Full wwPDB EM Validation Report ⓘ

Nov 2, 2022 – 07:17 AM EDT

PDB ID	:	5TC1
EMDB ID	:	EMD-8397
Title	:	In situ structures of the genome and genome-delivery apparatus in ssRNA bacteriophage MS2
Authors	:	Dai, X.H.; Li, Z.H.; Lai, M.; Shu, S.; Du, Y.S.; Zhou, Z.H.; Sun, R.
Deposited on	:	2016-09-13
Resolution	:	3.60 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:

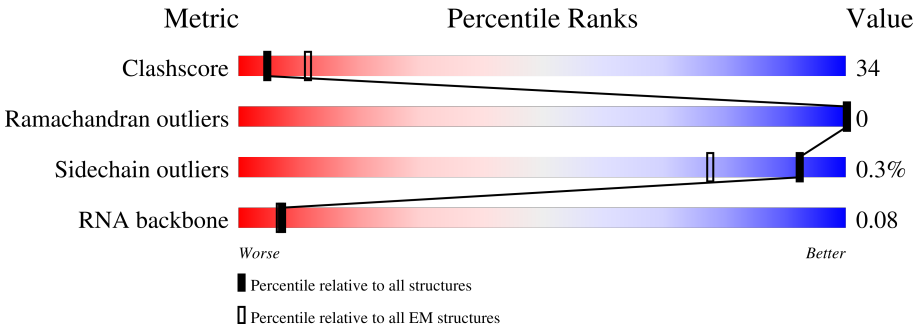
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.60 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	130	5% 89% 10%
1	B	130	80% 19%
1	C	130	8% 90% 9%
1	D	130	8% 75% 25%
1	E	130	10% 75% 25%
1	F	130	8% 74% 25%
1	G	130	5% 86% 5% 8%

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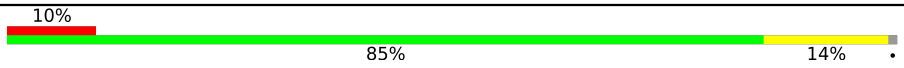
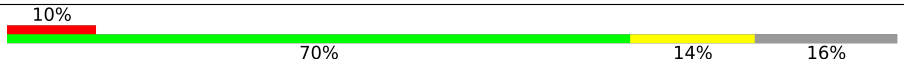
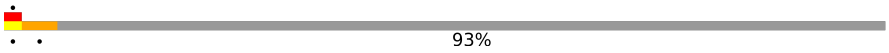
Mol	Chain	Length	Quality of chain
1	H	130	
2	M	393	
3	R	3569	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15393 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 Capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	129	Total	C	N	O	S	0	0
			965	606	165	190	4		
1	B	129	Total	C	N	O	S	0	0
			965	606	165	190	4		
1	C	129	Total	C	N	O	S	0	0
			965	606	165	190	4		
1	D	129	Total	C	N	O	S	0	0
			965	606	165	190	4		
1	E	129	Total	C	N	O	S	0	0
			965	606	165	190	4		
1	F	129	Total	C	N	O	S	0	0
			965	606	165	190	4		
1	G	119	Total	C	N	O	S	0	0
			898	565	154	175	4		
1	H	129	Total	C	N	O	S	0	0
			965	606	165	190	4		

- Molecule 2 is a protein called Maturation protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	330	Total	C	N	O	S	0	0
			2608	1664	465	468	11		

- Molecule 3 is a RNA chain called phage MS2 genome.

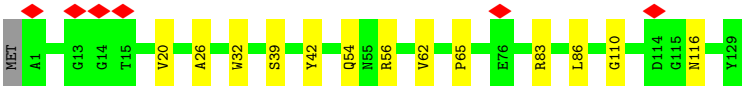
Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	242	Total	C	N	O	P	0	0
			5132	2297	897	1696	242		

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: Capsid protein

Chain A:

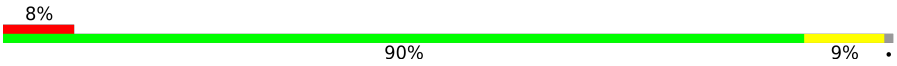


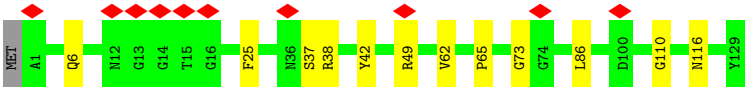
• Molecule 1: Capsid protein

Chain B:

• Molecule 1: Capsid protein

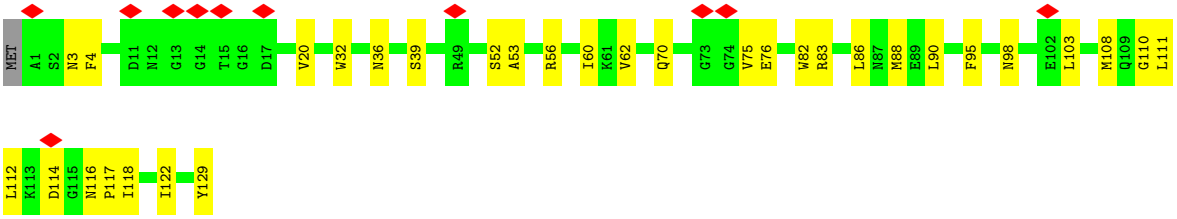
Chain C:





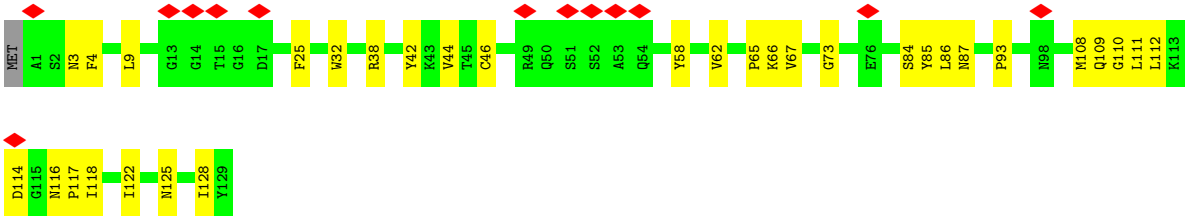
• Molecule 1: Capsid protein

Chain D:

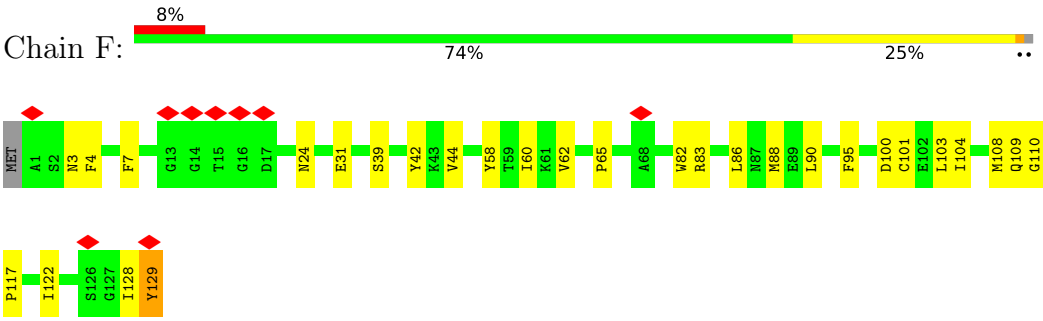


• Molecule 1: Capsid protein

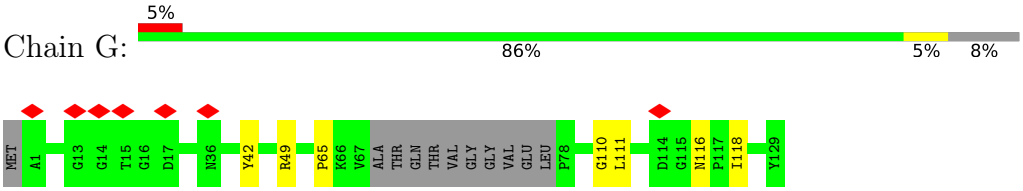
Chain E:



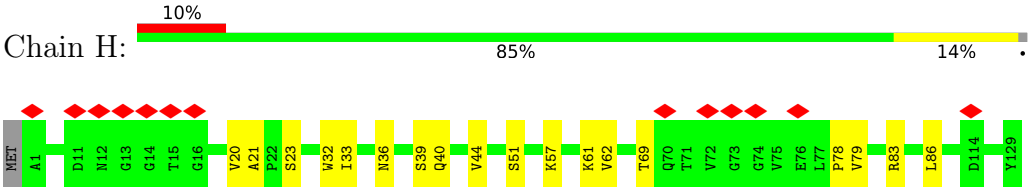
• Molecule 1: Capsid protein



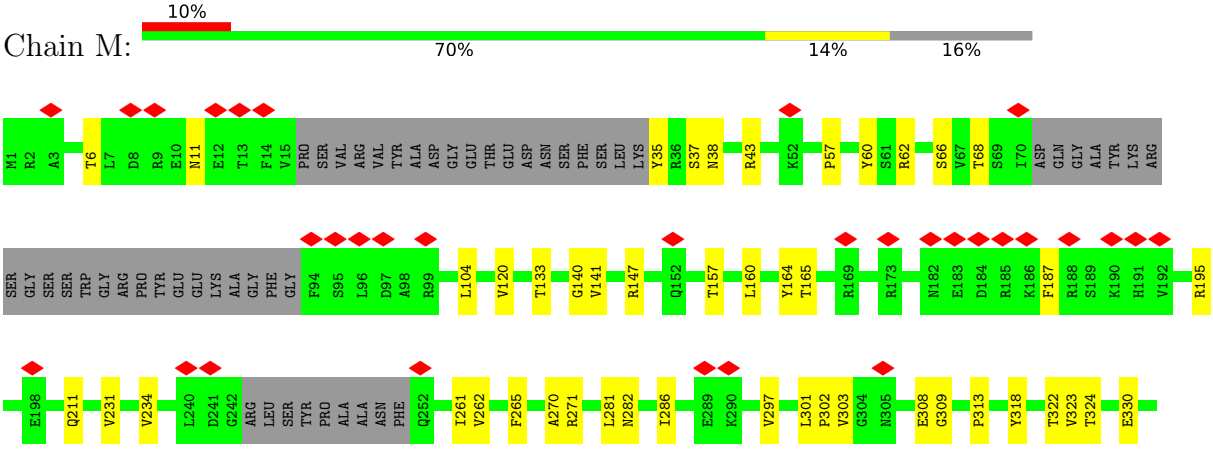
• Molecule 1: Capsid protein

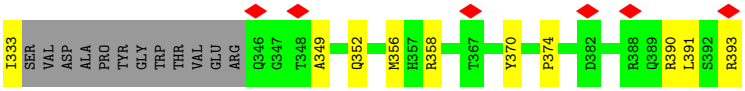


• Molecule 1: Capsid protein



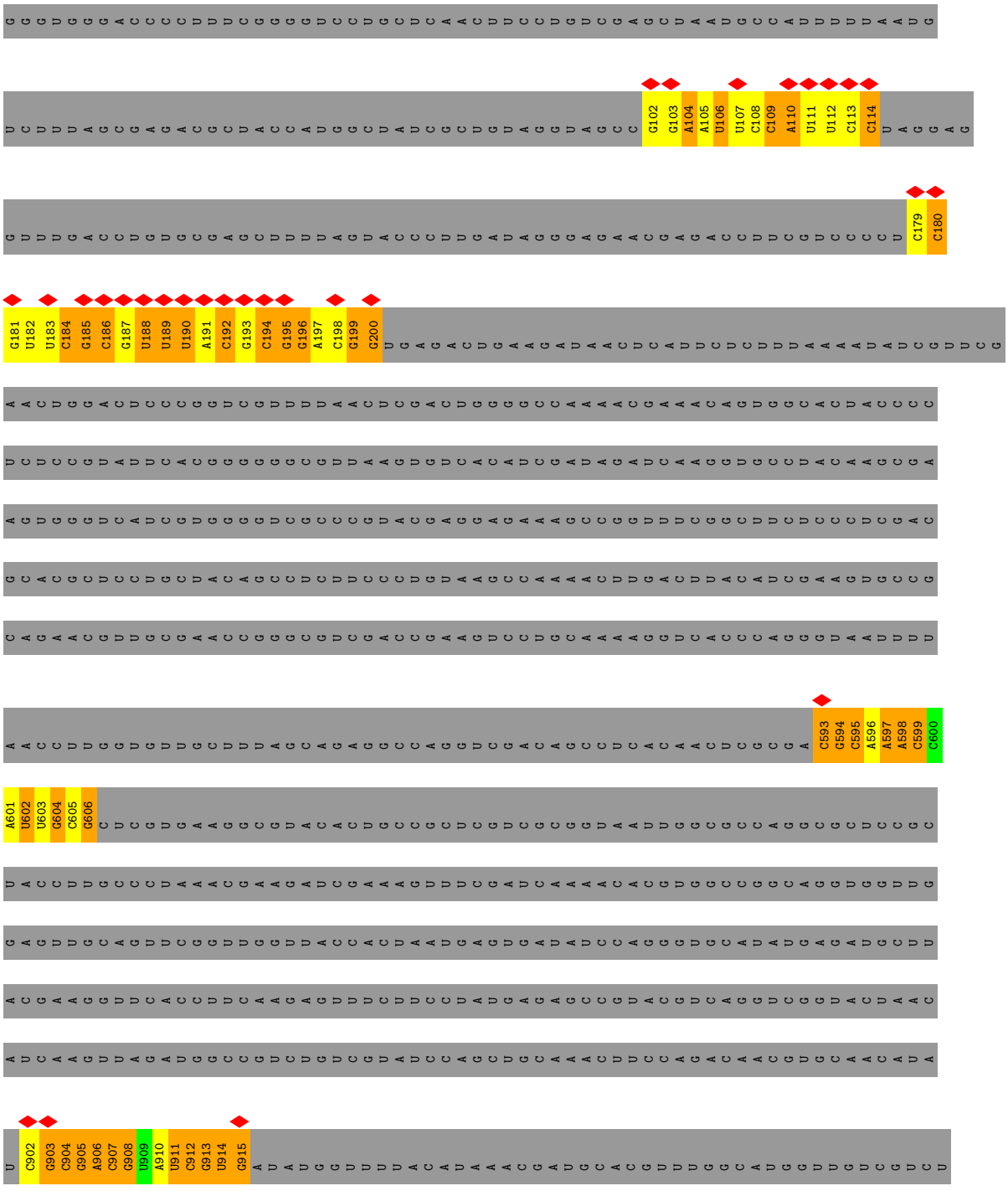
• Molecule 2: Maturation protein

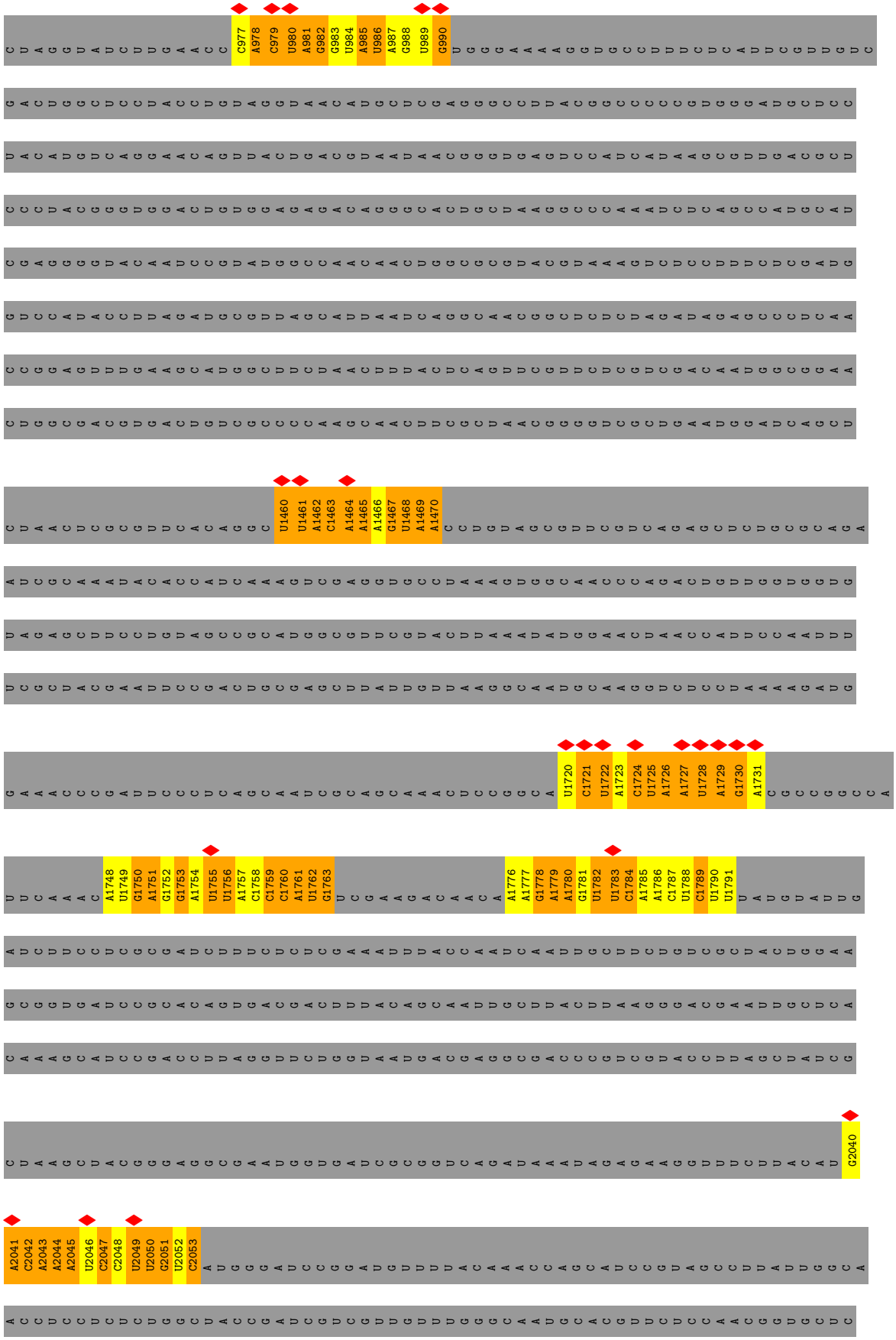




• Molecule 3: phage MS2 genome

Chain R: 93%




C977
A978
C979
U980
A981
G982
G983
U984
A985
U986
A987
G988
U989
G990
U1460
U1461
A1462
C1463
A1464
A1465
A1466
G1467
U1468
A1469
A1470
U1720
C1721
U1722
A1723
C1724
U1725
A1726
A1727
U1728
A1729
G1730
A1731
A1748
U1749
G1750
A1751
G1752
G1753
A1754
U1755
U1756
A1757
C1758
C1759
C1760
A1761
U1762
C1763
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A1777
G1778
A1779
A1780
G1781
U1782
U1783
C1784
A1785
A1786
C1787
U1788
C1789
U1790
U1791
G2040
A2041
C2042
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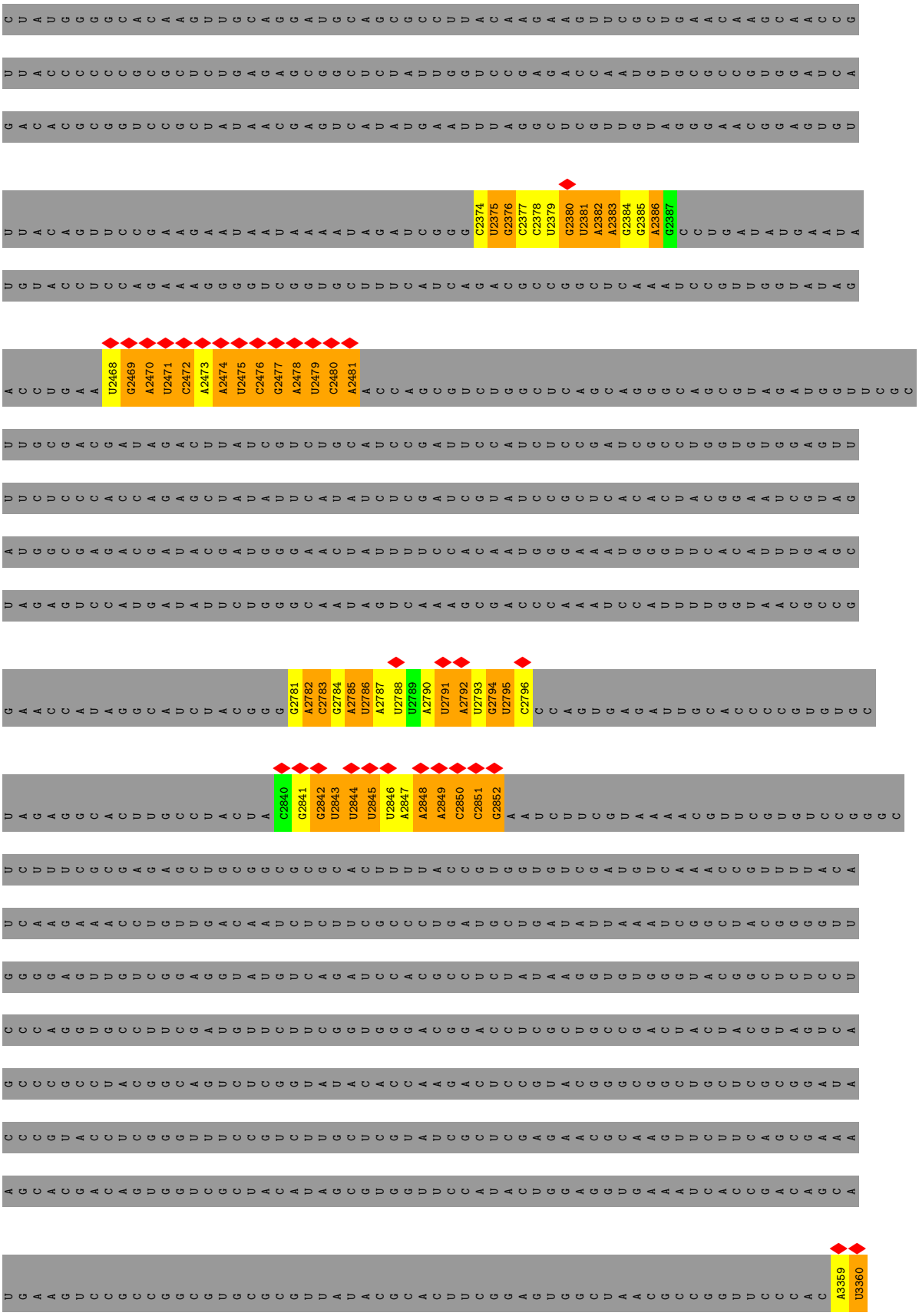
U2049
U2050
G2051
U2052
C2053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U2375
G2376
C2377
C2378
U2379
G2380
U2381
A2382
A2383
G2384
G2385
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G2387
U2468
G2469
A2470
U2471
C2472
A2473
A2474
U2475
C2476
G2477
A2478
U2479
C2480
A2481
G2781
A2782
C2783
G2784
A2785
U2786
A2787
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A2790
U2791
A2792
U2793
G2794
U2795
C2796
C2840
G2841
G2842
U2843
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A2849
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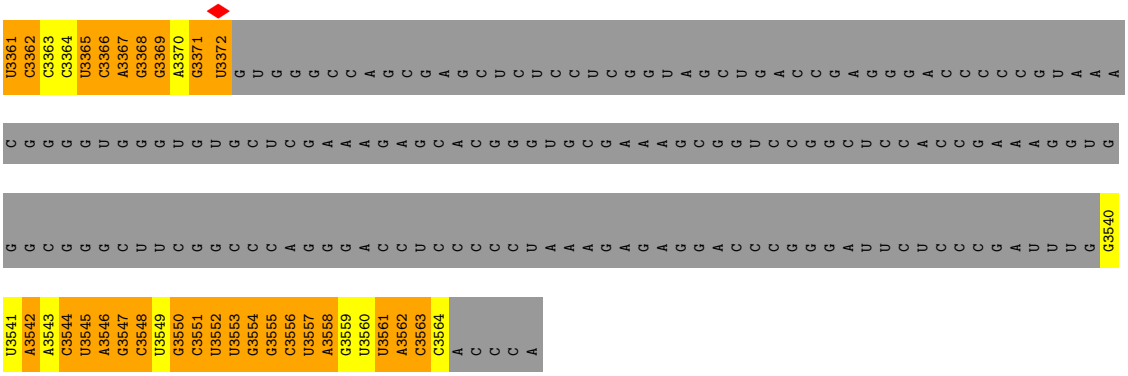
G2852
A3359
U3360


U3361 C3362 C3363 C3364 U3365 C3366 A3367 G3368 C3369 A3370 G3371 U3372
G3540
U3541 A3542 A3543 C3544 U3545 A3546 G3547 C3548 U3549 G3550 C3551 U3552 U3553 G3554 G3555 C3556 U3557 A3558 G3559 U3560 U3561 A3562 C3563 C3564

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	339718	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	47170	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	13.482	Depositor
Minimum map value	-7.572	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.0	Depositor
Map size (Å)	339.19998, 339.19998, 339.19998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	A	0.30	0/982	0.50	0/1337
1	B	0.30	0/982	0.51	0/1337
1	C	0.31	0/982	0.51	0/1337
1	D	0.35	0/982	0.52	0/1337
1	E	0.31	0/982	0.52	0/1337
1	F	0.31	0/982	0.51	0/1337
1	G	0.30	0/914	0.49	0/1241
1	H	0.29	0/982	0.50	0/1337
2	M	0.32	0/2665	0.53	1/3617 (0.0%)
3	R	0.17	0/5719	0.61	0/8867
All	All	0.27	0/16172	0.55	1/23084 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	M	104	LEU	C-N-CA	7.43	140.27	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	965	0	964	14	0
1	B	965	0	964	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	965	0	964	10	0
1	D	965	0	963	49	0
1	E	965	0	962	71	0
1	F	965	0	964	72	0
1	G	898	0	896	7	0
1	H	965	0	964	31	0
2	M	2608	0	2619	75	0
3	R	5132	0	2611	759	0
All	All	15393	0	12871	945	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 34.

All (945) 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:D:56:ARG:CZ	1:E:38:ARG:NH1	1.91	1.32
1:E:58:TYR:CE2	1:F:122:ILE:HG12	1.63	1.31
2:M:356:MET:SD	3:R:3554:G:H4'	1.71	1.29
3:R:106:U:C5	3:R:108:C:C5	2.20	1.29
1:E:114:ASP:OD1	1:F:109:GLN:NE2	1.65	1.26
1:D:76:GLU:OE1	2:M:68:THR:HG22	1.05	1.22
1:H:33:ILE:CD1	2:M:313:PRO:HG2	1.69	1.22
1:E:114:ASP:CG	1:F:109:GLN:HE22	1.45	1.20
1:D:76:GLU:OE1	2:M:68:THR:CG2	1.90	1.19
3:R:113:C:H2'	3:R:114:C:H5"	1.22	1.19
3:R:106:U:C5	3:R:108:C:C4	2.36	1.12
3:R:2851:C:H2'	3:R:2852:G:H5"	1.31	1.12
1:B:66:LYS:NZ	1:D:95:PHE:O	1.82	1.11
3:R:3558:A:C2	3:R:3559:G:C4	2.38	1.10
3:R:2792:A:H2'	3:R:2793:U:H6	1.12	1.09
3:R:981:A:N1	3:R:987:A:C2	2.20	1.09
1:D:56:ARG:NE	1:E:38:ARG:NH1	2.00	1.08
1:H:33:ILE:HD12	2:M:313:PRO:HG2	1.16	1.07
3:R:1728:U:H2'	3:R:1729:A:C8	1.90	1.06
3:R:2040:G:H2'	3:R:2041:A:C8	1.91	1.06
2:M:356:MET:SD	3:R:3554:G:C4'	2.44	1.05
3:R:2384:G:H2'	3:R:2385:G:C8	1.91	1.05
3:R:983:G:OP2	3:R:983:G:N2	1.88	1.04
3:R:2848:A:H2'	3:R:2849:A:C8	1.91	1.04
3:R:186:C:O2	3:R:193:G:N2	1.90	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:33:ILE:HD12	2:M:313:PRO:CG	1.87	1.03
3:R:185:G:N3	3:R:195:G:N2	2.06	1.03
3:R:902:C:H2'	3:R:903:G:H5'	1.39	1.03
2:M:60:TYR:OH	3:R:3553:U:OP2	1.77	1.02
1:D:56:ARG:NH2	1:E:38:ARG:HH12	1.55	1.02
1:B:108:MET:HG2	1:D:86:LEU:HD22	1.40	1.01
3:R:593:C:H2'	3:R:594:G:C8	1.95	1.01
1:D:56:ARG:CZ	1:E:38:ARG:HH12	1.60	1.01
3:R:2383:A:H2'	3:R:2384:G:H8	1.21	1.00
3:R:2787:A:C2	3:R:2792:A:N1	2.29	1.00
3:R:180:C:H2'	3:R:181:G:C8	1.94	1.00
3:R:1727:A:H2'	3:R:1728:U:C6	1.95	1.00
3:R:2050:U:H2'	3:R:2051:G:H5'	1.41	1.00
3:R:113:C:C2'	3:R:114:C:H5"	1.92	0.98
3:R:982:G:H3'	3:R:983:G:N2	1.79	0.98
3:R:982:G:H2'	3:R:983:G:H5'	1.45	0.98
2:M:358:ARG:HD3	3:R:3555:G:OP1	1.64	0.98
3:R:982:G:C2'	3:R:983:G:H5'	1.95	0.97
3:R:2849:A:C2	3:R:2850:C:N3	2.32	0.97
3:R:1468:U:O4	3:R:1469:A:N6	1.98	0.97
3:R:1722:U:H2'	3:R:1723:A:C8	1.98	0.97
3:R:593:C:O2	3:R:606:G:N2	1.98	0.97
3:R:2383:A:H2'	3:R:2384:G:C8	1.99	0.97
3:R:1782:U:C5	3:R:1784:C:C5	2.53	0.96
3:R:979:C:H2'	3:R:980:U:H6	1.26	0.96
3:R:1789:C:H2'	3:R:1790:U:C6	1.99	0.96
1:F:129:TYR:HE2	3:R:3547:G:OP2	1.47	0.96
3:R:979:C:H2'	3:R:980:U:C6	2.01	0.96
3:R:2477:G:H2'	3:R:2478:A:C8	2.02	0.95
3:R:597:A:H2'	3:R:598:A:C8	2.01	0.94
3:R:3558:A:C2	3:R:3559:G:C5	2.55	0.94
3:R:593:C:O2'	3:R:594:G:O5'	1.85	0.94
3:R:979:C:O2'	3:R:980:U:O5'	1.85	0.94
3:R:196:G:O2'	3:R:197:A:H5'	1.65	0.94
3:R:2792:A:H2'	3:R:2793:U:C6	2.02	0.94
3:R:2480:C:O2'	3:R:2481:A:O4'	1.85	0.93
1:E:66:LYS:NZ	1:F:95:PHE:O	2.02	0.93
3:R:106:U:H5	3:R:108:C:C4	1.80	0.93
3:R:2791:U:O2'	3:R:2792:A:O5'	1.85	0.93
3:R:2849:A:O2'	3:R:2850:C:O5'	1.85	0.93
3:R:2050:U:C2'	3:R:2051:G:H5'	1.99	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:2384:G:H2'	3:R:2385:G:H8	1.32	0.92
3:R:2470:A:C2	3:R:2471:U:C4	2.58	0.92
3:R:981:A:C2	3:R:987:A:C2	2.57	0.92
1:H:57:LYS:NZ	3:R:1781:G:P	2.43	0.91
3:R:106:U:C6	3:R:108:C:C5	2.58	0.91
3:R:902:C:C2'	3:R:903:G:H5'	1.99	0.91
3:R:904:C:H2'	3:R:905:G:C8	2.06	0.91
3:R:2379:U:H2'	3:R:2380:G:H5"	1.49	0.91
3:R:180:C:H2'	3:R:181:G:H8	1.31	0.91
3:R:2470:A:N3	3:R:2471:U:C5	2.38	0.91
3:R:593:C:H2'	3:R:594:G:H8	1.37	0.90
3:R:3558:A:N1	3:R:3559:G:C5	2.40	0.89
3:R:981:A:C2	3:R:987:A:H2	1.89	0.89
2:M:141:VAL:HG23	3:R:3558:A:H5'	1.54	0.89
3:R:2379:U:H2'	3:R:2380:G:C5'	2.02	0.89
2:M:43:ARG:HH12	3:R:3552:U:H5"	1.37	0.88
1:D:56:ARG:CZ	1:E:38:ARG:HH11	1.81	0.88
3:R:2782:A:N7	3:R:2783:C:N4	2.21	0.88
3:R:3370:A:H2'	3:R:3371:G:H5'	1.54	0.88
1:E:58:TYR:HE2	1:F:122:ILE:HG12	1.02	0.88
3:R:3545:U:O4	3:R:3558:A:N6	2.06	0.88
1:B:58:TYR:CE2	1:D:122:ILE:HG12	2.07	0.88
1:A:56:ARG:CZ	1:B:38:ARG:NH1	2.37	0.88
3:R:1760:C:O2'	3:R:1761:A:H5'	1.75	0.87
3:R:3560:U:O2'	3:R:3561:U:O5'	1.91	0.87
3:R:193:G:O2'	3:R:194:C:H5'	1.74	0.87
3:R:2851:C:H2'	3:R:2852:G:C5'	2.03	0.87
3:R:2477:G:H2'	3:R:2478:A:H8	1.39	0.87
3:R:1759:C:O2'	3:R:1760:C:H5'	1.75	0.87
3:R:2385:G:O2'	3:R:2386:A:H5'	1.75	0.87
3:R:3362:C:H2'	3:R:3363:C:C6	2.10	0.87
3:R:3368:G:H2'	3:R:3369:G:C8	2.08	0.87
1:E:67:VAL:HB	1:F:100:ASP:OD1	1.73	0.87
3:R:2044:A:O2'	3:R:2045:A:H5'	1.75	0.87
3:R:185:G:C2	3:R:195:G:N2	2.43	0.86
3:R:2848:A:H2'	3:R:2849:A:H8	1.34	0.86
3:R:2849:A:N3	3:R:2850:C:N3	2.23	0.86
3:R:1782:U:H5	3:R:1784:C:C5	1.92	0.86
3:R:905:G:C2	3:R:906:A:N7	2.43	0.86
1:F:129:TYR:OH	3:R:3548:C:N4	2.09	0.86
1:E:122:ILE:HG12	1:F:58:TYR:CE2	2.11	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:2470:A:N3	3:R:2471:U:C6	2.44	0.86
1:H:57:LYS:HZ2	3:R:1781:G:P	1.99	0.85
3:R:2478:A:C2	3:R:2479:U:C2	2.64	0.85
2:M:60:TYR:OH	3:R:3552:U:H3'	1.77	0.85
3:R:3370:A:C2'	3:R:3371:G:H5'	2.06	0.85
3:R:192:C:O2'	3:R:193:G:H5'	1.76	0.85
1:E:122:ILE:HG12	1:F:58:TYR:HE2	1.37	0.85
2:M:43:ARG:HH12	3:R:3552:U:C5'	1.90	0.84
3:R:1728:U:H2'	3:R:1729:A:H8	1.39	0.84
3:R:1469:A:H2'	3:R:1470:A:O4'	1.77	0.84
1:D:76:GLU:H	2:M:352:GLN:HE22	1.21	0.84
1:E:58:TYR:HE2	1:F:122:ILE:CG1	1.89	0.84
3:R:2469:G:C2	3:R:2470:A:N7	2.45	0.84
3:R:2470:A:C2	3:R:2471:U:C5	2.66	0.83
3:R:601:A:H4'	3:R:602:U:H5"	1.61	0.83
1:E:84:SER:OG	1:F:104:ILE:HD11	1.79	0.83
2:M:358:ARG:NH2	3:R:3555:G:OP1	2.12	0.83
3:R:1461:U:H2'	3:R:1462:A:H5"	1.59	0.83
1:E:67:VAL:HG21	1:F:103:LEU:HD22	1.61	0.83
3:R:2380:G:H3'	3:R:2381:U:H5'	1.61	0.83
3:R:1787:C:H2'	3:R:1788:U:C6	2.14	0.82
1:F:129:TYR:CE1	3:R:3548:C:N3	2.48	0.82
1:H:33:ILE:HD13	2:M:313:PRO:HG2	1.60	0.82
3:R:3368:G:H2'	3:R:3369:G:H8	1.43	0.82
1:H:57:LYS:NZ	3:R:1781:G:OP2	2.11	0.82
3:R:3551:C:H42	3:R:3555:G:H1	1.25	0.82
3:R:1760:C:H2'	3:R:1761:A:H8	1.44	0.82
2:M:62:ARG:NH1	3:R:3553:U:H5	1.77	0.82
3:R:186:C:O2'	3:R:187:G:H5'	1.80	0.81
3:R:2782:A:N7	3:R:2783:C:C4	2.48	0.81
1:D:56:ARG:NH2	1:E:38:ARG:NH1	2.19	0.81
3:R:2041:A:H2'	3:R:2042:C:H5'	1.63	0.81
3:R:1760:C:H2'	3:R:1761:A:C8	2.16	0.81
1:H:51:SER:HB2	3:R:1781:G:OP1	1.80	0.81
3:R:3555:G:O2'	3:R:3556:C:OP2	1.98	0.81
3:R:2480:C:H2'	3:R:2481:A:C8	2.15	0.81
3:R:2468:U:H3'	3:R:2469:G:H8	1.46	0.81
3:R:2383:A:O2'	3:R:2384:G:H5'	1.78	0.80
1:G:49:ARG:CZ	3:R:1751:A:H4'	2.11	0.80
3:R:3361:U:O4	3:R:3362:C:N4	2.14	0.80
3:R:3558:A:N1	3:R:3559:G:C6	2.48	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:75:VAL:HG22	2:M:330:GLU:OE2	1.81	0.80
3:R:1788:U:H2'	3:R:1789:C:H5'	1.64	0.80
3:R:103:G:O2'	3:R:104:A:H5'	1.82	0.80
3:R:184:C:H2'	3:R:185:G:H8	1.46	0.80
3:R:1729:A:H2'	3:R:1730:G:C8	2.17	0.80
1:E:3:ASN:O	1:F:117:PRO:HB3	1.82	0.80
3:R:112:U:O2'	3:R:113:C:H5'	1.81	0.80
3:R:2792:A:C2'	3:R:2793:U:H6	1.94	0.79
3:R:3547:G:OP2	3:R:3547:G:N2	2.14	0.79
1:H:79:VAL:O	2:M:301:LEU:HD13	1.83	0.79
2:M:43:ARG:NH1	3:R:3552:U:H5"	1.98	0.79
1:F:129:TYR:HH	3:R:3548:C:N4	1.81	0.78
3:R:1727:A:H2'	3:R:1728:U:C5	2.17	0.78
3:R:2468:U:H3'	3:R:2469:G:C8	2.18	0.78
3:R:2791:U:H4'	3:R:2792:A:OP1	1.83	0.78
3:R:182:U:O2'	3:R:183:U:H5'	1.84	0.78
3:R:1782:U:H5	3:R:1784:C:C4	2.01	0.78
1:B:108:MET:HG2	1:D:86:LEU:CD2	2.13	0.78
3:R:2795:U:O2'	3:R:2796:C:H5'	1.83	0.78
3:R:983:G:H21	3:R:983:G:P	2.08	0.77
3:R:1788:U:C2'	3:R:1789:C:H5'	2.14	0.77
3:R:2382:A:H4'	3:R:2383:A:O5'	1.84	0.77
1:B:108:MET:CG	1:D:86:LEU:HD22	2.14	0.77
1:E:128:ILE:HG21	1:F:4:PHE:CD1	2.19	0.77
3:R:2472:C:N4	3:R:2477:G:O6	2.17	0.77
3:R:179:C:H2'	3:R:180:C:H5'	1.65	0.77
2:M:356:MET:SD	3:R:3554:G:C5'	2.72	0.77
3:R:1752:G:H2'	3:R:1753:G:H5'	1.65	0.77
3:R:2843:U:H2'	3:R:2844:U:C6	2.20	0.77
3:R:593:C:H4'	3:R:594:G:OP1	1.84	0.77
3:R:3368:G:C2	3:R:3369:G:C5	2.73	0.77
3:R:979:C:H4'	3:R:980:U:OP1	1.84	0.76
3:R:104:A:H2'	3:R:105:A:C8	2.21	0.76
3:R:185:G:C2	3:R:195:G:C2	2.72	0.76
3:R:3362:C:O2'	3:R:3363:C:H5'	1.86	0.76
3:R:180:C:O2	3:R:199:G:N2	2.18	0.76
1:E:128:ILE:HG21	1:F:4:PHE:HD1	1.51	0.75
3:R:979:C:C2'	3:R:980:U:H6	1.99	0.75
3:R:2849:A:H4'	3:R:2850:C:OP1	1.84	0.75
1:E:128:ILE:CG2	1:F:4:PHE:CD1	2.69	0.75
3:R:3361:U:H2'	3:R:3362:C:H5'	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:21:ALA:HB3	2:M:370:TYR:HE2	1.50	0.75
1:F:129:TYR:CE1	3:R:3548:C:C2	2.74	0.75
3:R:2471:U:C3'	3:R:2472:C:H5"	2.17	0.75
3:R:2786:U:H2'	3:R:2787:A:C8	2.22	0.75
2:M:141:VAL:CG2	3:R:3558:A:H5'	2.16	0.75
1:E:128:ILE:CG2	1:F:4:PHE:HD1	2.00	0.75
3:R:3558:A:O2'	3:R:3559:G:H5'	1.87	0.75
3:R:2469:G:N1	3:R:2470:A:N7	2.35	0.74
3:R:2479:U:H2'	3:R:2480:C:C5	2.21	0.74
1:A:56:ARG:NH2	1:B:38:ARG:HH12	1.84	0.74
1:E:125:ASN:OD1	1:F:101:CYS:SG	2.45	0.74
3:R:2849:A:H2'	3:R:2850:C:C5	2.22	0.74
3:R:2051:G:N2	3:R:2052:U:O2	2.20	0.74
3:R:2045:A:H2'	3:R:2045:A:N3	2.00	0.74
3:R:907:C:C5	3:R:908:G:C2	2.76	0.74
3:R:3362:C:N3	3:R:3370:A:C2	2.55	0.74
3:R:3546:A:C6	3:R:3547:G:N7	2.56	0.74
2:M:60:TYR:CE1	3:R:3552:U:C2	2.76	0.74
3:R:3557:U:H5"	3:R:3558:A:H4'	1.69	0.74
1:H:36:ASN:OD1	2:M:270:ALA:HB3	1.88	0.73
3:R:2785:A:O2'	3:R:2786:U:H5'	1.87	0.73
3:R:1461:U:C2'	3:R:1462:A:H5"	2.17	0.73
1:H:51:SER:CB	3:R:1781:G:OP1	2.36	0.73
3:R:1780:A:O2'	3:R:1781:G:H5'	1.88	0.73
1:F:129:TYR:CE2	3:R:3547:G:OP2	2.37	0.73
3:R:3551:C:N4	3:R:3555:G:H1	1.86	0.73
3:R:1461:U:H2'	3:R:1462:A:C5'	2.19	0.72
3:R:1755:U:O2'	3:R:1756:U:OP1	2.05	0.72
1:B:97:THR:HG22	1:C:37:SER:OG	1.89	0.72
3:R:594:G:N2	3:R:595:C:O2	2.22	0.72
3:R:597:A:H2'	3:R:598:A:H8	1.55	0.72
1:H:36:ASN:OD1	2:M:270:ALA:CB	2.38	0.72
3:R:2478:A:C2	3:R:2479:U:N3	2.58	0.72
3:R:182:U:H2'	3:R:183:U:C6	2.25	0.71
3:R:1729:A:O2'	3:R:1730:G:OP1	2.08	0.71
3:R:2051:G:C2	3:R:2052:U:C2	2.78	0.71
3:R:3557:U:H5'	3:R:3558:A:O4'	1.90	0.71
3:R:179:C:C2'	3:R:180:C:H5'	2.21	0.71
3:R:2474:A:O2'	3:R:2475:U:H5'	1.90	0.71
2:M:393:ARG:NH2	3:R:1776:A:O2'	2.23	0.71
3:R:2476:C:H4'	3:R:2477:G:H5"	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:86:LEU:HD22	1:F:108:MET:HG2	1.70	0.71
2:M:60:TYR:CZ	3:R:3552:U:H3'	2.25	0.71
3:R:597:A:O2'	3:R:598:A:O4'	2.07	0.71
3:R:2844:U:O2'	3:R:2845:U:OP1	2.08	0.71
1:H:21:ALA:HB3	2:M:370:TYR:CE2	2.26	0.70
1:E:25:PHE:CE2	3:R:3547:G:N2	2.59	0.70
3:R:2374:C:C2'	3:R:2375:U:H5'	2.20	0.70
3:R:1790:U:O2'	3:R:1791:U:H5'	1.92	0.70
3:R:906:A:O2'	3:R:907:C:O4'	2.10	0.70
3:R:2473:A:H1'	3:R:2477:G:N2	2.07	0.70
3:R:2851:C:O2'	3:R:2852:G:OP1	2.07	0.70
2:M:141:VAL:HG23	3:R:3558:A:C5'	2.20	0.70
3:R:3361:U:C4	3:R:3362:C:C5	2.80	0.70
3:R:3559:G:C2	3:R:3560:U:N3	2.60	0.70
1:E:116:ASN:OD1	1:F:7:PHE:HB2	1.92	0.70
3:R:605:C:O2'	3:R:606:G:H5'	1.92	0.69
3:R:1722:U:H3	3:R:1729:A:H2	1.40	0.69
3:R:2374:C:O2'	3:R:2375:U:H5'	1.92	0.69
3:R:2786:U:H2'	3:R:2787:A:H8	1.55	0.69
3:R:2479:U:O2'	3:R:2480:C:OP1	2.08	0.69
3:R:1752:G:H4'	3:R:1752:G:OP2	1.90	0.69
1:A:56:ARG:NH2	1:B:38:ARG:NH1	2.40	0.69
3:R:184:C:H2'	3:R:185:G:C8	2.26	0.69
3:R:981:A:C6	3:R:987:A:C2	2.80	0.69
3:R:198:C:H2'	3:R:199:G:H5'	1.73	0.69
3:R:1789:C:O2'	3:R:1790:U:H5'	1.93	0.69
3:R:180:C:O2'	3:R:181:G:H5'	1.93	0.69
1:E:87:ASN:O	1:F:88:MET:HA	1.93	0.69
3:R:2471:U:H3'	3:R:2472:C:H5"	1.75	0.69
3:R:3558:A:C6	3:R:3559:G:C6	2.80	0.68
3:R:187:G:O2'	3:R:188:U:H5'	1.93	0.68
3:R:913:G:H2'	3:R:914:U:C6	2.28	0.68
3:R:1460:U:O2'	3:R:1461:U:OP1	2.08	0.68
1:F:129:TYR:OH	3:R:3548:C:C4	2.46	0.68
3:R:2478:A:N1	3:R:2479:U:N3	2.42	0.68
1:B:1:ALA:N	1:C:6:GLN:OE1	2.17	0.68
3:R:187:G:C2	3:R:190:U:C5	2.82	0.68
3:R:2849:A:H2'	3:R:2850:C:C6	2.29	0.68
3:R:1462:A:C6	3:R:1469:A:N1	2.62	0.68
3:R:106:U:C5	3:R:108:C:C6	2.82	0.68
3:R:199:G:H2'	3:R:200:G:C8	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:1789:C:H2'	3:R:1790:U:H6	1.55	0.68
1:B:125:ASN:HB3	1:E:38:ARG:HD3	1.76	0.68
1:G:49:ARG:HD3	3:R:1751:A:O2'	1.94	0.68
3:R:1782:U:O2'	3:R:1783:U:OP1	2.06	0.68
3:R:597:A:C2	3:R:598:A:C4	2.82	0.67
3:R:2783:C:O2'	3:R:2785:A:OP1	2.11	0.67
3:R:2040:G:H2'	3:R:2041:A:H8	1.54	0.67
3:R:2041:A:C2'	3:R:2042:C:H5'	2.25	0.67
3:R:2479:U:O2'	3:R:2480:C:H5'	1.94	0.67
3:R:112:U:H2'	3:R:113:C:C6	2.30	0.67
3:R:111:U:H2'	3:R:112:U:C6	2.30	0.67
1:B:58:TYR:HE2	1:D:122:ILE:HG12	1.59	0.66
1:F:129:TYR:CZ	3:R:3548:C:C4	2.83	0.66
3:R:102:G:H2'	3:R:103:G:C8	2.30	0.66
3:R:3541:U:H6	3:R:3541:U:O5'	1.78	0.66
3:R:185:G:N1	3:R:186:C:C4	2.64	0.66
3:R:3367:A:H4'	3:R:3368:G:O5'	1.95	0.66
3:R:113:C:H6	3:R:113:C:O5'	1.79	0.66
3:R:1783:U:O2'	3:R:1784:C:OP1	2.08	0.66
3:R:3363:C:O5'	3:R:3363:C:H6	1.79	0.66
1:E:25:PHE:CZ	3:R:3547:G:N2	2.62	0.65
3:R:605:C:C2'	3:R:606:G:H5'	2.26	0.65
3:R:905:G:C2	3:R:906:A:C5	2.84	0.65
3:R:1790:U:H6	3:R:1790:U:O5'	1.80	0.65
1:F:129:TYR:HE2	3:R:3547:G:P	2.19	0.65
3:R:989:U:O5'	3:R:989:U:H6	1.79	0.65
3:R:1782:U:C5	3:R:1784:C:C4	2.82	0.65
3:R:2480:C:O2'	3:R:2481:A:O5'	2.13	0.65
1:E:42:TYR:OH	1:F:103:LEU:HD21	1.96	0.65
3:R:192:C:O5'	3:R:192:C:H6	1.78	0.65
3:R:3361:U:H2'	3:R:3362:C:C5'	2.26	0.65
3:R:3558:A:C2	3:R:3559:G:N9	2.65	0.65
3:R:1777:A:H61	3:R:1790:U:H3	1.42	0.65
3:R:2844:U:H6	3:R:2844:U:O5'	1.79	0.65
3:R:1788:U:H6	3:R:1788:U:O5'	1.80	0.65
3:R:1729:A:O2'	3:R:1730:G:O4'	2.11	0.65
3:R:1755:U:H6	3:R:1755:U:O5'	1.80	0.64
3:R:1791:U:O5'	3:R:1791:U:H6	1.79	0.64
2:M:62:ARG:HD3	3:R:3553:U:OP2	1.98	0.64
3:R:903:G:H1'	3:R:904:C:O5'	1.97	0.64
1:B:125:ASN:ND2	1:D:98:ASN:OD1	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:105:A:O5'	3:R:105:A:H8	1.79	0.64
3:R:605:C:H6	3:R:605:C:O5'	1.80	0.64
3:R:979:C:H6	3:R:979:C:O5'	1.79	0.64
3:R:1727:A:O2'	3:R:1728:U:H5'	1.98	0.64
3:R:183:U:H6	3:R:183:U:O5'	1.80	0.64
3:R:2048:C:H4'	3:R:2049:U:H5'	1.78	0.64
3:R:982:G:O2'	3:R:983:G:H5'	1.98	0.64
3:R:2781:G:O5'	3:R:2781:G:H8	1.80	0.64
3:R:106:U:H5	3:R:108:C:N4	1.97	0.63
3:R:990:G:O5'	3:R:990:G:H8	1.80	0.63
3:R:1754:A:C2	3:R:1758:C:C2	2.86	0.63
2:M:57:PRO:HA	3:R:3556:C:H41	1.63	0.63
3:R:2385:G:C2'	3:R:2386:A:H5'	2.28	0.63
3:R:2795:U:H2'	3:R:2796:C:C6	2.34	0.63
1:B:58:TYR:CD2	1:D:122:ILE:HG12	2.34	0.63
1:E:114:ASP:CG	1:F:109:GLN:NE2	2.30	0.63
1:F:129:TYR:HH	3:R:3548:C:H42	1.44	0.63
1:H:23:SER:O	2:M:133:THR:HB	1.99	0.63
3:R:185:G:C2	3:R:186:C:C5	2.85	0.63
3:R:1786:A:C2	3:R:1787:C:N3	2.67	0.63
3:R:2472:C:N3	3:R:2477:G:N1	2.44	0.63
3:R:603:U:C2	3:R:604:G:C8	2.87	0.63
3:R:902:C:C4	3:R:903:G:N7	2.67	0.63
1:A:56:ARG:NE	1:B:38:ARG:NH1	2.47	0.62
3:R:105:A:H2'	3:R:106:U:O4'	1.98	0.62
3:R:2851:C:C2'	3:R:2852:G:H5"	2.20	0.62
1:B:60:ILE:HD13	1:D:118:ILE:HG21	1.79	0.62
3:R:3547:G:N3	3:R:3547:G:H2'	2.13	0.62
3:R:2793:U:H2'	3:R:2794:G:C8	2.35	0.62
3:R:3542:A:O5'	3:R:3542:A:H8	1.82	0.62
3:R:2481:A:O5'	3:R:2481:A:H8	1.83	0.62
3:R:3558:A:H2	3:R:3559:G:C4	2.09	0.62
3:R:2468:U:C3'	3:R:2469:G:H8	2.12	0.62
1:D:56:ARG:NE	1:E:38:ARG:HH12	1.76	0.62
3:R:102:G:O2'	3:R:103:G:H5'	2.00	0.62
1:B:94:ILE:HG22	1:C:38:ARG:HG2	1.82	0.62
3:R:2043:A:O5'	3:R:2043:A:H8	1.82	0.62
1:E:93:PRO:HG2	1:F:82:TRP:CE3	2.35	0.61
3:R:2479:U:H6	3:R:2479:U:O5'	1.82	0.61
3:R:104:A:O2'	3:R:105:A:H5'	2.00	0.61
3:R:2843:U:H6	3:R:2843:U:O5'	1.84	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:182:U:O5'	3:R:182:U:H6	1.84	0.61
3:R:1759:C:C2'	3:R:1760:C:H5'	2.29	0.61
3:R:912:C:O2'	3:R:913:G:H5'	2.00	0.61
2:M:324:THR:HG22	2:M:358:ARG:HG2	1.82	0.61
1:A:39:SER:O	1:A:83:ARG:NH2	2.33	0.61
1:B:87:ASN:O	1:D:88:MET:HA	2.00	0.61
1:H:33:ILE:HD12	2:M:313:PRO:CD	2.30	0.61
1:B:109:GLN:NE2	1:D:112:LEU:O	2.33	0.60
3:R:2380:G:H3'	3:R:2381:U:C5'	2.30	0.60
3:R:184:C:H6	3:R:184:C:O5'	1.83	0.60
3:R:181:G:H2'	3:R:182:U:C6	2.37	0.60
3:R:2851:C:H6	3:R:2851:C:O5'	1.84	0.60
3:R:2469:G:C6	3:R:2470:A:N7	2.68	0.60
3:R:3562:A:C6	3:R:3563:C:N3	2.69	0.60
3:R:914:U:H6	3:R:914:U:O5'	1.85	0.60
3:R:903:G:O2'	3:R:904:C:O5'	2.19	0.60
3:R:1722:U:H2'	3:R:1723:A:H8	1.61	0.60
3:R:2843:U:H3'	3:R:2844:U:C5	2.36	0.60
3:R:193:G:C2'	3:R:194:C:H5'	2.32	0.60
3:R:978:A:C6	3:R:979:C:C4	2.90	0.60
3:R:989:U:H2'	3:R:990:G:C8	2.36	0.60
3:R:3546:A:N7	3:R:3547:G:C6	2.69	0.60
3:R:3556:C:O2'	3:R:3557:U:OP1	2.20	0.60
3:R:595:C:H42	3:R:604:G:H1	1.48	0.59
3:R:2476:C:H5"	3:R:2476:C:O2	2.01	0.59
3:R:3546:A:H2'	3:R:3547:G:H5'	1.83	0.59
1:B:111:LEU:HD22	1:D:62:VAL:HG21	1.83	0.59
3:R:195:G:H2'	3:R:196:G:H8	1.67	0.59
3:R:1752:G:H2'	3:R:1753:G:C5'	2.33	0.59
1:E:108:MET:HB3	1:F:112:LEU:HD13	1.83	0.59
3:R:2043:A:H2'	3:R:2044:A:C8	2.38	0.59
3:R:185:G:H2'	3:R:186:C:H5'	1.83	0.59
3:R:595:C:C5	3:R:596:A:N7	2.71	0.59
1:B:85:TYR:O	1:D:90:LEU:HD12	2.02	0.59
3:R:2791:U:H2'	3:R:2792:A:C8	2.38	0.59
3:R:198:C:C2'	3:R:199:G:H5'	2.32	0.59
3:R:2849:A:N3	3:R:2850:C:C2	2.71	0.59
3:R:2385:G:H2'	3:R:2386:A:H8	1.68	0.59
3:R:2472:C:H42	3:R:2478:A:N6	2.01	0.59
3:R:2849:A:H2	3:R:2850:C:N3	1.98	0.59
3:R:2471:U:H3'	3:R:2472:C:C5'	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:183:U:H2'	3:R:184:C:C5	2.38	0.58
3:R:1757:A:H4'	3:R:1758:C:O5'	2.02	0.58
3:R:2374:C:H2'	3:R:2375:U:H5'	1.84	0.58
3:R:1467:G:N2	3:R:1468:U:O2	2.36	0.58
3:R:1467:G:O2'	3:R:1468:U:O5'	2.21	0.58
2:M:62:ARG:CZ	3:R:3553:U:H5	2.16	0.58
3:R:186:C:H2'	3:R:187:G:C8	2.37	0.58
3:R:984:U:O2'	3:R:985:A:H5'	2.04	0.58
3:R:2479:U:H2'	3:R:2480:C:C4	2.39	0.58
3:R:907:C:C5	3:R:908:G:N1	2.72	0.58
3:R:111:U:O2'	3:R:112:U:H5'	2.03	0.58
3:R:182:U:C5	3:R:183:U:C4	2.91	0.58
3:R:197:A:O5'	3:R:197:A:H8	1.87	0.58
3:R:2468:U:H2'	3:R:2469:G:O4'	2.04	0.58
3:R:2786:U:O2'	3:R:2787:A:O4'	2.21	0.58
1:H:83:ARG:HE	2:M:308:GLU:CD	2.07	0.57
3:R:977:C:C2	3:R:978:A:C8	2.92	0.57
3:R:2479:U:H4'	3:R:2480:C:OP1	2.03	0.57
3:R:106:U:C4	3:R:108:C:C6	2.91	0.57
3:R:1762:U:H2'	3:R:1763:G:H5'	1.85	0.57
3:R:195:G:H2'	3:R:196:G:C8	2.40	0.57
3:R:907:C:H6	3:R:907:C:O5'	1.87	0.57
3:R:2044:A:C2	3:R:2045:A:N6	2.73	0.57
3:R:3361:U:C2'	3:R:3362:C:H5'	2.34	0.57
3:R:3361:U:C5	3:R:3362:C:H5	2.23	0.57
2:M:62:ARG:NH1	3:R:3553:U:C5	2.66	0.57
3:R:1751:A:H5"	3:R:1752:G:O5'	2.05	0.57
1:B:67:VAL:HG21	1:D:103:LEU:CD2	2.33	0.57
1:E:86:LEU:CD2	1:F:108:MET:HG2	2.33	0.57
3:R:903:G:HO2'	3:R:904:C:C5'	2.18	0.57
3:R:1468:U:C4	3:R:1469:A:N6	2.73	0.57
3:R:1721:C:H3'	3:R:1722:U:H5"	1.87	0.57
3:R:2794:G:H2'	3:R:2795:U:C6	2.40	0.57
3:R:2844:U:H4'	3:R:2845:U:OP1	2.03	0.57
3:R:3555:G:C5	3:R:3556:C:N4	2.73	0.57
1:E:62:VAL:HG21	1:F:111:LEU:HD22	1.85	0.57
3:R:189:U:H4'	3:R:190:U:OP2	2.05	0.57
3:R:978:A:C6	3:R:979:C:N4	2.73	0.57
3:R:1729:A:H4'	3:R:1730:G:OP1	2.04	0.57
3:R:3368:G:N2	3:R:3369:G:C4	2.73	0.57
3:R:106:U:C4	3:R:108:C:C5	2.91	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:595:C:N4	3:R:596:A:C6	2.73	0.56
3:R:603:U:N3	3:R:604:G:N7	2.53	0.56
3:R:907:C:H3'	3:R:908:G:H21	1.70	0.56
3:R:912:C:O5'	3:R:912:C:H6	1.88	0.56
3:R:3551:C:N4	3:R:3552:U:C5	2.73	0.56
2:M:147:ARG:HD2	2:M:374:PRO:HB2	1.87	0.56
3:R:903:G:H1'	3:R:904:C:P	2.45	0.56
3:R:1759:C:HO2'	3:R:1760:C:H5'	1.68	0.56
3:R:2848:A:C6	3:R:2849:A:N6	2.73	0.56
3:R:1722:U:C4	3:R:1723:A:N6	2.73	0.56
3:R:2043:A:C6	3:R:2044:A:N6	2.73	0.56
3:R:2048:C:C4'	3:R:2049:U:H5'	2.35	0.56
3:R:2470:A:O2'	3:R:2471:U:O5'	2.22	0.56
3:R:2785:A:N1	3:R:2794:G:C6	2.74	0.56
3:R:3563:C:H6	3:R:3563:C:O5'	1.88	0.56
1:A:62:VAL:HB	1:A:86:LEU:HB3	1.87	0.56
1:E:66:LYS:HG2	1:F:100:ASP:OD2	2.06	0.56
3:R:1759:C:O5'	3:R:1759:C:H6	1.89	0.56
1:F:65:PRO:HB3	1:F:83:ARG:HG2	1.87	0.56
3:R:110:A:O2'	3:R:111:U:O4'	2.11	0.56
3:R:905:G:C6	3:R:913:G:N1	2.72	0.56
3:R:1460:U:H4'	3:R:1461:U:OP1	2.04	0.56
1:B:128:ILE:HG21	1:D:4:PHE:CD1	2.40	0.56
3:R:982:G:H3'	3:R:983:G:C2	2.41	0.56
3:R:982:G:N2	3:R:986:U:H3	2.04	0.56
3:R:2468:U:H2'	3:R:2469:G:C1'	2.35	0.56
3:R:2469:G:N2	3:R:2481:A:C2	2.73	0.56
3:R:2480:C:C2'	3:R:2481:A:C8	2.88	0.56
3:R:3546:A:C2'	3:R:3547:G:H5'	2.35	0.56
3:R:3550:G:C6	3:R:3551:C:N4	2.73	0.56
3:R:1721:C:N4	3:R:1722:U:C4	2.73	0.56
3:R:1762:U:C2'	3:R:1763:G:H5'	2.36	0.56
3:R:3558:A:C2	3:R:3559:G:C8	2.94	0.56
3:R:598:A:H8	3:R:598:A:O5'	1.89	0.56
3:R:3361:U:C4	3:R:3362:C:N4	2.74	0.56
3:R:905:G:O5'	3:R:905:G:H8	1.89	0.56
3:R:2472:C:N4	3:R:2477:G:C6	2.73	0.56
3:R:907:C:C6	3:R:908:G:N2	2.73	0.56
3:R:911:U:H2'	3:R:912:C:C6	2.41	0.56
1:F:110:GLY:O	1:F:116:ASN:ND2	2.38	0.55
3:R:1724:C:O2'	3:R:1725:U:OP1	2.23	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:102:G:N2	3:R:114:C:O2	2.38	0.55
3:R:2471:U:C2'	3:R:2472:C:H5"	2.36	0.55
1:E:85:TYR:O	1:F:90:LEU:HD12	2.06	0.55
2:M:62:ARG:HH21	3:R:3553:U:P	2.28	0.55
3:R:187:G:N2	3:R:190:U:C5	2.74	0.55
3:R:983:G:H1'	3:R:985:A:OP1	2.06	0.55
1:E:110:GLY:O	1:E:116:ASN:ND2	2.40	0.55
3:R:905:G:O2'	3:R:906:A:H5'	2.06	0.55
3:R:2050:U:O2'	3:R:2051:G:H5'	2.06	0.55
3:R:3558:A:N1	3:R:3559:G:C4	2.68	0.55
1:G:110:GLY:O	1:G:116:ASN:ND2	2.39	0.55
3:R:1720:U:O5'	3:R:1720:U:H6	1.90	0.55
3:R:2379:U:C2'	3:R:2380:G:H5"	2.32	0.55
3:R:181:G:C2	3:R:182:U:N3	2.74	0.55
3:R:980:U:H2'	3:R:980:U:O2	2.07	0.55
1:B:109:GLN:NE2	1:D:114:ASP:OD1	2.35	0.55
3:R:1778:G:O2'	3:R:1780:A:OP1	2.25	0.55
3:R:3360:U:H6	3:R:3360:U:O5'	1.90	0.55
1:E:117:PRO:HB3	1:F:3:ASN:O	2.06	0.55
3:R:3550:G:O2'	3:R:3551:C:OP1	2.19	0.55
3:R:2792:A:H2'	3:R:2793:U:O4'	2.07	0.55
3:R:3556:C:HO2'	3:R:3557:U:P	2.30	0.55
3:R:2471:U:H2'	3:R:2472:C:H5"	1.88	0.54
2:M:60:TYR:CE1	3:R:3552:U:N3	2.75	0.54
3:R:2468:U:C3'	3:R:2469:G:C8	2.88	0.54
3:R:3557:U:C5'	3:R:3558:A:H4'	2.35	0.54
3:R:3562:A:C2	3:R:3563:C:C2	2.94	0.54
3:R:905:G:N3	3:R:906:A:N7	2.54	0.54
2:M:271:ARG:NH1	2:M:309:GLY:O	2.40	0.54
1:B:3:ASN:O	1:D:117:PRO:HB3	2.08	0.54
1:E:58:TYR:CD2	1:F:122:ILE:HG12	2.34	0.54
3:R:593:C:O2'	3:R:594:G:O4'	2.21	0.54
3:R:603:U:H2'	3:R:603:U:O2	2.07	0.54
3:R:2793:U:H2'	3:R:2793:U:O2	2.07	0.54
1:D:39:SER:O	1:D:83:ARG:NH2	2.40	0.54
3:R:2385:G:H8	3:R:2385:G:O5'	1.90	0.54
3:R:2783:C:O2'	3:R:2785:A:H5"	2.08	0.54
3:R:1750:G:O2'	3:R:1752:G:O5'	2.21	0.54
3:R:1757:A:H4'	3:R:1758:C:C5'	2.38	0.54
1:E:32:TRP:HH2	1:F:128:ILE:HG21	1.72	0.54
1:B:118:ILE:HD11	1:D:32:TRP:CZ3	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:2471:U:H2'	3:R:2471:U:O2	2.07	0.54
1:F:129:TYR:CZ	3:R:3548:C:N3	2.76	0.53
3:R:1752:G:C2'	3:R:1753:G:H5'	2.35	0.53
1:B:129:TYR:CD2	1:E:4:PHE:HE2	2.27	0.53
3:R:3361:U:C2'	3:R:3362:C:C5'	2.86	0.53
3:R:2796:C:H6	3:R:2796:C:O5'	1.91	0.53
1:B:1:ALA:CB	1:C:6:GLN:OE1	2.56	0.53
3:R:3557:U:C5'	3:R:3558:A:C4'	2.87	0.53
3:R:1755:U:H4'	3:R:1756:U:OP1	2.08	0.53
3:R:1756:U:H4'	3:R:1757:A:OP1	2.09	0.53
2:M:43:ARG:NH1	3:R:3552:U:C5'	2.63	0.53
3:R:904:C:H2'	3:R:905:G:H8	1.67	0.53
3:R:1762:U:O5'	3:R:1762:U:H6	1.91	0.53
3:R:2479:U:C2'	3:R:2480:C:C5	2.91	0.53
3:R:196:G:HO2'	3:R:197:A:H5'	1.72	0.53
3:R:2376:G:H5'	3:R:2377:C:C5'	2.39	0.53
3:R:102:G:H2'	3:R:103:G:H8	1.74	0.52
3:R:3558:A:C6	3:R:3559:G:C5	2.97	0.52
2:M:6:THR:HG21	2:M:62:ARG:HH11	1.74	0.52
3:R:185:G:C2	3:R:186:C:C6	2.97	0.52
3:R:185:G:N1	3:R:186:C:C5	2.78	0.52
3:R:979:C:H2'	3:R:980:U:C5	2.44	0.52
3:R:3557:U:H3'	3:R:3557:U:H6	1.74	0.52
3:R:3558:A:H4'	3:R:3558:A:OP1	2.08	0.52
1:B:96:ALA:HB2	1:D:82:TRP:CH2	2.45	0.52
3:R:1464:A:O2'	3:R:1465:A:OP1	2.27	0.52
3:R:1724:C:H6	3:R:1724:C:O5'	1.93	0.52
3:R:2849:A:C2'	3:R:2850:C:C6	2.92	0.52
3:R:109:C:O2	3:R:109:C:H2'	2.09	0.52
3:R:194:C:H2'	3:R:195:G:O5'	2.10	0.52
3:R:2374:C:H6	3:R:2374:C:O5'	1.93	0.52
1:F:39:SER:O	1:F:83:ARG:NH2	2.43	0.52
3:R:981:A:C6	3:R:987:A:N1	2.78	0.52
3:R:986:U:O5'	3:R:986:U:H6	1.92	0.52
3:R:3561:U:H2'	3:R:3562:A:C8	2.45	0.52
3:R:594:G:C2	3:R:595:C:C2	2.98	0.51
3:R:3361:U:C4	3:R:3362:C:H5	2.29	0.51
1:B:111:LEU:HD21	1:D:60:ILE:HG21	1.91	0.51
3:R:196:G:O2'	3:R:197:A:C5'	2.50	0.51
3:R:595:C:H41	3:R:596:A:N6	2.08	0.51
2:M:211:GLN:HE22	2:M:282:ASN:HA	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:2377:C:H4'	3:R:2377:C:OP2	2.09	0.51
3:R:2479:U:H3'	3:R:2480:C:C5	2.46	0.51
1:E:67:VAL:H	1:F:100:ASP:CG	2.13	0.51
1:F:62:VAL:HB	1:F:86:LEU:HB3	1.92	0.51
1:H:33:ILE:CD1	2:M:313:PRO:CG	2.58	0.51
3:R:2050:U:H2'	3:R:2051:G:C5'	2.28	0.51
1:C:110:GLY:O	1:C:116:ASN:ND2	2.44	0.51
3:R:2479:U:C3'	3:R:2480:C:C5	2.94	0.51
1:E:67:VAL:CG2	1:F:103:LEU:HD22	2.37	0.51
3:R:2468:U:H2'	3:R:2469:G:C8	2.46	0.51
3:R:199:G:H2'	3:R:200:G:H8	1.73	0.51
3:R:1463:C:H6	3:R:1463:C:O5'	1.94	0.51
3:R:3369:G:H2'	3:R:3370:A:C8	2.46	0.51
3:R:2045:A:H1'	3:R:2046:U:C6	2.45	0.51
1:E:46:CYS:SG	1:F:128:ILE:HD11	2.51	0.50
2:M:62:ARG:NH2	3:R:3553:U:P	2.84	0.50
3:R:2782:A:C5	3:R:2783:C:C4	2.99	0.50
2:M:333:ILE:HB	2:M:349:ALA:HB3	1.93	0.50
3:R:3558:A:N3	3:R:3559:G:C8	2.80	0.50
1:B:66:LYS:HE2	1:E:73:GLY:O	2.12	0.50
1:E:86:LEU:HD13	1:F:90:LEU:HD13	1.93	0.50
3:R:1777:A:C3'	3:R:1778:G:H5'	2.41	0.50
3:R:2051:G:N2	3:R:2052:U:C2	2.79	0.50
3:R:3555:G:C4	3:R:3556:C:C4	3.00	0.50
1:D:56:ARG:HH21	1:E:38:ARG:HH12	1.51	0.50
3:R:982:G:H3'	3:R:983:G:H21	1.55	0.50
3:R:187:G:O5'	3:R:187:G:H8	1.95	0.50
3:R:1726:A:H4'	3:R:1727:A:O5'	2.11	0.50
3:R:182:U:C4	3:R:183:U:C4	3.00	0.49
3:R:3546:A:C5	3:R:3547:G:C5	3.00	0.49
3:R:905:G:N3	3:R:906:A:C8	2.80	0.49
3:R:1752:G:C2'	3:R:1753:G:C5'	2.90	0.49
3:R:179:C:O2'	3:R:180:C:H5'	2.12	0.49
3:R:1462:A:H2'	3:R:1463:C:C6	2.48	0.49
3:R:2480:C:H6	3:R:2480:C:H3'	1.77	0.49
3:R:3560:U:HO2'	3:R:3561:U:C5'	2.15	0.49
3:R:3560:U:HO2'	3:R:3561:U:P	2.32	0.49
1:E:118:ILE:HG21	1:F:60:ILE:HD13	1.95	0.49
2:M:38:ASN:HA	2:M:66:SER:HA	1.94	0.49
1:B:111:LEU:HD22	1:D:62:VAL:CG2	2.41	0.49
3:R:905:G:N1	3:R:913:G:N1	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:596:A:N6	3:R:597:A:N6	2.60	0.49
3:R:977:C:H2'	3:R:978:A:O4'	2.12	0.49
1:B:128:ILE:HG21	1:D:4:PHE:HD1	1.77	0.49
1:E:9:LEU:O	1:F:110:GLY:HA3	2.12	0.49
3:R:1755:U:OP2	3:R:1756:U:H5	1.96	0.49
3:R:2471:U:C4	3:R:2472:C:C5	3.01	0.49
3:R:3543:A:C2'	3:R:3544:C:H5'	2.42	0.49
1:D:110:GLY:O	1:D:116:ASN:ND2	2.46	0.49
2:M:231:VAL:HG22	2:M:262:VAL:HG22	1.95	0.49
3:R:905:G:C2	3:R:906:A:C8	3.00	0.49
3:R:2471:U:C3'	3:R:2472:C:C5'	2.90	0.49
1:E:67:VAL:CB	1:F:100:ASP:OD1	2.53	0.49
1:H:79:VAL:O	2:M:301:LEU:CD1	2.56	0.49
3:R:182:U:H2'	3:R:183:U:H6	1.75	0.49
3:R:3551:C:O2'	3:R:3552:U:OP1	2.28	0.49
3:R:601:A:C4'	3:R:602:U:H5"	2.38	0.49
3:R:2044:A:N1	3:R:2045:A:N6	2.61	0.49
3:R:3370:A:O5'	3:R:3370:A:H8	1.95	0.49
3:R:3556:C:H2'	3:R:3557:U:C4	2.47	0.49
3:R:3558:A:C2'	3:R:3559:G:H5'	2.41	0.49
1:E:58:TYR:CE2	1:F:122:ILE:CG1	2.60	0.48
1:E:84:SER:CB	1:F:104:ILE:HD11	2.44	0.48
3:R:3362:C:C4	3:R:3370:A:N1	2.81	0.48
3:R:3372:U:O5'	3:R:3372:U:H6	1.95	0.48
3:R:113:C:C3'	3:R:114:C:H5"	2.42	0.48
3:R:181:G:H8	3:R:181:G:O5'	1.96	0.48
3:R:903:G:C1'	3:R:904:C:P	3.00	0.48
3:R:902:C:O5'	3:R:902:C:H6	1.96	0.48
3:R:2849:A:N3	3:R:2850:C:C4	2.81	0.48
3:R:3363:C:O2'	3:R:3364:C:H5'	2.12	0.48
1:H:51:SER:HB3	3:R:1781:G:OP1	2.11	0.48
2:M:157:THR:HG21	2:M:303:VAL:HG11	1.95	0.48
3:R:2473:A:C8	3:R:2477:G:C2	3.02	0.48
3:R:3540:G:O5'	3:R:3540:G:H8	1.96	0.48
1:A:110:GLY:O	1:A:116:ASN:ND2	2.47	0.48
1:B:128:ILE:CG2	1:D:4:PHE:CD1	2.97	0.48
3:R:200:G:H8	3:R:200:G:O5'	1.96	0.48
3:R:3369:G:O2'	3:R:3370:A:H5'	2.14	0.48
1:B:129:TYR:CE1	1:D:3:ASN:ND2	2.82	0.48
3:R:2383:A:C4	3:R:2384:G:N7	2.81	0.48
3:R:2785:A:C2	3:R:2794:G:C2	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:2851:C:C2'	3:R:2852:G:C5'	2.86	0.48
1:H:21:ALA:CB	2:M:370:TYR:CE2	2.96	0.48
3:R:1722:U:C2	3:R:1730:G:N2	2.81	0.48
3:R:2478:A:C5	3:R:2479:U:C4	3.02	0.48
3:R:3553:U:H4'	3:R:3554:G:H5"	1.94	0.48
3:R:109:C:H4'	3:R:110:A:C8	2.49	0.48
3:R:905:G:N1	3:R:913:G:C6	2.82	0.48
3:R:3365:U:O2'	3:R:3366:C:H5'	2.13	0.48
3:R:182:U:C6	3:R:183:U:C5	3.01	0.47
3:R:1757:A:H4'	3:R:1758:C:H5"	1.94	0.47
2:M:165:THR:HG21	2:M:390:ARG:HB3	1.96	0.47
2:M:271:ARG:NH2	2:M:313:PRO:O	2.47	0.47
3:R:190:U:O2	3:R:190:U:O2'	2.27	0.47
3:R:2385:G:H2'	3:R:2386:A:C8	2.47	0.47
3:R:2843:U:C2'	3:R:2844:U:C6	2.94	0.47
1:B:67:VAL:HG21	1:D:103:LEU:HD22	1.95	0.47
1:H:32:TRP:HB2	1:H:44:VAL:HB	1.95	0.47
3:R:604:G:N2	3:R:605:C:C1'	2.78	0.47
3:R:2782:A:H61	3:R:2795:U:H3	1.63	0.47
1:B:62:VAL:HG21	1:D:111:LEU:HD22	1.95	0.47
1:E:32:TRP:CH2	1:F:128:ILE:HG21	2.49	0.47
2:M:140:GLY:HA2	3:R:3558:A:OP2	2.15	0.47
3:R:3369:G:N2	3:R:3370:A:C4	2.83	0.47
1:B:94:ILE:HB	1:C:38:ARG:HB3	1.95	0.47
1:E:109:GLN:NE2	1:F:114:ASP:OD1	2.34	0.47
3:R:2475:U:O2'	3:R:2476:C:O5'	2.27	0.47
3:R:2785:A:C2	3:R:2794:G:C6	3.03	0.47
3:R:3562:A:O5'	3:R:3562:A:H8	1.98	0.47
3:R:109:C:H5'	3:R:110:A:C8	2.50	0.47
3:R:2473:A:N6	3:R:2474:A:C6	2.83	0.47
3:R:3362:C:H2'	3:R:3363:C:H6	1.70	0.47
3:R:2473:A:H5"	3:R:2473:A:N3	2.29	0.47
3:R:1751:A:H5"	3:R:1752:G:C5'	2.45	0.46
3:R:2042:C:H2'	3:R:2043:A:C8	2.49	0.46
3:R:2046:U:O2'	3:R:2047:C:H5'	2.15	0.46
3:R:2792:A:C8	3:R:2793:U:C5	3.02	0.46
3:R:2793:U:H2'	3:R:2794:G:N7	2.30	0.46
1:A:56:ARG:CZ	1:B:38:ARG:HH11	2.24	0.46
2:M:11:ASN:ND2	2:M:37:SER:OG	2.48	0.46
3:R:905:G:C6	3:R:906:A:N6	2.83	0.46
3:R:2478:A:C6	3:R:2479:U:C4	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:2849:A:H2'	3:R:2850:C:C4	2.50	0.46
1:B:129:TYR:HB2	1:E:4:PHE:CE2	2.50	0.46
3:R:2376:G:H5'	3:R:2377:C:O5'	2.15	0.46
3:R:595:C:N4	3:R:604:G:H1	2.14	0.46
3:R:1468:U:H2'	3:R:1469:A:H5'	1.97	0.46
3:R:3559:G:O5'	3:R:3559:G:H8	1.99	0.46
2:M:356:MET:SD	3:R:3554:G:H5"	2.52	0.46
3:R:989:U:H5	3:R:989:U:OP2	1.98	0.46
3:R:2479:U:H2'	3:R:2480:C:C6	2.50	0.46
3:R:2782:A:C3'	3:R:2783:C:H5'	2.46	0.46
3:R:907:C:C6	3:R:908:G:C2	3.03	0.46
3:R:1754:A:C6	3:R:1756:U:C2	3.04	0.46
3:R:2041:A:H8	3:R:2041:A:O5'	1.98	0.46
1:C:62:VAL:HB	1:C:86:LEU:HB3	1.98	0.46
1:F:129:TYR:CE2	3:R:3547:G:P	3.05	0.46
2:M:11:ASN:HB2	2:M:35:TYR:HE2	1.81	0.46
3:R:1777:A:N6	3:R:1778:G:C6	2.83	0.46
3:R:113:C:H2'	3:R:114:C:C5'	2.17	0.46
3:R:605:C:H2'	3:R:606:G:C8	2.50	0.46
3:R:1760:C:C2'	3:R:1761:A:H5'	2.44	0.46
3:R:2043:A:H2'	3:R:2044:A:H8	1.79	0.46
1:H:20:VAL:HG22	1:H:32:TRP:HB3	1.98	0.46
3:R:1722:U:N3	3:R:1730:G:N2	2.64	0.46
3:R:2849:A:O2'	3:R:2850:C:O4'	2.34	0.46
3:R:3368:G:N3	3:R:3369:G:C8	2.84	0.46
1:B:88:MET:HG2	1:D:88:MET:HB3	1.97	0.45
3:R:902:C:C2'	3:R:903:G:C5'	2.86	0.45
3:R:977:C:H2'	3:R:978:A:O5'	2.16	0.45
3:R:1721:C:O5'	3:R:1721:C:H6	1.99	0.45
3:R:3562:A:C5	3:R:3563:C:C4	3.03	0.45
1:A:65:PRO:HB3	1:A:83:ARG:HG2	1.99	0.45
3:R:982:G:N2	3:R:986:U:N3	2.64	0.45
3:R:1758:C:H5"	3:R:1758:C:H6	1.82	0.45
2:M:43:ARG:NH1	3:R:3552:U:OP2	2.49	0.45
3:R:981:A:O2'	3:R:982:G:OP1	2.31	0.45
3:R:2476:C:H4'	3:R:2477:G:C5'	2.45	0.45
3:R:3557:U:H5"	3:R:3558:A:OP1	2.16	0.45
1:H:33:ILE:HD12	2:M:313:PRO:HD2	1.98	0.45
2:M:120:VAL:HG13	2:M:234:VAL:HG12	1.97	0.45
3:R:2380:G:C3'	3:R:2381:U:C5'	2.95	0.45
2:M:393:ARG:CZ	3:R:1776:A:O2'	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:1780:A:C2'	3:R:1781:G:H5'	2.47	0.45
3:R:2478:A:C6	3:R:2479:U:N3	2.85	0.45
1:E:84:SER:CB	1:F:104:ILE:CD1	2.95	0.45
3:R:1777:A:H3'	3:R:1778:G:H5'	1.97	0.45
3:R:2472:C:N4	3:R:2478:A:N6	2.64	0.45
3:R:3365:U:H6	3:R:3365:U:O5'	2.00	0.45
1:A:54:GLN:HE22	1:B:77:LEU:HD11	1.82	0.45
1:E:108:MET:CB	1:F:112:LEU:HD13	2.47	0.45
1:E:117:PRO:HD2	1:F:7:PHE:CD1	2.52	0.45
2:M:187:PHE:HD2	2:M:195:ARG:HH11	1.65	0.45
3:R:984:U:H2'	3:R:985:A:OP2	2.17	0.45
3:R:1724:C:O5'	3:R:1724:C:C6	2.71	0.45
3:R:3362:C:C4	3:R:3363:C:N4	2.85	0.45
1:B:4:PHE:CB	1:D:129:TYR:O	2.65	0.44
1:F:44:VAL:HG22	1:F:62:VAL:HG22	1.99	0.44
1:H:78:PRO:CG	2:M:302:PRO:HB3	2.46	0.44
2:M:62:ARG:HH12	3:R:3553:U:H5	1.63	0.44
3:R:111:U:H2'	3:R:112:U:H6	1.82	0.44
3:R:1729:A:H8	3:R:1729:A:O5'	2.00	0.44
3:R:1781:G:H2'	3:R:1782:U:O4'	2.17	0.44
3:R:1782:U:O4	3:R:1784:C:C2	2.70	0.44
3:R:2471:U:O4	3:R:2472:C:C4	2.70	0.44
3:R:104:A:C2	3:R:112:U:N3	2.76	0.44
3:R:989:U:H2'	3:R:990:G:N7	2.33	0.44
3:R:1461:U:C2'	3:R:1462:A:C5'	2.86	0.44
3:R:1469:A:H2'	3:R:1470:A:C4'	2.47	0.44
3:R:1754:A:C2	3:R:1758:C:O2	2.70	0.44
3:R:2479:U:C5	3:R:2479:U:OP2	2.70	0.44
3:R:2791:U:O2	3:R:2792:A:C6	2.70	0.44
3:R:3359:A:C2	3:R:3360:U:O2	2.71	0.44
3:R:3364:C:O2	3:R:3368:G:C2	2.70	0.44
3:R:1461:U:O5'	3:R:1461:U:C6	2.70	0.44
3:R:1722:U:C2'	3:R:1723:A:C8	2.86	0.44
3:R:3545:U:O4	3:R:3558:A:C6	2.70	0.44
3:R:106:U:C6	3:R:108:C:H5	2.28	0.44
3:R:106:U:O4	3:R:108:C:C2	2.71	0.44
3:R:3362:C:H5'	3:R:3362:C:H6	1.82	0.44
3:R:3372:U:O5'	3:R:3372:U:C6	2.70	0.44
3:R:3556:C:C6	3:R:3557:U:O4	2.70	0.44
1:H:69:THR:HG22	1:H:78:PRO:HA	2.00	0.44
3:R:598:A:O3'	3:R:599:C:H6	2.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:2041:A:H2'	3:R:2042:C:C5'	2.42	0.44
3:R:2470:A:HO2'	3:R:2471:U:P	2.39	0.44
3:R:3559:G:C6	3:R:3560:U:O4	2.71	0.44
1:D:20:VAL:HG22	1:D:32:TRP:HB3	1.98	0.44
2:M:265:PHE:HA	2:M:318:TYR:HA	1.99	0.44
2:M:281:LEU:HB3	2:M:286:ILE:HD11	2.00	0.44
3:R:112:U:HO2'	3:R:113:C:H5'	1.77	0.44
3:R:192:C:H2'	3:R:193:G:C8	2.53	0.44
3:R:3360:U:O5'	3:R:3360:U:C6	2.71	0.44
3:R:3368:G:N3	3:R:3369:G:N7	2.66	0.44
1:A:20:VAL:HG22	1:A:32:TRP:HB3	2.00	0.44
1:B:112:LEU:HD13	1:D:108:MET:HB3	1.99	0.44
1:E:32:TRP:HB2	1:E:44:VAL:HB	1.98	0.44
1:E:111:LEU:HD22	1:F:62:VAL:HG21	2.00	0.44
3:R:1462:A:C2	3:R:1463:C:O2	2.71	0.44
3:R:1468:U:H2'	3:R:1469:A:C5'	2.48	0.44
3:R:1789:C:C4	3:R:1790:U:O4	2.71	0.44
3:R:2052:U:C4	3:R:2053:C:N4	2.85	0.44
3:R:2783:C:H3'	3:R:2783:C:H6	1.83	0.44
3:R:2843:U:C4	3:R:2844:U:O4	2.71	0.44
3:R:3361:U:C4	3:R:3362:C:C4	3.05	0.44
3:R:111:U:C4	3:R:112:U:O4	2.71	0.44
3:R:182:U:C5	3:R:183:U:O4	2.70	0.44
3:R:194:C:C2'	3:R:195:G:O5'	2.65	0.44
3:R:1786:A:C2	3:R:1787:C:C4	3.06	0.44
3:R:2052:U:H5"	3:R:2052:U:H6	1.83	0.44
3:R:2383:A:C6	3:R:2384:G:O6	2.71	0.44
3:R:2794:G:C6	3:R:2795:U:O4	2.70	0.44
3:R:2842:G:C2	3:R:2851:C:O2	2.70	0.44
3:R:2844:U:O2'	3:R:2845:U:C6	2.71	0.44
1:B:66:LYS:CE	1:E:73:GLY:O	2.65	0.44
3:R:603:U:O2	3:R:604:G:C8	2.71	0.44
3:R:1463:C:O5'	3:R:1463:C:C6	2.70	0.44
3:R:1753:G:C2	3:R:1759:C:O2	2.71	0.44
3:R:2052:U:H2'	3:R:2053:C:H5'	1.99	0.44
3:R:2468:U:C2'	3:R:2469:G:C8	3.01	0.44
3:R:2842:G:C2	3:R:2843:U:O2	2.70	0.44
3:R:2843:U:C5	3:R:2844:U:O4	2.71	0.44
3:R:3555:G:O2'	3:R:3556:C:C6	2.70	0.44
1:B:108:MET:SD	1:D:86:LEU:HD22	2.58	0.43
1:E:42:TYR:CD1	1:E:65:PRO:HD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:605:C:H2'	3:R:606:G:H5'	2.00	0.43
3:R:1778:G:N2	3:R:1790:U:C2	2.85	0.43
3:R:2374:C:O5'	3:R:2374:C:C6	2.71	0.43
1:G:49:ARG:CZ	3:R:1751:A:C4'	2.92	0.43
3:R:2849:A:O2'	3:R:2850:C:C6	2.71	0.43
3:R:3562:A:C2	3:R:3563:C:O2	2.70	0.43
1:F:129:TYR:HD1	1:F:129:TYR:HA	1.70	0.43
1:G:49:ARG:NH1	3:R:1751:A:O4'	2.51	0.43
3:R:986:U:O5'	3:R:986:U:C6	2.70	0.43
1:E:108:MET:HB3	1:F:112:LEU:CD1	2.48	0.43
1:E:118:ILE:CG2	1:F:60:ILE:HD13	2.48	0.43
3:R:989:U:OP2	3:R:989:U:C5	2.71	0.43
3:R:2842:G:N2	3:R:2851:C:O2	2.52	0.43
3:R:3364:C:O5'	3:R:3364:C:C6	2.70	0.43
3:R:2045:A:N3	3:R:2045:A:C2'	2.75	0.43
3:R:905:G:C8	3:R:905:G:O5'	2.71	0.43
3:R:907:C:O5'	3:R:907:C:C6	2.70	0.43
3:R:979:C:HO2'	3:R:980:U:H6	1.64	0.43
3:R:1721:C:O5'	3:R:1721:C:C6	2.72	0.43
1:A:26:ALA:HA	1:C:25:PHE:CE2	2.54	0.43
1:A:42:TYR:CD1	1:A:65:PRO:HD2	2.53	0.43
3:R:905:G:N1	3:R:906:A:N6	2.67	0.43
3:R:190:U:H1'	3:R:192:C:N3	2.33	0.43
3:R:1759:C:O5'	3:R:1759:C:C6	2.71	0.43
3:R:2480:C:C6	3:R:2480:C:C3'	3.02	0.43
3:R:3540:G:O2'	3:R:3541:U:H5'	2.19	0.43
3:R:1729:A:C2'	3:R:1730:G:C8	2.96	0.43
3:R:3369:G:H2'	3:R:3370:A:H8	1.84	0.43
1:F:42:TYR:CD1	1:F:65:PRO:HD2	2.54	0.43
3:R:597:A:C2	3:R:598:A:C5	3.06	0.43
3:R:604:G:N2	3:R:605:C:H1'	2.33	0.43
3:R:913:G:N2	3:R:914:U:O2	2.52	0.43
3:R:1748:A:N6	3:R:1763:G:O6	2.51	0.43
3:R:2785:A:C6	3:R:2786:U:O4	2.71	0.43
3:R:3562:A:N1	3:R:3563:C:N3	2.67	0.43
3:R:1782:U:C4	3:R:1784:C:C5	3.04	0.42
3:R:2469:G:O6	3:R:2470:A:N6	2.39	0.42
3:R:2479:U:C2	3:R:2480:C:N4	2.87	0.42
3:R:2786:U:HO2'	3:R:2787:A:C4'	2.31	0.42
3:R:3555:G:O2'	3:R:3556:C:C5	2.72	0.42
3:R:1749:U:H6	3:R:1749:U:H5"	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:21:ALA:CB	2:M:370:TYR:HE2	2.26	0.42
3:R:192:C:H2'	3:R:193:G:H8	1.84	0.42
1:E:112:LEU:HD13	1:F:108:MET:HB3	2.00	0.42
1:G:111:LEU:HD11	1:G:118:ILE:HD12	2.01	0.42
3:R:1780:A:HO2'	3:R:1781:G:H5'	1.79	0.42
3:R:2045:A:C2	3:R:2047:C:N3	2.87	0.42
3:R:3361:U:C3'	3:R:3362:C:C5'	2.97	0.42
3:R:194:C:O5'	3:R:194:C:H6	2.03	0.42
3:R:984:U:O5'	3:R:984:U:H6	2.02	0.42
3:R:3361:U:C3'	3:R:3362:C:H5'	2.50	0.42
3:R:3560:U:O2'	3:R:3561:U:C6	2.71	0.42
3:R:604:G:H2'	3:R:605:C:H5'	2.01	0.42
3:R:1761:A:C2	3:R:1762:U:N3	2.87	0.42
1:A:56:ARG:HH21	1:B:38:ARG:HH12	1.63	0.42
1:G:42:TYR:CD1	1:G:65:PRO:HD2	2.55	0.42
2:M:261:ILE:HG12	2:M:323:VAL:HG22	2.00	0.42
3:R:1762:U:O5'	3:R:1762:U:C6	2.71	0.42
3:R:2843:U:H2'	3:R:2844:U:C5	2.54	0.42
1:C:73:GLY:O	1:D:70:GLN:HG3	2.20	0.42
3:R:1468:U:H2'	3:R:1469:A:O5'	2.19	0.42
3:R:3370:A:N6	3:R:3371:G:O6	2.52	0.42
3:R:3552:U:H3'	3:R:3552:U:O2	2.19	0.42
1:H:61:LYS:NZ	3:R:1779:A:OP1	2.49	0.42
3:R:106:U:C4	3:R:108:C:C4	3.03	0.42
3:R:1722:U:O4	3:R:1723:A:N6	2.53	0.42
3:R:3369:G:H8	3:R:3369:G:O5'	2.03	0.42
3:R:906:A:C2	3:R:907:C:C2	3.08	0.42
3:R:593:C:C2'	3:R:594:G:H8	2.20	0.41
3:R:913:G:C2	3:R:914:U:C2	3.08	0.41
3:R:1462:A:C6	3:R:1469:A:C2	3.07	0.41
3:R:1778:G:C5	3:R:1780:A:N7	2.87	0.41
3:R:1788:U:O2'	3:R:1789:C:H5'	2.19	0.41
3:R:2842:G:C2	3:R:2843:U:C2	3.08	0.41
3:R:3364:C:O5'	3:R:3364:C:H6	2.02	0.41
1:E:122:ILE:HG12	1:F:58:TYR:CD2	2.53	0.41
3:R:594:G:N1	3:R:595:C:C2	2.88	0.41
3:R:905:G:C4	3:R:906:A:N7	2.87	0.41
3:R:1785:A:H4'	3:R:1786:A:C8	2.55	0.41
3:R:2050:U:C2'	3:R:2051:G:C5'	2.86	0.41
3:R:903:G:H1'	3:R:904:C:OP1	2.20	0.41
3:R:2794:G:C5	3:R:2795:U:O4	2.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:62:VAL:HB	1:H:86:LEU:HB3	2.01	0.41
3:R:109:C:H4'	3:R:110:A:N7	2.35	0.41
3:R:199:G:H2'	3:R:200:G:O4'	2.21	0.41
3:R:905:G:H2'	3:R:906:A:H8	1.85	0.41
3:R:1729:A:O2'	3:R:1730:G:P	2.79	0.41
3:R:2469:G:N1	3:R:2470:A:C5	2.88	0.41
3:R:3362:C:C2	3:R:3370:A:C2	3.08	0.41
1:F:129:TYR:HE1	3:R:3548:C:N3	2.14	0.41
3:R:106:U:H5"	3:R:106:U:H6	1.86	0.41
3:R:1461:U:O5'	3:R:1461:U:H6	2.03	0.41
3:R:1789:C:C4	3:R:1790:U:C4	3.09	0.41
3:R:3557:U:H5'	3:R:3558:A:C4'	2.49	0.41
3:R:2785:A:C2	3:R:2794:G:N1	2.89	0.41
3:R:2844:U:O2'	3:R:2845:U:P	2.79	0.41
3:R:3361:U:C2'	3:R:3362:C:H5"	2.50	0.41
3:R:3557:U:C3'	3:R:3557:U:C6	3.03	0.41
2:M:160:LEU:O	2:M:164:TYR:N	2.45	0.41
3:R:2377:C:H6	3:R:2377:C:H5"	1.85	0.41
3:R:2845:U:O2	3:R:2845:U:O2'	2.27	0.41
3:R:179:C:H2'	3:R:180:C:C5'	2.44	0.41
3:R:593:C:O2'	3:R:594:G:P	2.79	0.41
3:R:1721:C:C4	3:R:1722:U:C5	3.09	0.41
3:R:2848:A:C5	3:R:2849:A:N6	2.89	0.41
1:B:111:LEU:HD21	1:D:60:ILE:CG2	2.51	0.41
1:B:117:PRO:HB3	1:D:3:ASN:O	2.21	0.41
1:C:42:TYR:CD1	1:C:65:PRO:HD2	2.56	0.41
2:M:322:THR:HG21	3:R:3555:G:H2'	2.03	0.41
3:R:181:G:C2	3:R:182:U:C4	3.09	0.41
3:R:912:C:O5'	3:R:912:C:C6	2.71	0.41
3:R:914:U:H2'	3:R:915:G:C8	2.56	0.41
3:R:1467:G:C2	3:R:1468:U:C2	3.09	0.41
3:R:2469:G:C2	3:R:2470:A:C8	3.08	0.41
3:R:2480:C:HO2'	3:R:2481:A:C4'	2.29	0.41
3:R:3368:G:C2	3:R:3369:G:N7	2.89	0.41
3:R:3368:G:N2	3:R:3369:G:C5	2.89	0.41
3:R:3369:G:C8	3:R:3369:G:O5'	2.74	0.41
3:R:3563:C:O5'	3:R:3563:C:C6	2.70	0.41
1:H:39:SER:OG	1:H:40:GLN:N	2.54	0.41
3:R:1460:U:O2'	3:R:1461:U:P	2.79	0.41
3:R:2479:U:O2'	3:R:2480:C:P	2.79	0.41
3:R:2783:C:C3'	3:R:2783:C:C6	3.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:3555:G:HO2'	3:R:3556:C:P	2.30	0.41
1:E:62:VAL:HB	1:E:86:LEU:HB3	2.03	0.40
1:F:24:ASN:HB3	1:F:31:GLU:HB3	2.03	0.40
3:R:109:C:H5'	3:R:110:A:N7	2.37	0.40
3:R:1729:A:H2'	3:R:1730:G:N9	2.35	0.40
3:R:2843:U:C3'	3:R:2844:U:C5	3.03	0.40
2:M:62:ARG:NH2	3:R:3553:U:OP2	2.38	0.40
2:M:297:VAL:HG22	2:M:391:LEU:HD22	2.02	0.40
3:R:188:U:O2	3:R:188:U:O2'	2.27	0.40
3:R:1786:A:C6	3:R:1787:C:N4	2.90	0.40
3:R:2045:A:O2'	3:R:2046:U:P	2.79	0.40
3:R:2849:A:O2'	3:R:2850:C:P	2.79	0.40
1:E:108:MET:HG2	1:F:86:LEU:HD22	2.03	0.40
3:R:2480:C:HO2'	3:R:2481:A:C5'	2.33	0.40
1:E:25:PHE:HZ	3:R:3547:G:H22	1.53	0.40
1:H:78:PRO:HG3	2:M:302:PRO:HA	2.03	0.40
3:R:907:C:C5	3:R:908:G:N2	2.89	0.40
1:D:52:SER:OG	1:D:53:ALA:N	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
1	B	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
1	C	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
1	D	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
1	E	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
1	F	127/130 (98%)	122 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	115/130 (88%)	108 (94%)	7 (6%)	0	100	100
1	H	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
2	M	320/393 (81%)	315 (98%)	5 (2%)	0	100	100
All	All	1324/1433 (92%)	1280 (97%)	44 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	106/107 (99%)	106 (100%)	0	100	100
1	B	106/107 (99%)	106 (100%)	0	100	100
1	C	106/107 (99%)	105 (99%)	1 (1%)	78	90
1	D	106/107 (99%)	105 (99%)	1 (1%)	78	90
1	E	106/107 (99%)	106 (100%)	0	100	100
1	F	106/107 (99%)	105 (99%)	1 (1%)	78	90
1	G	99/107 (92%)	99 (100%)	0	100	100
1	H	106/107 (99%)	106 (100%)	0	100	100
2	M	280/330 (85%)	280 (100%)	0	100	100
All	All	1121/1186 (94%)	1118 (100%)	3 (0%)	92	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	49	ARG
1	D	36	ASN
1	F	129	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	116	ASN
1	B	116	ASN
1	B	125	ASN
1	C	116	ASN
1	D	36	ASN
1	D	116	ASN
1	F	109	GLN
1	F	116	ASN
1	G	116	ASN
1	H	116	ASN
2	M	11	ASN
2	M	211	GLN
2	M	352	GLN
2	M	357	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	R	228/3569 (6%)	164 (71%)	16 (7%)

All (164) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	R	104	A
3	R	106	U
3	R	107	U
3	R	109	C
3	R	110	A
3	R	114	C
3	R	180	C
3	R	184	C
3	R	185	G
3	R	186	C
3	R	188	U
3	R	189	U
3	R	190	U
3	R	191	A
3	R	192	C
3	R	194	C
3	R	195	G
3	R	196	G

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Mol	Chain	Res	Type
3	R	199	G
3	R	200	G
3	R	594	G
3	R	595	C
3	R	597	A
3	R	598	A
3	R	599	C
3	R	602	U
3	R	604	G
3	R	606	G
3	R	903	G
3	R	904	C
3	R	905	G
3	R	906	A
3	R	907	C
3	R	908	G
3	R	910	A
3	R	911	U
3	R	912	C
3	R	913	G
3	R	914	U
3	R	915	G
3	R	978	A
3	R	980	U
3	R	981	A
3	R	982	G
3	R	985	A
3	R	986	U
3	R	988	G
3	R	990	G
3	R	1461	U
3	R	1462	A
3	R	1463	C
3	R	1464	A
3	R	1465	A
3	R	1466	A
3	R	1467	G
3	R	1468	U
3	R	1469	A
3	R	1470	A
3	R	1721	C
3	R	1722	U

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Mol	Chain	Res	Type
3	R	1725	U
3	R	1726	A
3	R	1727	A
3	R	1728	U
3	R	1729	A
3	R	1730	G
3	R	1731	A
3	R	1750	G
3	R	1751	A
3	R	1753	G
3	R	1755	U
3	R	1756	U
3	R	1759	C
3	R	1760	C
3	R	1761	A
3	R	1762	U
3	R	1763	G
3	R	1778	G
3	R	1779	A
3	R	1780	A
3	R	1783	U
3	R	1784	C
3	R	1789	C
3	R	2041	A
3	R	2042	C
3	R	2043	A
3	R	2044	A
3	R	2045	A
3	R	2047	C
3	R	2049	U
3	R	2050	U
3	R	2051	G
3	R	2053	C
3	R	2375	U
3	R	2376	G
3	R	2378	C
3	R	2380	G
3	R	2381	U
3	R	2382	A
3	R	2383	A
3	R	2386	A
3	R	2469	G

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Mol	Chain	Res	Type
3	R	2470	A
3	R	2471	U
3	R	2472	C
3	R	2474	A
3	R	2475	U
3	R	2476	C
3	R	2477	G
3	R	2478	A
3	R	2479	U
3	R	2480	C
3	R	2481	A
3	R	2782	A
3	R	2783	C
3	R	2784	G
3	R	2785	A
3	R	2786	U
3	R	2788	U
3	R	2790	A
3	R	2791	U
3	R	2792	A
3	R	2794	G
3	R	2795	U
3	R	2841	G
3	R	2842	G
3	R	2843	U
3	R	2845	U
3	R	2846	U
3	R	2847	A
3	R	2848	A
3	R	2849	A
3	R	2850	C
3	R	2852	G
3	R	3360	U
3	R	3361	U
3	R	3362	C
3	R	3365	U
3	R	3366	C
3	R	3367	A
3	R	3368	G
3	R	3369	G
3	R	3371	G
3	R	3372	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	R	3542	A
3	R	3544	C
3	R	3545	U
3	R	3546	A
3	R	3547	G
3	R	3548	C
3	R	3549	U
3	R	3550	G
3	R	3551	C
3	R	3552	U
3	R	3553	U
3	R	3554	G
3	R	3555	G
3	R	3556	C
3	R	3557	U
3	R	3558	A
3	R	3561	U
3	R	3562	A
3	R	3563	C
3	R	3564	C

All (16) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	R	191	A
3	R	593	C
3	R	903	G
3	R	979	C
3	R	1460	U
3	R	1724	C
3	R	1729	A
3	R	1755	U
3	R	1782	U
3	R	2479	U
3	R	2791	U
3	R	2844	U
3	R	2849	A
3	R	2851	C
3	R	3550	G
3	R	3551	C

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

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

5.5 Carbohydrates (i)

There are no monosaccharides 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.

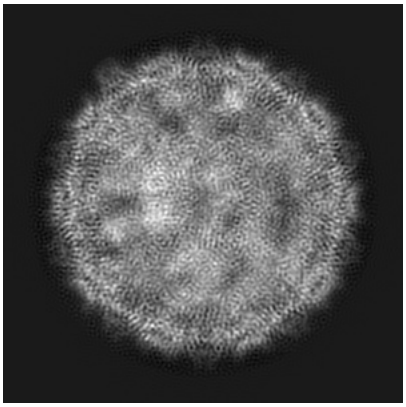
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-8397. These allow visual inspection of the internal detail of the map and identification of artifacts.

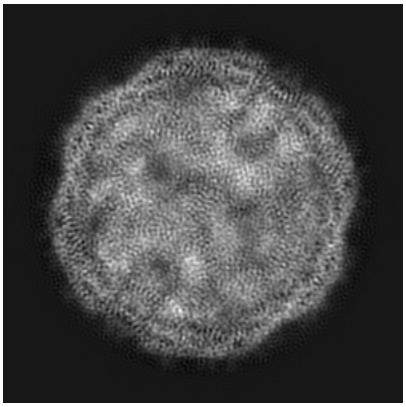
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

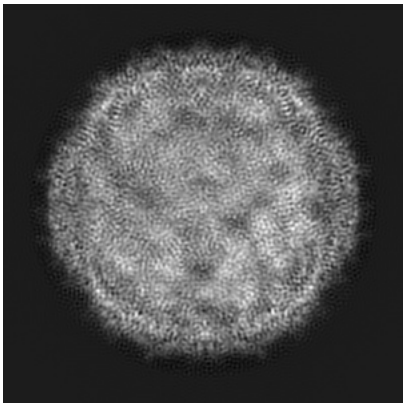
6.1.1 Primary map



X



Y

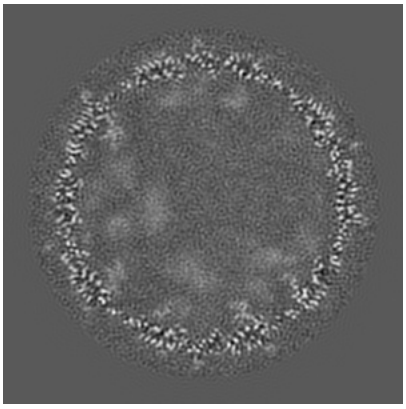


Z

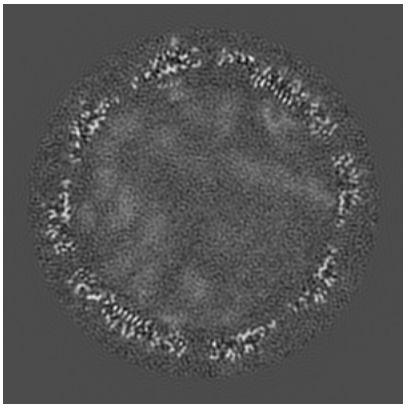
The images above show the map projected in three orthogonal directions.

6.2 Central slices

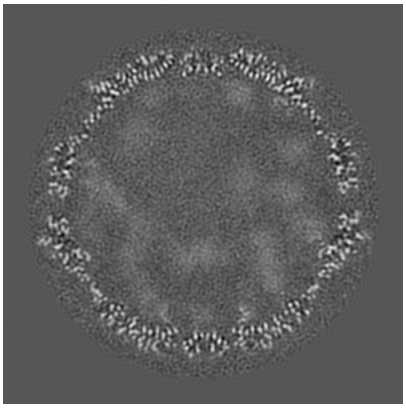
6.2.1 Primary map



X Index: 160



Y Index: 160

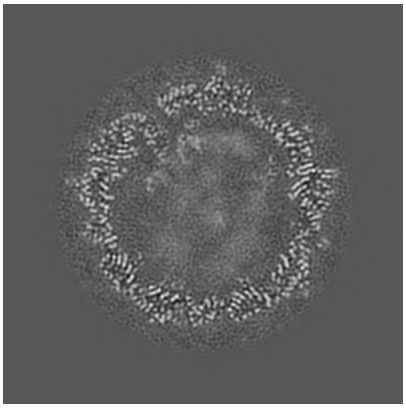


Z Index: 160

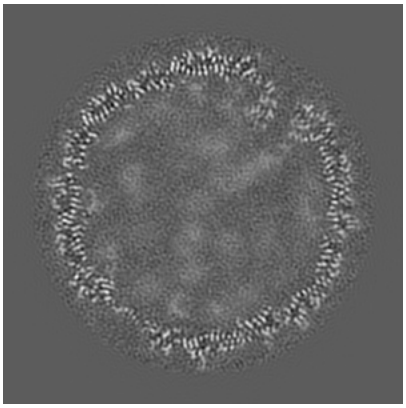
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

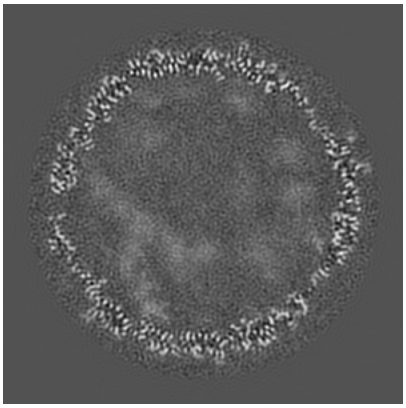
6.3.1 Primary map



X Index: 236



Y Index: 129



Z Index: 153

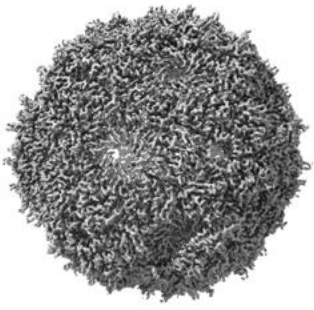
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

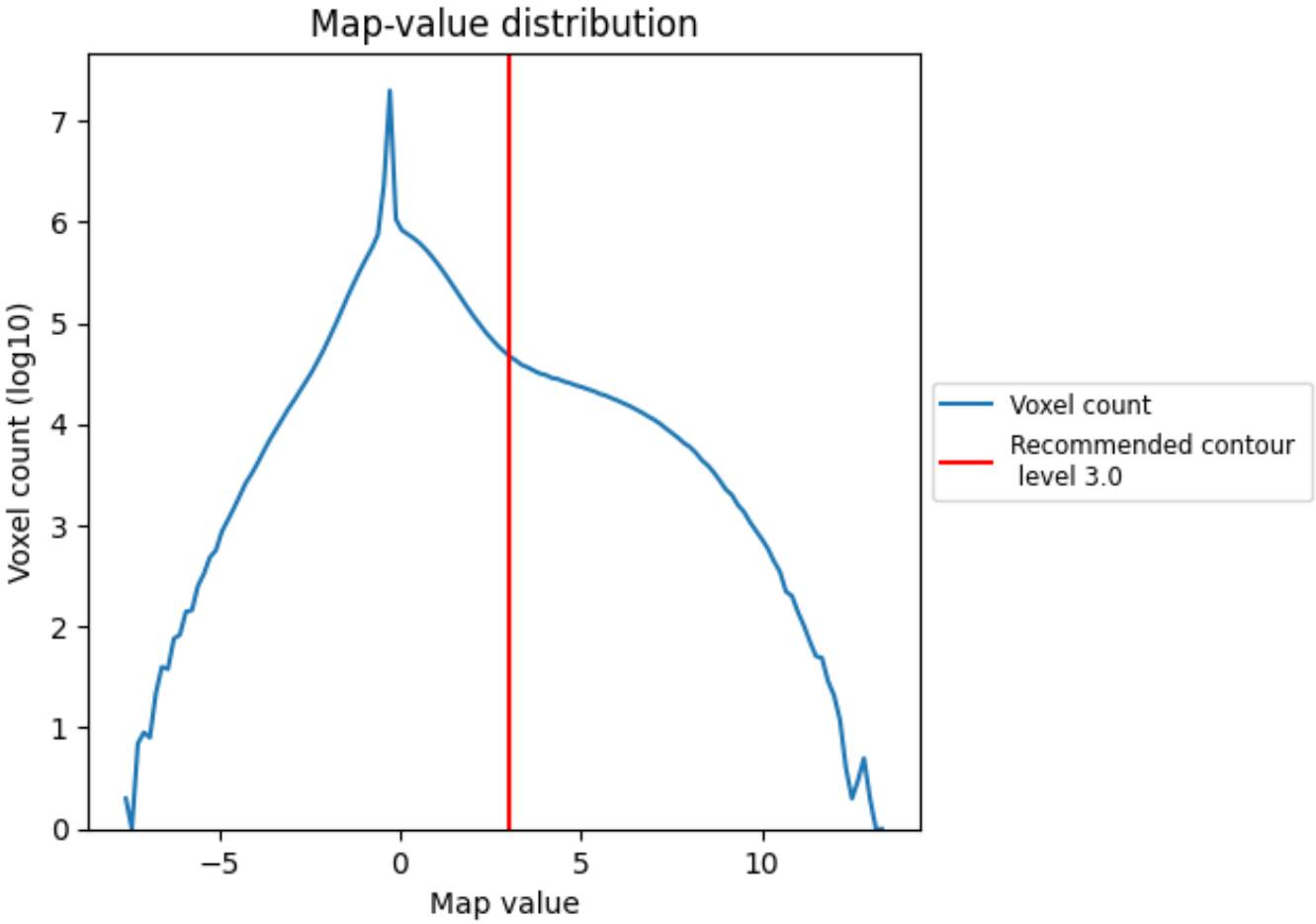
6.5 Mask visualisation (i)

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

7 Map analysis

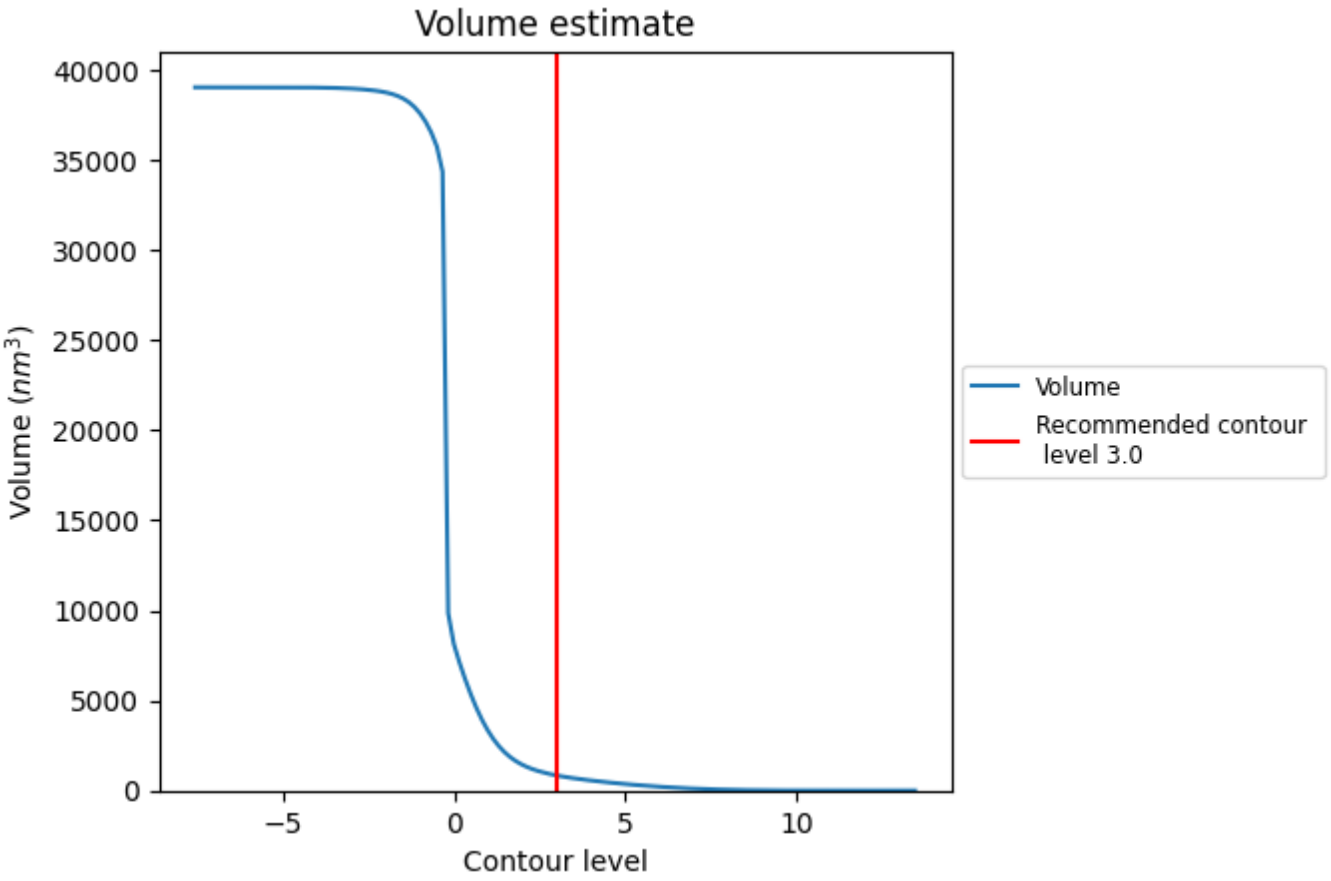
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

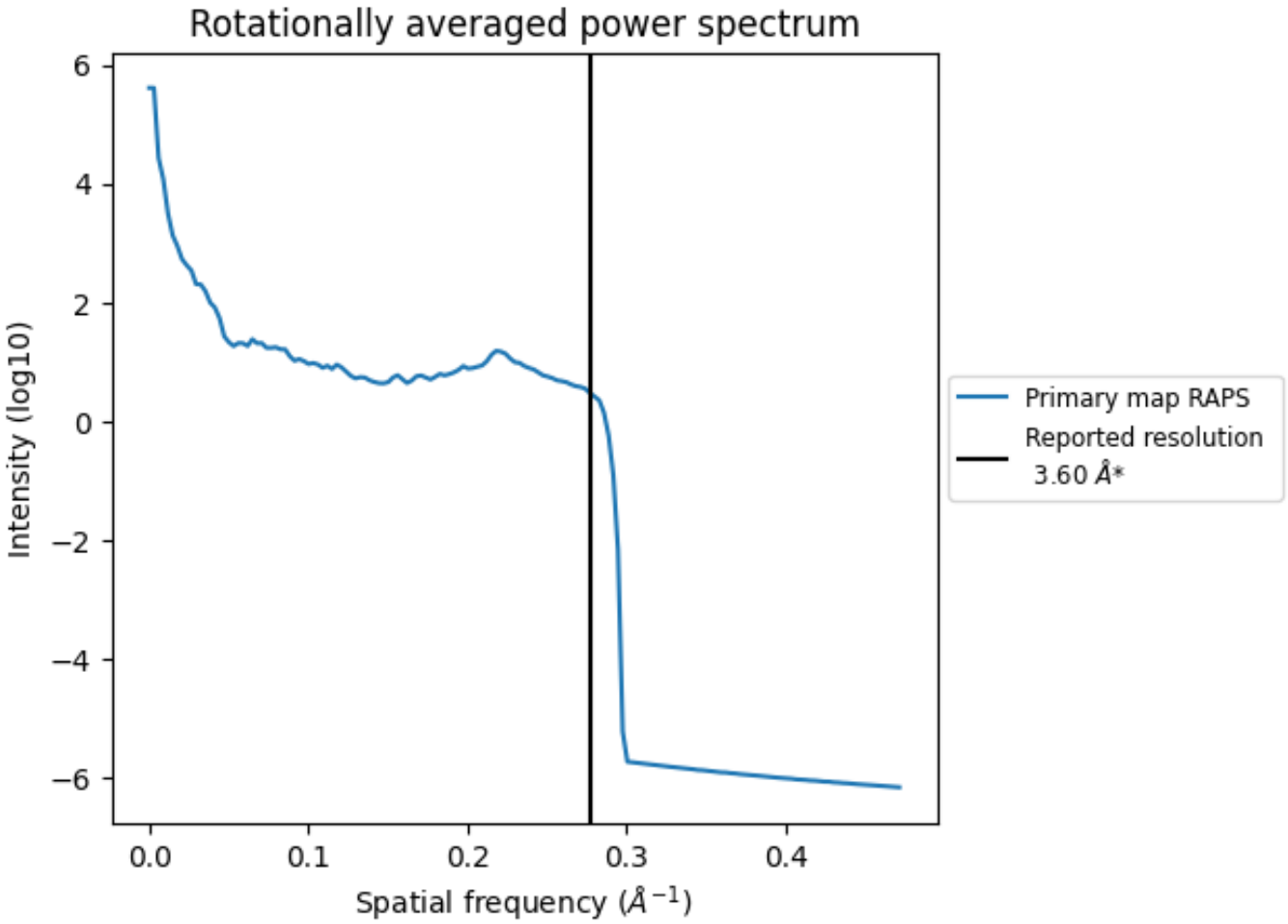
7.2 Volume estimate



The volume at the recommended contour level is 840 nm^3; this corresponds to an approximate mass of 759 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

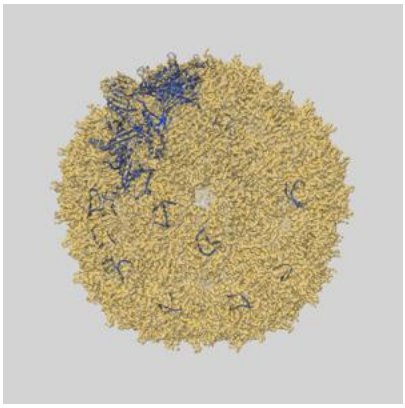
8 Fourier-Shell correlation

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

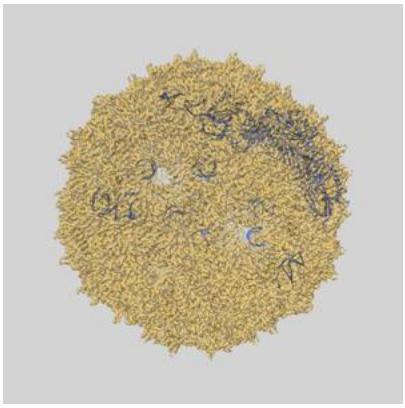
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-8397 and PDB model 5TC1. Per-residue inclusion information can be found in section 3 on page 5.

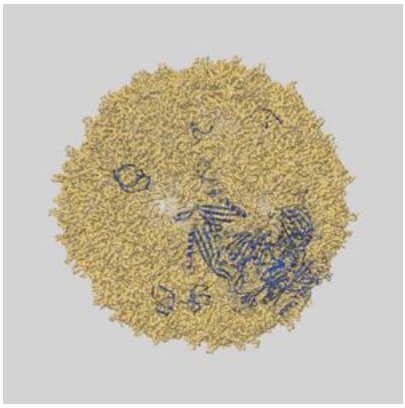
9.1 Map-model overlay



X



Y



Z

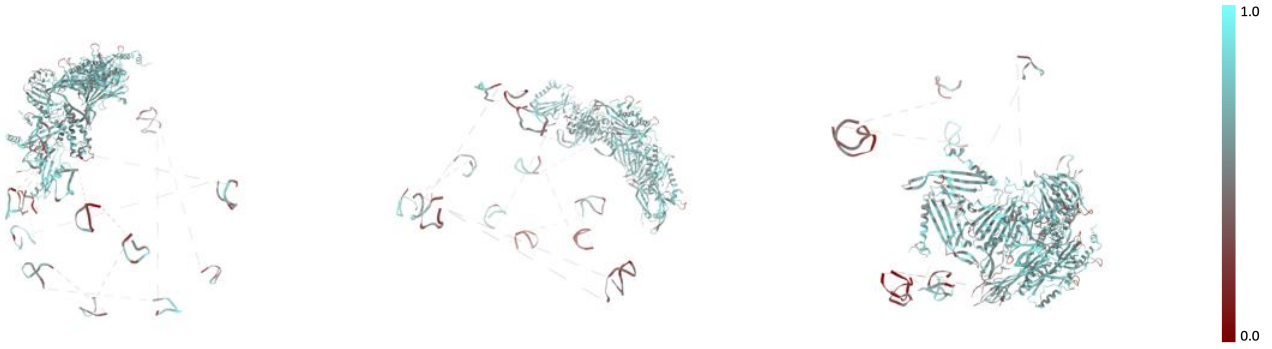
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)

X Y Z

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

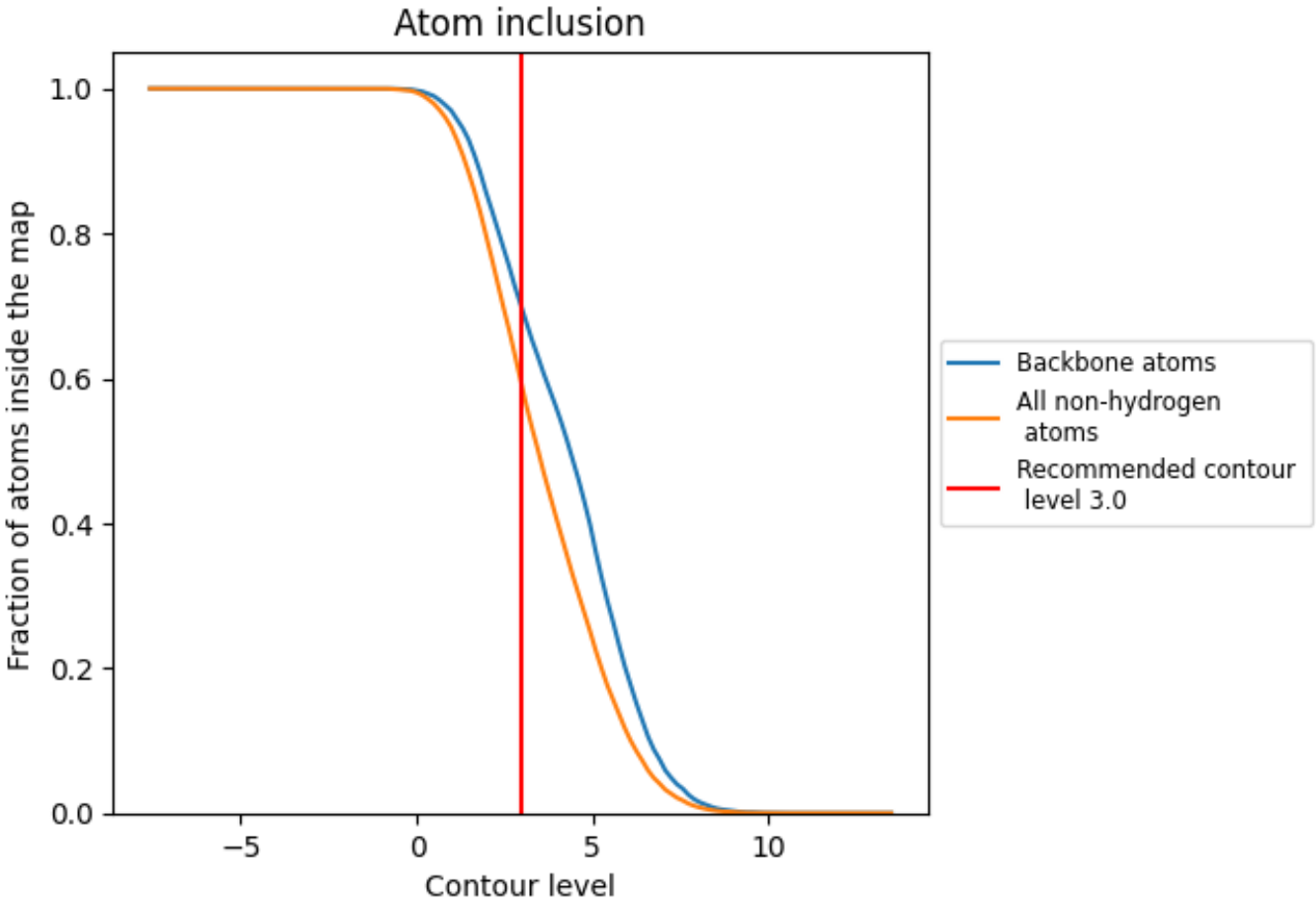
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.0).

9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 59% 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 (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5884	0.4830
A	0.6414	0.5210
B	0.6583	0.5190
C	0.6351	0.5110
D	0.6509	0.5190
E	0.6467	0.5080
F	0.6267	0.5100
G	0.6765	0.5130
H	0.6530	0.5180
M	0.6124	0.5020
R	0.4883	0.4270