



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 12:57 PM UTC

PDB ID : 7ZQ6 / pdb_00007zq6
EMDB ID : EMD-14865
Title : 70S E. coli ribosome with truncated uL23 and uL24 loops and a stalled filamin domain 5 nascent chain
Authors : Mitropoulou, A.; Wlodarski, T.; Ahn, M.; Becker, T.A.; Beckmann, R.; Cabrita, L.D.; Christodoulou, J.
Deposited on : 2022-04-29
Resolution : 2.75 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

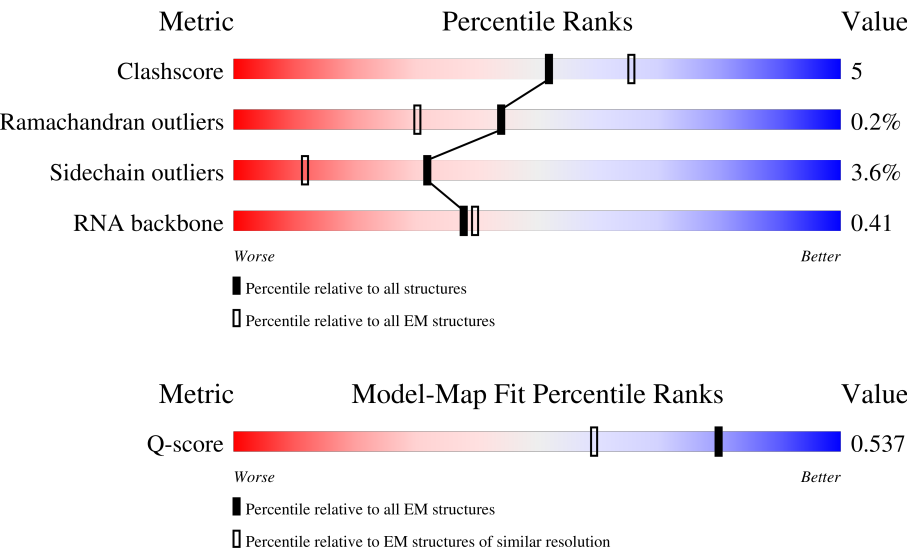
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.75 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	10570 (2.25 - 3.25)

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	0	78	
2	1	63	
3	2	59	

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Mol	Chain	Length	Quality of chain
4	3	57	
5	4	55	
6	6	46	
7	7	65	
8	8	50	
9	a	120	
10	b	2904	
11	c	273	
12	d	209	
13	e	201	
14	f	179	
15	g	177	
16	h	149	
17	j	142	
18	k	123	
19	l	144	
20	m	136	
21	n	127	
22	o	117	
23	p	115	
24	q	118	
25	r	103	
26	s	110	
27	t	100	
28	u	104	

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Mol	Chain	Length	Quality of chain
29	w	94	55% 79% 21%
30	y	85	5% 69% 16% 11%
31	M	76	47% 51% 41% 8%
32	z	3	67% 33%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 90507 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	57	Total	C	N	O	S	0	0
			439	276	86	75	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 9 is a RNA chain called 5S rRNA.

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

- Molecule 10 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	2901	Total	C	N	O	P	0	0
			62281	27784	11464	20132	2901		

- Molecule 11 is a protein called 50S ribosomal protein L2.

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

- Molecule 12 is a protein called 50S ribosomal protein L3.

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

- Molecule 13 is a protein called 50S ribosomal protein L4.

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

- Molecule 14 is a protein called 50S ribosomal protein L5.

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

- Molecule 15 is a protein called 50S ribosomal protein L6.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	39	Total	C	N	O	S	0	0
			287	184	51	51	1		

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

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

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	143	Total	C	N	O	S	0	0
			1043	649	206	186	2		

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

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

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	113	Total	C	N	O	S	0	0
			908	570	177	160	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	102	Total	C	N	O	S	0	0
			810	513	152	143	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	109	Total	C	N	O	S	0	0
			845	526	162	154	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	86	Total	C	N	O	S	0	0
			681	433	123	123	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	u	91	Total	C	N	O	0	0
			699	441	131	127		

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	y	76	Total	C	N	O	S	0	0
			578	358	117	102	1		

- Molecule 31 is a RNA chain called Gly-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	M	76	Total	C	N	O	P	0	0
			1621	722	287	536	76		

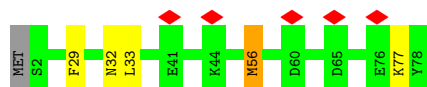
- Molecule 32 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	z	3	Total	C	N	O	0	0
			16	10	3	3		

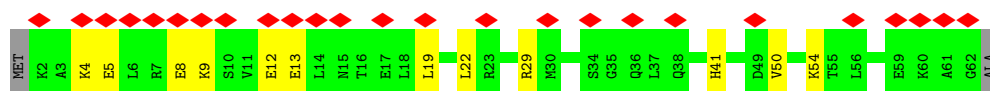
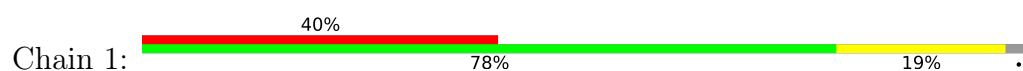
3 Residue-property plots [i](#)

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

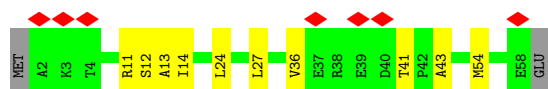
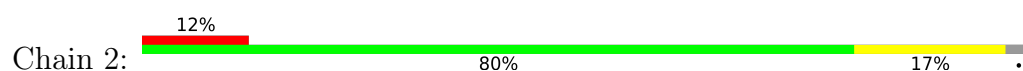
- Molecule 1: 50S ribosomal protein L28



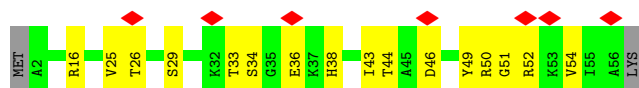
- Molecule 2: 50S ribosomal protein L29



- Molecule 3: 50S ribosomal protein L30



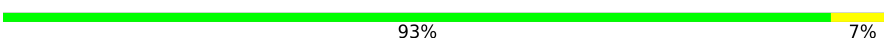
- Molecule 4: 50S ribosomal protein L32



- Molecule 5: 50S ribosomal protein L33



- Molecule 6: 50S ribosomal protein L34

Chain 6:  93% 7%



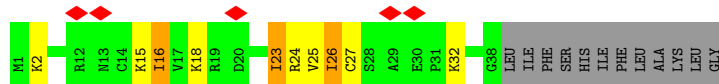
- Molecule 7: 50S ribosomal protein L35

Chain 7:  80% 18%



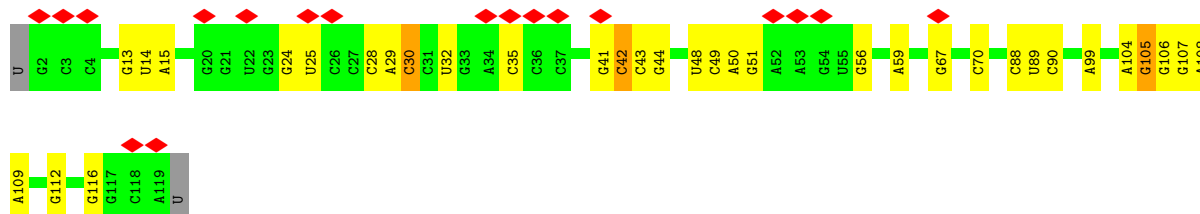
- Molecule 8: 50S ribosomal protein L36

Chain 8:  10% 56% 14% 6% 24%



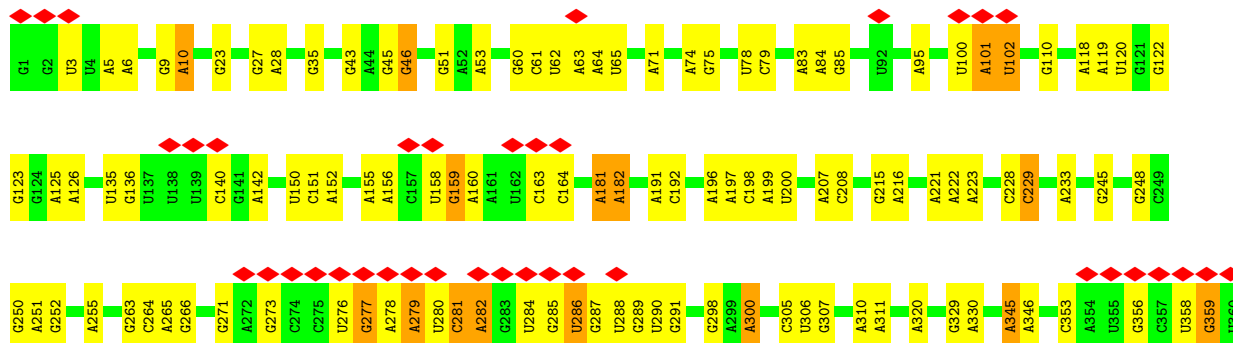
- Molecule 9: 5S rRNA

Chain a:  15% 70% 26%

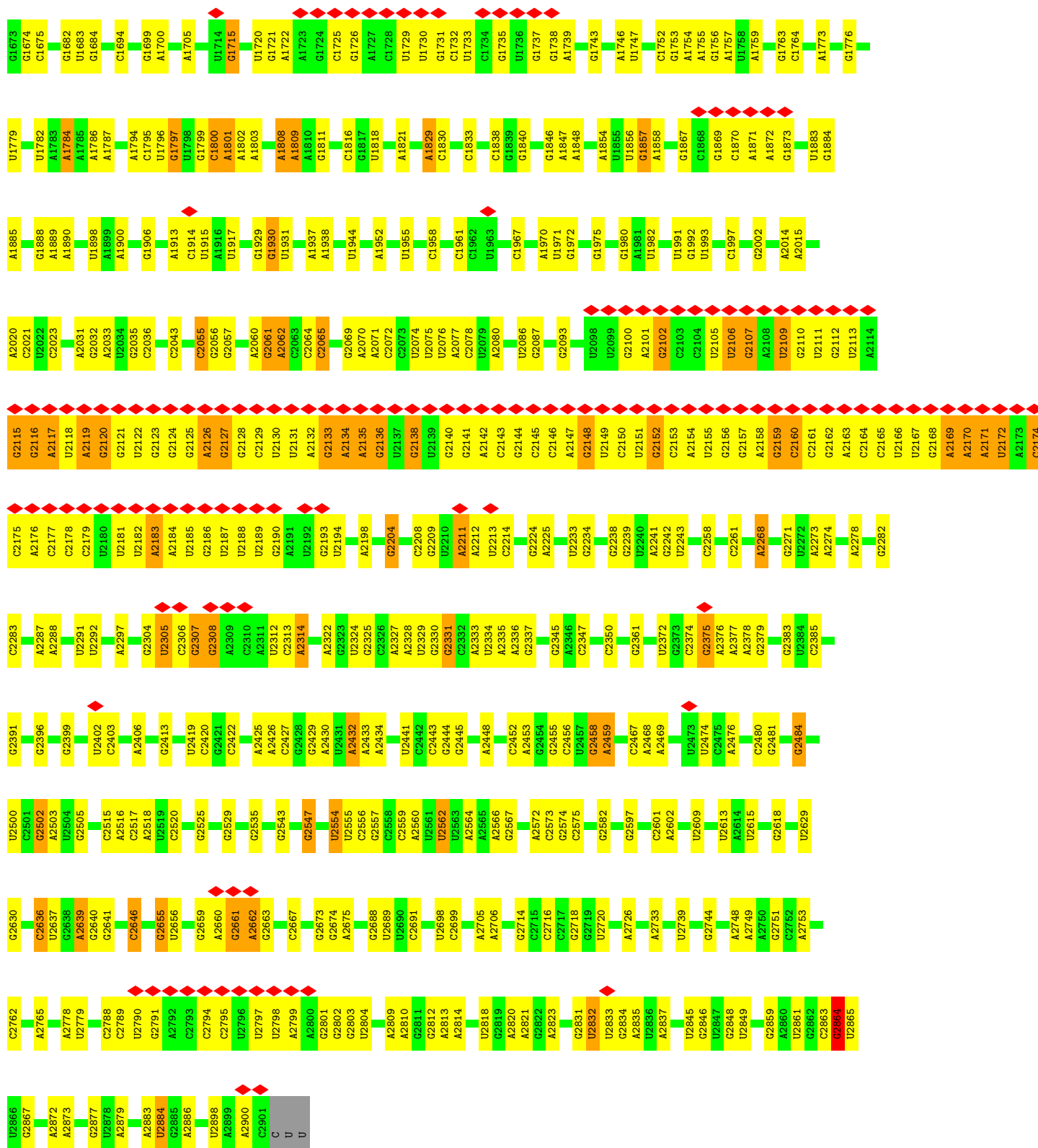


- Molecule 10: 23S rRNA

Chain b:  12% 63% 32% 6%

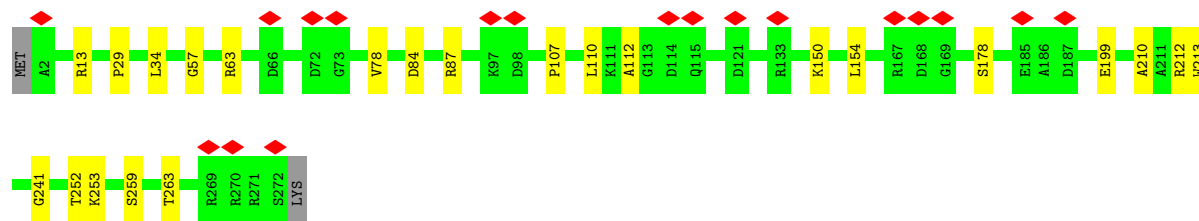




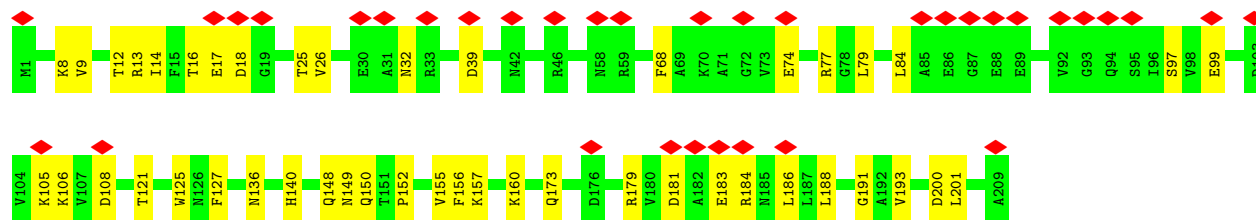
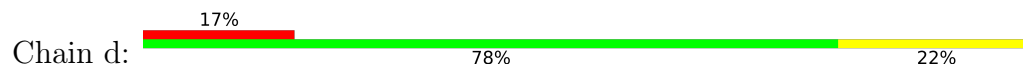


• Molecule 11: 50S ribosomal protein L2

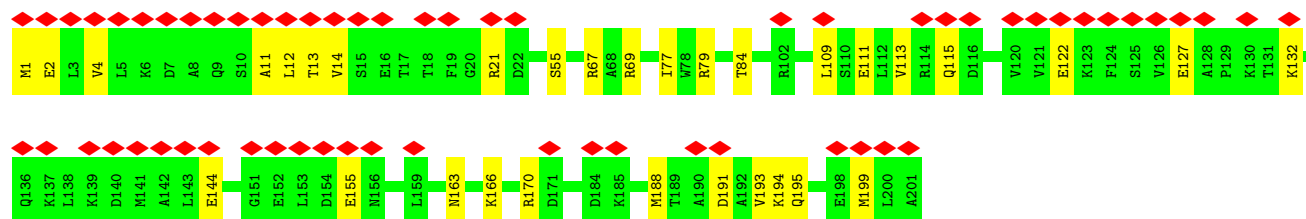
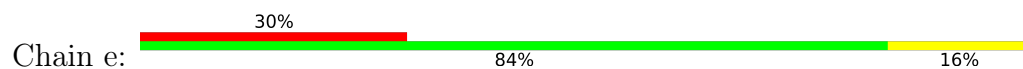




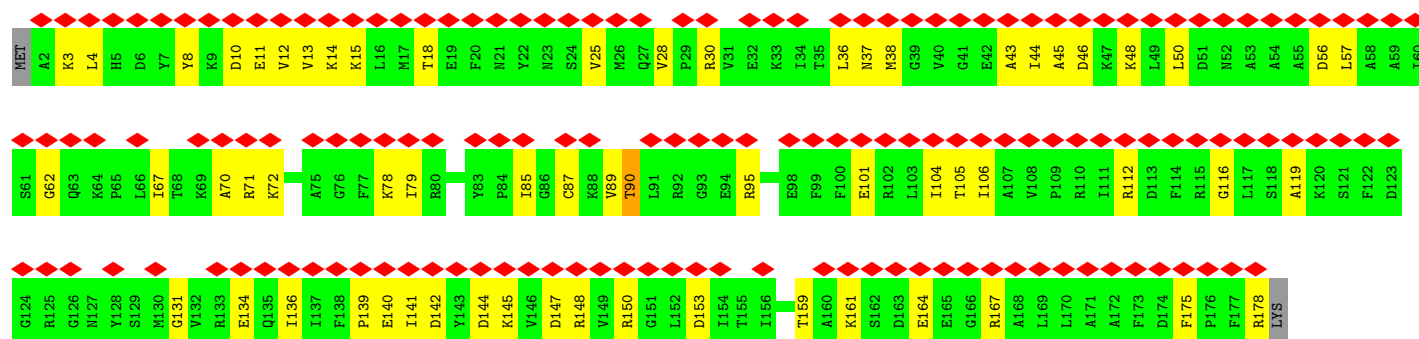
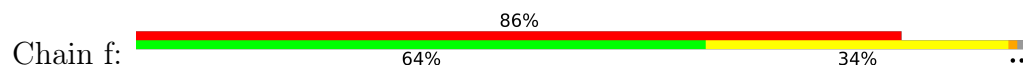
• Molecule 12: 50S ribosomal protein L3



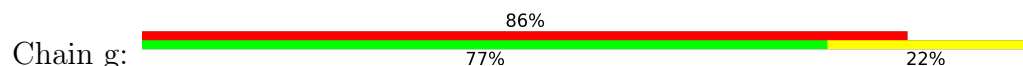
• Molecule 13: 50S ribosomal protein L4

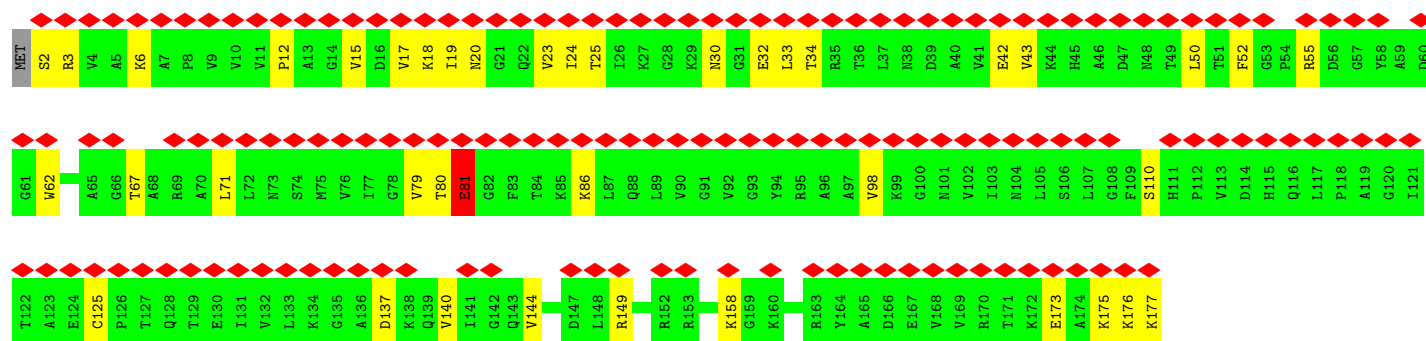


• Molecule 14: 50S ribosomal protein L5

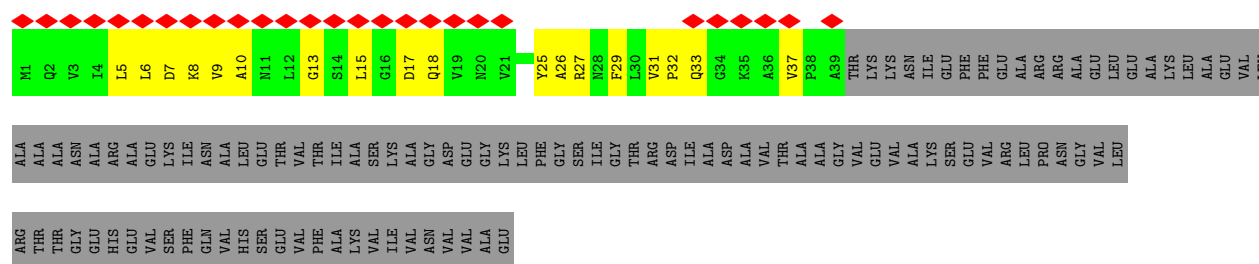


• Molecule 15: 50S ribosomal protein L6

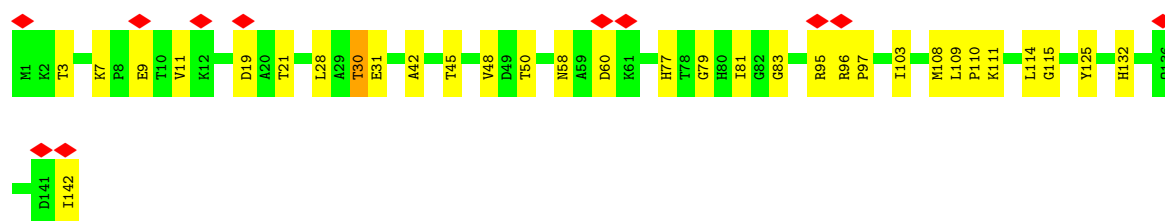
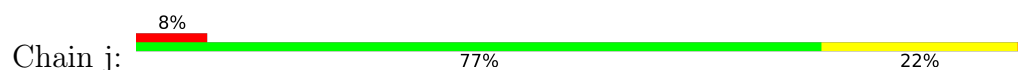




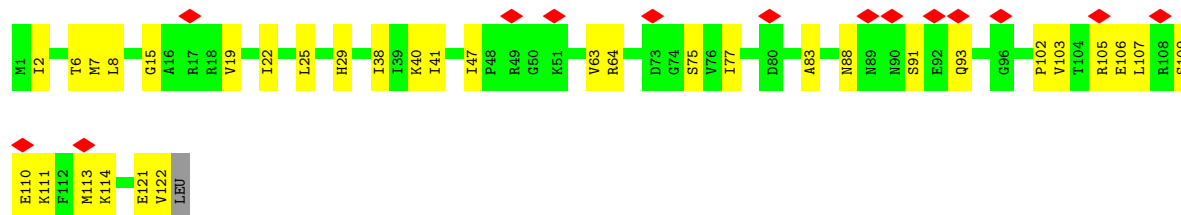
• Molecule 16: 50S ribosomal protein L9



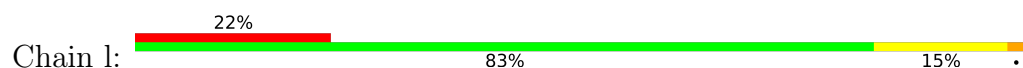
• Molecule 17: 50S ribosomal protein L13

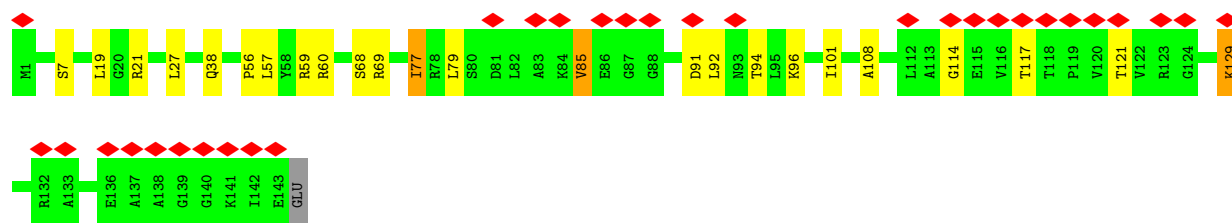


• Molecule 18: 50S ribosomal protein L14

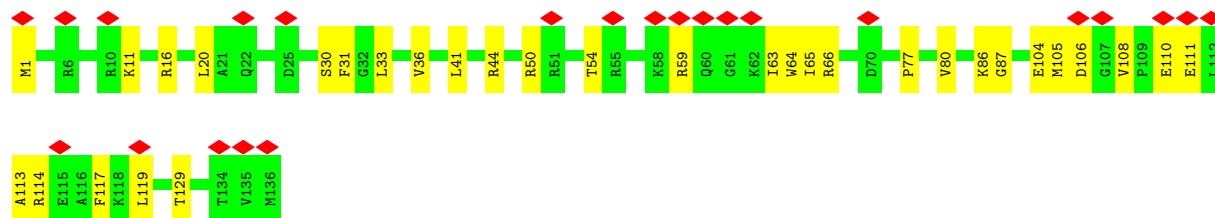
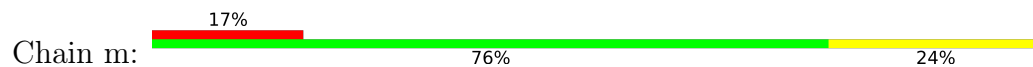


• Molecule 19: 50S ribosomal protein L15

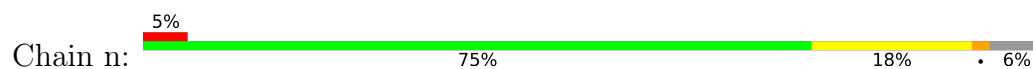




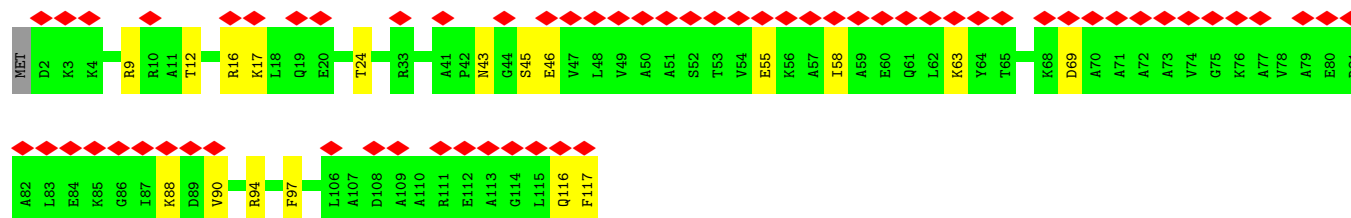
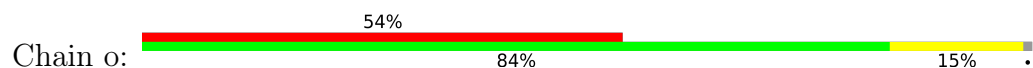
- Molecule 20: 50S ribosomal protein L16



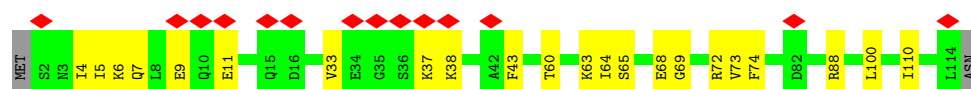
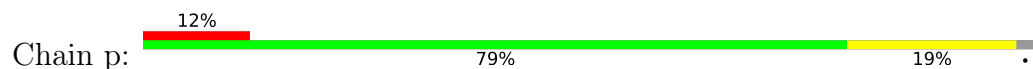
- Molecule 21: 50S ribosomal protein L17



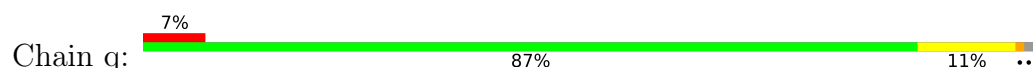
- Molecule 22: 50S ribosomal protein L18

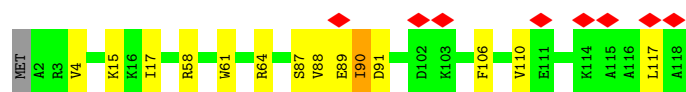


- Molecule 23: 50S ribosomal protein L19

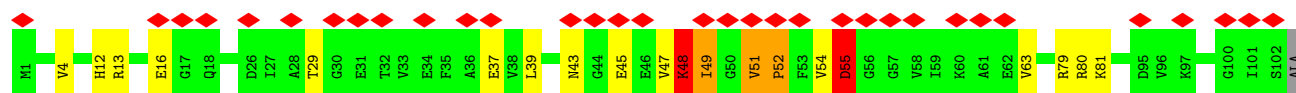
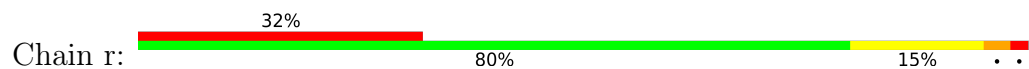


- Molecule 24: 50S ribosomal protein L20

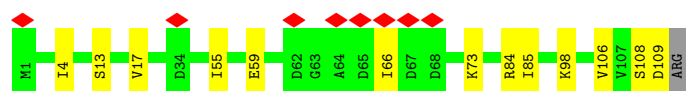
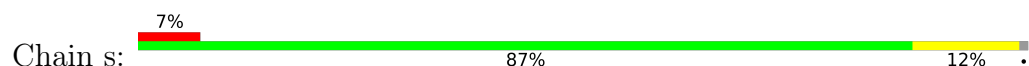




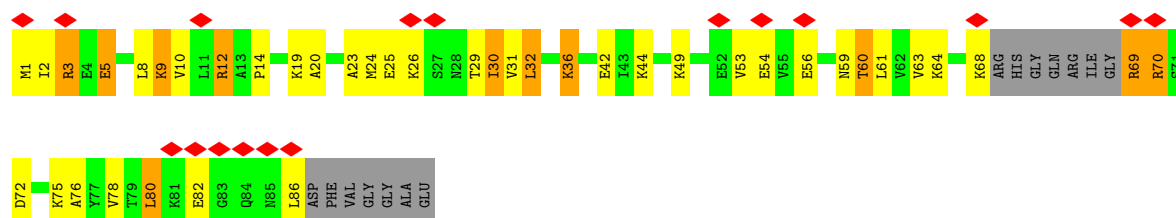
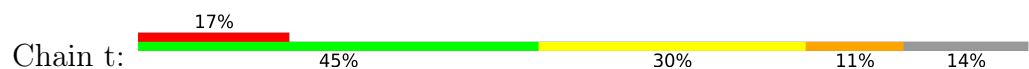
- Molecule 25: 50S ribosomal protein L21



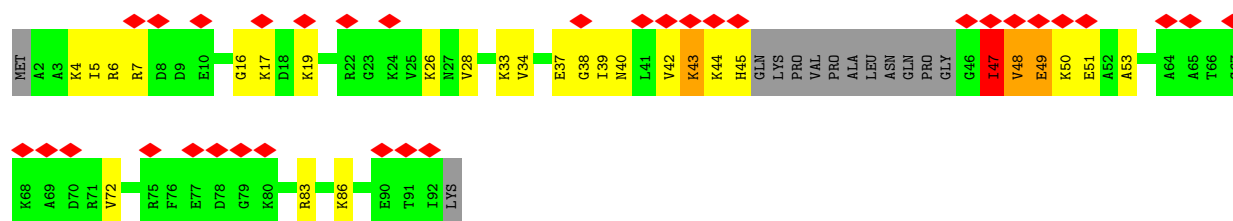
- Molecule 26: 50S ribosomal protein L22



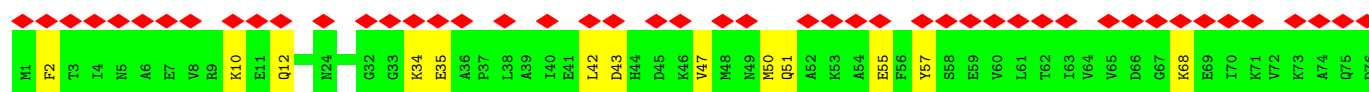
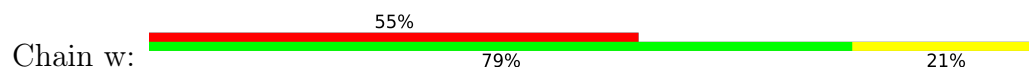
- Molecule 27: 50S ribosomal protein L23

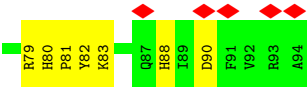


- Molecule 28: 50S ribosomal protein L24

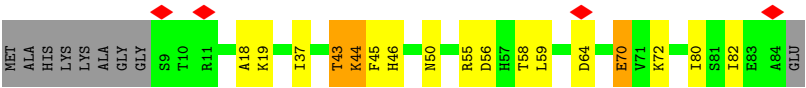


- Molecule 29: 50S ribosomal protein L25

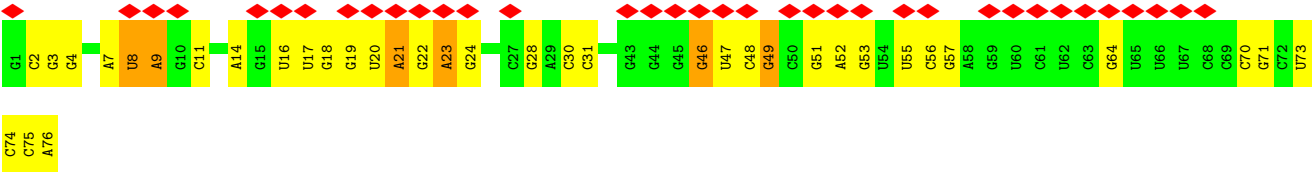




• Molecule 30: 50S ribosomal protein L27



• Molecule 31: Gly-tRNA



• Molecule 32: Nascent chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	109037	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.9	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.428	Depositor
Minimum map value	-0.110	Depositor
Average map value	-0.009	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.0806	Depositor
Map size ($\text{\AA}$)	399.28003, 399.28003, 399.28003	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.085, 1.085, 1.085	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.42	0/635	0.39	0/848
2	1	0.55	0/496	0.77	0/660
3	2	0.42	0/443	0.45	0/593
4	3	0.43	0/440	0.48	0/588
5	4	0.38	0/416	0.50	0/554
6	6	0.47	0/380	0.47	0/498
7	7	0.54	0/513	0.60	0/676
8	8	0.72	0/302	0.84	0/397
9	a	0.46	0/2828	0.45	0/4410
10	b	0.52	0/69757	0.58	17/108827 (0.0%)
11	c	0.46	0/2121	0.46	0/2852
12	d	0.44	0/1586	0.44	0/2134
13	e	0.40	0/1571	0.42	0/2113
14	f	0.32	0/1434	0.59	0/1926
15	g	0.31	0/1343	0.56	1/1816 (0.1%)
16	h	0.33	0/290	0.67	0/392
17	j	0.45	0/1152	0.44	0/1551
18	k	0.48	0/947	0.53	0/1268
19	l	0.51	0/1052	0.70	0/1401
20	m	0.41	0/1093	0.47	0/1460
21	n	0.46	0/973	0.50	0/1301
22	o	0.42	0/902	0.57	0/1209
23	p	0.45	0/920	0.44	0/1231
24	q	0.54	0/960	0.59	1/1278 (0.1%)
25	r	0.51	0/823	0.69	1/1100 (0.1%)
26	s	0.43	0/852	0.42	0/1142
27	t	0.95	0/686	1.16	0/918
28	u	0.52	0/704	0.62	0/936
29	w	0.38	0/766	0.49	0/1025
30	y	0.52	0/585	0.60	0/775
31	M	0.52	0/1810	0.72	0/2820
32	z	0.78	0/16	1.03	0/21
All	All	0.50	0/98796	0.58	20/148720 (0.0%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2864	G	C2'-C3'-O3'	9.00	127.20	113.70
10	b	2832	U	C2'-C3'-O3'	8.07	121.60	109.50
10	b	1626	A	C2'-C3'-O3'	7.78	125.36	113.70
10	b	390	U	C2'-C3'-O3'	7.71	121.06	109.50
10	b	2375	G	C4'-C3'-O3'	7.18	120.18	109.40
10	b	2655	G	C4'-C3'-O3'	7.01	119.92	109.40
25	r	48	LYS	CB-CA-C	-6.78	105.93	114.40
10	b	1930	G	C4'-C3'-O3'	6.51	119.16	109.40
10	b	479	A	C2'-C3'-O3'	-6.26	100.11	109.50
10	b	390	U	C4'-C3'-O3'	6.05	118.48	109.40
10	b	547	A	C4'-C3'-O3'	5.87	118.20	109.40
10	b	1299	G	C2'-C3'-O3'	5.81	122.42	113.70
10	b	2055	C	C2'-C3'-O3'	5.62	122.12	113.70
24	q	91	ASP	CB-CA-C	-5.41	99.20	110.40
10	b	464	U	C2'-C3'-O3'	-5.32	105.72	113.70
10	b	2055	C	C4'-C3'-O3'	5.22	120.83	113.00
10	b	2655	G	C2'-C3'-O3'	5.22	117.33	109.50
10	b	2575	C	C3'-C2'-O2'	-5.08	103.08	110.70
15	g	81	GLU	CA-CB-CG	5.07	124.24	114.10
10	b	1818	U	C4'-C3'-O3'	-5.05	105.42	113.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	625	0	652	5	0
2	1	495	0	526	10	0
3	2	439	0	482	7	0
4	3	434	0	445	11	0
5	4	409	0	440	16	0
6	6	377	0	418	3	0
7	7	504	0	572	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	8	301	0	341	5	0
9	a	2529	0	1281	7	0
10	b	62281	0	31323	394	0
11	c	2082	0	2154	19	0
12	d	1565	0	1616	36	0
13	e	1552	0	1619	27	0
14	f	1410	0	1444	51	0
15	g	1323	0	1371	30	0
16	h	287	0	307	12	0
17	j	1129	0	1162	25	0
18	k	938	0	1012	25	0
19	l	1043	0	1123	14	0
20	m	1074	0	1157	24	0
21	n	960	0	1000	18	0
22	o	892	0	923	9	0
23	p	908	0	956	19	0
24	q	947	0	1019	13	0
25	r	810	0	834	18	0
26	s	845	0	909	8	0
27	t	681	0	749	15	0
28	u	699	0	747	14	0
29	w	753	0	780	14	0
30	y	578	0	598	12	0
31	M	1621	0	820	5	0
32	z	16	0	14	1	0
All	All	90507	0	58794	800	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (800) 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)
10:b:874:G:C2'	10:b:875:G:H5'	1.80	1.10
10:b:874:G:O2'	10:b:875:G:H5'	1.61	1.00
10:b:901:C:H2'	10:b:902:C:C6	2.01	0.95
10:b:874:G:H2'	10:b:875:G:H5'	1.46	0.94
10:b:844:A:C2	10:b:845:A:N1	2.41	0.89
25:r:39:LEU:HB3	25:r:49:ILE:HD13	1.59	0.84
28:u:4:LYS:HD2	28:u:72:VAL:HG13	1.61	0.83
18:k:121:GLU:HG2	18:k:122:VAL:HG23	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:b:1439:A:H62	10:b:1552:A:H8	1.26	0.79
10:b:891:G:H5''	10:b:892:A:OP1	1.81	0.79
24:q:89:GLU:H	25:r:49:ILE:HD12	1.47	0.79
10:b:1053:C:H2'	10:b:1054:A:H4'	1.65	0.78
12:d:149:ASN:OD1	12:d:150:GLN:N	2.14	0.78
15:g:2:SER:HB2	15:g:62:TRP:HB3	1.66	0.77
13:e:122:GLU:OE2	13:e:122:GLU:N	2.17	0.76
21:n:37:THR:HG22	21:n:110:MET:HE1	1.67	0.76
16:h:7:ASP:OD1	16:h:8:LYS:N	2.18	0.76
25:r:51:VAL:HB	25:r:52:PRO:HD3	1.70	0.74
10:b:2125:G:H2'	10:b:2126:A:H4'	1.70	0.72
10:b:901:C:H2'	10:b:902:C:H6	1.50	0.72
10:b:874:G:O2'	10:b:875:G:C5'	2.36	0.72
10:b:1858:A:N6	10:b:1884:G:O2'	2.23	0.72
10:b:1054:A:N6	10:b:1055:G:H21	1.88	0.71
20:m:20:LEU:HD13	29:w:81:PRO:HG2	1.72	0.71
10:b:1093:G:O6	10:b:1099:G:N1	2.24	0.70
10:b:875:G:N2	10:b:903:C:C2	2.60	0.70
10:b:2100:G:H1	10:b:2189:U:H3	1.36	0.70
5:4:9:ILE:HD13	5:4:25:LYS:HB2	1.72	0.70
15:g:19:ILE:HD13	15:g:43:VAL:HG13	1.74	0.70
15:g:3:ARG:HA	15:g:6:LYS:HG2	1.75	0.69
22:o:9:ARG:HH11	22:o:9:ARG:HG2	1.57	0.69
14:f:116:GLY:HA3	14:f:178:ARG:HH12	1.58	0.69
12:d:77:ARG:NH2	12:d:200:ASP:OD1	2.25	0.69
10:b:101:A:H2'	10:b:102:U:H5	1.58	0.69
16:h:5:LEU:HD21	16:h:13:GLY:HA2	1.74	0.68
10:b:1069:A:N1	10:b:1095:A:H5''	2.09	0.68
19:l:56:PRO:HG2	19:l:59:ARG:HG3	1.75	0.68
10:b:875:G:C2	10:b:903:C:C2	2.83	0.67
17:j:77:HIS:CD2	17:j:79:GLY:H	2.13	0.67
18:k:110:GLU:HA	18:k:113:MET:HG2	1.77	0.67
2:1:4:LYS:H	2:1:4:LYS:HD2	1.60	0.67
10:b:901:C:C5	10:b:902:C:N4	2.64	0.66
17:j:125:TYR:HH	17:j:132:HIS:HE2	1.41	0.66
12:d:184:ARG:CZ	23:p:7:GLN:HE22	2.09	0.65
10:b:586:A:H5'	13:e:84:THR:HG21	1.77	0.65
2:1:5:GLU:HA	2:1:8:GLU:HG2	1.78	0.65
10:b:2749:A:H5''	15:g:2:SER:HB3	1.78	0.65
20:m:50:ARG:O	20:m:54:THR:HG22	1.97	0.65
17:j:3:THR:HG21	24:q:61:TRP:HE1	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:k:77:ILE:HG12	23:p:72:ARG:HG3	1.79	0.65
14:f:62:GLY:HA3	14:f:95:ARG:HH21	1.61	0.64
10:b:2305:U:H5''	14:f:131:GLY:HA3	1.79	0.64
26:s:59:GLU:HB2	26:s:66:ILE:HD11	1.78	0.64
10:b:901:C:C4	10:b:902:C:C4	2.86	0.64
10:b:101:A:H2'	10:b:102:U:C5	2.33	0.64
17:j:77:HIS:HD2	17:j:79:GLY:H	1.45	0.64
12:d:17:GLU:H	12:d:17:GLU:CD	2.05	0.64
20:m:111:GLU:H	20:m:111:GLU:CD	2.06	0.63
15:g:18:LYS:N	15:g:18:LYS:HE2	2.12	0.63
16:h:17:ASP:N	16:h:17:ASP:OD1	2.32	0.63
11:c:107:PRO:HD2	11:c:110:LEU:HD22	1.81	0.62
10:b:1738:G:HO2'	10:b:1739:A:H8	1.46	0.62
1:0:32:ASN:HB2	10:b:397:U:H5''	1.82	0.62
10:b:875:G:C2	10:b:903:C:O2	2.53	0.62
10:b:2102:G:H1	10:b:2187:U:H3	1.47	0.62
10:b:602:A:HO2'	10:b:604:G:HO2'	1.45	0.62
28:u:26:LYS:HD2	28:u:37:GLU:HG2	1.81	0.61
25:r:45:GLU:OE1	25:r:45:GLU:N	2.33	0.61
10:b:1093:G:H2'	10:b:1094:U:O4'	2.00	0.61
10:b:2100:G:H2'	10:b:2101:A:H8	1.64	0.61
14:f:30:ARG:H	14:f:159:THR:HB	1.65	0.61
31:M:9:A:H2'	31:M:11:C:H41	1.65	0.61
23:p:5:ILE:O	23:p:9:GLU:HG3	1.99	0.61
28:u:16:GLY:O	28:u:17:LYS:HG3	2.01	0.61
10:b:1857:G:H22	10:b:1884:G:H2'	1.65	0.61
12:d:183:GLU:CD	12:d:183:GLU:H	2.09	0.61
10:b:2291:U:H2'	10:b:2292:U:C6	2.36	0.60
25:r:4:VAL:HG12	25:r:13:ARG:HG3	1.83	0.60
10:b:281:C:H2'	10:b:282:A:H8	1.66	0.60
11:c:63:ARG:HD3	11:c:84:ASP:OD1	2.02	0.60
10:b:2061:G:H22	32:z:166:PRO:HB2	1.65	0.60
10:b:1005:C:O2'	17:j:30:THR:HG21	2.01	0.60
10:b:2327:A:H2'	10:b:2328:A:C8	2.36	0.60
10:b:2328:A:H2'	10:b:2329:U:C6	2.36	0.60
29:w:34:LYS:H	29:w:34:LYS:HD2	1.66	0.60
26:s:4:ILE:HG12	26:s:106:VAL:HG22	1.84	0.60
10:b:639:U:H2'	10:b:640:C:C6	2.36	0.60
13:e:1:MET:HG3	13:e:14:VAL:HG23	1.84	0.59
5:4:28:ARG:H	5:4:28:ARG:HD3	1.67	0.59
5:4:5:ILE:HG21	5:4:28:ARG:HH21	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:b:320:A:N3	13:e:163:ASN:ND2	2.50	0.59
10:b:875:G:N2	10:b:903:C:O2	2.36	0.59
12:d:125:TRP:CD2	12:d:160:LYS:HG2	2.37	0.59
4:3:16:ARG:NE	10:b:1266:G:OP1	2.35	0.59
14:f:14:LYS:O	14:f:18:THR:HG23	2.02	0.59
14:f:147:ASP:OD1	14:f:148:ARG:N	2.35	0.59
10:b:928:A:C6	10:b:929:U:C4	2.91	0.59
20:m:59:ARG:NH2	20:m:59:ARG:HB2	2.17	0.59
10:b:1494:A:O2'	10:b:1495:A:H8	1.86	0.58
10:b:1802:A:H2'	10:b:1803:A:C8	2.38	0.58
4:3:38:HIS:HB3	4:3:44:THR:HG22	1.84	0.58
7:7:54:ASP:HB3	19:l:57:LEU:HD22	1.86	0.58
10:b:883:G:H5''	10:b:884:U:H5	1.67	0.58
10:b:1060:U:H4'	10:b:1061:U:H4'	1.85	0.58
10:b:2204:G:H4'	11:c:150:LYS:HG3	1.85	0.58
10:b:2667:C:N3	15:g:110:SER:OG	2.35	0.58
10:b:281:C:H2'	10:b:282:A:C8	2.39	0.57
10:b:901:C:C5	10:b:902:C:C4	2.92	0.57
10:b:1102:C:N3	10:b:1103:A:N6	2.51	0.57
10:b:2273:A:H2'	10:b:2274:A:C8	2.38	0.57
10:b:1854:A:H62	10:b:1888:G:H8	1.53	0.57
27:t:3:ARG:HH21	27:t:5:GLU:HB2	1.69	0.57
10:b:874:G:C2'	10:b:875:G:C5'	2.71	0.57
14:f:134:GLU:OE1	14:f:136:ILE:HB	2.05	0.57
14:f:112:ARG:HH21	14:f:112:ARG:HG3	1.68	0.57
10:b:28:A:H61	10:b:512:G:H1'	1.70	0.57
12:d:26:VAL:HG11	23:p:4:ILE:HD11	1.87	0.57
15:g:20:ASN:HB2	15:g:23:VAL:HG13	1.87	0.57
20:m:64:TRP:HB2	20:m:104:GLU:HB2	1.87	0.57
13:e:21:ARG:NH2	13:e:21:ARG:HB3	2.19	0.56
10:b:2152:G:H2'	10:b:2153:C:C6	2.40	0.56
30:y:56:ASP:OD1	30:y:58:THR:HG23	2.06	0.56
20:m:33:LEU:HD13	20:m:117:PHE:HB3	1.88	0.56
23:p:7:GLN:NE2	23:p:11:GLU:OE1	2.38	0.56
10:b:191:A:H2'	10:b:192:C:C6	2.40	0.56
8:8:2:LYS:HE3	8:8:32:LYS:O	2.06	0.56
10:b:845:A:H2'	10:b:846:U:H4'	1.87	0.56
10:b:848:C:H2'	10:b:849:A:C8	2.40	0.56
10:b:1538:G:H2'	10:b:1539:U:C6	2.41	0.56
10:b:2120:G:H1	10:b:2179:C:H42	1.54	0.56
21:n:110:MET:HA	21:n:110:MET:HE2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:24:LEU:HD11	3:2:54:MET:HE2	1.88	0.56
10:b:901:C:O2'	10:b:902:C:H5'	2.05	0.56
14:f:164:GLU:H	14:f:164:GLU:CD	2.12	0.56
20:m:30:SER:OG	20:m:106:ASP:OD1	2.23	0.56
21:n:70:THR:O	21:n:70:THR:OG1	2.23	0.56
15:g:173:GLU:N	15:g:173:GLU:OE1	2.39	0.55
20:m:36:VAL:HG21	20:m:129:THR:HG23	1.87	0.55
21:n:41:ALA:O	21:n:42:LYS:HB2	2.06	0.55
5:4:51:GLU:OE2	5:4:53:LYS:HB2	2.06	0.55
10:b:2484:G:OP1	20:m:44:ARG:HG2	2.06	0.55
18:k:63:VAL:HG12	18:k:107:LEU:HD11	1.86	0.55
29:w:10:LYS:HA	29:w:10:LYS:HE3	1.88	0.55
10:b:555:G:HO2'	10:b:556:A:H8	1.53	0.55
10:b:1080:A:H3'	10:b:1081:U:C6	2.41	0.55
10:b:1199:U:H1'	24:q:4:VAL:HG22	1.87	0.55
17:j:31:GLU:HG2	17:j:142:ILE:HD12	1.88	0.55
31:M:21:A:H61	31:M:46:G:H2'	1.70	0.55
10:b:284:U:H3	10:b:356:G:H1	1.54	0.55
5:4:5:ILE:HG21	5:4:28:ARG:NH2	2.22	0.55
23:p:88:ARG:NH2	23:p:110:ILE:O	2.30	0.55
10:b:1171:G:O2'	10:b:1173:U:OP2	2.25	0.55
10:b:2467:C:H2'	10:b:2468:A:O4'	2.07	0.55
14:f:178:ARG:NH1	14:f:178:ARG:HA	2.22	0.55
20:m:11:LYS:HE2	20:m:87:GLY:O	2.07	0.55
23:p:63:LYS:HD3	23:p:65:SER:HB2	1.88	0.55
4:3:43:ILE:HG22	4:3:44:THR:O	2.07	0.55
12:d:9:VAL:HG11	23:p:4:ILE:HD11	1.88	0.55
10:b:1064:C:O2	10:b:1074:G:N1	2.40	0.55
10:b:1590:A:H2'	10:b:1591:A:C8	2.42	0.54
10:b:1386:C:H2'	10:b:1387:A:C8	2.41	0.54
10:b:1801:A:OP2	11:c:150:LYS:NZ	2.41	0.54
14:f:178:ARG:HA	14:f:178:ARG:CZ	2.37	0.54
31:M:8:U:H5'	31:M:49:G:H5'	1.89	0.54
10:b:1311:G:H21	10:b:1603:A:H62	1.55	0.54
13:e:122:GLU:H	13:e:122:GLU:CD	2.11	0.54
29:w:88:HIS:CE1	29:w:90:ASP:OD1	2.61	0.54
19:l:19:LEU:HD12	19:l:27:LEU:HD13	1.89	0.54
15:g:30:ASN:HB2	15:g:79:VAL:HA	1.89	0.54
16:h:6:LEU:HD11	16:h:37:VAL:HG13	1.88	0.54
10:b:373:U:H2'	10:b:374:A:H8	1.72	0.54
10:b:1054:A:H61	10:b:1055:G:H21	1.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:g:25:THR:HG23	15:g:34:THR:HB	1.89	0.54
17:j:95:ARG:HH21	17:j:96:ARG:HE	1.54	0.54
10:b:1080:A:H61	10:b:1088:A:H61	1.56	0.54
10:b:1149:G:H2'	10:b:1150:C:C6	2.43	0.54
14:f:105:THR:HG22	14:f:106:ILE:HD12	1.90	0.54
23:p:72:ARG:HD2	23:p:74:PHE:CE1	2.43	0.54
10:b:1078:U:H4'	10:b:1079:C:H5	1.73	0.54
10:b:1720:U:H2'	10:b:1721:G:O4'	2.08	0.54
10:b:2698:U:H2'	10:b:2699:C:C6	2.43	0.53
15:g:137:ASP:HB3	15:g:140:VAL:HB	1.90	0.53
17:j:77:HIS:CE1	17:j:83:GLY:HA3	2.42	0.53
10:b:844:A:H2	10:b:845:A:N1	2.01	0.53
10:b:1073:A:H3'	10:b:1074:G:C8	2.44	0.53
15:g:176:LYS:C	15:g:177:LYS:HD2	2.33	0.53
12:d:181:ASP:HB3	12:d:186:LEU:HB2	1.90	0.53
15:g:175:LYS:C	15:g:176:LYS:HD3	2.33	0.53
23:p:33:VAL:HG22	23:p:38:LYS:HG3	1.90	0.53
10:b:1538:G:H2'	10:b:1539:U:H6	1.73	0.53
15:g:98:VAL:HG23	15:g:125:CYS:SG	2.49	0.53
17:j:19:ASP:OD1	17:j:58:ASN:ND2	2.37	0.53
10:b:554:U:H2'	10:b:555:G:O4'	2.09	0.53
17:j:28:LEU:HD12	17:j:142:ILE:HG21	1.91	0.53
23:p:72:ARG:HD2	23:p:74:PHE:CZ	2.43	0.53
27:t:30:ILE:HB	27:t:80:LEU:HD11	1.91	0.53
5:4:37:LYS:HG3	5:4:48:ILE:HD13	1.90	0.53
10:b:2064:C:H2'	10:b:2065:C:C6	2.44	0.53
10:b:2597:G:H5'	11:c:241:GLY:HA3	1.91	0.53
10:b:2100:G:H2'	10:b:2101:A:C8	2.44	0.53
19:l:91:ASP:OD1	19:l:92:LEU:N	2.42	0.53
10:b:1857:G:O2'	10:b:1885:A:N6	2.42	0.53
10:b:2071:A:H2'	10:b:2072:C:C6	2.44	0.53
10:b:2233:U:H2'	10:b:2234:G:C8	2.44	0.53
12:d:179:ARG:HG2	12:d:179:ARG:HH11	1.72	0.53
10:b:955:U:H5''	20:m:86:LYS:HD2	1.90	0.53
10:b:1173:U:C2	10:b:1176:U:H2'	2.44	0.53
10:b:2127:G:O2'	10:b:2160:C:N4	2.42	0.52
28:u:39:ILE:HG13	28:u:40:ASN:H	1.73	0.52
10:b:287:G:H2'	10:b:288:U:C6	2.44	0.52
11:c:199:GLU:CD	11:c:199:GLU:H	2.17	0.52
11:c:259:SER:O	11:c:259:SER:OG	2.26	0.52
14:f:10:ASP:O	14:f:14:LYS:NZ	2.33	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:k:25:LEU:HD11	18:k:38:ILE:HG22	1.90	0.52
19:l:77:ILE:HD11	19:l:108:ALA:HB1	1.92	0.52
10:b:158:U:O2'	10:b:159:G:O5'	2.28	0.52
10:b:300:A:OP2	28:u:86:LYS:HE3	2.10	0.52
14:f:144:ASP:HB2	14:f:145:LYS:HD3	1.91	0.52
10:b:2122:U:O2'	10:b:2123:G:N2	2.42	0.52
10:b:2171:A:H1'	10:b:2172:U:O4'	2.10	0.52
10:b:2543:G:H21	10:b:2646:C:H5''	1.75	0.52
13:e:195:GLN:O	13:e:199:MET:HG3	2.09	0.52
16:h:7:ASP:OD1	16:h:9:VAL:HG22	2.10	0.52
10:b:901:C:C6	10:b:902:C:C5	2.98	0.52
14:f:11:GLU:N	14:f:11:GLU:OE1	2.43	0.52
20:m:66:ARG:NH1	20:m:104:GLU:OE2	2.42	0.52
10:b:1799:G:N7	11:c:178:SER:OG	2.42	0.52
10:b:2659:G:OP2	15:g:158:LYS:NZ	2.43	0.52
12:d:8:LYS:HB2	12:d:201:LEU:HD11	1.92	0.52
20:m:31:PHE:CE1	20:m:110:GLU:HG3	2.45	0.51
10:b:1738:G:O2'	10:b:1739:A:H8	1.93	0.51
10:b:2168:G:N1	10:b:2171:A:O5'	2.44	0.51
27:t:70:ARG:HE	27:t:70:ARG:H	1.59	0.51
10:b:1405:U:H2'	10:b:1406:U:C6	2.46	0.51
10:b:2062:A:H2'	10:b:2062:A:N3	2.25	0.51
10:b:2138:G:N1	10:b:2155:U:C2	2.78	0.51
14:f:141:ILE:HD12	14:f:141:ILE:O	2.10	0.51
10:b:155:A:H2'	10:b:156:A:C8	2.45	0.51
10:b:1570:A:H2'	10:b:1571:A:C8	2.45	0.51
10:b:1746:A:H2'	10:b:1747:U:C6	2.46	0.51
10:b:1076:C:H2'	10:b:1077:A:C8	2.46	0.51
10:b:1106:G:C2	10:b:1107:G:C8	2.99	0.51
10:b:1486:U:H2'	10:b:1487:U:H6	1.75	0.51
10:b:2661:G:H2'	10:b:2662:A:C8	2.46	0.51
15:g:42:GLU:O	15:g:52:PHE:HA	2.11	0.51
18:k:88:ASN:HB3	18:k:91:SER:O	2.11	0.51
25:r:43:ASN:OD1	25:r:43:ASN:N	2.44	0.51
12:d:16:THR:OG1	12:d:18:ASP:OD1	2.24	0.51
26:s:73:LYS:HB2	26:s:106:VAL:HB	1.93	0.51
10:b:287:G:H2'	10:b:288:U:H6	1.76	0.51
2:l:29:ARG:HD2	27:t:12:ARG:HA	1.91	0.50
10:b:1428:C:C5	10:b:1569:A:H5''	2.45	0.50
14:f:50:LEU:HD11	14:f:67:ILE:HD12	1.93	0.50
10:b:1028:A:H2'	10:b:1029:A:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:b:1093:G:N2	10:b:1098:A:H62	2.10	0.50
10:b:1098:A:H5''	10:b:1099:G:C8	2.46	0.50
10:b:1138:G:N2	17:j:108:MET:HE2	2.26	0.50
10:b:2172:U:H5''	10:b:2174:C:H41	1.76	0.50
18:k:64:ARG:HB2	18:k:83:ALA:HB3	1.93	0.50
29:w:88:HIS:HE1	29:w:90:ASP:OD1	1.93	0.50
3:2:41:THR:HG22	3:2:43:ALA:H	1.76	0.50
10:b:155:A:H2'	10:b:156:A:H8	1.76	0.50
15:g:149:ARG:HG2	15:g:149:ARG:HH11	1.76	0.50
20:m:110:GLU:O	20:m:114:ARG:HG3	2.11	0.50
10:b:2117:A:H61	10:b:2167:U:H3	1.59	0.50
28:u:38:GLY:H	28:u:51:GLU:HG2	1.76	0.50
2:1:50:VAL:O	2:1:54:LYS:HG2	2.12	0.50
5:4:10:LYS:HG2	5:4:12:VAL:HG23	1.94	0.50
10:b:5:A:H2'	10:b:6:A:C8	2.46	0.50
10:b:851:C:H2'	10:b:852:U:C6	2.46	0.50
10:b:2064:C:H2'	10:b:2065:C:H6	1.76	0.50
18:k:102:PRO:HD2	23:p:68:GLU:OE1	2.11	0.50
29:w:51:GLN:OE1	29:w:79:ARG:NH2	2.45	0.50
30:y:37:ILE:HG21	30:y:80:ILE:HG21	1.94	0.50
13:e:155:GLU:N	13:e:155:GLU:OE1	2.44	0.50
23:p:100:LEU:HD11	23:p:110:ILE:HD11	1.94	0.50
29:w:35:GLU:N	29:w:35:GLU:OE2	2.45	0.50
10:b:699:A:H2'	10:b:700:G:O4'	2.12	0.50
10:b:1450:G:H21	10:b:1452:G:H1	1.60	0.50
10:b:2181:U:H5''	10:b:2183:A:N1	2.27	0.50
13:e:21:ARG:HB3	13:e:21:ARG:HH21	1.76	0.50
14:f:71:ARG:O	14:f:71:ARG:HG2	2.12	0.50
24:q:88:VAL:HG13	25:r:49:ILE:HG13	1.94	0.50
15:g:42:GLU:OE2	15:g:55:ARG:NE	2.43	0.50
21:n:119:SER:O	21:n:119:SER:OG	2.18	0.50
14:f:37:ASN:OD1	14:f:38:MET:N	2.45	0.50
3:2:12:SER:OG	3:2:14:ILE:HG12	2.12	0.49
10:b:581:C:H2'	10:b:582:A:C8	2.47	0.49
10:b:1104:C:N4	10:b:1106:G:N7	2.58	0.49
10:b:1857:G:N2	10:b:1884:G:H2'	2.27	0.49
16:h:8:LYS:O	16:h:10:ALA:N	2.45	0.49
5:4:28:ARG:HD3	5:4:28:ARG:N	2.26	0.49
10:b:9:G:O2'	10:b:10:A:O5'	2.25	0.49
10:b:871:U:H2'	10:b:872:U:C6	2.48	0.49
10:b:2788:C:H2'	10:b:2789:C:C6	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:n:30:ARG:NH1	21:n:74:GLU:OE1	2.45	0.49
10:b:588:U:H2'	10:b:589:U:C6	2.47	0.49
10:b:1715:G:O2'	10:b:1743:G:O6	2.26	0.49
10:b:2312:U:H2'	14:f:37:ASN:HD21	1.76	0.49
12:d:12:THR:OG1	12:d:13:ARG:N	2.45	0.49
10:b:2636:C:H2'	10:b:2637:U:C6	2.48	0.49
18:k:91:SER:O	18:k:93:GLN:N	2.44	0.49
23:p:37:LYS:HB2	23:p:37:LYS:NZ	2.27	0.49
26:s:55:ILE:HG23	26:s:66:ILE:HD12	1.95	0.49
30:y:50:ASN:HB2	30:y:82:ILE:HB	1.94	0.49
10:b:2331:G:H4'	30:y:43:THR:H	1.78	0.49
13:e:4:VAL:HA	13:e:11:ALA:HA	1.94	0.49
14:f:119:ALA:O	14:f:167:ARG:NH1	2.44	0.49
15:g:67:THR:O	15:g:71:LEU:HG	2.12	0.49
25:r:39:LEU:HB3	25:r:49:ILE:CD1	2.37	0.49
28:u:28:VAL:HG22	28:u:34:VAL:HG12	1.94	0.49
19:l:85:VAL:HG22	19:l:94:THR:HG22	1.94	0.49
10:b:558:U:H2'	10:b:559:G:H8	1.78	0.49
10:b:2115:G:N2	10:b:2119:A:H62	2.10	0.49
12:d:32:ASN:N	12:d:32:ASN:HD22	2.11	0.49
14:f:104:ILE:HD11	14:f:175:PHE:CD1	2.47	0.49
9:a:51:G:OP1	22:o:63:LYS:NZ	2.27	0.49
10:b:2554:U:H2'	10:b:2555:U:C6	2.48	0.49
10:b:2562:U:OP1	18:k:40:LYS:HE3	2.13	0.49
24:q:58:ARG:HA	24:q:61:TRP:CE3	2.48	0.49
10:b:673:C:H4'	13:e:77:ILE:HD12	1.94	0.49
10:b:1093:G:O5'	10:b:1093:G:H8	1.96	0.49
10:b:1883:U:H2'	10:b:1884:G:O4'	2.13	0.49
10:b:2261:C:OP1	30:y:19:LYS:NZ	2.43	0.49
10:b:2660:A:O2'	10:b:2661:G:O4'	2.30	0.49
14:f:3:LYS:HE2	14:f:101:GLU:OE1	2.12	0.49
10:b:608:A:H2'	10:b:609:A:C8	2.48	0.48
10:b:1182:G:H2'	10:b:1183:U:O4'	2.13	0.48
14:f:38:MET:HG3	14:f:57:LEU:HD22	1.94	0.48
14:f:46:ASP:OD1	14:f:48:LYS:N	2.29	0.48
18:k:103:VAL:O	18:k:122:VAL:HB	2.12	0.48
10:b:391:A:H1'	10:b:411:G:O4'	2.13	0.48
10:b:1952:A:C5	18:k:22:ILE:HD12	2.49	0.48
10:b:2304:G:O2'	14:f:153:ASP:OD1	2.20	0.48
12:d:105:LYS:O	12:d:106:LYS:HG2	2.13	0.48
19:l:117:THR:O	19:l:117:THR:OG1	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:y:70:GLU:HG3	30:y:72:LYS:HG3	1.95	0.48
10:b:1083:U:H2'	10:b:1084:A:H2'	1.96	0.48
10:b:1594:U:H2'	10:b:1595:C:C6	2.48	0.48
10:b:2313:C:H2'	10:b:2314:A:C8	2.47	0.48
11:c:252:THR:OG1	11:c:253:LYS:N	2.47	0.48
18:k:105:ARG:NH2	18:k:122:VAL:HG13	2.28	0.48
12:d:99:GLU:CD	12:d:99:GLU:H	2.22	0.48
13:e:144:GLU:OE1	13:e:144:GLU:N	2.47	0.48
24:q:90:ILE:HG12	25:r:49:ILE:HD11	1.95	0.48
14:f:140:GLU:OE1	14:f:140:GLU:N	2.46	0.48
19:l:79:LEU:HB2	19:l:114:GLY:H	1.78	0.48
30:y:59:LEU:HD12	30:y:80:ILE:HD12	1.94	0.48
10:b:1079:C:H2'	10:b:1080:A:C4	2.49	0.48
10:b:1486:U:H2'	10:b:1487:U:C6	2.48	0.48
10:b:811:U:H2'	19:l:21:ARG:HA	1.96	0.48
10:b:1494:A:O2'	10:b:1495:A:O5'	2.30	0.48
10:b:2116:G:H4'	10:b:2146:C:H2'	1.96	0.48
10:b:2469:A:N6	10:b:2481:G:O2'	2.46	0.48
10:b:639:U:H2'	10:b:640:C:H6	1.77	0.48
10:b:2445:G:OP1	13:e:69:ARG:NH2	2.31	0.48
17:j:45:THR:HB	17:j:48:VAL:HG12	1.95	0.48
20:m:105:MET:HE3	20:m:108:VAL:HG21	1.95	0.48
10:b:1494:A:O2'	10:b:1495:A:C8	2.66	0.48
12:d:97:SER:OG	12:d:99:GLU:OE1	2.30	0.48
15:g:149:ARG:HG2	15:g:149:ARG:NH1	2.28	0.48
17:j:45:THR:HB	17:j:48:VAL:CG1	2.44	0.48
10:b:45:G:H5'	10:b:46:G:OP1	2.13	0.48
10:b:558:U:H2'	10:b:559:G:C8	2.49	0.48
10:b:713:G:H21	10:b:718:A:H2	1.60	0.48
10:b:721:A:H2'	10:b:722:A:C8	2.49	0.48
11:c:84:ASP:OD2	11:c:87:ARG:NE	2.42	0.48
15:g:2:SER:OG	15:g:3:ARG:N	2.44	0.48
4:3:25:VAL:O	4:3:26:THR:HG22	2.14	0.47
10:b:1545:A:H2'	10:b:1546:G:O4'	2.14	0.47
10:b:1794:A:H2'	10:b:1795:C:C6	2.49	0.47
10:b:1856:U:H2'	10:b:1857:G:O4'	2.14	0.47
10:b:2070:A:H2'	10:b:2071:A:C8	2.49	0.47
10:b:2138:G:C6	10:b:2155:U:N3	2.82	0.47
10:b:2618:G:H21	12:d:155:VAL:HG21	1.79	0.47
15:g:12:PRO:HD2	15:g:15:VAL:HG11	1.96	0.47
10:b:2329:U:H2'	10:b:2330:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:121:THR:HB	12:d:127:PHE:CD2	2.49	0.47
21:n:41:ALA:C	21:n:43:GLU:H	2.22	0.47
10:b:833:A:H2'	10:b:834:G:C8	2.50	0.47
13:e:188:MET:HE3	13:e:193:VAL:HG22	1.97	0.47
18:k:106:GLU:N	18:k:106:GLU:OE2	2.47	0.47
10:b:632:A:H2'	10:b:633:A:C8	2.49	0.47
10:b:1138:G:H21	17:j:108:MET:HE2	1.79	0.47
10:b:1847:A:H1'	10:b:1848:A:N7	2.29	0.47
10:b:2468:A:HO2'	10:b:2469:A:P	2.37	0.47
10:b:901:C:C2'	10:b:902:C:C6	2.88	0.47
10:b:973:A:H5''	25:r:81:LYS:HD2	1.96	0.47
10:b:1053:C:H41	10:b:1107:G:H21	1.62	0.47
10:b:2455:G:H2'	10:b:2456:C:C6	2.50	0.47
25:r:29:THR:HA	25:r:63:VAL:HG12	1.97	0.47
10:b:2831:G:OP1	10:b:2834:G:H4'	2.14	0.47
21:n:65:LEU:O	21:n:69:ARG:HG2	2.14	0.47
3:2:24:LEU:HD11	3:2:54:MET:CE	2.45	0.47
5:4:13:SER:HB2	5:4:49:TYR:CZ	2.50	0.47
10:b:1026:G:H2'	10:b:1027:A:C8	2.50	0.47
10:b:1073:A:OP2	10:b:1095:A:H2'	2.14	0.47
12:d:25:THR:HG21	12:d:193:VAL:HG22	1.97	0.47
18:k:64:ARG:HG3	18:k:64:ARG:HH11	1.79	0.47
22:o:55:GLU:HG2	22:o:58:ILE:HD12	1.96	0.47
10:b:307:G:N1	10:b:310:A:OP2	2.40	0.47
10:b:1084:A:O2'	10:b:1085:A:O4'	2.32	0.47
10:b:1270:C:H5''	10:b:1271:G:H5'	1.96	0.47
10:b:2120:G:H1	10:b:2179:C:N4	2.12	0.47
10:b:2312:U:H5'	14:f:85:ILE:HD11	1.97	0.47
10:b:2751:G:C6	15:g:3:ARG:NH1	2.83	0.47
24:q:87:SER:HB3	25:r:51:VAL:HA	1.96	0.47
10:b:263:G:H2'	10:b:264:C:O4'	2.15	0.47
10:b:2074:U:H2'	10:b:2075:U:C6	2.50	0.47
10:b:2133:G:C6	10:b:2159:G:H4'	2.50	0.47
20:m:36:VAL:HG13	29:w:82:TYR:CD2	2.50	0.47
10:b:839:U:H2'	10:b:840:C:C6	2.50	0.46
10:b:1548:A:H2'	10:b:1549:A:C8	2.50	0.46
10:b:2138:G:N1	10:b:2155:U:N3	2.62	0.46
21:n:37:THR:OG1	21:n:40:LYS:HG3	2.15	0.46
4:3:52:ARG:CZ	4:3:54:VAL:HG12	2.45	0.46
10:b:158:U:O2'	10:b:159:G:H8	1.99	0.46
10:b:1469:A:H2'	10:b:1470:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:w:68:LYS:HD2	29:w:68:LYS:N	2.29	0.46
10:b:2307:G:H4'	10:b:2308:G:O5'	2.15	0.46
13:e:194:LYS:HD2	13:e:194:LYS:N	2.29	0.46
14:f:78:LYS:HD3	14:f:78:LYS:N	2.29	0.46
14:f:106:ILE:HG21	14:f:139:PRO:HG3	1.97	0.46
27:t:3:ARG:HE	27:t:3:ARG:HB2	1.47	0.46
1:0:56:MET:HB2	1:0:56:MET:HE2	1.70	0.46
10:b:158:U:HO2'	10:b:159:G:H8	1.63	0.46
10:b:1115:G:H2'	10:b:1116:G:H8	1.80	0.46
10:b:1653:G:H3'	21:n:2:ARG:HG2	1.98	0.46
10:b:1980:G:O2'	10:b:1982:U:OP2	2.33	0.46
10:b:2109:U:O4	10:b:2182:U:O2'	2.28	0.46
10:b:2115:G:O6	10:b:2117:A:H2'	2.15	0.46
14:f:8:TYR:HA	14:f:12:VAL:CG2	2.46	0.46
17:j:9:GLU:H	17:j:9:GLU:CD	2.24	0.46
3:2:11:ARG:HG2	3:2:11:ARG:HH21	1.80	0.46
10:b:1590:A:H2'	10:b:1591:A:H8	1.80	0.46
12:d:148:GLN:HB2	12:d:152:PRO:HG2	1.97	0.46
9:a:106:G:H2'	9:a:107:G:O4'	2.16	0.46
10:b:1752:C:H2'	10:b:1753:G:C8	2.51	0.46
13:e:111:GLU:O	13:e:115:GLN:HG3	2.15	0.46
29:w:80:HIS:ND1	29:w:83:LYS:HB2	2.31	0.46
10:b:1000:A:H2'	10:b:1001:A:C8	2.51	0.46
13:e:12:LEU:HD12	13:e:13:THR:N	2.31	0.46
25:r:54:VAL:O	25:r:55:ASP:C	2.59	0.46
10:b:2515:C:H2'	10:b:2516:A:H8	1.81	0.46
14:f:56:ASP:OD2	14:f:150:ARG:NH1	2.42	0.46
21:n:56:LYS:NZ	21:n:94:TYR:OH	2.48	0.46
10:b:1537:G:C5	10:b:1538:G:H1'	2.51	0.46
15:g:32:GLU:O	15:g:33:LEU:HD23	2.16	0.46
17:j:110:PRO:O	17:j:115:GLY:HA3	2.16	0.46
18:k:109:SER:C	18:k:111:LYS:H	2.23	0.46
28:u:49:GLU:H	28:u:49:GLU:HG2	1.40	0.46
10:b:448:U:H1'	13:e:79:ARG:HG3	1.97	0.45
10:b:634:C:H2'	10:b:635:C:C6	2.51	0.45
10:b:657:U:H2'	10:b:658:U:C6	2.51	0.45
10:b:1341:G:H1'	27:t:59:ASN:HB3	1.98	0.45
14:f:144:ASP:HB2	14:f:145:LYS:HZ3	1.82	0.45
18:k:2:ILE:HG23	18:k:6:THR:HG21	1.98	0.45
18:k:19:VAL:HG11	18:k:41:ILE:HD12	1.98	0.45
10:b:2208:C:H2'	10:b:2209:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:b:589:U:H2'	10:b:590:A:C8	2.52	0.45
25:r:37:GLU:OE1	25:r:37:GLU:HA	2.15	0.45
29:w:55:GLU:H	29:w:55:GLU:CD	2.24	0.45
1:0:29:PHE:HB3	10:b:396:G:H1'	1.98	0.45
10:b:640:C:H2'	10:b:641:U:C6	2.51	0.45
10:b:674:G:H1'	13:e:69:ARG:HD3	1.98	0.45
10:b:1013:C:H2'	10:b:1014:A:C8	2.51	0.45
13:e:67:ARG:HE	13:e:67:ARG:HB3	1.56	0.45
28:u:33:LYS:HB3	28:u:53:ALA:HB1	1.98	0.45
29:w:51:GLN:OE1	29:w:57:TYR:OH	2.32	0.45
10:b:753:A:H2'	10:b:754:U:C6	2.51	0.45
10:b:1069:A:H5'	10:b:1096:A:H2	1.81	0.45
10:b:1082:U:H2'	10:b:1083:U:C2	2.51	0.45
10:b:2241:A:H2'	10:b:2242:G:C8	2.52	0.45
10:b:1482:G:C2	10:b:1508:A:H1'	2.52	0.45
10:b:1508:A:H3'	10:b:1509:A:H5'	1.98	0.45
12:d:156:PHE:CZ	17:j:81:ILE:HD13	2.52	0.45
13:e:109:LEU:O	13:e:113:VAL:HG23	2.17	0.45
14:f:36:LEU:HB2	14:f:89:VAL:HG12	1.98	0.45
21:n:32:GLU:HB3	21:n:115:LEU:HD12	1.99	0.45
21:n:106:ASP:OD1	21:n:106:ASP:N	2.46	0.45
27:t:23:ALA:HB1	27:t:29:THR:HB	1.98	0.45
10:b:2125:G:N2	10:b:2127:G:O4'	2.42	0.45
10:b:2138:G:O6	10:b:2155:U:C4	2.70	0.45
12:d:32:ASN:N	12:d:32:ASN:ND2	2.63	0.45
18:k:114:LYS:HE3	18:k:114:LYS:HB3	1.85	0.45
30:y:64:ASP:OD1	30:y:64:ASP:N	2.50	0.45
10:b:577:G:O2'	10:b:1254:A:OP1	2.34	0.45
10:b:1434:A:H62	10:b:1558:C:H42	1.65	0.45
10:b:2291:U:H2'	10:b:2292:U:H6	1.82	0.45
20:m:59:ARG:HB2	20:m:59:ARG:HH21	1.82	0.45
21:n:103:ARG:HD3	21:n:110:MET:SD	2.56	0.45
8:8:16:ILE:HD12	10:b:1032:A:H5''	1.99	0.45
10:b:1509:A:H4'	10:b:1510:G:OP2	2.17	0.45
10:b:2187:U:H2'	10:b:2188:U:C6	2.52	0.45
10:b:2432:A:H2'	10:b:2433:A:C8	2.51	0.45
10:b:78:U:H2'	10:b:79:C:C6	2.52	0.45
10:b:901:C:C4	10:b:902:C:N4	2.85	0.45
10:b:983:A:H3'	10:b:984:A:C8	2.51	0.45
10:b:1061:U:H3	10:b:1097:U:H3	1.65	0.45
10:b:2106:U:C2	10:b:2107:G:C8	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:50:ARG:HD2	10:b:2884:U:C6	2.52	0.44
10:b:1651:G:H4'	21:n:39:PRO:HG2	1.98	0.44
15:g:140:VAL:O	15:g:144:VAL:HG23	2.16	0.44
5:4:25:LYS:HE2	5:4:52:ALA:HB1	1.98	0.44
9:a:14:U:OP2	9:a:70:C:O2'	2.34	0.44
10:b:2116:G:N2	10:b:2148:G:H5'	2.32	0.44
21:n:57:THR:HG23	21:n:62:ASN:ND2	2.32	0.44
10:b:1421:G:H5'	10:b:2211:A:C8	2.52	0.44
10:b:1636:U:H2'	10:b:1637:A:C8	2.52	0.44
10:b:1808:A:H3'	10:b:1809:A:C8	2.53	0.44
12:d:108:ASP:OD1	12:d:173:GLN:HA	2.17	0.44
27:t:9:LYS:HA	27:t:9:LYS:HD3	1.89	0.44
10:b:749:A:H4'	10:b:1271:G:N3	2.32	0.44
10:b:1093:G:H21	10:b:1098:A:H62	1.65	0.44
10:b:1443:U:H2'	10:b:1444:G:H8	1.82	0.44
12:d:179:ARG:HG2	12:d:179:ARG:NH1	2.32	0.44
17:j:7:LYS:O	17:j:11:VAL:HG23	2.17	0.44
26:s:84:ARG:HG3	26:s:98:LYS:HD2	2.00	0.44
2:1:41:HIS:ND1	10:b:95:A:O2'	2.43	0.44
8:8:26:ILE:H	8:8:26:ILE:HG13	1.64	0.44
10:b:310:A:OP1	28:u:19:LYS:HD2	2.17	0.44
19:l:129:LYS:H	19:l:129:LYS:HG2	1.49	0.44
23:p:64:ILE:HD13	23:p:69:GLY:HA2	1.99	0.44
28:u:4:LYS:O	28:u:5:ILE:HG12	2.18	0.44
5:4:29:THR:HG22	5:4:30:LYS:HE3	2.00	0.44
10:b:28:A:N6	10:b:512:G:H1'	2.32	0.44
10:b:181:A:H2'	10:b:182:A:C8	2.53	0.44
10:b:2141:G:H2'	10:b:2142:A:C5	2.53	0.44
10:b:345:A:H1'	10:b:346:A:C2	2.53	0.44
10:b:1800:C:P	11:c:263:THR:HG21	2.58	0.44
10:b:2834:G:H2'	10:b:2879:A:H61	1.83	0.44
12:d:179:ARG:HB3	12:d:188:LEU:HB2	1.99	0.44
19:l:68:SER:O	19:l:69:ARG:HG2	2.18	0.44
5:4:23:THR:OG1	5:4:24:THR:N	2.51	0.44
10:b:2120:G:N1	10:b:2179:C:N3	2.62	0.44
3:2:12:SER:OG	3:2:13:ALA:N	2.49	0.44
10:b:135:U:H2'	10:b:136:G:O4'	2.18	0.44
10:b:228:C:H4'	10:b:229:C:O5'	2.17	0.44
10:b:476:G:H4'	10:b:502:A:N1	2.32	0.44
10:b:2135:A:N6	10:b:2136:G:O6	2.51	0.44
10:b:2306:C:H2'	10:b:2307:G:N2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:b:2502:G:H5''	10:b:2503:A:H5''	1.99	0.44
10:b:2863:C:H2'	10:b:2864:G:C8	2.53	0.44
14:f:15:LYS:NZ	14:f:15:LYS:HB3	2.33	0.44
17:j:3:THR:CG2	24:q:61:TRP:HE1	2.31	0.44
27:t:60:THR:HA	27:t:76:ALA:HA	2.00	0.44
10:b:902:C:H2'	10:b:903:C:C6	2.52	0.43
10:b:1496:A:H2'	10:b:1498:C:C5	2.53	0.43
24:q:117:LEU:HD23	24:q:117:LEU:HA	1.84	0.43
10:b:2061:G:N2	10:b:2062:A:N1	2.63	0.43
10:b:2100:G:C6	10:b:2190:G:C6	3.06	0.43
10:b:2458:G:H8	10:b:2459:A:H62	1.65	0.43
6:6:12:ARG:HH21	6:6:12:ARG:HG3	1.83	0.43
10:b:373:U:H2'	10:b:374:A:C8	2.53	0.43
10:b:1057:A:H62	10:b:1082:U:H5''	1.82	0.43
10:b:1070:A:OP2	10:b:1075:C:N4	2.52	0.43
10:b:1796:U:H2'	10:b:1797:G:C8	2.52	0.43
10:b:2172:U:C5'	10:b:2174:C:H41	2.31	0.43
18:k:7:MET:HE3	18:k:7:MET:HB3	1.80	0.43
25:r:79:ARG:HD2	25:r:80:ARG:NH1	2.34	0.43
10:b:277:G:N2	10:b:279:A:H5'	2.34	0.43
10:b:414:C:H2'	10:b:415:A:C8	2.54	0.43
10:b:191:A:H2'	10:b:192:C:H6	1.82	0.43
10:b:305:C:H2'	10:b:306:U:C6	2.54	0.43
10:b:831:G:O2'	19:l:38:GLN:OE1	2.36	0.43
10:b:602:A:O2'	10:b:604:G:O2'	2.22	0.43
10:b:927:A:H2'	10:b:928:A:C8	2.53	0.43
10:b:1026:G:H2'	10:b:1027:A:H8	1.83	0.43
10:b:2572:A:OP1	12:d:149:ASN:HB3	2.18	0.43
18:k:2:ILE:HD12	18:k:8:LEU:HD21	2.00	0.43
10:b:1073:A:H2'	10:b:1073:A:N3	2.34	0.43
10:b:1432:G:H2'	10:b:1433:A:C8	2.53	0.43
10:b:2193:G:H2'	10:b:2194:U:H6	1.83	0.43
17:j:11:VAL:HG11	17:j:50:THR:HA	2.01	0.43
17:j:109:LEU:O	17:j:111:LYS:NZ	2.48	0.43
20:m:16:ARG:HD3	20:m:16:ARG:HA	1.75	0.43
20:m:36:VAL:CG2	20:m:129:THR:HG23	2.49	0.43
30:y:44:LYS:HB2	30:y:45:PHE:H	1.72	0.43
12:d:14:ILE:HD13	12:d:14:ILE:HA	1.88	0.43
12:d:39:ASP:N	12:d:39:ASP:OD1	2.52	0.43
14:f:70:ALA:C	14:f:72:LYS:H	2.27	0.43
15:g:176:LYS:O	15:g:177:LYS:HD2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:j:42:ALA:O	24:q:64:ARG:HG2	2.18	0.43
20:m:63:ILE:HD13	20:m:63:ILE:HA	1.80	0.43
27:t:69:ARG:HB3	27:t:70:ARG:H	1.59	0.43
30:y:72:LYS:HB3	30:y:72:LYS:HE2	1.69	0.43
2:1:5:GLU:OE1	2:1:5:GLU:N	2.32	0.43
7:7:4:ILE:HG21	7:7:63:PRO:HG3	2.01	0.43
10:b:1537:G:H3'	10:b:1538:G:O4'	2.18	0.43
10:b:2639:A:H2'	10:b:2640:G:O4'	2.18	0.43
11:c:78:VAL:HG12	11:c:112:ALA:HA	2.01	0.43
27:t:14:PRO:HA	27:t:32:LEU:HG	2.01	0.43
9:a:104:A:H2'	9:a:105:G:O4'	2.19	0.43
10:b:2193:G:H2'	10:b:2194:U:C6	2.54	0.43
25:r:4:VAL:HA	25:r:12:HIS:O	2.19	0.43
3:2:27:LEU:HD23	3:2:27:LEU:HA	1.86	0.42
4:3:34:SER:OG	4:3:36:GLU:HG2	2.19	0.42
5:4:7:GLU:OE1	5:4:27:LYS:NZ	2.44	0.42
10:b:580:U:H2'	10:b:581:C:C6	2.54	0.42
10:b:832:U:H2'	10:b:833:A:C8	2.54	0.42
10:b:875:G:N1	10:b:903:C:N3	2.67	0.42
10:b:1952:A:C6	18:k:22:ILE:HD12	2.54	0.42
14:f:164:GLU:OE1	14:f:164:GLU:N	2.33	0.42
17:j:142:ILE:HD13	17:j:142:ILE:HA	1.82	0.42
21:n:36:THR:HG22	21:n:37:THR:H	1.84	0.42
4:3:36:GLU:OE2	4:3:46:ASP:HB2	2.19	0.42
10:b:1495:A:O2'	10:b:1496:A:C8	2.67	0.42
14:f:161:LYS:HB3	14:f:161:LYS:NZ	2.35	0.42
19:l:57:LEU:HD12	19:l:60:ARG:NH2	2.33	0.42
22:o:69:ASP:OD1	22:o:69:ASP:N	2.52	0.42
6:6:12:ARG:HG3	6:6:12:ARG:NH2	2.34	0.42
10:b:917:A:H5''	10:b:2268:A:H61	1.85	0.42
10:b:1064:C:H42	10:b:1095:A:N6	2.17	0.42
10:b:1079:C:H2'	10:b:1080:A:N3	2.35	0.42
10:b:1468:U:H2'	10:b:1522:A:N6	2.34	0.42
13:e:170:ARG:HD3	13:e:170:ARG:HA	1.76	0.42
14:f:46:ASP:OD1	14:f:46:ASP:C	2.61	0.42
19:l:96:LYS:HG3	19:l:101:ILE:HD11	2.01	0.42
24:q:15:LYS:HE2	24:q:15:LYS:HB3	1.75	0.42
25:r:48:LYS:HB3	25:r:49:ILE:H	1.64	0.42
31:M:23:A:H2'	31:M:24:G:C8	2.53	0.42
9:a:29:A:H2'	9:a:30:C:C6	2.55	0.42
10:b:1132:U:H3'	10:b:1133:A:H5''	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:25:THR:OG1	12:d:191:GLY:O	2.34	0.42
15:g:80:THR:C	15:g:81:GLU:OE2	2.61	0.42
16:h:18:GLN:HA	16:h:18:GLN:OE1	2.19	0.42
29:w:2:PHE:CD2	29:w:50:MET:HG2	2.54	0.42
2:1:22:LEU:HB3	27:t:8:LEU:HD13	2.01	0.42
10:b:27:G:H22	10:b:512:G:C2'	2.32	0.42
10:b:207:A:H2'	10:b:208:C:O4'	2.19	0.42
10:b:465:G:H2'	10:b:466:A:C8	2.54	0.42
10:b:1171:G:H4'	10:b:1172:C:C6	2.54	0.42
10:b:1533:C:H2'	10:b:1534:U:O4'	2.20	0.42
10:b:1799:G:C2	11:c:154:LEU:HD23	2.55	0.42
10:b:2377:A:H2'	10:b:2378:A:C8	2.54	0.42
12:d:136:ASN:HB3	12:d:140:HIS:CE1	2.54	0.42
14:f:44:ILE:HD12	14:f:45:ALA:N	2.35	0.42
31:M:70:C:H2'	31:M:71:G:C8	2.54	0.42
8:8:23:ILE:HD12	10:b:1032:A:H1'	2.01	0.42
9:a:42:C:N3	14:f:90:THR:HG22	2.34	0.42
10:b:1682:G:H2'	10:b:1683:U:C6	2.54	0.42
10:b:1838:C:N4	10:b:1898:U:H2'	2.34	0.42
12:d:74:GLU:OE1	12:d:74:GLU:HA	2.18	0.42
12:d:157:LYS:HE2	12:d:157:LYS:HB2	1.60	0.42
14:f:44:ILE:HG21	14:f:79:ILE:HG22	2.00	0.42
7:7:55:LEU:HD23	7:7:55:LEU:HA	1.73	0.42
8:8:16:ILE:HD13	8:8:25:VAL:HG22	2.02	0.42
10:b:645:C:H3'	10:b:646:U:H6	1.84	0.42
10:b:671:C:H2'	10:b:672:C:C6	2.54	0.42
10:b:2480:C:H2'	10:b:2481:G:O4'	2.20	0.42
10:b:2705:A:H2'	10:b:2706:A:O4'	2.19	0.42
10:b:2812:G:H2'	10:b:2813:A:C8	2.54	0.42
20:m:50:ARG:HG3	20:m:65:ILE:HD11	2.02	0.42
20:m:119:LEU:HD23	20:m:119:LEU:HA	1.88	0.42
10:b:27:G:H22	10:b:512:G:H2'	1.84	0.42
10:b:151:C:H2'	10:b:152:A:H8	1.84	0.42
10:b:2101:A:H2'	10:b:2102:G:C8	2.55	0.42
10:b:2183:A:O2'	10:b:2184:A:O4'	2.35	0.42
10:b:2674:G:H2'	10:b:2675:A:C8	2.55	0.42
10:b:2809:A:H2'	10:b:2810:A:C8	2.54	0.42
14:f:38:MET:HB2	14:f:87:CYS:SG	2.59	0.42
23:p:64:ILE:HD13	23:p:64:ILE:HA	1.86	0.42
24:q:106:PHE:O	24:q:110:VAL:HG23	2.20	0.42
5:4:34:LEU:HD12	5:4:35:GLU:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:b:27:G:H1'	10:b:513:A:N6	2.35	0.42
10:b:358:U:H2'	10:b:359:G:C8	2.55	0.42
10:b:1115:G:H2'	10:b:1116:G:C8	2.55	0.42
10:b:2123:G:N1	10:b:2176:A:N3	2.67	0.42
10:b:2312:U:C2'	14:f:37:ASN:HD21	2.32	0.42
25:r:39:LEU:HA	25:r:49:ILE:HG23	2.01	0.42
26:s:108:SER:OG	26:s:109:ASP:N	2.52	0.42
9:a:48:U:H2'	9:a:49:C:C6	2.55	0.42
10:b:1605:C:H2'	10:b:1606:C:O4'	2.20	0.42
10:b:1683:U:H2'	10:b:1684:G:C8	2.55	0.42
13:e:2:GLU:OE2	13:e:2:GLU:HA	2.18	0.42
13:e:132:LYS:HB2	13:e:132:LYS:HE3	1.66	0.42
14:f:104:ILE:HD11	14:f:175:PHE:CE1	2.55	0.42
17:j:60:ASP:HB3	17:j:97:PRO:HB3	2.01	0.42
4:3:43:ILE:CD1	4:3:49:TYR:HB2	2.50	0.41
10:b:796:C:H2'	10:b:797:G:C8	2.55	0.41
10:b:1096:A:H1'	10:b:1097:U:C6	2.55	0.41
11:c:29:PRO:HG2	11:c:34:LEU:HD11	2.01	0.41
14:f:4:LEU:HD23	14:f:4:LEU:HA	1.80	0.41
23:p:60:THR:HG23	23:p:73:VAL:HG22	2.02	0.41
24:q:17:ILE:HD13	24:q:17:ILE:HA	1.89	0.41
5:4:28:ARG:NH1	5:4:28:ARG:HG2	2.35	0.41
10:b:468:G:H5''	13:e:55:SER:HB3	2.01	0.41
10:b:602:A:H2'	10:b:655:A:N1	2.35	0.41
10:b:902:C:H2'	10:b:903:C:O4'	2.19	0.41
10:b:2794:C:H2'	10:b:2795:C:C6	2.55	0.41
12:d:184:ARG:CZ	23:p:7:GLN:NE2	2.80	0.41
15:g:32:GLU:OE1	15:g:32:GLU:HA	2.20	0.41
28:u:6:ARG:NH1	28:u:83:ARG:HD2	2.35	0.41
7:7:14:PHE:O	7:7:15:LYS:HD2	2.19	0.41
10:b:286:U:H2'	10:b:287:G:H8	1.86	0.41
10:b:457:A:N1	10:b:470:A:H5''	2.36	0.41
10:b:740:C:H5'	10:b:1784:A:H3'	2.02	0.41
15:g:17:VAL:HG11	15:g:50:LEU:HD21	2.02	0.41
18:k:91:SER:O	18:k:91:SER:OG	2.36	0.41
10:b:150:U:H2'	10:b:151:C:C6	2.56	0.41
10:b:602:A:H8	10:b:655:A:C2	2.38	0.41
10:b:2116:G:OP1	10:b:2166:U:N3	2.39	0.41
10:b:2186:G:H2'	10:b:2187:U:C6	2.55	0.41
14:f:43:ALA:HB2	14:f:50:LEU:HB2	2.02	0.41
2:1:19:LEU:HD12	2:1:19:LEU:HA	1.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:b:886:A:H2	10:b:889:C:H3'	1.85	0.41
10:b:1028:A:N6	10:b:1125:G:H2'	2.35	0.41
10:b:1083:U:HO2'	10:b:1085:A:N6	2.18	0.41
10:b:2169:A:H2'	10:b:2170:A:N7	2.36	0.41
27:t:5:GLU:HA	27:t:8:LEU:HD12	2.03	0.41
2:l:4:LYS:HD2	2:l:4:LYS:N	2.31	0.41
7:7:54:ASP:HA	7:7:57:LEU:HD12	2.03	0.41
10:b:1442:U:H2'	10:b:1443:U:C6	2.55	0.41
10:b:2271:G:OP1	30:y:18:ALA:HB1	2.20	0.41
14:f:13:VAL:HG13	14:f:28:VAL:HG21	2.03	0.41
16:h:26:ALA:O	16:h:27:ARG:HG2	2.21	0.41
22:o:94:ARG:HD2	22:o:97:PHE:O	2.21	0.41
27:t:20:ALA:HA	27:t:31:VAL:HG21	2.02	0.41
7:7:8:ARG:HD2	7:7:8:ARG:HA	1.75	0.41
10:b:1386:C:H2'	10:b:1387:A:H8	1.83	0.41
10:b:1889:A:H2'	10:b:1890:A:C8	2.56	0.41
10:b:2086:U:H2'	10:b:2087:G:C8	2.56	0.41
10:b:2106:U:N3	10:b:2184:A:C6	2.89	0.41
10:b:2134:A:N7	10:b:2135:A:O2'	2.44	0.41
10:b:2443:C:H2'	10:b:2444:G:C8	2.56	0.41
11:c:57:GLY:HA2	11:c:213:TRP:HA	2.02	0.41
11:c:210:ALA:HA	11:c:213:TRP:CE2	2.55	0.41
18:k:15:GLY:HA2	18:k:47:ILE:HG12	2.03	0.41
20:m:77:PRO:O	20:m:80:VAL:HG22	2.21	0.41
10:b:276:U:O2'	10:b:277:G:H4'	2.20	0.41
10:b:365:U:H2'	10:b:366:C:C6	2.55	0.41
10:b:741:U:H2'	10:b:742:A:C8	2.56	0.41
10:b:1059:G:H3'	10:b:1060:U:H5'	2.03	0.41
10:b:2189:U:H2'	10:b:2190:G:H8	1.86	0.41
10:b:2813:A:H2'	10:b:2814:A:C8	2.56	0.41
16:h:31:VAL:N	16:h:32:PRO:HD2	2.36	0.41
10:b:288:U:H2'	10:b:289:G:H8	1.85	0.41
10:b:499:U:H2'	10:b:500:G:O4'	2.21	0.41
10:b:1054:A:H1'	10:b:1106:G:H22	1.85	0.41
10:b:1183:U:H2'	10:b:1184:U:C6	2.55	0.41
10:b:2468:A:O2'	10:b:2469:A:H8	2.04	0.41
11:c:212:ARG:HD2	11:c:212:ARG:HA	1.79	0.41
12:d:68:PHE:CE1	12:d:79:LEU:HD21	2.56	0.41
14:f:142:ASP:OD2	14:f:145:LYS:NZ	2.48	0.41
20:m:105:MET:HE1	20:m:113:ALA:HA	2.02	0.41
22:o:43:ASN:O	22:o:45:SER:N	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:o:46:GLU:HA	22:o:46:GLU:OE2	2.21	0.41
22:o:88:LYS:NZ	22:o:116:GLN:HG2	2.35	0.41
23:p:43:PHE:CE1	23:p:63:LYS:HD2	2.56	0.41
26:s:85:ILE:HD13	26:s:85:ILE:HA	1.82	0.41
27:t:36:LYS:HE3	27:t:36:LYS:HB3	1.97	0.41
28:u:43:LYS:H	28:u:43:LYS:HG3	1.55	0.41
30:y:55:ARG:CZ	30:y:55:ARG:HB3	2.50	0.41
10:b:289:G:H2'	10:b:290:U:C6	2.56	0.41
10:b:504:A:N3	10:b:504:A:H2'	2.35	0.41
10:b:883:G:N3	10:b:883:G:H2'	2.36	0.41
10:b:1074:G:H2'	10:b:1075:C:C6	2.56	0.41
12:d:125:TRP:CG	12:d:160:LYS:HG2	2.56	0.41
10:b:555:G:O2'	10:b:556:A:H8	2.02	0.40
10:b:598:U:H2'	10:b:599:A:H8	1.85	0.40
10:b:1829:A:C8	10:b:1830:C:C5	3.09	0.40
10:b:2452:C:H2'	10:b:2453:A:C8	2.55	0.40
21:n:29:VAL:HG11	21:n:75:ILE:HG23	2.03	0.40
22:o:90:VAL:O	22:o:117:PHE:HB3	2.21	0.40
4:3:33:THR:HB	4:3:51:GLY:HA2	2.02	0.40
10:b:875:G:N2	10:b:903:C:H1'	2.36	0.40
11:c:13:ARG:HA	11:c:13:ARG:HD2	1.94	0.40
11:c:199:GLU:CD	11:c:199:GLU:N	2.79	0.40
13:e:127:GLU:OE1	13:e:127:GLU:N	2.45	0.40
13:e:166:LYS:HE2	13:e:166:LYS:HB3	1.64	0.40
17:j:114:LEU:HD12	17:j:114:LEU:HA	1.94	0.40
26:s:13:SER:O	26:s:17:VAL:HG23	2.21	0.40
28:u:47:ILE:HB	28:u:48:VAL:H	1.60	0.40
6:6:35:ARG:HG2	6:6:42:LEU:HD11	2.03	0.40
10:b:805:G:H22	10:b:828:U:H5''	1.86	0.40
10:b:2122:U:H2'	10:b:2176:A:C2	2.55	0.40
10:b:2556:C:H2'	10:b:2557:G:O4'	2.22	0.40
29:w:42:LEU:HD13	29:w:47:VAL:HG21	2.03	0.40
1:0:77:LYS:HD3	1:0:77:LYS:HA	1.84	0.40
4:3:36:GLU:HG2	4:3:36:GLU:H	1.62	0.40
5:4:40:ASP:HB3	5:4:43:VAL:HG12	2.04	0.40
10:b:250:G:H2'	10:b:251:A:C8	2.56	0.40
10:b:285:G:H2'	10:b:286:U:C6	2.57	0.40
10:b:892:A:H8	10:b:893:C:C6	2.40	0.40
10:b:1292:G:H2'	10:b:1293:C:C6	2.57	0.40
14:f:25:VAL:O	14:f:28:VAL:HG23	2.21	0.40
15:g:86:LYS:NZ	15:g:86:LYS:HB3	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:h:33:GLN:HE21	16:h:33:GLN:HB3	1.72	0.40
1:0:33:LEU:HD23	1:0:33:LEU:HA	1.90	0.40
2:1:9:LYS:HB3	2:1:9:LYS:HE3	1.95	0.40
7:7:9:GLY:O	7:7:13:ARG:HD2	2.22	0.40
10:b:640:C:H2'	10:b:641:U:H6	1.87	0.40
10:b:1080:A:H61	10:b:1088:A:N6	2.18	0.40
10:b:1301:A:H2	10:b:1626:A:H2	1.68	0.40
10:b:2014:A:H2'	10:b:2015:A:C8	2.56	0.40
10:b:2547:G:H4'	18:k:29:HIS:NE2	2.37	0.40
10:b:2845:U:H2'	10:b:2846:G:C8	2.57	0.40
14:f:8:TYR:HA	14:f:12:VAL:HG23	2.04	0.40
16:h:8:LYS:O	16:h:8:LYS:HD2	2.21	0.40
16:h:25:TYR:HE1	16:h:29:PHE:HD2	1.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	75/78 (96%)	75 (100%)	0	0	100	100
2	1	59/63 (94%)	56 (95%)	3 (5%)	0	100	100
3	2	55/59 (93%)	53 (96%)	2 (4%)	0	100	100
4	3	53/57 (93%)	50 (94%)	3 (6%)	0	100	100
5	4	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
6	6	44/46 (96%)	44 (100%)	0	0	100	100
7	7	62/65 (95%)	56 (90%)	6 (10%)	0	100	100
8	8	36/50 (72%)	34 (94%)	2 (6%)	0	100	100
11	c	269/273 (98%)	259 (96%)	10 (4%)	0	100	100
12	d	207/209 (99%)	200 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	e	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
14	f	175/179 (98%)	158 (90%)	17 (10%)	0	100	100
15	g	174/177 (98%)	160 (92%)	13 (8%)	1 (1%)	21	38
16	h	37/149 (25%)	31 (84%)	6 (16%)	0	100	100
17	j	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
18	k	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
19	l	141/144 (98%)	132 (94%)	9 (6%)	0	100	100
20	m	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
21	n	118/127 (93%)	111 (94%)	7 (6%)	0	100	100
22	o	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
23	p	111/115 (96%)	108 (97%)	3 (3%)	0	100	100
24	q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
25	r	100/103 (97%)	93 (93%)	4 (4%)	3 (3%)	3	6
26	s	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
27	t	84/100 (84%)	69 (82%)	14 (17%)	1 (1%)	10	20
28	u	89/104 (86%)	77 (86%)	11 (12%)	1 (1%)	11	22
29	w	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
30	y	74/85 (87%)	68 (92%)	5 (7%)	1 (1%)	9	17
32	z	1/3 (33%)	1 (100%)	0	0	100	100
All	All	3033/3282 (92%)	2874 (95%)	152 (5%)	7 (0%)	44	64

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	t	69	ARG
25	r	55	ASP
30	y	44	LYS
25	r	51	VAL
28	u	47	ILE
15	g	81	GLU
25	r	52	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	
1	0	67/68 (98%)	66 (98%)	1 (2%)	57	74
2	1	54/55 (98%)	52 (96%)	2 (4%)	30	54
3	2	47/49 (96%)	46 (98%)	1 (2%)	47	67
4	3	46/48 (96%)	45 (98%)	1 (2%)	45	67
5	4	45/49 (92%)	44 (98%)	1 (2%)	45	67
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	49 (96%)	2 (4%)	28	51
8	8	34/44 (77%)	27 (79%)	7 (21%)	1	2
11	c	216/218 (99%)	216 (100%)	0	100	100
12	d	164/164 (100%)	163 (99%)	1 (1%)	78	88
13	e	165/165 (100%)	164 (99%)	1 (1%)	78	88
14	f	148/150 (99%)	147 (99%)	1 (1%)	76	86
15	g	137/138 (99%)	136 (99%)	1 (1%)	76	86
16	h	30/114 (26%)	29 (97%)	1 (3%)	33	57
17	j	116/116 (100%)	113 (97%)	3 (3%)	40	63
18	k	103/104 (99%)	102 (99%)	1 (1%)	68	81
19	l	102/103 (99%)	97 (95%)	5 (5%)	22	43
20	m	109/109 (100%)	107 (98%)	2 (2%)	51	71
21	n	100/103 (97%)	98 (98%)	2 (2%)	48	69
22	o	86/87 (99%)	82 (95%)	4 (5%)	23	45
23	p	98/100 (98%)	97 (99%)	1 (1%)	68	81
24	q	89/90 (99%)	88 (99%)	1 (1%)	65	79
25	r	84/84 (100%)	79 (94%)	5 (6%)	17	32
26	s	92/93 (99%)	92 (100%)	0	100	100
27	t	75/84 (89%)	43 (57%)	32 (43%)	0	0
28	u	74/85 (87%)	65 (88%)	9 (12%)	5	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	w	78/78 (100%)	76 (97%)	2 (3%)	40	63
30	y	58/63 (92%)	55 (95%)	3 (5%)	21	39
32	z	1/1 (100%)	1 (100%)	0	100	100
All	All	2507/2652 (94%)	2417 (96%)	90 (4%)	32	55

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	56	MET
2	1	12	GLU
2	1	13	GLU
3	2	36	VAL
4	3	29	SER
5	4	36	LEU
7	7	30	ARG
7	7	32	ILE
8	8	15	LYS
8	8	16	ILE
8	8	18	LYS
8	8	23	ILE
8	8	24	ARG
8	8	26	ILE
8	8	27	CYS
12	d	84	LEU
13	e	191	ASP
14	f	90	THR
15	g	24	ILE
16	h	15	LEU
17	j	21	THR
17	j	30	THR
17	j	103	ILE
18	k	75	SER
19	l	7	SER
19	l	77	ILE
19	l	85	VAL
19	l	121	THR
19	l	129	LYS
20	m	1	MET
20	m	41	LEU
21	n	57	THR
21	n	65	LEU

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Mol	Chain	Res	Type
22	o	12	THR
22	o	16	ARG
22	o	17	LYS
22	o	24	THR
23	p	6	LYS
24	q	90	ILE
25	r	16	GLU
25	r	47	VAL
25	r	48	LYS
25	r	49	ILE
25	r	55	ASP
27	t	1	MET
27	t	2	ILE
27	t	3	ARG
27	t	5	GLU
27	t	9	LYS
27	t	10	VAL
27	t	12	ARG
27	t	19	LYS
27	t	24	MET
27	t	25	GLU
27	t	26	LYS
27	t	30	ILE
27	t	32	LEU
27	t	36	LYS
27	t	42	GLU
27	t	44	LYS
27	t	49	LYS
27	t	53	VAL
27	t	54	GLU
27	t	56	GLU
27	t	60	THR
27	t	61	LEU
27	t	63	VAL
27	t	64	LYS
27	t	68	LYS
27	t	70	ARG
27	t	72	ASP
27	t	75	LYS
27	t	78	VAL
27	t	80	LEU
27	t	82	GLU

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Mol	Chain	Res	Type
27	t	86	LEU
28	u	7	ARG
28	u	42	VAL
28	u	43	LYS
28	u	44	LYS
28	u	45	HIS
28	u	47	ILE
28	u	48	VAL
28	u	49	GLU
28	u	50	LYS
29	w	12	GLN
29	w	43	ASP
30	y	43	THR
30	y	46	HIS
30	y	70	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	34	HIS
2	1	15	ASN
2	1	45	GLN
4	3	4	GLN
4	3	6	ASN
4	3	19	HIS
5	4	19	HIS
6	6	6	GLN
6	6	26	ASN
6	6	29	GLN
11	c	134	ASN
11	c	153	GLN
11	c	251	GLN
11	c	260	ASN
12	d	150	GLN
12	d	173	GLN
13	e	195	GLN
14	f	5	HIS
14	f	23	ASN
15	g	64	GLN
15	g	104	ASN
16	h	33	GLN
17	j	47	HIS

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Mol	Chain	Res	Type
17	j	77	HIS
18	k	88	ASN
21	n	18	GLN
22	o	61	GLN
22	o	98	GLN
23	p	7	GLN
24	q	20	GLN
24	q	52	GLN
25	r	12	HIS
27	t	59	ASN
29	w	88	HIS
30	y	46	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	b	2900/2904 (99%)	741 (25%)	0
31	M	75/76 (98%)	33 (44%)	2 (2%)
9	a	117/120 (97%)	25 (21%)	0
All	All	3092/3100 (99%)	799 (25%)	2 (0%)

All (799) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	a	13	G
9	a	15	A
9	a	24	G
9	a	25	U
9	a	28	C
9	a	30	C
9	a	32	U
9	a	35	C
9	a	41	G
9	a	42	C
9	a	43	C
9	a	44	G
9	a	50	A
9	a	56	G
9	a	59	A
9	a	67	G
9	a	88	C

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Mol	Chain	Res	Type
9	a	89	U
9	a	90	C
9	a	99	A
9	a	105	G
9	a	108	A
9	a	109	A
9	a	112	G
9	a	116	G
10	b	3	U
10	b	10	A
10	b	23	G
10	b	35	G
10	b	43	G
10	b	46	G
10	b	51	G
10	b	53	A
10	b	60	G
10	b	61	C
10	b	62	U
10	b	63	A
10	b	64	A
10	b	65	U
10	b	71	A
10	b	74	A
10	b	75	G
10	b	83	A
10	b	84	A
10	b	85	G
10	b	100	U
10	b	101	A
10	b	102	U
10	b	110	G
10	b	118	A
10	b	119	A
10	b	120	U
10	b	122	G
10	b	123	G
10	b	125	A
10	b	126	A
10	b	140	C
10	b	142	A
10	b	159	G

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Mol	Chain	Res	Type
10	b	160	A
10	b	163	C
10	b	164	C
10	b	181	A
10	b	182	A
10	b	196	A
10	b	197	A
10	b	198	C
10	b	199	A
10	b	200	U
10	b	215	G
10	b	216	A
10	b	221	A
10	b	222	A
10	b	223	A
10	b	229	C
10	b	233	A
10	b	245	G
10	b	248	G
10	b	252	G
10	b	255	A
10	b	265	A
10	b	266	G
10	b	271	G
10	b	273	G
10	b	277	G
10	b	278	A
10	b	279	A
10	b	280	U
10	b	281	C
10	b	282	A
10	b	286	U
10	b	291	G
10	b	298	G
10	b	300	A
10	b	311	A
10	b	329	G
10	b	330	A
10	b	345	A
10	b	353	C
10	b	359	G
10	b	367	G

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Mol	Chain	Res	Type
10	b	371	A
10	b	372	G
10	b	383	C
10	b	386	G
10	b	387	U
10	b	390	U
10	b	391	A
10	b	396	G
10	b	397	U
10	b	400	G
10	b	401	A
10	b	403	U
10	b	405	U
10	b	406	G
10	b	411	G
10	b	412	A
10	b	416	U
10	b	417	C
10	b	418	C
10	b	445	C
10	b	446	G
10	b	447	A
10	b	449	A
10	b	451	U
10	b	454	A
10	b	455	C
10	b	457	A
10	b	467	G
10	b	471	A
10	b	474	G
10	b	475	C
10	b	479	A
10	b	480	A
10	b	481	G
10	b	491	G
10	b	493	G
10	b	505	A
10	b	508	A
10	b	509	C
10	b	511	U
10	b	513	A
10	b	514	A

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Mol	Chain	Res	Type
10	b	527	C
10	b	528	A
10	b	529	A
10	b	530	G
10	b	532	A
10	b	538	A
10	b	543	G
10	b	544	C
10	b	545	U
10	b	546	U
10	b	547	A
10	b	548	G
10	b	549	G
10	b	562	U
10	b	563	A
10	b	573	U
10	b	575	A
10	b	587	C
10	b	603	A
10	b	604	G
10	b	614	A
10	b	615	U
10	b	622	G
10	b	627	A
10	b	637	A
10	b	646	U
10	b	647	G
10	b	653	U
10	b	654	A
10	b	655	A
10	b	662	G
10	b	663	G
10	b	668	A
10	b	686	U
10	b	695	G
10	b	697	G
10	b	701	G
10	b	718	A
10	b	719	C
10	b	726	G
10	b	730	A
10	b	731	C

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Mol	Chain	Res	Type
10	b	740	C
10	b	746	U
10	b	747	U
10	b	757	G
10	b	764	A
10	b	765	C
10	b	771	G
10	b	775	G
10	b	776	G
10	b	782	A
10	b	783	A
10	b	784	G
10	b	785	G
10	b	789	A
10	b	791	C
10	b	792	A
10	b	805	G
10	b	811	U
10	b	812	C
10	b	819	A
10	b	827	U
10	b	828	U
10	b	830	G
10	b	839	U
10	b	841	G
10	b	842	U
10	b	845	A
10	b	846	U
10	b	847	U
10	b	848	C
10	b	854	C
10	b	855	G
10	b	856	G
10	b	858	G
10	b	859	G
10	b	866	A
10	b	869	G
10	b	872	U
10	b	873	C
10	b	875	G
10	b	876	C
10	b	877	A

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Mol	Chain	Res	Type
10	b	878	A
10	b	879	G
10	b	881	G
10	b	882	G
10	b	883	G
10	b	884	U
10	b	885	C
10	b	886	A
10	b	887	U
10	b	889	C
10	b	890	C
10	b	891	G
10	b	892	A
10	b	895	U
10	b	896	A
10	b	897	C
10	b	898	C
10	b	899	A
10	b	900	A
10	b	902	C
10	b	905	A
10	b	907	G
10	b	910	A
10	b	911	A
10	b	913	U
10	b	914	G
10	b	927	A
10	b	931	U
10	b	932	U
10	b	934	U
10	b	936	A
10	b	937	C
10	b	938	G
10	b	941	A
10	b	946	C
10	b	961	C
10	b	973	A
10	b	974	G
10	b	980	A
10	b	983	A
10	b	985	C
10	b	989	G

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Mol	Chain	Res	Type
10	b	990	A
10	b	996	A
10	b	1005	C
10	b	1009	A
10	b	1012	U
10	b	1013	C
10	b	1017	G
10	b	1020	A
10	b	1021	A
10	b	1022	G
10	b	1024	G
10	b	1026	G
10	b	1033	U
10	b	1034	G
10	b	1037	G
10	b	1038	G
10	b	1040	A
10	b	1044	C
10	b	1047	G
10	b	1048	A
10	b	1054	A
10	b	1055	G
10	b	1056	G
10	b	1058	U
10	b	1059	G
10	b	1060	U
10	b	1061	U
10	b	1062	G
10	b	1063	G
10	b	1064	C
10	b	1065	U
10	b	1066	U
10	b	1067	A
10	b	1068	G
10	b	1069	A
10	b	1070	A
10	b	1071	G
10	b	1072	C
10	b	1073	A
10	b	1074	G
10	b	1078	U
10	b	1079	C

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Mol	Chain	Res	Type
10	b	1080	A
10	b	1081	U
10	b	1082	U
10	b	1084	A
10	b	1086	A
10	b	1087	G
10	b	1088	A
10	b	1089	A
10	b	1095	A
10	b	1098	A
10	b	1099	G
10	b	1101	U
10	b	1102	C
10	b	1103	A
10	b	1104	C
10	b	1105	U
10	b	1106	G
10	b	1109	C
10	b	1110	G
10	b	1111	A
10	b	1112	G
10	b	1128	G
10	b	1130	U
10	b	1131	G
10	b	1132	U
10	b	1133	A
10	b	1134	A
10	b	1135	C
10	b	1142	A
10	b	1144	A
10	b	1156	A
10	b	1157	G
10	b	1172	C
10	b	1175	A
10	b	1176	U
10	b	1178	C
10	b	1185	G
10	b	1186	G
10	b	1195	G
10	b	1204	A
10	b	1206	G
10	b	1210	G

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Mol	Chain	Res	Type
10	b	1211	C
10	b	1212	G
10	b	1225	G
10	b	1227	G
10	b	1232	G
10	b	1238	G
10	b	1241	A
10	b	1250	G
10	b	1252	G
10	b	1253	A
10	b	1256	G
10	b	1262	A
10	b	1265	A
10	b	1266	G
10	b	1271	G
10	b	1272	A
10	b	1276	A
10	b	1300	G
10	b	1301	A
10	b	1312	U
10	b	1313	U
10	b	1318	U
10	b	1321	A
10	b	1324	G
10	b	1325	U
10	b	1329	U
10	b	1338	G
10	b	1352	U
10	b	1355	G
10	b	1359	A
10	b	1365	A
10	b	1368	G
10	b	1374	G
10	b	1378	A
10	b	1379	U
10	b	1383	A
10	b	1384	A
10	b	1388	G
10	b	1392	A
10	b	1395	A
10	b	1396	U
10	b	1416	G

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Mol	Chain	Res	Type
10	b	1419	A
10	b	1420	A
10	b	1421	G
10	b	1428	C
10	b	1429	G
10	b	1437	C
10	b	1452	G
10	b	1453	A
10	b	1459	G
10	b	1460	U
10	b	1461	C
10	b	1467	U
10	b	1469	A
10	b	1470	A
10	b	1476	U
10	b	1477	A
10	b	1482	G
10	b	1490	A
10	b	1491	G
10	b	1493	C
10	b	1494	A
10	b	1495	A
10	b	1496	A
10	b	1509	A
10	b	1512	C
10	b	1515	A
10	b	1523	U
10	b	1524	G
10	b	1529	G
10	b	1536	C
10	b	1537	G
10	b	1538	G
10	b	1539	U
10	b	1552	A
10	b	1554	U
10	b	1563	U
10	b	1566	A
10	b	1568	G
10	b	1569	A
10	b	1578	U
10	b	1583	A
10	b	1584	U

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Mol	Chain	Res	Type
10	b	1596	A
10	b	1608	A
10	b	1610	A
10	b	1613	G
10	b	1616	A
10	b	1618	A
10	b	1622	G
10	b	1627	G
10	b	1634	A
10	b	1642	G
10	b	1643	G
10	b	1647	U
10	b	1648	U
10	b	1649	G
10	b	1651	G
10	b	1664	A
10	b	1666	G
10	b	1667	G
10	b	1672	A
10	b	1674	G
10	b	1675	C
10	b	1694	C
10	b	1699	G
10	b	1700	A
10	b	1705	A
10	b	1715	G
10	b	1722	A
10	b	1725	C
10	b	1726	G
10	b	1729	U
10	b	1730	U
10	b	1731	G
10	b	1732	C
10	b	1733	U
10	b	1735	G
10	b	1737	G
10	b	1754	A
10	b	1755	A
10	b	1756	G
10	b	1757	A
10	b	1759	A
10	b	1763	G

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Mol	Chain	Res	Type
10	b	1764	C
10	b	1773	A
10	b	1776	G
10	b	1779	U
10	b	1782	U
10	b	1784	A
10	b	1786	A
10	b	1787	A
10	b	1797	G
10	b	1800	C
10	b	1801	A
10	b	1808	A
10	b	1809	A
10	b	1811	G
10	b	1816	C
10	b	1821	A
10	b	1829	A
10	b	1833	C
10	b	1840	G
10	b	1846	G
10	b	1857	G
10	b	1867	G
10	b	1869	G
10	b	1870	C
10	b	1871	A
10	b	1872	A
10	b	1873	G
10	b	1900	A
10	b	1906	G
10	b	1913	A
10	b	1914	C
10	b	1915	U
10	b	1917	U
10	b	1929	G
10	b	1930	G
10	b	1931	U
10	b	1937	A
10	b	1938	A
10	b	1944	U
10	b	1955	U
10	b	1958	C
10	b	1961	C

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Mol	Chain	Res	Type
10	b	1967	C
10	b	1970	A
10	b	1971	U
10	b	1972	G
10	b	1975	G
10	b	1991	U
10	b	1992	G
10	b	1993	U
10	b	1997	C
10	b	2002	G
10	b	2020	A
10	b	2021	C
10	b	2023	C
10	b	2031	A
10	b	2032	G
10	b	2033	A
10	b	2035	G
10	b	2036	C
10	b	2043	C
10	b	2055	C
10	b	2056	G
10	b	2057	G
10	b	2060	A
10	b	2061	G
10	b	2062	A
10	b	2065	C
10	b	2069	G
10	b	2076	U
10	b	2077	A
10	b	2078	C
10	b	2080	A
10	b	2093	G
10	b	2102	G
10	b	2105	U
10	b	2106	U
10	b	2107	G
10	b	2109	U
10	b	2110	G
10	b	2111	U
10	b	2112	G
10	b	2113	U
10	b	2115	G

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Mol	Chain	Res	Type
10	b	2116	G
10	b	2117	A
10	b	2118	U
10	b	2119	A
10	b	2120	G
10	b	2121	G
10	b	2124	G
10	b	2126	A
10	b	2127	G
10	b	2128	G
10	b	2129	C
10	b	2130	U
10	b	2131	U
10	b	2132	A
10	b	2133	G
10	b	2134	A
10	b	2135	A
10	b	2136	G
10	b	2138	G
10	b	2140	G
10	b	2143	C
10	b	2144	G
10	b	2145	C
10	b	2147	A
10	b	2148	G
10	b	2149	U
10	b	2150	C
10	b	2151	U
10	b	2152	G
10	b	2154	A
10	b	2156	G
10	b	2157	G
10	b	2158	A
10	b	2159	G
10	b	2160	C
10	b	2161	C
10	b	2162	G
10	b	2163	A
10	b	2164	C
10	b	2165	C
10	b	2169	A
10	b	2170	A

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Mol	Chain	Res	Type
10	b	2171	A
10	b	2172	U
10	b	2174	C
10	b	2175	C
10	b	2177	C
10	b	2178	C
10	b	2183	A
10	b	2185	U
10	b	2198	A
10	b	2204	G
10	b	2211	A
10	b	2212	A
10	b	2213	U
10	b	2214	C
10	b	2224	G
10	b	2225	A
10	b	2238	G
10	b	2239	G
10	b	2243	U
10	b	2258	C
10	b	2268	A
10	b	2278	A
10	b	2282	G
10	b	2283	C
10	b	2287	A
10	b	2288	A
10	b	2297	A
10	b	2305	U
10	b	2307	G
10	b	2308	G
10	b	2314	A
10	b	2322	A
10	b	2324	U
10	b	2325	G
10	b	2331	G
10	b	2333	A
10	b	2334	U
10	b	2335	A
10	b	2336	A
10	b	2337	G
10	b	2345	G
10	b	2347	C

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Mol	Chain	Res	Type
10	b	2350	C
10	b	2361	G
10	b	2372	U
10	b	2374	C
10	b	2375	G
10	b	2376	A
10	b	2379	G
10	b	2383	G
10	b	2385	C
10	b	2391	G
10	b	2396	G
10	b	2399	G
10	b	2402	U
10	b	2403	C
10	b	2406	A
10	b	2413	G
10	b	2419	U
10	b	2420	C
10	b	2422	C
10	b	2425	A
10	b	2426	A
10	b	2427	C
10	b	2429	G
10	b	2430	A
10	b	2432	A
10	b	2434	A
10	b	2441	U
10	b	2448	A
10	b	2458	G
10	b	2459	A
10	b	2474	U
10	b	2476	A
10	b	2484	G
10	b	2500	U
10	b	2502	G
10	b	2505	G
10	b	2517	C
10	b	2518	A
10	b	2520	C
10	b	2525	G
10	b	2529	G
10	b	2535	G

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Mol	Chain	Res	Type
10	b	2547	G
10	b	2554	U
10	b	2559	C
10	b	2560	A
10	b	2562	U
10	b	2564	A
10	b	2566	A
10	b	2567	G
10	b	2573	C
10	b	2574	G
10	b	2582	G
10	b	2601	C
10	b	2602	A
10	b	2609	U
10	b	2613	U
10	b	2615	U
10	b	2629	U
10	b	2630	G
10	b	2636	C
10	b	2639	A
10	b	2641	G
10	b	2646	C
10	b	2655	G
10	b	2656	U
10	b	2661	G
10	b	2662	A
10	b	2663	G
10	b	2673	G
10	b	2688	G
10	b	2689	U
10	b	2691	C
10	b	2714	G
10	b	2716	C
10	b	2718	G
10	b	2720	U
10	b	2726	A
10	b	2733	A
10	b	2739	U
10	b	2744	G
10	b	2748	A
10	b	2753	A
10	b	2762	C

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Mol	Chain	Res	Type
10	b	2765	A
10	b	2778	A
10	b	2779	U
10	b	2790	U
10	b	2791	G
10	b	2797	U
10	b	2798	U
10	b	2799	A
10	b	2801	G
10	b	2802	G
10	b	2803	G
10	b	2804	U
10	b	2818	U
10	b	2820	A
10	b	2821	A
10	b	2823	A
10	b	2832	U
10	b	2833	U
10	b	2835	A
10	b	2837	A
10	b	2848	G
10	b	2849	U
10	b	2859	G
10	b	2861	U
10	b	2864	G
10	b	2865	U
10	b	2867	G
10	b	2872	A
10	b	2873	A
10	b	2877	G
10	b	2883	A
10	b	2884	U
10	b	2886	A
10	b	2898	U
10	b	2900	A
31	M	2	C
31	M	3	G
31	M	4	G
31	M	7	A
31	M	8	U
31	M	9	A
31	M	14	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
31	M	16	U
31	M	17	U
31	M	18	G
31	M	19	G
31	M	20	U
31	M	21	A
31	M	22	G
31	M	23	A
31	M	28	G
31	M	30	C
31	M	31	C
31	M	46	G
31	M	47	U
31	M	48	C
31	M	49	G
31	M	51	G
31	M	52	A
31	M	53	G
31	M	55	U
31	M	56	C
31	M	57	G
31	M	64	G
31	M	73	U
31	M	74	C
31	M	75	C
31	M	76	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	M	16	U
31	M	74	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

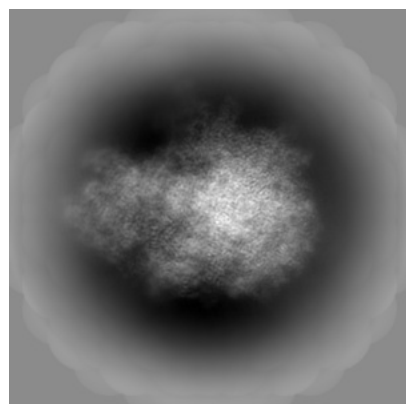
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14865. These allow visual inspection of the internal detail of the map and identification of artifacts.

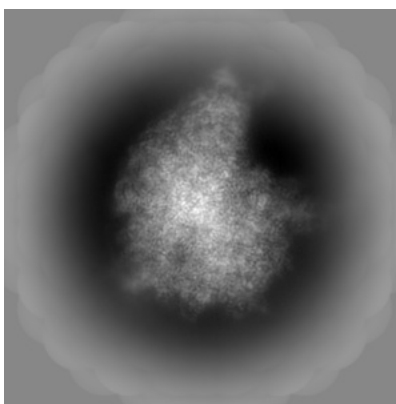
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

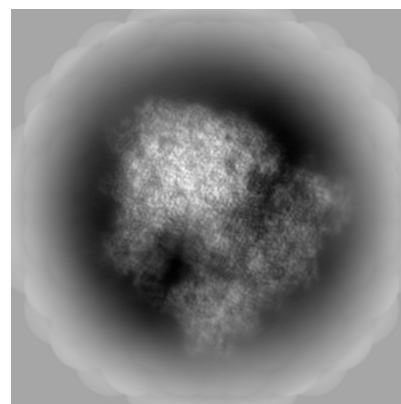
6.1.1 Primary map



X

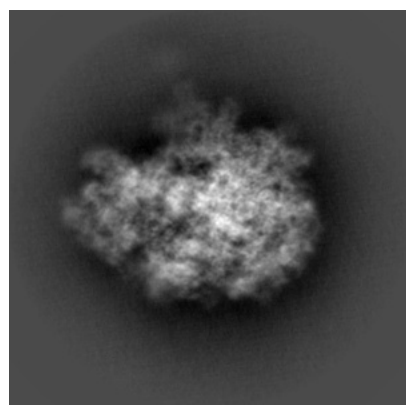


Y

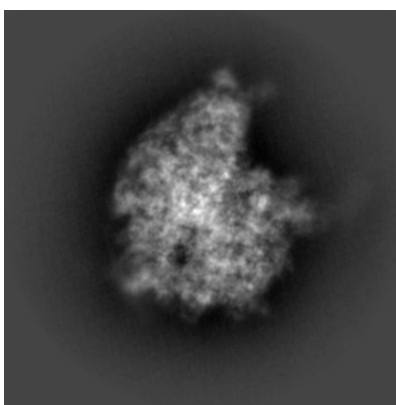


Z

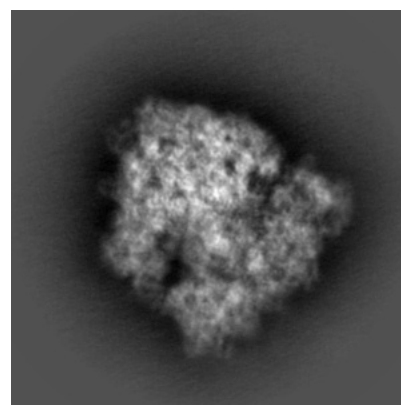
6.1.2 Raw map



X



Y

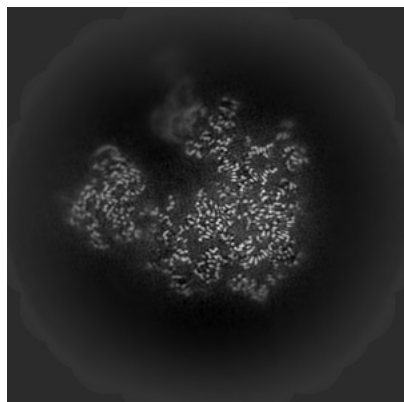


Z

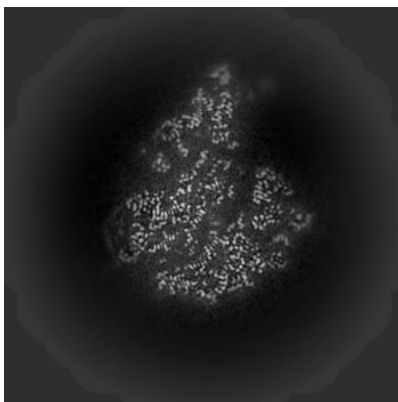
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

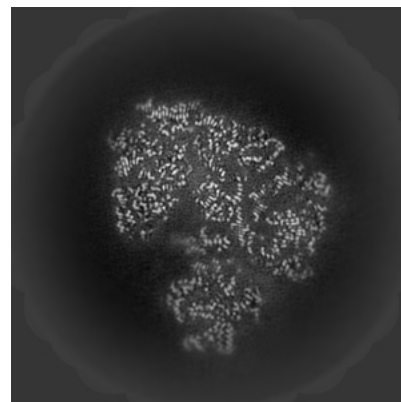
6.2.1 Primary map



X Index: 184

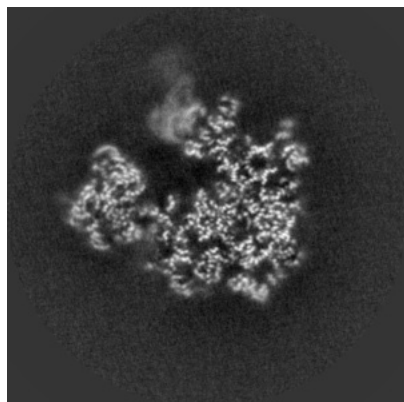


Y Index: 184

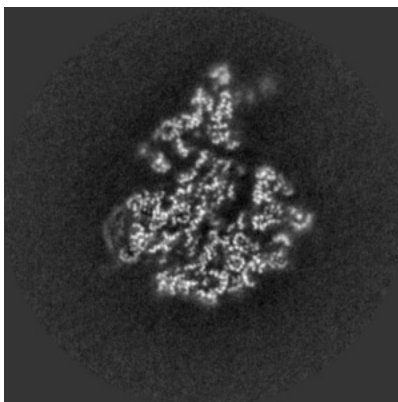


Z Index: 184

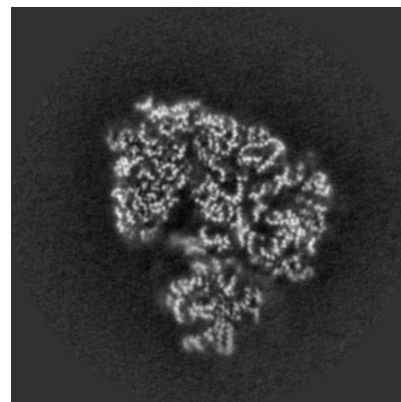
6.2.2 Raw map



X Index: 184



Y Index: 184

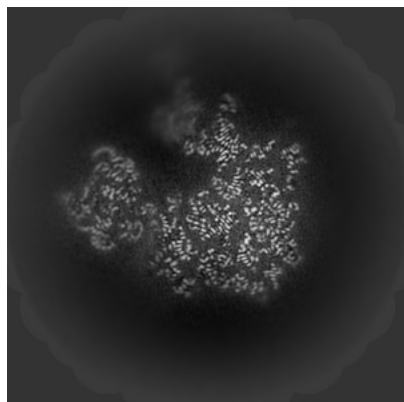


Z Index: 184

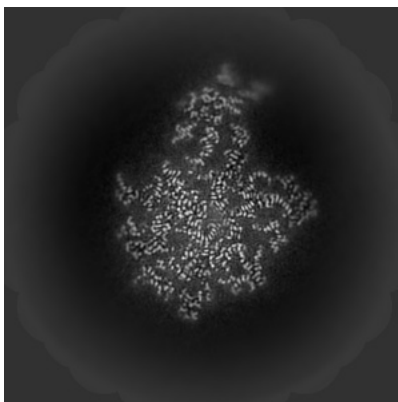
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

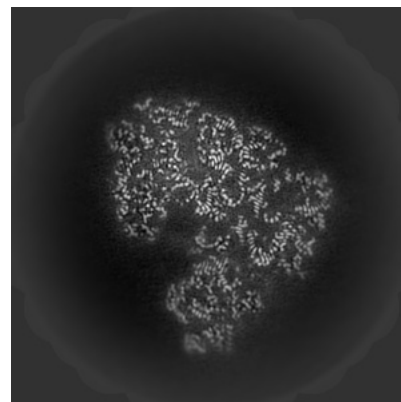
6.3.1 Primary map



X Index: 188

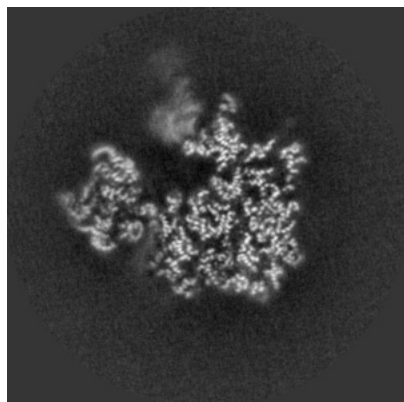


Y Index: 202

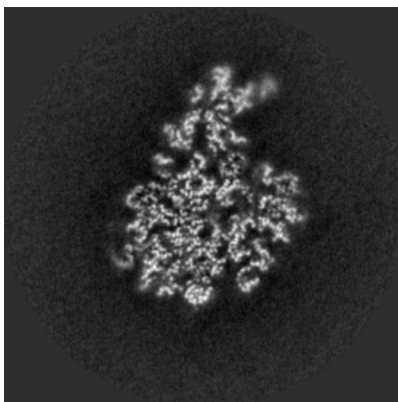


Z Index: 181

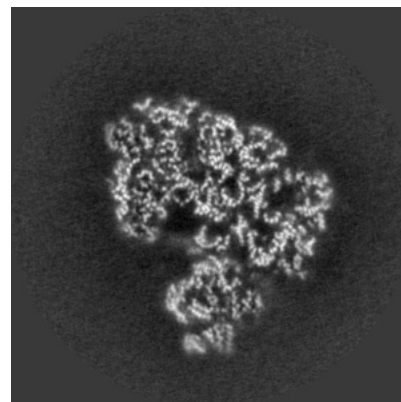
6.3.2 Raw map



X Index: 188



Y Index: 192

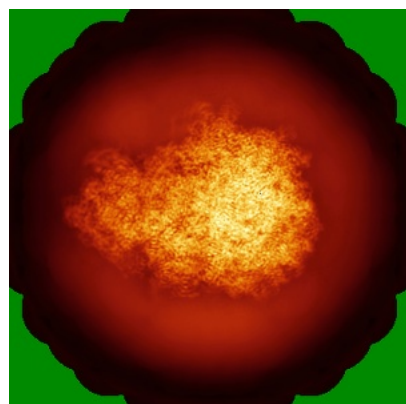


Z Index: 181

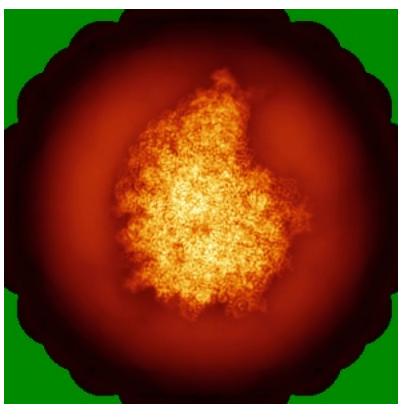
The images above show the largest variance slices of the map in three orthogonal directions.

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

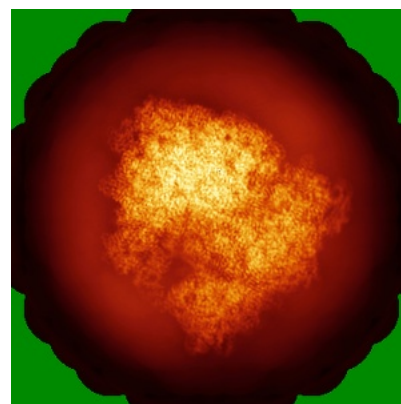
6.4.1 Primary map



X



Y

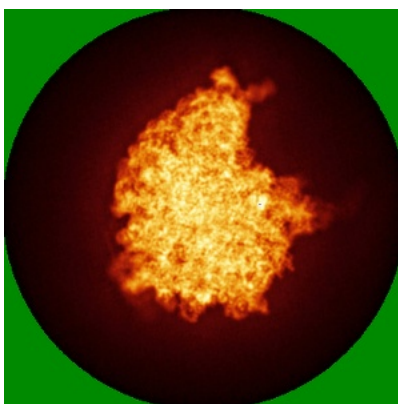


Z

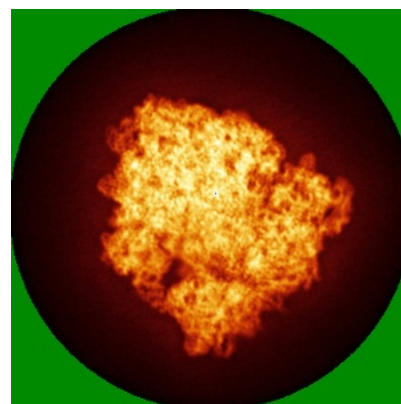
6.4.2 Raw map



X



Y

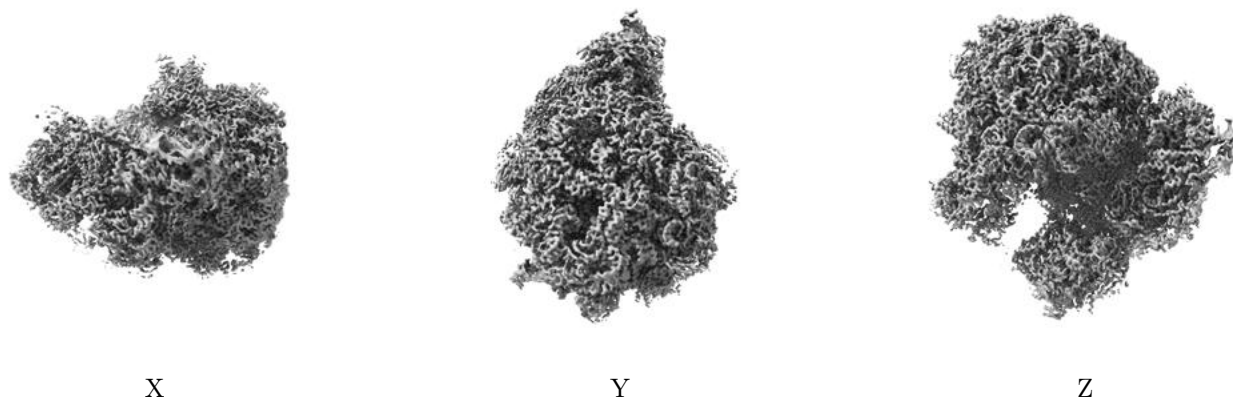


Z

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 0.0806. 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.

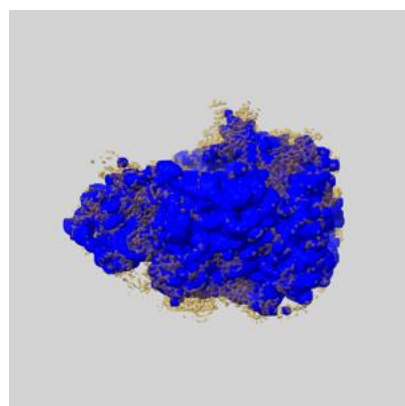
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

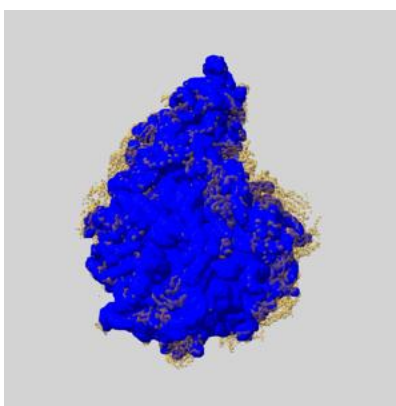
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

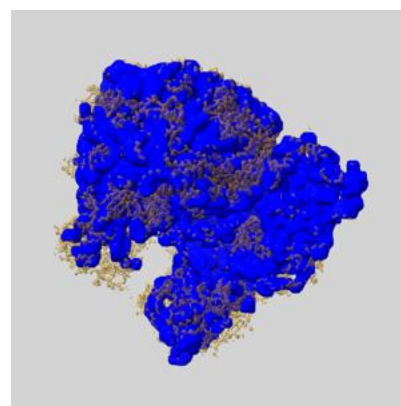
6.6.1 emd_14865_msk_1.map [i](#)



X



Y

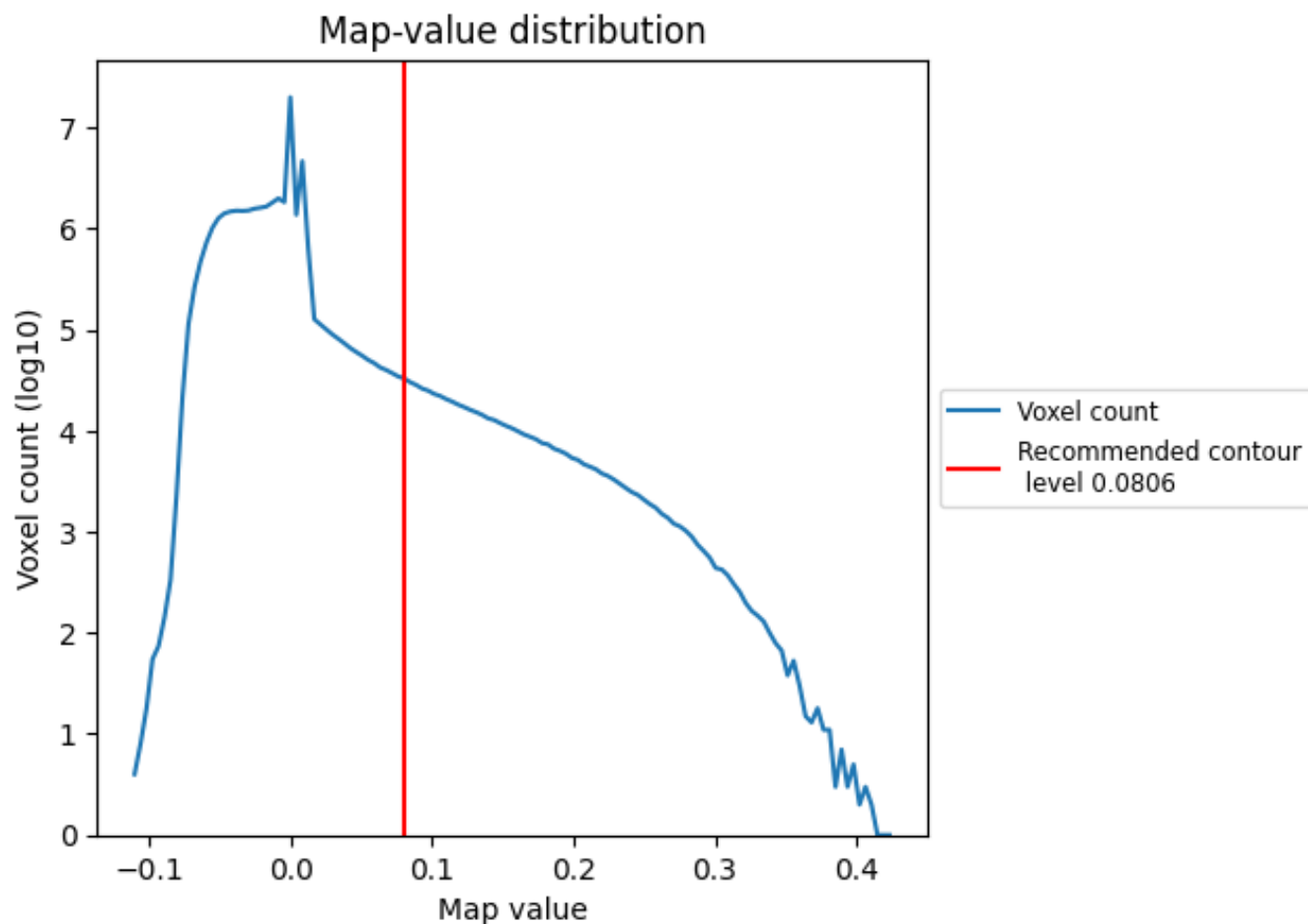


Z

7 Map analysis [i](#)

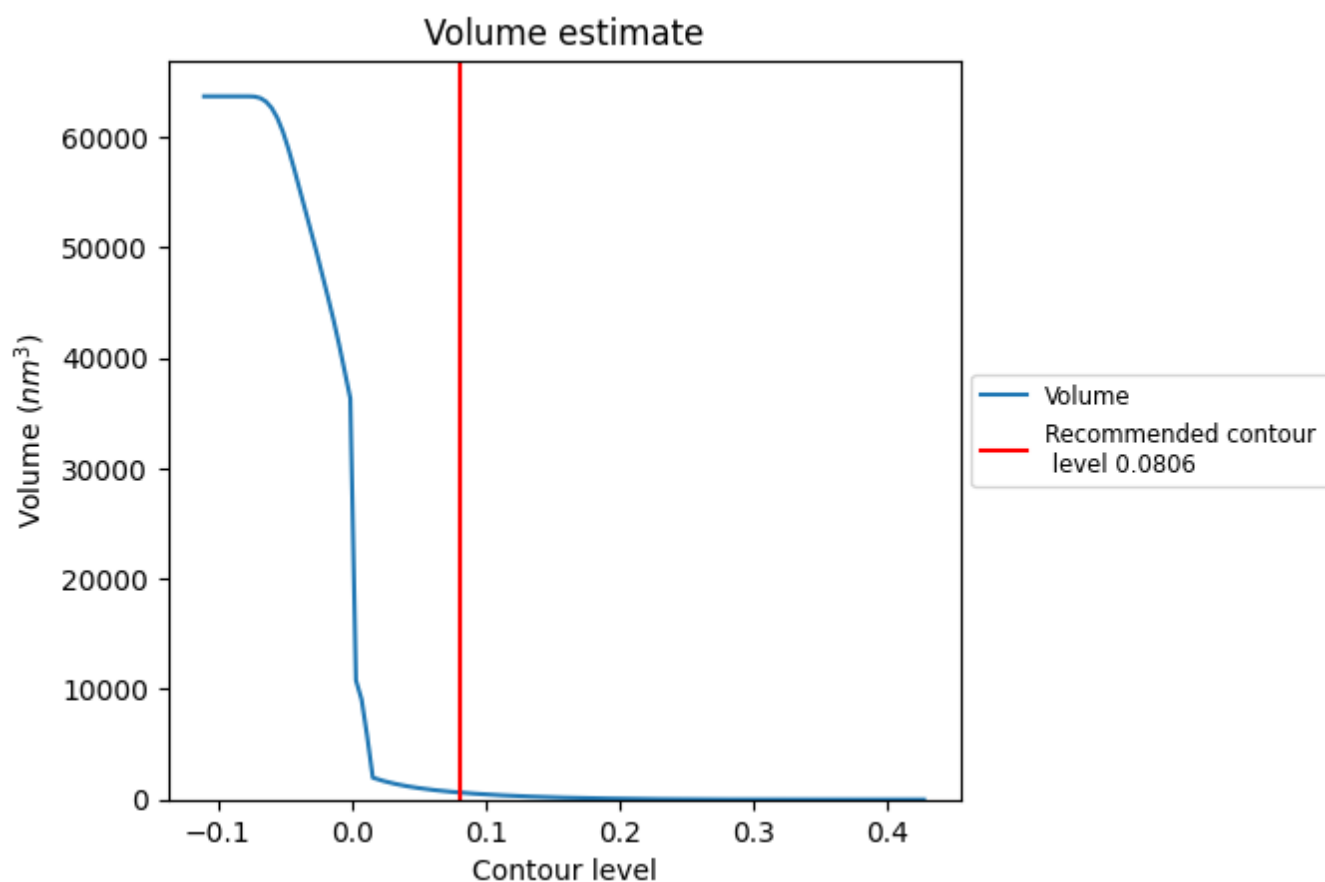
This section contains the results of statistical analysis of the map.

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.

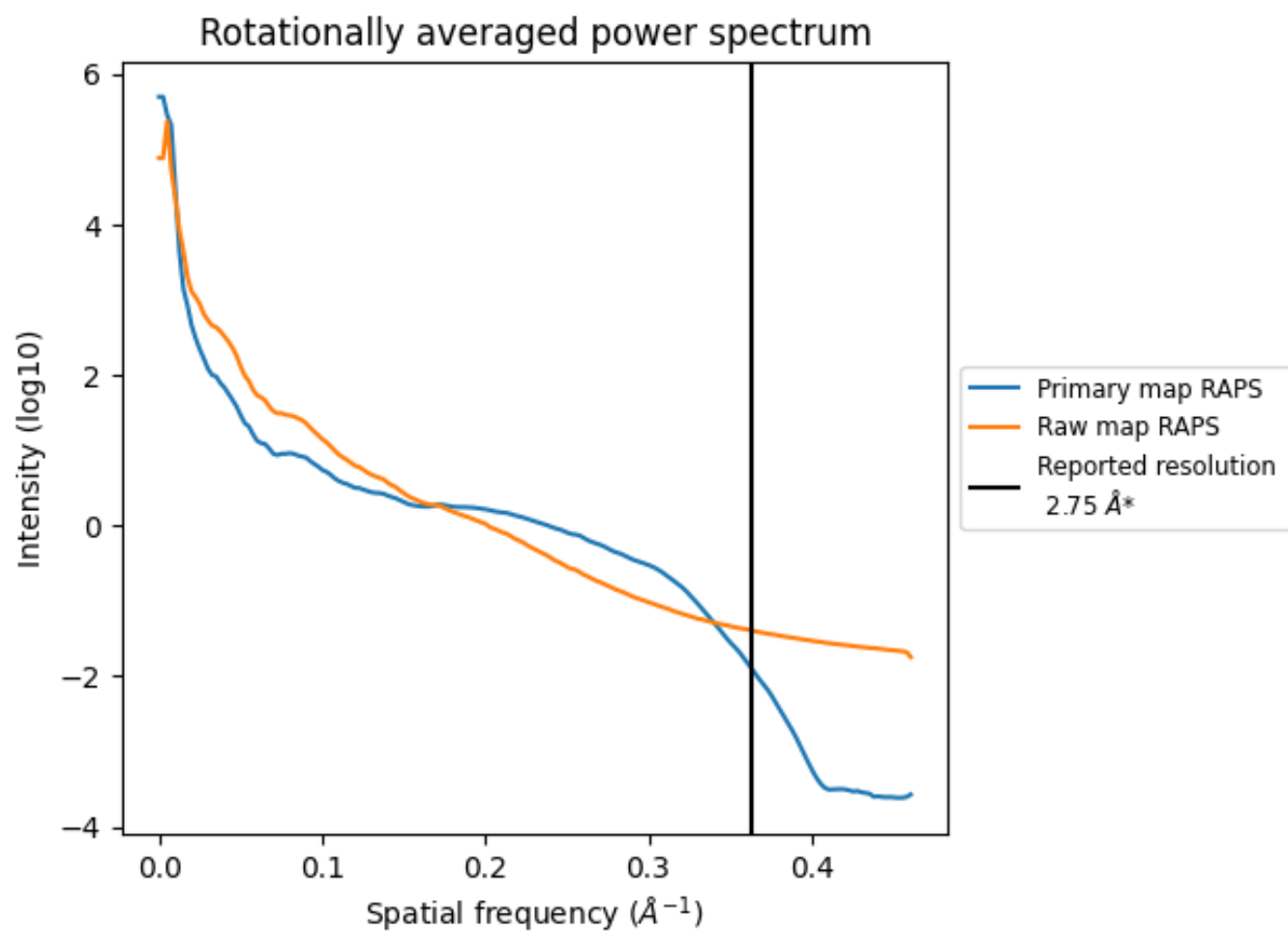
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 637 nm³; this corresponds to an approximate mass of 576 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 ⓘ

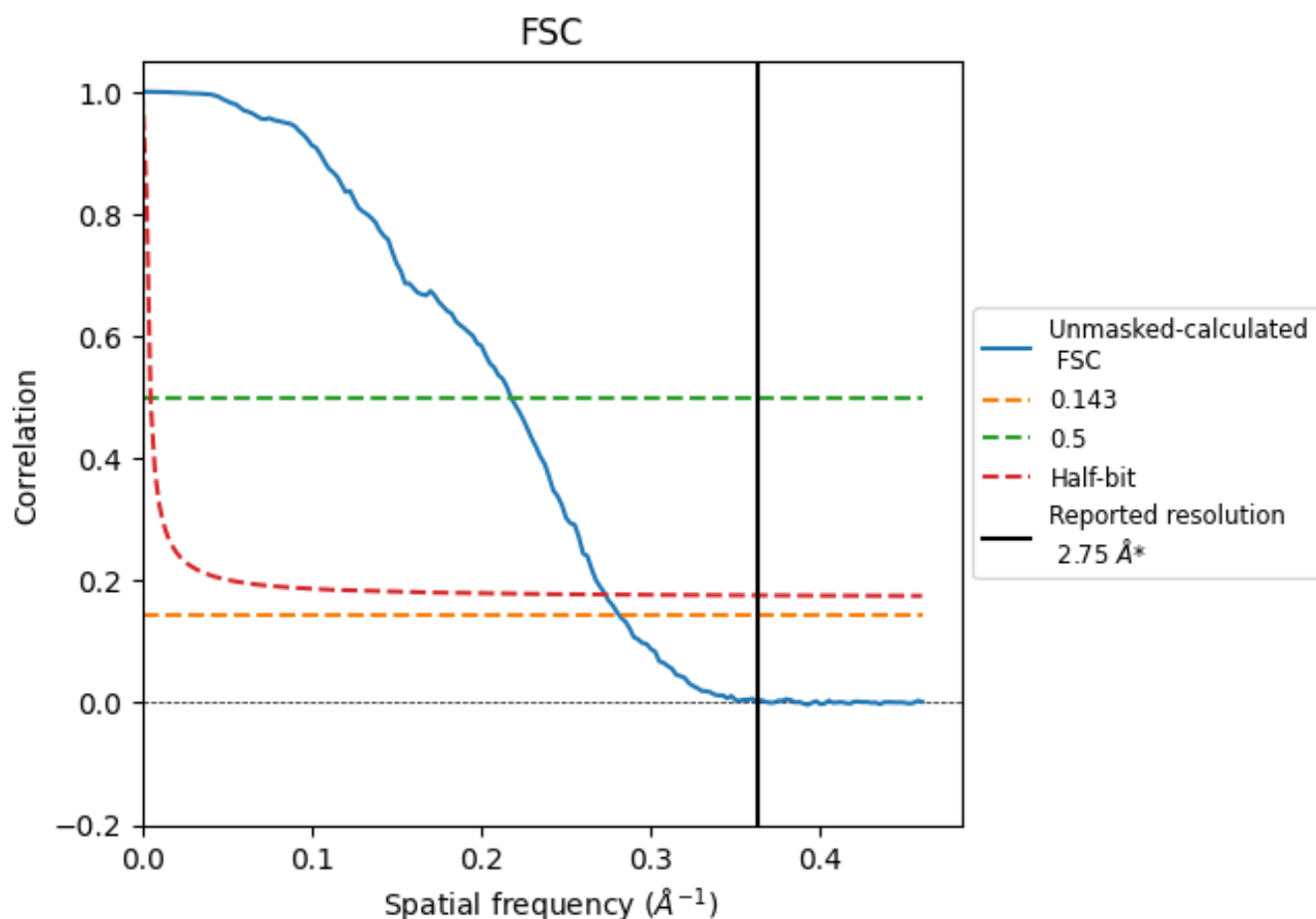


*Reported resolution corresponds to spatial frequency of 0.364 Å⁻¹

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 0.364 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

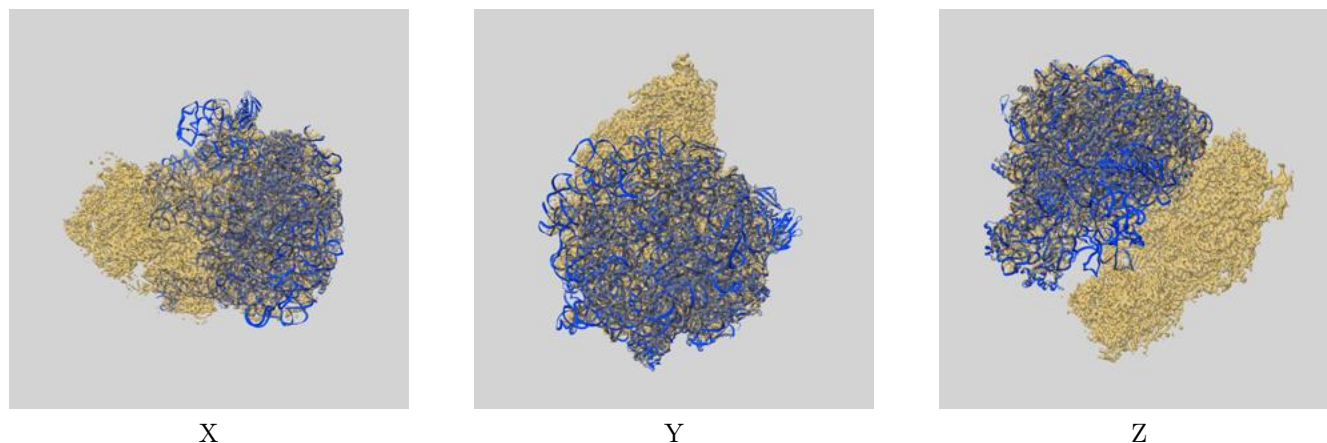
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.75	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.55	4.59	3.65

*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 3.55 differs from the reported value 2.75 by more than 10 %

9 Map-model fit [i](#)

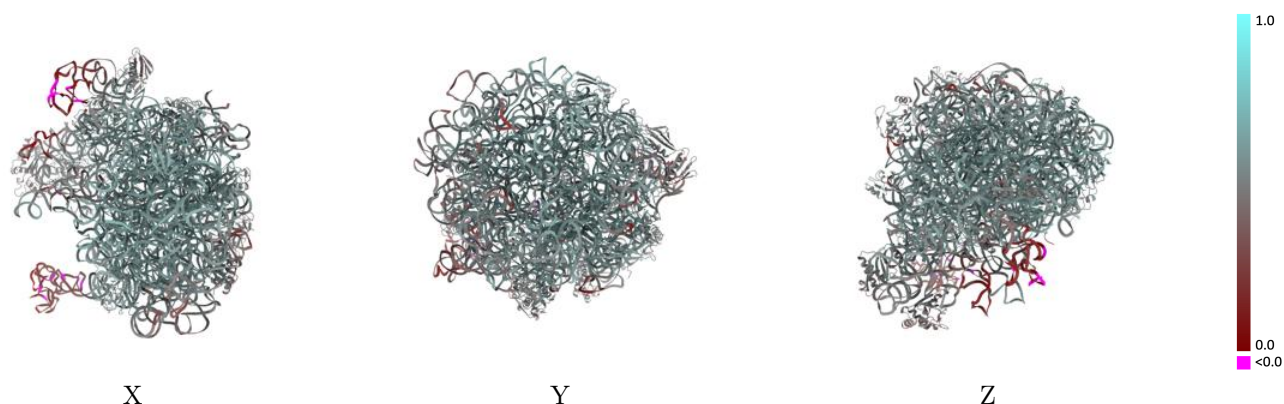
This section contains information regarding the fit between EMDB map EMD-14865 and PDB model 7ZQ6. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0806 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

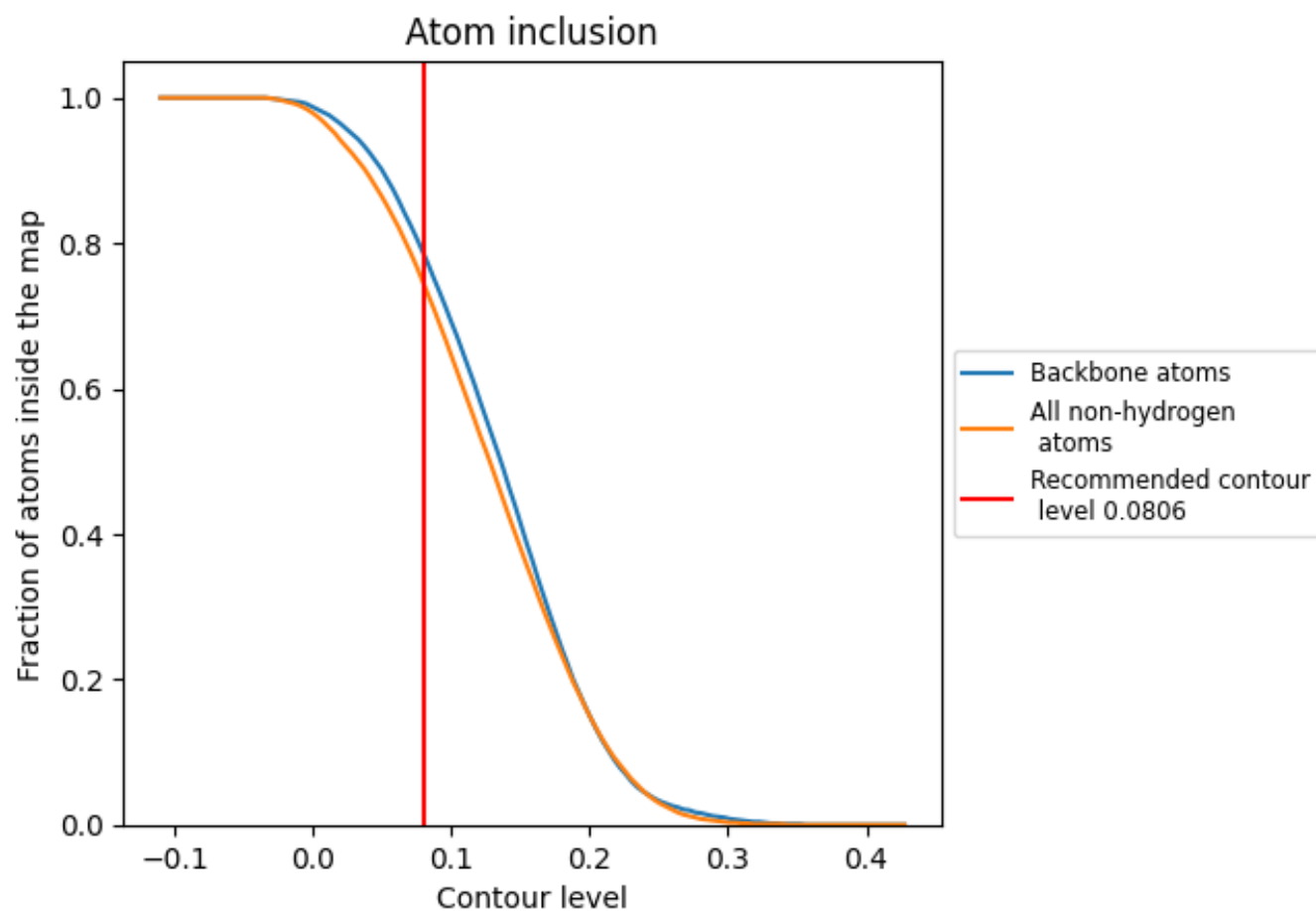


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 78% of all backbone atoms, 74% 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 (0.0806) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7410	 0.5370
0	 0.7240	 0.5710
1	 0.4470	 0.4620
2	 0.6600	 0.5650
3	 0.7420	 0.5680
4	 0.3440	 0.5160
6	 0.9630	 0.6090
7	 0.8700	 0.6050
8	 0.5600	 0.5470
M	 0.4460	 0.4200
a	 0.6500	 0.5140
b	 0.8100	 0.5400
c	 0.7660	 0.5890
d	 0.6670	 0.5770
e	 0.5880	 0.5230
f	 0.1830	 0.4500
g	 0.1730	 0.4690
h	 0.2010	 0.4600
j	 0.7010	 0.5630
k	 0.6630	 0.5750
l	 0.6750	 0.5660
m	 0.6080	 0.5670
n	 0.7650	 0.5750
o	 0.3650	 0.4820
p	 0.6380	 0.5670
q	 0.7600	 0.5720
r	 0.5730	 0.5440
s	 0.7610	 0.5650
t	 0.5520	 0.4370
u	 0.4540	 0.4550
w	 0.3930	 0.5160
y	 0.7100	 0.5690
z	 0.5000	 0.2990

