



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 09:21 AM UTC

PDB ID : 8I9R / pdb_00008i9r
EMDB ID : EMD-35281
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- State 5S RNP
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
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

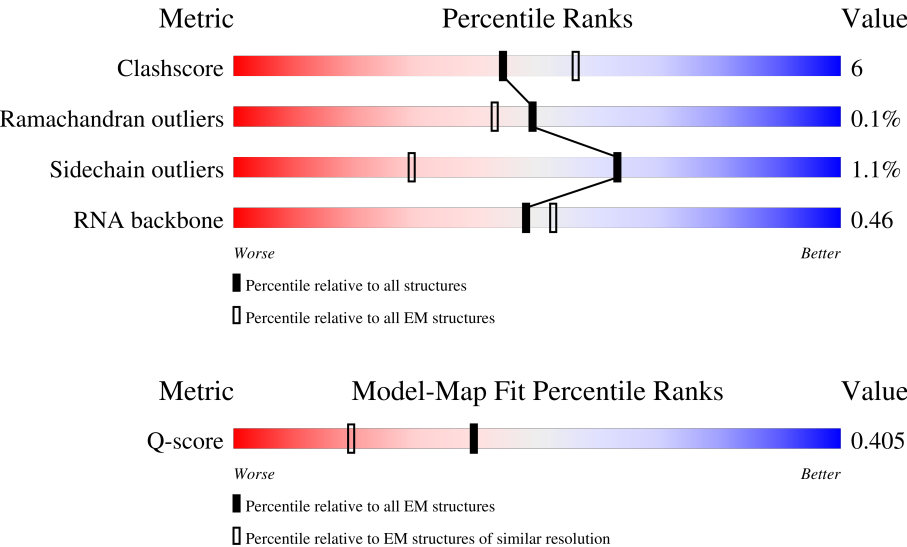
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	C1	3341	8% 36% 22% 39%
2	C2	256	54% 29% 5% 11%
3	CA	316	58% 24% 18%

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Mol	Chain	Length	Quality of chain
4	CB	391	
5	CC	801	
6	CE	598	
7	CH	661	
8	CI	414	
9	CJ	679	
10	CM	249	
10	LF	249	
11	CN	246	
12	CQ	225	
13	CR	237	
14	CU	451	
15	Ch	354	
16	LB	392	
17	LC	365	
18	LE	200	
19	LG	262	
20	LL	213	
21	LM	142	
22	LN	203	
23	LO	204	
24	LP	187	
25	LQ	213	
26	LS	174	
27	LT	160	

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Mol	Chain	Length	Quality of chain
28	LV	139	
29	LY	138	
30	Le	131	
31	Lf	109	
32	Lh	935	
33	Li	110	
34	Lj	95	
35	Cc	282	
36	Cd	436	
37	Ce	336	
38	Cf	570	
39	Cy	350	
40	Cg	478	
41	CP	751	
42	CG	184	
43	Lq	217	
44	Cx	202	
45	LJ	173	
46	LD	304	
47	C4	119	
48	CX	203	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 117417 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 RNA (3341-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	2048	Total	C	N	O	P	0	0
			43814	19561	7931	14274	2048		

- Molecule 2 is a RNA chain called RNA (256-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	228	Total	C	N	O	P	0	0
			4846	2162	864	1592	228		

- Molecule 3 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CA	260	Total	C	N	O	S	0	0
			2144	1371	393	373	7		

- Molecule 4 is a protein called Ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CB	260	Total	C	N	O	S	0	0
			2063	1322	367	371	3		

- Molecule 5 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CC	272	Total	C	N	O	S	0	0
			2258	1438	379	434	7		

- Molecule 6 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CE	463	Total	C	N	O	S	0	0
			3673	2352	643	667	11		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	543	LYS	-	insertion	UNP G0RYU9
CE	544	SER	-	insertion	UNP G0RYU9
CE	545	PHE	-	insertion	UNP G0RYU9
CE	546	GLY	-	insertion	UNP G0RYU9
CE	547	PHE	-	insertion	UNP G0RYU9
CE	548	SER	-	insertion	UNP G0RYU9
CE	549	THR	-	insertion	UNP G0RYU9
CE	550	PRO	-	insertion	UNP G0RYU9
CE	551	PRO	-	insertion	UNP G0RYU9
CE	552	ARG	-	insertion	UNP G0RYU9
CE	553	VAL	-	insertion	UNP G0RYU9
CE	554	ASP	-	insertion	UNP G0RYU9
CE	555	ILE	-	insertion	UNP G0RYU9
CE	556	THR	-	insertion	UNP G0RYU9
CE	557	LEU	-	insertion	UNP G0RYU9
CE	558	SER	-	insertion	UNP G0RYU9
CE	559	ALA	-	insertion	UNP G0RYU9
CE	560	SER	-	insertion	UNP G0RYU9
CE	561	LEU	-	insertion	UNP G0RYU9
CE	562	SER	-	insertion	UNP G0RYU9
CE	563	ARG	-	insertion	UNP G0RYU9
CE	564	ASP	-	insertion	UNP G0RYU9
CE	565	LYS	-	insertion	UNP G0RYU9
CE	566	LYS	-	insertion	UNP G0RYU9
CE	567	PRO	-	insertion	UNP G0RYU9
CE	568	GLN	-	insertion	UNP G0RYU9
CE	569	GLY	-	insertion	UNP G0RYU9
CE	570	ARG	-	insertion	UNP G0RYU9
CE	571	ARG	-	insertion	UNP G0RYU9
CE	572	ALA	-	insertion	UNP G0RYU9
CE	573	TYR	-	insertion	UNP G0RYU9
CE	574	GLY	-	insertion	UNP G0RYU9
CE	575	SER	-	insertion	UNP G0RYU9
CE	576	GLN	-	insertion	UNP G0RYU9
CE	577	PRO	-	insertion	UNP G0RYU9
CE	578	ARG	-	insertion	UNP G0RYU9
CE	579	GLN	-	insertion	UNP G0RYU9
CE	580	GLY	-	insertion	UNP G0RYU9
CE	581	GLY	-	insertion	UNP G0RYU9
CE	582	ARG	-	insertion	UNP G0RYU9
CE	583	TYR	-	insertion	UNP G0RYU9
CE	584	LYS	-	insertion	UNP G0RYU9

- Molecule 7 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CH	108	Total	C	N	O	S	0	0
			891	561	146	183	1		

- Molecule 8 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CI	146	Total	C	N	O	S	0	0
			1196	763	224	204	5		

- Molecule 9 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CJ	380	Total	C	N	O	S	0	0
			3109	2003	547	549	10		

- Molecule 10 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CM	187	Total	C	N	O	S	0	0
			1525	987	278	257	3		
10	LF	240	Total	C	N	O	S	0	0
			1967	1264	368	332	3		

- Molecule 11 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CN	246	Total	C	N	O	S	0	0
			1856	1158	322	369	7		

- Molecule 12 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CQ	112	Total	C	N	O	S	0	0
			960	607	195	148	10		

- Molecule 13 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CR	167	Total	C	N	O	S	0	0
			1354	827	278	247	2		

- Molecule 14 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CU	121	Total	C	N	O	S	0	0
			969	604	179	183	3		

- Molecule 15 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ch	71	Total	C	N	O	S	0	0
			562	350	109	102	1		

- Molecule 16 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LB	341	Total	C	N	O	S	0	0
			2708	1721	493	482	12		

- Molecule 17 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LC	362	Total	C	N	O	S	0	0
			2752	1738	526	479	9		

- Molecule 18 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LE	170	Total	C	N	O	S	0	0
			1338	861	241	233	3		

- Molecule 19 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LG	183	Total	C	N	O	S	0	0
			1470	951	263	252	4		

- Molecule 20 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	117	Total	C	N	O	S	0	0
			964	608	206	148	2		

- Molecule 21 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	137	Total	C	N	O	S	0	0
			1101	699	211	190	1		

- Molecule 22 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	183	Total	C	N	O	S	0	0
			1563	974	332	253	4		

- Molecule 23 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	204	Total	C	N	O	S	0	0
			1618	1039	306	267	6		

- Molecule 24 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	154	Total	C	N	O	S	0	0
			1212	758	233	218	3		

- Molecule 25 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	129	Total	C	N	O	S	0	0
			1021	646	200	173	2		

- Molecule 26 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	174	Total	C	N	O	S	0	0
			1433	922	267	239	5		

- Molecule 27 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	126	Total	C	N	O	S	0	0
			1014	643	196	173	2		

- Molecule 28 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LV	135	Total	C	N	O	S	0	0
			995	633	185	170	7		

- Molecule 29 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LY	134	Total	C	N	O	S	0	0
			1065	664	215	184	2		

- Molecule 30 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Le	131	Total	C	N	O	S	0	0
			1055	663	213	172	7		

- Molecule 31 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lf	108	Total	C	N	O	S	0	0
			862	546	171	144	1		

- Molecule 32 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Lh	121	Total	C	N	O	0	0
			995	633	196	166		

- Molecule 33 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Li	88	Total	C	N	O	S	0	0
			731	449	162	119	1		

- Molecule 34 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lj	74	Total	C	N	O	S	0	0
			595	365	132	93	5		

- Molecule 35 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Cc	236	Total	C	N	O	S	0	0
			1898	1208	337	343	10		

- Molecule 36 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Cd	347	Total	C	N	O	S	0	0
			2800	1764	538	494	4		

- Molecule 37 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ce	194	Total	C	N	O	S	0	0
			1609	1020	304	276	9		

- Molecule 38 is a protein called 60S ribosome biogenesis protein Rrp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Cf	147	Total	C	N	O	S	0	0
			1225	755	245	224	1		

- Molecule 39 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Cy	244	Total	C	N	O		0	0
			1210	722	244	244			

- Molecule 40 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Cg	233	Total	C	N	O	S	0	0
			1850	1168	348	324	10		

- Molecule 41 is a protein called RNA methyltransferase nop2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CP	324	Total	C	N	O		0	0
			1596	948	324	324			

- Molecule 42 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	CG	177	Total	C	N	O	0	0
			873	519	177	177		

- Molecule 43 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	Lq	207	Total	C	N	O	0	0
			1021	607	207	207		

- Molecule 44 is a protein called Ribosome biogenesis regulatory protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	Cx	102	Total	C	N	O	0	0
			565	340	114	111		

- Molecule 45 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	LJ	169	Total	C	N	O	0	0
			831	492	169	170		

- Molecule 46 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	LD	273	Total	C	N	O	0	0
			1346	801	273	272		

- Molecule 47 is a RNA chain called RNA (119-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	C4	119	Total	C	N	O	P	0	0
			2536	1131	453	833	119		

- Molecule 48 is a protein called 60S ribosomal subunit-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	CX	63	Total	C	N	O	0	0
			375	233	68	74		

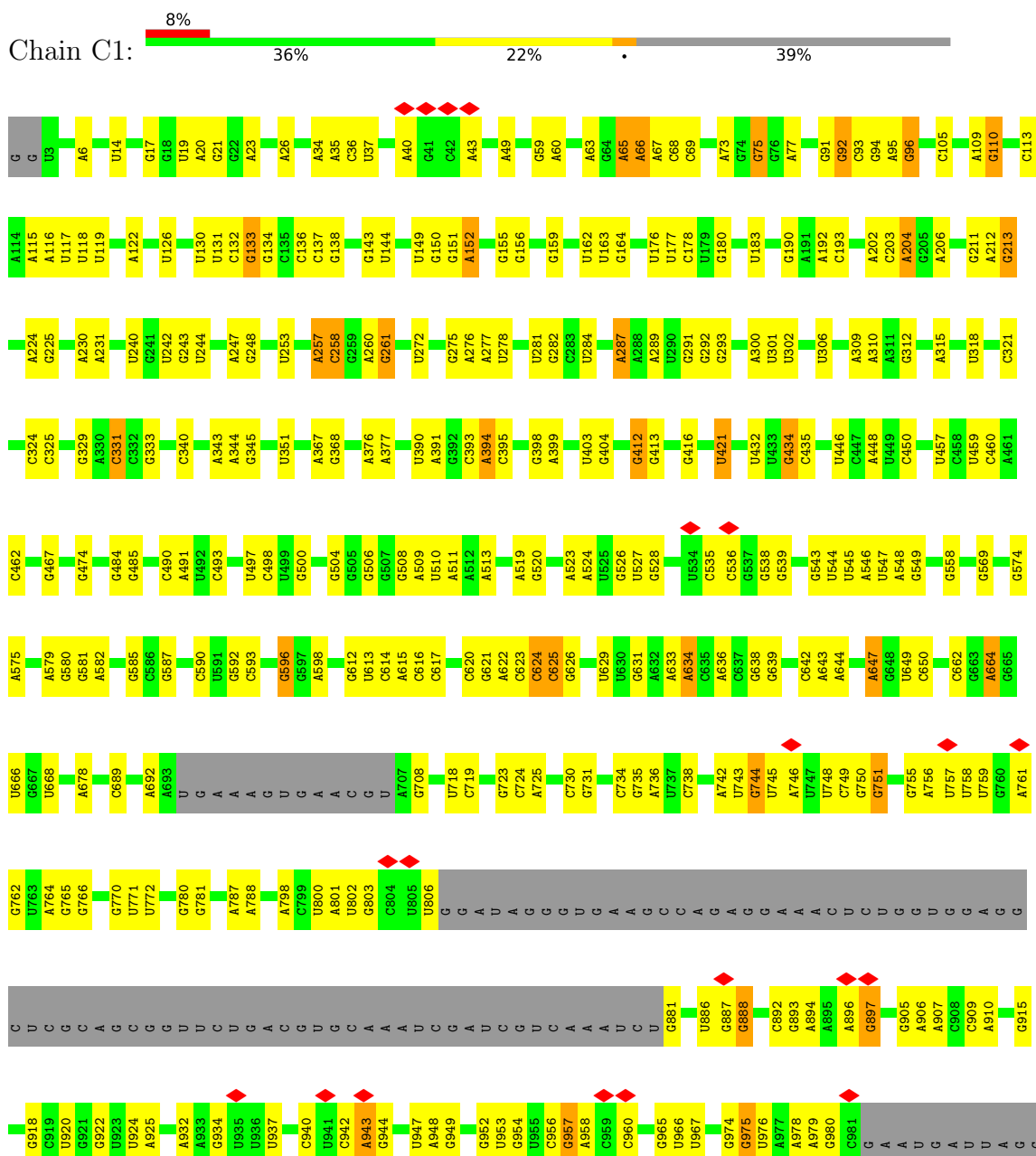
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

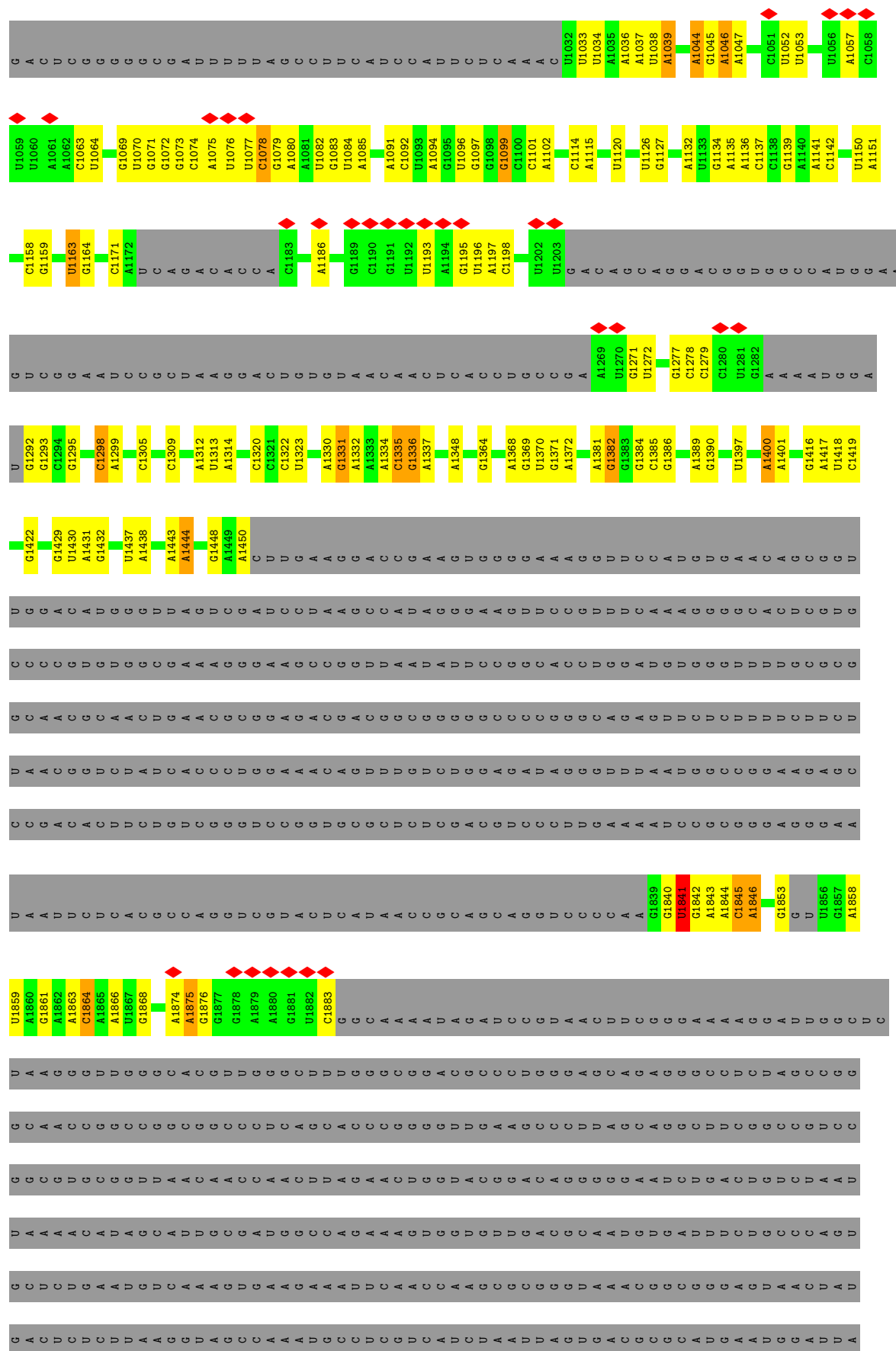
Mol	Chain	Residues	Atoms		AltConf
49	C1	1	Total 1	Zn 1	0
49	Lj	1	Total 1	Zn 1	0
49	Ce	1	Total 1	Zn 1	0

3 Residue-property plots

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

• Molecule 1: RNA (3341-MER)

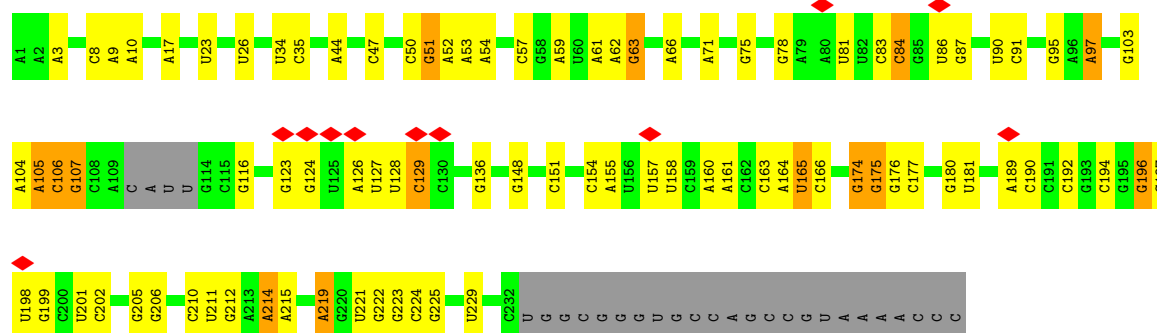








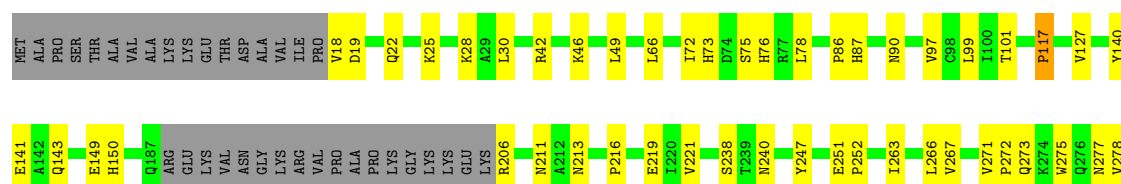
• Molecule 2: RNA (256-MER)



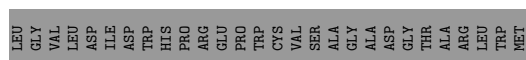
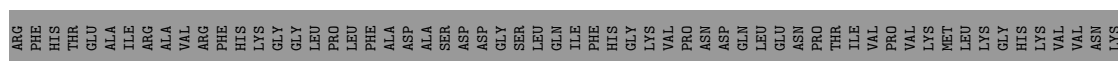
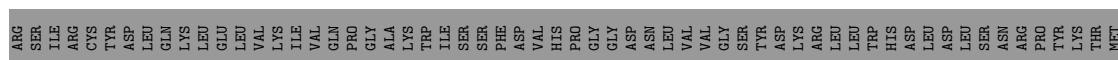
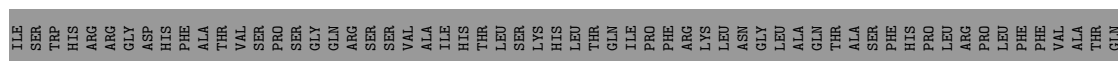
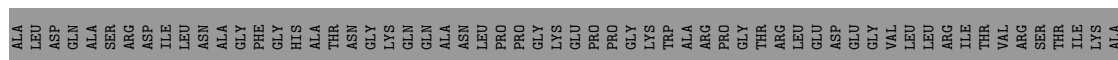
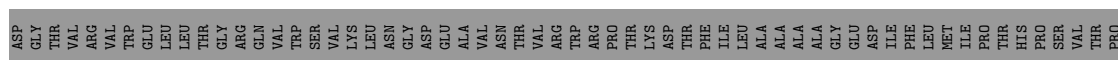
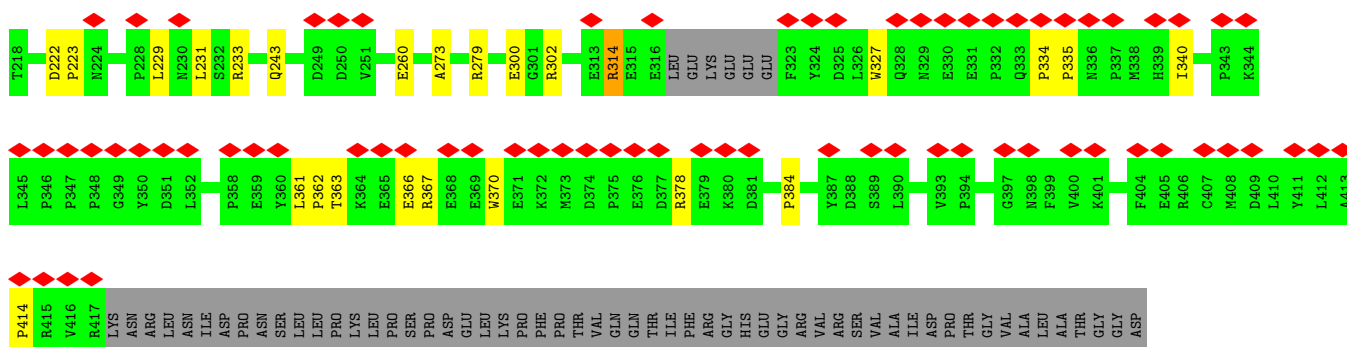
• Molecule 3: Brix domain-containing protein



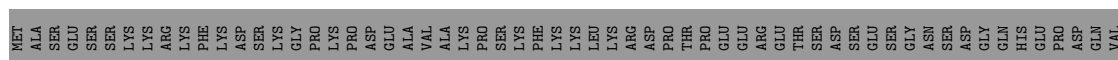
• Molecule 4: Ribosome biogenesis protein C8F11.04



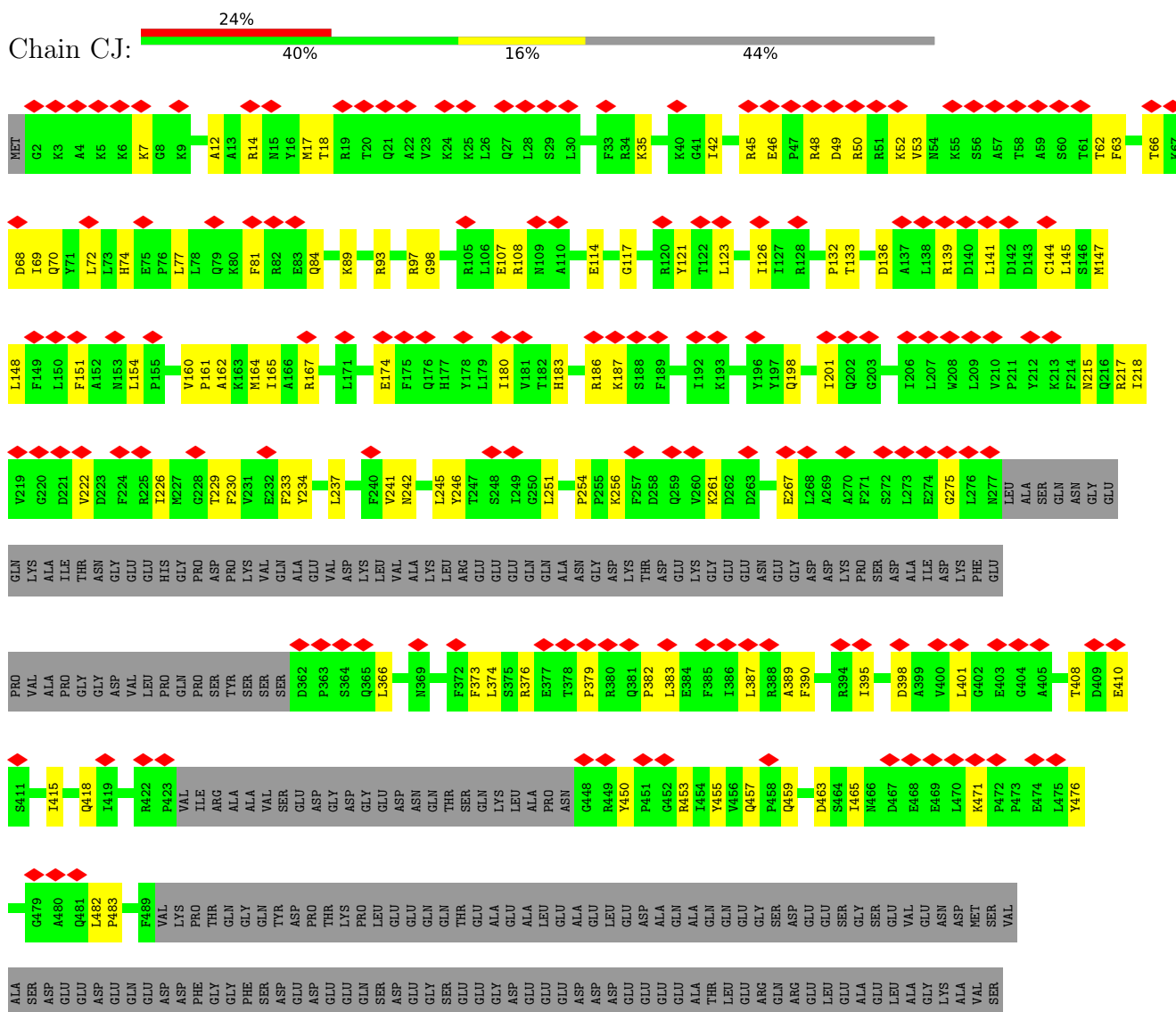
- Molecule 5: Ribosome biogenesis protein ERB1

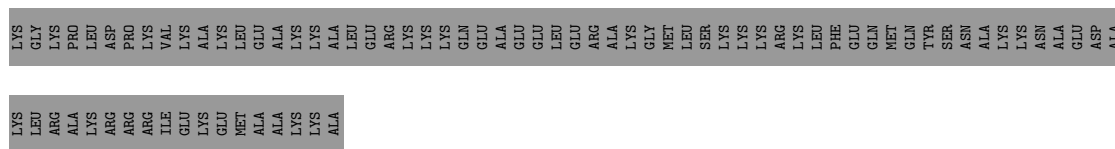


- Molecule 6: RNA helicase

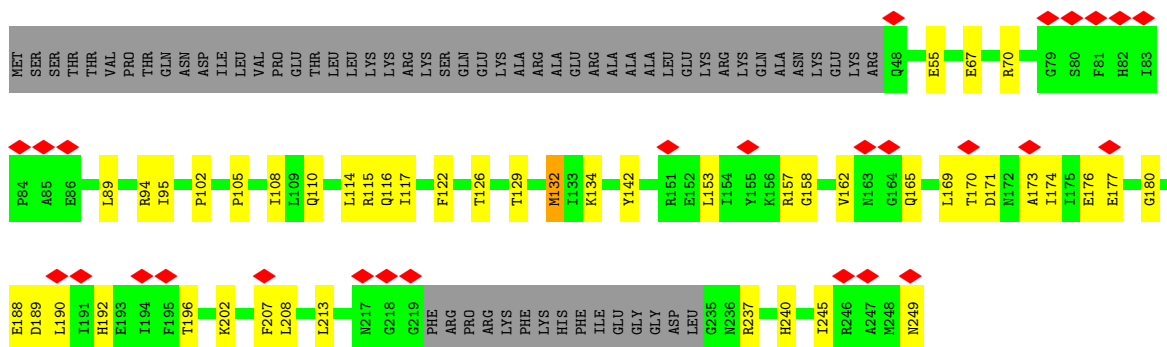


- Molecule 9: Pescadillo homolog

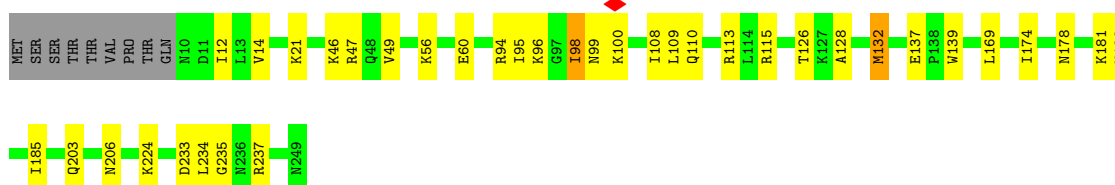
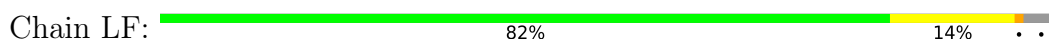




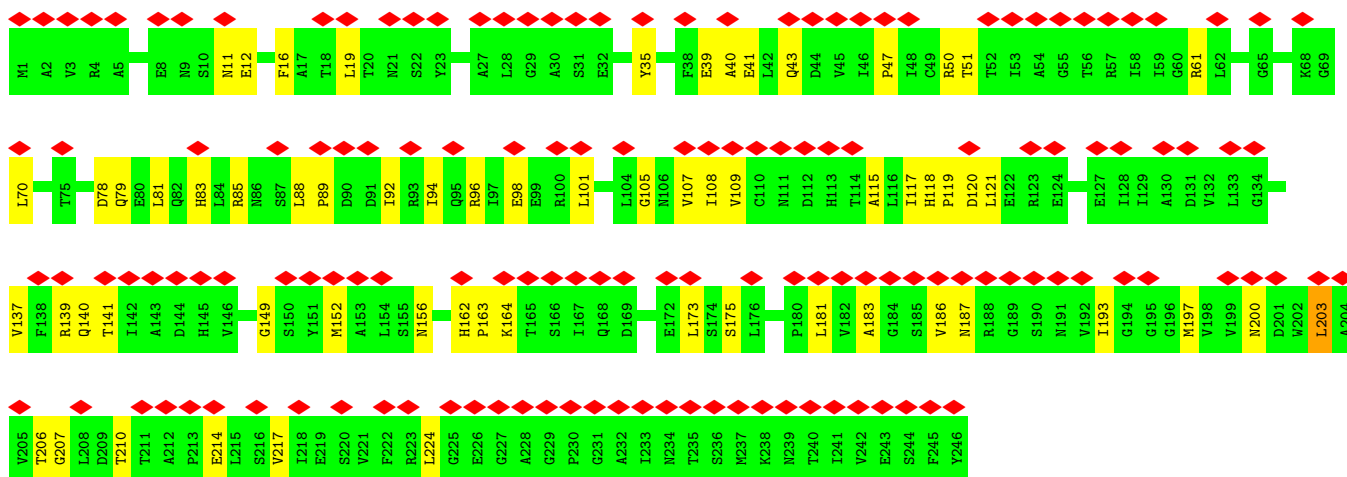
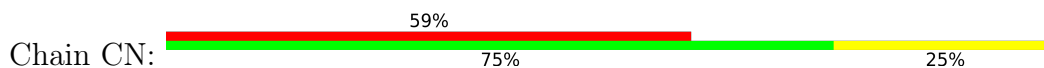
- Molecule 10: 60S ribosomal protein l7-like protein



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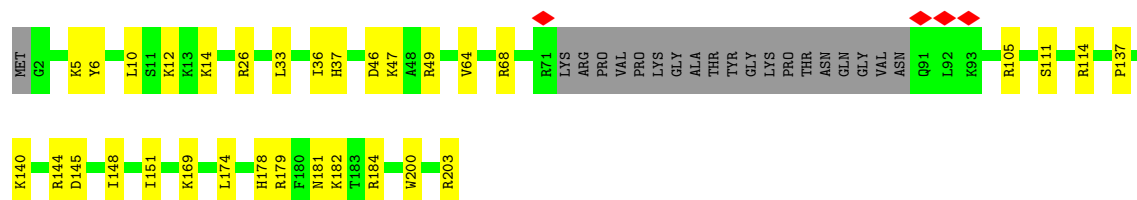


- Molecule 11: Eukaryotic translation initiation factor 6

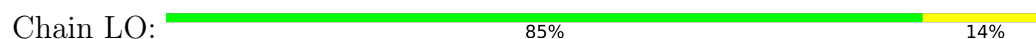


- Molecule 12: Ribosome biogenesis protein RLP24

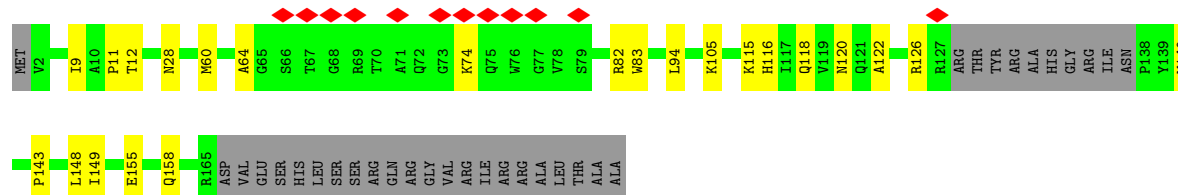
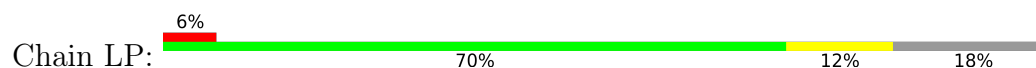
- Chain LN:



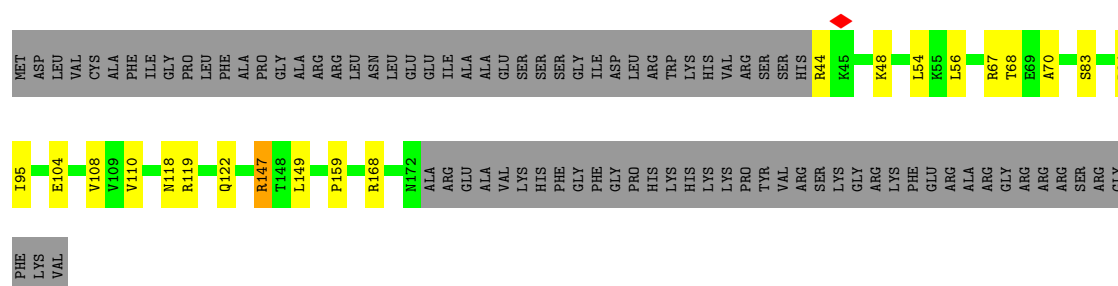
- Molecule 23: 60S ribosomal protein L16-like protein



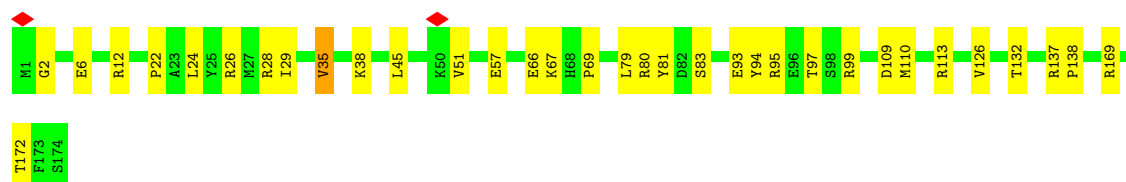
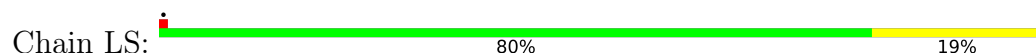
- Molecule 24: 60S ribosomal protein l17-like protein



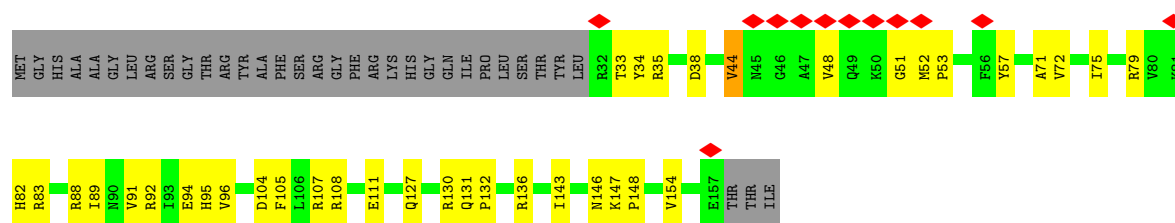
- Molecule 25: Ribosomal protein L18-like protein



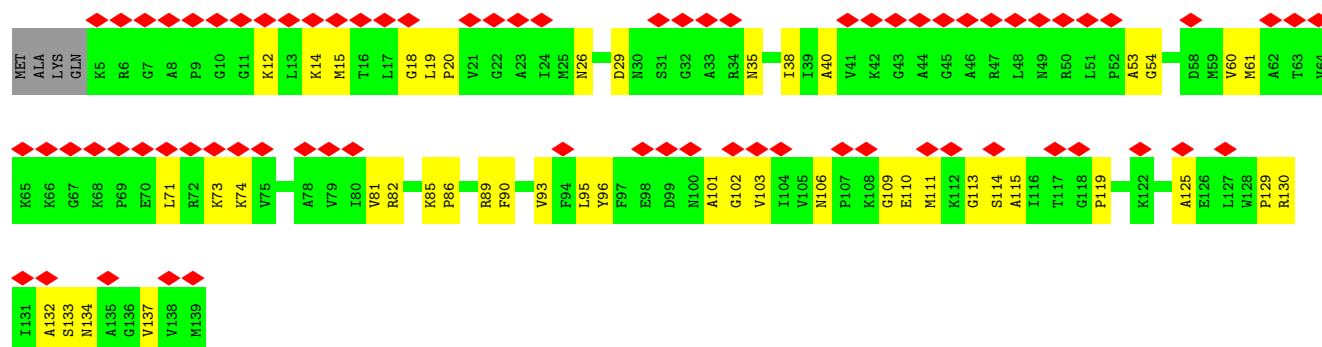
- Molecule 26: 60S ribosomal protein L20



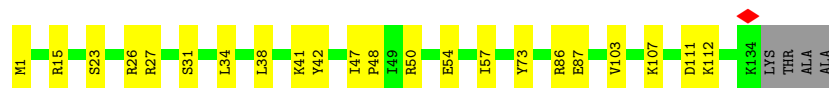
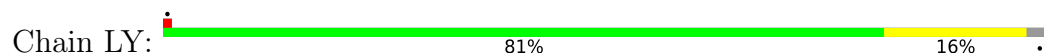
- Molecule 27: 60S ribosomal protein l21-like protein



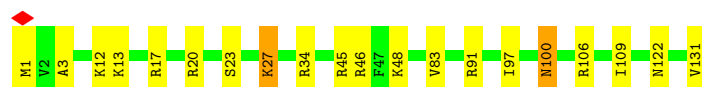
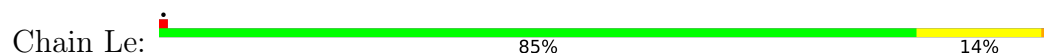
- Molecule 28: 60S ribosomal protein l23-like protein



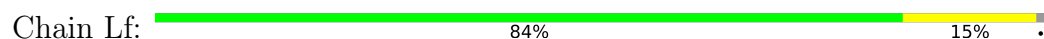
- Molecule 29: 60S ribosomal protein L26-like protein



- Molecule 30: 60S ribosomal protein L32-like protein



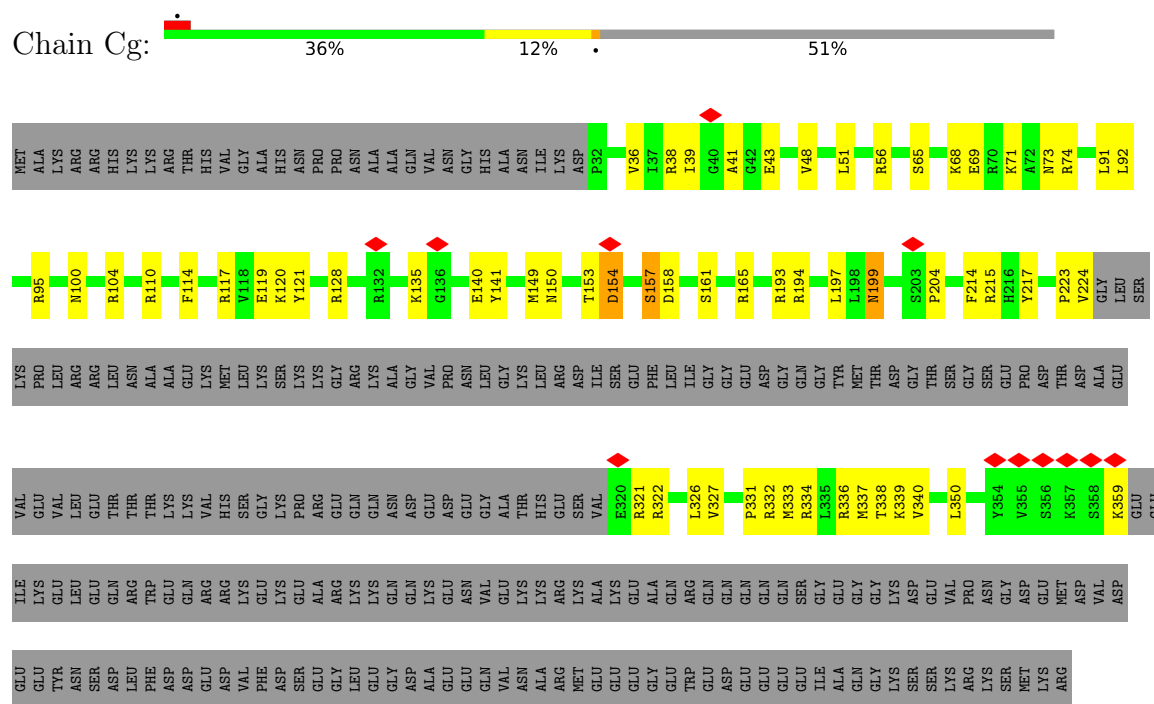
- Molecule 31: 60S ribosomal protein l33-like protein



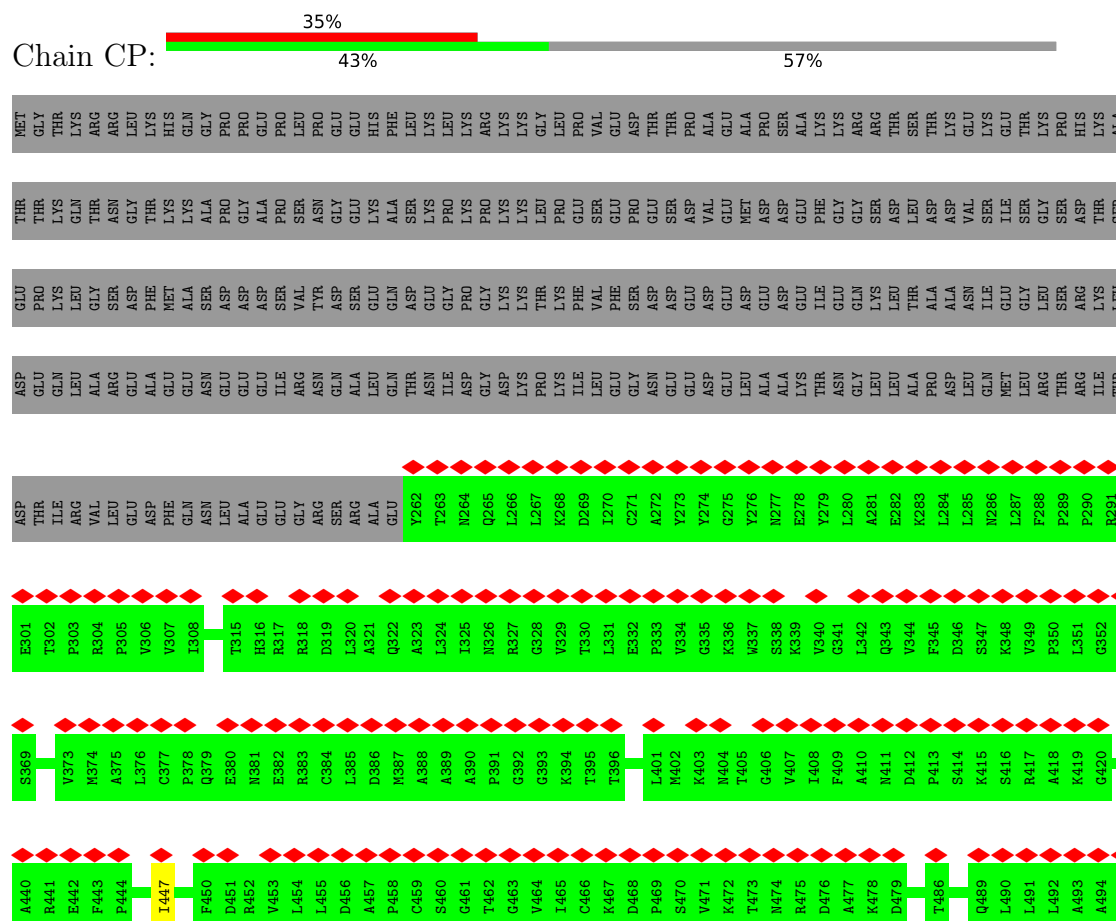
- Molecule 32: dolichyl-diphosphooligosaccharide--protein glycotransferase

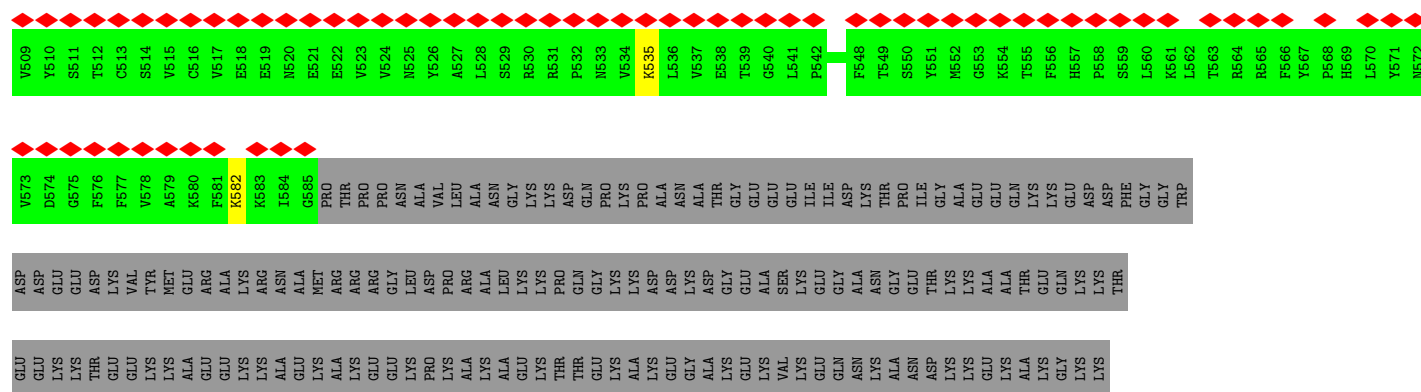


● Molecule 40: Brix domain-containing protein

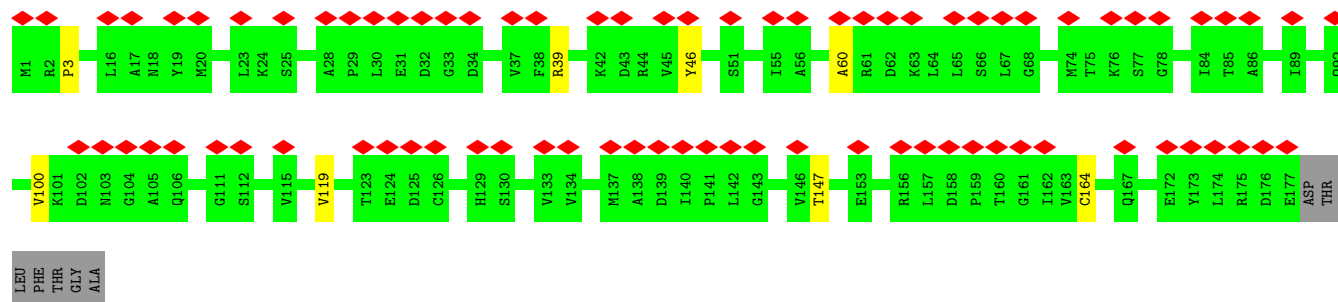
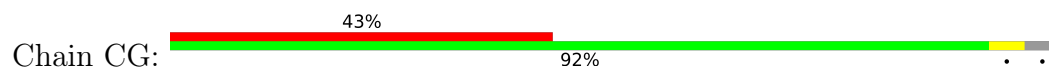


● Molecule 41: RNA methyltransferase nop2-like protein

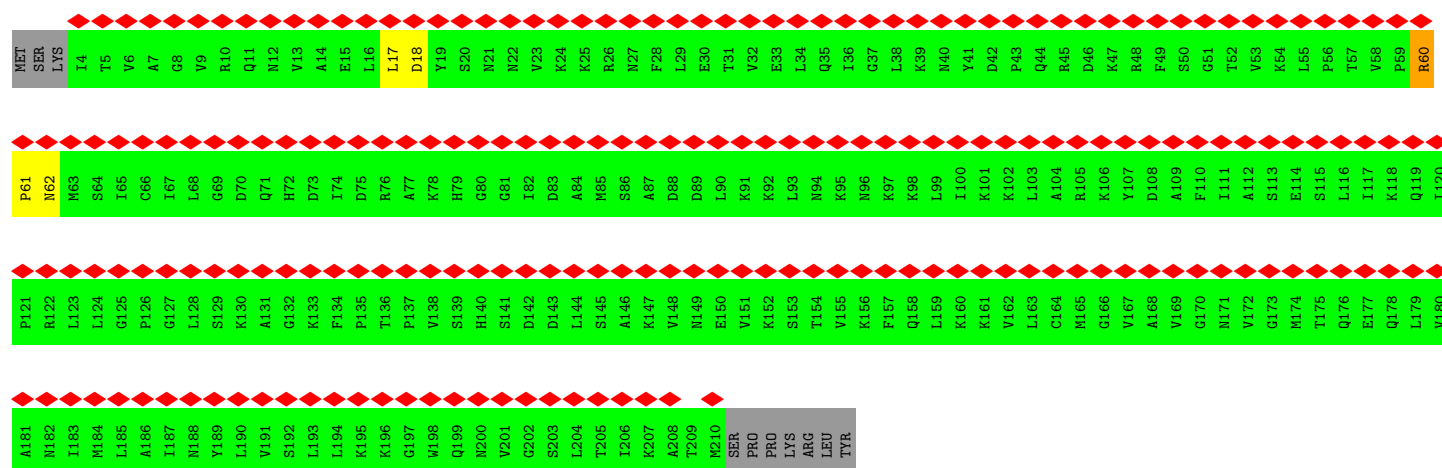




• Molecule 42: 60S ribosome subunit biogenesis protein NIP7

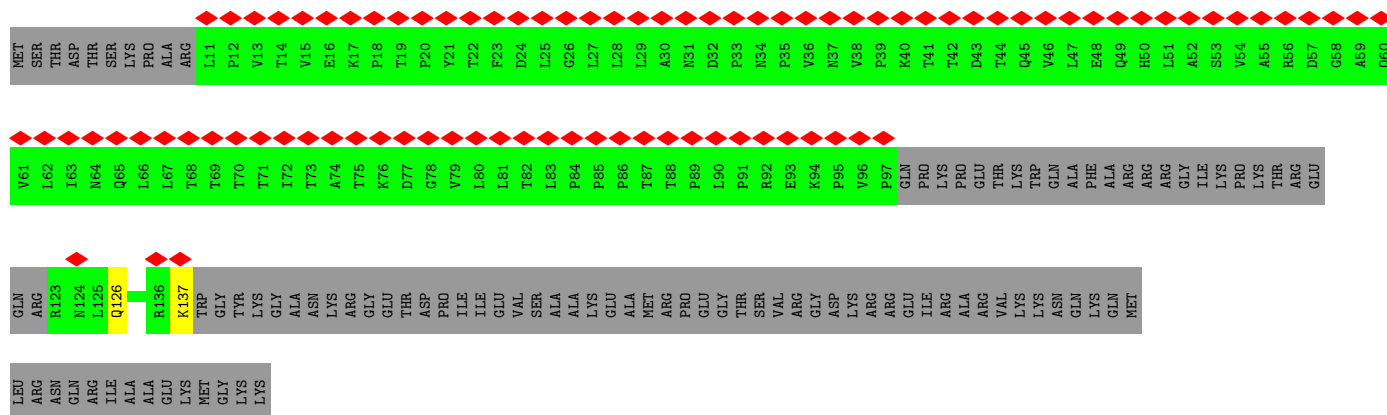


• Molecule 43: Ribosomal protein

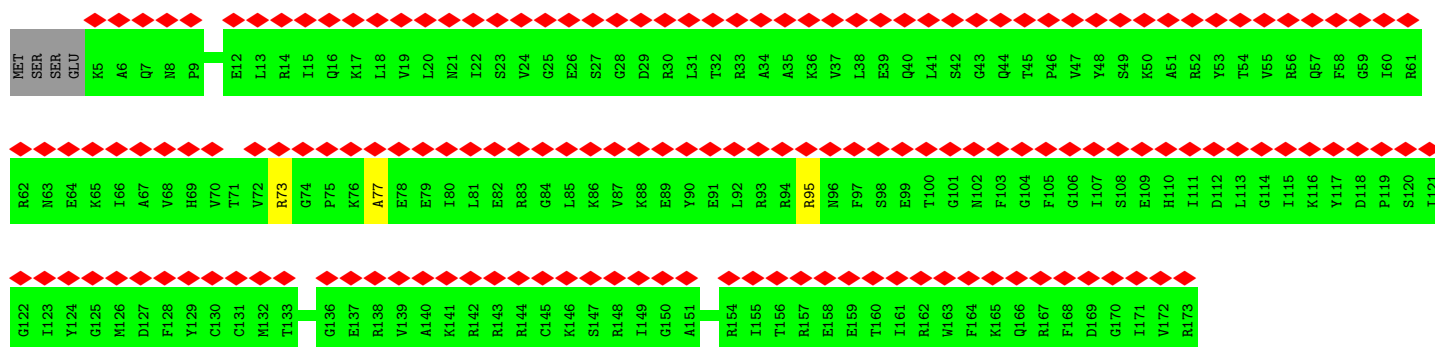


• Molecule 44: Ribosome biogenesis regulatory protein

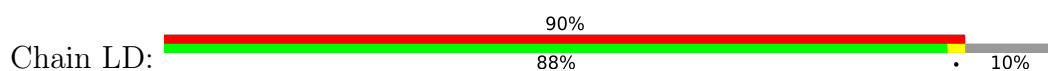




• Molecule 45: Putative ribosomal protein



• Molecule 46: 60S ribosomal protein 15-like protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41599	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 ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.491	Depositor
Minimum map value	-0.237	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	438.9, 438.9, 438.9	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	C1	0.27	1/48945 (0.0%)	0.37	4/76270 (0.0%)
2	C2	0.28	0/5415	0.37	0/8436
3	CA	0.26	0/2190	0.60	0/2940
4	CB	0.27	0/2109	0.61	2/2866 (0.1%)
5	CC	0.23	0/2325	0.53	1/3164 (0.0%)
6	CE	0.26	0/3743	0.52	0/5045
7	CH	0.22	0/909	0.65	0/1229
8	CI	0.25	0/1225	0.53	1/1645 (0.1%)
9	CJ	0.18	0/3189	0.48	2/4309 (0.0%)
10	CM	0.27	0/1555	0.65	0/2091
10	LF	0.29	0/2004	0.50	0/2686
11	CN	0.20	0/1881	0.57	0/2560
12	CQ	0.24	0/981	0.63	2/1301 (0.2%)
13	CR	0.26	0/1369	0.43	0/1828
14	CU	0.20	0/980	0.54	0/1314
15	Ch	0.19	0/563	0.64	0/746
16	LB	0.29	0/2760	0.68	2/3701 (0.1%)
17	LC	0.28	0/2809	0.50	1/3787 (0.0%)
18	LE	0.26	0/1363	0.48	0/1833
19	LG	0.29	0/1492	0.55	1/2003 (0.0%)
20	LL	0.29	0/983	0.44	0/1318
21	LM	0.26	0/1120	0.47	0/1507
22	LN	0.28	0/1595	0.39	0/2132
23	LO	0.27	0/1652	0.52	0/2215
24	LP	0.20	0/1231	0.40	0/1658
25	LQ	0.28	0/1033	0.44	0/1391
26	LS	0.26	0/1468	0.53	0/1975
27	LT	0.21	0/1033	0.50	0/1389
28	LV	0.22	0/1013	0.57	1/1361 (0.1%)
29	LY	0.25	0/1079	0.45	0/1443
30	Le	0.27	0/1073	0.42	0/1431
31	Lf	0.29	0/883	0.45	0/1187

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Lh	0.22	0/1006	0.38	0/1338
33	Li	0.24	0/738	0.41	0/971
34	Lj	0.27	0/606	0.43	0/803
35	Cc	0.27	0/1934	0.48	0/2614
36	Cd	0.26	0/2857	0.48	1/3843 (0.0%)
37	Ce	0.29	0/1638	0.73	2/2196 (0.1%)
38	Cf	0.22	0/1238	0.61	4/1631 (0.2%)
39	Cy	0.11	0/1208	0.31	0/1682
40	Cg	0.46	2/1887 (0.1%)	0.78	4/2544 (0.2%)
41	CP	0.17	0/1595	0.43	0/2217
42	CG	0.21	0/872	0.48	1/1212 (0.1%)
43	Lq	0.18	0/1020	0.50	0/1418
44	Cx	0.13	0/567	0.33	0/783
45	LJ	0.12	0/830	0.34	0/1150
46	LD	0.10	0/1344	0.29	0/1868
47	C4	0.15	0/2833	0.34	0/4414
48	CX	0.80	0/377	1.16	0/518
All	All	0.26	3/124520 (0.0%)	0.46	29/179963 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	CB	0	1
15	Ch	0	1
16	LB	0	1
19	LG	0	1
25	LQ	0	1
40	Cg	0	1
43	Lq	0	1
All	All	0	7

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	Cg	204	PRO	CG-CD	-14.81	1.00	1.50
40	Cg	204	PRO	N-CD	6.99	1.57	1.47
1	C1	3215	U	C1'-N1	6.85	1.58	1.48

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	Ce	186	CYS	CA-C-N	18.28	146.80	121.20
37	Ce	186	CYS	C-N-CA	18.28	146.80	121.20
40	Cg	204	PRO	N-CD-CG	-16.54	78.39	103.20
40	Cg	204	PRO	CA-N-CD	-10.36	97.49	112.00
40	Cg	204	PRO	CA-CB-CG	-10.12	85.28	104.50
17	LC	163	VAL	N-CA-C	-7.61	105.90	113.20
1	C1	2931	G	P-O3'-C3'	-7.41	109.09	120.20
1	C1	2932	U	P-O3'-C3'	-7.23	109.35	120.20
28	LV	73	LYS	CA-CB-CG	6.57	127.23	114.10
38	Cf	459	PRO	CA-N-CD	-6.22	103.30	112.00
36	Cd	417	ASP	N-CA-C	-6.12	103.05	110.88
40	Cg	157	SER	CB-CA-C	-6.10	108.53	115.79
16	LB	212	LYS	CA-CB-CG	6.09	126.28	114.10
19	LG	77	ALA	N-CA-C	-5.97	106.98	114.56
5	CC	314	ARG	CA-CB-CG	5.86	125.83	114.10
1	C1	2930	G	P-O3'-C3'	-5.77	111.55	120.20
38	Cf	412	ASN	CA-C-N	-5.76	115.58	122.44
38	Cf	412	ASN	C-N-CA	-5.76	115.58	122.44
4	CB	141	GLU	CA-CB-CG	5.68	125.46	114.10
38	Cf	459	PRO	N-CD-CG	-5.62	94.76	103.20
9	CJ	261	LYS	CA-CB-CG	5.59	125.28	114.10
12	CQ	64	VAL	N-CA-C	-5.44	108.20	113.53
42	CG	3	PRO	N-CA-CB	-5.41	97.57	103.25
4	CB	251	GLU	CA-CB-CG	5.39	124.88	114.10
12	CQ	11	ARG	CB-CG-CD	5.32	123.54	111.30
1	C1	1841	U	N1-C1'-C2'	5.32	119.98	112.00
9	CJ	35	LYS	CA-CB-CG	5.31	124.71	114.10
8	CI	284	PRO	CA-N-CD	-5.19	104.74	112.00
16	LB	197	ARG	CB-CG-CD	5.12	123.06	111.30

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	CB	42	ARG	Peptide
40	Cg	154	ASP	Peptide
15	Ch	282	LEU	Peptide
16	LB	58	ARG	Sidechain
19	LG	161	ASP	Peptide
25	LQ	147	ARG	Sidechain
43	Lq	60	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	C1	43814	0	22091	436	0
2	C2	4846	0	2449	35	0
3	CA	2144	0	2178	59	0
4	CB	2063	0	2131	27	0
5	CC	2258	0	2180	33	0
6	CE	3673	0	3778	45	0
7	CH	891	0	844	21	0
8	CI	1196	0	1202	17	0
9	CJ	3109	0	3122	71	0
10	CM	1525	0	1604	35	0
10	LF	1967	0	2080	23	0
11	CN	1856	0	1856	44	0
12	CQ	960	0	1001	29	0
13	CR	1354	0	1400	18	0
14	CU	969	0	1005	12	0
15	Ch	562	0	611	9	0
16	LB	2708	0	2811	82	0
17	LC	2752	0	2878	34	0
18	LE	1338	0	1423	22	0
19	LG	1470	0	1598	21	0
20	LL	964	0	1041	12	0
21	LM	1101	0	1170	23	0
22	LN	1563	0	1618	24	0
23	LO	1618	0	1714	22	0
24	LP	1212	0	1250	14	0
25	LQ	1021	0	1118	15	0
26	LS	1433	0	1496	28	0
27	LT	1014	0	1073	26	0
28	LV	995	0	1055	31	0
29	LY	1065	0	1156	16	0
30	Le	1055	0	1133	19	0
31	Lf	862	0	891	12	0
32	Lh	995	0	1110	19	0
33	Li	731	0	797	10	0
34	Lj	595	0	625	8	0
35	Cc	1898	0	1931	29	0
36	Cd	2800	0	2889	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	Ce	1609	0	1682	24	0
38	Cf	1225	0	1291	24	0
39	Cy	1210	0	527	0	0
40	Cg	1850	0	1937	41	0
41	CP	1596	0	733	2	0
42	CG	873	0	406	4	0
43	Lq	1021	0	461	2	0
44	Cx	565	0	304	2	0
45	LJ	831	0	371	2	0
46	LD	1346	0	641	4	0
47	C4	2536	0	1286	21	0
48	CX	375	0	286	6	0
49	C1	1	0	0	0	0
49	Ce	1	0	0	0	0
49	Lj	1	0	0	0	0
All	All	117417	0	90234	1298	0

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

All (1298) 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)
1:C1:975:G:N2	1:C1:1037:A:C6	2.12	1.16
1:C1:975:G:C2	1:C1:1037:A:N6	2.19	1.10
1:C1:631:G:N2	1:C1:1135:A:H62	1.50	1.10
6:CE:111:GLN:HE21	6:CE:111:GLN:N	1.51	1.09
1:C1:788:A:N6	1:C1:915:G:H1	1.51	1.08
1:C1:631:G:H21	1:C1:1135:A:N6	1.54	1.04
1:C1:2590:G:N2	1:C1:2605:A:C6	2.26	1.03
1:C1:1046:A:N1	1:C1:1074:C:C4	2.31	0.98
1:C1:3023:U:H3	1:C1:3032:G:H1	1.09	0.92
1:C1:2922:G:O6	1:C1:2926:G:C6	2.24	0.91
1:C1:2404:G:H1	1:C1:2467:U:H3	1.20	0.89
1:C1:2587:U:H3	1:C1:2607:G:H1	0.89	0.89
1:C1:800:U:H3	1:C1:888:G:H1	1.13	0.88
1:C1:2590:G:C2	1:C1:2605:A:C6	2.62	0.87
6:CE:111:GLN:N	6:CE:111:GLN:NE2	2.24	0.86
1:C1:3020:U:H3	1:C1:3037:G:H1	1.16	0.86
2:C2:196:G:H1	2:C2:201:U:H3	1.24	0.85
1:C1:788:A:H62	1:C1:915:G:H1	0.86	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2387:G:O6	1:C1:2563:G:C2	2.32	0.83
1:C1:1053:U:H3	1:C1:1069:G:H1	1.27	0.81
10:LF:94:ARG:HH22	10:LF:98:ILE:HG23	1.45	0.79
1:C1:2590:G:C2	1:C1:2605:A:N6	2.50	0.79
1:C1:2933:U:H2'	1:C1:2934:A:H8	1.47	0.79
1:C1:2590:G:N2	1:C1:2605:A:N6	2.29	0.78
1:C1:974:G:H1	1:C1:1038:U:H3	0.86	0.78
1:C1:975:G:N2	1:C1:1037:A:C5	2.50	0.78
1:C1:2433:U:C4	1:C1:2436:G:C6	2.72	0.77
1:C1:1046:A:N6	1:C1:1074:C:C2	2.54	0.76
1:C1:631:G:N2	1:C1:1135:A:N6	2.21	0.75
1:C1:975:G:C2	1:C1:1037:A:C6	2.71	0.75
11:CN:203:LEU:HA	11:CN:224:LEU:HD11	1.68	0.75
7:CH:425:TRP:HB2	7:CH:433:LYS:HE2	1.69	0.73
11:CN:96:ARG:O	12:CQ:76:ASN:ND2	2.21	0.73
40:Cg:100:ASN:HD21	40:Cg:117:ARG:HE	1.35	0.73
1:C1:2590:G:N2	1:C1:2605:A:C5	2.56	0.72
1:C1:2933:U:H2'	1:C1:2934:A:C8	2.24	0.72
1:C1:130:U:O2	1:C1:133:G:N2	2.23	0.71
1:C1:2389:U:O2	1:C1:2561:G:C6	2.43	0.71
11:CN:119:PRO:HA	11:CN:139:ARG:HD2	1.73	0.71
1:C1:2390:U:C4	1:C1:2560:G:O6	2.43	0.71
1:C1:2376:G:H1	1:C1:2764:U:H3	1.39	0.70
40:Cg:92:LEU:HB2	40:Cg:104:ARG:HB3	1.74	0.70
3:CA:121:HIS:HB2	3:CA:237:ARG:HB2	1.73	0.70
1:C1:788:A:N6	1:C1:915:G:N1	2.35	0.69
1:C1:634:A:N6	1:C1:2332:G:N2	2.40	0.69
1:C1:1450:A:C5	1:C1:1840:G:N2	2.61	0.69
1:C1:1864:C:O2'	40:Cg:110:ARG:NH1	2.25	0.69
5:CC:414:PRO:HB2	9:CJ:46:GLU:HG2	1.75	0.69
11:CN:140:GLN:NE2	11:CN:141:THR:O	2.26	0.69
1:C1:3235:A:OP1	16:LB:128:LYS:NZ	2.27	0.68
3:CA:102:MET:HB2	3:CA:115:PHE:HB2	1.74	0.68
1:C1:1195:G:OP2	26:LS:137:ARG:NH1	2.27	0.68
7:CH:422:ARG:HD2	7:CH:434:TYR:H	1.59	0.67
18:LE:172:ASN:OD1	18:LE:175:LYS:NZ	2.28	0.67
5:CC:340:ILE:H	9:CJ:45:ARG:HD3	1.60	0.67
10:CM:108:ILE:HD12	10:CM:132:MET:HB3	1.76	0.67
17:LC:100:MET:HE3	17:LC:103:PRO:HA	1.77	0.67
1:C1:3270:C:H42	1:C1:3314:U:H3	1.43	0.67
1:C1:3173:C:N3	1:C1:3198:U:O2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Cd:238:LYS:O	37:Ce:132:ARG:NH2	2.27	0.66
1:C1:1046:A:C2	1:C1:1074:C:N4	2.62	0.66
1:C1:2387:G:O6	1:C1:2563:G:N2	2.28	0.66
12:CQ:63:MET:N	12:CQ:63:MET:SD	2.68	0.66
5:CC:229:LEU:HD13	5:CC:231:LEU:HG	1.76	0.66
6:CE:532:ASP:HB3	6:CE:535:LYS:HG3	1.77	0.66
10:CM:67:GLU:OE2	10:CM:70:ARG:NH2	2.29	0.66
1:C1:2922:G:C6	1:C1:2926:G:C6	2.83	0.66
10:CM:153:LEU:HA	10:CM:157:ARG:HB2	1.78	0.66
2:C2:78:G:O2'	32:Lh:47:ASN:ND2	2.29	0.66
9:CJ:376:ARG:HH21	10:CM:189:ASP:HA	1.61	0.66
17:LC:136:LEU:HB3	17:LC:143:VAL:HG11	1.76	0.66
1:C1:2433:U:O4	1:C1:2436:G:C6	2.50	0.65
1:C1:3127:A:H62	31:Lf:56:ARG:HH22	1.43	0.65
26:LS:6:GLU:OE2	26:LS:99:ARG:NH1	2.29	0.65
1:C1:331:C:H3'	17:LC:199:ARG:HH12	1.61	0.65
3:CA:25:ASN:HB2	3:CA:170:LYS:HD2	1.78	0.65
37:Ce:81:ILE:HD13	37:Ce:97:ARG:HE	1.61	0.65
16:LB:222:THR:HG22	16:LB:274:HIS:H	1.62	0.65
1:C1:243:G:N2	13:CR:191:GLU:OE1	2.30	0.65
13:CR:43:GLU:O	20:LL:40:ARG:NH2	2.30	0.65
16:LB:95:THR:HG22	16:LB:97:ARG:H	1.62	0.65
24:LP:9:ILE:HD13	24:LP:115:LYS:HE2	1.78	0.65
36:Cd:371:ASN:OD1	36:Cd:384:LYS:NZ	2.28	0.65
1:C1:3020:U:O2	1:C1:3037:G:N2	2.28	0.65
35:Cc:129:LYS:HD3	35:Cc:149:ALA:HA	1.78	0.65
2:C2:214:A:H5'	8:CI:193:ARG:HG2	1.80	0.64
19:LG:84:THR:HG21	19:LG:184:LYS:HG3	1.80	0.64
25:LQ:147:ARG:HH12	25:LQ:149:LEU:HD21	1.63	0.64
1:C1:949:G:H4'	27:LT:83:ARG:HH12	1.61	0.64
15:Ch:273:GLU:OE1	15:Ch:274:GLN:NE2	2.31	0.64
1:C1:1348:A:O2'	30:Le:46:ARG:NH2	2.31	0.64
1:C1:2416:G:O6	1:C1:2446:A:N1	2.30	0.64
3:CA:138:PRO:HD2	3:CA:165:VAL:HG11	1.78	0.64
8:CI:251:TYR:HB3	8:CI:258:LEU:HD12	1.78	0.64
4:CB:66:LEU:HD22	4:CB:266:LEU:HD21	1.78	0.64
1:C1:144:U:OP2	22:LN:49:ARG:NH2	2.31	0.63
36:Cd:200:LYS:HB3	36:Cd:253:TYR:HA	1.79	0.63
1:C1:2399:G:H1	1:C1:2472:U:H3	1.47	0.63
1:C1:3149:C:OP1	21:LM:98:ASN:ND2	2.32	0.63
7:CH:427:LEU:HD13	7:CH:432:TRP:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CH:415:GLY:O	16:LB:349:ARG:NH1	2.30	0.63
35:Cc:199:ASP:OD2	35:Cc:244:ARG:NH1	2.32	0.63
40:Cg:56:ARG:HD3	40:Cg:65:SER:HA	1.80	0.63
1:C1:19:U:OP1	32:Lh:95:ARG:NH1	2.31	0.63
1:C1:3036:U:H5'	40:Cg:74:ARG:HH12	1.64	0.63
38:Cf:435:LYS:O	38:Cf:477:ARG:NH1	2.31	0.63
32:Lh:12:LEU:HD11	32:Lh:59:VAL:HG22	1.81	0.62
35:Cc:47:VAL:HG21	35:Cc:89:TRP:HA	1.81	0.62
36:Cd:410:ARG:NH2	36:Cd:422:GLU:OE2	2.32	0.62
1:C1:68:C:OP2	1:C1:293:G:N2	2.31	0.62
1:C1:738:C:N4	1:C1:756:A:H61	1.95	0.62
25:LQ:68:THR:HG22	25:LQ:70:ALA:H	1.64	0.62
1:C1:3268:G:H21	16:LB:310:GLY:HA2	1.64	0.62
40:Cg:41:ALA:HB1	40:Cg:71:LYS:HA	1.82	0.62
1:C1:765:G:H21	25:LQ:119:ARG:HB3	1.65	0.62
1:C1:3159:A:OP2	21:LM:125:LYS:NZ	2.32	0.62
6:CE:463:GLN:HB2	6:CE:466:GLU:HG3	1.80	0.62
10:CM:176:GLU:HA	10:CM:180:GLY:HA3	1.82	0.62
24:LP:11:PRO:O	24:LP:105:LYS:NZ	2.32	0.62
1:C1:735:G:H1	1:C1:759:U:H3	1.47	0.62
3:CA:181:SER:HB3	3:CA:192:ARG:HB2	1.81	0.62
4:CB:273:GLN:HB2	4:CB:277:ASN:HB2	1.80	0.62
1:C1:272:U:O2'	22:LN:182:LYS:NZ	2.33	0.62
10:CM:237:ARG:HG2	10:CM:240:HIS:HB2	1.80	0.62
1:C1:258:C:O2	33:Li:39:LYS:NZ	2.32	0.62
1:C1:1046:A:C2	1:C1:1074:C:C4	2.87	0.62
1:C1:738:C:N4	1:C1:756:A:N6	2.47	0.61
5:CC:314:ARG:O	5:CC:314:ARG:NE	2.32	0.61
6:CE:170:VAL:HG22	6:CE:207:MET:HE2	1.81	0.61
13:CR:40:ASN:HB3	13:CR:43:GLU:HG3	1.81	0.61
1:C1:6:A:OP1	9:CJ:93:ARG:NH1	2.32	0.61
10:CM:162:VAL:O	10:CM:165:GLN:NE2	2.33	0.61
35:Cc:174:ARG:HH12	35:Cc:184:GLU:HA	1.64	0.61
2:C2:219:A:N6	8:CI:218:VAL:O	2.34	0.61
9:CJ:84:GLN:HG3	9:CJ:121:TYR:HE1	1.65	0.61
15:Ch:275:ILE:HA	15:Ch:278:ARG:HG3	1.80	0.61
28:LV:111:MET:HB3	28:LV:130:ARG:HH22	1.65	0.61
1:C1:1437:U:H2'	1:C1:1438:A:H8	1.66	0.61
13:CR:131:VAL:HG12	13:CR:133:GLN:H	1.66	0.61
1:C1:152:A:OP2	33:Li:32:LYS:NZ	2.34	0.61
12:CQ:45:ASN:HD22	12:CQ:48:LYS:HG2	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LF:46:LYS:HE2	10:LF:185:ILE:HD12	1.82	0.61
1:C1:631:G:H21	1:C1:1135:A:H62	0.73	0.61
1:C1:1139:G:OP1	10:LF:96:LYS:NZ	2.33	0.61
1:C1:2922:G:O6	1:C1:2926:G:O6	2.19	0.61
40:Cg:214:PHE:HB3	40:Cg:333:MET:HB2	1.83	0.61
1:C1:37:U:O2	20:LL:15:ARG:NH2	2.34	0.60
1:C1:66:A:N6	1:C1:75:G:N2	2.48	0.60
16:LB:92:TYR:HB3	16:LB:99:LEU:HD22	1.83	0.60
37:Ce:39:ASN:OD1	37:Ce:42:SER:OG	2.19	0.60
3:CA:35:ARG:NH2	3:CA:84:TYR:O	2.34	0.60
16:LB:122:TRP:O	16:LB:127:LYS:NZ	2.30	0.60
2:C2:165:U:O2'	4:CB:206:ARG:NH1	2.35	0.60
1:C1:735:G:N2	1:C1:759:U:O2	2.35	0.60
7:CH:422:ARG:NH2	7:CH:435:ASP:O	2.34	0.60
26:LS:99:ARG:NH2	26:LS:126:VAL:O	2.34	0.60
4:CB:284:LYS:HB2	4:CB:290:ALA:HA	1.83	0.60
11:CN:85:ARG:NH1	12:CQ:78:PRO:O	2.35	0.60
5:CC:367:ARG:NH1	5:CC:384:PRO:O	2.35	0.60
3:CA:310:ASP:HB3	3:CA:313:GLU:HG3	1.84	0.60
26:LS:81:TYR:HE1	26:LS:83:SER:HB3	1.67	0.60
27:LT:44:VAL:H	27:LT:95:HIS:HB3	1.66	0.59
16:LB:90:VAL:HG23	16:LB:104:THR:HB	1.83	0.59
11:CN:88:LEU:HD12	11:CN:92:ILE:HG21	1.83	0.59
1:C1:624:C:C4	1:C1:2323:A:C6	2.91	0.59
3:CA:51:LEU:HD22	3:CA:120:LEU:HD11	1.84	0.59
27:LT:92:ARG:HD3	27:LT:92:ARG:H	1.66	0.59
9:CJ:410:GLU:O	9:CJ:453:ARG:NH1	2.35	0.59
36:Cd:88:ASP:HB3	36:Cd:91:GLU:HB2	1.84	0.59
40:Cg:140:GLU:HB3	40:Cg:193:ARG:HD2	1.84	0.59
1:C1:947:U:H2'	1:C1:948:A:H8	1.67	0.59
1:C1:1331:G:H2'	10:LF:21:LYS:HG3	1.83	0.59
3:CA:109:ASN:O	5:CC:148:ARG:NH2	2.36	0.59
1:C1:3042:G:H2'	1:C1:3043:A:H8	1.68	0.59
1:C1:3307:C:H5'	12:CQ:111:ARG:HH21	1.68	0.59
26:LS:57:GLU:OE1	27:LT:136:ARG:NH2	2.36	0.59
1:C1:642:C:H2'	1:C1:643:A:H8	1.68	0.59
16:LB:290:ASP:OD1	16:LB:290:ASP:N	2.34	0.59
35:Cc:83:ARG:O	35:Cc:83:ARG:NH1	2.36	0.59
35:Cc:106:VAL:HG13	35:Cc:107:LEU:HD12	1.83	0.59
1:C1:806:U:H3	1:C1:881:G:H1	1.50	0.58
1:C1:2390:U:N3	1:C1:2560:G:C6	2.71	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Ch:275:ILE:O	15:Ch:279:GLU:N	2.35	0.58
1:C1:1134:G:OP2	1:C1:1134:G:N2	2.34	0.58
5:CC:273:ALA:HB2	6:CE:552:ARG:HG2	1.86	0.58
12:CQ:6:CYS:HB3	12:CQ:11:ARG:H	1.67	0.58
6:CE:457:ARG:NH2	6:CE:483:TYR:OH	2.36	0.58
47:C4:73:U:O2	47:C4:105:C:N3	2.36	0.58
16:LB:26:ARG:HA	16:LB:336:ILE:HG21	1.86	0.58
29:LY:23:SER:HA	29:LY:26:ARG:HB2	1.84	0.58
1:C1:126:U:OP1	22:LN:144:ARG:NH1	2.37	0.58
3:CA:227:THR:HG23	14:CU:255:ARG:HH22	1.69	0.58
4:CB:99:LEU:HB3	4:CB:127:VAL:HG12	1.84	0.58
17:LC:301:ARG:O	25:LQ:67:ARG:NH1	2.36	0.58
33:Li:81:PHE:HA	33:Li:84:LYS:HE3	1.85	0.58
1:C1:3169:U:O2'	1:C1:3200:A:N1	2.33	0.58
16:LB:206:ILE:HD11	16:LB:321:ASP:HB3	1.86	0.58
10:CM:94:ARG:NH1	10:CM:95:ILE:O	2.37	0.58
1:C1:3306:G:O2'	12:CQ:111:ARG:NH2	2.37	0.58
40:Cg:120:LYS:HD2	40:Cg:334:ARG:HG3	1.85	0.58
17:LC:364:GLU:O	26:LS:28:ARG:NH1	2.37	0.58
1:C1:2618:G:N3	1:C1:2702:U:O2'	2.36	0.57
1:C1:110:G:OP2	20:LL:73:ARG:NH2	2.37	0.57
1:C1:745:U:O2	1:C1:749:C:N3	2.37	0.57
1:C1:956:C:OP1	25:LQ:44:ARG:NH2	2.37	0.57
20:LL:53:LYS:HB2	20:LL:55:ARG:HH12	1.68	0.57
1:C1:897:G:O6	1:C1:2937:U:O2	2.23	0.57
1:C1:1841:U:C4	1:C1:1842:G:N2	2.72	0.57
1:C1:243:G:O6	13:CR:185:ARG:NH2	2.36	0.57
1:C1:2618:G:H1'	1:C1:2702:U:H1'	1.85	0.57
12:CQ:6:CYS:SG	12:CQ:9:CYS:N	2.77	0.57
16:LB:58:ARG:HB3	16:LB:72:VAL:HG23	1.87	0.57
1:C1:1842:G:N3	38:Cf:469:LYS:NZ	2.45	0.57
1:C1:2389:U:O2	1:C1:2560:G:O6	2.22	0.57
27:LT:75:ILE:HG12	27:LT:88:ARG:HG2	1.87	0.57
1:C1:345:G:O6	34:Lj:55:ARG:NH1	2.37	0.57
1:C1:1845:C:O2	38:Cf:421:HIS:ND1	2.37	0.57
4:CB:216:PRO:HB2	4:CB:219:GLU:HG2	1.87	0.57
24:LP:118:GLN:NE2	24:LP:120:ASN:OD1	2.38	0.57
28:LV:26:ASN:HA	28:LV:35:ASN:HA	1.86	0.57
40:Cg:36:VAL:HG12	40:Cg:91:LEU:HB2	1.85	0.57
1:C1:1444:A:N6	1:C1:1853:G:N1	2.50	0.57
3:CA:191:VAL:O	3:CA:192:ARG:NE	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CM:170:THR:HB	10:CM:174:ILE:HG13	1.87	0.56
36:Cd:357:ARG:HB3	36:Cd:394:GLY:HA3	1.85	0.56
1:C1:780:G:O2'	20:LL:18:TRP:NE1	2.37	0.56
1:C1:1193:U:O2'	26:LS:113:ARG:NH1	2.39	0.56
1:C1:2478:U:O4	1:C1:2550:G:N2	2.38	0.56
4:CB:117:PRO:HD2	4:CB:221:VAL:HG21	1.87	0.56
5:CC:300:GLU:OE1	5:CC:302:ARG:NH1	2.39	0.56
9:CJ:141:LEU:HA	9:CJ:144:CYS:HB3	1.88	0.56
17:LC:233:GLU:OE1	17:LC:244:GLN:NE2	2.31	0.56
38:Cf:499:GLU:N	38:Cf:499:GLU:OE1	2.38	0.56
1:C1:2463:U:O2'	1:C1:2465:G:OP2	2.22	0.56
1:C1:975:G:N1	1:C1:1037:A:N6	2.54	0.56
3:CA:177:ASP:OD1	3:CA:177:ASP:N	2.37	0.56
5:CC:183:TYR:O	5:CC:197:ARG:NH2	2.38	0.56
7:CH:419:VAL:HG22	11:CN:50:ARG:HH21	1.70	0.56
10:CM:94:ARG:HG2	10:CM:117:ILE:HA	1.87	0.56
1:C1:2955:U:C2	1:C1:3337:C:N3	2.74	0.56
9:CJ:215:ASN:ND2	10:CM:158:GLY:O	2.39	0.56
26:LS:35:VAL:HA	26:LS:38:LYS:HZ2	1.69	0.56
11:CN:109:VAL:HB	11:CN:149:GLY:HA2	1.88	0.56
28:LV:82:ARG:HB2	28:LV:101:ALA:HB3	1.87	0.56
1:C1:1390:G:O6	30:Le:17:ARG:NH2	2.38	0.56
8:CI:214:THR:OG1	8:CI:234:GLU:OE1	2.23	0.56
1:C1:974:G:O6	1:C1:1038:U:O4	2.24	0.56
1:C1:1074:C:H2'	1:C1:1078:C:H5	1.71	0.56
1:C1:3298:U:H2'	1:C1:3299:A:H8	1.70	0.56
26:LS:79:LEU:HD13	26:LS:110:MET:HE2	1.87	0.56
9:CJ:141:LEU:HD11	9:CJ:241:VAL:HG11	1.87	0.55
40:Cg:157:SER:OG	40:Cg:165:ARG:NE	2.39	0.55
1:C1:261:G:N2	1:C1:287:A:OP2	2.32	0.55
1:C1:1444:A:H61	1:C1:1853:G:H1	1.54	0.55
1:C1:3008:U:H2'	1:C1:3009:G:H8	1.70	0.55
3:CA:247:GLU:OE2	5:CC:148:ARG:NH1	2.40	0.55
6:CE:416:VAL:HG12	6:CE:419:ARG:HH22	1.71	0.55
1:C1:725:A:OP1	25:LQ:94:ARG:NH1	2.40	0.55
1:C1:2380:G:H5''	1:C1:2381:A:H5'	1.88	0.55
1:C1:3270:C:N3	1:C1:3314:U:O2	2.38	0.55
40:Cg:158:ASP:HB3	40:Cg:161:SER:HB2	1.87	0.55
9:CJ:180:ILE:HA	9:CJ:389:ALA:HA	1.88	0.55
10:CM:245:ILE:O	10:CM:249:ASN:N	2.35	0.55
13:CR:69:ASN:HD21	13:CR:72:LEU:HD12	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:92:G:H5'	1:C1:93:C:H5''	1.88	0.55
1:C1:2326:G:N2	1:C1:2328:C:OP2	2.40	0.55
10:LF:56:LYS:NZ	10:LF:60:GLU:OE2	2.40	0.55
36:Cd:284:THR:OG1	36:Cd:407:GLY:O	2.24	0.55
1:C1:2389:U:C2	1:C1:2561:G:O6	2.60	0.55
3:CA:291:ALA:O	3:CA:295:GLN:NE2	2.39	0.55
4:CB:211:ASN:ND2	4:CB:213:ASN:OD1	2.40	0.55
38:Cf:417:THR:HG22	38:Cf:428:SER:HA	1.89	0.55
3:CA:103:TRP:CZ2	3:CA:114:LYS:HD2	2.42	0.55
11:CN:118:HIS:HE1	11:CN:120:ASP:HB2	1.71	0.55
26:LS:22:PRO:O	27:LT:146:ASN:ND2	2.39	0.55
31:Lf:49:LYS:NZ	31:Lf:106:PRO:O	2.37	0.55
1:C1:3269:U:H4'	16:LB:309:MET:HB3	1.88	0.55
9:CJ:70:GLN:O	9:CJ:74:HIS:ND1	2.40	0.55
9:CJ:133:THR:OG1	9:CJ:136:ASP:OD2	2.23	0.55
10:CM:110:GLN:HG3	10:CM:115:ARG:HH12	1.72	0.55
18:LE:49:ARG:NH1	31:Lf:109:ILE:O	2.40	0.55
40:Cg:340:VAL:HG13	40:Cg:350:LEU:HB2	1.88	0.55
4:CB:49:LEU:HD22	6:CE:337:VAL:HG21	1.89	0.55
11:CN:61:ARG:HD3	28:LV:133:SER:HA	1.89	0.55
11:CN:162:HIS:HE1	11:CN:164:LYS:HB2	1.70	0.55
28:LV:106:ASN:OD1	28:LV:110:GLU:N	2.40	0.55
2:C2:75:G:OP2	29:LY:73:TYR:OH	2.25	0.54
16:LB:222:THR:OG1	16:LB:223:LYS:N	2.40	0.54
35:Cc:175:ILE:HG22	35:Cc:176:THR:HG23	1.89	0.54
38:Cf:526:LYS:HE2	38:Cf:530:ASN:HD21	1.70	0.54
47:C4:80:U:H3	47:C4:98:G:H1	1.54	0.54
1:C1:1372:A:N6	1:C1:1400:A:O2'	2.40	0.54
2:C2:129:C:H5''	9:CJ:7:LYS:HE2	1.88	0.54
16:LB:63:PRO:O	16:LB:349:ARG:NH2	2.38	0.54
1:C1:260:A:N7	22:LN:12:LYS:NZ	2.55	0.54
1:C1:340:C:O2	1:C1:344:A:O2'	2.25	0.54
1:C1:3227:C:H2'	1:C1:3228:G:H8	1.72	0.54
7:CH:395:LYS:HA	7:CH:400:ARG:HH21	1.72	0.54
16:LB:381:MET:SD	16:LB:381:MET:N	2.81	0.54
1:C1:920:U:OP1	38:Cf:538:LYS:NZ	2.35	0.54
1:C1:3042:G:H2'	1:C1:3043:A:C8	2.43	0.54
3:CA:41:SER:OG	3:CA:42:ARG:N	2.37	0.54
17:LC:361:LEU:HD11	27:LT:148:PRO:HG2	1.89	0.54
10:LF:108:ILE:HG23	10:LF:132:MET:HG2	1.88	0.54
3:CA:36:VAL:HG12	3:CA:88:ASN:HD22	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:403:U:H2'	1:C1:404:G:H8	1.72	0.54
1:C1:1386:G:O6	30:Le:17:ARG:NH2	2.41	0.54
9:CJ:183:HIS:O	9:CJ:186:ARG:NH1	2.40	0.54
16:LB:92:TYR:HE2	16:LB:160:ARG:HE	1.55	0.54
27:LT:104:ASP:OD1	27:LT:107:ARG:NH2	2.41	0.54
46:LD:13:TYR:O	47:C4:11:A:N6	2.33	0.54
16:LB:293:ALA:HA	16:LB:304:LYS:H	1.72	0.54
16:LB:295:ALA:HB3	16:LB:304:LYS:HG3	1.89	0.54
1:C1:1150:U:H2'	1:C1:1151:A:H8	1.72	0.54
2:C2:196:G:O6	2:C2:201:U:O4	2.25	0.54
17:LC:154:ASP:N	17:LC:154:ASP:OD1	2.40	0.54
27:LT:79:ARG:HH22	27:LT:82:HIS:HA	1.73	0.54
37:Ce:83:LEU:HD21	37:Ce:94:ILE:HD11	1.90	0.54
6:CE:136:GLU:OE2	6:CE:139:ARG:NH2	2.40	0.54
40:Cg:224:VAL:N	40:Cg:321:ARG:O	2.39	0.54
8:CI:316:ARG:HA	8:CI:319:LYS:HG2	1.90	0.54
9:CJ:136:ASP:HA	9:CJ:139:ARG:HD2	1.90	0.54
11:CN:40:ALA:O	11:CN:43:GLN:NE2	2.41	0.54
37:Ce:10:ILE:HG23	37:Ce:15:CYS:HB2	1.89	0.54
1:C1:3134:A:OP2	23:LO:173:LYS:NZ	2.33	0.53
7:CH:474:TYR:OH	12:CQ:102:ARG:NH1	2.41	0.53
9:CJ:450:TYR:N	9:CJ:455:TYR:OH	2.39	0.53
17:LC:284:GLN:NE2	35:Cc:102:THR:O	2.41	0.53
1:C1:1046:A:N1	1:C1:1074:C:N3	2.56	0.53
1:C1:1158:C:OP1	23:LO:26:LYS:NZ	2.39	0.53
1:C1:3326:C:H2'	1:C1:3327:G:H8	1.73	0.53
16:LB:43:LEU:HD22	16:LB:209:ILE:HG12	1.91	0.53
1:C1:3023:U:O2	1:C1:3032:G:N2	2.32	0.53
1:C1:3274:U:H3	1:C1:3309:G:H5''	1.73	0.53
10:CM:192:HIS:O	10:CM:196:THR:OG1	2.23	0.53
40:Cg:39:ILE:HB	40:Cg:92:LEU:HD12	1.90	0.53
47:C4:45:U:H2'	47:C4:46:G:H8	1.74	0.53
1:C1:3138:U:HO2'	26:LS:172:THR:HG1	1.51	0.53
9:CJ:161:PRO:HG2	9:CJ:164:MET:HB2	1.91	0.53
1:C1:118:U:O3'	5:CC:279:ARG:NH1	2.42	0.53
1:C1:3039:C:H2'	1:C1:3040:G:H8	1.74	0.53
11:CN:152:MET:HE1	11:CN:173:LEU:HD21	1.91	0.53
13:CR:198:LEU:HD22	13:CR:209:MET:HG2	1.91	0.53
1:C1:770:G:O2'	17:LC:115:ASN:OD1	2.23	0.53
9:CJ:162:ALA:HA	9:CJ:165:ILE:HD12	1.91	0.53
16:LB:47:MET:H	16:LB:84:MET:HE1	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LT:38:ASP:OD1	27:LT:38:ASP:N	2.42	0.53
1:C1:638:G:O2'	1:C1:1417:A:OP1	2.27	0.53
1:C1:2404:G:O6	1:C1:2467:U:O4	2.27	0.53
2:C2:128:U:O4	9:CJ:48:ARG:NH1	2.41	0.53
1:C1:634:A:N6	1:C1:2332:G:C2	2.77	0.53
1:C1:2387:G:C6	1:C1:2563:G:N2	2.77	0.53
2:C2:154:C:H2'	2:C2:155:A:C8	2.44	0.53
4:CB:275:TRP:HE3	4:CB:278:VAL:HG11	1.74	0.53
5:CC:414:PRO:HD3	9:CJ:62:THR:HG22	1.91	0.53
9:CJ:45:ARG:NH2	9:CJ:68:ASP:OD2	2.42	0.53
16:LB:185:ASN:OD1	16:LB:185:ASN:N	2.42	0.53
28:LV:125:ALA:HB1	28:LV:132:ALA:HB2	1.91	0.53
1:C1:281:U:H2'	1:C1:282:G:H8	1.74	0.52
1:C1:3011:U:H3	1:C1:3045:G:H1	1.57	0.52
1:C1:3263:A:O2'	40:Cg:128:ARG:NH1	2.42	0.52
3:CA:243:ILE:HG22	3:CA:244:ILE:HG12	1.91	0.52
1:C1:2700:C:H2'	1:C1:2701:A:H8	1.74	0.52
2:C2:50:C:OP2	2:C2:51:G:N2	2.41	0.52
7:CH:461:LEU:HD13	12:CQ:71:PHE:HE2	1.74	0.52
9:CJ:98:GLY:O	19:LG:101:ARG:NH1	2.40	0.52
21:LM:130:GLU:HA	21:LM:133:LYS:NZ	2.24	0.52
26:LS:12:ARG:HG2	26:LS:24:LEU:HD12	1.90	0.52
1:C1:351:U:HO2'	34:Lj:16:HIS:HD1	1.51	0.52
1:C1:1196:U:H2'	1:C1:1197:A:H8	1.74	0.52
1:C1:2433:U:O4	1:C1:2436:G:O6	2.27	0.52
9:CJ:226:ILE:O	9:CJ:229:THR:OG1	2.27	0.52
35:Cc:54:LEU:HD13	35:Cc:74:LEU:HD22	1.90	0.52
1:C1:744:G:C6	1:C1:750:G:C2	2.97	0.52
24:LP:12:THR:HG21	37:Ce:161:LYS:HA	1.92	0.52
31:Lf:16:LEU:HD11	31:Lf:33:LYS:HB2	1.91	0.52
33:Li:38:ARG:NH2	33:Li:42:GLN:OE1	2.34	0.52
9:CJ:218:ILE:HG22	9:CJ:222:VAL:HG21	1.91	0.52
2:C2:194:C:OP2	8:CI:316:ARG:NH2	2.37	0.52
23:LO:17:LEU:HD12	23:LO:42:LEU:HD23	1.91	0.52
27:LT:127:GLN:OE1	27:LT:131:GLN:NE2	2.42	0.52
1:C1:1292:G:H2'	1:C1:1293:G:C8	2.45	0.52
4:CB:22:GLN:HA	4:CB:25:LYS:HG2	1.91	0.52
5:CC:137:TYR:HB3	5:CC:151:TYR:HE1	1.74	0.52
11:CN:70:LEU:HB3	11:CN:94:ILE:HG12	1.91	0.52
12:CQ:14:TRP:O	12:CQ:30:ARG:NH2	2.43	0.52
40:Cg:223:PRO:HA	40:Cg:322:ARG:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CQ:22:MET:HE1	28:LV:95:LEU:HB2	1.92	0.52
23:LO:39:CYS:HA	23:LO:42:LEU:HD13	1.90	0.52
37:Ce:182:GLN:H	37:Ce:191:TRP:HZ3	1.58	0.52
1:C1:63:A:H5'	22:LN:174:LEU:HD13	1.91	0.52
1:C1:213:G:C6	1:C1:1371:G:C2	2.97	0.52
1:C1:1046:A:N1	1:C1:1074:C:C5	2.78	0.52
1:C1:1386:G:OP2	30:Le:12:LYS:NZ	2.43	0.52
5:CC:137:TYR:HB3	5:CC:151:TYR:CE1	2.45	0.52
9:CJ:46:GLU:OE2	9:CJ:50:ARG:NH1	2.43	0.52
10:CM:142:TYR:H	10:CM:237:ARG:HH21	1.56	0.52
16:LB:83:PRO:O	16:LB:166:GLN:NE2	2.42	0.52
1:C1:34:A:H2'	1:C1:35:A:C8	2.44	0.52
1:C1:738:C:H42	1:C1:756:A:N6	2.08	0.52
2:C2:175:G:H2'	2:C2:176:G:O4'	2.10	0.52
3:CA:252:GLY:O	6:CE:579:GLN:NE2	2.38	0.52
6:CE:172:MET:HE2	6:CE:259:LYS:HB2	1.90	0.52
8:CI:217:ARG:NH1	8:CI:272:LEU:O	2.43	0.52
8:CI:299:GLU:OE1	8:CI:299:GLU:N	2.41	0.52
1:C1:2741:U:H2'	1:C1:2742:G:H8	1.75	0.51
2:C2:176:G:H2'	2:C2:177:C:H6	1.75	0.51
6:CE:415:ASP:OD1	6:CE:415:ASP:N	2.43	0.51
21:LM:98:ASN:HA	21:LM:101:LYS:HG3	1.92	0.51
24:LP:60:MET:HB3	24:LP:64:ALA:HA	1.91	0.51
27:LT:33:THR:HG23	27:LT:35:ARG:HH12	1.74	0.51
34:Lj:64:MET:O	34:Lj:68:SER:OG	2.22	0.51
6:CE:316:LEU:HG	6:CE:318:ILE:HD11	1.92	0.51
22:LN:46:ASP:OD1	22:LN:47:LYS:N	2.44	0.51
40:Cg:157:SER:OG	40:Cg:158:ASP:N	2.39	0.51
1:C1:3331:A:N6	16:LB:123:TYR:OH	2.42	0.51
12:CQ:106:VAL:HA	12:CQ:109:LYS:HE3	1.92	0.51
16:LB:63:PRO:HA	16:LB:68:HIS:NE2	2.25	0.51
29:LY:41:LYS:HE3	29:LY:42:TYR:CZ	2.45	0.51
32:Lh:12:LEU:HB3	32:Lh:62:VAL:HG21	1.91	0.51
1:C1:781:G:H22	17:LC:102:ALA:HA	1.75	0.51
5:CC:142:ASP:HB3	5:CC:148:ARG:HB2	1.92	0.51
6:CE:193:ARG:NH1	6:CE:219:GLY:O	2.42	0.51
10:CM:94:ARG:HB2	10:CM:114:LEU:HD22	1.93	0.51
16:LB:144:SER:O	16:LB:148:GLU:N	2.41	0.51
29:LY:86:ARG:NH1	29:LY:87:GLU:O	2.43	0.51
1:C1:2768:C:H2'	1:C1:2769:A:C8	2.46	0.51
9:CJ:148:LEU:HD21	9:CJ:234:TYR:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Le:97:ILE:HG21	30:Le:106:ARG:HG2	1.93	0.51
1:C1:2587:U:O4	1:C1:2607:G:O6	2.29	0.51
1:C1:3326:C:H2'	1:C1:3327:G:C8	2.45	0.51
3:CA:142:PHE:O	14:CU:246:GLN:NE2	2.43	0.51
12:CQ:93:MET:HA	12:CQ:96:ILE:HB	1.92	0.51
20:LL:42:LYS:HD2	20:LL:51:VAL:HG13	1.93	0.51
1:C1:1101:C:H2'	1:C1:1102:A:H8	1.74	0.51
2:C2:66:A:OP1	34:Lj:87:ARG:NH1	2.42	0.51
11:CN:193:ILE:O	11:CN:197:MET:N	2.43	0.51
24:LP:126:ARG:HA	24:LP:140:MET:HE1	1.92	0.51
35:Cc:117:ARG:HH21	35:Cc:200:ILE:HG22	1.74	0.51
1:C1:289:A:O2'	33:Li:41:ALA:O	2.28	0.51
1:C1:3192:C:H2'	1:C1:3193:G:H8	1.76	0.51
10:CM:89:LEU:HD21	10:CM:122:PHE:HD1	1.75	0.51
16:LB:21:ARG:HE	16:LB:273:TYR:HD2	1.59	0.51
18:LE:61:LEU:HD11	18:LE:103:ILE:HG13	1.91	0.51
1:C1:66:A:N6	1:C1:75:G:C2	2.79	0.51
6:CE:266:ALA:HB3	6:CE:296:SER:HB2	1.92	0.51
11:CN:96:ARG:NH1	11:CN:98:GLU:OE2	2.43	0.51
47:C4:16:C:N3	47:C4:64:A:N6	2.58	0.51
6:CE:248:LEU:HB3	6:CE:284:ILE:HD13	1.93	0.51
35:Cc:151:ASP:OD1	35:Cc:153:SER:OG	2.29	0.51
1:C1:202:A:N3	17:LC:228:ASN:ND2	2.58	0.50
11:CN:61:ARG:NH2	11:CN:105:GLY:O	2.38	0.50
36:Cd:14:LEU:HB3	36:Cd:24:ARG:HG3	1.93	0.50
4:CB:90:ASN:OD1	4:CB:247:TYR:OH	2.28	0.50
13:CR:206:VAL:HA	13:CR:209:MET:HE2	1.93	0.50
21:LM:33:ILE:O	26:LS:95:ARG:NH1	2.44	0.50
24:LP:122:ALA:HB3	24:LP:143:PRO:HB2	1.93	0.50
1:C1:324:C:H4'	34:Lj:71:PRO:HB3	1.91	0.50
3:CA:35:ARG:HB2	3:CA:86:CYS:HA	1.93	0.50
10:CM:174:ILE:HA	10:CM:177:GLU:HB2	1.93	0.50
11:CN:207:GLY:O	11:CN:210:THR:OG1	2.29	0.50
36:Cd:388:ALA:HB3	37:Ce:167:GLU:HG3	1.92	0.50
2:C2:210:C:OP1	6:CE:488:ASN:ND2	2.44	0.50
5:CC:370:TRP:O	5:CC:378:ARG:NH1	2.44	0.50
36:Cd:380:MET:SD	37:Ce:175:ARG:NH2	2.84	0.50
1:C1:1370:U:O2'	30:Le:100:ASN:O	2.26	0.50
1:C1:2562:U:H4'	42:CG:60:ALA:HA	1.91	0.50
11:CN:156:ASN:OD1	11:CN:156:ASN:N	2.44	0.50
16:LB:297:THR:OG1	16:LB:298:GLU:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LG:90:ALA:HB1	19:LG:188:ARG:HH12	1.76	0.50
48:CX:76:THR:HG23	48:CX:78:THR:H	1.75	0.50
1:C1:788:A:H61	1:C1:915:G:H22	1.60	0.50
1:C1:2390:U:C4	1:C1:2560:G:C6	3.00	0.50
1:C1:3016:G:C6	1:C1:3042:G:N1	2.80	0.50
5:CC:180:TYR:HB3	5:CC:186:ILE:HG22	1.93	0.50
1:C1:2735:G:H1	1:C1:2741:U:H3	1.58	0.50
32:Lh:68:ARG:NH2	32:Lh:84:ASP:O	2.45	0.50
38:Cf:448:LEU:HD13	38:Cf:488:GLU:HG2	1.94	0.50
3:CA:73:ARG:N	3:CA:76:GLU:OE2	2.41	0.50
8:CI:292:GLN:HA	8:CI:295:ARG:HE	1.76	0.50
26:LS:80:ARG:NH1	27:LT:154:VAL:O	2.44	0.50
27:LT:71:ALA:HA	27:LT:92:ARG:HA	1.94	0.50
32:Lh:48:LYS:HG3	32:Lh:52:LEU:HD23	1.93	0.50
28:LV:20:PRO:HA	28:LV:53:ALA:HA	1.93	0.50
29:LY:34:LEU:HD23	29:LY:38:LEU:HB3	1.92	0.50
36:Cd:310:GLU:OE2	37:Ce:173:ARG:NH1	2.41	0.50
40:Cg:135:LYS:HD2	40:Cg:327:VAL:HG21	1.93	0.50
1:C1:1044:A:H4'	27:LT:105:PHE:CE1	2.48	0.49
1:C1:2480:C:H2'	1:C1:2481:A:H8	1.77	0.49
1:C1:2548:A:H2'	1:C1:2549:A:C8	2.47	0.49
17:LC:21:GLU:OE1	17:LC:263:LYS:NZ	2.45	0.49
22:LN:181:ASN:OD1	22:LN:184:ARG:NH2	2.44	0.49
42:CG:147:THR:HA	42:CG:164:CYS:HA	1.93	0.49
1:C1:744:G:C6	1:C1:750:G:N1	2.80	0.49
1:C1:2435:C:H2'	1:C1:2436:G:H21	1.76	0.49
9:CJ:201:ILE:HG21	9:CJ:245:LEU:HD11	1.94	0.49
47:C4:85:U:C4	47:C4:86:C:N4	2.81	0.49
15:Ch:273:GLU:HA	15:Ch:276:ILE:HD12	1.94	0.49
1:C1:2306:U:H2'	1:C1:2307:A:C8	2.46	0.49
1:C1:2425:G:N1	1:C1:2455:U:N3	2.61	0.49
11:CN:187:ASN:H	11:CN:210:THR:HG22	1.77	0.49
17:LC:20:THR:OG1	35:Cc:12:LYS:NZ	2.45	0.49
21:LM:76:ALA:HB1	21:LM:80:ALA:HB3	1.95	0.49
42:CG:100:VAL:HA	42:CG:119:VAL:HA	1.94	0.49
47:C4:29:G:H2'	47:C4:30:G:H8	1.76	0.49
1:C1:3151:C:O2'	1:C1:3153:U:OP1	2.30	0.49
5:CC:361:LEU:HD12	5:CC:362:PRO:HD2	1.94	0.49
6:CE:515:TYR:HE1	6:CE:541:VAL:HG23	1.77	0.49
33:Li:36:SER:O	33:Li:36:SER:OG	2.30	0.49
36:Cd:28:TYR:CE2	36:Cd:32:LYS:HD2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1429:G:O2'	1:C1:2317:G:O6	2.28	0.49
1:C1:3267:G:H2'	1:C1:3268:G:H8	1.77	0.49
4:CB:28:LYS:HD3	4:CB:252:PRO:HG3	1.94	0.49
5:CC:138:ARG:NH1	5:CC:140:GLU:OE2	2.45	0.49
10:CM:70:ARG:NH1	10:CM:134:LYS:O	2.45	0.49
11:CN:11:ASN:HB3	11:CN:207:GLY:HA3	1.94	0.49
11:CN:107:VAL:HG23	11:CN:108:ILE:HG13	1.94	0.49
27:LT:51:GLY:O	27:LT:92:ARG:NH1	2.46	0.49
1:C1:284:U:OP2	22:LN:68:ARG:NH2	2.45	0.49
18:LE:139:GLU:HG2	36:Cd:247:PHE:HD1	1.78	0.49
10:LF:94:ARG:HD2	10:LF:109:LEU:HD13	1.95	0.49
23:LO:199:LEU:HD12	23:LO:204:TYR:HB2	1.93	0.49
27:LT:53:PRO:HD3	27:LT:92:ARG:HH12	1.77	0.49
38:Cf:454:ARG:HH12	38:Cf:458:LEU:HD22	1.76	0.49
6:CE:270:LEU:HD12	6:CE:275:GLU:HG3	1.94	0.49
7:CH:437:ILE:HD11	11:CN:79:GLN:HE22	1.78	0.49
11:CN:115:ALA:HB3	11:CN:137:VAL:HG22	1.94	0.49
10:LF:113:ARG:NH1	10:LF:206:ASN:OD1	2.46	0.49
30:Le:131:VAL:HG12	37:Ce:135:GLU:HG2	1.95	0.49
35:Cc:203:ASP:OD1	35:Cc:253:ARG:NH1	2.33	0.49
7:CH:445:ASN:HD21	12:CQ:2:ARG:HG2	1.78	0.49
12:CQ:32:CYS:SG	12:CQ:33:ARG:N	2.86	0.49
16:LB:58:ARG:NH1	16:LB:355:VAL:HG22	2.28	0.49
22:LN:36:ILE:HD11	22:LN:105:ARG:HB3	1.95	0.49
27:LT:72:VAL:N	27:LT:91:VAL:O	2.40	0.49
35:Cc:225:ILE:HA	35:Cc:228:MET:HE3	1.95	0.49
9:CJ:242:ASN:O	9:CJ:246:TYR:HB2	2.12	0.48
9:CJ:379:PRO:HB2	9:CJ:382:PRO:HD2	1.94	0.48
9:CJ:387:LEU:HD13	9:CJ:395:ILE:HG12	1.95	0.48
18:LE:57:VAL:HB	18:LE:107:VAL:HG13	1.95	0.48
1:C1:190:G:H5''	36:Cd:429:LYS:HG3	1.93	0.48
1:C1:1320:C:O2	30:Le:13:LYS:NZ	2.46	0.48
1:C1:2695:C:H2'	1:C1:2696:A:C8	2.48	0.48
1:C1:3254:A:O3'	16:LB:175:LYS:NZ	2.46	0.48
1:C1:3323:C:N4	1:C1:3326:C:OP2	2.46	0.48
1:C1:3328:C:H2'	1:C1:3329:C:C6	2.49	0.48
12:CQ:67:SER:HA	12:CQ:70:GLN:HG2	1.95	0.48
36:Cd:301:HIS:O	36:Cd:391:GLN:NE2	2.47	0.48
37:Ce:114:THR:O	37:Ce:118:GLN:HG3	2.13	0.48
38:Cf:539:LEU:HA	38:Cf:542:LYS:HZ3	1.78	0.48
40:Cg:117:ARG:HD3	40:Cg:336:ARG:HH21	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:363:THR:HB	5:CC:366:GLU:HG3	1.94	0.48
10:CM:102:PRO:HB2	10:CM:105:PRO:HD2	1.95	0.48
16:LB:220:ALA:HB2	16:LB:337:MET:HE1	1.95	0.48
18:LE:200:PHE:OXT	21:LM:113:THR:OG1	2.31	0.48
26:LS:99:ARG:NH2	26:LS:126:VAL:HG13	2.28	0.48
27:LT:108:ARG:HD3	27:LT:130:ARG:HD2	1.95	0.48
36:Cd:272:VAL:HG22	36:Cd:284:THR:HG23	1.94	0.48
46:LD:158:THR:O	47:C4:35:C:O2'	2.27	0.48
1:C1:892:C:H2'	1:C1:893:G:C8	2.48	0.48
1:C1:2693:U:H2'	1:C1:2694:A:H8	1.78	0.48
1:C1:3201:U:OP1	21:LM:122:ARG:NH1	2.46	0.48
13:CR:27:LEU:HD22	20:LL:37:LEU:HD22	1.95	0.48
16:LB:373:THR:HG23	16:LB:376:GLU:H	1.78	0.48
40:Cg:39:ILE:HG21	40:Cg:104:ARG:HH12	1.78	0.48
1:C1:23:A:OP2	34:Lj:43:LYS:NZ	2.42	0.48
1:C1:1127:G:OP1	30:Le:45:ARG:NH2	2.47	0.48
1:C1:1417:A:H5''	1:C1:1418:U:H5''	1.95	0.48
1:C1:1846:A:OP1	38:Cf:425:TYR:OH	2.32	0.48
1:C1:2396:U:H5'	1:C1:2551:A:H2	1.79	0.48
2:C2:9:A:H2'	2:C2:10:A:C8	2.49	0.48
3:CA:133:LEU:HB3	3:CA:173:LYS:HE2	1.93	0.48
1:C1:2385:U:H2'	1:C1:2386:A:H8	1.77	0.48
1:C1:2389:U:O2	1:C1:2561:G:O6	2.31	0.48
4:CB:72:ILE:HG22	4:CB:272:PRO:HD2	1.95	0.48
9:CJ:117:GLY:HA3	9:CJ:167:ARG:HE	1.78	0.48
1:C1:484:G:H4'	30:Le:1:MET:HE3	1.95	0.48
1:C1:612:G:H21	1:C1:1382:G:H5'	1.78	0.48
23:LO:13:LYS:O	26:LS:169:ARG:NH2	2.43	0.48
1:C1:1450:A:C6	1:C1:1840:G:N2	2.81	0.48
1:C1:3189:G:H2'	1:C1:3190:G:H8	1.77	0.48
7:CH:374:MET:HE2	11:CN:175:SER:HB3	1.96	0.48
10:CM:129:THR:HG22	10:CM:132:MET:HE2	1.95	0.48
14:CU:267:ARG:NH2	48:CX:75:ASN:OD1	2.47	0.48
10:LF:110:GLN:HG3	10:LF:115:ARG:HH22	1.77	0.48
23:LO:79:SER:HB3	23:LO:108:GLU:HG3	1.94	0.48
3:CA:133:LEU:HB2	3:CA:136:SER:HB3	1.94	0.48
25:LQ:95:ILE:HG23	25:LQ:108:VAL:HG21	1.94	0.48
28:LV:109:GLY:O	28:LV:130:ARG:NH1	2.47	0.48
38:Cf:442:LYS:HD2	38:Cf:495:LEU:HD11	1.94	0.48
40:Cg:48:VAL:HA	40:Cg:51:LEU:HB3	1.96	0.48
1:C1:36:C:O2'	1:C1:915:G:N2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:278:U:O2'	22:LN:179:ARG:O	2.32	0.48
1:C1:1845:C:O2'	38:Cf:476:ARG:NH2	2.47	0.48
2:C2:23:U:OP1	29:LY:15:ARG:NH1	2.46	0.48
9:CJ:415:ILE:HB	9:CJ:453:ARG:HD2	1.96	0.48
28:LV:81:VAL:H	28:LV:102:GLY:HA2	1.78	0.48
1:C1:318:U:OP1	20:LL:31:LYS:NZ	2.42	0.47
1:C1:647:A:N1	1:C1:922:G:O2'	2.45	0.47
1:C1:2433:U:C4	1:C1:2436:G:O6	2.67	0.47
1:C1:2996:G:H2'	1:C1:2997:A:H8	1.79	0.47
1:C1:3195:C:H2'	1:C1:3196:G:H8	1.79	0.47
1:C1:3309:G:N2	16:LB:381:MET:O	2.47	0.47
16:LB:66:LYS:H	16:LB:66:LYS:HG2	1.37	0.47
1:C1:1305:C:H4'	26:LS:2:GLY:H	1.79	0.47
3:CA:51:LEU:HB3	3:CA:92:PHE:HE2	1.78	0.47
4:CB:75:SER:OG	4:CB:76:HIS:N	2.46	0.47
6:CE:223:ARG:NH1	6:CE:246:ASP:OD1	2.48	0.47
11:CN:19:LEU:HG	11:CN:200:ASN:HB3	1.95	0.47
25:LQ:48:LYS:HZ3	25:LQ:83:SER:HB3	1.79	0.47
32:Lh:31:LEU:HD21	32:Lh:35:ARG:HH21	1.77	0.47
32:Lh:100:GLU:OE1	32:Lh:104:ARG:NH2	2.48	0.47
42:CG:39:ARG:O	42:CG:46:TYR:N	2.42	0.47
1:C1:1083:G:H5''	10:LF:113:ARG:HD3	1.97	0.47
1:C1:2433:U:O2	1:C1:2437:G:O6	2.32	0.47
3:CA:74:LEU:HB3	3:CA:250:PHE:HB3	1.96	0.47
5:CC:184:PRO:HA	5:CC:197:ARG:HH12	1.80	0.47
9:CJ:187:LYS:HB2	9:CJ:198:GLN:HB3	1.96	0.47
18:LE:152:LYS:H	18:LE:152:LYS:HG2	1.53	0.47
1:C1:1101:C:H2'	1:C1:1102:A:C8	2.48	0.47
1:C1:1336:G:OP1	37:Ce:41:GLN:NE2	2.38	0.47
1:C1:3002:G:O3'	16:LB:276:ARG:NH1	2.47	0.47
1:C1:3283:G:H21	1:C1:3302:A:H2	1.62	0.47
6:CE:387:LEU:HD12	6:CE:411:LEU:HD21	1.95	0.47
15:Ch:283:ARG:NH2	40:Cg:326:LEU:O	2.41	0.47
10:LF:233:ASP:OD1	10:LF:237:ARG:NH2	2.44	0.47
21:LM:119:LYS:O	21:LM:123:LEU:N	2.45	0.47
22:LN:5:LYS:HE3	33:Li:46:THR:HG22	1.95	0.47
45:LJ:73:ARG:HA	45:LJ:77:ALA:HB2	1.96	0.47
1:C1:159:G:OP2	13:CR:227:ARG:NH1	2.47	0.47
1:C1:506:G:H5''	17:LC:346:ALA:HB2	1.95	0.47
1:C1:966:U:H2'	1:C1:967:U:H6	1.78	0.47
3:CA:139:ILE:HD11	3:CA:176:ILE:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CN:214:GLU:HA	11:CN:217:VAL:HG12	1.96	0.47
40:Cg:217:TYR:HB3	40:Cg:326:LEU:HB3	1.96	0.47
1:C1:634:A:H61	1:C1:2332:G:N2	2.12	0.47
1:C1:947:U:H2'	1:C1:948:A:C8	2.48	0.47
1:C1:1052:U:H3	1:C1:1070:U:H3	1.62	0.47
1:C1:3188:U:H2'	1:C1:3189:G:C8	2.49	0.47
2:C2:205:G:H4'	4:CB:238:SER:HB2	1.97	0.47
3:CA:247:GLU:HB3	3:CA:253:PRO:HD2	1.96	0.47
5:CC:173:GLY:HA3	14:CU:274:GLU:HB2	1.96	0.47
6:CE:133:LYS:HB3	6:CE:133:LYS:HE3	1.67	0.47
8:CI:214:THR:OG1	8:CI:215:ARG:N	2.48	0.47
40:Cg:141:TYR:HA	40:Cg:194:ARG:HH11	1.78	0.47
1:C1:35:A:H2'	1:C1:36:C:H6	1.80	0.47
1:C1:66:A:H61	1:C1:75:G:N2	2.11	0.47
1:C1:585:G:H1	1:C1:596:G:H5''	1.80	0.47
1:C1:965:G:H22	1:C1:1120:U:H5''	1.79	0.47
1:C1:1114:C:H2'	1:C1:1115:A:H8	1.79	0.47
4:CB:149:GLU:HG2	4:CB:150:HIS:ND1	2.29	0.47
27:LT:48:VAL:HG21	27:LT:94:GLU:HG2	1.97	0.47
29:LY:1:MET:HE3	29:LY:1:MET:HB2	1.88	0.47
29:LY:57:ILE:HA	29:LY:103:VAL:HG12	1.97	0.47
29:LY:111:ASP:N	29:LY:111:ASP:OD1	2.46	0.47
32:Lh:15:LYS:HB2	32:Lh:15:LYS:HE2	1.72	0.47
32:Lh:99:LYS:HB2	32:Lh:99:LYS:HE2	1.69	0.47
1:C1:692:A:N3	3:CA:285:GLN:NE2	2.52	0.47
1:C1:1046:A:C6	1:C1:1074:C:N3	2.83	0.47
1:C1:1422:G:OP1	17:LC:84:HIS:NE2	2.45	0.47
21:LM:123:LEU:HD21	23:LO:195:VAL:HB	1.96	0.47
1:C1:230:A:H2'	1:C1:231:A:C8	2.50	0.47
1:C1:664:A:H3'	25:LQ:118:ASN:HD21	1.79	0.47
1:C1:781:G:O6	17:LC:105:LYS:NZ	2.48	0.47
1:C1:2566:G:H2'	1:C1:2567:A:H8	1.78	0.47
2:C2:106:C:H4'	2:C2:107:G:H5''	1.97	0.47
3:CA:36:VAL:HG12	3:CA:88:ASN:HB2	1.96	0.47
3:CA:63:ARG:HH11	3:CA:63:ARG:HB3	1.80	0.47
11:CN:47:PRO:HG3	11:CN:89:PRO:HD3	1.96	0.47
36:Cd:404:VAL:HG13	36:Cd:420:LYS:HB2	1.97	0.47
6:CE:150:ASP:OD1	6:CE:312:ARG:NH2	2.38	0.47
16:LB:50:LYS:HA	16:LB:79:ILE:HD12	1.96	0.47
16:LB:89:LEU:HD12	16:LB:161:VAL:HA	1.97	0.47
16:LB:111:SER:OG	16:LB:112:ASP:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LY:34:LEU:HD11	29:LY:47:ILE:HG12	1.95	0.47
35:Cc:105:ASP:OD1	35:Cc:105:ASP:N	2.43	0.47
1:C1:1292:G:H2'	1:C1:1293:G:H8	1.80	0.46
6:CE:537:ASP:OD2	6:CE:540:LYS:NZ	2.36	0.46
9:CJ:49:ASP:HB3	9:CJ:52:LYS:HB2	1.96	0.46
10:LF:95:ILE:HD11	10:LF:234:LEU:HD23	1.97	0.46
21:LM:33:ILE:HG23	21:LM:39:VAL:HG12	1.96	0.46
24:LP:94:LEU:HB3	24:LP:148:LEU:HD21	1.96	0.46
28:LV:82:ARG:NH1	28:LV:119:PRO:O	2.39	0.46
29:LY:54:GLU:HB3	29:LY:107:LYS:HB3	1.96	0.46
1:C1:65:A:H1'	1:C1:77:A:H1'	1.97	0.46
1:C1:3212:C:OP2	18:LE:96:ARG:NH1	2.48	0.46
5:CC:182:SER:HB2	48:CX:85:PRO:HG3	1.97	0.46
10:CM:126:THR:N	10:CM:129:THR:OG1	2.34	0.46
47:C4:11:A:N1	47:C4:67:G:O2'	2.43	0.46
11:CN:162:HIS:HD1	11:CN:164:LYS:H	1.63	0.46
19:LG:164:GLU:OE2	22:LN:26:ARG:NH2	2.41	0.46
31:Lf:18:TYR:OH	31:Lf:91:LEU:O	2.29	0.46
37:Ce:69:GLU:OE1	37:Ce:69:GLU:N	2.39	0.46
40:Cg:73:ASN:O	40:Cg:74:ARG:NE	2.47	0.46
40:Cg:120:LYS:HB2	40:Cg:334:ARG:HG3	1.98	0.46
1:C1:434:G:H2'	1:C1:435:C:C6	2.49	0.46
1:C1:538:G:H2'	1:C1:539:G:H8	1.80	0.46
1:C1:800:U:O4	1:C1:888:G:O6	2.33	0.46
1:C1:2726:U:H2'	1:C1:2727:A:C8	2.50	0.46
3:CA:144:ALA:HB3	14:CU:225:ARG:HA	1.98	0.46
15:Ch:304:ALA:O	15:Ch:308:GLU:N	2.47	0.46
16:LB:160:ARG:HA	16:LB:183:GLN:HA	1.98	0.46
30:Le:20:ARG:O	30:Le:23:SER:OG	2.24	0.46
30:Le:100:ASN:OD1	30:Le:100:ASN:N	2.43	0.46
1:C1:394:A:OP2	36:Cd:25:GLN:NE2	2.48	0.46
1:C1:886:U:H2'	1:C1:888:G:H1'	1.97	0.46
1:C1:1298:C:H5''	1:C1:1299:A:H5''	1.98	0.46
16:LB:299:THR:HG21	16:LB:358:LYS:HD3	1.96	0.46
20:LL:77:LEU:HD22	20:LL:87:ARG:HD2	1.98	0.46
3:CA:40:SER:HB2	3:CA:52:LEU:HD21	1.97	0.46
6:CE:450:ARG:HH22	6:CE:455:LYS:HE2	1.81	0.46
11:CN:206:THR:OG1	11:CN:207:GLY:N	2.47	0.46
16:LB:282:LYS:HD3	16:LB:284:TYR:HE1	1.81	0.46
19:LG:155:LEU:HD13	19:LG:183:ILE:HD13	1.98	0.46
30:Le:20:ARG:HH21	30:Le:34:ARG:HG3	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Cc:8:MET:HB2	35:Cc:8:MET:HE3	1.77	0.46
35:Cc:63:ARG:HB2	35:Cc:66:PRO:HG2	1.98	0.46
1:C1:523:A:H2'	1:C1:524:A:C8	2.50	0.46
1:C1:802:U:H2'	1:C1:803:G:C8	2.51	0.46
1:C1:956:C:H2'	1:C1:957:G:H8	1.80	0.46
40:Cg:43:GLU:O	40:Cg:95:ARG:NH2	2.44	0.46
1:C1:1158:C:O3'	23:LO:91:PRO:HG3	2.15	0.46
1:C1:2343:G:N2	1:C1:2348:A:N6	2.64	0.46
1:C1:2555:U:H2'	1:C1:2556:G:C8	2.50	0.46
2:C2:47:C:H1'	2:C2:61:A:H2'	1.97	0.46
4:CB:86:PRO:HB2	4:CB:87:HIS:CE1	2.51	0.46
8:CI:195:PRO:HG2	8:CI:253:LEU:HD23	1.98	0.46
11:CN:162:HIS:CE1	11:CN:164:LYS:HB2	2.50	0.46
16:LB:14:LEU:HA	16:LB:17:LEU:HG	1.98	0.46
16:LB:60:LEU:HD23	16:LB:67:ALA:HB3	1.97	0.46
18:LE:182:TYR:OH	21:LM:114:ASP:OD2	2.21	0.46
28:LV:29:ASP:HB3	28:LV:103:VAL:HG23	1.98	0.46
38:Cf:419:LEU:HD12	38:Cf:426:ALA:HB2	1.97	0.46
1:C1:800:U:H2'	1:C1:801:A:C8	2.51	0.46
1:C1:1845:C:N4	38:Cf:424:THR:OG1	2.46	0.46
1:C1:2626:U:H2'	1:C1:2627:G:H8	1.80	0.46
2:C2:81:U:H4'	32:Lh:6:LYS:HD3	1.97	0.46
9:CJ:254:PRO:O	9:CJ:256:LYS:NZ	2.49	0.46
12:CQ:38:LYS:HA	12:CQ:41:LYS:HB2	1.98	0.46
12:CQ:86:TRP:O	12:CQ:90:LEU:N	2.43	0.46
18:LE:76:LEU:HD21	18:LE:123:ALA:HB1	1.97	0.46
43:Lq:17:LEU:HA	43:Lq:18:ASP:HA	1.60	0.46
1:C1:620:C:O2'	31:Lf:23:ARG:O	2.32	0.46
3:CA:106:LYS:HB2	3:CA:110:GLY:HA3	1.98	0.46
4:CB:46:LYS:HE2	6:CE:482:GLU:OE2	2.16	0.46
16:LB:117:ARG:HE	16:LB:176:LYS:HD3	1.80	0.46
10:LF:96:LYS:HG2	10:LF:139:TRP:CD1	2.51	0.46
19:LG:146:ILE:HG23	19:LG:178:ILE:HD12	1.97	0.46
28:LV:18:GLY:HA3	28:LV:85:LYS:HG3	1.97	0.46
36:Cd:189:ASN:OD1	36:Cd:190:LEU:N	2.49	0.46
40:Cg:121:TYR:HB2	40:Cg:333:MET:HE1	1.98	0.46
1:C1:19:U:H2'	1:C1:20:A:C8	2.50	0.45
10:CM:134:LYS:HE3	10:CM:134:LYS:HB3	1.75	0.45
10:LF:99:ASN:OD1	10:LF:100:LYS:N	2.49	0.45
10:LF:126:THR:HG22	10:LF:128:ALA:H	1.80	0.45
3:CA:115:PHE:HE2	3:CA:189:ILE:HD12	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CB:18:VAL:HG22	4:CB:295:GLN:HE21	1.81	0.45
10:CM:153:LEU:HD11	10:CM:245:ILE:HG21	1.98	0.45
19:LG:159:ASP:OD1	19:LG:159:ASP:N	2.50	0.45
33:Li:53:ILE:HA	33:Li:56:VAL:HG22	1.98	0.45
1:C1:3053:C:H4'	16:LB:327:GLY:HA2	1.99	0.45
3:CA:108:PRO:HG3	5:CC:154:ILE:HG12	1.98	0.45
3:CA:133:LEU:HD22	14:CU:273:ALA:HB3	1.98	0.45
8:CI:323:MET:HE2	8:CI:323:MET:HB3	1.88	0.45
12:CQ:85:LEU:HA	12:CQ:88:LYS:HG2	1.98	0.45
16:LB:117:ARG:HH21	16:LB:176:LYS:HD3	1.81	0.45
37:Ce:107:HIS:NE2	37:Ce:111:GLN:OE1	2.50	0.45
1:C1:2352:A:N6	1:C1:2948:G:O6	2.49	0.45
1:C1:2357:G:N2	1:C1:2941:C:O2'	2.48	0.45
1:C1:3105:C:H2'	1:C1:3106:G:H8	1.82	0.45
2:C2:83:C:O2	29:LY:50:ARG:NH2	2.49	0.45
16:LB:283:ILE:HG12	16:LB:325:ILE:HD12	1.97	0.45
40:Cg:38:ARG:NH1	40:Cg:69:GLU:OE1	2.49	0.45
4:CB:76:HIS:HB3	4:CB:78:LEU:HD13	1.97	0.45
10:LF:178:ASN:O	10:LF:181:LYS:NZ	2.49	0.45
19:LG:68:LEU:HD22	19:LG:72:LEU:HG	1.99	0.45
21:LM:35:ASP:OD2	21:LM:38:ARG:NH1	2.49	0.45
1:C1:616:C:H2'	1:C1:617:C:H6	1.82	0.45
1:C1:2959:C:OP1	16:LB:26:ARG:NH2	2.43	0.45
1:C1:3103:G:H2'	1:C1:3104:A:H8	1.82	0.45
1:C1:3254:A:H5''	16:LB:175:LYS:HG3	1.97	0.45
2:C2:84:C:H1'	29:LY:112:LYS:HE3	1.97	0.45
12:CQ:22:MET:HE1	28:LV:95:LEU:HD12	1.97	0.45
16:LB:58:ARG:NH1	16:LB:357:LEU:HD22	2.32	0.45
44:Cx:126:GLN:OE1	44:Cx:126:GLN:N	2.50	0.45
48:CX:69:LEU:HD23	48:CX:69:LEU:HA	1.86	0.45
1:C1:621:G:O2'	30:Le:48:LYS:NZ	2.48	0.45
1:C1:2617:G:N1	1:C1:2670:U:N3	2.65	0.45
9:CJ:217:ARG:NH1	10:CM:169:LEU:O	2.49	0.45
13:CR:28:ASN:ND2	13:CR:41:LYS:HG2	2.32	0.45
16:LB:48:GLY:N	16:LB:337:MET:O	2.40	0.45
38:Cf:420:SER:OG	38:Cf:423:LEU:N	2.50	0.45
1:C1:115:A:N6	1:C1:149:U:C2	2.85	0.45
1:C1:202:A:H4'	1:C1:204:A:N7	2.32	0.45
1:C1:462:C:O3'	37:Ce:58:LYS:NZ	2.49	0.45
8:CI:211:GLY:HA3	8:CI:240:VAL:HG21	1.98	0.45
10:CM:110:GLN:HG3	10:CM:115:ARG:NH1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LS:45:LEU:HD23	26:LS:45:LEU:HA	1.80	0.45
41:CP:535:LYS:O	41:CP:582:LYS:N	2.45	0.45
47:C4:2:C:H2'	47:C4:3:G:H8	1.81	0.45
1:C1:724:C:N3	25:LQ:168:ARG:NH2	2.65	0.45
1:C1:3020:U:O4	1:C1:3037:G:O6	2.35	0.45
3:CA:63:ARG:HD3	3:CA:84:TYR:HD2	1.81	0.45
11:CN:186:VAL:HG21	11:CN:197:MET:HE3	1.98	0.45
16:LB:43:LEU:HB2	16:LB:209:ILE:HG23	1.98	0.45
17:LC:244:GLN:O	17:LC:253:ARG:NH1	2.49	0.45
18:LE:84:THR:HB	18:LE:94:LEU:HD23	1.98	0.45
33:Li:68:GLU:OE2	33:Li:71:ARG:NH2	2.50	0.45
1:C1:642:C:H2'	1:C1:643:A:C8	2.49	0.45
6:CE:157:THR:OG1	6:CE:265:GLU:OE2	2.34	0.45
9:CJ:390:PHE:CG	9:CJ:465:ILE:HD11	2.52	0.45
11:CN:12:GLU:OE1	11:CN:12:GLU:N	2.50	0.45
16:LB:127:LYS:HA	16:LB:127:LYS:HD3	1.87	0.45
18:LE:139:GLU:HG2	36:Cd:247:PHE:CD1	2.51	0.45
30:Le:83:VAL:HG21	30:Le:109:ILE:HG23	1.99	0.45
32:Lh:89:LEU:HD23	32:Lh:93:LEU:HB3	1.99	0.45
1:C1:155:G:H2'	1:C1:156:G:C8	2.52	0.44
1:C1:952:G:H2'	1:C1:953:U:C6	2.52	0.44
23:LO:196:SER:OG	23:LO:197:GLU:OE2	2.34	0.44
32:Lh:34:LEU:HD13	32:Lh:37:GLN:HE21	1.82	0.44
36:Cd:290:ARG:HA	36:Cd:290:ARG:HH11	1.82	0.44
1:C1:115:A:H2'	1:C1:257:A:H2'	1.99	0.44
1:C1:909:C:H2'	1:C1:910:A:C8	2.52	0.44
1:C1:2353:G:N1	1:C1:2946:C:O2	2.47	0.44
1:C1:3118:A:OP1	36:Cd:301:HIS:NE2	2.47	0.44
6:CE:538:LEU:HA	6:CE:541:VAL:HG22	1.99	0.44
9:CJ:373:PHE:HB2	9:CJ:415:ILE:HD13	2.00	0.44
14:CU:282:MET:HA	14:CU:285:VAL:HG12	1.97	0.44
16:LB:57:VAL:HG12	16:LB:359:TRP:HD1	1.81	0.44
16:LB:216:ILE:N	16:LB:281:HIS:O	2.41	0.44
21:LM:16:VAL:HG11	21:LM:74:ARG:HA	2.00	0.44
28:LV:40:ALA:HB3	28:LV:61:MET:HB2	1.98	0.44
28:LV:85:LYS:HE2	28:LV:86:PRO:HD2	2.00	0.44
38:Cf:407:ALA:HB3	40:Cg:149:MET:HB2	1.99	0.44
40:Cg:150:ASN:HB3	40:Cg:199:ASN:HB2	1.99	0.44
1:C1:1196:U:H2'	1:C1:1197:A:C8	2.52	0.44
2:C2:26:U:O2'	17:LC:52:ALA:O	2.34	0.44
3:CA:160:LEU:HD23	3:CA:161:HIS:HD2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CA:192:ARG:NE	3:CA:237:ARG:HD2	2.33	0.44
8:CI:309:GLU:O	8:CI:313:ARG:HG3	2.17	0.44
9:CJ:17:MET:HE2	9:CJ:66:THR:HA	2.00	0.44
15:Ch:274:GLN:HA	15:Ch:277:GLU:OE2	2.17	0.44
18:LE:100:ARG:HB3	31:Lf:106:PRO:HB3	1.98	0.44
35:Cc:58:LEU:HG	35:Cc:111:LYS:HD2	1.99	0.44
1:C1:3127:A:H62	31:Lf:56:ARG:NH2	2.11	0.44
5:CC:334:PRO:HA	5:CC:335:PRO:HD3	1.92	0.44
11:CN:117:ILE:HG12	11:CN:121:LEU:HD22	1.98	0.44
16:LB:76:VAL:HG12	16:LB:326:LYS:HA	2.00	0.44
28:LV:71:LEU:HA	28:LV:74:LYS:HD2	2.00	0.44
35:Cc:127:MET:HE2	35:Cc:155:VAL:HG22	2.00	0.44
37:Ce:33:SER:OG	37:Ce:35:SER:O	2.36	0.44
1:C1:312:G:OP1	22:LN:169:LYS:NZ	2.49	0.44
1:C1:662:C:O2'	1:C1:666:U:OP1	2.32	0.44
1:C1:892:C:H2'	1:C1:893:G:H8	1.82	0.44
1:C1:2344:G:H1'	1:C1:2348:A:H62	1.82	0.44
2:C2:201:U:H2'	2:C2:202:C:C6	2.52	0.44
3:CA:188:LYS:HE3	3:CA:239:VAL:HG11	1.98	0.44
9:CJ:230:PHE:HA	9:CJ:233:PHE:HD2	1.83	0.44
12:CQ:96:ILE:HD13	12:CQ:99:ILE:HD11	2.00	0.44
17:LC:13:ASP:OD1	17:LC:13:ASP:N	2.48	0.44
36:Cd:357:ARG:HG2	36:Cd:393:ILE:HG13	1.99	0.44
1:C1:750:G:H2'	1:C1:751:G:C4	2.53	0.44
1:C1:979:A:H2'	1:C1:980:G:C8	2.53	0.44
1:C1:3217:U:H4'	31:Lf:66:ILE:HD12	2.00	0.44
3:CA:194:TYR:HA	3:CA:233:GLU:HA	1.98	0.44
5:CC:327:TRP:NE1	9:CJ:132:PRO:O	2.51	0.44
9:CJ:141:LEU:HD22	9:CJ:145:LEU:HG	1.99	0.44
11:CN:118:HIS:CE1	11:CN:120:ASP:HB2	2.52	0.44
16:LB:132:LYS:HA	16:LB:135:LYS:HB2	1.99	0.44
47:C4:59:C:H2'	47:C4:60:A:H8	1.83	0.44
1:C1:893:G:H2'	1:C1:894:A:H8	1.82	0.44
1:C1:1364:G:OP2	17:LC:204:ARG:NH1	2.50	0.44
1:C1:2772:G:H2'	1:C1:2773:G:H8	1.81	0.44
1:C1:3262:G:O2'	1:C1:3263:A:O5'	2.33	0.44
9:CJ:410:GLU:OE2	9:CJ:418:GLN:NE2	2.51	0.44
28:LV:38:ILE:HG12	28:LV:60:VAL:HG11	2.00	0.44
35:Cc:110:GLU:N	35:Cc:110:GLU:OE1	2.51	0.44
1:C1:67:A:N1	1:C1:292:G:O2'	2.48	0.44
1:C1:247:A:H2'	1:C1:248:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:966:U:H2'	1:C1:967:U:C6	2.52	0.44
1:C1:2327:C:H2'	1:C1:2328:C:C6	2.53	0.44
1:C1:3335:U:H2'	1:C1:3336:U:C6	2.52	0.44
2:C2:71:A:OP1	29:LY:27:ARG:NH1	2.51	0.44
3:CA:240:LEU:HD23	3:CA:240:LEU:HA	1.89	0.44
7:CH:421:LEU:HD23	16:LB:69:LYS:HE3	1.99	0.44
10:CM:173:ALA:HA	10:CM:176:GLU:HG2	1.98	0.44
27:LT:131:GLN:HA	27:LT:132:PRO:HD3	1.79	0.44
1:C1:20:A:H2'	1:C1:21:G:C8	2.52	0.44
1:C1:399:A:C2	2:C2:17:A:H1'	2.53	0.44
1:C1:580:G:H21	18:LE:37:LYS:HD3	1.83	0.44
1:C1:612:G:H2'	1:C1:613:U:C6	2.53	0.44
1:C1:742:A:H2'	1:C1:743:U:C6	2.52	0.44
1:C1:1444:A:N6	1:C1:1853:G:H1	2.14	0.44
3:CA:104:PHE:HB2	3:CA:113:VAL:HG12	2.00	0.44
5:CC:185:HIS:CD2	5:CC:194:LYS:HE2	2.53	0.44
9:CJ:14:ARG:O	9:CJ:66:THR:OG1	2.32	0.44
13:CR:195:LEU:HD11	13:CR:228:ARG:HB3	2.00	0.44
19:LG:104:THR:HG23	19:LG:107:GLU:H	1.83	0.44
25:LQ:104:GLU:H	25:LQ:104:GLU:HG3	1.65	0.44
26:LS:66:GLU:HB3	26:LS:69:PRO:HG3	1.98	0.44
28:LV:115:ALA:HA	28:LV:134:ASN:HD21	1.83	0.44
1:C1:510:U:C4	17:LC:351:PRO:HB3	2.53	0.43
1:C1:2729:U:C4	1:C1:2731:C:N4	2.86	0.43
1:C1:3008:U:H2'	1:C1:3009:G:C8	2.51	0.43
16:LB:62:ARG:NH1	16:LB:353:GLU:OE1	2.51	0.43
18:LE:50:LYS:HE2	18:LE:50:LYS:HB2	1.61	0.43
22:LN:33:LEU:HD23	22:LN:37:HIS:CD2	2.53	0.43
28:LV:81:VAL:HG13	28:LV:82:ARG:HG3	2.00	0.43
40:Cg:338:THR:OG1	40:Cg:339:LYS:HG2	2.18	0.43
1:C1:1071:G:H2'	1:C1:1072:G:C8	2.52	0.43
1:C1:2930:G:H2'	1:C1:2931:G:O4'	2.18	0.43
1:C1:3043:A:OP1	16:LB:368:HIS:NE2	2.52	0.43
16:LB:92:TYR:HB2	16:LB:158:VAL:HB	2.00	0.43
27:LT:147:LYS:HD3	27:LT:148:PRO:HD2	1.99	0.43
28:LV:114:SER:O	28:LV:134:ASN:ND2	2.51	0.43
36:Cd:207:ILE:HD11	36:Cd:238:LYS:HD3	2.00	0.43
3:CA:79:GLU:HG3	6:CE:573:TYR:HB3	2.01	0.43
3:CA:112:THR:OG1	3:CA:113:VAL:N	2.49	0.43
7:CH:467:ARG:HA	7:CH:470:LYS:HB2	2.00	0.43
9:CJ:459:GLN:HE22	9:CJ:482:LEU:HD13	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CQ:56:ARG:HA	12:CQ:59:ALA:HB3	2.00	0.43
13:CR:206:VAL:HG11	13:CR:226:LYS:HE2	2.01	0.43
19:LG:156:ILE:HG12	19:LG:169:LEU:HD23	2.00	0.43
32:Lh:54:LYS:HA	32:Lh:54:LYS:HD3	1.80	0.43
43:Lq:60:ARG:O	43:Lq:62:ASN:N	2.51	0.43
1:C1:745:U:O2	1:C1:749:C:C4	2.72	0.43
1:C1:2695:C:H2'	1:C1:2696:A:H8	1.83	0.43
2:C2:97:A:OP1	32:Lh:72:ARG:NH2	2.42	0.43
5:CC:370:TRP:CD1	5:CC:378:ARG:HG2	2.53	0.43
13:CR:57:LYS:HB2	13:CR:72:LEU:HD23	1.99	0.43
16:LB:291:ASP:HB3	16:LB:294:ASN:HD21	1.84	0.43
27:LT:33:THR:OG1	27:LT:35:ARG:NH2	2.50	0.43
1:C1:3217:U:OP1	1:C1:3218:A:N6	2.52	0.43
4:CB:73:HIS:O	4:CB:75:SER:N	2.48	0.43
28:LV:89:ARG:NH2	28:LV:90:PHE:HB3	2.33	0.43
38:Cf:464:LYS:HD3	40:Cg:359:LYS:HB3	2.00	0.43
47:C4:59:C:H2'	47:C4:60:A:C8	2.53	0.43
47:C4:88:G:N2	47:C4:90:G:H3'	2.33	0.43
1:C1:117:U:O2'	1:C1:119:U:OP2	2.29	0.43
1:C1:942:C:H1'	1:C1:943:A:H2'	2.00	0.43
6:CE:337:VAL:HG22	6:CE:483:TYR:HB2	1.99	0.43
9:CJ:374:LEU:HD22	9:CJ:383:LEU:HD13	2.00	0.43
12:CQ:6:CYS:HB3	12:CQ:11:ARG:N	2.33	0.43
24:LP:116:HIS:HB3	24:LP:149:ILE:HB	2.00	0.43
35:Cc:67:GLN:HG2	35:Cc:111:LYS:HD3	2.00	0.43
1:C1:3103:G:H2'	1:C1:3104:A:C8	2.53	0.43
3:CA:76:GLU:HA	3:CA:79:GLU:OE1	2.19	0.43
17:LC:148:GLU:HG3	17:LC:150:PRO:HD2	2.01	0.43
30:Le:122:ASN:OD1	30:Le:122:ASN:N	2.45	0.43
35:Cc:161:LEU:HD12	35:Cc:161:LEU:HA	1.83	0.43
40:Cg:114:PHE:HB3	40:Cg:337:MET:HE1	2.00	0.43
1:C1:68:C:N4	1:C1:306:U:O2'	2.52	0.43
1:C1:421:U:O2'	31:Lf:90:PRO:O	2.34	0.43
1:C1:3195:C:H2'	1:C1:3196:G:C8	2.54	0.43
3:CA:198:GLU:OE1	14:CU:255:ARG:NH2	2.52	0.43
15:Ch:276:ILE:HG22	15:Ch:280:ARG:HH11	1.84	0.43
16:LB:287:GLY:HA3	16:LB:322:TYR:CE1	2.54	0.43
18:LE:98:ASN:HB3	18:LE:101:TYR:HD1	1.84	0.43
19:LG:68:LEU:HD23	19:LG:68:LEU:HA	1.83	0.43
20:LL:53:LYS:HD3	20:LL:94:GLY:HA2	1.99	0.43
22:LN:10:LEU:HG	33:Li:53:ILE:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Lh:6:LYS:HE2	32:Lh:8:LYS:HE3	2.00	0.43
47:C4:63:G:H2'	47:C4:64:A:C8	2.53	0.43
1:C1:1099:G:O3'	38:Cf:545:LYS:NZ	2.44	0.43
1:C1:2390:U:O2'	41:CP:447:ILE:O	2.30	0.43
1:C1:2391:G:H2'	1:C1:2392:A:C8	2.53	0.43
2:C2:103:G:OP2	2:C2:105:A:O2'	2.32	0.43
2:C2:154:C:H2'	2:C2:155:A:H8	1.82	0.43
3:CA:173:LYS:HE3	14:CU:273:ALA:HB1	2.00	0.43
7:CH:431:GLU:HG2	12:CQ:83:ARG:HH22	1.84	0.43
8:CI:286:ASN:OD1	8:CI:286:ASN:N	2.51	0.43
13:CR:4:GLU:CD	13:CR:4:GLU:H	2.27	0.43
21:LM:71:LYS:HE2	21:LM:71:LYS:HB3	1.84	0.43
21:LM:128:ARG:HD2	21:LM:132:ARG:NH2	2.34	0.43
24:LP:74:LYS:HE2	24:LP:74:LYS:HB3	1.92	0.43
28:LV:12:LYS:HE2	28:LV:14:LYS:HA	2.00	0.43
37:Ce:136:LYS:HB2	37:Ce:136:LYS:HE2	1.76	0.43
47:C4:35:C:O2	47:C4:45:U:O2'	2.37	0.43
1:C1:2347:A:H4'	1:C1:2348:A:H5'	2.01	0.43
1:C1:2366:A:H62	1:C1:2775:A:H2	1.65	0.43
1:C1:3002:G:OP1	16:LB:19:ARG:NH2	2.52	0.43
1:C1:3162:A:H5''	1:C1:3163:G:C5	2.54	0.43
6:CE:361:ILE:HD12	6:CE:426:VAL:HG11	1.99	0.43
9:CJ:114:GLU:HA	9:CJ:161:PRO:HG3	2.01	0.43
10:CM:245:ILE:HD12	10:CM:245:ILE:H	1.84	0.43
11:CN:51:THR:HA	11:CN:83:HIS:CE1	2.53	0.43
16:LB:126:LYS:HE3	16:LB:126:LYS:HB3	1.90	0.43
35:Cc:251:ASP:OD1	35:Cc:252:ASP:N	2.52	0.43
47:C4:92:C:H2'	47:C4:93:G:H8	1.83	0.43
48:CX:74:LEU:HD23	48:CX:74:LEU:HA	1.85	0.43
1:C1:403:U:H2'	1:C1:404:G:C8	2.53	0.42
16:LB:14:LEU:HD22	16:LB:17:LEU:HD11	2.01	0.42
16:LB:58:ARG:HH11	16:LB:356:GLU:N	2.17	0.42
16:LB:111:SER:OG	16:LB:113:GLU:OE1	2.36	0.42
16:LB:126:LYS:O	16:LB:128:LYS:NZ	2.52	0.42
22:LN:145:ASP:HB3	22:LN:148:ILE:HG22	2.01	0.42
36:Cd:328:MET:HG3	36:Cd:346:LEU:HD22	2.01	0.42
1:C1:462:C:OP1	37:Ce:62:TYR:OH	2.32	0.42
1:C1:527:U:H2'	1:C1:528:G:H8	1.84	0.42
1:C1:643:A:H2'	1:C1:644:A:C8	2.54	0.42
1:C1:3053:C:O3'	16:LB:326:LYS:NZ	2.52	0.42
1:C1:3115:C:H5''	24:LP:158:GLN:HE21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3183:C:OP2	16:LB:154:LYS:NZ	2.52	0.42
5:CC:223:PRO:HG2	19:LG:239:GLY:HA3	2.00	0.42
6:CE:261:LEU:HB3	6:CE:292:THR:HG23	2.01	0.42
6:CE:274:PHE:HD1	6:CE:277:GLU:HG3	1.82	0.42
10:CM:157:ARG:HD2	10:CM:213:LEU:HD13	2.00	0.42
11:CN:78:ASP:HA	11:CN:81:LEU:HB3	2.00	0.42
11:CN:121:LEU:HB3	11:CN:139:ARG:HH12	1.84	0.42
16:LB:304:LYS:HE3	16:LB:304:LYS:HB2	1.51	0.42
21:LM:123:LEU:HB3	23:LO:199:LEU:HD21	1.99	0.42
44:Cx:126:GLN:HE22	44:Cx:137:LYS:HA	1.83	0.42
1:C1:910:A:O2'	34:Lj:49:TRP:O	2.32	0.42
10:CM:202:LYS:HE2	10:CM:202:LYS:HB2	1.63	0.42
12:CQ:37:HIS:NE2	28:LV:96:TYR:OH	2.45	0.42
18:LE:25:GLN:HB2	18:LE:26:LYS:H	1.65	0.42
31:Lf:75:ARG:HD3	31:Lf:84:ARG:HD2	2.01	0.42
40:Cg:39:ILE:HD12	40:Cg:39:ILE:HA	1.87	0.42
1:C1:69:C:OP1	22:LN:178:HIS:ND1	2.53	0.42
1:C1:3192:C:H2'	1:C1:3193:G:C8	2.53	0.42
4:CB:30:LEU:HD13	4:CB:291:LEU:HG	2.02	0.42
14:CU:248:LEU:HD12	14:CU:248:LEU:HA	1.91	0.42
16:LB:304:LYS:NZ	16:LB:372:GLN:HB3	2.35	0.42
23:LO:151:TYR:HB3	23:LO:154:VAL:HB	2.00	0.42
1:C1:1158:C:H2'	1:C1:1159:G:N2	2.35	0.42
1:C1:2641:U:H2'	1:C1:2642:C:H6	1.84	0.42
5:CC:121:PHE:HB2	6:CE:439:ARG:HG3	2.00	0.42
23:LO:185:LYS:HD3	23:LO:185:LYS:HA	1.88	0.42
26:LS:137:ARG:HG3	26:LS:138:PRO:HD2	2.01	0.42
1:C1:614:C:H2'	1:C1:615:A:C8	2.55	0.42
1:C1:1151:A:H4'	10:LF:224:LYS:HD3	2.01	0.42
6:CE:474:LYS:HE3	6:CE:474:LYS:HB3	1.89	0.42
7:CH:445:ASN:ND2	12:CQ:2:ARG:HG2	2.34	0.42
16:LB:295:ALA:HA	16:LB:360:ILE:HD13	2.02	0.42
17:LC:296:ILE:HD13	25:LQ:159:PRO:HB3	2.02	0.42
18:LE:39:VAL:HG22	18:LE:41:LYS:HG2	2.01	0.42
10:LF:182:TYR:CZ	10:LF:203:GLN:HG2	2.55	0.42
26:LS:67:LYS:HB2	26:LS:67:LYS:HE2	1.76	0.42
38:Cf:456:GLU:HA	38:Cf:463:ARG:NH2	2.34	0.42
1:C1:580:G:N2	18:LE:37:LYS:HD3	2.34	0.42
1:C1:1163:U:O4	23:LO:22:SER:OG	2.26	0.42
1:C1:2590:G:N3	1:C1:2605:A:N1	2.66	0.42
1:C1:3016:G:C6	1:C1:3042:G:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:57:C:H4'	2:C2:63:G:N7	2.35	0.42
2:C2:174:G:H1'	2:C2:175:G:C8	2.54	0.42
3:CA:51:LEU:HG	3:CA:55:LEU:HD13	2.02	0.42
3:CA:235:GLY:HA3	3:CA:236:PRO:HD3	1.79	0.42
4:CB:99:LEU:HG	4:CB:101:THR:HG23	2.01	0.42
11:CN:41:GLU:HB3	11:CN:203:LEU:HD22	2.01	0.42
12:CQ:17:LYS:O	12:CQ:30:ARG:NH2	2.35	0.42
26:LS:81:TYR:CD2	26:LS:110:MET:HE1	2.53	0.42
36:Cd:195:PRO:HB3	36:Cd:330:ILE:HD11	2.02	0.42
47:C4:23:A:N3	47:C4:119:U:O2'	2.50	0.42
1:C1:2355:G:O2'	1:C1:2356:G:O5'	2.38	0.42
1:C1:2356:G:H2'	1:C1:2357:G:C8	2.54	0.42
8:CI:292:GLN:HG3	8:CI:295:ARG:HH21	1.84	0.42
11:CN:101:LEU:HA	28:LV:137:VAL:HG22	2.02	0.42
16:LB:143:ALA:O	16:LB:147:ARG:N	2.47	0.42
18:LE:107:VAL:HG21	18:LE:179:LEU:HD11	2.02	0.42
23:LO:62:MET:HE2	23:LO:65:TYR:HA	2.02	0.42
36:Cd:383:VAL:HG21	37:Ce:171:LEU:HB3	2.02	0.42
1:C1:689:C:H41	3:CA:282:ARG:HH21	1.68	0.42
1:C1:2389:U:H2'	1:C1:2390:U:C6	2.55	0.42
1:C1:3264:A:H8	1:C1:3264:A:OP1	2.03	0.42
6:CE:359:LYS:NZ	6:CE:406:ALA:O	2.34	0.42
9:CJ:398:ASP:HA	9:CJ:408:THR:HG23	2.01	0.42
17:LC:287:LEU:HD13	25:LQ:56:LEU:HG	2.02	0.42
21:LM:42:ASP:HB2	21:LM:54:ARG:HG3	2.02	0.42
35:Cc:118:ARG:HD3	35:Cc:118:ARG:HA	1.90	0.42
35:Cc:126:TRP:CE2	35:Cc:154:LYS:HD3	2.55	0.42
1:C1:333:G:C6	17:LC:198:MET:HE3	2.55	0.42
1:C1:1386:G:N2	1:C1:1389:A:OP2	2.40	0.42
1:C1:2764:U:H2'	1:C1:2765:U:C6	2.55	0.42
1:C1:3235:A:H2'	1:C1:3236:A:C8	2.54	0.42
4:CB:140:TYR:HA	4:CB:143:GLN:HG2	2.01	0.42
14:CU:282:MET:HB3	48:CX:74:LEU:HD13	2.02	0.42
16:LB:32:PHE:CE2	16:LB:183:GLN:HB2	2.55	0.42
16:LB:218:VAL:O	16:LB:278:SER:N	2.53	0.42
21:LM:16:VAL:HG13	21:LM:31:VAL:HA	2.02	0.42
47:C4:77:U:H2'	47:C4:78:A:H8	1.85	0.42
1:C1:622:A:H2'	1:C1:623:C:O4'	2.20	0.41
1:C1:649:U:H2'	1:C1:650:C:C6	2.55	0.41
1:C1:1858:A:O2'	38:Cf:440:ASP:OD1	2.38	0.41
1:C1:2469:U:H2'	1:C1:2470:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3092:U:H2'	1:C1:3093:G:C8	2.55	0.41
3:CA:48:HIS:CD2	3:CA:100:LEU:HD22	2.55	0.41
9:CJ:42:ILE:HD12	9:CJ:68:ASP:HB3	2.01	0.41
9:CJ:366:LEU:HD23	9:CJ:366:LEU:HA	1.94	0.41
13:CR:151:LEU:HD23	13:CR:151:LEU:HA	1.85	0.41
24:LP:28:ASN:OD1	24:LP:82:ARG:NH1	2.52	0.41
1:C1:260:A:C5	22:LN:12:LYS:HG2	2.54	0.41
1:C1:579:A:H8	1:C1:580:G:C8	2.37	0.41
1:C1:1875:A:H2'	1:C1:1876:G:C8	2.55	0.41
1:C1:3136:A:P	23:LO:38:ARG:HH22	2.42	0.41
9:CJ:77:LEU:O	9:CJ:81:PHE:N	2.50	0.41
9:CJ:107:GLU:HG3	9:CJ:108:ARG:HH11	1.86	0.41
9:CJ:183:HIS:ND1	9:CJ:389:ALA:O	2.53	0.41
9:CJ:256:LYS:HD3	9:CJ:256:LYS:HA	1.83	0.41
10:CM:171:ASP:HB2	10:CM:174:ILE:HG12	2.02	0.41
11:CN:163:PRO:HA	11:CN:183:ALA:HB1	2.02	0.41
17:LC:133:ALA:HA	17:LC:149:VAL:HG21	2.01	0.41
23:LO:170:TYR:O	23:LO:174:LYS:N	2.44	0.41
26:LS:45:LEU:HD13	26:LS:51:VAL:HG11	2.02	0.41
35:Cc:244:ARG:HA	35:Cc:244:ARG:HD3	1.74	0.41
38:Cf:528:GLU:OE1	38:Cf:528:GLU:N	2.54	0.41
1:C1:764:A:H5''	1:C1:765:G:H5'	2.01	0.41
1:C1:1038:U:H2'	1:C1:1039:A:C8	2.56	0.41
2:C2:8:C:H2'	2:C2:9:A:H8	1.85	0.41
3:CA:109:ASN:OD1	3:CA:109:ASN:N	2.54	0.41
4:CB:19:ASP:OD1	4:CB:22:GLN:HB3	2.19	0.41
6:CE:384:VAL:HA	6:CE:410:THR:HG23	2.02	0.41
7:CH:404:ALA:HA	7:CH:407:ILE:HB	2.01	0.41
7:CH:413:GLY:H	7:CH:416:VAL:HB	1.84	0.41
9:CJ:147:MET:O	9:CJ:151:PHE:N	2.41	0.41
22:LN:200:TRP:O	22:LN:203:ARG:NH1	2.47	0.41
25:LQ:54:LEU:HD12	25:LQ:54:LEU:HA	1.88	0.41
35:Cc:33:LEU:HD12	35:Cc:77:LEU:HD22	2.01	0.41
36:Cd:402:ARG:NH2	37:Ce:141:MET:HE1	2.35	0.41
38:Cf:456:GLU:HA	38:Cf:463:ARG:HH21	1.85	0.41
46:LD:106:ALA:HB2	46:LD:169:ALA:HA	2.02	0.41
47:C4:17:A:H2'	47:C4:18:G:C8	2.55	0.41
1:C1:367:A:O2'	29:LY:86:ARG:NH1	2.52	0.41
1:C1:398:G:OP1	1:C1:1397:U:O2'	2.36	0.41
1:C1:967:U:O2'	10:LF:128:ALA:O	2.36	0.41
1:C1:2294:A:H2'	1:C1:2295:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2424:G:O6	1:C1:2455:U:C2	2.73	0.41
3:CA:182:PHE:CD1	3:CA:191:VAL:HG12	2.55	0.41
7:CH:470:LYS:HD3	7:CH:470:LYS:HA	1.90	0.41
9:CJ:151:PHE:HD1	9:CJ:154:LEU:HD12	1.85	0.41
16:LB:70:LYS:HB3	28:LV:90:PHE:CZ	2.55	0.41
27:LT:57:TYR:HD2	27:LT:89:ILE:HD13	1.85	0.41
32:Lh:108:LYS:H	32:Lh:108:LYS:HG2	1.67	0.41
34:Lj:64:MET:SD	34:Lj:67:LEU:HB3	2.60	0.41
47:C4:17:A:H2'	47:C4:18:G:H8	1.84	0.41
1:C1:301:U:H5''	6:CE:578:ARG:HD3	2.01	0.41
1:C1:581:G:O2'	18:LE:35:GLN:O	2.35	0.41
1:C1:1385:C:H42	30:Le:17:ARG:HH22	1.68	0.41
1:C1:3006:A:H2'	1:C1:3007:U:O4'	2.21	0.41
1:C1:3157:C:OP1	21:LM:132:ARG:NH2	2.54	0.41
1:C1:3262:G:O2'	1:C1:3263:A:H8	2.03	0.41
3:CA:194:TYR:HB3	3:CA:231:LEU:HB3	2.02	0.41
3:CA:314:LEU:HD12	3:CA:314:LEU:HA	1.88	0.41
7:CH:402:VAL:O	7:CH:406:ASP:HB2	2.21	0.41
9:CJ:89:LYS:HE3	9:CJ:89:LYS:HB3	1.92	0.41
12:CQ:48:LYS:HA	12:CQ:48:LYS:HD3	1.74	0.41
17:LC:146:VAL:HB	17:LC:151:LEU:HD13	2.02	0.41
23:LO:73:PHE:O	23:LO:80:ARG:HD2	2.21	0.41
28:LV:111:MET:SD	28:LV:113:GLY:N	2.93	0.41
31:Lf:45:PHE:HZ	31:Lf:109:ILE:HD11	1.86	0.41
1:C1:490:C:H2'	1:C1:491:A:H8	1.86	0.41
1:C1:2387:G:C6	1:C1:2563:G:C2	3.08	0.41
1:C1:3042:G:O2'	1:C1:3271:C:H4'	2.21	0.41
4:CB:263:ILE:O	4:CB:267:VAL:HG22	2.21	0.41
13:CR:9:LYS:H	13:CR:9:LYS:HG3	1.58	0.41
16:LB:53:MET:HE1	16:LB:75:ALA:HB1	2.01	0.41
28:LV:93:VAL:HG12	28:LV:95:LEU:HB3	2.03	0.41
46:LD:186:TYR:HA	46:LD:193:LEU:HA	2.02	0.41
1:C1:17:G:H4'	32:Lh:80:TYR:CZ	2.56	0.41
1:C1:2671:U:H5'	1:C1:2672:G:H5'	2.01	0.41
9:CJ:160:VAL:HA	9:CJ:164:MET:HE2	2.03	0.41
9:CJ:230:PHE:HA	9:CJ:233:PHE:HB2	2.03	0.41
19:LG:178:ILE:H	19:LG:178:ILE:HG13	1.68	0.41
19:LG:216:LYS:HB2	19:LG:216:LYS:HE2	1.86	0.41
47:C4:84:G:HO2'	47:C4:85:U:C5'	2.34	0.41
1:C1:497:U:H2'	1:C1:498:C:C6	2.56	0.41
1:C1:639:G:H2'	1:C1:2323:A:H5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:735:G:H2'	1:C1:736:A:C8	2.56	0.41
1:C1:1322:C:H2'	1:C1:1323:U:C6	2.56	0.41
1:C1:1845:C:H1'	38:Cf:421:HIS:CE1	2.56	0.41
1:C1:2567:A:H2'	1:C1:2568:G:H8	1.86	0.41
1:C1:2700:C:H2'	1:C1:2701:A:C8	2.54	0.41
1:C1:2702:U:H2'	1:C1:2703:G:C8	2.56	0.41
1:C1:3023:U:O4	1:C1:3032:G:O6	2.38	0.41
1:C1:3106:G:H4'	16:LB:130:PHE:CD1	2.56	0.41
9:CJ:237:LEU:HD12	9:CJ:237:LEU:HA	1.91	0.41
9:CJ:401:LEU:HD22	10:CM:188:GLU:HG2	2.02	0.41
11:CN:16:PHE:CE1	28:LV:129:PRO:HB3	2.55	0.41
11:CN:35:TYR:O	11:CN:39:GLU:HG3	2.21	0.41
18:LE:170:ILE:HA	18:LE:173:ILE:HB	2.03	0.41
21:LM:121:MET:HE3	21:LM:121:MET:HB3	1.95	0.41
27:LT:52:MET:HA	27:LT:92:ARG:HH12	1.85	0.41
36:Cd:196:PRO:HA	36:Cd:197:PRO:HD3	1.93	0.41
40:Cg:332:ARG:NH1	40:Cg:334:ARG:HH22	2.19	0.41
1:C1:137:C:H2'	1:C1:138:G:O4'	2.21	0.41
1:C1:177:U:H2'	1:C1:178:C:C6	2.56	0.41
1:C1:527:U:H2'	1:C1:528:G:C8	2.56	0.41
1:C1:613:U:H2'	1:C1:614:C:C6	2.56	0.41
1:C1:738:C:N3	1:C1:756:A:N1	2.69	0.41
1:C1:893:G:H2'	1:C1:894:A:C8	2.55	0.41
1:C1:956:C:H2'	1:C1:957:G:C8	2.56	0.41
1:C1:1171:C:N4	1:C1:1298:C:OP2	2.53	0.41
1:C1:1335:C:H4'	37:Ce:39:ASN:HD22	1.86	0.41
1:C1:2314:A:OP1	24:LP:82:ARG:HG2	2.20	0.41
1:C1:2431:G:OP2	1:C1:2439:G:N2	2.54	0.41
1:C1:2590:G:C2	1:C1:2605:A:N1	2.88	0.41
1:C1:2639:U:H2'	1:C1:2640:C:H6	1.85	0.41
1:C1:2974:G:H2'	1:C1:2975:C:C6	2.55	0.41
1:C1:3030:G:H2'	1:C1:3031:G:H8	1.86	0.41
1:C1:3215:U:OP1	1:C1:3215:U:H6	2.03	0.41
1:C1:3227:C:H2'	1:C1:3228:G:C8	2.52	0.41
1:C1:3270:C:N4	1:C1:3314:U:H3	2.14	0.41
1:C1:3313:G:C6	1:C1:3314:U:N3	2.89	0.41
2:C2:8:C:H2'	2:C2:9:A:C8	2.56	0.41
6:CE:173:LEU:HD21	6:CE:185:GLY:HA3	2.03	0.41
9:CJ:12:ALA:HB1	9:CJ:53:VAL:HG22	2.02	0.41
9:CJ:463:ASP:HB3	9:CJ:471:LYS:HD3	2.03	0.41
15:Ch:297:VAL:O	15:Ch:301:GLN:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LC:5:PRO:HG2	35:Cc:15:ALA:HB1	2.03	0.41
17:LC:236:PRO:HG2	17:LC:239:ALA:HB3	2.03	0.41
17:LC:331:PRO:HB3	10:LF:47:ARG:HH21	1.86	0.41
17:LC:361:LEU:O	26:LS:26:ARG:NH2	2.53	0.41
26:LS:29:ILE:HD13	26:LS:29:ILE:HA	1.91	0.41
26:LS:94:TYR:OH	26:LS:109:ASP:OD2	2.25	0.41
27:LT:34:TYR:OH	27:LT:96:VAL:O	2.29	0.41
36:Cd:311:LEU:HD12	36:Cd:311:LEU:HA	1.85	0.41
36:Cd:364:GLU:HA	36:Cd:386:ILE:HG22	2.02	0.41
36:Cd:392:GLU:OE2	36:Cd:396:ARG:NH2	2.54	0.41
37:Ce:65:ILE:HD12	37:Ce:81:ILE:HD12	2.03	0.41
40:Cg:215:ARG:HG2	40:Cg:332:ARG:HH11	1.86	0.41
40:Cg:331:PRO:HB2	40:Cg:333:MET:HE3	2.01	0.41
1:C1:734:C:H2'	1:C1:735:G:C8	2.56	0.41
1:C1:2768:C:H2'	1:C1:2769:A:H8	1.84	0.41
1:C1:3092:U:H2'	1:C1:3093:G:H8	1.86	0.41
3:CA:154:VAL:HG21	14:CU:196:LEU:HG	2.03	0.41
7:CH:371:ALA:HB3	11:CN:181:LEU:H	1.86	0.41
9:CJ:18:THR:HA	9:CJ:63:PHE:HA	2.02	0.41
10:CM:190:LEU:HD11	10:CM:207:PHE:HE2	1.84	0.41
19:LG:119:ILE:HD13	19:LG:119:ILE:HA	1.89	0.41
22:LN:114:ARG:HG2	22:LN:137:PRO:HG3	2.03	0.41
26:LS:66:GLU:OE1	26:LS:99:ARG:HG3	2.21	0.41
28:LV:19:LEU:O	28:LV:54:GLY:N	2.42	0.41
1:C1:2618:G:O2'	1:C1:2702:U:O2	2.39	0.40
1:C1:3117:C:H5''	36:Cd:301:HIS:O	2.21	0.40
3:CA:91:PHE:HB3	3:CA:103:TRP:HB2	2.03	0.40
5:CC:135:ARG:NH2	6:CE:569:GLY:O	2.54	0.40
6:CE:368:ASN:ND2	6:CE:513:GLU:HB3	2.36	0.40
9:CJ:69:ILE:HD13	9:CJ:72:LEU:HD12	2.02	0.40
9:CJ:123:LEU:HA	9:CJ:126:ILE:HD12	2.02	0.40
17:LC:151:LEU:HD23	17:LC:256:VAL:HG22	2.03	0.40
19:LG:85:LEU:HD13	19:LG:181:ALA:HB1	2.03	0.40
22:LN:14:LYS:HB3	22:LN:14:LYS:HE3	1.86	0.40
30:Le:27:LYS:HE3	30:Le:27:LYS:HB2	1.90	0.40
35:Cc:249:LEU:O	35:Cc:257:ASN:ND2	2.54	0.40
1:C1:574:G:H2'	1:C1:575:A:H8	1.86	0.40
1:C1:625:C:H2'	1:C1:626:G:C8	2.57	0.40
5:CC:229:LEU:HD22	19:LG:71:ARG:HE	1.86	0.40
6:CE:342:ASP:HB3	6:CE:540:LYS:HG2	2.04	0.40
9:CJ:97:ARG:HB3	19:LG:191:THR:HG23	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CJ:174:GLU:OE1	9:CJ:242:ASN:ND2	2.53	0.40
9:CJ:251:LEU:HG	9:CJ:275:GLY:HA2	2.03	0.40
13:CR:132:PRO:HG2	20:LL:106:GLU:HB3	2.03	0.40
16:LB:32:PHE:CD2	16:LB:183:GLN:HB2	2.57	0.40
10:LF:137:GLU:HG2	10:LF:235:GLY:HA2	2.02	0.40
19:LG:147:GLU:OE2	22:LN:6:TYR:OH	2.26	0.40
20:LL:126:PHE:HA	20:LL:127:PRO:HD3	1.96	0.40
24:LP:82:ARG:HG2	24:LP:83:TRP:H	1.86	0.40
25:LQ:149:LEU:HD23	25:LQ:149:LEU:HA	1.81	0.40
1:C1:95:A:C5	1:C1:96:G:H1'	2.55	0.40
1:C1:734:C:H2'	1:C1:735:G:H8	1.86	0.40
1:C1:771:U:H2'	1:C1:772:U:C6	2.57	0.40
1:C1:1150:U:H2'	1:C1:1151:A:C8	2.56	0.40
1:C1:3036:U:O4'	40:Cg:74:ARG:NH2	2.54	0.40
5:CC:222:ASP:HA	19:LG:240:ILE:HD11	2.03	0.40
6:CE:336:TYR:CZ	6:CE:482:GLU:HB2	2.57	0.40
19:LG:80:GLN:NE2	19:LG:170:PRO:HG2	2.36	0.40
23:LO:194:LYS:HD3	23:LO:194:LYS:HA	1.70	0.40
29:LY:31:SER:HA	29:LY:48:PRO:HA	2.01	0.40
37:Ce:108:LYS:HA	37:Ce:108:LYS:HD2	1.91	0.40
1:C1:412:G:O2'	1:C1:2346:A:N6	2.54	0.40
1:C1:1082:U:H2'	1:C1:1083:G:H8	1.87	0.40
1:C1:2300:C:H2'	1:C1:2301:C:H6	1.86	0.40
1:C1:2385:U:H2'	1:C1:2386:A:C8	2.55	0.40
1:C1:2626:U:H2'	1:C1:2627:G:C8	2.55	0.40
1:C1:3136:A:H2'	1:C1:3137:A:H8	1.86	0.40
8:CI:316:ARG:O	8:CI:320:LEU:HG	2.22	0.40
9:CJ:457:GLN:OE1	9:CJ:457:GLN:N	2.55	0.40
9:CJ:476:TYR:HE1	9:CJ:483:PRO:HD2	1.86	0.40
10:CM:208:LEU:HD12	10:CM:208:LEU:HA	1.93	0.40
17:LC:197:LYS:HB2	17:LC:197:LYS:HE2	1.83	0.40
10:LF:46:LYS:HA	10:LF:49:VAL:HG12	2.04	0.40
10:LF:169:LEU:HD23	10:LF:174:ILE:HD11	2.04	0.40
21:LM:109:ARG:HD2	23:LO:204:TYR:CZ	2.56	0.40
22:LN:114:ARG:NH1	22:LN:151:ILE:O	2.54	0.40
22:LN:169:LYS:HG2	22:LN:174:LEU:HD12	2.01	0.40
28:LV:12:LYS:HG3	28:LV:15:MET:HE1	2.02	0.40
30:Le:3:ALA:O	30:Le:91:ARG:NH1	2.53	0.40
32:Lh:34:LEU:O	32:Lh:38:LYS:N	2.55	0.40
1:C1:1430:U:H2'	1:C1:1431:A:H8	1.87	0.40
1:C1:2480:C:H2'	1:C1:2481:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2630:G:O2'	45:LJ:95:ARG:O	2.39	0.40
1:C1:2933:U:C2	1:C1:2934:A:N7	2.90	0.40
6:CE:478:VAL:HA	6:CE:479:PRO:HD3	1.96	0.40
10:CM:129:THR:HA	10:CM:132:MET:HE2	2.04	0.40
16:LB:94:GLU:OE2	23:LO:157:ARG:NH2	2.55	0.40
21:LM:135:LEU:HD12	21:LM:135:LEU:HA	1.94	0.40
23:LO:174:LYS:O	23:LO:178:ARG:HG2	2.22	0.40
26:LS:93:GLU:HB2	26:LS:137:ARG:HD2	2.03	0.40
40:Cg:119:GLU:HG2	40:Cg:120:LYS:HE3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CA	254/316 (80%)	236 (93%)	18 (7%)	0	100	100
4	CB	256/391 (66%)	235 (92%)	20 (8%)	1 (0%)	30	61
5	CC	264/801 (33%)	250 (95%)	14 (5%)	0	100	100
6	CE	459/598 (77%)	440 (96%)	19 (4%)	0	100	100
7	CH	106/661 (16%)	101 (95%)	4 (4%)	1 (1%)	14	44
8	CI	144/414 (35%)	133 (92%)	10 (7%)	1 (1%)	18	49
9	CJ	374/679 (55%)	357 (96%)	16 (4%)	1 (0%)	36	67
10	CM	183/249 (74%)	171 (93%)	12 (7%)	0	100	100
10	LF	238/249 (96%)	230 (97%)	7 (3%)	1 (0%)	30	61
11	CN	244/246 (99%)	228 (93%)	16 (7%)	0	100	100
12	CQ	110/225 (49%)	107 (97%)	3 (3%)	0	100	100
13	CR	159/237 (67%)	153 (96%)	6 (4%)	0	100	100
14	CU	119/451 (26%)	113 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	Ch	69/354 (20%)	66 (96%)	3 (4%)	0	100	100
16	LB	337/392 (86%)	319 (95%)	18 (5%)	0	100	100
17	LC	360/365 (99%)	349 (97%)	11 (3%)	0	100	100
18	LE	166/200 (83%)	161 (97%)	5 (3%)	0	100	100
19	LG	179/262 (68%)	174 (97%)	5 (3%)	0	100	100
20	LL	115/213 (54%)	111 (96%)	4 (4%)	0	100	100
21	LM	135/142 (95%)	131 (97%)	4 (3%)	0	100	100
22	LN	179/203 (88%)	175 (98%)	4 (2%)	0	100	100
23	LO	202/204 (99%)	194 (96%)	8 (4%)	0	100	100
24	LP	150/187 (80%)	148 (99%)	2 (1%)	0	100	100
25	LQ	127/213 (60%)	123 (97%)	4 (3%)	0	100	100
26	LS	172/174 (99%)	164 (95%)	8 (5%)	0	100	100
27	LT	124/160 (78%)	115 (93%)	8 (6%)	1 (1%)	16	47
28	LV	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
29	LY	132/138 (96%)	128 (97%)	4 (3%)	0	100	100
30	Le	129/131 (98%)	127 (98%)	2 (2%)	0	100	100
31	Lf	106/109 (97%)	102 (96%)	2 (2%)	2 (2%)	6	27
32	Lh	119/935 (13%)	117 (98%)	2 (2%)	0	100	100
33	Li	86/110 (78%)	84 (98%)	2 (2%)	0	100	100
34	Lj	72/95 (76%)	71 (99%)	1 (1%)	0	100	100
35	Cc	232/282 (82%)	222 (96%)	10 (4%)	0	100	100
36	Cd	343/436 (79%)	321 (94%)	22 (6%)	0	100	100
37	Ce	192/336 (57%)	188 (98%)	4 (2%)	0	100	100
38	Cf	145/570 (25%)	136 (94%)	9 (6%)	0	100	100
39	Cy	240/350 (69%)	238 (99%)	2 (1%)	0	100	100
40	Cg	229/478 (48%)	215 (94%)	12 (5%)	2 (1%)	14	44
41	CP	322/751 (43%)	314 (98%)	8 (2%)	0	100	100
42	CG	175/184 (95%)	171 (98%)	4 (2%)	0	100	100
43	Lq	205/217 (94%)	183 (89%)	21 (10%)	1 (0%)	24	57
44	Cx	98/202 (48%)	98 (100%)	0	0	100	100
45	LJ	167/173 (96%)	167 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	LD	269/304 (88%)	266 (99%)	3 (1%)	0	100	100
48	CX	59/203 (29%)	56 (95%)	3 (5%)	0	100	100
All	All	8678/14729 (59%)	8315 (96%)	352 (4%)	11 (0%)	49	78

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CB	117	PRO
8	CI	268	VAL
40	Cg	154	ASP
31	Lf	93	ALA
7	CH	403	LEU
10	LF	12	ILE
9	CJ	267	GLU
40	Cg	153	THR
27	LT	44	VAL
31	Lf	92	PRO
43	Lq	61	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CA	231/276 (84%)	230 (100%)	1 (0%)	84	86
4	CB	222/329 (68%)	218 (98%)	4 (2%)	51	73
5	CC	252/710 (36%)	246 (98%)	6 (2%)	43	69
6	CE	398/517 (77%)	395 (99%)	3 (1%)	73	81
7	CH	95/575 (16%)	95 (100%)	0	100	100
8	CI	121/336 (36%)	121 (100%)	0	100	100
9	CJ	332/579 (57%)	332 (100%)	0	100	100
10	CM	161/215 (75%)	158 (98%)	3 (2%)	50	73
10	LF	206/215 (96%)	203 (98%)	3 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	CN	206/206 (100%)	205 (100%)	1 (0%)	81	85
12	CQ	100/192 (52%)	100 (100%)	0	100	100
13	CR	144/206 (70%)	141 (98%)	3 (2%)	47	71
14	CU	104/376 (28%)	104 (100%)	0	100	100
15	Ch	58/291 (20%)	58 (100%)	0	100	100
16	LB	290/331 (88%)	284 (98%)	6 (2%)	47	71
17	LC	283/285 (99%)	280 (99%)	3 (1%)	65	78
18	LE	143/166 (86%)	141 (99%)	2 (1%)	59	76
19	LG	157/222 (71%)	154 (98%)	3 (2%)	50	73
20	LL	99/176 (56%)	98 (99%)	1 (1%)	68	79
21	LM	115/117 (98%)	115 (100%)	0	100	100
22	LN	164/180 (91%)	161 (98%)	3 (2%)	51	73
23	LO	163/163 (100%)	160 (98%)	3 (2%)	51	73
24	LP	125/152 (82%)	124 (99%)	1 (1%)	73	81
25	LQ	110/178 (62%)	108 (98%)	2 (2%)	51	73
26	LS	154/154 (100%)	151 (98%)	3 (2%)	50	73
27	LT	109/135 (81%)	107 (98%)	2 (2%)	51	73
28	LV	99/102 (97%)	99 (100%)	0	100	100
29	LY	117/119 (98%)	117 (100%)	0	100	100
30	Le	114/114 (100%)	112 (98%)	2 (2%)	51	73
31	Lf	89/90 (99%)	89 (100%)	0	100	100
32	Lh	108/781 (14%)	107 (99%)	1 (1%)	70	80
33	Li	75/93 (81%)	75 (100%)	0	100	100
34	Lj	61/78 (78%)	61 (100%)	0	100	100
35	Cc	204/244 (84%)	204 (100%)	0	100	100
36	Cd	295/367 (80%)	292 (99%)	3 (1%)	68	79
37	Ce	173/297 (58%)	171 (99%)	2 (1%)	63	78
38	Cf	127/482 (26%)	125 (98%)	2 (2%)	55	75
40	Cg	210/417 (50%)	207 (99%)	3 (1%)	59	76
44	Cx	14/176 (8%)	14 (100%)	0	100	100
48	CX	22/172 (13%)	22 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	6250/10814 (58%)	6184 (99%)	66 (1%)	63	78

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	CA	52	LEU
4	CB	97	VAL
4	CB	240	ASN
4	CB	271	VAL
4	CB	283	VAL
5	CC	155	ASP
5	CC	167	VAL
5	CC	171	THR
5	CC	233	ARG
5	CC	243	GLN
5	CC	260	GLU
6	CE	111	GLN
6	CE	430	VAL
6	CE	478	VAL
10	CM	55	GLU
10	CM	116	GLN
10	CM	132	MET
11	CN	203	LEU
13	CR	152	GLU
13	CR	187	GLN
13	CR	230	LYS
16	LB	66	LYS
16	LB	68	HIS
16	LB	166	GLN
16	LB	172	LEU
16	LB	324	MET
16	LB	338	THR
17	LC	137	MET
17	LC	149	VAL
17	LC	290	LEU
18	LE	109	VAL
18	LE	152	LYS
10	LF	14	VAL
10	LF	98	ILE
10	LF	132	MET
19	LG	52	MET
19	LG	161	ASP

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Mol	Chain	Res	Type
19	LG	183	ILE
20	LL	22	VAL
22	LN	64	VAL
22	LN	111	SER
22	LN	140	LYS
23	LO	8	VAL
23	LO	153	ASP
23	LO	199	LEU
24	LP	155	GLU
25	LQ	110	VAL
25	LQ	122	GLN
26	LS	35	VAL
26	LS	97	THR
26	LS	132	THR
27	LT	111	GLU
27	LT	143	ILE
30	Le	27	LYS
30	Le	100	ASN
32	Lh	105	VAL
36	Cd	186	GLN
36	Cd	261	GLU
36	Cd	263	GLN
37	Ce	11	ASN
37	Ce	77	TRP
38	Cf	476	ARG
38	Cf	523	ARG
40	Cg	68	LYS
40	Cg	197	LEU
40	Cg	199	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
3	CA	34	GLN
4	CB	143	GLN
5	CC	243	GLN
6	CE	280	GLN
6	CE	492	ASN
6	CE	504	ASN
8	CI	267	GLN
8	CI	311	GLN
9	CJ	153	ASN

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Mol	Chain	Res	Type
9	CJ	177	HIS
10	CM	118	ASN
10	CM	249	ASN
11	CN	95	GLN
12	CQ	39	ASN
12	CQ	45	ASN
13	CR	187	GLN
13	CR	202	HIS
14	CU	238	GLN
14	CU	305	GLN
15	Ch	321	GLN
17	LC	46	ASN
17	LC	315	GLN
17	LC	363	HIS
10	LF	77	GLN
10	LF	119	ASN
19	LG	80	GLN
21	LM	5	ASN
22	LN	32	GLN
22	LN	37	HIS
22	LN	156	HIS
23	LO	74	HIS
23	LO	145	HIS
24	LP	89	GLN
24	LP	116	HIS
25	LQ	118	ASN
27	LT	45	ASN
30	Le	72	HIS
31	Lf	58	GLN
32	Lh	37	GLN
32	Lh	47	ASN
35	Cc	37	GLN
37	Ce	8	GLN
37	Ce	85	GLN
38	Cf	524	GLN
40	Cg	100	ASN
40	Cg	102	ASN
40	Cg	133	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2026/3341 (60%)	482 (23%)	17 (0%)
2	C2	225/256 (87%)	61 (27%)	1 (0%)
47	C4	118/119 (99%)	23 (19%)	0
All	All	2369/3716 (63%)	566 (23%)	18 (0%)

All (566) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	14	U
1	C1	26	A
1	C1	40	A
1	C1	43	A
1	C1	49	A
1	C1	59	G
1	C1	60	A
1	C1	65	A
1	C1	66	A
1	C1	73	A
1	C1	75	G
1	C1	91	G
1	C1	92	G
1	C1	94	G
1	C1	96	G
1	C1	105	C
1	C1	109	A
1	C1	110	G
1	C1	113	C
1	C1	116	A
1	C1	122	A
1	C1	131	U
1	C1	132	C
1	C1	133	G
1	C1	134	G
1	C1	136	C
1	C1	143	G
1	C1	150	G
1	C1	151	G
1	C1	152	A
1	C1	162	U
1	C1	163	U
1	C1	164	G
1	C1	176	U
1	C1	180	G

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Mol	Chain	Res	Type
1	C1	183	U
1	C1	192	A
1	C1	193	C
1	C1	203	C
1	C1	204	A
1	C1	206	A
1	C1	211	G
1	C1	212	A
1	C1	213	G
1	C1	224	A
1	C1	225	G
1	C1	240	U
1	C1	242	U
1	C1	244	U
1	C1	253	U
1	C1	257	A
1	C1	258	C
1	C1	261	G
1	C1	275	G
1	C1	276	A
1	C1	277	A
1	C1	287	A
1	C1	291	G
1	C1	300	A
1	C1	302	U
1	C1	309	A
1	C1	310	A
1	C1	315	A
1	C1	321	C
1	C1	325	C
1	C1	329	G
1	C1	331	C
1	C1	343	A
1	C1	368	G
1	C1	376	A
1	C1	377	A
1	C1	390	U
1	C1	391	A
1	C1	393	C
1	C1	394	A
1	C1	395	C
1	C1	412	G

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Mol	Chain	Res	Type
1	C1	413	G
1	C1	416	G
1	C1	421	U
1	C1	432	U
1	C1	434	G
1	C1	446	U
1	C1	448	A
1	C1	450	C
1	C1	457	U
1	C1	459	U
1	C1	460	C
1	C1	467	G
1	C1	474	G
1	C1	485	G
1	C1	493	C
1	C1	500	G
1	C1	504	G
1	C1	508	G
1	C1	509	A
1	C1	511	A
1	C1	513	A
1	C1	520	G
1	C1	526	G
1	C1	535	C
1	C1	536	C
1	C1	543	G
1	C1	544	U
1	C1	545	U
1	C1	546	A
1	C1	547	U
1	C1	548	A
1	C1	549	G
1	C1	558	G
1	C1	569	G
1	C1	582	A
1	C1	587	G
1	C1	590	C
1	C1	592	G
1	C1	593	C
1	C1	596	G
1	C1	598	A
1	C1	624	C

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Mol	Chain	Res	Type
1	C1	625	C
1	C1	629	U
1	C1	633	A
1	C1	634	A
1	C1	636	A
1	C1	647	A
1	C1	664	A
1	C1	668	U
1	C1	678	A
1	C1	708	G
1	C1	718	U
1	C1	719	C
1	C1	723	G
1	C1	730	C
1	C1	731	G
1	C1	744	G
1	C1	746	A
1	C1	748	U
1	C1	751	G
1	C1	755	G
1	C1	757	U
1	C1	758	U
1	C1	761	A
1	C1	762	G
1	C1	766	G
1	C1	787	A
1	C1	798	A
1	C1	887	G
1	C1	888	G
1	C1	896	A
1	C1	897	G
1	C1	905	G
1	C1	906	A
1	C1	907	A
1	C1	918	G
1	C1	924	U
1	C1	925	A
1	C1	932	A
1	C1	934	G
1	C1	937	U
1	C1	940	C
1	C1	943	A

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Mol	Chain	Res	Type
1	C1	944	G
1	C1	954	G
1	C1	957	G
1	C1	958	A
1	C1	960	C
1	C1	975	G
1	C1	976	U
1	C1	978	A
1	C1	1033	U
1	C1	1034	U
1	C1	1036	A
1	C1	1039	A
1	C1	1045	G
1	C1	1046	A
1	C1	1047	A
1	C1	1057	A
1	C1	1063	C
1	C1	1064	U
1	C1	1073	G
1	C1	1075	A
1	C1	1076	U
1	C1	1077	U
1	C1	1078	C
1	C1	1079	G
1	C1	1080	A
1	C1	1084	U
1	C1	1085	A
1	C1	1091	A
1	C1	1092	C
1	C1	1094	A
1	C1	1096	U
1	C1	1097	G
1	C1	1099	G
1	C1	1126	U
1	C1	1132	A
1	C1	1136	A
1	C1	1137	C
1	C1	1141	A
1	C1	1142	C
1	C1	1163	U
1	C1	1164	G
1	C1	1186	A

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Mol	Chain	Res	Type
1	C1	1198	C
1	C1	1271	G
1	C1	1272	U
1	C1	1277	G
1	C1	1278	C
1	C1	1279	C
1	C1	1295	G
1	C1	1298	C
1	C1	1309	C
1	C1	1312	A
1	C1	1313	U
1	C1	1314	A
1	C1	1330	A
1	C1	1331	G
1	C1	1332	A
1	C1	1334	A
1	C1	1335	C
1	C1	1336	G
1	C1	1337	A
1	C1	1368	A
1	C1	1369	G
1	C1	1381	A
1	C1	1382	G
1	C1	1384	G
1	C1	1400	A
1	C1	1401	A
1	C1	1416	G
1	C1	1419	C
1	C1	1432	G
1	C1	1443	A
1	C1	1444	A
1	C1	1448	G
1	C1	1841	U
1	C1	1843	A
1	C1	1844	A
1	C1	1845	C
1	C1	1846	A
1	C1	1859	U
1	C1	1861	G
1	C1	1863	A
1	C1	1864	C
1	C1	1866	A

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Mol	Chain	Res	Type
1	C1	1868	G
1	C1	1874	A
1	C1	1875	A
1	C1	1883	C
1	C1	2297	G
1	C1	2302	U
1	C1	2309	U
1	C1	2310	A
1	C1	2325	A
1	C1	2326	G
1	C1	2327	C
1	C1	2332	G
1	C1	2334	A
1	C1	2335	A
1	C1	2336	C
1	C1	2337	G
1	C1	2339	G
1	C1	2346	A
1	C1	2347	A
1	C1	2348	A
1	C1	2349	A
1	C1	2350	U
1	C1	2351	C
1	C1	2352	A
1	C1	2353	G
1	C1	2355	G
1	C1	2356	G
1	C1	2358	G
1	C1	2365	G
1	C1	2376	G
1	C1	2388	U
1	C1	2396	U
1	C1	2402	A
1	C1	2407	A
1	C1	2414	G
1	C1	2415	U
1	C1	2421	A
1	C1	2422	U
1	C1	2423	A
1	C1	2424	G
1	C1	2425	G
1	C1	2428	G

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Mol	Chain	Res	Type
1	C1	2429	G
1	C1	2430	A
1	C1	2432	C
1	C1	2433	U
1	C1	2434	U
1	C1	2435	C
1	C1	2436	G
1	C1	2438	C
1	C1	2439	G
1	C1	2443	G
1	C1	2449	U
1	C1	2450	A
1	C1	2452	C
1	C1	2453	A
1	C1	2455	U
1	C1	2456	A
1	C1	2457	C
1	C1	2459	C
1	C1	2465	G
1	C1	2466	U
1	C1	2467	U
1	C1	2484	G
1	C1	2551	A
1	C1	2558	C
1	C1	2560	G
1	C1	2564	G
1	C1	2565	G
1	C1	2570	U
1	C1	2581	G
1	C1	2583	C
1	C1	2584	A
1	C1	2588	C
1	C1	2605	A
1	C1	2608	U
1	C1	2614	A
1	C1	2630	G
1	C1	2632	A
1	C1	2634	A
1	C1	2635	G
1	C1	2645	G
1	C1	2646	U
1	C1	2650	A

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Mol	Chain	Res	Type
1	C1	2655	A
1	C1	2656	G
1	C1	2657	G
1	C1	2662	A
1	C1	2663	A
1	C1	2666	C
1	C1	2670	U
1	C1	2671	U
1	C1	2672	G
1	C1	2673	A
1	C1	2674	U
1	C1	2679	A
1	C1	2688	G
1	C1	2689	OMU
1	C1	2690	G
1	C1	2707	G
1	C1	2712	G
1	C1	2713	C
1	C1	2730	C
1	C1	2735	G
1	C1	2739	U
1	C1	2749	G
1	C1	2759	A
1	C1	2766	A
1	C1	2916	A
1	C1	2917	C
1	C1	2919	G
1	C1	2925	A
1	C1	2929	A
1	C1	2930	G
1	C1	2931	G
1	C1	2932	U
1	C1	2933	U
1	C1	2942	C
1	C1	2944	U
1	C1	2950	U
1	C1	2954	C
1	C1	2955	U
1	C1	2969	A
1	C1	2970	U
1	C1	2973	A
1	C1	2974	G

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Mol	Chain	Res	Type
1	C1	2978	A
1	C1	2979	G
1	C1	2993	G
1	C1	2994	C
1	C1	2996	G
1	C1	3000	C
1	C1	3008	U
1	C1	3012	U
1	C1	3015	U
1	C1	3016	G
1	C1	3022	G
1	C1	3031	G
1	C1	3032	G
1	C1	3033	C
1	C1	3034	A
1	C1	3035	G
1	C1	3036	U
1	C1	3037	G
1	C1	3040	G
1	C1	3047	U
1	C1	3048	A
1	C1	3049	C
1	C1	3050	C
1	C1	3056	C
1	C1	3057	U
1	C1	3058	G
1	C1	3091	A
1	C1	3099	A
1	C1	3100	C
1	C1	3101	G
1	C1	3109	A
1	C1	3113	C
1	C1	3117	C
1	C1	3118	A
1	C1	3124	U
1	C1	3126	G
1	C1	3130	U
1	C1	3134	A
1	C1	3139	A
1	C1	3140	G
1	C1	3144	C
1	C1	3145	C

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Mol	Chain	Res	Type
1	C1	3146	G
1	C1	3147	G
1	C1	3154	A
1	C1	3159	A
1	C1	3161	C
1	C1	3162	A
1	C1	3163	G
1	C1	3167	A
1	C1	3171	C
1	C1	3181	C
1	C1	3183	C
1	C1	3187	G
1	C1	3189	G
1	C1	3199	A
1	C1	3200	A
1	C1	3205	C
1	C1	3206	G
1	C1	3209	U
1	C1	3212	C
1	C1	3213	A
1	C1	3215	U
1	C1	3218	A
1	C1	3219	G
1	C1	3221	C
1	C1	3223	C
1	C1	3224	G
1	C1	3226	G
1	C1	3229	G
1	C1	3231	A
1	C1	3232	U
1	C1	3244	C
1	C1	3248	C
1	C1	3249	G
1	C1	3254	A
1	C1	3256	A
1	C1	3257	U
1	C1	3258	G
1	C1	3259	U
1	C1	3260	G
1	C1	3262	G
1	C1	3263	A
1	C1	3264	A

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Mol	Chain	Res	Type
1	C1	3270	C
1	C1	3274	U
1	C1	3281	U
1	C1	3282	A
1	C1	3285	G
1	C1	3290	C
1	C1	3291	U
1	C1	3292	U
1	C1	3295	U
1	C1	3296	G
1	C1	3297	U
1	C1	3298	U
1	C1	3302	A
1	C1	3303	U
1	C1	3308	U
1	C1	3309	G
1	C1	3316	A
1	C1	3318	C
1	C1	3322	C
1	C1	3323	C
1	C1	3324	U
1	C1	3328	C
1	C1	3330	U
1	C1	3331	A
1	C1	3332	G
1	C1	3333	A
1	C1	3337	C
2	C2	3	A
2	C2	34	U
2	C2	35	C
2	C2	44	A
2	C2	51	G
2	C2	52	A
2	C2	53	A
2	C2	54	A
2	C2	59	A
2	C2	62	A
2	C2	63	G
2	C2	84	C
2	C2	86	U
2	C2	87	G
2	C2	90	U

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Mol	Chain	Res	Type
2	C2	91	C
2	C2	95	G
2	C2	97	A
2	C2	104	A
2	C2	105	A
2	C2	106	C
2	C2	107	G
2	C2	116	G
2	C2	124	G
2	C2	126	A
2	C2	127	U
2	C2	129	C
2	C2	136	G
2	C2	148	G
2	C2	151	C
2	C2	157	U
2	C2	158	U
2	C2	160	A
2	C2	161	A
2	C2	163	C
2	C2	164	A
2	C2	165	U
2	C2	166	C
2	C2	174	G
2	C2	175	G
2	C2	180	G
2	C2	181	U
2	C2	189	A
2	C2	190	C
2	C2	192	C
2	C2	196	G
2	C2	197	C
2	C2	198	U
2	C2	199	G
2	C2	206	G
2	C2	211	U
2	C2	212	G
2	C2	214	A
2	C2	215	A
2	C2	219	A
2	C2	221	U
2	C2	222	G

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Mol	Chain	Res	Type
2	C2	223	G
2	C2	224	C
2	C2	225	G
2	C2	229	U
47	C4	7	G
47	C4	9	C
47	C4	22	A
47	C4	29	G
47	C4	54	U
47	C4	55	A
47	C4	64	A
47	C4	66	G
47	C4	75	A
47	C4	76	G
47	C4	82	G
47	C4	83	G
47	C4	84	G
47	C4	85	U
47	C4	86	C
47	C4	89	U
47	C4	92	C
47	C4	93	G
47	C4	94	A
47	C4	99	C
47	C4	100	G
47	C4	101	A
47	C4	111	G

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	150	G
1	C1	519	A
1	C1	887	G
1	C1	896	A
1	C1	906	A
1	C1	1044	A
1	C1	1046	A
1	C1	2301	C
1	C1	2569	U
1	C1	2929	A
1	C1	2932	U

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Mol	Chain	Res	Type
1	C1	3015	U
1	C1	3162	A
1	C1	3255	G
1	C1	3257	U
1	C1	3296	G
1	C1	3297	U
2	C2	123	G

5.4 Non-standard residues in protein, DNA, RNA chains

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMU	C1	2689	1	19,22,23	3.02	8 (42%)	25,31,34	1.79	5 (20%)
1	OMU	C1	2687	1	19,22,23	3.01	8 (42%)	25,31,34	1.78	5 (20%)
1	OMU	C1	2682	1	19,22,23	3.02	8 (42%)	25,31,34	1.74	4 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	C1	2689	1	-	2/9/27/28	0/2/2/2
1	OMU	C1	2687	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2682	1	-	1/9/27/28	0/2/2/2

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	2682	OMU	C2-N1	7.37	1.50	1.38
1	C1	2689	OMU	C2-N1	7.36	1.50	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	2687	OMU	C2-N1	7.32	1.49	1.38
1	C1	2689	OMU	C2-N3	6.88	1.49	1.38
1	C1	2682	OMU	C2-N3	6.87	1.49	1.38
1	C1	2687	OMU	C2-N3	6.86	1.49	1.38
1	C1	2682	OMU	C6-C5	5.93	1.48	1.35
1	C1	2689	OMU	C6-C5	5.92	1.48	1.35
1	C1	2687	OMU	C6-C5	5.90	1.48	1.35
1	C1	2689	OMU	C4-N3	3.74	1.45	1.38
1	C1	2687	OMU	C4-N3	3.69	1.44	1.38
1	C1	2682	OMU	C4-N3	3.63	1.44	1.38
1	C1	2682	OMU	O2-C2	-2.67	1.18	1.23
1	C1	2689	OMU	O2-C2	-2.63	1.18	1.23
1	C1	2687	OMU	O2-C2	-2.62	1.18	1.23
1	C1	2687	OMU	O4-C4	-2.57	1.19	1.24
1	C1	2689	OMU	O4-C4	-2.57	1.19	1.24
1	C1	2682	OMU	O4-C4	-2.56	1.19	1.24
1	C1	2687	OMU	C5-C4	2.14	1.48	1.43
1	C1	2687	OMU	C6-N1	2.13	1.43	1.38
1	C1	2682	OMU	C6-N1	2.13	1.43	1.38
1	C1	2689	OMU	C5-C4	2.12	1.48	1.43
1	C1	2689	OMU	C6-N1	2.10	1.43	1.38
1	C1	2682	OMU	C5-C4	2.06	1.48	1.43

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	2689	OMU	C4-N3-C2	-5.48	119.80	126.61
1	C1	2687	OMU	C4-N3-C2	-5.47	119.83	126.61
1	C1	2682	OMU	C4-N3-C2	-5.32	120.01	126.61
1	C1	2689	OMU	N3-C2-N1	3.79	119.82	114.89
1	C1	2687	OMU	N3-C2-N1	3.74	119.77	114.89
1	C1	2682	OMU	N3-C2-N1	3.66	119.66	114.89
1	C1	2687	OMU	C5-C4-N3	3.54	119.76	114.80
1	C1	2682	OMU	C5-C4-N3	3.53	119.75	114.80
1	C1	2689	OMU	C5-C4-N3	3.52	119.73	114.80
1	C1	2687	OMU	O4-C4-C5	-2.92	120.12	125.16
1	C1	2689	OMU	O4-C4-C5	-2.92	120.13	125.16
1	C1	2682	OMU	O4-C4-C5	-2.91	120.14	125.16
1	C1	2687	OMU	O2-C2-N1	-2.04	120.14	122.80
1	C1	2689	OMU	O2-C2-N1	-2.04	120.14	122.80

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C1	2682	OMU	C1'-C2'-O2'-CM2
1	C1	2689	OMU	C3'-C4'-C5'-O5'
1	C1	2689	OMU	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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.

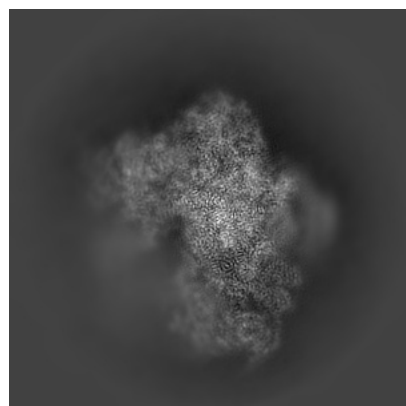
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35281. These allow visual inspection of the internal detail of the map and identification of artifacts.

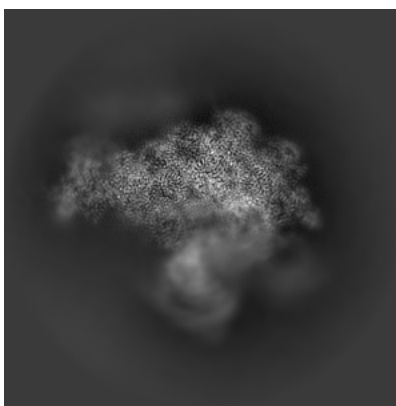
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

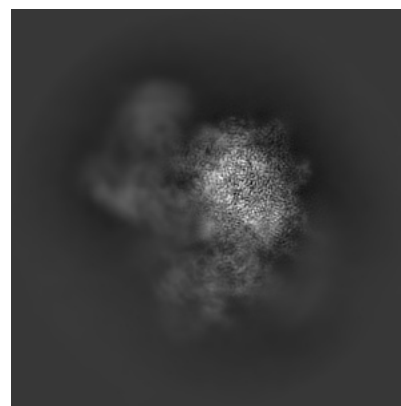
6.1.1 Primary map



X

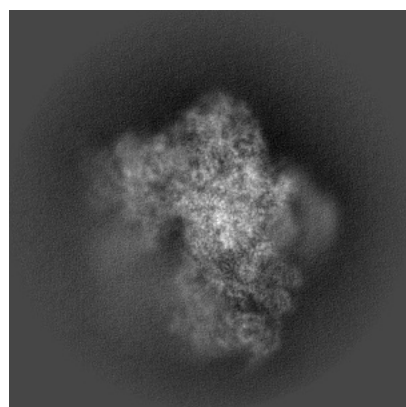


Y

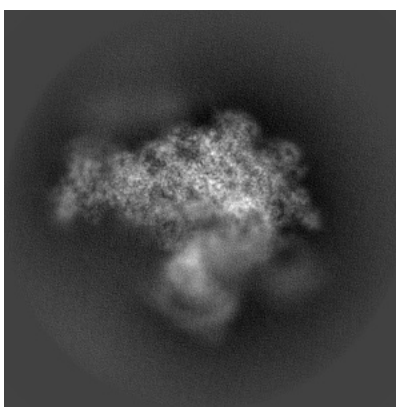


Z

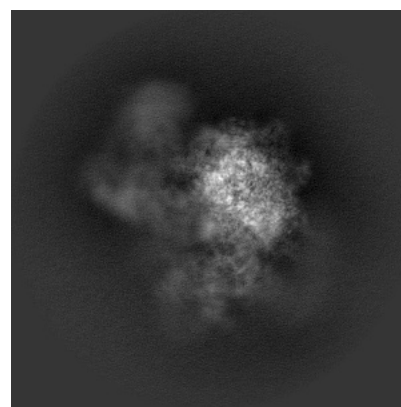
6.1.2 Raw map



X



Y



Z

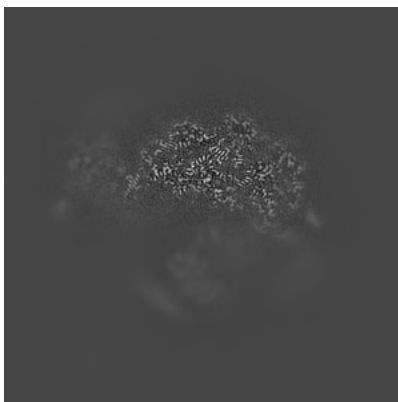
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

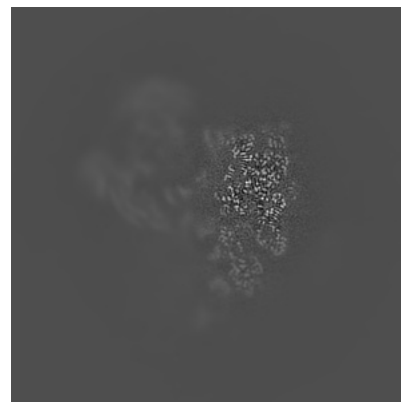
6.2.1 Primary map



X Index: 210

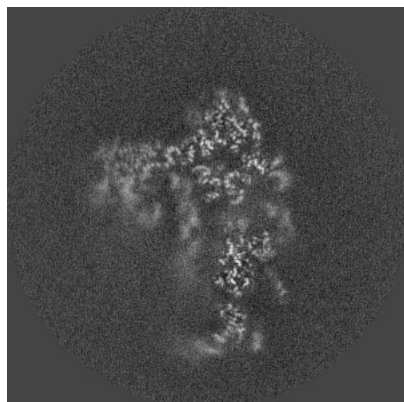


Y Index: 210

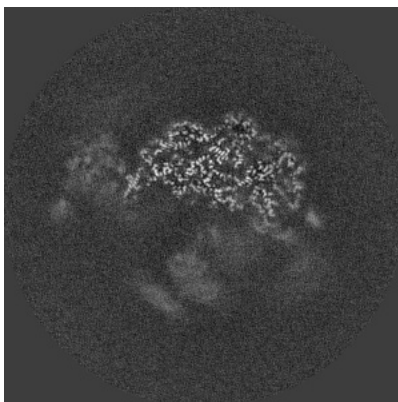


Z Index: 210

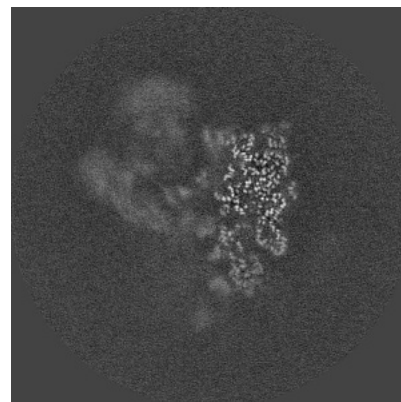
6.2.2 Raw map



X Index: 210



Y Index: 210

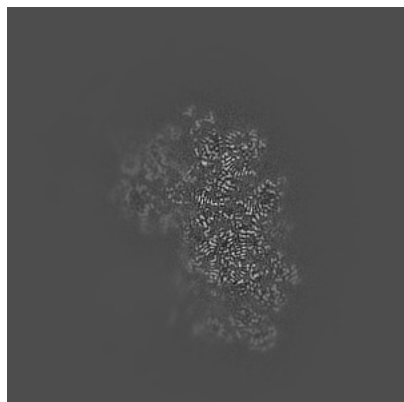


Z Index: 210

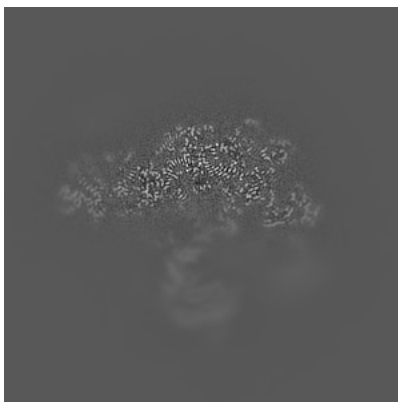
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

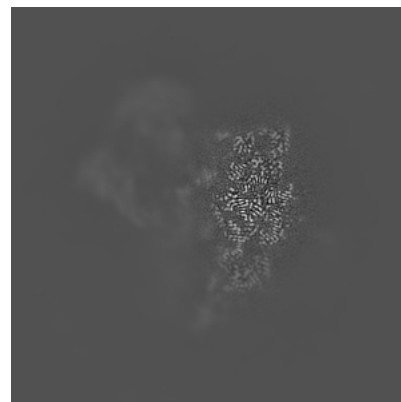
6.3.1 Primary map



X Index: 243

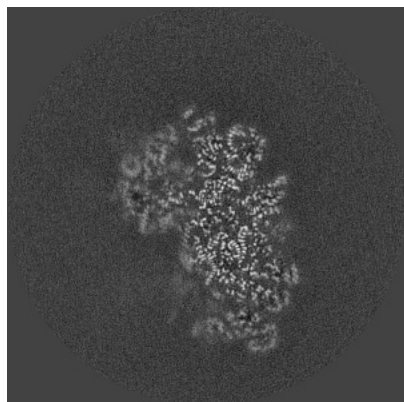


Y Index: 229

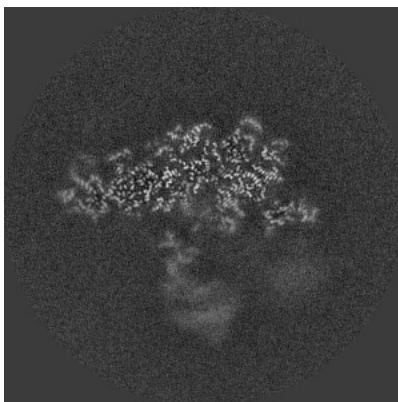


Z Index: 216

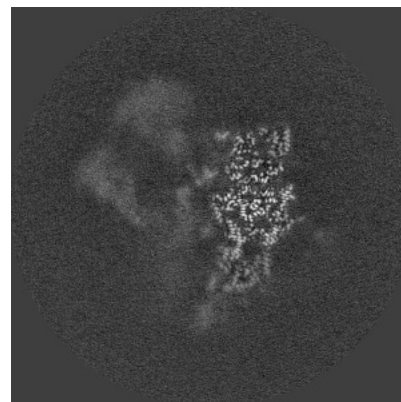
6.3.2 Raw map



X Index: 241



Y Index: 233

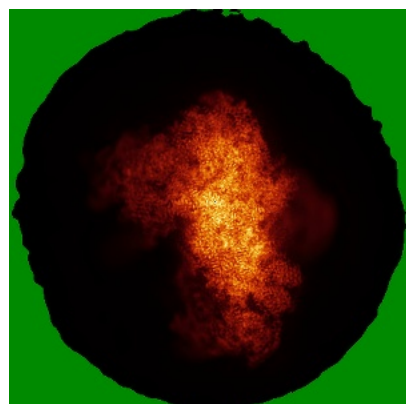


Z Index: 217

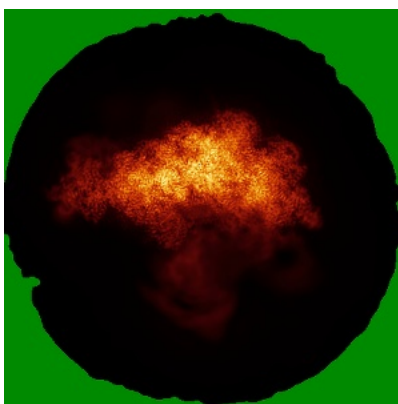
The images above show the largest variance slices of the map in three orthogonal directions.

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

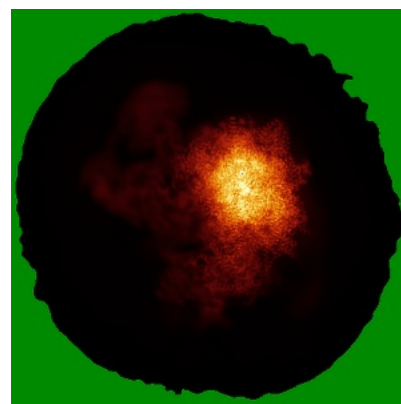
6.4.1 Primary map



X

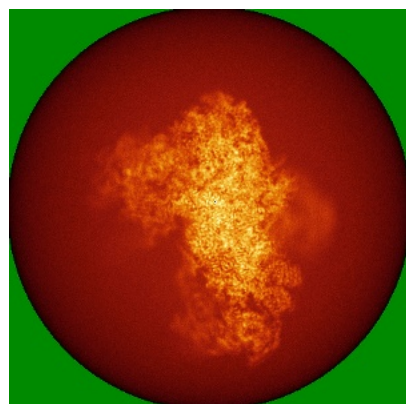


Y

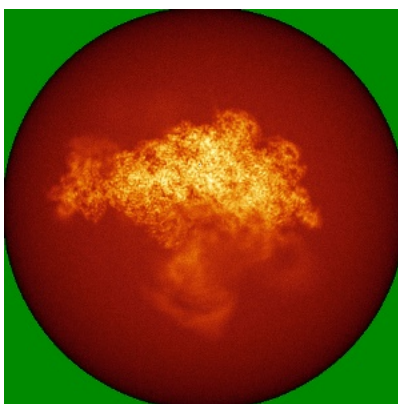


Z

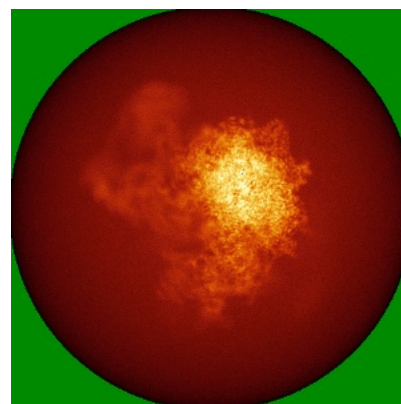
6.4.2 Raw map



X



Y

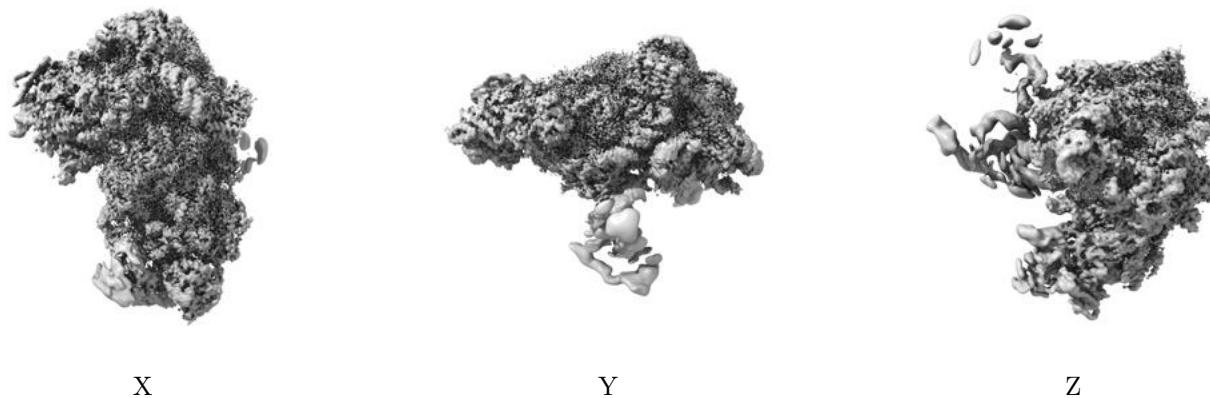


Z

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

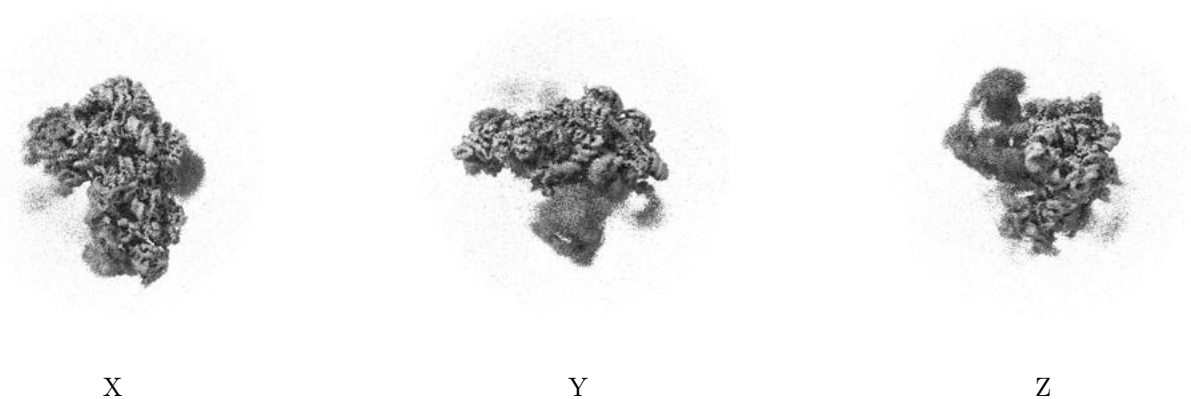
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

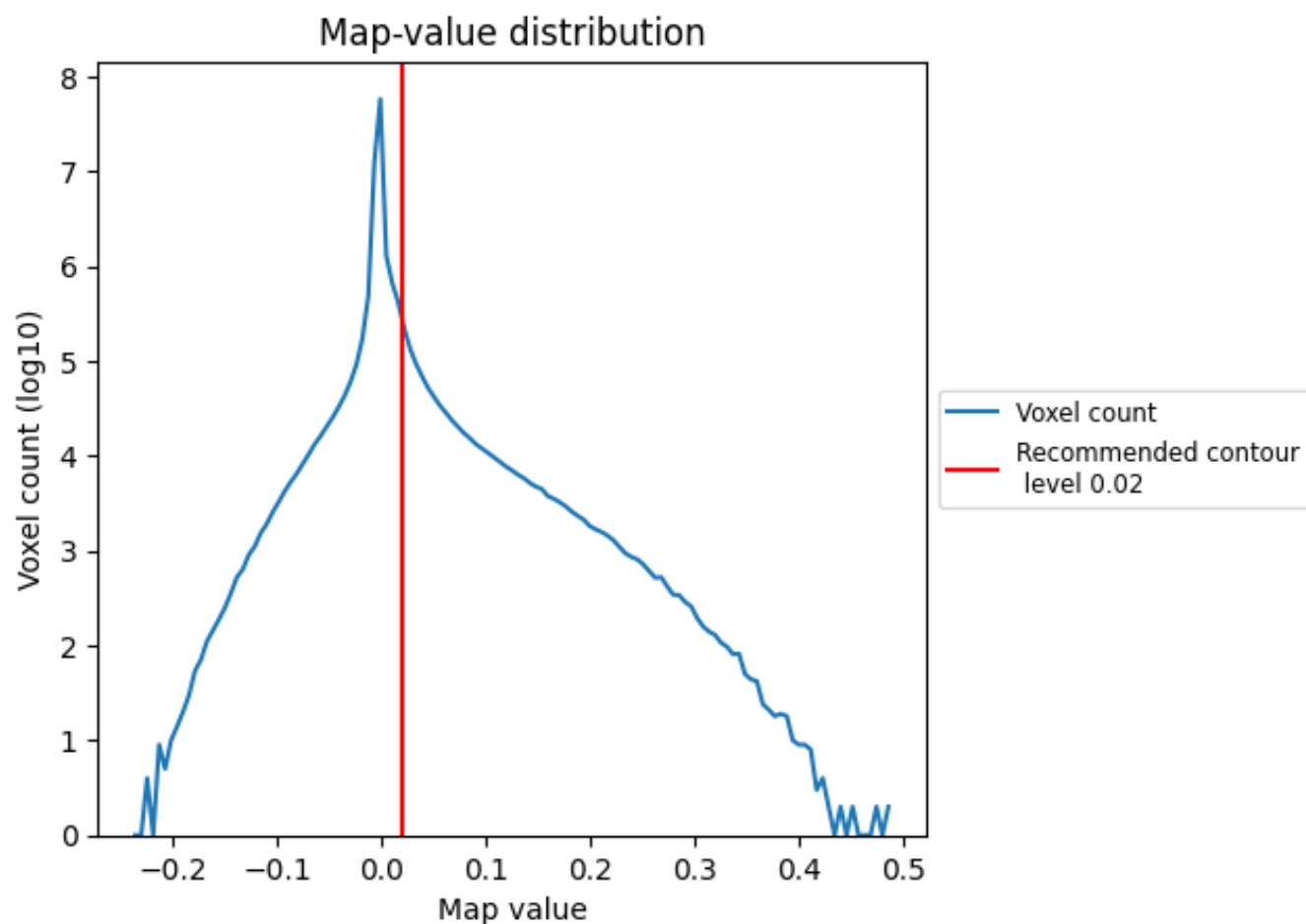
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

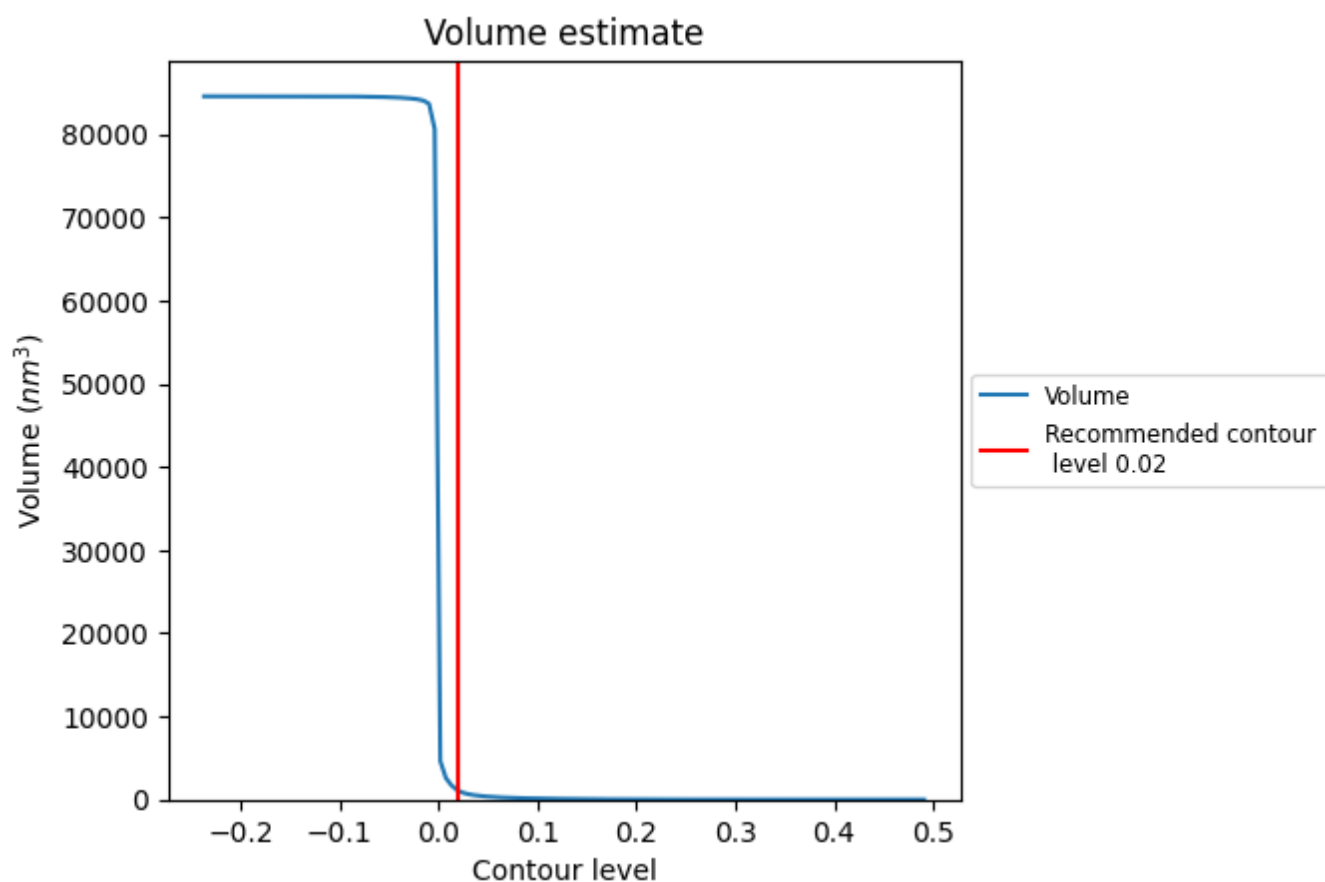
This section contains the results of statistical analysis of the map.

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.

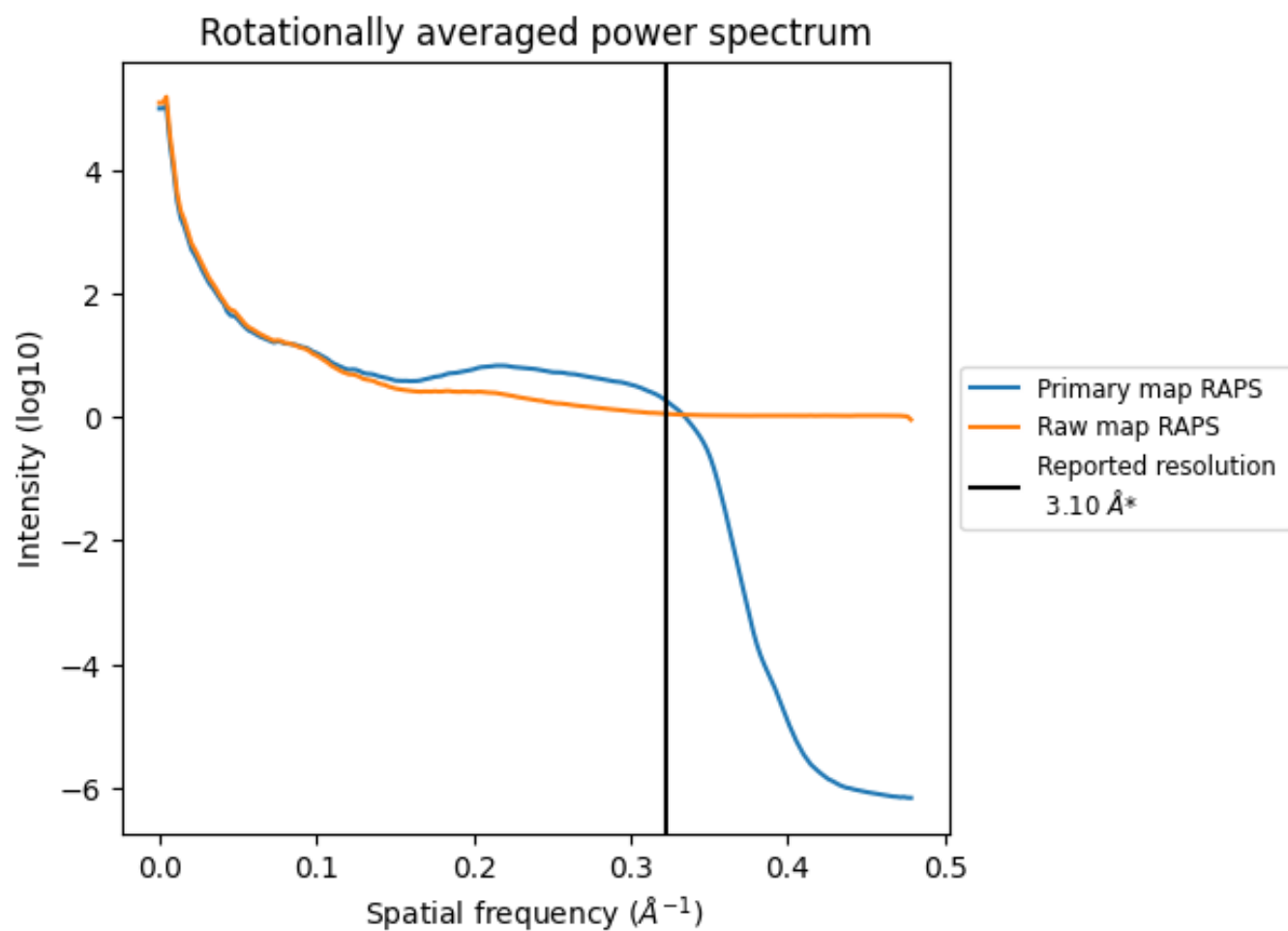
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1087 nm^3 ; this corresponds to an approximate mass of 982 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 ⓘ

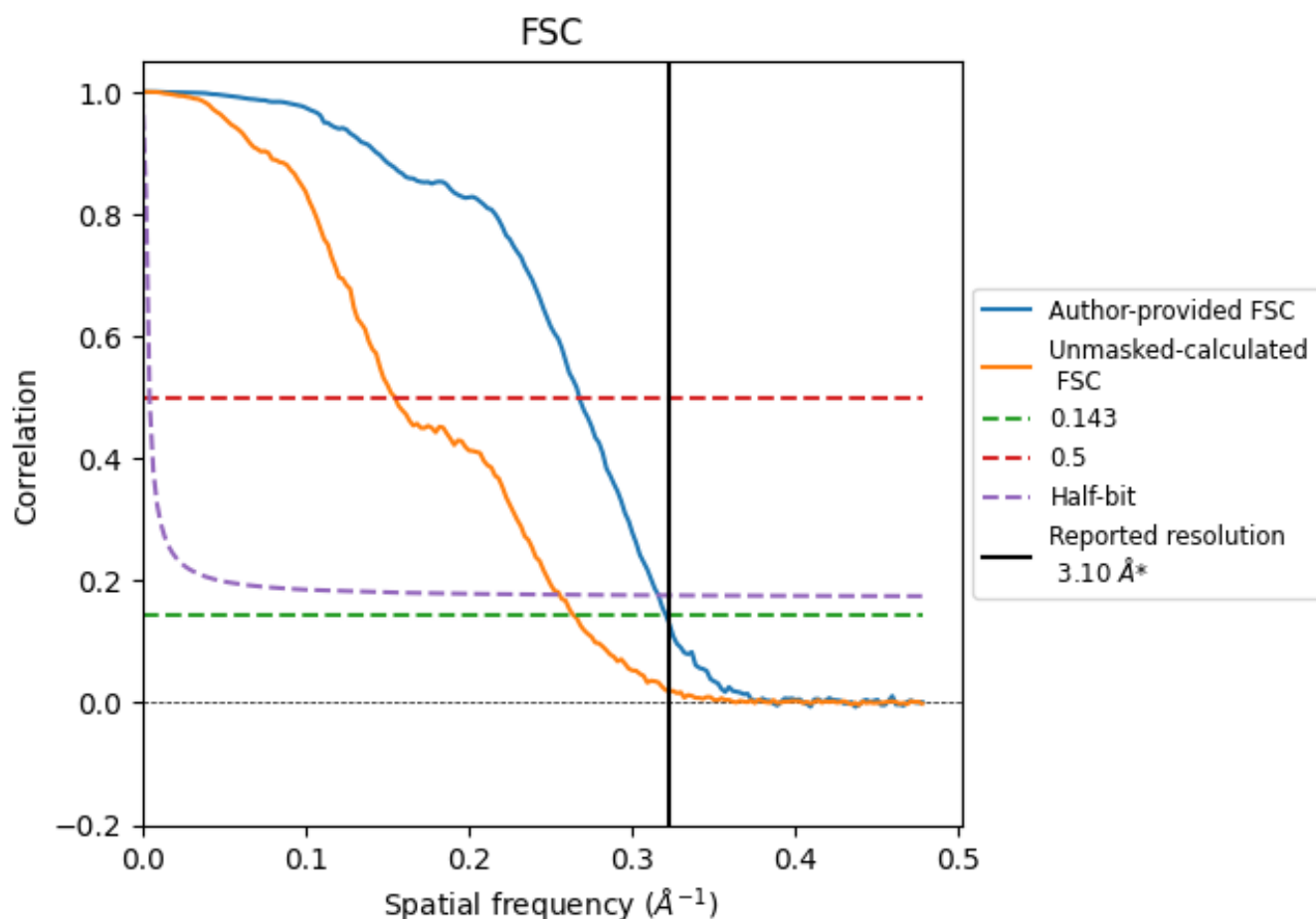


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

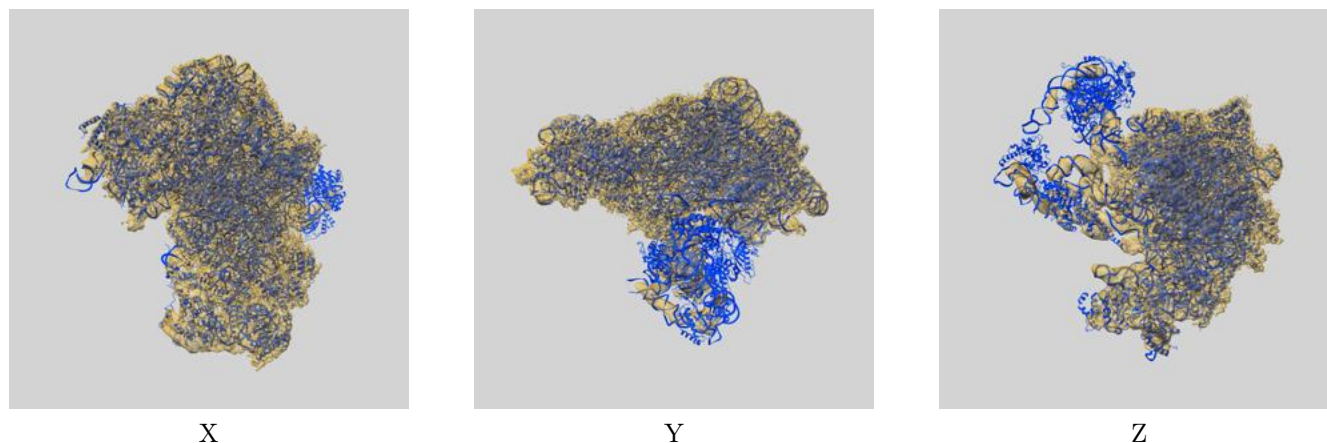
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.11	3.73	3.16
Unmasked-calculated*	3.78	6.45	3.91

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.78 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

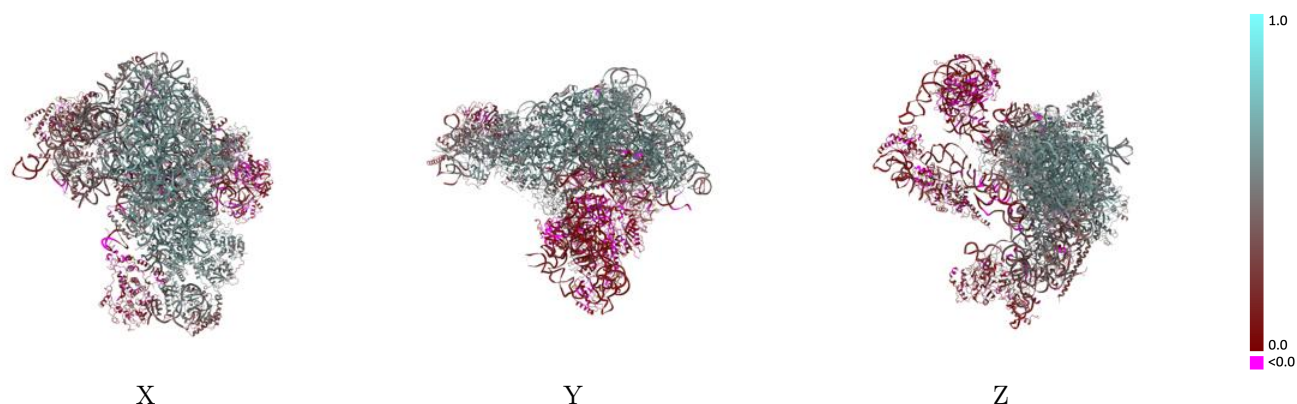
This section contains information regarding the fit between EMDB map EMD-35281 and PDB model 8I9R. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



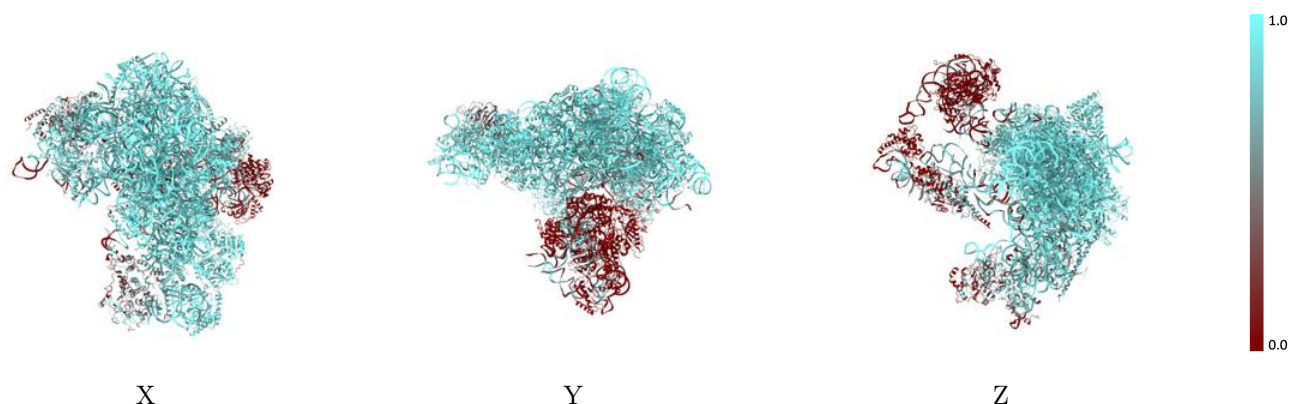
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



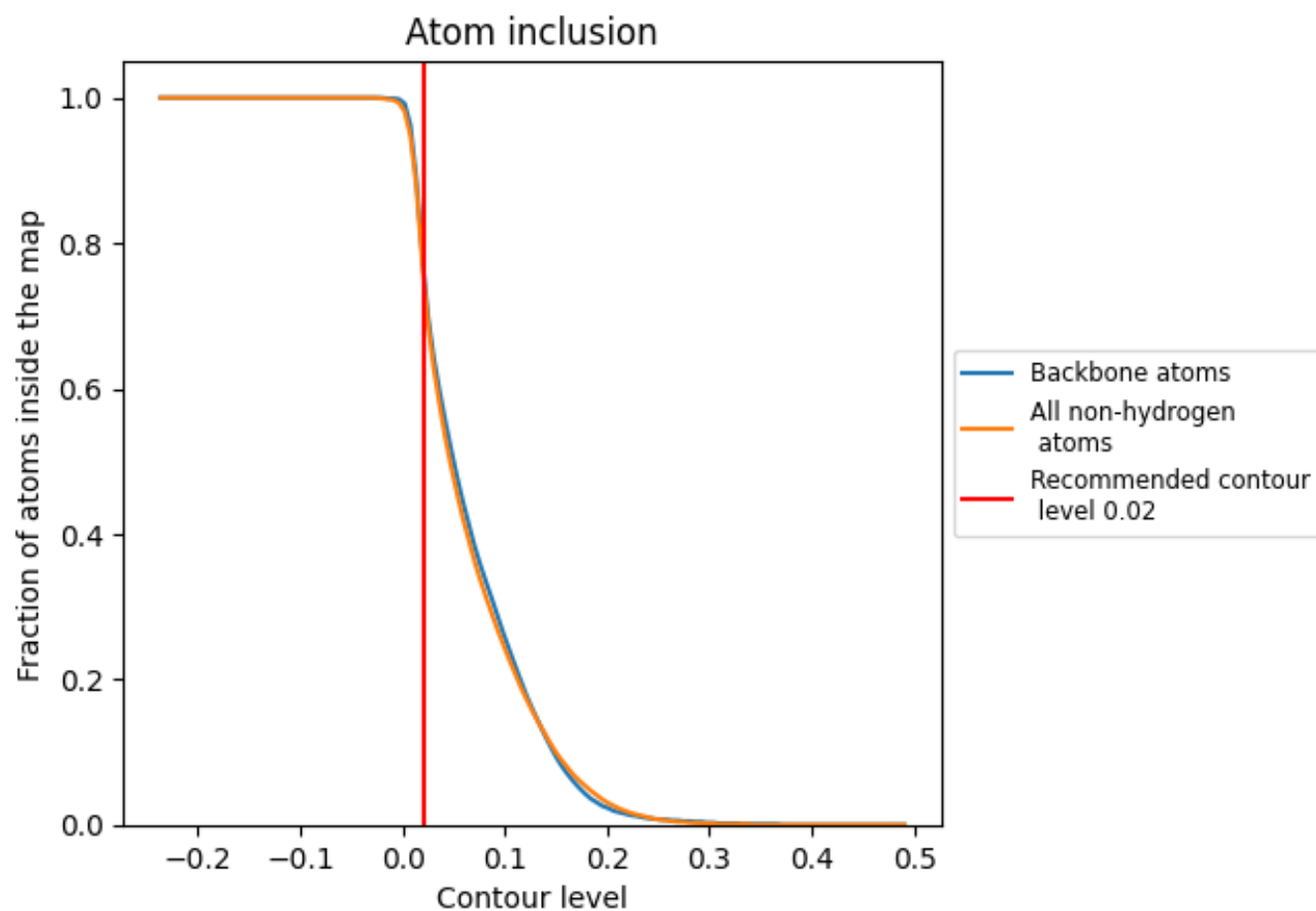
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 76% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7610	 0.4050
C1	 0.8260	 0.4090
C2	 0.9150	 0.4740
C4	 0.1690	 0.1000
CA	 0.8840	 0.4900
CB	 0.8480	 0.4450
CC	 0.6290	 0.3320
CE	 0.9000	 0.5130
CG	 0.5290	 0.1640
CH	 0.3820	 0.2080
CI	 0.8720	 0.4490
CJ	 0.4900	 0.1550
CM	 0.6900	 0.3100
CN	 0.3660	 0.1790
CP	 0.1970	 0.1380
CQ	 0.6160	 0.2450
CR	 0.9140	 0.5420
CU	 0.8040	 0.4050
CX	 0.6150	 0.3430
Cc	 0.8530	 0.5030
Cd	 0.9130	 0.5400
Ce	 0.9410	 0.5680
Cf	 0.7690	 0.4040
Cg	 0.7650	 0.3980
Ch	 0.7200	 0.3060
Cx	 0.1520	 0.1030
Cy	 0.0000	 0.0720
LB	 0.7710	 0.3770
LC	 0.9510	 0.5860
LD	 0.0010	 0.0380
LE	 0.9140	 0.5320
LF	 0.9320	 0.5550
LG	 0.9050	 0.5480
LJ	 0.0380	 0.0310
LL	 0.9420	 0.5770



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Chain	Atom inclusion	Q-score
LM	 0.8660	 0.4960
LN	 0.9470	 0.5970
LO	 0.9350	 0.5440
LP	 0.8320	 0.4810
LQ	 0.9480	 0.5760
LS	 0.9110	 0.5070
LT	 0.7370	 0.3560
LV	 0.3700	 0.1870
LY	 0.9300	 0.5690
Le	 0.9430	 0.5900
Lf	 0.9470	 0.5880
Lh	 0.8670	 0.4900
Li	 0.8930	 0.5270
Lj	 0.9590	 0.6060
Lq	 0.0080	 0.0760