol	Chain	Res	Type
1	A	101	A
1	A	118	A
1	A	119	A
1	A	120	U
1	A	125	A
1	A	139	U
1	A	140	C
1	A	141	G
1	A	142	A
1	A	143	C
1	A	149	A
1	A	158	U
1	A	162	U
1	A	163	C
1	A	172	A
1	A	182	A
1	A	185	G
1	A	188	G
1	A	196	A
1	A	199	A
1	A	215	G
1	A	216	A
1	A	219	A
1	A	221	A
1	A	222	A
1	A	226	A
1	A	227	A
1	A	228	C
1	A	233	A
1	A	242	G
1	A	243	U
1	A	248	G
1	A	249	C
1	A	250	G
1	A	255	A
1	A	265	A
1	A	266	G
1	A	267	C
1	A	275	C
1	A	276	U
1	A	277	G
1	A	289	G

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Mol	Chain	Res	Type
1	A	294	A
1	A	302	C
1	A	310	A
1	A	311	A
1	A	312	G
1	A	322	A
1	A	323	C
1	A	329	G
1	A	330	A
1	A	335	C
1	A	345	A
1	A	349	U
1	A	353	C
1	A	356	G
1	A	361	G
1	A	362	A
1	A	367	G
1	A	371	A
1	A	372	G
1	A	373	U
1	A	384	A
1	A	386	G
1	A	387	U
1	A	391	A
1	A	396	G
1	A	401	A
1	A	404	A
1	A	405	U
1	A	406	G
1	A	411	G
1	A	421	C
1	A	424	G
1	A	425	G
1	A	428	A
1	A	436	C
1	A	448	U
1	A	452	G
1	A	456	C
1	A	457	A
1	A	458	G
1	A	473	G
1	A	480	A

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Mol	Chain	Res	Type
1	A	481	G
1	A	483	A
1	A	490	C
1	A	491	G
1	A	504	A
1	A	505	A
1	A	506	G
1	A	508	A
1	A	509	C
1	A	518	G
1	A	529	A
1	A	531	C
1	A	532	A
1	A	533	G
1	A	543	G
1	A	545	U
1	A	546	U
1	A	547	A
1	A	550	C
1	A	556	A
1	A	563	A
1	A	572	A
1	A	573	U
1	A	575	A
1	A	584	C
1	A	588	U
1	A	603	A
1	A	609	A
1	A	614	A
1	A	615	U
1	A	616	A
1	A	621	A
1	A	622	G
1	A	627	A
1	A	631	A
1	A	634	C
1	A	636	G
1	A	637	A
1	A	644	A
1	A	645	C
1	A	646	U
1	A	651	G

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Mol	Chain	Res	Type
1	A	654	A
1	A	655	A
1	A	659	G
1	A	668	A
1	A	670	A
1	A	686	U
1	A	687	C
1	A	695	G
1	A	704	G
1	A	711	G
1	A	715	A
1	A	717	C
1	A	730	A
1	A	734	A
1	A	746	U
1	A	747	C
1	A	748	G
1	A	749	A
1	A	750	A
1	A	752	A
1	A	754	U
1	A	762	U
1	A	764	A
1	A	765	C
1	A	772	C
1	A	775	G
1	A	776	G
1	A	782	A
1	A	784	G
1	A	785	G
1	A	800	A
1	A	801	G
1	A	802	A
1	A	805	G
1	A	812	C
1	A	819	A
1	A	822	G
1	A	827	U
1	A	828	U
1	A	829	A
1	A	831	G
1	A	845	A

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Mol	Chain	Res	Type
1	A	846	U
1	A	847	U
1	A	856	G
1	A	857	G
1	A	858	G
1	A	859	G
1	A	860	U
1	A	869	G
1	A	877	A
1	A	878	A
1	A	879	G
1	A	881	G
1	A	883	G
1	A	885	C
1	A	891	G
1	A	892	A
1	A	896	A
1	A	897	C
1	A	902	C
1	A	904	G
1	A	907	G
1	A	910	A
1	A	915	C
1	A	927	A
1	A	931	U
1	A	932	U
1	A	933	A
1	A	941	A
1	A	945	A
1	A	946	C
1	A	957	C
1	A	958	U
1	A	961	C
1	A	973	A
1	A	974	G
1	A	980	A
1	A	983	A
1	A	984	A
1	A	989	G
1	A	990	A
1	A	995	C
1	A	996	A

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Mol	Chain	Res	Type
1	A	999	U
1	A	1005	C
1	A	1012	U
1	A	1013	C
1	A	1021	A
1	A	1022	G
1	A	1023	U
1	A	1025	G
1	A	1026	G
1	A	1033	U
1	A	1040	A
1	A	1045	C
1	A	1046	A
1	A	1047	G
1	A	1050	A
1	A	1053	C
1	A	1054	A
1	A	1057	A
1	A	1059	G
1	A	1060	U
1	A	1061	U
1	A	1062	G
1	A	1065	U
1	A	1066	U
1	A	1068	G
1	A	1069	A
1	A	1071	G
1	A	1072	C
1	A	1073	A
1	A	1075	C
1	A	1076	C
1	A	1078	U
1	A	1079	C
1	A	1083	U
1	A	1084	A
1	A	1088	A
1	A	1089	A
1	A	1090	A
1	A	1092	C
1	A	1093	G
1	A	1095	A
1	A	1097	U

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Mol	Chain	Res	Type
1	A	1098	A
1	A	1101	U
1	A	1102	C
1	A	1104	C
1	A	1111	A
1	A	1112	G
1	A	1119	U
1	A	1130	U
1	A	1131	G
1	A	1132	U
1	A	1135	C
1	A	1139	G
1	A	1142	A
1	A	1143	A
1	A	1149	G
1	A	1151	A
1	A	1155	A
1	A	1171	G
1	A	1173	U
1	A	1174	U
1	A	1175	A
1	A	1176	U
1	A	1177	G
1	A	1178	C
1	A	1180	U
1	A	1181	U
1	A	1183	U
1	A	1206	G
1	A	1211	C
1	A	1212	G
1	A	1224	U
1	A	1236	G
1	A	1237	A
1	A	1244	A
1	A	1247	A
1	A	1248	G
1	A	1250	G
1	A	1253	A
1	A	1256	G
1	A	1257	C
1	A	1265	A
1	A	1271	G

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Mol	Chain	Res	Type
1	A	1272	A
1	A	1273	U
1	A	1275	A
1	A	1300	G
1	A	1301	A
1	A	1305	C
1	A	1306	C
1	A	1311	G
1	A	1321	A
1	A	1325	U
1	A	1326	U
1	A	1332	G
1	A	1341	G
1	A	1345	C
1	A	1360	G
1	A	1365	A
1	A	1366	A
1	A	1368	G
1	A	1375	U
1	A	1378	A
1	A	1379	U
1	A	1383	A
1	A	1387	A
1	A	1392	A
1	A	1395	A
1	A	1416	G
1	A	1419	A
1	A	1420	A
1	A	1421	G
1	A	1424	G
1	A	1427	A
1	A	1428	C
1	A	1434	A
1	A	1437	C
1	A	1454	C
1	A	1455	G
1	A	1458	U
1	A	1460	U
1	A	1461	C
1	A	1467	U
1	A	1475	G
1	A	1482	G

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Mol	Chain	Res	Type
1	A	1490	A
1	A	1491	G
1	A	1494	A
1	A	1504	A
1	A	1506	U
1	A	1507	C
1	A	1509	A
1	A	1515	A
1	A	1523	U
1	A	1524	G
1	A	1529	G
1	A	1530	G
1	A	1534	U
1	A	1535	A
1	A	1536	C
1	A	1537	G
1	A	1545	A
1	A	1546	G
1	A	1555	G
1	A	1556	C
1	A	1558	C
1	A	1559	U
1	A	1560	G
1	A	1565	C
1	A	1566	A
1	A	1567	G
1	A	1569	A
1	A	1584	U
1	A	1585	C
1	A	1586	A
1	A	1587	G
1	A	1592	C
1	A	1593	A
1	A	1608	A
1	A	1611	C
1	A	1627	G
1	A	1634	A
1	A	1646	C
1	A	1647	U
1	A	1648	U
1	A	1649	G
1	A	1652	A

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Mol	Chain	Res	Type
1	A	1669	A
1	A	1674	G
1	A	1675	C
1	A	1682	G
1	A	1693	U
1	A	1694	C
1	A	1695	G
1	A	1698	A
1	A	1699	G
1	A	1707	G
1	A	1715	G
1	A	1727	C
1	A	1729	U
1	A	1730	C
1	A	1731	G
1	A	1732	C
1	A	1738	G
1	A	1757	A
1	A	1758	U
1	A	1764	C
1	A	1769	U
1	A	1773	A
1	A	1776	G
1	A	1781	U
1	A	1786	A
1	A	1800	C
1	A	1801	A
1	A	1802	A
1	A	1807	G
1	A	1808	A
1	A	1811	G
1	A	1812	U
1	A	1816	C
1	A	1826	G
1	A	1828	G
1	A	1829	A
1	A	1842	G
1	A	1857	G
1	A	1869	G
1	A	1871	A
1	A	1884	G
1	A	1888	G

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Mol	Chain	Res	Type
1	A	1897	G
1	A	1900	A
1	A	1901	A
1	A	1906	G
1	A	1907	G
1	A	1912	A
1	A	1919	A
1	A	1927	A
1	A	1929	G
1	A	1930	G
1	A	1937	A
1	A	1938	A
1	A	1940	U
1	A	1941	C
1	A	1942	C
1	A	1945	G
1	A	1955	U
1	A	1966	A
1	A	1967	C
1	A	1970	A
1	A	1971	U
1	A	1972	G
1	A	1991	U
1	A	1992	G
1	A	1993	U
1	A	1997	C
1	A	2015	A
1	A	2020	A
1	A	2022	U
1	A	2023	C
1	A	2031	A
1	A	2033	A
1	A	2043	C
1	A	2044	C
1	A	2046	G
1	A	2052	A
1	A	2053	G
1	A	2055	C
1	A	2056	G
1	A	2060	A
1	A	2061	G
1	A	2069	G

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Mol	Chain	Res	Type
1	A	2072	C
1	A	2080	A
1	A	2092	U
1	A	2093	G
1	A	2096	C
1	A	2100	G
1	A	2104	C
1	A	2105	U
1	A	2106	U
1	A	2108	A
1	A	2110	G
1	A	2111	U
1	A	2112	G
1	A	2113	U
1	A	2115	G
1	A	2117	A
1	A	2118	U
1	A	2119	A
1	A	2123	G
1	A	2125	G
1	A	2127	G
1	A	2128	G
1	A	2131	U
1	A	2132	U
1	A	2133	G
1	A	2137	U
1	A	2138	G
1	A	2139	U
1	A	2145	C
1	A	2146	C
1	A	2147	A
1	A	2148	G
1	A	2157	G
1	A	2162	G
1	A	2164	C
1	A	2167	U
1	A	2168	G
1	A	2169	A
1	A	2170	A
1	A	2172	U
1	A	2173	A
1	A	2174	C

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Mol	Chain	Res	Type
1	A	2175	C
1	A	2176	A
1	A	2178	C
1	A	2179	C
1	A	2189	U
1	A	2192	U
1	A	2198	A
1	A	2203	U
1	A	2204	G
1	A	2210	U
1	A	2212	A
1	A	2213	U
1	A	2225	A
1	A	2226	C
1	A	2228	G
1	A	2229	U
1	A	2238	G
1	A	2239	G
1	A	2250	G
1	A	2251	G
1	A	2266	A
1	A	2279	G
1	A	2283	C
1	A	2286	G
1	A	2287	A
1	A	2305	U
1	A	2308	G
1	A	2309	A
1	A	2320	U
1	A	2325	G
1	A	2326	C
1	A	2327	A
1	A	2331	G
1	A	2333	A
1	A	2334	U
1	A	2335	A
1	A	2344	U
1	A	2345	G
1	A	2350	C
1	A	2354	C
1	A	2357	G
1	A	2358	A

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Mol	Chain	Res	Type
1	A	2359	C
1	A	2361	G
1	A	2377	A
1	A	2383	G
1	A	2385	C
1	A	2391	G
1	A	2392	A
1	A	2402	U
1	A	2403	C
1	A	2405	G
1	A	2406	A
1	A	2407	A
1	A	2419	U
1	A	2422	C
1	A	2423	U
1	A	2424	C
1	A	2425	A
1	A	2426	A
1	A	2428	G
1	A	2429	G
1	A	2430	A
1	A	2434	A
1	A	2435	A
1	A	2440	C
1	A	2441	U
1	A	2445	G
1	A	2448	A
1	A	2464	G
1	A	2470	G
1	A	2475	C
1	A	2476	A
1	A	2488	G
1	A	2494	G
1	A	2502	G
1	A	2503	A
1	A	2504	U
1	A	2505	G
1	A	2506	U
1	A	2518	A
1	A	2520	C
1	A	2529	G
1	A	2534	A

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Mol	Chain	Res	Type
1	A	2535	G
1	A	2547	A
1	A	2554	U
1	A	2564	A
1	A	2567	G
1	A	2569	G
1	A	2572	A
1	A	2573	C
1	A	2574	G
1	A	2582	G
1	A	2585	U
1	A	2602	A
1	A	2608	G
1	A	2609	U
1	A	2613	U
1	A	2614	A
1	A	2629	U
1	A	2646	C
1	A	2655	G
1	A	2661	G
1	A	2663	G
1	A	2668	G
1	A	2689	U
1	A	2690	U
1	A	2707	U
1	A	2714	G
1	A	2718	G
1	A	2724	U
1	A	2726	A
1	A	2727	A
1	A	2732	G
1	A	2733	A
1	A	2744	G
1	A	2748	A
1	A	2750	A
1	A	2752	C
1	A	2761	A
1	A	2762	C
1	A	2764	A
1	A	2765	A
1	A	2778	A
1	A	2779	U

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Mol	Chain	Res	Type
1	A	2780	G
1	A	2791	G
1	A	2792	A
1	A	2794	C
1	A	2796	U
1	A	2797	U
1	A	2798	U
1	A	2799	A
1	A	2800	A
1	A	2801	G
1	A	2808	G
1	A	2809	A
1	A	2811	G
1	A	2818	U
1	A	2820	A
1	A	2833	U
1	A	2836	U
1	A	2849	U
1	A	2851	A
1	A	2861	U
1	A	2866	U
1	A	2867	G
1	A	2868	A
1	A	2873	A
1	A	2880	C
1	A	2884	U
1	A	2887	A
1	A	2891	U
1	A	2894	G
1	A	2902	C
1	A	2903	U
2	B	4	C
2	B	9	G
2	B	12	C
2	B	13	G
2	B	15	A
2	B	19	C
2	B	21	G
2	B	24	G
2	B	30	C
2	B	34	A
2	B	35	C

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Mol	Chain	Res	Type
2	B	42	C
2	B	44	G
2	B	45	A
2	B	53	A
2	B	59	A
2	B	66	A
2	B	67	G
2	B	68	C
2	B	69	G
2	B	88	C
2	B	89	U
2	B	90	C
2	B	91	C
2	B	105	G
2	B	108	A
2	B	109	A
2	B	112	G
2	B	118	C
2	B	120	A
34	7	27	C
34	7	29	A
34	7	30	G
34	7	31	A
35	a	5	U
35	a	6	G
35	a	7	A
35	a	9	G
35	a	22	G
35	a	27	G
35	a	31	G
35	a	32	A
35	a	39	G
35	a	47	C
35	a	48	C
35	a	49	U
35	a	50	A
35	a	51	A
35	a	58	C
35	a	59	A
35	a	69	G
35	a	71	A
35	a	73	C

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Mol	Chain	Res	Type
35	a	78	A
35	a	79	G
35	a	80	A
35	a	81	A
35	a	82	G
35	a	86	G
35	a	87	C
35	a	88	U
35	a	89	U
35	a	92	U
35	a	95	C
35	a	96	U
35	a	121	U
35	a	130	A
35	a	132	C
35	a	134	G
35	a	149	A
35	a	154	U
35	a	163	C
35	a	164	G
35	a	173	U
35	a	174	A
35	a	181	A
35	a	183	C
35	a	184	G
35	a	197	A
35	a	199	A
35	a	200	G
35	a	205	A
35	a	207	C
35	a	209	U
35	a	210	C
35	a	212	G
35	a	215	C
35	a	219	U
35	a	226	G
35	a	240	G
35	a	245	U
35	a	247	G
35	a	251	G
35	a	257	G
35	a	263	A

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Mol	Chain	Res	Type
35	a	266	G
35	a	267	C
35	a	268	U
35	a	281	G
35	a	282	A
35	a	289	G
35	a	306	A
35	a	327	A
35	a	328	C
35	a	345	C
35	a	346	G
35	a	347	G
35	a	350	G
35	a	352	C
35	a	353	A
35	a	354	G
35	a	358	U
35	a	367	U
35	a	368	U
35	a	369	G
35	a	372	C
35	a	376	G
35	a	382	A
35	a	385	C
35	a	388	G
35	a	392	C
35	a	397	A
35	a	406	G
35	a	411	A
35	a	412	A
35	a	413	G
35	a	414	A
35	a	422	C
35	a	424	G
35	a	427	U
35	a	428	G
35	a	429	U
35	a	430	A
35	a	435	A
35	a	438	U
35	a	439	U
35	a	442	G

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Mol	Chain	Res	Type
35	a	451	A
35	a	452	A
35	a	460	A
35	a	462	G
35	a	467	U
35	a	468	A
35	a	473	U
35	a	477	C
35	a	479	U
35	a	480	U
35	a	482	A
35	a	484	G
35	a	486	U
35	a	487	A
35	a	489	C
35	a	492	C
35	a	495	A
35	a	496	A
35	a	497	G
35	a	508	U
35	a	509	A
35	a	511	C
35	a	516	U
35	a	518	C
35	a	519	C
35	a	521	G
35	a	524	G
35	a	527	G
35	a	528	C
35	a	531	U
35	a	532	A
35	a	533	A
35	a	547	A
35	a	561	U
35	a	562	U
35	a	564	C
35	a	572	A
35	a	573	A
35	a	575	G
35	a	576	C
35	a	577	G
35	a	596	A

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Mol	Chain	Res	Type
35	a	607	A
35	a	632	U
35	a	633	G
35	a	639	G
35	a	642	A
35	a	652	U
35	a	665	A
35	a	695	A
35	a	703	G
35	a	713	G
35	a	714	G
35	a	718	A
35	a	721	G
35	a	724	G
35	a	731	G
35	a	733	G
35	a	748	G
35	a	753	A
35	a	754	C
35	a	755	G
35	a	766	A
35	a	777	A
35	a	792	A
35	a	793	U
35	a	814	A
35	a	817	C
35	a	820	U
35	a	826	C
35	a	836	G
35	a	843	U
35	a	844	G
35	a	845	A
35	a	846	G
35	a	851	G
35	a	871	U
35	a	873	A
35	a	876	C
35	a	884	U
35	a	885	G
35	a	887	G
35	a	889	A
35	a	890	G

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Mol	Chain	Res	Type
35	a	902	G
35	a	916	U
35	a	926	G
35	a	931	C
35	a	934	C
35	a	935	A
35	a	939	G
35	a	942	G
35	a	960	U
35	a	961	U
35	a	966	G
35	a	968	A
35	a	969	A
35	a	974	A
35	a	975	A
35	a	976	G
35	a	977	A
35	a	983	A
35	a	989	U
35	a	992	U
35	a	993	G
35	a	994	A
35	a	999	C
35	a	1004	A
35	a	1005	A
35	a	1013	G
35	a	1020	G
35	a	1026	G
35	a	1027	C
35	a	1028	C
35	a	1030	U
35	a	1031	C
35	a	1033	G
35	a	1034	G
35	a	1036	A
35	a	1042	A
35	a	1053	G
35	a	1056	U
35	a	1064	G
35	a	1065	U
35	a	1085	U
35	a	1089	G

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Mol	Chain	Res	Type
35	a	1094	G
35	a	1095	U
35	a	1101	A
35	a	1104	G
35	a	1129	C
35	a	1130	A
35	a	1132	C
35	a	1136	C
35	a	1137	C
35	a	1138	G
35	a	1139	G
35	a	1140	C
35	a	1143	G
35	a	1146	A
35	a	1151	A
35	a	1152	A
35	a	1158	C
35	a	1159	U
35	a	1168	U
35	a	1171	A
35	a	1183	U
35	a	1184	G
35	a	1191	A
35	a	1196	A
35	a	1197	A
35	a	1200	C
35	a	1201	A
35	a	1202	U
35	a	1212	U
35	a	1213	A
35	a	1225	A
35	a	1226	C
35	a	1227	A
35	a	1228	C
35	a	1236	A
35	a	1238	A
35	a	1240	U
35	a	1241	G
35	a	1256	A
35	a	1258	G
35	a	1260	G
35	a	1261	A

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Mol	Chain	Res	Type
35	a	1262	C
35	a	1278	G
35	a	1280	A
35	a	1281	C
35	a	1282	C
35	a	1287	A
35	a	1289	A
35	a	1291	U
35	a	1294	G
35	a	1298	U
35	a	1300	G
35	a	1301	U
35	a	1302	C
35	a	1309	G
35	a	1311	A
35	a	1312	G
35	a	1315	U
35	a	1317	C
35	a	1320	C
35	a	1322	C
35	a	1323	G
35	a	1334	G
35	a	1335	U
35	a	1336	C
35	a	1340	A
35	a	1346	A
35	a	1347	G
35	a	1348	U
35	a	1353	G
35	a	1363	A
35	a	1364	U
35	a	1368	A
35	a	1370	G
35	a	1378	C
35	a	1381	U
35	a	1384	C
35	a	1386	G
35	a	1387	G
35	a	1394	A
35	a	1395	C
35	a	1397	C
35	a	1399	C

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Mol	Chain	Res	Type
35	a	1400	C
35	a	1401	G
35	a	1402	C
35	a	1406	U
35	a	1418	A
35	a	1419	G
35	a	1440	U
35	a	1441	A
35	a	1442	G
35	a	1443	C
35	a	1445	U
35	a	1446	A
35	a	1452	C
35	a	1455	G
35	a	1484	C
35	a	1487	G
35	a	1492	A
35	a	1493	A
35	a	1494	G
35	a	1497	G
35	a	1499	A
35	a	1502	A
35	a	1503	A
35	a	1506	U
35	a	1517	G
35	a	1529	G
35	a	1530	G
35	a	1531	A
35	a	1534	A
35	a	1535	C
35	a	1536	C
35	a	1540	U
57	x	3	G
57	x	4	C
57	x	5	U
57	x	6	U
57	x	14	A
57	x	15	G
57	x	16	G
57	x	17	U
57	x	17(A)	G
57	x	19	U

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Mol	Chain	Res	Type
57	x	21	A
57	x	22	G
57	x	34	G
57	x	42	U
57	x	46	G
57	x	47	U
57	x	48	C
57	x	50	G
57	x	62	C
57	x	65	U
57	x	76	A

All (32) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	86	G
1	A	227	A
1	A	242	G
1	A	372	G
1	A	490	C
1	A	549	G
1	A	555	G
1	A	846	U
1	A	858	G
1	A	859	G
1	A	931	U
1	A	1020	A
1	A	1022	G
1	A	1130	U
1	A	1182	G
1	A	1190	G
1	A	1300	G
1	A	1378	A
1	A	1399	C
1	A	1565	C
1	A	1566	A
1	A	1913	A
1	A	1940	U
1	A	2326	C
1	A	2347	C
1	A	2566	A
1	A	2808	G

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Mol	Chain	Res	Type
2	B	3	C
2	B	12	C
2	B	52	A
2	B	66	A
2	B	88	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	L	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L	60:ARG	C	61:LEU	N	1.18

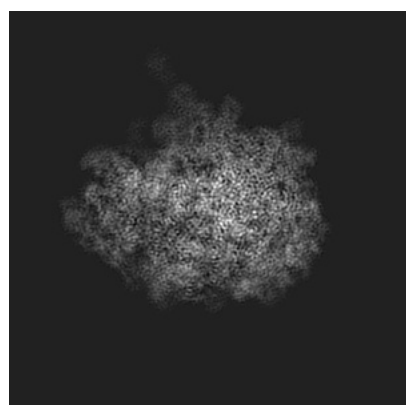
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3730. These allow visual inspection of the internal detail of the map and identification of artifacts.

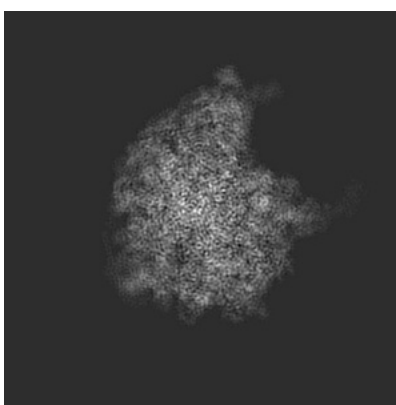
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

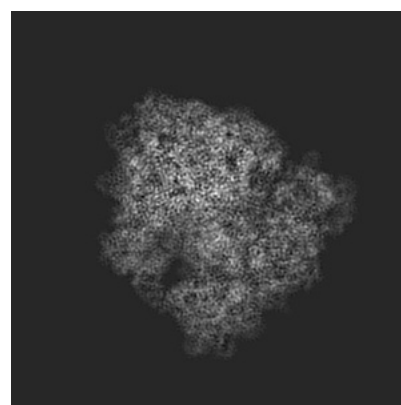
6.1.1 Primary map



X



Y

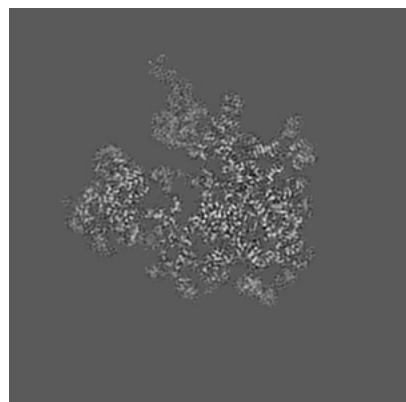


Z

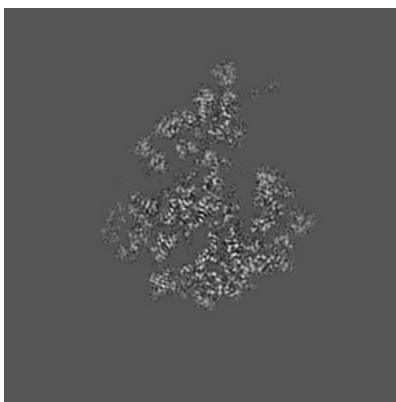
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 180



Y Index: 180

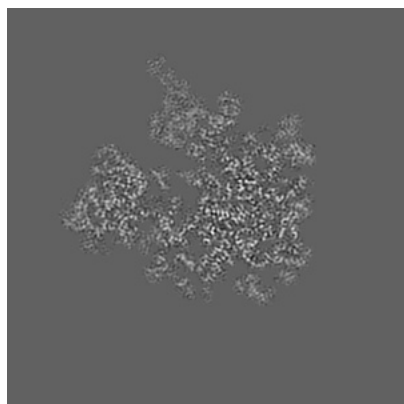


Z Index: 180

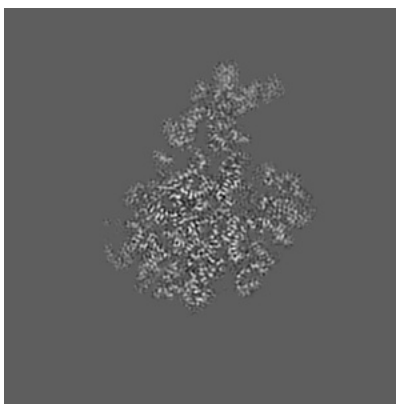
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

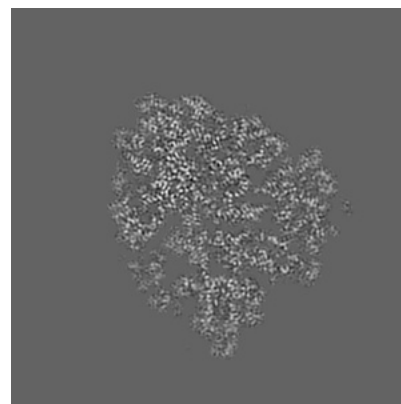
6.3.1 Primary map



X Index: 178



Y Index: 190

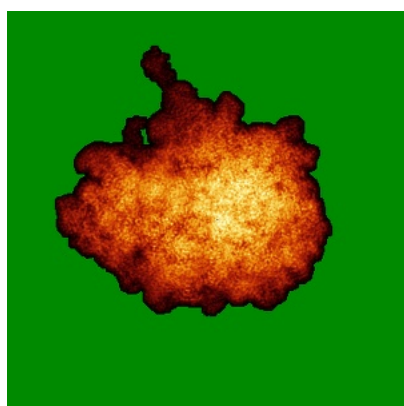


Z Index: 186

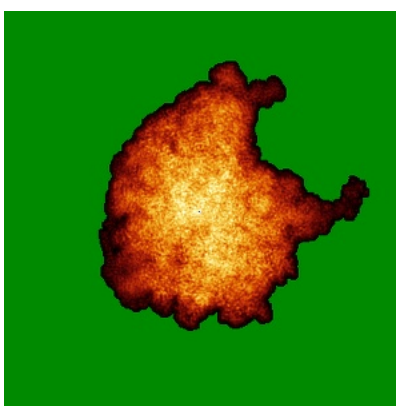
The images above show the largest variance slices of the map in three orthogonal directions.

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

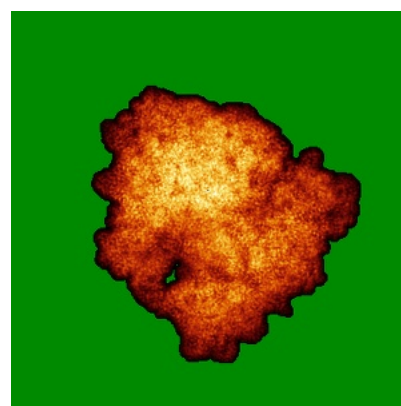
6.4.1 Primary map



X



Y

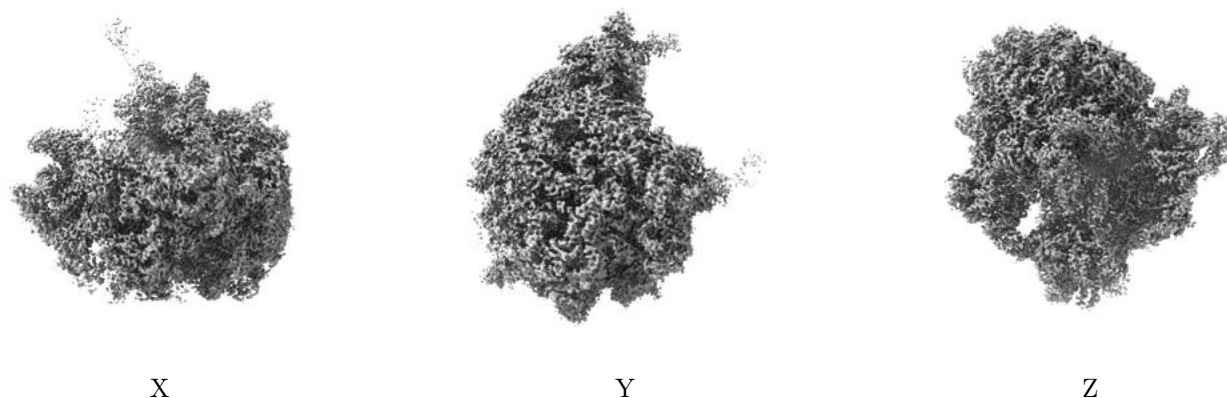


Z

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

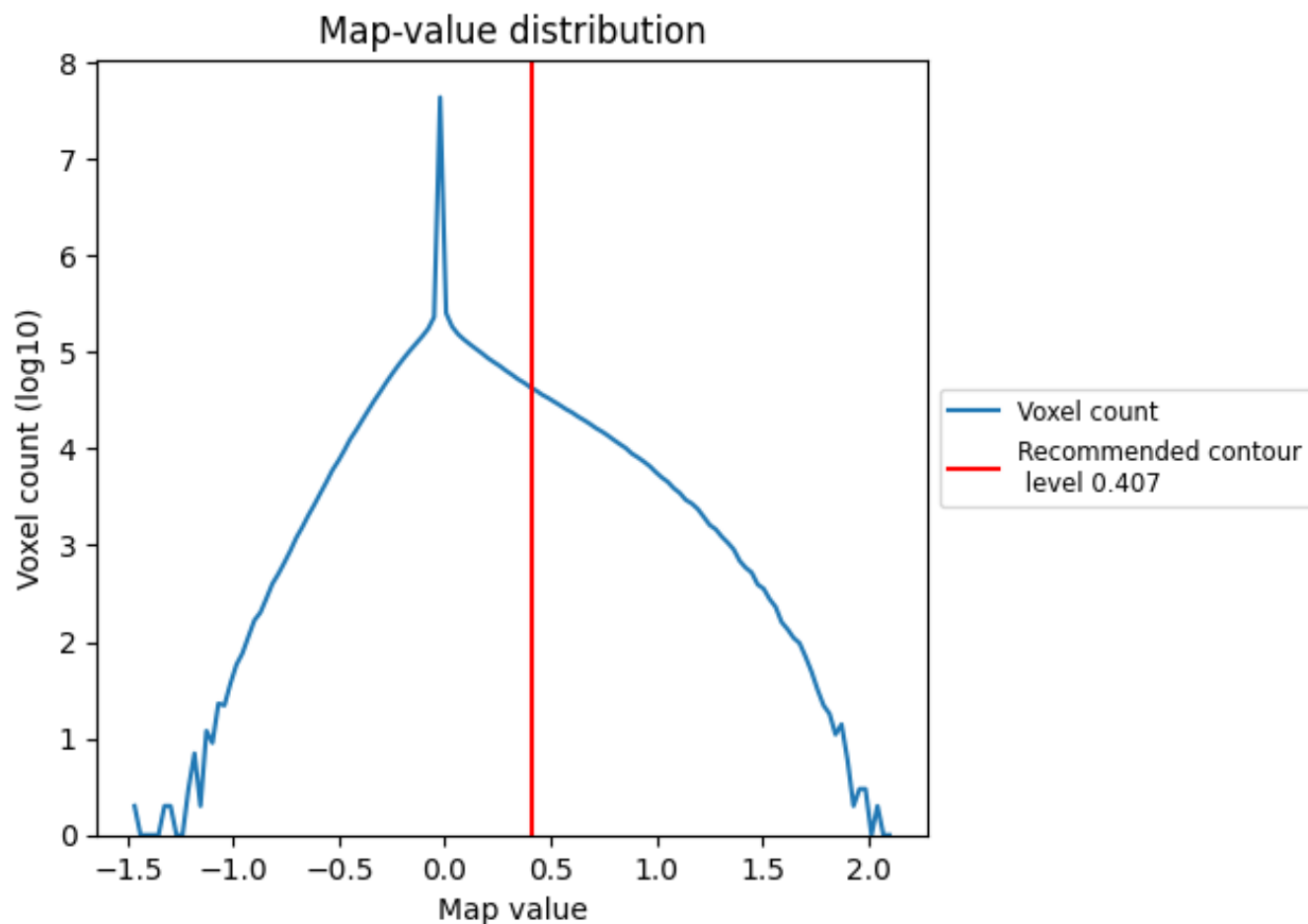
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

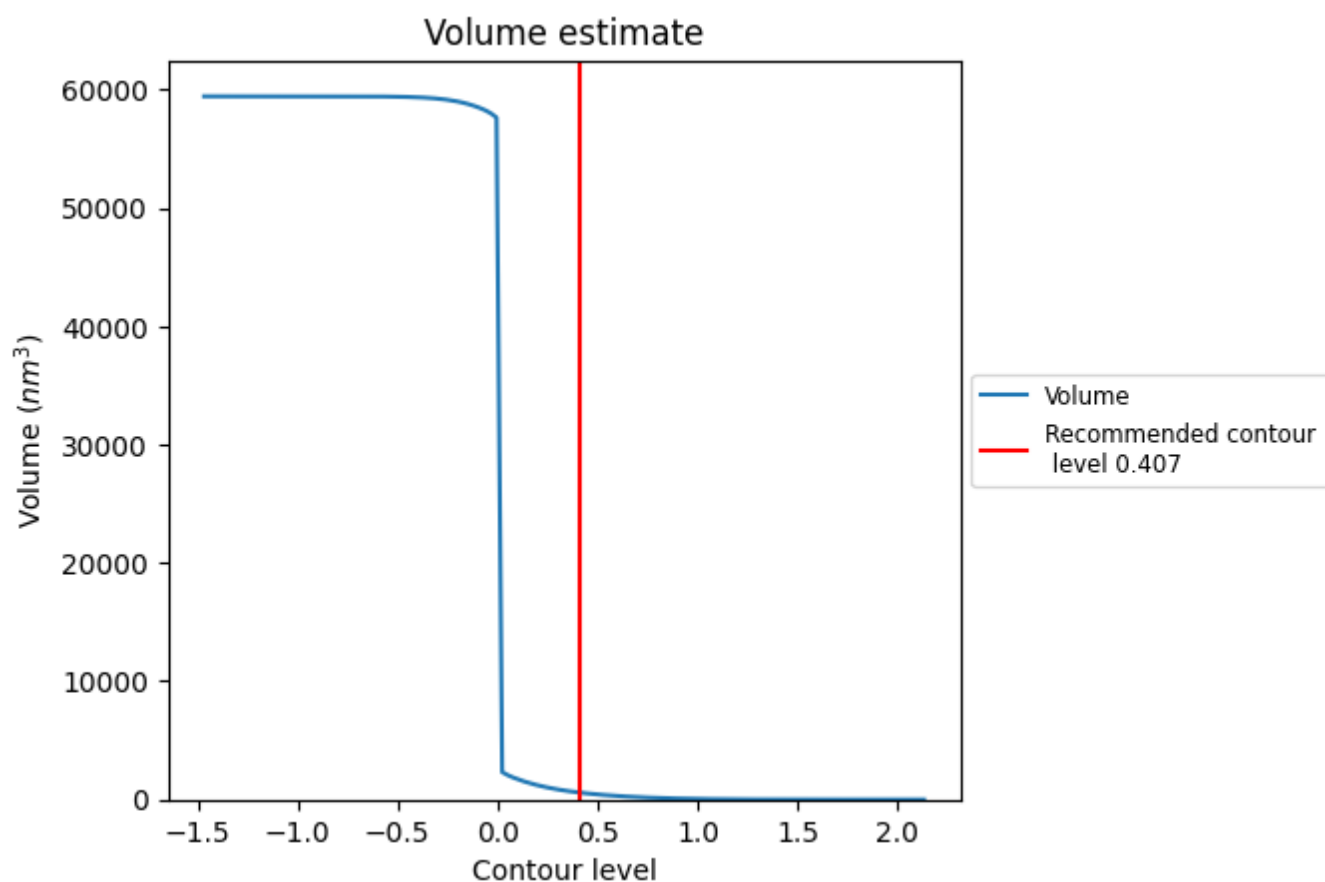
This section contains the results of statistical analysis of the map.

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.

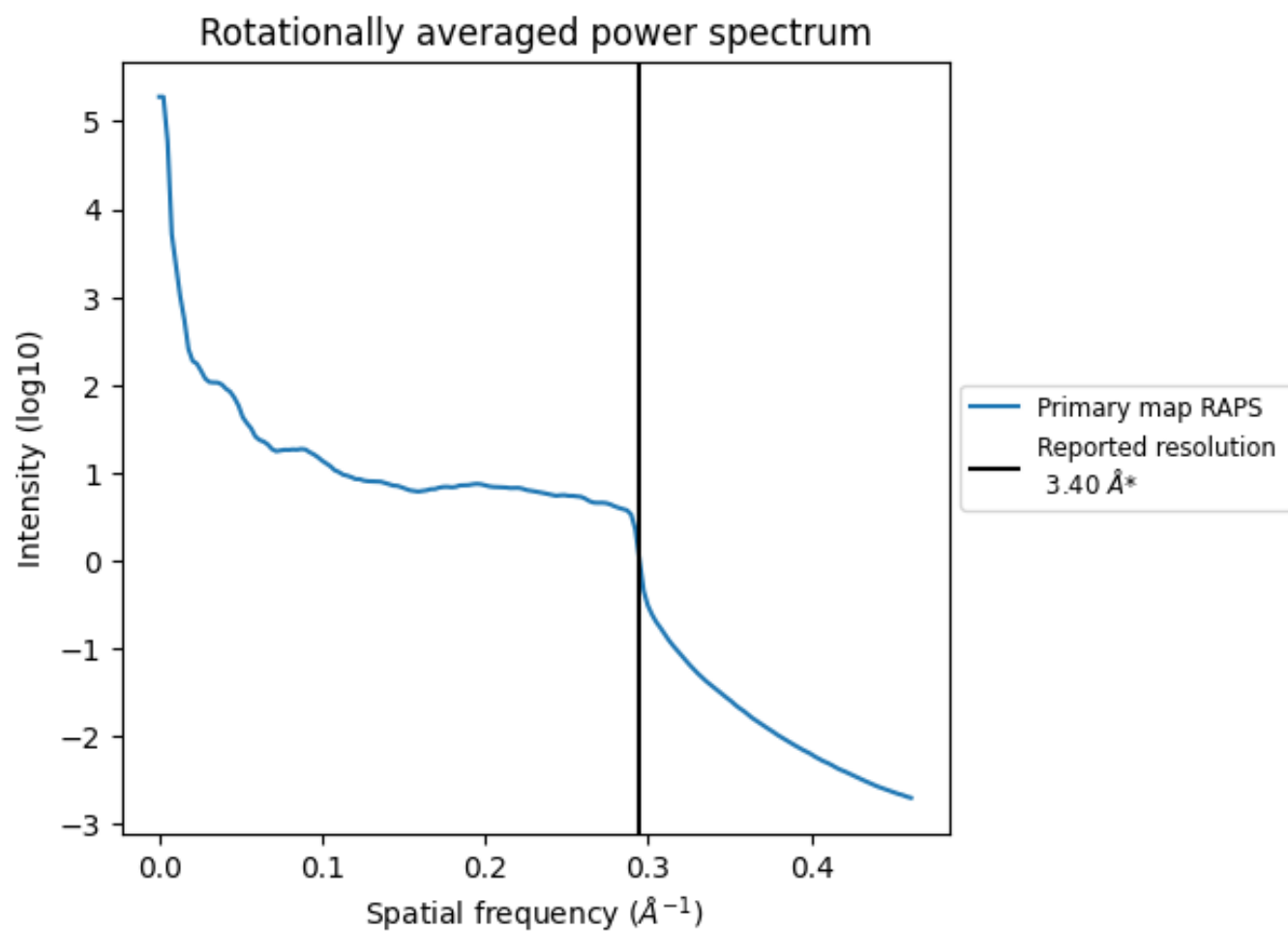
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 595 nm³; this corresponds to an approximate mass of 537 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 0.294 Å⁻¹

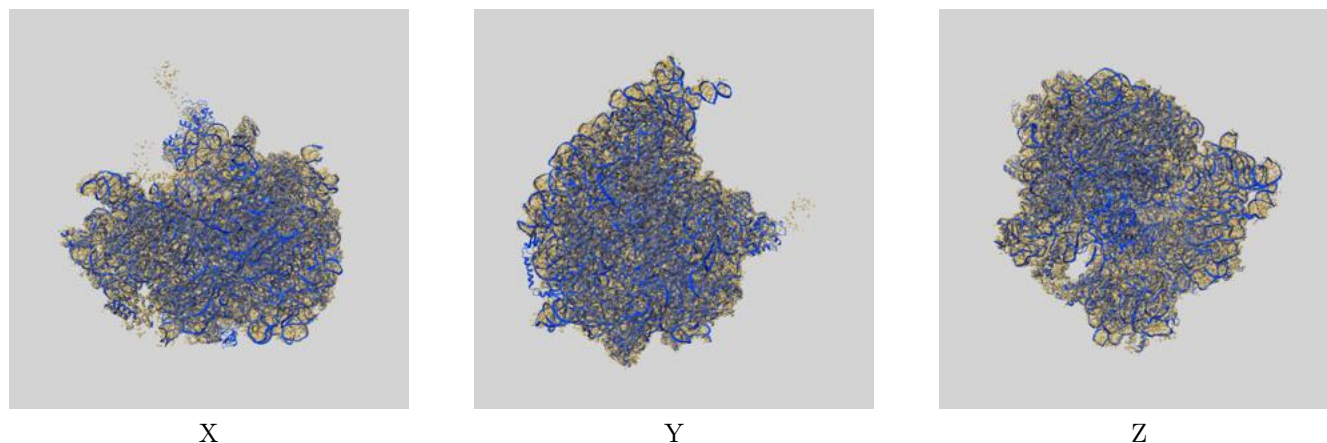
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

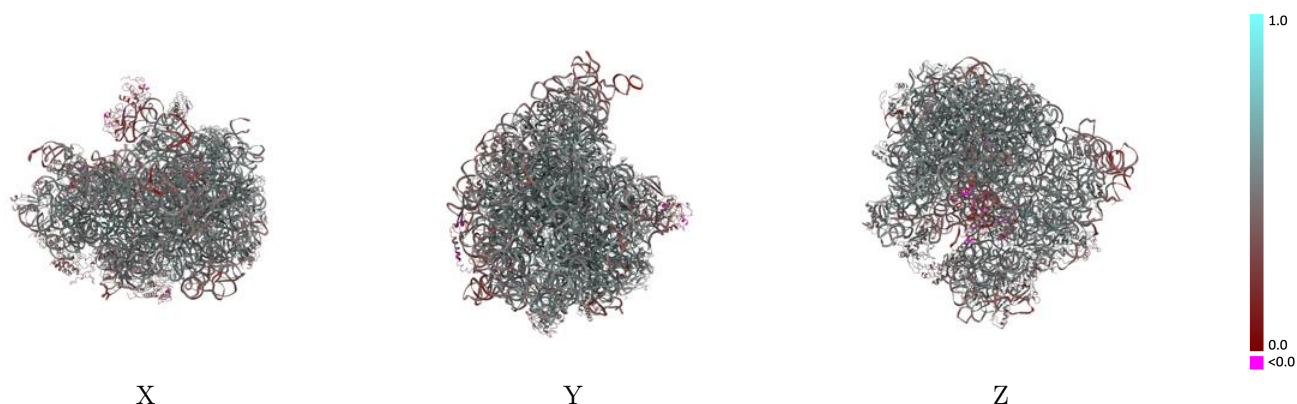
This section contains information regarding the fit between EMDB map EMD-3730 and PDB model 5O2R. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



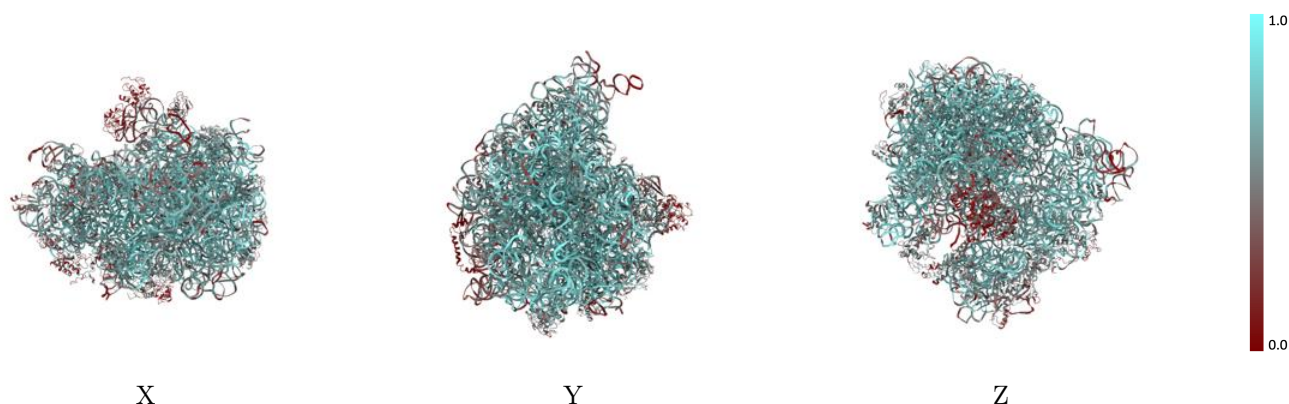
The images above show the 3D surface view of the map at the recommended contour level 0.407 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



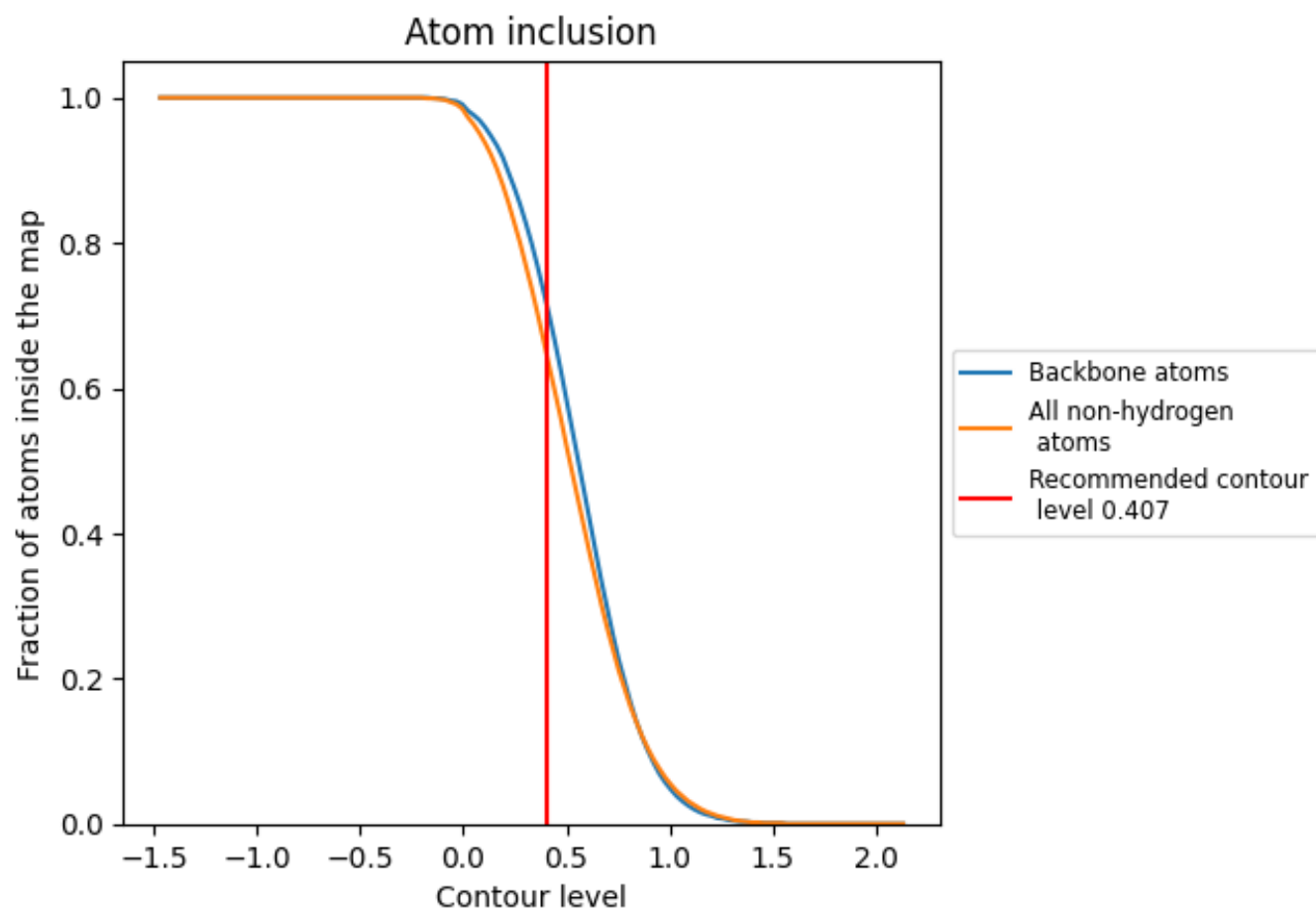
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.407).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 64% 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 (0.407) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6430	 0.4760
0	 0.6100	 0.5100
1	 0.5010	 0.4880
2	 0.6790	 0.5170
3	 0.6720	 0.5400
4	 0.5750	 0.5170
5	 0.0680	 0.2130
6	 0.3520	 0.3920
7	 0.8120	 0.5450
A	 0.7200	 0.4880
B	 0.7080	 0.4730
C	 0.6040	 0.5210
D	 0.5980	 0.5120
E	 0.5530	 0.4840
F	 0.4840	 0.4530
G	 0.3760	 0.4170
H	 0.1120	 0.2790
I	 0.0620	 0.2140
J	 0.5970	 0.5110
K	 0.5820	 0.5030
L	 0.5840	 0.5060
M	 0.5970	 0.5180
N	 0.6410	 0.5220
O	 0.5420	 0.4760
P	 0.5830	 0.5040
Q	 0.6560	 0.5180
R	 0.5520	 0.4840
S	 0.6010	 0.5050
T	 0.5280	 0.4810
U	 0.4890	 0.4640
V	 0.5460	 0.4820
W	 0.6440	 0.5380
X	 0.5470	 0.4820
Y	 0.4450	 0.4330
Z	 0.6130	 0.5050



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Chain	Atom inclusion	Q-score
a	 0.7030	 0.4770
b	 0.3550	 0.3970
c	 0.5210	 0.4600
d	 0.4430	 0.4240
e	 0.5860	 0.4980
f	 0.4330	 0.4270
g	 0.3930	 0.4250
h	 0.5380	 0.4820
i	 0.4710	 0.4450
j	 0.4390	 0.4410
k	 0.4960	 0.4620
l	 0.5790	 0.4960
m	 0.4850	 0.4370
n	 0.5660	 0.4680
o	 0.5430	 0.4700
p	 0.5290	 0.4710
q	 0.4700	 0.4610
r	 0.5380	 0.4760
s	 0.5040	 0.4620
t	 0.5030	 0.4530
u	 0.3130	 0.3610
v	 0.5060	 0.4820
x	 0.6130	 0.4550
z	 0.4780	 0.4720