



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 12:31 AM UTC

PDB ID : 7QG8 / pdb_00007qg8
EMDB ID : EMD-13952
Title : Structure of the collided E. coli disome - VemP-stalled 70S ribosome
Authors : Kratzat, H.; Buschauer, R.; Berninghausen, O.; Beckmann, R.
Deposited on : 2021-12-07
Resolution : 3.97 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

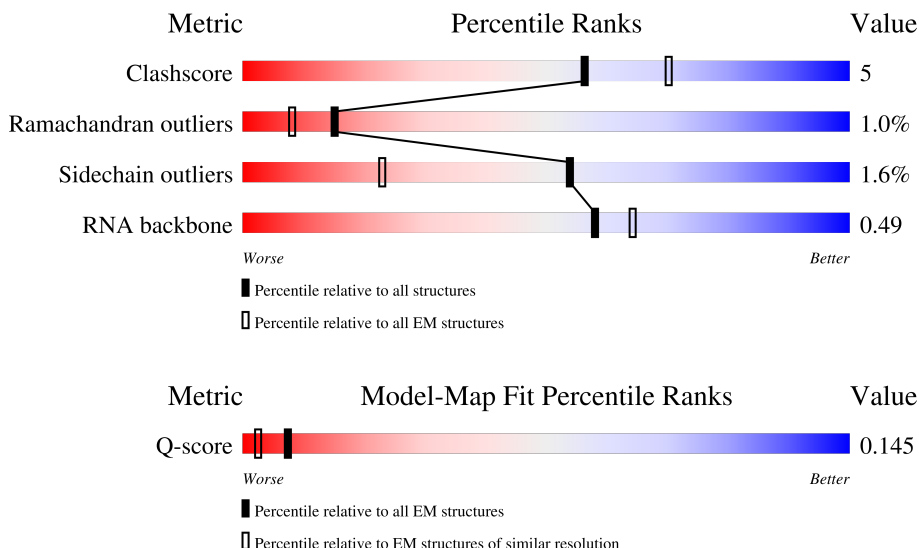
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.97 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.



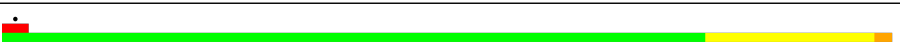
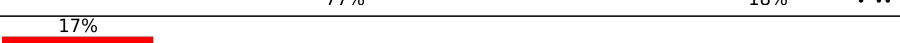
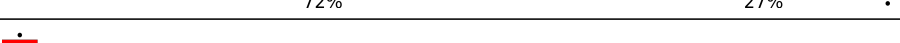
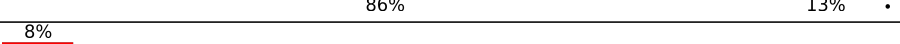
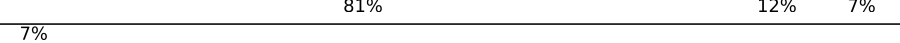
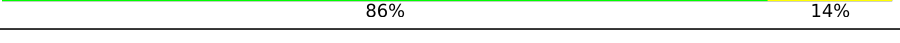
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7578 (3.47 - 4.47)

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

Mol	Chain	Length	Quality of chain
1	A	73	
2	s	179	
3	M	75	

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Mol	Chain	Length	Quality of chain
4	O	120	
5	P	273	
6	Q	209	
7	R	201	
8	S	179	
9	T	177	
10	U	149	
11	V	142	
12	W	142	
13	X	123	
14	Y	144	
15	Z	136	
16	a	127	
17	b	117	
18	c	115	
19	d	118	
20	e	103	
21	f	110	
22	g	100	
23	h	104	
24	i	94	
25	j	85	
26	k	78	
27	l	63	
28	m	59	

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Mol	Chain	Length	Quality of chain
29	n	57	
30	o	55	
31	p	46	
32	q	65	
33	r	55	
34	N	2903	
35	L	70	
36	C	223	
37	0	1539	
38	1	239	
39	2	218	
40	3	206	
41	4	162	
42	5	131	
43	6	156	
44	7	130	
45	8	130	
46	9	103	
47	D	129	
48	E	124	
49	F	118	
50	G	101	
51	H	89	
52	I	82	
53	J	84	

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Mol	Chain	Length	Quality of chain
54	K	75	11% 47% 25% • 27%
55	t	92	12% 64% 17% • • 14%
56	u	87	10% 74% 22% • • •
57	v	88	18% 38% 16% • • 42%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 147108 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called A-site tRNA.

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

- Molecule 2 is a protein called VemP nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	s	37	Total	C	N	O	S	0	0
			316	198	58	58	2		

- Molecule 3 is a RNA chain called P-site tRNA.

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

- Molecule 4 is a RNA chain called 5S rRNA.

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

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

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

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L11.

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

- Molecule 12 is a protein called 50S ribosomal protein L13.

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

- Molecule 13 is a protein called 50S ribosomal protein L14.

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

- Molecule 14 is a protein called 50S ribosomal protein L15.

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

- Molecule 15 is a protein called 50S ribosomal protein L16.

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

- Molecule 16 is a protein called 50S ribosomal protein L17.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	123	ALA	GLU	variant	UNP P0AG44

- Molecule 17 is a protein called 50S ribosomal protein L18.

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

- Molecule 18 is a protein called 50S ribosomal protein L19.

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

- Molecule 19 is a protein called 50S ribosomal protein L20.

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

- Molecule 20 is a protein called 50S ribosomal protein L21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	98	SER	GLY	variant	UNP P0ADZ0

- Molecule 23 is a protein called 50S ribosomal protein L24.

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

- Molecule 24 is a protein called 50S ribosomal protein L25.

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

- Molecule 25 is a protein called 50S ribosomal protein L27.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	3	UNK	HIS	variant	UNP P0A7L8

- Molecule 26 is a protein called 50S ribosomal protein L28.

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

- Molecule 27 is a protein called 50S ribosomal protein L29.

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

- Molecule 28 is a protein called 50S ribosomal protein L30.

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

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

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

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a RNA chain called 23S rRNA.

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

- Molecule 35 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L	55	Total	C	N	O	S	0	0
			419	258	76	79	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	68	SER	GLY	variant	UNP P0A7M9

- Molecule 36 is a protein called 50S ribosomal protein L1.

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

- Molecule 37 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	0	1532	Total	C	N	O	P	0	0
			32873	14661	6031	10649	1532		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	1	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	2	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	3	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	4	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	4	MET	ILE	variant	UNP P0A7W1

- Molecule 42 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	6	144	Total	C	N	O	S	0	0
			1129	705	213	207	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	78	HIS	ARG	variant	UNP P02359

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	7	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 45 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	8	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	3	ASP	GLU	variant	UNP P0A7X3

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	9	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 47 is a protein called 30S ribosomal protein S11.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	5	ALA	PRO	variant	UNP P0A7R9

- Molecule 48 is a protein called 30S ribosomal protein S12.

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

- Molecule 49 is a protein called 30S ribosomal protein S13.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	1	VAL	MET	variant	UNP P0A7S9

- Molecule 50 is a protein called 30S ribosomal protein S14.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	40	ALA	ASP	variant	UNP P0AG59

- Molecule 51 is a protein called 30S ribosomal protein S15.

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

- Molecule 52 is a protein called 30S ribosomal protein S16.

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

- Molecule 53 is a protein called 30S ribosomal protein S17.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	2	ALA	THR	variant	UNP P0AG63

- Molecule 54 is a protein called 30S ribosomal protein S18.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	15	THR	ALA	variant	UNP P0A7T7
K	19	VAL	GLN	variant	UNP P0A7T7

- Molecule 55 is a protein called 30S ribosomal protein S19.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	82	TYR	GLY	variant	UNP P0A7U3
t	83	TYR	HIS	variant	UNP P0A7U3

- Molecule 56 is a protein called 30S ribosomal protein S20.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	1	LEU	MET	variant	UNP P0A7U7

- Molecule 57 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	v	51	Total	C	N	O	S	0	0
			421	263	86	71	1		

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

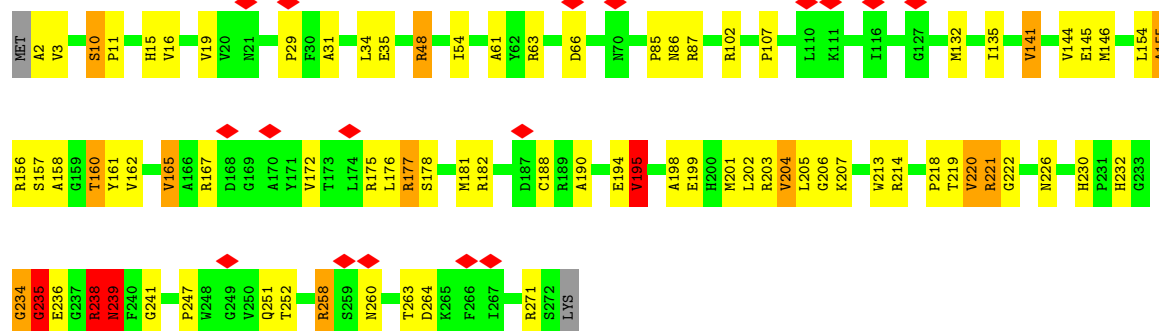
Mol	Chain	Residues	Atoms		AltConf
58	A	2	Total	Mg	0
			2	2	

- Molecule 59 is POTASSIUM ION (CCD ID: K) (formula: K).

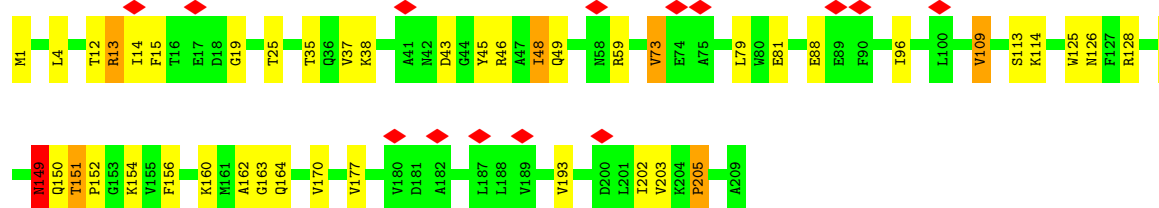
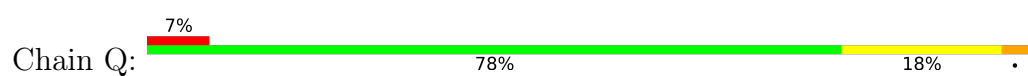
Mol	Chain	Residues	Atoms		AltConf
59	A	1	Total	K	0
			1	1	

- Molecule 60 is water.

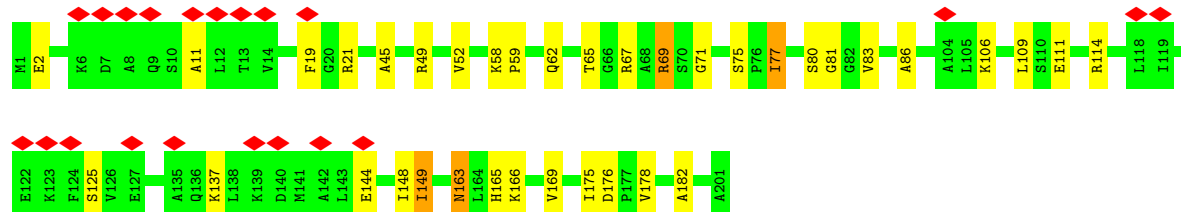
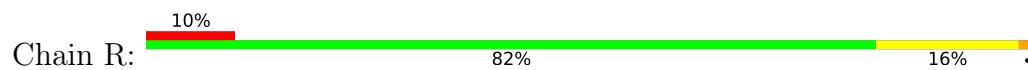
Mol	Chain	Residues	Atoms		AltConf
60	A	9	Total	O	0
			9	9	



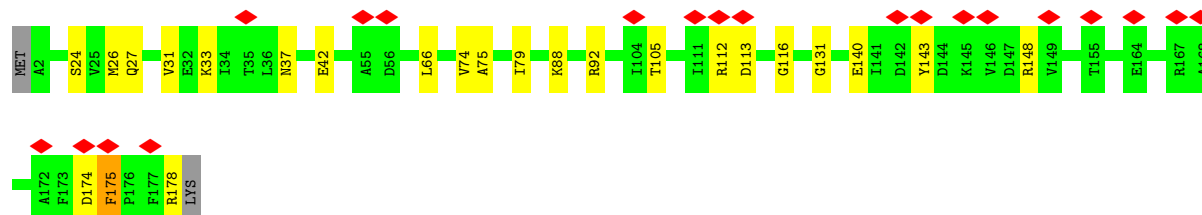
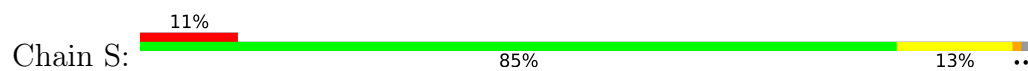
• Molecule 6: 50S ribosomal protein L3



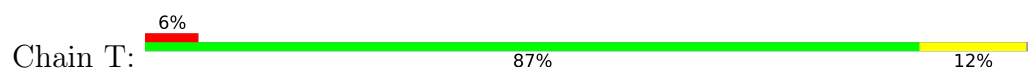
• Molecule 7: 50S ribosomal protein L4

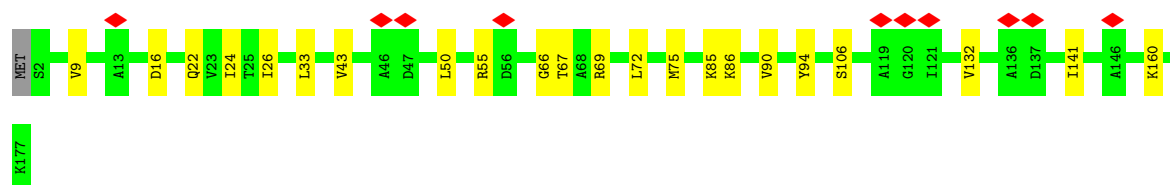


• Molecule 8: 50S ribosomal protein L5

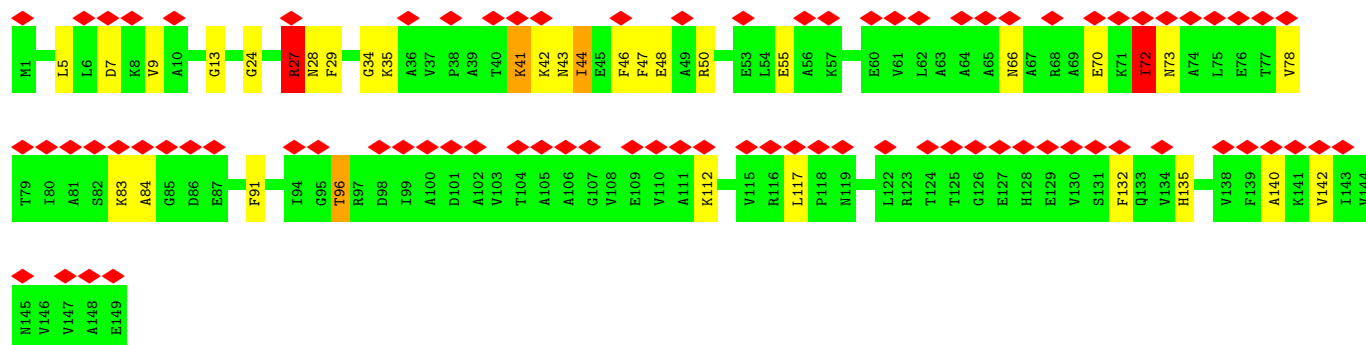
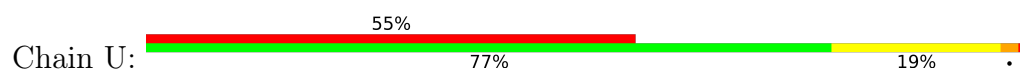


• Molecule 9: 50S ribosomal protein L6

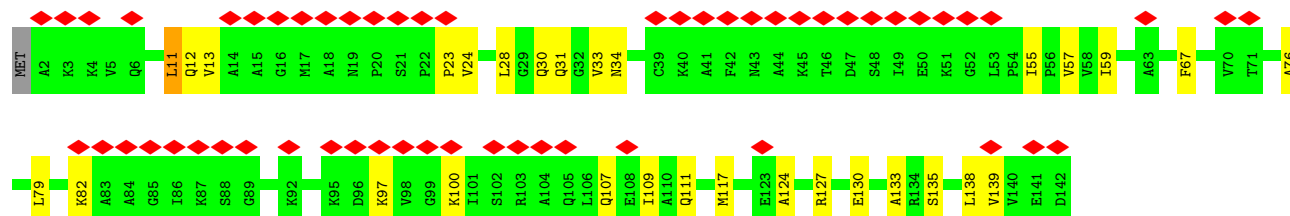
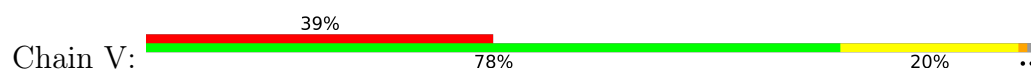




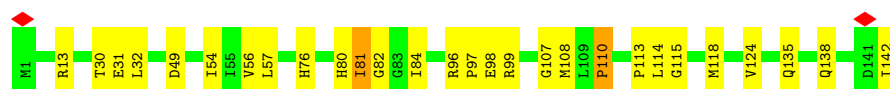
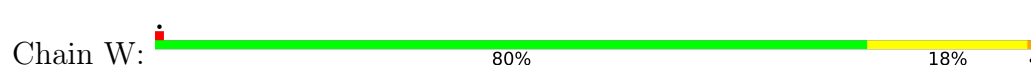
- Molecule 10: 50S ribosomal protein L9



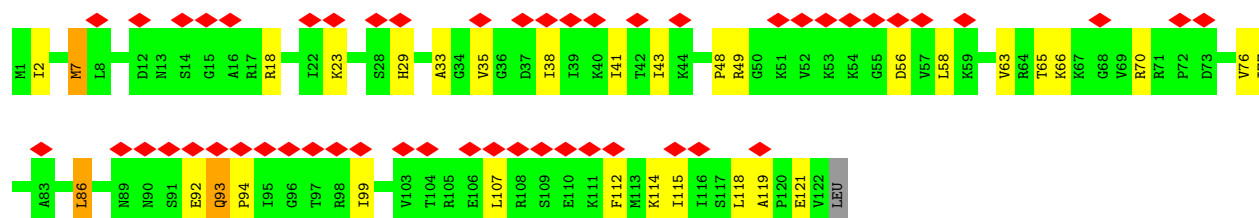
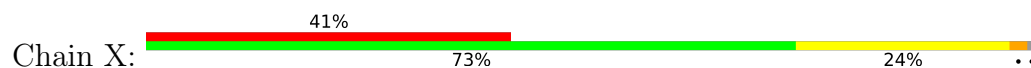
- Molecule 11: 50S ribosomal protein L11



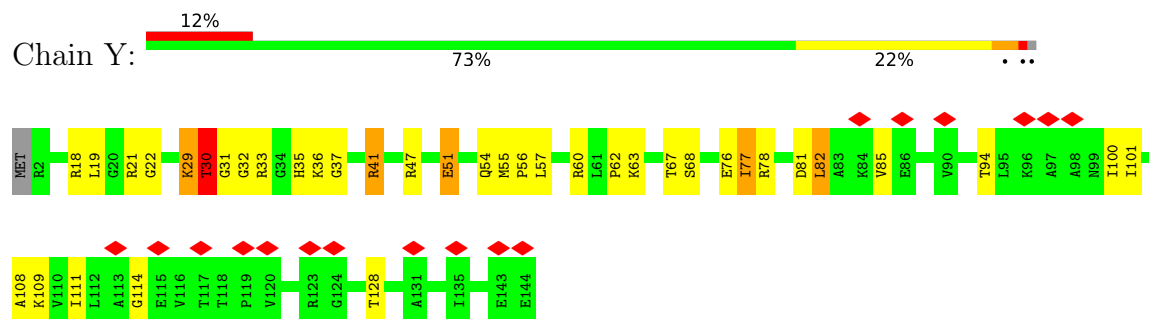
- Molecule 12: 50S ribosomal protein L13



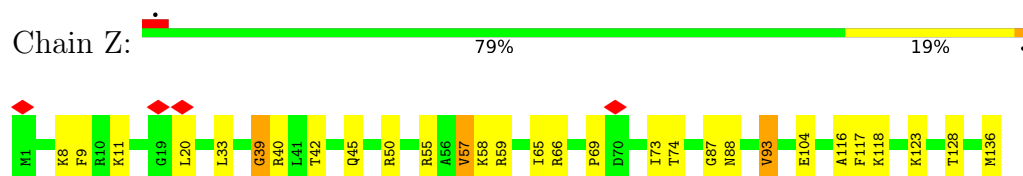
- Molecule 13: 50S ribosomal protein L14



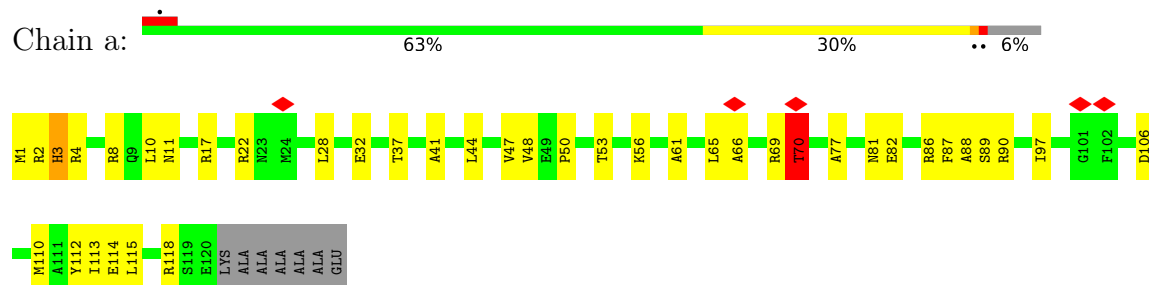
- Molecule 14: 50S ribosomal protein L15



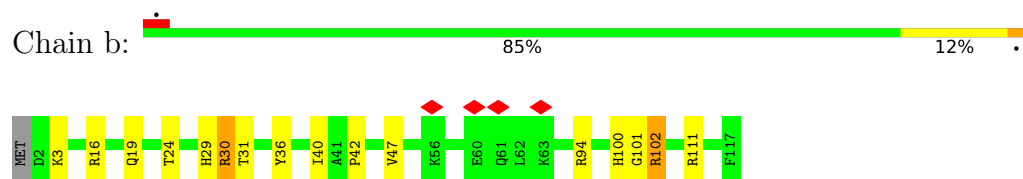
- Molecule 15: 50S ribosomal protein L16



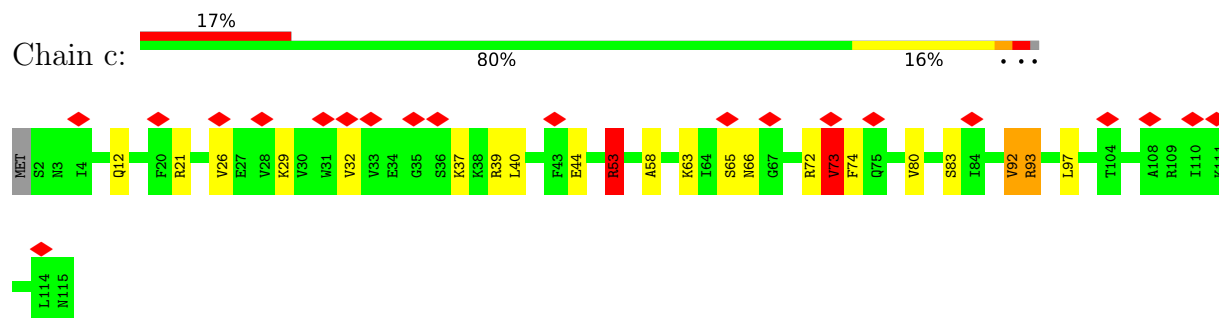
- Molecule 16: 50S ribosomal protein L17



- Molecule 17: 50S ribosomal protein L18



- Molecule 18: 50S ribosomal protein L19



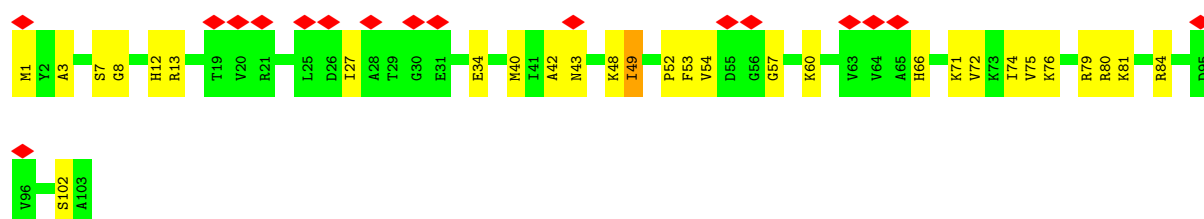
- Molecule 19: 50S ribosomal protein L20

Chain d:  77% 18% ..



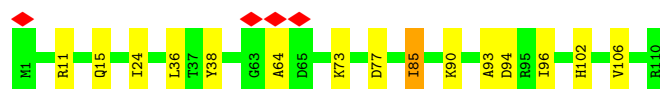
- Molecule 20: 50S ribosomal protein L21

Chain e:  17% 72% 27% .



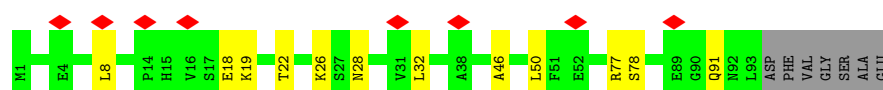
- Molecule 21: 50S ribosomal protein L22

Chain f:  86% 13% .



- Molecule 22: 50S ribosomal protein L23

Chain g:  8% 81% 12% 7%



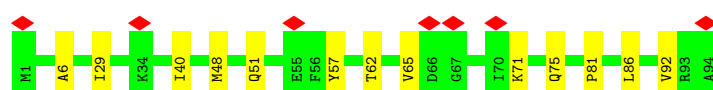
- Molecule 23: 50S ribosomal protein L24

Chain h:  7% 77% 20% ..



- Molecule 24: 50S ribosomal protein L25

Chain i:  7% 86% 14%



- Molecule 25: 50S ribosomal protein L27

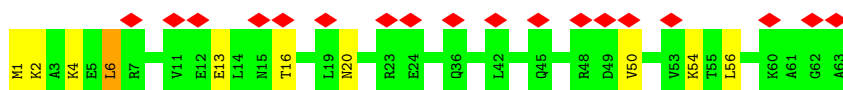
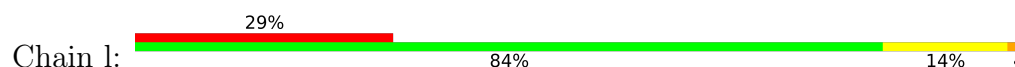
Chain j:  69% 15% .. 12%



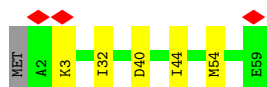
- Molecule 26: 50S ribosomal protein L28



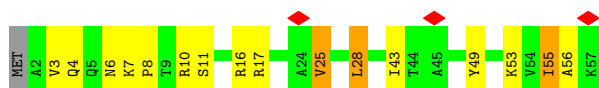
- Molecule 27: 50S ribosomal protein L29



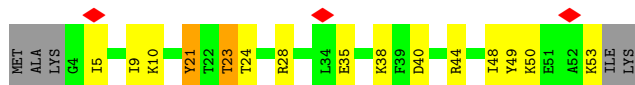
- Molecule 28: 50S ribosomal protein L30



- Molecule 29: 50S ribosomal protein L32



- Molecule 30: 50S ribosomal protein L33

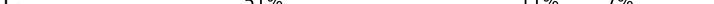


- Molecule 31: 50S ribosomal protein L34

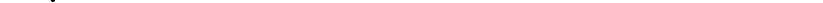


- Molecule 32: 50S ribosomal protein L35

Sequence logo for the 12-mer motif. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows positions 1 to 12. The sequence METP2K5R8K12K16G20H31I32L33K36D54A65 is displayed above the bars. Position 12 (I32) has the highest information content, exceeding 1.5 bits.

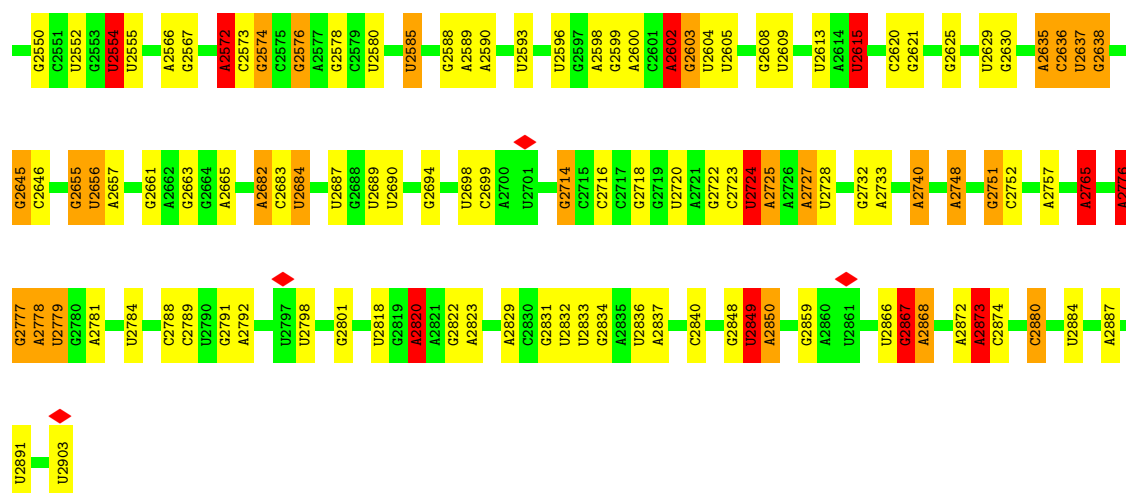
- Chain r:  51% 11% 7% 31%

M1	K2	V3	V7	C11	C14	I26	K34	Q35	Q36	Q37	G38	CYS	I1E	PHE	SER	SER	TVR	PHE	SER	SER	CYS	LYS	VAL	GLY	LEU	SER	TRP	LEU	ASP
----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

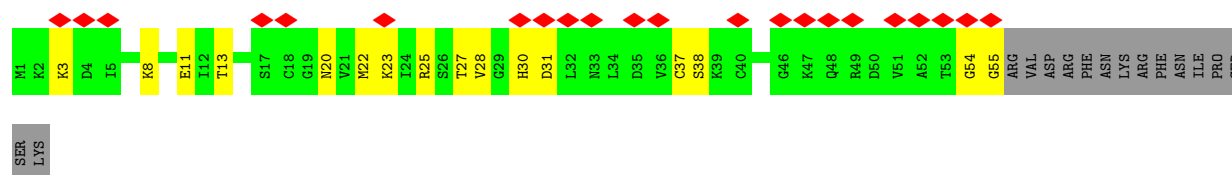
- Chain N:  64% 28% 7%

[illegible]

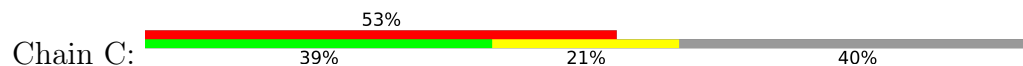
G2458	C2354	C2263	U2105	G2021	C1924	A1805	C1708	G1416	C1295	A1175	U1078
A2459	G2357	C2264	U2106	U2022	A1927	A1808	A1713	A1419	G1296	U1176	
U2460	A2358	U2265	C2174	C2023	A1928	A1809	U1714	G1421	C1297	C1177	U1081
C2466	C2359	A2267	A2175	C2025	G1929	A1810	G1715	G1421	C1298	U1082	U1083
C2467	G2360	C2268	G2110	U2028	U1930	G1811	C1586	A1427	G1299	G1179	
A2468	C2361	G2269	G2111	G2029	U1931	U1812	A1586	C1428	A1301	U1180	A1088
A2469		A2273	G2112	A2030	A1936	G1813	G1587		A1302		A1089
G2470	C2364	A2274	U2113	G2030	A1937	U1814	U1724		G1186	G1187	A1090
	A2376		A2114	A2031	A1938	G1816	U1725	G1432	G1309		
U2474		A2278	U2118	G2032	A1938	G1817	C1726	G1433	G1310	G1093	
C2475	G2383	G2279	A2119	A2033	U1939	U1818	C1727	A1434	G1311	U1094	
A2476	U2384		G2120	U2034		G1819	C1728		G1190	A1095	
G2481	C2385	G2282	G2121	G2035	C1942	A1819	U1729	C1437	U1313	A1096	
A2482	A2386	C2283	U2122		U1943		G1730		C1314	U1097	
C2483	U2387	C2284	G2123	G2038			G1731	C1447	C1315	A1098	
G2484	A2285	U2187	G2124		G1949	G1822	C1732		U1199	G1099	
C2485	C2286	U2188	G2125	A2042	U1955	G1824	C1811	G1450	A1321	C1100	
C2486	A2287	U2189	U2126	C2043	U1956	U1825	C1812	A1204	A1327	C1104	
	A2288	G2190	G2127	C2044	C1958	G1826	G1735	G1452	A1328	U1105	
	C2394	A2191	G2128	G2046	G1959	G1828	U1736	A1453	U1329	G1106	
U2489		U2192	C2129	C2047	A1960	A1829	G1738		G1620	G1210	
A2497	U2402	G2193	U2130	G2048	G1964	C1830	U1621		G1332	G1211	
C2498	C2403	U2194	U2131	G2049		G1831	G1822	C1461	G1333	G1212	
C2499	G2404		U2132	C2050	C1967	C1833	A1626		A1204		
U2500	G2405	A2198	G2133	A2051	G1968	U1834	G1757	G1475	G1334	G1206	
C2501	A2406	A2199	A2052	A2052	G1969	G1835	U1758	G1478	U1340		
G2502	A2407	C2200	G2134		U1971	G1847	C1639		A1341	G1227	
A2503			A2135	C2055	A1972	A1848	U1760	G1482	G1343	G1122	
U2504	G2411	U2203	G2136	G2056	A1977	A1853	C1764		U1344	A1126	
C2505	C2420	G2204	U2137		A1981	G1857	U1772		G1345		
U2506	G2421	C2208	G2138	A2060	U1982	U1865	C1774	A1504	U1352	A1129	
	C2422		U2139	G2061	U1983		C1777		A1509	U1130	
G2509	U2424	A2211	G2140	C2062	A1984	G1868	U1778	A1508	G1363	G1131	
U2514	A2425	A2212	G2141	C2063	U1985	C1869	U1779	A1510	G1364	U1132	
C2515	A2426	C2214	G2142	G2069	U1986	C1870	U1780		A1365	A1133	
A2516	G2427		C2143	A2070	U1991	G1875	U1781	U1534	G1251	G1152	
C2517	G2428	A2225	G2144	C2071	G1992	U1913	U1782	A1535	G1252	C1153	
A2518	G2429	C2226	G2145	C2072	U1993	U1914	A1783	C1536	A1263	G1154	
U2519	A2430		C2146	U2074	C1994	U1915	U1784	G1537	G1264	G1155	
C2520	U2431	C2232	C2147			U1919	C1795	A1544	U1267	A1156	
G2521		U2233	A2148	A2077	C1997	A1901	U1794	U1554	A1268	G1168	
U2522	A2435		G2149		A1998	A1906	A1678		A1392	A1269	
	G2436	G2238	U2151	U2081	C1999	G1906	U1677		A1393	C1270	
G2529	G2437	G2239	C2150	A2088	A2005	U1915	U1681	A1566	A1394	G1171	
	U2441	U2243	U2152	G2087	C2006	U1915	G1799	G1567	A1395	C1172	
U2532	C2442	U2244	C2153	A2092	A2006	U1915	C1795	A1403		U1174	
A2533	C2443	G2245	A2154	A2094	A2007	U1915					
G2534	G2444	G2246	U2155	A2094	A2008	U1915					
U2535	G2445	A2247	U2156	A2097	A2009	U1915					
C2539	G2446	C2248	G2157	U2098	U2015	U1919					
G2540	G2447	U2249	U2158	U2099	U2016						
A2541	A2448	G2250	C2159		A2019						
A2542		G2251	G2160		A2020						
G2543	C2452	C2261	C2161	C2104							
A2547	U2457	U2262	G2162								
			A2163								
			C2164								
			A2171								



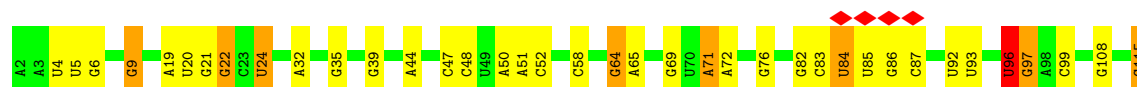
• Molecule 35: 50S ribosomal protein L31

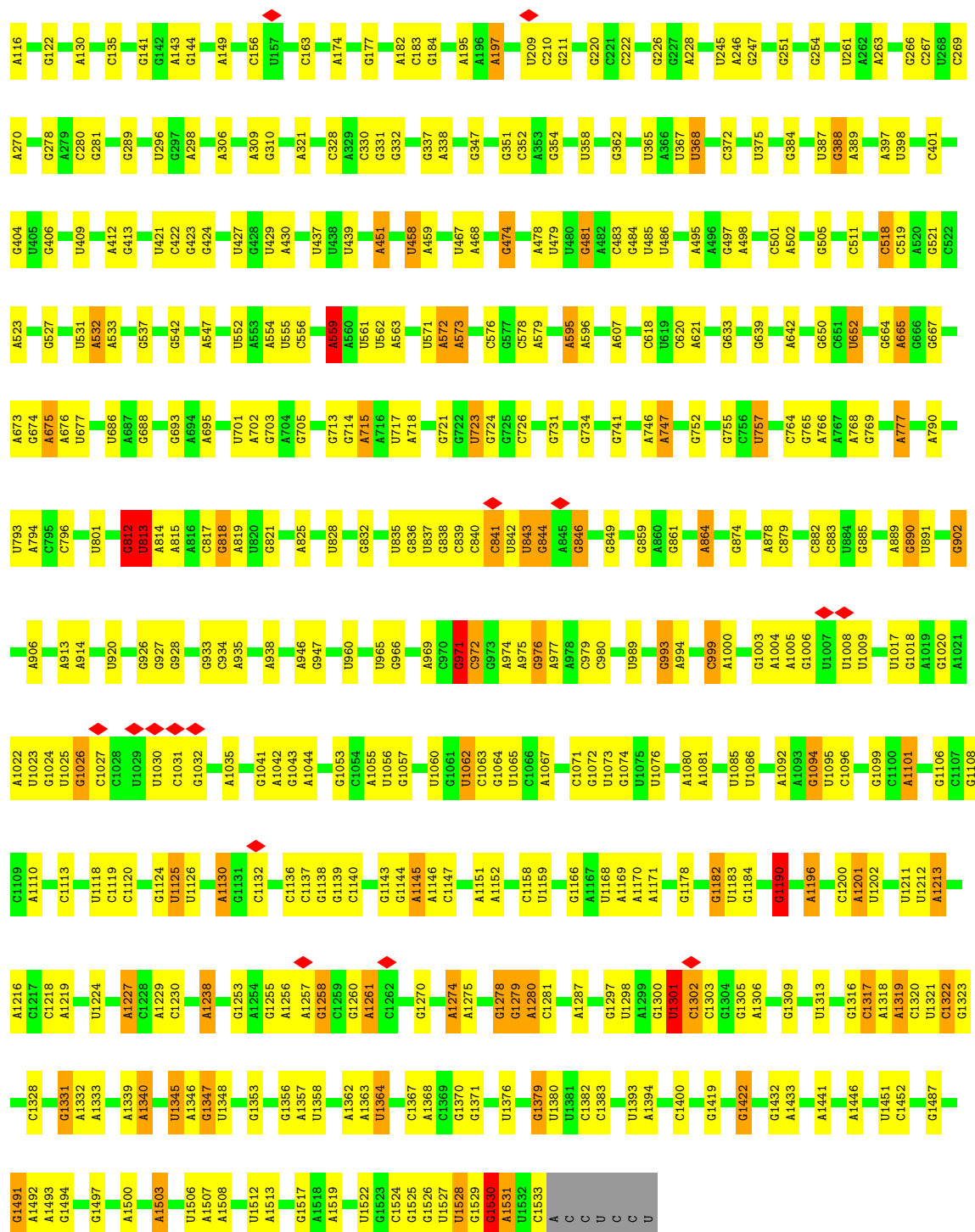


• Molecule 36: 50S ribosomal protein L1

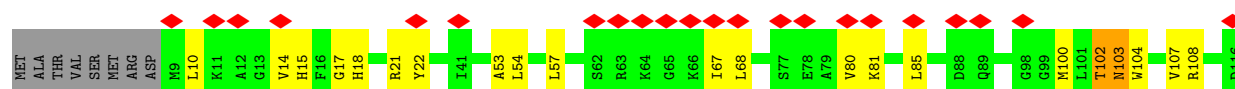


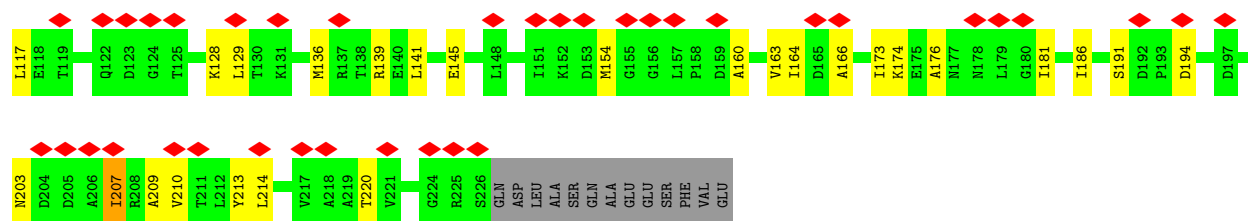
• Molecule 37: 16S rRNA



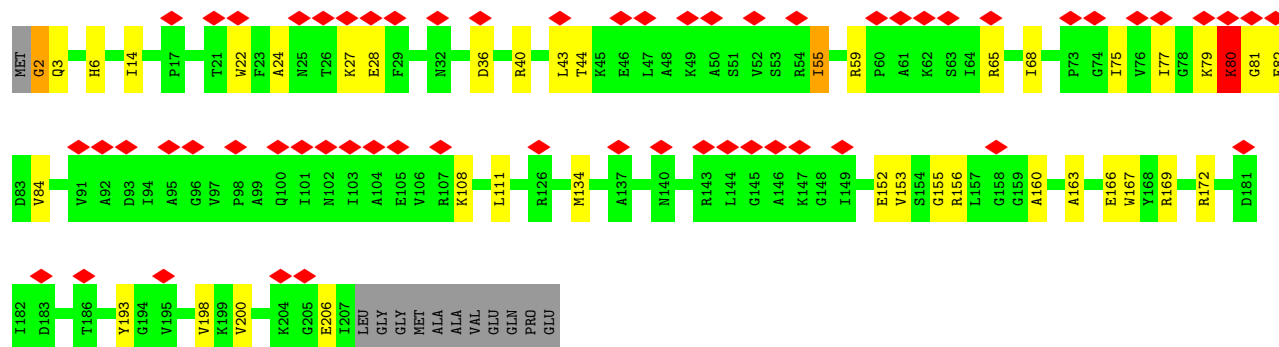
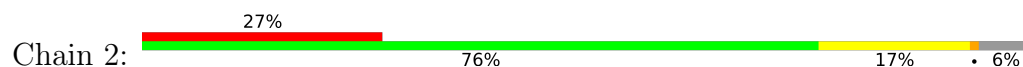


• Molecule 38: 30S ribosomal protein S2

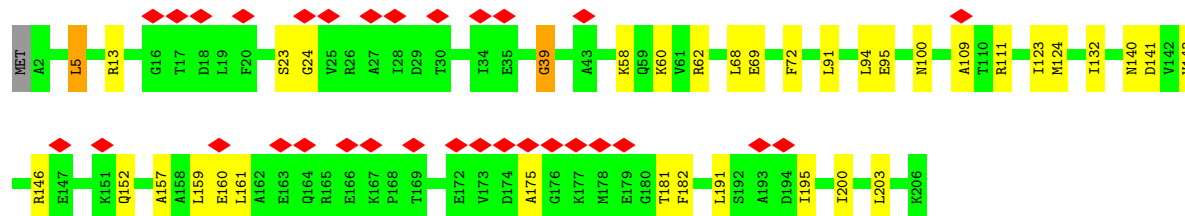
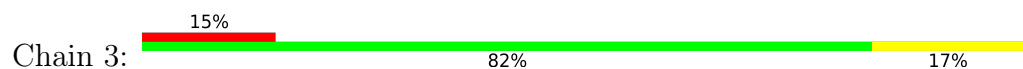




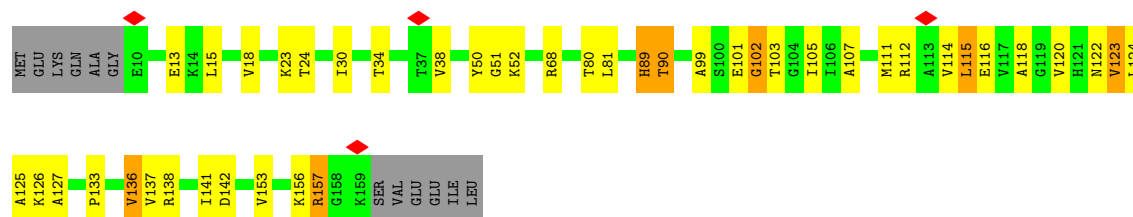
• Molecule 39: 30S ribosomal protein S3



• Molecule 40: 30S ribosomal protein S4

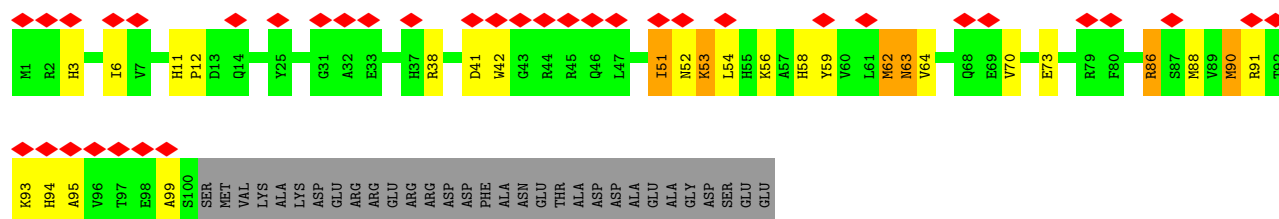


• Molecule 41: 30S ribosomal protein S5

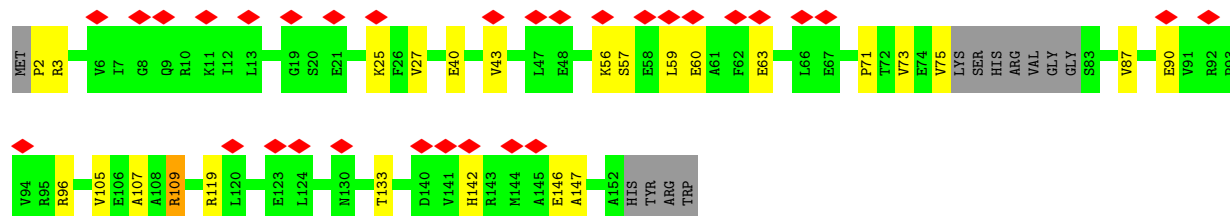
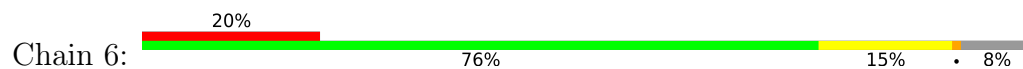


• Molecule 42: 30S ribosomal protein S6, non-modified isoform

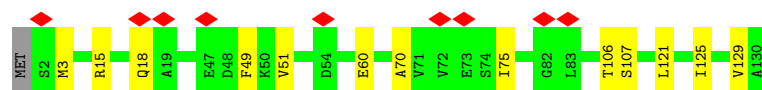
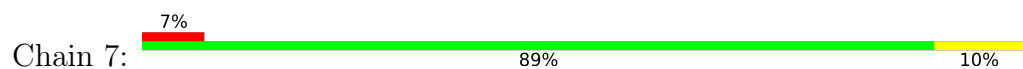




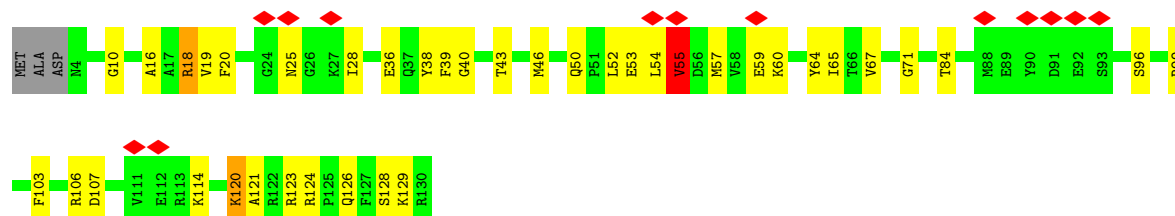
- Molecule 43: 30S ribosomal protein S7



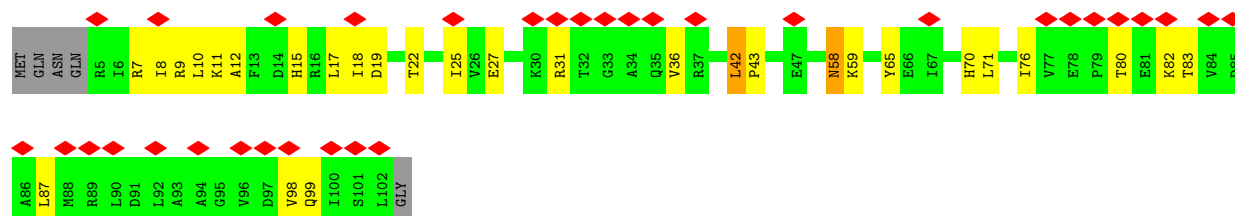
- Molecule 44: 30S ribosomal protein S8



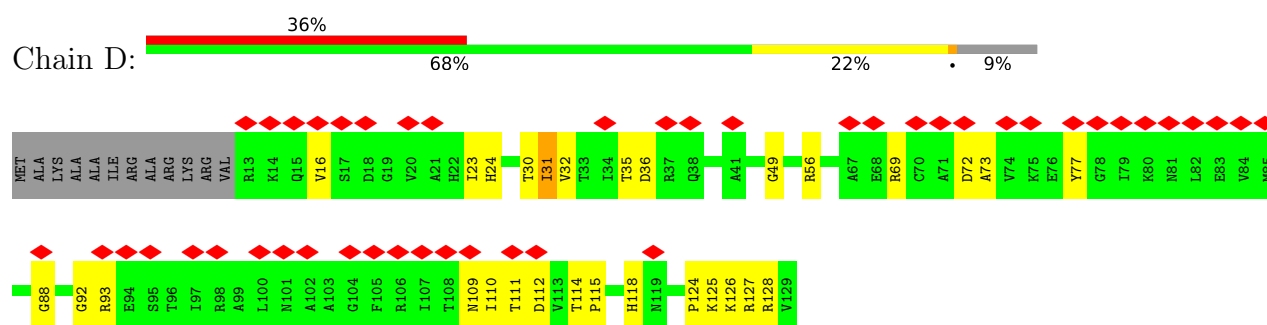
- Molecule 45: 30S ribosomal protein S9



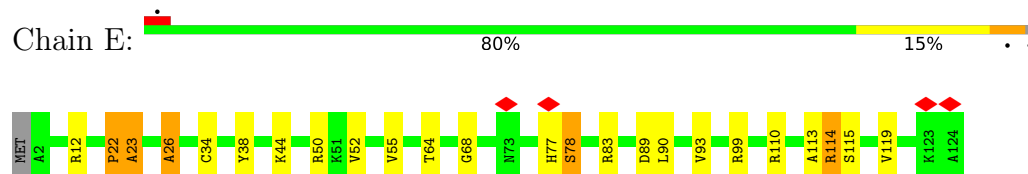
- Molecule 46: 30S ribosomal protein S10



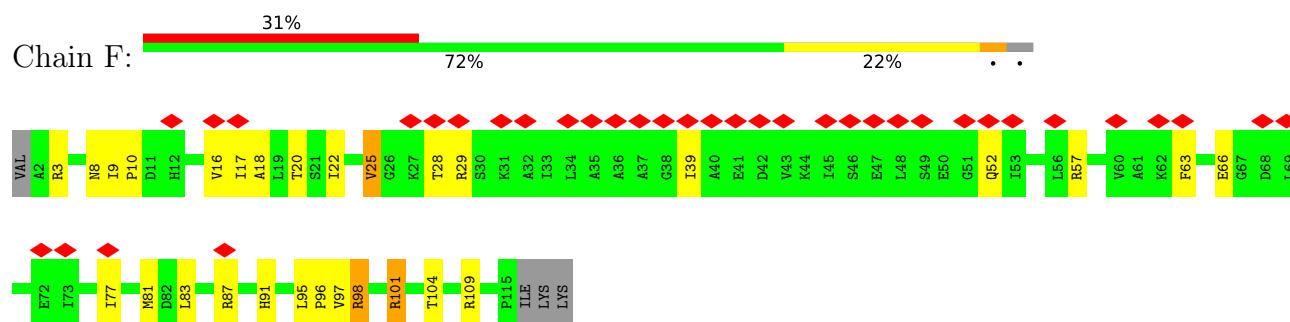
- Molecule 47: 30S ribosomal protein S11



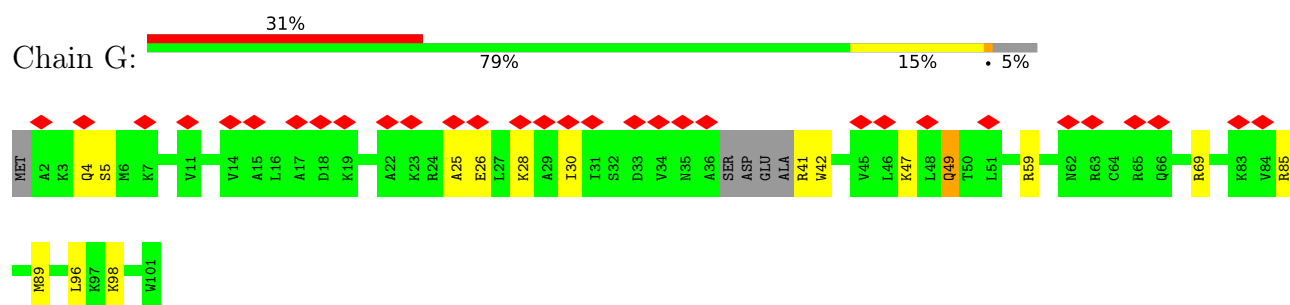
- Molecule 48: 30S ribosomal protein S12



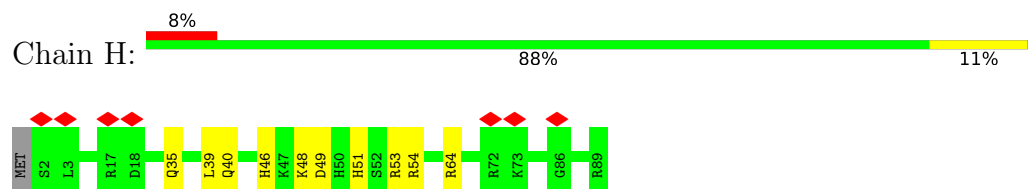
- Molecule 49: 30S ribosomal protein S13



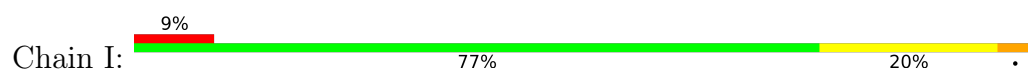
- Molecule 50: 30S ribosomal protein S14

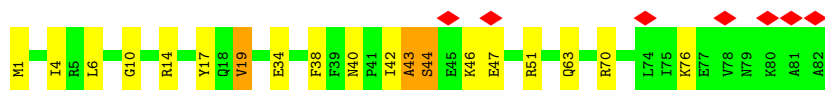


- Molecule 51: 30S ribosomal protein S15

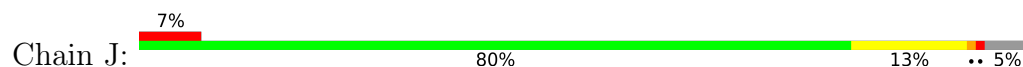


- Molecule 52: 30S ribosomal protein S16





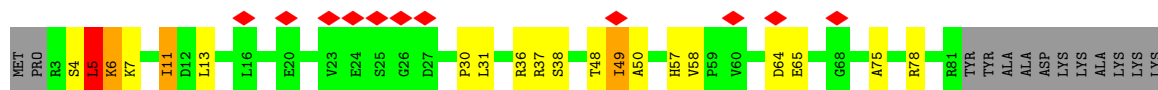
- Molecule 53: 30S ribosomal protein S17



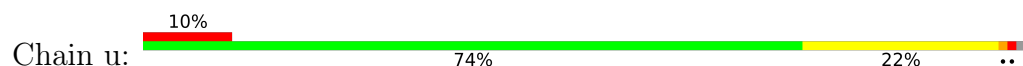
- Molecule 54: 30S ribosomal protein S18



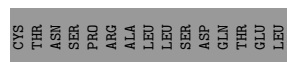
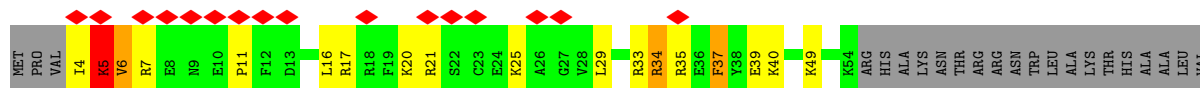
- Molecule 55: 30S ribosomal protein S19



- Molecule 56: 30S ribosomal protein S20



- Molecule 57: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75081	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	2.540	Depositor
Minimum map value	-0.736	Depositor
Average map value	-0.008	Depositor
Map value standard deviation	0.148	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	654.0, 654.0, 654.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.51	0/1744	0.72	0/2716
2	s	0.96	1/326 (0.3%)	0.92	0/441
3	M	0.51	0/1779	0.77	3/2768 (0.1%)
4	O	0.65	1/2828 (0.0%)	0.83	7/4410 (0.2%)
5	P	1.72	39/2121 (1.8%)	1.42	17/2852 (0.6%)
6	Q	1.54	14/1585 (0.9%)	1.29	10/2134 (0.5%)
7	R	1.21	8/1571 (0.5%)	1.09	5/2113 (0.2%)
8	S	0.84	0/1434	0.89	0/1926
9	T	0.83	0/1342	0.86	0/1816
10	U	0.68	1/1122 (0.1%)	1.02	3/1515 (0.2%)
11	V	0.77	0/1045	0.74	0/1410
12	W	1.42	10/1151 (0.9%)	1.10	0/1551
13	X	1.53	8/947 (0.8%)	1.28	4/1268 (0.3%)
14	Y	1.65	14/1053 (1.3%)	1.44	7/1403 (0.5%)
15	Z	1.42	4/1092 (0.4%)	1.20	2/1460 (0.1%)
16	a	1.65	11/973 (1.1%)	1.35	5/1301 (0.4%)
17	b	1.05	2/901 (0.2%)	1.04	5/1209 (0.4%)
18	c	1.38	4/927 (0.4%)	1.21	4/1240 (0.3%)
19	d	1.57	7/959 (0.7%)	1.32	7/1278 (0.5%)
20	e	1.39	6/828 (0.7%)	1.21	1/1107 (0.1%)
21	f	1.33	2/864 (0.2%)	1.14	1/1156 (0.1%)
22	g	1.22	0/744	1.10	0/994
23	h	1.00	1/787 (0.1%)	1.06	0/1051
24	i	0.96	0/765	0.90	0/1025
25	j	1.50	5/575 (0.9%)	1.38	6/762 (0.8%)
26	k	1.35	1/634 (0.2%)	1.16	2/848 (0.2%)
27	l	0.89	0/509	1.00	0/677
28	m	1.18	0/452	1.14	1/605 (0.2%)
29	n	1.48	2/449 (0.4%)	1.40	6/599 (1.0%)
30	o	1.45	5/416 (1.2%)	1.02	0/554
31	p	1.73	5/379 (1.3%)	1.61	5/498 (1.0%)
32	q	1.50	0/512	1.35	2/676 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	r	1.43	3/302 (1.0%)	1.34	3/397 (0.8%)
34	N	0.95	271/69681 (0.4%)	0.95	171/108706 (0.2%)
35	L	0.78	0/426	0.90	1/570 (0.2%)
36	C	0.32	0/1034	0.81	1/1387 (0.1%)
37	0	0.76	28/36809 (0.1%)	0.85	49/57423 (0.1%)
38	1	1.02	1/1735 (0.1%)	0.99	2/2338 (0.1%)
39	2	1.08	4/1651 (0.2%)	0.97	3/2225 (0.1%)
40	3	0.95	2/1664 (0.1%)	1.03	2/2227 (0.1%)
41	4	1.53	6/1118 (0.5%)	1.35	7/1504 (0.5%)
42	5	1.16	5/835 (0.6%)	1.14	3/1128 (0.3%)
43	6	0.83	0/1142	0.86	1/1532 (0.1%)
44	7	1.15	1/988 (0.1%)	1.04	0/1326
45	8	1.09	1/1033 (0.1%)	1.13	2/1375 (0.1%)
46	9	0.95	1/796 (0.1%)	1.02	2/1077 (0.2%)
47	D	1.11	0/892	1.12	3/1205 (0.2%)
48	E	1.37	6/968 (0.6%)	1.25	3/1300 (0.2%)
49	F	1.09	1/892 (0.1%)	1.07	0/1193
50	G	1.10	0/784	1.14	1/1043 (0.1%)
51	H	1.20	2/717 (0.3%)	1.03	1/959 (0.1%)
52	I	1.18	3/658 (0.5%)	1.19	5/884 (0.6%)
53	J	1.08	1/657 (0.2%)	1.06	1/881 (0.1%)
54	K	1.20	0/462	1.15	1/621 (0.2%)
55	t	1.02	1/652 (0.2%)	1.00	1/877 (0.1%)
56	u	1.19	2/670 (0.3%)	1.20	2/888 (0.2%)
57	v	1.24	5/426 (1.2%)	1.27	3/565 (0.5%)
All	All	0.99	495/159806 (0.3%)	0.97	371/238994 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	P	0	3
6	Q	0	1
8	S	0	2
10	U	0	1
11	V	0	1
14	Y	0	2
15	Z	0	2
23	h	0	1
32	q	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	N	0	6
37	0	0	5
38	1	0	3
39	2	0	2
41	4	0	5
42	5	0	2
45	8	0	4
47	D	0	1
48	E	0	2
53	J	0	2
55	t	0	1
56	u	0	1
57	v	0	1
All	All	0	49

All (495) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	2502	G	P-OP2	14.12	1.77	1.49
34	N	1156	A	P-OP2	12.93	1.74	1.49
34	N	1333	G	P-OP2	10.88	1.70	1.49
34	N	783	A	P-OP2	10.82	1.70	1.49
41	4	127	ALA	C-O	-10.60	1.10	1.23
5	P	221	ARG	CA-C	-10.45	1.38	1.53
34	N	945	A	P-OP2	10.42	1.69	1.49
34	N	1639	C	P-OP1	10.27	1.69	1.49
14	Y	51	GLU	C-O	10.23	1.37	1.23
34	N	1664	A	P-OP2	10.14	1.69	1.49
5	P	219	THR	C-O	10.06	1.35	1.24
34	N	945	A	P-OP1	10.05	1.69	1.49
34	N	1670	C	P-OP1	9.82	1.68	1.49
48	E	23	ALA	N-CA	9.72	1.58	1.46
5	P	213	TRP	CD2-CE2	9.65	1.57	1.41
34	N	2074	U	P-OP1	9.65	1.68	1.49
16	a	2	ARG	C-O	-9.60	1.11	1.24
34	N	2588	G	P-OP1	9.38	1.67	1.49
42	5	63	ASN	C-O	-9.36	1.09	1.23
34	N	2005	A	P-OP1	9.15	1.67	1.49
34	N	827	U	P-OP1	9.02	1.67	1.49
34	N	450	G	P-OP2	9.01	1.67	1.49
30	o	50	LYS	C-O	-8.90	1.14	1.24
34	N	943	A	P-OP2	8.78	1.66	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	u	5	LYS	C-O	-8.71	1.17	1.24
34	N	828	U	O3'-P	-8.69	1.48	1.61
34	N	2349	G	O3'-P	-8.59	1.48	1.61
34	N	2445	G	O3'-P	-8.59	1.48	1.61
34	N	2025	C	P-OP2	8.56	1.66	1.49
34	N	567	U	P-OP1	8.52	1.66	1.49
37	0	578	C	P-OP1	8.51	1.66	1.49
34	N	800	A	P-OP1	8.46	1.65	1.49
5	P	213	TRP	CA-C	-8.45	1.39	1.52
34	N	963	U	O3'-P	-8.35	1.48	1.61
5	P	48	ARG	C-O	-8.28	1.13	1.23
6	Q	162	ALA	CA-C	-8.26	1.41	1.52
34	N	1604	C	P-OP1	8.26	1.65	1.49
33	r	38	GLY	N-CA	8.25	1.58	1.45
34	N	2615	U	P-OP1	8.22	1.65	1.49
34	N	1774	C	P-OP1	8.22	1.65	1.49
37	0	21	G	P-OP1	8.21	1.65	1.49
34	N	2589	A	O3'-P	-8.20	1.48	1.61
34	N	2060	A	O3'-P	-8.15	1.49	1.61
34	N	1777	U	O3'-P	-8.14	1.49	1.61
7	R	80	SER	C-O	-8.10	1.12	1.23
34	N	2502	G	O5'-C5'	-8.05	1.30	1.42
37	0	757	U	O3'-P	-8.05	1.49	1.61
14	Y	22	GLY	C-O	-8.03	1.11	1.23
5	P	238	ARG	C-O	8.01	1.34	1.24
34	N	782	A	O3'-P	-7.91	1.49	1.61
34	N	963	U	P-OP1	7.90	1.64	1.49
37	0	20	U	O3'-P	-7.89	1.49	1.61
34	N	1968	G	O3'-P	-7.87	1.49	1.61
5	P	204	VAL	CA-C	-7.87	1.42	1.52
34	N	1828	G	P-OP2	7.86	1.64	1.49
34	N	787	C	O3'-P	-7.85	1.49	1.61
14	Y	62	PRO	C-O	7.84	1.33	1.23
34	N	576	U	P-OP1	7.82	1.64	1.49
34	N	692	C	O3'-P	-7.82	1.49	1.61
5	P	230	HIS	CA-C	-7.81	1.43	1.52
34	N	2687	U	O3'-P	-7.80	1.49	1.61
34	N	825	A	O3'-P	-7.77	1.49	1.61
14	Y	18	ARG	CZ-NH1	7.76	1.43	1.32
34	N	1009	A	O3'-P	-7.75	1.49	1.61
41	4	30	ILE	C-O	-7.73	1.16	1.24
34	N	1269	A	P-OP2	7.71	1.64	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	585	G	O3'-P	-7.68	1.49	1.61
34	N	948	C	P-OP1	7.68	1.64	1.49
34	N	1257	C	O3'-P	-7.60	1.49	1.61
5	P	11	PRO	N-CA	7.44	1.56	1.47
34	N	554	U	O3'-P	-7.44	1.50	1.61
34	N	2588	G	P-OP2	7.43	1.63	1.49
34	N	2019	A	O3'-P	-7.43	1.50	1.61
34	N	809	G	O3'-P	-7.41	1.50	1.61
34	N	2025	C	O3'-P	-7.39	1.50	1.61
34	N	2550	G	O3'-P	-7.38	1.50	1.61
34	N	2543	G	P-OP1	7.36	1.63	1.49
34	N	2593	U	O3'-P	-7.35	1.50	1.61
31	p	38	GLY	CA-C	-7.34	1.41	1.51
12	W	97	PRO	C-O	7.32	1.33	1.24
18	c	93	ARG	CD-NE	-7.31	1.36	1.46
37	0	667	G	O3'-P	-7.31	1.50	1.61
34	N	2576	G	P-OP1	7.30	1.63	1.49
34	N	116	C	O3'-P	-7.30	1.50	1.61
34	N	120	U	P-OP1	7.29	1.63	1.49
34	N	2050	C	O3'-P	-7.28	1.50	1.61
34	N	445	C	O3'-P	-7.25	1.50	1.61
34	N	984	A	O3'-P	-7.25	1.50	1.61
37	0	882	C	O3'-P	-7.22	1.50	1.61
34	N	2714	G	P-OP2	7.22	1.63	1.49
34	N	1664	A	P-OP1	7.22	1.63	1.49
14	Y	19	LEU	C-O	7.19	1.32	1.23
5	P	213	TRP	CZ3-CH2	7.19	1.58	1.40
17	b	30	ARG	CZ-NH1	7.18	1.42	1.32
34	N	1375	U	O3'-P	-7.15	1.50	1.61
42	5	63	ASN	N-CA	7.15	1.55	1.46
34	N	1152	C	O3'-P	-7.14	1.50	1.61
34	N	2873	A	C6-N1	-7.14	1.21	1.35
34	N	673	C	O3'-P	-7.08	1.50	1.61
34	N	2588	G	O3'-P	-7.07	1.50	1.61
13	X	86	LEU	C-O	-7.07	1.15	1.24
34	N	2503	A	P-OP2	7.00	1.62	1.49
34	N	397	U	O3'-P	-6.99	1.50	1.61
34	N	859	G	O3'-P	6.99	1.71	1.61
16	a	47	VAL	C-O	-6.97	1.15	1.23
34	N	2498	C	P-OP2	6.97	1.62	1.49
34	N	826	U	P-OP1	6.97	1.62	1.49
7	R	77	ILE	CB-CG1	-6.96	1.39	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	j	14	ARG	C-O	-6.95	1.15	1.23
34	N	1780	A	P-OP1	6.93	1.62	1.49
29	n	11	SER	N-CA	-6.93	1.38	1.46
6	Q	125	TRP	CA-C	-6.93	1.43	1.52
34	N	453	A	P-OP1	6.93	1.62	1.49
34	N	1019	U	O3'-P	-6.92	1.50	1.61
34	N	2022	U	P-OP1	6.92	1.62	1.49
34	N	2052	A	O3'-P	-6.91	1.50	1.61
34	N	1774	C	O3'-P	-6.88	1.50	1.61
34	N	1612	C	O3'-P	-6.86	1.50	1.61
53	J	71	LYS	C-O	-6.83	1.15	1.24
34	N	1658	C	P-OP1	6.80	1.62	1.49
48	E	22	PRO	CA-C	6.79	1.62	1.52
5	P	222	GLY	C-O	-6.79	1.14	1.23
34	N	2698	U	O3'-P	-6.78	1.50	1.61
34	N	2635	A	O3'-P	-6.77	1.50	1.61
12	W	81	ILE	C-O	6.77	1.32	1.24
5	P	86	ASN	C-O	-6.76	1.15	1.24
34	N	200	U	O3'-P	-6.75	1.51	1.61
16	a	66	ALA	CA-C	-6.75	1.43	1.52
5	P	221	ARG	C-O	-6.73	1.15	1.23
5	P	15	HIS	C-O	-6.72	1.14	1.24
34	N	2006	C	P-OP1	6.69	1.62	1.49
34	N	1994	C	O3'-P	-6.68	1.51	1.61
34	N	1658	C	O3'-P	-6.67	1.51	1.61
23	h	68	SER	CB-OG	6.66	1.55	1.42
37	0	812	G	O3'-P	6.66	1.71	1.61
16	a	2	ARG	C-N	-6.63	1.24	1.33
19	d	49	ASP	CA-C	-6.63	1.43	1.52
34	N	1751	U	O3'-P	-6.63	1.51	1.61
37	0	1500	A	O3'-P	-6.63	1.51	1.61
34	N	2466	C	O3'-P	-6.63	1.51	1.61
34	N	1831	G	O3'-P	-6.62	1.51	1.61
19	d	49	ASP	C-O	6.62	1.32	1.24
34	N	641	U	O3'-P	-6.61	1.51	1.61
34	N	1993	U	O5'-C5'	-6.61	1.32	1.42
34	N	955	U	O3'-P	-6.61	1.51	1.61
34	N	192	C	P-OP1	6.59	1.62	1.49
34	N	2062	A	P-OP2	6.59	1.62	1.49
29	n	10	ARG	CA-C	6.59	1.61	1.52
34	N	1900	A	O3'-P	6.58	1.71	1.61
34	N	2035	G	O5'-C5'	-6.58	1.32	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	1782	U	P-OP1	6.57	1.62	1.49
34	N	2740	A	O3'-P	-6.57	1.51	1.61
34	N	2765	A	C6-N1	-6.50	1.22	1.35
34	N	1268	A	P-OP1	6.49	1.61	1.49
13	X	66	LYS	CA-C	-6.49	1.44	1.52
18	c	21	ARG	C-O	-6.49	1.18	1.24
5	P	221	ARG	CB-CG	-6.49	1.32	1.52
34	N	1353	A	O3'-P	-6.48	1.51	1.61
34	N	2518	A	P-OP2	6.46	1.61	1.49
16	a	1	MET	C-O	6.46	1.36	1.23
34	N	2489	U	O3'-P	-6.45	1.51	1.61
34	N	810	U	P-OP1	6.44	1.61	1.49
5	P	213	TRP	CB-CG	-6.43	1.30	1.50
13	X	7	MET	N-CA	6.42	1.54	1.46
34	N	2543	G	O5'-C5'	-6.42	1.32	1.42
15	Z	39	GLY	C-O	-6.40	1.15	1.23
45	8	121	ALA	C-O	-6.40	1.16	1.24
34	N	2605	U	O3'-P	-6.40	1.51	1.61
34	N	2437	G	O3'-P	-6.38	1.51	1.61
34	N	1254	A	O3'-P	-6.38	1.51	1.61
5	P	204	VAL	N-CA	-6.36	1.39	1.46
20	e	79	ARG	C-O	6.35	1.31	1.23
34	N	1970	A	P-OP2	6.35	1.61	1.49
14	Y	62	PRO	CA-CB	-6.34	1.45	1.53
34	N	2031	A	P-OP1	-6.33	1.36	1.49
5	P	234	GLY	C-O	-6.31	1.15	1.23
34	N	1678	A	P-OP2	6.31	1.61	1.49
34	N	2264	C	O3'-P	-6.30	1.51	1.61
6	Q	126	ASN	CA-C	-6.30	1.45	1.53
5	P	271	ARG	CZ-NH1	6.29	1.41	1.32
34	N	1813	G	O3'-P	-6.29	1.51	1.61
34	N	1828	G	P-OP1	6.29	1.61	1.49
48	E	114	ARG	C-O	-6.29	1.16	1.24
34	N	975	A	P-OP2	6.27	1.61	1.49
34	N	839	U	O3'-P	-6.26	1.51	1.61
18	c	53	ARG	N-CA	-6.26	1.36	1.46
34	N	2590	A	O3'-P	-6.26	1.51	1.61
31	p	39	ARG	NE-CZ	6.23	1.39	1.33
34	N	733	G	O3'-P	-6.22	1.51	1.61
34	N	2265	U	O3'-P	-6.22	1.51	1.61
5	P	220	VAL	CA-CB	-6.21	1.46	1.54
14	Y	41	ARG	CA-C	-6.20	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	192	C	O3'-P	-6.20	1.51	1.61
37	0	726	C	O3'-P	-6.20	1.51	1.61
26	k	22	LEU	C-O	-6.18	1.14	1.23
16	a	112	TYR	CA-C	-6.17	1.45	1.52
6	Q	163	GLY	N-CA	6.17	1.52	1.45
34	N	1794	A	O3'-P	-6.17	1.51	1.61
34	N	1189	A	O3'-P	-6.17	1.51	1.61
19	d	10	ALA	C-O	6.15	1.31	1.24
41	4	24	THR	C-O	-6.15	1.14	1.23
34	N	2447	G	O3'-P	-6.15	1.51	1.61
34	N	372	G	O3'-P	6.14	1.70	1.61
30	o	10	LYS	C-O	-6.13	1.16	1.24
33	r	37	GLN	CA-C	-6.12	1.44	1.52
37	0	24	U	N3-C4	-6.12	1.26	1.38
34	N	515	A	O3'-P	-6.12	1.51	1.61
12	W	138	GLN	C-O	-6.11	1.16	1.23
34	N	1778	U	O3'-P	-6.11	1.51	1.61
34	N	569	U	O3'-P	-6.11	1.51	1.61
57	v	34	ARG	CZ-NH1	6.09	1.41	1.32
34	N	832	U	O3'-P	-6.08	1.52	1.61
34	N	254	G	O3'-P	-6.08	1.52	1.61
34	N	572	A	P-OP1	6.08	1.61	1.49
12	W	107	GLY	C-O	-6.08	1.17	1.24
12	W	98	GLU	N-CA	-6.07	1.38	1.46
34	N	2572	A	O3'-P	-6.06	1.52	1.61
34	N	1790	C	O3'-P	-6.06	1.52	1.61
7	R	75	SER	CA-C	-6.06	1.46	1.53
5	P	10	SER	CA-CB	6.05	1.62	1.53
34	N	464	U	O3'-P	-6.05	1.52	1.61
34	N	997	G	O3'-P	-6.05	1.52	1.61
41	4	24	THR	CA-C	-6.04	1.47	1.53
34	N	2822	G	O3'-P	-6.02	1.52	1.61
14	Y	37	GLY	C-O	-6.01	1.16	1.23
12	W	84	ILE	CA-C	-6.01	1.46	1.53
37	0	1367	C	O3'-P	-6.00	1.52	1.61
34	N	821	A	O3'-P	-6.00	1.52	1.61
34	N	2620	C	O3'-P	-6.00	1.52	1.61
34	N	818	G	P-OP2	6.00	1.60	1.49
14	Y	29	LYS	C-O	5.99	1.31	1.24
34	N	1771	C	O3'-P	-5.98	1.52	1.61
34	N	2867	G	O3'-P	5.98	1.70	1.61
34	N	671	C	P-OP2	5.97	1.60	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	v	37	PHE	N-CA	5.97	1.53	1.46
42	5	51	ILE	C-O	-5.96	1.17	1.24
34	N	2406	A	P-OP1	5.95	1.60	1.49
14	Y	51	GLU	N-CA	-5.95	1.39	1.46
5	P	214	ARG	CZ-NH1	5.94	1.41	1.32
39	2	3	GLN	N-CA	-5.94	1.39	1.46
34	N	2385	C	P-OP1	5.93	1.60	1.49
34	N	2081	U	O3'-P	-5.93	1.52	1.61
34	N	2625	G	O3'-P	-5.93	1.52	1.61
46	9	58	ASN	CA-C	-5.93	1.44	1.52
37	0	1393	U	O3'-P	-5.93	1.52	1.61
34	N	2499	C	P-OP2	5.92	1.60	1.49
34	N	676	A	O3'-P	-5.91	1.52	1.61
34	N	2025	C	O5'-C5'	-5.91	1.33	1.42
34	N	538	A	O3'-P	-5.90	1.52	1.61
34	N	2061	G	C2'-O2'	5.90	1.51	1.42
5	P	158	ALA	CA-C	-5.89	1.45	1.52
34	N	566	U	O3'-P	-5.89	1.52	1.61
34	N	2072	C	O5'-C5'	-5.89	1.33	1.42
34	N	2837	A	O3'-P	-5.88	1.52	1.61
34	N	2637	U	O3'-P	-5.88	1.52	1.61
48	E	23	ALA	C-O	-5.87	1.16	1.24
34	N	730	A	P-OP2	5.86	1.60	1.49
34	N	2444	G	O3'-P	-5.86	1.52	1.61
34	N	2359	C	O3'-P	-5.85	1.52	1.61
33	r	36	ARG	CD-NE	-5.85	1.38	1.46
30	o	48	ILE	C-O	-5.85	1.17	1.24
55	t	6	LYS	N-CA	5.84	1.53	1.46
41	4	50	TYR	C-O	5.83	1.31	1.24
5	P	235	GLY	C-N	-5.83	1.25	1.33
5	P	235	GLY	CA-C	-5.83	1.43	1.51
34	N	1822	C	O3'-P	-5.83	1.52	1.61
34	N	2232	C	O3'-P	-5.82	1.52	1.61
34	N	2062	A	O5'-C5'	-5.82	1.34	1.42
34	N	2072	C	O3'-P	-5.82	1.52	1.61
37	0	980	C	P-OP1	5.80	1.60	1.49
5	P	258	ARG	NE-CZ	-5.80	1.26	1.33
34	N	2247	A	O3'-P	-5.79	1.52	1.61
34	N	2598	A	O3'-P	-5.79	1.52	1.61
5	P	204	VAL	C-N	-5.78	1.25	1.33
34	N	1824	G	P-OP2	5.78	1.60	1.49
37	0	22	G	O3'-P	-5.78	1.52	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	P	160	THR	C-O	-5.78	1.16	1.24
34	N	198	C	O3'-P	-5.77	1.52	1.61
16	a	106	ASP	N-CA	-5.77	1.40	1.46
52	I	4	ILE	C-O	-5.77	1.17	1.23
34	N	1261	C	O3'-P	-5.77	1.52	1.61
7	R	62	GLN	N-CA	5.76	1.53	1.46
34	N	2457	U	O3'-P	-5.75	1.52	1.61
34	N	2542	A	O3'-P	-5.75	1.52	1.61
34	N	2684	U	O3'-P	-5.75	1.52	1.61
34	N	1298	C	O3'-P	-5.74	1.52	1.61
34	N	2572	A	P-OP1	-5.74	1.37	1.49
37	0	387	U	O3'-P	-5.74	1.52	1.61
39	2	2	GLY	N-CA	5.74	1.54	1.45
13	X	65	THR	C-O	-5.73	1.16	1.23
12	W	30	THR	CB-CG2	-5.73	1.33	1.52
34	N	940	G	O3'-P	-5.73	1.52	1.61
34	N	2602	A	O3'-P	5.73	1.69	1.61
30	o	23	THR	C-O	-5.71	1.20	1.24
34	N	2268	A	P-OP1	5.71	1.60	1.49
7	R	81	GLY	C-N	-5.71	1.25	1.33
34	N	578	G	P-OP2	5.70	1.60	1.49
34	N	2016	U	O3'-P	-5.70	1.52	1.61
13	X	23	LYS	CA-C	-5.70	1.45	1.52
34	N	783	A	C4'-O4'	5.69	1.54	1.45
34	N	1662	U	P-OP2	5.69	1.60	1.49
34	N	796	C	O3'-P	-5.69	1.52	1.61
34	N	1805	A	O3'-P	-5.69	1.52	1.61
34	N	1681	G	O3'-P	-5.68	1.52	1.61
34	N	2013	A	O3'-P	-5.68	1.52	1.61
37	0	505	G	O3'-P	-5.67	1.52	1.61
34	N	25	U	O3'-P	-5.66	1.52	1.61
34	N	126	A	O3'-P	-5.66	1.52	1.61
31	p	34	ARG	CG-CD	-5.65	1.35	1.52
34	N	29	U	O3'-P	-5.65	1.52	1.61
37	0	814	A	P-OP2	5.64	1.60	1.49
34	N	571	U	O3'-P	-5.64	1.52	1.61
51	H	49	ASP	C-O	5.64	1.31	1.23
34	N	966	G	O3'-P	-5.64	1.52	1.61
13	X	41	ILE	C-O	-5.63	1.17	1.23
15	Z	93	VAL	CA-CB	5.63	1.63	1.54
52	I	10	GLY	N-CA	5.63	1.51	1.45
6	Q	164	GLN	C-O	5.63	1.30	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	761	A	P-OP1	5.63	1.60	1.49
25	j	42	GLY	N-CA	5.62	1.55	1.45
51	H	51	HIS	C-O	5.62	1.30	1.24
34	N	1795	C	O3'-P	-5.61	1.52	1.61
34	N	2499	C	P-OP1	5.61	1.60	1.49
4	O	83	G	O3'-P	-5.61	1.52	1.61
34	N	2049	G	O3'-P	-5.60	1.52	1.61
16	a	17	ARG	C-O	5.59	1.30	1.24
34	N	773	U	O3'-P	-5.57	1.52	1.61
15	Z	11	LYS	C-O	-5.56	1.17	1.24
34	N	2072	C	P-OP1	5.55	1.60	1.49
5	P	205	LEU	N-CA	5.55	1.53	1.46
12	W	80	HIS	CA-C	-5.55	1.45	1.53
6	Q	162	ALA	C-O	-5.54	1.17	1.23
34	N	1009	A	P-OP2	5.54	1.60	1.49
12	W	110	PRO	CA-C	-5.54	1.45	1.52
19	d	51	ARG	CA-CB	-5.53	1.44	1.53
34	N	393	C	P-OP1	5.53	1.60	1.49
34	N	680	C	O3'-P	-5.53	1.52	1.61
34	N	2332	C	O3'-P	-5.53	1.52	1.61
34	N	2051	A	O3'-P	5.53	1.69	1.61
37	0	765	G	O3'-P	-5.53	1.52	1.61
34	N	2829	A	O3'-P	-5.52	1.52	1.61
48	E	113	ALA	CA-C	-5.51	1.46	1.53
6	Q	109	VAL	C-O	-5.51	1.18	1.24
34	N	1010	A	P-OP2	5.51	1.59	1.49
34	N	2436	G	O3'-P	-5.51	1.52	1.61
14	Y	35	HIS	CA-C	-5.49	1.45	1.53
34	N	784	G	O3'-P	5.49	1.69	1.61
34	N	1949	G	O3'-P	-5.49	1.52	1.61
34	N	2248	C	P-OP2	5.49	1.59	1.49
6	Q	126	ASN	N-CA	5.49	1.54	1.46
42	5	99	ALA	CA-C	5.49	1.56	1.52
19	d	32	TYR	C-N	-5.48	1.25	1.33
5	P	198	ALA	C-O	5.48	1.30	1.24
37	0	764	C	O3'-P	-5.47	1.52	1.61
5	P	155	ALA	CA-C	-5.47	1.47	1.53
34	N	1186	G	P-OP2	5.44	1.59	1.49
34	N	1255	U	O5'-C5'	-5.44	1.34	1.42
13	X	114	LYS	C-O	-5.43	1.17	1.24
42	5	62	MET	C-N	-5.43	1.27	1.33
5	P	239	ASN	CA-C	5.42	1.60	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	2	166	GLU	C-O	-5.41	1.17	1.24
40	3	123	ILE	C-O	-5.39	1.18	1.24
34	N	2243	U	P-OP1	5.39	1.59	1.49
20	e	12	HIS	C-O	5.38	1.30	1.23
34	N	1394	U	O3'-P	-5.38	1.53	1.61
34	N	688	U	O3'-P	-5.38	1.53	1.61
34	N	2516	A	O3'-P	-5.38	1.53	1.61
20	e	72	VAL	C-O	-5.38	1.18	1.24
5	P	54	ILE	N-CA	5.37	1.52	1.46
20	e	75	VAL	C-O	-5.37	1.18	1.24
34	N	2554	U	P-OP2	-5.37	1.38	1.49
34	N	2048	G	O3'-P	-5.37	1.53	1.61
34	N	923	G	O3'-P	-5.37	1.53	1.61
34	N	419	U	O3'-P	-5.36	1.53	1.61
25	j	15	ASP	N-CA	-5.36	1.39	1.45
34	N	1671	U	P-OP2	5.36	1.59	1.49
6	Q	126	ASN	C-O	-5.36	1.16	1.23
31	p	34	ARG	C-O	-5.35	1.17	1.24
57	v	40	LYS	CA-C	5.35	1.59	1.52
6	Q	170	VAL	CA-C	-5.34	1.46	1.52
6	Q	149	ASN	CA-CB	-5.34	1.44	1.53
34	N	1327	A	P-OP2	5.33	1.59	1.49
34	N	1782	U	O3'-P	-5.33	1.53	1.61
34	N	503	A	C6-N1	-5.33	1.24	1.35
34	N	1026	G	P-OP2	-5.33	1.38	1.49
14	Y	101	ILE	N-CA	-5.32	1.40	1.46
13	X	35	VAL	C-O	5.32	1.29	1.24
34	N	239	C	O3'-P	-5.32	1.53	1.61
34	N	2694	G	O3'-P	-5.32	1.53	1.61
37	0	1182	G	O3'-P	5.32	1.69	1.61
12	W	76	HIS	C-O	-5.31	1.17	1.23
20	e	54	VAL	C-O	5.31	1.29	1.24
21	f	96	ILE	N-CA	-5.29	1.39	1.46
31	p	42	LEU	N-CA	-5.29	1.41	1.46
34	N	120	U	P-OP2	5.29	1.59	1.49
37	0	572	A	P-OP1	5.29	1.59	1.49
34	N	1977	A	O3'-P	-5.28	1.53	1.61
34	N	2045	C	O3'-P	-5.28	1.53	1.61
7	R	45	ALA	N-CA	-5.28	1.40	1.46
34	N	2260	C	O3'-P	-5.27	1.53	1.61
5	P	195	VAL	CB-CG1	-5.27	1.35	1.52
34	N	1342	A	P-OP2	5.27	1.59	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	2289	G	O3'-P	-5.27	1.53	1.61
34	N	117	G	O3'-P	-5.26	1.53	1.61
7	R	81	GLY	N-CA	-5.26	1.37	1.45
25	j	72	LYS	C-O	5.26	1.30	1.23
34	N	1649	G	O3'-P	-5.26	1.53	1.61
5	P	156	ARG	CD-NE	-5.26	1.38	1.46
34	N	1191	G	O3'-P	-5.26	1.53	1.61
19	d	49	ASP	CB-CG	5.25	1.65	1.52
34	N	1960	A	O3'-P	-5.25	1.53	1.61
34	N	698	C	O3'-P	-5.25	1.53	1.61
34	N	2285	C	O3'-P	-5.25	1.53	1.61
34	N	411	G	P-OP1	5.24	1.59	1.49
34	N	946	C	P-OP2	5.24	1.59	1.49
5	P	175	ARG	CA-C	-5.24	1.46	1.52
57	v	35	ARG	CA-C	-5.24	1.46	1.52
21	f	85	ILE	C-O	-5.24	1.18	1.24
34	N	2074	U	O3'-P	-5.24	1.53	1.61
40	3	39	GLY	N-CA	5.24	1.52	1.45
34	N	2682	A	P-OP2	5.24	1.59	1.49
16	a	8	ARG	NE-CZ	-5.23	1.27	1.33
34	N	1234	U	O3'-P	-5.23	1.53	1.61
34	N	2028	U	O3'-P	-5.23	1.53	1.61
34	N	2723	C	O3'-P	-5.23	1.53	1.61
34	N	2452	C	O3'-P	-5.23	1.53	1.61
34	N	1968	G	P-OP1	5.23	1.59	1.49
5	P	195	VAL	C-O	-5.22	1.17	1.24
18	c	92	VAL	CA-C	-5.22	1.46	1.52
14	Y	62	PRO	N-CA	-5.21	1.41	1.46
34	N	2426	A	O3'-P	-5.20	1.53	1.61
52	I	34	GLU	CA-C	-5.20	1.46	1.52
30	o	21	TYR	CE2-CZ	-5.20	1.25	1.38
34	N	193	U	O3'-P	-5.20	1.53	1.61
37	0	715	A	O3'-P	-5.19	1.53	1.61
34	N	2732	G	C3'-O3'	5.19	1.50	1.42
34	N	1432	G	O3'-P	-5.19	1.53	1.61
34	N	1153	C	P-OP2	5.18	1.59	1.49
5	P	239	ASN	N-CA	-5.17	1.39	1.46
19	d	21	ALA	C-O	-5.17	1.16	1.23
34	N	694	U	O3'-P	-5.17	1.53	1.61
57	v	34	ARG	CA-C	5.17	1.59	1.52
34	N	1680	U	O3'-P	-5.17	1.53	1.61
34	N	1677	A	O3'-P	-5.16	1.53	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	Q	150	GLN	N-CA	5.16	1.52	1.46
34	N	960	A	O3'-P	-5.16	1.53	1.61
34	N	1141	U	N3-C4	-5.16	1.28	1.38
34	N	1334	G	O3'-P	-5.16	1.53	1.61
34	N	2727	A	O3'-P	-5.15	1.53	1.61
5	P	213	TRP	CD1-NE1	5.15	1.48	1.37
6	Q	12	THR	CA-CB	5.14	1.61	1.54
34	N	2699	C	O3'-P	-5.14	1.53	1.61
37	0	559	A	N1-C2	5.14	1.44	1.34
15	Z	73	ILE	C-O	-5.13	1.18	1.24
34	N	2262	U	O3'-P	-5.13	1.53	1.61
20	e	43	ASN	CA-C	5.13	1.56	1.52
34	N	2502	G	O3'-P	-5.13	1.53	1.61
34	N	2503	A	P-OP1	5.12	1.59	1.49
37	0	1062	U	O3'-P	-5.11	1.53	1.61
34	N	632	A	O3'-P	-5.11	1.53	1.61
7	R	52	VAL	C-O	-5.11	1.18	1.24
34	N	1296	G	O3'-P	-5.11	1.53	1.61
37	0	1110	A	P-OP2	5.11	1.59	1.49
34	N	1648	U	P-OP2	5.11	1.59	1.49
34	N	1652	A	O3'-P	-5.10	1.53	1.61
34	N	208	C	O3'-P	-5.09	1.53	1.61
34	N	234	U	N3-C4	-5.09	1.28	1.38
2	s	152	ALA	C-O	5.09	1.30	1.24
44	7	106	THR	CA-C	-5.09	1.46	1.53
34	N	727	A	P-OP1	5.09	1.59	1.49
37	0	368	U	N3-C4	-5.09	1.28	1.38
34	N	963	U	P-OP2	5.08	1.59	1.49
38	1	18	HIS	C-O	-5.08	1.20	1.24
16	a	10	LEU	CA-C	-5.08	1.45	1.53
34	N	1142	A	O3'-P	5.08	1.68	1.61
56	u	10	ARG	CD-NE	-5.08	1.39	1.46
34	N	745	G	O3'-P	-5.08	1.53	1.61
34	N	1650	A	O3'-P	-5.07	1.53	1.61
37	0	19	A	O3'-P	-5.06	1.53	1.61
34	N	1367	A	O3'-P	-5.06	1.53	1.61
25	j	45	PHE	CA-CB	-5.05	1.45	1.53
39	2	152	GLU	CA-C	-5.04	1.47	1.53
10	U	29	PHE	CA-C	-5.04	1.48	1.52
16	a	11	ASN	CA-C	-5.04	1.46	1.53
17	b	102	ARG	CZ-NH2	5.03	1.40	1.33
14	Y	63	LYS	N-CA	-5.03	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	1186	G	O3'-P	-5.03	1.53	1.61
34	N	408	G	O3'-P	-5.03	1.53	1.61
6	Q	131	ASP	C-O	-5.03	1.17	1.23
49	F	101	ARG	CZ-NH1	5.01	1.39	1.32
37	O	920	U	O3'-P	-5.01	1.53	1.61
34	N	1004	U	O3'-P	-5.00	1.53	1.61
34	N	1187	G	P-OP2	5.00	1.58	1.49
41	4	50	TYR	CA-C	-5.00	1.46	1.52
48	E	26	ALA	CA-C	5.00	1.58	1.53

All (371) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	73	C	O3'-P-O5'	18.16	131.23	104.00
6	Q	151	THR	CA-C-N	12.76	134.27	119.47
6	Q	151	THR	C-N-CA	12.76	134.27	119.47
34	N	1936	A	C4'-C3'-O3'	-11.05	96.42	113.00
34	N	2725	A	C3'-C2'-O2'	-10.56	94.86	110.70
34	N	242	G	C4'-C3'-O3'	9.99	124.39	109.40
56	u	10	ARG	CB-CG-CD	-9.41	89.65	111.30
34	N	774	G	C1'-C2'-O2'	-9.41	94.29	108.40
57	v	5	LYS	N-CA-C	9.35	124.02	110.10
34	N	2251	G	C3'-C2'-O2'	9.31	124.67	110.70
34	N	774	G	C4'-C3'-O3'	-9.29	99.07	113.00
37	O	561	U	C4'-C3'-O3'	-9.17	99.25	113.00
34	N	995	C	C4'-C3'-O3'	-8.79	96.21	109.40
34	N	2776	A	C2'-C3'-O3'	8.72	122.59	109.50
34	N	670	A	C2'-C3'-O3'	8.68	122.51	109.50
5	P	204	VAL	N-CA-C	8.57	120.31	112.43
34	N	2732	G	C4'-C3'-O3'	-8.46	100.31	113.00
37	O	1528	U	C1'-C2'-O2'	-8.46	99.11	111.80
34	N	1937	A	C4'-C3'-O3'	-8.40	100.40	113.00
34	N	2060	A	O3'-P-O5'	8.31	116.46	104.00
37	O	1347	G	C4'-C3'-O3'	8.30	121.85	109.40
34	N	1136	G	P-O5'-C5'	-8.23	108.56	120.90
34	N	784	G	C2'-C3'-O3'	8.22	126.03	113.70
37	O	717	U	C4'-C3'-O3'	-8.03	100.95	113.00
34	N	1236	G	C4'-C3'-O3'	-8.03	100.95	113.00
37	O	1345	U	C4'-C3'-O3'	8.00	121.40	109.40
34	N	2324	U	C4'-C3'-O3'	-7.99	101.02	113.00
5	P	221	ARG	CG-CD-NE	-7.95	94.52	112.00
34	N	746	U	C4'-C3'-O3'	-7.91	101.14	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	P	232	HIS	O-C-N	-7.86	113.85	123.04
34	N	1141	U	C2'-C3'-O3'	7.81	121.21	109.50
13	X	94	PRO	N-CA-C	7.75	122.88	110.40
42	5	90	MET	CA-C-N	7.62	136.09	121.54
42	5	90	MET	C-N-CA	7.62	136.09	121.54
34	N	2266	A	C4'-C3'-O3'	-7.61	97.99	109.40
34	N	2406	A	C2'-C3'-O3'	-7.56	102.36	113.70
4	O	44	G	C4'-C3'-O3'	-7.55	101.67	113.00
13	X	35	VAL	O-C-N	7.47	129.94	121.94
37	0	115	G	C2'-C3'-O3'	7.45	120.68	109.50
34	N	1142	A	C2'-C3'-O3'	7.41	120.61	109.50
37	0	518	C	C4'-C3'-O3'	7.40	120.50	109.40
32	q	8	ARG	CD-NE-CZ	-7.39	114.05	124.40
17	b	101	GLY	O-C-N	7.33	125.95	121.85
7	R	81	GLY	O-C-N	-7.32	113.19	122.70
37	0	1278	G	C4'-C3'-O3'	-7.30	102.04	113.00
55	t	5	LEU	CB-CG-CD2	7.27	132.50	110.70
7	R	81	GLY	CA-C-N	-7.21	107.28	121.41
7	R	81	GLY	C-N-CA	-7.21	107.28	121.41
34	N	2543	G	P-O5'-C5'	-7.21	110.09	120.90
34	N	2497	A	C5'-C4'-C3'	-7.19	104.42	115.20
37	0	752	G	C4'-C3'-O3'	-7.16	102.27	113.00
34	N	33	C	C4'-C3'-O3'	-7.10	102.35	113.00
34	N	2225	A	C2'-C3'-O3'	7.07	120.10	109.50
5	P	239	ASN	N-CA-C	7.06	125.85	110.80
34	N	227	A	C4'-C3'-O3'	-7.03	102.45	113.00
31	p	39	ARG	NE-CZ-NH2	-7.03	112.87	119.20
47	D	126	LYS	N-CA-C	7.01	120.72	109.79
37	0	1362	A	C4'-C3'-O3'	-7.00	102.50	113.00
41	4	111	MET	CG-SD-CE	-6.98	85.55	100.90
34	N	1648	U	P-O5'-C5'	-6.97	110.44	120.90
34	N	2732	G	C1'-C2'-O2'	-6.96	97.96	108.40
37	0	878	A	C3'-C2'-O2'	6.96	121.14	110.70
25	j	14	ARG	CG-CD-NE	-6.96	96.69	112.00
34	N	1993	U	C3'-C2'-O2'	-6.92	100.32	110.70
6	Q	13	ARG	NE-CZ-NH2	6.92	125.42	119.20
5	P	157	SER	N-CA-C	-6.90	100.59	110.59
19	d	22	LYS	N-CA-C	-6.86	100.32	110.48
34	N	1666	G	C3'-C2'-O2'	6.86	120.99	110.70
37	0	1279	G	N9-C1'-C2'	6.86	122.29	112.00
3	M	73	C	OP1-P-O3'	-6.85	87.44	108.00
34	N	1865	U	C4'-C3'-O3'	-6.85	102.72	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	p	39	ARG	NE-CZ-NH1	6.85	128.35	121.50
19	d	6	ARG	NE-CZ-NH2	6.80	125.32	119.20
34	N	989	G	C4'-C3'-O3'	-6.77	102.84	113.00
34	N	995	C	C2'-C3'-O3'	6.76	119.64	109.50
5	P	241	GLY	N-CA-C	6.75	124.67	114.61
34	N	2061	G	C4'-C3'-O3'	-6.74	102.89	113.00
43	6	109	ARG	CG-CD-NE	-6.73	97.19	112.00
37	0	1190	G	C1'-C2'-O2'	-6.72	101.71	111.80
57	v	21	ARG	N-CA-C	6.72	118.69	111.36
7	R	65	THR	O-C-N	-6.72	114.55	122.81
34	N	1313	U	N1-C1'-C2'	6.71	122.06	112.00
34	N	974	G	N9-C1'-C2'	6.70	124.05	114.00
31	p	34	ARG	NE-CZ-NH1	-6.67	114.83	121.50
34	N	2832	U	C4'-C3'-O3'	-6.66	103.01	113.00
34	N	2238	G	C2'-C3'-O3'	6.64	119.47	109.50
18	c	93	ARG	CG-CD-NE	-6.63	97.41	112.00
37	0	1190	G	C4'-C3'-O3'	-6.62	99.46	109.40
4	O	108	A	C2'-C3'-O3'	-6.57	103.85	113.70
34	N	1666	G	O4'-C4'-C3'	-6.57	97.43	104.00
37	0	388	G	C2'-C3'-O3'	6.55	119.32	109.50
45	8	18	ARG	CB-CG-CD	-6.55	96.24	111.30
34	N	2509	G	C3'-C2'-O2'	6.54	120.52	110.70
34	N	421	C	C2'-C3'-O3'	6.54	119.31	109.50
35	L	54	GLY	N-CA-C	6.51	120.98	112.25
34	N	2071	A	C3'-C2'-O2'	6.51	120.47	110.70
17	b	102	ARG	NE-CZ-NH2	6.51	125.06	119.20
37	0	1145	A	C4'-C3'-O3'	-6.47	103.30	113.00
37	0	665	A	C2'-C3'-O3'	-6.46	104.01	113.70
37	0	1301	U	N1-C1'-C2'	6.46	121.68	112.00
14	Y	30	THR	N-CA-CB	6.45	121.38	110.49
56	u	69	LYS	N-CA-C	6.43	124.51	110.80
14	Y	68	SER	N-CA-C	6.43	118.37	111.36
37	0	1151	A	C4'-C3'-O3'	-6.43	103.36	113.00
34	N	1452	G	C4'-C3'-O3'	-6.41	103.38	113.00
14	Y	47	ARG	NE-CZ-NH2	6.41	124.97	119.20
34	N	2443	C	O4'-C4'-C3'	-6.40	97.60	104.00
34	N	1212	G	C4'-C3'-O3'	-6.38	103.43	113.00
37	0	818	G	C4'-C3'-O3'	-6.37	103.45	113.00
18	c	73	VAL	N-CA-CB	6.35	117.64	110.72
29	n	25	VAL	CA-C-N	6.31	133.05	121.70
29	n	25	VAL	C-N-CA	6.31	133.05	121.70
26	k	57	ARG	NE-CZ-NH2	6.30	124.87	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	N	404	A	C4'-C3'-O3'	6.29	118.84	109.40
54	K	57	ARG	CA-CB-CG	6.29	126.68	114.10
37	0	1213	A	C4'-C3'-O3'	-6.28	103.58	113.00
52	I	43	ALA	CA-C-N	6.28	133.53	121.54
52	I	43	ALA	C-N-CA	6.28	133.53	121.54
4	O	44	G	N9-C1'-C2'	6.27	121.41	112.00
41	4	127	ALA	N-CA-C	6.27	119.45	110.24
5	P	11	PRO	CB-CA-C	-6.26	103.37	111.39
25	j	41	ARG	CD-NE-CZ	6.24	133.14	124.40
39	2	167	TRP	N-CA-C	6.22	119.68	110.48
34	N	2364	C	O4'-C4'-C3'	-6.21	97.79	104.00
34	N	2728	U	C2'-C3'-O3'	-6.19	104.41	113.70
34	N	859	G	C1'-C2'-O2'	-6.19	102.52	111.80
48	E	22	PRO	O-C-N	-6.15	114.34	122.64
34	N	446	G	C2'-C3'-O3'	6.14	118.71	109.50
34	N	2501	C	C4'-C3'-O3'	-6.14	103.80	113.00
37	0	818	G	N9-C1'-C2'	6.14	121.20	112.00
14	Y	78	ARG	NE-CZ-NH2	6.13	124.71	119.20
10	U	72	ILE	N-CA-C	6.12	122.08	109.34
25	j	41	ARG	CB-CG-CD	6.12	125.38	111.30
37	0	1201	A	C2'-C3'-O3'	6.08	118.63	109.50
48	E	44	LYS	N-CA-C	6.08	120.49	112.35
34	N	1352	U	O4'-C1'-C2'	-6.07	101.53	107.60
34	N	2728	U	C4'-C3'-O3'	-6.07	103.90	113.00
31	p	12	ARG	CA-CB-CG	6.06	126.22	114.10
34	N	2725	A	C1'-C2'-O2'	-6.05	99.32	108.40
34	N	2319	G	C4'-C3'-O3'	-6.04	103.94	113.00
47	D	124	PRO	CA-C-N	6.03	128.97	120.28
47	D	124	PRO	C-N-CA	6.03	128.97	120.28
5	P	221	ARG	N-CA-CB	6.03	120.11	110.46
10	U	27	ARG	NE-CZ-NH1	-6.03	115.47	121.50
41	4	138	ARG	N-CA-CB	6.02	120.66	110.49
52	I	44	SER	N-CA-C	-6.00	98.02	110.80
34	N	2034	U	C4'-C3'-O3'	-5.98	104.03	113.00
16	a	70	THR	N-CA-C	5.97	123.52	110.80
34	N	827	U	C2'-C3'-O3'	-5.96	104.76	113.70
16	a	69	ARG	NE-CZ-NH2	5.95	124.55	119.20
34	N	2246	G	O4'-C4'-C3'	-5.94	98.06	104.00
34	N	1567	G	C1'-C2'-O2'	-5.93	102.90	111.80
37	0	64	G	C2'-C3'-O3'	-5.93	104.80	113.70
28	m	32	ILE	N-CA-CB	5.91	116.98	110.53
34	N	2468	A	C4'-C3'-O3'	-5.91	104.13	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	r	36	ARG	NE-CZ-NH1	-5.91	115.59	121.50
34	N	782	A	C4'-C3'-O3'	-5.91	100.54	109.40
25	j	19	LYS	N-CA-C	5.90	120.48	113.16
34	N	2518	A	C1'-C2'-O2'	-5.90	102.95	111.80
34	N	2543	G	C5'-C4'-C3'	-5.89	107.16	116.00
34	N	974	G	C4'-C3'-O3'	-5.88	100.58	109.40
34	N	1254	A	C4'-C3'-O3'	-5.88	104.18	113.00
34	N	871	U	P-O5'-C5'	-5.87	112.09	120.90
34	N	1626	A	C2'-C3'-O3'	-5.86	104.92	113.70
34	N	2035	G	C4'-C3'-O3'	-5.86	100.62	109.40
37	0	330	C	P-O5'-C5'	-5.84	112.14	120.90
34	N	820	A	O4'-C4'-C3'	-5.83	98.17	104.00
5	P	258	ARG	NE-CZ-NH1	-5.83	115.67	121.50
34	N	974	G	C2'-C3'-O3'	5.82	118.23	109.50
29	n	25	VAL	N-CA-C	5.82	116.46	110.82
25	j	41	ARG	N-CA-C	5.81	120.66	112.93
34	N	301	G	C4'-C3'-O3'	-5.79	104.31	113.00
41	4	38	VAL	CG1-CB-CG2	-5.78	98.08	110.80
6	Q	113	SER	N-CA-C	5.77	117.51	110.41
5	P	177	ARG	CG-CD-NE	-5.77	99.31	112.00
34	N	1970	A	C2'-C3'-O3'	5.76	118.14	109.50
34	N	2447	G	P-O3'-C3'	5.76	128.84	120.20
34	N	2873	A	P-O5'-C5'	-5.75	112.27	120.90
34	N	782	A	C2'-C3'-O3'	5.75	118.12	109.50
5	P	238	ARG	N-CA-C	5.74	123.03	110.80
19	d	33	ARG	CB-CG-CD	-5.74	98.10	111.30
5	P	31	ALA	CA-C-N	-5.73	114.98	120.83
5	P	31	ALA	C-N-CA	-5.73	114.98	120.83
6	Q	151	THR	O-C-N	-5.73	115.01	121.43
34	N	2267	A	N9-C1'-C2'	5.73	120.59	112.00
34	N	140	C	N1-C1'-C2'	5.72	120.59	112.00
20	e	79	ARG	CD-NE-CZ	-5.72	116.39	124.40
34	N	512	G	P-O3'-C3'	5.71	128.76	120.20
34	N	2035	G	C1'-C2'-O2'	-5.70	103.25	111.80
5	P	156	ARG	CB-CG-CD	-5.70	98.20	111.30
34	N	2049	G	C3'-C2'-O2'	5.70	119.24	110.70
37	0	96	U	C2'-C3'-O3'	5.69	122.24	113.70
34	N	2543	G	O5'-C5'-C4'	5.68	120.03	111.50
29	n	7	LYS	CD-CE-NZ	5.68	130.08	111.90
41	4	24	THR	N-CA-C	5.66	117.53	110.91
37	0	1196	A	C4'-C3'-O3'	-5.66	104.52	113.00
4	O	88	C	C4'-C3'-O3'	-5.65	104.52	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	2	6	HIS	N-CA-C	-5.65	102.53	109.65
34	N	555	G	C4'-C3'-O3'	-5.64	104.53	113.00
34	N	301	G	N9-C1'-C2'	5.64	120.46	112.00
37	0	971	G	C2'-C3'-O3'	-5.64	105.24	113.70
37	0	1280	A	C4'-C3'-O3'	-5.63	104.56	113.00
17	b	100	HIS	CA-C-N	-5.63	115.51	123.95
17	b	100	HIS	C-N-CA	-5.63	115.51	123.95
19	d	13	ARG	NE-CZ-NH2	5.63	124.26	119.20
34	N	1661	G	C3'-C2'-O2'	5.63	119.14	110.70
34	N	2776	A	C4-N9-C1'	5.62	143.18	126.30
39	2	3	GLN	N-CA-C	5.62	122.08	113.19
17	b	102	ARG	NE-CZ-NH1	-5.62	115.88	121.50
34	N	2776	A	C8-N9-C1'	-5.62	110.83	127.70
16	a	69	ARG	CG-CD-NE	5.62	124.36	112.00
34	N	1900	A	P-O3'-C3'	5.62	128.63	120.20
37	0	1432	G	C4'-C3'-O3'	-5.62	104.58	113.00
34	N	2019	A	C3'-C2'-O2'	5.61	119.12	110.70
4	O	24	G	C2'-C3'-O3'	-5.61	105.29	113.70
18	c	53	ARG	CB-CG-CD	-5.61	98.40	111.30
34	N	1261	C	O4'-C4'-C3'	-5.58	98.42	104.00
34	N	1565	C	C2'-C3'-O3'	5.58	117.87	109.50
34	N	2517	C	O3'-P-O5'	-5.55	95.67	104.00
32	q	8	ARG	CG-CD-NE	5.55	124.22	112.00
29	n	55	ILE	N-CA-C	5.55	120.89	109.34
34	N	784	G	P-O3'-C3'	5.55	128.52	120.20
34	N	1205	A	C4'-C3'-O3'	5.55	117.72	109.40
34	N	2034	U	O3'-P-O5'	-5.54	95.68	104.00
42	5	63	ASN	N-CA-C	5.54	117.39	110.91
34	N	752	A	N9-C1'-C2'	5.54	122.31	114.00
34	N	727	A	N9-C1'-C2'	5.54	120.30	112.00
34	N	2645	G	C5'-C4'-C3'	-5.54	106.90	115.20
34	N	1565	C	C5'-C4'-C3'	-5.52	106.92	115.20
34	N	2645	G	P-O5'-C5'	-5.51	112.63	120.90
37	0	686	U	C4'-C3'-O3'	-5.51	104.73	113.00
18	c	21	ARG	NE-CZ-NH1	-5.49	116.01	121.50
34	N	372	G	C1'-C2'-O2'	-5.48	103.58	111.80
37	0	665	A	C3'-C2'-O2'	5.48	118.92	110.70
34	N	1012	U	C2'-C3'-O3'	-5.47	105.49	113.70
34	N	2724	U	C2'-C3'-O3'	-5.47	105.49	113.70
45	8	126	GLN	CA-C-O	-5.47	115.03	121.16
34	N	1428	C	C2'-C3'-O3'	-5.47	105.49	113.70
34	N	645	C	N1-C1'-C2'	5.47	120.20	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Q	160	LYS	CG-CD-CE	5.47	123.88	111.30
37	0	1491	G	C4'-C3'-O3'	5.46	121.19	113.00
34	N	2751	G	C2'-C3'-O3'	-5.46	105.52	113.70
38	1	17	GLY	CA-C-O	-5.45	117.88	122.29
41	4	157	ARG	NE-CZ-NH1	-5.44	116.06	121.50
37	0	1125	U	N1-C1'-C2'	5.44	120.16	112.00
34	N	923	G	C3'-C2'-O2'	5.44	118.86	110.70
34	N	947	A	C3'-C2'-O2'	-5.43	102.55	110.70
34	N	962	G	C3'-C2'-O2'	5.43	118.85	110.70
37	0	813	U	C4'-C3'-O3'	-5.42	104.86	113.00
53	J	71	LYS	N-CA-C	5.42	122.34	110.80
33	r	1	MET	CB-CG-SD	-5.41	96.47	112.70
37	0	1211	U	C2'-C3'-O3'	-5.41	105.58	113.70
29	n	7	LYS	CG-CD-CE	-5.40	98.89	111.30
37	0	563	A	N9-C1'-C2'	5.39	120.09	112.00
25	j	41	ARG	NH1-CZ-NH2	-5.39	112.29	119.30
34	N	51	G	C4'-C3'-O3'	-5.39	104.91	113.00
34	N	983	A	C5'-C4'-O4'	-5.38	101.73	109.80
34	N	2497	A	C2'-C3'-O3'	5.38	117.57	109.50
34	N	2820	A	C4'-C3'-O3'	-5.37	104.94	113.00
37	0	5	U	C2'-C3'-O3'	-5.35	105.67	113.70
34	N	2038	G	C3'-C2'-O2'	5.34	118.72	110.70
34	N	2354	C	C5'-C4'-C3'	-5.34	107.98	116.00
34	N	2645	G	C2'-C3'-O3'	5.34	117.51	109.50
34	N	1819	A	C1'-C2'-O2'	-5.33	103.80	111.80
34	N	2552	U	C3'-C2'-O2'	5.33	118.70	110.70
34	N	1937	A	N9-C1'-C2'	5.32	119.99	112.00
34	N	783	A	O4'-C1'-C2'	-5.32	102.28	107.60
34	N	1620	G	C3'-C2'-O2'	5.32	118.68	110.70
14	Y	29	LYS	CD-CE-NZ	-5.31	94.89	111.90
34	N	1236	G	P-O3'-C3'	5.31	128.17	120.20
46	9	42	LEU	CA-C-N	5.31	126.48	119.84
46	9	42	LEU	C-N-CA	5.31	126.48	119.84
37	0	388	G	O3'-P-O5'	-5.31	96.04	104.00
34	N	2092	U	P-O5'-C5'	-5.30	112.95	120.90
34	N	310	A	C1'-C2'-O2'	-5.29	100.46	108.40
31	p	12	ARG	CB-CG-CD	-5.29	99.14	111.30
34	N	1770	G	C3'-C2'-O2'	5.28	118.62	110.70
34	N	2394	C	O4'-C4'-C3'	-5.28	98.72	104.00
34	N	1977	A	C2'-C3'-O3'	-5.27	105.79	113.70
15	Z	118	LYS	CB-CG-CD	-5.27	99.19	111.30
51	H	64	ARG	CG-CD-NE	-5.27	100.41	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	N	2498	C	C3'-C2'-O2'	5.26	118.59	110.70
34	N	669	G	N9-C1'-C2'	5.26	119.89	112.00
36	C	55	SER	N-CA-C	5.26	117.01	111.28
37	0	1094	G	C4'-C3'-O3'	-5.25	105.12	113.00
34	N	2430	A	C3'-C2'-O2'	5.25	118.58	110.70
34	N	2497	A	C4'-C3'-O3'	-5.25	101.53	109.40
37	0	652	U	C2'-C3'-O3'	-5.24	105.84	113.70
34	N	2849	U	P-O5'-C5'	5.24	128.75	120.90
5	P	226	ASN	CA-C-N	-5.23	114.27	119.56
5	P	226	ASN	C-N-CA	-5.23	114.27	119.56
6	Q	12	THR	N-CA-C	-5.23	101.44	108.19
6	Q	114	LYS	CA-CB-CG	5.23	124.56	114.10
34	N	1650	A	C3'-C2'-O2'	5.23	118.54	110.70
7	R	49	ARG	NE-CZ-NH1	-5.22	116.28	121.50
14	Y	18	ARG	NE-CZ-NH2	-5.22	114.50	119.20
34	N	785	G	P-O5'-C5'	-5.22	113.07	120.90
34	N	2502	G	C3'-C2'-O2'	-5.21	102.88	110.70
34	N	1343	G	N9-C1'-C2'	5.20	119.80	112.00
34	N	2474	U	N1-C1'-C2'	5.20	119.80	112.00
34	N	421	C	C4'-C3'-O3'	5.20	117.20	109.40
48	E	12	ARG	NE-CZ-NH1	-5.20	116.30	121.50
37	0	812	G	C1'-C2'-O2'	-5.20	100.60	108.40
37	0	1530	G	C4'-C3'-O3'	-5.20	105.20	113.00
13	X	29	HIS	CB-CA-C	-5.20	103.50	111.66
34	N	2311	A	P-O3'-C3'	5.20	127.99	120.20
34	N	2638	G	C4'-C3'-O3'	-5.20	105.21	113.00
34	N	372	G	C2'-C3'-O3'	5.19	117.29	109.50
19	d	3	ARG	NE-CZ-NH1	-5.19	116.31	121.50
26	k	28	ARG	NE-CZ-NH2	-5.19	114.53	119.20
4	O	41	G	C4'-C3'-O3'	-5.18	105.22	113.00
34	N	27	G	C5'-C4'-O4'	-5.18	102.03	109.80
34	N	2596	U	C2'-C3'-O3'	-5.18	105.94	113.70
5	P	156	ARG	CG-CD-NE	5.17	123.38	112.00
34	N	278	A	N9-C1'-C2'	5.17	119.76	112.00
40	3	5	LEU	CB-CA-C	-5.17	104.55	112.11
34	N	2867	G	C4'-C3'-O3'	5.17	117.15	109.40
37	0	1303	C	N1-C1'-C2'	5.17	119.75	112.00
34	N	2621	G	C3'-C2'-O2'	5.17	118.45	110.70
21	f	11	ARG	N-CA-CB	5.16	118.01	110.58
50	G	49	GLN	N-CA-C	-5.16	104.28	110.88
34	N	1676	A	C3'-C2'-O2'	5.15	118.43	110.70
57	v	33	ARG	CA-CB-CG	5.15	124.40	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	X	35	VAL	CA-C-O	-5.14	115.21	121.18
34	N	2580	U	N1-C1'-C2'	5.14	119.71	112.00
34	N	1180	U	N1-C1'-C2'	5.13	119.70	112.00
37	0	971	G	P-O5'-C5'	-5.13	113.20	120.90
34	N	2035	G	C2'-C3'-O3'	5.13	117.20	109.50
6	Q	128	ARG	CA-C-N	5.13	127.99	120.71
6	Q	128	ARG	C-N-CA	5.13	127.99	120.71
16	a	69	ARG	N-CA-C	-5.13	103.27	110.50
34	N	2019	A	C2'-C3'-O3'	-5.13	106.00	113.70
34	N	481	G	C2'-C3'-O3'	-5.13	106.01	113.70
34	N	2049	G	O4'-C4'-C3'	-5.13	98.87	104.00
14	Y	41	ARG	CA-CB-CG	-5.13	103.85	114.10
34	N	566	U	C2'-C3'-O3'	-5.12	106.02	113.70
34	N	1998	A	O4'-C4'-C3'	-5.12	98.88	104.00
4	O	100	G	C3'-C2'-O2'	5.12	118.38	110.70
10	U	96	THR	N-CA-C	-5.12	106.89	113.23
34	N	123	G	C3'-C2'-O2'	5.11	118.37	110.70
40	3	23	SER	O-C-N	5.10	128.02	122.11
34	N	2732	G	C3'-C2'-O2'	-5.09	103.06	110.70
37	0	595	A	C4'-C3'-O3'	5.09	117.04	109.40
34	N	2238	G	C4'-C3'-O3'	-5.09	101.77	109.40
37	0	812	G	P-O3'-C3'	5.07	127.81	120.20
52	I	42	ILE	CA-C-N	5.07	131.23	121.54
52	I	42	ILE	C-N-CA	5.07	131.23	121.54
33	r	36	ARG	CG-CD-NE	-5.07	100.84	112.00
34	N	1928	A	C3'-C2'-O2'	5.07	118.30	110.70
41	4	30	ILE	CB-CA-C	5.07	117.72	110.33
34	N	1997	C	O4'-C4'-C3'	-5.06	98.94	104.00
34	N	1253	A	C2'-C3'-O3'	5.05	117.08	109.50
34	N	2049	G	C2'-C3'-O3'	-5.05	106.12	113.70
3	M	9	C	C2'-C3'-O3'	-5.05	106.12	113.70
34	N	1131	G	O3'-P-O5'	-5.05	96.42	104.00
34	N	2502	G	P-O5'-C5'	5.05	128.47	120.90
34	N	820	A	O4'-C1'-C2'	-5.04	102.56	107.60
34	N	2062	A	O4'-C4'-C3'	-5.04	101.06	106.10
19	d	9	ILE	N-CA-C	5.04	117.38	111.09
34	N	683	U	N1-C1'-C2'	5.03	119.55	112.00
34	N	750	A	C2'-C3'-O3'	-5.03	106.15	113.70
19	d	32	TYR	CA-C-O	5.03	125.78	120.10
15	Z	8	LYS	CB-CG-CD	-5.02	99.75	111.30
16	a	1	MET	CB-CG-SD	-5.02	97.63	112.70
34	N	995	C	C1'-C2'-O2'	-5.02	104.27	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	0	801	U	C2'-C3'-O3'	-5.02	106.17	113.70
34	N	60	G	C1'-C2'-O2'	-5.02	104.27	111.80
38	1	103	ASN	N-CA-CB	5.02	119.89	110.56
37	0	532	A	C2'-C3'-O3'	-5.01	106.19	113.70
34	N	1937	A	P-O5'-C5'	-5.00	113.39	120.90
34	N	1968	G	O4'-C4'-C3'	-5.00	99.00	104.00

There are no chirality outliers.

All (49) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
37	0	24	U	Sidechain
37	0	368	U	Sidechain
37	0	559	A	Sidechain
37	0	571	U	Sidechain
37	0	864	A	Sidechain
38	1	10	LEU	Peptide
38	1	102	THR	Peptide
38	1	14	VAL	Peptide
39	2	79	LYS	Peptide
39	2	80	LYS	Peptide
41	4	102	GLY	Peptide
41	4	136	VAL	Peptide
41	4	137	VAL	Peptide
41	4	142	ASP	Peptide
41	4	89	HIS	Peptide
42	5	52	ASN	Peptide
42	5	93	LYS	Peptide
45	8	128	SER	Peptide
45	8	53	GLU	Peptide
45	8	54	LEU	Peptide
45	8	55	VAL	Peptide
47	D	125	LYS	Peptide
48	E	22	PRO	Peptide
48	E	77	HIS	Peptide
53	J	17	MET	Peptide
53	J	69	LYS	Peptide
34	N	1802	A	Sidechain
34	N	2522	U	Sidechain
34	N	2765	A	Sidechain
34	N	586	A	Sidechain
34	N	850	U	Sidechain

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Mol	Chain	Res	Type	Group
34	N	927	A	Sidechain
5	P	195	VAL	Peptide
5	P	234	GLY	Peptide
5	P	238	ARG	Peptide
6	Q	151	THR	Peptide
8	S	174	ASP	Peptide
8	S	175	PHE	Peptide
10	U	34	GLY	Peptide
11	V	11	LEU	Peptide
14	Y	114	GLY	Peptide
14	Y	82	LEU	Peptide
15	Z	57	VAL	Peptide,Mainchain
23	h	52	LEU	Peptide
32	q	31	HIS	Peptide
55	t	37	ARG	Peptide
56	u	3	ASN	Peptide
57	v	34	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1561	0	788	14	0
2	s	316	0	283	7	0
3	M	1594	0	809	65	0
4	O	2529	0	1281	13	0
5	P	2082	0	2154	39	0
6	Q	1564	0	1616	24	0
7	R	1552	0	1619	21	0
8	S	1410	0	1444	27	0
9	T	1322	0	1371	13	0
10	U	1111	0	1148	28	0
11	V	1031	0	1085	22	0
12	W	1128	0	1162	15	0
13	X	938	0	1012	17	0
14	Y	1044	0	1117	18	0
15	Z	1073	0	1157	16	0
16	a	960	0	1000	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	b	891	0	923	10	0
18	c	915	0	958	14	0
19	d	946	0	1019	23	0
20	e	815	0	839	18	0
21	f	857	0	922	10	0
22	g	738	0	807	6	0
23	h	779	0	831	11	0
24	i	752	0	780	9	0
25	j	568	0	581	10	0
26	k	624	0	652	11	0
27	l	508	0	543	7	0
28	m	448	0	488	3	0
29	n	443	0	458	12	0
30	o	409	0	440	6	0
31	p	376	0	418	17	0
32	q	503	0	572	12	0
33	r	301	0	341	8	0
34	N	62215	0	31275	411	0
35	L	419	0	418	12	0
36	C	1027	0	1091	43	0
37	0	32873	0	16532	180	0
38	1	1704	0	1732	28	0
39	2	1624	0	1696	24	0
40	3	1642	0	1707	22	0
41	4	1105	0	1148	19	0
42	5	817	0	808	14	0
43	6	1129	0	1178	16	0
44	7	978	0	1031	6	0
45	8	1021	0	1070	23	0
46	9	786	0	828	21	0
47	D	876	0	887	23	0
48	E	954	0	1016	17	0
49	F	883	0	941	20	0
50	G	773	0	824	12	0
51	H	709	0	728	12	0
52	I	648	0	666	11	0
53	J	648	0	691	5	0
54	K	455	0	478	12	0
55	t	637	0	665	11	0
56	u	664	0	714	15	0
57	v	421	0	445	15	0
58	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	A	1	0	0	0	0
60	A	9	0	0	0	0
All	All	147108	0	99187	1167	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 5.

All (1167) 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)
3:M:75:A:H5''	34:N:2602:A:C5	1.40	1.55
34:N:306:U:H3	34:N:310:A:N6	1.15	1.40
37:O:1238:A:N6	37:O:1301:U:H3	1.22	1.37
3:M:75:A:H3'	34:N:2602:A:N6	1.36	1.37
10:U:43:ASN:HB3	10:U:47:PHE:CE2	1.62	1.32
3:M:12:C:O2'	34:N:1923:U:H1'	1.34	1.25
3:M:12:C:O2'	34:N:1923:U:C1'	1.84	1.25
3:M:75:A:H5''	34:N:2602:A:N7	1.53	1.24
34:N:499:U:H3	34:N:503:A:N6	1.38	1.21
34:N:715:A:C1'	51:H:40:GLN:HE22	1.52	1.21
34:N:715:A:H1'	51:H:40:GLN:NE2	1.53	1.21
3:M:56:G:H5'	8:S:75:ALA:HB3	1.27	1.16
3:M:75:A:C5'	34:N:2602:A:N7	2.12	1.12
3:M:12:C:HO2'	34:N:1923:U:C1'	1.60	1.11
3:M:75:A:C5'	34:N:2602:A:C5	2.36	1.08
34:N:715:A:H1'	51:H:40:GLN:HE22	1.00	1.07
3:M:12:C:O2'	34:N:1923:U:O2'	1.74	1.04
10:U:43:ASN:CB	10:U:47:PHE:HE2	1.71	1.03
3:M:75:A:H3'	34:N:2602:A:C6	1.96	0.99
34:N:306:U:N3	34:N:310:A:N6	1.86	0.99
3:M:15:G:H5''	3:M:15:G:H8	1.31	0.96
3:M:15:G:H5''	3:M:15:G:C8	2.02	0.93
10:U:42:LYS:O	10:U:46:PHE:CD2	2.23	0.92
3:M:56:G:H5'	8:S:75:ALA:CB	2.00	0.91
10:U:42:LYS:O	10:U:46:PHE:HD2	1.51	0.91
34:N:715:A:H1'	51:H:40:GLN:CD	1.89	0.91
37:O:1060:U:C5	39:2:2:GLY:HA3	2.07	0.90
3:M:12:C:O2'	34:N:1923:U:C2'	2.19	0.89
3:M:75:A:C3'	34:N:2602:A:N6	2.31	0.89
34:N:715:A:C1'	51:H:40:GLN:NE2	2.22	0.86
10:U:43:ASN:O	10:U:47:PHE:HD2	1.57	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:U:43:ASN:O	10:U:47:PHE:CD2	2.29	0.86
3:M:31:U:H5'	37:0:1340:A:O2'	1.74	0.86
3:M:75:A:H5''	34:N:2602:A:C6	2.10	0.86
34:N:2304:G:H22	34:N:2312:U:H3	1.23	0.85
34:N:2177:C:O3'	36:C:211:LYS:HE2	1.76	0.85
1:A:12:U:H4'	34:N:1915:U:H4'	1.58	0.84
46:9:83:THR:O	46:9:87:LEU:HB2	1.79	0.83
5:P:35:GLU:OE2	34:N:1816:C:N4	2.10	0.83
3:M:30:A:O4'	37:0:1339:A:C2	2.34	0.80
3:M:15:G:H5'	3:M:16:C:OP2	1.81	0.80
3:M:56:G:C5'	8:S:75:ALA:HB3	2.10	0.79
3:M:12:C:HO2'	34:N:1923:U:H1'	1.27	0.79
49:F:101:ARG:NH1	49:F:104:THR:OG1	2.17	0.78
16:a:53:THR:HG21	34:N:2840:C:H5''	1.66	0.77
33:r:3:VAL:HG21	34:N:2539:C:H5'	1.67	0.77
37:0:1279:G:OP1	46:9:9:ARG:NH2	2.18	0.77
37:0:1238:A:N7	37:0:1301:U:O4	2.18	0.76
13:X:49:ARG:NH2	37:0:1422:G:O3'	2.18	0.76
34:N:306:U:C2	34:N:310:A:N6	2.54	0.76
36:C:3:LYS:HG3	36:C:4:LEU:H	1.50	0.75
5:P:221:ARG:NH1	34:N:1789:A:OP2	2.20	0.75
34:N:2112:G:H2'	34:N:2113:U:H5'	1.69	0.74
41:4:101:GLU:OE2	41:4:103:THR:OG1	2.05	0.74
3:M:16:C:H3'	3:M:17:G:H5'	1.68	0.74
34:N:284:U:H3	34:N:356:G:H1	1.30	0.74
1:A:64:A:H5'	34:N:2482:A:O2'	1.88	0.74
37:0:673:A:O3'	42:5:86:ARG:NH2	2.20	0.74
3:M:56:G:C5'	8:S:75:ALA:CB	2.66	0.73
55:t:30:PRO:HA	55:t:48:THR:O	1.88	0.73
6:Q:14:ILE:HA	18:c:12:GLN:HE22	1.52	0.73
34:N:1093:G:N2	34:N:1098:A:H62	1.85	0.73
49:F:87:ARG:O	49:F:91:HIS:HB2	1.87	0.73
46:9:65:TYR:HB3	50:G:96:LEU:HD11	1.69	0.73
55:t:6:LYS:HG3	55:t:7:LYS:HG2	1.70	0.73
3:M:75:A:H5'	34:N:2602:A:N7	2.04	0.73
10:U:42:LYS:HB3	10:U:46:PHE:HE2	1.52	0.73
37:0:1527:U:OP2	57:v:39:GLU:OE1	2.07	0.72
1:A:72:C:OP1	34:N:1942:C:O3'	2.08	0.72
37:0:664:G:H22	37:0:741:G:H1	1.37	0.72
37:0:1238:A:N6	37:0:1301:U:N3	2.01	0.72
16:a:77:ALA:O	16:a:81:ASN:HB2	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:4:81:LEU:HD13	41:4:123:VAL:HG11	1.72	0.71
50:G:47:LYS:HB3	55:t:13:LEU:HD12	1.72	0.71
3:M:16:C:C3'	3:M:17:G:H5'	2.20	0.71
37:0:1147:C:O2	45:8:18:ARG:NH2	2.22	0.71
3:M:12:C:C2'	34:N:1923:U:O2'	2.38	0.71
37:0:404:G:O2'	37:0:498:A:N1	2.23	0.71
34:N:1093:G:H21	34:N:1098:A:N6	1.87	0.71
37:0:1081:A:OP2	41:4:52:LYS:NZ	2.23	0.71
8:S:37:ASN:ND2	34:N:2312:U:O2	2.24	0.70
32:q:8:ARG:NH2	34:N:243:U:OP1	2.24	0.70
34:N:499:U:N3	34:N:503:A:N6	2.11	0.70
37:0:1309:G:OP2	49:F:98:ARG:NH1	2.25	0.70
3:M:12:C:H4'	34:N:1922:G:H21	1.57	0.69
13:X:48:PRO:HB3	37:0:1422:G:OP1	1.92	0.69
21:f:15:GLN:HE22	34:N:1266:G:H5''	1.56	0.69
5:P:258:ARG:NH1	5:P:264:ASP:OD1	2.23	0.69
34:N:715:A:C6	51:H:53:ARG:NH1	2.60	0.69
34:N:2128:G:H21	34:N:2173:A:H1'	1.57	0.69
34:N:2637:U:N3	34:N:2776:A:N6	2.40	0.69
10:U:43:ASN:CB	10:U:47:PHE:CE2	2.57	0.69
5:P:87:ARG:NH2	34:N:1817:G:OP1	2.26	0.69
34:N:2134:A:N6	34:N:2157:G:H4'	2.09	0.69
34:N:613:A:N7	34:N:616:A:N1	2.41	0.68
1:A:72:C:OP2	34:N:1943:U:OP2	2.11	0.68
37:0:501:C:OP1	48:E:114:ARG:NH2	2.26	0.68
49:F:29:ARG:HH21	49:F:63:PHE:HB2	1.59	0.68
34:N:2177:C:H4'	36:C:211:LYS:HZ1	1.58	0.68
7:R:163:ASN:ND2	34:N:323:C:H2'	2.07	0.68
22:g:46:ALA:O	22:g:50:LEU:HB2	1.94	0.68
34:N:2107:G:OP1	36:C:3:LYS:HE3	1.94	0.68
4:O:48:U:OP1	17:b:30:ARG:NH2	2.26	0.68
3:M:75:A:C5'	34:N:2602:A:C8	2.76	0.67
37:0:1064:G:N2	37:0:1190:G:O2'	2.28	0.67
12:W:113:PRO:HD2	34:N:558:U:OP1	1.94	0.67
3:M:56:G:O4'	8:S:75:ALA:HB1	1.95	0.67
45:8:84:THR:HG21	45:8:103:PHE:HB3	1.75	0.67
38:1:209:ALA:O	38:1:213:TYR:HB2	1.94	0.67
50:G:26:GLU:HG2	50:G:30:ILE:HD12	1.77	0.67
6:Q:45:TYR:HH	34:N:2636:C:HO2'	1.40	0.67
34:N:962:G:H21	34:N:2250:G:H1	1.41	0.67
3:M:75:A:H5''	34:N:2602:A:C8	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:N:2156:G:H2'	34:N:2157:G:H5'	1.78	0.66
37:0:427:U:OP1	40:3:13:ARG:NH2	2.28	0.66
10:U:43:ASN:C	10:U:47:PHE:HD2	2.02	0.66
37:0:458:U:H3	37:0:474:G:H1	1.44	0.66
3:M:74:C:H2'	3:M:75:A:H1'	1.78	0.66
34:N:499:U:C2	34:N:503:A:N6	2.63	0.66
9:T:67:THR:HG21	34:N:2757:A:N1	2.10	0.65
44:7:75:ILE:HD13	44:7:129:VAL:HG22	1.79	0.65
37:0:554:A:H5'	48:E:26:ALA:HB1	1.78	0.65
34:N:1019:U:H3	34:N:1142:A:N6	1.95	0.65
1:A:21:A:H4'	1:A:22:G:OP1	1.96	0.65
10:U:84:ALA:HA	10:U:91:PHE:H	1.62	0.65
31:p:37:LYS:HE2	34:N:469:G:O6	1.97	0.65
34:N:2178:C:P	36:C:211:LYS:HE2	2.37	0.64
4:O:31:C:H4'	8:S:26:MET:HE1	1.79	0.64
32:q:8:ARG:NH2	34:N:243:U:P	2.70	0.64
37:0:974:A:OP1	50:G:69:ARG:NH2	2.30	0.64
34:N:140:C:OP1	34:N:141:G:N2	2.30	0.64
34:N:2121:G:H4'	36:C:167:LYS:HD3	1.79	0.64
34:N:2637:U:H3	34:N:2776:A:N6	1.96	0.64
44:7:15:ARG:NH1	44:7:75:ILE:O	2.30	0.64
47:D:24:HIS:HB3	47:D:31:ILE:HG23	1.78	0.64
5:P:29:PRO:HG2	5:P:34:LEU:HD11	1.78	0.64
3:M:75:A:H5''	34:N:2602:A:C4	2.24	0.64
34:N:2405:G:O2'	34:N:2411:A:N6	2.30	0.64
45:8:123:ARG:NH1	45:8:124:ARG:O	2.31	0.64
37:0:437:U:OP1	40:3:152:GLN:NE2	2.30	0.64
3:M:75:A:H3'	34:N:2602:A:H61	1.55	0.64
34:N:1311:G:H21	34:N:1603:A:H62	1.45	0.63
6:Q:38:LYS:O	6:Q:46:ARG:HA	1.97	0.63
13:X:92:GLU:O	13:X:93:GLN:HB2	1.99	0.63
34:N:2141:G:H2'	34:N:2142:A:H8	1.63	0.63
8:S:88:LYS:HD3	34:N:2313:C:H5''	1.80	0.63
19:d:6:ARG:NH1	34:N:585:G:N7	2.47	0.63
37:0:1060:U:OP1	50:G:85:ARG:NH2	2.30	0.63
45:8:46:MET:HE2	45:8:50:GLN:HE21	1.63	0.63
1:A:12:U:C4'	34:N:1915:U:H4'	2.28	0.63
15:Z:55:ARG:NH2	34:N:2469:A:O2'	2.32	0.63
37:0:972:C:OP2	46:9:59:LYS:HD3	1.98	0.63
55:t:11:ILE:HG22	55:t:38:SER:HB3	1.81	0.63
31:p:44:VAL:HG13	31:p:44:VAL:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:8:25:ASN:HA	45:8:59:GLU:HG3	1.81	0.63
6:Q:49:GLN:HE21	6:Q:79:LEU:HB3	1.64	0.62
13:X:2:ILE:HB	13:X:33:ALA:HB3	1.80	0.62
34:N:1105:U:H2'	34:N:1106:G:H8	1.64	0.62
2:s:132:TYR:OH	7:R:67:ARG:NH1	2.33	0.62
53:J:9:GLN:HG2	53:J:60:GLU:HG2	1.81	0.62
9:T:86:LYS:HG3	9:T:132:VAL:HG22	1.81	0.62
37:0:1527:U:OP2	57:v:39:GLU:CD	2.42	0.62
43:6:147:ALA:O	47:D:56:ARG:NH2	2.32	0.62
22:g:28:ASN:OD1	22:g:91:GLN:NE2	2.31	0.62
34:N:1315:C:O2'	34:N:1392:A:N3	2.30	0.62
3:M:31:U:C5'	37:0:1340:A:O2'	2.48	0.62
15:Z:20:LEU:HD13	24:i:81:PRO:HG2	1.82	0.62
34:N:2849:U:O2'	34:N:2866:U:O2	2.15	0.62
37:0:1238:A:N6	37:0:1301:U:C2	2.68	0.62
17:b:16:ARG:NH2	17:b:19:GLN:OE1	2.33	0.62
10:U:5:LEU:HD13	10:U:13:GLY:HA2	1.82	0.61
34:N:1066:U:O2'	34:N:1074:G:N2	2.32	0.61
35:L:20:ASN:ND2	35:L:37:CYS:SG	2.73	0.61
26:k:16:ASN:HA	26:k:25:THR:O	2.01	0.61
34:N:475:C:O2	34:N:479:A:N6	2.33	0.61
46:9:19:ASP:HA	46:9:22:THR:HG22	1.83	0.61
21:f:15:GLN:NE2	34:N:1266:G:H5''	2.16	0.61
34:N:1093:G:H21	34:N:1098:A:H62	1.46	0.61
34:N:1779:U:H5	34:N:1784:A:N7	1.99	0.61
45:8:52:LEU:HB3	45:8:57:MET:HB3	1.81	0.61
24:i:51:GLN:HE22	24:i:86:LEU:HD21	1.65	0.61
34:N:693:A:O2'	34:N:1353:A:N3	2.33	0.61
34:N:2127:G:H4'	36:C:38:PHE:CD1	2.36	0.61
10:U:42:LYS:HB3	10:U:46:PHE:CE2	2.36	0.60
37:0:933:G:N7	43:6:3:ARG:NH1	2.49	0.60
1:A:72:C:P	34:N:1942:C:O3'	2.59	0.60
6:Q:156:PHE:CE1	12:W:81:ILE:HD12	2.37	0.60
37:0:1270:G:HO2'	37:0:1313:U:HO2'	1.49	0.60
56:u:59:ASP:OD1	56:u:76:LYS:NZ	2.33	0.60
32:q:12:LYS:NZ	34:N:249:C:O2	2.33	0.60
4:O:24:G:O2'	4:O:27:C:N4	2.34	0.60
11:V:135:SER:OG	34:N:1062:G:N3	2.34	0.60
26:k:12:PRO:HB3	26:k:30:LEU:HD23	1.82	0.60
11:V:31:GLN:NE2	34:N:1097:U:O4	2.34	0.60
37:0:1055:A:HI'	39:2:156:ARG:HH21	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:0:1086:U:H3	37:0:1099:G:H22	1.46	0.60
48:E:50:ARG:NH1	48:E:89:ASP:OD2	2.35	0.60
34:N:613:A:H62	34:N:616:A:H61	1.50	0.59
34:N:1068:G:N1	34:N:1073:A:N6	2.50	0.59
40:3:60:LYS:HE3	40:3:195:ILE:HG22	1.84	0.59
31:p:9:VAL:HG23	34:N:1309:G:OP1	2.01	0.59
37:0:812:G:OP1	37:0:902:G:N2	2.34	0.59
37:0:769:G:H4'	37:0:1513:A:H4'	1.84	0.59
37:0:946:A:H2'	37:0:947:G:C8	2.38	0.59
37:0:1526:G:H3'	57:v:39:GLU:OE1	2.03	0.59
5:P:236:GLU:HG2	34:N:2600:A:N7	2.17	0.59
34:N:1019:U:N3	34:N:1142:A:N6	2.50	0.59
34:N:2128:G:H4'	36:C:218:MET:HE1	1.85	0.59
37:0:693:G:OP1	47:D:127:ARG:NH2	2.36	0.59
39:2:40:ARG:NH1	39:2:55:ILE:O	2.36	0.59
25:j:15:ASP:OD1	34:N:2263:C:N4	2.35	0.59
48:E:68:GLY:O	48:E:99:ARG:NH1	2.36	0.59
34:N:1212:G:O2'	34:N:1237:A:N6	2.36	0.59
38:1:141:LEU:O	38:1:145:GLU:HB2	2.02	0.59
34:N:1093:G:N2	34:N:1098:A:N6	2.48	0.59
37:0:675:A:H1'	47:D:118:HIS:CD2	2.38	0.59
2:s:124:TRP:HB2	21:f:85:ILE:HD11	1.85	0.58
19:d:88:VAL:HA	20:e:49:ILE:HD12	1.85	0.58
51:H:46:HIS:O	51:H:48:LYS:N	2.36	0.58
55:t:31:LEU:HB2	55:t:49:ILE:HG22	1.84	0.58
49:F:83:LEU:HD21	55:t:65:GLU:HG2	1.85	0.58
4:O:43:C:O2	8:S:92:ARG:NH2	2.36	0.58
12:W:32:LEU:HD22	12:W:54:ILE:HG21	1.85	0.58
25:j:18:ALA:O	25:j:20:ARG:NH1	2.35	0.58
3:M:13:A:H4'	34:N:1924:C:H5'	1.85	0.58
10:U:43:ASN:C	10:U:47:PHE:CD2	2.81	0.58
38:1:81:LYS:O	38:1:85:LEU:HB2	2.04	0.58
34:N:1726:C:N4	34:N:1735:A:N6	2.51	0.58
37:0:890:G:O2'	37:0:906:A:N6	2.36	0.58
54:K:26:ILE:O	54:K:30:LYS:HB2	2.03	0.58
15:Z:66:ARG:NH1	15:Z:104:GLU:OE2	2.36	0.58
34:N:1019:U:C4	34:N:1142:A:N6	2.71	0.58
6:Q:46:ARG:NH2	6:Q:88:GLU:O	2.36	0.58
10:U:96:THR:HG23	10:U:112:LYS:HE2	1.84	0.58
37:0:1224:U:O2'	37:0:1322:C:OP1	2.21	0.58
37:0:1302:C:C5	49:F:17:ILE:HD13	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:O:579:A:O2'	51:H:54:ARG:NH1	2.36	0.58
47:D:93:ARG:HH12	57:v:25:LYS:HD3	1.68	0.58
26:k:10:LYS:NZ	34:N:396:G:OP2	2.37	0.58
32:q:5:LYS:HE2	34:N:254:G:N7	2.19	0.58
32:q:16:LYS:HE2	32:q:20:GLY:HA2	1.84	0.58
34:N:2848:G:O2'	34:N:2867:G:N2	2.36	0.58
3:M:30:A:C1'	37:O:1339:A:C2	2.86	0.57
34:N:481:G:O2'	34:N:506:G:N2	2.37	0.57
19:d:92:ARG:HG2	34:N:997:G:OP1	2.03	0.57
36:C:201:PRO:HB2	36:C:204:ALA:HB2	1.86	0.57
40:3:91:LEU:HD13	40:3:191:LEU:HD11	1.86	0.57
9:T:24:ILE:HD11	9:T:43:VAL:HG11	1.87	0.57
36:C:54:LYS:HD2	36:C:57:GLN:HG3	1.86	0.57
36:C:63:THR:HG22	36:C:163:TYR:HE1	1.69	0.57
37:O:246:A:N1	37:O:278:G:O2'	2.35	0.57
37:O:1261:A:N6	37:O:1274:A:O2'	2.35	0.57
3:M:12:C:H2'	34:N:1923:U:O2'	2.04	0.57
24:i:62:THR:HG22	24:i:71:LYS:HG2	1.86	0.57
32:q:32:ILE:O	32:q:36:LYS:NZ	2.36	0.57
13:X:70:ARG:NH1	34:N:2684:U:O4'	2.37	0.57
34:N:1332:G:N7	34:N:1609:A:O2'	2.37	0.57
36:C:54:LYS:HD2	36:C:57:GLN:HE21	1.70	0.57
36:C:213:SER:C	36:C:214:ILE:HD12	2.30	0.57
37:O:1316:G:H22	37:O:1319:A:H5''	1.69	0.57
37:O:1368:A:OP2	45:8:114:LYS:HD3	2.05	0.57
12:W:135:GLN:NE2	34:N:6:A:N3	2.53	0.57
46:9:27:GLU:O	46:9:31:ARG:HB2	2.04	0.57
25:j:23:VAL:HG22	25:j:38:VAL:HG22	1.87	0.57
34:N:805:G:N2	34:N:829:A:OP1	2.38	0.57
34:N:2506[A]:U:OP2	34:N:2576:G:N1	2.33	0.56
3:M:75:A:C3'	34:N:2602:A:C6	2.80	0.56
11:V:34:ASN:H	11:V:67:PHE:HE2	1.52	0.56
15:Z:50:ARG:HD3	15:Z:65:ILE:HD11	1.87	0.56
26:k:6:GLN:O	26:k:74:ARG:NH1	2.37	0.56
31:p:34:ARG:HD3	34:N:467:G:OP2	2.05	0.56
34:N:2176:A:H5''	36:C:221:GLY:N	2.20	0.56
39:2:36:ASP:OD1	39:2:59:ARG:NH2	2.34	0.56
34:N:370:G:O2'	34:N:424:G:OP1	2.22	0.56
14:Y:111:ILE:HD12	14:Y:111:ILE:H	1.70	0.56
39:2:156:ARG:HD3	39:2:193:TYR:HB3	1.86	0.56
3:M:30:A:O4'	37:O:1339:A:H2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:N:2177:C:O3'	36:C:211:LYS:CE	2.53	0.56
42:5:38:ARG:HG2	42:5:63:ASN:HB2	1.85	0.56
45:8:36:GLU:HA	45:8:40:GLY:HA3	1.87	0.56
10:U:132:PHE:HB2	10:U:140:ALA:HB3	1.87	0.56
26:k:45:ARG:HH21	26:k:47:VAL:HG22	1.71	0.56
34:N:1070:A:N7	34:N:1096:A:O2'	2.36	0.56
36:C:67:HIS:HB2	36:C:188:ASN:HD21	1.71	0.56
4:O:42:C:C5	8:S:66:LEU:HD22	2.40	0.56
37:0:409:U:OP1	40:3:24:GLY:HA3	2.06	0.56
43:6:40:GLU:OE2	45:8:43:THR:HG23	2.06	0.56
7:R:149:ILE:HD12	7:R:175:ILE:HG21	1.88	0.56
15:Z:45:GLN:NE2	34:N:2485:G:OP1	2.34	0.56
8:S:140:GLU:OE2	35:L:27:THR:HG23	2.07	0.55
34:N:1980:G:O2'	34:N:1982:U:OP2	2.22	0.55
5:P:2:ALA:N	5:P:199:GLU:OE1	2.39	0.55
16:a:53:THR:HA	16:a:56:LYS:HD3	1.88	0.55
34:N:1724:G:O6	34:N:1737:G:C2	2.59	0.55
34:N:2156:G:C2'	34:N:2157:G:H5'	2.36	0.55
37:0:451:A:H61	37:0:481:G:H5'	1.70	0.55
3:M:13:A:H4'	34:N:1924:C:C4'	2.37	0.55
34:N:2163:A:H2'	34:N:2164:C:H5'	1.88	0.55
7:R:69:ARG:HG3	34:N:674:G:O2'	2.05	0.55
37:0:993:G:O2'	37:0:994:A:N7	2.40	0.55
11:V:97:LYS:HD2	11:V:139:VAL:HG21	1.87	0.55
14:Y:76:GLU:OE2	34:N:627:A:O2'	2.23	0.55
47:D:93:ARG:NH2	47:D:112:ASP:OD1	2.39	0.55
4:O:72:G:H21	4:O:104:A:H62	1.55	0.55
5:P:144:VAL:HB	5:P:154:LEU:HB2	1.86	0.55
31:p:31:LEU:HD22	31:p:42:LEU:HD23	1.88	0.55
34:N:837:C:N3	34:N:941:A:N6	2.54	0.55
37:0:673:A:H2'	37:0:674:G:C8	2.42	0.55
41:4:13:GLU:OE1	41:4:68:ARG:NH2	2.39	0.55
5:P:235:GLY:O	5:P:239:ASN:ND2	2.39	0.55
15:Z:74:THR:HA	15:Z:88:ASN:O	2.07	0.55
33:r:36:ARG:HD2	33:r:37:GLN:HB2	1.89	0.55
34:N:715:A:C1'	51:H:40:GLN:CD	2.65	0.55
37:0:1166:G:N1	37:0:1169:A:OP2	2.40	0.55
37:0:1522:U:OP1	47:D:128:ARG:NH1	2.40	0.55
20:e:49:ILE:HB	20:e:52:PRO:HA	1.89	0.54
34:N:1726:C:H42	34:N:1735:A:N6	2.04	0.54
6:Q:13:ARG:NH1	34:N:2683:C:H4'	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:N:1536:C:O2	34:N:1537:G:N2	2.41	0.54
25:j:19:LYS:NZ	34:N:2261:C:OP1	2.33	0.54
29:n:43:ILE:HG22	29:n:49:TYR:HB2	1.89	0.54
34:N:413:C:HO2'	34:N:1880:U:HO2'	1.54	0.54
46:9:10:LEU:HG	46:9:98:VAL:HG12	1.88	0.54
11:V:100:LYS:HA	11:V:139:VAL:O	2.08	0.54
13:X:43:ILE:HD12	13:X:56:ASP:HB2	1.89	0.54
26:k:72:ARG:NH2	26:k:78:TYR:OH	2.33	0.54
42:5:11:HIS:HD2	42:5:12:PRO:HD2	1.72	0.54
34:N:2162:G:H2'	34:N:2163:A:H8	1.73	0.54
3:M:12:C:C2'	34:N:1923:U:HO2'	2.15	0.54
3:M:74:C:H2'	3:M:75:A:C1'	2.38	0.54
34:N:306:U:O4	34:N:310:A:N7	2.41	0.54
37:0:979:C:O2	50:G:59:ARG:NH1	2.35	0.54
5:P:204:VAL:O	5:P:206:GLY:N	2.40	0.54
7:R:178:VAL:O	7:R:182:ALA:HB2	2.08	0.54
12:W:56:VAL:HB	12:W:124:VAL:HG12	1.88	0.54
34:N:1450:G:N2	34:N:1452:G:O6	2.40	0.54
46:9:8:ILE:HA	46:9:99:GLN:O	2.08	0.54
49:F:77:ILE:HG22	49:F:81:MET:HE2	1.89	0.54
1:A:72:C:OP2	34:N:1943:U:P	2.66	0.53
14:Y:21:ARG:HA	34:N:811:U:H2'	1.90	0.53
34:N:987:C:O2'	34:N:1000:A:N3	2.36	0.53
34:N:2850:A:N7	34:N:2868:A:O2'	2.35	0.53
37:0:796:C:O3'	47:D:127:ARG:NH1	2.38	0.53
3:M:16:C:O2	3:M:16:C:H5''	2.07	0.53
7:R:176:ASP:OD1	7:R:176:ASP:N	2.40	0.53
9:T:33:LEU:HD22	9:T:75:MET:HG2	1.89	0.53
50:G:41:ARG:NH1	50:G:42:TRP:O	2.41	0.53
2:s:150:TYR:O	2:s:154:ASN:ND2	2.35	0.53
3:M:15:G:C8	3:M:15:G:C5'	2.86	0.53
8:S:143:TYR:CE2	49:F:9:ILE:HD12	2.44	0.53
11:V:12:GLN:HE21	11:V:55:ILE:H	1.57	0.53
41:4:99:ALA:O	41:4:102:GLY:N	2.39	0.53
5:P:160:THR:HG23	5:P:177:ARG:HG2	1.90	0.53
14:Y:76:GLU:HG3	14:Y:111:ILE:HD13	1.91	0.53
20:e:1:MET:HA	20:e:42:ALA:O	2.07	0.53
33:r:3:VAL:HG12	33:r:36:ARG:HE	1.73	0.53
37:0:1067:A:N1	37:0:1108:G:O2'	2.34	0.53
37:0:1003:G:H21	37:0:1005:A:H5'	1.73	0.53
37:0:263:A:OP2	56:u:74:ARG:NH1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:41:ASP:OD1	42:5:58:HIS:NE2	2.41	0.53
13:X:77:ILE:HG12	18:c:72:ARG:HD2	1.91	0.53
34:N:1726:C:N4	34:N:1735:A:H61	2.06	0.53
5:P:48:ARG:HD3	34:N:773:U:O2'	2.09	0.53
37:0:502:A:OP1	48:E:115:SER:HB3	2.09	0.53
38:1:67:ILE:HD12	38:1:160:ALA:HB3	1.91	0.53
7:R:163:ASN:HD21	34:N:323:C:H2'	1.74	0.53
9:T:24:ILE:HG21	9:T:72:LEU:HD21	1.91	0.53
16:a:22:ARG:HG3	16:a:70:THR:HA	1.91	0.53
23:h:86:ARG:NH1	23:h:100:SER:OG	2.42	0.53
37:0:768:A:N3	37:0:1512:U:O2'	2.40	0.53
38:1:117:LEU:HB3	38:1:141:LEU:HD11	1.89	0.53
56:u:28:MET:HE1	56:u:67:ILE:HG12	1.91	0.53
1:A:20:U:O2'	1:A:21:A:P	2.68	0.52
10:U:42:LYS:C	10:U:46:PHE:HD2	2.15	0.52
16:a:41:ALA:HB1	16:a:97:ILE:HD12	1.92	0.52
19:d:37:GLN:HE21	34:N:1252:G:H1	1.55	0.52
47:D:30:THR:HG21	47:D:92:GLY:HA3	1.89	0.52
3:M:29:G:H4'	37:0:1230:C:OP1	2.10	0.52
20:e:74:ILE:HD13	34:N:992:C:H4'	1.90	0.52
34:N:51:G:O2'	34:N:118:A:N6	2.42	0.52
34:N:1028:A:N3	34:N:2486:C:O2'	2.42	0.52
46:9:80:THR:HG22	46:9:82:LYS:H	1.74	0.52
49:F:39:ILE:HD12	49:F:52:GLN:HE21	1.73	0.52
51:H:46:HIS:C	51:H:48:LYS:H	2.17	0.52
25:j:41:ARG:HH11	34:N:2387:U:H1'	1.74	0.52
29:n:53:LYS:HE2	29:n:56:ALA:HB2	1.89	0.52
31:p:29:GLN:NE2	34:N:210:C:OP1	2.40	0.52
34:N:1939:U:OP1	34:N:2604:U:O2'	2.27	0.52
37:0:76:G:H1	37:0:93:U:H3	1.56	0.52
37:0:927:G:O2'	37:0:1503:A:N7	2.35	0.52
37:0:1006:G:O6	37:0:1023:U:O2	2.27	0.52
4:O:89:U:H6	34:N:958:U:H2'	1.74	0.52
10:U:83:LYS:HG3	10:U:91:PHE:HB3	1.92	0.52
34:N:28:A:N6	34:N:512:G:H1'	2.24	0.52
38:1:68:LEU:HD12	38:1:154:MET:HE1	1.92	0.52
47:D:109:ASN:HA	57:v:6:VAL:O	2.09	0.52
55:t:36:ARG:NH2	55:t:75:ALA:O	2.42	0.52
38:1:54:LEU:HG	38:1:220:THR:HG21	1.92	0.52
7:R:144:GLU:HG2	7:R:166:LYS:HD2	1.92	0.52
11:V:76:ALA:HA	11:V:79:LEU:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:f:73:LYS:HB2	21:f:106:VAL:HB	1.90	0.52
23:h:86:ARG:NH2	23:h:102:THR:OG1	2.43	0.52
7:R:19:PHE:HE1	7:R:109:LEU:HD13	1.75	0.52
31:p:12:ARG:NH1	34:N:465:G:OP1	2.42	0.52
5:P:3:VAL:HG12	5:P:19:VAL:HG22	1.92	0.52
19:d:88:VAL:HG22	20:e:49:ILE:O	2.09	0.52
20:e:57:GLY:HA2	20:e:102:SER:O	2.10	0.52
32:q:8:ARG:HH21	34:N:243:U:P	2.33	0.52
34:N:1070:A:H2'	34:N:1097:U:H4'	1.92	0.52
37:0:1527:U:OP2	57:v:39:GLU:OE2	2.28	0.52
12:W:13:ARG:NH1	12:W:49:ASP:O	2.39	0.52
18:c:37:LYS:HD2	18:c:39:ARG:HH11	1.75	0.52
38:1:80:VAL:HG12	38:1:214:LEU:HD21	1.91	0.52
3:M:30:A:H4'	37:0:1339:A:N1	2.25	0.51
7:R:2:GLU:HB3	7:R:11:ALA:HB1	1.92	0.51
22:g:8:LEU:HD23	22:g:50:LEU:HD21	1.91	0.51
29:n:4:GLN:HA	34:N:2615:U:C2	2.45	0.51
34:N:639:U:H2'	34:N:640:C:C6	2.45	0.51
34:N:948:C:O2	34:N:984:A:O2'	2.28	0.51
34:N:1363:C:O2'	34:N:1809:A:N3	2.41	0.51
34:N:1936:A:H2	34:N:1943:U:H3	1.56	0.51
47:D:111:THR:HG22	57:v:5:LYS:CA	2.40	0.51
46:9:15:HIS:HA	46:9:18:ILE:HG22	1.93	0.51
53:J:17:MET:HG3	53:J:20:SER:HB3	1.92	0.51
37:0:676:A:H5''	47:D:115:PRO:HB3	1.90	0.51
42:5:90:MET:SD	54:K:61:ARG:NH1	2.83	0.51
1:A:20:U:HO2'	1:A:21:A:P	2.34	0.51
5:P:220:VAL:HG21	34:N:782:A:N7	2.26	0.51
8:S:116:GLY:HA3	8:S:178:ARG:HB3	1.91	0.51
27:l:6:LEU:HD13	27:l:56:LEU:HD22	1.93	0.51
34:N:877:A:O2'	34:N:900:A:N6	2.43	0.51
34:N:2638:G:O2'	34:N:2778:A:N6	2.44	0.51
39:2:55:ILE:HG22	39:2:68:ILE:HG12	1.92	0.51
41:4:122:ASN:N	41:4:122:ASN:OD1	2.42	0.51
45:8:19:VAL:HA	45:8:65:ILE:HG22	1.92	0.51
54:K:32:TYR:HB3	54:K:55:LEU:HD21	1.93	0.51
13:X:77:ILE:HG12	18:c:72:ARG:CD	2.41	0.51
16:a:114:GLU:OE1	16:a:118:ARG:NH2	2.42	0.51
34:N:2114:A:N3	34:N:2114:A:H2'	2.25	0.51
39:2:156:ARG:NH1	39:2:160:ALA:O	2.43	0.51
3:M:16:C:H4'	3:M:17:G:OP2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:O:552:U:H5'	48:E:83:ARG:HH11	1.76	0.51
3:M:56:G:C4'	8:S:75:ALA:HB1	2.41	0.51
3:M:13:A:H4'	34:N:1924:C:C5'	2.41	0.51
13:X:76:VAL:HG12	18:c:73:VAL:HG22	1.93	0.51
32:q:8:ARG:NH2	34:N:243:U:OP2	2.44	0.51
34:N:612:G:N2	34:N:614:A:O2'	2.44	0.51
47:D:35:THR:OG1	47:D:36:ASP:N	2.44	0.51
3:M:30:A:C4'	37:O:1339:A:C2	2.93	0.51
11:V:117:MET:HA	34:N:1058:U:O2'	2.11	0.51
20:e:76:LYS:O	20:e:84:ARG:HA	2.11	0.51
48:E:34:CYS:SG	48:E:78:SER:OG	2.67	0.51
36:C:23:ILE:HG12	36:C:224:VAL:HB	1.93	0.51
40:3:58:LYS:NZ	40:3:69:GLU:OE1	2.44	0.51
43:6:109:ARG:O	43:6:119:ARG:NH2	2.44	0.51
53:J:59:VAL:HG21	53:J:75:LEU:HD22	1.92	0.51
13:X:99:ILE:HD12	13:X:118:LEU:HB2	1.93	0.50
34:N:1534:U:O2'	34:N:1537:G:O6	2.29	0.50
43:6:57:SER:HB3	43:6:60:GLU:HG2	1.93	0.50
23:h:11:VAL:HG12	23:h:72:ILE:HG22	1.94	0.50
37:O:938:A:N3	37:O:1376:U:O2'	2.40	0.50
16:a:32:GLU:HG2	16:a:115:LEU:HD12	1.94	0.50
34:N:527:C:N4	34:N:2779:U:OP2	2.44	0.50
45:8:55:VAL:O	45:8:60:LYS:NZ	2.43	0.50
46:9:11:LYS:HA	46:9:70:HIS:O	2.12	0.50
47:D:72:ASP:O	47:D:73:ALA:HB3	2.12	0.50
27:l:54:LYS:HE3	34:N:72:U:OP2	2.11	0.50
34:N:698:C:O2'	34:N:734:A:N6	2.44	0.50
34:N:2185:U:H2'	34:N:2186:G:C8	2.47	0.50
45:8:120:LYS:HG2	45:8:123:ARG:HB3	1.94	0.50
54:K:42:SER:HB3	54:K:52:GLN:HE21	1.75	0.50
17:b:40:ILE:HG12	17:b:47:VAL:HG12	1.94	0.50
34:N:306:U:H3	34:N:310:A:H62	0.61	0.50
34:N:2105:U:H2'	34:N:2106:U:O4'	2.12	0.50
34:N:2113:U:H2'	34:N:2114:A:H8	1.77	0.50
35:L:37:CYS:SG	35:L:38:SER:N	2.85	0.50
36:C:183:ASP:O	36:C:187:GLU:HG2	2.12	0.50
23:h:7:ARG:NH2	23:h:26:LYS:O	2.45	0.50
34:N:500:G:N1	34:N:503:A:OP2	2.42	0.50
39:2:172:ARG:NH2	39:2:206:GLU:OE2	2.44	0.50
52:I:6:LEU:HG	52:I:17:TYR:HB3	1.93	0.50
5:P:165:VAL:HG21	5:P:181:MET:HE1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:e:7:SER:OG	20:e:8:GLY:N	2.45	0.50
22:g:18:GLU:OE2	34:N:1392:A:N6	2.42	0.50
23:h:34:VAL:HG13	23:h:67:VAL:HG22	1.93	0.50
23:h:51:ALA:O	23:h:54:GLN:NE2	2.44	0.50
37:0:542:G:H5'	40:3:39:GLY:HA3	1.94	0.50
10:U:72:ILE:HG22	10:U:73:ASN:N	2.27	0.50
12:W:108:MET:HE2	34:N:1138:G:N3	2.27	0.50
39:2:77:ILE:HA	39:2:84:VAL:HG23	1.92	0.50
3:M:16:C:O2	3:M:16:C:H2'	2.11	0.49
28:m:3:LYS:HE2	28:m:40:ASP:HB3	1.94	0.49
29:n:3:VAL:HG23	34:N:2015:A:C6	2.47	0.49
34:N:299:A:N3	34:N:319:G:O2'	2.37	0.49
34:N:1297:C:O2'	34:N:1302:A:N1	2.39	0.49
37:0:1076:U:OP1	38:1:174:LYS:NZ	2.43	0.49
11:V:124:ALA:HB1	34:N:1081:U:H4'	1.93	0.49
38:1:141:LEU:O	38:1:145:GLU:CB	2.61	0.49
56:u:54:MET:HE3	56:u:58:VAL:HG21	1.94	0.49
7:R:21:ARG:HD3	7:R:106:LYS:HB3	1.93	0.49
34:N:2533:U:OP1	34:N:2665:A:O2'	2.29	0.49
37:0:401:C:O2'	37:0:621:A:N3	2.40	0.49
46:9:27:GLU:O	46:9:31:ARG:CB	2.61	0.49
7:R:58:LYS:HG3	7:R:71:GLY:HA2	1.95	0.49
34:N:2106:U:H2'	34:N:2107:G:C8	2.48	0.49
47:D:109:ASN:OD1	57:v:7:ARG:HA	2.13	0.49
34:N:2150:C:H2'	34:N:2151:U:O4'	2.13	0.49
24:i:6:ALA:HB1	24:i:40:ILE:HG23	1.95	0.49
29:n:17:ARG:NE	34:N:1266:G:OP2	2.40	0.49
37:0:976:G:OP2	37:0:1358:U:O2'	2.29	0.49
43:6:142:HIS:O	43:6:146:GLU:HB2	2.13	0.49
56:u:69:LYS:O	56:u:72:ALA:HB3	2.12	0.49
36:C:212:VAL:HG23	36:C:224:VAL:HG23	1.95	0.49
37:0:835:U:OP1	54:K:53:ARG:NH2	2.32	0.49
41:4:99:ALA:HB2	41:4:124:LEU:HG	1.94	0.49
45:8:38:TYR:HD2	45:8:39:PHE:HD1	1.61	0.49
7:R:83:VAL:HB	7:R:86:ALA:HB2	1.95	0.49
38:1:176:ALA:HB1	38:1:181:ILE:HB	1.94	0.49
47:D:110:ILE:HD12	57:v:17:ARG:HD2	1.94	0.49
49:F:10:PRO:HB2	49:F:18:ALA:HB1	1.94	0.49
11:V:127:ARG:HA	11:V:130:GLU:HB2	1.94	0.49
34:N:1047:G:O2'	34:N:1111:A:N6	2.46	0.49
4:O:74:U:O2	24:i:29:ILE:HD13	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:P:207:LYS:HB2	34:N:729:G:C6	2.48	0.49
34:N:1868:C:N4	34:N:1869:G:O6	2.46	0.49
34:N:2149:U:H2'	34:N:2150:C:O4'	2.13	0.49
37:0:972:C:P	46:9:59:LYS:HD3	2.53	0.49
40:3:141:ASP:O	40:3:181:THR:HA	2.12	0.49
53:J:31:HIS:HD2	53:J:34:TYR:H	1.59	0.49
3:M:37:U:O2'	37:0:790:A:OP1	2.30	0.48
9:T:67:THR:HG22	34:N:2748:A:H1'	1.95	0.48
10:U:7:ASP:HB3	10:U:9:VAL:HG23	1.94	0.48
20:e:71:LYS:NZ	34:N:1223:G:N7	2.61	0.48
14:Y:51:GLU:OE1	14:Y:60:ARG:NH1	2.46	0.48
37:0:642:A:C5	44:7:107:SER:HA	2.49	0.48
45:8:28:ILE:HD11	45:8:57:MET:HE1	1.96	0.48
5:P:66:ASP:OD2	5:P:102:ARG:NH1	2.46	0.48
5:P:235:GLY:O	34:N:2599:G:N7	2.47	0.48
34:N:1724:G:C6	34:N:1737:G:N2	2.81	0.48
34:N:2128:G:N2	34:N:2173:A:H1'	2.27	0.48
10:U:27:ARG:NH2	26:k:56:MET:HE2	2.29	0.48
19:d:51:ARG:HG2	34:N:1156:A:C8	2.49	0.48
31:p:18:PHE:HA	31:p:43:THR:HG21	1.95	0.48
36:C:25:GLU:O	36:C:29:LEU:HG	2.13	0.48
17:b:31:THR:O	17:b:102:ARG:NH1	2.41	0.48
34:N:2139:U:H2'	34:N:2140:G:C8	2.49	0.48
50:G:89:MET:HE1	50:G:98:LYS:HD3	1.96	0.48
16:a:61:ALA:O	16:a:65:LEU:HB2	2.13	0.48
25:j:41:ARG:NH1	34:N:2262:U:OP1	2.47	0.48
1:A:72:C:OP1	34:N:1942:C:H4'	2.14	0.48
3:M:1:U:H2'	3:M:2:G:H8	1.78	0.48
3:M:55:C:H4'	8:S:74:VAL:HA	1.96	0.48
11:V:55:ILE:HG22	11:V:57:VAL:HB	1.94	0.48
20:e:27:ILE:O	20:e:66:HIS:NE2	2.42	0.48
30:o:35:GLU:HA	30:o:49:TYR:O	2.13	0.48
34:N:1447:C:O2'	34:N:1544:A:N3	2.39	0.48
37:0:812:G:O2'	37:0:813:U:H6	1.96	0.48
37:0:1130:A:H61	37:0:1144:G:H1'	1.79	0.48
12:W:81:ILE:O	34:N:1131:G:OP1	2.32	0.48
27:l:2:LYS:HD3	34:N:77:G:OP1	2.13	0.48
34:N:355:U:H2'	34:N:356:G:H8	1.78	0.48
34:N:2176:A:H2'	34:N:2177:C:C6	2.49	0.48
37:0:757:U:O2'	37:0:879:C:O2	2.31	0.48
15:Z:33:LEU:HD13	15:Z:117:PHE:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:N:1783:A:H5'	34:N:2608:G:H4'	1.95	0.48
38:1:207:ILE:HA	38:1:210:VAL:HG22	1.96	0.48
39:2:108:LYS:HD3	39:2:111:LEU:HD12	1.96	0.48
47:D:16:VAL:HG12	47:D:77:TYR:HB3	1.96	0.48
47:D:111:THR:HG22	57:v:5:LYS:HA	1.95	0.48
48:E:64:THR:HG23	48:E:93:VAL:HG12	1.95	0.48
52:I:46:LYS:HG3	52:I:47:GLU:H	1.79	0.48
14:Y:57:LEU:HD22	32:q:54:ASP:HB3	1.96	0.47
14:Y:111:ILE:HD11	34:N:636:G:C6	2.49	0.47
15:Z:57:VAL:HG13	15:Z:116:ALA:HB2	1.96	0.47
16:a:82:GLU:OE2	16:a:86:ARG:NH2	2.47	0.47
19:d:4:VAL:HG22	34:N:1199:U:H1'	1.95	0.47
23:h:45:HIS:HB3	23:h:58:ILE:HG12	1.95	0.47
31:p:1:MET:SD	34:N:752:A:H3'	2.53	0.47
34:N:33:C:O2	34:N:447:A:N6	2.47	0.47
34:N:270:A:N1	34:N:369:U:O2'	2.38	0.47
34:N:528:A:C2	34:N:2042:A:H2'	2.50	0.47
37:O:254:G:O3'	53:J:71:LYS:NZ	2.47	0.47
47:D:23:ILE:HG22	47:D:32:VAL:HG13	1.96	0.47
10:U:43:ASN:HB3	10:U:47:PHE:HE2	0.74	0.47
14:Y:67:THR:HG21	34:N:244:A:H5''	1.95	0.47
18:c:26:VAL:O	18:c:44:GLU:HA	2.14	0.47
22:g:22:THR:O	22:g:26:LYS:HB3	2.15	0.47
25:j:65:GLY:HA3	25:j:83:GLU:O	2.15	0.47
31:p:33:ARG:NH2	34:N:467:G:OP1	2.46	0.47
35:L:55:GLY:C	55:t:64:ASP:OD2	2.57	0.47
5:P:132:MET:HG2	5:P:135:ILE:HD12	1.96	0.47
5:P:167:ARG:HG2	5:P:172:VAL:HG12	1.96	0.47
8:S:42:GLU:OE1	8:S:148:ARG:NH1	2.48	0.47
11:V:33:VAL:HG13	11:V:59:ILE:HG21	1.96	0.47
34:N:910:A:H2'	34:N:911:A:C8	2.50	0.47
31:p:19:ARG:HG2	34:N:126:A:O5'	2.14	0.47
34:N:503:A:H4'	34:N:504:A:H5'	1.97	0.47
36:C:171:ILE:HD13	36:C:196:LEU:HD11	1.96	0.47
37:O:1073:U:O2	38:1:103:ASN:ND2	2.48	0.47
38:1:81:LYS:O	38:1:85:LEU:CB	2.62	0.47
40:3:95:GLU:HA	40:3:100:ASN:ND2	2.29	0.47
5:P:155:ALA:HB2	5:P:162:VAL:HG23	1.97	0.47
21:f:90:LYS:NZ	34:N:746:U:O2'	2.47	0.47
34:N:1724:G:O6	34:N:1737:G:N2	2.47	0.47
34:N:2177:C:H4'	36:C:211:LYS:NZ	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:O:705:G:H21	47:D:31:ILE:HD11	1.78	0.47
54:K:51:TYR:O	54:K:55:LEU:HB2	2.15	0.47
34:N:2189:U:H2'	34:N:2190:G:C8	2.49	0.47
34:N:2243:U:H2'	34:N:2244:U:C6	2.50	0.47
34:N:2540:C:O2'	34:N:2740:A:N3	2.42	0.47
37:O:261:U:OP2	56:u:74:ARG:NH2	2.47	0.47
5:P:251:GLN:NE2	5:P:252:THR:O	2.48	0.47
6:Q:35:THR:HG22	6:Q:73:VAL:HG11	1.96	0.47
14:Y:81:ASP:HB2	14:Y:100:ILE:HD11	1.96	0.47
33:r:11:CYS:SG	33:r:14:CYS:N	2.88	0.47
34:N:284:U:O4	34:N:356:G:O6	2.33	0.47
34:N:1187:G:N2	34:N:1188:U:O4	2.47	0.47
34:N:2776:A:O5'	34:N:2776:A:H8	1.97	0.47
37:O:677:U:H3	37:O:713:G:H22	1.62	0.47
37:O:1006:G:O6	37:O:1023:U:C2	2.67	0.47
37:O:1302:C:C6	49:F:17:ILE:HD13	2.50	0.47
42:5:88:MET:HE3	54:K:64:TYR:CD2	2.49	0.47
19:d:37:GLN:HE21	34:N:1252:G:H22	1.62	0.47
34:N:548:G:H5''	34:N:549:G:H5'	1.97	0.47
35:L:13:THR:HA	35:L:23:LYS:HA	1.97	0.47
36:C:55:SER:O	36:C:58:ASN:ND2	2.48	0.47
54:K:34:THR:HG23	54:K:36:SER:H	1.79	0.47
23:h:41:LEU:HA	23:h:61:LYS:O	2.15	0.47
29:n:25:VAL:HG21	29:n:28:LEU:HD23	1.97	0.47
31:p:1:MET:HE2	31:p:1:MET:HB3	1.83	0.47
34:N:1853:A:N3	34:N:2233:U:O2'	2.43	0.47
37:O:999:C:N3	37:O:1042:A:N6	2.63	0.47
38:1:136:MET:SD	38:1:139:ARG:NH2	2.87	0.47
18:c:29:LYS:HD3	18:c:40:LEU:HD21	1.97	0.47
29:n:6:ASN:ND2	34:N:2020:A:H62	2.12	0.47
34:N:160:A:N3	34:N:2208:C:O2'	2.44	0.47
34:N:1999:C:O3'	34:N:2722:G:N2	2.48	0.47
34:N:2273:A:H2'	34:N:2274:A:C8	2.50	0.47
41:4:89:HIS:CD2	41:4:90:THR:H	2.33	0.47
41:4:105:ILE:HD11	41:4:115:LEU:HD23	1.96	0.47
8:S:74:VAL:HG22	8:S:79:ILE:HD11	1.97	0.46
10:U:24:GLY:O	10:U:28:ASN:HB2	2.15	0.46
37:O:197:A:N1	37:O:220:G:O2'	2.45	0.46
37:O:618:C:O2'	52:I:14:ARG:NH2	2.47	0.46
37:O:1227:A:OP2	49:F:95:LEU:HD21	2.15	0.46
48:E:38:TYR:HB2	48:E:52:VAL:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:F:8:ASN:HD22	49:F:22:ILE:HG13	1.78	0.46
15:Z:136:MET:HE3	24:i:57:TYR:HB3	1.96	0.46
33:r:36:ARG:HH11	33:r:36:ARG:HD3	1.53	0.46
34:N:476:G:N1	34:N:479:A:OP2	2.46	0.46
34:N:1900:A:H1'	34:N:1970:A:H2'	1.97	0.46
36:C:163:TYR:CD2	36:C:171:ILE:HD11	2.50	0.46
37:O:523:A:N1	48:E:89:ASP:HB2	2.31	0.46
37:O:1006:G:C6	37:O:1023:U:O2	2.68	0.46
15:Z:42:THR:HG22	15:Z:93:VAL:HG12	1.97	0.46
31:p:12:ARG:CZ	31:p:44:VAL:HG21	2.45	0.46
34:N:2180:U:H2'	34:N:2181:U:O4'	2.16	0.46
8:S:24:SER:HB3	8:S:27:GLN:HB2	1.97	0.46
11:V:30:GLN:OE1	34:N:1095:A:N6	2.48	0.46
12:W:114:LEU:HG	12:W:118:MET:HE3	1.97	0.46
34:N:1847:A:O2'	34:N:1848:A:H8	1.98	0.46
19:d:16:LYS:NZ	34:N:1227:G:OP2	2.48	0.46
37:O:296:U:O2'	37:O:556:C:O2	2.33	0.46
8:S:140:GLU:CD	35:L:27:THR:HG23	2.41	0.46
14:Y:41:ARG:NH1	34:N:807:U:OP2	2.48	0.46
15:Z:55:ARG:NH2	34:N:2469:A:O3'	2.49	0.46
34:N:715:A:N6	51:H:53:ARG:NH1	2.64	0.46
34:N:857:G:N2	34:N:2269:G:O4'	2.49	0.46
34:N:1266:G:O2'	34:N:2012:G:O6	2.22	0.46
36:C:163:TYR:HD2	36:C:171:ILE:HD11	1.79	0.46
37:O:71:A:N1	37:O:99:C:O2'	2.47	0.46
37:O:1113:C:H4'	39:2:14:ILE:HD12	1.97	0.46
57:v:37:PHE:HB3	57:v:39:GLU:H	1.79	0.46
5:P:260:ASN:ND2	5:P:263:THR:OG1	2.49	0.46
24:i:48:MET:SD	24:i:51:GLN:NE2	2.89	0.46
34:N:2104:C:H2'	34:N:2105:U:C6	2.51	0.46
36:C:163:TYR:HB2	36:C:171:ILE:HD11	1.97	0.46
40:3:140:ASN:N	40:3:182:PHE:O	2.48	0.46
18:c:92:VAL:HG21	18:c:97:LEU:HD21	1.98	0.46
34:N:1509:A:H2'	34:N:1510:G:C8	2.50	0.46
34:N:1733:G:H2'	34:N:1734:G:C8	2.51	0.46
34:N:2177:C:O2'	36:C:170:ILE:HG12	2.15	0.46
37:O:1126:U:OP1	46:9:7:ARG:NH2	2.49	0.46
39:2:65:ARG:O	39:2:65:ARG:HG3	2.16	0.46
42:5:62:MET:HG2	42:5:64:VAL:HG23	1.97	0.46
46:9:10:LEU:O	46:9:71:LEU:HA	2.15	0.46
52:I:70:ARG:HD2	52:I:70:ARG:HA	1.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:148:ILE:HB	7:R:169:VAL:HG22	1.98	0.46
12:W:31:GLU:HG2	12:W:142:ILE:HG12	1.97	0.46
29:n:16:ARG:NE	34:N:1266:G:OP1	2.37	0.46
32:q:5:LYS:CE	34:N:254:G:N7	2.78	0.46
34:N:881:G:N2	34:N:895:U:O2	2.49	0.46
34:N:1064:C:N4	34:N:1070:A:OP2	2.49	0.46
34:N:2006:C:O2'	34:N:2823:A:N3	2.48	0.46
34:N:2506[A]:U:OP2	34:N:2576:G:N2	2.47	0.46
37:0:1218:C:H2'	37:0:1219:A:C8	2.51	0.46
21:f:38:TYR:CD2	29:n:28:LEU:HD22	2.51	0.46
31:p:35:ARG:HG3	31:p:42:LEU:HD21	1.98	0.46
34:N:1475:G:H1'	34:N:1732:C:H41	1.79	0.46
34:N:2126:A:H2'	34:N:2162:G:C2	2.50	0.46
37:0:674:G:P	42:5:86:ARG:HH22	2.38	0.46
38:1:163:VAL:HG21	38:1:173:ILE:HD11	1.98	0.46
39:2:155:GLY:HA2	39:2:163:ALA:HB1	1.98	0.46
49:F:3:ARG:O	49:F:57:ARG:NH1	2.37	0.46
4:O:7:G:H5'	17:b:29:HIS:CE1	2.51	0.45
34:N:1176:U:H2'	34:N:1177:G:C8	2.51	0.45
37:0:1106:G:O2'	39:2:169:ARG:NH1	2.50	0.45
54:K:33:ILE:HD13	54:K:33:ILE:HG21	1.68	0.45
8:S:131:GLY:HA3	34:N:2305:U:H5''	1.98	0.45
11:V:107:GLN:O	11:V:111:GLN:HB2	2.15	0.45
34:N:1077:A:N6	34:N:1089:A:OP1	2.46	0.45
37:0:1356:G:H2'	37:0:1357:A:C8	2.51	0.45
38:1:104:TRP:O	38:1:108:ARG:N	2.47	0.45
41:4:153:VAL:HG12	41:4:156:LYS:HZ1	1.80	0.45
12:W:82:GLY:HA2	34:N:1131:G:OP1	2.17	0.45
37:0:573:A:N3	37:0:883:C:O2'	2.47	0.45
55:t:50:ALA:HB1	55:t:57:HIS:HB3	1.97	0.45
3:M:16:C:H3'	3:M:17:G:C5'	2.40	0.45
6:Q:149:ASN:HD22	34:N:2572:A:H2'	1.81	0.45
15:Z:9:PHE:HZ	34:N:911:A:H2'	1.80	0.45
15:Z:123:LYS:HE3	34:N:2483:C:N3	2.32	0.45
33:r:1:MET:HE2	33:r:34:LYS:HD3	1.98	0.45
34:N:2183:A:H2'	34:N:2184:A:C8	2.51	0.45
36:C:184:LYS:O	36:C:188:ASN:ND2	2.50	0.45
40:3:58:LYS:HD3	40:3:203:LEU:HD23	1.98	0.45
1:A:12:U:C5'	34:N:1915:U:H4'	2.47	0.45
2:s:155:SER:HB3	34:N:2061:G:H22	1.81	0.45
5:P:182:ARG:NH1	34:N:1800:C:OP2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:Y:33:ARG:NH1	34:N:587:C:O2	2.46	0.45
34:N:2186:G:H2'	34:N:2187:U:O4'	2.16	0.45
34:N:2514:U:H2'	34:N:2515:C:C6	2.51	0.45
37:0:861:G:O2'	37:0:874:G:O2'	2.31	0.45
3:M:34:U:OP1	45:8:129:LYS:NZ	2.40	0.45
34:N:1078:U:O2'	34:N:1088:A:OP1	2.34	0.45
14:Y:54:GLN:HE21	34:N:2428:G:N2	2.14	0.45
14:Y:82:LEU:HA	14:Y:85:VAL:HG13	1.99	0.45
16:a:44:LEU:HD23	16:a:113:ILE:HD13	1.98	0.45
34:N:499:U:O4	34:N:503:A:N7	2.49	0.45
37:0:928:G:O2'	37:0:1533:C:OP1	2.34	0.45
37:0:1379:G:O6	43:6:2:PRO:HB2	2.17	0.45
47:D:49:GLY:O	47:D:69:ARG:NH1	2.50	0.45
11:V:11:LEU:HD23	34:N:1097:U:O2	2.16	0.45
33:r:7:VAL:HG22	33:r:38:GLY:HA3	1.99	0.45
34:N:2777:G:OP2	34:N:2781:A:O2'	2.26	0.45
38:1:53:ALA:O	38:1:57:LEU:CB	2.65	0.45
38:1:100:MET:HA	38:1:107:VAL:HG21	1.99	0.45
41:4:107:ALA:HA	41:4:125:ALA:HB3	1.98	0.45
5:P:19:VAL:HG23	5:P:203:ARG:HB3	1.99	0.45
18:c:63:LYS:HE3	18:c:65:SER:HB2	1.99	0.45
19:d:31:VAL:HG13	34:N:580:U:O3'	2.17	0.45
27:l:56:LEU:HD23	27:l:56:LEU:HA	1.86	0.45
37:0:1062:U:H2'	37:0:1063:C:C6	2.52	0.45
41:4:133:PRO:HA	41:4:136:VAL:HG12	1.97	0.45
34:N:1794:A:H2'	34:N:1795:C:C6	2.52	0.45
38:1:53:ALA:O	38:1:57:LEU:HB2	2.16	0.45
41:4:18:VAL:HA	41:4:34:THR:O	2.16	0.45
48:E:114:ARG:HG2	48:E:119:VAL:HB	1.99	0.45
1:A:56:C:H6	34:N:896:A:C2	2.27	0.44
7:R:165:HIS:CD2	34:N:1205:A:C6	3.05	0.44
11:V:11:LEU:HD11	11:V:28:LEU:HB3	1.99	0.44
29:n:16:ARG:HA	34:N:2046:G:H5'	1.99	0.44
34:N:569:U:H5''	34:N:821:A:C2	2.52	0.44
37:0:309:A:H2'	37:0:310:G:H8	1.81	0.44
37:0:1101:A:H61	38:1:102:THR:HG21	1.81	0.44
40:3:62:ARG:HH21	40:3:68:LEU:HA	1.82	0.44
46:9:12:ALA:HB3	46:9:18:ILE:HB	1.99	0.44
15:Z:9:PHE:CZ	34:N:911:A:H2'	2.52	0.44
37:0:1074:G:O2'	37:0:1101:A:N1	2.44	0.44
37:0:1096:C:O2	37:0:1170:A:O2'	2.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:F:17:ILE:O	49:F:20:THR:OG1	2.33	0.44
52:I:38:PHE:CE1	52:I:51:ARG:HG2	2.52	0.44
10:U:72:ILE:HG22	10:U:73:ASN:H	1.82	0.44
13:X:63:VAL:HG12	13:X:107:LEU:HD21	2.00	0.44
18:c:29:LYS:HB2	18:c:83:SER:HB2	1.98	0.44
19:d:37:GLN:NE2	34:N:1252:G:H22	2.14	0.44
26:k:37:ARG:HG2	26:k:46:PHE:HB3	1.98	0.44
34:N:45:G:H5''	34:N:46:G:H5'	1.98	0.44
34:N:613:A:N7	34:N:616:A:C6	2.85	0.44
34:N:2458:G:O2'	34:N:2460:U:O4	2.34	0.44
37:0:362:G:N1	37:0:365:U:OP2	2.43	0.44
37:0:723:U:C5'	57:v:49:LYS:HE2	2.48	0.44
38:1:166:ALA:HB3	38:1:191:SER:HB3	2.00	0.44
5:P:145:GLU:HB2	5:P:188:CYS:HB3	1.98	0.44
7:R:165:HIS:CD2	34:N:1205:A:C5	3.06	0.44
10:U:44:ILE:O	10:U:48:GLU:HG3	2.18	0.44
17:b:29:HIS:HB3	17:b:36:TYR:HB2	2.00	0.44
19:d:48:ARG:NE	19:d:49:ASP:OD1	2.49	0.44
19:d:88:VAL:HA	20:e:49:ILE:CD1	2.47	0.44
43:6:59:LEU:O	43:6:63:GLU:HB2	2.18	0.44
56:u:12:ILE:HD13	56:u:12:ILE:HG21	1.72	0.44
2:s:153:LEU:HD21	34:N:2585:U:O2'	2.17	0.44
3:M:9:C:O2'	3:M:44:A:O2'	2.33	0.44
3:M:30:A:C4'	37:0:1339:A:N1	2.80	0.44
21:f:77:ASP:HB2	21:f:102:HIS:HB2	2.00	0.44
30:o:40:ASP:O	30:o:44:ARG:N	2.50	0.44
34:N:514:A:N3	34:N:581:C:O2'	2.44	0.44
36:C:5:THR:OG1	36:C:6:LYS:N	2.49	0.44
39:2:40:ARG:O	39:2:44:THR:OG1	2.34	0.44
43:6:56:LYS:HE3	43:6:60:GLU:HG3	1.99	0.44
5:P:141:VAL:HG13	5:P:190:ALA:HB1	1.99	0.44
9:T:66:GLY:O	9:T:69:ARG:HB3	2.17	0.44
14:Y:100:ILE:HG21	14:Y:100:ILE:HD13	1.75	0.44
27:l:1:MET:HG2	27:l:4:LYS:HD3	2.00	0.44
31:p:16:HIS:ND1	34:N:684:G:OP1	2.48	0.44
34:N:2130:U:H5'	34:N:2159:G:N2	2.33	0.44
37:0:481:G:O2'	37:0:483:C:N4	2.50	0.44
37:0:1080:A:OP1	41:4:52:LYS:HD2	2.18	0.44
43:6:73:VAL:HG12	43:6:90:GLU:HA	2.00	0.44
6:Q:43:ASP:OD1	34:N:2784:U:H4'	2.17	0.44
11:V:133:ALA:O	11:V:138:LEU:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Z:40:ARG:HD3	15:Z:93:VAL:HG21	2.00	0.44
34:N:2123:G:H2'	34:N:2124:G:C8	2.52	0.44
37:0:9:G:OP2	41:4:126:LYS:HD2	2.18	0.44
37:0:71:A:H61	37:0:99:C:H1'	1.83	0.44
37:0:766:A:OP2	37:0:812:G:N2	2.49	0.44
37:0:1060:U:P	50:G:85:ARG:HH22	2.41	0.44
40:3:109:ALA:HA	40:3:161:LEU:HD11	2.00	0.44
45:8:16:ALA:O	45:8:67:VAL:HA	2.17	0.44
3:M:30:A:H1'	37:0:1339:A:C2	2.53	0.44
6:Q:13:ARG:HD2	6:Q:15:PHE:CZ	2.53	0.44
11:V:79:LEU:HD21	11:V:109:ILE:HG21	1.99	0.44
34:N:499:U:H3	34:N:503:A:H62	0.54	0.44
34:N:1275:A:N1	34:N:1295:C:O2'	2.47	0.44
34:N:2029:G:N1	34:N:2033:A:OP2	2.34	0.44
37:0:714:G:H2'	37:0:715:A:C8	2.53	0.44
40:3:100:ASN:OD1	40:3:111:ARG:NH1	2.51	0.44
55:t:4:SER:HB3	55:t:5:LEU:HD12	2.00	0.44
6:Q:37:VAL:HG22	6:Q:48:ILE:HG22	2.00	0.44
19:d:15:LYS:HB2	19:d:15:LYS:HE2	1.80	0.44
20:e:3:ALA:HA	20:e:40:MET:O	2.17	0.44
25:j:33:ALA:N	25:j:64:ASP:OD1	2.51	0.44
36:C:3:LYS:HG3	36:C:4:LEU:N	2.25	0.44
37:0:1178:G:C5	45:8:99:ARG:NH2	2.86	0.44
43:6:71:PRO:O	43:6:96:ARG:NH1	2.51	0.44
56:u:67:ILE:HG13	56:u:71:LYS:HD3	2.00	0.44
5:P:85:PRO:HG3	34:N:1567:G:H2'	2.00	0.43
9:T:9:VAL:HB	9:T:50:LEU:HB2	2.00	0.43
11:V:24:VAL:HG12	34:N:1070:A:H61	1.83	0.43
19:d:97:ASP:OD2	20:e:13:ARG:NE	2.47	0.43
20:e:34:GLU:HG2	20:e:60:LYS:HG2	1.98	0.43
27:l:20:ASN:HB3	27:l:50:VAL:HG22	2.00	0.43
29:n:4:GLN:NE2	34:N:2016:U:O2	2.49	0.43
34:N:58:G:O2'	34:N:73:A:N1	2.46	0.43
34:N:84:A:N1	34:N:98:G:O2'	2.46	0.43
34:N:1044:C:O2'	34:N:1111:A:N1	2.48	0.43
36:C:45:ALA:HA	36:C:172:HIS:CD2	2.52	0.43
41:4:114:VAL:O	41:4:118:ALA:HB2	2.18	0.43
2:s:153:LEU:C	2:s:153:LEU:HD23	2.43	0.43
6:Q:19:GLY:HA3	18:c:80:VAL:HG23	2.01	0.43
7:R:69:ARG:NH2	34:N:2445:G:OP1	2.47	0.43
19:d:11:ARG:HA	19:d:11:ARG:HD2	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:d:113:ALA:O	19:d:117:LEU:HB2	2.18	0.43
37:0:971:G:O6	37:0:1364:U:O2'	2.35	0.43
37:0:1317:C:H4'	50:G:49:GLN:HE21	1.83	0.43
37:0:1321:U:O2'	55:t:78:ARG:NH1	2.51	0.43
37:0:1507:A:H2'	37:0:1508:A:C8	2.53	0.43
49:F:16:VAL:HG23	49:F:17:ILE:HG13	2.00	0.43
5:P:61:ALA:O	5:P:63:ARG:NH2	2.52	0.43
6:Q:1:MET:HG2	6:Q:205:PRO:HG2	2.00	0.43
6:Q:4:LEU:HD21	6:Q:96:ILE:HG22	1.99	0.43
13:X:70:ARG:NH2	34:N:2683:C:O2	2.52	0.43
13:X:99:ILE:HD13	13:X:115:ILE:HG23	1.99	0.43
30:o:21:TYR:HE2	30:o:38:LYS:HB3	1.83	0.43
41:4:80:THR:OG1	41:4:81:LEU:N	2.50	0.43
45:8:106:ARG:NH1	45:8:107:ASP:O	2.50	0.43
27:l:13:GLU:HA	27:l:16:THR:HG22	1.99	0.43
34:N:247:G:OP2	34:N:249:C:N4	2.47	0.43
34:N:299:A:N1	34:N:322:A:O2'	2.46	0.43
37:0:825:A:H4'	44:7:3:MET:HE2	1.99	0.43
42:5:70:VAL:HA	42:5:73:GLU:HG2	1.99	0.43
32:q:33:LEU:HB2	34:N:2420:C:OP2	2.19	0.43
34:N:675:A:N3	34:N:2443:C:O2'	2.47	0.43
34:N:749:A:N1	34:N:753:A:O2'	2.43	0.43
34:N:1072:C:H42	34:N:1098:A:N6	2.16	0.43
34:N:2602:A:H4'	34:N:2603:G:H5'	2.01	0.43
37:0:552:U:H5'	48:E:83:ARG:NH1	2.32	0.43
37:0:1380:U:O2	37:0:1382:C:N4	2.49	0.43
38:1:186:ILE:HB	38:1:213:TYR:CZ	2.54	0.43
43:6:105:VAL:O	43:6:109:ARG:HG2	2.19	0.43
45:8:129:LYS:HB2	45:8:129:LYS:HE3	1.71	0.43
54:K:71:THR:HG23	54:K:73:ARG:H	1.82	0.43
57:v:17:ARG:H	57:v:17:ARG:HD3	1.82	0.43
18:c:53:ARG:NH2	34:N:2720:U:OP1	2.51	0.43
34:N:629:G:N3	34:N:639:U:O2'	2.52	0.43
34:N:1437:C:O2'	34:N:1516:G:O2'	2.35	0.43
35:L:11:GLU:HA	35:L:25:ARG:HA	2.01	0.43
38:1:15:HIS:HB2	38:1:203:ASN:HD22	1.84	0.43
43:6:107:ALA:HB1	43:6:133:THR:HB	2.00	0.43
47:D:31:ILE:HG21	47:D:31:ILE:HD13	1.70	0.43
51:H:35:GLN:HE21	51:H:39:LEU:HD13	1.84	0.43
52:I:6:LEU:HD12	52:I:19:VAL:HB	1.99	0.43
8:S:105:THR:HG21	35:L:22:MET:SD	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:Y:77:ILE:CD1	14:Y:108:ALA:HB1	2.48	0.43
16:a:3:HIS:CD2	34:N:2820:A:H4'	2.54	0.43
19:d:112:LYS:HG3	20:e:48:LYS:HE2	2.01	0.43
34:N:373:U:H2'	34:N:374:A:H8	1.84	0.43
34:N:537:G:O2'	34:N:556:A:N6	2.50	0.43
34:N:2141:G:H2'	34:N:2142:A:C8	2.48	0.43
36:C:46:VAL:HG13	36:C:212:VAL:HG12	2.01	0.43
37:O:228:A:H5'	52:I:63:GLN:NE2	2.34	0.43
37:O:620:C:C2	40:3:132:ILE:HD13	2.53	0.43
37:O:1064:G:O2'	37:O:1190:G:N2	2.51	0.43
44:7:49:PHE:HA	44:7:60:GLU:O	2.19	0.43
46:9:83:THR:O	46:9:87:LEU:CB	2.58	0.43
3:M:12:C:H4'	34:N:1922:G:N2	2.31	0.43
3:M:29:G:OP1	37:O:1229:A:O2'	2.36	0.43
9:T:85:LYS:HG2	9:T:141:ILE:HD12	1.99	0.43
14:Y:30:THR:O	14:Y:32:GLY:N	2.52	0.43
30:o:23:THR:OG1	30:o:24:THR:N	2.52	0.43
34:N:526:A:O2'	34:N:2043:C:O2	2.34	0.43
34:N:1826:G:O2'	34:N:1971:U:OP2	2.35	0.43
37:O:96:U:H2'	37:O:97:G:C8	2.54	0.43
37:O:838:G:H2'	37:O:839:C:C6	2.54	0.43
37:O:1081:A:H5'	41:4:23:LYS:HG3	2.01	0.43
40:3:159:LEU:HD13	40:3:175:ALA:HB1	2.01	0.43
5:P:201:MET:HG3	5:P:202:LEU:HD12	2.01	0.43
8:S:140:GLU:HA	35:L:28:VAL:HG22	2.01	0.43
12:W:113:PRO:HD2	34:N:558:U:P	2.58	0.43
19:d:37:GLN:NE2	34:N:1252:G:H1	2.17	0.43
34:N:372:G:HO2'	34:N:400:G:H1	1.61	0.43
34:N:2291:U:H2'	34:N:2292:U:C6	2.54	0.43
37:O:837:U:H2'	37:O:838:G:C8	2.54	0.43
37:O:841:C:H2'	37:O:843:U:H5''	2.00	0.43
37:O:1143:G:H2'	37:O:1144:G:H8	1.83	0.43
37:O:1255:G:O2'	37:O:1258:G:N3	2.46	0.43
49:F:96:PRO:HA	49:F:109:ARG:HG2	2.01	0.43
16:a:3:HIS:O	16:a:4:ARG:HB2	2.17	0.43
16:a:90:ARG:HD2	34:N:2880:C:O2'	2.18	0.43
23:h:72:ILE:HD13	23:h:72:ILE:HG21	1.79	0.43
26:k:17:ASN:HB2	26:k:25:THR:HB	1.99	0.43
34:N:1769:U:O2'	34:N:1958:C:OP1	2.36	0.43
37:O:1380:U:C5	43:6:3:ARG:HA	2.54	0.43
3:M:13:A:H4'	34:N:1924:C:H4'	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:45:TYR:OH	34:N:2636:C:O2'	2.07	0.42
6:Q:152:PRO:HG2	6:Q:156:PHE:CZ	2.54	0.42
9:T:22:GLN:HE22	9:T:55:ARG:HH21	1.66	0.42
34:N:285:G:O6	34:N:355:U:O2	2.36	0.42
34:N:828:U:H2'	34:N:829:A:C8	2.53	0.42
37:O:269:C:H2'	37:O:270:A:C8	2.54	0.42
37:O:537:G:H5''	48:E:110:ARG:HH12	1.84	0.42
37:O:746:A:H2'	37:O:747:A:C8	2.54	0.42
5:P:161:TYR:HB3	5:P:194:GLU:HB3	2.01	0.42
6:Q:109:VAL:HG22	6:Q:203:VAL:HG22	2.00	0.42
7:R:77:ILE:HD13	7:R:77:ILE:HG21	1.24	0.42
10:U:66:ASN:CG	10:U:135:HIS:HD2	2.26	0.42
28:m:54:MET:HE3	28:m:54:MET:HB2	1.75	0.42
34:N:221:A:N1	34:N:265:A:O2'	2.51	0.42
36:C:7:ARG:O	36:C:11:ILE:HG12	2.19	0.42
37:O:35:G:O2'	48:E:115:SER:O	2.31	0.42
37:O:1026:G:C6	37:O:1035:A:C6	3.06	0.42
37:O:1118:U:H2'	37:O:1119:C:C6	2.54	0.42
37:O:1119:C:H2'	37:O:1120:C:H6	1.84	0.42
48:E:34:CYS:HA	48:E:55:VAL:HA	2.01	0.42
48:E:50:ARG:HG3	48:E:90:LEU:HD11	2.01	0.42
5:P:236:GLU:HB3	34:N:2599:G:N7	2.35	0.42
14:Y:55:MET:HA	14:Y:56:PRO:HD3	1.90	0.42
16:a:37:THR:HG22	16:a:110:MET:HE1	2.00	0.42
21:f:93:ALA:HB2	34:N:1614:A:C2	2.55	0.42
26:k:31:PRO:HG2	26:k:33:LEU:HD13	2.01	0.42
34:N:219:A:N3	34:N:234:U:O2'	2.41	0.42
34:N:1075:C:H2'	34:N:1076:C:C6	2.54	0.42
34:N:1509:A:H2'	34:N:1510:G:H8	1.84	0.42
34:N:2469:A:N6	34:N:2481:G:O2'	2.50	0.42
35:L:30:HIS:ND1	35:L:31:ASP:O	2.52	0.42
36:C:42:VAL:HG12	36:C:216:THR:HG22	2.00	0.42
44:7:18:GLN:NE2	44:7:70:ALA:HB1	2.35	0.42
6:Q:149:ASN:ND2	34:N:2572:A:H2'	2.35	0.42
24:i:75:GLN:HB2	24:i:92:VAL:HG23	2.01	0.42
30:o:9:ILE:HG22	30:o:53:LYS:HB2	2.01	0.42
34:N:2170:A:H2'	34:N:2171:A:O4'	2.19	0.42
34:N:2174:C:O2'	34:N:2175:C:H5'	2.19	0.42
56:u:51:PHE:HA	56:u:54:MET:HG2	2.01	0.42
5:P:146:MET:HE1	34:N:1800:C:C5'	2.50	0.42
6:Q:156:PHE:CD1	12:W:81:ILE:HD12	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:X:7:MET:HB3	13:X:18:ARG:HD2	2.02	0.42
37:0:135:C:O2	52:I:1:MET:HB2	2.20	0.42
37:0:713:G:H2'	37:0:714:G:C8	2.54	0.42
8:S:37:ASN:ND2	34:N:2313:C:O4'	2.52	0.42
10:U:41:LYS:HD3	10:U:41:LYS:HA	1.90	0.42
10:U:78:VAL:HG23	10:U:142:VAL:HG11	2.01	0.42
34:N:190:A:N3	34:N:679:C:O2'	2.49	0.42
37:0:555:U:H2'	37:0:556:C:C6	2.54	0.42
37:0:812:G:HO2'	37:0:813:U:P	2.43	0.42
37:0:1101:A:H61	38:1:102:THR:CG2	2.32	0.42
56:u:56:PRO:O	56:u:60:ARG:HB2	2.20	0.42
6:Q:25:THR:HG21	6:Q:193:VAL:HG22	2.00	0.42
9:T:16:ASP:O	9:T:26:ILE:HA	2.19	0.42
13:X:38:ILE:HD11	13:X:112:PHE:HZ	1.84	0.42
18:c:58:ALA:HA	18:c:74:PHE:O	2.20	0.42
25:j:37:ILE:HG22	25:j:38:VAL:HG23	2.01	0.42
34:N:1058:U:H2'	34:N:1059:G:C8	2.55	0.42
37:0:1216:A:H5''	50:G:5:SER:HB2	2.02	0.42
39:2:22:TRP:NE1	39:2:36:ASP:OD2	2.50	0.42
40:3:95:GLU:HA	40:3:100:ASN:HD22	1.84	0.42
11:V:79:LEU:O	11:V:82:LYS:NZ	2.52	0.42
21:f:85:ILE:HA	21:f:94:ASP:O	2.19	0.42
29:n:8:PRO:HD2	34:N:1263:U:O2'	2.19	0.42
31:p:19:ARG:NH2	34:N:125:A:OP2	2.53	0.42
37:0:1041:G:H2'	37:0:1042:A:C8	2.55	0.42
40:3:95:GLU:HG3	40:3:191:LEU:HD22	2.00	0.42
40:3:157:ALA:O	40:3:160:GLU:HB3	2.19	0.42
56:u:33:LYS:O	56:u:37:ALA:HB3	2.19	0.42
6:Q:154:LYS:HE2	34:N:2024:G:O3'	2.20	0.42
8:S:33:LYS:HD3	8:S:92:ARG:NH1	2.35	0.42
9:T:94:TYR:HA	9:T:106:SER:O	2.19	0.42
11:V:13:VAL:HG21	11:V:23:PRO:HG2	2.02	0.42
34:N:284:U:O2	34:N:356:G:N2	2.49	0.42
34:N:2866:U:H4'	34:N:2867:G:H5'	2.02	0.42
37:0:22:G:O2'	37:0:913:A:N1	2.47	0.42
37:0:228:A:C4'	52:I:63:GLN:HE21	2.32	0.42
37:0:1118:U:H2'	37:0:1119:C:H6	1.85	0.42
38:1:128:LYS:HG3	38:1:129:LEU:HG	2.01	0.42
39:2:153:VAL:HG12	39:2:198:VAL:HG22	2.01	0.42
54:K:21:ILE:HD12	54:K:22:ASP:HB2	2.01	0.42
54:K:26:ILE:HG21	54:K:67:LEU:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:1:U:H2'	3:M:2:G:C8	2.54	0.42
21:f:24:ILE:HD13	21:f:36:LEU:HD11	2.02	0.42
34:N:320:A:H4'	34:N:322:A:C8	2.54	0.42
34:N:372:G:H1'	34:N:373:U:H5	1.85	0.42
34:N:1394:U:H4'	34:N:1603:A:H4'	2.02	0.42
34:N:2328:A:H2'	34:N:2329:U:C6	2.55	0.42
37:0:844:G:C5	37:0:846:G:H4'	2.55	0.42
37:0:1530:G:H2'	37:0:1531:A:C8	2.54	0.42
38:1:164:ILE:HD11	38:1:210:VAL:HB	2.02	0.42
56:u:33:LYS:O	56:u:37:ALA:CB	2.68	0.42
5:P:16:VAL:HG22	5:P:206:GLY:HA3	2.02	0.41
12:W:96:ARG:HH21	12:W:99:ARG:HG2	1.84	0.41
33:r:3:VAL:HG12	33:r:36:ARG:HB3	2.02	0.41
35:L:8:LYS:HA	35:L:8:LYS:HD3	1.82	0.41
41:4:112:ARG:O	41:4:116:GLU:HB2	2.19	0.41
25:j:41:ARG:HH12	34:N:2262:U:H5''	1.84	0.41
37:0:839:C:H2'	37:0:840:C:C6	2.55	0.41
37:0:1306:A:N6	37:0:1331:G:H1'	2.35	0.41
42:5:3:HIS:CE1	42:5:95:ALA:HB2	2.55	0.41
52:I:76:LYS:HE3	52:I:76:LYS:HB3	1.87	0.41
56:u:79:LEU:HA	56:u:79:LEU:HD23	1.83	0.41
12:W:110:PRO:O	12:W:115:GLY:HA3	2.20	0.41
13:X:121:GLU:HG3	18:c:66:ASN:HD21	1.85	0.41
19:d:17:ILE:HD13	19:d:17:ILE:HA	1.91	0.41
20:e:80:ARG:NH2	34:N:572:A:OP2	2.47	0.41
34:N:1173:U:H3'	34:N:1174:U:H4'	2.02	0.41
34:N:2176:A:H4'	36:C:215:SER:CB	2.50	0.41
36:C:60:ARG:HE	36:C:162:ARG:HH11	1.68	0.41
37:0:337:G:H2'	37:0:338:A:C8	2.56	0.41
37:0:723:U:H5''	57:v:49:LYS:HE2	2.01	0.41
42:5:42:TRP:HB2	42:5:59:TYR:HB2	2.01	0.41
2:s:153:LEU:O	34:N:2585:U:O2	2.37	0.41
16:a:28:LEU:HD23	16:a:48:VAL:HG21	2.01	0.41
20:e:81:LYS:HD2	34:N:973:A:OP2	2.20	0.41
34:N:859:G:HO2'	34:N:916:G:H1	1.68	0.41
34:N:1236:G:O2'	34:N:1237:A:O5'	2.37	0.41
38:1:21:ARG:HG3	38:1:22:TYR:CD2	2.55	0.41
40:3:72:PHE:HE1	40:3:94:LEU:HD11	1.84	0.41
42:5:6:ILE:HB	42:5:62:MET:HB3	2.02	0.41
42:5:51:ILE:N	42:5:53:LYS:O	2.52	0.41
9:T:90:VAL:O	9:T:160:LYS:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:b:94:ARG:HH12	34:N:2294:G:P	2.43	0.41
30:o:5:ILE:HG21	30:o:28:ARG:HH12	1.85	0.41
36:C:195:ALA:O	36:C:198:LYS:HB2	2.20	0.41
36:C:211:LYS:HB3	36:C:211:LYS:HE3	1.83	0.41
37:0:331:G:H2'	56:u:5:LYS:NZ	2.35	0.41
37:0:946:A:O2'	37:0:1333:A:N3	2.45	0.41
37:0:1371:G:O3'	45:8:71:GLY:HA3	2.20	0.41
46:9:22:THR:HA	46:9:25:ILE:HG22	2.02	0.41
4:O:42:C:C6	8:S:66:LEU:HB2	2.56	0.41
5:P:154:LEU:HD13	5:P:176:LEU:HD21	2.03	0.41
6:Q:81:GLU:OE1	34:N:2635:A:O2'	2.30	0.41
34:N:927:A:H2'	34:N:928:A:C8	2.56	0.41
34:N:2155:U:H2'	34:N:2156:G:H5'	2.01	0.41
34:N:2175:C:OP1	36:C:8:MET:HG2	2.20	0.41
37:0:837:U:H2'	37:0:838:G:H8	1.85	0.41
39:2:24:ALA:HB1	39:2:28:GLU:HG2	2.03	0.41
42:5:90:MET:HE3	42:5:90:MET:HB2	1.92	0.41
46:9:36:VAL:HG22	46:9:76:ILE:HG12	2.02	0.41
50:G:25:ALA:O	50:G:28:LYS:HG2	2.21	0.41
5:P:107:PRO:HA	5:P:195:VAL:HA	2.03	0.41
8:S:112:ARG:NH2	8:S:113:ASP:OD2	2.53	0.41
8:S:140:GLU:OE1	35:L:27:THR:HG23	2.21	0.41
26:k:37:ARG:HG3	26:k:48:THR:HB	2.02	0.41
34:N:2087:G:H2'	34:N:2088:A:H8	1.86	0.41
49:F:87:ARG:HG3	49:F:97:VAL:HG13	2.03	0.41
56:u:62:ALA:HA	56:u:67:ILE:HG22	2.02	0.41
5:P:146:MET:HE1	34:N:1800:C:H5'	2.02	0.41
5:P:178:SER:HB2	34:N:1799:G:N7	2.36	0.41
5:P:247:PRO:HD3	34:N:1824:G:O3'	2.20	0.41
11:V:12:GLN:HE21	11:V:55:ILE:N	2.19	0.41
22:g:19:LYS:NZ	34:N:1340:U:OP1	2.52	0.41
34:N:1212:G:H2'	34:N:1236:G:H22	1.85	0.41
34:N:2131:U:O5'	34:N:2133:G:H4'	2.21	0.41
34:N:2532:G:O2'	34:N:2657:A:N1	2.52	0.41
34:N:2572:A:OP1	34:N:2574:G:H4'	2.20	0.41
37:0:195:A:N3	37:0:222:C:O2'	2.51	0.41
39:2:55:ILE:HG21	39:2:55:ILE:HD13	1.65	0.41
49:F:25:VAL:HG23	49:F:29:ARG:HB3	2.03	0.41
52:I:40:ASN:HB3	52:I:43:ALA:HB2	2.03	0.41
57:v:17:ARG:HD3	57:v:17:ARG:N	2.36	0.41
13:X:49:ARG:HH21	37:0:1422:G:H4'	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Z:136:MET:SD	24:i:75:GLN:O	2.78	0.41
19:d:24:TYR:CD1	34:N:533:G:H5'	2.55	0.41
19:d:24:TYR:CE1	34:N:533:G:H5'	2.56	0.41
23:h:11:VAL:HA	23:h:72:ILE:HA	2.03	0.41
31:p:24:THR:HG23	31:p:27:GLY:H	1.86	0.41
34:N:301:G:O2'	34:N:302:C:O4'	2.34	0.41
34:N:2124:G:O2'	36:C:41:SER:HB3	2.20	0.41
34:N:2193:G:H2'	34:N:2194:U:C6	2.56	0.41
37:0:1071:C:H2'	37:0:1072:G:H8	1.86	0.41
39:2:134:MET:HE2	39:2:134:MET:HB3	1.91	0.41
4:O:49:C:OP1	17:b:102:ARG:HG2	2.21	0.41
7:R:111:GLU:OE2	7:R:114:ARG:NH1	2.49	0.41
17:b:24:THR:HG22	17:b:42:PRO:HD3	2.03	0.41
20:e:49:ILE:H	20:e:49:ILE:HG13	1.70	0.41
34:N:657:U:H2'	34:N:658:U:C6	2.56	0.41
34:N:932:U:O2'	34:N:934:U:O4	2.36	0.41
37:0:677:U:O2	37:0:777:A:O2'	2.38	0.41
43:6:75:VAL:HA	43:6:87:VAL:O	2.21	0.41
46:9:11:LYS:HG2	46:9:71:LEU:HG	2.03	0.41
6:Q:59:ARG:NH1	34:N:2831:G:OP2	2.42	0.40
28:m:44:ILE:HD13	28:m:44:ILE:HA	1.96	0.40
34:N:227:A:O2'	34:N:228:C:O5'	2.38	0.40
34:N:373:U:H2'	34:N:374:A:C8	2.56	0.40
34:N:568:U:O5'	34:N:945:A:N6	2.54	0.40
34:N:1875:G:O3'	36:C:205:LYS:HE3	2.13	0.40
34:N:2122:U:H2'	34:N:2123:G:O4'	2.21	0.40
37:0:1524:C:H2'	37:0:1525:G:C8	2.56	0.40
40:3:124:MET:HE3	40:3:146:ARG:HG2	2.03	0.40
7:R:125:SER:O	7:R:137:LYS:NZ	2.54	0.40
19:d:33:ARG:HG2	34:N:1252:G:N3	2.35	0.40
34:N:851:C:H2'	34:N:852:U:C6	2.57	0.40
34:N:1028:A:OP2	34:N:1126:A:N6	2.46	0.40
34:N:2092:U:N3	34:N:2226:C:OP2	2.44	0.40
34:N:2724:U:H2'	34:N:2725:A:C8	2.56	0.40
34:N:2788:C:H2'	34:N:2789:C:C6	2.56	0.40
39:2:43:LEU:HD21	39:2:68:ILE:HD11	2.04	0.40
45:8:20:PHE:HB2	45:8:64:TYR:O	2.21	0.40
47:D:88:GLY:H	47:D:114:THR:HG22	1.87	0.40
1:A:20:U:O2'	1:A:21:A:OP1	2.38	0.40
14:Y:109:LYS:HE2	14:Y:128:THR:HG22	2.02	0.40
23:h:16:GLY:C	23:h:18:ASP:H	2.28	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:N:493:G:H2'	34:N:494:G:O4'	2.21	0.40
34:N:704:G:H1'	34:N:727:A:N6	2.36	0.40
34:N:770:G:H1'	34:N:1379:U:C4	2.57	0.40
34:N:2177:C:H5''	36:C:211:LYS:HZ3	1.86	0.40
34:N:2554:U:H2'	34:N:2555:U:C6	2.55	0.40
39:2:80:LYS:O	39:2:82:GLU:N	2.54	0.40
45:8:96:SER:O	45:8:99:ARG:HB3	2.21	0.40
3:M:34:U:P	45:8:129:LYS:HZ3	2.45	0.40
4:O:80:U:H2'	4:O:81:G:H8	1.87	0.40
4:O:89:U:H1'	34:N:958:U:H2'	2.02	0.40
7:R:58:LYS:HA	7:R:59:PRO:HD3	1.93	0.40
10:U:96:THR:HB	10:U:117:LEU:HD21	2.03	0.40
16:a:87:PHE:O	16:a:89:SER:N	2.49	0.40
17:b:111:ARG:NH1	34:N:2376:A:N3	2.69	0.40
32:q:54:ASP:OD2	34:N:2359:C:O2'	2.30	0.40
34:N:632:A:H2'	34:N:633:A:C8	2.56	0.40
34:N:2655:G:O2'	34:N:2656:U:O5'	2.38	0.40
34:N:2873:A:H8	34:N:2873:A:H2'	1.77	0.40
36:C:171:ILE:O	36:C:171:ILE:HG23	2.22	0.40
37:0:552:U:O2'	48:E:83:ARG:O	2.40	0.40
37:0:1057:G:H5'	39:2:155:GLY:HA3	2.04	0.40
39:2:27:LYS:HB3	39:2:27:LYS:HE3	1.88	0.40
40:3:200:ILE:HD13	40:3:200:ILE:HG21	1.76	0.40
43:6:27:VAL:HG12	43:6:43:VAL:HG21	2.02	0.40
34:N:1129:A:O2'	34:N:2515:C:O2	2.38	0.40
34:N:1779:U:OP2	34:N:1784:A:N6	2.50	0.40
37:0:82:G:N2	37:0:84:U:O4	2.55	0.40
37:0:1152:A:OP1	46:9:70:HIS:ND1	2.55	0.40
37:0:1328:C:H5''	49:F:28:THR:HG21	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
2	s	35/179 (20%)	32 (91%)	3 (9%)	0	100	100
5	P	269/273 (98%)	247 (92%)	18 (7%)	4 (2%)	8	38
6	Q	207/209 (99%)	195 (94%)	11 (5%)	1 (0%)	24	60
7	R	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
8	S	175/179 (98%)	163 (93%)	11 (6%)	1 (1%)	21	57
9	T	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
10	U	147/149 (99%)	125 (85%)	19 (13%)	3 (2%)	6	33
11	V	139/142 (98%)	112 (81%)	27 (19%)	0	100	100
12	W	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
13	X	120/123 (98%)	109 (91%)	9 (8%)	2 (2%)	7	36
14	Y	141/144 (98%)	121 (86%)	16 (11%)	4 (3%)	4	28
15	Z	134/136 (98%)	119 (89%)	10 (8%)	5 (4%)	2	23
16	a	118/127 (93%)	102 (86%)	14 (12%)	2 (2%)	7	36
17	b	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
18	c	112/115 (97%)	104 (93%)	8 (7%)	0	100	100
19	d	115/118 (98%)	115 (100%)	0	0	100	100
20	e	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	12	45
21	f	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	14	48
22	g	91/100 (91%)	80 (88%)	9 (10%)	2 (2%)	5	31
23	h	100/104 (96%)	84 (84%)	14 (14%)	2 (2%)	6	33
24	i	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
25	j	73/85 (86%)	71 (97%)	2 (3%)	0	100	100
26	k	75/78 (96%)	71 (95%)	3 (4%)	1 (1%)	9	41
27	l	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
28	m	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
29	n	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	34
30	o	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
31	p	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
32	q	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	7	37
33	r	36/55 (66%)	35 (97%)	1 (3%)	0	100	100
35	L	53/70 (76%)	45 (85%)	7 (13%)	1 (2%)	6	34
36	C	130/223 (58%)	123 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	1	216/239 (90%)	187 (87%)	28 (13%)	1 (0%)	24	60
39	2	204/218 (94%)	186 (91%)	16 (8%)	2 (1%)	12	45
40	3	203/206 (98%)	182 (90%)	21 (10%)	0	100	100
41	4	148/162 (91%)	116 (78%)	30 (20%)	2 (1%)	9	39
42	5	98/131 (75%)	81 (83%)	11 (11%)	6 (6%)	1	16
43	6	140/156 (90%)	130 (93%)	10 (7%)	0	100	100
44	7	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
45	8	125/130 (96%)	103 (82%)	20 (16%)	2 (2%)	7	37
46	9	96/103 (93%)	84 (88%)	9 (9%)	3 (3%)	3	26
47	D	115/129 (89%)	102 (89%)	13 (11%)	0	100	100
48	E	121/124 (98%)	104 (86%)	15 (12%)	2 (2%)	7	36
49	F	112/118 (95%)	103 (92%)	8 (7%)	1 (1%)	14	48
50	G	92/101 (91%)	77 (84%)	14 (15%)	1 (1%)	11	44
51	H	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
52	I	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	9	41
53	J	78/84 (93%)	66 (85%)	9 (12%)	3 (4%)	2	22
54	K	53/75 (71%)	49 (92%)	3 (6%)	1 (2%)	6	34
55	t	77/92 (84%)	73 (95%)	4 (5%)	0	100	100
56	u	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	10	42
57	v	49/88 (56%)	41 (84%)	7 (14%)	1 (2%)	6	33
All	All	5826/6442 (90%)	5264 (90%)	503 (9%)	59 (1%)	15	45

All (59) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	P	239	ASN
10	U	72	ILE
14	Y	36	LYS
15	Z	58	LYS
20	e	53	PHE
29	n	55	ILE
32	q	32	ILE
42	5	53	LYS
46	9	58	ASN
52	I	44	SER

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Mol	Chain	Res	Type
53	J	70	THR
57	v	11	PRO
10	U	41	LYS
15	Z	59	ARG
16	a	3	HIS
39	2	81	GLY
42	5	56	LYS
42	5	91	ARG
45	8	55	VAL
48	E	23	ALA
53	J	18	GLU
56	u	69	LYS
5	P	235	GLY
15	Z	39	GLY
22	g	78	SER
23	h	99	ASN
26	k	3	ARG
39	2	80	LYS
42	5	54	LEU
42	5	94	HIS
46	9	43	PRO
48	E	78	SER
53	J	71	LYS
54	K	48	ARG
5	P	10	SER
5	P	238	ARG
6	Q	149	ASN
8	S	175	PHE
10	U	35	LYS
13	X	93	GLN
14	Y	29	LYS
14	Y	30	THR
14	Y	31	GLY
15	Z	69	PRO
22	g	77	ARG
35	L	3	LYS
41	4	51	GLY
42	5	86	ARG
49	F	66	GLU
16	a	88	ALA
21	f	64	ALA
23	h	53	ASN

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Mol	Chain	Res	Type
38	1	194	ASP
41	4	90	THR
50	G	4	GLN
15	Z	87	GLY
46	9	42	LEU
45	8	10	GLY
13	X	119	ALA

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	s	34/158 (22%)	34 (100%)	0	100	100
5	P	216/218 (99%)	213 (99%)	3 (1%)	59	71
6	Q	164/164 (100%)	159 (97%)	5 (3%)	36	57
7	R	165/165 (100%)	162 (98%)	3 (2%)	51	67
8	S	148/150 (99%)	147 (99%)	1 (1%)	76	79
9	T	137/138 (99%)	137 (100%)	0	100	100
10	U	114/114 (100%)	109 (96%)	5 (4%)	25	48
11	V	109/110 (99%)	109 (100%)	0	100	100
12	W	116/116 (100%)	115 (99%)	1 (1%)	70	76
13	X	103/104 (99%)	101 (98%)	2 (2%)	50	67
14	Y	102/103 (99%)	100 (98%)	2 (2%)	48	66
15	Z	109/109 (100%)	108 (99%)	1 (1%)	70	76
16	a	100/102 (98%)	98 (98%)	2 (2%)	48	66
17	b	86/87 (99%)	85 (99%)	1 (1%)	63	73
18	c	98/100 (98%)	94 (96%)	4 (4%)	27	49
19	d	89/90 (99%)	87 (98%)	2 (2%)	45	64
20	e	84/84 (100%)	83 (99%)	1 (1%)	63	73
21	f	93/93 (100%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	g	80/85 (94%)	79 (99%)	1 (1%)	61	72
23	h	83/85 (98%)	81 (98%)	2 (2%)	43	63
24	i	78/78 (100%)	77 (99%)	1 (1%)	61	72
25	j	56/62 (90%)	55 (98%)	1 (2%)	51	67
26	k	67/68 (98%)	67 (100%)	0	100	100
27	l	55/55 (100%)	54 (98%)	1 (2%)	51	67
28	m	48/49 (98%)	48 (100%)	0	100	100
29	n	47/48 (98%)	46 (98%)	1 (2%)	47	65
30	o	45/49 (92%)	45 (100%)	0	100	100
31	p	38/38 (100%)	38 (100%)	0	100	100
32	q	51/52 (98%)	49 (96%)	2 (4%)	28	50
33	r	34/50 (68%)	33 (97%)	1 (3%)	37	58
35	L	48/63 (76%)	48 (100%)	0	100	100
36	C	110/174 (63%)	109 (99%)	1 (1%)	70	76
38	1	180/198 (91%)	179 (99%)	1 (1%)	78	81
39	2	170/178 (96%)	167 (98%)	3 (2%)	51	67
40	3	172/173 (99%)	170 (99%)	2 (1%)	63	73
41	4	113/123 (92%)	107 (95%)	6 (5%)	20	44
42	5	87/112 (78%)	87 (100%)	0	100	100
43	6	119/129 (92%)	118 (99%)	1 (1%)	73	77
44	7	104/105 (99%)	101 (97%)	3 (3%)	37	58
45	8	105/107 (98%)	104 (99%)	1 (1%)	68	76
46	9	86/90 (96%)	85 (99%)	1 (1%)	63	73
47	D	90/98 (92%)	89 (99%)	1 (1%)	65	74
48	E	103/104 (99%)	103 (100%)	0	100	100
49	F	92/96 (96%)	90 (98%)	2 (2%)	45	64
50	G	79/83 (95%)	79 (100%)	0	100	100
51	H	75/77 (97%)	75 (100%)	0	100	100
52	I	65/65 (100%)	64 (98%)	1 (2%)	57	70
53	J	74/77 (96%)	73 (99%)	1 (1%)	59	71
54	K	48/66 (73%)	47 (98%)	1 (2%)	47	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	t	70/80 (88%)	66 (94%)	4 (6%)	18	42
56	u	65/66 (98%)	65 (100%)	0	100	100
57	v	43/76 (57%)	37 (86%)	6 (14%)	3	17
All	All	4847/5264 (92%)	4769 (98%)	78 (2%)	54	70

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	P	141	VAL
5	P	165	VAL
5	P	218	PRO
6	Q	48	ILE
6	Q	73	VAL
6	Q	177	VAL
6	Q	202	ILE
6	Q	205	PRO
7	R	69	ARG
7	R	149	ILE
7	R	163	ASN
8	S	31	VAL
10	U	27	ARG
10	U	44	ILE
10	U	50	ARG
10	U	55	GLU
10	U	70	GLU
12	W	57	LEU
13	X	58	LEU
13	X	86	LEU
14	Y	77	ILE
14	Y	94	THR
15	Z	128	THR
16	a	50	PRO
16	a	70	THR
17	b	3	LYS
18	c	32	VAL
18	c	53	ARG
18	c	73	VAL
18	c	93	ARG
19	d	16	LYS
19	d	33	ARG
20	e	49	ILE

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Mol	Chain	Res	Type
22	g	32	LEU
23	h	28	VAL
23	h	68	SER
24	i	65	VAL
25	j	41	ARG
27	l	6	LEU
29	n	28	LEU
32	q	2	PRO
32	q	32	ILE
33	r	26	ILE
36	C	33	LEU
38	1	207	ILE
39	2	55	ILE
39	2	75	ILE
39	2	200	VAL
40	3	5	LEU
40	3	143	VAL
41	4	15	LEU
41	4	115	LEU
41	4	120	VAL
41	4	123	VAL
41	4	141	ILE
41	4	157	ARG
43	6	25	LYS
44	7	51	VAL
44	7	121	LEU
44	7	125	ILE
45	8	120	LYS
46	9	17	LEU
47	D	31	ILE
49	F	25	VAL
49	F	98	ARG
52	I	19	VAL
53	J	61	ILE
54	K	21	ILE
55	t	5	LEU
55	t	11	ILE
55	t	49	ILE
55	t	58	VAL
57	v	4	ILE
57	v	5	LYS
57	v	6	VAL

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Mol	Chain	Res	Type
57	v	16	LEU
57	v	20	LYS
57	v	29	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (68) such sidechains are listed below:

Mol	Chain	Res	Type
2	s	126	HIS
5	P	53	HIS
5	P	86	ASN
5	P	260	ASN
6	Q	32	ASN
6	Q	49	GLN
6	Q	149	ASN
6	Q	150	GLN
7	R	136	GLN
7	R	163	ASN
7	R	165	HIS
9	T	22	GLN
9	T	73	ASN
9	T	143	GLN
10	U	2	GLN
10	U	11	ASN
10	U	135	HIS
11	V	12	GLN
12	W	40	HIS
12	W	86	GLN
16	a	73	ASN
18	c	12	GLN
18	c	15	GLN
18	c	52	ASN
19	d	37	GLN
20	e	12	HIS
21	f	15	GLN
24	i	51	GLN
26	k	36	HIS
29	n	6	ASN
29	n	38	HIS
30	o	19	HIS
35	L	20	ASN
36	C	57	GLN
36	C	67	HIS

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Mol	Chain	Res	Type
36	C	172	HIS
36	C	188	ASN
38	1	15	HIS
38	1	177	ASN
38	1	203	ASN
39	2	8	ASN
39	2	123	GLN
39	2	190	HIS
41	4	73	ASN
41	4	89	HIS
41	4	121	HIS
42	5	11	HIS
42	5	55	HIS
43	6	28	ASN
43	6	148	ASN
45	8	32	GLN
45	8	50	GLN
46	9	56	HIS
46	9	58	ASN
47	D	118	HIS
49	F	8	ASN
50	G	49	GLN
50	G	66	GLN
51	H	35	GLN
51	H	37	ASN
52	I	63	GLN
53	J	31	HIS
54	K	52	GLN
54	K	54	GLN
55	t	56	GLN
56	u	20	HIS
56	u	48	GLN
56	u	78	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	72/73 (98%)	20 (27%)	8 (11%)
3	M	74/75 (98%)	11 (14%)	0
34	N	2894/2903 (99%)	521 (18%)	34 (1%)
37	0	1531/1539 (99%)	277 (18%)	22 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	O	117/120 (97%)	21 (17%)	1 (0%)
All	All	4688/4710 (99%)	850 (18%)	65 (1%)

All (850) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	C
1	A	14	A
1	A	16	U
1	A	17	C
1	A	18	G
1	A	19	G
1	A	20	U
1	A	21	A
1	A	22	G
1	A	36	A
1	A	45	U
1	A	46	G
1	A	47	U
1	A	48	C
1	A	52	G
1	A	60	U
1	A	61	C
1	A	62	C
1	A	63	G
1	A	73	A
3	M	9	C
3	M	10	G
3	M	15	G
3	M	16	C
3	M	17	G
3	M	19	U
3	M	20	A
3	M	42	G
3	M	47	C
3	M	74	C
3	M	75	A
4	O	13	G
4	O	25	U
4	O	31	C
4	O	35	C
4	O	41	G

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Mol	Chain	Res	Type
4	O	44	G
4	O	45	A
4	O	51	G
4	O	53	A
4	O	56	G
4	O	57	A
4	O	64	G
4	O	66	A
4	O	67	G
4	O	88	C
4	O	89	U
4	O	90	C
4	O	91	C
4	O	99	A
4	O	108	A
4	O	109	A
34	N	10	A
34	N	23	G
34	N	28	A
34	N	35	G
34	N	36	G
34	N	42	A
34	N	46	G
34	N	51	G
34	N	55	G
34	N	60	G
34	N	61	C
34	N	63	A
34	N	71	A
34	N	74	A
34	N	75	G
34	N	84	A
34	N	96	C
34	N	101	A
34	N	102	U
34	N	103	A
34	N	118	A
34	N	119	A
34	N	120	U
34	N	125	A
34	N	138	U
34	N	139	U

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Mol	Chain	Res	Type
34	N	140	C
34	N	141	G
34	N	142	A
34	N	162	U
34	N	163	C
34	N	165	A
34	N	166	U
34	N	188	G
34	N	196	A
34	N	199	A
34	N	201	C
34	N	215	G
34	N	216	A
34	N	221	A
34	N	222	A
34	N	223	A
34	N	224	U
34	N	228	C
34	N	241	A
34	N	242	G
34	N	243	U
34	N	248	G
34	N	255	A
34	N	265	A
34	N	266	G
34	N	267	C
34	N	271	G
34	N	272	A
34	N	276	U
34	N	278	A
34	N	281	C
34	N	284	U
34	N	294	A
34	N	301	G
34	N	311	A
34	N	323	C
34	N	329	G
34	N	330	A
34	N	332	A
34	N	346	A
34	N	361	G
34	N	362	A

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Mol	Chain	Res	Type
34	N	371	A
34	N	372	G
34	N	373	U
34	N	386	G
34	N	396	G
34	N	399	U
34	N	403	U
34	N	404	A
34	N	405	U
34	N	406	G
34	N	411	G
34	N	412	A
34	N	421	C
34	N	422	A
34	N	424	G
34	N	435	C
34	N	447	A
34	N	455	C
34	N	456	C
34	N	457	A
34	N	467	G
34	N	471	A
34	N	473	G
34	N	481	G
34	N	491	G
34	N	501	A
34	N	504	A
34	N	505	A
34	N	509	C
34	N	513	A
34	N	529	A
34	N	531	C
34	N	532	A
34	N	543	G
34	N	544	C
34	N	546	U
34	N	548	G
34	N	549	G
34	N	550	C
34	N	556	A
34	N	563	A
34	N	573	U

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Mol	Chain	Res	Type
34	N	575	A
34	N	578	G
34	N	586	A
34	N	603	A
34	N	613	A
34	N	614	A
34	N	616	A
34	N	622	G
34	N	627	A
34	N	637	A
34	N	645	C
34	N	646	U
34	N	647	G
34	N	648	G
34	N	654	A
34	N	655	A
34	N	669	G
34	N	670	A
34	N	671	C
34	N	677	A
34	N	686	U
34	N	695	G
34	N	696	G
34	N	717	C
34	N	729	G
34	N	730	A
34	N	738	G
34	N	747	U
34	N	764	A
34	N	765	C
34	N	775	G
34	N	776	G
34	N	782	A
34	N	783	A
34	N	784	G
34	N	785	G
34	N	792	A
34	N	800	A
34	N	805	G
34	N	806	C
34	N	812	C
34	N	819	A

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Mol	Chain	Res	Type
34	N	827	U
34	N	828	U
34	N	829	A
34	N	845	A
34	N	846	U
34	N	858	G
34	N	860	U
34	N	866	A
34	N	869	G
34	N	878	A
34	N	885	C
34	N	896	A
34	N	897	C
34	N	907	G
34	N	910	A
34	N	914	G
34	N	919	U
34	N	932	U
34	N	941	A
34	N	945	A
34	N	946	C
34	N	953	G
34	N	961	C
34	N	973	A
34	N	974	G
34	N	983	A
34	N	985	C
34	N	989	G
34	N	995	C
34	N	996	A
34	N	997	G
34	N	1004	U
34	N	1012	U
34	N	1013	C
34	N	1020	A
34	N	1021	A
34	N	1022	G
34	N	1023	U
34	N	1025	G
34	N	1026	G
34	N	1033	U
34	N	1046	A

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Mol	Chain	Res	Type
34	N	1047	G
34	N	1057	A
34	N	1060	U
34	N	1062	G
34	N	1064	C
34	N	1066	U
34	N	1067	A
34	N	1068	G
34	N	1070	A
34	N	1077	A
34	N	1082	U
34	N	1083	U
34	N	1088	A
34	N	1089	A
34	N	1090	A
34	N	1094	U
34	N	1096	A
34	N	1097	U
34	N	1100	C
34	N	1104	C
34	N	1110	G
34	N	1111	A
34	N	1112	G
34	N	1119	U
34	N	1122	G
34	N	1130	U
34	N	1132	U
34	N	1133	A
34	N	1135	C
34	N	1136	G
34	N	1141	U
34	N	1142	A
34	N	1143	A
34	N	1155	A
34	N	1168	G
34	N	1171	G
34	N	1173	U
34	N	1174	U
34	N	1175	A
34	N	1180	U
34	N	1186	G
34	N	1195	G

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Mol	Chain	Res	Type
34	N	1204	A
34	N	1205	A
34	N	1206	G
34	N	1210	G
34	N	1212	G
34	N	1237	A
34	N	1238	G
34	N	1250	G
34	N	1251	C
34	N	1253	A
34	N	1256	G
34	N	1257	C
34	N	1265	A
34	N	1266	G
34	N	1268	A
34	N	1271	G
34	N	1272	A
34	N	1275	A
34	N	1300	G
34	N	1301	A
34	N	1321	A
34	N	1329	U
34	N	1332	G
34	N	1345	C
34	N	1352	U
34	N	1365	A
34	N	1368	G
34	N	1376	C
34	N	1379	U
34	N	1383	A
34	N	1386	C
34	N	1395	A
34	N	1403	A
34	N	1416	G
34	N	1419	A
34	N	1420	A
34	N	1421	G
34	N	1427	A
34	N	1428	C
34	N	1434	A
34	N	1437	C
34	N	1453	A

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Mol	Chain	Res	Type
34	N	1458	U
34	N	1461	C
34	N	1478	G
34	N	1482	G
34	N	1504	A
34	N	1508	A
34	N	1509	A
34	N	1515	A
34	N	1524	G
34	N	1529	G
34	N	1535	A
34	N	1536	C
34	N	1537	G
34	N	1538	G
34	N	1554	U
34	N	1565	C
34	N	1566	A
34	N	1569	A
34	N	1578	U
34	N	1583	A
34	N	1584	U
34	N	1585	C
34	N	1587	G
34	N	1607	C
34	N	1608	A
34	N	1610	A
34	N	1613	G
34	N	1622	G
34	N	1647	U
34	N	1648	U
34	N	1651	G
34	N	1674	G
34	N	1675	C
34	N	1676	A
34	N	1698	A
34	N	1699	G
34	N	1713	A
34	N	1715	G
34	N	1728	C
34	N	1729	U
34	N	1730	C
34	N	1733	G

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Mol	Chain	Res	Type
34	N	1738	G
34	N	1757	A
34	N	1758	U
34	N	1760	C
34	N	1764	C
34	N	1773	A
34	N	1784	A
34	N	1787	A
34	N	1800	C
34	N	1801	A
34	N	1802	A
34	N	1808	A
34	N	1811	G
34	N	1816	C
34	N	1829	A
34	N	1833	C
34	N	1835	G
34	N	1857	G
34	N	1869	G
34	N	1870	C
34	N	1900	A
34	N	1901	A
34	N	1906	G
34	N	1913	A
34	N	1919	A
34	N	1927	A
34	N	1929	G
34	N	1930	G
34	N	1931	U
34	N	1938	A
34	N	1955	U
34	N	1964	G
34	N	1967	C
34	N	1970	A
34	N	1971	U
34	N	1972	G
34	N	1991	U
34	N	1993	U
34	N	1997	C
34	N	2004	G
34	N	2006	C
34	N	2020	A

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Mol	Chain	Res	Type
34	N	2022	U
34	N	2023	C
34	N	2031	A
34	N	2033	A
34	N	2043	C
34	N	2046	G
34	N	2055	C
34	N	2056	G
34	N	2060	A
34	N	2061	G
34	N	2062	A
34	N	2063	C
34	N	2069	G
34	N	2072	C
34	N	2077	A
34	N	2092	U
34	N	2094	A
34	N	2097	A
34	N	2099	U
34	N	2110	G
34	N	2111	U
34	N	2112	G
34	N	2113	U
34	N	2118	U
34	N	2119	A
34	N	2132	U
34	N	2133	G
34	N	2145	C
34	N	2147	A
34	N	2162	G
34	N	2171	A
34	N	2172	U
34	N	2173	A
34	N	2190	G
34	N	2191	A
34	N	2194	U
34	N	2198	A
34	N	2200	C
34	N	2203	U
34	N	2204	G
34	N	2211	A
34	N	2212	A

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Mol	Chain	Res	Type
34	N	2214	C
34	N	2225	A
34	N	2226	C
34	N	2238	G
34	N	2239	G
34	N	2266	A
34	N	2278	A
34	N	2279	G
34	N	2283	C
34	N	2286	G
34	N	2287	A
34	N	2288	A
34	N	2297	A
34	N	2305	U
34	N	2307	G
34	N	2309	A
34	N	2312	U
34	N	2325	G
34	N	2333	A
34	N	2334	U
34	N	2345	G
34	N	2347	C
34	N	2350	C
34	N	2354	C
34	N	2357	G
34	N	2361	G
34	N	2383	G
34	N	2385	C
34	N	2391	G
34	N	2402	U
34	N	2403	C
34	N	2406	A
34	N	2407	A
34	N	2422	C
34	N	2423	U
34	N	2425	A
34	N	2426	A
34	N	2427	C
34	N	2429	G
34	N	2430	A
34	N	2431	U
34	N	2435	A

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Mol	Chain	Res	Type
34	N	2441	U
34	N	2448	A
34	N	2470	G
34	N	2476	A
34	N	2498	C
34	N	2502	G
34	N	2503	A
34	N	2504	U
34	N	2505	G
34	N	2518	A
34	N	2520	C
34	N	2529	G
34	N	2535	G
34	N	2547	A
34	N	2554	U
34	N	2566	A
34	N	2567	G
34	N	2572	A
34	N	2573	C
34	N	2574	G
34	N	2578	G
34	N	2585	U
34	N	2602	A
34	N	2603	G
34	N	2609	U
34	N	2613	U
34	N	2615	U
34	N	2629	U
34	N	2630	G
34	N	2636	C
34	N	2645	G
34	N	2646	C
34	N	2655	G
34	N	2656	U
34	N	2661	G
34	N	2663	G
34	N	2682	A
34	N	2689	U
34	N	2690	U
34	N	2714	G
34	N	2716	C
34	N	2718	G

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Mol	Chain	Res	Type
34	N	2724	U
34	N	2727	A
34	N	2733	A
34	N	2748	A
34	N	2751	G
34	N	2752	C
34	N	2765	A
34	N	2776	A
34	N	2777	G
34	N	2778	A
34	N	2779	U
34	N	2791	G
34	N	2792	A
34	N	2798	U
34	N	2801	G
34	N	2818	U
34	N	2820	A
34	N	2833	U
34	N	2834	G
34	N	2836	U
34	N	2849	U
34	N	2850	A
34	N	2859	G
34	N	2867	G
34	N	2868	A
34	N	2872	A
34	N	2873	A
34	N	2874	C
34	N	2880	C
34	N	2884	U
34	N	2887	A
34	N	2891	U
34	N	2903	U
37	0	4	U
37	0	6	G
37	0	9	G
37	0	32	A
37	0	39	G
37	0	44	A
37	0	47	C
37	0	48	C
37	0	50	A

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Mol	Chain	Res	Type
37	0	51	A
37	0	52	C
37	0	58	C
37	0	65	A
37	0	69	G
37	0	71	A
37	0	72	A
37	0	83	C
37	0	84	U
37	0	85	U
37	0	86	G
37	0	87	C
37	0	92	U
37	0	97	G
37	0	108	G
37	0	115	G
37	0	116	A
37	0	122	G
37	0	130	A
37	0	141	G
37	0	143	A
37	0	144	G
37	0	149	A
37	0	156	C
37	0	163	C
37	0	174	A
37	0	177	G
37	0	182	A
37	0	183	C
37	0	184	G
37	0	197	A
37	0	209	U
37	0	210	C
37	0	211	G
37	0	226	G
37	0	245	U
37	0	247	G
37	0	251	G
37	0	266	G
37	0	267	C
37	0	280	C
37	0	281	G

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Mol	Chain	Res	Type
37	0	289	G
37	0	298	A
37	0	306	A
37	0	321	A
37	0	328	C
37	0	332	G
37	0	347	G
37	0	351	G
37	0	352	C
37	0	354	G
37	0	358	U
37	0	367	U
37	0	372	C
37	0	375	U
37	0	384	G
37	0	388	G
37	0	389	A
37	0	397	A
37	0	398	U
37	0	406	G
37	0	412	A
37	0	413	G
37	0	421	U
37	0	422	C
37	0	423	G
37	0	424	G
37	0	429	U
37	0	430	A
37	0	439	U
37	0	451	A
37	0	458	U
37	0	459	A
37	0	467	U
37	0	468	A
37	0	474	G
37	0	478	A
37	0	479	U
37	0	481	G
37	0	484	G
37	0	485	U
37	0	486	U
37	0	495	A

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Mol	Chain	Res	Type
37	0	497	G
37	0	511	C
37	0	518	C
37	0	519	C
37	0	521	G
37	0	527	G
37	0	531	U
37	0	532	A
37	0	533	A
37	0	547	A
37	0	559	A
37	0	562	U
37	0	572	A
37	0	573	A
37	0	576	C
37	0	595	A
37	0	596	A
37	0	607	A
37	0	633	G
37	0	639	G
37	0	650	G
37	0	652	U
37	0	665	A
37	0	675	A
37	0	688	G
37	0	695	A
37	0	701	U
37	0	702	A
37	0	703	G
37	0	718	A
37	0	721	G
37	0	723	U
37	0	724	G
37	0	731	G
37	0	734	G
37	0	747	A
37	0	755	G
37	0	777	A
37	0	793	U
37	0	794	A
37	0	813	U
37	0	815	A

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Mol	Chain	Res	Type
37	0	817	C
37	0	818	G
37	0	819	A
37	0	821	G
37	0	828	U
37	0	832	G
37	0	836	G
37	0	841	C
37	0	842	U
37	0	843	U
37	0	844	G
37	0	846	G
37	0	849	G
37	0	859	G
37	0	864	A
37	0	885	G
37	0	889	A
37	0	890	G
37	0	891	U
37	0	902	G
37	0	914	A
37	0	926	G
37	0	934	C
37	0	935	A
37	0	960	U
37	0	965	U
37	0	966	G
37	0	969	A
37	0	971	G
37	0	972	C
37	0	975	A
37	0	976	G
37	0	977	A
37	0	989	U
37	0	993	G
37	0	999	C
37	0	1000	A
37	0	1004	A
37	0	1008	U
37	0	1009	U
37	0	1017	U
37	0	1018	G

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Mol	Chain	Res	Type
37	0	1020	G
37	0	1022	A
37	0	1024	G
37	0	1025	U
37	0	1026	G
37	0	1027	C
37	0	1030	U
37	0	1031	C
37	0	1032	G
37	0	1043	G
37	0	1044	A
37	0	1053	G
37	0	1056	U
37	0	1065	U
37	0	1085	U
37	0	1092	A
37	0	1094	G
37	0	1095	U
37	0	1101	A
37	0	1125	U
37	0	1130	A
37	0	1132	C
37	0	1136	C
37	0	1137	C
37	0	1138	G
37	0	1139	G
37	0	1140	C
37	0	1146	A
37	0	1158	C
37	0	1159	U
37	0	1168	U
37	0	1171	A
37	0	1182	G
37	0	1183	U
37	0	1184	G
37	0	1190	G
37	0	1196	A
37	0	1200	C
37	0	1201	A
37	0	1202	U
37	0	1212	U
37	0	1213	A

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Mol	Chain	Res	Type
37	0	1227	A
37	0	1238	A
37	0	1253	G
37	0	1256	A
37	0	1257	A
37	0	1258	G
37	0	1260	G
37	0	1261	A
37	0	1274	A
37	0	1275	A
37	0	1278	G
37	0	1280	A
37	0	1281	C
37	0	1287	A
37	0	1297	G
37	0	1298	U
37	0	1300	G
37	0	1301	U
37	0	1302	C
37	0	1305	G
37	0	1317	C
37	0	1318	A
37	0	1319	A
37	0	1320	C
37	0	1322	C
37	0	1323	G
37	0	1331	G
37	0	1332	A
37	0	1340	A
37	0	1346	A
37	0	1347	G
37	0	1348	U
37	0	1353	G
37	0	1363	A
37	0	1364	U
37	0	1370	G
37	0	1379	G
37	0	1383	C
37	0	1394	A
37	0	1400	C
37	0	1419	G
37	0	1422	G

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Mol	Chain	Res	Type
37	0	1433	A
37	0	1441	A
37	0	1446	A
37	0	1451	U
37	0	1452	C
37	0	1487	G
37	0	1492	A
37	0	1494	G
37	0	1497	G
37	0	1503	A
37	0	1506	U
37	0	1517	G
37	0	1519	A
37	0	1529	G
37	0	1530	G
37	0	1531	A

All (65) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	16	U
1	A	19	G
1	A	20	U
1	A	21	A
1	A	44	G
1	A	45	U
1	A	46	G
1	A	60	U
4	O	52	A
34	N	60	G
34	N	227	A
34	N	242	G
34	N	249	C
34	N	372	G
34	N	404	A
34	N	421	C
34	N	446	G
34	N	456	C
34	N	474	G
34	N	503	A
34	N	512	G
34	N	555	G

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Mol	Chain	Res	Type
34	N	670	A
34	N	774	G
34	N	784	G
34	N	859	G
34	N	995	C
34	N	1020	A
34	N	1134	A
34	N	1141	U
34	N	1142	A
34	N	1236	G
34	N	1900	A
34	N	2062	A
34	N	2225	A
34	N	2282	G
34	N	2286	G
34	N	2311	A
34	N	2405	G
34	N	2655	G
34	N	2776	A
34	N	2867	G
34	N	2873	A
37	0	64	G
37	0	85	U
37	0	96	U
37	0	115	G
37	0	388	G
37	0	429	U
37	0	518	C
37	0	595	A
37	0	812	G
37	0	890	G
37	0	965	U
37	0	1124	G
37	0	1145	A
37	0	1182	G
37	0	1190	G
37	0	1201	A
37	0	1300	G
37	0	1345	U
37	0	1347	G
37	0	1491	G
37	0	1493	A

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Mol	Chain	Res	Type
37	0	1528	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

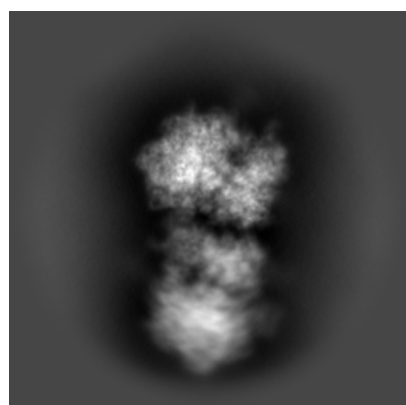
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13952. These allow visual inspection of the internal detail of the map and identification of artifacts.

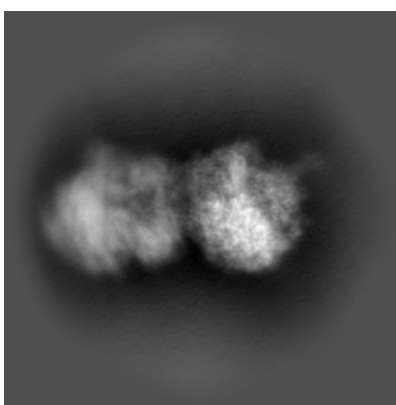
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

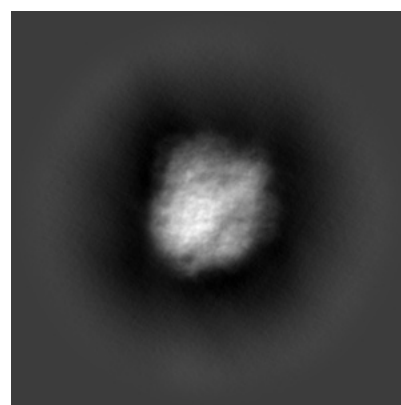
6.1.1 Primary map



X



Y

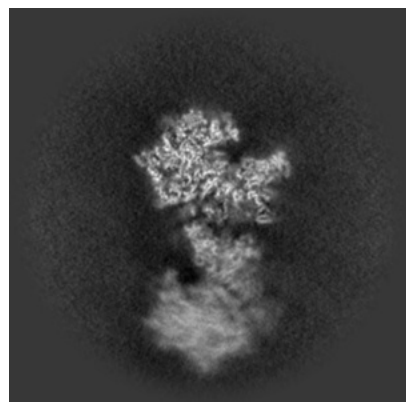


Z

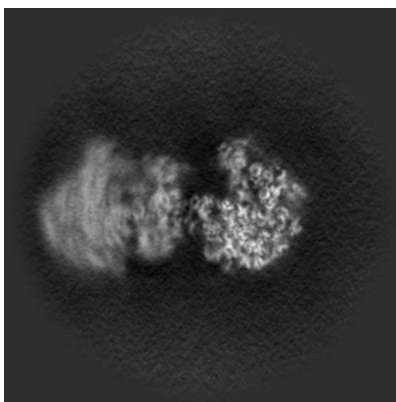
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

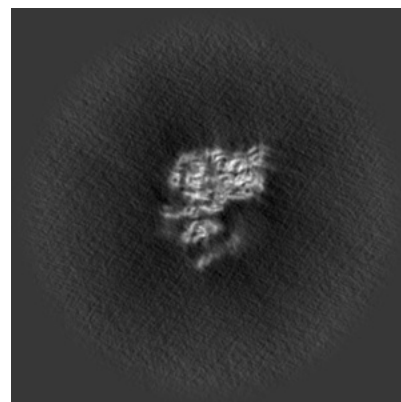
6.2.1 Primary map



X Index: 300



Y Index: 300

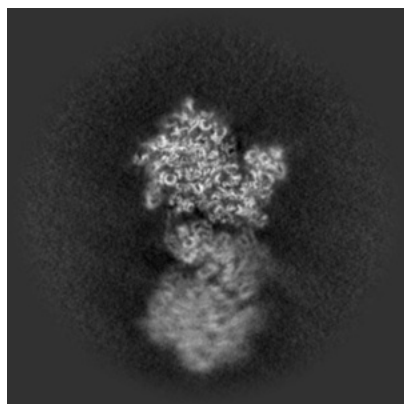


Z Index: 300

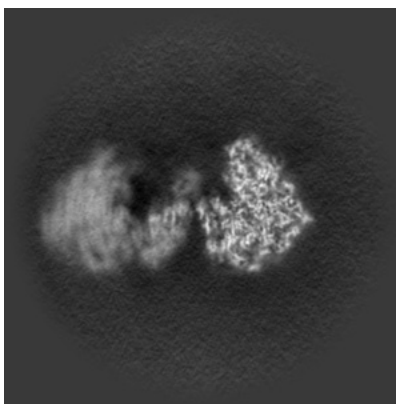
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

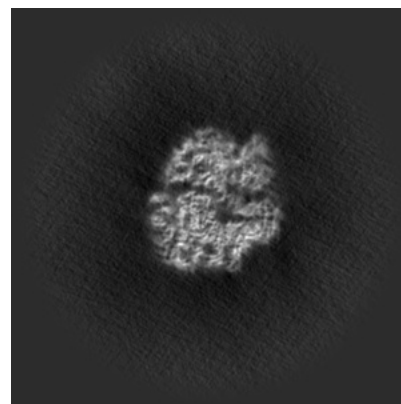
6.3.1 Primary map



X Index: 282



Y Index: 275

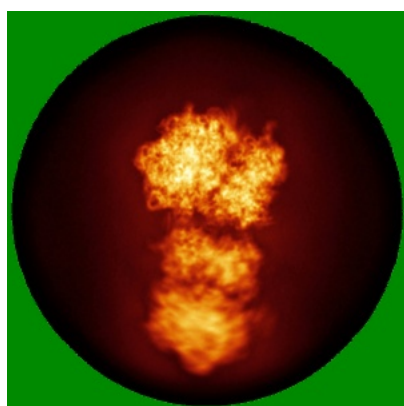


Z Index: 348

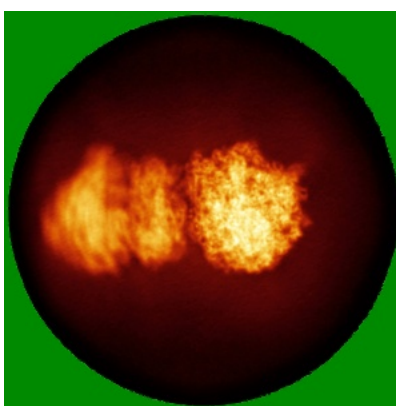
The images above show the largest variance slices of the map in three orthogonal directions.

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

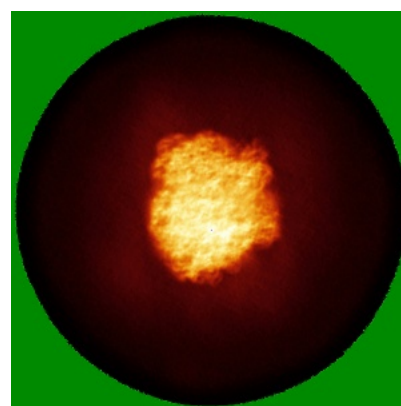
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

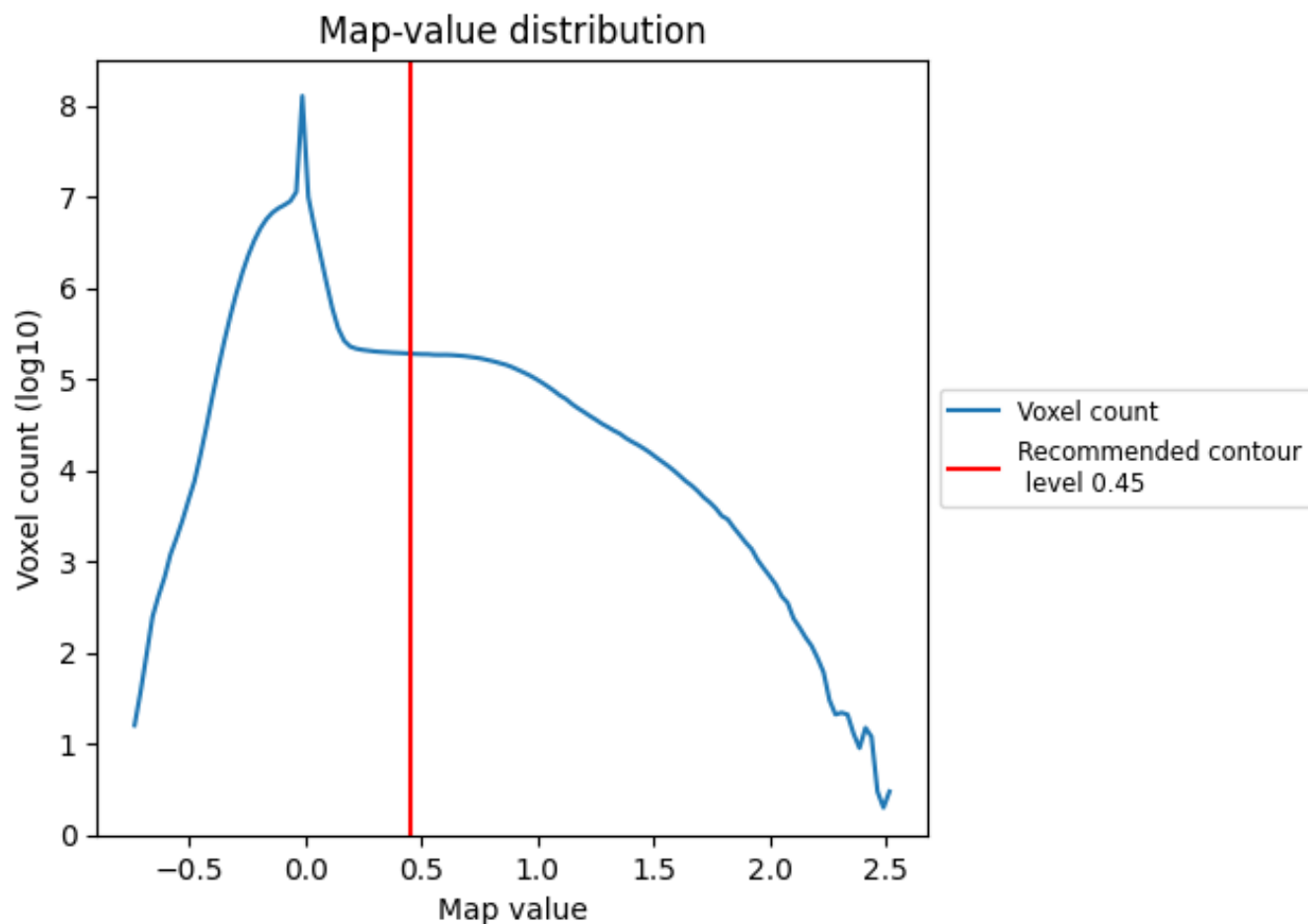
6.6 Mask visualisation

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

7 Map analysis [i](#)

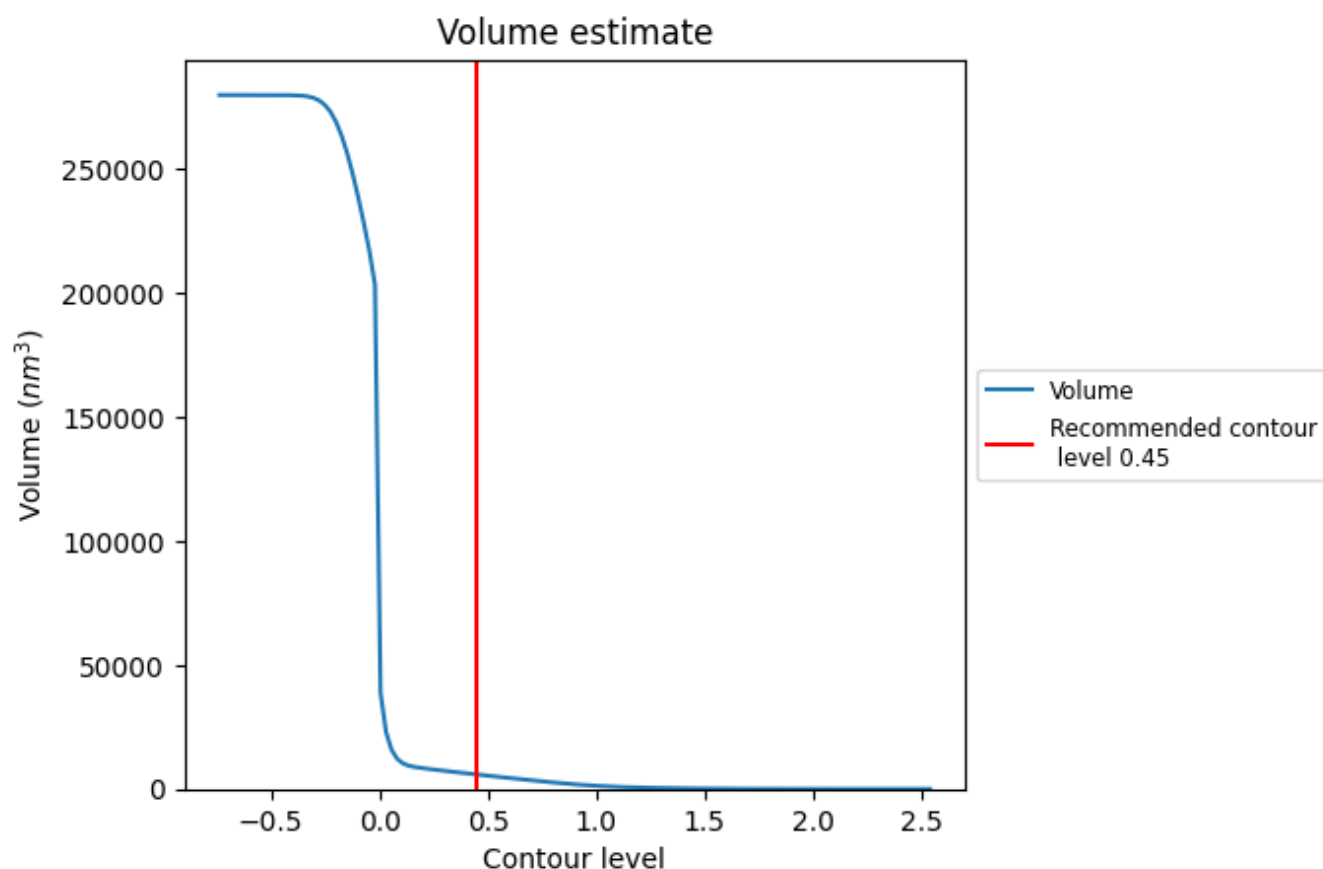
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

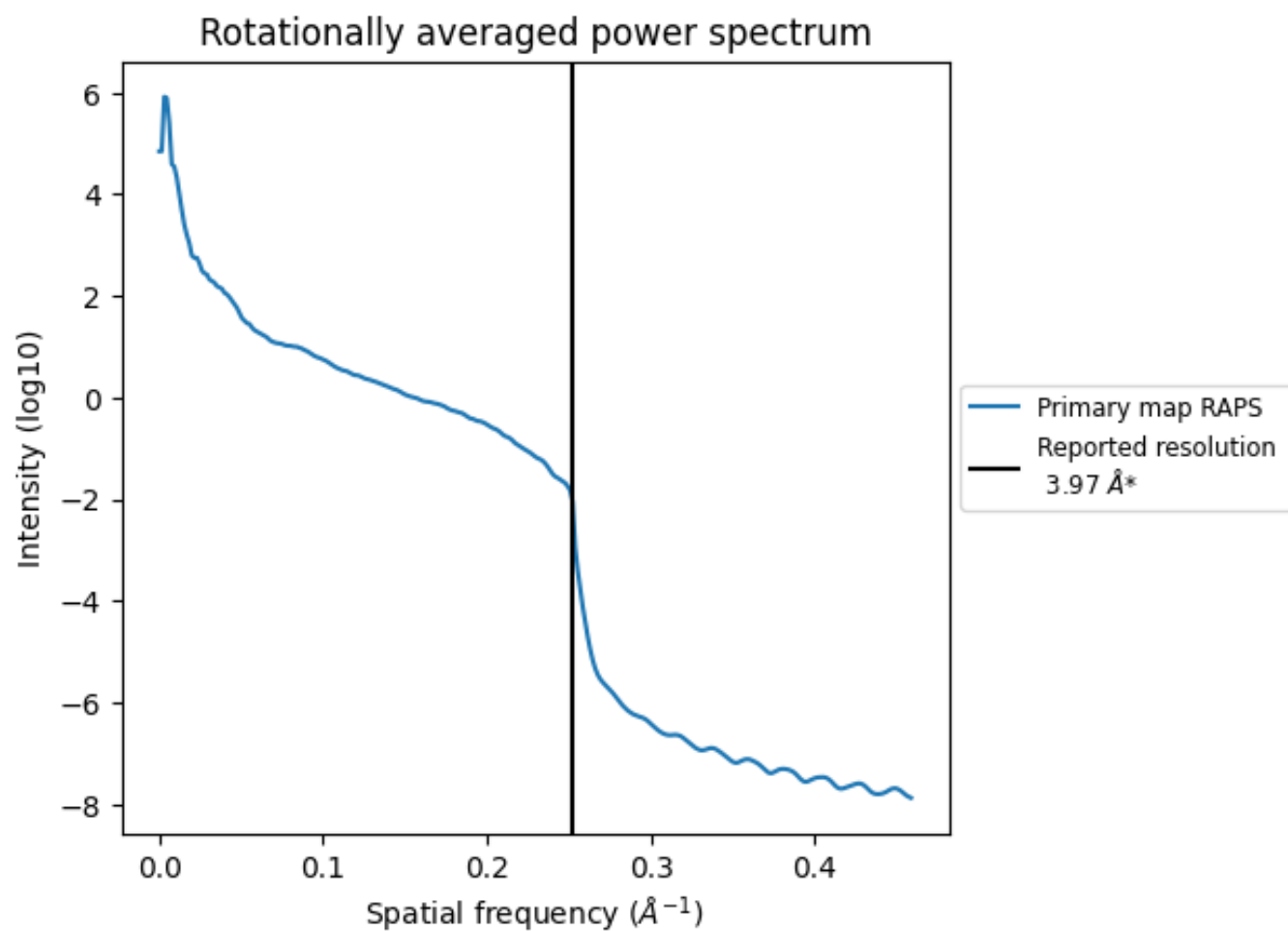
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5826 nm^3 ; this corresponds to an approximate mass of 5263 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.252 Å⁻¹

8 Fourier-Shell correlation

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

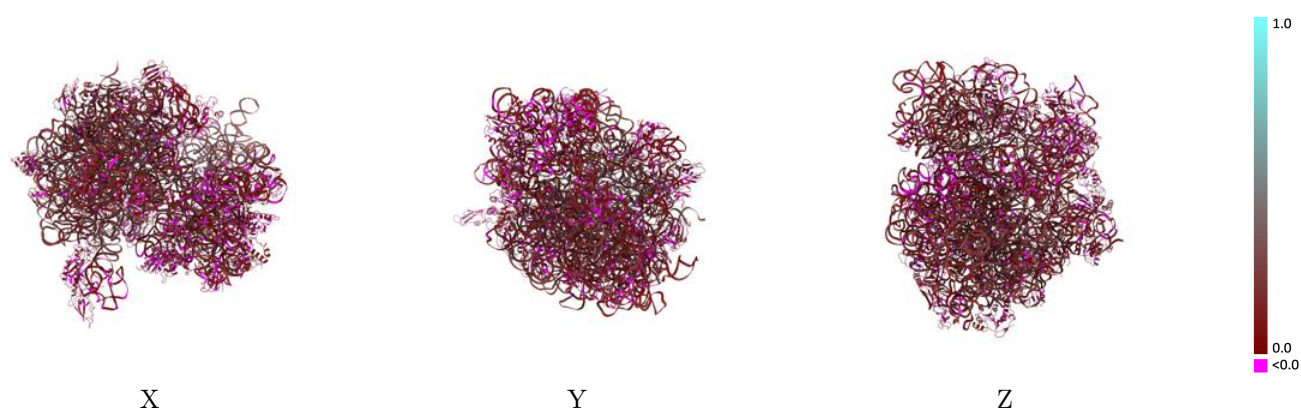
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-13952 and PDB model 7QG8. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)

This section was not generated.

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

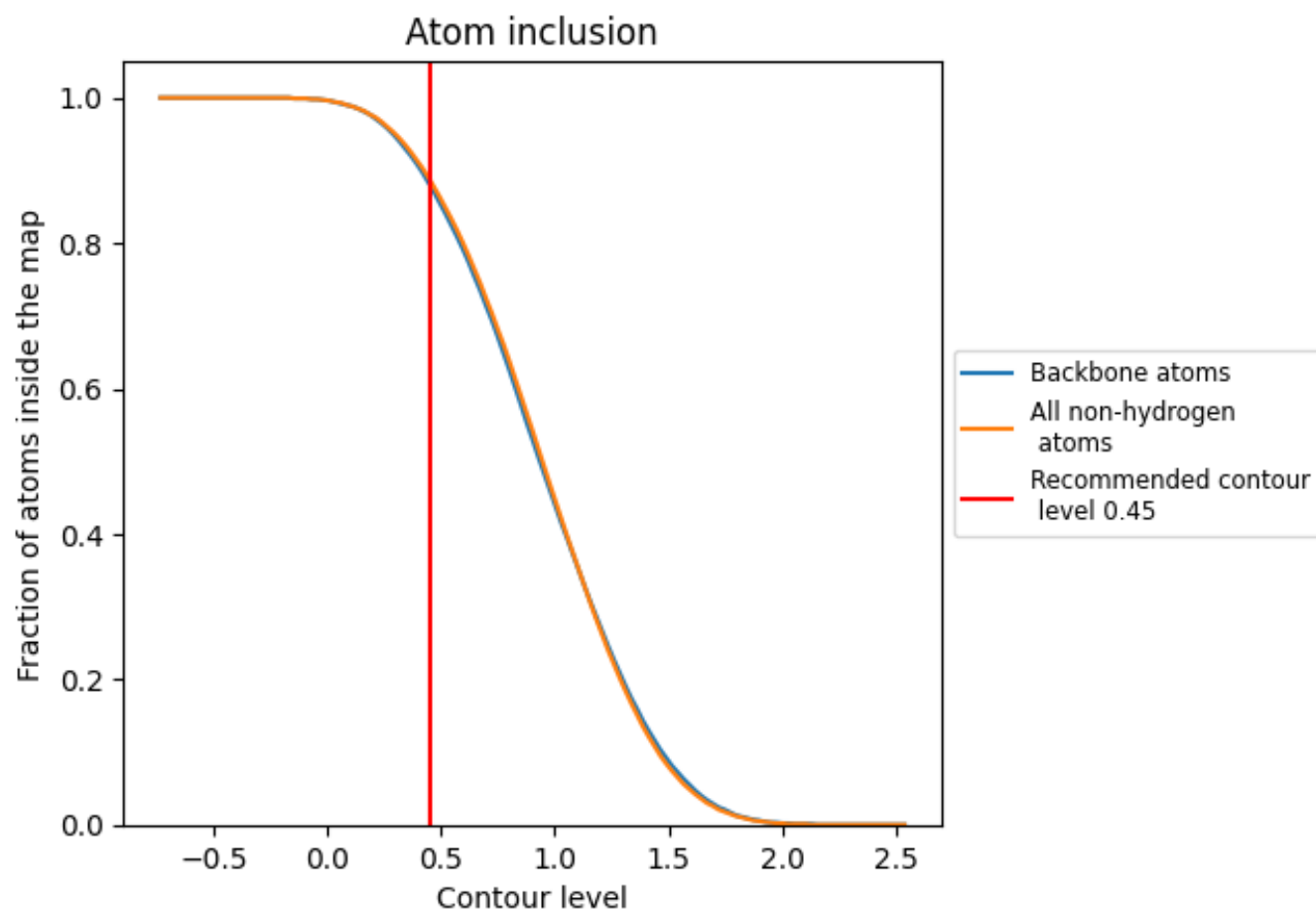


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8870	 0.1450
0	 0.9490	 0.1580
1	 0.5930	 0.1110
2	 0.6140	 0.0610
3	 0.7810	 0.1020
4	 0.9050	 0.1390
5	 0.5230	 0.1150
6	 0.6800	 0.0780
7	 0.8020	 0.1190
8	 0.8100	 0.0840
9	 0.5700	 0.0820
A	 0.7540	 0.1560
C	 0.0970	 0.0690
D	 0.5490	 0.0490
E	 0.8960	 0.0910
F	 0.6170	 0.0710
G	 0.6480	 0.0470
H	 0.8100	 0.1300
I	 0.8750	 0.1250
J	 0.8260	 0.0380
K	 0.6810	 0.1310
L	 0.5070	 0.1250
M	 0.9150	 0.1840
N	 0.9560	 0.1680
O	 0.9550	 0.1550
P	 0.8630	 0.0740
Q	 0.8170	 0.0790
R	 0.7890	 0.1310
S	 0.7900	 0.0960
T	 0.8470	 0.1070
U	 0.3990	 0.1080
V	 0.5640	 0.0520
W	 0.9230	 0.1590
X	 0.5170	 0.0200
Y	 0.8110	 0.1500



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Chain	Atom inclusion	Q-score
Z	 0.8730	 0.1730
a	 0.9130	 0.0930
b	 0.8500	 0.1160
c	 0.7270	 0.0160
d	 0.9130	 0.1470
e	 0.7430	 0.1710
f	 0.8900	 0.1250
g	 0.7700	 0.0810
h	 0.8570	 0.1110
i	 0.8560	 0.1420
j	 0.9820	 0.1180
k	 0.7880	 0.1460
l	 0.6030	 0.1020
m	 0.8900	 0.1580
n	 0.8500	 0.0900
o	 0.8700	 0.1480
p	 0.9660	 0.1100
q	 0.9740	 0.1670
r	 0.9490	 0.1150
s	 0.9480	 0.1080
t	 0.7970	 0.0600
u	 0.7810	 0.1080
v	 0.5870	 0.1390