Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 03:29 AM UTC

PDB ID	:	9E0N / pdb_00009e0n
EMDB ID	:	EMD-47363
Title	:	M. smegmatis unmethylated 70S ribosome structure
Authors	:	Nandi, S.; Conn, G.L.
Deposited on	:	2024-10-18
Resolution	:	3.24 Å(reported)
Based on initial model	:	5ZEB

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:

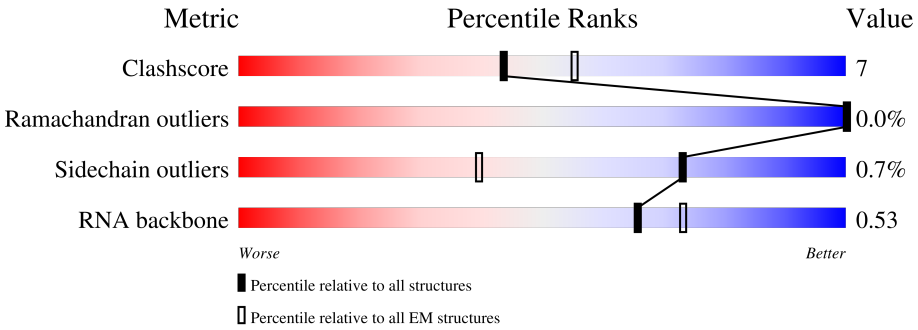
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

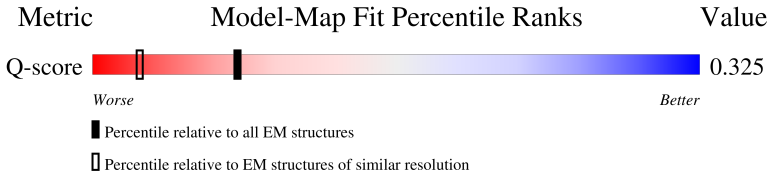
1 Overall quality at a glance

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

The reported resolution of this entry is 3.24 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	14594 (2.74 - 3.74)

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

Mol	Chain	Length	Quality of chain
1	1	61	92% 7%
2	2	75	19% 71% 17% 12%
3	3	57	89% 5% 5%

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Mol	Chain	Length	Quality of chain
4	4	55	71% 20% 9%
5	5	47	81% 15%
6	6	64	83% 16%
7	7	37	86% 11%
8	8	24	8% 71% 25%
9	A	3120	61% 32% 6%
10	B	118	63% 29% 8%
11	C	278	81% 17%
12	D	217	86% 12%
13	E	215	77% 19%
14	F	187	75% 21%
15	G	179	87% 11%
16	H	151	12% 93% 7%
17	I	174	66% 67% 5% 28%
18	J	142	75% 82% 11% 6%
19	K	147	92% 8%
20	L	122	89% 11%
21	M	147	91% 7%
22	N	138	83% 14%
23	O	174	55% 11% 33%
24	P	127	83% 16%
25	Q	113	83% 17%
26	R	129	86% 10%
27	S	103	81% 18%
28	T	153	65% 9% 25%

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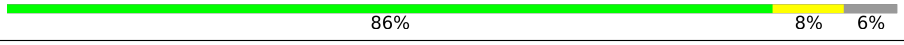
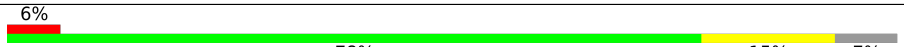
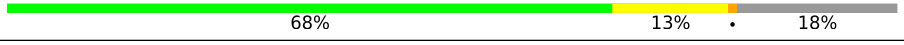
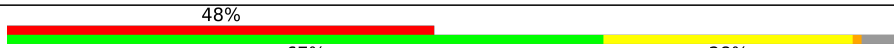
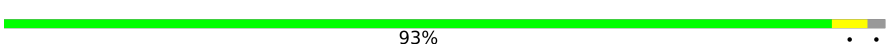
Mol	Chain	Length	Quality of chain
29	U	100	
30	V	105	
31	W	215	
32	X	88	
33	Y	64	
34	Z	77	
35	a	1528	
36	b	277	
37	c	275	
38	d	201	
39	e	214	
40	f	96	
41	g	156	
42	h	132	
43	i	150	
44	j	101	
45	k	138	
46	l	124	
47	m	124	
48	n	61	
49	o	89	
50	p	156	
51	q	98	
52	r	84	
53	s	93	

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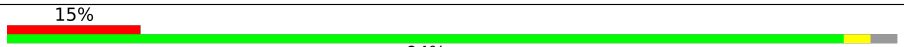
Mol	Chain	Length	Quality of chain
54	t	86	
55	u	33	

2 Entry composition (i)

There are 56 unique types of molecules in this entry. The entry contains 148775 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	1	60	483	298	97	88	0	0

- Molecule 2 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	2	66	510	316	93	96	5	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	54	423	260	93	69	1	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	50	416	254	86	72	4	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	45	372	222	96	53	1	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	6	63	502	302	115	85	0	0

- Molecule 7 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	37	Total	C	N	O	S	0	0
			298	181	66	46	5		

- Molecule 8 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	8	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 9 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	3102	Total	C	N	O	P	0	0
			66623	29694	12253	21574	3102		

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	117	Total	C	N	O	P	0	0
			2501	1116	462	806	117		

- Molecule 11 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	273	Total	C	N	O	S	0	0
			2097	1290	435	368	4		

- Molecule 12 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 13 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	207	Total	C	N	O	S	0	0
			1553	959	292	300	2		

- Molecule 14 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	181	Total	C	N	O	S	0	0
			1437	903	269	259	6		

- Molecule 15 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 17 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 18 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 19 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	147	Total	C	N	O	S	0	0
			1127	719	207	199	2		

- Molecule 20 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	121	Total	C	N	O	S	0	0
			930	580	178	169	3		

- Molecule 21 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 22 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	134	Total	C	N	O	S	0	0
			1068	677	211	178	2		

- Molecule 23 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	P	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 25 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 26 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	R	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 27 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	S	102	Total	C	N	O	0	0
			768	487	140	141		

- Molecule 28 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	T	114	Total 873	C 543	N 171	O 159	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	U	94	Total 739	C 469	N 135	O 135	0	0

- Molecule 30 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	97	Total 731	C 456	N 137	O 136	S 2	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	W	188	Total 1407	C 869	N 251	O 287	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	X	82	Total 604	C 372	N 127	O 105	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	63	Total 470	C 283	N 103	O 80	S 4	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	63	Total 527	C 322	N 102	O 102	S 1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	1506	Total	C	N	O	P	0	0
			32341	14404	5921	10510	1506		

- Molecule 36 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 37 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c	210	Total	C	N	O	S	0	0
			1672	1043	324	300	5		

- Molecule 38 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 39 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	198	Total	C	N	O	S	0	0
			1433	885	282	262	4		

- Molecule 40 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 41 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	156	Total	C	N	O	S	0	0
			1240	773	242	222	3		

- Molecule 42 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	130	Total	C	N	O	S	0	0
			1003	629	188	185	1		

- Molecule 43 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	i	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 44 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	97	Total	C	N	O	S	0	0
			775	488	143	141	3		

- Molecule 45 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	117	Total	C	N	O	S	0	0
			871	539	173	158	1		

- Molecule 46 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	l	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 47 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 48 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	n	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 49 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	o	87	Total 709	C 443	N 143	O 123	0	0

- Molecule 50 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	p	113	Total 891	C 570	N 162	O 159	0	0

- Molecule 51 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	92	Total 730	C 458	N 138	O 132	S 2	0	0

- Molecule 52 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	64	Total 512	C 319	N 102	O 88	S 3	0	0

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	78	Total 630	C 405	N 117	O 107	S 1	0	0

- Molecule 54 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	t	84	Total 655	C 399	N 138	O 118	0	0

- Molecule 55 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	u	32	Total 280	C 172	N 71	O 36	S 1	0	0

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
56	2	1	Total Mg 1 1	0
56	A	76	Total Mg 76 76	0
56	C	1	Total Mg 1 1	0
56	D	1	Total Mg 1 1	0
56	a	28	Total Mg 28 28	0

3 Residue-property plots (i)

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

• Molecule 1: Large ribosomal subunit protein uL30

Chain 1:

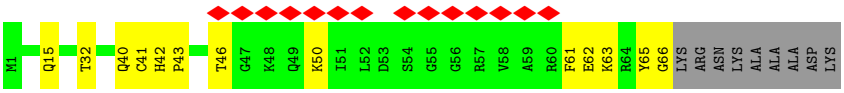




• Molecule 2: Large ribosomal subunit protein bL31

Chain 2:

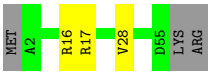




• Molecule 3: Large ribosomal subunit protein bL32

Chain 3:

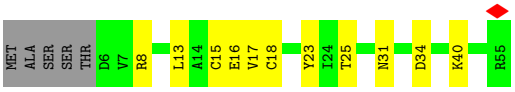




• Molecule 4: Large ribosomal subunit protein bL33A

Chain 4:

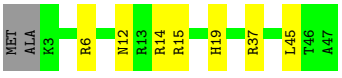




• Molecule 5: Large ribosomal subunit protein bL34

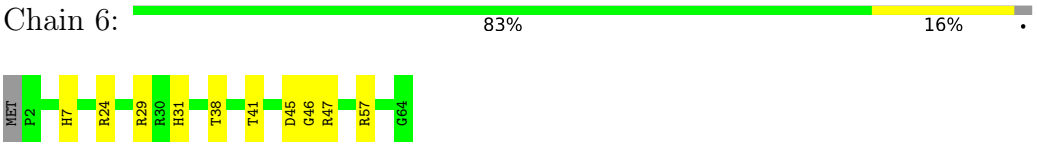
Chain 5:





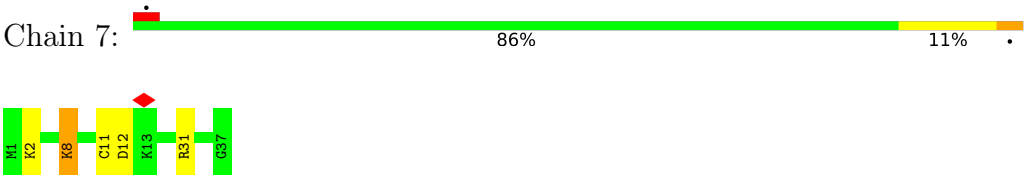
• Molecule 6: Large ribosomal subunit protein bL35

Chain 6:



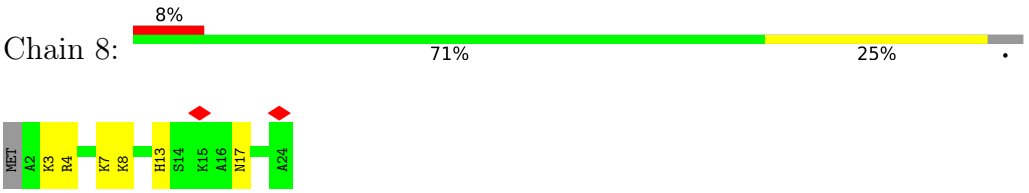
• Molecule 7: 50S ribosomal protein L36

Chain 7:



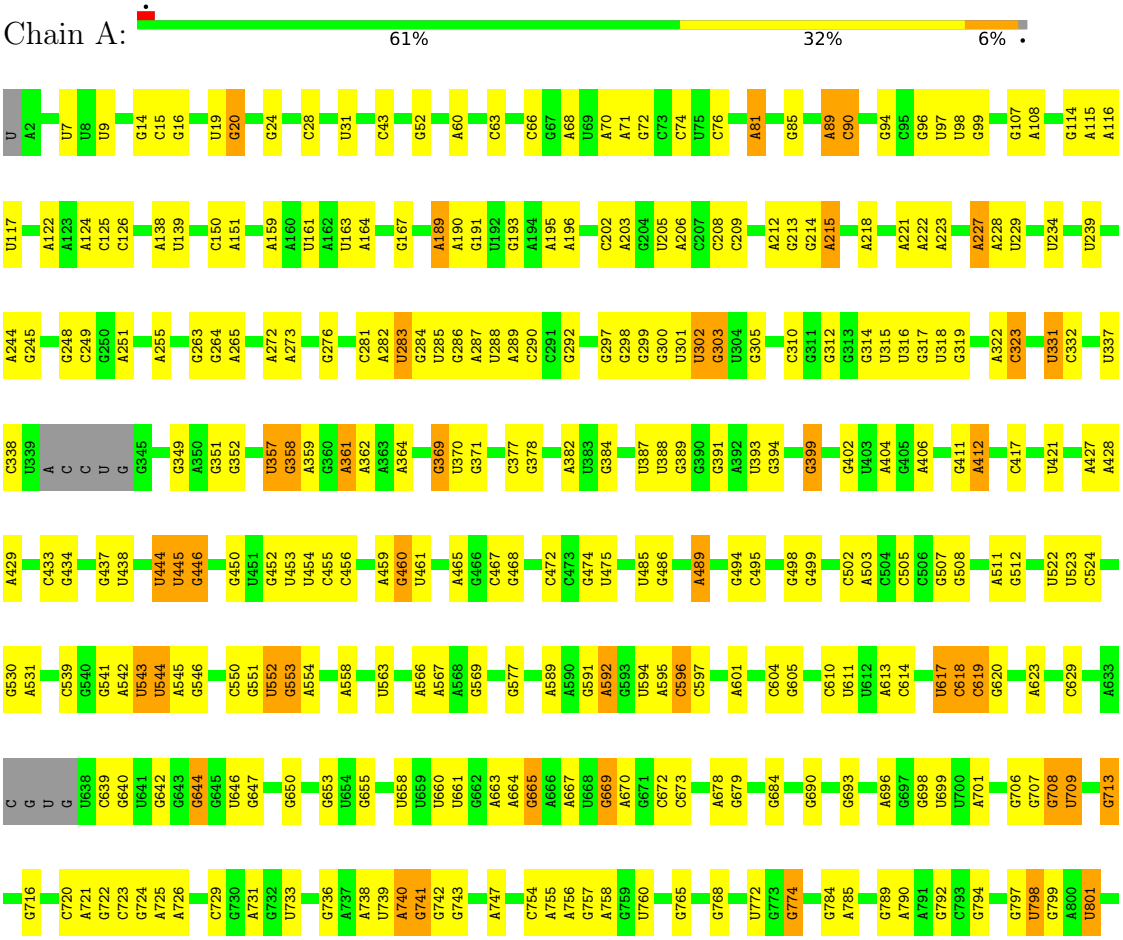
• Molecule 8: 50S ribosomal protein bL37

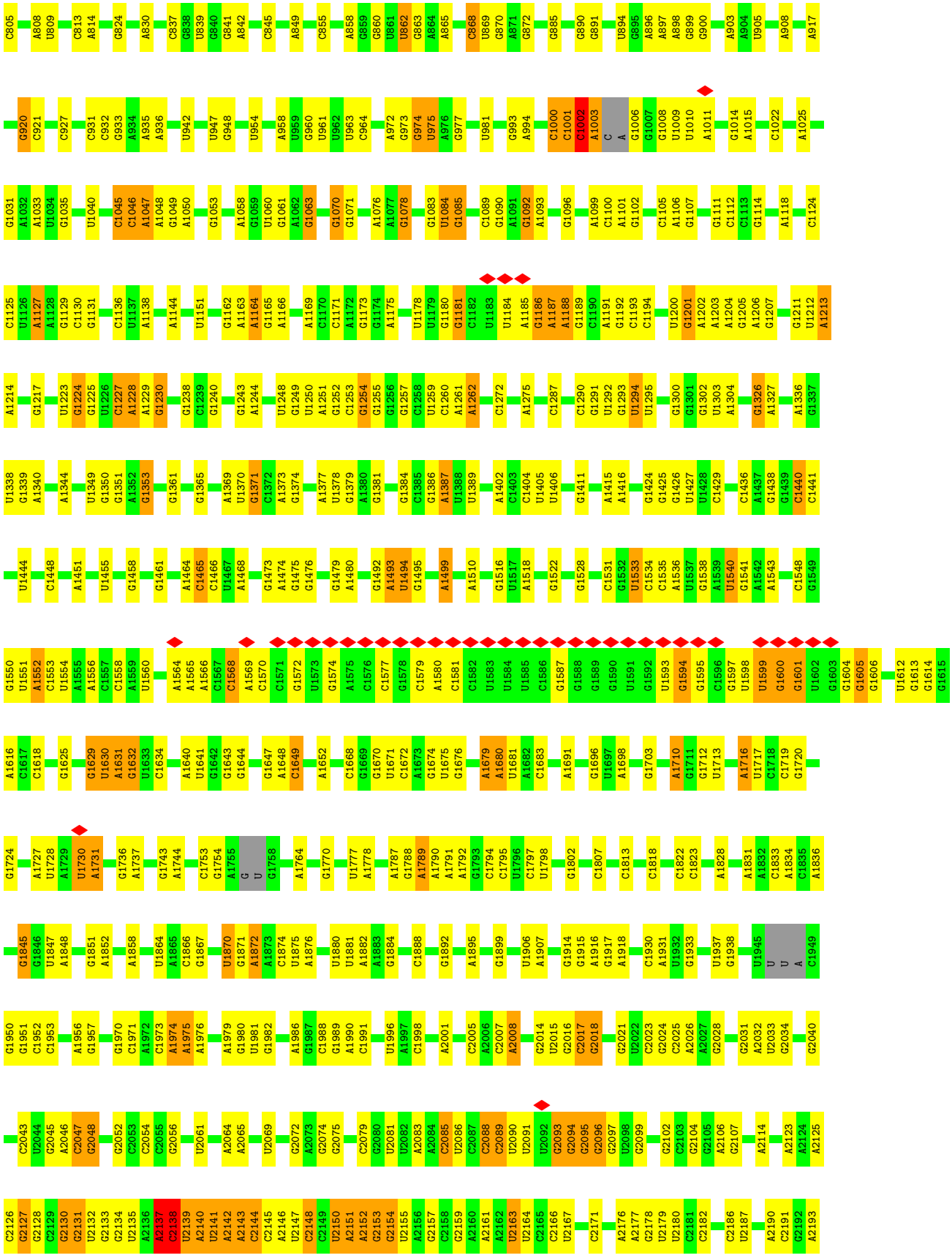
Chain 8:

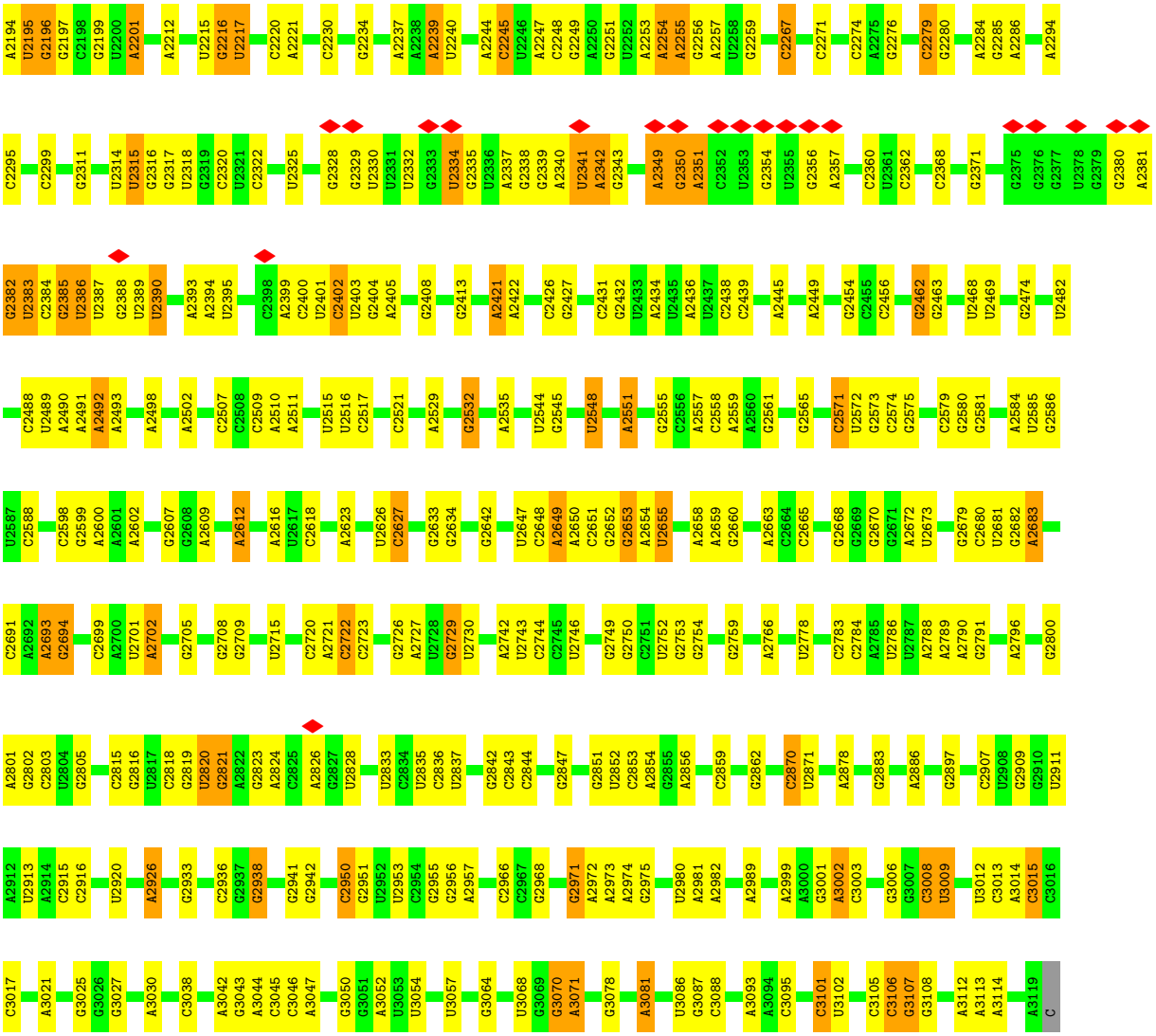


• Molecule 9: 23S rRNA

Chain A:



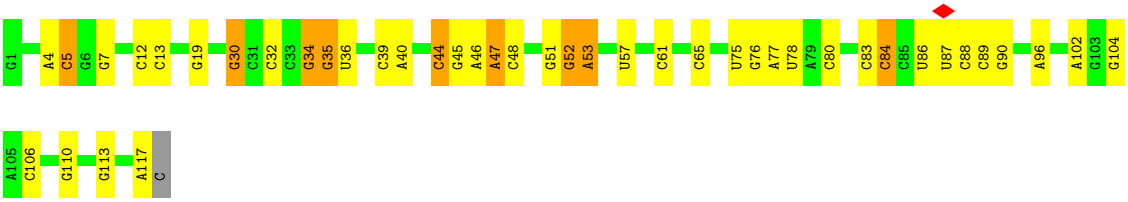




• Molecule 10: 5S rRNA

Chain B:

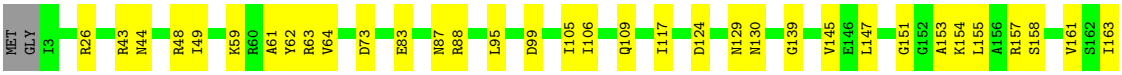


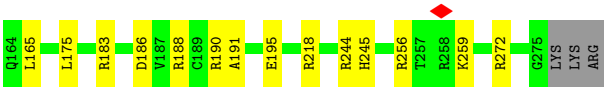


• Molecule 11: Large ribosomal subunit protein uL2

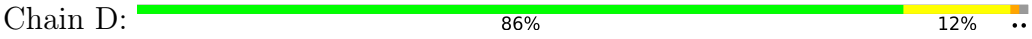
Chain C:







• Molecule 12: Large ribosomal subunit protein uL3

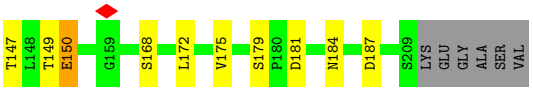




• Molecule 13: Large ribosomal subunit protein uL4



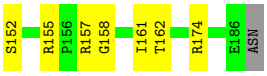




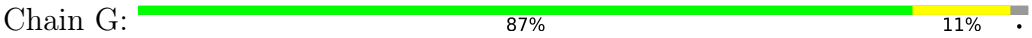
• Molecule 14: Large ribosomal subunit protein uL5





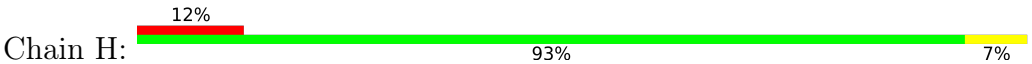


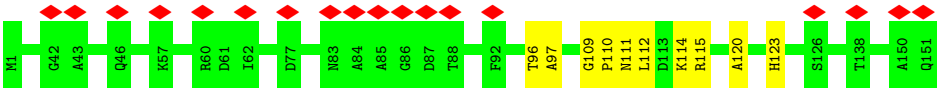
• Molecule 15: Large ribosomal subunit protein uL6





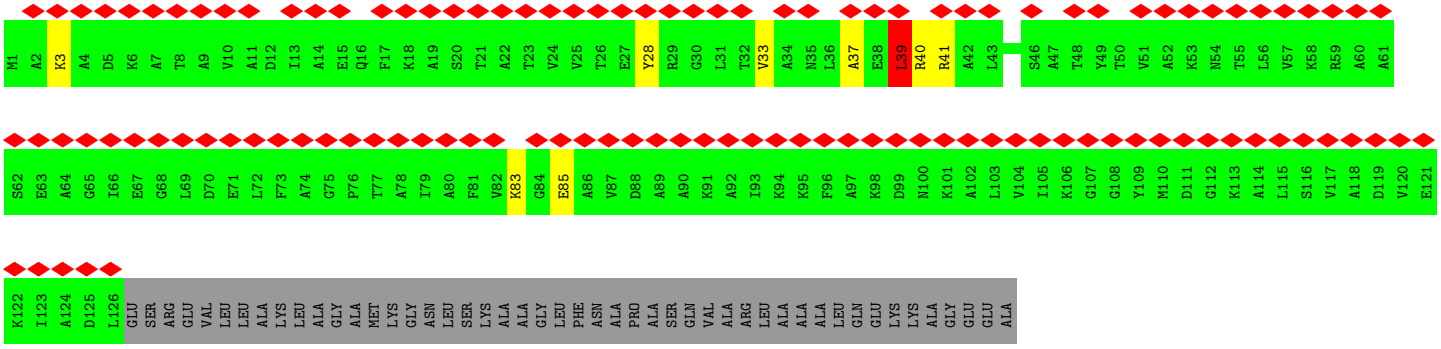
• Molecule 16: 50S ribosomal protein L9





• Molecule 17: Large ribosomal subunit protein uL10

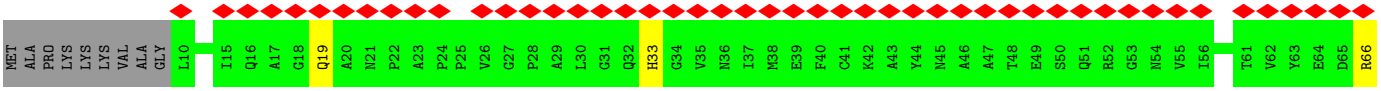


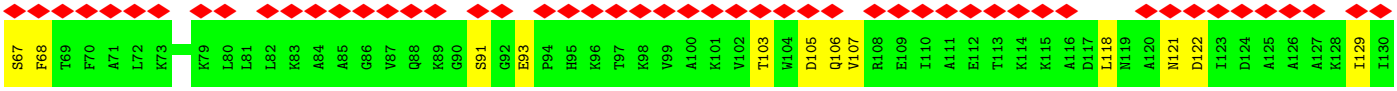


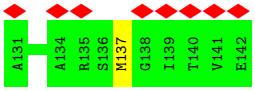
• Molecule 18: Large ribosomal subunit protein uL11

Chain J:



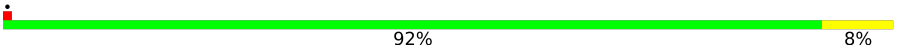


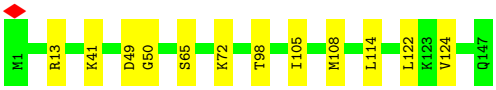




• Molecule 19: Large ribosomal subunit protein uL13

Chain K:

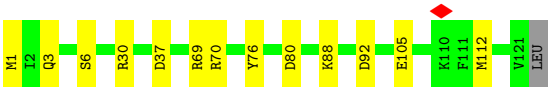




• Molecule 20: Large ribosomal subunit protein uL14

Chain L:

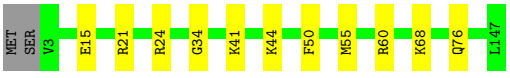




• Molecule 21: Large ribosomal subunit protein uL15

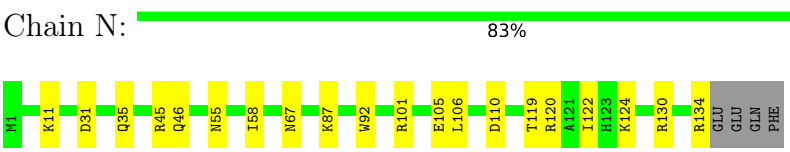
Chain M:





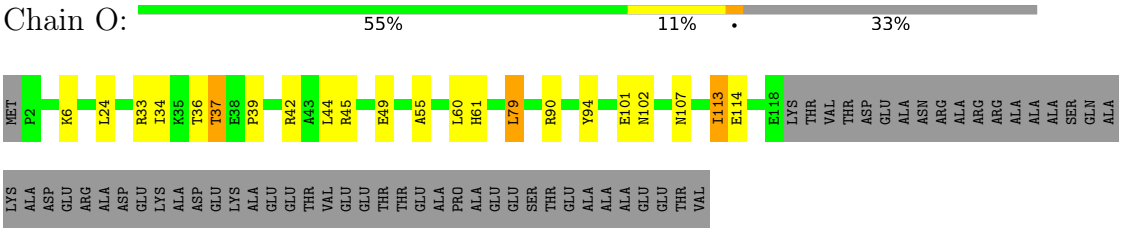
• Molecule 22: Large ribosomal subunit protein uL16

Chain N:



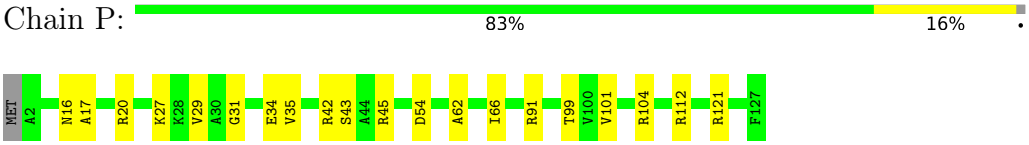
• Molecule 23: Large ribosomal subunit protein bL17

Chain O:



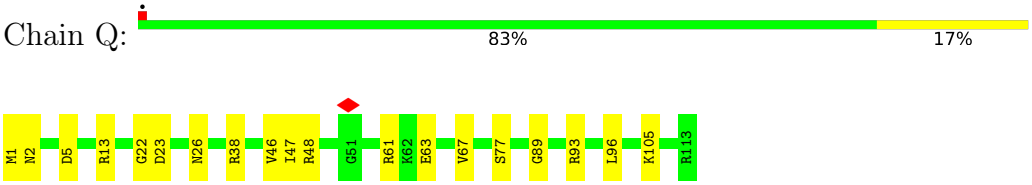
• Molecule 24: Large ribosomal subunit protein uL18

Chain P:



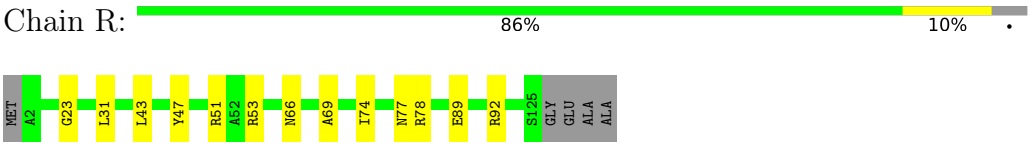
• Molecule 25: Large ribosomal subunit protein bL19

Chain Q:



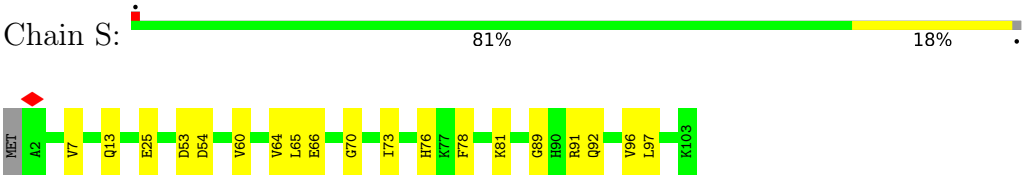
• Molecule 26: Large ribosomal subunit protein bL20

Chain R:



• Molecule 27: Large ribosomal subunit protein bL21

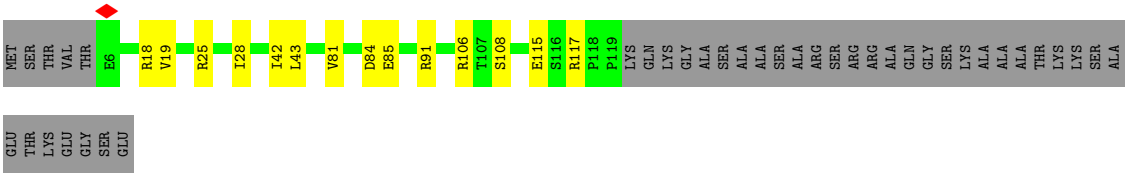
Chain S:



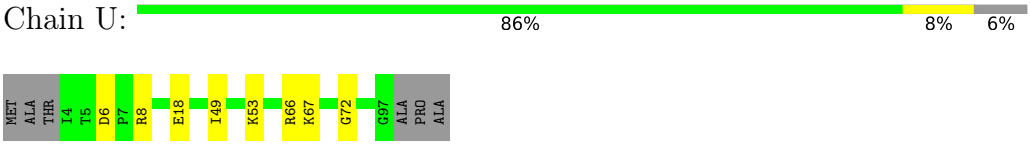
• Molecule 28: Large ribosomal subunit protein uL22

Chain T:

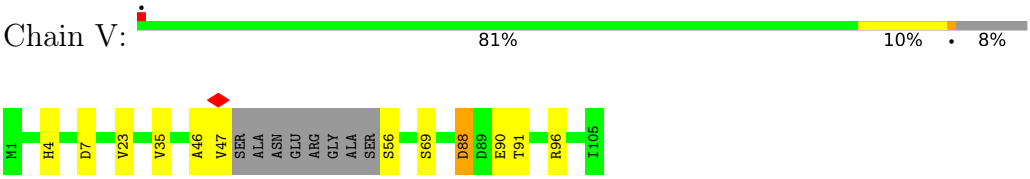




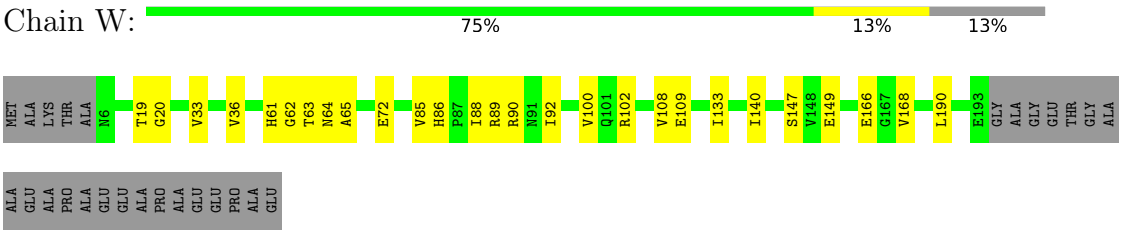
• Molecule 29: Large ribosomal subunit protein uL23



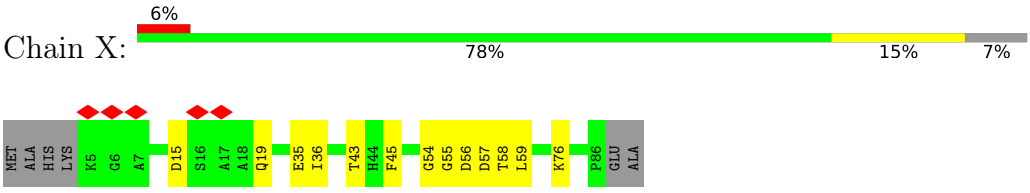
• Molecule 30: Large ribosomal subunit protein uL24



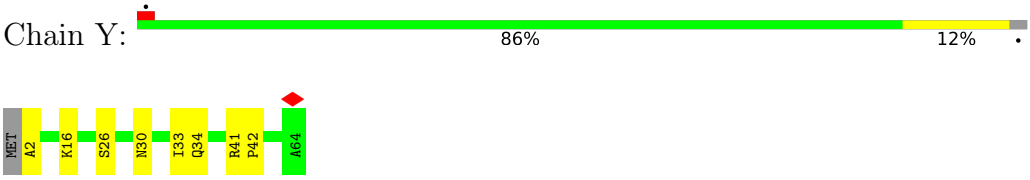
• Molecule 31: Large ribosomal subunit protein bL25



• Molecule 32: Large ribosomal subunit protein bL27



• Molecule 33: Large ribosomal subunit protein bL28



• Molecule 34: Large ribosomal subunit protein uL29

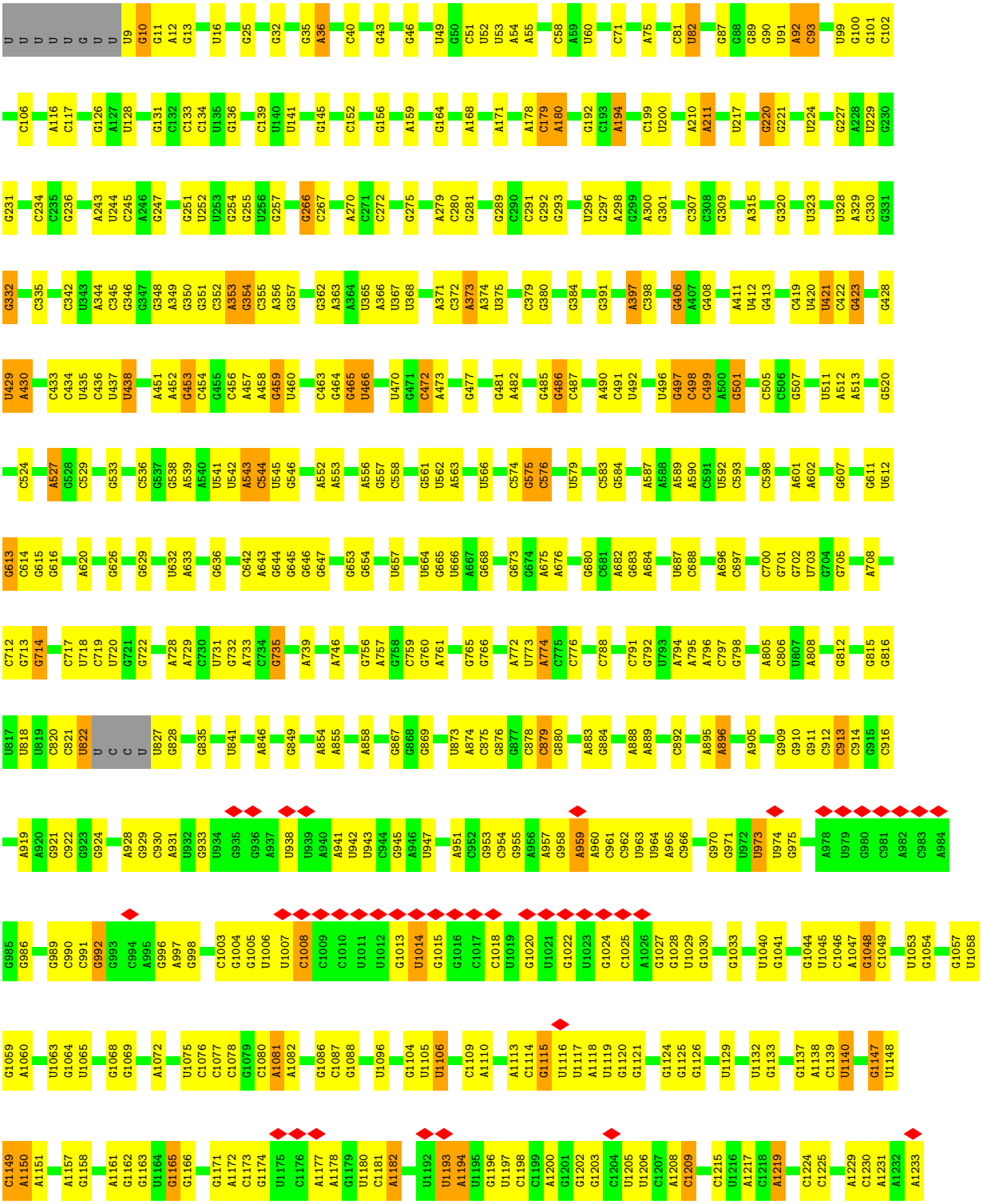


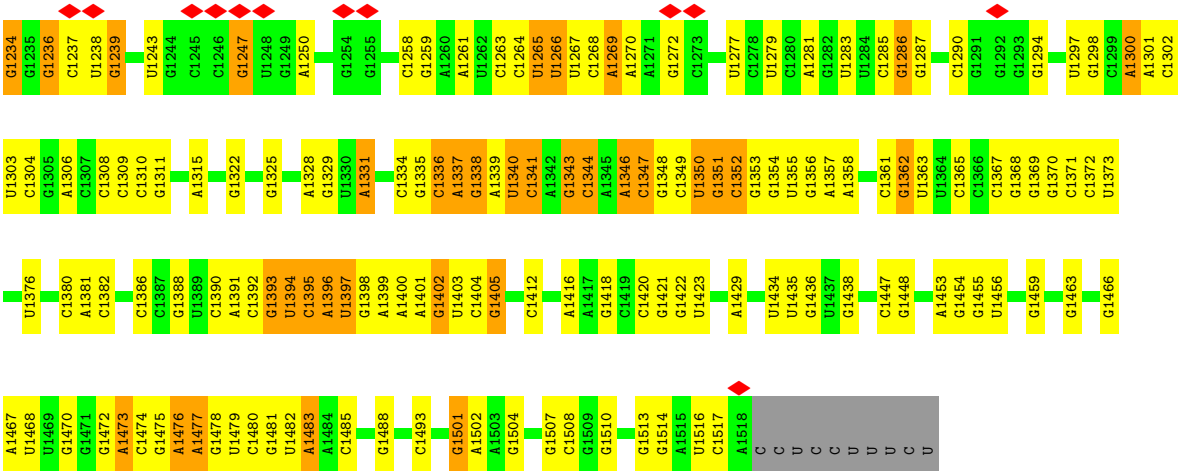


• Molecule 35: 16S rRNA

Chain a:



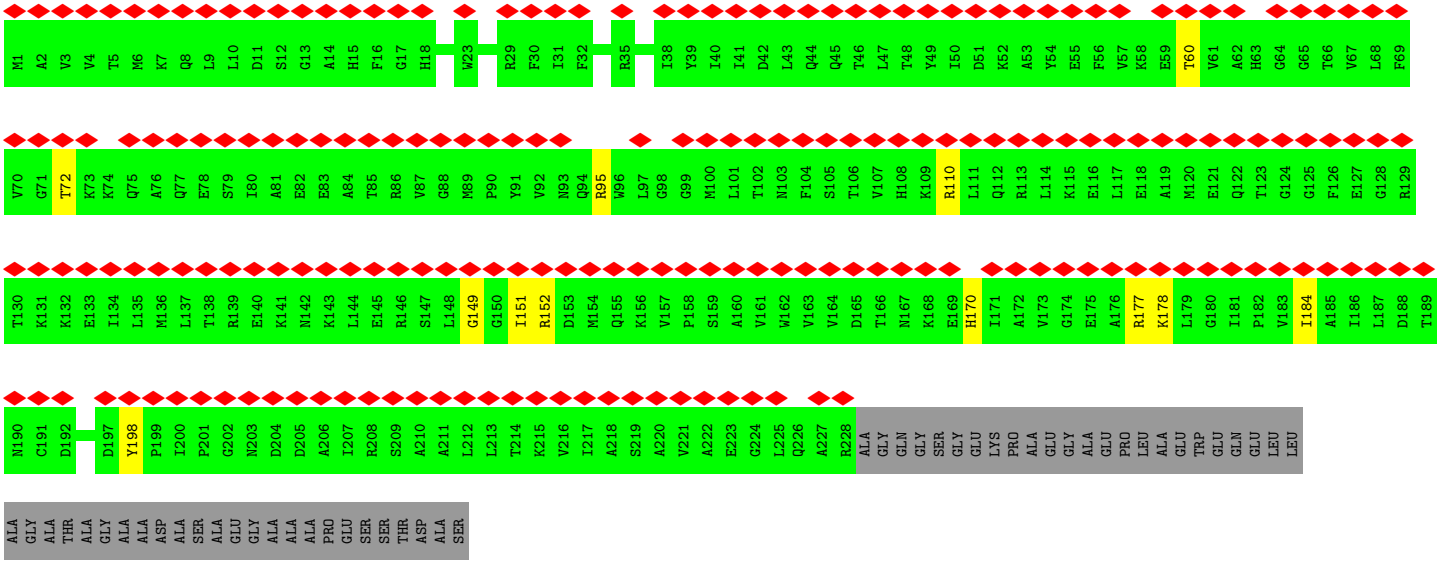




• Molecule 36: Small ribosomal subunit protein uS2

Chain b:

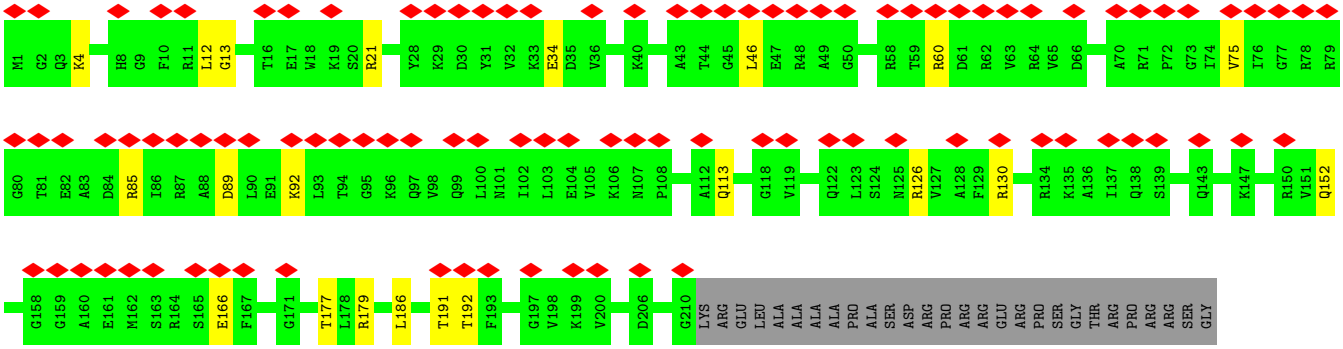




• Molecule 37: Small ribosomal subunit protein uS3

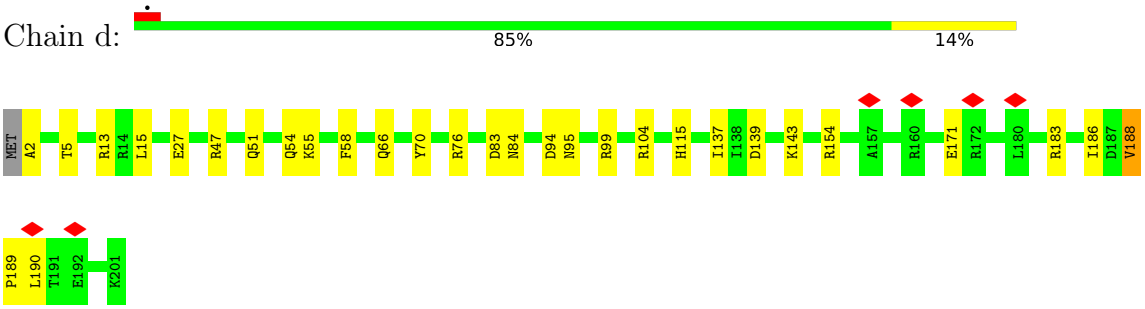
Chain c:



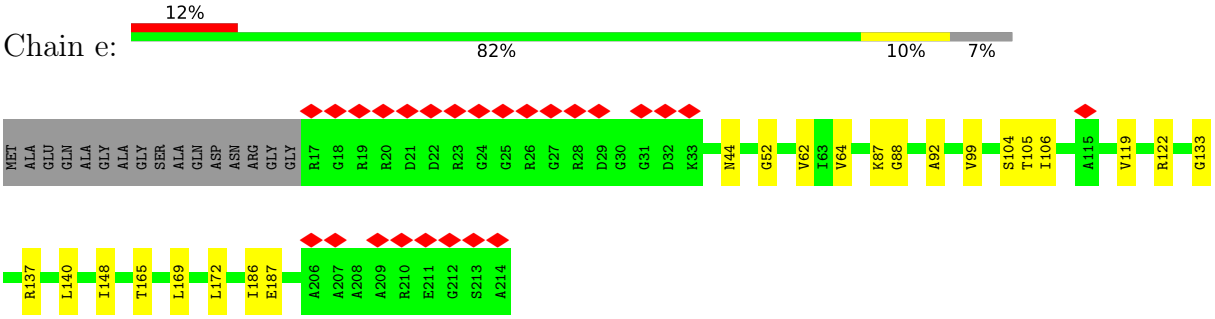




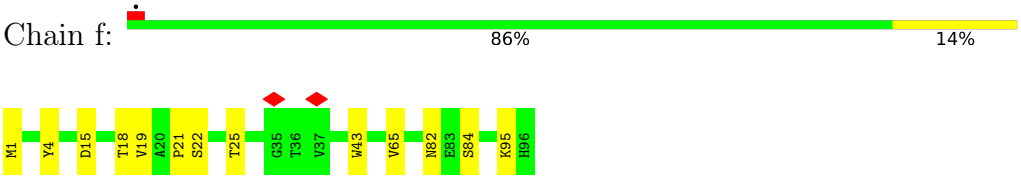
• Molecule 38: Small ribosomal subunit protein uS4



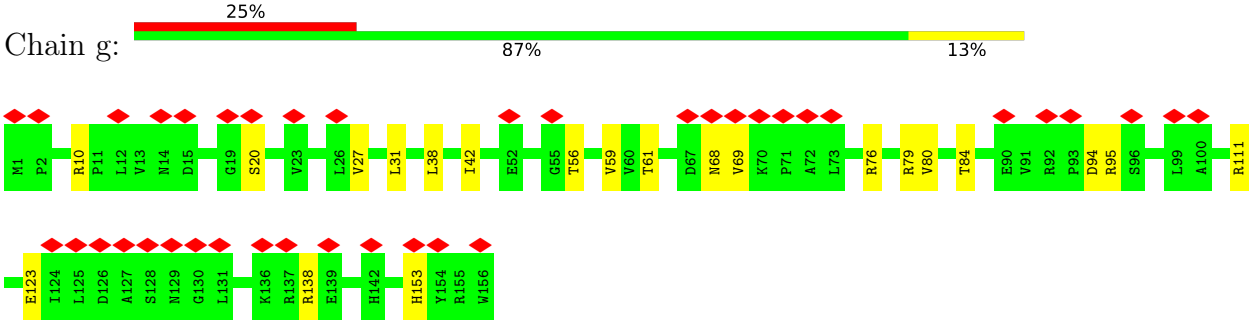
• Molecule 39: Small ribosomal subunit protein uS5



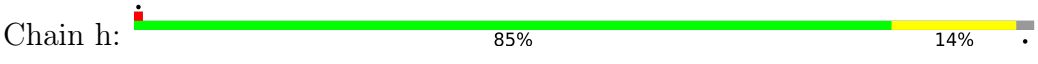
• Molecule 40: Small ribosomal subunit protein bS6

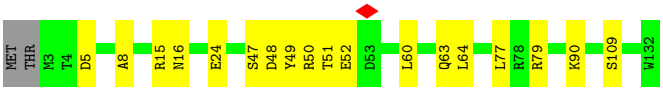


• Molecule 41: Small ribosomal subunit protein uS7



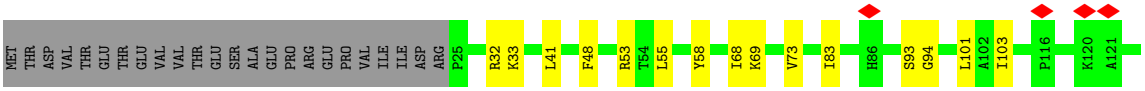
• Molecule 42: Small ribosomal subunit protein uS8

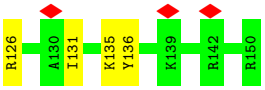




• Molecule 43: Small ribosomal subunit protein uS9

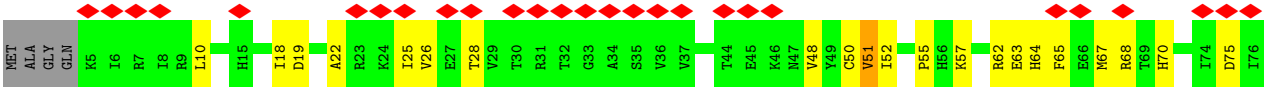


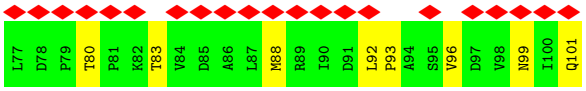




• Molecule 44: Small ribosomal subunit protein uS10

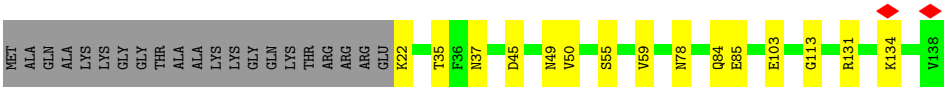




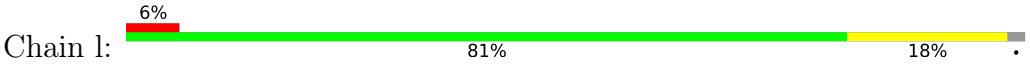


• Molecule 45: Small ribosomal subunit protein uS11



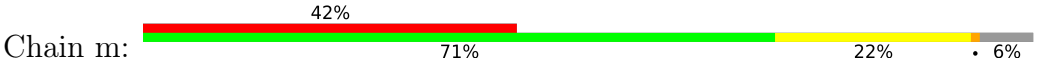


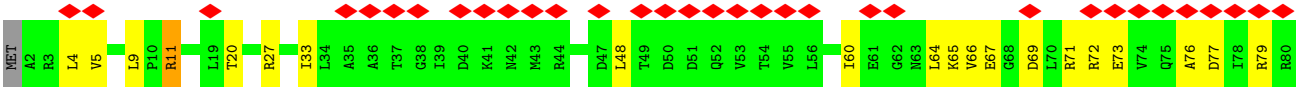
• Molecule 46: Small ribosomal subunit protein uS12

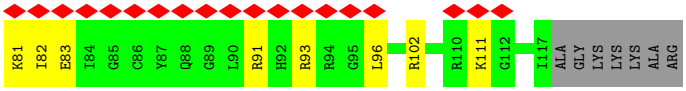




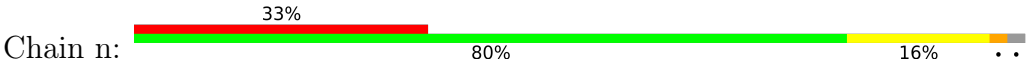
• Molecule 47: Small ribosomal subunit protein uS13



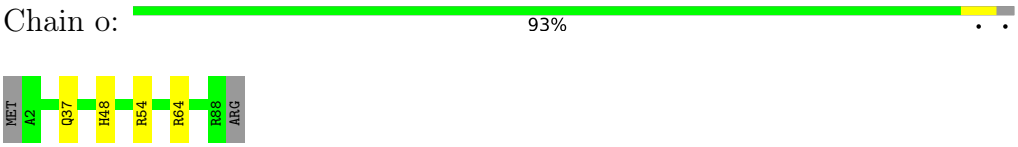




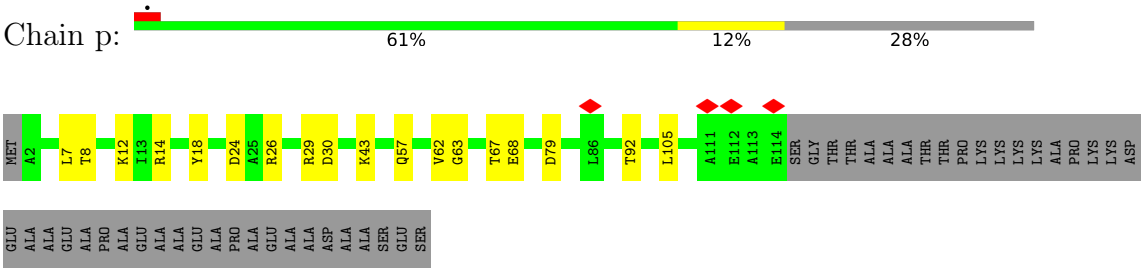
• Molecule 48: Small ribosomal subunit protein uS14B



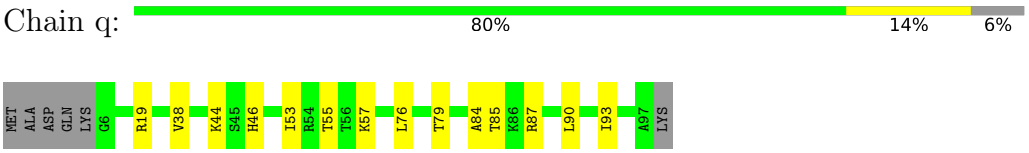
• Molecule 49: Small ribosomal subunit protein uS15



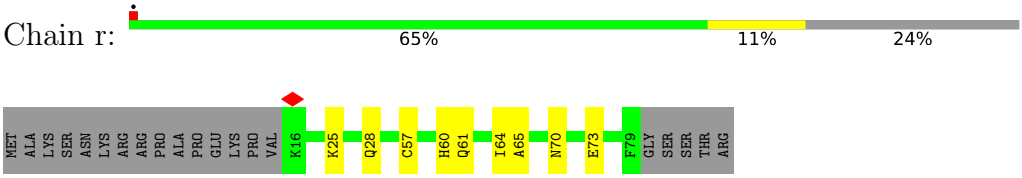
• Molecule 50: Small ribosomal subunit protein bS16



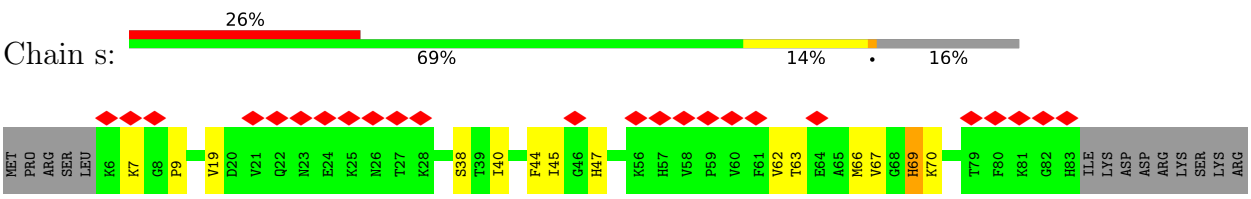
• Molecule 51: Small ribosomal subunit protein uS17



• Molecule 52: Small ribosomal subunit protein bS18B

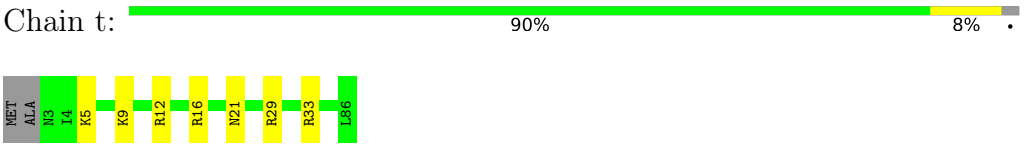


• Molecule 53: Small ribosomal subunit protein uS19

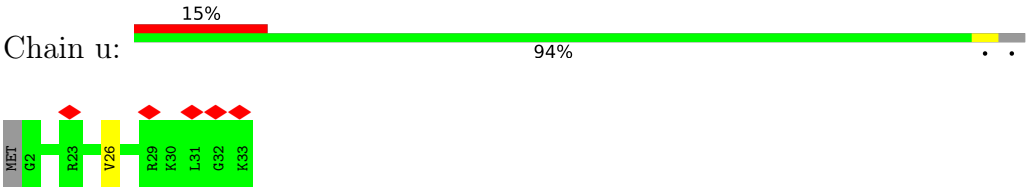




• Molecule 54: Small ribosomal subunit protein bS20



• Molecule 55: Conserved domain protein



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	227969	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	52.51	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.059	Depositor
Minimum map value	-0.026	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	427.6, 427.6, 427.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.069, 1.069, 1.069	Depositor

5 Model quality

5.1 Standard geometry

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

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	1	0.12	0/486	0.28	0/651
2	2	0.16	0/520	0.31	0/698
3	3	0.10	0/427	0.24	0/572
4	4	0.11	0/424	0.29	0/567
5	5	0.13	0/375	0.33	0/493
6	6	0.10	0/507	0.31	0/672
7	7	0.16	0/302	0.38	0/401
8	8	0.11	0/191	0.27	0/247
9	A	0.10	3/74597 (0.0%)	0.27	22/116386 (0.0%)
10	B	0.06	0/2797	0.17	0/4357
11	C	0.10	0/2140	0.27	0/2879
12	D	0.09	0/1609	0.23	0/2165
13	E	0.10	0/1576	0.27	0/2132
14	F	0.12	0/1459	0.34	0/1962
15	G	0.10	0/1369	0.22	0/1848
16	H	0.11	0/1027	0.24	0/1398
17	I	0.12	0/925	0.27	0/1246
18	J	0.10	0/1006	0.23	0/1364
19	K	0.10	0/1154	0.22	0/1565
20	L	0.11	0/938	0.27	0/1257
21	M	0.08	0/1091	0.20	0/1457
22	N	0.12	0/1094	0.27	0/1474
23	O	0.09	0/936	0.26	0/1256
24	P	0.10	0/966	0.22	0/1298
25	Q	0.11	0/921	0.24	0/1236
26	R	0.11	0/1000	0.23	0/1341
27	S	0.07	0/778	0.19	0/1048
28	T	0.10	0/887	0.28	0/1204
29	U	0.09	0/749	0.24	0/1006
30	V	0.12	0/737	0.26	0/987
31	W	0.10	0/1422	0.24	0/1941
32	X	0.12	0/613	0.32	0/821

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Y	0.10	0/478	0.27	0/641
34	Z	0.10	0/530	0.26	0/708
35	a	0.13	3/36201 (0.0%)	0.31	11/56488 (0.0%)
36	b	0.09	0/1822	0.21	0/2457
37	c	0.11	0/1696	0.30	0/2276
38	d	0.10	0/1672	0.24	0/2251
39	e	0.09	0/1449	0.27	0/1949
40	f	0.11	0/782	0.23	0/1059
41	g	0.11	0/1260	0.28	0/1701
42	h	0.09	0/1018	0.24	0/1375
43	i	0.11	0/1012	0.32	0/1362
44	j	0.14	0/789	0.38	0/1069
45	k	0.08	0/889	0.24	0/1201
46	l	0.11	0/969	0.33	0/1294
47	m	0.15	0/942	0.34	0/1260
48	n	0.09	0/488	0.24	0/650
49	o	0.09	0/718	0.27	0/963
50	p	0.10	0/908	0.24	0/1226
51	q	0.09	0/741	0.25	0/993
52	r	0.10	0/517	0.28	0/691
53	s	0.13	0/647	0.34	0/871
54	t	0.10	0/658	0.26	0/875
55	u	0.12	0/280	0.29	0/359
All	All	0.11	6/161489 (0.0%)	0.28	33/241648 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2137	A	O3'-P	-10.55	1.45	1.61
35	a	1171	G	C6-O6	-8.58	1.06	1.24
35	a	1236	G	N9-C4	8.06	1.54	1.38
9	A	1224	G	N9-C4	7.85	1.53	1.38
35	a	1236	G	N9-C8	-7.67	1.22	1.37
9	A	1224	G	N9-C8	-7.65	1.22	1.37

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	1224	G	N7-C8-N9	-26.15	34.66	113.10
35	a	1236	G	N7-C8-N9	-26.00	35.10	113.10
9	A	1224	G	C4-C5-N7	-22.59	43.02	110.80
35	a	1236	G	C4-C5-N7	-22.58	43.05	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
35	a	1171	G	N1-C6-O6	-22.45	52.53	119.90
35	a	1171	G	C5-C6-O6	-20.33	67.60	128.60
35	a	1236	G	C8-N9-C4	-19.19	48.83	106.40
9	A	1224	G	C8-N9-C4	-19.01	49.36	106.40
9	A	2138	C	P-O3'-C3'	17.05	145.78	120.20
9	A	2137	A	O3'-P-O5'	14.06	125.09	104.00
9	A	2137	A	P-O3'-C3'	13.90	141.05	120.20
9	A	1224	G	OP1-P-OP2	-13.24	79.89	119.60
9	A	1224	G	O5'-P-OP1	-11.22	74.33	108.00
9	A	1223	U	OP2-P-O3'	-10.65	76.05	108.00
9	A	1224	G	C4-N9-C1'	8.95	153.36	126.50
9	A	1223	U	OP1-P-O3'	8.92	134.76	108.00
35	a	1331	A	OP2-P-O3'	-8.81	81.58	108.00
35	a	1331	A	OP1-P-O3'	-8.70	81.91	108.00
35	a	1236	G	C4-N9-C1'	8.70	152.59	126.50
35	a	1236	G	C6-C5-N7	8.66	156.37	130.40
9	A	2137	A	OP1-P-O3'	-8.65	82.05	108.00
9	A	1224	G	O5'-P-OP2	8.65	133.95	108.00
9	A	1224	G	C6-C5-N7	8.59	156.16	130.40
9	A	2138	C	OP1-P-O3'	8.06	132.18	108.00
35	a	1236	G	C8-N9-C1'	-7.75	103.77	127.00
9	A	1224	G	C8-N9-C1'	-7.67	104.00	127.00
9	A	2138	C	O3'-P-O5'	-6.52	94.21	104.00
9	A	1224	G	C5-N7-C8	6.35	123.36	104.30
9	A	1002	C	C4'-C3'-O3'	6.23	118.75	109.40
35	a	1236	G	C5-N7-C8	6.19	122.87	104.30
9	A	2138	C	OP2-P-O3'	-5.99	90.04	108.00
9	A	1223	U	O3'-P-O5'	-5.29	96.07	104.00
9	A	1002	C	C2'-C3'-O3'	5.05	117.08	109.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	483	0	513	4	0
2	2	510	0	501	18	0
3	3	423	0	463	3	0
4	4	416	0	422	8	0
5	5	372	0	406	7	0
6	6	502	0	541	8	0
7	7	298	0	321	4	0
8	8	189	0	205	7	0
9	A	66623	0	33523	700	0
10	B	2501	0	1273	29	0
11	C	2097	0	2149	38	0
12	D	1587	0	1630	23	0
13	E	1553	0	1587	34	0
14	F	1437	0	1470	40	0
15	G	1348	0	1399	19	0
16	H	1018	0	988	7	0
17	I	918	0	959	8	0
18	J	990	0	1021	10	0
19	K	1127	0	1154	8	0
20	L	930	0	989	11	0
21	M	1078	0	1151	11	0
22	N	1068	0	1107	16	0
23	O	919	0	959	16	0
24	P	956	0	991	15	0
25	Q	907	0	938	13	0
26	R	988	0	1038	11	0
27	S	768	0	820	15	0
28	T	873	0	909	11	0
29	U	739	0	785	6	0
30	V	731	0	782	8	0
31	W	1407	0	1423	20	0
32	X	604	0	622	9	0
33	Y	470	0	484	6	0
34	Z	527	0	538	6	0
35	a	32341	0	16271	418	0
36	b	1793	0	1839	9	0
37	c	1672	0	1722	15	0
38	d	1641	0	1668	25	0
39	e	1433	0	1490	12	0
40	f	771	0	797	8	0
41	g	1240	0	1293	14	0
42	h	1003	0	1039	12	0
43	i	994	0	1050	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	j	775	0	808	31	0
45	k	871	0	885	10	0
46	l	958	0	1045	19	0
47	m	935	0	986	35	0
48	n	477	0	503	9	0
49	o	709	0	747	3	0
50	p	891	0	935	13	0
51	q	730	0	774	9	0
52	r	512	0	543	5	0
53	s	630	0	640	21	0
54	t	655	0	707	7	0
55	u	280	0	342	1	0
56	2	1	0	0	0	0
56	A	76	0	0	0	0
56	C	1	0	0	0	0
56	D	1	0	0	0	0
56	a	28	0	0	0	0
All	All	148775	0	100145	1525	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 (1525) 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)
9:A:1171:C:O2	9:A:1224:G:N2	1.85	1.10
9:A:592:A:HO2'	9:A:596:C:HO2'	1.14	0.95
35:a:1139:C:O2	35:a:1162:G:N2	2.00	0.94
35:a:1335:G:N2	44:j:63:GLU:O	2.01	0.94
9:A:1558:C:O2	9:A:1613:G:N2	2.02	0.93
35:a:1352:C:O2'	44:j:65:PHE:N	2.02	0.92
9:A:2482:U:O2'	9:A:2651:C:OP2	1.87	0.92
9:A:2322:C:O2	9:A:2413:G:N2	2.03	0.91
35:a:139:C:O2	35:a:221:G:N2	2.04	0.91
35:a:485:G:O2'	35:a:486:G:OP1	1.87	0.91
35:a:990:C:O2	35:a:1005:G:N2	2.04	0.91
35:a:1390:C:H2'	35:a:1391:A:C8	2.04	0.91
35:a:991:C:O2	35:a:1004:G:N2	2.03	0.90
35:a:913:C:O2	35:a:1369:G:N2	2.05	0.90
35:a:1007:U:O2'	35:a:1008:C:OP2	1.90	0.90
9:A:1001:C:O2	9:A:1006:G:N2	2.05	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2144:C:H5”	35:a:1501:G:C6	2.07	0.89
9:A:369:G:N2	9:A:433:C:O2	2.05	0.89
9:A:973:G:HO2’	9:A:2492:A:HO2’	1.05	0.89
9:A:2907:C:O2	20:L:76:TYR:OH	1.89	0.89
9:A:3015:C:O2	9:A:3027:G:N2	2.05	0.89
9:A:2138:C:H5	35:a:1392:C:HO2’	0.95	0.89
35:a:1290:C:O2	35:a:1311:G:N2	2.04	0.89
35:a:766:G:N2	35:a:776:C:O2	2.05	0.88
9:A:1528:G:N2	9:A:1807:C:O2	2.07	0.88
35:a:524:C:OP1	38:d:54:GLN:NE2	2.07	0.88
9:A:1092:G:OP1	9:A:1302:G:O2’	1.92	0.87
35:a:1027:G:HO2’	35:a:1196:G:HO2’	1.22	0.87
9:A:332:C:O2	9:A:349:G:N2	2.07	0.87
9:A:255:A:O2’	9:A:472:C:OP2	1.94	0.86
35:a:291:C:O2	35:a:309:G:N2	2.07	0.86
35:a:454:C:O2	35:a:459:G:N2	2.08	0.86
9:A:2085:C:O2	9:A:2097:G:N2	2.07	0.86
9:A:3017:C:O2	9:A:3025:G:N2	2.09	0.86
9:A:1461:G:N2	9:A:1818:C:O2	2.08	0.86
9:A:2031:G:OP2	9:A:2032:A:O2’	1.94	0.86
9:A:1201:G:N2	9:A:1204:A:OP2	2.08	0.86
35:a:583:C:O2	35:a:615:G:N2	2.09	0.85
9:A:842:A:OP2	9:A:1652:A:O2’	1.94	0.85
9:A:601:A:N3	9:A:673:C:O2’	2.08	0.84
9:A:1880:U:O2’	9:A:2911:U:OP1	1.95	0.84
9:A:2580:G:N2	9:A:2586:G:O6	2.10	0.84
35:a:1157:A:O2’	35:a:1158:G:O4’	1.94	0.84
35:a:254:G:N2	35:a:272:C:O2	2.11	0.84
35:a:676:A:N3	35:a:766:G:O2’	2.11	0.83
35:a:911:G:N2	35:a:1371:C:O2	2.09	0.83
35:a:1386:C:O2	35:a:1483:A:N6	2.10	0.83
9:A:2043:C:O2’	9:A:2195:U:OP2	1.95	0.83
9:A:3052:A:OP1	12:D:60:ARG:NH2	2.11	0.83
35:a:9:U:O2’	35:a:10:G:OP1	1.97	0.83
35:a:820:C:O2	35:a:828:G:N2	2.12	0.83
35:a:1048:G:N2	35:a:1087:C:O2	2.11	0.83
35:a:1337:A:O2’	35:a:1338:G:O5’	1.96	0.83
9:A:2663:A:O2’	9:A:2824:A:OP1	1.96	0.83
9:A:276:G:N2	9:A:310:C:O2	2.11	0.83
9:A:1974:A:O2’	9:A:1975:A:OP1	1.97	0.83
9:A:2749:G:HO2’	9:A:2966:C:HO2’	1.24	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:361:A:O2'	9:A:362:A:O4'	1.97	0.82
14:F:108:ASP:OD1	14:F:109:ARG:N	2.11	0.82
9:A:159:A:N3	9:A:2431:C:O2'	2.12	0.82
9:A:661:U:O2'	9:A:1063:G:N2	2.11	0.82
35:a:1341:C:O2'	35:a:1343:G:N7	2.13	0.82
35:a:1412:C:O2	35:a:1455:G:N2	2.13	0.82
9:A:3086:U:OP2	9:A:3087:G:O2'	1.98	0.82
9:A:1670:G:N2	9:A:1683:C:O2	2.13	0.81
9:A:1971:C:N4	9:A:2941:G:O4'	2.13	0.81
35:a:543:A:O2'	35:a:546:G:O2'	1.93	0.81
9:A:2279:C:N4	9:A:2723:C:O2	2.13	0.81
9:A:1466:C:HO2'	9:A:1791:A:HO2'	1.28	0.81
35:a:538:G:OP2	35:a:539:A:O2'	1.98	0.81
9:A:660:U:O2	9:A:2254:A:N6	2.13	0.81
9:A:2818:C:O2	9:A:2823:G:N2	2.11	0.81
9:A:1730:U:O2'	9:A:1731:A:OP2	1.97	0.81
9:A:1339:G:O2'	9:A:1340:A:O4'	1.98	0.81
9:A:3012:U:O2'	9:A:3030:A:N3	2.14	0.81
37:c:21:ARG:NH1	48:n:52:GLU:O	2.14	0.81
4:4:25:THR:OG1	9:A:2510:A:N6	2.12	0.81
35:a:1270:A:O2'	35:a:1334:C:O2'	1.98	0.81
9:A:234:U:O4	9:A:263:G:N2	2.14	0.81
9:A:1996:U:OP2	9:A:2001:A:N6	2.13	0.81
9:A:1466:C:O2'	9:A:1791:A:O2'	1.97	0.80
35:a:1310:C:OP1	47:m:27:ARG:NH1	2.13	0.80
10:B:83:C:N4	10:B:84:C:N4	2.28	0.80
35:a:566:U:O2	35:a:735:G:O6	1.98	0.80
35:a:1349:C:O2'	35:a:1350:U:OP1	1.97	0.80
9:A:114:G:OP2	9:A:116:A:O2'	1.98	0.80
35:a:806:C:O2	42:h:16:ASN:ND2	2.14	0.80
35:a:1421:G:N2	35:a:1447:C:O2	2.13	0.80
9:A:2166:C:OP2	9:A:2167:U:O2'	1.97	0.80
9:A:2079:C:O2	9:A:2104:G:N2	2.15	0.80
35:a:961:C:O2'	35:a:1200:A:OP2	1.99	0.80
9:A:3078:G:N2	9:A:3081:A:OP2	2.15	0.79
35:a:558:C:O2'	35:a:708:A:N3	2.14	0.79
35:a:1087:C:O2'	35:a:1172:A:O2'	1.97	0.79
35:a:1063:U:O2'	35:a:1082:A:OP2	2.00	0.79
35:a:1149:C:O2'	35:a:1150:A:OP2	1.99	0.79
9:A:1870:U:O2'	9:A:1872:A:OP2	2.00	0.79
35:a:705:G:OP1	35:a:835:G:N2	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2047:C:O2'	9:A:2048:G:O5'	1.98	0.79
38:d:188:VAL:HG22	38:d:189:PRO:HD2	1.65	0.79
9:A:63:C:O2	9:A:85:G:N2	2.15	0.79
9:A:1127:A:N3	9:A:1272:C:O2'	2.16	0.79
9:A:1165:G:O2'	9:A:1228:A:N6	2.16	0.79
35:a:905:A:O2'	35:a:1382:C:OP2	1.99	0.79
9:A:664:A:OP2	27:S:81:LYS:NZ	2.15	0.79
35:a:1087:C:HO2'	35:a:1172:A:HO2'	1.18	0.79
9:A:1112:C:OP1	26:R:53:ARG:NH2	2.16	0.78
9:A:1441:C:O2'	9:A:2234:G:O2'	2.00	0.78
35:a:10:G:O2'	35:a:298:A:O4'	2.01	0.78
9:A:2386:U:OP1	9:A:2393:A:O2'	2.01	0.78
9:A:239:U:HO2'	9:A:716:G:HO2'	1.23	0.78
9:A:63:C:N3	9:A:85:G:N1	2.32	0.78
9:A:218:A:N3	9:A:234:U:O2'	2.16	0.78
9:A:15:C:N4	9:A:16:G:O6	2.16	0.78
9:A:2088:C:O2'	9:A:2089:C:OP1	2.02	0.78
9:A:2216:G:N2	9:A:2220:C:O2'	2.17	0.78
35:a:849:G:O2'	35:a:855:A:N1	2.16	0.77
35:a:970:G:N2	35:a:1198:C:O2	2.13	0.77
9:A:1915:G:OP2	9:A:1916:A:O2'	2.00	0.77
35:a:989:G:O6	35:a:1006:U:O2	2.01	0.77
35:a:1049:C:O2	35:a:1086:G:N2	2.17	0.77
9:A:1516:G:O2'	9:A:1744:A:OP2	2.01	0.77
35:a:593:C:O2	35:a:607:G:N2	2.18	0.77
9:A:485:U:O2'	9:A:2454:G:N2	2.18	0.77
9:A:1186:G:N2	9:A:1213:A:N3	2.32	0.77
35:a:997:A:O2'	35:a:1200:A:O4'	2.03	0.77
9:A:222:A:O2'	9:A:508:G:N3	2.17	0.77
9:A:1136:C:O2'	9:A:1238:G:N2	2.18	0.77
9:A:244:A:OP1	21:M:68:LYS:NZ	2.18	0.77
9:A:2551:A:N6	9:A:2612:A:C6	2.53	0.77
35:a:912:C:O2	35:a:1370:G:N2	2.14	0.76
35:a:1234:G:O6	35:a:1265:U:O2	2.03	0.76
9:A:693:G:N2	9:A:698:G:O3'	2.18	0.76
35:a:1363:U:O2	35:a:1365:C:N4	2.19	0.76
9:A:2350:G:O2'	9:A:2351:A:OP1	2.03	0.76
35:a:654:G:O6	35:a:696:A:N1	2.18	0.76
9:A:2164:U:O2	9:A:2166:C:N4	2.18	0.76
35:a:991:C:N3	35:a:1004:G:N1	2.33	0.76
42:h:50:ARG:NH1	42:h:52:GLU:OE2	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:293:G:O3'	35:a:590:A:O2'	2.03	0.76
35:a:1388:G:O2'	35:a:1502:A:O2'	2.03	0.76
9:A:1426:G:OP2	9:A:1426:G:N2	2.19	0.76
9:A:2072:G:O2'	9:A:2311:G:O2'	2.04	0.76
35:a:963:U:OP2	35:a:964:U:O2'	2.01	0.76
35:a:1390:C:H2'	35:a:1391:A:H8	1.44	0.76
9:A:1105:C:O2'	9:A:1118:A:N3	2.19	0.76
35:a:102:C:O2'	35:a:379:C:OP1	2.04	0.76
9:A:551:G:N2	9:A:554:A:OP2	2.19	0.75
9:A:610:C:O2	9:A:646:U:O2'	2.03	0.75
20:L:69:ARG:NH2	20:L:105:GLU:OE1	2.20	0.75
35:a:106:C:O2'	50:p:26:ARG:O	2.03	0.75
35:a:335:C:O2'	35:a:1416:A:N3	2.18	0.75
35:a:463:C:OP2	35:a:464:G:O2'	2.03	0.75
9:A:908:A:OP2	9:A:2294:A:O2'	2.04	0.75
9:A:1612:U:O4	9:A:1613:G:O6	2.03	0.75
9:A:1884:G:HO2'	20:L:6:SER:HG	1.24	0.75
9:A:2163:U:OP1	9:A:2828:U:O2'	2.03	0.75
9:A:1716:A:N3	9:A:1797:C:O2'	2.18	0.75
9:A:2176:A:N3	9:A:2784:C:O2'	2.19	0.75
35:a:990:C:N3	35:a:1005:G:N1	2.35	0.75
2:2:63:LYS:O	53:s:69:HIS:N	2.20	0.75
35:a:957:A:O3'	35:a:1340:U:O2'	2.01	0.75
9:A:1249:G:O6	9:A:2248:C:O2'	2.04	0.74
35:a:1105:U:O2'	35:a:1106:U:O5'	2.04	0.74
9:A:2065:A:C6	35:a:682:A:N6	2.55	0.74
35:a:869:G:N2	35:a:892:C:O2	2.19	0.74
9:A:1914:G:N2	9:A:2201:A:O2'	2.20	0.74
35:a:465:G:O2'	35:a:466:U:O5'	2.06	0.74
35:a:620:A:N3	42:h:109:SER:OG	2.19	0.74
9:A:742:G:O2'	9:A:2575:G:OP1	2.06	0.74
9:A:2852:U:O2'	9:A:3006:G:OP1	2.01	0.74
35:a:1277:U:O2	47:m:11:ARG:NH2	2.19	0.74
9:A:2008:A:N6	9:A:2045:G:O2'	2.20	0.74
9:A:2125:A:H2'	9:A:2126:C:C6	2.22	0.74
10:B:34:G:O2'	10:B:35:G:O5'	2.05	0.74
9:A:993:G:O2'	9:A:1015:A:N6	2.21	0.74
9:A:2140:A:H3'	9:A:2141:U:H6	1.52	0.74
9:A:213:G:HO2'	9:A:215:A:HO2'	1.35	0.74
9:A:592:A:O2'	9:A:596:C:O2'	1.99	0.74
9:A:2847:G:OP1	9:A:3047:A:O2'	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:211:A:N1	35:a:220:G:O2'	2.18	0.74
35:a:971:G:O6	35:a:1197:U:O2	2.04	0.74
52:r:25:LYS:NZ	52:r:28:GLN:OE1	2.21	0.74
9:A:213:G:O2'	9:A:215:A:O2'	2.05	0.74
9:A:1436:C:O2'	28:T:18:ARG:NH1	2.20	0.74
9:A:2015:U:OP2	11:C:272:ARG:NH1	2.20	0.74
9:A:2177:A:O2'	9:A:2783:C:O2	2.05	0.73
14:F:142:GLN:NE2	14:F:155:ARG:O	2.20	0.73
9:A:417:C:O2	30:V:69:SER:OG	2.03	0.73
9:A:1558:C:N3	9:A:1613:G:N1	2.35	0.73
9:A:2125:A:H2'	9:A:2126:C:H6	1.52	0.73
37:c:60:ARG:NH1	44:j:88:MET:O	2.21	0.73
9:A:723:C:O3'	9:A:743:G:N2	2.21	0.73
9:A:2135:U:H2'	9:A:2142:A:N1	2.03	0.73
35:a:869:G:N1	35:a:892:C:N3	2.36	0.73
51:q:44:LYS:NZ	51:q:55:THR:OG1	2.21	0.73
9:A:623:A:OP1	26:R:53:ARG:NH1	2.20	0.73
9:A:2255:A:N3	9:A:2679:G:O2'	2.21	0.73
35:a:485:G:HO2'	35:a:486:G:P	2.11	0.73
35:a:821:C:N3	35:a:827:U:O4	2.22	0.73
5:5:14:ARG:NH2	9:A:885:G:OP2	2.22	0.73
9:A:1538:G:N2	9:A:1634:C:O2	2.15	0.73
46:l:68:PRO:O	46:l:99:ARG:NH2	2.22	0.73
9:A:284:G:N2	9:A:302:U:O2	2.22	0.72
9:A:2065:A:C5	35:a:682:A:C6	2.77	0.72
31:W:89:ARG:O	31:W:90:ARG:NH2	2.21	0.72
35:a:1078:C:O2	36:b:95:ARG:NH2	2.21	0.72
7:7:31:ARG:NH1	9:A:2753:G:O6	2.22	0.72
35:a:1040:U:O2'	43:i:136:TYR:OH	2.00	0.72
9:A:1163:A:OP1	9:A:1164:A:O2'	2.07	0.72
9:A:1479:G:OP1	33:Y:2:ALA:N	2.23	0.72
9:A:1495:G:O2'	9:A:1789:A:N6	2.22	0.72
35:a:139:C:N3	35:a:221:G:N1	2.37	0.72
4:4:31:ASN:ND2	9:A:2509:C:OP1	2.22	0.72
9:A:249:C:OP2	9:A:2618:C:O2'	2.02	0.72
9:A:2126:C:H1'	11:C:245:HIS:CD2	2.24	0.72
9:A:1000:C:OP2	9:A:1002:C:N4	2.14	0.72
9:A:2544:U:O4	9:A:2557:A:O2'	2.02	0.72
35:a:613:G:O2'	35:a:614:C:O4'	2.02	0.72
35:a:657:U:O2	35:a:757:A:O2'	2.08	0.72
9:A:614:C:N4	9:A:3003:C:OP2	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:974:G:O2'	9:A:975:U:O5'	2.08	0.72
9:A:973:G:OP1	32:X:76:LYS:NZ	2.23	0.71
35:a:320:G:O2'	35:a:1418:G:O2'	2.08	0.71
35:a:544:C:OP2	46:l:12:ARG:NH2	2.23	0.71
9:A:1083:G:O4'	9:A:2491:A:N6	2.23	0.71
9:A:89:A:O2'	9:A:90:C:OP1	2.08	0.71
9:A:824:G:N2	9:A:837:C:O2	2.15	0.71
9:A:1743:G:OP2	9:A:1744:A:O2'	2.07	0.71
9:A:1899:G:O2'	9:A:1979:A:N3	2.18	0.71
9:A:2069:U:O2	9:A:2114:A:N6	2.20	0.71
11:C:73:ASP:OD2	11:C:190:ARG:NH1	2.23	0.71
35:a:728:A:O2'	35:a:729:A:N7	2.22	0.71
35:a:1303:U:OP2	35:a:1304:C:O2'	2.04	0.71
15:G:150:ARG:NE	15:G:163:VAL:O	2.24	0.71
9:A:2699:C:O2'	9:A:2701:U:OP2	2.06	0.71
9:A:2800:G:O2'	9:A:2803:C:OP2	2.08	0.71
9:A:2859:C:O2'	12:D:83:GLU:OE1	2.09	0.71
9:A:963:U:O2	9:A:1050:A:O2'	2.07	0.70
18:J:91:SER:OG	18:J:137:MET:O	2.09	0.70
35:a:1247:G:N2	35:a:1250:A:OP2	2.23	0.70
9:A:1162:G:OP2	17:I:3:LYS:NZ	2.23	0.70
35:a:642:C:OP2	40:f:95:LYS:NZ	2.17	0.70
35:a:371:A:O2'	35:a:373:A:N7	2.23	0.70
50:p:8:THR:OG1	50:p:30:ASP:OD1	2.10	0.70
9:A:2083:A:N6	9:A:2099:G:O2'	2.25	0.70
35:a:958:G:O4'	35:a:1346:A:N6	2.23	0.70
9:A:865:A:OP1	9:A:1833:C:N4	2.23	0.70
35:a:49:U:OP1	35:a:307:C:O2'	2.09	0.70
35:a:194:A:N1	51:q:79:THR:OG1	2.21	0.70
35:a:1395:C:H3'	35:a:1396:A:H8	1.56	0.70
9:A:138:A:O2'	9:A:139:U:O4'	2.09	0.70
9:A:541:G:N2	9:A:546:G:OP2	2.25	0.69
9:A:1612:U:C4	9:A:1613:G:O6	2.45	0.69
9:A:1691:A:N6	9:A:1743:G:O2'	2.25	0.69
41:g:68:ASN:O	41:g:138:ARG:NH1	2.25	0.69
14:F:140:ASN:OD1	47:m:79:ARG:NH1	2.25	0.69
35:a:1096:U:O2	35:a:1165:G:O6	2.08	0.69
10:B:83:C:C4	10:B:84:C:N4	2.60	0.69
21:M:55:MET:O	21:M:60:ARG:NH1	2.25	0.69
35:a:139:C:O2'	35:a:210:A:N1	2.25	0.69
35:a:1208:A:O2'	35:a:1209:C:OP1	2.11	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:498:C:O2	46:l:47:SER:OG	2.09	0.69
35:a:858:A:O5'	42:h:15:ARG:NH1	2.24	0.69
35:a:1396:A:H3'	35:a:1397:U:C6	2.27	0.69
9:A:1188:A:N7	9:A:1214:A:O2'	2.24	0.69
9:A:1379:G:N2	9:A:2240:U:O4	2.25	0.69
9:A:2805:G:N2	9:A:2805:G:OP2	2.21	0.69
35:a:1355:U:OP1	43:i:94:GLY:N	2.26	0.69
48:n:7:VAL:O	48:n:11:ASN:ND2	2.25	0.69
9:A:2085:C:N3	9:A:2097:G:N1	2.40	0.69
35:a:1137:G:O2'	35:a:1161:A:N6	2.26	0.69
9:A:784:G:N2	9:A:785:A:O4'	2.25	0.68
35:a:1420:C:OP1	54:t:29:ARG:NH1	2.26	0.68
9:A:2555:G:O2'	32:X:43:THR:OG1	2.11	0.68
35:a:1132:U:OP1	44:j:70:HIS:ND1	2.26	0.68
9:A:1541:G:N2	9:A:1631:A:H62	1.89	0.68
35:a:1229:A:O2'	43:i:53:ARG:NH1	2.26	0.68
9:A:2017:C:OP1	11:C:259:LYS:NZ	2.26	0.68
28:T:115:GLU:OE2	28:T:117:ARG:NH1	2.27	0.68
35:a:254:G:N1	35:a:272:C:N3	2.39	0.68
35:a:1322:G:OP1	41:g:84:THR:HG21	1.93	0.68
41:g:79:ARG:O	41:g:79:ARG:NH2	2.26	0.68
9:A:619:C:OP1	9:A:653:G:N2	2.27	0.68
9:A:809:U:OP1	11:C:59:LYS:NZ	2.27	0.68
9:A:1194:C:O2'	18:J:93:GLU:OE2	2.11	0.68
9:A:2843:C:O2'	12:D:166:MET:SD	2.47	0.68
35:a:1147:G:N2	35:a:1151:A:OP2	2.16	0.68
9:A:2023:C:O2	11:C:44:ASN:ND2	2.27	0.67
9:A:3050:G:N2	9:A:3057:U:O2'	2.27	0.67
9:A:2883:G:N2	9:A:2886:A:OP2	2.28	0.67
44:j:50:CYS:SG	44:j:64:HIS:NE2	2.68	0.67
9:A:331:U:O4	9:A:332:C:N4	2.27	0.67
35:a:236:G:O3'	51:q:57:LYS:NZ	2.27	0.67
9:A:2818:C:N4	9:A:2819:G:O6	2.28	0.67
35:a:100:G:OP1	54:t:16:ARG:NH1	2.28	0.67
35:a:297:G:N2	35:a:300:A:OP2	2.27	0.67
35:a:815:G:C6	35:a:816:G:O6	2.47	0.67
9:A:191:G:O2'	9:A:792:G:N2	2.26	0.67
9:A:896:A:O2'	9:A:2005:C:O2	2.12	0.67
35:a:593:C:N3	35:a:607:G:N1	2.40	0.67
9:A:1630:U:C2	9:A:1631:A:H1'	2.30	0.67
35:a:888:A:O2'	35:a:889:A:O4'	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:910:G:O2'	36:b:177:ARG:NH2	2.27	0.67
46:l:71:GLY:O	46:l:99:ARG:NH1	2.28	0.67
46:l:79:MET:N	46:l:103:ASP:OD2	2.28	0.67
9:A:1031:G:O2'	10:B:96:A:O2'	2.13	0.67
9:A:921:C:O2	9:A:2668:G:O2'	2.13	0.67
9:A:1033:A:N3	10:B:80:C:O2'	2.28	0.67
9:A:1411:G:OP1	9:A:2933:G:O2'	2.07	0.66
29:U:66:ARG:NH1	29:U:72:GLY:O	2.27	0.66
4:4:8:ARG:NH2	9:A:2509:C:OP2	2.28	0.66
9:A:2017:C:OP2	11:C:183:ARG:NH1	2.29	0.66
9:A:81:A:OP1	30:V:4:HIS:NE2	2.29	0.66
9:A:1930:C:OP2	9:A:1931:A:O2'	2.05	0.66
10:B:48:C:OP2	24:P:42:ARG:NH2	2.28	0.66
35:a:1080:C:OP1	36:b:110:ARG:NH2	2.29	0.66
35:a:420:U:O2'	35:a:423:G:O6	2.12	0.66
35:a:1139:C:N3	35:a:1162:G:N1	2.43	0.66
9:A:935:A:N3	9:A:1060:U:O2'	2.27	0.66
9:A:2151:A:H2'	9:A:2152:A:C8	2.31	0.66
35:a:643:A:H61	35:a:722:G:H22	1.42	0.66
9:A:2975:G:N2	9:A:2975:G:OP1	2.28	0.66
11:C:61:ALA:O	11:C:87:ASN:ND2	2.28	0.66
13:E:138:THR:HG21	13:E:168:SER:OG	1.95	0.66
35:a:227:G:N2	50:p:62:VAL:O	2.27	0.66
6:6:24:ARG:NH1	9:A:2584:A:OP1	2.30	0.65
9:A:190:A:N7	9:A:203:A:N6	2.42	0.65
9:A:613:A:O2'	9:A:2267:C:O2	2.13	0.65
22:N:35:GLN:OE1	22:N:130:ARG:NH1	2.29	0.65
35:a:156:G:N2	35:a:159:A:OP2	2.29	0.65
9:A:1201:G:N2	9:A:1203:A:OP2	2.30	0.65
9:A:1683:C:HO2'	9:A:2926:A:HO2'	1.44	0.65
35:a:315:A:O2'	35:a:330:C:O2'	2.13	0.65
35:a:357:G:OP1	35:a:366:A:O2'	2.13	0.65
35:a:1277:U:O2'	47:m:11:ARG:NH1	2.30	0.65
9:A:2130:G:N7	9:A:2153:G:N2	2.44	0.65
22:N:58:ILE:CD1	22:N:106:LEU:HD21	2.27	0.65
8:8:17:ASN:OD1	9:A:1096:G:N2	2.30	0.65
2:2:62:GLU:HA	53:s:66:MET:HA	1.78	0.65
9:A:522:U:O2	9:A:524:C:N4	2.30	0.65
9:A:1777:U:OP2	9:A:1778:A:O2'	2.08	0.65
35:a:1373:U:O3'	36:b:178:LYS:NZ	2.30	0.65
9:A:281:C:OP1	16:H:114:LYS:NZ	2.21	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:1053:U:OP1	39:e:87:LYS:NZ	2.30	0.65
9:A:2551:A:C6	9:A:2612:A:N1	2.65	0.64
35:a:397:A:N7	35:a:527:A:O2'	2.30	0.64
35:a:1396:A:H3'	35:a:1397:U:H6	1.60	0.64
35:a:1422:G:OP1	54:t:33:ARG:NH2	2.30	0.64
13:E:138:THR:HG21	13:E:168:SER:CB	2.27	0.64
14:F:119:ARG:HB2	47:m:76:ALA:HB3	1.80	0.64
35:a:374:A:N6	35:a:391:G:O4'	2.31	0.64
35:a:718:U:OP1	40:f:4:TYR:OH	2.13	0.64
35:a:973:U:N3	35:a:1193:U:O2'	2.31	0.64
38:d:188:VAL:HG22	38:d:189:PRO:CD	2.27	0.64
13:E:97:ASP:OD2	13:E:99:SER:OG	2.14	0.64
35:a:1388:G:HO2'	35:a:1502:A:HO2'	1.38	0.64
9:A:2126:C:H4'	11:C:244:ARG:O	1.96	0.64
40:f:21:PRO:O	40:f:25:THR:HG23	1.98	0.64
9:A:543:U:O2'	9:A:544:U:OP1	2.15	0.64
9:A:273:A:O2'	9:A:455:C:O2	2.13	0.64
9:A:698:G:N3	9:A:772:U:O2'	2.31	0.64
35:a:766:G:N1	35:a:776:C:N3	2.42	0.64
35:a:1398:G:C5	35:a:1470:G:C6	2.86	0.64
35:a:1472:G:H2'	35:a:1473:A:C8	2.33	0.64
9:A:2916:C:O2	9:A:3068:U:O2'	2.14	0.64
2:2:65:TYR:H	53:s:66:MET:HB3	1.61	0.64
9:A:808:A:O2'	9:A:1468:A:N3	2.30	0.64
9:A:1099:A:N1	9:A:2251:G:O2'	2.28	0.64
10:B:51:G:O2'	10:B:52:G:O4'	2.12	0.64
9:A:2588:C:O3'	32:X:55:GLY:N	2.31	0.64
22:N:58:ILE:HD11	22:N:106:LEU:HD21	1.80	0.64
9:A:323:C:N4	9:A:453:U:O4	2.30	0.63
9:A:2599:G:N2	9:A:2602:A:OP2	2.30	0.63
9:A:2133:G:C4	9:A:2146:A:C2	2.86	0.63
35:a:880:G:N2	35:a:883:A:OP2	2.32	0.63
23:O:34:ILE:HG22	23:O:113:ILE:HG22	1.80	0.63
9:A:461:U:O2'	9:A:511:A:N3	2.25	0.63
3:3:16:ARG:NH2	9:A:1379:G:OP1	2.31	0.63
9:A:1644:G:HO2'	9:A:1719:C:HO2'	1.45	0.63
9:A:2551:A:C6	9:A:2612:A:C6	2.86	0.63
9:A:2721:A:N3	9:A:2722:C:N4	2.46	0.63
9:A:830:A:OP2	49:o:64:ARG:NH2	2.31	0.63
9:A:2065:A:N7	35:a:682:A:C6	2.66	0.63
8:8:8:LYS:NZ	9:A:2253:A:OP2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2815:C:N4	9:A:2816:G:O6	2.31	0.63
35:a:1048:G:OP1	35:a:1370:G:O2'	2.16	0.63
35:a:1047:A:N6	35:a:1088:G:O2'	2.30	0.63
35:a:1395:C:H6	35:a:1395:C:O5'	1.81	0.62
44:j:67:MET:O	44:j:68:ARG:NH2	2.31	0.62
9:A:1063:G:O6	9:A:1090:G:N2	2.32	0.62
13:E:139:LYS:O	13:E:143:THR:HG23	1.98	0.62
38:d:99:ARG:NH2	38:d:186:ILE:O	2.31	0.62
9:A:2548:U:O2'	9:A:2561:G:OP1	2.17	0.62
22:N:67:ASN:ND2	22:N:105:GLU:OE2	2.33	0.62
35:a:583:C:N4	35:a:584:G:O6	2.32	0.62
8:8:13:HIS:ND1	10:B:87:U:OP1	2.32	0.62
9:A:2469:U:O2'	9:A:2660:G:OP2	2.14	0.62
9:A:2648:C:O2	9:A:2653:G:O2'	2.12	0.62
35:a:1358:A:OP2	41:g:10:ARG:NH2	2.32	0.62
9:A:799:G:O2'	9:A:903:A:N7	2.33	0.62
35:a:1259:G:O2'	44:j:99:ASN:OD1	2.17	0.62
23:O:102:ASN:ND2	23:O:107:ASN:OD1	2.32	0.62
9:A:1365:G:OP2	21:M:24:ARG:NH1	2.32	0.62
9:A:1568:C:N4	9:A:1604:G:O2'	2.26	0.62
31:W:61:HIS:O	31:W:65:ALA:HB2	2.00	0.62
9:A:1552:A:O2'	9:A:1618:C:N4	2.32	0.62
10:B:34:G:HO2'	10:B:35:G:P	2.23	0.62
9:A:1670:G:N1	9:A:1683:C:N3	2.41	0.62
9:A:2551:A:C5	9:A:2612:A:N1	2.68	0.62
10:B:39:C:O2'	10:B:46:A:N1	2.31	0.62
53:s:9:PRO:HG2	53:s:40:ILE:HG21	1.81	0.62
30:V:46:ALA:O	30:V:47:VAL:C	2.43	0.62
35:a:911:G:N1	35:a:1371:C:N3	2.46	0.62
35:a:913:C:N3	35:a:1369:G:N1	2.48	0.61
9:A:2844:C:O2'	12:D:167:SER:O	2.16	0.61
38:d:47:ARG:NH1	38:d:51:GLN:OE1	2.33	0.61
35:a:973:U:O2	35:a:1194:A:N7	2.33	0.61
9:A:1257:G:OP2	19:K:72:LYS:NZ	2.32	0.61
9:A:2870:C:OP2	9:A:2956:G:O2'	2.17	0.61
9:A:66:C:O2	9:A:70:A:O2'	2.14	0.61
35:a:375:U:O2	50:p:29:ARG:NH1	2.33	0.61
35:a:1054:G:O2'	35:a:1081:A:N1	2.33	0.61
39:e:99:VAL:HG21	39:e:169:LEU:HD22	1.82	0.61
46:l:31:ARG:O	46:l:58:THR:OG1	2.15	0.61
9:A:2125:A:C4	9:A:2126:C:C5	2.88	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:C:95:LEU:HD11	11:C:105:ILE:HG13	1.80	0.61
9:A:1475:G:O6	9:A:2438:C:O2	2.19	0.61
35:a:178:A:O2'	35:a:180:A:N1	2.29	0.61
35:a:924:G:OP1	44:j:57:LYS:NZ	2.33	0.61
9:A:2016:G:O2'	11:C:183:ARG:NH2	2.33	0.61
35:a:1233:A:N3	44:j:48:VAL:HG13	2.15	0.61
47:m:102:ARG:O	47:m:111:LYS:NZ	2.33	0.61
2:2:65:TYR:CD1	53:s:45:ILE:HD11	2.36	0.61
9:A:2007:C:OP2	9:A:2045:G:N1	2.34	0.61
35:a:1049:C:N3	35:a:1086:G:N1	2.43	0.61
45:k:55:SER:O	45:k:59:VAL:HG23	2.00	0.61
6:6:57:ARG:NH1	21:M:50:PHE:O	2.34	0.61
9:A:3009:U:OP1	12:D:38:ARG:NH2	2.33	0.61
9:A:3102:U:O2	23:O:45:ARG:NH1	2.34	0.61
10:B:5:C:OP1	10:B:61:C:O2'	2.18	0.61
18:J:33:HIS:O	18:J:66:ARG:NH1	2.34	0.61
9:A:896:A:OP1	11:C:218:ARG:NH2	2.34	0.60
35:a:352:C:O2'	35:a:353:A:O5'	2.17	0.60
35:a:454:C:N3	35:a:459:G:N1	2.45	0.60
9:A:20:G:N2	28:T:84:ASP:OD1	2.17	0.60
9:A:2649:A:OP2	9:A:2650:A:O2'	2.03	0.60
13:E:131:VAL:HG21	13:E:138:THR:HG22	1.83	0.60
9:A:618:C:OP1	9:A:653:G:N1	2.34	0.60
9:A:1888:C:O2	9:A:2217:U:O2'	2.18	0.60
14:F:119:ARG:HB2	47:m:76:ALA:H	1.65	0.60
18:J:105:ASP:OD1	18:J:106:GLN:N	2.33	0.60
35:a:1482:U:O2'	35:a:1483:A:OP2	2.14	0.60
39:e:104:SER:O	39:e:105:THR:OG1	2.18	0.60
9:A:2141:U:H2'	9:A:2142:A:C8	2.36	0.60
11:C:153:ALA:O	11:C:157:ARG:NH2	2.35	0.60
35:a:989:G:O6	35:a:1006:U:C2	2.55	0.60
9:A:427:A:N3	9:A:429:A:N6	2.50	0.60
9:A:531:A:OP1	13:E:47:GLN:N	2.35	0.60
9:A:2754:G:OP2	9:A:2759:G:N2	2.35	0.60
9:A:460:G:N2	9:A:489:A:OP2	2.35	0.60
35:a:697:C:O2'	35:a:714:G:O4'	2.09	0.60
33:Y:16:LYS:NZ	33:Y:26:SER:OG	2.31	0.60
9:A:931:C:OP1	9:A:1300:G:O2'	2.11	0.59
9:A:2230:C:O2'	9:A:3044:A:N3	2.33	0.59
53:s:9:PRO:HG2	53:s:40:ILE:HD13	1.83	0.59
9:A:1070:G:O2'	9:A:2490:A:OP2	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:F:69:GLY:O	14:F:102:ARG:NH1	2.35	0.59
9:A:3043:G:O6	23:O:6:LYS:NZ	2.35	0.59
14:F:63:ASP:OD2	14:F:157:ARG:NH1	2.35	0.59
28:T:85:GLU:OE2	28:T:106:ARG:NH2	2.36	0.59
9:A:1336:A:OP1	27:S:91:ARG:NH1	2.32	0.59
9:A:920:G:OP1	21:M:44:LYS:NZ	2.35	0.59
9:A:1379:G:N2	9:A:2239:A:OP2	2.35	0.59
9:A:2558:C:OP2	24:P:20:ARG:NH2	2.35	0.59
35:a:1057:G:N2	35:a:1060:A:OP2	2.34	0.59
9:A:2973:A:O2'	15:G:63:ARG:NH1	2.36	0.59
28:T:28:ILE:HD12	28:T:81:VAL:HG21	1.84	0.59
35:a:664:U:O2'	45:k:50:VAL:O	2.18	0.59
6:6:31:HIS:NE2	9:A:2616:A:OP2	2.35	0.59
9:A:1092:G:O2'	9:A:1093:A:OP2	2.16	0.59
9:A:1907:A:OP2	9:A:1916:A:N6	2.35	0.59
14:F:119:ARG:HA	47:m:72:ARG:O	2.03	0.59
9:A:2093:G:O2'	9:A:2094:G:OP2	2.15	0.59
10:B:52:G:O6	24:P:45:ARG:NE	2.35	0.59
35:a:429:U:O2'	35:a:430:A:OP2	2.15	0.59
7:7:8:LYS:NZ	9:A:2691:C:OP1	2.35	0.58
9:A:3038:C:OP1	23:O:42:ARG:NH1	2.35	0.58
14:F:114:ALA:O	14:F:118:ILE:N	2.35	0.58
26:R:89:GLU:O	27:S:13:GLN:NE2	2.34	0.58
35:a:16:U:O2'	35:a:896:A:OP1	2.14	0.58
35:a:562:U:O4	35:a:563:A:N6	2.36	0.58
9:A:2551:A:N6	9:A:2612:A:C5	2.71	0.58
9:A:3054:U:O2'	12:D:60:ARG:NH1	2.34	0.58
15:G:19:ILE:HG12	15:G:24:LEU:HD13	1.84	0.58
9:A:2130:G:C5	9:A:2153:G:N2	2.72	0.58
9:A:2137:A:H2	35:a:1392:C:O2	1.87	0.58
14:F:113:ILE:O	14:F:117:ARG:N	2.35	0.58
35:a:101:G:N2	35:a:379:C:O3'	2.36	0.58
35:a:965:A:O2'	35:a:1029:U:O3'	2.21	0.58
9:A:723:C:N4	9:A:724:G:O6	2.36	0.58
9:A:1720:G:N2	11:C:99:ASP:O	2.34	0.58
35:a:437:U:O2'	38:d:115:HIS:ND1	2.34	0.58
53:s:45:ILE:HD12	53:s:63:THR:O	2.03	0.58
9:A:2135:U:H3	9:A:2142:A:H2'	1.67	0.58
9:A:2154:G:H22	9:A:2193:A:C5'	2.17	0.58
35:a:1140:U:O4'	35:a:1163:G:N2	2.37	0.58
50:p:67:THR:HG22	50:p:68:GLU:H	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:38:THR:HG21	9:A:2572:U:OP2	2.02	0.58
35:a:342:C:N4	35:a:348:G:O6	2.37	0.58
35:a:1048:G:N1	35:a:1087:C:N3	2.48	0.58
35:a:1473:A:O2'	35:a:1474:C:H5'	2.03	0.58
9:A:1249:G:O2'	9:A:2249:G:O2'	2.20	0.58
9:A:1899:G:N2	9:A:1980:G:OP2	2.32	0.58
35:a:481:G:O2'	35:a:529:C:O2	2.22	0.58
9:A:1058:A:O2'	21:M:34:GLY:O	2.20	0.58
9:A:2746:U:O2'	9:A:2871:U:OP1	2.15	0.58
9:A:2975:G:H4'	15:G:4:ILE:HD11	1.86	0.58
9:A:3043:G:O2'	9:A:3045:C:OP2	2.18	0.58
9:A:2802:G:N2	12:D:135:GLN:OE1	2.37	0.58
12:D:85:ARG:O	12:D:209:ARG:NH2	2.37	0.58
22:N:110:ASP:N	22:N:110:ASP:OD1	2.37	0.58
9:A:164:A:O3'	33:Y:41:ARG:NH1	2.37	0.57
9:A:2565:G:N2	9:A:2598:C:O3'	2.37	0.57
13:E:37:VAL:HG23	13:E:107:ILE:HG22	1.85	0.57
35:a:960:A:N7	35:a:1300:A:N6	2.51	0.57
41:g:111:ARG:NH1	41:g:123:GLU:OE1	2.37	0.57
4:4:15:CYS:SG	4:4:16:GLU:N	2.77	0.57
9:A:1631:A:N3	9:A:1631:A:H2'	2.18	0.57
9:A:2516:U:N3	9:A:2565:G:O6	2.37	0.57
9:A:797:G:O2'	9:A:798:U:O5'	2.22	0.57
9:A:1162:G:O2'	9:A:1229:A:N7	2.36	0.57
14:F:122:ARG:NH2	47:m:77:ASP:O	2.37	0.57
25:Q:105:LYS:NZ	35:a:1448:G:OP2	2.36	0.57
35:a:92:A:O2'	35:a:93:C:O5'	2.23	0.57
35:a:1230:C:O2'	43:i:58:TYR:OH	2.20	0.57
35:a:1476:A:H2'	35:a:1477:A:C8	2.39	0.57
35:a:1508:C:OP1	45:k:131:ARG:NH1	2.37	0.57
17:I:28:TYR:OH	17:I:39:LEU:HD21	2.04	0.57
9:A:202:C:OP2	9:A:203:A:O2'	2.12	0.57
9:A:1476:G:O2'	9:A:2439:C:O2'	2.09	0.57
31:W:85:VAL:HG23	31:W:86:HIS:H	1.69	0.57
35:a:846:A:O2'	35:a:1058:U:O4	2.12	0.57
9:A:2140:A:H3'	9:A:2141:U:C6	2.38	0.57
18:J:118:LEU:HD22	18:J:129:ILE:HG21	1.86	0.57
35:a:574:C:N4	35:a:626:G:O6	2.38	0.57
35:a:1306:A:O4'	35:a:1344:C:O2'	2.22	0.57
11:C:130:ASN:OD1	11:C:190:ARG:NH2	2.38	0.57
39:e:133:GLY:O	39:e:137:ARG:N	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2139:U:H2'	9:A:2140:A:O4'	2.04	0.57
9:A:1093:A:H62	9:A:1107:G:H21	1.53	0.57
9:A:1093:A:O2'	9:A:1275:A:N1	2.36	0.57
35:a:541:U:H4'	35:a:543:A:H62	1.70	0.57
37:c:113:GLN:NE2	37:c:186:LEU:O	2.38	0.57
9:A:1438:G:OP1	28:T:91:ARG:NH2	2.38	0.56
24:P:62:ALA:O	24:P:91:ARG:NH1	2.38	0.56
25:Q:38:ARG:NH2	35:a:346:G:OP1	2.37	0.56
35:a:332:G:OP1	54:t:5:LYS:NZ	2.38	0.56
35:a:362:G:OP1	46:l:31:ARG:NH2	2.38	0.56
35:a:636:G:N1	35:a:731:U:O4	2.38	0.56
30:V:90:GLU:O	30:V:91:THR:OG1	2.16	0.56
35:a:1302:C:OP1	53:s:70:LYS:NZ	2.38	0.56
4:4:40:LYS:NZ	9:A:2571:C:OP1	2.36	0.56
9:A:577:G:N2	9:A:1436:C:OP1	2.39	0.56
9:A:723:C:O2	9:A:733:U:O2'	2.22	0.56
9:A:747:A:N6	9:A:768:G:O2'	2.38	0.56
9:A:1541:G:N7	9:A:1629:G:H1'	2.20	0.56
14:F:119:ARG:CB	47:m:76:ALA:HB3	2.36	0.56
35:a:795:A:N7	35:a:1493:C:O2'	2.37	0.56
35:a:869:G:O6	35:a:892:C:N4	2.38	0.56
42:h:5:ASP:OD2	42:h:79:ARG:NH2	2.36	0.56
9:A:1906:U:O2'	9:A:1918:A:N7	2.34	0.56
35:a:598:C:N4	35:a:601:A:OP2	2.38	0.56
9:A:947:U:OP2	9:A:1061:G:N1	2.36	0.56
9:A:1402:A:N6	9:A:1867:G:O4'	2.39	0.56
35:a:1208:A:HO2'	35:a:1209:C:P	2.27	0.56
9:A:932:C:O2'	9:A:954:U:OP1	2.23	0.56
9:A:1813:C:OP1	29:U:53:LYS:NZ	2.26	0.56
20:L:88:LYS:N	20:L:92:ASP:O	2.33	0.56
9:A:530:G:N3	13:E:49:THR:OG1	2.35	0.56
9:A:2137:A:N7	35:a:1478:G:C8	2.74	0.56
32:X:35:GLU:OE2	32:X:36:ILE:N	2.39	0.56
35:a:1352:C:H3'	44:j:63:GLU:HB3	1.88	0.56
9:A:2079:C:N3	9:A:2104:G:N1	2.48	0.56
9:A:2788:A:N6	9:A:2789:A:N1	2.54	0.56
35:a:257:G:O6	35:a:270:A:N6	2.39	0.56
35:a:1339:A:OP2	35:a:1341:C:N4	2.37	0.56
46:l:16:ILE:HG23	46:l:18:LYS:CG	2.36	0.56
9:A:14:G:C2	9:A:611:U:C2	2.94	0.56
9:A:2316:G:O2'	9:A:2421:A:N1	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:O:101:GLU:N	23:O:101:GLU:OE1	2.39	0.56
5:5:19:HIS:NE2	9:A:552:U:O2	2.39	0.56
9:A:2754:G:N7	15:G:173:LYS:NZ	2.54	0.56
35:a:255:G:O6	35:a:266:G:O6	2.23	0.56
46:l:37:VAL:HG23	46:l:37:VAL:O	2.05	0.56
9:A:552:U:O2'	9:A:553:G:OP1	2.21	0.55
9:A:898:A:O2'	9:A:900:G:OP1	2.18	0.55
9:A:1427:U:N3	9:A:1455:U:O4	2.40	0.55
9:A:2133:G:C2	9:A:2146:A:C2	2.94	0.55
35:a:805:A:N6	35:a:858:A:N1	2.54	0.55
41:g:94:ASP:OD1	41:g:95:ARG:N	2.39	0.55
44:j:101:GLN:N	44:j:101:GLN:OE1	2.39	0.55
2:2:40:GLN:OE1	2:2:41:CYS:N	2.39	0.55
18:J:19:GLN:N	18:J:19:GLN:OE1	2.39	0.55
45:k:35:THR:HG23	45:k:37:ASN:H	1.71	0.55
9:A:629:C:N4	9:A:644:G:O6	2.39	0.55
9:A:1458:G:O2'	9:A:1499:A:N1	2.35	0.55
9:A:2981:A:N1	15:G:68:LEU:HD22	2.21	0.55
10:B:52:G:O2'	10:B:53:A:O5'	2.21	0.55
9:A:1440:C:OP2	9:A:1834:A:O2'	2.15	0.55
9:A:2982:A:C4	15:G:68:LEU:HD21	2.40	0.55
9:A:2137:A:H1'	35:a:1477:A:C2	2.42	0.55
35:a:501:G:OP2	46:l:51:LYS:NZ	2.40	0.55
26:R:47:TYR:OH	26:R:51:ARG:NH2	2.39	0.55
40:f:1:MET:SD	40:f:1:MET:N	2.77	0.55
9:A:1577:C:N4	9:A:1594:G:O6	2.39	0.55
9:A:2350:G:HO2'	9:A:2351:A:P	2.25	0.55
9:A:14:G:N1	9:A:611:U:C2	2.75	0.55
9:A:1259:U:OP2	19:K:65:SER:OG	2.22	0.55
35:a:40:C:OP1	46:l:120:LYS:NZ	2.26	0.55
35:a:1475:G:H21	35:a:1476:A:H62	1.53	0.55
9:A:332:C:N3	9:A:349:G:N1	2.48	0.55
9:A:977:G:O2'	10:B:78:U:O2	2.22	0.55
13:E:9:THR:HG22	13:E:13:LYS:O	2.07	0.55
35:a:1215:C:O2'	44:j:55:PRO:O	2.22	0.55
9:A:63:C:N4	9:A:85:G:O6	2.37	0.55
9:A:2851:G:N2	9:A:3001:G:OP2	2.40	0.55
13:E:27:VAL:HG11	13:E:112:ARG:HB3	1.89	0.55
35:a:680:G:O2'	35:a:684:A:O4'	2.22	0.55
35:a:1007:U:HO2'	35:a:1008:C:P	2.28	0.55
9:A:1698:A:N1	9:A:1777:U:O2'	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2133:G:N3	9:A:2146:A:C2	2.75	0.54
9:A:2145:C:H2'	9:A:2146:A:C8	2.42	0.54
9:A:2750:G:OP2	15:G:154:ARG:NH2	2.39	0.54
2:2:65:TYR:N	53:s:66:MET:O	2.40	0.54
9:A:369:G:N1	9:A:433:C:N3	2.47	0.54
9:A:1540:U:C5	9:A:1629:G:H8	2.25	0.54
9:A:2178:G:O2'	9:A:2180:U:O4	2.20	0.54
9:A:2708:G:OP1	22:N:45:ARG:NH2	2.40	0.54
35:a:309:G:O2'	35:a:587:A:N1	2.37	0.54
35:a:323:U:OP1	54:t:21:ASN:ND2	2.39	0.54
9:A:193:G:N2	9:A:251:A:N3	2.55	0.54
9:A:2130:G:C8	9:A:2153:G:C2	2.95	0.54
14:F:86:LEU:HD22	14:F:92:ILE:HD13	1.90	0.54
14:F:126:PRO:O	14:F:174:ARG:NE	2.39	0.54
35:a:362:G:N1	35:a:365:U:OP2	2.40	0.54
35:a:991:C:N4	35:a:992:G:O6	2.40	0.54
44:j:96:VAL:HG23	44:j:96:VAL:O	2.07	0.54
5:5:12:ASN:ND2	9:A:1424:G:OP1	2.41	0.54
9:A:3009:U:O2	12:D:69:GLN:NE2	2.37	0.54
35:a:796:A:OP2	35:a:1510:G:O2'	2.25	0.54
15:G:2:SER:OG	15:G:3:ARG:N	2.40	0.54
28:T:19:VAL:O	28:T:108:SER:OG	2.16	0.54
8:8:4:ARG:NH1	9:A:2680:C:OP1	2.40	0.54
9:A:28:C:O2'	9:A:1353:G:OP1	2.23	0.54
9:A:891:G:N1	9:A:2295:C:OP1	2.39	0.54
9:A:1604:G:N2	9:A:1605:G:O6	2.41	0.54
9:A:1631:A:C8	9:A:1632:G:C8	2.96	0.54
30:V:4:HIS:O	30:V:23:VAL:HG11	2.07	0.54
35:a:429:U:OP1	38:d:13:ARG:NH1	2.40	0.54
35:a:632:U:O4	35:a:733:A:N7	2.41	0.54
47:m:60:ILE:HG13	47:m:66:VAL:HG22	1.89	0.54
9:A:283:U:O2	9:A:303:G:O6	2.25	0.54
9:A:2159:G:H1	9:A:2186:C:HO2'	1.56	0.54
10:B:83:C:N4	10:B:84:C:H41	2.03	0.54
24:P:16:ASN:OD1	24:P:17:ALA:N	2.40	0.54
35:a:46:G:O2'	35:a:602:A:N1	2.36	0.54
35:a:791:C:O2'	35:a:883:A:N1	2.41	0.54
35:a:1311:G:OP1	47:m:20:THR:HG21	2.08	0.54
5:5:37:ARG:NE	5:5:45:LEU:O	2.41	0.54
35:a:421:U:O4	37:c:126:ARG:NH1	2.39	0.54
35:a:1393:G:H8	35:a:1393:G:OP2	1.91	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2132:U:H5"	9:A:2132:U:H6	1.73	0.53
12:D:19:GLU:OE2	12:D:20:ASN:ND2	2.41	0.53
13:E:143:THR:O	13:E:147:THR:HG23	2.08	0.53
14:F:130:ASP:OD2	14:F:134:ASN:ND2	2.40	0.53
35:a:598:C:O2	50:p:12:LYS:NZ	2.41	0.53
52:r:57:CYS:SG	52:r:60:HIS:ND1	2.81	0.53
9:A:2138:C:N4	35:a:1393:G:OP1	2.41	0.53
9:A:2142:A:OP2	9:A:2142:A:H8	1.92	0.53
35:a:1354:G:OP2	43:i:131:ILE:HD11	2.09	0.53
9:A:650:G:H5'	19:K:114:LEU:HD12	1.89	0.53
9:A:1211:G:N2	9:A:1217:G:O6	2.41	0.53
9:A:1533:U:P	9:A:1536:A:H61	2.32	0.53
9:A:2138:C:H41	35:a:1392:C:H4'	1.74	0.53
9:A:2143:A:C3'	9:A:2144:C:H5'	2.39	0.53
9:A:3038:C:OP1	23:O:42:ARG:NH2	2.41	0.53
25:Q:47:ILE:O	25:Q:96:LEU:N	2.40	0.53
35:a:373:A:O2'	35:a:451:A:N7	2.41	0.53
9:A:2955:G:O2'	9:A:2956:G:O4'	2.25	0.53
35:a:1403:U:H2'	35:a:1404:C:C6	2.43	0.53
9:A:539:C:N4	9:A:542:A:OP2	2.35	0.53
9:A:2600:A:N3	24:P:121:ARG:NH2	2.57	0.53
9:A:3070:G:O2'	9:A:3087:G:N2	2.42	0.53
15:G:65:LEU:HD13	15:G:68:LEU:HD23	1.91	0.53
35:a:929:G:H22	35:a:1215:C:N4	2.05	0.53
32:X:45:PHE:O	32:X:59:LEU:HD11	2.09	0.53
35:a:32:G:O2'	35:a:296:U:OP1	2.24	0.53
35:a:1069:G:O2'	35:a:1151:A:N1	2.39	0.53
14:F:130:ASP:OD1	14:F:134:ASN:N	2.40	0.53
24:P:31:GLY:N	24:P:54:ASP:OD2	2.39	0.53
9:A:2054:C:C2	9:A:2128:G:C2	2.96	0.53
9:A:2693:A:O2'	9:A:2694:G:OP1	2.23	0.53
9:A:2871:U:O2	9:A:2897:G:O6	2.26	0.53
14:F:147:GLU:N	14:F:147:GLU:OE1	2.42	0.53
35:a:356:A:O2'	35:a:368:U:O2'	2.26	0.53
37:c:12:LEU:HD21	48:n:51:GLY:HA3	1.91	0.53
38:d:183:ARG:O	38:d:183:ARG:NH1	2.41	0.53
40:f:15:ASP:OD1	40:f:18:THR:OG1	2.21	0.53
9:A:14:G:N1	9:A:611:U:N3	2.57	0.53
9:A:1129:G:OP2	26:R:66:ASN:ND2	2.41	0.53
9:A:272:A:N3	9:A:456:C:O2'	2.38	0.52
9:A:699:U:OP2	13:E:105:LYS:NZ	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1272:C:OP1	26:R:92:ARG:NH2	2.42	0.52
9:A:2150:U:O2	9:A:2153:G:C6	2.62	0.52
9:A:1186:G:O2'	9:A:1187:A:N7	2.42	0.52
9:A:1845:G:N1	9:A:1858:A:N7	2.58	0.52
9:A:2454:G:O2'	33:Y:30:ASN:O	2.27	0.52
37:c:130:ARG:NE	37:c:166:GLU:OE2	2.41	0.52
9:A:1822:C:O2'	9:A:1828:A:N1	2.36	0.52
9:A:2133:G:C6	9:A:2146:A:N1	2.77	0.52
9:A:2031:G:P	9:A:2032:A:HO2'	2.26	0.52
9:A:2317:G:O2'	9:A:2318:U:O4'	2.23	0.52
9:A:2137:A:C2	35:a:1391:A:C2	2.97	0.52
9:A:2157:G:H5"	55:u:26:VAL:HG21	1.91	0.52
9:A:663:A:O2'	9:A:665:G:OP2	2.28	0.52
9:A:1872:A:O2'	12:D:123:PHE:O	2.26	0.52
9:A:2159:G:N1	9:A:2186:C:O2'	2.43	0.52
15:G:17:VAL:CG1	15:G:24:LEU:HD11	2.40	0.52
15:G:120:GLU:N	15:G:120:GLU:OE1	2.43	0.52
9:A:2334:U:OP1	9:A:2341:U:O2'	2.24	0.52
9:A:2382:G:O2'	9:A:2383:U:O5'	2.28	0.52
44:j:80:THR:O	44:j:83:THR:OG1	2.28	0.52
9:A:1696:G:O2'	9:A:1736:G:O6	2.26	0.52
9:A:2130:G:C4	9:A:2153:G:N1	2.77	0.52
44:j:18:ILE:HG23	44:j:19:ASP:N	2.24	0.52
7:7:2:LYS:NZ	9:A:2702:A:OP2	2.42	0.52
9:A:276:G:N1	9:A:310:C:N3	2.48	0.52
35:a:292:G:O2'	35:a:589:A:N6	2.41	0.52
9:A:14:G:C2	9:A:611:U:O2	2.63	0.51
9:A:388:U:H2'	9:A:389:G:O4'	2.10	0.51
9:A:1668:C:O2'	9:A:1764:A:N3	2.38	0.51
2:2:65:TYR:CE1	53:s:45:ILE:HD11	2.45	0.51
2:2:66:GLY:C	53:s:62:VAL:HG22	2.36	0.51
9:A:2054:C:C1'	9:A:2152:A:H1'	2.40	0.51
35:a:453:G:O6	35:a:460:U:O2	2.27	0.51
35:a:878:C:H2'	35:a:879:C:C1'	2.40	0.51
46:l:16:ILE:HG23	46:l:18:LYS:HG3	1.92	0.51
9:A:81:A:N1	9:A:96:G:O2'	2.41	0.51
9:A:2054:C:H1'	9:A:2152:A:H1'	1.93	0.51
16:H:120:ALA:O	16:H:123:HIS:NE2	2.43	0.51
26:R:77:ASN:OD1	26:R:78:ARG:N	2.43	0.51
35:a:772:A:O2'	35:a:774:A:N7	2.42	0.51
39:e:62:VAL:HG21	39:e:88:GLY:C	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2445:A:O3'	11:C:188:ARG:NH2	2.42	0.51
31:W:166:GLU:OE1	31:W:166:GLU:N	2.40	0.51
35:a:545:U:OP2	35:a:546:G:O2'	2.28	0.51
35:a:1507:G:OP1	45:k:134:LYS:NZ	2.43	0.51
44:j:93:PRO:HG2	44:j:96:VAL:HG22	1.92	0.51
51:q:46:HIS:ND1	51:q:53:ILE:HD11	2.25	0.51
35:a:989:G:C6	35:a:1006:U:O2	2.63	0.51
36:b:184:ILE:HG22	36:b:198:TYR:HB2	1.93	0.51
9:A:472:C:H2'	9:A:472:C:O2	2.09	0.51
14:F:135:TYR:O	14:F:162:THR:OG1	2.12	0.51
35:a:922:C:N4	35:a:1325:G:O6	2.43	0.51
43:i:55:LEU:HD11	43:i:68:ILE:HD12	1.93	0.51
9:A:2061:U:O3'	11:C:256:ARG:NH1	2.44	0.51
27:S:65:LEU:HB2	27:S:96:VAL:HG23	1.92	0.51
35:a:145:G:O6	35:a:171:A:N1	2.44	0.51
32:X:54:GLY:N	32:X:58:THR:O	2.39	0.51
35:a:943:U:O2	35:a:1182:A:N6	2.44	0.51
9:A:1046:C:O2'	9:A:1287:C:O2	2.28	0.51
9:A:2144:C:H5"	35:a:1501:G:C5	2.44	0.51
35:a:962:C:O2'	48:n:21:TYR:OH	2.01	0.51
9:A:974:G:HO2'	9:A:975:U:P	2.34	0.51
9:A:1381:G:N2	9:A:2237:A:OP2	2.44	0.51
9:A:2135:U:H3	9:A:2142:A:C2'	2.24	0.51
13:E:14:THR:HG23	13:E:15:ASP:H	1.76	0.51
24:P:43:SER:O	24:P:112:ARG:NH1	2.43	0.51
9:A:245:G:N2	9:A:472:C:O2'	2.43	0.50
9:A:1475:G:N1	9:A:2438:C:N3	2.60	0.50
9:A:1679:A:O2'	9:A:1680:A:OP2	2.23	0.50
9:A:2691:C:O2	22:N:124:LYS:NZ	2.38	0.50
27:S:64:VAL:HG12	27:S:97:LEU:CD2	2.41	0.50
9:A:1938:G:N2	9:A:1957:G:O6	2.43	0.50
9:A:2054:C:O2	9:A:2151:A:H2	1.94	0.50
14:F:73:GLU:OE2	14:F:95:ARG:NE	2.44	0.50
31:W:85:VAL:HG23	31:W:86:HIS:N	2.26	0.50
37:c:85:ARG:NH1	37:c:89:ASP:OD2	2.45	0.50
9:A:485:U:O3'	9:A:2454:G:N2	2.44	0.50
9:A:1257:G:O2'	9:A:1262:A:N1	2.41	0.50
11:C:95:LEU:HD13	11:C:117:ILE:HD11	1.93	0.50
15:G:18:THR:O	15:G:24:LEU:HD12	2.12	0.50
35:a:1311:G:OP1	47:m:27:ARG:NH2	2.44	0.50
35:a:1475:G:N2	35:a:1476:A:H62	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:g:79:ARG:O	41:g:80:VAL:HG23	2.12	0.50
9:A:1249:G:HO2'	9:A:2249:G:HO2'	1.57	0.50
9:A:1451:A:OP2	29:U:67:LYS:NZ	2.25	0.50
9:A:2125:A:C6	9:A:2126:C:C4	2.99	0.50
9:A:2133:G:C6	9:A:2146:A:C6	2.99	0.50
9:A:2535:A:C2	14:F:86:LEU:HD21	2.46	0.50
9:A:2551:A:C6	9:A:2612:A:C2	3.00	0.50
9:A:3071:A:OP2	9:A:3087:G:N1	2.43	0.50
30:V:7:ASP:OD2	30:V:96:ARG:NH2	2.43	0.50
35:a:583:C:N3	35:a:615:G:N1	2.45	0.50
35:a:1229:A:N6	35:a:1272:G:O6	2.45	0.50
5:5:15:ARG:NH2	9:A:553:G:OP1	2.42	0.50
9:A:2133:G:C5	9:A:2146:A:N1	2.80	0.50
24:P:34:GLU:HG2	24:P:35:VAL:HG23	1.92	0.50
35:a:1403:U:H2'	35:a:1404:C:H6	1.77	0.50
9:A:167:G:HO2'	9:A:2432:G:HO2'	1.54	0.50
9:A:726:A:N3	9:A:2627:C:O2'	2.36	0.50
47:m:82:ILE:HG22	47:m:83:GLU:N	2.27	0.50
9:A:1475:G:C6	9:A:2438:C:O2	2.65	0.50
35:a:291:C:N3	35:a:309:G:N1	2.51	0.50
50:p:14:ARG:O	50:p:43:LYS:NZ	2.42	0.50
9:A:740:A:O2'	9:A:741:G:OP2	2.25	0.50
9:A:1788:G:OP2	11:C:63:ARG:NH1	2.45	0.50
9:A:3070:G:O3'	9:A:3087:G:N2	2.44	0.50
10:B:76:G:OP1	31:W:20:GLY:N	2.45	0.50
35:a:301:G:N2	35:a:536:C:O3'	2.45	0.50
40:f:82:ASN:OD1	40:f:84:SER:N	2.42	0.50
9:A:1558:C:C2	9:A:1613:G:N2	2.76	0.50
9:A:1630:U:OP1	9:A:1631:A:H8	1.95	0.50
9:A:2859:C:O2	12:D:40:ARG:NH2	2.45	0.50
35:a:592:U:OP1	38:d:76:ARG:NH1	2.45	0.50
35:a:1517:C:OP1	36:b:177:ARG:NE	2.39	0.50
41:g:69:VAL:HG12	41:g:69:VAL:O	2.12	0.50
13:E:27:VAL:HG12	13:E:116:SER:OG	2.12	0.49
9:A:282:A:N6	9:A:305:G:O6	2.45	0.49
9:A:1290:C:H41	9:A:1291:G:H21	1.61	0.49
9:A:2515:U:O2'	9:A:2598:C:O2	2.29	0.49
9:A:2670:G:N2	9:A:2673:U:O2	2.42	0.49
11:C:26:ARG:NH2	11:C:83:GLU:OE2	2.45	0.49
23:O:49:GLU:OE2	23:O:94:TYR:N	2.44	0.49
32:X:15:ASP:OD1	32:X:15:ASP:C	2.54	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:472:C:N3	35:a:473:A:N6	2.59	0.49
39:e:44:ASN:OD1	39:e:44:ASN:N	2.45	0.49
43:i:135:LYS:O	48:n:60:SER:OG	2.30	0.49
47:m:4:LEU:HD22	47:m:9:LEU:HD11	1.93	0.49
9:A:357:U:H4'	9:A:358:G:O5'	2.12	0.49
9:A:1111:G:N2	27:S:25:GLU:OE2	2.44	0.49
9:A:1468:A:OP2	9:A:1492:G:N1	2.42	0.49
13:E:138:THR:HG21	13:E:168:SER:HB3	1.94	0.49
35:a:1224:C:H2'	35:a:1225:C:C1'	2.42	0.49
23:O:33:ARG:NH2	23:O:114:GLU:OE2	2.46	0.49
35:a:990:C:C2	35:a:1005:G:N2	2.77	0.49
35:a:1396:A:H2'	35:a:1396:A:N3	2.27	0.49
35:a:1473:A:H2'	35:a:1474:C:H6	1.78	0.49
9:A:663:A:O2'	27:S:81:LYS:NZ	2.44	0.49
9:A:1022:C:O2'	22:N:101:ARG:NH2	2.45	0.49
9:A:2147:U:H2'	9:A:2148:C:C6	2.48	0.49
12:D:110:ALA:O	12:D:182:VAL:HG12	2.12	0.49
9:A:701:A:OP2	9:A:713:G:N1	2.40	0.49
9:A:2801:A:O4'	9:A:2836:C:N4	2.45	0.49
25:Q:23:ASP:OD1	25:Q:89:GLY:N	2.44	0.49
9:A:2196:G:N1	9:A:2197:G:O6	2.45	0.49
35:a:252:U:O2	35:a:275:G:N2	2.45	0.49
35:a:438:U:OP1	38:d:143:LYS:NZ	2.44	0.49
35:a:1398:G:C2	35:a:1399:A:C8	3.01	0.49
35:a:1473:A:H2'	35:a:1474:C:C6	2.47	0.49
9:A:227:A:N1	9:A:505:C:O2'	2.44	0.49
9:A:1181:G:O6	9:A:1193:C:N4	2.38	0.49
9:A:2474:G:O2'	9:A:2720:C:OP1	2.22	0.49
9:A:3101:C:O3'	23:O:90:ARG:NH1	2.46	0.49
11:C:124:ASP:O	11:C:129:ASN:ND2	2.45	0.49
25:Q:22:GLY:N	25:Q:46:VAL:O	2.44	0.49
35:a:938:U:O2	35:a:1206:U:N3	2.46	0.49
47:m:69:ASP:HA	47:m:72:ARG:HG2	1.95	0.49
9:A:1540:U:C4	9:A:1629:G:H2'	2.47	0.49
35:a:408:G:O3'	38:d:104:ARG:NH1	2.46	0.49
44:j:25:ILE:O	44:j:28:THR:HG22	2.12	0.49
53:s:38:SER:OG	53:s:40:ILE:HG23	2.12	0.49
2:2:42:HIS:O	2:2:46:THR:HG23	2.13	0.49
9:A:196:A:O2'	9:A:2468:U:OP1	2.29	0.49
9:A:357:U:H1'	9:A:358:G:OP2	2.13	0.49
9:A:2133:G:N1	9:A:2134:G:C5	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2138:C:H2'	9:A:2139:U:C5	2.48	0.49
9:A:2907:C:N3	9:A:2951:G:O2'	2.35	0.49
11:C:147:LEU:HD21	11:C:155:LEU:HD21	1.95	0.49
19:K:98:THR:HG23	19:K:124:VAL:HB	1.95	0.49
35:a:579:U:OP1	42:h:90:LYS:NZ	2.43	0.49
9:A:2065:A:N7	35:a:682:A:N1	2.61	0.48
9:A:2171:C:O2	35:a:1467:A:O2'	2.29	0.48
9:A:2299:C:OP2	9:A:2462:G:N2	2.45	0.48
35:a:496:U:O2'	35:a:497:G:OP1	2.20	0.48
38:d:94:ASP:OD1	38:d:95:ASN:N	2.46	0.48
42:h:24:GLU:OE1	42:h:63:GLN:NE2	2.46	0.48
2:2:15:GLN:NE2	2:2:32:THR:OG1	2.44	0.48
9:A:387:U:O2	9:A:394:G:O6	2.31	0.48
35:a:1027:G:O2'	35:a:1196:G:O2'	2.01	0.48
9:A:1770:G:OP1	9:A:1937:U:O2'	2.19	0.48
9:A:2065:A:C5	35:a:682:A:N6	2.81	0.48
13:E:20:LEU:O	13:E:20:LEU:HD12	2.13	0.48
25:Q:2:ASN:O	25:Q:5:ASP:N	2.38	0.48
35:a:408:G:O2'	38:d:104:ARG:NH1	2.46	0.48
36:b:149:GLY:O	36:b:152:ARG:NH2	2.46	0.48
44:j:51:VAL:O	44:j:52:ILE:HG12	2.13	0.48
5:5:6:ARG:NH1	9:A:1831:A:O2'	2.46	0.48
9:A:76:C:O2'	9:A:428:A:N3	2.42	0.48
9:A:862:U:OP2	9:A:2835:U:O2'	2.29	0.48
9:A:2130:G:H2'	9:A:2131:G:C5'	2.43	0.48
9:A:2138:C:H3'	9:A:2139:U:C5	2.49	0.48
35:a:406:G:OP1	38:d:5:THR:HG21	2.14	0.48
35:a:945:G:O2'	35:a:1180:U:OP1	2.20	0.48
9:A:552:U:O4	9:A:799:G:O2'	2.32	0.48
34:Z:5:THR:OG1	34:Z:6:THR:N	2.46	0.48
39:e:140:LEU:HD22	39:e:148:ILE:CD1	2.44	0.48
47:m:66:VAL:O	47:m:69:ASP:N	2.47	0.48
47:m:91:ARG:NE	47:m:96:LEU:HD23	2.29	0.48
9:A:1649:C:N4	9:A:1790:A:OP2	2.39	0.48
9:A:2244:A:N6	9:A:2259:G:O6	2.47	0.48
35:a:292:G:HO2'	35:a:589:A:N6	2.10	0.48
9:A:2145:C:H2'	9:A:2146:A:H8	1.78	0.48
12:D:88:ASP:OD1	12:D:88:ASP:N	2.46	0.48
42:h:48:ASP:OD1	42:h:49:TYR:N	2.45	0.48
9:A:550:C:N4	9:A:551:G:O6	2.46	0.48
9:A:860:G:N2	9:A:868:C:N3	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1045:C:O2'	9:A:1047:A:N6	2.47	0.48
9:A:2018:G:O4'	9:A:2426:C:O2'	2.32	0.48
9:A:2693:A:OP1	22:N:120:ARG:NH2	2.46	0.48
10:B:7:G:H22	10:B:110:G:N2	2.11	0.48
19:K:41:LYS:NZ	19:K:50:GLY:O	2.41	0.48
35:a:673:G:O2'	41:g:153:HIS:NE2	2.47	0.48
35:a:919:A:O3'	41:g:76:ARG:NH1	2.47	0.48
35:a:1234:G:O6	35:a:1265:U:C2	2.66	0.48
9:A:708:G:N2	13:E:187:ASP:OD2	2.45	0.48
9:A:2088:C:H3'	9:A:2089:C:C6	2.49	0.48
9:A:2138:C:H2'	9:A:2139:U:C6	2.48	0.48
9:A:2140:A:H5"	9:A:2140:A:N3	2.29	0.48
24:P:34:GLU:OE2	24:P:34:GLU:N	2.40	0.48
35:a:1269:A:H2'	35:a:1270:A:O4'	2.14	0.48
35:a:1353:G:H5"	44:j:63:GLU:HA	1.96	0.48
35:a:1367:C:N4	35:a:1368:G:O6	2.47	0.48
38:d:15:LEU:HD11	38:d:58:PHE:CD2	2.48	0.48
45:k:22:LYS:NZ	45:k:85:GLU:OE2	2.44	0.48
50:p:57:GLN:NE2	50:p:79:ASP:O	2.46	0.48
9:A:1986:A:O2'	9:A:2182:C:OP1	2.28	0.48
35:a:352:C:HO2'	35:a:353:A:P	2.36	0.48
35:a:1325:G:N2	35:a:1331:A:O2'	2.43	0.48
9:A:558:A:OP2	13:E:80:ARG:NH2	2.47	0.47
9:A:814:A:N3	9:A:1851:G:O2'	2.45	0.47
9:A:1952:C:H2'	9:A:1953:C:C6	2.50	0.47
9:A:2130:G:N7	9:A:2153:G:C2	2.82	0.47
20:L:30:ARG:NH1	20:L:37:ASP:OD2	2.47	0.47
9:A:1089:C:H2'	9:A:1090:G:O4'	2.14	0.47
15:G:47:GLU:N	15:G:47:GLU:OE2	2.45	0.47
18:J:121:ASN:OD1	18:J:122:ASP:N	2.47	0.47
28:T:42:ILE:HG22	28:T:43:LEU:N	2.29	0.47
35:a:1337:A:O2'	35:a:1338:G:P	2.71	0.47
9:A:1528:G:N1	9:A:1807:C:N3	2.51	0.47
9:A:2709:G:OP1	22:N:46:GLN:NE2	2.42	0.47
35:a:561:G:N1	35:a:739:A:OP2	2.44	0.47
38:d:15:LEU:HD13	38:d:55:LYS:HA	1.96	0.47
7:7:11:CYS:SG	7:7:12:ASP:N	2.87	0.47
9:A:16:G:OP1	26:R:23:GLY:N	2.47	0.47
9:A:1248:U:N3	9:A:2249:G:OP1	2.46	0.47
9:A:1371:G:O2'	13:E:83:GLN:OE1	2.21	0.47
9:A:1788:G:OP1	11:C:61:ALA:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:717:C:C2	35:a:718:U:C5	3.03	0.47
50:p:68:GLU:N	50:p:68:GLU:OE2	2.47	0.47
9:A:2743:U:O4'	9:A:2766:A:N6	2.47	0.47
20:L:70:ARG:NH2	20:L:76:TYR:OH	2.47	0.47
27:S:7:VAL:HG12	27:S:60:VAL:HG11	1.97	0.47
35:a:499:C:OP2	46:l:47:SER:OG	2.31	0.47
43:i:101:LEU:HD13	43:i:126:ARG:HG2	1.97	0.47
8:8:3:LYS:NZ	9:A:1252:G:OP1	2.25	0.47
9:A:1647:G:O2'	9:A:1792:A:N6	2.45	0.47
12:D:102:THR:HG23	12:D:104:GLU:H	1.80	0.47
14:F:151:ASP:OD2	14:F:152:SER:N	2.48	0.47
47:m:79:ARG:HA	47:m:82:ILE:HG12	1.96	0.47
9:A:1111:G:N3	27:S:92:GLN:NE2	2.62	0.47
9:A:1173:G:H21	9:A:1203:A:C1'	2.27	0.47
9:A:2154:G:H22	9:A:2193:A:H5"	1.79	0.47
9:A:2752:U:O2'	9:A:2754:G:OP1	2.25	0.47
11:C:186:ASP:N	11:C:186:ASP:OD1	2.44	0.47
15:G:19:ILE:CG1	15:G:24:LEU:HD13	2.44	0.47
23:O:24:LEU:HD22	23:O:36:THR:HG21	1.97	0.47
35:a:1265:U:OP2	35:a:1266:U:O2'	2.19	0.47
35:a:1353:G:O5'	44:j:64:HIS:N	2.31	0.47
35:a:1402:G:N2	35:a:1466:G:H1'	2.30	0.47
48:n:60:SER:OG	48:n:60:SER:O	2.30	0.47
9:A:552:U:HO2'	9:A:553:G:P	2.36	0.47
9:A:2350:G:O2'	9:A:2351:A:P	2.71	0.47
20:L:112:MET:SD	20:L:112:MET:N	2.88	0.47
27:S:53:ASP:OD1	27:S:54:ASP:N	2.48	0.47
27:S:66:GLU:O	27:S:96:VAL:HG22	2.13	0.47
35:a:36:A:N6	35:a:533:G:O6	2.48	0.47
35:a:354:G:C2	35:a:355:C:C5	3.03	0.47
35:a:665:G:N1	35:a:684:A:OP2	2.43	0.47
35:a:1478:G:O2'	35:a:1479:U:H5'	2.14	0.47
9:A:2018:G:N2	9:A:2028:G:OP2	2.42	0.47
35:a:437:U:HO2'	38:d:115:HIS:CE1	2.31	0.47
35:a:756:G:O2'	35:a:757:A:N7	2.48	0.47
35:a:1236:G:H8	35:a:1239:G:H21	1.62	0.47
39:e:119:VAL:HG11	39:e:165:THR:HG22	1.95	0.47
3:3:17:ARG:NH2	9:A:1378:U:OP1	2.42	0.47
9:A:406:A:N6	9:A:421:U:O4'	2.48	0.47
9:A:1541:G:H21	9:A:1631:A:H62	1.61	0.47
22:N:31:ASP:OD1	22:N:134:ARG:NH1	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:739:A:O2'	46:l:9:ARG:NH1	2.48	0.47
9:A:1227:C:O3'	9:A:1228:A:O4'	2.33	0.46
9:A:1630:U:OP2	9:A:1630:U:H6	1.98	0.46
44:j:18:ILE:HG23	44:j:19:ASP:H	1.81	0.46
8:8:7:LYS:NZ	9:A:1252:G:OP2	2.40	0.46
9:A:1326:G:O2'	9:A:1327:A:OP2	2.26	0.46
9:A:1556:A:N6	9:A:1616:A:N1	2.64	0.46
9:A:2034:G:OP1	11:C:88:ARG:NH1	2.49	0.46
19:K:13:ARG:NH2	19:K:49:ASP:O	2.45	0.46
29:U:18:GLU:OE1	29:U:18:GLU:N	2.48	0.46
35:a:788:C:OP1	49:o:48:HIS:NE2	2.48	0.46
35:a:792:G:OP1	35:a:884:G:N2	2.43	0.46
9:A:699:U:O2	9:A:716:G:O6	2.32	0.46
9:A:1404:C:C2	9:A:1405:U:C5	3.04	0.46
9:A:1643:G:O3'	9:A:1712:G:O2'	2.33	0.46
9:A:2133:G:C2	9:A:2134:G:C8	3.03	0.46
31:W:64:ASN:OD1	31:W:64:ASN:C	2.58	0.46
35:a:25:G:H21	35:a:896:A:H62	1.63	0.46
35:a:1480:C:O2'	35:a:1501:G:O6	2.34	0.46
44:j:67:MET:SD	44:j:68:ARG:N	2.87	0.46
4:4:13:LEU:N	4:4:23:TYR:O	2.48	0.46
9:A:1003:A:O2'	9:A:1006:G:O6	2.21	0.46
9:A:1165:G:HO2'	9:A:1228:A:H61	1.61	0.46
9:A:1166:A:H1'	9:A:1230:G:H21	1.80	0.46
9:A:1884:G:O2'	20:L:6:SER:OG	2.06	0.46
29:U:6:ASP:O	29:U:8:ARG:N	2.47	0.46
31:W:108:VAL:HG22	31:W:109:GLU:N	2.31	0.46
35:a:1396:A:C6	35:a:1397:U:C4	3.03	0.46
37:c:4:LYS:NZ	37:c:152:GLN:OE1	2.48	0.46
2:2:50:LYS:HD3	14:F:122:ARG:HH11	1.79	0.46
9:A:936:A:N6	9:A:1090:G:O2'	2.47	0.46
9:A:3013:C:O2'	9:A:3113:A:N6	2.48	0.46
9:A:3086:U:P	9:A:3087:G:H2'	2.55	0.46
35:a:60:U:O4	35:a:352:C:N4	2.49	0.46
35:a:815:G:C6	35:a:816:G:C6	3.03	0.46
9:A:189:A:N6	9:A:206:A:C4	2.84	0.46
9:A:223:A:OP2	9:A:507:G:N2	2.48	0.46
9:A:541:G:N3	9:A:545:A:O2'	2.48	0.46
9:A:604:C:O2'	28:T:25:ARG:NH1	2.43	0.46
9:A:1200:U:O2'	17:I:83:LYS:NZ	2.40	0.46
10:B:113:G:H4'	24:P:66:ILE:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:4:ILE:HD12	15:G:4:ILE:H	1.79	0.46
9:A:1710:A:N6	9:A:1716:A:OP1	2.49	0.46
35:a:928:A:O2'	35:a:1315:A:N3	2.37	0.46
35:a:1109:C:O2	35:a:1125:G:N2	2.48	0.46
6:6:47:ARG:NH1	9:A:725:A:OP2	2.49	0.46
12:D:89:GLU:HA	12:D:92:VAL:HG12	1.97	0.46
13:E:149:THR:O	13:E:150:GLU:HG3	2.15	0.46
14:F:119:ARG:N	47:m:76:ALA:HB3	2.31	0.46
9:A:163:U:O2	16:H:115:ARG:NH1	2.49	0.46
9:A:189:A:H62	9:A:205:U:H3	1.63	0.46
9:A:729:C:O2'	9:A:733:U:OP1	2.34	0.46
9:A:869:U:O2'	9:A:1387:A:N1	2.48	0.46
9:A:1493:A:O2'	9:A:1495:G:OP2	2.33	0.46
9:A:2081:U:OP1	9:A:2634:G:O2'	2.34	0.46
9:A:2135:U:H2'	9:A:2142:A:C2	2.50	0.46
9:A:2802:G:O2'	12:D:147:ARG:NH2	2.45	0.46
9:A:3064:G:N3	25:Q:1:MET:N	2.63	0.46
18:J:103:THR:O	18:J:107:VAL:HG23	2.15	0.46
22:N:130:ARG:NH2	31:W:88:ILE:O	2.49	0.46
23:O:60:LEU:O	23:O:61:HIS:HB3	2.15	0.46
35:a:465:G:HO2'	35:a:466:U:P	2.39	0.46
39:e:64:VAL:HG22	39:e:92:ALA:HB1	1.98	0.46
40:f:19:VAL:O	40:f:22:SER:OG	2.28	0.46
9:A:720:C:N4	21:M:76:GLN:OE1	2.43	0.46
15:G:8:PRO:O	15:G:70:ARG:NH2	2.47	0.46
35:a:644:G:O2'	35:a:646:G:OP2	2.29	0.46
53:s:19:VAL:HG11	53:s:44:PHE:HD1	1.81	0.46
2:2:62:GLU:O	53:s:67:VAL:O	2.33	0.45
9:A:1535:C:O2	9:A:1535:C:O4'	2.34	0.45
9:A:2056:G:C6	9:A:2151:A:C6	3.04	0.45
11:C:139:GLY:N	11:C:165:LEU:O	2.47	0.45
14:F:141:GLU:O	14:F:142:GLN:HB3	2.17	0.45
35:a:1362:G:O2'	35:a:1363:U:O4'	2.31	0.45
35:a:1388:G:N2	35:a:1502:A:N3	2.64	0.45
44:j:92:LEU:N	44:j:93:PRO:CD	2.80	0.45
9:A:150:C:H2'	9:A:151:A:H8	1.81	0.45
9:A:1405:U:C2	9:A:1406:U:C5	3.04	0.45
9:A:2065:A:N6	35:a:682:A:N6	2.65	0.45
9:A:2314:U:OP2	9:A:2315:U:O2'	2.31	0.45
13:E:179:SER:OG	13:E:181:ASP:OD1	2.34	0.45
14:F:142:GLN:OE1	14:F:143:SER:OG	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Z:16:ASP:OD1	34:Z:17:GLU:N	2.49	0.45
35:a:1376:U:O2'	35:a:1485:C:O2'	2.15	0.45
38:d:27:GLU:OE2	38:d:27:GLU:N	2.49	0.45
9:A:774:G:N2	13:E:36:GLN:OE1	2.49	0.45
9:A:2842:G:O2'	12:D:160:VAL:HG22	2.17	0.45
35:a:482:A:OP1	46:l:115:SER:OG	2.32	0.45
35:a:616:G:O3'	51:q:19:ARG:NH1	2.49	0.45
35:a:1401:A:N6	35:a:1466:G:O2'	2.42	0.45
9:A:1377:A:C6	9:A:1378:U:C4	3.04	0.45
9:A:2357:A:H8	9:A:2380:G:H21	1.64	0.45
31:W:62:GLY:O	31:W:63:THR:OG1	2.27	0.45
35:a:136:G:O6	35:a:224:U:O2	2.34	0.45
44:j:10:LEU:H	44:j:10:LEU:HD23	1.82	0.45
47:m:82:ILE:HD12	47:m:93:ARG:HG2	1.98	0.45
9:A:1629:G:H4'	9:A:1630:U:OP2	2.16	0.45
35:a:465:G:O2'	35:a:466:U:P	2.75	0.45
35:a:1401:A:C8	35:a:1401:A:H3'	2.52	0.45
9:A:1099:A:OP2	9:A:1100:C:N4	2.50	0.45
9:A:1974:A:HO2'	9:A:1975:A:P	2.35	0.45
9:A:2154:G:H1'	9:A:2155:U:H5	1.81	0.45
1:1:13:ILE:HD12	9:A:1107:G:C8	2.51	0.45
6:6:29:ARG:NH1	6:6:41:THR:O	2.50	0.45
9:A:2133:G:C2	9:A:2134:G:C4	3.05	0.45
9:A:2138:C:C2'	9:A:2138:C:O2	2.64	0.45
14:F:86:LEU:HD22	14:F:92:ILE:CD1	2.46	0.45
34:Z:28:GLU:OE2	34:Z:46:ARG:NH1	2.49	0.45
35:a:912:C:N3	35:a:1370:G:N1	2.46	0.45
2:2:65:TYR:CG	53:s:67:VAL:HA	2.52	0.45
9:A:1493:A:O2'	9:A:1494:U:OP2	2.32	0.45
9:A:1599:U:O2'	9:A:1600:G:O5'	2.23	0.45
9:A:2137:A:H1'	35:a:1477:A:N1	2.31	0.45
13:E:14:THR:HG23	13:E:15:ASP:N	2.32	0.45
31:W:147:SER:OG	31:W:149:GLU:OE1	2.35	0.45
35:a:71:C:O2'	35:a:168:A:N3	2.49	0.45
2:2:42:HIS:N	2:2:43:PRO:HD2	2.32	0.45
9:A:672:C:H4'	26:R:31:LEU:HD13	1.97	0.45
9:A:789:G:O2'	13:E:68:GLN:OE1	2.34	0.45
10:B:7:G:H1	10:B:110:G:H22	1.64	0.45
35:a:687:U:C2	35:a:688:C:C5	3.05	0.45
35:a:708:A:N7	49:o:54:ARG:NE	2.65	0.45
9:A:669:G:O2'	9:A:1369:A:OP1	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:32:C:C4	10:B:51:G:N2	2.85	0.45
35:a:296:U:O2'	35:a:536:C:O2'	2.07	0.45
35:a:1336:C:O3'	44:j:50:CYS:HA	2.18	0.45
35:a:1396:A:N1	35:a:1472:G:C6	2.85	0.45
37:c:92:LYS:O	37:c:92:LYS:NZ	2.37	0.45
9:A:1630:U:H2'	9:A:1631:A:O4'	2.16	0.44
9:A:2271:C:O2'	9:A:3044:A:N1	2.50	0.44
9:A:2517:C:OP1	24:P:104:ARG:NH1	2.47	0.44
9:A:2862:G:O2'	9:A:3002:A:N6	2.49	0.44
2:2:65:TYR:HA	53:s:66:MET:HB2	1.99	0.44
9:A:663:A:N3	9:A:663:A:H2'	2.32	0.44
9:A:2142:A:C2	9:A:2143:A:N6	2.86	0.44
31:W:140:ILE:HG23	31:W:140:ILE:O	2.17	0.44
35:a:89:G:N1	35:a:90:G:O6	2.50	0.44
35:a:1007:U:H4'	35:a:1008:C:O5'	2.17	0.44
35:a:1014:U:H2'	35:a:1015:G:C8	2.52	0.44
42:h:5:ASP:HB3	42:h:8:ALA:HB3	2.00	0.44
9:A:1243:G:OP2	9:A:1244:A:O2'	2.31	0.44
9:A:3008:C:HO2'	9:A:3009:U:P	2.39	0.44
12:D:19:GLU:OE1	12:D:19:GLU:N	2.46	0.44
13:E:172:LEU:O	13:E:175:VAL:HG12	2.17	0.44
23:O:24:LEU:HB3	23:O:44:LEU:HD22	1.99	0.44
32:X:19:GLN:N	32:X:19:GLN:OE1	2.50	0.44
35:a:1335:G:H3'	35:a:1336:C:H5"	1.98	0.44
35:a:1352:C:H3'	44:j:63:GLU:CB	2.47	0.44
2:2:65:TYR:HB2	53:s:66:MET:O	2.18	0.44
9:A:52:G:O2'	9:A:124:A:N1	2.46	0.44
9:A:2074:G:O6	9:A:2075:G:N1	2.49	0.44
9:A:2123:A:C4	9:A:2127:G:C6	3.06	0.44
13:E:37:VAL:CG2	13:E:107:ILE:HG22	2.46	0.44
23:O:55:ALA:HB2	23:O:79:LEU:HD21	2.00	0.44
25:Q:13:ARG:NH1	25:Q:77:SER:O	2.49	0.44
35:a:1047:A:OP1	35:a:1072:A:O2'	2.36	0.44
9:A:265:A:N6	9:A:359:A:N7	2.65	0.44
9:A:619:C:N4	9:A:2244:A:N3	2.66	0.44
9:A:2025:C:O2	9:A:2025:C:O4'	2.35	0.44
9:A:2133:G:N1	9:A:2146:A:C6	2.86	0.44
11:C:109:GLN:N	11:C:195:GLU:O	2.45	0.44
37:c:12:LEU:HD23	37:c:13:GLY:N	2.32	0.44
3:3:28:VAL:HG13	9:A:3107:G:O3'	2.17	0.44
9:A:1303:U:C2	9:A:1304:A:C8	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1365:G:N7	21:M:21:ARG:NH1	2.66	0.44
9:A:2065:A:N6	35:a:682:A:H61	2.15	0.44
9:A:2332:U:O4	9:A:2402:C:N4	2.50	0.44
13:E:41:GLN:NE2	13:E:184:ASN:OD1	2.51	0.44
24:P:29:VAL:HG23	24:P:101:VAL:HG21	1.99	0.44
35:a:1405:G:C6	35:a:1463:G:C6	3.05	0.44
41:g:20:SER:CB	41:g:59:VAL:HG11	2.47	0.44
47:m:33:ILE:HG12	47:m:64:LEU:HD12	2.00	0.44
6:6:7:HIS:NE2	9:A:251:A:OP1	2.49	0.44
9:A:617:U:O2	9:A:2245:C:N4	2.50	0.44
14:F:119:ARG:NH1	47:m:71:ARG:O	2.51	0.44
30:V:88:ASP:OD1	30:V:88:ASP:N	2.51	0.44
35:a:354:G:H2'	35:a:354:G:N3	2.32	0.44
35:a:719:C:H2'	35:a:720:U:O4'	2.18	0.44
35:a:1109:C:O2'	35:a:1110:A:O5'	2.35	0.44
35:a:1285:C:O2'	35:a:1286:G:OP1	2.28	0.44
45:k:103:GLU:OE1	45:k:103:GLU:N	2.44	0.44
9:A:2139:U:C6	9:A:2140:A:C2	3.06	0.44
9:A:2579:C:H2'	9:A:2580:G:O4'	2.18	0.44
35:a:133:C:O2'	50:p:63:GLY:O	2.27	0.44
35:a:139:C:C2	35:a:221:G:N2	2.79	0.44
35:a:152:C:N4	35:a:164:G:O6	2.51	0.44
35:a:1268:C:N3	44:j:48:VAL:HG22	2.33	0.44
37:c:177:THR:HG22	37:c:179:ARG:H	1.82	0.44
51:q:38:VAL:HG21	51:q:76:LEU:HD11	2.00	0.44
6:6:45:ASP:OD1	6:6:46:GLY:N	2.47	0.44
14:F:120:ASP:N	47:m:73:GLU:HA	2.32	0.44
16:H:115:ARG:NH2	33:Y:42:PRO:O	2.45	0.44
35:a:1347:C:P	44:j:52:ILE:HD12	2.58	0.44
35:a:1401:A:H61	35:a:1466:G:C2'	2.31	0.44
41:g:56:THR:OG1	41:g:61:THR:OG1	2.33	0.44
53:s:47:HIS:O	53:s:62:VAL:HG21	2.18	0.44
9:A:2144:C:O2'	9:A:2145:C:H5'	2.18	0.43
9:A:2730:U:OP2	9:A:2800:G:N1	2.47	0.43
10:B:19:G:N2	10:B:65:C:O2	2.51	0.43
11:C:158:SER:O	11:C:161:VAL:HG12	2.18	0.43
35:a:895:A:H4'	35:a:896:A:O5'	2.18	0.43
35:a:1049:C:O2'	35:a:1173:C:O2	2.32	0.43
37:c:34:GLU:N	37:c:34:GLU:OE1	2.50	0.43
46:l:44:LYS:N	46:l:45:PRO:CD	2.80	0.43
9:A:805:C:O2'	11:C:43:ARG:NH2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1538:G:N1	9:A:1634:C:N3	2.45	0.43
9:A:2133:G:N2	9:A:2134:G:C4	2.85	0.43
9:A:2862:G:H22	9:A:2999:A:H2'	1.82	0.43
17:I:40:ARG:O	17:I:41:ARG:C	2.60	0.43
17:I:85:GLU:OE1	17:I:85:GLU:N	2.51	0.43
28:T:42:ILE:HG22	28:T:43:LEU:H	1.83	0.43
35:a:380:G:N1	35:a:384:G:O6	2.51	0.43
35:a:1202:G:H2'	35:a:1203:G:C1'	2.48	0.43
35:a:1308:C:H2'	35:a:1309:C:O4'	2.17	0.43
38:d:189:PRO:O	38:d:190:LEU:C	2.62	0.43
4:4:17:VAL:HG23	4:4:18:CYS:N	2.33	0.43
4:4:34:ASP:OD1	4:4:34:ASP:N	2.51	0.43
9:A:391:G:N2	9:A:411:G:O3'	2.51	0.43
9:A:1105:C:H2'	9:A:1106:A:O4'	2.16	0.43
9:A:1875:U:O4	9:A:1876:A:N6	2.49	0.43
9:A:1938:G:H21	9:A:1956:A:H62	1.65	0.43
9:A:2130:G:C5	9:A:2131:G:C8	3.06	0.43
9:A:2140:A:C6	9:A:2141:U:C4	3.06	0.43
12:D:86:LEU:HD12	12:D:92:VAL:HA	2.00	0.43
22:N:58:ILE:HD13	22:N:106:LEU:HD21	1.99	0.43
35:a:575:G:H21	35:a:576:C:N4	2.16	0.43
35:a:958:G:P	35:a:1340:U:HO2'	2.35	0.43
35:a:1396:A:N6	35:a:1472:G:O6	2.51	0.43
9:A:2623:A:N6	9:A:2642:G:O6	2.52	0.43
27:S:70:GLY:O	27:S:91:ARG:NH2	2.45	0.43
34:Z:14:THR:OG1	34:Z:15:ASP:N	2.52	0.43
35:a:244:U:H3	35:a:875:C:H42	1.66	0.43
35:a:746:A:OP2	35:a:792:G:N2	2.48	0.43
39:e:106:ILE:HD11	39:e:122:ARG:C	2.44	0.43
42:h:47:SER:OG	42:h:64:LEU:O	2.29	0.43
47:m:65:LYS:HB3	47:m:69:ASP:HB3	2.00	0.43
9:A:444:U:OP1	9:A:446:G:H4'	2.19	0.43
9:A:1035:G:N2	9:A:2493:A:O4'	2.51	0.43
9:A:2342:A:H61	9:A:2390:U:H1'	1.83	0.43
10:B:44:C:O2'	10:B:47:A:N6	2.51	0.43
1:1:10:ARG:NH1	9:A:1118:A:O2'	2.51	0.43
9:A:1938:G:H21	9:A:1956:A:N6	2.17	0.43
9:A:2699:C:H42	9:A:2753:G:N2	2.16	0.43
11:C:105:ILE:HG22	11:C:106:ILE:N	2.33	0.43
13:E:54:THR:O	13:E:58:VAL:HG23	2.19	0.43
20:L:80:ASP:OD2	25:Q:61:ARG:NH2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:a:81:C:H3'	35:a:82:U:H5"	2.00	0.43
35:a:234:C:O3'	51:q:87:ARG:NH2	2.50	0.43
35:a:1058:U:O4	35:a:1059:G:N2	2.52	0.43
9:A:190:A:H2'	9:A:191:G:N3	2.34	0.43
9:A:1169:A:N6	9:A:1227:C:N3	2.66	0.43
9:A:1254:G:H2'	9:A:1255:G:C8	2.53	0.43
9:A:1874:C:OP1	12:D:146:ARG:NE	2.47	0.43
47:m:72:ARG:O	47:m:72:ARG:HG3	2.18	0.43
9:A:1373:A:N6	9:A:1374:G:O6	2.52	0.43
9:A:1612:U:N3	9:A:1613:G:O6	2.50	0.43
9:A:1971:C:OP1	25:Q:93:ARG:NE	2.48	0.43
10:B:7:G:H22	10:B:110:G:H22	1.67	0.43
10:B:34:G:N2	10:B:36:U:O4	2.50	0.43
25:Q:63:GLU:OE2	25:Q:67:VAL:N	2.51	0.43
35:a:134:C:N4	35:a:227:G:O6	2.52	0.43
35:a:873:U:O2	35:a:874:A:C8	2.71	0.43
42:h:15:ARG:NH2	42:h:77:LEU:O	2.52	0.43
43:i:48:PHE:HE2	43:i:103:ILE:HD11	1.83	0.43
46:l:90:LEU:O	46:l:93:VAL:HG12	2.18	0.43
9:A:208:C:C2	9:A:209:C:C5	3.06	0.43
9:A:391:G:N7	9:A:412:A:N6	2.67	0.43
9:A:445:U:H4'	9:A:446:G:O5'	2.19	0.43
9:A:2024:G:OP1	11:C:48:ARG:NH1	2.52	0.43
10:B:34:G:O2'	10:B:35:G:P	2.74	0.43
12:D:161:PHE:O	12:D:162:LYS:C	2.62	0.43
14:F:122:ARG:NH2	47:m:77:ASP:OD2	2.51	0.43
28:T:84:ASP:OD2	28:T:85:GLU:N	2.47	0.43
35:a:199:C:H3'	35:a:200:U:C5'	2.49	0.43
35:a:731:U:H2'	35:a:732:G:O4'	2.19	0.43
36:b:151:ILE:O	36:b:151:ILE:HG22	2.18	0.43
38:d:137:ILE:HG22	38:d:139:ASP:OD1	2.19	0.43
40:f:15:ASP:OD1	40:f:15:ASP:N	2.50	0.43
9:A:858:A:N6	9:A:870:G:O6	2.51	0.43
9:A:1071:G:O2'	9:A:2498:A:N1	2.29	0.43
9:A:2245:C:H2'	9:A:2245:C:O2	2.19	0.43
9:A:2920:U:O4	9:A:2938:G:N1	2.52	0.43
14:F:108:ASP:OD1	14:F:108:ASP:C	2.60	0.43
15:G:23:ASN:OD1	15:G:24:LEU:N	2.51	0.43
31:W:85:VAL:HG12	31:W:92:ILE:HD13	2.01	0.43
1:1:21:GLU:OE1	9:A:964:C:O2'	2.32	0.42
9:A:736:G:HO2'	9:A:2573:G:HO2'	1.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2021:G:O6	9:A:2031:G:N2	2.52	0.42
14:F:122:ARG:NH2	47:m:81:LYS:HB2	2.34	0.42
16:H:109:GLY:N	16:H:110:PRO:CD	2.81	0.42
17:I:37:ALA:O	17:I:39:LEU:O	2.37	0.42
35:a:664:U:O2	45:k:50:VAL:HG12	2.19	0.42
35:a:1174:G:O2'	39:e:52:GLY:O	2.37	0.42
38:d:15:LEU:HD11	38:d:58:PHE:HD2	1.83	0.42
52:r:61:GLN:O	52:r:61:GLN:NE2	2.52	0.42
9:A:1338:U:O3'	27:S:89:GLY:N	2.51	0.42
9:A:2349:A:N6	9:A:2385:G:O3'	2.52	0.42
14:F:119:ARG:CA	47:m:76:ALA:HB3	2.49	0.42
23:O:61:HIS:O	23:O:61:HIS:CG	2.72	0.42
9:A:2125:A:C2	9:A:2126:C:C2	3.06	0.42
9:A:2150:U:O2	9:A:2153:G:C5	2.72	0.42
16:H:111:ASN:OD1	16:H:112:LEU:N	2.52	0.42
35:a:220:G:C2	35:a:221:G:C8	3.08	0.42
35:a:355:C:C2	35:a:356:A:C8	3.06	0.42
41:g:38:LEU:HD23	41:g:42:ILE:HD12	2.00	0.42
47:m:69:ASP:O	47:m:73:GLU:HG2	2.20	0.42
9:A:905:U:O2	9:A:905:U:H2'	2.19	0.42
9:A:1165:G:HO2'	9:A:1228:A:N6	2.15	0.42
9:A:2980:U:H4'	9:A:2981:A:OP1	2.19	0.42
14:F:85:LYS:O	14:F:86:LEU:HD23	2.19	0.42
35:a:1105:U:HO2'	35:a:1106:U:P	2.36	0.42
35:a:1119:U:O2	35:a:1119:U:H2'	2.20	0.42
38:d:66:GLN:NE2	38:d:70:TYR:OH	2.52	0.42
44:j:62:ARG:O	44:j:63:GLU:OE2	2.36	0.42
9:A:167:G:O2'	9:A:2432:G:O2'	2.23	0.42
9:A:2134:G:C2	9:A:2145:C:O2	2.73	0.42
9:A:2515:U:O2	9:A:2598:C:O2'	2.35	0.42
9:A:2558:C:O3'	24:P:27:LYS:NZ	2.53	0.42
9:A:2655:U:N3	9:A:2658:A:OP2	2.48	0.42
35:a:229:U:O2'	50:p:24:ASP:OD2	2.21	0.42
35:a:991:C:N4	35:a:1004:G:O6	2.52	0.42
42:h:50:ARG:O	42:h:60:LEU:HD12	2.20	0.42
9:A:1001:C:H3'	9:A:1002:C:C5'	2.50	0.42
9:A:1084:U:H4'	9:A:1085:G:OP2	2.19	0.42
9:A:1192:G:C2	9:A:1193:C:C5	3.08	0.42
9:A:2488:C:H2'	9:A:2489:U:O4'	2.19	0.42
30:V:46:ALA:C	30:V:56:SER:HA	2.45	0.42
33:Y:33:ILE:O	33:Y:34:GLN:NE2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:e:186:ILE:HG22	39:e:187:GLU:N	2.34	0.42
45:k:45:ASP:OD1	45:k:49:ASN:N	2.53	0.42
9:A:107:G:C2	9:A:108:A:C8	3.08	0.42
9:A:563:U:O4	9:A:567:A:N7	2.53	0.42
9:A:679:G:OP2	21:M:24:ARG:NH2	2.52	0.42
9:A:1294:U:H2'	9:A:1295:U:C6	2.55	0.42
9:A:1613:G:H2'	9:A:1614:G:C8	2.55	0.42
9:A:2132:U:H5"	9:A:2132:U:C6	2.53	0.42
9:A:2720:C:H2'	9:A:2721:A:O4'	2.19	0.42
22:N:11:LYS:NZ	22:N:87:LYS:O	2.44	0.42
35:a:759:C:H2'	35:a:760:G:O4'	2.20	0.42
35:a:930:C:O2	35:a:931:A:C8	2.73	0.42
35:a:1473:A:H8	35:a:1473:A:OP2	2.02	0.42
45:k:84:GLN:NE2	45:k:113:GLY:O	2.53	0.42
9:A:755:A:C6	9:A:756:A:N6	2.88	0.42
13:E:131:VAL:O	13:E:132:GLU:C	2.63	0.42
14:F:141:GLU:O	14:F:158:GLY:N	2.53	0.42
35:a:590:A:N3	35:a:590:A:H2'	2.35	0.42
35:a:941:A:O2'	35:a:966:C:O2'	2.16	0.42
35:a:1391:A:H8	35:a:1391:A:O5'	2.00	0.42
43:i:69:LYS:O	43:i:73:VAL:N	2.53	0.42
9:A:222:A:N1	9:A:495:C:O2'	2.40	0.42
9:A:2682:G:H21	9:A:2683:A:N6	2.18	0.42
14:F:43:VAL:HG12	14:F:161:ILE:HG23	2.01	0.42
16:H:96:THR:OG1	16:H:97:ALA:N	2.52	0.42
35:a:587:A:OP1	35:a:611:G:N2	2.38	0.42
35:a:1114:C:H3'	35:a:1115:G:H5"	2.01	0.42
35:a:1118:A:N6	35:a:1243:U:O4'	2.50	0.42
9:A:797:G:C2'	9:A:798:U:O5'	2.68	0.42
9:A:894:U:H5"	11:C:49:ILE:HD12	2.01	0.42
9:A:1461:G:N1	9:A:1818:C:N3	2.47	0.42
9:A:1464:A:H3'	9:A:1465:C:C5'	2.50	0.42
11:C:106:ILE:HG22	11:C:106:ILE:O	2.19	0.42
13:E:27:VAL:HG13	13:E:113:GLY:HA2	2.01	0.42
35:a:99:U:OP1	54:t:12:ARG:NH2	2.53	0.42
35:a:821:C:O2'	35:a:822:U:OP1	2.35	0.42
38:d:83:ASP:OD1	38:d:84:ASN:N	2.53	0.42
2:2:65:TYR:HA	53:s:66:MET:CB	2.50	0.41
9:A:709:U:O2'	13:E:184:ASN:ND2	2.47	0.41
9:A:1102:G:OP2	9:A:1102:G:N2	2.44	0.41
9:A:1951:G:C2	9:A:1952:C:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2143:A:H3'	9:A:2144:C:H5'	2.02	0.41
9:A:2973:A:OP2	9:A:2974:A:O2'	2.36	0.41
9:A:3046:C:O2	9:A:3046:C:O4'	2.37	0.41
11:C:151:GLY:O	11:C:154:LYS:NZ	2.53	0.41
35:a:436:C:H2'	35:a:437:U:C6	2.55	0.41
37:c:191:THR:OG1	37:c:192:THR:N	2.51	0.41
50:p:92:THR:HG22	50:p:92:THR:O	2.20	0.41
5:5:14:ARG:NH1	9:A:801:U:O4'	2.46	0.41
9:A:690:G:N2	21:M:15:GLU:O	2.53	0.41
9:A:1787:A:O2'	11:C:63:ARG:NH1	2.53	0.41
10:B:89:C:C2	10:B:90:G:C8	3.08	0.41
11:C:145:VAL:HG22	11:C:191:ALA:CB	2.51	0.41
34:Z:13:LEU:O	34:Z:64:ARG:NH1	2.49	0.41
35:a:973:U:H3	35:a:1193:U:HO2'	1.51	0.41
35:a:1068:G:C6	35:a:1069:G:C6	3.08	0.41
35:a:1219:A:N1	35:a:1281:A:N6	2.68	0.41
35:a:1297:U:H2'	35:a:1298:G:O4'	2.20	0.41
35:a:1337:A:O2'	35:a:1338:G:C5'	2.68	0.41
38:d:154:ARG:NH1	38:d:171:GLU:OE2	2.53	0.41
9:A:74:C:O3'	34:Z:11:ARG:NH1	2.53	0.41
9:A:382:A:N6	9:A:399:G:O6	2.53	0.41
9:A:736:G:N2	9:A:739:U:OP2	2.49	0.41
9:A:932:C:H2'	9:A:933:G:O4'	2.20	0.41
9:A:1675:U:O2'	9:A:1676:G:N7	2.53	0.41
9:A:2137:A:C4	35:a:1477:A:C5	3.08	0.41
10:B:75:U:H1'	31:W:36:VAL:HG21	2.03	0.41
11:C:62:TYR:CE2	11:C:64:VAL:HG12	2.55	0.41
14:F:117:ARG:NH1	14:F:145:PHE:O	2.53	0.41
17:I:37:ALA:O	17:I:41:ARG:HB2	2.20	0.41
26:R:69:ALA:HB1	26:R:74:ILE:HG23	2.02	0.41
31:W:33:VAL:O	31:W:33:VAL:HG23	2.20	0.41
31:W:100:VAL:HG23	31:W:102:ARG:H	1.85	0.41
35:a:875:C:C2	35:a:876:G:C8	3.08	0.41
35:a:1076:C:H2'	35:a:1077:C:C6	2.55	0.41
35:a:1353:G:O4'	44:j:64:HIS:N	2.53	0.41
37:c:46:LEU:HD11	37:c:75:VAL:HG21	2.02	0.41
47:m:4:LEU:HG	47:m:5:VAL:H	1.85	0.41
51:q:84:ALA:O	51:q:85:THR:OG1	2.33	0.41
2:2:62:GLU:O	53:s:67:VAL:C	2.63	0.41
8:8:8:LYS:NZ	9:A:1078:G:O6	2.51	0.41
9:A:14:G:C6	9:A:611:U:N3	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1225:G:H21	17:I:33:VAL:CG1	2.33	0.41
9:A:1227:C:H4'	9:A:1228:A:OP1	2.20	0.41
9:A:1361:G:O2'	13:E:46:ARG:NH2	2.44	0.41
9:A:2138:C:C5	35:a:1392:C:O3'	2.74	0.41
14:F:47:VAL:HG22	14:F:93:GLY:N	2.35	0.41
35:a:544:C:OP1	46:l:12:ARG:NE	2.53	0.41
35:a:1350:U:C2'	35:a:1351:G:OP1	2.68	0.41
35:a:1392:C:O2	35:a:1392:C:H2'	2.19	0.41
35:a:1393:G:H4'	35:a:1394:U:OP1	2.20	0.41
35:a:1401:A:C8	35:a:1401:A:C3'	3.04	0.41
37:c:12:LEU:HD21	48:n:51:GLY:O	2.21	0.41
9:A:191:G:N2	9:A:191:G:OP2	2.53	0.41
9:A:502:C:O3'	9:A:2102:G:N2	2.53	0.41
9:A:665:G:N1	9:A:2255:A:OP1	2.52	0.41
9:A:958:A:N6	9:A:1053:G:O6	2.53	0.41
9:A:1989:G:H21	9:A:1991:C:H5"	1.86	0.41
35:a:496:U:O4	35:a:513:A:N7	2.53	0.41
35:a:574:C:O3'	35:a:575:G:O4'	2.39	0.41
35:a:647:G:OP1	35:a:712:C:O2'	2.28	0.41
9:A:670:A:OP1	9:A:1370:U:O2'	2.38	0.41
9:A:1425:G:O6	9:A:1823:C:N4	2.54	0.41
9:A:1794:C:C2	9:A:1795:C:C5	3.08	0.41
9:A:2065:A:C8	35:a:682:A:C4	3.09	0.41
25:Q:26:ASN:OD1	25:Q:26:ASN:N	2.51	0.41
32:X:56:ASP:OD1	32:X:57:ASP:N	2.48	0.41
35:a:632:U:O4	35:a:732:G:O2'	2.38	0.41
35:a:941:A:N3	35:a:1202:G:N2	2.69	0.41
35:a:1263:C:H2'	35:a:1264:C:O4'	2.21	0.41
46:l:14:ASP:OD1	46:l:15:LYS:N	2.50	0.41
47:m:82:ILE:CG2	47:m:83:GLU:N	2.83	0.41
9:A:2095:G:C2	9:A:2096:G:N7	2.88	0.41
9:A:2950:C:O3'	20:L:1:MET:HE1	2.19	0.41
11:C:163:ILE:HG21	11:C:175:LEU:HB3	2.03	0.41
14:F:120:ASP:HB3	47:m:77:ASP:HB2	2.01	0.41
35:a:1372:C:H2'	35:a:1373:U:O4'	2.20	0.41
35:a:1402:G:O2'	35:a:1403:U:H5'	2.20	0.41
43:i:32:ARG:HG3	43:i:33:LYS:H	1.85	0.41
48:n:23:ARG:O	48:n:24:CYS:C	2.64	0.41
9:A:813:C:O2'	9:A:849:A:N6	2.54	0.41
9:A:1378:U:H2'	9:A:1379:G:O4'	2.21	0.41
9:A:1884:G:N3	20:L:3:GLN:NE2	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2727:A:O2'	9:A:2729:G:OP2	2.28	0.41
10:B:30:G:H2'	10:B:30:G:N3	2.36	0.41
13:E:41:GLN:OE1	13:E:184:ASN:ND2	2.53	0.41
23:O:37:THR:HG22	23:O:39:PRO:HD2	2.03	0.41
35:a:1349:C:C2'	35:a:1350:U:OP1	2.67	0.41
44:j:22:ALA:O	44:j:26:VAL:HG12	2.21	0.41
1:1:21:GLU:HA	1:1:24:ARG:HG2	2.02	0.41
9:A:1124:C:O2'	19:K:108:MET:O	2.26	0.41
9:A:1173:G:H21	9:A:1203:A:H1'	1.86	0.41
9:A:1349:U:H2'	9:A:1350:G:O4'	2.21	0.41
9:A:1598:U:N3	9:A:1601:G:O6	2.53	0.41
9:A:1847:U:O4	9:A:1848:A:N6	2.52	0.41
9:A:1982:G:C6	9:A:2212:A:N6	2.89	0.41
9:A:2014:G:C6	9:A:2040:G:C6	3.09	0.41
9:A:2125:A:N3	9:A:2126:C:C6	2.89	0.41
9:A:2909:G:OP1	25:Q:48:ARG:NH1	2.54	0.41
9:A:3106:C:H3'	9:A:3107:G:C5'	2.51	0.41
19:K:105:ILE:HG21	19:K:122:LEU:HD22	2.03	0.41
26:R:43:LEU:HD13	27:S:76:HIS:HB2	2.03	0.41
29:U:8:ARG:NE	29:U:49:ILE:HD12	2.36	0.41
35:a:1063:U:H3'	35:a:1064:G:C8	2.55	0.41
35:a:1338:G:N3	35:a:1338:G:H2'	2.36	0.41
35:a:1400:A:C2	35:a:1468:U:O4	2.74	0.41
47:m:66:VAL:O	47:m:67:GLU:C	2.63	0.41
48:n:4:LYS:HA	48:n:7:VAL:HG22	2.03	0.41
9:A:402:G:O6	13:E:142:LYS:NZ	2.43	0.41
9:A:2532:G:H2'	9:A:2532:G:N3	2.36	0.41
9:A:3008:C:O2'	9:A:3009:U:OP1	2.36	0.41
35:a:527:A:OP2	38:d:2:ALA:N	2.54	0.41
52:r:64:ILE:O	52:r:65:ALA:C	2.63	0.41
9:A:465:A:N6	9:A:486:G:O6	2.54	0.40
9:A:503:A:N6	9:A:2633:G:O6	2.55	0.40
9:A:2128:G:H1'	9:A:2151:A:N1	2.36	0.40
9:A:2973:A:O3'	15:G:63:ARG:NH1	2.54	0.40
12:D:28:VAL:HG13	12:D:191:VAL:HG13	2.04	0.40
35:a:100:G:N7	54:t:9:LYS:NZ	2.65	0.40
35:a:179:C:O2	35:a:179:C:H2'	2.21	0.40
51:q:90:LEU:HD21	51:q:93:ILE:CD1	2.51	0.40
53:s:7:LYS:C	53:s:9:PRO:HD3	2.46	0.40
9:A:1111:G:H4'	27:S:73:ILE:HD12	2.02	0.40
10:B:76:G:H2'	10:B:77:A:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:P:99:THR:O	24:P:99:THR:HG23	2.21	0.40
31:W:72:GLU:OE1	31:W:72:GLU:N	2.55	0.40
35:a:365:U:H2'	35:a:365:U:O2	2.21	0.40
35:a:496:U:H3	35:a:513:A:H62	1.70	0.40
35:a:1453:A:C2	35:a:1454:G:C8	3.09	0.40
35:a:1455:G:H2'	35:a:1456:U:C6	2.56	0.40
43:i:41:LEU:HD12	43:i:83:ILE:HD13	2.02	0.40
9:A:377:C:H2'	9:A:378:G:H8	1.87	0.40
9:A:467:C:O2'	9:A:2456:C:OP1	2.36	0.40
9:A:1124:C:H2'	9:A:1125:C:C1'	2.51	0.40
9:A:1950:G:C2	9:A:1951:G:N7	2.90	0.40
9:A:2820:U:H4'	9:A:2821:G:OP1	2.20	0.40
14:F:42:VAL:HG12	14:F:97:THR:HG23	2.02	0.40
18:J:67:SER:OG	18:J:68:PHE:N	2.55	0.40
18:J:118:LEU:CD2	18:J:129:ILE:HG21	2.50	0.40
22:N:55:ASN:ND2	31:W:190:LEU:O	2.55	0.40
31:W:19:THR:OG1	31:W:20:GLY:N	2.55	0.40
31:W:133:ILE:HG23	31:W:168:VAL:CG1	2.52	0.40
35:a:933:G:OP1	35:a:959:A:N6	2.54	0.40
35:a:991:C:C2	35:a:1004:G:N2	2.83	0.40
9:A:948:G:OP2	21:M:41:LYS:NZ	2.35	0.40
9:A:2150:U:H2'	9:A:2152:A:N7	2.36	0.40
9:A:2971:G:H21	9:A:2981:A:H62	1.70	0.40
35:a:653:G:H2'	35:a:654:G:H8	1.85	0.40
35:a:714:G:N2	52:r:73:GLU:OE1	2.54	0.40
35:a:911:G:O3'	36:b:170:HIS:NE2	2.55	0.40
47:m:48:LEU:HD12	47:m:48:LEU:C	2.46	0.40
9:A:1988:C:H2'	9:A:1989:G:O4'	2.22	0.40
9:A:2680:C:N3	9:A:2681:U:C5	2.89	0.40
14:F:43:VAL:O	14:F:43:VAL:HG23	2.20	0.40
22:N:119:THR:HA	22:N:122:ILE:HG22	2.04	0.40
41:g:27:VAL:O	41:g:31:LEU:HG	2.22	0.40
50:p:7:LEU:HD12	50:p:18:TYR:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
2	2	64/75 (85%)	61 (95%)	3 (5%)	0	100	100
3	3	52/57 (91%)	52 (100%)	0	0	100	100
4	4	48/55 (87%)	40 (83%)	8 (17%)	0	100	100
5	5	43/47 (92%)	42 (98%)	1 (2%)	0	100	100
6	6	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
7	7	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
8	8	21/24 (88%)	21 (100%)	0	0	100	100
11	C	271/278 (98%)	259 (96%)	12 (4%)	0	100	100
12	D	212/217 (98%)	201 (95%)	11 (5%)	0	100	100
13	E	205/215 (95%)	185 (90%)	20 (10%)	0	100	100
14	F	179/187 (96%)	161 (90%)	18 (10%)	0	100	100
15	G	174/179 (97%)	171 (98%)	3 (2%)	0	100	100
16	H	149/151 (99%)	140 (94%)	9 (6%)	0	100	100
17	I	124/174 (71%)	119 (96%)	4 (3%)	1 (1%)	16	47
18	J	131/142 (92%)	128 (98%)	3 (2%)	0	100	100
19	K	145/147 (99%)	140 (97%)	5 (3%)	0	100	100
20	L	119/122 (98%)	108 (91%)	11 (9%)	0	100	100
21	M	143/147 (97%)	138 (96%)	5 (4%)	0	100	100
22	N	132/138 (96%)	126 (96%)	6 (4%)	0	100	100
23	O	115/174 (66%)	110 (96%)	5 (4%)	0	100	100
24	P	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
25	Q	111/113 (98%)	107 (96%)	4 (4%)	0	100	100
26	R	122/129 (95%)	121 (99%)	1 (1%)	0	100	100
27	S	100/103 (97%)	99 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	T	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
29	U	92/100 (92%)	84 (91%)	8 (9%)	0	100	100
30	V	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
31	W	186/215 (86%)	178 (96%)	8 (4%)	0	100	100
32	X	80/88 (91%)	68 (85%)	12 (15%)	0	100	100
33	Y	61/64 (95%)	61 (100%)	0	0	100	100
34	Z	61/77 (79%)	59 (97%)	2 (3%)	0	100	100
36	b	226/277 (82%)	222 (98%)	4 (2%)	0	100	100
37	c	208/275 (76%)	190 (91%)	18 (9%)	0	100	100
38	d	198/201 (98%)	192 (97%)	6 (3%)	0	100	100
39	e	196/214 (92%)	190 (97%)	6 (3%)	0	100	100
40	f	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
41	g	154/156 (99%)	149 (97%)	5 (3%)	0	100	100
42	h	128/132 (97%)	124 (97%)	4 (3%)	0	100	100
43	i	124/150 (83%)	116 (94%)	8 (6%)	0	100	100
44	j	95/101 (94%)	82 (86%)	13 (14%)	0	100	100
45	k	115/138 (83%)	110 (96%)	5 (4%)	0	100	100
46	l	120/124 (97%)	108 (90%)	12 (10%)	0	100	100
47	m	114/124 (92%)	102 (90%)	12 (10%)	0	100	100
48	n	58/61 (95%)	52 (90%)	6 (10%)	0	100	100
49	o	85/89 (96%)	84 (99%)	1 (1%)	0	100	100
50	p	111/156 (71%)	105 (95%)	6 (5%)	0	100	100
51	q	90/98 (92%)	87 (97%)	3 (3%)	0	100	100
52	r	62/84 (74%)	55 (89%)	7 (11%)	0	100	100
53	s	76/93 (82%)	69 (91%)	7 (9%)	0	100	100
54	t	82/86 (95%)	82 (100%)	0	0	100	100
55	u	30/33 (91%)	29 (97%)	1 (3%)	0	100	100
All	All	5989/6653 (90%)	5688 (95%)	300 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	I	39	LEU

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	53/54 (98%)	53 (100%)	0	100	100
2	2	57/63 (90%)	56 (98%)	1 (2%)	51	71
3	3	43/46 (94%)	43 (100%)	0	100	100
4	4	48/52 (92%)	48 (100%)	0	100	100
5	5	35/36 (97%)	35 (100%)	0	100	100
6	6	53/54 (98%)	53 (100%)	0	100	100
7	7	35/35 (100%)	34 (97%)	1 (3%)	37	63
8	8	18/19 (95%)	18 (100%)	0	100	100
11	C	214/218 (98%)	214 (100%)	0	100	100
12	D	160/163 (98%)	158 (99%)	2 (1%)	61	75
13	E	167/173 (96%)	163 (98%)	4 (2%)	43	67
14	F	150/156 (96%)	150 (100%)	0	100	100
15	G	148/150 (99%)	147 (99%)	1 (1%)	76	81
16	H	90/116 (78%)	90 (100%)	0	100	100
17	I	89/120 (74%)	88 (99%)	1 (1%)	65	77
18	J	102/108 (94%)	102 (100%)	0	100	100
19	K	117/120 (98%)	117 (100%)	0	100	100
20	L	99/100 (99%)	99 (100%)	0	100	100
21	M	112/114 (98%)	112 (100%)	0	100	100
22	N	110/116 (95%)	109 (99%)	1 (1%)	70	79
23	O	96/138 (70%)	93 (97%)	3 (3%)	35	62
24	P	93/94 (99%)	93 (100%)	0	100	100
25	Q	100/100 (100%)	100 (100%)	0	100	100
26	R	97/99 (98%)	97 (100%)	0	100	100
27	S	82/83 (99%)	81 (99%)	1 (1%)	63	76
28	T	90/117 (77%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	U	82/85 (96%)	82 (100%)	0	100	100
30	V	81/86 (94%)	79 (98%)	2 (2%)	42	66
31	W	154/168 (92%)	154 (100%)	0	100	100
32	X	59/63 (94%)	59 (100%)	0	100	100
33	Y	50/51 (98%)	50 (100%)	0	100	100
34	Z	58/66 (88%)	57 (98%)	1 (2%)	53	72
36	b	191/218 (88%)	189 (99%)	2 (1%)	68	78
37	c	171/212 (81%)	171 (100%)	0	100	100
38	d	175/176 (99%)	174 (99%)	1 (1%)	78	83
39	e	139/147 (95%)	138 (99%)	1 (1%)	76	81
40	f	85/85 (100%)	83 (98%)	2 (2%)	43	67
41	g	132/132 (100%)	132 (100%)	0	100	100
42	h	106/108 (98%)	105 (99%)	1 (1%)	70	79
43	i	102/125 (82%)	101 (99%)	1 (1%)	68	78
44	j	88/90 (98%)	86 (98%)	2 (2%)	44	68
45	k	91/105 (87%)	90 (99%)	1 (1%)	65	77
46	l	103/105 (98%)	103 (100%)	0	100	100
47	m	99/104 (95%)	98 (99%)	1 (1%)	68	78
48	n	49/50 (98%)	46 (94%)	3 (6%)	17	47
49	o	75/77 (97%)	74 (99%)	1 (1%)	61	75
50	p	92/118 (78%)	91 (99%)	1 (1%)	65	77
51	q	78/83 (94%)	78 (100%)	0	100	100
52	r	55/72 (76%)	54 (98%)	1 (2%)	51	71
53	s	69/84 (82%)	68 (99%)	1 (1%)	59	74
54	t	69/70 (99%)	69 (100%)	0	100	100
55	u	30/31 (97%)	30 (100%)	0	100	100
All	All	4941/5355 (92%)	4904 (99%)	37 (1%)	73	81

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	2	61	PHE
7	7	8	LYS

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Mol	Chain	Res	Type
12	D	92	VAL
12	D	182	VAL
13	E	33	LEU
13	E	37	VAL
13	E	78	SER
13	E	150	GLU
15	G	137	ILE
17	I	39	LEU
22	N	92	TRP
23	O	37	THR
23	O	79	LEU
23	O	113	ILE
27	S	78	PHE
30	V	35	VAL
30	V	88	ASP
34	Z	5	THR
36	b	60	THR
36	b	72	THR
38	d	188	VAL
39	e	172	LEU
40	f	43	TRP
40	f	65	VAL
42	h	51	THR
43	i	93	SER
44	j	51	VAL
44	j	75	ASP
45	k	78	ASN
47	m	11	ARG
48	n	3	LYS
48	n	12	LYS
48	n	24	CYS
49	o	37	GLN
50	p	105	LEU
52	r	70	ASN
53	s	69	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	8	GLN
12	D	178	GLN
13	E	47	GLN

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Mol	Chain	Res	Type
13	E	151	ASN
13	E	208	ASN
14	F	34	GLN
16	H	130	HIS
17	I	100	ASN
20	L	51	ASN
21	M	7	HIS
21	M	107	ASN
22	N	96	ASN
26	R	27	GLN
29	U	41	GLN
29	U	58	ASN
31	W	161	GLN
33	Y	20	HIS
36	b	94	GLN
36	b	167	ASN
37	c	27	GLN
38	d	66	GLN
38	d	117	HIS
39	e	163	HIS
41	g	68	ASN
42	h	35	ASN
43	i	146	GLN
45	k	84	GLN
45	k	110	GLN
49	o	42	HIS
52	r	61	GLN
54	t	52	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	116/118 (98%)	19 (16%)	2 (1%)
35	a	1504/1528 (98%)	275 (18%)	0
9	A	3096/3120 (99%)	534 (17%)	32 (1%)
All	All	4716/4766 (98%)	828 (17%)	34 (0%)

All (828) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	7	U

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Mol	Chain	Res	Type
9	A	19	U
9	A	20	G
9	A	24	G
9	A	31	U
9	A	43	C
9	A	60	A
9	A	68	A
9	A	71	A
9	A	72	G
9	A	81	A
9	A	90	C
9	A	94	G
9	A	98	U
9	A	99	G
9	A	115	A
9	A	117	U
9	A	122	A
9	A	125	C
9	A	126	C
9	A	161	U
9	A	189	A
9	A	195	A
9	A	212	A
9	A	214	G
9	A	215	A
9	A	221	A
9	A	227	A
9	A	228	A
9	A	229	U
9	A	248	G
9	A	264	G
9	A	283	U
9	A	285	U
9	A	286	G
9	A	287	A
9	A	288	U
9	A	289	A
9	A	290	C
9	A	292	G
9	A	297	G
9	A	298	G
9	A	299	G

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Mol	Chain	Res	Type
9	A	300	G
9	A	301	U
9	A	302	U
9	A	303	G
9	A	312	G
9	A	314	G
9	A	315	U
9	A	317	G
9	A	318	U
9	A	319	G
9	A	322	A
9	A	323	C
9	A	331	U
9	A	337	U
9	A	338	C
9	A	351	G
9	A	352	G
9	A	357	U
9	A	358	G
9	A	361	A
9	A	364	A
9	A	370	U
9	A	371	G
9	A	384	G
9	A	393	U
9	A	399	G
9	A	404	A
9	A	412	A
9	A	434	G
9	A	437	G
9	A	438	U
9	A	444	U
9	A	445	U
9	A	446	G
9	A	450	G
9	A	452	G
9	A	454	U
9	A	459	A
9	A	460	G
9	A	468	G
9	A	474	G
9	A	475	U

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Mol	Chain	Res	Type
9	A	489	A
9	A	494	G
9	A	498	G
9	A	499	G
9	A	512	G
9	A	523	U
9	A	543	U
9	A	544	U
9	A	552	U
9	A	553	G
9	A	566	A
9	A	569	G
9	A	589	A
9	A	591	G
9	A	592	A
9	A	594	U
9	A	595	A
9	A	596	C
9	A	597	C
9	A	605	G
9	A	617	U
9	A	618	C
9	A	619	C
9	A	620	G
9	A	639	C
9	A	640	G
9	A	642	G
9	A	644	G
9	A	647	G
9	A	655	G
9	A	658	U
9	A	665	G
9	A	667	A
9	A	669	G
9	A	678	A
9	A	684	G
9	A	696	A
9	A	706	G
9	A	707	G
9	A	708	G
9	A	709	U
9	A	721	A

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Mol	Chain	Res	Type
9	A	722	G
9	A	731	A
9	A	738	A
9	A	740	A
9	A	741	G
9	A	754	C
9	A	757	G
9	A	758	A
9	A	760	U
9	A	765	G
9	A	774	G
9	A	790	A
9	A	794	G
9	A	798	U
9	A	801	U
9	A	839	U
9	A	841	G
9	A	845	C
9	A	855	C
9	A	862	U
9	A	863	G
9	A	868	C
9	A	872	G
9	A	890	G
9	A	897	A
9	A	899	G
9	A	917	A
9	A	920	G
9	A	927	C
9	A	942	U
9	A	960	G
9	A	961	U
9	A	972	A
9	A	974	G
9	A	975	U
9	A	981	U
9	A	994	A
9	A	1000	C
9	A	1001	C
9	A	1002	C
9	A	1003	A
9	A	1008	G

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Mol	Chain	Res	Type
9	A	1009	U
9	A	1011	A
9	A	1014	G
9	A	1025	A
9	A	1045	C
9	A	1046	C
9	A	1047	A
9	A	1048	A
9	A	1049	G
9	A	1063	G
9	A	1070	G
9	A	1076	A
9	A	1078	G
9	A	1085	G
9	A	1092	G
9	A	1101	A
9	A	1114	G
9	A	1127	A
9	A	1130	C
9	A	1131	G
9	A	1138	A
9	A	1144	A
9	A	1151	U
9	A	1164	A
9	A	1175	A
9	A	1178	U
9	A	1180	G
9	A	1181	G
9	A	1184	U
9	A	1185	A
9	A	1186	G
9	A	1187	A
9	A	1188	A
9	A	1189	G
9	A	1191	A
9	A	1201	G
9	A	1202	A
9	A	1205	G
9	A	1206	A
9	A	1207	G
9	A	1212	U
9	A	1213	A

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Mol	Chain	Res	Type
9	A	1228	A
9	A	1230	G
9	A	1240	G
9	A	1250	U
9	A	1251	A
9	A	1253	C
9	A	1254	G
9	A	1260	C
9	A	1261	A
9	A	1262	A
9	A	1292	U
9	A	1293	G
9	A	1294	U
9	A	1326	G
9	A	1344	A
9	A	1351	G
9	A	1353	G
9	A	1371	G
9	A	1384	G
9	A	1386	G
9	A	1387	A
9	A	1389	U
9	A	1415	A
9	A	1416	A
9	A	1429	C
9	A	1440	C
9	A	1444	U
9	A	1448	C
9	A	1465	C
9	A	1474	A
9	A	1480	A
9	A	1493	A
9	A	1494	U
9	A	1499	A
9	A	1510	A
9	A	1518	A
9	A	1522	G
9	A	1531	C
9	A	1533	U
9	A	1534	C
9	A	1540	U
9	A	1543	A

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Mol	Chain	Res	Type
9	A	1548	C
9	A	1550	G
9	A	1551	U
9	A	1552	A
9	A	1553	C
9	A	1554	U
9	A	1560	U
9	A	1564	A
9	A	1565	A
9	A	1566	A
9	A	1568	C
9	A	1569	A
9	A	1570	C
9	A	1572	G
9	A	1574	G
9	A	1579	C
9	A	1580	A
9	A	1581	C
9	A	1587	G
9	A	1593	U
9	A	1594	G
9	A	1595	G
9	A	1597	G
9	A	1599	U
9	A	1600	G
9	A	1601	G
9	A	1605	G
9	A	1606	G
9	A	1625	G
9	A	1629	G
9	A	1630	U
9	A	1631	A
9	A	1632	G
9	A	1640	A
9	A	1641	U
9	A	1648	A
9	A	1649	C
9	A	1671	U
9	A	1672	C
9	A	1674	G
9	A	1679	A
9	A	1680	A

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Mol	Chain	Res	Type
9	A	1681	U
9	A	1703	G
9	A	1710	A
9	A	1713	U
9	A	1716	A
9	A	1717	U
9	A	1724	G
9	A	1727	A
9	A	1728	U
9	A	1731	A
9	A	1737	A
9	A	1753	C
9	A	1754	G
9	A	1789	A
9	A	1798	U
9	A	1802	G
9	A	1836	A
9	A	1845	G
9	A	1852	A
9	A	1864	U
9	A	1866	C
9	A	1870	U
9	A	1871	G
9	A	1872	A
9	A	1882	A
9	A	1892	G
9	A	1895	A
9	A	1917	G
9	A	1933	G
9	A	1970	G
9	A	1973	C
9	A	1975	A
9	A	1976	A
9	A	1981	U
9	A	1990	A
9	A	1998	C
9	A	2008	A
9	A	2017	C
9	A	2018	G
9	A	2026	A
9	A	2033	U
9	A	2046	A

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Mol	Chain	Res	Type
9	A	2048	G
9	A	2052	G
9	A	2064	A
9	A	2085	C
9	A	2086	U
9	A	2088	C
9	A	2089	C
9	A	2090	U
9	A	2091	U
9	A	2093	G
9	A	2094	G
9	A	2095	G
9	A	2096	G
9	A	2106	A
9	A	2107	G
9	A	2127	G
9	A	2130	G
9	A	2131	G
9	A	2137	A
9	A	2138	C
9	A	2139	U
9	A	2140	A
9	A	2141	U
9	A	2142	A
9	A	2143	A
9	A	2144	C
9	A	2148	C
9	A	2150	U
9	A	2151	A
9	A	2152	A
9	A	2153	G
9	A	2154	G
9	A	2161	A
9	A	2163	U
9	A	2179	U
9	A	2187	U
9	A	2190	A
9	A	2191	C
9	A	2194	A
9	A	2195	U
9	A	2196	G
9	A	2199	G

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Mol	Chain	Res	Type
9	A	2201	A
9	A	2215	U
9	A	2216	G
9	A	2217	U
9	A	2221	A
9	A	2239	A
9	A	2245	C
9	A	2247	A
9	A	2254	A
9	A	2255	A
9	A	2256	G
9	A	2257	A
9	A	2267	C
9	A	2274	C
9	A	2276	G
9	A	2279	C
9	A	2280	G
9	A	2284	A
9	A	2285	G
9	A	2286	A
9	A	2315	U
9	A	2320	C
9	A	2325	U
9	A	2328	G
9	A	2329	G
9	A	2330	U
9	A	2334	U
9	A	2335	G
9	A	2337	A
9	A	2338	G
9	A	2339	G
9	A	2340	A
9	A	2341	U
9	A	2342	A
9	A	2343	G
9	A	2349	A
9	A	2351	A
9	A	2354	G
9	A	2356	G
9	A	2360	C
9	A	2362	C
9	A	2368	C

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Mol	Chain	Res	Type
9	A	2371	G
9	A	2382	G
9	A	2383	U
9	A	2384	C
9	A	2385	G
9	A	2386	U
9	A	2387	U
9	A	2388	G
9	A	2390	U
9	A	2394	A
9	A	2395	U
9	A	2399	A
9	A	2400	C
9	A	2401	U
9	A	2402	C
9	A	2403	U
9	A	2404	G
9	A	2405	A
9	A	2408	G
9	A	2421	A
9	A	2422	A
9	A	2427	G
9	A	2434	A
9	A	2436	A
9	A	2449	A
9	A	2462	G
9	A	2463	G
9	A	2492	A
9	A	2502	A
9	A	2507	C
9	A	2511	A
9	A	2521	C
9	A	2529	A
9	A	2532	G
9	A	2545	G
9	A	2548	U
9	A	2551	A
9	A	2559	A
9	A	2571	C
9	A	2574	C
9	A	2581	G
9	A	2585	U

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Mol	Chain	Res	Type
9	A	2607	G
9	A	2609	A
9	A	2612	A
9	A	2626	U
9	A	2627	C
9	A	2647	U
9	A	2649	A
9	A	2652	G
9	A	2653	G
9	A	2654	A
9	A	2655	U
9	A	2659	A
9	A	2665	C
9	A	2672	A
9	A	2683	A
9	A	2693	A
9	A	2694	G
9	A	2702	A
9	A	2705	G
9	A	2715	U
9	A	2722	C
9	A	2726	G
9	A	2729	G
9	A	2742	A
9	A	2744	C
9	A	2778	U
9	A	2786	U
9	A	2790	A
9	A	2791	G
9	A	2796	A
9	A	2821	G
9	A	2826	A
9	A	2833	U
9	A	2837	U
9	A	2853	C
9	A	2854	A
9	A	2856	A
9	A	2870	C
9	A	2878	A
9	A	2913	U
9	A	2915	C
9	A	2926	A

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Mol	Chain	Res	Type
9	A	2936	C
9	A	2938	G
9	A	2942	G
9	A	2950	C
9	A	2953	U
9	A	2957	A
9	A	2968	G
9	A	2971	G
9	A	2972	A
9	A	2989	A
9	A	3002	A
9	A	3009	U
9	A	3014	A
9	A	3015	C
9	A	3021	A
9	A	3042	A
9	A	3070	G
9	A	3071	A
9	A	3081	A
9	A	3088	C
9	A	3093	A
9	A	3095	C
9	A	3101	C
9	A	3105	C
9	A	3106	C
9	A	3107	G
9	A	3108	G
9	A	3112	A
9	A	3114	A
10	B	4	A
10	B	5	C
10	B	12	C
10	B	13	C
10	B	30	G
10	B	35	G
10	B	40	A
10	B	44	C
10	B	45	G
10	B	47	A
10	B	53	A
10	B	57	U
10	B	84	C

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Mol	Chain	Res	Type
10	B	86	U
10	B	88	C
10	B	102	A
10	B	104	G
10	B	106	C
10	B	117	A
35	a	10	G
35	a	11	G
35	a	12	A
35	a	13	G
35	a	35	G
35	a	36	A
35	a	43	G
35	a	51	C
35	a	52	U
35	a	53	U
35	a	54	A
35	a	55	A
35	a	58	C
35	a	75	A
35	a	82	U
35	a	87	G
35	a	91	U
35	a	92	A
35	a	93	C
35	a	116	A
35	a	117	C
35	a	126	G
35	a	128	U
35	a	131	G
35	a	141	U
35	a	179	C
35	a	180	A
35	a	192	G
35	a	194	A
35	a	211	A
35	a	217	U
35	a	220	G
35	a	231	G
35	a	243	A
35	a	245	C
35	a	247	G

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Mol	Chain	Res	Type
35	a	251	G
35	a	266	G
35	a	267	C
35	a	279	A
35	a	280	C
35	a	281	G
35	a	289	G
35	a	328	U
35	a	329	A
35	a	332	G
35	a	344	A
35	a	345	C
35	a	349	A
35	a	350	G
35	a	351	G
35	a	353	A
35	a	354	G
35	a	363	A
35	a	367	U
35	a	372	C
35	a	373	A
35	a	397	A
35	a	398	C
35	a	406	G
35	a	411	A
35	a	412	U
35	a	413	G
35	a	419	C
35	a	421	U
35	a	422	C
35	a	423	G
35	a	428	G
35	a	429	U
35	a	430	A
35	a	433	C
35	a	434	C
35	a	435	U
35	a	438	U
35	a	452	A
35	a	453	G
35	a	456	C
35	a	457	A

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Mol	Chain	Res	Type
35	a	458	A
35	a	459	G
35	a	465	G
35	a	466	U
35	a	470	U
35	a	472	C
35	a	477	G
35	a	486	G
35	a	487	C
35	a	490	A
35	a	491	C
35	a	492	U
35	a	497	G
35	a	498	C
35	a	499	C
35	a	501	G
35	a	505	C
35	a	507	G
35	a	511	U
35	a	512	A
35	a	520	G
35	a	527	A
35	a	542	U
35	a	543	A
35	a	544	C
35	a	552	A
35	a	553	A
35	a	556	A
35	a	557	G
35	a	575	G
35	a	576	C
35	a	612	U
35	a	613	G
35	a	629	G
35	a	633	A
35	a	645	G
35	a	666	U
35	a	668	G
35	a	675	A
35	a	683	G
35	a	700	C
35	a	701	G

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Mol	Chain	Res	Type
35	a	702	G
35	a	703	U
35	a	713	G
35	a	714	G
35	a	735	G
35	a	761	A
35	a	765	G
35	a	773	U
35	a	774	A
35	a	794	A
35	a	797	C
35	a	798	G
35	a	808	A
35	a	812	G
35	a	818	U
35	a	822	U
35	a	841	U
35	a	854	A
35	a	867	G
35	a	879	C
35	a	896	A
35	a	909	G
35	a	913	C
35	a	914	C
35	a	916	C
35	a	921	G
35	a	942	U
35	a	947	U
35	a	951	A
35	a	953	G
35	a	954	C
35	a	955	G
35	a	959	A
35	a	973	U
35	a	974	U
35	a	975	G
35	a	986	G
35	a	992	G
35	a	996	G
35	a	998	G
35	a	1003	C
35	a	1008	C

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Mol	Chain	Res	Type
35	a	1013	G
35	a	1014	U
35	a	1018	C
35	a	1020	G
35	a	1022	G
35	a	1024	G
35	a	1025	C
35	a	1028	G
35	a	1030	G
35	a	1033	G
35	a	1041	G
35	a	1044	G
35	a	1045	U
35	a	1046	C
35	a	1048	G
35	a	1065	U
35	a	1075	U
35	a	1081	A
35	a	1104	G
35	a	1106	U
35	a	1113	A
35	a	1115	G
35	a	1116	U
35	a	1117	U
35	a	1120	G
35	a	1121	G
35	a	1124	G
35	a	1126	G
35	a	1129	U
35	a	1133	G
35	a	1138	A
35	a	1140	U
35	a	1147	G
35	a	1148	U
35	a	1149	C
35	a	1150	A
35	a	1165	G
35	a	1166	G
35	a	1177	A
35	a	1178	A
35	a	1181	C
35	a	1182	A

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Mol	Chain	Res	Type
35	a	1193	U
35	a	1194	A
35	a	1205	U
35	a	1209	C
35	a	1217	A
35	a	1219	A
35	a	1231	A
35	a	1234	G
35	a	1237	C
35	a	1238	U
35	a	1239	G
35	a	1247	G
35	a	1258	C
35	a	1261	A
35	a	1265	U
35	a	1266	U
35	a	1267	U
35	a	1269	A
35	a	1279	U
35	a	1283	U
35	a	1286	G
35	a	1287	G
35	a	1294	G
35	a	1300	A
35	a	1301	A
35	a	1328	A
35	a	1329	G
35	a	1336	C
35	a	1337	A
35	a	1338	G
35	a	1340	U
35	a	1341	C
35	a	1343	G
35	a	1344	C
35	a	1346	A
35	a	1347	C
35	a	1348	G
35	a	1350	U
35	a	1351	G
35	a	1352	C
35	a	1356	G
35	a	1357	A

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Mol	Chain	Res	Type
35	a	1361	C
35	a	1362	G
35	a	1380	C
35	a	1381	A
35	a	1393	G
35	a	1394	U
35	a	1395	C
35	a	1396	A
35	a	1397	U
35	a	1402	G
35	a	1405	G
35	a	1423	U
35	a	1429	A
35	a	1434	U
35	a	1435	U
35	a	1436	G
35	a	1438	G
35	a	1459	G
35	a	1473	A
35	a	1476	A
35	a	1477	A
35	a	1481	G
35	a	1483	A
35	a	1488	G
35	a	1501	G
35	a	1504	G
35	a	1513	G
35	a	1514	G
35	a	1516	U

All (34) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	9	U
9	A	89	A
9	A	97	U
9	A	316	U
9	A	357	U
9	A	369	G
9	A	445	U
9	A	552	U
9	A	713	G

Continued on next page...

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Mol	Chain	Res	Type
9	A	974	G
9	A	1002	C
9	A	1010	U
9	A	1040	U
9	A	1084	U
9	A	1227	C
9	A	1473	G
9	A	1629	G
9	A	1730	U
9	A	1881	U
9	A	1974	A
9	A	2047	C
9	A	2088	C
9	A	2094	G
9	A	2142	A
9	A	2342	A
9	A	2350	G
9	A	2381	A
9	A	2389	U
9	A	2626	U
9	A	2693	A
9	A	2820	U
9	A	3008	C
10	B	34	G
10	B	52	G

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 107 ligands modelled in this entry, 107 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

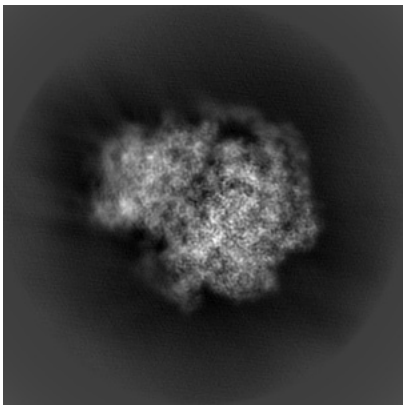
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-47363. These allow visual inspection of the internal detail of the map and identification of artifacts.

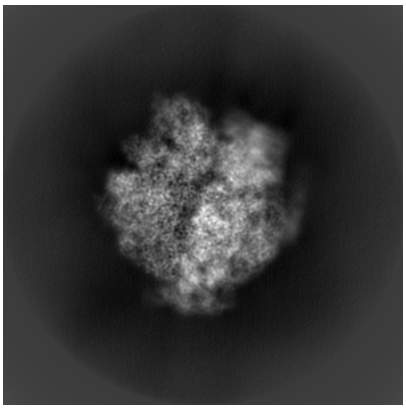
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

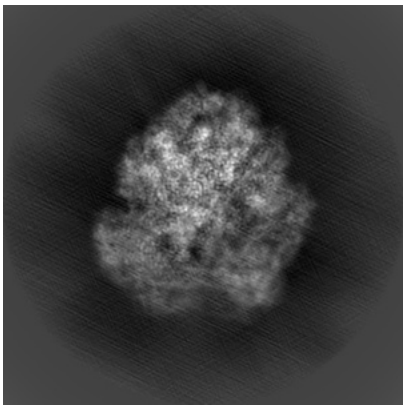
6.1.1 Primary map



X

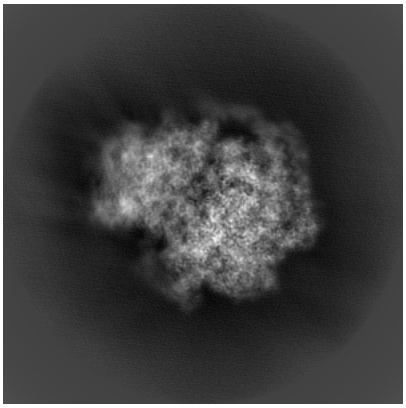


Y

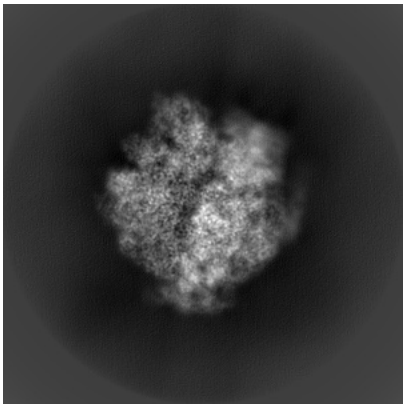


Z

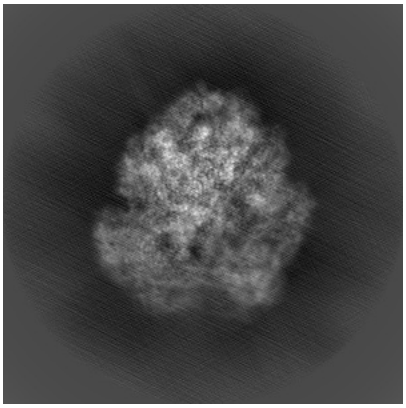
6.1.2 Raw map



X



Y

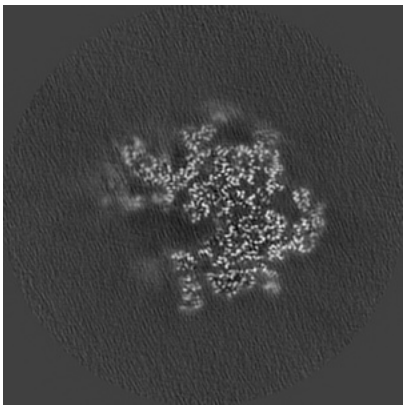


Z

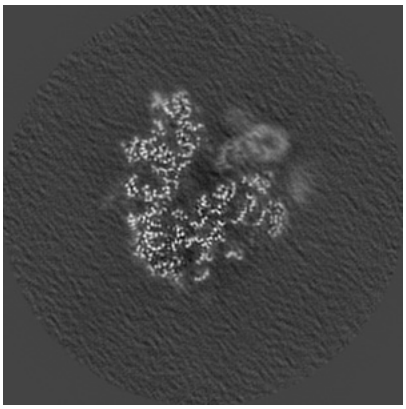
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

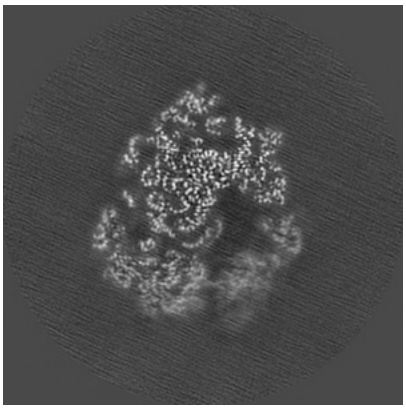
6.2.1 Primary map



X Index: 200

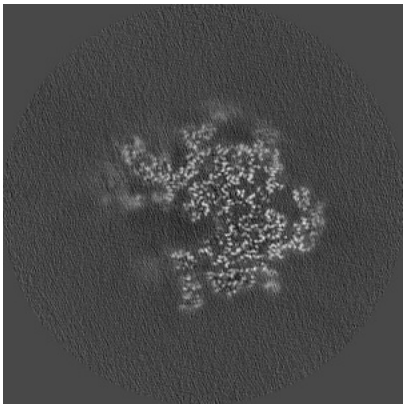


Y Index: 200

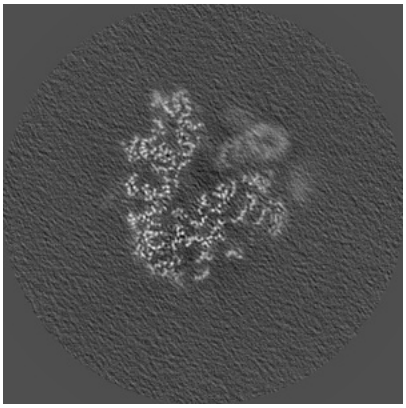


Z Index: 200

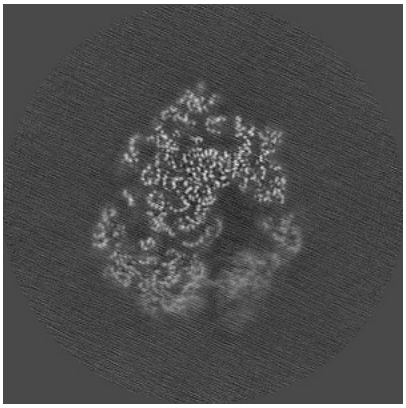
6.2.2 Raw map



X Index: 200



Y Index: 200

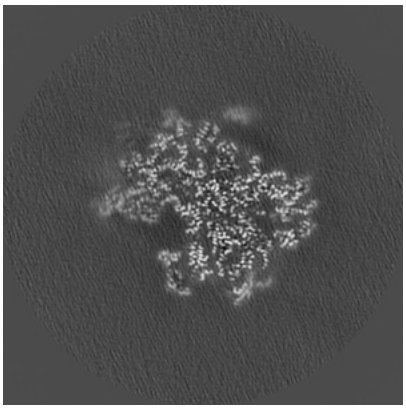


Z Index: 200

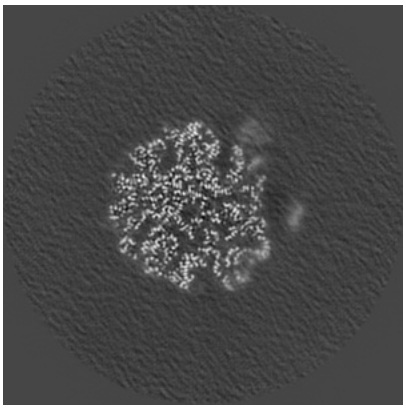
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

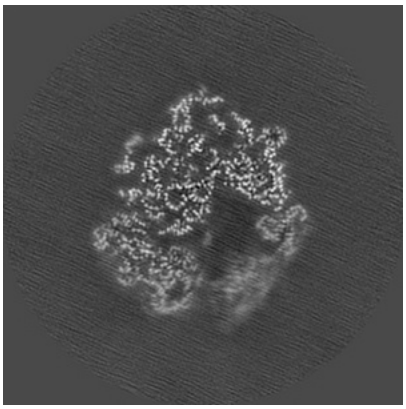
6.3.1 Primary map



X Index: 183

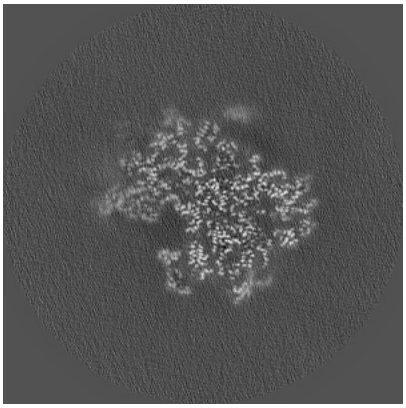


Y Index: 229

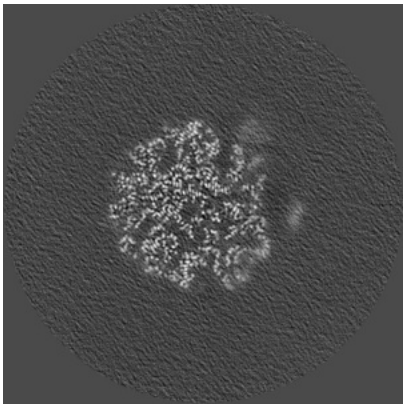


Z Index: 194

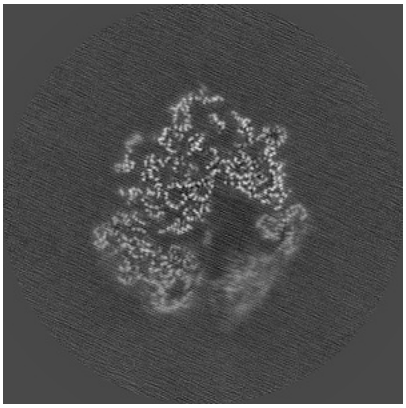
6.3.2 Raw map



X Index: 183



Y Index: 229

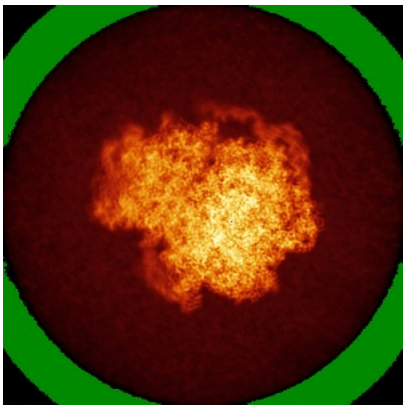


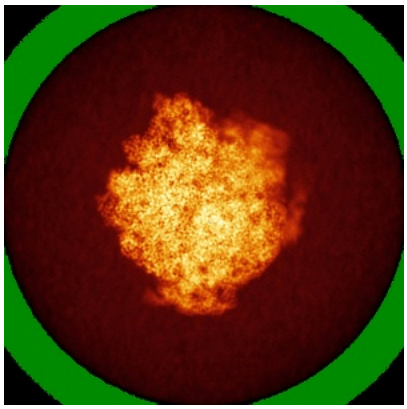
Z Index: 194

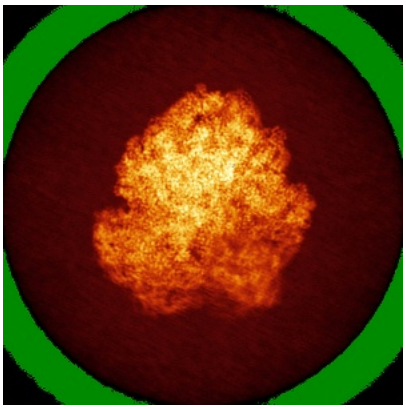
The images above show the largest variance slices of the map in three orthogonal directions.

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

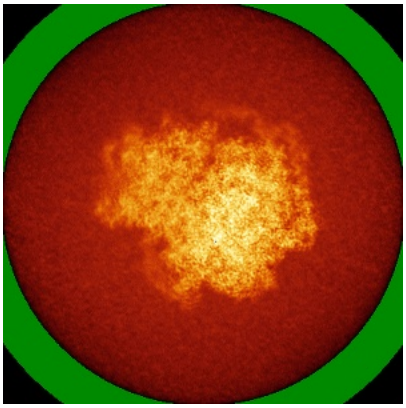
6.4.1 Primary map

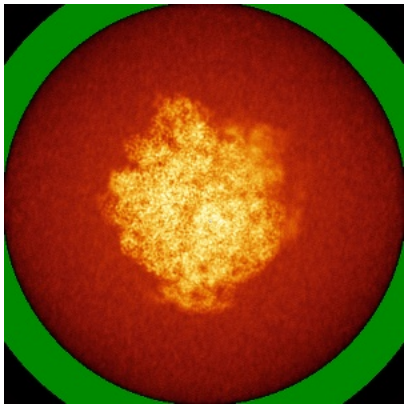

X

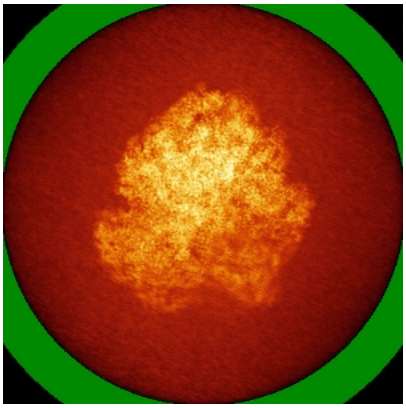

Y


Z

6.4.2 Raw map


X


Y


Z

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

6.5 Orthogonal surface views (i)

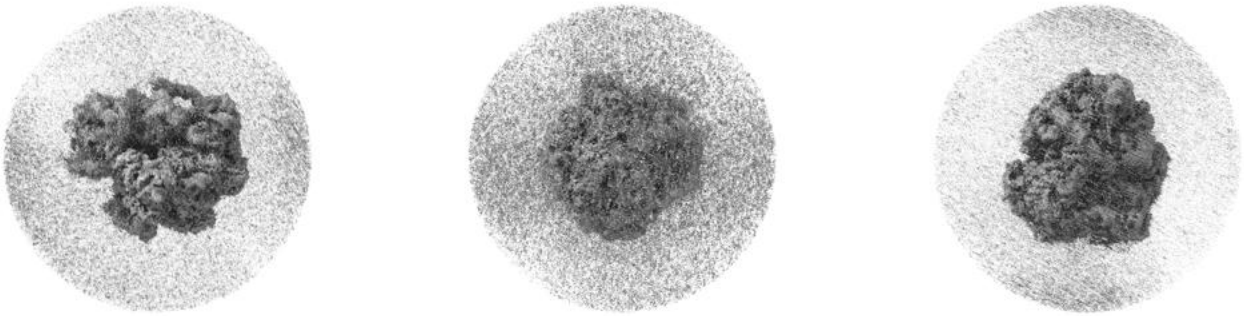
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

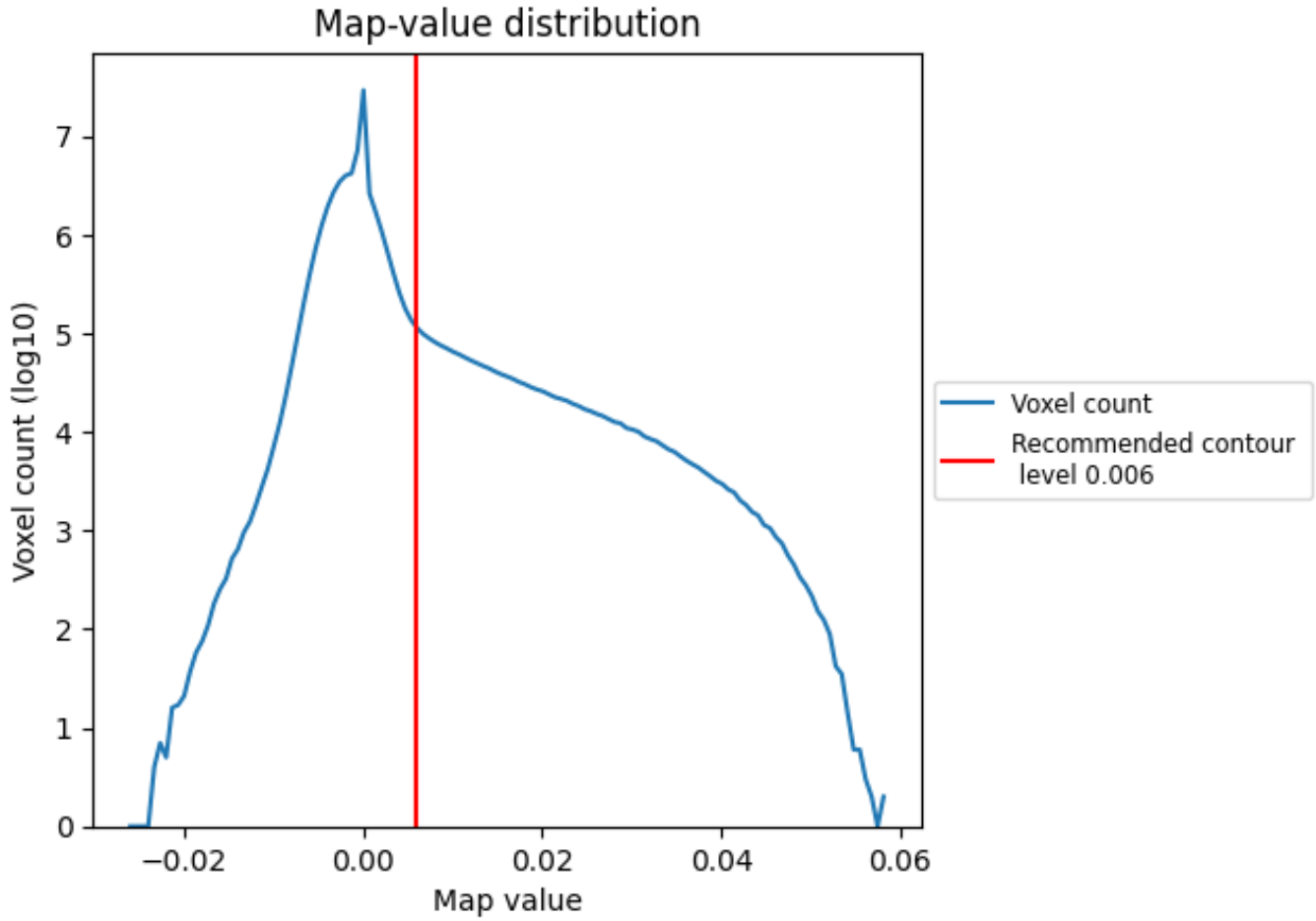
6.6 Mask visualisation (i)

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

7 Map analysis

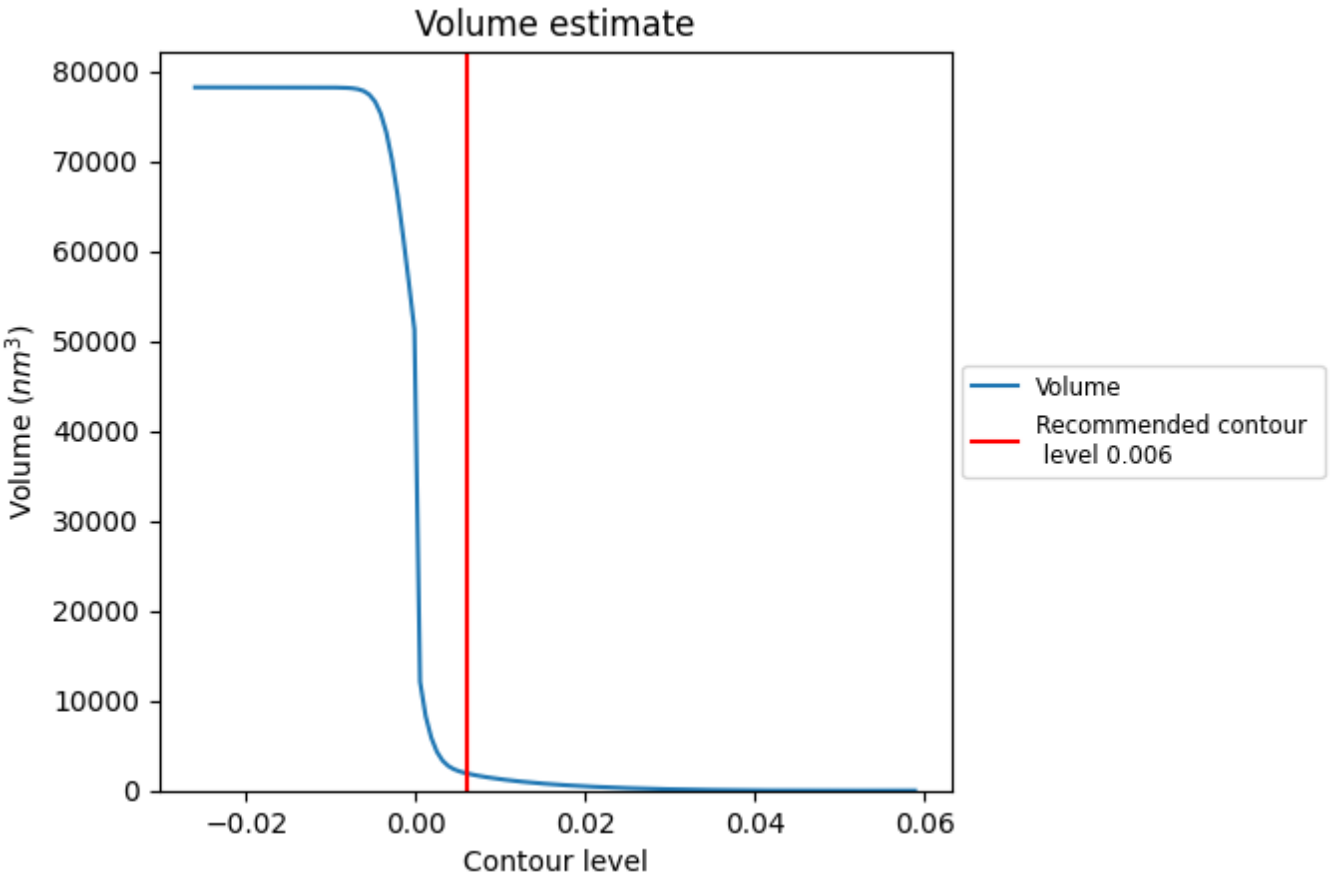
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

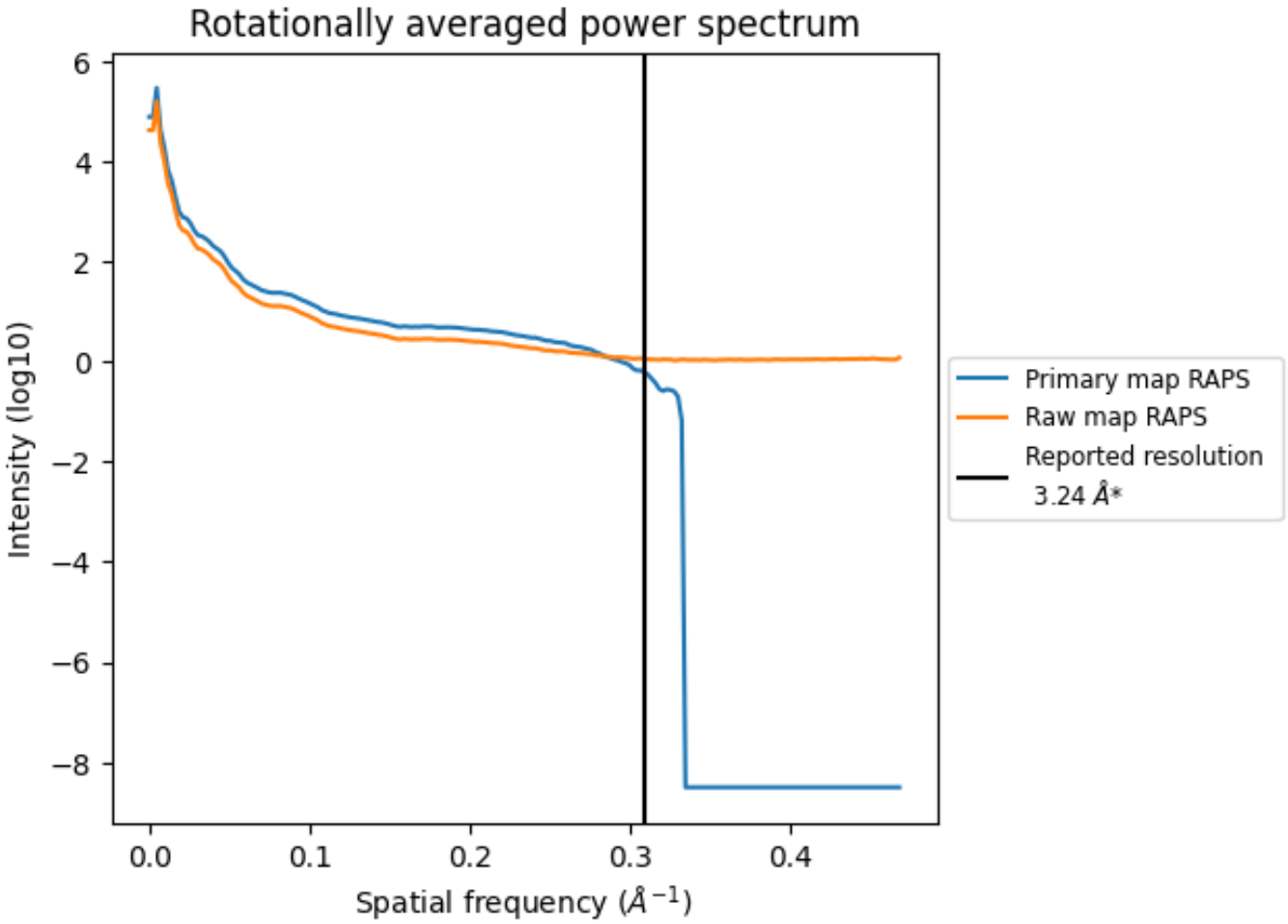
7.2 Volume estimate



The volume at the recommended contour level is 1913 nm^3; this corresponds to an approximate mass of 1728 kDa.

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

7.3 Rotationally averaged power spectrum (i)

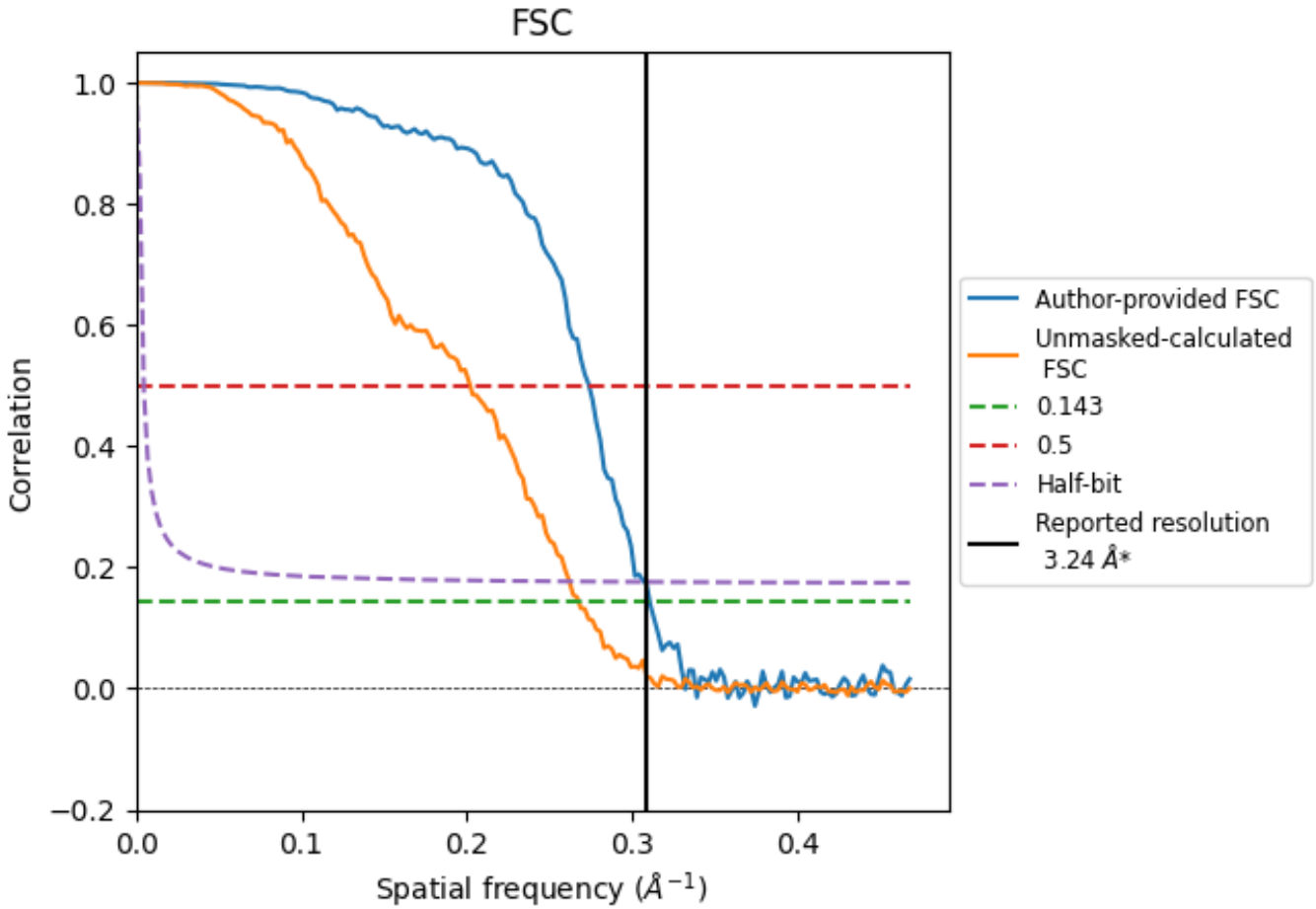


*Reported resolution corresponds to spatial frequency of 0.309 Å^{-1}

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.309 Å^{-1}

8.2 Resolution estimates (i)

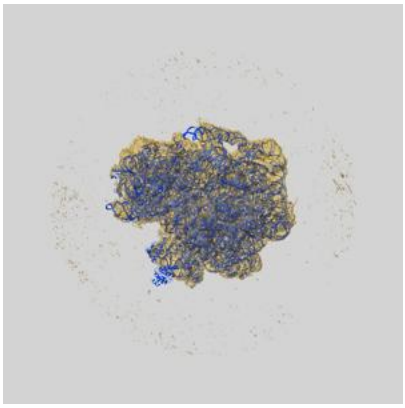
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.24	-	-
Author-provided FSC curve	3.22	3.65	3.26
Unmasked-calculated*	3.74	4.95	3.82

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.74 differs from the reported value 3.24 by more than 10 %

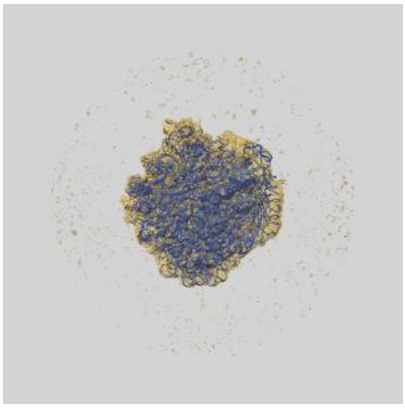
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-47363 and PDB model 9E0N. Per-residue inclusion information can be found in section 3 on page 15.

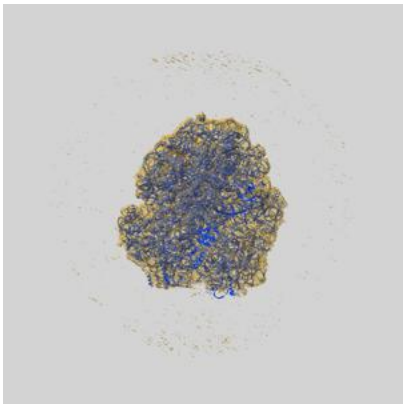
9.1 Map-model overlay



X



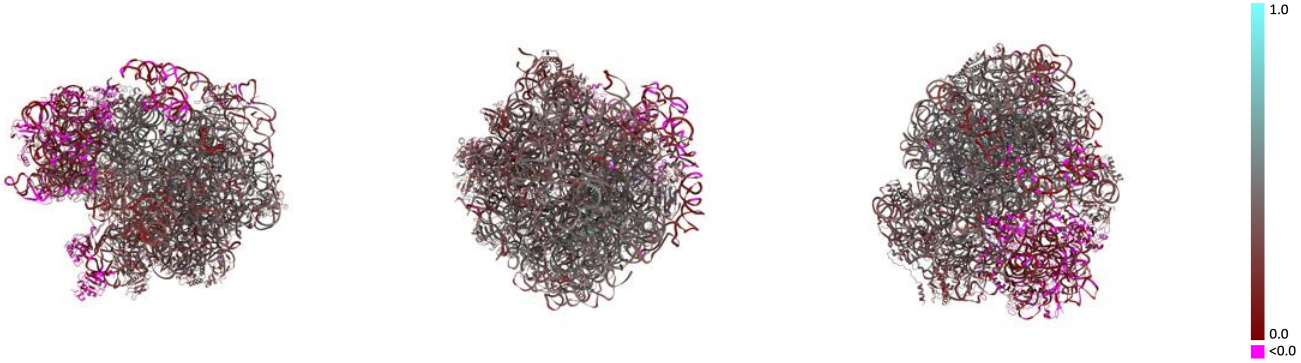
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.006 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.

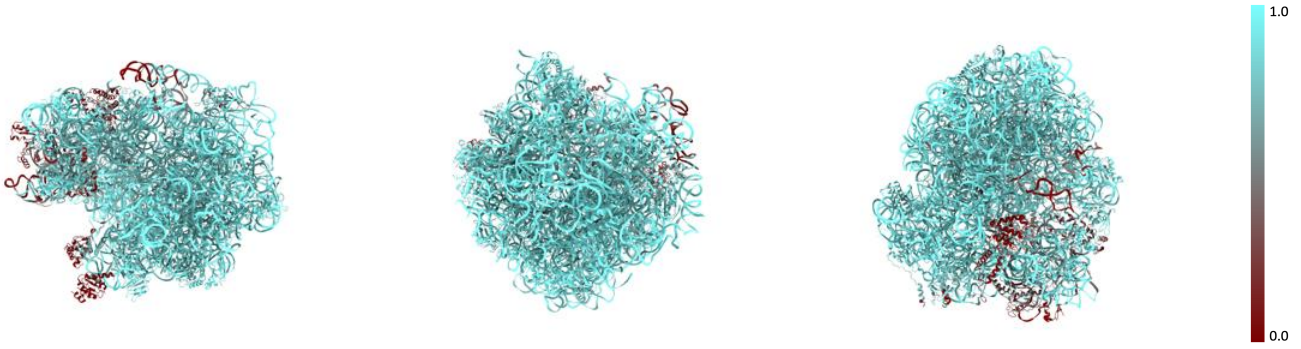
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

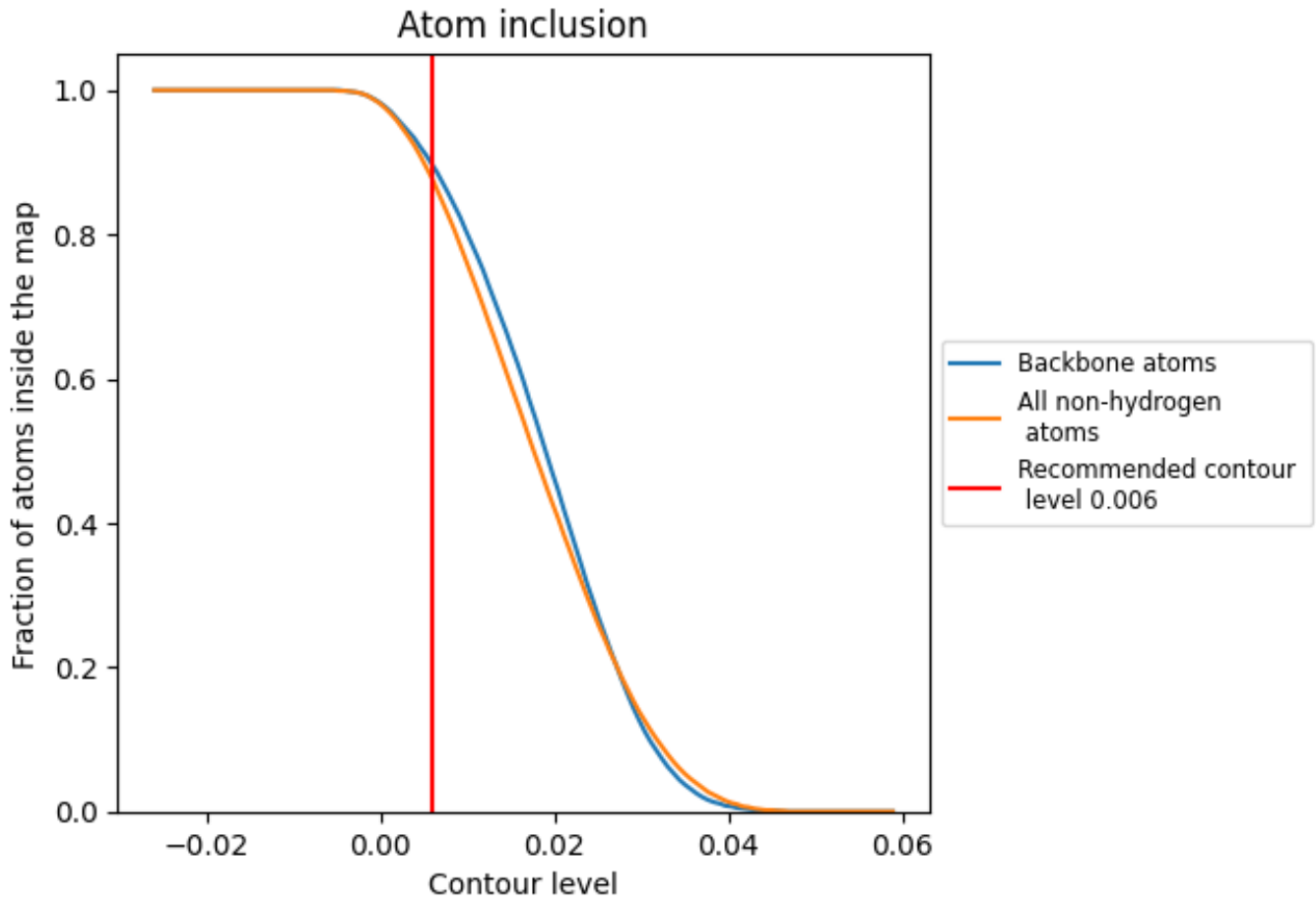
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.006).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8750	0.3250
1	0.8180	0.3150
2	0.7440	0.1580
3	0.9180	0.4070
4	0.9060	0.3460
5	0.9100	0.4610
6	0.8460	0.3800
7	0.8710	0.3280
8	0.8100	0.3610
A	0.9310	0.3580
B	0.9340	0.2580
C	0.9070	0.4570
D	0.9130	0.4070
E	0.8730	0.3620
F	0.8540	0.2670
G	0.8930	0.3280
H	0.6840	0.3380
I	0.0860	0.0190
J	0.1820	0.0250
K	0.8730	0.3540
L	0.8480	0.4080
M	0.8800	0.3600
N	0.8420	0.3600
O	0.9190	0.4200
P	0.9100	0.2970
Q	0.9040	0.4100
R	0.8950	0.3840
S	0.8880	0.3810
T	0.8780	0.4110
U	0.8930	0.4090
V	0.9110	0.3920
W	0.8330	0.2960
X	0.8060	0.3020
Y	0.8940	0.4430
Z	0.9110	0.4200



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Chain	Atom inclusion	Q-score
a	0.9090	0.3050
b	0.1170	0.0360
c	0.4340	0.1290
d	0.8270	0.3310
e	0.7520	0.2990
f	0.9000	0.3860
g	0.6870	0.0560
h	0.9120	0.3860
i	0.8480	0.1070
j	0.4510	0.0110
k	0.8480	0.3660
l	0.7800	0.3300
m	0.5020	0.0330
n	0.5410	0.1160
o	0.9150	0.4020
p	0.8620	0.3690
q	0.8800	0.3710
r	0.9290	0.3740
s	0.6220	0.0540
t	0.9040	0.3510
u	0.6410	0.3470