



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 06:26 AM UTC

PDB ID : 7OHY / pdb_00007ohy
EMDB ID : EMD-12913
Title : Nog1-TAP associated immature ribosomal particles from *S. cerevisiae* after rpL34 expression shut down, population B
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-11
Resolution : 3.90 Å(reported)
Based on initial model : 6EM1

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

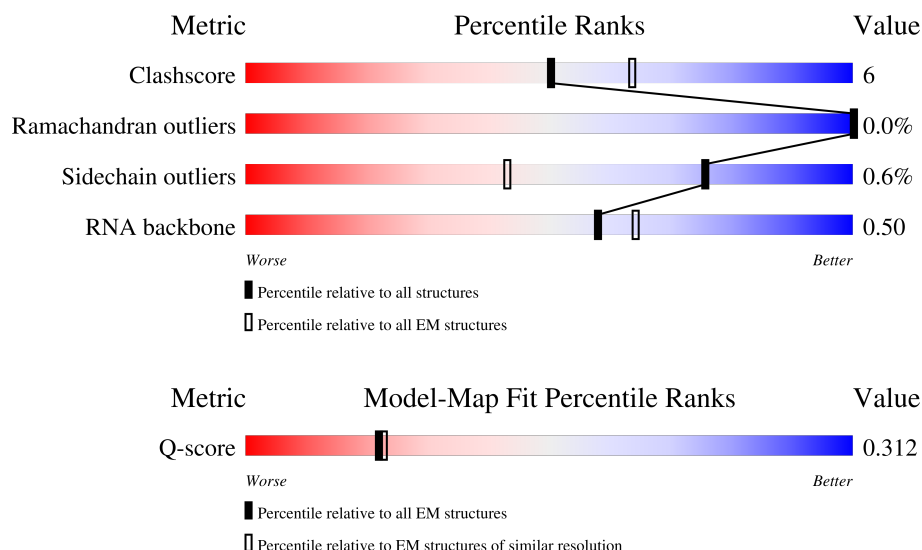
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.



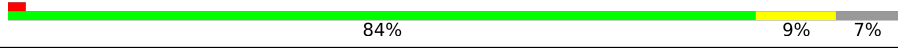
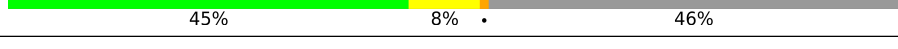
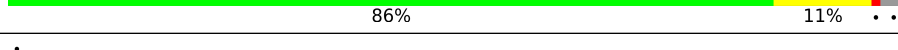
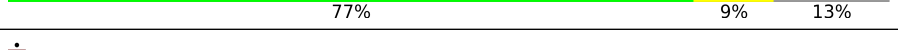
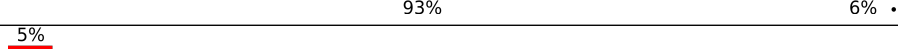
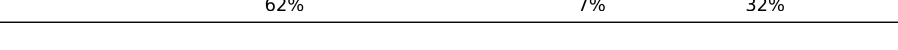
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	1	3396	
2	2	158	
3	B	387	

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Mol	Chain	Length	Quality of chain
4	C	362	
5	E	176	
6	F	244	
7	G	256	
8	H	191	
9	L	199	
10	M	138	
11	N	204	
12	O	199	
13	P	184	
14	Q	186	
15	S	172	
16	V	137	
17	W	236	
18	Y	127	
19	b	647	
20	e	130	
21	f	107	
22	h	120	
23	j	88	
24	r	261	
25	u	199	
26	y	245	

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 125318 atoms, of which 53608 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 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	1689	Total	C	H	N	O	P	0	0
			54311	16140	18161	6526	11795	1689		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	148	Total	C	H	N	O	P	0	0
			4733	1406	1590	554	1035	148		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	B	333	Total	C	H	N	O	S	0	0
			5374	1680	2728	490	470	6		

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	C	343	Total	C	H	N	O	S	0	0
			5336	1643	2725	499	466	3		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	151	Total	C	H	N	O	S	0	0
			2497	780	1292	215	209	1		

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	228	Total	C	H	N	O	S	0	0
			3749	1180	1917	334	317	1		

- Molecule 7 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	108	Total	C	H	N	O	S	0	0
			1751	544	911	147	147	2		

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	190	Total	C	H	N	O	S	0	0
			3086	957	1576	273	276	4		

- Molecule 9 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	L	108	Total	C	H	N	O	S	0	0
			1782	541	918	180	143			

- Molecule 10 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	M	134	Total	C	H	N	O	S	0	0
			2179	668	1138	197	174	2		

- Molecule 11 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	N	177	Total	C	H	N	O	S	0	0
			3079	948	1566	320	244	1		

- Molecule 12 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	O	197	Total	C	H	N	O	S	0	0
			3215	1003	1660	289	262	1		

- Molecule 13 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	P	126	Total	C	H	N	O	S	0	0
			1998	624	1005	186	183			

- Molecule 14 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	131	Total	C	H	N	O	S	
			2101	645	1092	190	173	1	0 0

- Molecule 15 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	170	Total	C	H	N	O	S	
			2904	922	1472	265	242	3	0 0

- Molecule 16 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	V	111	Total	C	H	N	O	S	
			1693	522	867	151	146	7	0 0

- Molecule 17 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	W	227	Total	C	H	N	O	S	
			3683	1157	1852	315	354	5	0 0

- Molecule 18 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Y	125	Total	C	H	N	O		
			2060	620	1076	191	173		0 0

- Molecule 19 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	b	375	Total	C	H	N	O	S	
			6144	1950	3104	515	557	18	0 0

- Molecule 20 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	e	125	Total	C	H	N	O	S	
			2090	641	1081	203	164	1	0 0

- Molecule 21 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	f	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 22 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	h	119	Total	C	H	N	O	S	0	0
			2048	615	1079	186	167	1		

- Molecule 23 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	j	71	Total	C	H	N	O	S	0	0
			1137	344	571	123	94	5		

- Molecule 24 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	r	71	Total	C	H	N	O	S	0	0
			1250	377	638	130	104	1		

- Molecule 25 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	u	116	Total	C	H	N	O	S	0	0
			1987	612	1011	200	155	9		

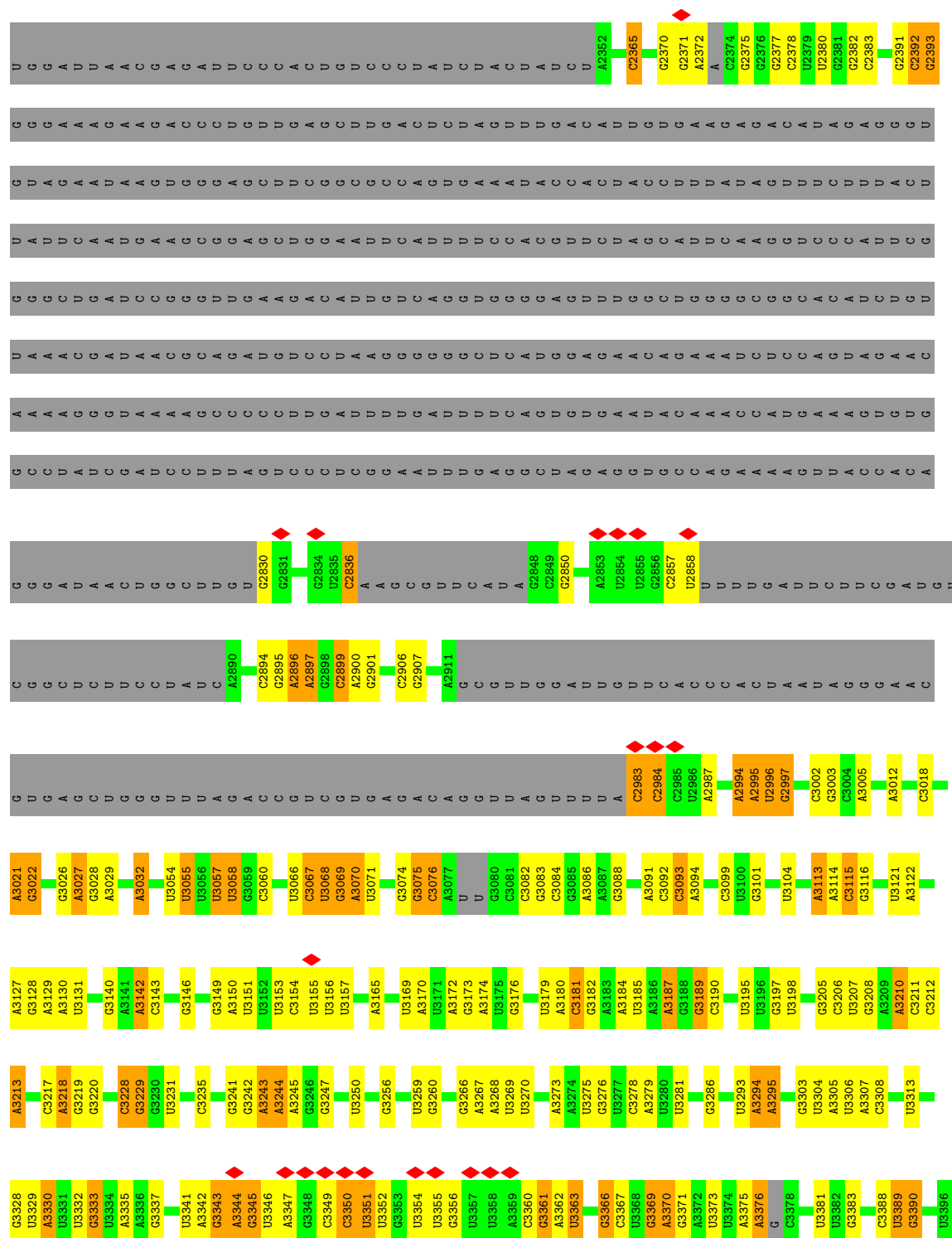
- Molecule 26 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	y	225	Total	C	H	N	O	S	0	0
			3398	1056	1697	295	343	7		

- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

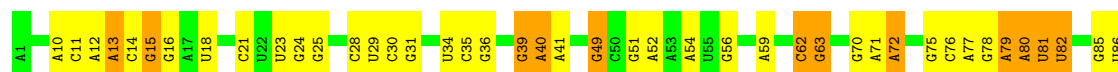
Mol	Chain	Residues	Atoms		AltConf
27	j	1	Total	Zn	0
			1	1	
27	u	1	Total	Zn	0
			1	1	

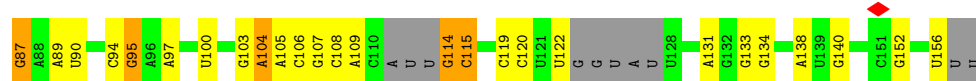




• Molecule 2: 5.8S rRNA

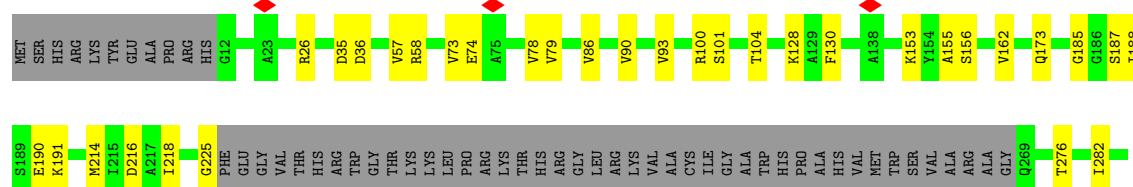
Chain 2: 50% 33% 11% 6%





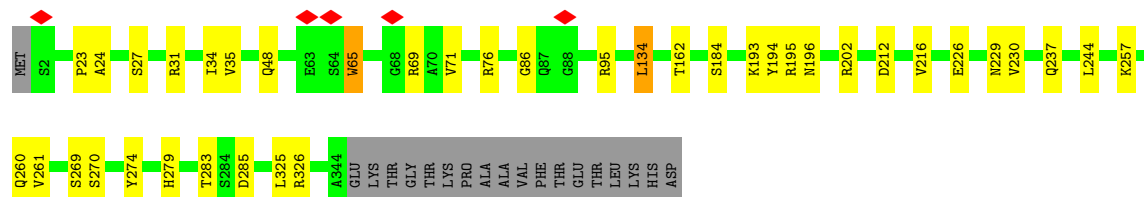
• Molecule 3: 60S ribosomal protein L3

Chain B: 73% 13% 14%



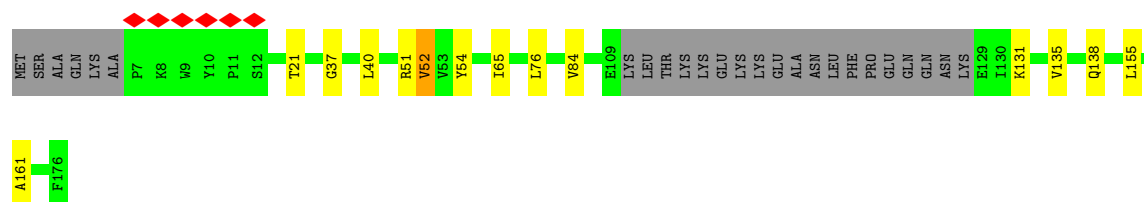
• Molecule 4: 60S ribosomal protein L4-A

Chain C: 84% 10% 5%



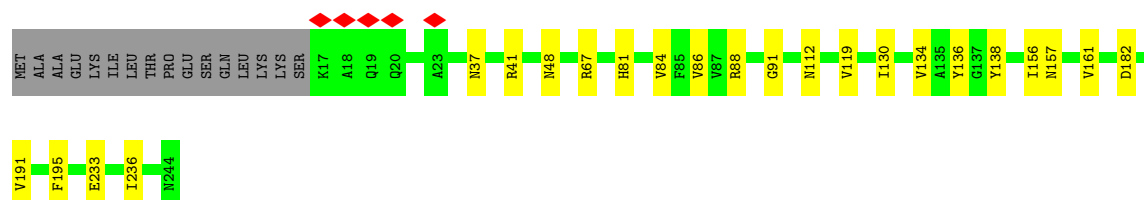
• Molecule 5: 60S ribosomal protein L6-A

Chain E: 78% 7% 14%

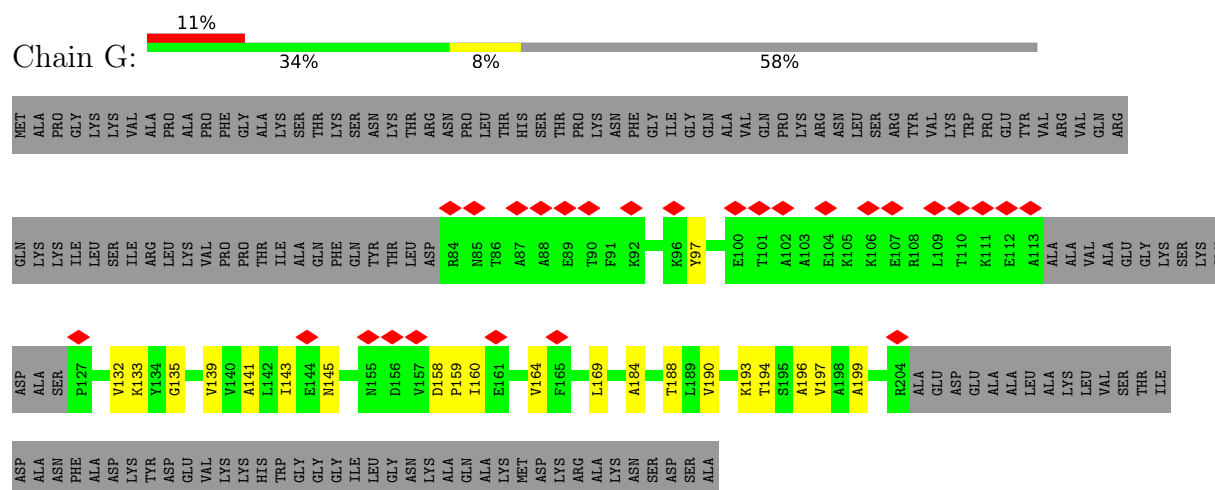


• Molecule 6: 60S ribosomal protein L7-A

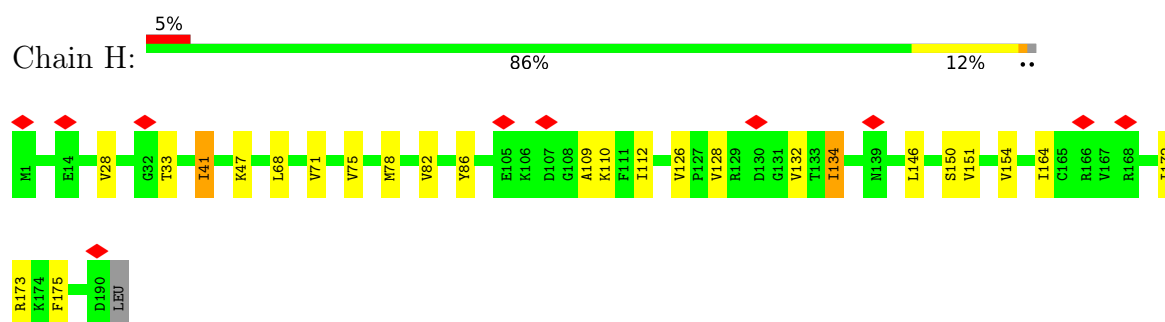
Chain F: 84% 9% 7%



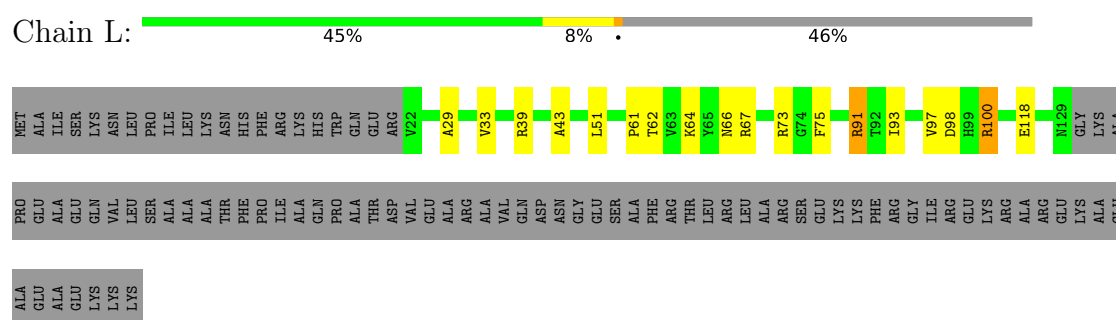
- Molecule 7: 60S ribosomal protein L8-A



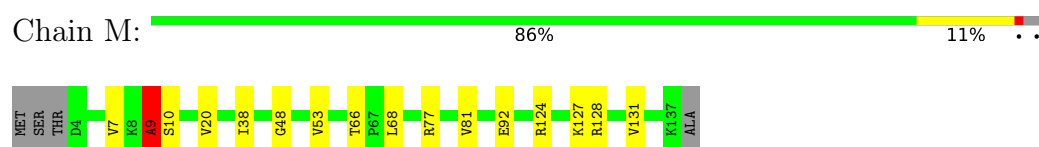
- Molecule 8: 60S ribosomal protein L9-A



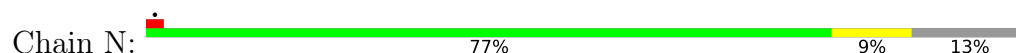
- Molecule 9: 60S ribosomal protein L13-A

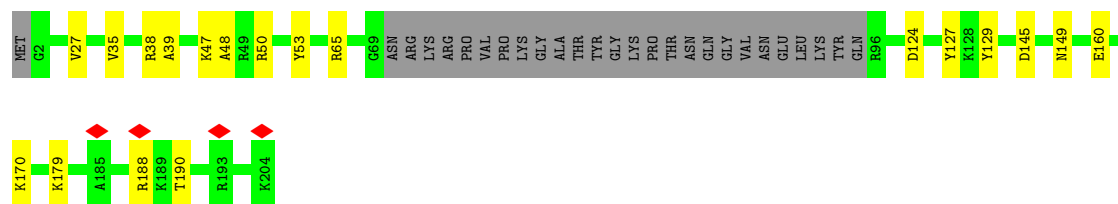


- Molecule 10: 60S ribosomal protein L14-A

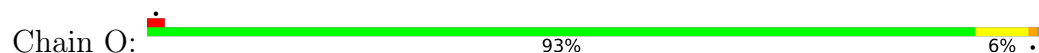


- Molecule 11: 60S ribosomal protein L15-A

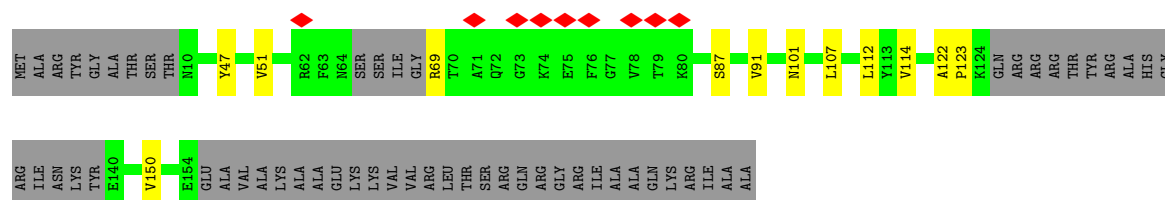




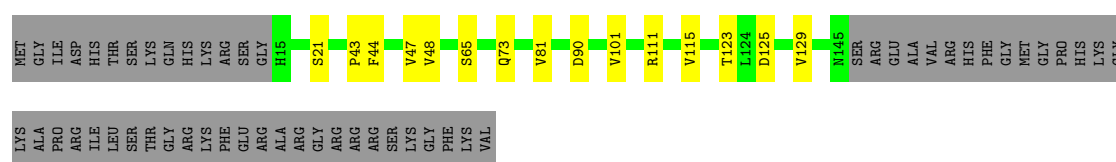
- Molecule 12: 60S ribosomal protein L16-A



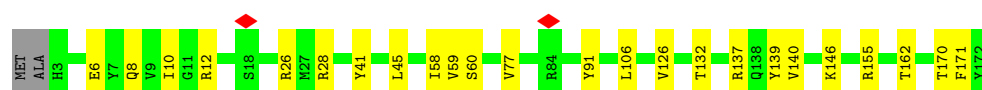
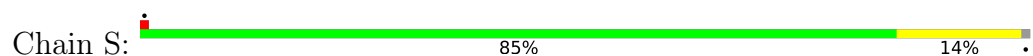
- Molecule 13: 60S ribosomal protein L17-A



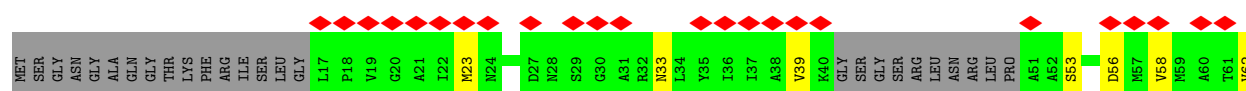
- Molecule 14: 60S ribosomal protein L18-A

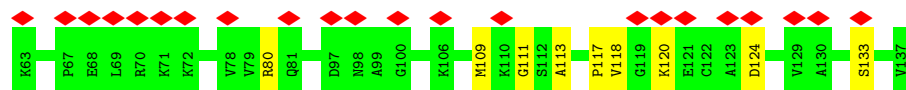


- Molecule 15: 60S ribosomal protein L20-A

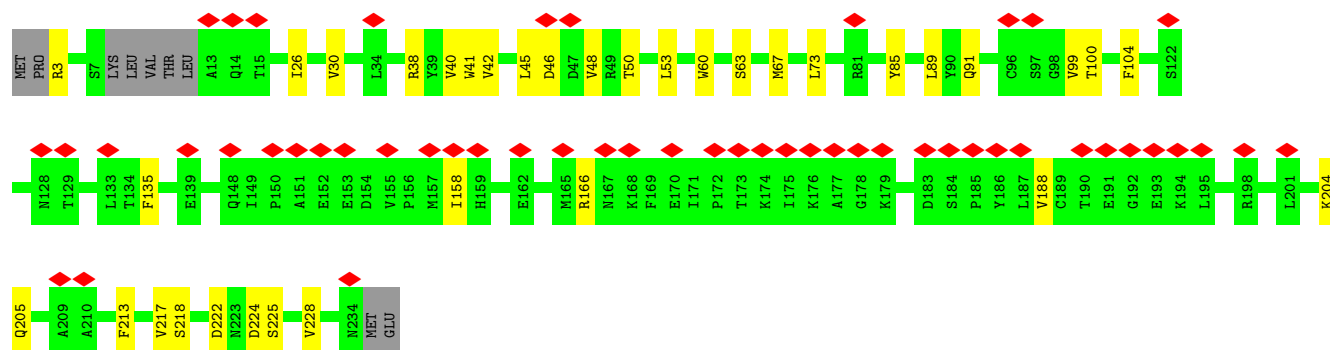
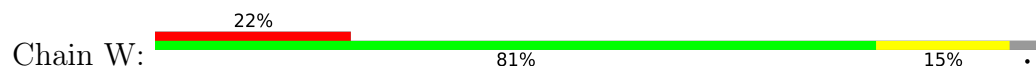


- Molecule 16: 60S ribosomal protein L23-A

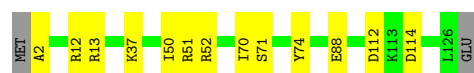
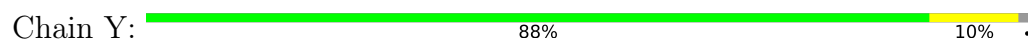




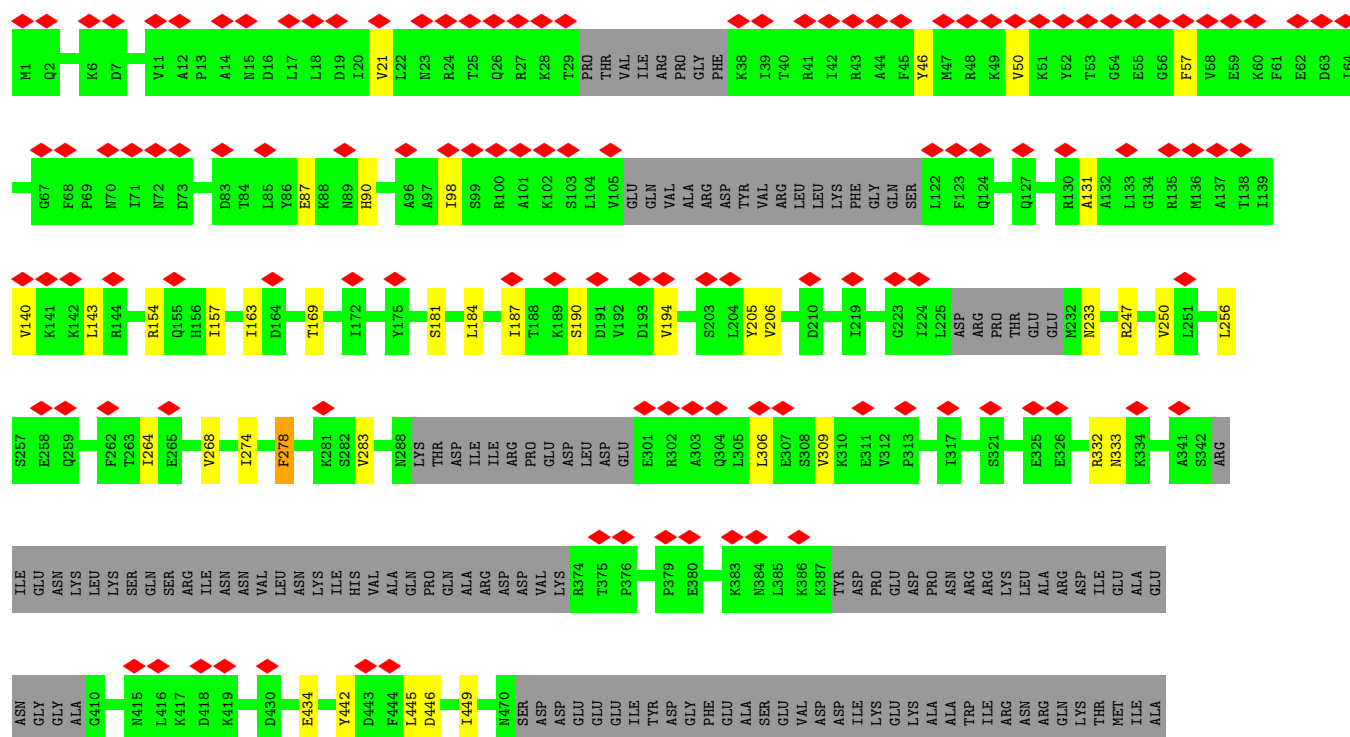
• Molecule 17: Ribosome assembly factor MRT4



• Molecule 18: 60S ribosomal protein L26-A

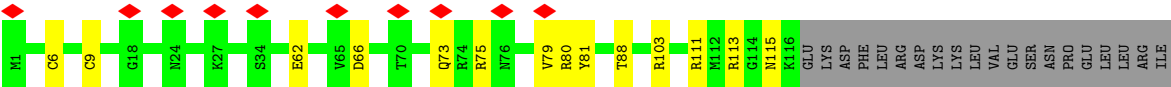


• Molecule 19: Nucleolar GTP-binding protein 1



GLN
LEU
GLY
VAL
LEU
THR
LYS
GLY
THR
ILE
ILE
GLU
VAL
ASN
VAL
SER
GLU
LEU
GLY
MET
VAL
THR
ALA
GLY
GLY
LYS
VAL
VAL
TRP
GLY
LYS
TYR
ALA
GLN
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ASP
GLY
CYS
VAL
ASN
ALA
VAL
LEU
LEU
VAL

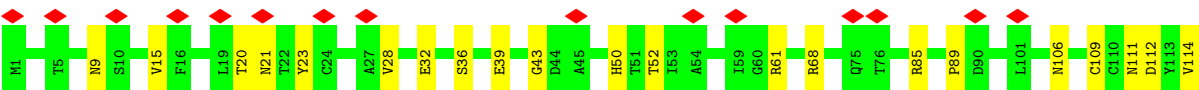
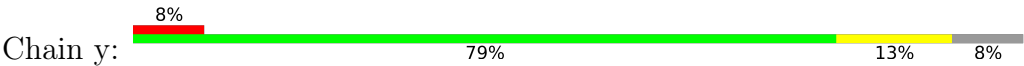
• Molecule 25: Ribosome biogenesis protein RLP24



ARG
GLU
VAL
GLU
ILE
ALA
ARG
LYS
LEU
ALA
LYS
GLU
GLN
GLU
ARG
ALA
GLU
SER
VAL
SER
GLU
GLN
GLU
SER
GLU
GLU
GLU
ASP
GLU
MET
ILE
ASP
SER
ASP
GLU
GLU
GLU
GLU
GLN
LEU
GLU
LYS
PHE
GLN
LYS
ILE
ARG
ASP
LYS
LYS
VAL
GLU
SER
ASN
PRO
GLU
LEU
ARG
ILE

ILE
ALA
PHE

• Molecule 26: Eukaryotic translation initiation factor 6



A115 L116 D122 V135 S143 G144 N145 I146 L173 L177 V182 N200 L203 I221 Q225
ASP
ALA
GLN
PRO
GLU
SER
ILE
SER
GLY
ASN
LEU
ARG
ASP
THR
LEU
ILE
GLU
THR
TYR
SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18398	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 ($e^-/\text{\AA}^2$)	88	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.128	Depositor
Minimum map value	-0.043	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.021	Depositor
Map size (Å)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.07	0/40444	0.22	0/63013
2	2	0.09	0/3510	0.25	0/5460
3	B	0.11	0/2699	0.27	0/3626
4	C	0.10	0/2660	0.25	0/3601
5	E	0.10	0/1226	0.23	0/1648
6	F	0.10	0/1869	0.24	0/2514
7	G	0.12	0/852	0.27	0/1148
8	H	0.09	0/1531	0.27	0/2062
9	L	0.12	0/877	0.28	0/1179
10	M	0.11	0/1056	0.24	0/1421
11	N	0.12	0/1544	0.24	0/2065
12	O	0.10	0/1585	0.23	0/2128
13	P	0.10	0/1010	0.22	0/1359
14	Q	0.10	0/1024	0.22	0/1385
15	S	0.10	0/1468	0.26	0/1973
16	V	0.10	0/838	0.24	0/1128
17	W	0.10	0/1862	0.26	0/2508
18	Y	0.11	0/995	0.25	0/1329
19	b	0.09	0/3093	0.26	0/4163
20	e	0.10	0/1030	0.22	0/1379
21	f	0.12	0/868	0.27	0/1168
22	h	0.11	0/978	0.28	0/1301
23	j	0.12	0/578	0.25	0/767
24	r	0.10	0/622	0.23	0/816
25	u	0.11	0/996	0.31	0/1324
26	y	0.08	0/1722	0.24	0/2343
All	All	0.09	0/76937	0.23	0/112808

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
10	M	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	M	9	ALA	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	1	36150	18161	18183	386	0
2	2	3143	1590	1593	47	0
3	B	2646	2728	2726	36	0
4	C	2611	2725	2724	28	0
5	E	1205	1292	1291	8	0
6	F	1832	1917	1916	18	0
7	G	840	911	910	14	0
8	H	1510	1576	1576	19	0
9	L	864	918	917	14	0
10	M	1041	1138	1137	11	0
11	N	1513	1566	1564	13	0
12	O	1555	1660	1659	10	0
13	P	993	1005	1002	8	0
14	Q	1009	1092	1091	9	0
15	S	1432	1472	1470	17	0
16	V	826	867	865	9	0
17	W	1831	1852	1850	26	0
18	Y	984	1076	1075	10	0
19	b	3040	3104	3098	27	0
20	e	1009	1081	1080	6	0
21	f	850	881	880	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	h	969	1079	1078	10	0
23	j	566	571	566	14	0
24	r	612	638	638	8	0
25	u	976	1011	1007	13	0
26	y	1701	1697	1697	18	0
27	j	1	0	0	0	0
27	u	1	0	0	0	0
All	All	71710	53608	53593	668	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 (668) 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)
1:1:1259:A:O2'	1:1:1260:A:O5'	1.78	1.00
2:2:114:G:O2'	2:2:115:C:OP1	1.88	0.92
1:1:3084:C:O2'	1:1:3332:U:OP1	1.88	0.91
1:1:408:A:N3	1:1:655:C:O2'	2.08	0.87
1:1:1310:G:O2'	1:1:2380:U:O2'	1.92	0.87
1:1:282:G:O2'	1:1:283:G:O5'	1.94	0.86
1:1:3228:C:O2'	1:1:3229:G:OP2	1.92	0.86
1:1:691:A:N1	2:2:28:C:O2'	2.09	0.86
1:1:1188:U:OP1	1:1:1210:U:O2'	1.93	0.85
1:1:3069:G:O2'	1:1:3070:A:OP1	1.93	0.85
1:1:3116:G:N2	1:1:3116:G:OP1	2.10	0.85
1:1:518:G:OP2	1:1:518:G:N2	2.11	0.84
1:1:542:G:O6	1:1:549:U:O2	1.96	0.84
1:1:1347:U:O2'	1:1:1348:U:OP1	1.94	0.83
1:1:376:G:N2	1:1:400:G:O2'	2.12	0.82
17:W:38:ARG:NH2	17:W:224:ASP:OD2	2.12	0.82
1:1:296:A:O2'	1:1:297:G:O4'	1.96	0.82
1:1:3114:A:OP2	1:1:3115:C:O2'	1.97	0.82
1:1:1243:G:N2	1:1:1270:A:O2'	2.13	0.82
26:y:32:GLU:OE2	26:y:36:SER:OG	1.99	0.81
1:1:188:U:O2'	1:1:207:U:O2	1.99	0.81
1:1:3083:G:N2	1:1:3333:G:OP2	2.13	0.80
18:Y:52:ARG:NH2	18:Y:71:SER:O	2.15	0.80
1:1:480:C:O2'	1:1:481:U:O4'	1.99	0.80
1:1:68:C:OP2	1:1:301:G:N2	2.15	0.80
1:1:633:C:O2'	21:f:21:ARG:O	2.00	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:95:G:O2'	23:j:81:GLY:O	2.02	0.78
1:1:3369:G:N2	3:B:380:MET:O	2.17	0.78
1:1:3241:G:OP2	3:B:153:LYS:NZ	2.15	0.77
1:1:3150:A:O2'	1:1:3295:A:OP1	2.03	0.77
1:1:3054:U:O2	1:1:3088:G:O6	2.02	0.77
1:1:3305:A:O2'	1:1:3306:U:O4'	2.01	0.77
7:G:160:ILE:O	7:G:164:VAL:HG13	1.84	0.77
1:1:760:G:O3'	1:1:770:G:N2	2.18	0.76
1:1:3332:U:O2	1:1:3370:A:N6	2.19	0.76
1:1:3150:A:HO2'	1:1:3294:A:HO2'	1.23	0.76
2:2:103:G:OP2	2:2:105:A:O2'	2.03	0.76
1:1:1259:A:N6	17:W:67:MET:SD	2.59	0.76
1:1:1310:G:HO2'	1:1:2380:U:HO2'	1.31	0.76
1:1:3293:U:OP1	3:B:128:LYS:NZ	2.18	0.75
1:1:3303:G:O2'	1:1:3305:A:N6	2.19	0.75
2:2:21:C:OP2	4:C:194:TYR:OH	2.03	0.75
1:1:2365:C:O2	12:O:68:ARG:NH2	2.20	0.75
1:1:1196:C:OP1	1:1:1309:U:O2'	2.03	0.75
3:B:57:VAL:HG12	3:B:73:VAL:HG23	1.69	0.74
1:1:268:A:OP1	11:N:47:LYS:NZ	2.19	0.74
1:1:3018:C:OP1	26:y:9:ASN:ND2	2.20	0.74
1:1:1224:C:H41	1:1:1285:G:H21	1.35	0.74
1:1:2392:C:O2'	1:1:2393:G:O4'	2.05	0.74
1:1:164:A:O2'	1:1:166:C:O4'	2.05	0.74
1:1:3332:U:O2	1:1:3371:G:O6	2.06	0.73
1:1:358:G:N2	1:1:361:A:OP2	2.21	0.73
1:1:239:G:O2'	1:1:240:U:OP1	2.05	0.73
1:1:2994:A:OP2	1:1:3142:A:N6	2.22	0.73
1:1:1260:A:O2'	1:1:1261:G:O4'	2.06	0.72
1:1:751:A:N1	1:1:753:C:N4	2.38	0.72
1:1:1112:A:N3	1:1:1370:G:O2'	2.20	0.72
1:1:2997:G:O6	1:1:3151:U:O2	2.08	0.71
2:2:75:G:OP2	18:Y:74:TYR:OH	2.07	0.71
1:1:1276:U:O2'	1:1:1277:C:OP1	2.06	0.71
1:1:807:A:C6	1:1:935:U:N3	2.59	0.71
1:1:3149:G:O2'	3:B:130:PHE:N	2.23	0.71
1:1:701:G:N2	1:1:788:C:O3'	2.23	0.71
1:1:1176:C:OP2	1:1:1177:G:O2'	2.04	0.71
1:1:1274:A:O2'	17:W:205:GLN:OE1	2.09	0.71
17:W:224:ASP:OD2	17:W:225:SER:N	2.24	0.70
26:y:21:ASN:ND2	26:y:112:ASP:OD2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:644:G:O2'	1:1:1117:G:N2	2.24	0.70
1:1:3082:C:N4	1:1:3083:G:O6	2.24	0.70
1:1:348:A:N3	1:1:352:A:O2'	2.24	0.70
1:1:1178:G:N3	1:1:1328:C:O2'	2.25	0.70
15:S:155:ARG:NE	15:S:171:PHE:O	2.23	0.70
21:f:49:ILE:HD11	21:f:71:VAL:HG22	1.73	0.70
1:1:3308:C:N3	13:P:69:ARG:NH1	2.40	0.69
1:1:3366:G:OP1	25:u:113:ARG:NH2	2.25	0.69
1:1:3343:G:O2'	1:1:3362:A:N1	2.23	0.69
1:1:3366:G:O2'	25:u:115:ASN:OD1	2.11	0.69
1:1:3027:A:O2'	19:b:190:SER:OG	2.10	0.68
1:1:3362:A:O2'	1:1:3363:U:O4'	2.10	0.68
1:1:949:C:O2'	1:1:971:G:OP1	2.11	0.68
1:1:2995:A:O2'	1:1:2996:U:O5'	2.11	0.68
1:1:807:A:N6	1:1:935:U:N3	2.41	0.68
1:1:1221:A:O2'	1:1:1222:G:OP1	2.11	0.68
1:1:1151:U:OP1	21:f:21:ARG:NH2	2.26	0.67
10:M:38:ILE:HD12	10:M:38:ILE:O	1.93	0.67
1:1:1120:A:N6	1:1:1139:G:O6	2.26	0.67
1:1:533:A:O2'	1:1:535:G:O5'	2.12	0.67
1:1:3344:A:OP2	1:1:3361:G:N2	2.27	0.67
1:1:720:A:O2'	1:1:783:A:O3'	2.08	0.67
1:1:63:A:N3	1:1:78:U:O2'	2.27	0.67
1:1:3344:A:N1	1:1:3361:G:O2'	2.27	0.67
1:1:741:U:O2'	14:Q:73:GLN:OE1	2.10	0.67
1:1:1245:A:N7	1:1:1271:A:O2'	2.27	0.67
1:1:3306:U:O2'	1:1:3308:C:OP2	2.13	0.66
1:1:1405:U:H3	20:e:55:ILE:HD12	1.60	0.66
15:S:91:TYR:O	15:S:137:ARG:NH2	2.28	0.66
1:1:1333:C:O2'	6:F:112:ASN:ND2	2.29	0.66
1:1:3067:C:O2'	1:1:3068:U:O4'	2.14	0.66
8:H:175:PHE:O	24:r:17:ARG:NH1	2.27	0.66
1:1:1403:C:N4	1:1:1404:G:O6	2.29	0.66
1:1:2894:C:N4	1:1:2895:G:O6	2.28	0.66
4:C:325:LEU:O	6:F:41:ARG:NH2	2.28	0.66
1:1:1242:G:OP2	19:b:233:ASN:ND2	2.28	0.66
1:1:2994:A:O2'	1:1:2995:A:OP1	2.13	0.66
1:1:75:G:O2'	1:1:76:G:OP1	2.12	0.66
1:1:169:U:O2'	1:1:170:G:O5'	2.12	0.66
6:F:48:ASN:ND2	6:F:182:ASP:OD1	2.29	0.66
1:1:542:G:O6	1:1:549:U:C2	2.49	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1174:G:N2	12:O:87:MET:SD	2.69	0.65
1:1:1129:A:O2'	1:1:1130:A:OP1	2.11	0.65
1:1:517:G:OP1	6:F:67:ARG:NH2	2.29	0.65
15:S:77:VAL:HG13	15:S:126:VAL:HG22	1.78	0.65
1:1:3345:G:N2	1:1:3361:G:O4'	2.29	0.65
1:1:110:G:OP2	9:L:73:ARG:NH1	2.29	0.65
1:1:753:C:O2'	1:1:754:G:O5'	2.12	0.65
3:B:187:SER:O	3:B:190:GLU:N	2.29	0.65
1:1:1116:G:O2'	1:1:1117:G:O4'	2.11	0.64
1:1:476:G:O2'	1:1:477:A:OP1	2.12	0.63
1:1:726:G:N1	1:1:743:C:OP2	2.29	0.63
1:1:3275:U:O2'	21:f:99:ARG:NH1	2.30	0.63
1:1:929:A:O2'	23:j:49:TRP:O	2.16	0.63
1:1:111:C:OP2	1:1:156:G:N1	2.32	0.63
1:1:2983:C:O2'	1:1:2984:C:O5'	2.13	0.63
9:L:93:ILE:HG22	9:L:93:ILE:O	1.97	0.63
14:Q:65:SER:OG	14:Q:90:ASP:OD2	2.14	0.63
1:1:3002:C:OP1	3:B:26:ARG:NH2	2.31	0.63
1:1:107:A:OP1	9:L:39:ARG:NE	2.32	0.63
1:1:3370:A:OP2	3:B:384:LYS:N	2.32	0.63
1:1:543:C:N4	1:1:548:G:O6	2.32	0.62
1:1:3054:U:O2'	1:1:3055:U:O5'	2.12	0.62
7:G:141:ALA:O	7:G:145:ASN:ND2	2.33	0.62
1:1:23:A:OP1	23:j:44:THR:N	2.32	0.62
1:1:345:G:O2'	2:2:25:G:N3	2.32	0.62
10:M:20:VAL:HG13	10:M:66:THR:OG1	1.99	0.62
1:1:399:A:O2'	1:1:403:C:O2'	2.18	0.62
1:1:3146:G:N3	3:B:101:SER:OG	2.31	0.62
26:y:85:ARG:NH1	26:y:89:PRO:O	2.33	0.62
1:1:1329:U:OP1	21:f:17:GLN:NE2	2.32	0.62
6:F:191:VAL:HG22	6:F:195:PHE:CD1	2.35	0.61
1:1:1445:U:OP2	1:1:1446:A:O2'	2.11	0.61
1:1:3306:U:OP1	3:B:225:GLY:N	2.33	0.61
6:F:86:VAL:HG22	6:F:136:TYR:HB3	1.81	0.61
3:B:296:THR:OG1	3:B:299:ASP:OD1	2.10	0.61
1:1:406:G:O2'	1:1:407:A:OP2	2.17	0.61
14:Q:123:THR:OG1	14:Q:125:ASP:OD1	2.18	0.61
1:1:39:A:O3'	1:1:95:A:O2'	2.18	0.61
16:V:53:SER:N	16:V:56:ASP:OD2	2.33	0.61
1:1:1158:A:OP1	6:F:91:GLY:N	2.33	0.61
1:1:3350:C:O2'	1:1:3351:U:O5'	2.17	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:269:SER:OG	4:C:274:TYR:O	2.16	0.61
1:1:3205:G:OP2	1:1:3206:C:N4	2.34	0.61
1:1:456:U:O2'	1:1:457:C:OP1	2.18	0.60
26:y:109:CYS:O	26:y:116:LEU:N	2.33	0.60
1:1:310:U:O2'	1:1:311:C:O5'	2.17	0.60
1:1:2896:A:O3'	1:1:2899:C:N4	2.34	0.60
5:E:40:LEU:HD11	5:E:54:TYR:HB2	1.84	0.60
16:V:39:VAL:HA	16:V:58:VAL:HG12	1.83	0.60
7:G:184:ALA:O	7:G:188:THR:HG23	2.02	0.60
2:2:104:A:OP1	23:j:21:ARG:NH2	2.35	0.60
5:E:51:ARG:NH1	5:E:161:ALA:O	2.36	0.59
1:1:1153:A:H62	1:1:1154:A:H62	1.51	0.59
26:y:200:ASN:OD1	26:y:203:LEU:N	2.33	0.59
4:C:65:TRP:CE3	4:C:71:VAL:HG11	2.37	0.59
1:1:1408:G:OP2	20:e:31:ASN:ND2	2.36	0.59
19:b:445:LEU:O	25:u:75:ARG:NE	2.36	0.59
8:H:134:ILE:HG22	8:H:146:LEU:HG	1.84	0.58
1:1:3060:C:O3'	1:1:3371:G:N2	2.36	0.58
1:1:428:A:N6	1:1:632:G:O6	2.35	0.58
1:1:591:G:N2	1:1:612:U:OP1	2.36	0.58
3:B:86:VAL:HG22	3:B:162:VAL:HG12	1.83	0.58
3:B:90:VAL:HG13	3:B:104:THR:HG22	1.85	0.58
16:V:118:VAL:HG21	16:V:133:SER:OG	2.04	0.58
20:e:100:ILE:O	20:e:105:ARG:NE	2.36	0.58
1:1:1145:G:N2	1:1:1331:U:O2'	2.36	0.58
1:1:77:A:OP2	9:L:73:ARG:NH2	2.36	0.58
1:1:3369:G:N2	25:u:62:GLU:OE2	2.37	0.58
1:1:1207:G:O2'	24:r:36:SER:OG	2.19	0.57
1:1:3313:U:OP1	3:B:173:GLN:NE2	2.37	0.57
1:1:751:A:N1	1:1:781:G:O6	2.37	0.57
1:1:1395:G:O2'	2:2:18:U:O2	2.20	0.57
1:1:3184:A:N3	1:1:3187:A:O2'	2.37	0.57
13:P:114:VAL:HA	13:P:150:VAL:HG12	1.86	0.57
17:W:26:ILE:O	17:W:30:VAL:HG23	2.03	0.57
2:2:56:G:N2	2:2:62:C:O4'	2.38	0.57
16:V:120:LYS:NZ	16:V:124:ASP:OD2	2.37	0.57
1:1:195:U:O2'	1:1:1391:C:OP1	2.14	0.57
1:1:346:C:N4	1:1:349:A:OP2	2.36	0.57
17:W:42:VAL:HG23	17:W:218:SER:HG	1.69	0.57
8:H:112:ILE:HD11	8:H:134:ILE:HG21	1.86	0.57
19:b:205:TYR:OH	24:r:5:ASP:OD2	2.21	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:299:ASP:OD1	3:B:300:ARG:N	2.37	0.56
1:1:1152:G:OP2	1:1:1152:G:N2	2.33	0.56
15:S:77:VAL:HG11	15:S:106:LEU:HD22	1.87	0.56
1:1:673:U:O3'	4:C:34:ILE:HD11	2.05	0.56
1:1:1188:U:O2'	1:1:1190:A:N7	2.36	0.56
1:1:1180:A:OP1	21:f:78:SER:N	2.39	0.56
23:j:67:LEU:HD13	23:j:67:LEU:O	2.03	0.56
1:1:3212:C:C2'	1:1:3213:A:O5'	2.53	0.56
1:1:815:G:OP2	23:j:31:LYS:NZ	2.33	0.56
1:1:1237:G:O6	1:1:1251:A:N1	2.39	0.56
2:2:12:A:C2	2:2:13:A:N7	2.73	0.56
6:F:86:VAL:HG22	6:F:136:TYR:CB	2.36	0.56
9:L:43:ALA:HA	9:L:51:LEU:HD21	1.88	0.56
1:1:2896:A:O2'	1:1:2897:A:P	2.64	0.56
5:E:76:LEU:N	5:E:138:GLN:OE1	2.37	0.56
2:2:72:A:OP2	18:Y:52:ARG:NH1	2.37	0.55
21:f:49:ILE:HD11	21:f:71:VAL:CG2	2.36	0.55
1:1:189:G:O2'	1:1:190:U:O4'	2.25	0.55
1:1:807:A:C6	1:1:935:U:C4	2.95	0.55
1:1:3267:A:OP1	1:1:3268:A:N6	2.36	0.55
4:C:35:VAL:HG11	4:C:244:LEU:HD21	1.89	0.55
1:1:782:U:O2'	1:1:783:A:O4'	2.17	0.55
17:W:40:VAL:HG22	17:W:104:PHE:HD1	1.72	0.55
17:W:46:ASP:HA	17:W:99:VAL:HG21	1.88	0.55
26:y:15:VAL:HG22	26:y:61:ARG:HD3	1.89	0.54
17:W:158:ILE:O	17:W:158:ILE:HD12	2.08	0.54
25:u:66:ASP:OD2	25:u:103:ARG:NH1	2.41	0.54
3:B:312:VAL:HG12	3:B:313:HIS:ND1	2.23	0.54
13:P:87:SER:O	13:P:91:VAL:HG23	2.07	0.54
1:1:209:A:O2'	1:1:211:A:OP2	2.25	0.54
1:1:343:U:O4'	4:C:95:ARG:NE	2.40	0.54
1:1:359:U:O2'	23:j:16:HIS:ND1	2.40	0.54
2:2:49:G:C6	2:2:77:A:N1	2.76	0.54
11:N:27:VAL:HG23	11:N:129:TYR:CE1	2.43	0.54
1:1:361:A:O3'	23:j:45:ARG:NH2	2.40	0.54
4:C:283:THR:HG22	4:C:285:ASP:H	1.72	0.54
1:1:117:U:O2'	1:1:119:U:OP2	2.15	0.54
1:1:388:G:N2	13:P:101:ASN:OD1	2.38	0.54
4:C:260:GLN:O	4:C:270:SER:OG	2.24	0.53
15:S:139:TYR:CD2	15:S:140:VAL:HG23	2.43	0.53
1:1:1062:A:O2'	1:1:1098:A:O5'	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3231:U:O2	1:1:3256:G:O6	2.25	0.53
1:1:282:G:O2'	1:1:283:G:P	2.67	0.53
1:1:1224:C:N4	1:1:1285:G:H21	2.04	0.53
1:1:3195:U:O2'	1:1:3197:G:N2	2.41	0.53
4:C:65:TRP:HE3	4:C:71:VAL:HG11	1.73	0.53
1:1:164:A:N6	1:1:258:G:O6	2.40	0.53
1:1:649:A:O2'	1:1:650:C:P	2.66	0.53
1:1:3333:G:O4'	1:1:3370:A:N6	2.41	0.53
15:S:41:TYR:HE2	15:S:58:ILE:HD12	1.73	0.53
1:1:213:A:OP1	18:Y:2:ALA:N	2.42	0.53
1:1:649:A:O2'	1:1:650:C:OP1	2.27	0.53
13:P:47:TYR:O	13:P:51:VAL:HG23	2.08	0.53
9:L:61:PRO:O	9:L:62:THR:OG1	2.26	0.53
1:1:596:C:OP1	6:F:37:ASN:ND2	2.41	0.53
1:1:615:U:O2'	1:1:616:G:P	2.67	0.53
1:1:1203:A:O2'	1:1:1300:G:N2	2.42	0.53
1:1:3091:A:O2'	1:1:3093:C:OP1	2.26	0.53
17:W:60:TRP:CD1	17:W:63:SER:HG	2.27	0.53
2:2:94:C:OP1	23:j:76:ASN:ND2	2.41	0.52
1:1:3190:C:OP1	12:O:172:ARG:NH1	2.36	0.52
1:1:2896:A:O2'	1:1:2897:A:OP1	2.23	0.52
1:1:2899:C:O2	8:H:173:ARG:NH1	2.42	0.52
3:B:306:THR:OG1	3:B:317:ILE:O	2.27	0.52
1:1:1419:A:O5'	4:C:193:LYS:NZ	2.43	0.52
1:1:271:C:OP1	11:N:170:LYS:NZ	2.29	0.52
2:2:41:A:N6	2:2:103:G:O2'	2.31	0.52
26:y:182:VAL:HG23	26:y:221:ILE:HD13	1.90	0.52
1:1:705:A:O4'	1:1:715:A:N6	2.43	0.52
1:1:3213:A:OP1	10:M:128:ARG:NE	2.42	0.52
1:1:267:G:O4'	11:N:50:ARG:NH1	2.43	0.52
1:1:760:G:HO3'	1:1:770:G:N2	2.08	0.52
17:W:166:ARG:NH1	24:r:18:LEU:O	2.42	0.52
1:1:1347:U:HO2'	1:1:1348:U:P	2.29	0.51
1:1:3337:G:N1	1:1:3367:C:O2	2.43	0.51
1:1:276:U:C2	1:1:290:G:N1	2.78	0.51
1:1:1129:A:HO2'	1:1:1130:A:P	2.32	0.51
7:G:143:ILE:HG22	7:G:169:LEU:HD22	1.92	0.51
1:1:807:A:N6	1:1:935:U:C4	2.79	0.51
2:2:87:G:OP2	22:h:5:LYS:NZ	2.43	0.51
1:1:1278:A:O2'	1:1:1279:C:O5'	2.23	0.51
3:B:282:ILE:HA	3:B:324:VAL:HG12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:b:256:LEU:HD13	19:b:306:LEU:HD11	1.91	0.51
26:y:28:VAL:HG13	26:y:52:THR:HG23	1.93	0.51
1:1:370:U:O4	1:1:374:A:N7	2.43	0.51
1:1:2382:G:OP2	12:O:90:HIS:NE2	2.44	0.51
1:1:3208:G:O4'	1:1:3210:A:C8	2.63	0.51
3:B:214:MET:O	3:B:341:SER:OG	2.20	0.51
25:u:6:CYS:SG	25:u:9:CYS:N	2.80	0.51
1:1:1111:U:O2'	1:1:1112:A:O5'	2.28	0.51
1:1:1404:G:N2	1:1:1407:A:OP2	2.44	0.51
2:2:12:A:C2	2:2:13:A:C8	2.98	0.51
1:1:18:G:OP1	22:h:81:ARG:NH1	2.39	0.51
1:1:1222:G:O2'	1:1:1223:A:OP2	2.26	0.51
1:1:3350:C:O2'	1:1:3351:U:P	2.69	0.51
1:1:421:G:O6	1:1:2383:C:O2'	2.20	0.51
1:1:625:G:N2	1:1:1401:A:OP1	2.40	0.51
1:1:1209:G:N7	17:W:3:ARG:NE	2.58	0.51
4:C:257:LYS:O	4:C:261:VAL:HG23	2.11	0.51
25:u:73:GLN:O	25:u:75:ARG:NH2	2.43	0.51
2:2:120:C:O2'	2:2:133:G:N1	2.44	0.50
3:B:218:ILE:HG22	3:B:276:THR:OG1	2.12	0.50
1:1:164:A:HO2'	1:1:166:C:C1'	2.20	0.50
1:1:2906:C:N4	1:1:2907:G:O6	2.45	0.50
1:1:102:C:O2'	9:L:62:THR:OG1	2.10	0.50
1:1:608:A:O3'	4:C:326:ARG:NH1	2.44	0.50
1:1:1300:G:OP1	24:r:44:GLY:N	2.44	0.50
1:1:276:U:N3	1:1:290:G:C6	2.80	0.50
1:1:282:G:HO2'	1:1:283:G:C5'	2.19	0.50
1:1:674:G:OP1	4:C:31:ARG:NH1	2.45	0.50
1:1:3165:A:N6	1:1:3286:G:O6	2.45	0.50
15:S:41:TYR:CE2	15:S:45:LEU:HD11	2.46	0.50
19:b:169:THR:OG1	19:b:247:ARG:O	2.28	0.50
4:C:27:SER:O	4:C:279:HIS:NE2	2.43	0.50
1:1:1259:A:O2'	1:1:1260:A:P	2.70	0.50
8:H:134:ILE:HD12	8:H:134:ILE:O	2.11	0.50
1:1:336:A:O2'	4:C:48:GLN:NE2	2.43	0.49
1:1:807:A:N6	1:1:935:U:C2	2.80	0.49
7:G:143:ILE:CG2	7:G:169:LEU:HD22	2.42	0.49
15:S:139:TYR:CE2	15:S:140:VAL:HG23	2.47	0.49
1:1:1413:G:C2	1:1:1414:G:N7	2.80	0.49
16:V:109:MET:SD	16:V:111:GLY:N	2.84	0.49
1:1:1259:A:HO2'	1:1:1260:A:P	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3211:C:C2	1:1:3212:C:C5	3.01	0.49
3:B:93:VAL:HG12	3:B:155:ALA:HB2	1.94	0.49
8:H:126:VAL:CG2	8:H:164:ILE:HG21	2.42	0.49
1:1:341:G:H21	1:1:349:A:N6	2.11	0.49
7:G:158:ASP:HB3	7:G:159:PRO:HD3	1.93	0.49
18:Y:51:ARG:NH1	18:Y:112:ASP:OD2	2.45	0.49
22:h:62:GLN:O	22:h:66:VAL:HG23	2.12	0.49
23:j:19:CYS:O	23:j:23:GLY:N	2.42	0.49
1:1:378:A:N6	1:1:391:A:O2'	2.46	0.49
1:1:409:A:O2'	1:1:654:C:O2'	2.23	0.49
1:1:599:C:N4	1:1:600:G:O6	2.46	0.49
21:f:3:GLU:N	21:f:3:GLU:OE1	2.45	0.49
26:y:61:ARG:NE	26:y:106:ASN:OD1	2.41	0.49
1:1:600:G:N2	1:1:603:A:OP2	2.41	0.49
1:1:934:G:N2	1:1:935:U:C5	2.80	0.49
12:O:120:VAL:HG13	15:S:162:THR:O	2.12	0.49
14:Q:44:PHE:O	14:Q:48:VAL:HG23	2.13	0.49
1:1:337:G:OP2	4:C:196:ASN:ND2	2.46	0.49
1:1:673:U:OP1	14:Q:21:SER:OG	2.25	0.49
3:B:156:SER:C	3:B:188:ILE:HG21	2.38	0.49
15:S:41:TYR:CE2	15:S:58:ILE:HD12	2.48	0.49
1:1:472:A:O2'	1:1:473:G:O4'	2.31	0.49
1:1:3169:U:OP2	21:f:56:SER:OG	2.29	0.49
3:B:216:ASP:OD1	3:B:216:ASP:N	2.46	0.49
1:1:36:C:HO2'	1:1:37:U:P	2.36	0.48
1:1:36:C:O2'	1:1:37:U:OP1	2.28	0.48
1:1:2836:C:N4	1:1:2850:G:O2'	2.45	0.48
1:1:3181:C:C2	1:1:3182:G:C8	3.01	0.48
10:M:77:ARG:O	10:M:81:VAL:HG23	2.12	0.48
2:2:95:G:OP2	23:j:72:ARG:NH1	2.45	0.48
17:W:41:TRP:HE3	17:W:217:VAL:HG11	1.77	0.48
1:1:1167:U:OP2	21:f:73:ARG:NH1	2.43	0.48
3:B:156:SER:CA	3:B:188:ILE:HG21	2.42	0.48
4:C:76:ARG:NE	4:C:86:GLY:O	2.39	0.48
1:1:412:G:N1	2:2:12:A:N7	2.61	0.48
1:1:210:U:OP2	4:C:162:THR:OG1	2.26	0.48
1:1:359:U:H4'	1:1:360:G:OP1	2.13	0.48
2:2:11:C:O2	2:2:12:A:H8	1.96	0.48
1:1:1229:G:OP1	17:W:204:LYS:NZ	2.47	0.48
1:1:1336:U:O2	1:1:1337:A:C8	2.65	0.48
1:1:1384:U:OP2	4:C:202:ARG:NE	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:65:TRP:O	4:C:69:ARG:NH1	2.44	0.48
5:E:40:LEU:HB3	5:E:84:VAL:HG13	1.93	0.48
8:H:41:ILE:HD13	8:H:71:VAL:HG22	1.95	0.48
8:H:86:TYR:CG	8:H:151:VAL:HG22	2.48	0.48
1:1:431:U:OP1	21:f:65:ARG:NH1	2.41	0.48
1:1:3220:G:C6	1:1:3266:G:O6	2.67	0.48
6:F:84:VAL:HG12	6:F:138:TYR:CD1	2.49	0.48
19:b:87:GLU:OE1	19:b:90:HIS:N	2.46	0.48
2:2:108:C:H2'	2:2:109:A:O4'	2.13	0.48
25:u:81:TYR:CG	25:u:81:TYR:O	2.66	0.48
2:2:85:G:O6	18:Y:114:ASP:N	2.41	0.47
3:B:185:GLY:O	3:B:191:LYS:NZ	2.40	0.47
1:1:35:A:H1'	1:1:809:G:H21	1.78	0.47
1:1:1278:A:O2'	1:1:1279:C:P	2.72	0.47
1:1:3068:U:O2	1:1:3075:G:C6	2.67	0.47
1:1:3362:A:O2'	1:1:3363:U:O5'	2.32	0.47
2:2:97:A:OP1	22:h:63:ARG:NE	2.44	0.47
6:F:156:ILE:HG22	6:F:157:ASN:N	2.29	0.47
19:b:256:LEU:HD13	19:b:306:LEU:CD1	2.44	0.47
26:y:111:ASN:OD1	26:y:114:VAL:N	2.40	0.47
1:1:931:C:OP2	1:1:932:U:O2'	2.20	0.47
1:1:3332:U:O2	1:1:3371:G:C6	2.66	0.47
6:F:84:VAL:HG12	6:F:138:TYR:HD1	1.79	0.47
17:W:40:VAL:HG22	17:W:104:PHE:CD1	2.49	0.47
1:1:340:C:OP2	4:C:195:ARG:NH1	2.45	0.47
11:N:38:ARG:NH1	11:N:39:ALA:O	2.45	0.47
23:j:66:TYR:OH	23:j:73:ARG:NH2	2.48	0.47
1:1:100:A:H3'	1:1:101:G:H21	1.80	0.47
1:1:1333:C:C2	1:1:1334:U:C5	3.03	0.47
4:C:35:VAL:HG11	4:C:244:LEU:CD2	2.45	0.47
11:N:124:ASP:N	11:N:127:TYR:O	2.45	0.47
19:b:332:ARG:NH1	19:b:333:ASN:OD1	2.47	0.47
1:1:282:G:N2	11:N:179:LYS:O	2.45	0.47
1:1:501:A:N6	1:1:613:G:O6	2.47	0.47
1:1:716:A:O2'	1:1:717:C:O3'	2.32	0.47
3:B:156:SER:O	3:B:188:ILE:HG21	2.13	0.47
13:P:107:LEU:HD23	13:P:112:LEU:HD13	1.96	0.47
1:1:3127:A:H2'	1:1:3128:G:O4'	2.15	0.47
19:b:264:ILE:O	19:b:268:VAL:HG23	2.15	0.47
1:1:621:A:O2'	1:1:623:U:O4	2.32	0.47
1:1:1221:A:HO2'	1:1:1222:G:P	2.36	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1416:C:O3'	1:1:1417:G:O4'	2.33	0.47
2:2:63:G:H22	2:2:97:A:H2	1.62	0.47
1:1:32:U:C2	1:1:53:G:N1	2.83	0.47
1:1:1235:U:N3	1:1:1237:G:O4'	2.48	0.47
7:G:193:LYS:O	7:G:194:THR:HG23	2.14	0.47
1:1:534:U:OP1	15:S:132:THR:OG1	2.28	0.46
1:1:637:C:O2'	1:1:638:C:OP2	2.24	0.46
2:2:76:C:H2'	2:2:77:A:C8	2.49	0.46
1:1:807:A:C5	1:1:935:U:O4	2.68	0.46
1:1:1152:G:H21	1:1:1152:G:P	2.38	0.46
8:H:71:VAL:O	8:H:75:VAL:HG23	2.15	0.46
1:1:615:U:O2'	1:1:616:G:OP1	2.33	0.46
1:1:655:C:OP1	20:e:27:ARG:N	2.48	0.46
3:B:79:VAL:HG13	3:B:79:VAL:O	2.16	0.46
5:E:131:LYS:O	5:E:135:VAL:HG23	2.15	0.46
19:b:250:VAL:CG1	19:b:283:VAL:HG22	2.45	0.46
1:1:84:U:OP2	1:1:85:A:O2'	2.19	0.46
3:B:156:SER:HA	3:B:188:ILE:HG21	1.97	0.46
16:V:23:MET:SD	16:V:23:MET:N	2.89	0.46
1:1:75:G:HO2'	1:1:76:G:P	2.36	0.46
2:2:41:A:H61	2:2:103:G:C2'	2.28	0.46
1:1:1193:A:O2'	1:1:1194:G:OP1	2.28	0.46
1:1:2896:A:HO2'	1:1:2897:A:P	2.37	0.46
13:P:107:LEU:CD2	13:P:112:LEU:HD13	2.46	0.46
9:L:62:THR:O	9:L:64:LYS:N	2.49	0.46
19:b:250:VAL:HG11	19:b:278:PHE:CE1	2.51	0.46
1:1:353:G:O6	23:j:55:ARG:NH2	2.48	0.46
1:1:3244:A:OP2	3:B:100:ARG:NH1	2.48	0.46
1:1:93:C:H1'	1:1:94:G:OP2	2.16	0.46
1:1:751:A:N1	1:1:781:G:C6	2.84	0.46
1:1:1278:A:HO2'	1:1:1279:C:P	2.38	0.46
15:S:155:ARG:O	15:S:170:THR:OG1	2.28	0.46
17:W:42:VAL:HG23	17:W:218:SER:OG	2.15	0.46
1:1:50:U:OP2	11:N:188:ARG:NH1	2.49	0.46
1:1:3243:A:C4	12:O:156:LEU:HD11	2.51	0.46
15:S:8:GLN:OE1	15:S:26:ARG:NH2	2.48	0.46
22:h:50:SER:O	22:h:54:VAL:HG23	2.16	0.46
1:1:1116:G:N2	1:1:1142:G:O2'	2.49	0.45
10:M:92:GLU:OE1	10:M:92:GLU:N	2.48	0.45
20:e:23:ASP:OD2	20:e:24:ARG:N	2.49	0.45
21:f:16:TYR:OH	21:f:91:ALA:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3294:A:O2'	1:1:3295:A:OP1	2.33	0.45
2:2:81:U:O2	2:2:82:U:O2'	2.35	0.45
3:B:35:ASP:OD1	3:B:36:ASP:N	2.49	0.45
17:W:45:LEU:HD12	17:W:53:LEU:CD2	2.46	0.45
8:H:172:ILE:O	24:r:17:ARG:NH1	2.46	0.45
1:1:91:G:H22	1:1:94:G:H5''	1.80	0.45
1:1:543:C:O2	1:1:549:U:N3	2.49	0.45
1:1:2896:A:C3'	1:1:2899:C:H41	2.30	0.45
1:1:3369:G:OP1	25:u:111:ARG:NH1	2.47	0.45
3:B:287:LYS:O	3:B:293:ASN:ND2	2.48	0.45
10:M:127:LYS:O	10:M:131:VAL:HG23	2.16	0.45
11:N:145:ASP:O	11:N:149:ASN:N	2.49	0.45
19:b:449:ILE:HD11	25:u:88:THR:OG1	2.16	0.45
17:W:73:LEU:HD12	17:W:100:THR:HB	1.98	0.45
1:1:715:A:N1	1:1:781:G:O2'	2.41	0.45
1:1:725:G:H2'	1:1:726:G:O4'	2.17	0.45
1:1:1416:C:H2'	1:1:1417:G:C4	2.52	0.45
2:2:14:C:O2	2:2:14:C:H2'	2.17	0.45
17:W:38:ARG:NH2	17:W:222:ASP:OD1	2.49	0.45
17:W:48:VAL:HG22	17:W:213:PHE:CZ	2.52	0.45
1:1:18:G:OP1	22:h:81:ARG:NH2	2.48	0.45
1:1:945:C:HO2'	1:1:1406:A:HO2'	1.60	0.45
1:1:1232:C:H1'	17:W:50:THR:HG21	1.99	0.45
1:1:3212:C:O2'	1:1:3213:A:O5'	2.32	0.45
2:2:119:C:O2	2:2:134:G:N2	2.48	0.45
9:L:91:ARG:NH2	9:L:97:VAL:O	2.49	0.45
1:1:39:A:H2'	1:1:39:A:N3	2.32	0.44
1:1:340:C:H2'	1:1:341:G:O4'	2.17	0.44
1:1:954:U:O2	1:1:954:U:H2'	2.17	0.44
1:1:3005:A:O2'	1:1:3140:G:N2	2.50	0.44
1:1:3069:G:O2'	1:1:3070:A:P	2.74	0.44
6:F:156:ILE:O	6:F:157:ASN:C	2.59	0.44
26:y:39:GLU:O	26:y:43:GLY:N	2.51	0.44
1:1:198:A:C2'	1:1:218:G:HO2'	2.29	0.44
1:1:208:C:H2'	1:1:209:A:O4'	2.17	0.44
1:1:790:U:O2	1:1:791:A:C8	2.70	0.44
1:1:3022:G:N2	1:1:3032:A:OP2	2.45	0.44
6:F:156:ILE:HG22	6:F:157:ASN:H	1.82	0.44
1:1:1412:G:C2	1:1:1413:G:C8	3.05	0.44
1:1:3373:U:O2'	1:1:3376:A:N1	2.50	0.44
8:H:78:MET:O	8:H:82:VAL:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:812:G:C6	1:1:929:A:N6	2.85	0.44
1:1:3218:A:O2'	1:1:3278:C:N4	2.50	0.44
1:1:3389:U:O2	1:1:3390:G:C8	2.71	0.44
9:L:75:PHE:O	9:L:98:ASP:N	2.44	0.44
14:Q:125:ASP:O	14:Q:129:VAL:HG23	2.17	0.44
1:1:412:G:O6	2:2:12:A:N6	2.50	0.44
1:1:1124:U:O2	1:1:1124:U:O4'	2.36	0.44
1:1:1259:A:C6	17:W:67:MET:SD	3.10	0.44
1:1:1282:G:C2	1:1:1283:C:C5	3.05	0.44
1:1:1414:G:C2	1:1:1415:U:C4	3.06	0.44
1:1:3329:U:O3'	1:1:3330:A:O4'	2.36	0.44
9:L:66:ASN:OD1	9:L:67:ARG:N	2.51	0.44
19:b:256:LEU:HD12	19:b:256:LEU:O	2.16	0.44
19:b:163:ILE:HG22	19:b:206:VAL:HG21	1.98	0.44
19:b:442:TYR:O	25:u:75:ARG:NH2	2.51	0.44
2:2:156:U:O2	2:2:156:U:H2'	2.18	0.44
10:M:20:VAL:HG12	10:M:68:LEU:O	2.17	0.44
17:W:135:PHE:HB3	17:W:188:VAL:HG22	2.00	0.44
24:r:5:ASP:OD1	24:r:9:ARG:NH2	2.47	0.44
1:1:640:U:O2'	1:1:941:G:OP2	2.32	0.44
1:1:3228:C:H4'	1:1:3229:G:O5'	2.18	0.44
7:G:190:VAL:O	7:G:190:VAL:HG12	2.18	0.44
19:b:181:SER:HB3	19:b:194:VAL:HG13	1.99	0.44
1:1:144:A:OP1	7:G:193:LYS:NZ	2.45	0.44
1:1:154:U:OP2	22:h:103:LYS:NZ	2.48	0.44
1:1:456:U:HO2'	1:1:457:C:P	2.39	0.44
1:1:1119:C:N4	1:1:1120:A:H62	2.15	0.44
1:1:3228:C:O2'	1:1:3229:G:P	2.76	0.44
10:M:48:GLY:HA3	10:M:53:VAL:HG13	1.99	0.44
26:y:20:THR:OG1	26:y:23:TYR:O	2.31	0.44
1:1:106:A:N3	1:1:325:A:O2'	2.42	0.43
1:1:2896:A:H3'	1:1:2899:C:H41	1.83	0.43
1:1:406:G:OP1	1:1:1415:U:O2'	2.24	0.43
1:1:611:A:O2'	1:1:612:U:OP2	2.25	0.43
11:N:35:VAL:HG22	11:N:65:ARG:HH22	1.83	0.43
19:b:46:TYR:O	19:b:50:VAL:HG23	2.17	0.43
9:L:29:ALA:O	9:L:33:VAL:HG23	2.17	0.43
11:N:35:VAL:HG22	11:N:65:ARG:NH2	2.33	0.43
17:W:60:TRP:CG	17:W:63:SER:HG	2.37	0.43
19:b:274:ILE:HG22	19:b:278:PHE:HB3	1.99	0.43
1:1:476:G:HO2'	1:1:477:A:P	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:48:ALA:HB1	11:N:53:TYR:HB3	2.00	0.43
19:b:57:PHE:CE1	19:b:140:VAL:HG21	2.54	0.43
26:y:68:ARG:NH1	26:y:112:ASP:O	2.47	0.43
1:1:612:U:H4'	5:E:21:THR:HG21	2.00	0.43
7:G:196:ALA:O	7:G:197:VAL:HG13	2.17	0.43
1:1:989:A:O2'	1:1:990:U:O4'	2.36	0.43
1:1:1276:U:O2'	1:1:1277:C:P	2.76	0.43
1:1:1405:U:H4'	1:1:1406:A:OP1	2.17	0.43
4:C:134:LEU:HD21	4:C:244:LEU:HB2	2.01	0.43
8:H:109:ALA:O	8:H:110:LYS:C	2.62	0.43
18:Y:88:GLU:OE1	18:Y:88:GLU:N	2.52	0.43
21:f:31:LYS:NZ	21:f:78:SER:O	2.44	0.43
1:1:1242:G:N3	1:1:1242:G:H2'	2.34	0.43
18:Y:50:ILE:HD11	18:Y:70:ILE:HD11	2.00	0.43
1:1:1176:C:O2'	12:O:89:SER:OG	1.99	0.43
1:1:1280:C:O2	1:1:1281:G:C8	2.72	0.43
1:1:1315:U:O2	1:1:1317:A:N6	2.51	0.43
1:1:2830:G:H1'	19:b:131:ALA:HA	2.00	0.43
2:2:28:C:N3	2:2:29:U:C5	2.87	0.43
5:E:37:GLY:N	5:E:54:TYR:O	2.47	0.43
5:E:52:VAL:CG1	5:E:65:ILE:HB	2.49	0.43
1:1:1415:U:C4	1:1:1416:C:C4	3.07	0.43
1:1:2900:A:C2	1:1:2901:G:C8	3.07	0.43
1:1:3328:G:N2	3:B:309:GLY:O	2.46	0.43
1:1:3153:U:OP2	1:1:3293:U:O2'	2.32	0.43
14:Q:43:PRO:O	14:Q:47:VAL:HG23	2.19	0.43
1:1:126:U:C2	1:1:127:G:C8	3.07	0.42
1:1:1398:U:O2	1:1:1412:G:O6	2.37	0.42
1:1:3121:U:H4'	1:1:3122:A:OP1	2.19	0.42
2:2:114:G:O2'	2:2:115:C:P	2.76	0.42
1:1:359:U:HO2'	23:j:16:HIS:CE1	2.36	0.42
9:L:98:ASP:OD1	9:L:100:ARG:NE	2.48	0.42
16:V:80:ARG:NH1	16:V:117:PRO:O	2.52	0.42
26:y:115:ALA:HB2	26:y:135:VAL:HG21	2.01	0.42
10:M:9:ALA:O	10:M:10:SER:CB	2.66	0.42
13:P:122:ALA:HB1	13:P:123:PRO:HD2	2.00	0.42
15:S:10:ILE:HD11	15:S:60:SER:HB3	2.00	0.42
1:1:733:G:N2	1:1:736:A:OP2	2.45	0.42
1:1:3021:A:O2'	1:1:3022:G:OP2	2.27	0.42
1:1:3026:G:N2	1:1:3029:A:OP2	2.52	0.42
4:C:23:PRO:O	4:C:24:ALA:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:128:VAL:HG13	8:H:132:VAL:HG13	2.01	0.42
1:1:82:C:C4	1:1:83:U:C4	3.07	0.42
1:1:476:G:H21	1:1:477:A:H1'	1.84	0.42
1:1:3388:C:H5''	1:1:3389:U:O4'	2.20	0.42
2:2:79:A:H2'	2:2:80:A:O4'	2.20	0.42
8:H:47:LYS:HB2	10:M:7:VAL:HG21	2.01	0.42
8:H:126:VAL:HG23	8:H:164:ILE:HG21	2.02	0.42
14:Q:81:VAL:HG13	14:Q:101:VAL:HG13	2.01	0.42
22:h:18:ALA:O	22:h:22:VAL:HG23	2.18	0.42
1:1:1241:U:N3	1:1:1244:A:OP1	2.53	0.42
1:1:3066:U:O2	1:1:3076:C:N4	2.53	0.42
3:B:287:LYS:N	3:B:293:ASN:OD1	2.53	0.42
2:2:11:C:O2	2:2:11:C:H2'	2.20	0.42
1:1:43:A:N3	1:1:43:A:H2'	2.34	0.42
1:1:1340:G:OP2	20:e:61:LYS:NZ	2.44	0.42
1:1:3242:G:OP1	12:O:159:LYS:NZ	2.52	0.42
1:1:535:G:OP1	15:S:146:LYS:NZ	2.41	0.42
1:1:1255:C:O2	1:1:1255:C:O4'	2.37	0.42
1:1:2994:A:H2'	1:1:2994:A:N3	2.34	0.42
2:2:10:A:C5	2:2:11:C:C5	3.08	0.42
8:H:86:TYR:CD2	8:H:151:VAL:HG22	2.55	0.42
16:V:33:ASN:O	16:V:62:VAL:HG22	2.20	0.42
26:y:114:VAL:HG21	26:y:177:LEU:HD23	2.01	0.42
1:1:215:G:OP1	18:Y:12:ARG:NH1	2.50	0.42
1:1:500:C:N4	1:1:501:A:H62	2.18	0.42
1:1:621:A:OP1	21:f:60:ARG:NH1	2.41	0.42
1:1:1108:U:O2	1:1:1108:U:O4'	2.38	0.42
11:N:160:GLU:OE1	11:N:160:GLU:N	2.50	0.42
17:W:91:GLN:CB	17:W:228:VAL:HG21	2.50	0.42
19:b:154:ARG:HA	19:b:157:ILE:HG22	2.01	0.42
1:1:76:G:O2'	9:L:98:ASP:OD2	2.28	0.41
1:1:310:U:H4'	1:1:311:C:OP1	2.20	0.41
2:2:36:G:O2'	2:2:104:A:N1	2.52	0.41
3:B:78:VAL:HG11	3:B:305:ILE:HD13	2.02	0.41
2:2:77:A:H2'	2:2:78:G:O4'	2.20	0.41
7:G:97:TYR:HB3	7:G:132:VAL:HG13	2.02	0.41
21:f:90:PRO:O	21:f:91:ALA:HB3	2.19	0.41
22:h:53:CYS:O	22:h:57:VAL:HG23	2.21	0.41
25:u:79:VAL:HG12	25:u:80:ARG:H	1.84	0.41
1:1:81:C:C2	1:1:82:C:C5	3.09	0.41
1:1:187:A:N3	1:1:208:C:O2'	2.42	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:454:C:H2'	1:1:455:C:C6	2.55	0.41
8:H:28:VAL:HG22	8:H:33:THR:HG22	2.03	0.41
1:1:144:A:H2'	1:1:145:G:O4'	2.20	0.41
1:1:1299:U:H4'	24:r:43:THR:HG22	2.03	0.41
2:2:24:G:OP2	18:Y:13:ARG:NE	2.46	0.41
2:2:97:A:O2'	22:h:59:ASN:ND2	2.53	0.41
4:C:226:GLU:OE1	4:C:237:GLN:NE2	2.50	0.41
7:G:133:LYS:N	7:G:199:ALA:O	2.41	0.41
8:H:68:LEU:C	8:H:68:LEU:HD13	2.45	0.41
16:V:113:ALA:HB2	26:y:146:ILE:HG21	2.02	0.41
1:1:32:U:O2	1:1:53:G:C2	2.74	0.41
1:1:406:G:HO2'	1:1:407:A:P	2.43	0.41
1:1:1335:C:N3	1:1:1336:U:C5	2.89	0.41
1:1:1281:G:C2	1:1:1282:G:C8	3.08	0.41
1:1:2995:A:O2'	1:1:2996:U:O4'	2.36	0.41
2:2:39:G:O2'	2:2:40:A:OP2	2.35	0.41
1:1:170:G:N3	1:1:170:G:H2'	2.36	0.41
19:b:309:VAL:HG12	19:b:309:VAL:O	2.21	0.41
1:1:1281:G:C2	1:1:1282:G:N7	2.88	0.41
1:1:3332:U:O2'	1:1:3333:G:O5'	2.38	0.41
3:B:319:ASN:OD1	3:B:319:ASN:N	2.53	0.41
6:F:81:HIS:O	6:F:119:VAL:HG21	2.20	0.41
7:G:160:ILE:HG22	7:G:164:VAL:CG1	2.51	0.41
1:1:14:U:O2'	1:1:15:C:OP1	2.37	0.41
1:1:20:A:N6	2:2:140:G:O6	2.54	0.41
1:1:220:G:N7	1:1:1389:G:N1	2.66	0.41
1:1:754:G:O2'	1:1:755:A:O4'	2.26	0.41
1:1:779:G:C6	1:1:781:G:N7	2.88	0.41
1:1:3058:U:O2	1:1:3058:U:H2'	2.21	0.41
1:1:3185:U:H2'	12:O:126:VAL:HG23	2.03	0.41
1:1:3332:U:O2'	1:1:3333:G:O4'	2.38	0.41
2:2:30:C:O2	2:2:31:G:C8	2.74	0.41
6:F:233:GLU:O	6:F:236:ILE:HG22	2.21	0.41
14:Q:111:ARG:O	14:Q:115:VAL:HG23	2.20	0.41
17:W:85:TYR:HB3	17:W:89:LEU:HD23	2.03	0.41
1:1:1299:U:O5'	1:1:1299:U:O2	2.38	0.41
1:1:3113:A:H2'	1:1:3114:A:O4'	2.21	0.41
1:1:3211:C:O2	1:1:3212:C:C5	2.74	0.41
1:1:725:G:C6	1:1:746:A:N6	2.89	0.40
1:1:3057:U:H3'	1:1:3058:U:C5'	2.51	0.40
2:2:14:C:H2'	2:2:15:G:O5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:107:G:H4'	2:2:138:A:H5'	2.03	0.40
15:S:6:GLU:OE2	15:S:28:ARG:NE	2.55	0.40
15:S:12:ARG:HG3	15:S:59:VAL:HG13	2.03	0.40
19:b:21:VAL:HG11	19:b:57:PHE:CZ	2.56	0.40
1:1:537:A:H61	1:1:554:A:C2'	2.35	0.40
26:y:50:HIS:O	26:y:50:HIS:ND1	2.55	0.40
3:B:58:ARG:NE	3:B:74:GLU:OE1	2.49	0.40
7:G:135:GLY:O	7:G:139:VAL:HG23	2.20	0.40
8:H:150:SER:O	8:H:154:VAL:HG23	2.22	0.40
19:b:98:ILE:HD13	19:b:143:LEU:HD21	2.03	0.40
1:1:543:C:N3	1:1:549:U:O4	2.54	0.40
1:1:754:G:OP2	1:1:754:G:C8	2.75	0.40
1:1:1358:C:O2'	1:1:1359:C:OP1	2.29	0.40
1:1:3212:C:OP1	10:M:124:ARG:NH2	2.54	0.40
4:C:229:ASN:OD1	4:C:230:VAL:N	2.54	0.40
6:F:88:ARG:NH1	6:F:91:GLY:O	2.52	0.40
6:F:156:ILE:HD12	6:F:161:VAL:HG21	2.04	0.40
19:b:184:LEU:HA	19:b:187:ILE:HG22	2.03	0.40
21:f:49:ILE:HD12	21:f:83:ALA:HB1	2.03	0.40
1:1:806:A:N3	1:1:936:A:N6	2.69	0.40
1:1:1263:A:H2'	1:1:1263:A:N3	2.36	0.40
1:1:1299:U:H2'	1:1:1300:G:O4'	2.22	0.40
1:1:3181:C:C6	12:O:168:TYR:CG	3.10	0.40
1:1:3189:G:H2'	1:1:3189:G:N3	2.36	0.40
2:2:28:C:C2	2:2:29:U:C5	3.10	0.40
4:C:212:ASP:OD1	4:C:216:VAL:HG22	2.22	0.40
19:b:446:ASP:CG	25:u:75:ARG:HE	2.29	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	
3	B	329/387 (85%)	309 (94%)	20 (6%)	0	100	100
4	C	341/362 (94%)	325 (95%)	16 (5%)	0	100	100
5	E	147/176 (84%)	143 (97%)	4 (3%)	0	100	100
6	F	226/244 (93%)	217 (96%)	9 (4%)	0	100	100
7	G	104/256 (41%)	98 (94%)	6 (6%)	0	100	100
8	H	188/191 (98%)	176 (94%)	12 (6%)	0	100	100
9	L	106/199 (53%)	98 (92%)	8 (8%)	0	100	100
10	M	132/138 (96%)	126 (96%)	5 (4%)	1 (1%)	16	50
11	N	173/204 (85%)	171 (99%)	2 (1%)	0	100	100
12	O	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
13	P	120/184 (65%)	119 (99%)	1 (1%)	0	100	100
14	Q	129/186 (69%)	128 (99%)	1 (1%)	0	100	100
15	S	168/172 (98%)	155 (92%)	13 (8%)	0	100	100
16	V	107/137 (78%)	105 (98%)	2 (2%)	0	100	100
17	W	223/236 (94%)	218 (98%)	5 (2%)	0	100	100
18	Y	123/127 (97%)	120 (98%)	3 (2%)	0	100	100
19	b	361/647 (56%)	347 (96%)	14 (4%)	0	100	100
20	e	123/130 (95%)	120 (98%)	3 (2%)	0	100	100
21	f	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
22	h	117/120 (98%)	107 (92%)	10 (8%)	0	100	100
23	j	69/88 (78%)	67 (97%)	2 (3%)	0	100	100
24	r	69/261 (26%)	63 (91%)	6 (9%)	0	100	100
25	u	114/199 (57%)	108 (95%)	6 (5%)	0	100	100
26	y	223/245 (91%)	214 (96%)	9 (4%)	0	100	100
All	All	3991/5195 (77%)	3824 (96%)	166 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	M	9	ALA

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	B	280/323 (87%)	280 (100%)	0	100	100
4	C	273/289 (94%)	270 (99%)	3 (1%)	65	74
5	E	131/153 (86%)	129 (98%)	2 (2%)	57	70
6	F	191/205 (93%)	189 (99%)	2 (1%)	68	75
7	G	89/208 (43%)	89 (100%)	0	100	100
8	H	170/171 (99%)	168 (99%)	2 (1%)	63	72
9	L	87/159 (55%)	84 (97%)	3 (3%)	32	55
10	M	106/109 (97%)	106 (100%)	0	100	100
11	N	153/176 (87%)	152 (99%)	1 (1%)	76	78
12	O	160/162 (99%)	157 (98%)	3 (2%)	50	66
13	P	103/146 (70%)	103 (100%)	0	100	100
14	Q	107/151 (71%)	107 (100%)	0	100	100
15	S	155/156 (99%)	155 (100%)	0	100	100
16	V	86/105 (82%)	86 (100%)	0	100	100
17	W	204/213 (96%)	204 (100%)	0	100	100
18	Y	108/110 (98%)	107 (99%)	1 (1%)	70	75
19	b	339/573 (59%)	337 (99%)	2 (1%)	78	80
20	e	108/111 (97%)	108 (100%)	0	100	100
21	f	90/91 (99%)	90 (100%)	0	100	100
22	h	104/105 (99%)	103 (99%)	1 (1%)	68	75
23	j	59/71 (83%)	59 (100%)	0	100	100
24	r	63/229 (28%)	63 (100%)	0	100	100
25	u	101/180 (56%)	101 (100%)	0	100	100
26	y	193/211 (92%)	192 (100%)	1 (0%)	81	82
All	All	3460/4407 (78%)	3439 (99%)	21 (1%)	76	80

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	C	65	TRP
4	C	134	LEU
4	C	184	SER
5	E	52	VAL
5	E	155	LEU
6	F	130	ILE
6	F	134	VAL
8	H	41	ILE
8	H	134	ILE
9	L	91	ARG
9	L	100	ARG
9	L	118	GLU
11	N	190	THR
12	O	143	THR
12	O	156	LEU
12	O	164	SER
18	Y	37	LYS
19	b	278	PHE
19	b	434	GLU
22	h	85	THR
26	y	173	LEU

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

Mol	Chain	Res	Type
3	B	121	ASN
3	B	198	HIS
4	C	48	GLN
4	C	116	ASN
4	C	196	ASN
5	E	57	HIS
5	E	172	HIS
6	F	112	ASN
6	F	209	ASN
8	H	64	HIS
8	H	157	ASN
9	L	103	ASN
11	N	117	ASN
11	N	195	ASN
12	O	50	ASN
12	O	122	GLN
13	P	54	HIS
14	Q	58	ASN

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Mol	Chain	Res	Type
15	S	89	ASN
15	S	114	HIS
17	W	148	GLN
18	Y	4	GLN
18	Y	110	HIS
19	b	208	HIS
19	b	429	ASN
19	b	440	ASN
20	e	26	HIS
21	f	106	ASN
22	h	59	ASN
22	h	104	GLN
24	r	10	HIS
24	r	49	GLN
26	y	82	GLN
26	y	168	GLN
26	y	178	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1668/3396 (49%)	343 (20%)	43 (2%)
2	2	146/158 (92%)	34 (23%)	2 (1%)
All	All	1814/3554 (51%)	377 (20%)	45 (2%)

All (377) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	3	U
1	1	15	C
1	1	18	G
1	1	20	A
1	1	26	A
1	1	37	U
1	1	39	A
1	1	44	U
1	1	48	A
1	1	49	A
1	1	50	U
1	1	60	A

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Mol	Chain	Res	Type
1	1	65	A
1	1	66	A
1	1	72	C
1	1	74	G
1	1	76	G
1	1	92	G
1	1	93	C
1	1	94	G
1	1	109	A
1	1	110	G
1	1	115	A
1	1	117	U
1	1	118	U
1	1	122	A
1	1	135	C
1	1	136	G
1	1	150	A
1	1	156	G
1	1	157	A
1	1	168	U
1	1	170	G
1	1	190	U
1	1	191	U
1	1	200	C
1	1	210	U
1	1	213	A
1	1	218	G
1	1	219	A
1	1	221	A
1	1	222	A
1	1	240	U
1	1	243	G
1	1	246	U
1	1	251	G
1	1	252	U
1	1	254	A
1	1	265	A
1	1	266	A
1	1	268	A
1	1	269	G
1	1	282	G
1	1	283	G

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Mol	Chain	Res	Type
1	1	284	A
1	1	285	A
1	1	295	A
1	1	298	U
1	1	299	G
1	1	305	U
1	1	311	C
1	1	315	C
1	1	323	A
1	1	325	A
1	1	329	U
1	1	351	A
1	1	352	A
1	1	360	G
1	1	376	G
1	1	381	U
1	1	383	G
1	1	384	A
1	1	385	A
1	1	387	A
1	1	388	G
1	1	398	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	404	G
1	1	420	G
1	1	421	G
1	1	436	A
1	1	438	A
1	1	439	C
1	1	441	U
1	1	442	G
1	1	446	U
1	1	453	C
1	1	454	C
1	1	457	C
1	1	477	A
1	1	478	A
1	1	481	U
1	1	482	C
1	1	495	G

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Mol	Chain	Res	Type
1	1	521	A
1	1	544	C
1	1	546	C
1	1	547	G
1	1	550	A
1	1	552	G
1	1	557	A
1	1	559	A
1	1	578	A
1	1	579	G
1	1	592	A
1	1	593	C
1	1	604	G
1	1	611	A
1	1	612	U
1	1	616	G
1	1	620	U
1	1	621	A
1	1	623	U
1	1	636	C
1	1	638	C
1	1	644	G
1	1	647	A
1	1	648	C
1	1	650	C
1	1	660	A
1	1	661	G
1	1	677	A
1	1	681	U
1	1	691	A
1	1	705	A
1	1	706	A
1	1	708	G
1	1	719	U
1	1	720	A
1	1	721	G
1	1	722	G
1	1	753	C
1	1	754	G
1	1	758	C
1	1	783	A
1	1	784	A

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Mol	Chain	Res	Type
1	1	785	G
1	1	808	A
1	1	817	A
1	1	926	A
1	1	930	U
1	1	932	U
1	1	933	A
1	1	936	A
1	1	944	C
1	1	957	C
1	1	959	C
1	1	961	C
1	1	962	A
1	1	977	C
1	1	978	G
1	1	979	U
1	1	980	A
1	1	984	G
1	1	985	U
1	1	1098	A
1	1	1103	A
1	1	1104	G
1	1	1111	U
1	1	1112	A
1	1	1116	G
1	1	1124	U
1	1	1125	U
1	1	1127	G
1	1	1129	A
1	1	1130	A
1	1	1131	G
1	1	1139	G
1	1	1143	A
1	1	1144	U
1	1	1153	A
1	1	1154	A
1	1	1159	A
1	1	1180	A
1	1	1181	U
1	1	1191	U
1	1	1192	C
1	1	1193	A

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Mol	Chain	Res	Type
1	1	1194	G
1	1	1196	C
1	1	1217	A
1	1	1220	U
1	1	1221	A
1	1	1222	G
1	1	1241	U
1	1	1242	G
1	1	1243	G
1	1	1244	A
1	1	1245	A
1	1	1246	G
1	1	1252	A
1	1	1253	U
1	1	1258	U
1	1	1259	A
1	1	1260	A
1	1	1262	G
1	1	1277	C
1	1	1278	A
1	1	1279	C
1	1	1282	G
1	1	1284	C
1	1	1285	G
1	1	1286	A
1	1	1287	A
1	1	1313	G
1	1	1330	A
1	1	1332	A
1	1	1348	U
1	1	1349	G
1	1	1350	A
1	1	1355	A
1	1	1357	G
1	1	1359	C
1	1	1386	A
1	1	1390	A
1	1	1399	A
1	1	1400	G
1	1	1406	A
1	1	1408	G
1	1	1417	G

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Mol	Chain	Res	Type
1	1	1418	A
1	1	1419	A
1	1	1436	U
1	1	1437	C
1	1	2365	C
1	1	2370	G
1	1	2371	G
1	1	2372	A
1	1	2375	G
1	1	2377	G
1	1	2378	C
1	1	2391	G
1	1	2392	C
1	1	2393	G
1	1	2836	C
1	1	2858	U
1	1	2897	A
1	1	2899	C
1	1	2984	C
1	1	2987	A
1	1	2995	A
1	1	2996	U
1	1	2997	G
1	1	3003	G
1	1	3012	A
1	1	3021	A
1	1	3022	G
1	1	3027	A
1	1	3028	G
1	1	3032	A
1	1	3055	U
1	1	3057	U
1	1	3058	U
1	1	3067	C
1	1	3068	U
1	1	3069	G
1	1	3070	A
1	1	3071	U
1	1	3074	G
1	1	3075	G
1	1	3076	C
1	1	3086	A

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Mol	Chain	Res	Type
1	1	3092	C
1	1	3093	C
1	1	3094	A
1	1	3099	C
1	1	3101	G
1	1	3104	U
1	1	3113	A
1	1	3115	C
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3154	C
1	1	3155	U
1	1	3156	U
1	1	3157	U
1	1	3170	A
1	1	3172	A
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3179	U
1	1	3180	A
1	1	3181	C
1	1	3187	A
1	1	3189	G
1	1	3198	U
1	1	3207	U
1	1	3210	A
1	1	3213	A
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3229	G
1	1	3235	C
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3247	G
1	1	3250	U
1	1	3259	U

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Mol	Chain	Res	Type
1	1	3260	G
1	1	3270	U
1	1	3273	A
1	1	3276	G
1	1	3279	A
1	1	3281	U
1	1	3295	A
1	1	3304	U
1	1	3307	A
1	1	3330	A
1	1	3333	G
1	1	3335	A
1	1	3341	U
1	1	3342	A
1	1	3343	G
1	1	3344	A
1	1	3345	G
1	1	3346	U
1	1	3347	A
1	1	3349	C
1	1	3351	U
1	1	3352	U
1	1	3354	U
1	1	3355	U
1	1	3356	G
1	1	3361	G
1	1	3363	U
1	1	3366	G
1	1	3369	G
1	1	3370	A
1	1	3375	A
1	1	3376	A
1	1	3381	U
1	1	3383	G
1	1	3389	U
1	1	3390	G
2	2	13	A
2	2	15	G
2	2	16	G
2	2	23	U
2	2	34	U
2	2	35	C

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Mol	Chain	Res	Type
2	2	39	G
2	2	40	A
2	2	49	G
2	2	51	G
2	2	52	A
2	2	54	A
2	2	59	A
2	2	62	C
2	2	63	G
2	2	70	G
2	2	71	A
2	2	72	A
2	2	79	A
2	2	80	A
2	2	81	U
2	2	82	U
2	2	86	U
2	2	87	G
2	2	89	A
2	2	90	U
2	2	95	G
2	2	100	U
2	2	104	A
2	2	106	C
2	2	115	C
2	2	122	U
2	2	131	A
2	2	152	G

All (45) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	14	U
1	1	36	C
1	1	75	G
1	1	93	C
1	1	239	G
1	1	282	G
1	1	304	G
1	1	310	U
1	1	359	U
1	1	387	A

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Mol	Chain	Res	Type
1	1	438	A
1	1	441	U
1	1	456	U
1	1	476	G
1	1	615	U
1	1	649	A
1	1	659	G
1	1	705	A
1	1	753	C
1	1	1102	A
1	1	1128	U
1	1	1129	A
1	1	1193	A
1	1	1241	U
1	1	1259	A
1	1	1276	U
1	1	1347	U
1	1	1358	C
1	1	1385	C
1	1	1405	U
1	1	2371	G
1	1	2857	C
1	1	2896	A
1	1	2983	C
1	1	2994	A
1	1	2995	A
1	1	3069	G
1	1	3228	C
1	1	3269	U
1	1	3294	A
1	1	3350	C
1	1	3360	C
1	1	3369	G
2	2	71	A
2	2	114	G

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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.

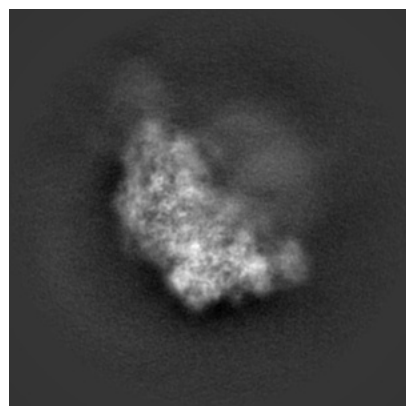
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12913. These allow visual inspection of the internal detail of the map and identification of artifacts.

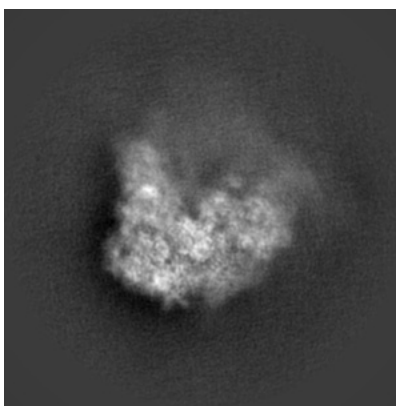
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

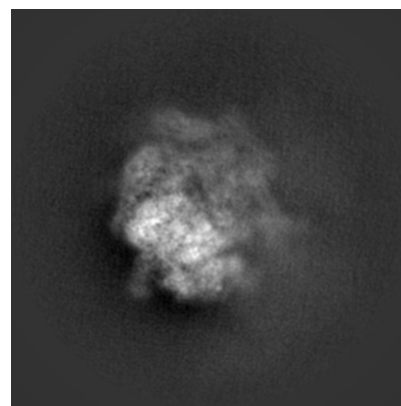
6.1.1 Primary map



X

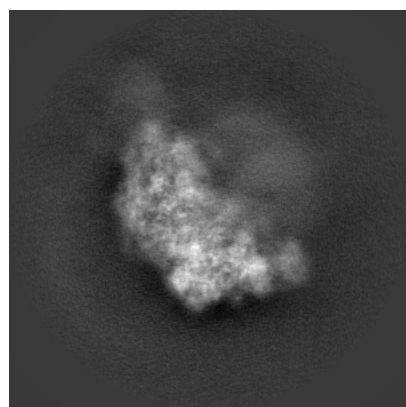


Y

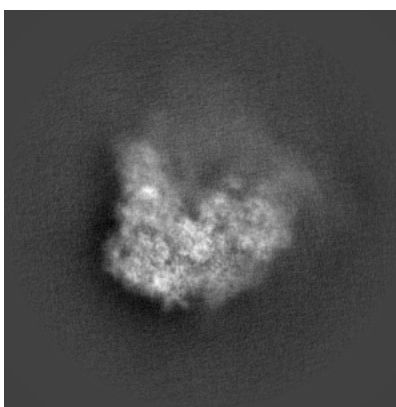


Z

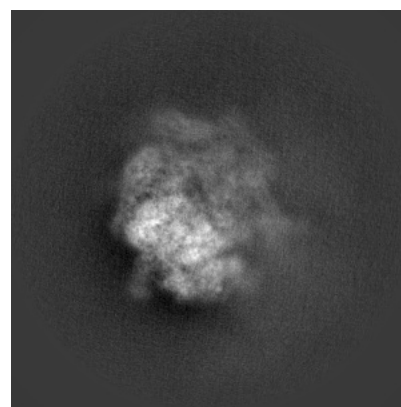
6.1.2 Raw map



X



Y

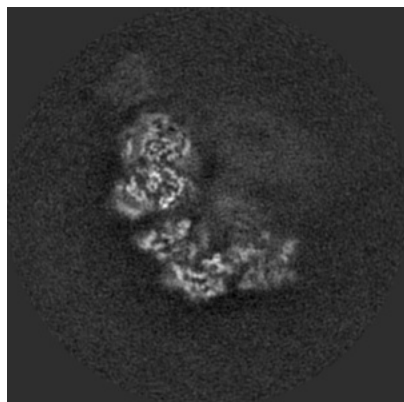


Z

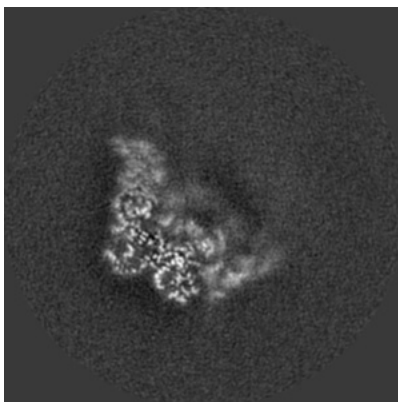
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

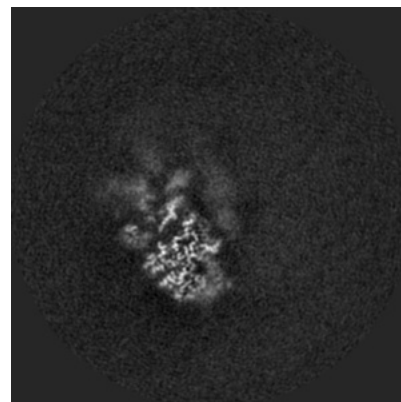
6.2.1 Primary map



X Index: 200

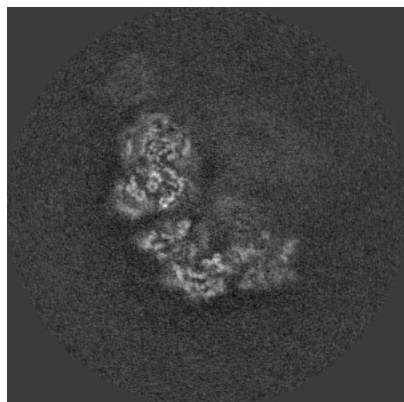


Y Index: 200

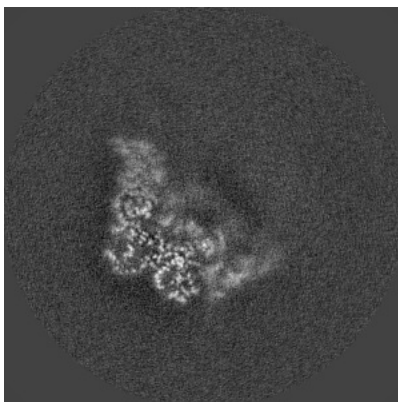


Z Index: 200

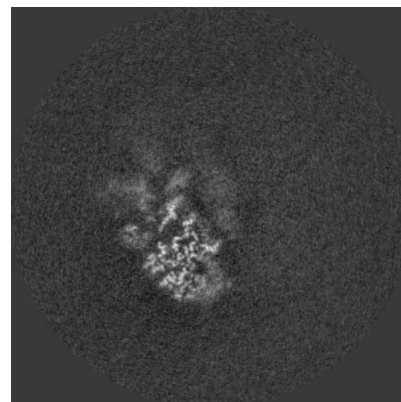
6.2.2 Raw map



X Index: 200



Y Index: 200

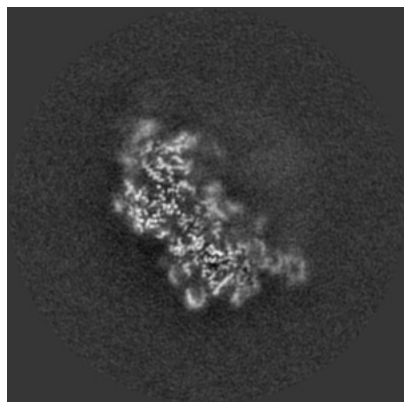


Z Index: 200

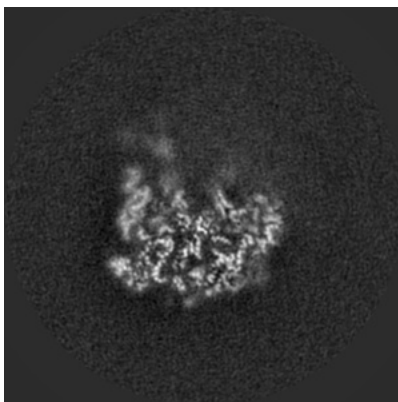
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

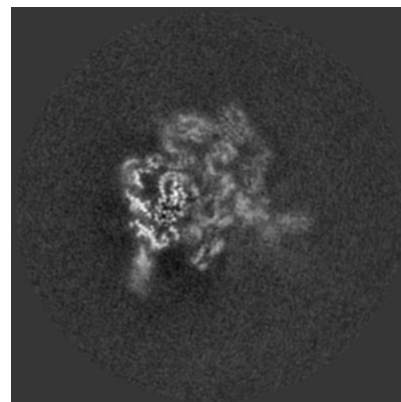
6.3.1 Primary map



X Index: 165

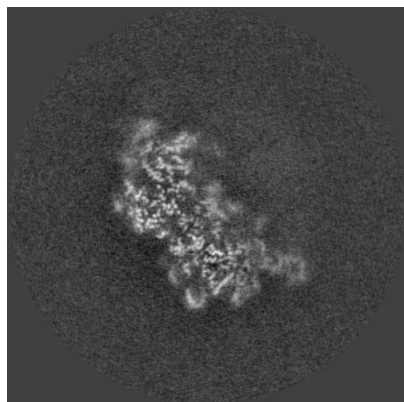


Y Index: 172

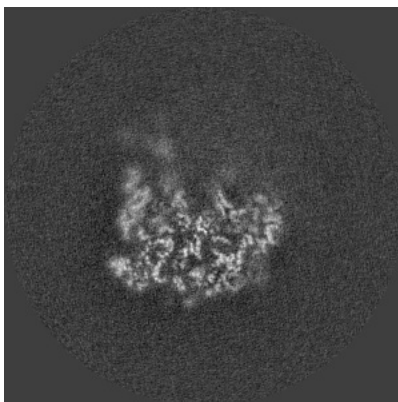


Z Index: 153

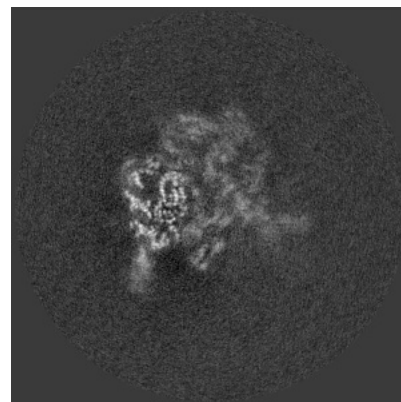
6.3.2 Raw map



X Index: 165



Y Index: 172

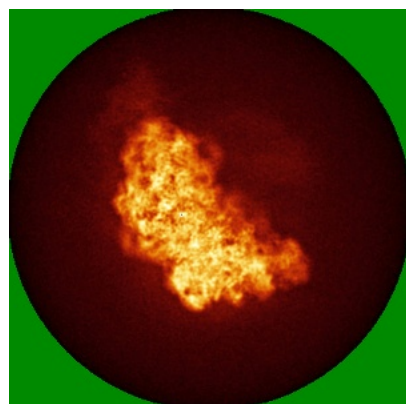


Z Index: 154

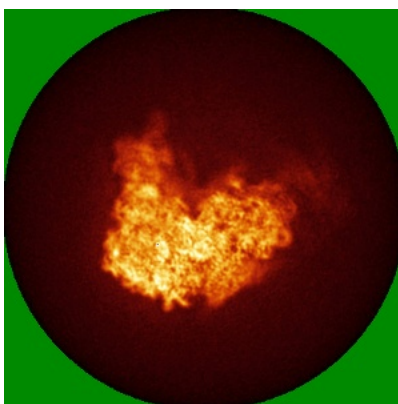
The images above show the largest variance slices of the map in three orthogonal directions.

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

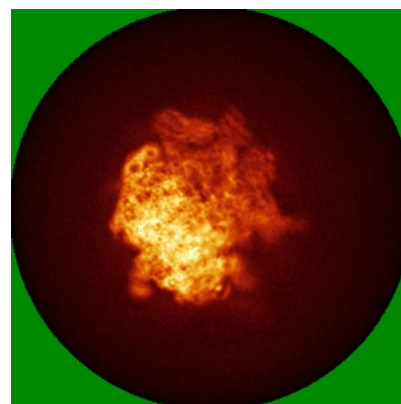
6.4.1 Primary map



X

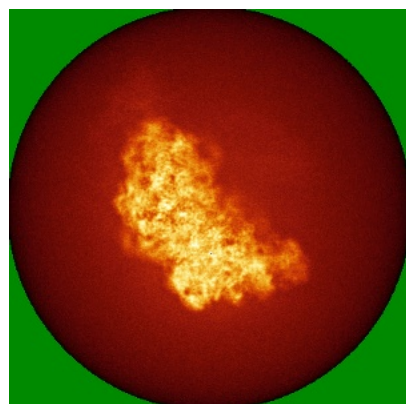


Y

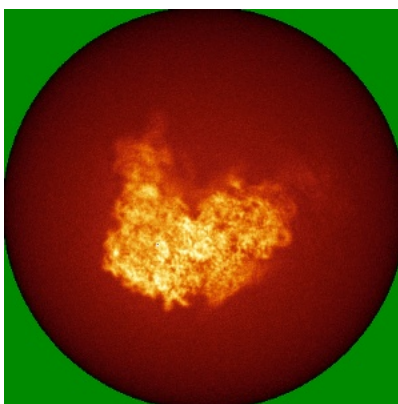


Z

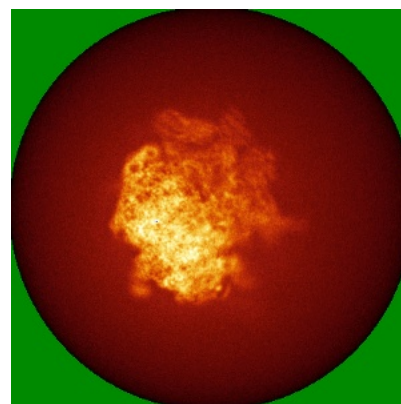
6.4.2 Raw map



X



Y

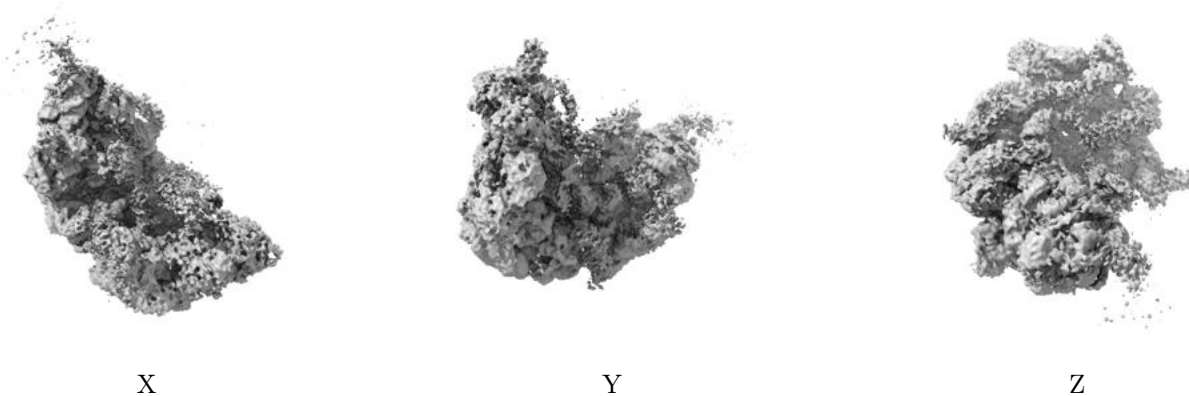


Z

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.

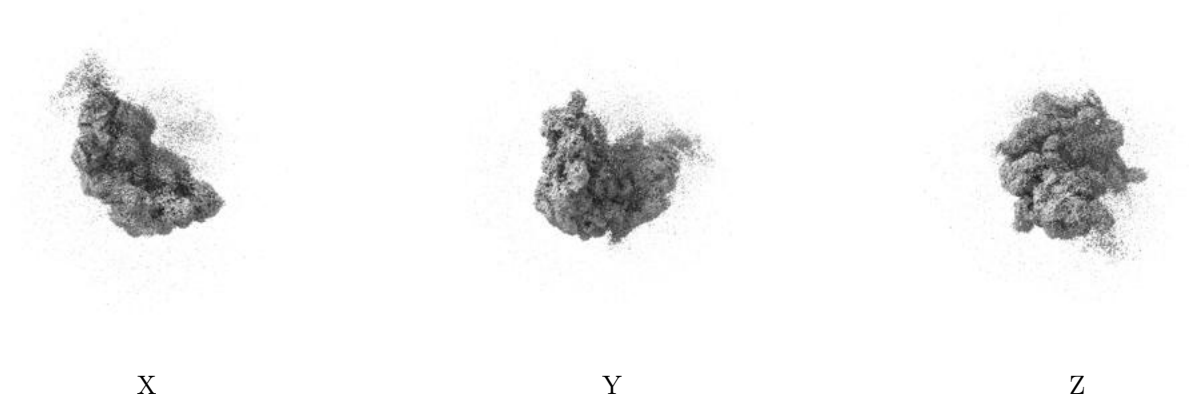
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.021. 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.

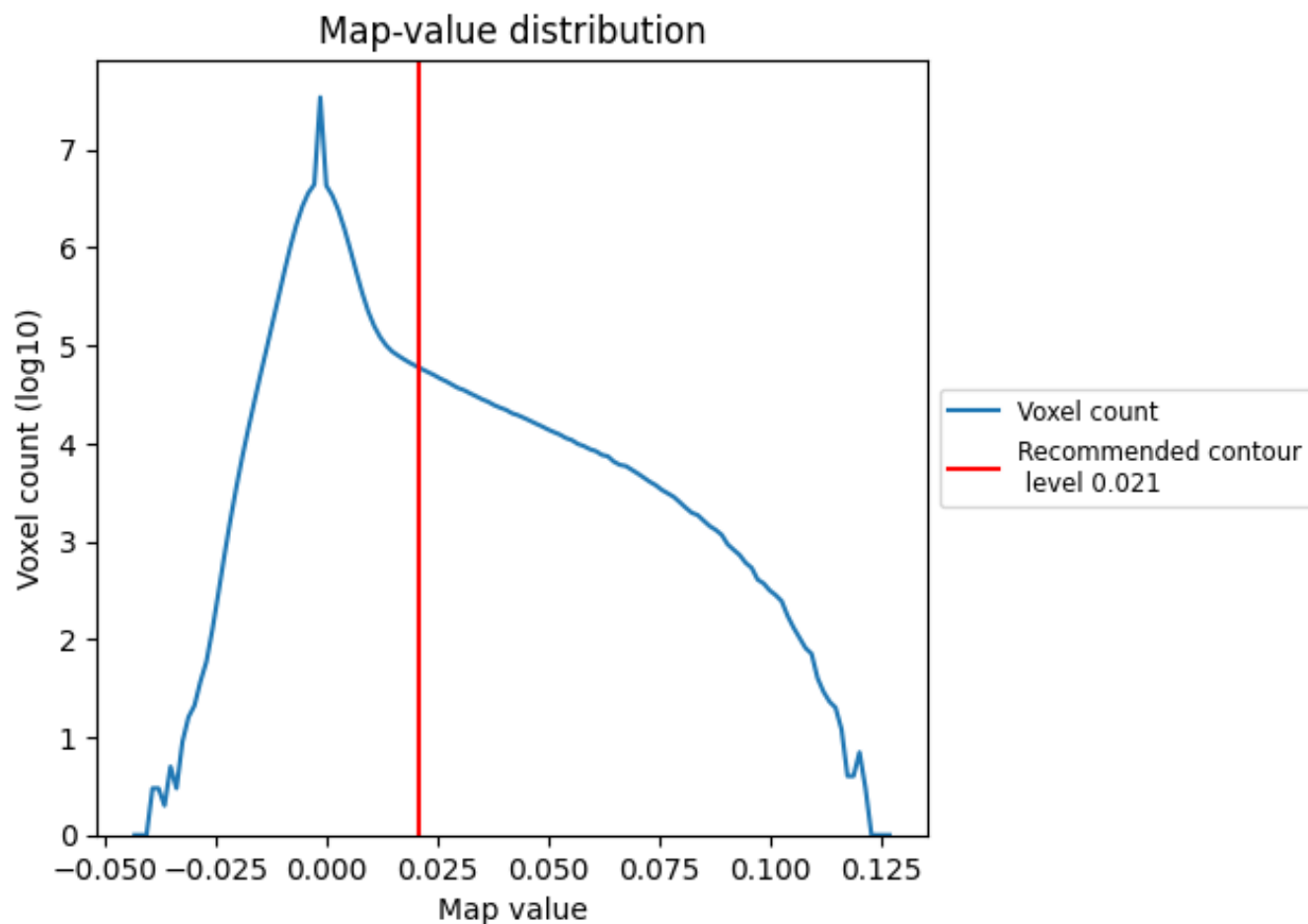
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

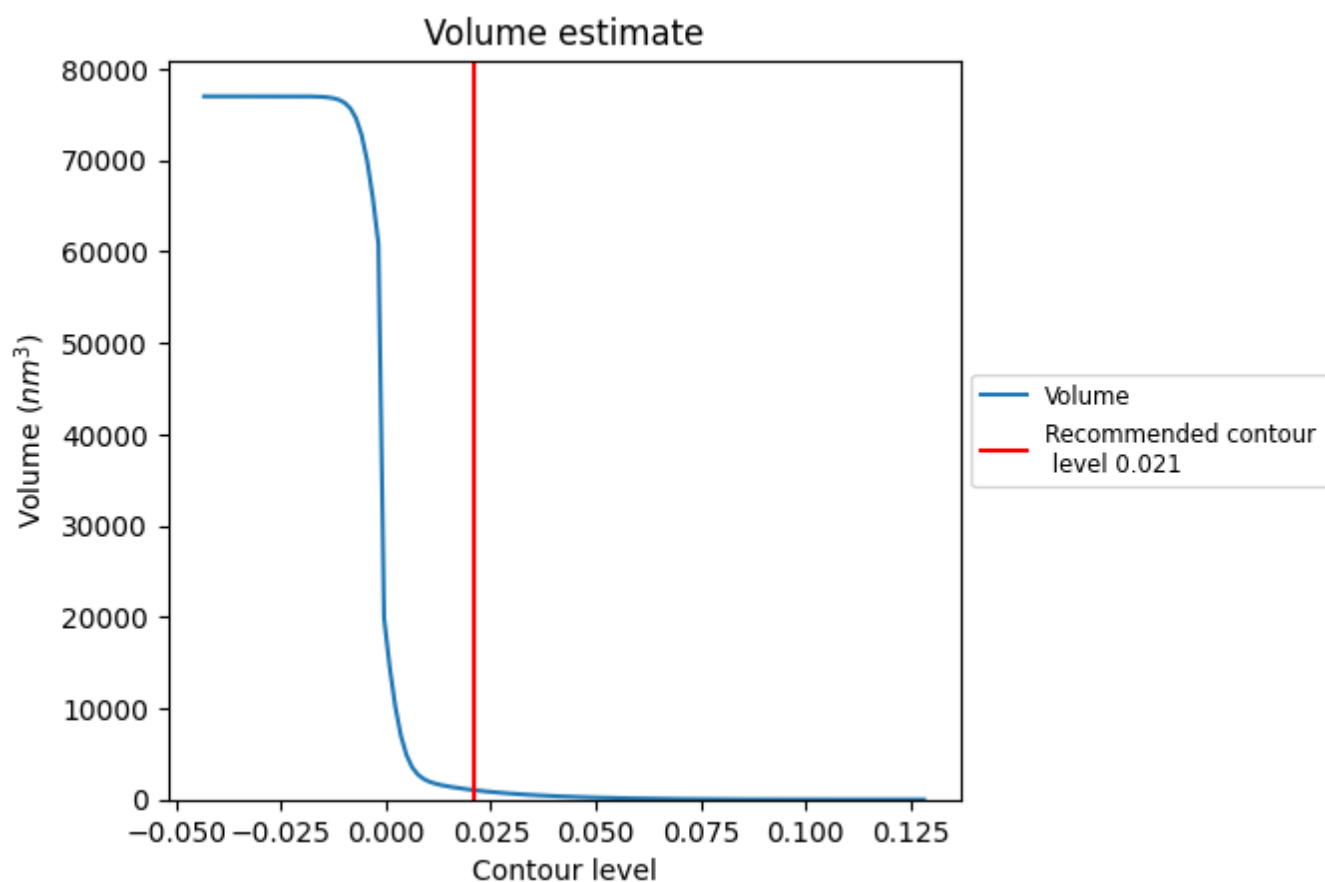
This section contains the results of statistical analysis of the map.

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.

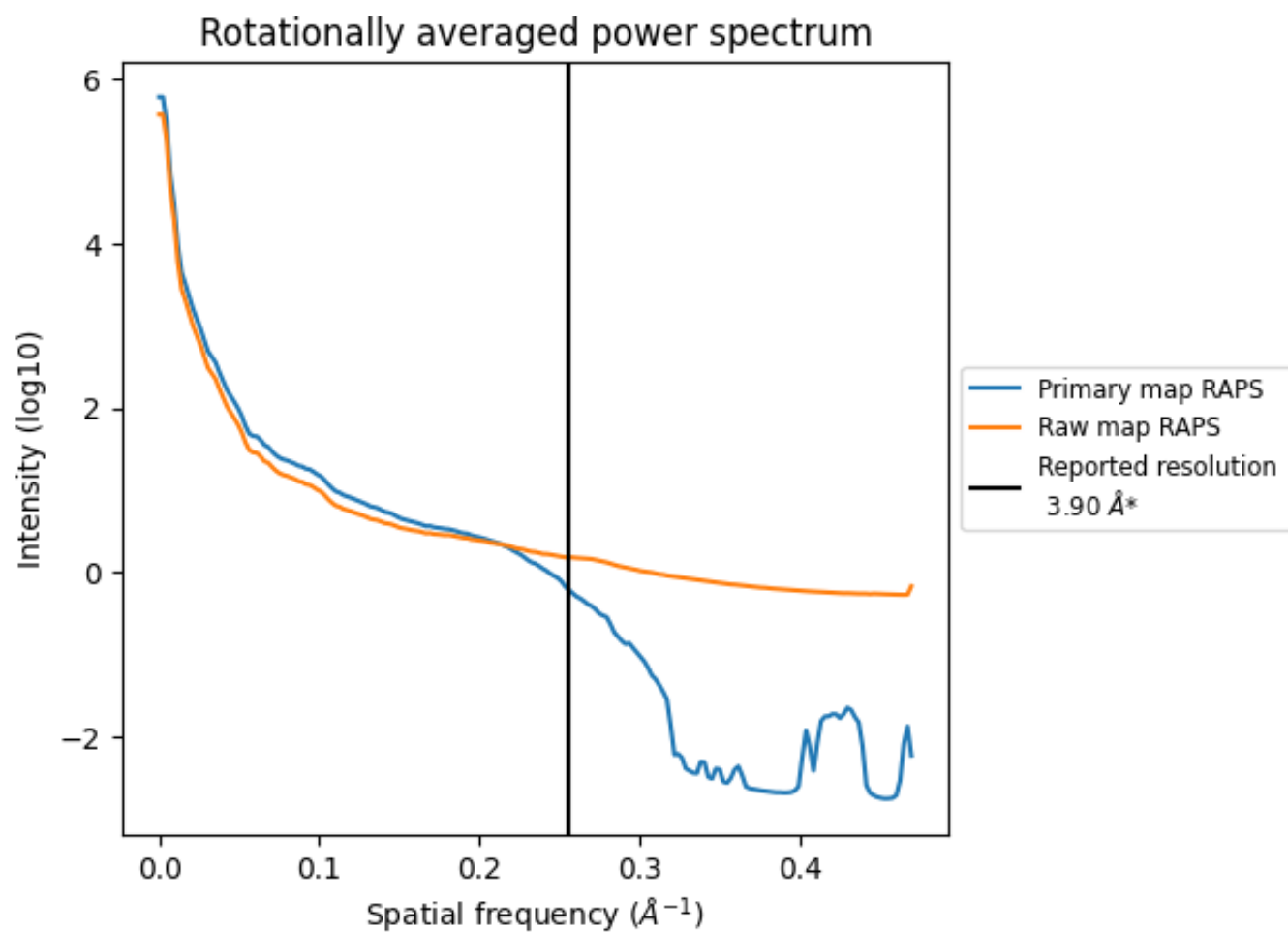
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1034 nm³; this corresponds to an approximate mass of 934 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 ⓘ

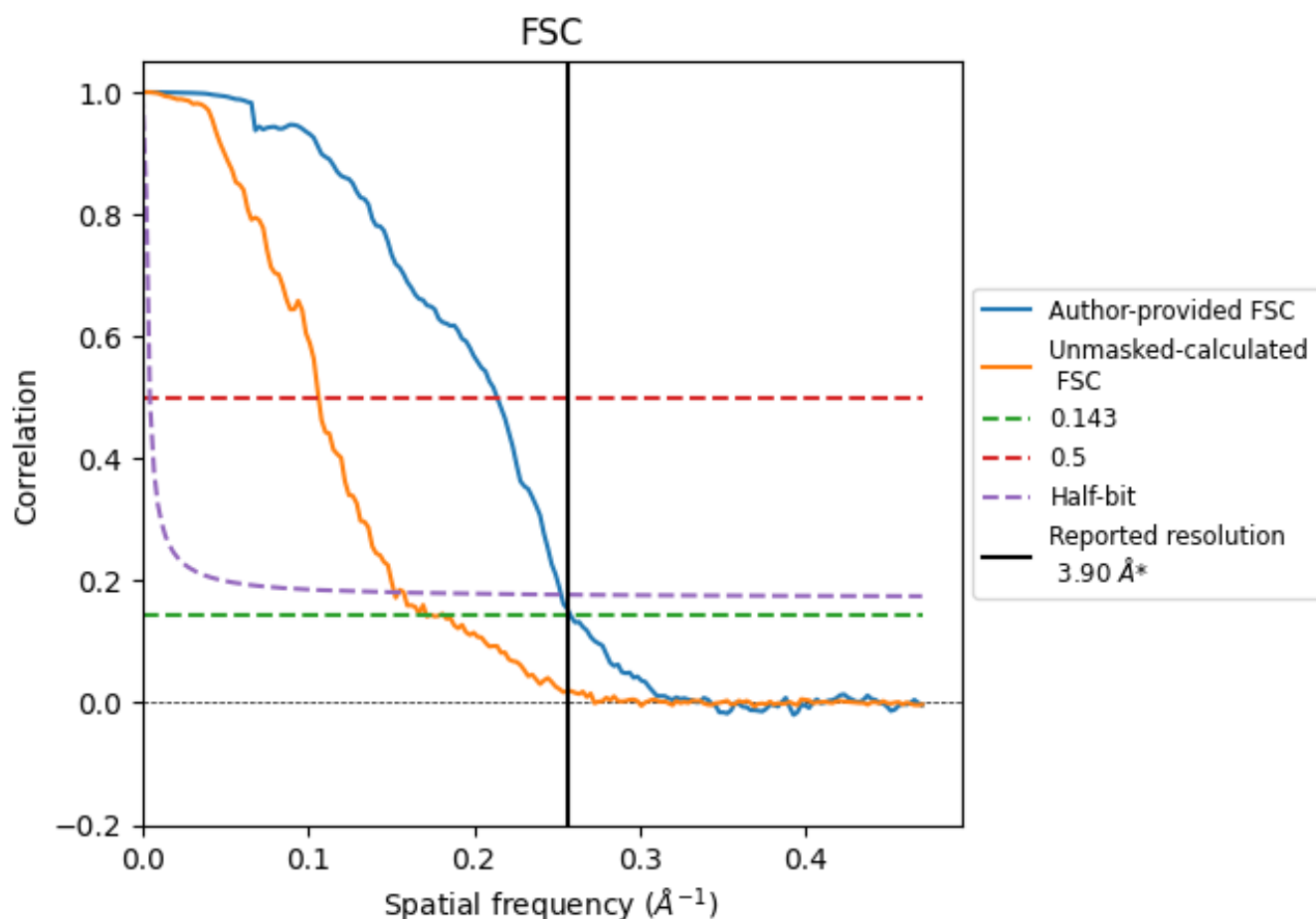


*Reported resolution corresponds to spatial frequency of 0.256 $\text{\AA}^{-1}$

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 0.256 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

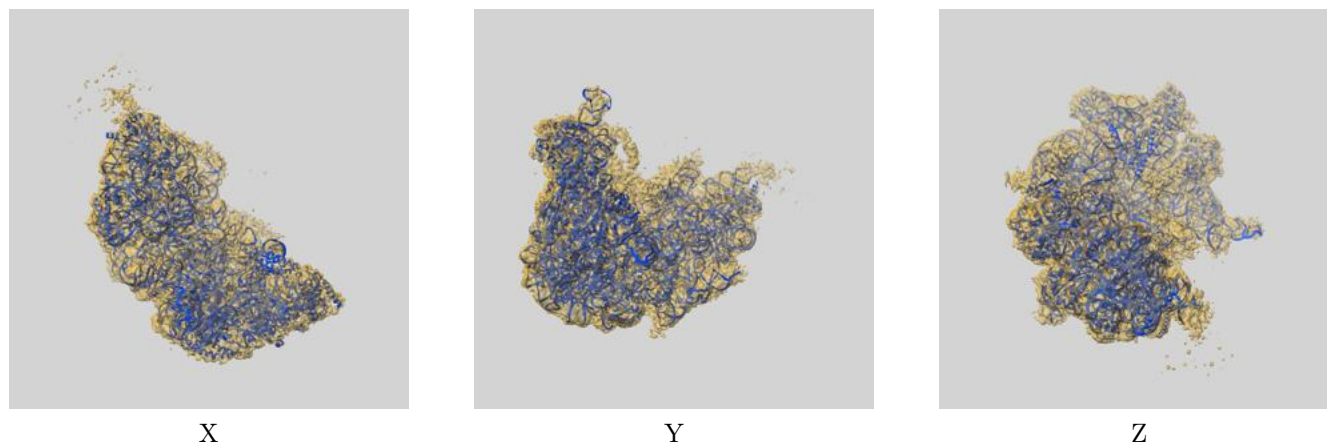
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.87	4.68	3.96
Unmasked-calculated*	5.83	9.41	6.58

*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 5.83 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

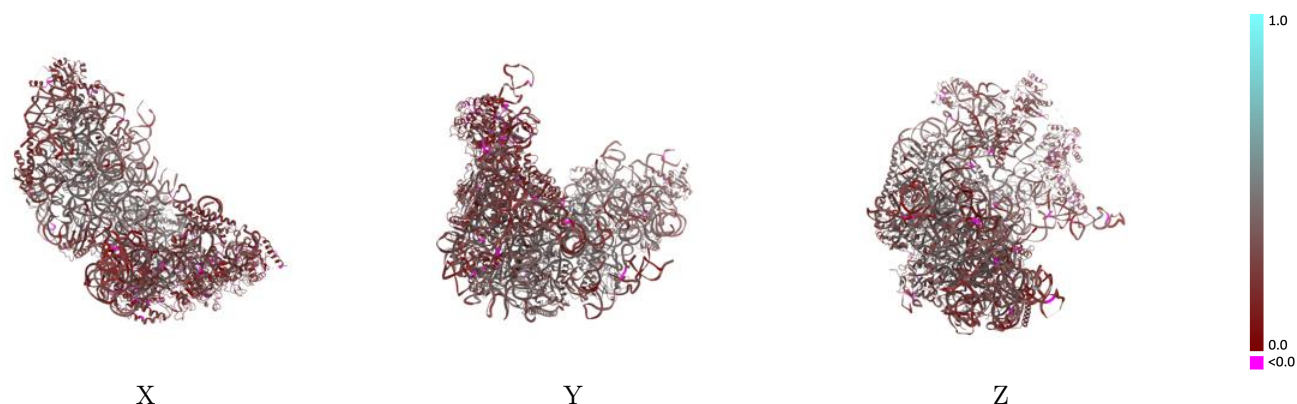
This section contains information regarding the fit between EMDB map EMD-12913 and PDB model 7OHY. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



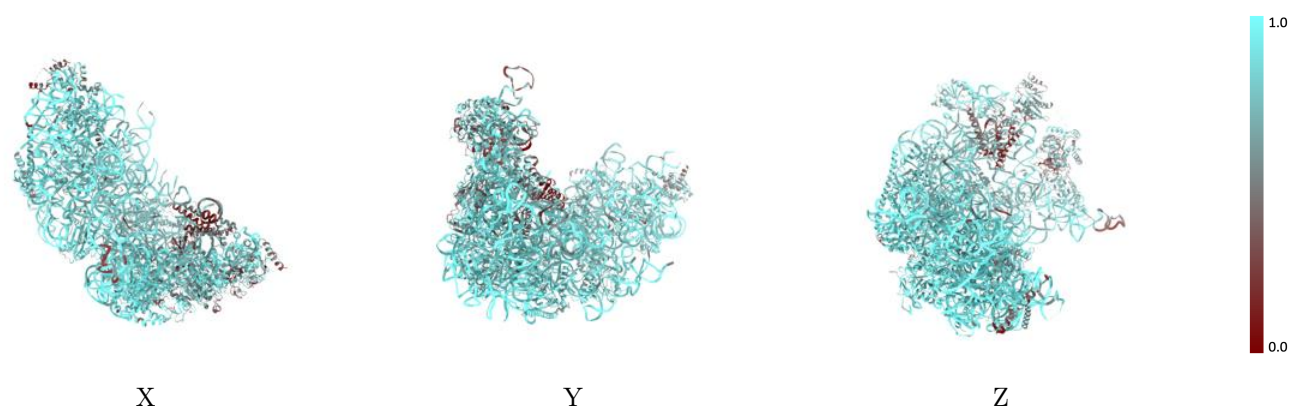
The images above show the 3D surface view of the map at the recommended contour level 0.021 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



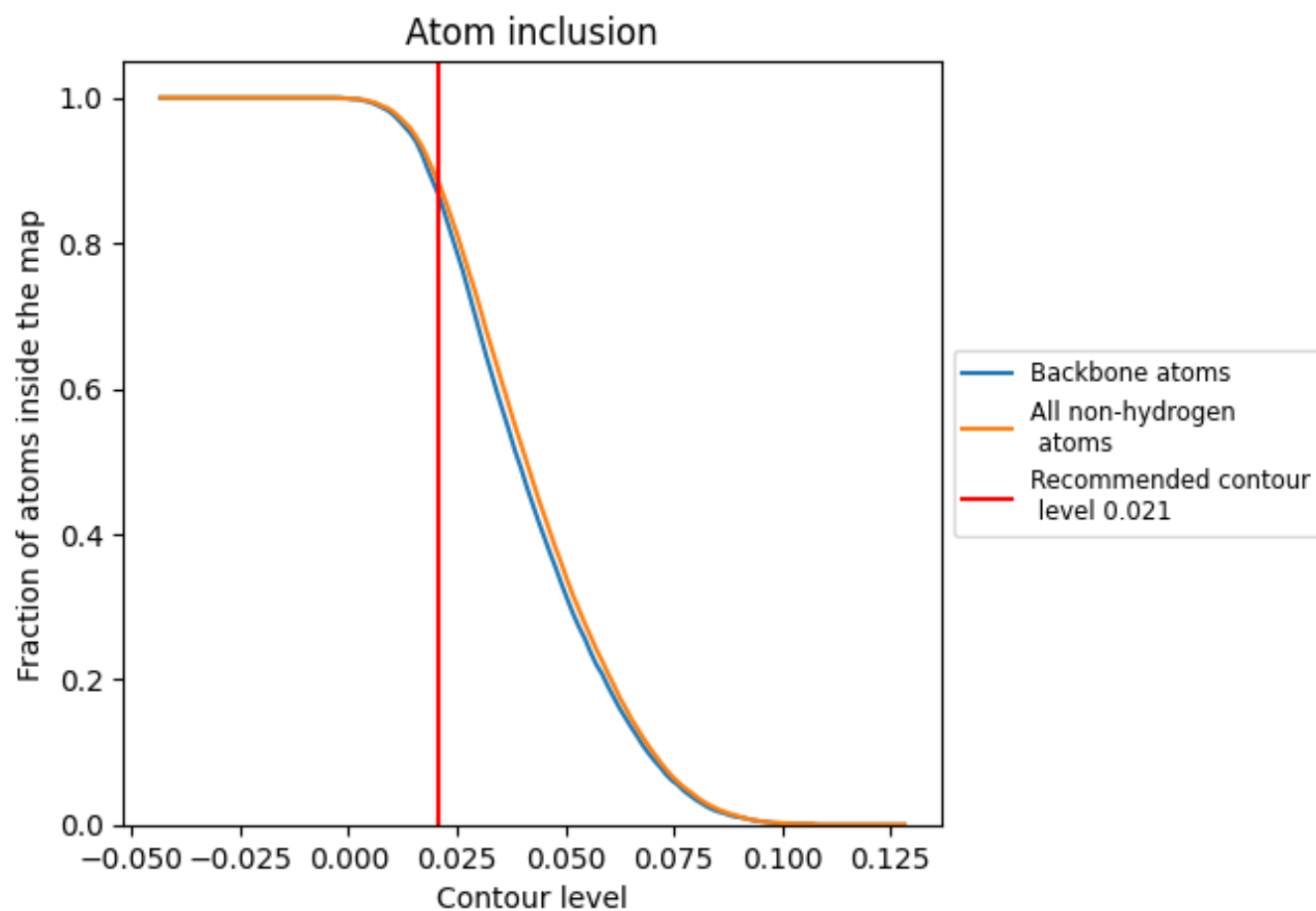
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.021).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8810	 0.3120
1	 0.9440	 0.3060
2	 0.9450	 0.3010
B	 0.8980	 0.3040
C	 0.8880	 0.4000
E	 0.8870	 0.3850
F	 0.8780	 0.3780
G	 0.5970	 0.2570
H	 0.7480	 0.3300
L	 0.9180	 0.3530
M	 0.9120	 0.3870
N	 0.8340	 0.3200
O	 0.8640	 0.3820
P	 0.7850	 0.3190
Q	 0.8950	 0.3720
S	 0.8900	 0.3650
V	 0.4940	 0.2360
W	 0.6400	 0.2340
Y	 0.9130	 0.3660
b	 0.5330	 0.2190
e	 0.8580	 0.4180
f	 0.8920	 0.4390
h	 0.7590	 0.2770
j	 0.8580	 0.3820
r	 0.5230	 0.2860
u	 0.8000	 0.1770
y	 0.7000	 0.2270

