



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 01:30 PM UTC

PDB ID : 5IT9 / pdb_00005it9
EMDB ID : EMD-8124
Title : Structure of the yeast *Kluyveromyces lactis* small ribosomal subunit in complex with the cricket paralysis virus IRES.
Authors : Murray, J.; Savva, C.G.; Shin, B.S.; Dever, T.E.; Ramakrishnan, V.; Fernandez, I.S.
Deposited on : 2016-03-16
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

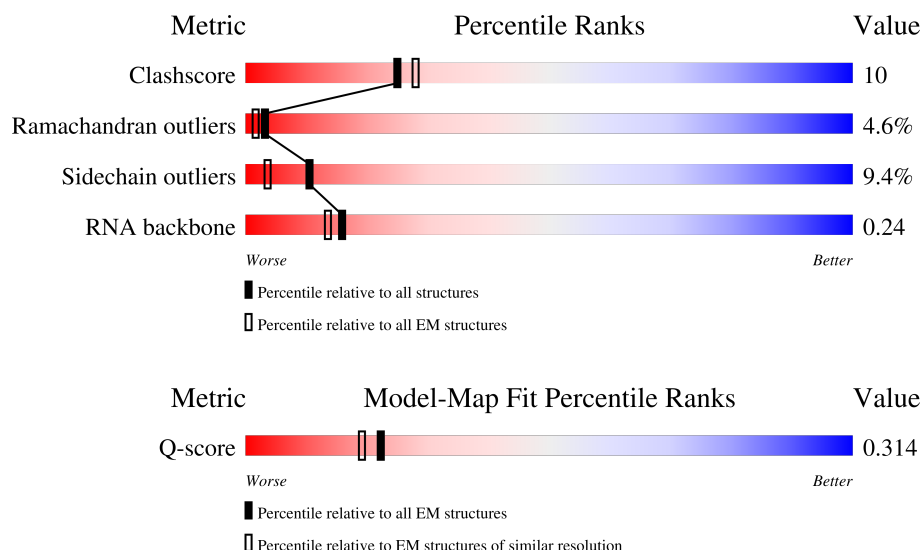
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	A	206	
2	B	214	
3	C	217	

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Mol	Chain	Length	Quality of chain
4	D	223	
5	E	260	
6	F	206	
7	G	226	
8	H	184	
9	I	200	
10	J	182	
11	K	96	
12	L	155	
13	M	122	
14	N	150	
15	O	127	
16	P	123	
17	Q	141	
18	R	129	
19	S	145	
20	T	143	
21	U	106	
22	V	87	
23	W	129	
24	X	145	
25	Y	134	
26	Z	70	
27	a	100	
28	b	82	

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Mol	Chain	Length	Quality of chain
29	c	63	13% 90% 10%
30	d	53	• 89% 9% •
31	e	55	25% 91% 9%
32	f	69	64% 71% 22% 7%
33	g	324	18% 90% 8% •
34	2	1780	13% 36% 46% 16% •
35	i	192	69% 27% 38% 35% •

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 80144 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 Ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	206	Total	C	N	O	S	0	0
			1616	1035	285	294	2		

- Molecule 2 is a protein called Ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	214	Total	C	N	O	S	0	0
			1722	1089	313	317	3		

- Molecule 3 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	217	Total	C	N	O	S	0	0
			1629	1041	287	297	4		

- Molecule 4 is a protein called Ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	223	Total	C	N	O	S	0	0
			1744	1108	313	318	5		

- Molecule 5 is a protein called Ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	260	Total	C	N	O	S	0	0
			2078	1322	393	359	4		

- Molecule 6 is a protein called Ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	206	Total	C	N	O	S	0	0
			1609	1008	298	300	3		

- Molecule 7 is a protein called Ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	226	Total	C	N	O	S	0	0
			1812	1134	348	326	4		

- Molecule 8 is a protein called Ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	184	Total	C	N	O	S	0	0
			1483	950	270	263			

- Molecule 9 is a protein called Ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	188	Total	C	N	O	S	0	0
			1493	926	301	265	1		

- Molecule 10 is a protein called Ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	182	Total	C	N	O	S	0	0
			1471	929	287	254	1		

- Molecule 11 is a protein called Ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	96	Total	C	N	O	S	0	0
			809	533	129	146	1		

- Molecule 12 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	155	Total	C	N	O	S	0	0
			1248	798	237	210	3		

- Molecule 13 is a protein called Ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	122	Total	C	N	O	S	0	0
			922	575	167	180			

- Molecule 14 is a protein called Ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	150	Total	C	N	O	S	0	0
			1187	756	223	206	2		

- Molecule 15 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	127	Total	C	N	O	S	0	0
			942	578	188	173	3		

- Molecule 16 is a protein called Ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	123	Total	C	N	O	S	0	0
			980	628	179	168	5		

- Molecule 17 is a protein called Ribosomal protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	141	Total	C	N	O		
			1105	709	204	192	0	0

- Molecule 18 is a protein called Ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	129	Total	C	N	O	S	0	0
			1031	641	193	194	3		

- Molecule 19 is a protein called Ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	145	Total	C	N	O	S	0	0
			1193	741	240	210	2		

- Molecule 20 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	143	Total	C	N	O		
			1110	693	210	207	0	0

- Molecule 21 is a protein called Ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 22 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 23 is a protein called Ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 24 is a protein called Ribosomal protein uS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	145	Total	C	N	O	S	0	0
			1127	713	219	192	3		

- Molecule 25 is a protein called Ribosomal protein eS24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	134	Total	C	N	O	0	0
			1061	665	207	189		

- Molecule 26 is a protein called Ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	70	Total	C	N	O	S	0	0
			558	355	104	98	1		

- Molecule 27 is a protein called Ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	100	Total	C	N	O	S	0	0
			798	491	170	131	6		

- Molecule 28 is a protein called Ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	82	Total	C	N	O	S	0	0
			617	384	113	114	6		

- Molecule 29 is a protein called Ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	63	Total	C	N	O	S	0	0
			494	305	98	90	1		

- Molecule 30 is a protein called Ribosomal protein eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	53	Total	C	N	O	S	0	0
			446	280	89	76	1		

- Molecule 31 is a protein called Ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	55	Total	C	N	O	S	0	0
			443	276	90	76	1		

- Molecule 32 is a protein called Ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	69	Total	C	N	O	S	0	0
			549	352	102	91	4		

- Molecule 33 is a protein called Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	318	Total	C	N	O	S	0	0
			2466	1561	430	470	5		

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2	1780	Total	C	N	O	P	0	0
			37797	16892	6658	12467	1780		

- Molecule 35 is a RNA chain called Cricket paralysis virus IRES RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	192	Total	C	N	O	P	0	0
			3968	1774	669	1333	192		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
i	6176	C	U	conflict	GB 8895506

- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	G	1	Total	Mg	0
			1	1	
36	N	1	Total	Mg	0
			1	1	
36	T	1	Total	Mg	0
			1	1	
36	X	1	Total	Mg	0
			1	1	
36	2	76	Total	Mg	0
			76	76	

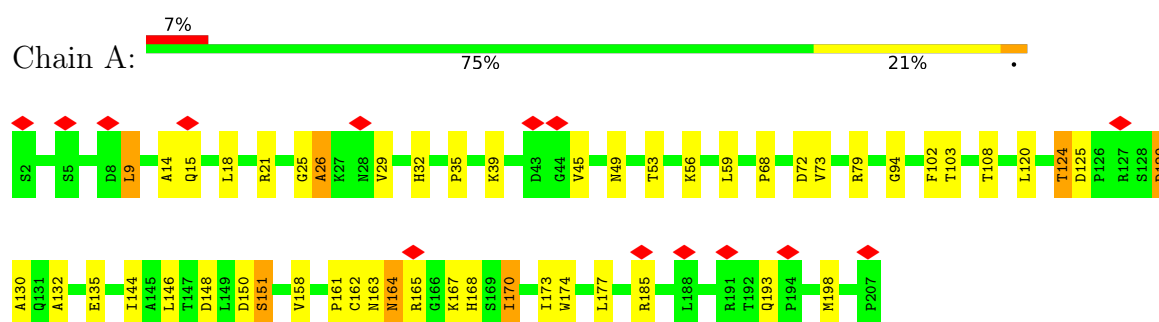
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	a	1	Total	Zn	0
			1	1	
37	b	1	Total	Zn	0
			1	1	
37	f	1	Total	Zn	0
			1	1	

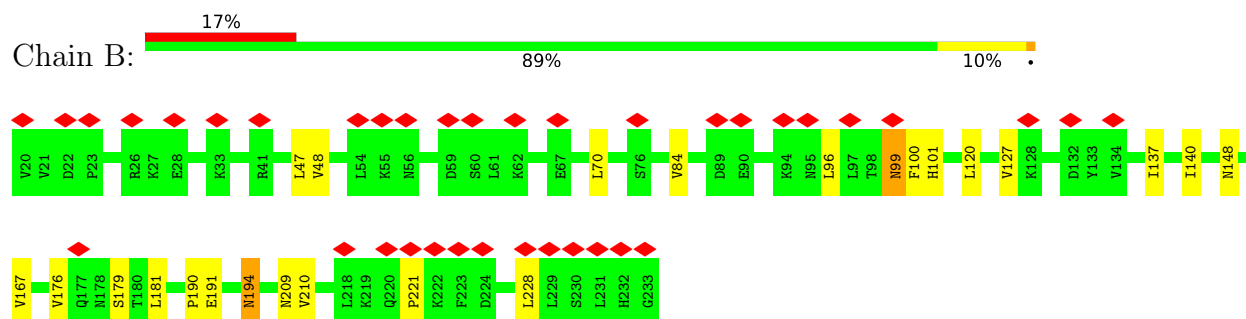
3 Residue-property plots

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

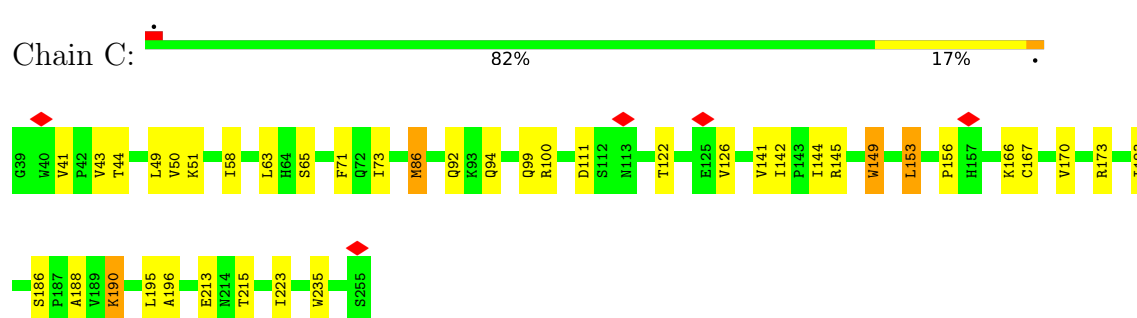
• Molecule 1: Ribosomal protein uS2



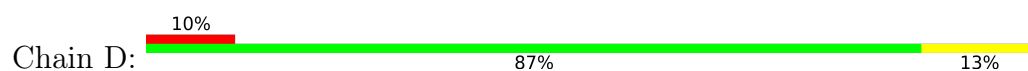
• Molecule 2: Ribosomal protein eS1

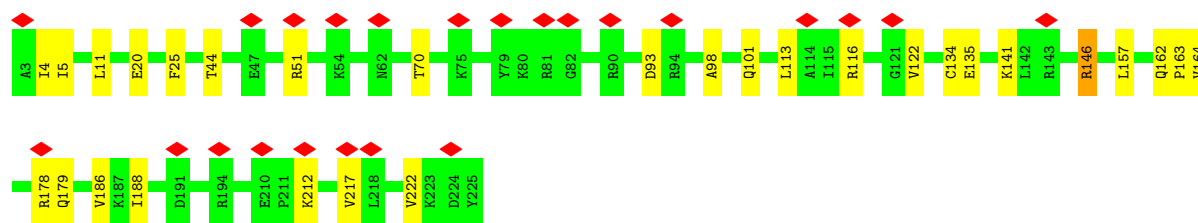


• Molecule 3: Ribosomal protein uS5

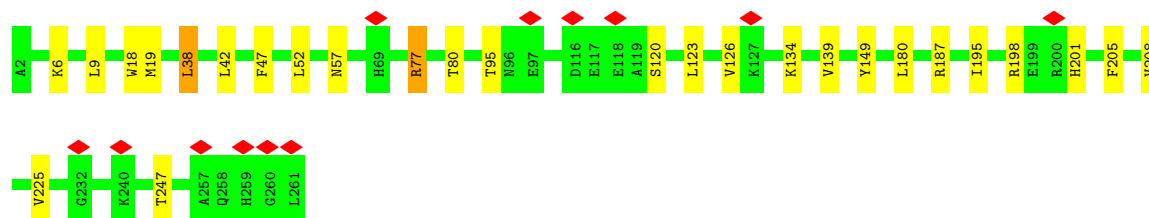
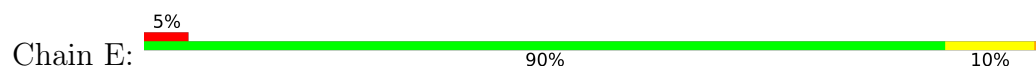


• Molecule 4: Ribosomal protein uS3

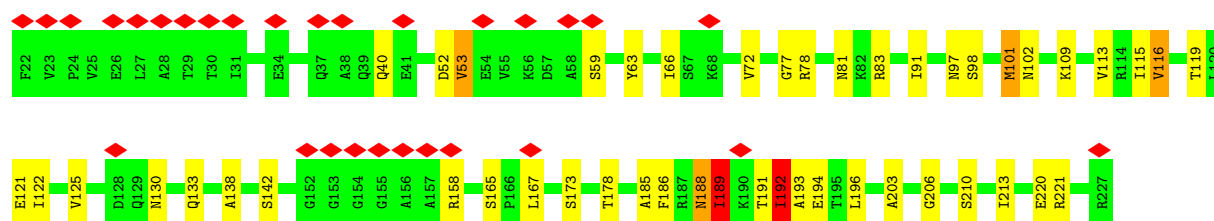
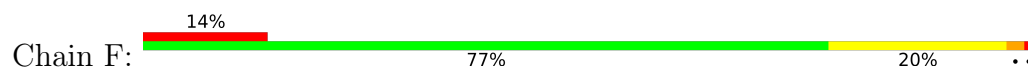




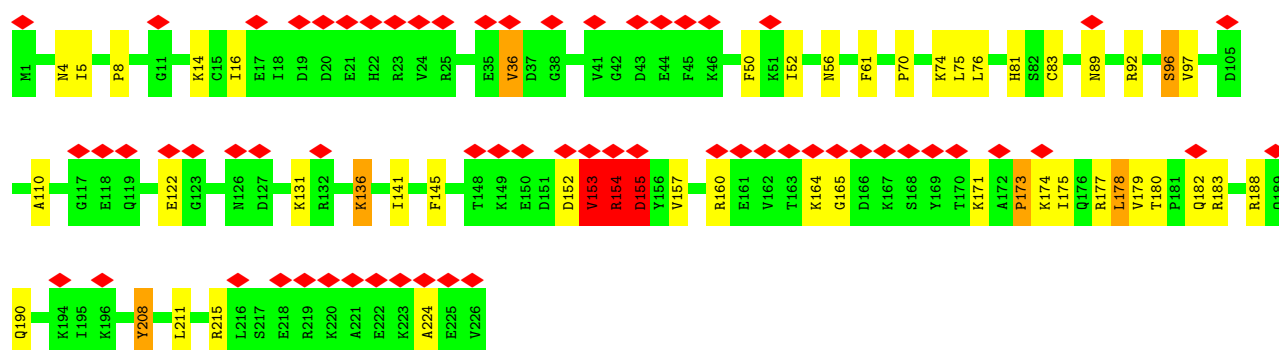
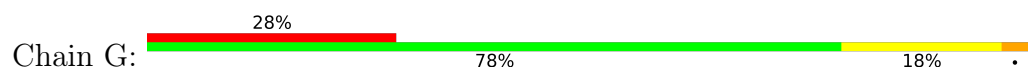
• Molecule 5: Ribosomal protein eS4



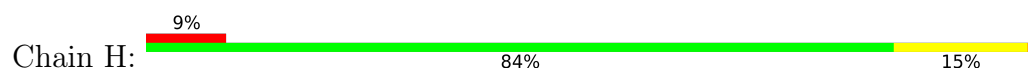
• Molecule 6: Ribosomal protein uS7

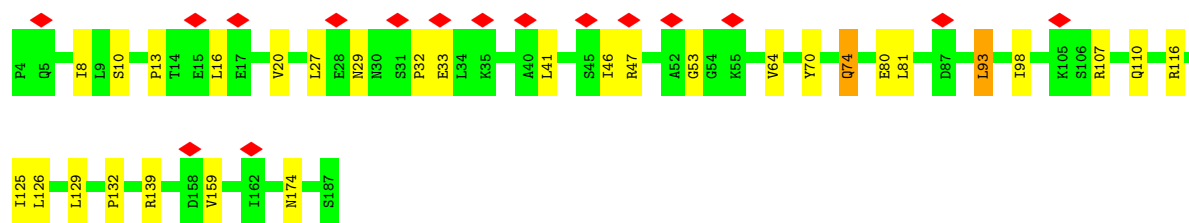


• Molecule 7: Ribosomal protein eS6

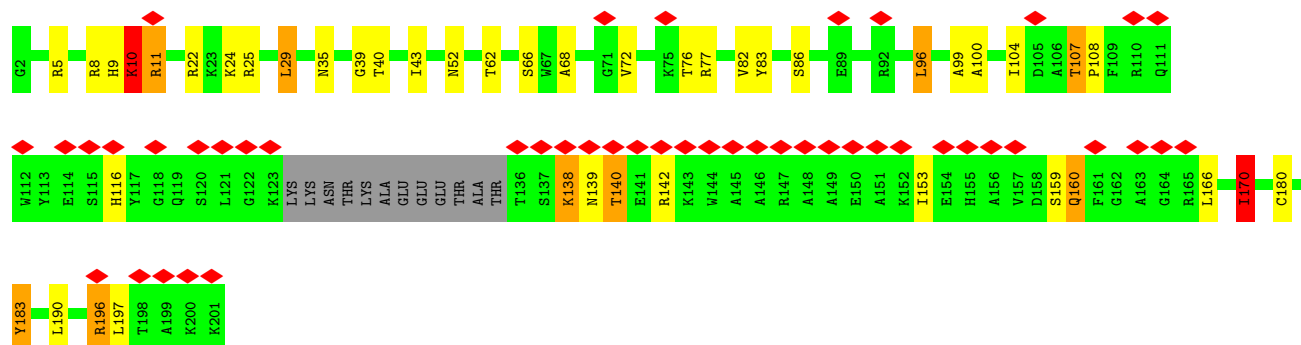
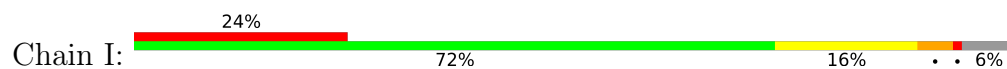


• Molecule 8: Ribosomal protein eS7

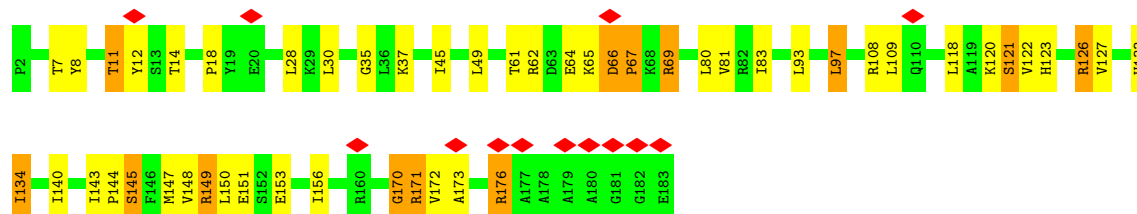




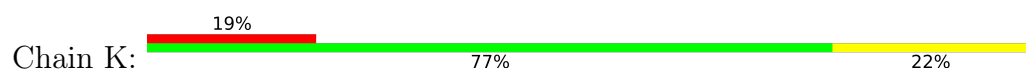
• Molecule 9: Ribosomal protein eS8



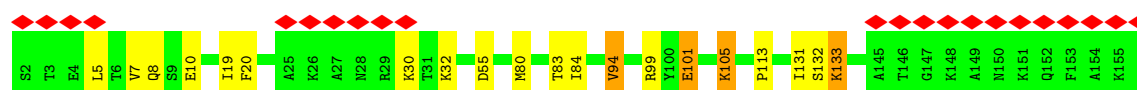
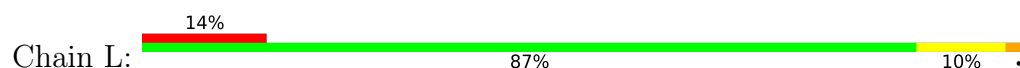
• Molecule 10: Ribosomal protein uS4



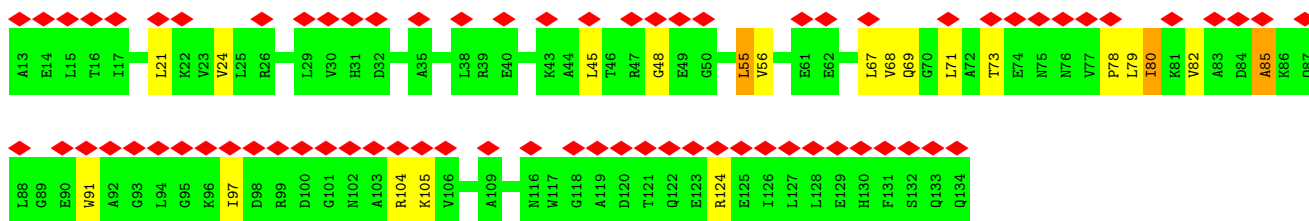
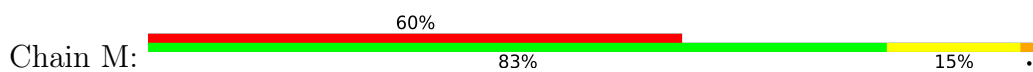
• Molecule 11: Ribosomal protein eS10



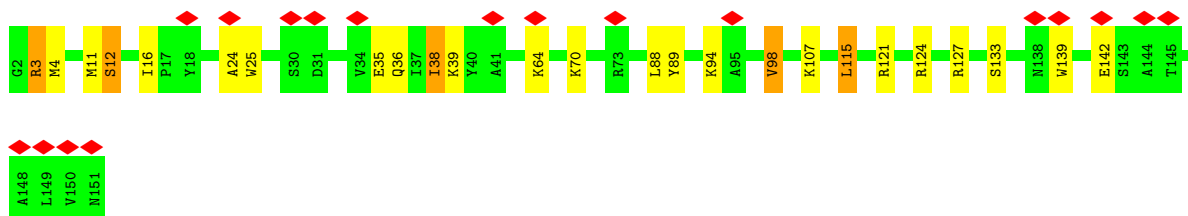
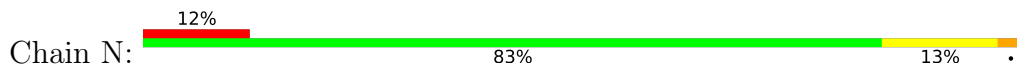
• Molecule 12: Ribosomal protein uS17



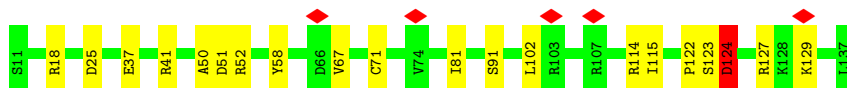
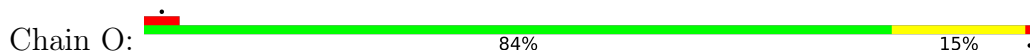
• Molecule 13: Ribosomal protein eS12



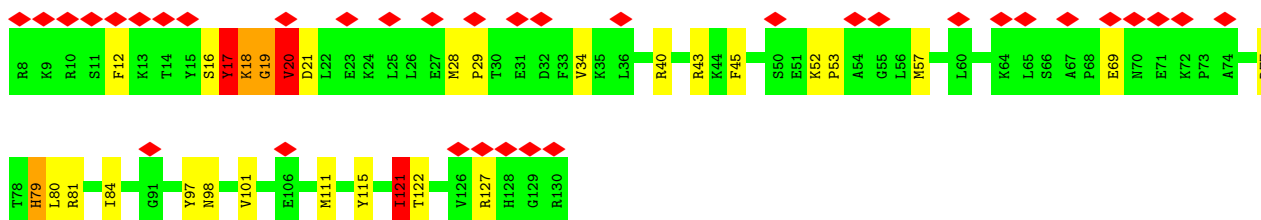
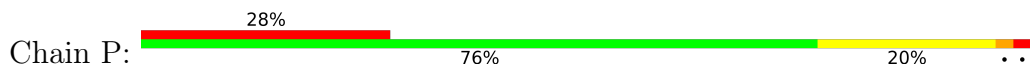
• Molecule 14: Ribosomal protein uS15



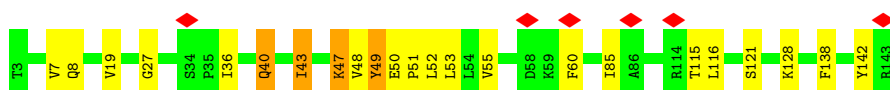
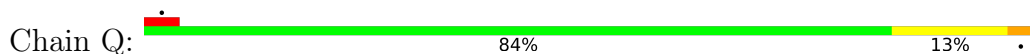
• Molecule 15: Ribosomal protein uS14



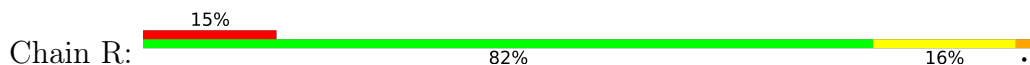
• Molecule 16: Ribosomal protein uS19

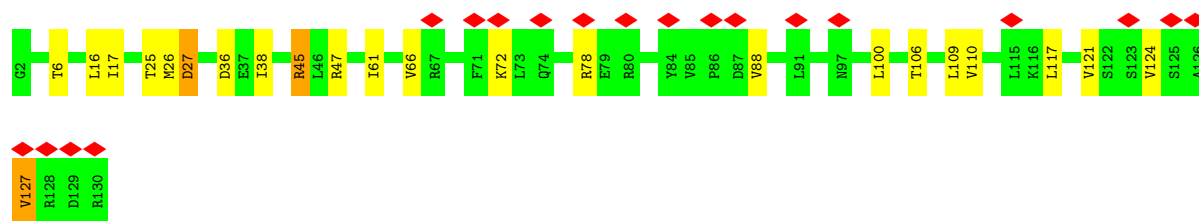


• Molecule 17: Ribosomal protein uS9

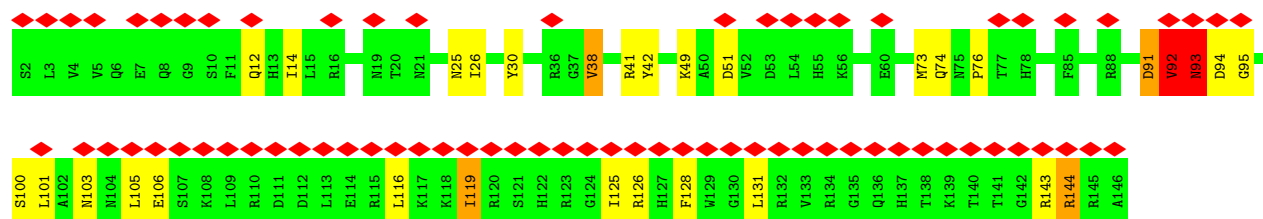
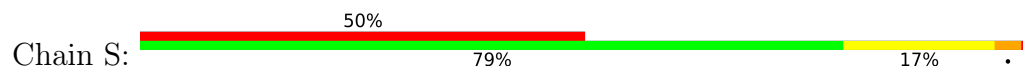


• Molecule 18: Ribosomal protein eS17

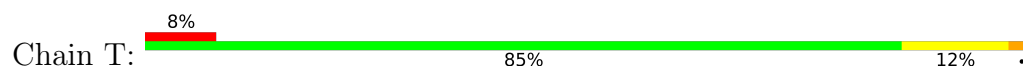




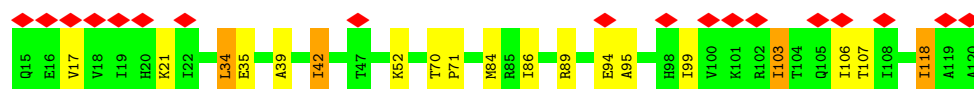
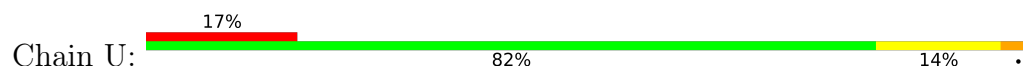
• Molecule 19: Ribosomal protein uS13



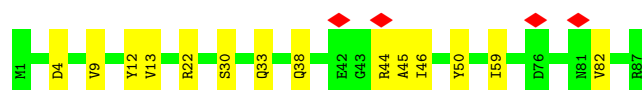
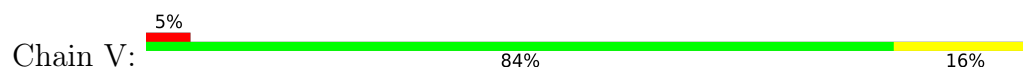
• Molecule 20: Ribosomal protein eS19



• Molecule 21: Ribosomal protein uS10



• Molecule 22: Ribosomal protein eS21



• Molecule 23: Ribosomal protein uS8





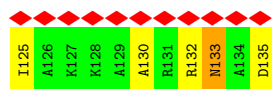
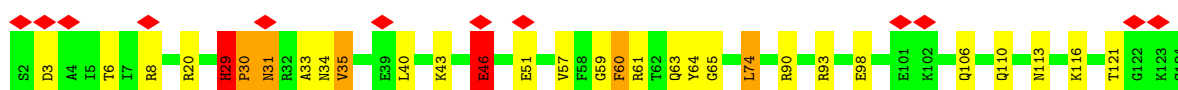
- Molecule 24: Ribosomal protein uS21

Chain X: 77% 18% . .



- Molecule 25: Ribosomal protein eS24

Chain Y: 17% 74% 20% . .



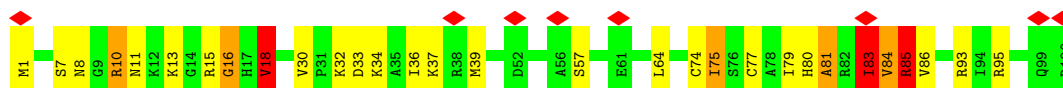
- Molecule 26: Ribosomal protein eS25

Chain Z: 29% 56% 33% 10% .



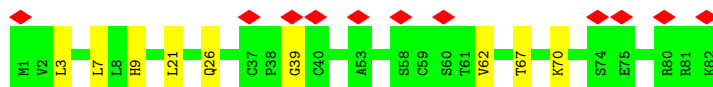
- Molecule 27: Ribosomal protein eS26

Chain a: 8% 70% 22% 5% .



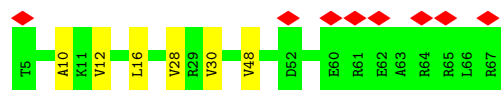
- Molecule 28: Ribosomal protein eS27

Chain b: 13% 89% 11%

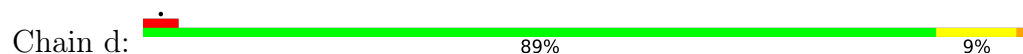


- Molecule 29: Ribosomal protein eS28

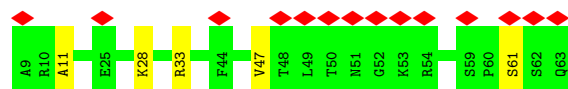
Chain c: 13% 90% 10%



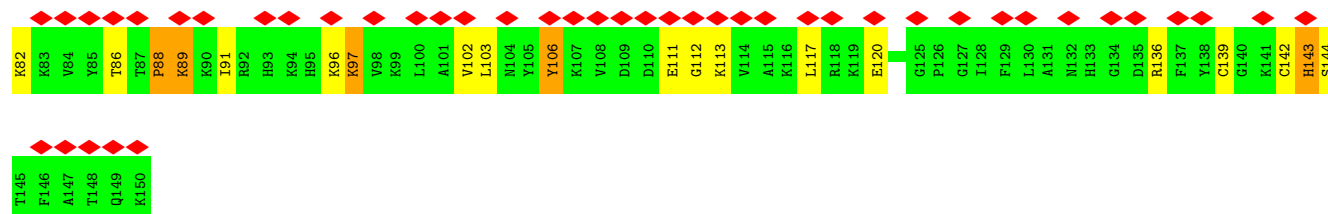
- Molecule 30: Ribosomal protein eS29



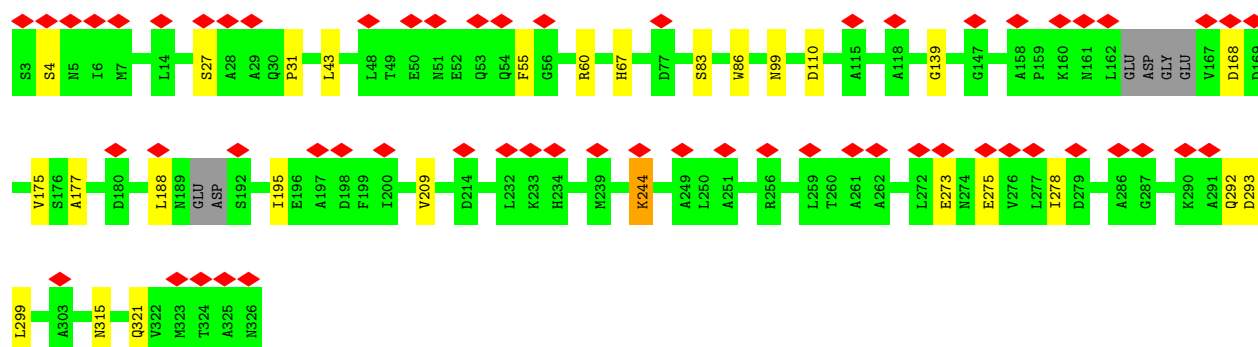
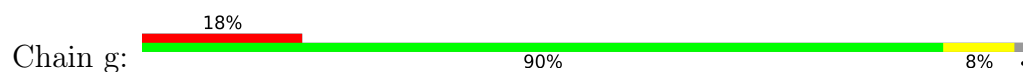
- Molecule 31: Ribosomal protein eS30



- Molecule 32: Ribosomal protein eS31

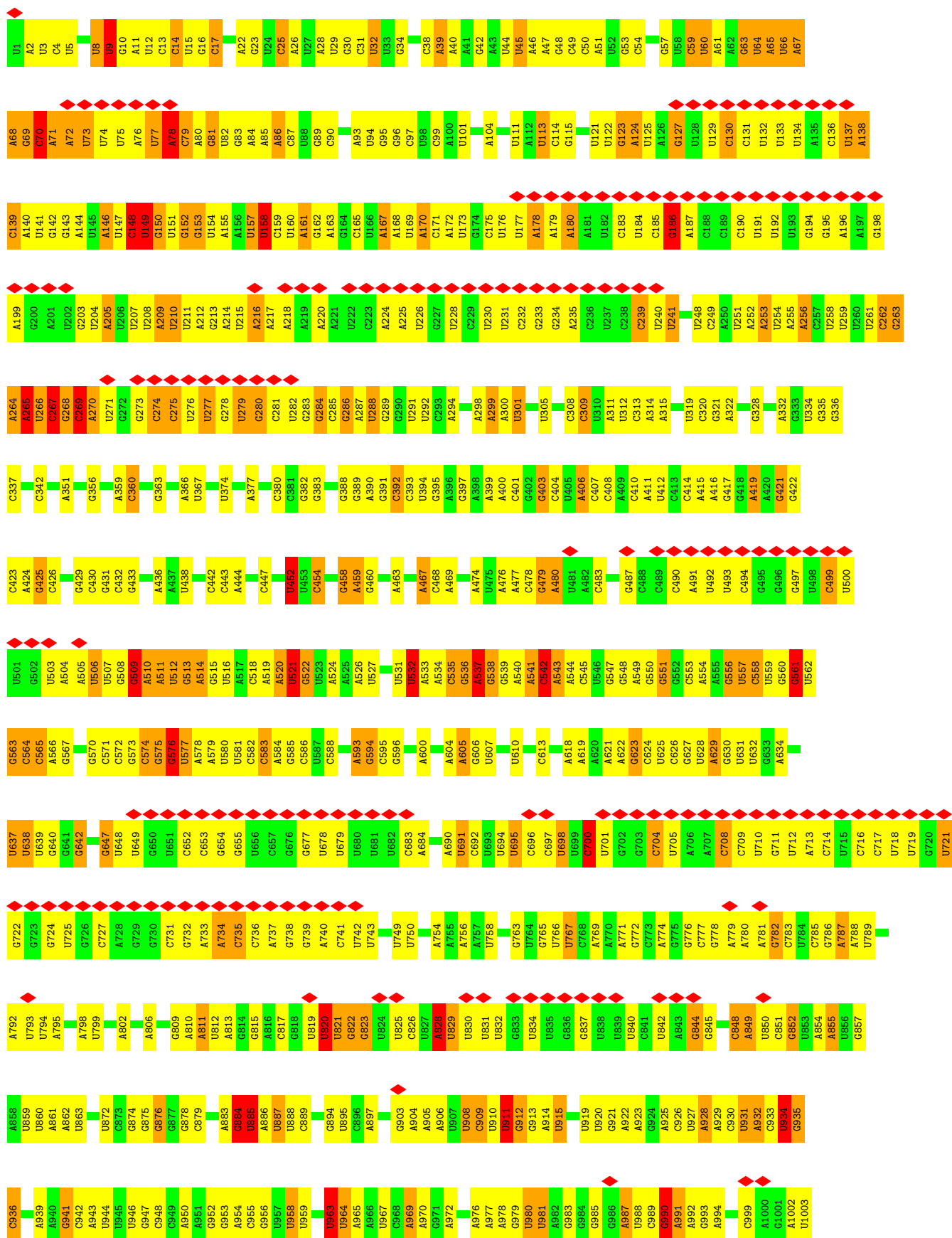


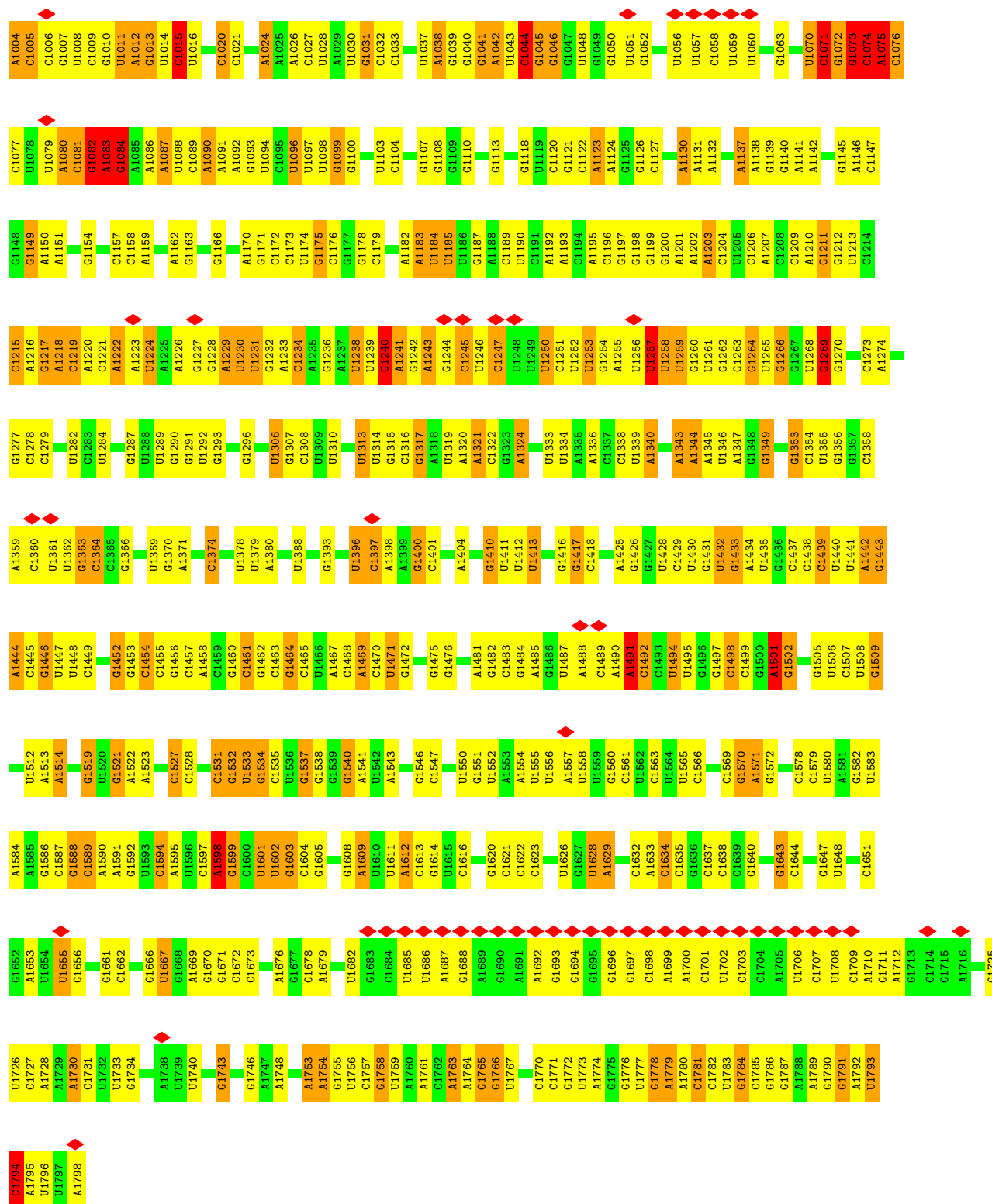
- Molecule 33: Ribosomal protein RACK1



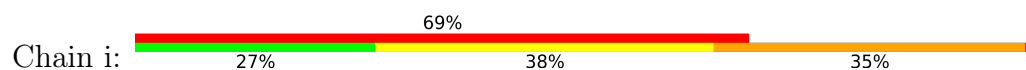
- Molecule 34: 18S ribosomal RNA

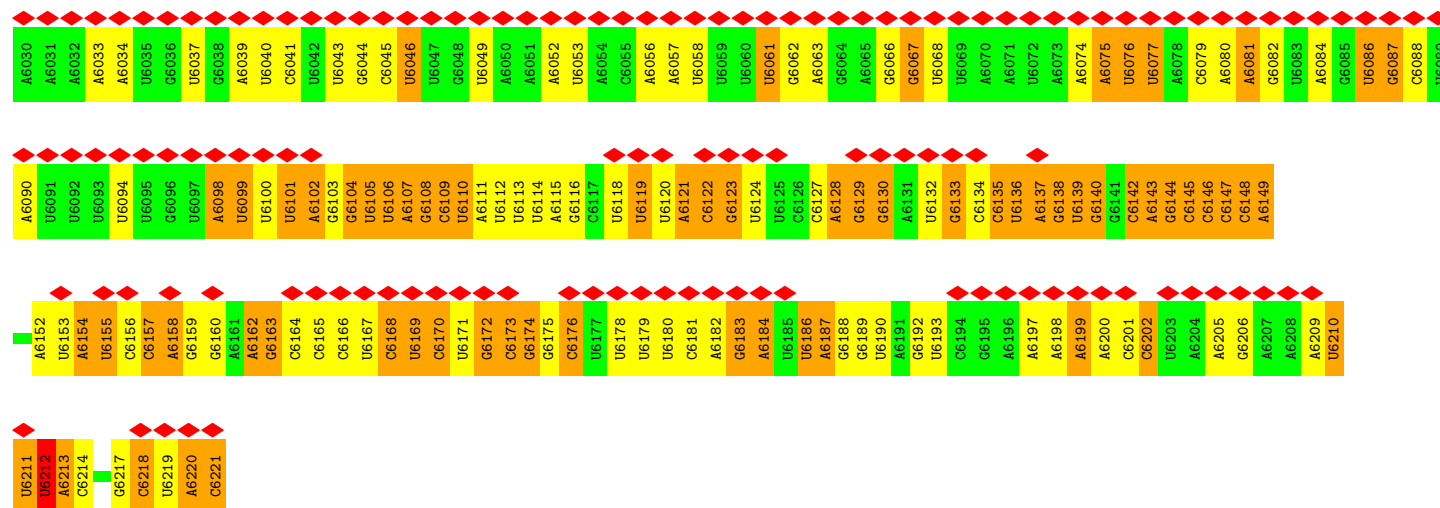






• Molecule 35: Cricket paralysis virus IRES RNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54481	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.973	Depositor
Minimum map value	-0.641	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	375.2, 375.2, 375.2	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	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, MG

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	0.56	0/1656	1.06	4/2264 (0.2%)
2	B	0.54	0/1747	0.94	0/2353
3	C	0.50	0/1659	0.98	0/2252
4	D	0.49	0/1769	0.93	1/2378 (0.0%)
5	E	0.52	0/2122	0.84	2/2861 (0.1%)
6	F	0.52	0/1628	1.15	6/2198 (0.3%)
7	G	0.72	3/1835 (0.2%)	1.05	12/2451 (0.5%)
8	H	0.53	0/1507	1.00	0/2028
9	I	0.55	0/1519	1.00	3/2033 (0.1%)
10	J	0.59	1/1495 (0.1%)	1.17	3/2001 (0.1%)
11	K	0.53	0/831	1.05	2/1123 (0.2%)
12	L	0.50	0/1276	0.77	0/1718
13	M	0.56	0/929	1.05	0/1255
14	N	0.54	0/1210	1.17	2/1628 (0.1%)
15	O	0.58	0/953	0.99	0/1279
16	P	0.79	5/1000 (0.5%)	1.05	3/1343 (0.2%)
17	Q	0.53	0/1125	1.04	0/1510
18	R	0.56	0/1042	1.16	1/1399 (0.1%)
19	S	0.68	4/1212 (0.3%)	1.11	4/1629 (0.2%)
20	T	0.47	0/1129	1.09	2/1520 (0.1%)
21	U	0.53	0/857	0.95	1/1158 (0.1%)
22	V	0.51	0/696	0.90	1/938 (0.1%)
23	W	0.52	0/1039	1.12	1/1399 (0.1%)
24	X	0.50	0/1145	0.99	3/1526 (0.2%)
25	Y	0.53	0/1075	1.02	1/1433 (0.1%)
26	Z	0.57	0/567	1.28	4/762 (0.5%)
27	a	0.60	0/810	0.98	3/1084 (0.3%)
28	b	0.48	0/627	0.82	0/847
29	c	0.54	0/496	0.77	0/666
30	d	0.49	0/457	0.80	0/607
31	e	0.48	0/450	0.90	0/599
32	f	0.65	0/562	0.85	0/751

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.50	0/2521	0.69	0/3431
34	2	0.41	8/42269 (0.0%)	0.83	88/65862 (0.1%)
35	i	0.25	1/4425 (0.0%)	0.35	2/6875 (0.0%)
All	All	0.48	22/85640 (0.0%)	0.89	149/125161 (0.1%)

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
1	A	0	2
7	G	0	1
10	J	0	1
15	O	0	1
17	Q	0	2
22	V	0	1
23	W	0	1
26	Z	0	1
27	a	0	1
34	2	0	7
All	All	0	18

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	154	ARG	CA-C	14.08	1.71	1.52
7	G	154	ARG	N-CA	9.13	1.57	1.46
34	2	934	U	O3'-P	-8.14	1.49	1.61
19	S	93	ASN	N-CA	7.88	1.56	1.46
35	i	6109	C	O3'-P	-7.73	1.49	1.61
16	P	18	LYS	CA-C	7.51	1.62	1.53
7	G	155	ASP	N-CA	7.27	1.55	1.46
16	P	20	VAL	N-CA	7.27	1.55	1.46
34	2	1073	G	C2-N2	-6.81	1.21	1.34
19	S	93	ASN	CA-C	6.66	1.61	1.52
16	P	19	GLY	N-CA	6.62	1.54	1.45
34	2	78	A	O5'-C5'	6.37	1.52	1.42
34	2	511	A	O5'-C5'	5.86	1.51	1.42
16	P	20	VAL	CA-C	5.82	1.60	1.52
10	J	170	GLY	CA-C	5.74	1.59	1.51
34	2	8	U	O3'-P	-5.63	1.52	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	P	17	TYR	CA-C	5.53	1.60	1.52
34	2	1072	G	C2-N2	5.35	1.45	1.34
34	2	1074	C	C4-N4	5.21	1.44	1.33
19	S	92	VAL	CA-C	5.07	1.59	1.52
19	S	92	VAL	N-CA	5.06	1.52	1.46
34	2	520	A	O3'-P	-5.03	1.53	1.61

All (149) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	Z	68	ARG	N-CA-C	-19.50	88.93	112.92
34	2	1074	C	C2'-C3'-O3'	13.55	134.03	113.70
34	2	78	A	C4'-C3'-O3'	10.58	128.88	113.00
34	2	1534	G	C2'-C3'-O3'	9.24	123.36	109.50
34	2	1075	A	C4'-C3'-O3'	8.87	122.70	109.40
34	2	704	C	C4'-C3'-O3'	8.71	122.47	109.40
34	2	1083	A	C4'-C3'-O3'	-8.54	100.20	113.00
35	i	6212	U	C2'-C3'-O3'	-8.49	100.97	113.70
34	2	828	A	C2'-C3'-O3'	8.44	122.17	109.50
34	2	113	U	C4'-C3'-O3'	-8.32	100.53	113.00
16	P	16	SER	N-CA-C	8.29	119.57	108.38
34	2	963	U	C2'-C3'-O3'	8.21	121.82	109.50
6	F	192	ILE	N-CA-CB	7.99	120.46	110.47
34	2	1532	G	C2'-C3'-O3'	7.98	121.47	109.50
34	2	279	U	C2'-C3'-O3'	7.89	121.33	109.50
16	P	18	LYS	N-CA-C	7.78	123.88	109.56
20	T	80	TYR	N-CA-C	7.78	119.83	111.36
34	2	73	U	C2'-C3'-O3'	7.77	121.15	109.50
34	2	239	C	C4'-C3'-O3'	7.67	120.91	109.40
34	2	79	C	C3'-C2'-O2'	7.61	122.12	110.70
34	2	1501	A	C2'-C3'-O3'	7.59	120.88	109.50
34	2	1655	U	C4'-C3'-O3'	7.57	120.76	109.40
34	2	78	A	C5'-C4'-C3'	7.56	127.34	116.00
34	2	1243	A	C2'-C3'-O3'	7.53	120.79	109.50
34	2	532	U	C2'-C3'-O3'	-7.50	102.44	113.70
16	P	20	VAL	N-CA-C	7.35	124.63	109.34
34	2	885	U	C1'-C2'-O2'	-7.27	97.49	108.40
34	2	1074	C	N1-C1'-C2'	-7.22	101.17	112.00
6	F	192	ILE	CB-CA-C	-7.20	102.61	112.04
7	G	145	PHE	N-CA-C	7.16	118.98	111.03
34	2	931	U	C3'-C2'-O2'	-7.16	103.86	114.60
34	2	934	U	C2'-C3'-O3'	-7.16	102.96	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	130	ASN	CA-C-N	7.14	126.64	118.85
6	F	130	ASN	C-N-CA	7.14	126.64	118.85
34	2	1073	G	C1'-C2'-O2'	-7.11	101.14	111.80
34	2	700	C	C2'-C3'-O3'	6.95	119.92	109.50
10	J	176	ARG	N-CA-CB	6.84	119.92	110.01
34	2	1071	C	C4'-C3'-O3'	-6.82	102.77	113.00
34	2	1628	U	C4'-C3'-O3'	6.77	123.16	113.00
34	2	78	A	C2'-C3'-O3'	-6.75	103.58	113.70
5	E	57	ASN	CA-C-N	6.70	127.38	119.94
5	E	57	ASN	C-N-CA	6.70	127.38	119.94
34	2	1433	G	C2'-C3'-O3'	-6.70	103.66	113.70
19	S	93	ASN	N-CA-C	6.68	125.04	110.80
34	2	209	A	C3'-C2'-O2'	6.67	120.71	110.70
34	2	537	A	C4'-C3'-O3'	6.58	119.27	109.40
34	2	1794	C	C2'-C3'-O3'	6.54	119.32	109.50
34	2	269	C	C4'-C3'-O3'	6.52	119.17	109.40
34	2	884	G	C1'-C2'-O2'	6.44	118.06	108.40
34	2	78	A	P-O5'-C5'	6.41	130.51	120.90
24	X	41	SER	CA-C-N	6.40	127.84	119.84
24	X	41	SER	C-N-CA	6.40	127.84	119.84
34	2	1071	C	C3'-C2'-O2'	-6.35	101.17	110.70
1	A	170	ILE	CB-CA-C	-6.32	103.89	111.97
19	S	30	TYR	CB-CA-C	6.31	121.26	110.79
7	G	153	VAL	N-CA-C	6.29	118.19	108.44
34	2	277	U	C2'-C3'-O3'	6.27	118.91	109.50
34	2	149	U	C1'-C2'-O2'	-6.25	102.42	111.80
34	2	1791	G	C4'-C3'-O3'	6.22	118.73	109.40
34	2	186	G	C4'-C3'-O3'	6.20	118.70	109.40
7	G	154	ARG	CA-C-N	6.20	133.38	121.54
7	G	154	ARG	C-N-CA	6.20	133.38	121.54
24	X	64	PRO	CA-N-CD	-6.17	103.36	112.00
26	Z	54	ALA	N-CA-C	-6.15	104.43	113.16
34	2	113	U	C2'-C3'-O3'	6.15	122.92	113.70
34	2	577	U	C4'-C3'-O3'	6.10	118.55	109.40
34	2	557	U	C2'-C3'-O3'	6.06	118.59	109.50
14	N	38	ILE	N-CA-CB	6.05	117.63	110.55
34	2	1491	A	C3'-C2'-O2'	6.00	119.71	110.70
34	2	542	C	C3'-C2'-O2'	5.99	123.58	114.60
34	2	522	G	C1'-C2'-O2'	-5.98	99.42	108.40
1	A	165	ARG	N-CA-C	-5.97	104.69	111.14
21	U	42	ILE	N-CA-CB	5.96	118.65	110.54
34	2	1149	G	C2'-C3'-O3'	-5.91	104.83	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	81	VAL	N-CA-CB	5.91	118.58	110.54
11	K	87	PHE	CA-C-N	5.89	127.20	119.84
11	K	87	PHE	C-N-CA	5.89	127.20	119.84
7	G	153	VAL	CA-C-N	5.87	132.76	121.54
7	G	153	VAL	C-N-CA	5.87	132.76	121.54
7	G	155	ASP	N-CA-C	5.87	123.30	110.80
34	2	721	U	C2'-C3'-O3'	5.86	118.29	109.50
14	N	98	VAL	N-CA-CB	5.86	118.50	110.54
7	G	154	ARG	N-CA-C	5.83	123.22	110.80
27	a	57	SER	N-CA-C	5.82	117.57	110.41
9	I	183	TYR	N-CA-C	5.82	118.14	108.13
34	2	1609	A	C3'-C2'-O2'	5.82	119.42	110.70
7	G	14	LYS	N-CA-C	5.81	117.68	108.79
20	T	11	ALA	N-CA-C	5.79	123.13	110.80
9	I	138	LYS	N-CA-C	5.76	119.49	112.23
7	G	155	ASP	CB-CA-C	-5.75	98.99	110.42
34	2	1084	G	C3'-C2'-O2'	5.75	119.32	110.70
23	W	44	HIS	CB-CA-C	5.74	119.90	110.88
6	F	142	SER	N-CA-C	5.72	119.52	112.54
34	2	708	C	C4'-C3'-O3'	5.71	117.96	109.40
6	F	189	ILE	CB-CA-C	-5.69	104.46	112.14
34	2	269	C	C2'-C3'-O3'	5.69	118.03	109.50
19	S	119	ILE	N-CA-CB	5.68	118.27	110.54
34	2	1257	U	C3'-C2'-O2'	5.68	119.21	110.70
26	Z	54	ALA	CA-C-N	-5.67	113.94	119.78
26	Z	54	ALA	C-N-CA	-5.67	113.94	119.78
9	I	170	ILE	N-CA-CB	5.66	116.70	110.53
34	2	1601	U	C4'-C3'-O3'	-5.65	104.53	113.00
34	2	452	U	N1-C1'-C2'	5.62	120.44	112.00
34	2	1015	C	C1'-C2'-O2'	5.60	116.80	108.40
34	2	265	A	C2'-C3'-O3'	5.59	117.89	109.50
35	i	6210	U	C4'-C3'-O3'	-5.58	104.63	113.00
4	D	25	PHE	CB-CA-C	5.58	120.05	110.79
34	2	421	G	C4'-C3'-O3'	-5.57	104.64	113.00
7	G	208	TYR	CA-CB-CG	-5.57	103.87	113.90
34	2	912	G	C3'-C2'-O2'	5.57	119.05	110.70
34	2	911	U	N1-C1'-C2'	5.56	122.34	114.00
34	2	1082	G	P-O3'-C3'	-5.55	111.88	120.20
34	2	1240	G	C4'-C3'-O3'	5.52	121.28	113.00
18	R	78	ARG	O-C-N	5.51	127.75	122.07
34	2	695	U	C2'-C3'-O3'	5.49	117.74	109.50
34	2	1598	A	C4'-C3'-O3'	5.47	117.61	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	2	509	G	C2'-C3'-O3'	-5.42	105.57	113.70
34	2	1011	U	C4'-C3'-O3'	-5.38	104.94	113.00
34	2	9	U	C3'-C2'-O2'	-5.37	102.64	110.70
27	a	18	VAL	N-CA-C	5.37	120.50	109.34
34	2	511	A	P-O5'-C5'	5.36	128.93	120.90
34	2	299	A	C4'-C3'-O3'	-5.33	105.00	113.00
10	J	170	GLY	N-CA-C	5.33	125.81	113.18
34	2	1634	C	C4'-C3'-O3'	5.33	117.40	109.40
34	2	1521	G	C2'-C3'-O3'	-5.31	105.73	113.70
34	2	158	U	C2'-C3'-O3'	5.31	117.46	109.50
34	2	1071	C	C2'-C3'-O3'	5.31	121.66	113.70
34	2	990	G	C2'-C3'-O3'	-5.30	105.75	113.70
22	V	59	ILE	N-CA-CB	5.28	116.73	110.55
34	2	1074	C	C3'-C2'-C1'	5.28	106.58	101.30
34	2	521	U	C4'-C3'-O3'	-5.23	105.16	113.00
34	2	148	C	C2'-C3'-O3'	5.23	121.54	113.70
34	2	1045	G	C4'-C3'-O3'	-5.18	105.24	113.00
34	2	267	C	C3'-C2'-O2'	5.14	118.41	110.70
19	S	91	ASP	N-CA-C	5.13	116.87	108.76
34	2	277	U	C4'-C3'-O3'	5.13	117.10	109.40
34	2	130	C	C4'-C3'-O3'	5.12	117.08	109.40
34	2	78	A	O4'-C4'-C3'	-5.12	98.88	104.00
34	2	638	U	C4'-C3'-O3'	5.10	117.05	109.40
1	A	129	ASP	CA-C-N	5.09	131.26	121.54
1	A	129	ASP	C-N-CA	5.09	131.26	121.54
25	Y	46	GLU	N-CA-CB	5.09	117.60	110.12
34	2	576	G	C4'-C3'-O3'	5.08	117.02	109.40
7	G	208	TYR	CB-CA-C	5.08	119.22	110.79
34	2	820	U	N1-C1'-C2'	5.07	119.61	112.00
34	2	70	C	C2'-C3'-O3'	5.06	121.29	113.70
27	a	83	ILE	CB-CA-C	-5.05	103.00	111.29
34	2	1074	C	O4'-C4'-C3'	5.02	109.02	104.00
34	2	884	G	C3'-C2'-O2'	5.00	118.20	110.70

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	2	1044	C	Sidechain
34	2	1073	G	Sidechain
34	2	1074	C	Sidechain
34	2	1269	G	Sidechain

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Mol	Chain	Res	Type	Group
34	2	1439	C	Sidechain
34	2	561	G	Sidechain
34	2	583	C	Sidechain
1	A	164	ASN	Peptide
1	A	168	HIS	Peptide
7	G	155	ASP	Peptide
10	J	66	ASP	Peptide
15	O	122	PRO	Peptide
17	Q	40	GLN	Peptide
17	Q	49	TYR	Peptide
22	V	13	VAL	Peptide
23	W	75	ILE	Peptide
26	Z	68	ARG	Sidechain
27	a	83	ILE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1616	0	1636	18	0
2	B	1722	0	1795	3	0
3	C	1629	0	1710	8	0
4	D	1744	0	1825	22	0
5	E	2078	0	2157	5	0
6	F	1609	0	1679	28	0
7	G	1812	0	1911	58	0
8	H	1483	0	1579	6	0
9	I	1493	0	1515	20	0
10	J	1471	0	1554	39	0
11	K	809	0	810	4	0
12	L	1248	0	1311	6	0
13	M	922	0	953	7	0
14	N	1187	0	1251	6	0
15	O	942	0	979	27	0
16	P	980	0	1026	23	0
17	Q	1105	0	1170	6	0
18	R	1031	0	1082	6	0
19	S	1193	0	1217	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	T	1110	0	1124	4	0
21	U	845	0	913	5	0
22	V	687	0	682	2	0
23	W	1021	0	1056	12	0
24	X	1127	0	1210	23	0
25	Y	1061	0	1111	15	0
26	Z	558	0	585	77	0
27	a	798	0	855	15	0
28	b	617	0	642	1	0
29	c	494	0	534	2	0
30	d	446	0	436	2	0
31	e	443	0	481	1	0
32	f	549	0	564	8	0
33	g	2466	0	2406	2	0
34	2	37797	0	19010	969	0
35	i	3968	0	1986	204	0
36	2	76	0	0	0	0
36	G	1	0	0	0	0
36	N	1	0	0	0	0
36	T	1	0	0	0	0
36	X	1	0	0	0	0
37	a	1	0	0	0	0
37	b	1	0	0	0	0
37	f	1	0	0	0	0
All	All	80144	0	60755	1441	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 10.

All (1441) 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)
4:D:116:ARG:CZ	35:i:6220:A:C2	1.74	1.62
4:D:116:ARG:NH2	35:i:6220:A:C2	1.70	1.49
4:D:116:ARG:CZ	35:i:6220:A:N1	1.70	1.46
26:Z:52:LYS:HA	26:Z:53:GLU:CG	1.47	1.43
34:2:513:G:H1	34:2:542:C:N4	1.27	1.31
15:O:58:TYR:HB2	35:i:6111:A:N6	1.42	1.30
24:X:63:GLN:NE2	34:2:1753:A:OP1	1.64	1.29
34:2:480:A:N1	34:2:506:U:C4	2.04	1.26
4:D:116:ARG:NE	35:i:6220:A:N1	1.83	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:51:MET:O	26:Z:53:GLU:HA	1.13	1.26
34:2:1072:G:N2	34:2:1073:G:N7	1.84	1.24
34:2:480:A:N1	34:2:506:U:O4	1.72	1.22
26:Z:58:ARG:NH1	26:Z:103:ARG:HH22	1.40	1.20
10:J:170:GLY:O	34:2:511:A:H5''	1.39	1.18
34:2:1044:C:N3	34:2:1072:G:N2	1.90	1.18
34:2:1292:U:O4	34:2:1321:A:N1	1.77	1.17
4:D:116:ARG:NH1	35:i:6220:A:C2	2.13	1.17
10:J:170:GLY:O	34:2:511:A:P	2.05	1.15
34:2:1044:C:N4	34:2:1072:G:H1	1.44	1.15
10:J:170:GLY:O	34:2:511:A:C5'	1.93	1.14
34:2:1221:C:O2	34:2:1261:U:O2	1.67	1.13
34:2:1754:A:N1	35:i:6189:G:O2'	1.83	1.12
7:G:155:ASP:N	34:2:78:A:O5'	1.83	1.11
4:D:146:ARG:HH21	35:i:6218:C:N4	1.49	1.10
26:Z:53:GLU:HB3	26:Z:55:PRO:HD2	1.34	1.10
10:J:170:GLY:C	34:2:511:A:P	2.36	1.08
26:Z:51:MET:O	26:Z:53:GLU:CA	2.02	1.08
7:G:136:LYS:NZ	34:2:65:A:OP1	1.87	1.08
34:2:955:C:O2'	34:2:1046:G:O2'	1.71	1.08
26:Z:52:LYS:HA	26:Z:53:GLU:HG3	1.08	1.07
7:G:154:ARG:N	34:2:78:A:O5'	1.87	1.07
24:X:63:GLN:HE21	34:2:1753:A:P	1.77	1.07
10:J:170:GLY:HA3	34:2:511:A:H5'	1.36	1.07
7:G:155:ASP:H	34:2:78:A:C5'	1.68	1.07
26:Z:58:ARG:NH1	26:Z:103:ARG:NH2	2.02	1.06
26:Z:63:SER:O	26:Z:66:VAL:O	1.70	1.06
34:2:1292:U:C4	34:2:1321:A:N1	2.23	1.06
15:O:58:TYR:CG	35:i:6111:A:C5	2.44	1.06
26:Z:52:LYS:CA	26:Z:53:GLU:HG3	1.87	1.05
26:Z:54:ALA:HB2	26:Z:83:LEU:HD22	1.39	1.05
26:Z:52:LYS:HA	26:Z:53:GLU:HG2	1.37	1.04
34:2:138:A:N7	34:2:265:A:H2	1.55	1.03
34:2:1072:G:C2	34:2:1073:G:N7	2.24	1.03
26:Z:51:MET:C	26:Z:53:GLU:HA	1.83	1.02
10:J:170:GLY:C	34:2:511:A:OP1	2.03	1.02
34:2:511:A:H2'	34:2:512:U:H5'	1.42	1.01
34:2:513:G:N2	34:2:542:C:C5	2.28	1.01
34:2:883:A:H2'	34:2:884:G:H5'	1.41	1.01
26:Z:58:ARG:O	26:Z:102:THR:HG23	1.60	1.01
35:i:6183:G:N2	35:i:6211:U:O4	1.95	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:116:ARG:CZ	35:i:6220:A:H2	1.35	0.99
15:O:58:TYR:HB2	35:i:6111:A:C6	1.98	0.99
10:J:170:GLY:HA3	34:2:511:A:C5'	1.91	0.99
35:i:6212:U:HO2'	35:i:6213:A:H8	1.10	0.99
34:2:935:G:OP2	34:2:1074:C:N3	1.96	0.98
34:2:537:A:C8	34:2:542:C:N3	2.33	0.96
26:Z:60:VAL:HG12	26:Z:80:LEU:HD21	1.44	0.96
34:2:513:G:C2	34:2:542:C:H5	1.82	0.96
34:2:1084:G:N2	34:2:1088:U:C2	2.34	0.96
34:2:1044:C:N4	34:2:1072:G:N1	2.14	0.95
26:Z:52:LYS:CA	26:Z:53:GLU:CG	2.42	0.95
34:2:1218:A:N6	34:2:1263:G:O2'	2.00	0.94
4:D:116:ARG:NH1	35:i:6220:A:H2	1.55	0.94
34:2:264:A:N1	34:2:288:U:O4	1.98	0.94
34:2:1082:G:O2'	34:2:1093:G:O2'	1.84	0.94
34:2:1082:G:H2'	34:2:1083:A:H5''	1.49	0.94
26:Z:49:ARG:HH11	26:Z:49:ARG:HG2	1.32	0.92
4:D:146:ARG:NH2	35:i:6218:C:N4	2.16	0.92
34:2:1012:A:H2'	34:2:1013:G:O4'	1.70	0.92
34:2:513:G:N2	34:2:542:C:H5	1.68	0.91
34:2:1040:G:C2	34:2:1076:C:N3	2.39	0.91
10:J:170:GLY:CA	34:2:511:A:H5'	2.02	0.90
34:2:480:A:C2	34:2:506:U:O4	2.25	0.90
4:D:116:ARG:NH2	35:i:6220:A:H2	1.27	0.90
15:O:58:TYR:HB2	35:i:6111:A:H62	1.29	0.90
26:Z:104:ALA:HB1	26:Z:105:THR:HA	1.52	0.90
34:2:143:G:O6	34:2:170:A:N6	2.05	0.90
34:2:267:C:N4	34:2:286:G:H1	1.69	0.89
7:G:154:ARG:CA	34:2:78:A:O5'	2.19	0.89
34:2:269:C:H2'	34:2:270:A:H8	1.35	0.89
34:2:1072:G:N2	34:2:1073:G:C5	2.39	0.89
34:2:1258:U:C5	34:2:1259:U:O4	2.25	0.89
34:2:1040:G:C6	34:2:1076:C:N4	2.41	0.88
10:J:170:GLY:C	34:2:511:A:C5'	2.46	0.88
34:2:935:G:OP1	34:2:1044:C:C1'	2.21	0.88
34:2:1273:C:O2'	35:i:6187:A:H5'	1.72	0.88
34:2:884:G:H5'	34:2:884:G:H8	1.36	0.88
7:G:154:ARG:HA	34:2:78:A:H3'	1.56	0.88
35:i:6212:U:O2'	35:i:6213:A:O5'	1.91	0.88
4:D:146:ARG:NH2	35:i:6218:C:H42	1.71	0.87
35:i:6209:A:C3'	35:i:6210:U:H5'	2.05	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:511:A:C2'	34:2:512:U:H5'	2.04	0.87
34:2:1229:A:N3	34:2:1257:U:C5	2.43	0.86
34:2:560:G:HO2'	34:2:561:G:H8	1.23	0.86
34:2:1258:U:O2'	34:2:1259:U:C5	2.29	0.86
7:G:155:ASP:N	34:2:78:A:C5'	2.39	0.85
35:i:6183:G:N2	35:i:6211:U:C4	2.44	0.85
34:2:1044:C:C2	34:2:1072:G:N2	2.35	0.85
34:2:1040:G:C2	34:2:1076:C:C4	2.63	0.85
34:2:513:G:C2	34:2:542:C:C5	2.64	0.85
34:2:1229:A:C2	34:2:1257:U:C6	2.64	0.85
34:2:1292:U:O4	34:2:1321:A:C6	2.29	0.85
10:J:170:GLY:CA	34:2:511:A:OP1	2.25	0.85
34:2:1042:A:N1	34:2:1075:A:C2	2.44	0.85
4:D:146:ARG:CZ	35:i:6218:C:H42	1.88	0.84
35:i:6142:C:O2'	35:i:6143:A:OP1	1.95	0.84
34:2:1292:U:O4	34:2:1321:A:C2	2.30	0.84
34:2:513:G:N1	34:2:542:C:N4	2.07	0.84
7:G:171:LYS:HE3	34:2:71:A:H61	1.41	0.84
34:2:1082:G:C2'	34:2:1083:A:H5''	2.07	0.83
34:2:884:G:H5'	34:2:884:G:C8	2.13	0.83
4:D:146:ARG:NE	35:i:6218:C:H42	1.76	0.83
7:G:155:ASP:H	34:2:78:A:P	2.02	0.83
34:2:8:U:C3'	34:2:9:U:H5'	2.09	0.83
35:i:6211:U:O2'	35:i:6212:U:OP2	1.95	0.83
34:2:1222:A:C6	34:2:1260:G:C6	2.67	0.82
34:2:566:A:H2'	34:2:567:G:O4'	1.80	0.82
34:2:1258:U:O2'	34:2:1259:U:C6	2.32	0.82
34:2:65:A:H2'	34:2:83:G:H1	1.45	0.82
34:2:1292:U:C4	34:2:1321:A:C2	2.68	0.82
34:2:1040:G:N2	34:2:1076:C:C2	2.48	0.81
34:2:513:G:H1	34:2:542:C:H41	0.85	0.81
15:O:58:TYR:CD2	35:i:6111:A:C8	2.67	0.81
26:Z:54:ALA:HB3	26:Z:88:ILE:CG2	2.10	0.81
10:J:170:GLY:CA	34:2:511:A:C5'	2.57	0.81
34:2:883:A:C2'	34:2:884:G:H5'	2.09	0.81
7:G:155:ASP:N	34:2:78:A:P	2.53	0.81
34:2:935:G:OP1	34:2:1044:C:H1'	1.80	0.80
26:Z:54:ALA:CB	26:Z:83:LEU:HD22	2.10	0.80
34:2:480:A:C6	34:2:506:U:O4	2.33	0.80
34:2:1230:U:O3'	34:2:1257:U:O2'	1.99	0.80
26:Z:54:ALA:HB2	26:Z:83:LEU:CD2	2.11	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1040:G:N1	34:2:1076:C:C4	2.50	0.80
34:2:560:G:C2'	34:2:561:G:H8	1.95	0.80
4:D:146:ARG:HH21	35:i:6218:C:H41	1.26	0.80
7:G:154:ARG:C	34:2:78:A:O5'	2.24	0.79
34:2:511:A:H2'	34:2:512:U:C5'	2.13	0.79
34:2:513:G:N1	34:2:542:C:C5	2.50	0.79
34:2:138:A:N7	34:2:265:A:C2	2.46	0.79
34:2:537:A:H4'	34:2:538:G:OP1	1.80	0.79
34:2:8:U:O4	34:2:15:U:O4	2.01	0.79
35:i:6134:C:N3	35:i:6152:A:O2'	2.16	0.79
34:2:264:A:C2	34:2:287:A:N6	2.50	0.78
6:F:125:VAL:HG11	26:Z:59:TYR:HB3	1.65	0.78
35:i:6143:A:O2'	35:i:6144:G:H3'	1.84	0.78
34:2:564:C:H2'	34:2:576:G:N2	1.98	0.78
34:2:1258:U:C2'	34:2:1259:U:C5	2.66	0.78
34:2:1258:U:C6	34:2:1259:U:O4	2.36	0.78
34:2:883:A:H2'	34:2:884:G:C5'	2.12	0.78
15:O:58:TYR:CD2	35:i:6111:A:N7	2.53	0.77
15:O:58:TYR:CD1	35:i:6111:A:C5	2.71	0.77
34:2:267:C:H42	34:2:286:G:H1	1.29	0.77
34:2:565:C:H2'	34:2:566:A:C8	2.19	0.77
34:2:883:A:C2'	34:2:884:G:C5'	2.62	0.77
34:2:1173:C:N3	34:2:1464:G:C2	2.53	0.77
34:2:1258:U:H2'	34:2:1259:U:H5	1.49	0.77
10:J:14:THR:HG21	34:2:23:G:OP1	1.83	0.77
34:2:1229:A:H2	34:2:1257:U:H6	1.33	0.77
34:2:1082:G:C3'	34:2:1083:A:H5''	2.14	0.77
34:2:70:C:H2'	34:2:71:A:O4'	1.85	0.77
34:2:1229:A:C2	34:2:1257:U:H6	2.02	0.77
10:J:170:GLY:N	34:2:511:A:OP1	2.19	0.76
15:O:58:TYR:CD1	35:i:6111:A:C6	2.74	0.76
34:2:935:G:OP2	34:2:1073:G:N2	2.18	0.76
16:P:18:LYS:O	19:S:95:GLY:N	2.18	0.76
26:Z:58:ARG:HH12	26:Z:103:ARG:HH22	1.29	0.76
34:2:888:U:H2'	34:2:889:C:C6	2.21	0.76
34:2:1070:U:H5''	34:2:1071:C:OP1	1.86	0.76
8:H:70:TYR:O	8:H:74:GLN:N	2.19	0.76
26:Z:53:GLU:HB3	26:Z:55:PRO:CD	2.15	0.76
34:2:1229:A:N3	34:2:1257:U:C6	2.54	0.76
34:2:1590:A:H2'	34:2:1591:A:C8	2.21	0.76
34:2:65:A:H2'	34:2:83:G:N1	2.01	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:208:U:C4	34:2:209:A:N7	2.54	0.75
26:Z:52:LYS:HD2	26:Z:53:GLU:HG3	1.67	0.75
34:2:1754:A:H2	35:i:6189:G:N3	1.85	0.75
26:Z:58:ARG:CZ	26:Z:103:ARG:HH22	1.99	0.75
34:2:884:G:C2'	34:2:885:U:H4'	2.16	0.75
26:Z:104:ALA:HB1	26:Z:105:THR:CA	2.16	0.75
15:O:58:TYR:CG	35:i:6111:A:C6	2.74	0.75
34:2:556:G:C6	34:2:558:C:N4	2.55	0.74
26:Z:60:VAL:HG12	26:Z:80:LEU:CD2	2.16	0.74
34:2:70:C:N4	34:2:71:A:N1	2.36	0.74
35:i:6217:G:O2'	35:i:6218:C:OP1	2.05	0.74
34:2:1255:A:N3	34:2:1257:U:O4	2.20	0.74
35:i:6145:C:O2'	35:i:6146:C:OP2	2.06	0.73
34:2:267:C:N3	34:2:286:G:N2	2.35	0.73
15:O:58:TYR:CB	35:i:6111:A:C6	2.70	0.73
34:2:8:U:O2'	34:2:9:U:H5'	1.89	0.73
34:2:1754:A:C2	35:i:6189:G:N3	2.55	0.73
35:i:6137:A:H4'	35:i:6138:G:O5'	1.89	0.73
34:2:264:A:H2	34:2:288:U:H3	1.37	0.73
10:J:170:GLY:O	34:2:511:A:OP2	2.07	0.73
34:2:558:C:H2'	34:2:559:U:C6	2.24	0.72
24:X:63:GLN:NE2	34:2:1753:A:H5'	2.05	0.72
34:2:560:G:H2'	34:2:561:G:H8	1.54	0.72
35:i:6186:U:O2'	35:i:6187:A:O5'	2.07	0.72
34:2:560:G:H2'	34:2:561:G:C8	2.23	0.72
35:i:6186:U:H4'	35:i:6186:U:OP1	1.90	0.72
10:J:170:GLY:O	34:2:511:A:O5'	2.07	0.72
34:2:1221:C:O2	34:2:1261:U:C2	2.43	0.72
34:2:884:G:H2'	34:2:885:U:H4'	1.71	0.72
34:2:884:G:H8	34:2:884:G:C5'	2.03	0.71
9:I:160:GLN:HB3	9:I:166:LEU:HA	1.73	0.71
34:2:150:G:O6	34:2:162:G:O6	2.08	0.71
34:2:884:G:C3'	34:2:885:U:H4'	2.20	0.71
10:J:170:GLY:CA	34:2:511:A:P	2.78	0.71
26:Z:54:ALA:HB3	26:Z:88:ILE:HG21	1.72	0.71
34:2:1082:G:O6	34:2:1083:A:C6	2.44	0.71
34:2:1043:U:N3	34:2:1044:C:N4	2.38	0.71
4:D:146:ARG:HE	35:i:6218:C:N4	1.88	0.70
7:G:154:ARG:CA	34:2:78:A:H3'	2.21	0.70
7:G:155:ASP:N	34:2:77:U:O3'	2.24	0.70
34:2:214:A:N7	34:2:241:U:H2'	2.06	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:6162:A:O2'	35:i:6163:G:OP1	2.07	0.70
26:Z:60:VAL:CG1	26:Z:80:LEU:HD21	2.21	0.70
34:2:1083:A:N1	34:2:1089:C:C4	2.59	0.70
26:Z:49:ARG:HG2	26:Z:49:ARG:NH1	1.96	0.70
35:i:6183:G:C2	35:i:6211:U:O4	2.44	0.70
35:i:6122:C:OP2	35:i:6122:C:O3'	2.09	0.70
34:2:564:C:H2'	34:2:576:G:C2	2.25	0.70
34:2:264:A:N1	34:2:287:A:N6	2.40	0.69
34:2:1363:G:N2	34:2:1364:C:C2	2.60	0.69
35:i:6154:A:C8	35:i:6154:A:OP2	2.44	0.69
35:i:6076:U:HO2'	35:i:6130:G:HO2'	1.39	0.69
35:i:6172:G:O2'	35:i:6173:C:OP1	2.10	0.69
35:i:6210:U:H4'	35:i:6211:U:H4'	1.75	0.69
34:2:537:A:C8	34:2:542:C:C4	2.80	0.69
34:2:1082:G:C6	34:2:1083:A:C5	2.80	0.69
34:2:515:G:C6	34:2:536:G:N2	2.61	0.69
16:P:19:GLY:N	19:S:93:ASN:N	2.41	0.69
35:i:6183:G:N2	35:i:6211:U:C5	2.61	0.69
27:a:85:ARG:HA	27:a:85:ARG:NE	2.07	0.69
26:Z:61:SER:O	26:Z:64:VAL:N	2.25	0.68
34:2:542:C:O2'	34:2:543:A:P	2.50	0.68
34:2:1229:A:C2	34:2:1257:U:C5	2.82	0.68
35:i:6172:G:O2'	35:i:6173:C:P	2.50	0.68
34:2:148:C:H2'	34:2:149:U:C6	2.28	0.68
34:2:261:U:C4	34:2:262:C:N4	2.61	0.68
34:2:559:U:H2'	34:2:560:G:H8	1.58	0.68
34:2:884:G:H2'	34:2:885:U:C4'	2.23	0.68
34:2:1499:C:C2	34:2:1505:G:N2	2.62	0.68
35:i:6061:U:O2	35:i:6061:U:H3'	1.93	0.68
34:2:628:U:N3	34:2:969:A:N6	2.41	0.68
34:2:1258:U:H2'	34:2:1259:U:C5	2.28	0.68
9:I:82:VAL:HG12	9:I:197:LEU:HD21	1.76	0.68
34:2:1042:A:N1	34:2:1075:A:N1	2.42	0.68
34:2:511:A:C3'	34:2:512:U:H5'	2.23	0.68
26:Z:53:GLU:CB	26:Z:55:PRO:HD2	2.20	0.68
35:i:6155:U:H4'	35:i:6155:U:OP1	1.93	0.67
4:D:146:ARG:HE	35:i:6218:C:H42	1.40	0.67
34:2:537:A:N7	34:2:542:C:N4	2.42	0.67
35:i:6173:C:O2'	35:i:6174:G:N7	2.27	0.67
35:i:6186:U:O2'	35:i:6188:G:OP2	2.06	0.67
26:Z:61:SER:HB3	26:Z:64:VAL:HG23	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:261:U:C4	34:2:262:C:C4	2.82	0.67
34:2:299:A:H2'	34:2:300:A:C8	2.30	0.67
34:2:269:C:H2'	34:2:270:A:C8	2.25	0.67
34:2:406:A:O2'	34:2:1669:A:N3	2.26	0.67
35:i:6143:A:H5''	35:i:6146:C:H42	1.60	0.67
35:i:6210:U:O3'	35:i:6211:U:O4'	2.13	0.67
34:2:144:A:C2	34:2:170:A:C2	2.83	0.66
34:2:883:A:C3'	34:2:884:G:C5'	2.73	0.66
34:2:1082:G:O6	34:2:1083:A:C5	2.48	0.66
34:2:1215:C:O2'	34:2:1442:A:N6	2.28	0.66
34:2:1218:A:N6	34:2:1263:G:C2'	2.58	0.66
4:D:116:ARG:NH2	35:i:6220:A:N1	2.13	0.66
34:2:1223:A:N6	34:2:1224:U:C4	2.64	0.66
35:i:6135:C:H2'	35:i:6136:U:C2	2.31	0.66
34:2:139:C:H42	34:2:280:G:P	2.19	0.66
15:O:58:TYR:CG	35:i:6111:A:N7	2.64	0.66
34:2:1084:G:N2	34:2:1088:U:N3	2.44	0.66
35:i:6106:U:O2'	35:i:6107:A:OP1	2.12	0.66
10:J:170:GLY:HA3	34:2:511:A:O5'	1.96	0.65
16:P:17:TYR:N	19:S:92:VAL:O	2.29	0.65
34:2:1074:C:C2'	34:2:1074:C:O2	2.42	0.65
34:2:1215:C:HO2'	34:2:1442:A:N6	1.93	0.65
16:P:17:TYR:C	19:S:92:VAL:O	2.39	0.65
34:2:537:A:N7	34:2:542:C:C4	2.65	0.65
34:2:1183:A:C2	34:2:1453:G:O4'	2.48	0.65
34:2:264:A:N1	34:2:288:U:C4	2.63	0.65
26:Z:60:VAL:CG1	26:Z:80:LEU:CD2	2.75	0.65
34:2:560:G:N3	34:2:561:G:C8	2.64	0.65
34:2:1417:G:C6	34:2:1418:C:N3	2.64	0.65
34:2:556:G:C2	34:2:558:C:C4	2.84	0.65
34:2:1223:A:C6	34:2:1224:U:C4	2.85	0.65
34:2:1044:C:C4	34:2:1072:G:N1	2.56	0.65
26:Z:61:SER:O	26:Z:62:VAL:C	2.40	0.65
34:2:480:A:C2	34:2:506:U:C4	2.82	0.65
34:2:935:G:P	34:2:1074:C:N4	2.70	0.65
34:2:1040:G:N1	34:2:1076:C:N4	2.42	0.65
34:2:883:A:C6	34:2:884:G:C6	2.84	0.65
34:2:8:U:C2'	34:2:9:U:H5'	2.27	0.65
34:2:360:C:C2	34:2:383:G:N2	2.65	0.65
34:2:535:C:H2'	34:2:536:G:O4'	1.96	0.65
34:2:1601:U:H2'	34:2:1602:U:C6	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1040:G:N2	34:2:1076:C:N3	2.44	0.64
26:Z:54:ALA:CB	26:Z:88:ILE:CG2	2.75	0.64
26:Z:55:PRO:O	26:Z:56:THR:OG1	2.12	0.64
35:i:6074:A:O2'	35:i:6157:C:O4'	2.15	0.64
34:2:1217:G:C8	34:2:1442:A:C5	2.85	0.64
34:2:1082:G:H3'	34:2:1083:A:C5'	2.27	0.64
34:2:560:G:O2'	34:2:561:G:H8	1.80	0.64
35:i:6157:C:H3'	35:i:6158:A:H4'	1.80	0.64
35:i:6182:A:H2'	35:i:6183:G:C8	2.33	0.63
34:2:1464:G:N2	34:2:1465:C:C2	2.66	0.63
34:2:67:A:OP2	34:2:83:G:N2	2.31	0.63
35:i:6210:U:O3'	35:i:6211:U:C4'	2.47	0.63
34:2:152:G:C6	34:2:161:A:C6	2.87	0.63
34:2:363:G:N2	34:2:380:C:C2	2.67	0.63
35:i:6201:C:C2'	35:i:6202:C:OP1	2.46	0.63
26:Z:58:ARG:CZ	26:Z:103:ARG:NH2	2.60	0.63
34:2:151:U:N3	34:2:162:G:N7	2.47	0.63
34:2:537:A:C8	34:2:542:C:N4	2.67	0.63
34:2:883:A:C2'	34:2:884:G:H5''	2.28	0.63
35:i:6144:G:H4'	35:i:6145:C:OP1	1.97	0.63
7:G:174:LYS:HA	34:2:79:C:O2'	1.99	0.63
34:2:559:U:H2'	34:2:560:G:C8	2.34	0.63
35:i:6075:A:O2'	35:i:6076:U:P	2.56	0.63
35:i:6212:U:O2'	35:i:6213:A:P	2.57	0.63
34:2:264:A:H2	34:2:288:U:N3	1.96	0.62
34:2:70:C:C5	34:2:71:A:C5	2.87	0.62
34:2:264:A:C2	34:2:288:U:N3	2.67	0.62
35:i:6075:A:O2'	35:i:6076:U:OP2	2.18	0.62
35:i:6098:A:H2'	35:i:6099:U:H5'	1.81	0.62
34:2:363:G:C2	34:2:380:C:C2	2.88	0.62
35:i:6067:G:H4'	35:i:6067:G:OP1	2.00	0.62
7:G:154:ARG:HB3	34:2:77:U:H4'	1.80	0.62
34:2:168:A:C4	34:2:170:A:C8	2.87	0.62
34:2:823:G:N2	34:2:848:C:C2	2.67	0.62
34:2:1220:A:N1	34:2:1261:U:N3	2.48	0.62
35:i:6172:G:HO2'	35:i:6173:C:P	2.21	0.62
24:X:102:VAL:HG22	24:X:124:VAL:HG13	1.81	0.62
7:G:155:ASP:H	34:2:78:A:H5''	1.60	0.62
35:i:6106:U:O2	35:i:6106:U:O4'	2.18	0.62
34:2:1632:C:N4	35:i:6217:G:OP2	2.30	0.62
7:G:188:ARG:NH1	34:2:283:G:O6	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:58:TYR:CE2	35:i:6111:A:C8	2.88	0.62
34:2:207:U:H2'	34:2:208:U:C6	2.35	0.61
31:e:28:LYS:HD3	34:2:541:A:H61	1.65	0.61
34:2:171:C:O2'	34:2:172:A:O4'	2.15	0.61
34:2:1220:A:C6	34:2:1262:G:C6	2.88	0.61
34:2:1222:A:C4	34:2:1260:G:C2	2.88	0.61
34:2:1222:A:C5	34:2:1260:G:N1	2.68	0.61
34:2:1223:A:C6	34:2:1259:U:N3	2.68	0.61
35:i:6140:G:N7	35:i:6143:A:N6	2.47	0.61
35:i:6139:U:C5	35:i:6143:A:N6	2.59	0.61
27:a:85:ARG:HA	27:a:85:ARG:CZ	2.30	0.61
6:F:53:VAL:HG13	6:F:133:GLN:HA	1.81	0.61
26:Z:67:ASP:C	26:Z:69:PHE:H	1.82	0.61
16:P:19:GLY:H	19:S:93:ASN:N	1.99	0.61
34:2:1229:A:H2	34:2:1257:U:C6	2.08	0.61
34:2:1378:U:O2'	34:2:1514:A:N1	2.32	0.61
34:2:480:A:C6	34:2:506:U:C4	2.86	0.61
6:F:188:ASN:HA	34:2:1533:U:C6	2.36	0.60
24:X:96:VAL:HA	24:X:127:VAL:HG11	1.82	0.60
26:Z:54:ALA:N	26:Z:55:PRO:HD2	2.16	0.60
34:2:65:A:N1	34:2:83:G:H2'	2.16	0.60
34:2:209:A:C2'	34:2:210:U:H5'	2.31	0.60
34:2:513:G:N7	34:2:536:G:N2	2.49	0.60
34:2:1082:G:C3'	34:2:1083:A:C5'	2.78	0.60
7:G:154:ARG:H	34:2:78:A:C4'	2.14	0.60
34:2:65:A:C2'	34:2:83:G:H1	2.10	0.60
34:2:267:C:O2'	34:2:268:G:H5'	2.02	0.60
35:i:6144:G:H1'	35:i:6145:C:H4'	1.83	0.60
7:G:154:ARG:N	34:2:78:A:C5'	2.64	0.60
35:i:6143:A:H5''	35:i:6146:C:N4	2.14	0.60
3:C:126:VAL:HG11	35:i:6221:C:H4'	1.82	0.60
20:T:68:ARG:NH1	34:2:1519:G:O6	2.33	0.60
34:2:69:G:C6	34:2:70:C:C4	2.88	0.60
34:2:560:G:C4	34:2:561:G:N7	2.69	0.60
34:2:1130:A:H2'	34:2:1131:A:O4'	2.01	0.60
34:2:811:A:O4'	34:2:857:G:N2	2.34	0.60
34:2:1044:C:C4	34:2:1072:G:N2	2.61	0.60
16:P:19:GLY:HA3	19:S:94:ASP:C	2.26	0.60
34:2:987:A:H2'	34:2:988:U:C6	2.36	0.60
34:2:1219:C:N3	34:2:1262:G:O6	2.35	0.60
7:G:154:ARG:CB	34:2:77:U:H4'	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:58:TYR:CD1	35:i:6111:A:C4	2.89	0.60
34:2:1754:A:O2'	35:i:6190:U:O2	2.20	0.60
34:2:561:G:H2'	34:2:562:U:H6	1.67	0.59
34:2:969:A:N6	34:2:970:A:C4	2.70	0.59
34:2:1220:A:C5	34:2:1262:G:C6	2.90	0.59
34:2:1230:U:H5'	34:2:1258:U:H4'	1.83	0.59
27:a:10:ARG:CZ	34:2:1795:A:OP1	2.50	0.59
34:2:12:U:H2'	34:2:13:C:C6	2.37	0.59
34:2:1024:A:O2'	34:2:1771:C:O2'	2.20	0.59
35:i:6145:C:O2'	35:i:6146:C:P	2.60	0.59
34:2:70:C:H42	34:2:81:G:H1	1.50	0.59
34:2:1218:A:N6	34:2:1263:G:HO2'	2.01	0.59
9:I:107:THR:N	9:I:108:PRO:HD2	2.17	0.59
26:Z:59:TYR:CZ	26:Z:64:VAL:CG2	2.85	0.59
34:2:65:A:C2'	34:2:83:G:N1	2.66	0.59
34:2:70:C:N4	34:2:71:A:C6	2.70	0.59
26:Z:59:TYR:CZ	26:Z:64:VAL:HG21	2.37	0.59
34:2:1464:G:N1	34:2:1465:C:C4	2.71	0.59
7:G:154:ARG:H	34:2:78:A:C5'	2.16	0.59
10:J:173:ALA:HA	34:2:510:A:OP2	2.03	0.59
34:2:157:U:C4	34:2:419:A:H4'	2.38	0.59
34:2:1231:U:OP1	34:2:1257:U:O3'	2.21	0.59
34:2:886:A:H2'	34:2:887:U:O4'	2.02	0.59
34:2:1671:G:C6	34:2:1672:C:N4	2.70	0.59
35:i:6182:A:O2'	35:i:6183:G:O5'	2.21	0.59
4:D:116:ARG:NH2	35:i:6221:C:O2'	2.36	0.59
24:X:41:SER:O	24:X:43:PHE:N	2.36	0.59
26:Z:54:ALA:HB1	26:Z:89:ILE:HD11	1.83	0.59
32:f:142:CYS:O	32:f:144:SER:N	2.35	0.59
34:2:266:U:O2	34:2:287:A:C2	2.56	0.59
34:2:1217:G:O6	34:2:1442:A:H5''	2.03	0.59
34:2:1462:G:N2	34:2:1463:C:C2	2.71	0.59
17:Q:36:ILE:HD11	17:Q:48:VAL:HG12	1.85	0.58
34:2:749:U:H2'	34:2:750:U:C6	2.37	0.58
34:2:1218:A:H62	34:2:1263:G:H2'	1.68	0.58
3:C:50:VAL:HG21	3:C:73:ILE:HG23	1.85	0.58
15:O:58:TYR:CD2	35:i:6111:A:C5	2.89	0.58
34:2:1082:G:C6	34:2:1083:A:N7	2.71	0.58
35:i:6182:A:O2'	35:i:6183:G:P	2.61	0.58
9:I:83:TYR:CZ	9:I:196:ARG:HG2	2.37	0.58
34:2:958:U:H2'	34:2:958:U:O2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:6122:C:O2'	35:i:6123:G:P	2.61	0.58
34:2:1215:C:H2'	34:2:1442:A:N1	2.19	0.58
35:i:6205:A:H5'	35:i:6206:G:P	2.44	0.58
34:2:1103:U:H2'	34:2:1104:C:O4'	2.04	0.58
34:2:1120:C:C2	34:2:1126:G:C2	2.92	0.58
34:2:1349:G:C2	34:2:1374:C:O2	2.57	0.58
24:X:63:GLN:HG3	24:X:64:PRO:HD2	1.84	0.58
26:Z:105:THR:HG22	26:Z:105:THR:O	2.01	0.58
34:2:1462:G:N1	34:2:1463:C:C4	2.72	0.58
35:i:6167:U:O2'	35:i:6168:C:O5'	2.18	0.58
7:G:171:LYS:CE	34:2:71:A:H61	2.12	0.58
34:2:291:U:H2'	34:2:292:U:C6	2.39	0.58
34:2:1086:A:H2'	34:2:1087:A:C8	2.38	0.58
15:O:58:TYR:CE1	35:i:6111:A:C4	2.91	0.58
34:2:561:G:C2	34:2:583:C:C2	2.93	0.57
34:2:561:G:C2	34:2:583:C:O2	2.57	0.57
34:2:1223:A:N6	34:2:1224:U:O4	2.37	0.57
35:i:6122:C:O2	35:i:6122:C:O4'	2.20	0.57
34:2:1222:A:N1	34:2:1260:G:C5	2.73	0.57
34:2:1256:U:C6	34:2:1257:U:H1'	2.40	0.57
15:O:81:ILE:HB	15:O:115:ILE:HG22	1.87	0.57
1:A:120:LEU:HD11	1:A:144:ILE:HD12	1.87	0.57
27:a:79:ILE:HG12	27:a:84:VAL:HG11	1.86	0.57
34:2:70:C:C4	34:2:71:A:C6	2.93	0.57
34:2:556:G:N2	34:2:558:C:C2	2.73	0.57
35:i:6212:U:O2'	35:i:6213:A:H8	1.82	0.57
9:I:76:THR:HG21	9:I:104:ILE:HG23	1.86	0.57
26:Z:54:ALA:CB	26:Z:88:ILE:HG21	2.32	0.57
34:2:1757:C:H2'	34:2:1758:G:O4'	2.05	0.57
35:i:6148:C:H5''	35:i:6148:C:H6	1.69	0.57
34:2:513:G:N7	34:2:536:G:C2	2.73	0.57
34:2:1215:C:O2'	34:2:1442:A:C6	2.58	0.57
34:2:1793:U:O3'	34:2:1795:A:N1	2.38	0.57
1:A:129:ASP:O	1:A:132:ALA:N	2.35	0.56
1:A:18:LEU:HD22	18:R:106:THR:HG23	1.86	0.56
25:Y:40:LEU:HD13	25:Y:60:PHE:CZ	2.39	0.56
34:2:1349:G:C6	34:2:1374:C:N3	2.73	0.56
35:i:6061:U:OP1	35:i:6061:U:C2	2.58	0.56
9:I:99:ALA:N	9:I:170:ILE:O	2.36	0.56
12:L:99:ARG:HB2	24:X:12:ALA:HB2	1.87	0.56
15:O:58:TYR:CB	35:i:6111:A:N6	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:121:ILE:HD11	19:S:125:ILE:HD13	1.88	0.56
34:2:137:U:N3	34:2:138:A:N6	2.53	0.56
34:2:1671:G:C2	34:2:1672:C:C2	2.94	0.56
35:i:6201:C:O2'	35:i:6202:C:OP1	2.17	0.56
24:X:69:ARG:NH1	24:X:116:ASP:OD2	2.38	0.56
34:2:1182:A:N3	34:2:1209:C:O2'	2.26	0.56
34:2:1218:A:N6	34:2:1263:G:H2'	2.19	0.56
34:2:1012:A:H2'	34:2:1013:G:C1'	2.36	0.56
35:i:6106:U:HO2'	35:i:6107:A:P	2.28	0.56
34:2:908:U:H2'	34:2:909:C:C5	2.40	0.56
3:C:170:VAL:HG11	3:C:215:THR:HA	1.87	0.56
23:W:40:VAL:HG11	23:W:103:ILE:HD12	1.86	0.56
34:2:884:G:H2'	34:2:885:U:O2'	2.06	0.56
34:2:1218:A:N7	34:2:1264:G:H1'	2.20	0.56
35:i:6103:G:C2'	35:i:6104:G:O5'	2.53	0.56
35:i:6103:G:O2'	35:i:6104:G:O5'	2.22	0.56
35:i:6106:U:O4	35:i:6119:U:H2'	2.04	0.56
7:G:153:VAL:HG21	7:G:178:LEU:HD11	1.87	0.56
23:W:82:LYS:O	23:W:84:ALA:N	2.37	0.56
34:2:556:G:C2	34:2:558:C:N3	2.74	0.56
34:2:564:C:O2'	34:2:565:C:OP2	2.22	0.56
34:2:823:G:C2	34:2:848:C:N3	2.74	0.56
35:i:6134:C:H2'	35:i:6135:C:H4'	1.87	0.56
34:2:1154:G:C2	34:2:1622:C:C2	2.94	0.56
35:i:6074:A:O2'	35:i:6157:C:C4'	2.53	0.55
34:2:511:A:C2'	34:2:512:U:C5'	2.76	0.55
34:2:1277:G:C2	34:2:1278:C:C2	2.95	0.55
7:G:136:LYS:HZ2	34:2:65:A:P	2.20	0.55
34:2:1042:A:C6	34:2:1043:U:C4	2.93	0.55
34:2:1758:G:O2'	34:2:1779:A:N1	2.35	0.55
1:A:14:ALA:O	1:A:18:LEU:HG	2.06	0.55
34:2:209:A:C6	34:2:210:U:C4	2.94	0.55
34:2:1173:C:N4	34:2:1464:G:C6	2.75	0.55
34:2:1230:U:C5'	34:2:1258:U:H4'	2.35	0.55
34:2:1239:U:O2'	34:2:1241:A:C8	2.59	0.55
34:2:1586:G:N1	34:2:1587:C:C2	2.73	0.55
23:W:55:ASP:O	23:W:57:ARG:N	2.39	0.55
34:2:50:C:O2	34:2:429:G:C2	2.60	0.55
34:2:150:G:C2	34:2:163:A:C5	2.95	0.55
35:i:6133:G:H2'	35:i:6134:C:C5	2.41	0.55
35:i:6143:A:C5'	35:i:6146:C:H42	2.19	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:185:ALA:HB2	6:F:192:ILE:HG23	1.89	0.55
34:2:1042:A:C2	34:2:1043:U:C2	2.95	0.55
34:2:1173:C:C2	34:2:1464:G:C2	2.94	0.55
34:2:1223:A:C4	34:2:1259:U:O2	2.59	0.55
11:K:46:LEU:HD13	11:K:66:TYR:CE2	2.42	0.55
34:2:976:A:H2'	34:2:977:A:O4'	2.07	0.55
34:2:1081:C:O2'	34:2:1082:G:H5''	2.06	0.55
34:2:1292:U:O4	34:2:1293:G:C4	2.60	0.55
34:2:884:G:C3'	34:2:885:U:C4'	2.85	0.55
35:i:6145:C:HO2'	35:i:6146:C:P	2.27	0.55
26:Z:58:ARG:NH1	26:Z:103:ARG:CZ	2.68	0.55
34:2:884:G:H3'	34:2:885:U:C4'	2.37	0.55
34:2:990:G:O2'	34:2:1012:A:N6	2.39	0.55
34:2:1042:A:C6	34:2:1043:U:N3	2.75	0.55
34:2:1257:U:H2'	34:2:1258:U:O4'	2.06	0.55
3:C:86:MET:HE1	3:C:188:ALA:HA	1.90	0.54
7:G:154:ARG:C	34:2:78:A:H3'	2.32	0.54
34:2:69:G:C2	34:2:70:C:C2	2.95	0.54
35:i:6104:G:O2'	35:i:6105:U:OP2	2.22	0.54
25:Y:121:THR:OG1	34:2:148:C:OP1	2.20	0.54
34:2:262:C:O2'	34:2:263:G:O4'	2.25	0.54
34:2:1183:A:C2	34:2:1452:G:N3	2.74	0.54
34:2:1343:A:H2'	34:2:1344:A:C8	2.42	0.54
34:2:1778:G:HO2'	34:2:1779:A:H8	1.53	0.54
1:A:49:ASN:O	1:A:53:THR:HG23	2.08	0.54
28:b:70:LYS:N	34:2:1048:U:OP1	2.40	0.54
34:2:161:A:C6	34:2:162:G:C6	2.95	0.54
35:i:6135:C:H5''	35:i:6136:U:C4	2.43	0.54
35:i:6183:G:C4	35:i:6184:A:H1'	2.43	0.54
34:2:562:U:H2'	34:2:563:G:C8	2.43	0.54
7:G:131:LYS:HB3	34:2:165:C:O2'	2.07	0.54
10:J:170:GLY:CA	34:2:511:A:O5'	2.56	0.54
34:2:594:G:C6	34:2:595:C:N4	2.76	0.54
35:i:6102:A:N1	35:i:6136:U:N3	2.55	0.54
24:X:63:GLN:NE2	34:2:1753:A:P	2.54	0.54
34:2:147:U:H2'	34:2:148:C:O4'	2.08	0.54
34:2:1072:G:N2	34:2:1073:G:C6	2.75	0.54
34:2:1220:A:H2'	34:2:1221:C:C6	2.43	0.54
35:i:6169:U:H2'	35:i:6170:C:H5''	1.90	0.54
34:2:268:G:C6	34:2:269:C:C4	2.96	0.54
34:2:1043:U:H3	34:2:1044:C:N4	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1726:U:H2'	34:2:1727:C:C6	2.43	0.54
3:C:173:ARG:NH1	34:2:1096:U:O3'	2.41	0.54
34:2:65:A:H2'	34:2:83:G:C6	2.43	0.54
34:2:168:A:C5	34:2:170:A:C8	2.95	0.54
35:i:6157:C:C3'	35:i:6158:A:H4'	2.37	0.54
34:2:922:A:N1	34:2:923:A:C6	2.76	0.54
34:2:1219:C:O2	34:2:1262:G:N1	2.41	0.54
34:2:1333:U:H2'	34:2:1334:U:O4'	2.08	0.54
34:2:1499:C:C2	34:2:1505:G:C2	2.95	0.54
35:i:6110:U:H3'	35:i:6111:A:H5''	1.90	0.54
7:G:155:ASP:HB2	34:2:78:A:OP2	2.08	0.53
26:Z:52:LYS:HD2	26:Z:53:GLU:CG	2.37	0.53
34:2:1222:A:C2	34:2:1260:G:C4	2.96	0.53
34:2:1378:U:H2'	34:2:1379:U:C6	2.44	0.53
34:2:121:U:H2'	34:2:122:U:C6	2.43	0.53
34:2:1754:A:C6	35:i:6189:G:O2'	2.57	0.53
35:i:6122:C:OP2	35:i:6122:C:C3'	2.57	0.53
7:G:171:LYS:HE3	34:2:71:A:N6	2.18	0.53
15:O:58:TYR:CB	35:i:6111:A:C5	2.90	0.53
34:2:1772:G:H2'	34:2:1773:U:O4'	2.08	0.53
35:i:6162:A:C2	35:i:6163:G:H1'	2.43	0.53
34:2:150:G:C6	34:2:163:A:C6	2.96	0.53
23:W:75:ILE:HD11	23:W:125:ILE:HB	1.90	0.53
35:i:6163:G:H2'	35:i:6164:C:H5'	1.91	0.53
6:F:53:VAL:HG12	6:F:53:VAL:O	2.08	0.53
23:W:16:ASN:O	23:W:20:THR:HG23	2.08	0.53
9:I:82:VAL:HG12	9:I:197:LEU:CD2	2.37	0.53
34:2:70:C:N4	34:2:71:A:C2	2.77	0.53
34:2:394:U:H2'	34:2:395:G:O4'	2.08	0.53
34:2:1363:G:N1	34:2:1364:C:C4	2.77	0.53
34:2:1794:C:O4'	34:2:1794:C:O2	2.25	0.53
26:Z:104:ALA:CB	26:Z:105:THR:HA	2.21	0.53
34:2:143:G:C6	34:2:170:A:N6	2.68	0.53
34:2:1671:G:C6	34:2:1672:C:C4	2.97	0.53
34:2:1671:G:C5	34:2:1672:C:C4	2.97	0.53
6:F:97:ASN:HB3	34:2:1609:A:O2'	2.09	0.53
34:2:22:A:C2	34:2:23:G:C8	2.97	0.53
34:2:170:A:H2'	34:2:171:C:C6	2.44	0.53
34:2:1653:A:N6	34:2:1743:G:O2'	2.42	0.53
35:i:6122:C:H4'	35:i:6123:G:O5'	2.09	0.53
34:2:1494:U:O2	34:2:1509:G:O6	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:6120:U:O4	35:i:6127:C:H3'	2.09	0.53
7:G:155:ASP:O	7:G:157:VAL:HB	2.08	0.52
10:J:121:SER:O	10:J:123:HIS:N	2.41	0.52
34:2:406:A:H2'	34:2:407:C:C6	2.44	0.52
34:2:478:C:H2'	34:2:479:G:O4'	2.09	0.52
34:2:1231:U:C4	34:2:1253:U:C6	2.97	0.52
7:G:190:GLN:NE2	34:2:266:U:O4	2.42	0.52
34:2:150:G:N1	34:2:162:G:N7	2.57	0.52
34:2:582:C:H2'	34:2:582:C:O2	2.08	0.52
34:2:1277:G:C6	34:2:1278:C:C4	2.97	0.52
35:i:6099:U:H5''	35:i:6100:U:O4'	2.10	0.52
6:F:115:ILE:O	6:F:119:THR:HG23	2.08	0.52
34:2:467:A:N1	34:2:593:A:O2'	2.38	0.52
34:2:565:C:H2'	34:2:566:A:H8	1.74	0.52
34:2:700:C:C2	34:2:739:G:N1	2.77	0.52
34:2:886:A:C5	34:2:887:U:C4	2.98	0.52
34:2:1074:C:O2'	34:2:1075:A:OP1	2.27	0.52
34:2:1146:A:H2'	34:2:1147:C:O4'	2.09	0.52
5:E:149:TYR:HB3	7:G:208:TYR:CD1	2.44	0.52
6:F:221:ARG:CZ	35:i:6115:A:H4'	2.40	0.52
26:Z:56:THR:O	26:Z:57:TYR:HB2	2.10	0.52
34:2:25:C:O2	34:2:25:C:O4'	2.26	0.52
34:2:86:A:H2'	34:2:87:C:C6	2.45	0.52
34:2:150:G:C6	34:2:163:A:N6	2.77	0.52
34:2:268:G:C2	34:2:269:C:C2	2.97	0.52
34:2:628:U:C2	34:2:969:A:N6	2.77	0.52
34:2:1338:C:O2'	34:2:1340:A:N7	2.29	0.52
34:2:266:U:O2	34:2:267:C:C5	2.63	0.52
9:I:142:ARG:NH2	34:2:196:A:N1	2.57	0.52
34:2:519:A:N1	34:2:532:U:C2	2.77	0.52
34:2:700:C:N3	34:2:739:G:C6	2.78	0.52
34:2:884:G:C4	34:2:885:U:H1'	2.44	0.52
34:2:1771:C:C2	34:2:1787:G:C2	2.97	0.52
4:D:146:ARG:NE	35:i:6218:C:N4	2.46	0.52
26:Z:54:ALA:N	26:Z:55:PRO:CD	2.73	0.52
34:2:360:C:C2	34:2:383:G:C2	2.97	0.52
34:2:1137:A:H2'	34:2:1138:A:C8	2.44	0.52
34:2:1671:G:H2'	34:2:1672:C:C6	2.45	0.52
9:I:10:LYS:O	9:I:11:ARG:C	2.52	0.52
34:2:255:A:H2'	34:2:256:A:C8	2.45	0.52
34:2:560:G:O6	34:2:584:A:C6	2.63	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1041:G:H2'	34:2:1042:A:O4'	2.10	0.52
34:2:508:G:H2'	34:2:509:G:O4'	2.09	0.52
34:2:214:A:C5	34:2:241:U:C6	2.97	0.52
34:2:431:G:C6	34:2:432:C:N3	2.78	0.52
34:2:509:G:C6	34:2:510:A:N7	2.78	0.52
34:2:1014:U:C6	34:2:1015:C:N3	2.78	0.52
34:2:1586:G:C6	34:2:1587:C:C4	2.97	0.52
15:O:123:SER:O	34:2:884:G:N2	2.41	0.51
26:Z:103:ARG:O	26:Z:104:ALA:O	2.28	0.51
34:2:309:C:C2	34:2:356:G:C2	2.98	0.51
34:2:624:C:H2'	34:2:625:U:C6	2.45	0.51
35:i:6209:A:C3'	35:i:6210:U:C5'	2.86	0.51
8:H:93:LEU:HD21	8:H:125:ILE:HG23	1.92	0.51
12:L:101:GLU:OE2	24:X:13:ARG:N	2.43	0.51
14:N:94:LYS:O	14:N:98:VAL:HG23	2.09	0.51
34:2:820:U:H2'	34:2:821:U:C6	2.45	0.51
34:2:1137:A:C4	34:2:1138:A:N7	2.78	0.51
34:2:1651:C:C2	34:2:1746:G:C2	2.98	0.51
7:G:83:CYS:N	34:2:161:A:OP1	2.43	0.51
7:G:174:LYS:HD3	34:2:65:A:H5'	1.93	0.51
9:I:68:ALA:HB1	12:L:20:PHE:CZ	2.46	0.51
34:2:1012:A:C2'	34:2:1013:G:O4'	2.53	0.51
35:i:6157:C:H2'	35:i:6158:A:H4'	1.92	0.51
2:B:99:ASN:O	2:B:101:HIS:N	2.43	0.51
34:2:520:A:C2	34:2:531:U:N3	2.78	0.51
34:2:1266:G:O2'	34:2:1446:G:O2'	2.27	0.51
34:2:28:A:H2'	34:2:29:U:O4'	2.10	0.51
34:2:849:A:C2	34:2:850:U:C2	2.98	0.51
34:2:1349:G:N1	34:2:1374:C:C2	2.78	0.51
26:Z:67:ASP:C	26:Z:69:PHE:N	2.52	0.51
34:2:214:A:C5	34:2:215:U:C5	2.98	0.51
34:2:776:G:N2	34:2:777:C:C2	2.79	0.51
34:2:928:A:P	34:2:930:C:N4	2.84	0.51
34:2:1070:U:H5''	34:2:1071:C:P	2.50	0.51
15:O:123:SER:HB3	34:2:884:G:H1'	1.92	0.51
34:2:150:G:N2	34:2:163:A:C4	2.79	0.51
34:2:480:A:N1	34:2:506:U:C5	2.76	0.51
34:2:273:G:C6	34:2:274:C:N4	2.79	0.51
34:2:425:G:N2	34:2:426:C:C2	2.79	0.51
34:2:885:U:H2'	34:2:886:A:O4'	2.10	0.51
34:2:1020:C:C4	34:2:1021:C:C4	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1120:C:O2	34:2:1126:G:C2	2.63	0.51
34:2:1353:G:C6	34:2:1354:C:C4	2.99	0.51
8:H:107:ARG:HD3	34:2:698:U:H1'	1.93	0.51
27:a:10:ARG:NH1	34:2:1794:C:O3'	2.43	0.51
34:2:541:A:H2'	34:2:542:C:H3'	1.93	0.51
34:2:642:G:C2	34:2:692:C:O2	2.63	0.51
34:2:1558:U:O2	34:2:1558:U:O4'	2.28	0.51
16:P:34:VAL:HG21	16:P:45:PHE:CG	2.45	0.51
24:X:63:GLN:HB3	24:X:64:PRO:HD2	1.93	0.51
34:2:70:C:C4	34:2:71:A:C5	2.98	0.51
34:2:85:A:O2'	34:2:147:U:O3'	2.22	0.51
34:2:1611:U:C5	34:2:1612:A:C2	2.98	0.51
35:i:6045:C:C2'	35:i:6046:U:OP1	2.59	0.51
1:A:148:ASP:OD1	1:A:151:SER:N	2.44	0.50
26:Z:54:ALA:CB	26:Z:88:ILE:HG22	2.41	0.50
34:2:565:C:O2'	34:2:566:A:O4'	2.25	0.50
34:2:1137:A:H2'	34:2:1138:A:H8	1.76	0.50
34:2:1363:G:C2	34:2:1364:C:C4	2.99	0.50
35:i:6040:U:H2'	35:i:6041:C:O4'	2.11	0.50
35:i:6129:G:H2'	35:i:6130:G:C8	2.46	0.50
24:X:65:ASN:HB3	34:2:574:C:H41	1.76	0.50
34:2:72:A:N3	34:2:72:A:H2'	2.26	0.50
34:2:980:U:O2'	34:2:1122:C:N3	2.45	0.50
30:d:43:PHE:O	30:d:47:ALA:N	2.44	0.50
34:2:89:G:C6	34:2:90:C:C4	3.00	0.50
34:2:887:U:O4	34:2:888:U:O4	2.28	0.50
24:X:63:GLN:HG3	24:X:64:PRO:CD	2.41	0.50
26:Z:104:ALA:HB1	26:Z:105:THR:OG1	2.12	0.50
34:2:1173:C:C2	34:2:1464:G:N2	2.79	0.50
6:F:192:ILE:HD11	34:2:1471:U:H5'	1.94	0.50
15:O:129:LYS:HA	34:2:989:C:H4'	1.94	0.50
23:W:87:GLU:O	23:W:90:THR:HG22	2.12	0.50
34:2:65:A:C5	34:2:83:G:C5	3.00	0.50
34:2:281:C:H2'	34:2:282:U:O4'	2.12	0.50
34:2:1353:G:C2	34:2:1354:C:C2	2.99	0.50
1:A:18:LEU:HD22	18:R:106:THR:CG2	2.41	0.50
21:U:34:LEU:HD11	21:U:89:ARG:HG3	1.94	0.50
34:2:137:U:C2	34:2:138:A:C6	2.99	0.50
34:2:150:G:N1	34:2:163:A:C6	2.80	0.50
34:2:1666:G:H2'	34:2:1667:U:O4'	2.11	0.50
7:G:155:ASP:N	34:2:78:A:H5''	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:261:U:N3	34:2:262:C:C4	2.80	0.50
34:2:508:G:H2'	34:2:509:G:C8	2.47	0.50
34:2:542:C:HO2'	34:2:543:A:P	2.33	0.50
34:2:883:A:C3'	34:2:884:G:H5'	2.40	0.50
34:2:1471:U:O2	34:2:1471:U:C2'	2.59	0.50
35:i:6133:G:H2'	35:i:6134:C:C6	2.46	0.50
6:F:194:GLU:OE2	26:Z:59:TYR:HE2	1.95	0.50
16:P:18:LYS:C	19:S:93:ASN:C	2.80	0.50
17:Q:50:GLU:N	17:Q:51:PRO:CD	2.74	0.50
34:2:515:G:O6	34:2:536:G:N2	2.45	0.50
34:2:700:C:O2	34:2:739:G:C2	2.65	0.50
35:i:6061:U:O2	35:i:6061:U:C3'	2.60	0.50
7:G:173:PRO:HA	34:2:66:U:O4'	2.11	0.49
34:2:1238:U:H1'	34:2:1247:C:N4	2.27	0.49
27:a:84:VAL:CG1	34:2:1793:U:H4'	2.42	0.49
34:2:564:C:C4	34:2:575:G:C8	3.00	0.49
34:2:1005:C:C6	34:2:1006:C:C5	3.00	0.49
34:2:1417:G:C2	34:2:1418:C:O2	2.65	0.49
34:2:1661:G:C6	34:2:1662:C:C4	3.00	0.49
1:A:73:VAL:HG13	1:A:120:LEU:HD12	1.94	0.49
13:M:56:VAL:HG22	13:M:85:ALA:HB2	1.94	0.49
34:2:38:C:O2	34:2:469:A:N1	2.44	0.49
34:2:150:G:C2	34:2:163:A:C4	3.00	0.49
34:2:266:U:H3	34:2:267:C:H41	1.60	0.49
34:2:1611:U:O2	34:2:1611:U:O4'	2.27	0.49
34:2:39:A:O2'	34:2:468:C:N4	2.46	0.49
34:2:782:G:N2	34:2:783:C:C2	2.81	0.49
34:2:921:G:C6	34:2:922:A:C6	3.00	0.49
34:2:1015:C:O4'	34:2:1015:C:O2	2.29	0.49
35:i:6155:U:H2'	35:i:6156:C:C6	2.47	0.49
6:F:189:ILE:HG23	34:2:1533:U:O2	2.12	0.49
10:J:62:ARG:HB2	10:J:69:ARG:HG2	1.95	0.49
17:Q:52:LEU:HD22	17:Q:60:PHE:CZ	2.47	0.49
34:2:561:G:H2'	34:2:562:U:C6	2.46	0.49
34:2:1292:U:C5	34:2:1321:A:C2	3.01	0.49
34:2:1396:U:H3'	34:2:1397:C:H5'	1.95	0.49
34:2:1527:C:H2'	34:2:1528:C:C6	2.46	0.49
35:i:6143:A:C2'	35:i:6144:G:H3'	2.42	0.49
15:O:123:SER:HA	34:2:928:A:C5	2.47	0.49
34:2:70:C:C5	34:2:71:A:C6	3.00	0.49
34:2:932:A:N7	34:2:934:U:H1'	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1183:A:H2	34:2:1453:G:O4'	1.95	0.49
35:i:6144:G:H1'	35:i:6145:C:C4'	2.42	0.49
16:P:115:TYR:OH	34:2:1554:A:OP1	2.29	0.49
34:2:30:G:H2'	34:2:31:C:O4'	2.13	0.49
34:2:922:A:C2	34:2:923:A:C6	3.01	0.49
34:2:1083:A:H2'	34:2:1084:G:O4'	2.13	0.49
34:2:1346:U:O2	34:2:1514:A:H5'	2.13	0.49
7:G:171:LYS:CE	34:2:71:A:N6	2.75	0.49
13:M:24:VAL:HG22	13:M:124:ARG:HD3	1.94	0.49
26:Z:103:ARG:C	26:Z:104:ALA:O	2.54	0.49
34:2:560:G:N3	34:2:561:G:N7	2.60	0.49
34:2:874:G:O2'	34:2:876:G:OP2	2.28	0.49
34:2:886:A:C6	34:2:887:U:C4	3.01	0.49
34:2:1222:A:N6	34:2:1260:G:O6	2.46	0.49
34:2:1571:A:O4'	34:2:1572:G:C2	2.65	0.49
34:2:1671:G:C5	34:2:1672:C:N4	2.80	0.49
35:i:6205:A:H5'	35:i:6206:G:OP1	2.12	0.49
27:a:74:CYS:O	27:a:77:CYS:N	2.46	0.49
34:2:94:U:H2'	34:2:95:G:O4'	2.13	0.49
34:2:767:U:O2	34:2:767:U:O4'	2.30	0.49
34:2:925:A:H4'	34:2:1015:C:O2'	2.13	0.49
34:2:1255:A:H1'	34:2:1257:U:O4	2.12	0.49
35:i:6045:C:H2'	35:i:6046:U:OP1	2.13	0.49
34:2:207:U:O2'	34:2:208:U:O4'	2.18	0.49
34:2:334:U:H2'	34:2:335:G:O4'	2.12	0.49
34:2:390:A:O2'	34:2:1728:A:O2'	2.31	0.49
34:2:1131:A:C2	34:2:1132:A:C4	3.01	0.49
20:T:31:PRO:HG3	20:T:54:PHE:CZ	2.48	0.48
34:2:261:U:O4	34:2:262:C:N4	2.46	0.48
35:i:6140:G:C2	35:i:6149:A:C2	3.01	0.48
27:a:11:ASN:O	27:a:15:ARG:NH1	2.47	0.48
34:2:1501:A:O2'	34:2:1502:G:OP1	2.26	0.48
34:2:1637:C:H2'	34:2:1638:C:O4'	2.13	0.48
16:P:18:LYS:HA	19:S:91:ASP:C	2.37	0.48
25:Y:132:ARG:O	25:Y:135:ASP:N	2.46	0.48
34:2:89:G:C2	34:2:90:C:C2	3.01	0.48
34:2:522:G:O5'	34:2:522:G:H8	1.97	0.48
34:2:1046:G:N1	34:2:1071:C:C2	2.81	0.48
34:2:150:G:N1	34:2:163:A:C5	2.81	0.48
34:2:1175:G:C2	34:2:1176:C:C2	3.02	0.48
35:i:6100:U:H2'	35:i:6101:U:H5'	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:136:LYS:HB3	34:2:167:A:H4'	1.96	0.48
16:P:19:GLY:C	19:S:93:ASN:H	2.21	0.48
34:2:1032:C:N4	34:2:1033:C:N4	2.61	0.48
34:2:1306:U:O2	34:2:1306:U:O4'	2.31	0.48
14:N:35:GLU:HA	14:N:38:ILE:HG12	1.95	0.48
19:S:143:ARG:NH1	34:2:1460:G:N7	2.62	0.48
34:2:888:U:O4'	34:2:987:A:H4'	2.14	0.48
6:F:203:ALA:HA	6:F:213:ILE:HD11	1.96	0.48
34:2:14:C:C2	34:2:1140:G:C2	3.02	0.48
34:2:487:G:C2	34:2:499:C:C2	3.02	0.48
34:2:594:G:C2	34:2:595:C:N3	2.81	0.48
34:2:637:U:O2	34:2:637:U:O4'	2.31	0.48
34:2:763:G:O6	34:2:772:G:O6	2.30	0.48
34:2:1222:A:C6	34:2:1260:G:N1	2.82	0.48
34:2:1400:G:C6	34:2:1401:C:C4	3.02	0.48
35:i:6176:C:N3	35:i:6199:A:N6	2.62	0.48
4:D:116:ARG:HH12	35:i:6220:A:H2	1.51	0.48
10:J:80:LEU:O	10:J:83:ILE:HG22	2.13	0.48
34:2:9:U:H2'	34:2:11:A:OP2	2.13	0.48
34:2:388:G:C2	34:2:408:C:C2	3.02	0.48
34:2:963:U:O4'	34:2:964:U:C5	2.66	0.48
34:2:1220:A:C5	34:2:1221:C:C4	3.02	0.48
34:2:1786:G:H2'	34:2:1787:G:O4'	2.14	0.48
25:Y:43:LYS:O	25:Y:46:GLU:HG3	2.14	0.48
34:2:1255:A:O4'	34:2:1257:U:C5	2.67	0.48
34:2:1499:C:N3	34:2:1505:G:C2	2.82	0.48
34:2:1661:G:C2	34:2:1662:C:C2	3.02	0.48
35:i:6174:G:H1'	35:i:6175:G:N7	2.28	0.48
35:i:6212:U:O2'	35:i:6213:A:C5'	2.62	0.48
19:S:42:TYR:CE1	19:S:101:LEU:HD11	2.49	0.48
34:2:511:A:C6	34:2:512:U:C4	3.02	0.48
24:X:19:ARG:HA	24:X:19:ARG:HD2	1.57	0.47
24:X:65:ASN:CB	34:2:574:C:H41	2.27	0.47
34:2:151:U:O2	34:2:162:G:C8	2.67	0.47
34:2:152:G:H2'	34:2:153:G:C8	2.49	0.47
34:2:1620:G:C2	34:2:1621:C:C2	3.02	0.47
35:i:6172:G:O2'	35:i:6173:C:O5'	2.32	0.47
10:J:170:GLY:C	34:2:511:A:O5'	2.56	0.47
18:R:25:THR:O	18:R:27:ASP:N	2.47	0.47
34:2:30:G:C6	34:2:31:C:C4	3.02	0.47
34:2:84:A:H2'	34:2:85:A:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:921:G:H2'	34:2:922:A:C8	2.49	0.47
34:2:1138:A:H2'	34:2:1139:G:O4'	2.14	0.47
34:2:1586:G:C2	34:2:1587:C:C2	3.02	0.47
34:2:1670:G:C2	34:2:1671:G:C5	3.03	0.47
13:M:55:LEU:HD22	13:M:79:LEU:HD22	1.96	0.47
34:2:1002:A:O2'	34:2:1004:A:N7	2.44	0.47
34:2:1262:G:C2	34:2:1263:G:H1'	2.49	0.47
35:i:6135:C:H2'	35:i:6136:U:N3	2.29	0.47
35:i:6146:C:C6	35:i:6146:C:O5'	2.67	0.47
27:a:85:ARG:CZ	34:2:1151:A:O2'	2.62	0.47
34:2:204:U:C2	34:2:205:A:C8	3.03	0.47
34:2:1044:C:C4	34:2:1072:G:C2	3.02	0.47
35:i:6128:A:H2'	35:i:6129:G:H1'	1.96	0.47
35:i:6154:A:H3'	35:i:6155:U:C4'	2.44	0.47
35:i:6156:C:H2'	35:i:6157:C:H5''	1.96	0.47
34:2:96:G:C6	34:2:97:C:C4	3.03	0.47
34:2:212:A:C6	34:2:252:A:C6	3.03	0.47
34:2:560:G:C2'	34:2:561:G:C8	2.82	0.47
34:2:1083:A:N6	34:2:1089:C:N4	2.62	0.47
34:2:1497:G:C6	34:2:1498:C:C4	3.02	0.47
34:2:1533:U:O2	34:2:1533:U:O4'	2.31	0.47
26:Z:52:LYS:CD	26:Z:53:GLU:HG3	2.41	0.47
30:d:21:CYS:SG	30:d:24:SER:N	2.88	0.47
34:2:207:U:O2	34:2:208:U:C2	2.67	0.47
34:2:360:C:N3	34:2:383:G:C2	2.82	0.47
34:2:1042:A:C5	34:2:1043:U:C4	3.02	0.47
34:2:1220:A:N6	34:2:1261:U:O4	2.47	0.47
34:2:1240:G:H2'	34:2:1241:A:O5'	2.15	0.47
7:G:179:VAL:HG11	34:2:139:C:H1'	1.97	0.47
26:Z:52:LYS:O	26:Z:52:LYS:HG3	2.14	0.47
26:Z:104:ALA:CB	26:Z:105:THR:CA	2.85	0.47
34:2:567:G:C6	34:2:575:G:C2	3.03	0.47
34:2:935:G:OP1	34:2:1044:C:O4'	2.33	0.47
34:2:988:U:C4	34:2:989:C:N4	2.83	0.47
34:2:1218:A:C5	34:2:1264:G:H1'	2.49	0.47
34:2:1231:U:C2	34:2:1253:U:H1'	2.50	0.47
34:2:1437:C:H2'	34:2:1438:C:C6	2.49	0.47
7:G:136:LYS:NZ	34:2:65:A:P	2.84	0.47
7:G:173:PRO:HB2	7:G:175:ILE:HD12	1.95	0.47
16:P:19:GLY:H	19:S:92:VAL:C	2.22	0.47
32:f:91:ILE:HG12	34:2:1443:G:C5	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:71:A:C2	34:2:72:A:C6	3.02	0.47
34:2:564:C:H2'	34:2:576:G:H21	1.75	0.47
34:2:925:A:H3'	34:2:926:C:C6	2.50	0.47
34:2:1038:A:N6	34:2:1077:C:H42	2.12	0.47
34:2:1444:A:N7	34:2:1446:G:C5	2.82	0.47
34:2:1454:C:O2	34:2:1454:C:O4'	2.33	0.47
35:i:6104:G:H1'	35:i:6152:A:N1	2.29	0.47
35:i:6127:C:H5'	35:i:6128:A:OP2	2.15	0.47
9:I:100:ALA:O	9:I:170:ILE:HD12	2.14	0.47
10:J:148:VAL:HG11	10:J:156:ILE:HD11	1.96	0.47
33:g:177:ALA:HB2	33:g:209:VAL:HG23	1.97	0.47
34:2:1040:G:H2'	34:2:1041:G:C8	2.50	0.47
34:2:1222:A:N6	34:2:1260:G:C6	2.82	0.47
34:2:1400:G:C2	34:2:1401:C:C2	3.03	0.47
34:2:1588:G:C2	34:2:1589:C:C2	3.03	0.47
35:i:6205:A:C5'	35:i:6206:G:P	3.03	0.47
1:A:164:ASN:HA	1:A:170:ILE:HD11	1.96	0.47
26:Z:104:ALA:HB1	26:Z:105:THR:CB	2.45	0.47
34:2:1183:A:C2	34:2:1452:G:N2	2.82	0.47
34:2:214:A:C5	34:2:241:U:C5	3.03	0.46
34:2:1081:C:O2'	34:2:1082:G:C5'	2.62	0.46
34:2:1239:U:O4'	34:2:1245:C:N4	2.48	0.46
34:2:1560:G:C6	34:2:1561:C:C4	3.03	0.46
35:i:6066:G:H3'	35:i:6067:G:H5''	1.97	0.46
35:i:6183:G:H5''	35:i:6184:A:OP2	2.15	0.46
10:J:66:ASP:HB3	10:J:67:PRO:CD	2.45	0.46
10:J:172:VAL:N	34:2:511:A:OP2	2.48	0.46
20:T:18:TYR:CD2	20:T:135:ILE:HD13	2.50	0.46
34:2:967:U:H5''	34:2:1032:C:O2'	2.16	0.46
34:2:1598:A:H1'	34:2:1599:G:H5'	1.98	0.46
35:i:6120:U:C2	35:i:6128:A:N7	2.84	0.46
35:i:6154:A:OP2	35:i:6154:A:H8	1.97	0.46
35:i:6156:C:H3'	35:i:6157:C:H5'	1.97	0.46
34:2:142:G:H2'	34:2:143:G:C8	2.50	0.46
34:2:274:C:N4	34:2:275:C:N4	2.64	0.46
34:2:585:G:C6	34:2:586:C:C4	3.03	0.46
34:2:980:U:H2'	34:2:981:U:C6	2.50	0.46
34:2:1175:G:C6	34:2:1176:C:C4	3.04	0.46
34:2:1578:C:H2'	34:2:1579:C:O4'	2.15	0.46
7:G:160:ARG:NE	34:2:68:A:C8	2.83	0.46
7:G:175:ILE:HG22	34:2:78:A:N3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:68:ALA:HB2	9:I:183:TYR:OH	2.14	0.46
25:Y:33:ALA:CB	34:2:532:U:H4'	2.46	0.46
27:a:79:ILE:CG1	27:a:84:VAL:HG11	2.45	0.46
29:c:10:ALA:HB1	29:c:30:VAL:CG1	2.45	0.46
34:2:254:U:C4	34:2:255:A:N7	2.84	0.46
34:2:585:G:C2	34:2:586:C:C2	3.03	0.46
34:2:884:G:C8	34:2:884:G:C5'	2.85	0.46
34:2:935:G:C6	34:2:936:C:C4	3.03	0.46
34:2:1222:A:N3	34:2:1260:G:C2	2.84	0.46
34:2:1363:G:C6	34:2:1364:C:N4	2.83	0.46
34:2:1620:G:C6	34:2:1621:C:C4	3.04	0.46
34:2:1670:G:H2'	34:2:1671:G:C8	2.50	0.46
35:i:6081:A:O2'	35:i:6082:G:C8	2.66	0.46
16:P:79:HIS:O	16:P:81:ARG:N	2.49	0.46
25:Y:90:ARG:HA	25:Y:93:ARG:HD3	1.98	0.46
32:f:143:HIS:HB2	34:2:1233:A:H4'	1.98	0.46
34:2:149:U:O2'	34:2:150:G:O4'	2.23	0.46
34:2:266:U:O2	34:2:287:A:N1	2.48	0.46
34:2:284:G:N2	34:2:285:C:C2	2.84	0.46
34:2:887:U:C4	34:2:888:U:C4	3.04	0.46
34:2:1203:A:N3	34:2:1203:A:H2'	2.31	0.46
34:2:1290:G:H2'	34:2:1291:G:H8	1.81	0.46
35:i:6210:U:O5'	35:i:6211:U:OP1	2.32	0.46
7:G:155:ASP:HB2	34:2:78:A:P	2.55	0.46
21:U:95:ALA:HB1	21:U:99:ILE:HG21	1.96	0.46
24:X:7:ARG:NH2	34:2:1099:G:O4'	2.48	0.46
34:2:30:G:C2	34:2:31:C:C2	3.04	0.46
34:2:210:U:H2'	34:2:211:U:C6	2.51	0.46
34:2:268:G:O6	34:2:285:C:N3	2.49	0.46
34:2:458:G:H3'	34:2:459:A:C5'	2.45	0.46
34:2:642:G:N1	34:2:692:C:C2	2.84	0.46
35:i:6157:C:C2'	35:i:6158:A:H4'	2.45	0.46
35:i:6212:U:O2'	35:i:6213:A:C8	2.63	0.46
9:I:139:ASN:HB2	34:2:186:G:H2'	1.98	0.46
16:P:122:THR:HG21	34:2:1452:G:H4'	1.98	0.46
24:X:63:GLN:CB	24:X:64:PRO:HD2	2.46	0.46
26:Z:54:ALA:HB1	26:Z:89:ILE:CD1	2.46	0.46
34:2:89:G:N1	34:2:90:C:C2	2.84	0.46
34:2:266:U:C2	34:2:287:A:N1	2.83	0.46
34:2:1643:G:N2	34:2:1644:C:C2	2.84	0.46
7:G:74:LYS:HA	7:G:96:SER:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:98:VAL:CG1	14:N:115:LEU:HB2	2.46	0.46
25:Y:59:GLY:O	25:Y:60:PHE:HB2	2.16	0.46
34:2:1289:U:H2'	34:2:1290:G:C8	2.51	0.46
35:i:6128:A:H2'	35:i:6129:G:C1'	2.46	0.46
7:G:4:ASN:HB3	7:G:110:ALA:HA	1.98	0.46
34:2:209:A:O2'	34:2:210:U:H5'	2.15	0.46
34:2:214:A:C4	34:2:241:U:C5	3.04	0.46
34:2:988:U:H2'	34:2:989:C:C2	2.51	0.46
34:2:1589:C:C2	34:2:1590:A:C8	3.04	0.46
7:G:153:VAL:HA	34:2:78:A:H5'	1.98	0.46
34:2:987:A:C2	34:2:988:U:C2	3.04	0.46
34:2:1082:G:O6	34:2:1083:A:N6	2.49	0.46
34:2:1083:A:H2'	34:2:1084:G:C8	2.51	0.46
34:2:1603:G:C6	34:2:1604:C:C4	3.03	0.46
34:2:1778:G:O2'	34:2:1779:A:H8	1.98	0.46
19:S:41:ARG:HD2	34:2:1563:C:H5''	1.97	0.45
34:2:935:G:OP1	34:2:1074:C:N4	2.49	0.45
6:F:119:THR:HG22	6:F:193:ALA:O	2.16	0.45
21:U:103:ILE:O	21:U:106:ILE:O	2.34	0.45
23:W:4:THR:O	23:W:5:SER:C	2.58	0.45
34:2:991:A:H4'	34:2:1783:U:O2'	2.16	0.45
34:2:1074:C:O2	34:2:1074:C:H2'	2.10	0.45
34:2:1647:G:H2'	34:2:1648:U:C6	2.51	0.45
34:2:1733:U:H2'	34:2:1734:G:O4'	2.16	0.45
35:i:6146:C:O2	35:i:6147:C:C2	2.69	0.45
35:i:6155:U:H2'	35:i:6156:C:C5	2.51	0.45
35:i:6163:G:C2'	35:i:6164:C:H5'	2.46	0.45
8:H:116:ARG:NH2	34:2:855:A:O2'	2.49	0.45
15:O:41:ARG:NH2	34:2:915:U:O2	2.49	0.45
34:2:85:A:N3	34:2:147:U:H1'	2.31	0.45
34:2:89:G:C6	34:2:90:C:N3	2.84	0.45
34:2:623:G:C2	34:2:624:C:C2	3.04	0.45
34:2:1042:A:N1	34:2:1043:U:C2	2.84	0.45
34:2:1223:A:C6	34:2:1259:U:C2	3.04	0.45
34:2:1439:C:H2'	34:2:1440:U:O4'	2.16	0.45
35:i:6134:C:C2	35:i:6152:A:O2'	2.69	0.45
5:E:19:MET:HE2	34:2:787:A:H2'	1.99	0.45
10:J:62:ARG:HB2	10:J:69:ARG:CG	2.46	0.45
34:2:123:G:C5	34:2:124:A:C8	3.04	0.45
34:2:403:G:C2	34:2:404:C:C2	3.05	0.45
34:2:1730:A:H2'	34:2:1731:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:6122:C:O2'	35:i:6123:G:O5'	2.32	0.45
6:F:63:TYR:CE1	6:F:167:LEU:HD11	2.52	0.45
12:L:94:VAL:CG2	24:X:12:ALA:HB1	2.47	0.45
19:S:116:LEU:HA	19:S:119:ILE:HG12	1.97	0.45
25:Y:130:ALA:O	25:Y:133:ASN:HB2	2.16	0.45
34:2:626:C:H2'	34:2:627:G:O4'	2.16	0.45
34:2:1220:A:C2	34:2:1262:G:C4	3.05	0.45
34:2:1491:A:O2'	34:2:1492:C:OP2	2.28	0.45
34:2:1598:A:H1'	34:2:1599:G:C5'	2.47	0.45
34:2:1783:U:H2'	34:2:1784:G:C8	2.52	0.45
3:C:183:ILE:HG21	3:C:190:LYS:HA	1.98	0.45
25:Y:29:HIS:CD2	25:Y:35:VAL:HG13	2.51	0.45
34:2:96:G:C2	34:2:97:C:C2	3.05	0.45
34:2:266:U:C2	34:2:267:C:C5	3.04	0.45
34:2:1185:U:C4	34:2:1207:A:N6	2.84	0.45
34:2:1217:G:C4	34:2:1442:A:C8	3.04	0.45
7:G:183:ARG:NH1	34:2:266:U:OP1	2.50	0.45
34:2:45:U:O2'	34:2:46:A:H2'	2.17	0.45
34:2:137:U:O2	34:2:137:U:C2'	2.64	0.45
34:2:269:C:C2'	34:2:270:A:H8	2.17	0.45
34:2:1007:G:H2'	34:2:1008:U:C6	2.51	0.45
34:2:1220:A:N1	34:2:1261:U:C4	2.85	0.45
34:2:1269:G:C2	34:2:1439:C:O2	2.70	0.45
2:B:194:ASN:OD1	2:B:194:ASN:N	2.48	0.45
16:P:79:HIS:CE1	16:P:97:TYR:CD2	3.04	0.45
26:Z:54:ALA:HB1	26:Z:89:ILE:CG1	2.47	0.45
34:2:1170:A:H2'	34:2:1171:G:C8	2.52	0.45
34:2:1560:G:C2	34:2:1561:C:C2	3.05	0.45
35:i:6135:C:H5''	35:i:6136:U:C5	2.52	0.45
34:2:1447:U:H2'	34:2:1448:U:O4'	2.17	0.45
34:2:1497:G:C2	34:2:1498:C:C2	3.05	0.45
35:i:6154:A:H3'	35:i:6155:U:C5'	2.47	0.45
5:E:134:LYS:N	34:2:252:A:OP1	2.50	0.45
9:I:76:THR:HG23	9:I:108:PRO:HG2	1.99	0.45
10:J:108:ARG:NH2	10:J:145:SER:OG	2.50	0.45
23:W:99:PHE:HB3	23:W:130:TYR:CE1	2.52	0.45
34:2:48:G:C6	34:2:49:C:C4	3.05	0.45
34:2:48:G:C2	34:2:49:C:C2	3.05	0.45
34:2:782:G:C2	34:2:783:C:C2	3.05	0.45
4:D:98:ALA:HA	4:D:188:ILE:HD13	1.98	0.44
26:Z:63:SER:O	26:Z:66:VAL:C	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:70:C:N4	34:2:81:G:H1	2.14	0.44
34:2:208:U:N3	34:2:209:A:N7	2.65	0.44
34:2:520:A:C2'	34:2:521:U:O5'	2.65	0.44
34:2:932:A:C6	34:2:934:U:C2	3.05	0.44
34:2:991:A:C5'	34:2:991:A:N3	2.80	0.44
34:2:1223:A:N6	34:2:1259:U:H3	2.14	0.44
34:2:1442:A:H2'	34:2:1442:A:N3	2.32	0.44
34:2:1781:C:H2'	34:2:1782:C:C6	2.51	0.44
1:A:124:THR:OG1	1:A:125:ASP:N	2.51	0.44
7:G:155:ASP:OD2	34:2:77:U:O2'	2.34	0.44
9:I:140:THR:CG2	34:2:185:C:H3'	2.47	0.44
26:Z:97:LYS:NZ	34:2:1471:U:OP2	2.49	0.44
34:2:1126:G:C6	34:2:1127:C:C4	3.05	0.44
34:2:1269:G:C2	34:2:1439:C:C2	3.06	0.44
35:i:6146:C:O5'	35:i:6146:C:H6	2.00	0.44
26:Z:51:MET:O	26:Z:53:GLU:CB	2.64	0.44
34:2:798:A:C2	34:2:799:U:C2	3.05	0.44
34:2:878:G:C2	34:2:879:C:C2	3.05	0.44
34:2:1307:G:C2	34:2:1308:C:C2	3.05	0.44
34:2:1584:A:C2	34:2:1609:A:N7	2.86	0.44
35:i:6110:U:C4	35:i:6113:U:C5	3.05	0.44
35:i:6122:C:OP2	35:i:6122:C:H3'	2.17	0.44
35:i:6122:C:O2'	35:i:6123:G:OP2	2.34	0.44
6:F:109:LYS:HB2	34:2:1608:G:C5'	2.48	0.44
13:M:73:THR:OG1	32:f:112:GLY:O	2.35	0.44
24:X:91:GLY:C	24:X:93:LEU:H	2.26	0.44
26:Z:59:TYR:HA	26:Z:101:TYR:O	2.17	0.44
34:2:515:G:O6	34:2:536:G:C2	2.70	0.44
34:2:560:G:C6	34:2:584:A:C6	3.06	0.44
34:2:883:A:N6	34:2:884:G:C6	2.84	0.44
34:2:935:G:C2	34:2:936:C:C2	3.05	0.44
34:2:1603:G:C2	34:2:1604:C:C2	3.05	0.44
6:F:78:ARG:NH2	34:2:1410:G:OP1	2.51	0.44
7:G:175:ILE:HD13	34:2:78:A:O2'	2.16	0.44
10:J:140:ILE:HD12	25:Y:65:GLY:HA3	1.99	0.44
16:P:43:ARG:NH2	34:2:1550:U:OP2	2.50	0.44
21:U:39:ALA:HA	21:U:42:ILE:HG12	1.99	0.44
26:Z:49:ARG:HH11	26:Z:49:ARG:CG	2.12	0.44
27:a:13:LYS:HB3	34:2:1075:A:P	2.57	0.44
34:2:269:C:H42	34:2:284:G:H1	1.64	0.44
34:2:567:G:O6	34:2:575:G:N1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:954:A:H2'	34:2:955:C:O4'	2.17	0.44
34:2:1031:G:C6	34:2:1032:C:C4	3.05	0.44
34:2:1042:A:C6	34:2:1075:A:N1	2.85	0.44
35:i:6057:A:N6	35:i:6162:A:H1'	2.33	0.44
35:i:6074:A:O2'	35:i:6157:C:H4'	2.17	0.44
35:i:6106:U:O2	35:i:6106:U:C5'	2.66	0.44
23:W:75:ILE:HA	34:2:1099:G:O2'	2.17	0.44
32:f:86:THR:HG23	32:f:88:PRO:HD3	1.98	0.44
34:2:251:U:O2'	34:2:252:A:O4'	2.31	0.44
34:2:267:C:N4	34:2:286:G:N1	2.47	0.44
34:2:288:U:C2	34:2:289:G:C8	3.06	0.44
34:2:560:G:C6	34:2:584:A:N1	2.86	0.44
34:2:734:A:H2'	34:2:735:C:C6	2.53	0.44
34:2:952:G:H2'	34:2:953:G:C8	2.52	0.44
34:2:1218:A:N6	34:2:1264:G:H4'	2.32	0.44
34:2:1219:C:C4	34:2:1263:G:N2	2.86	0.44
34:2:1498:C:N3	34:2:1499:C:C5	2.86	0.44
35:i:6155:U:OP1	35:i:6155:U:C4'	2.63	0.44
6:F:125:VAL:CG1	26:Z:59:TYR:HB3	2.44	0.44
8:H:41:LEU:HD22	8:H:70:TYR:CD2	2.52	0.44
26:Z:61:SER:O	26:Z:63:SER:N	2.51	0.44
34:2:268:G:O6	34:2:286:G:C4	2.71	0.44
34:2:268:G:N2	34:2:269:C:C2	2.86	0.44
34:2:508:G:H2'	34:2:509:G:C1'	2.47	0.44
34:2:564:C:C5	34:2:575:G:C8	3.06	0.44
34:2:1014:U:C5	34:2:1015:C:N3	2.86	0.44
34:2:1080:A:C6	34:2:1090:A:C6	3.06	0.44
34:2:1209:C:H2'	34:2:1210:A:C8	2.52	0.44
35:i:6143:A:O3'	35:i:6144:G:H2'	2.18	0.44
7:G:5:ILE:HD12	7:G:16:ILE:HD13	2.00	0.44
34:2:157:U:H4'	34:2:158:U:OP1	2.18	0.44
34:2:514:A:C6	34:2:542:C:C6	3.06	0.44
34:2:515:G:C6	34:2:536:G:C2	3.06	0.44
34:2:922:A:C6	34:2:923:A:N6	2.86	0.44
34:2:1218:A:C8	34:2:1263:G:N2	2.85	0.44
19:S:103:ASN:O	19:S:106:GLU:HG2	2.18	0.44
25:Y:29:HIS:O	25:Y:30:PRO:C	2.61	0.44
34:2:8:U:H3'	34:2:9:U:H5'	1.97	0.44
34:2:53:G:C6	34:2:54:C:C4	3.05	0.44
34:2:407:C:O2'	34:2:1730:A:O2'	2.34	0.44
34:2:955:C:H2'	34:2:956:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1232:G:N2	34:2:1252:U:H1'	2.32	0.44
34:2:1287:G:N7	34:2:1313:U:H2'	2.33	0.44
34:2:1671:G:C4	34:2:1672:C:C5	3.06	0.44
35:i:6182:A:HO2'	35:i:6183:G:P	2.40	0.44
34:2:168:A:C8	34:2:170:A:N7	2.86	0.43
34:2:911:U:O2	34:2:911:U:C2'	2.66	0.43
34:2:979:G:H2'	34:2:980:U:O4'	2.18	0.43
34:2:1042:A:C6	34:2:1075:A:C2	3.06	0.43
35:i:6133:G:C2	35:i:6134:C:N4	2.86	0.43
35:i:6162:A:HO2'	35:i:6163:G:P	2.35	0.43
6:F:113:VAL:HG12	17:Q:43:ILE:HD11	2.00	0.43
6:F:194:GLU:CD	26:Z:59:TYR:OH	2.61	0.43
10:J:11:THR:HB	10:J:12:TYR:CE1	2.53	0.43
26:Z:96:SER:O	26:Z:97:LYS:HG3	2.18	0.43
27:a:15:ARG:O	27:a:16:GLY:C	2.61	0.43
34:2:53:G:C2	34:2:54:C:C2	3.06	0.43
34:2:151:U:O2	34:2:162:G:H8	2.00	0.43
34:2:429:G:C2	34:2:430:C:C2	3.06	0.43
34:2:519:A:C2	34:2:532:U:O2	2.71	0.43
34:2:623:G:C6	34:2:624:C:C4	3.06	0.43
34:2:776:G:N1	34:2:777:C:C4	2.86	0.43
34:2:782:G:C6	34:2:783:C:C4	3.05	0.43
34:2:1217:G:C5'	34:2:1442:A:H62	2.31	0.43
34:2:1316:C:H2'	34:2:1317:G:O4'	2.18	0.43
25:Y:121:THR:N	34:2:148:C:OP1	2.50	0.43
34:2:1015:C:H2'	34:2:1016:U:O4'	2.18	0.43
34:2:1123:A:C6	34:2:1124:A:C6	3.06	0.43
7:G:136:LYS:O	7:G:175:ILE:HG23	2.18	0.43
9:I:139:ASN:CG	34:2:196:A:N1	2.77	0.43
20:T:99:SER:HA	20:T:102:ARG:NH2	2.33	0.43
34:2:1046:G:C2	34:2:1071:C:O2	2.72	0.43
34:2:1437:C:C2	34:2:1438:C:C5	3.06	0.43
14:N:127:ARG:NH2	34:2:628:U:OP1	2.51	0.43
34:2:551:G:C2	34:2:572:C:C2	3.06	0.43
34:2:886:A:C2	34:2:925:A:C2	3.06	0.43
34:2:1031:G:C2	34:2:1032:C:C2	3.06	0.43
34:2:1270:G:C2	34:2:1438:C:C2	3.06	0.43
34:2:1417:G:H2'	34:2:1418:C:O4'	2.18	0.43
35:i:6213:A:H2'	35:i:6214:C:O4'	2.19	0.43
1:A:29:VAL:HG13	1:A:150:ASP:HB3	2.00	0.43
1:A:162:CYS:SG	1:A:163:ASN:N	2.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:109:LEU:HD11	10:J:134:ILE:HG21	1.98	0.43
34:2:213:G:C5'	34:2:241:U:O2	2.66	0.43
34:2:266:U:H3	34:2:267:C:N4	2.17	0.43
34:2:452:U:O2	34:2:452:U:H2'	2.19	0.43
34:2:1217:G:C5	34:2:1442:A:C8	3.06	0.43
34:2:1222:A:C2	34:2:1260:G:C2	3.07	0.43
34:2:1482:G:N2	34:2:1483:C:C2	2.86	0.43
34:2:1540:G:O2'	34:2:1541:A:O4'	2.35	0.43
34:2:1546:G:C2	34:2:1547:C:C2	3.07	0.43
35:i:6142:C:HO2'	35:i:6143:A:P	2.30	0.43
1:A:53:THR:HA	1:A:161:PRO:HD2	2.00	0.43
6:F:194:GLU:OE2	26:Z:59:TYR:CE2	2.72	0.43
34:2:207:U:N3	34:2:208:U:C4	2.87	0.43
34:2:560:G:O6	34:2:584:A:N6	2.51	0.43
34:2:1222:A:N1	34:2:1259:U:C2	2.86	0.43
35:i:6193:U:O2	35:i:6211:U:C5	2.72	0.43
2:B:137:ILE:HG21	2:B:176:VAL:HG21	1.99	0.43
7:G:174:LYS:CD	34:2:65:A:H5'	2.48	0.43
17:Q:47:LYS:O	17:Q:50:GLU:HB2	2.18	0.43
23:W:17:ALA:O	23:W:20:THR:OG1	2.33	0.43
26:Z:61:SER:H	26:Z:64:VAL:HB	1.84	0.43
27:a:80:HIS:O	27:a:81:ALA:HB3	2.19	0.43
34:2:366:A:H2'	34:2:367:U:O4'	2.19	0.43
34:2:828:A:O2'	34:2:829:U:OP2	2.37	0.43
34:2:1182:A:C2	34:2:1209:C:O2	2.72	0.43
34:2:1210:A:H2'	34:2:1211:G:O4'	2.18	0.43
16:P:79:HIS:HB2	34:2:1240:G:C8	2.54	0.43
34:2:429:G:C6	34:2:430:C:C4	3.07	0.43
34:2:452:U:O2	34:2:452:U:C2'	2.66	0.43
34:2:1220:A:C4	34:2:1262:G:C2	3.07	0.43
34:2:1292:U:O4	34:2:1293:G:C5	2.72	0.43
34:2:1598:A:H4'	34:2:1599:G:OP1	2.18	0.43
34:2:1785:C:H2'	34:2:1786:G:C8	2.54	0.43
7:G:173:PRO:HG3	34:2:66:U:C2	2.54	0.43
10:J:126:ARG:HD3	10:J:144:PRO:HB3	2.01	0.43
10:J:149:ARG:O	10:J:151:GLU:N	2.49	0.43
11:K:42:VAL:HG12	11:K:46:LEU:HD12	2.01	0.43
15:O:58:TYR:CD1	35:i:6111:A:C2	3.06	0.43
34:2:978:A:N3	34:2:1773:U:O2'	2.42	0.43
34:2:1171:G:C2	34:2:1172:C:C2	3.06	0.43
34:2:1178:G:C2	34:2:1179:C:C2	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1222:A:N1	34:2:1260:G:C6	2.87	0.43
34:2:1258:U:C6	34:2:1259:U:C4	3.06	0.43
34:2:1783:U:H2'	34:2:1784:G:H8	1.83	0.43
1:A:25:GLY:O	1:A:26:ALA:HB3	2.19	0.42
9:I:9:HIS:O	9:I:10:LYS:HB2	2.19	0.42
34:2:851:C:H2'	34:2:852:G:O4'	2.19	0.42
34:2:1073:G:O2'	34:2:1074:C:H5''	2.19	0.42
34:2:1240:G:C2'	34:2:1241:A:O5'	2.65	0.42
34:2:1551:G:N1	34:2:1554:A:OP2	2.52	0.42
35:i:6201:C:H2'	35:i:6202:C:OP1	2.19	0.42
1:A:15:GLN:HG3	18:R:117:LEU:HD23	2.00	0.42
6:F:125:VAL:HG11	26:Z:59:TYR:CB	2.43	0.42
7:G:153:VAL:C	34:2:78:A:OP1	2.62	0.42
10:J:7:THR:HG21	34:2:758:U:H5''	2.00	0.42
10:J:170:GLY:C	34:2:511:A:H5''	2.17	0.42
14:N:4:MET:SD	14:N:124:ARG:NH1	2.92	0.42
34:2:144:A:C6	34:2:170:A:C6	3.07	0.42
34:2:535:C:C2'	34:2:536:G:O4'	2.65	0.42
34:2:556:G:N1	34:2:558:C:C4	2.87	0.42
34:2:571:C:C4	34:2:572:C:C5	3.07	0.42
34:2:1079:U:H3	34:2:1090:A:H61	1.67	0.42
34:2:1482:G:C6	34:2:1483:C:N4	2.88	0.42
34:2:1590:A:C2	34:2:1602:U:N3	2.87	0.42
34:2:1784:G:C6	34:2:1785:C:N3	2.87	0.42
35:i:6115:A:H2'	35:i:6116:G:H8	1.83	0.42
12:L:99:ARG:CB	24:X:12:ALA:HB2	2.49	0.42
16:P:18:LYS:N	19:S:93:ASN:O	2.41	0.42
25:Y:29:HIS:N	25:Y:30:PRO:CD	2.82	0.42
34:2:513:G:N1	34:2:542:C:C4	2.57	0.42
34:2:515:G:C5	34:2:536:G:N2	2.85	0.42
34:2:549:A:C2	34:2:588:C:C6	3.07	0.42
34:2:566:A:C2	34:2:582:C:H1'	2.55	0.42
34:2:1083:A:C2	34:2:1089:C:N3	2.87	0.42
34:2:1218:A:H62	34:2:1263:G:C2'	2.26	0.42
34:2:1460:G:C2	34:2:1461:C:C2	3.07	0.42
9:I:96:LEU:HD11	9:I:180:CYS:SG	2.59	0.42
33:g:86:TRP:HA	33:g:110:ASP:HB2	2.02	0.42
34:2:1460:G:C6	34:2:1461:C:C4	3.07	0.42
34:2:1672:C:H2'	34:2:1673:C:C6	2.54	0.42
7:G:96:SER:OG	34:2:419:A:OP1	2.34	0.42
34:2:127:G:O2'	34:2:178:A:N7	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:506:U:O2	34:2:506:U:O4'	2.37	0.42
34:2:630:G:C5	34:2:631:U:C4	3.07	0.42
34:2:1073:G:O2'	34:2:1074:C:O5'	2.37	0.42
34:2:1074:C:O2	34:2:1074:C:O2'	2.37	0.42
34:2:1083:A:C2	34:2:1089:C:C2	3.07	0.42
34:2:1126:G:C2	34:2:1127:C:C2	3.08	0.42
34:2:1154:G:N2	34:2:1622:C:C2	2.87	0.42
34:2:1230:U:O3'	34:2:1258:U:H5'	2.19	0.42
34:2:1307:G:C6	34:2:1308:C:N4	2.87	0.42
34:2:1444:A:C8	34:2:1446:G:C5	3.08	0.42
35:i:6120:U:O4	35:i:6127:C:H5''	2.19	0.42
16:P:17:TYR:CA	19:S:92:VAL:O	2.68	0.42
16:P:20:VAL:N	19:S:94:ASP:H	2.18	0.42
18:R:45:ARG:NH2	34:2:1413:U:OP1	2.52	0.42
34:2:647:G:N3	34:2:647:G:H2'	2.34	0.42
34:2:1147:C:O2'	34:2:1763:A:C2	2.71	0.42
34:2:1171:G:C6	34:2:1172:C:C4	3.07	0.42
34:2:1315:G:C2	34:2:1316:C:C2	3.07	0.42
6:F:138:ALA:HA	6:F:203:ALA:HB1	2.01	0.42
7:G:160:ARG:HB3	7:G:171:LYS:HB2	2.01	0.42
17:Q:49:TYR:O	17:Q:52:LEU:HG	2.20	0.42
32:f:136:ARG:NH1	34:2:1234:C:O2	2.53	0.42
34:2:16:G:C2	34:2:17:C:N3	2.87	0.42
34:2:564:C:C4	34:2:576:G:C5	3.07	0.42
34:2:1588:G:N2	34:2:1589:C:C2	2.87	0.42
34:2:1629:A:N6	34:2:1761:A:O2'	2.53	0.42
13:M:21:LEU:HD21	13:M:80:ILE:HD13	2.01	0.42
19:S:38:VAL:HG22	19:S:101:LEU:HB3	2.02	0.42
34:2:86:A:O2'	34:2:146:A:O2'	2.36	0.42
34:2:549:A:C6	34:2:556:G:O6	2.73	0.42
34:2:566:A:C2'	34:2:567:G:O4'	2.60	0.42
34:2:885:U:N3	34:2:886:A:C5	2.87	0.42
34:2:1217:G:H2'	34:2:1442:A:N6	2.34	0.42
34:2:1378:U:H2'	34:2:1379:U:O4'	2.19	0.42
34:2:1582:G:O2'	34:2:1608:G:O6	2.36	0.42
35:i:6210:U:O2	35:i:6210:U:C2'	2.68	0.42
34:2:922:A:H2'	34:2:923:A:O4'	2.19	0.42
34:2:941:G:C2	34:2:942:C:C2	3.08	0.42
34:2:1431:G:H2'	34:2:1432:U:O4'	2.19	0.42
34:2:1531:C:H4'	34:2:1537:G:C6	2.55	0.42
34:2:1602:U:C4	34:2:1603:G:N7	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:6066:G:H5''	35:i:6067:G:OP2	2.19	0.42
35:i:6110:U:C3'	35:i:6111:A:H5''	2.50	0.42
35:i:6134:C:C2'	35:i:6135:C:H4'	2.50	0.42
34:2:63:G:O2'	34:2:64:U:O5'	2.38	0.42
34:2:1070:U:O3'	34:2:1071:C:O4'	2.38	0.42
10:J:127:VAL:HG21	34:2:477:A:H5'	2.02	0.41
15:O:58:TYR:CE2	35:i:6111:A:N9	2.88	0.41
18:R:110:VAL:HG13	18:R:117:LEU:HD22	2.02	0.41
24:X:63:GLN:CG	24:X:64:PRO:HD2	2.49	0.41
27:a:80:HIS:O	27:a:81:ALA:CB	2.68	0.41
34:2:15:U:H2'	34:2:16:G:O4'	2.21	0.41
34:2:60:U:H4'	34:2:454:C:N4	2.35	0.41
34:2:363:G:C2	34:2:380:C:N3	2.88	0.41
34:2:629:A:C8	34:2:630:G:C8	3.08	0.41
34:2:922:A:N1	34:2:923:A:N6	2.67	0.41
34:2:1083:A:C6	34:2:1089:C:N4	2.88	0.41
34:2:1220:A:C2	34:2:1262:G:C5	3.08	0.41
34:2:1255:A:C1'	34:2:1257:U:C5	3.02	0.41
9:I:5:ARG:NH1	9:I:29:LEU:O	2.44	0.41
10:J:171:ARG:N	10:J:171:ARG:HD2	2.35	0.41
23:W:76:SER:CB	23:W:77:PRO:CD	2.98	0.41
34:2:50:C:N3	34:2:429:G:C6	2.88	0.41
34:2:391:G:C2	34:2:392:C:C2	3.08	0.41
34:2:584:A:N6	34:2:585:G:O6	2.53	0.41
34:2:1040:G:C5	34:2:1076:C:N4	2.86	0.41
34:2:1183:A:O2'	34:2:1184:U:H4'	2.21	0.41
34:2:1260:G:C5	34:2:1261:U:C4	3.08	0.41
1:A:185:ARG:HG3	22:V:45:ALA:HB3	2.01	0.41
32:f:102:VAL:HG12	32:f:102:VAL:O	2.20	0.41
34:2:31:C:N4	34:2:32:U:C4	2.88	0.41
34:2:268:G:C5	34:2:269:C:C5	3.09	0.41
34:2:300:A:H2'	34:2:301:U:O4'	2.20	0.41
34:2:407:C:H2'	34:2:408:C:C6	2.54	0.41
34:2:1073:G:O2'	34:2:1074:C:C5'	2.68	0.41
34:2:1222:A:C2	34:2:1260:G:N3	2.88	0.41
34:2:1441:U:H4'	34:2:1444:A:N3	2.35	0.41
1:A:124:THR:HG22	1:A:174:TRP:HE1	1.85	0.41
3:C:144:ILE:CD1	3:C:196:ALA:HB1	2.51	0.41
13:M:45:LEU:HD13	13:M:71:LEU:HB3	2.02	0.41
26:Z:66:VAL:HA	26:Z:67:ASP:HA	1.56	0.41
34:2:511:A:C3'	34:2:512:U:C5'	2.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:642:G:C6	34:2:692:C:N3	2.88	0.41
34:2:878:G:C6	34:2:879:C:C4	3.08	0.41
34:2:978:A:C2	34:2:1773:U:H4'	2.55	0.41
34:2:1206:C:C2	34:2:1207:A:C6	3.09	0.41
34:2:1315:G:C6	34:2:1316:C:C4	3.08	0.41
34:2:1469:A:N3	34:2:1472:G:O2'	2.49	0.41
34:2:1560:G:N2	34:2:1561:C:C2	2.89	0.41
35:i:6086:U:H2'	35:i:6087:G:H5''	2.03	0.41
5:E:47:PHE:CE2	5:E:52:LEU:HD11	2.56	0.41
6:F:116:VAL:O	6:F:119:THR:OG1	2.32	0.41
10:J:133:HIS:HB2	10:J:134:ILE:HD12	2.02	0.41
24:X:53:VAL:HG13	24:X:72:VAL:HG13	2.02	0.41
27:a:95:ARG:CZ	34:2:933:C:C2	3.03	0.41
34:2:146:A:C5	34:2:147:U:C5	3.08	0.41
34:2:146:A:C6	34:2:147:U:C5	3.08	0.41
34:2:1471:U:O2	34:2:1471:U:H2'	2.19	0.41
35:i:6086:U:H2'	35:i:6087:G:C5'	2.50	0.41
35:i:6172:G:C2'	35:i:6173:C:O5'	2.68	0.41
14:N:12:SER:OG	34:2:956:G:N7	2.48	0.41
16:P:98:ASN:O	34:2:1182:A:N6	2.54	0.41
34:2:8:U:C3'	34:2:9:U:C5'	2.90	0.41
34:2:59:C:O2'	34:2:60:U:C6	2.72	0.41
34:2:690:A:H2'	34:2:691:U:O4'	2.20	0.41
34:2:1290:G:C2	34:2:1324:A:C2	3.08	0.41
34:2:1463:C:C5	34:2:1464:G:C8	3.09	0.41
35:i:6043:U:H6	35:i:6043:U:O5'	2.03	0.41
12:L:132:SER:O	12:L:133:LYS:C	2.63	0.41
23:W:8:ALA:HA	23:W:74:VAL:HG21	2.01	0.41
34:2:46:A:N1	34:2:431:G:O2'	2.45	0.41
34:2:209:A:H2'	34:2:210:U:H5'	2.00	0.41
34:2:211:U:C2	34:2:253:A:C2	3.09	0.41
34:2:566:A:C8	34:2:575:G:N2	2.86	0.41
34:2:776:G:C2	34:2:777:C:C2	3.08	0.41
34:2:1250:U:C2	34:2:1251:C:C5	3.08	0.41
34:2:1307:G:C6	34:2:1308:C:C4	3.09	0.41
34:2:1546:G:N2	34:2:1547:C:C2	2.89	0.41
1:A:102:PHE:CE2	1:A:132:ALA:HA	2.55	0.41
4:D:20:GLU:HG2	11:K:61:TRP:CZ3	2.55	0.41
6:F:191:THR:O	6:F:192:ILE:C	2.64	0.41
15:O:124:ASP:OD1	34:2:926:C:O2'	2.33	0.41
19:S:41:ARG:NH1	34:2:1563:C:OP1	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:70:THR:HG22	34:2:1279:C:O2'	2.20	0.41
26:Z:52:LYS:HD2	26:Z:53:GLU:CD	2.45	0.41
34:2:556:G:N2	34:2:558:C:N3	2.68	0.41
34:2:564:C:C2'	34:2:576:G:N2	2.78	0.41
34:2:885:U:O4	34:2:886:A:N6	2.54	0.41
34:2:1255:A:O4'	34:2:1257:U:H5	2.04	0.41
7:G:36:VAL:HB	7:G:50:PHE:HB2	2.03	0.41
7:G:56:ASN:ND2	7:G:61:PHE:O	2.54	0.41
10:J:173:ALA:HB3	34:2:511:A:OP1	2.20	0.41
11:K:3:ILE:HG21	11:K:8:ARG:HB2	2.02	0.41
15:O:50:ALA:O	15:O:52:ARG:N	2.53	0.41
25:Y:35:VAL:HG21	25:Y:40:LEU:HD11	2.02	0.41
34:2:151:U:C2	34:2:162:G:C8	3.08	0.41
34:2:185:C:O2	34:2:185:C:H2'	2.21	0.41
34:2:216:A:N1	34:2:844:G:H1'	2.36	0.41
34:2:391:G:C6	34:2:392:C:C4	3.08	0.41
34:2:564:C:C5	34:2:576:G:C5	3.09	0.41
34:2:935:G:P	34:2:1074:C:N3	2.91	0.41
34:2:1041:G:H1	34:2:1075:A:H2	1.69	0.41
34:2:1245:C:C4	34:2:1246:U:O2	2.74	0.41
34:2:1464:G:C6	34:2:1465:C:C4	3.08	0.41
34:2:1592:G:OP2	34:2:1594:C:N4	2.54	0.41
35:i:6077:U:OP2	35:i:6077:U:H6	2.04	0.41
13:M:55:LEU:HB3	13:M:68:VAL:HG11	2.03	0.41
32:f:96:LYS:O	32:f:97:LYS:HB3	2.21	0.41
34:2:268:G:O6	34:2:286:G:N3	2.54	0.41
34:2:403:G:C6	34:2:404:C:C4	3.09	0.41
34:2:425:G:C2	34:2:426:C:C2	3.09	0.41
34:2:425:G:C6	34:2:426:C:C4	3.09	0.41
34:2:821:U:C4	34:2:822:G:C2	3.09	0.41
34:2:1038:A:H61	34:2:1077:C:N4	2.19	0.41
34:2:1187:G:C6	34:2:1197:G:C6	3.09	0.41
35:i:6176:C:OP2	35:i:6176:C:C6	2.74	0.41
8:H:20:VAL:HG21	8:H:46:ILE:HD13	2.02	0.40
25:Y:20:ARG:CZ	25:Y:74:LEU:HD13	2.51	0.40
34:2:99:C:C2	34:2:360:C:C5	3.09	0.40
34:2:179:A:H2'	34:2:180:A:O4'	2.20	0.40
34:2:883:A:O2'	34:2:884:G:H5''	2.21	0.40
34:2:947:G:C2	34:2:948:C:C2	3.09	0.40
34:2:1570:G:H5''	34:2:1570:G:N3	2.36	0.40
3:C:156:PRO:HG3	22:V:9:VAL:HG11	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:122:ILE:HD12	26:Z:59:TYR:CE2	2.55	0.40
34:2:16:G:C2	34:2:17:C:C2	3.09	0.40
34:2:16:G:C6	34:2:17:C:N4	2.89	0.40
5:E:126:VAL:HG13	5:E:139:VAL:CG2	2.52	0.40
6:F:66:ILE:O	6:F:66:ILE:HG22	2.21	0.40
6:F:98:SER:HB2	6:F:178:THR:HG21	2.03	0.40
9:I:138:LYS:NZ	34:2:186:G:O2'	2.45	0.40
29:c:12:VAL:HG13	29:c:28:VAL:CG1	2.51	0.40
34:2:65:A:H2	34:2:84:A:N7	2.19	0.40
34:2:149:U:C4	34:2:150:G:N7	2.90	0.40
34:2:392:C:H2'	34:2:393:C:C6	2.56	0.40
34:2:531:U:H2'	34:2:532:U:O4'	2.21	0.40
34:2:566:A:N1	34:2:582:C:H1'	2.36	0.40
34:2:776:G:C6	34:2:777:C:C4	3.09	0.40
34:2:946:U:H2'	34:2:947:G:O4'	2.21	0.40
34:2:958:U:O2	34:2:958:U:C2'	2.69	0.40
34:2:1140:G:H2'	34:2:1141:A:C8	2.57	0.40
34:2:1354:C:H2'	34:2:1355:U:O4'	2.21	0.40
34:2:1437:C:H2'	34:2:1438:C:H6	1.86	0.40
34:2:1588:G:C6	34:2:1589:C:C4	3.10	0.40
35:i:6107:A:H2'	35:i:6108:G:O4'	2.21	0.40
35:i:6154:A:C3'	35:i:6155:U:H4'	2.51	0.40
34:2:208:U:C2	34:2:209:A:C8	3.09	0.40
34:2:941:G:C6	34:2:942:C:C4	3.09	0.40
34:2:1020:C:H2'	34:2:1021:C:O4'	2.22	0.40
34:2:1231:U:P	34:2:1258:U:H5'	2.62	0.40
34:2:1256:U:C5	34:2:1257:U:H1'	2.57	0.40
6:F:138:ALA:HA	6:F:203:ALA:CB	2.51	0.40
16:P:18:LYS:H	19:S:93:ASN:C	2.28	0.40
34:2:65:A:O2'	34:2:83:G:N1	2.55	0.40
34:2:214:A:C4	34:2:241:U:C4	3.09	0.40
34:2:252:A:O2'	34:2:253:A:O4'	2.35	0.40
34:2:604:A:C4	34:2:605:A:C2	3.09	0.40
34:2:1040:G:C6	34:2:1041:G:C6	3.09	0.40
34:2:1072:G:N3	34:2:1073:G:N7	2.64	0.40
34:2:1765:G:H4'	34:2:1766:G:O5'	2.21	0.40
35:i:6121:A:N3	35:i:6122:C:H3'	2.36	0.40
35:i:6134:C:N4	35:i:6135:C:C2	2.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	204/206 (99%)	168 (82%)	25 (12%)	11 (5%)	1	16
2	B	212/214 (99%)	174 (82%)	32 (15%)	6 (3%)	4	26
3	C	215/217 (99%)	187 (87%)	21 (10%)	7 (3%)	3	24
4	D	221/223 (99%)	198 (90%)	17 (8%)	6 (3%)	4	27
5	E	258/260 (99%)	214 (83%)	36 (14%)	8 (3%)	3	25
6	F	204/206 (99%)	174 (85%)	21 (10%)	9 (4%)	2	19
7	G	224/226 (99%)	186 (83%)	29 (13%)	9 (4%)	2	20
8	H	182/184 (99%)	155 (85%)	16 (9%)	11 (6%)	1	14
9	I	184/200 (92%)	154 (84%)	22 (12%)	8 (4%)	2	19
10	J	180/182 (99%)	151 (84%)	17 (9%)	12 (7%)	1	13
11	K	94/96 (98%)	80 (85%)	7 (7%)	7 (7%)	1	11
12	L	153/155 (99%)	129 (84%)	17 (11%)	7 (5%)	2	18
13	M	120/122 (98%)	94 (78%)	21 (18%)	5 (4%)	2	19
14	N	148/150 (99%)	130 (88%)	14 (10%)	4 (3%)	4	27
15	O	125/127 (98%)	108 (86%)	11 (9%)	6 (5%)	2	17
16	P	121/123 (98%)	96 (79%)	16 (13%)	9 (7%)	1	11
17	Q	139/141 (99%)	122 (88%)	12 (9%)	5 (4%)	2	22
18	R	127/129 (98%)	106 (84%)	14 (11%)	7 (6%)	1	16
19	S	143/145 (99%)	119 (83%)	17 (12%)	7 (5%)	1	17
20	T	141/143 (99%)	126 (89%)	10 (7%)	5 (4%)	3	23
21	U	104/106 (98%)	93 (89%)	7 (7%)	4 (4%)	2	21
22	V	85/87 (98%)	69 (81%)	10 (12%)	6 (7%)	1	12
23	W	127/129 (98%)	107 (84%)	14 (11%)	6 (5%)	2	18
24	X	143/145 (99%)	121 (85%)	15 (10%)	7 (5%)	1	17
25	Y	132/134 (98%)	113 (86%)	9 (7%)	10 (8%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Z	68/70 (97%)	58 (85%)	5 (7%)	5 (7%)	1	11
27	a	98/100 (98%)	74 (76%)	13 (13%)	11 (11%)	0	5
28	b	80/82 (98%)	64 (80%)	12 (15%)	4 (5%)	1	17
29	c	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
30	d	51/53 (96%)	41 (80%)	10 (20%)	0	100	100
31	e	53/55 (96%)	47 (89%)	3 (6%)	3 (6%)	1	15
32	f	67/69 (97%)	50 (75%)	11 (16%)	6 (9%)	0	8
33	g	312/324 (96%)	261 (84%)	44 (14%)	7 (2%)	5	30
All	All	4776/4866 (98%)	4024 (84%)	534 (11%)	218 (5%)	3	18

All (218) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	130	ALA
2	B	100	PHE
3	C	149	TRP
4	D	164	VAL
6	F	59	SER
6	F	206	GLY
7	G	154	ARG
8	H	32	PRO
8	H	64	VAL
8	H	74	GLN
9	I	10	LYS
10	J	121	SER
11	K	88	PRO
12	L	105	LYS
14	N	24	ALA
14	N	133	SER
15	O	91	SER
16	P	20	VAL
16	P	29	PRO
17	Q	40	GLN
17	Q	138	PHE
18	R	26	MET
18	R	121	VAL
19	S	92	VAL
20	T	11	ALA
21	U	107	THR

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Mol	Chain	Res	Type
21	U	118	ILE
22	V	30	SER
23	W	83	ILE
24	X	42	PRO
24	X	64	PRO
24	X	131	SER
25	Y	30	PRO
25	Y	60	PHE
26	Z	73	GLY
26	Z	104	ALA
27	a	18	VAL
27	a	75	ILE
27	a	81	ALA
27	a	86	VAL
28	b	21	LEU
32	f	143	HIS
1	A	26	ALA
1	A	72	ASP
1	A	94	GLY
3	C	141	VAL
3	C	153	LEU
4	D	217	VAL
5	E	38	LEU
5	E	195	ILE
5	E	201	HIS
7	G	122	GLU
8	H	10	SER
8	H	13	PRO
8	H	53	GLY
8	H	132	PRO
9	I	11	ARG
9	I	153	ILE
10	J	65	LYS
10	J	118	LEU
11	K	81	ASN
11	K	83	PRO
12	L	5	LEU
12	L	7	VAL
12	L	55	ASP
13	M	48	GLY
13	M	82	VAL
13	M	85	ALA

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Mol	Chain	Res	Type
16	P	12	PHE
16	P	101	VAL
17	Q	27	GLY
18	R	127	VAL
19	S	26	ILE
19	S	51	ASP
20	T	43	ASN
22	V	22	ARG
23	W	5	SER
23	W	57	ARG
23	W	120	HIS
24	X	130	VAL
25	Y	64	TYR
27	a	10	ARG
27	a	83	ILE
27	a	85	ARG
32	f	89	LYS
32	f	97	LYS
32	f	111	GLU
33	g	293	ASP
1	A	35	PRO
2	B	209	ASN
3	C	41	VAL
3	C	111	ASP
4	D	44	THR
4	D	93	ASP
5	E	80	THR
5	E	95	THR
5	E	120	SER
5	E	205	PHE
6	F	53	VAL
6	F	101	MET
7	G	89	ASN
8	H	29	ASN
9	I	22	ARG
9	I	40	THR
9	I	52	ASN
10	J	97	LEU
10	J	171	ARG
12	L	133	LYS
13	M	78	PRO
15	O	18	ARG

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Mol	Chain	Res	Type
15	O	124	ASP
17	Q	116	LEU
20	T	50	SER
22	V	4	ASP
22	V	44	ARG
23	W	107	SER
25	Y	61	ARG
25	Y	63	GLN
27	a	8	ASN
31	e	11	ALA
31	e	61	SER
32	f	88	PRO
33	g	4	SER
33	g	244	LYS
1	A	9	LEU
1	A	39	LYS
1	A	103	THR
1	A	167	LYS
1	A	193	GLN
2	B	148	ASN
2	B	210	VAL
5	E	77	ARG
6	F	83	ARG
7	G	165	GLY
7	G	173	PRO
7	G	177	ARG
8	H	110	GLN
9	I	116	HIS
10	J	35	GLY
10	J	120	LYS
10	J	147	MET
15	O	51	ASP
16	P	28	MET
16	P	80	LEU
16	P	121	ILE
17	Q	115	THR
18	R	100	LEU
20	T	39	THR
21	U	21	LYS
25	Y	34	ASN
26	Z	56	THR
26	Z	57	TYR

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Mol	Chain	Res	Type
27	a	16	GLY
28	b	3	LEU
32	f	106	TYR
33	g	168	ASP
1	A	68	PRO
2	B	190	PRO
3	C	44	THR
3	C	65	SER
6	F	40	GLN
6	F	52	ASP
6	F	102	ASN
7	G	8	PRO
7	G	70	PRO
7	G	224	ALA
10	J	18	PRO
10	J	67	PRO
10	J	122	VAL
10	J	134	ILE
11	K	54	PHE
11	K	87	PHE
11	K	94	GLY
12	L	30	LYS
14	N	70	LYS
15	O	114	ARG
18	R	72	LYS
19	S	14	ILE
19	S	144	ARG
21	U	71	PRO
24	X	4	GLY
25	Y	51	GLU
25	Y	133	ASN
28	b	62	VAL
31	e	47	VAL
2	B	221	PRO
4	D	4	ILE
11	K	2	LEU
12	L	113	PRO
14	N	3	ARG
15	O	25	ASP
16	P	69	GLU
19	S	12	GLN
20	T	45	LEU

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Mol	Chain	Res	Type
22	V	46	ILE
22	V	82	VAL
24	X	144	ARG
25	Y	31	ASN
26	Z	62	VAL
27	a	84	VAL
33	g	139	GLY
27	a	36	ILE
33	g	278	ILE
6	F	77	GLY
8	H	8	ILE
13	M	97	ILE
18	R	38	ILE
18	R	124	VAL
23	W	76	SER
4	D	163	PRO
8	H	98	ILE
9	I	39	GLY
24	X	63	GLN
28	b	39	GLY
33	g	31	PRO
16	P	53	PRO
19	S	76	PRO
25	Y	29	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	174/174 (100%)	158 (91%)	16 (9%)	8	31
2	B	196/196 (100%)	181 (92%)	15 (8%)	12	37
3	C	176/176 (100%)	152 (86%)	24 (14%)	3	18
4	D	185/185 (100%)	167 (90%)	18 (10%)	8	29
5	E	223/223 (100%)	210 (94%)	13 (6%)	18	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	174/174 (100%)	158 (91%)	16 (9%)	8	31
7	G	192/192 (100%)	173 (90%)	19 (10%)	7	28
8	H	164/164 (100%)	152 (93%)	12 (7%)	13	39
9	I	148/158 (94%)	128 (86%)	20 (14%)	4	19
10	J	153/153 (100%)	134 (88%)	19 (12%)	4	21
11	K	88/88 (100%)	79 (90%)	9 (10%)	7	27
12	L	136/136 (100%)	125 (92%)	11 (8%)	11	35
13	M	97/97 (100%)	90 (93%)	7 (7%)	13	39
14	N	127/127 (100%)	112 (88%)	15 (12%)	5	22
15	O	96/96 (100%)	90 (94%)	6 (6%)	16	42
16	P	105/106 (99%)	94 (90%)	11 (10%)	6	26
17	Q	117/117 (100%)	106 (91%)	11 (9%)	8	30
18	R	117/117 (100%)	105 (90%)	12 (10%)	7	27
19	S	128/128 (100%)	116 (91%)	12 (9%)	8	30
20	T	117/117 (100%)	106 (91%)	11 (9%)	8	30
21	U	96/96 (100%)	87 (91%)	9 (9%)	8	30
22	V	73/73 (100%)	69 (94%)	4 (6%)	19	45
23	W	110/110 (100%)	93 (84%)	17 (16%)	2	15
24	X	120/120 (100%)	105 (88%)	15 (12%)	4	21
25	Y	108/108 (100%)	93 (86%)	15 (14%)	3	18
26	Z	60/60 (100%)	57 (95%)	3 (5%)	22	47
27	a	85/85 (100%)	72 (85%)	13 (15%)	3	16
28	b	72/72 (100%)	68 (94%)	4 (6%)	19	45
29	c	55/55 (100%)	53 (96%)	2 (4%)	31	54
30	d	46/46 (100%)	43 (94%)	3 (6%)	15	42
31	e	49/49 (100%)	48 (98%)	1 (2%)	48	65
32	f	58/60 (97%)	50 (86%)	8 (14%)	3	18
33	g	265/270 (98%)	248 (94%)	17 (6%)	16	42
All	All	4110/4128 (100%)	3722 (91%)	388 (9%)	10	30

All (388) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	21	ARG
1	A	32	HIS
1	A	45	VAL
1	A	56	LYS
1	A	59	LEU
1	A	79	ARG
1	A	108	THR
1	A	124	THR
1	A	135	GLU
1	A	146	LEU
1	A	151	SER
1	A	158	VAL
1	A	173	ILE
1	A	177	LEU
1	A	198	MET
2	B	47	LEU
2	B	48	VAL
2	B	70	LEU
2	B	84	VAL
2	B	96	LEU
2	B	99	ASN
2	B	120	LEU
2	B	127	VAL
2	B	140	ILE
2	B	167	VAL
2	B	179	SER
2	B	181	LEU
2	B	191	GLU
2	B	194	ASN
2	B	228	LEU
3	C	43	VAL
3	C	49	LEU
3	C	51	LYS
3	C	58	ILE
3	C	63	LEU
3	C	71	PHE
3	C	86	MET
3	C	92	GLN
3	C	94	GLN
3	C	99	GLN
3	C	100	ARG
3	C	122	THR

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Mol	Chain	Res	Type
3	C	142	ILE
3	C	145	ARG
3	C	149	TRP
3	C	153	LEU
3	C	166	LYS
3	C	167	CYS
3	C	186	SER
3	C	190	LYS
3	C	195	LEU
3	C	213	GLU
3	C	223	ILE
3	C	235	TRP
4	D	5	ILE
4	D	11	LEU
4	D	51	ARG
4	D	70	THR
4	D	101	GLN
4	D	113	LEU
4	D	122	VAL
4	D	134	CYS
4	D	135	GLU
4	D	141	LYS
4	D	146	ARG
4	D	157	LEU
4	D	162	GLN
4	D	178	ARG
4	D	179	GLN
4	D	186	VAL
4	D	212	LYS
4	D	222	VAL
5	E	6	LYS
5	E	9	LEU
5	E	18	TRP
5	E	38	LEU
5	E	42	LEU
5	E	77	ARG
5	E	123	LEU
5	E	180	LEU
5	E	187	ARG
5	E	198	ARG
5	E	208	VAL
5	E	225	VAL

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Mol	Chain	Res	Type
5	E	247	THR
6	F	72	VAL
6	F	81	ASN
6	F	91	ILE
6	F	101	MET
6	F	116	VAL
6	F	121	GLU
6	F	158	ARG
6	F	165	SER
6	F	173	SER
6	F	186	PHE
6	F	188	ASN
6	F	189	ILE
6	F	192	ILE
6	F	196	LEU
6	F	210	SER
6	F	220	GLU
7	G	36	VAL
7	G	52	ILE
7	G	75	LEU
7	G	76	LEU
7	G	81	HIS
7	G	92	ARG
7	G	96	SER
7	G	97	VAL
7	G	136	LYS
7	G	141	ILE
7	G	152	ASP
7	G	153	VAL
7	G	155	ASP
7	G	164	LYS
7	G	178	LEU
7	G	180	THR
7	G	182	GLN
7	G	211	LEU
7	G	215	ARG
8	H	16	LEU
8	H	27	LEU
8	H	33	GLU
8	H	47	ARG
8	H	80	GLU
8	H	81	LEU

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Mol	Chain	Res	Type
8	H	93	LEU
8	H	126	LEU
8	H	129	LEU
8	H	139	ARG
8	H	159	VAL
8	H	174	ASN
9	I	8	ARG
9	I	10	LYS
9	I	24	LYS
9	I	25	ARG
9	I	29	LEU
9	I	35	ASN
9	I	43	ILE
9	I	62	THR
9	I	66	SER
9	I	72	VAL
9	I	77	ARG
9	I	86	SER
9	I	96	LEU
9	I	107	THR
9	I	140	THR
9	I	159	SER
9	I	160	GLN
9	I	170	ILE
9	I	190	LEU
9	I	196	ARG
10	J	8	TYR
10	J	11	THR
10	J	28	LEU
10	J	30	LEU
10	J	37	LYS
10	J	45	ILE
10	J	49	LEU
10	J	61	THR
10	J	64	GLU
10	J	69	ARG
10	J	93	LEU
10	J	97	LEU
10	J	126	ARG
10	J	143	ILE
10	J	145	SER
10	J	149	ARG

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Mol	Chain	Res	Type
10	J	150	LEU
10	J	153	GLU
10	J	176	ARG
11	K	15	LEU
11	K	17	GLN
11	K	20	VAL
11	K	21	LEU
11	K	40	LEU
11	K	59	PHE
11	K	76	LEU
11	K	80	LEU
11	K	86	ILE
12	L	8	GLN
12	L	10	GLU
12	L	19	ILE
12	L	32	LYS
12	L	80	MET
12	L	83	THR
12	L	84	ILE
12	L	94	VAL
12	L	101	GLU
12	L	105	LYS
12	L	131	ILE
13	M	55	LEU
13	M	67	LEU
13	M	69	GLN
13	M	80	ILE
13	M	91	TRP
13	M	104	ARG
13	M	105	LYS
14	N	3	ARG
14	N	11	MET
14	N	12	SER
14	N	16	ILE
14	N	25	TRP
14	N	36	GLN
14	N	39	LYS
14	N	64	LYS
14	N	88	LEU
14	N	89	TYR
14	N	107	LYS
14	N	115	LEU

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Mol	Chain	Res	Type
14	N	121	ARG
14	N	139	TRP
14	N	142	GLU
15	O	37	GLU
15	O	67	VAL
15	O	71	CYS
15	O	102	LEU
15	O	124	ASP
15	O	127	ARG
16	P	17	TYR
16	P	21	ASP
16	P	40	ARG
16	P	52	LYS
16	P	57	MET
16	P	77	ARG
16	P	79	HIS
16	P	84	ILE
16	P	111	MET
16	P	121	ILE
16	P	127	ARG
17	Q	7	VAL
17	Q	8	GLN
17	Q	19	VAL
17	Q	43	ILE
17	Q	47	LYS
17	Q	53	LEU
17	Q	55	VAL
17	Q	85	ILE
17	Q	121	SER
17	Q	128	LYS
17	Q	142	TYR
18	R	6	THR
18	R	16	LEU
18	R	17	ILE
18	R	27	ASP
18	R	36	ASP
18	R	45	ARG
18	R	47	ARG
18	R	61	ILE
18	R	66	VAL
18	R	88	VAL
18	R	109	LEU

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Mol	Chain	Res	Type
18	R	127	VAL
19	S	25	ASN
19	S	38	VAL
19	S	49	LYS
19	S	73	MET
19	S	74	GLN
19	S	93	ASN
19	S	100	SER
19	S	105	LEU
19	S	126	ARG
19	S	128	PHE
19	S	131	LEU
19	S	144	ARG
20	T	45	LEU
20	T	53	TRP
20	T	57	ARG
20	T	63	ARG
20	T	68	ARG
20	T	85	ASN
20	T	86	ARG
20	T	100	ILE
20	T	102	ARG
20	T	124	ILE
20	T	139	THR
21	U	17	VAL
21	U	34	LEU
21	U	35	GLU
21	U	52	LYS
21	U	84	MET
21	U	86	ILE
21	U	94	GLU
21	U	103	ILE
21	U	118	ILE
22	V	12	TYR
22	V	33	GLN
22	V	38	GLN
22	V	50	TYR
23	W	6	VAL
23	W	7	LEU
23	W	11	LEU
23	W	15	ASN
23	W	19	LYS

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Mol	Chain	Res	Type
23	W	23	ARG
23	W	24	GLN
23	W	25	VAL
23	W	28	ARG
23	W	40	VAL
23	W	47	ILE
23	W	51	GLU
23	W	61	ILE
23	W	66	ASN
23	W	70	ASN
23	W	107	SER
23	W	119	LYS
24	X	9	LEU
24	X	17	VAL
24	X	19	ARG
24	X	55	GLU
24	X	63	GLN
24	X	64	PRO
24	X	70	LYS
24	X	73	ARG
24	X	93	LEU
24	X	98	GLU
24	X	99	ASN
24	X	102	VAL
24	X	107	PHE
24	X	109	ARG
24	X	130	VAL
25	Y	3	ASP
25	Y	6	THR
25	Y	8	ARG
25	Y	29	HIS
25	Y	31	ASN
25	Y	35	VAL
25	Y	46	GLU
25	Y	57	VAL
25	Y	74	LEU
25	Y	98	GLU
25	Y	106	GLN
25	Y	110	GLN
25	Y	113	ASN
25	Y	116	LYS
25	Y	125	ILE

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Mol	Chain	Res	Type
26	Z	49	ARG
26	Z	68	ARG
26	Z	97	LYS
27	a	1	MET
27	a	7	SER
27	a	18	VAL
27	a	30	VAL
27	a	32	LYS
27	a	33	ASP
27	a	34	LYS
27	a	37	LYS
27	a	39	MET
27	a	64	LEU
27	a	75	ILE
27	a	85	ARG
27	a	93	ARG
28	b	7	LEU
28	b	9	HIS
28	b	26	GLN
28	b	67	THR
29	c	16	LEU
29	c	48	VAL
30	d	21	CYS
30	d	40	ARG
30	d	45	GLU
31	e	33	ARG
32	f	82	LYS
32	f	89	LYS
32	f	103	LEU
32	f	106	TYR
32	f	113	LYS
32	f	117	LEU
32	f	120	GLU
32	f	139	CYS
33	g	27	SER
33	g	43	LEU
33	g	55	PHE
33	g	60	ARG
33	g	67	HIS
33	g	83	SER
33	g	99	ASN
33	g	175	VAL

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Mol	Chain	Res	Type
33	g	188	LEU
33	g	195	ILE
33	g	244	LYS
33	g	273	GLU
33	g	275	GLU
33	g	292	GLN
33	g	299	LEU
33	g	315	ASN
33	g	321	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	GLN
1	A	168	HIS
2	B	124	ASN
2	B	157	GLN
2	B	160	HIS
2	B	208	GLN
3	C	80	ASN
3	C	115	HIS
3	C	152	ASN
4	D	165	ASN
4	D	195	ASN
5	E	188	ASN
5	E	201	HIS
6	F	81	ASN
6	F	130	ASN
6	F	141	ASN
6	F	188	ASN
6	F	202	ASN
7	G	176	GLN
8	H	19	GLN
8	H	74	GLN
8	H	122	HIS
10	J	124	HIS
11	K	62	GLN
12	L	14	GLN
14	N	78	ASN
15	O	12	GLN
15	O	29	HIS
16	P	79	HIS

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Mol	Chain	Res	Type
17	Q	40	GLN
17	Q	83	GLN
18	R	31	ASN
18	R	56	HIS
18	R	105	GLN
19	S	12	GLN
19	S	89	GLN
20	T	64	HIS
20	T	106	GLN
21	U	40	ASN
22	V	3	ASN
22	V	21	ASN
23	W	24	GLN
23	W	92	ASN
24	X	10	ASN
24	X	18	HIS
24	X	22	ASN
24	X	63	GLN
25	Y	29	HIS
25	Y	31	ASN
25	Y	34	ASN
25	Y	110	GLN
25	Y	113	ASN
30	d	10	HIS
33	g	99	ASN
33	g	203	ASN
33	g	292	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	2	1778/1780 (99%)	772 (43%)	111 (6%)
35	i	183/192 (95%)	106 (57%)	0
All	All	1961/1972 (99%)	878 (44%)	111 (5%)

All (878) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	2	2	A
34	2	3	U
34	2	4	C

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Mol	Chain	Res	Type
34	2	5	U
34	2	9	U
34	2	10	G
34	2	14	C
34	2	17	C
34	2	25	C
34	2	26	A
34	2	32	U
34	2	34	G
34	2	39	A
34	2	40	A
34	2	42	G
34	2	45	U
34	2	47	A
34	2	51	A
34	2	57	G
34	2	59	C
34	2	60	U
34	2	61	A
34	2	63	G
34	2	64	U
34	2	65	A
34	2	66	U
34	2	67	A
34	2	68	A
34	2	69	G
34	2	71	A
34	2	72	A
34	2	73	U
34	2	74	U
34	2	75	U
34	2	76	A
34	2	77	U
34	2	78	A
34	2	80	A
34	2	81	G
34	2	82	U
34	2	86	A
34	2	93	A
34	2	101	U
34	2	104	A
34	2	111	U

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Mol	Chain	Res	Type
34	2	113	U
34	2	114	C
34	2	115	G
34	2	123	G
34	2	124	A
34	2	125	U
34	2	127	G
34	2	129	U
34	2	130	C
34	2	131	C
34	2	132	U
34	2	133	U
34	2	134	U
34	2	136	C
34	2	137	U
34	2	138	A
34	2	139	C
34	2	140	A
34	2	141	U
34	2	146	A
34	2	148	C
34	2	149	U
34	2	150	G
34	2	152	G
34	2	153	G
34	2	154	U
34	2	155	A
34	2	157	U
34	2	158	U
34	2	159	C
34	2	160	U
34	2	161	A
34	2	167	A
34	2	169	U
34	2	170	A
34	2	173	U
34	2	175	C
34	2	176	U
34	2	177	U
34	2	178	A
34	2	180	A
34	2	183	C

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Mol	Chain	Res	Type
34	2	184	U
34	2	186	G
34	2	187	A
34	2	190	C
34	2	191	U
34	2	192	U
34	2	194	G
34	2	195	G
34	2	198	G
34	2	199	A
34	2	203	G
34	2	205	A
34	2	210	U
34	2	217	A
34	2	218	A
34	2	220	A
34	2	224	A
34	2	225	A
34	2	226	U
34	2	228	U
34	2	230	U
34	2	231	U
34	2	232	C
34	2	233	G
34	2	234	G
34	2	235	A
34	2	239	C
34	2	240	U
34	2	241	U
34	2	249	C
34	2	253	A
34	2	256	A
34	2	259	U
34	2	264	A
34	2	265	A
34	2	266	U
34	2	267	C
34	2	268	G
34	2	269	C
34	2	270	A
34	2	274	C
34	2	275	C

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Mol	Chain	Res	Type
34	2	276	U
34	2	277	U
34	2	278	G
34	2	279	U
34	2	280	G
34	2	284	G
34	2	286	G
34	2	288	U
34	2	294	A
34	2	298	A
34	2	301	U
34	2	305	U
34	2	308	C
34	2	309	C
34	2	311	A
34	2	312	U
34	2	313	C
34	2	314	A
34	2	315	A
34	2	319	U
34	2	320	C
34	2	321	G
34	2	322	A
34	2	328	G
34	2	332	A
34	2	336	G
34	2	337	C
34	2	342	C
34	2	351	A
34	2	359	A
34	2	360	C
34	2	374	U
34	2	377	A
34	2	382	G
34	2	389	G
34	2	392	C
34	2	397	G
34	2	399	A
34	2	400	A
34	2	401	C
34	2	403	G
34	2	406	A

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Mol	Chain	Res	Type
34	2	410	C
34	2	411	A
34	2	412	U
34	2	414	C
34	2	415	A
34	2	416	A
34	2	417	G
34	2	419	A
34	2	421	G
34	2	422	G
34	2	423	C
34	2	424	A
34	2	425	G
34	2	433	G
34	2	436	A
34	2	438	U
34	2	442	C
34	2	443	C
34	2	444	A
34	2	447	C
34	2	452	U
34	2	458	G
34	2	459	A
34	2	460	G
34	2	463	A
34	2	467	A
34	2	474	A
34	2	476	A
34	2	479	G
34	2	480	A
34	2	483	C
34	2	490	C
34	2	491	A
34	2	492	U
34	2	493	U
34	2	494	C
34	2	497	G
34	2	499	C
34	2	500	U
34	2	503	U
34	2	504	A
34	2	505	A

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Mol	Chain	Res	Type
34	2	506	U
34	2	507	U
34	2	509	G
34	2	510	A
34	2	512	U
34	2	513	G
34	2	514	A
34	2	516	U
34	2	518	C
34	2	521	U
34	2	524	A
34	2	526	A
34	2	527	U
34	2	532	U
34	2	533	A
34	2	534	A
34	2	535	C
34	2	536	G
34	2	537	A
34	2	538	G
34	2	539	G
34	2	540	A
34	2	541	A
34	2	542	C
34	2	543	A
34	2	544	A
34	2	545	C
34	2	547	G
34	2	548	G
34	2	550	G
34	2	551	G
34	2	553	C
34	2	554	A
34	2	556	G
34	2	557	U
34	2	558	C
34	2	561	G
34	2	564	C
34	2	565	C
34	2	570	G
34	2	573	G
34	2	574	C

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Mol	Chain	Res	Type
34	2	575	G
34	2	576	G
34	2	577	U
34	2	578	A
34	2	579	A
34	2	580	U
34	2	581	U
34	2	593	A
34	2	594	G
34	2	596	G
34	2	600	A
34	2	605	A
34	2	606	G
34	2	607	U
34	2	610	U
34	2	613	C
34	2	618	A
34	2	619	A
34	2	622	A
34	2	623	G
34	2	629	A
34	2	632	U
34	2	634	A
34	2	637	U
34	2	638	U
34	2	639	U
34	2	640	G
34	2	642	G
34	2	647	G
34	2	648	U
34	2	649	U
34	2	652	C
34	2	653	C
34	2	654	G
34	2	655	G
34	2	677	G
34	2	678	U
34	2	679	U
34	2	683	C
34	2	684	A
34	2	691	U
34	2	694	U

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Mol	Chain	Res	Type
34	2	695	U
34	2	696	C
34	2	697	C
34	2	698	U
34	2	701	U
34	2	704	C
34	2	705	U
34	2	708	C
34	2	709	C
34	2	710	U
34	2	711	G
34	2	712	U
34	2	713	A
34	2	714	C
34	2	716	C
34	2	717	C
34	2	718	U
34	2	719	U
34	2	722	G
34	2	724	G
34	2	725	U
34	2	727	C
34	2	731	C
34	2	732	G
34	2	733	A
34	2	734	A
34	2	735	C
34	2	736	C
34	2	737	A
34	2	738	G
34	2	740	A
34	2	741	C
34	2	742	U
34	2	743	U
34	2	754	A
34	2	756	A
34	2	765	G
34	2	766	U
34	2	767	U
34	2	769	A
34	2	771	A
34	2	774	A

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Mol	Chain	Res	Type
34	2	778	G
34	2	779	A
34	2	780	A
34	2	781	A
34	2	782	G
34	2	785	C
34	2	786	G
34	2	787	A
34	2	788	A
34	2	789	U
34	2	792	A
34	2	793	U
34	2	794	U
34	2	795	A
34	2	802	A
34	2	806	A
34	2	809	G
34	2	810	A
34	2	811	A
34	2	812	U
34	2	813	A
34	2	815	G
34	2	817	C
34	2	819	U
34	2	820	U
34	2	821	U
34	2	822	G
34	2	823	G
34	2	825	U
34	2	826	C
34	2	828	A
34	2	829	U
34	2	830	U
34	2	831	U
34	2	832	U
34	2	834	U
34	2	837	G
34	2	840	U
34	2	842	U
34	2	844	G
34	2	845	G
34	2	848	C

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Mol	Chain	Res	Type
34	2	849	A
34	2	852	G
34	2	855	A
34	2	859	U
34	2	860	U
34	2	861	A
34	2	862	A
34	2	863	U
34	2	872	U
34	2	875	G
34	2	876	G
34	2	884	G
34	2	885	U
34	2	887	U
34	2	894	G
34	2	895	U
34	2	897	A
34	2	903	G
34	2	904	A
34	2	905	A
34	2	906	A
34	2	908	U
34	2	909	C
34	2	910	U
34	2	912	G
34	2	913	G
34	2	914	A
34	2	915	U
34	2	919	U
34	2	920	U
34	2	927	U
34	2	928	A
34	2	929	A
34	2	931	U
34	2	932	A
34	2	934	U
34	2	935	G
34	2	936	C
34	2	939	A
34	2	941	G
34	2	943	A
34	2	944	U

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Mol	Chain	Res	Type
34	2	950	A
34	2	958	U
34	2	959	U
34	2	964	U
34	2	965	A
34	2	969	A
34	2	972	A
34	2	980	U
34	2	981	U
34	2	983	G
34	2	985	G
34	2	987	A
34	2	990	G
34	2	991	A
34	2	992	A
34	2	993	G
34	2	994	A
34	2	999	C
34	2	1003	U
34	2	1004	A
34	2	1005	C
34	2	1009	C
34	2	1010	G
34	2	1011	U
34	2	1012	A
34	2	1013	G
34	2	1015	C
34	2	1020	C
34	2	1024	A
34	2	1026	A
34	2	1027	C
34	2	1028	U
34	2	1030	U
34	2	1031	G
34	2	1037	U
34	2	1038	A
34	2	1039	G
34	2	1041	G
34	2	1042	A
34	2	1044	C
34	2	1045	G
34	2	1046	G

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Mol	Chain	Res	Type
34	2	1050	G
34	2	1051	U
34	2	1052	G
34	2	1056	U
34	2	1057	U
34	2	1058	C
34	2	1059	U
34	2	1060	U
34	2	1063	G
34	2	1070	U
34	2	1071	C
34	2	1073	G
34	2	1074	C
34	2	1075	A
34	2	1076	C
34	2	1080	A
34	2	1081	C
34	2	1082	G
34	2	1083	A
34	2	1084	G
34	2	1087	A
34	2	1090	A
34	2	1091	A
34	2	1092	A
34	2	1094	U
34	2	1096	U
34	2	1097	U
34	2	1098	U
34	2	1099	G
34	2	1100	G
34	2	1107	G
34	2	1108	G
34	2	1110	G
34	2	1113	G
34	2	1118	G
34	2	1121	G
34	2	1123	A
34	2	1130	A
34	2	1137	A
34	2	1142	A
34	2	1145	G
34	2	1149	G

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Mol	Chain	Res	Type
34	2	1150	A
34	2	1157	C
34	2	1158	C
34	2	1159	A
34	2	1162	A
34	2	1163	G
34	2	1166	G
34	2	1174	U
34	2	1175	G
34	2	1183	A
34	2	1184	U
34	2	1185	U
34	2	1189	C
34	2	1190	U
34	2	1192	A
34	2	1193	A
34	2	1195	A
34	2	1196	C
34	2	1198	G
34	2	1199	G
34	2	1200	G
34	2	1201	A
34	2	1202	A
34	2	1203	A
34	2	1204	C
34	2	1211	G
34	2	1212	G
34	2	1213	U
34	2	1215	C
34	2	1216	A
34	2	1217	G
34	2	1218	A
34	2	1219	C
34	2	1222	A
34	2	1224	U
34	2	1226	A
34	2	1227	G
34	2	1228	G
34	2	1229	A
34	2	1230	U
34	2	1231	U
34	2	1234	C

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Mol	Chain	Res	Type
34	2	1236	G
34	2	1238	U
34	2	1240	G
34	2	1241	A
34	2	1242	G
34	2	1243	A
34	2	1244	G
34	2	1245	C
34	2	1247	C
34	2	1250	U
34	2	1253	U
34	2	1254	G
34	2	1257	U
34	2	1258	U
34	2	1259	U
34	2	1264	G
34	2	1265	U
34	2	1266	G
34	2	1268	U
34	2	1269	G
34	2	1274	A
34	2	1282	U
34	2	1284	U
34	2	1296	G
34	2	1306	U
34	2	1310	U
34	2	1313	U
34	2	1314	U
34	2	1317	G
34	2	1319	U
34	2	1320	A
34	2	1321	A
34	2	1322	C
34	2	1324	A
34	2	1336	A
34	2	1339	U
34	2	1340	A
34	2	1343	A
34	2	1344	A
34	2	1345	A
34	2	1347	A
34	2	1349	G

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Mol	Chain	Res	Type
34	2	1353	G
34	2	1356	G
34	2	1358	C
34	2	1359	A
34	2	1360	C
34	2	1361	U
34	2	1362	U
34	2	1363	G
34	2	1364	C
34	2	1366	G
34	2	1369	U
34	2	1370	G
34	2	1371	A
34	2	1374	C
34	2	1380	A
34	2	1388	U
34	2	1393	G
34	2	1396	U
34	2	1397	C
34	2	1398	A
34	2	1400	G
34	2	1404	A
34	2	1410	G
34	2	1411	U
34	2	1412	U
34	2	1413	U
34	2	1416	G
34	2	1417	G
34	2	1425	A
34	2	1426	G
34	2	1428	U
34	2	1430	U
34	2	1432	U
34	2	1433	G
34	2	1434	A
34	2	1435	U
34	2	1442	A
34	2	1443	G
34	2	1444	A
34	2	1445	C
34	2	1446	G
34	2	1449	C

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Mol	Chain	Res	Type
34	2	1452	G
34	2	1454	C
34	2	1455	C
34	2	1456	G
34	2	1457	C
34	2	1458	A
34	2	1461	C
34	2	1464	G
34	2	1467	A
34	2	1468	C
34	2	1469	A
34	2	1471	U
34	2	1475	G
34	2	1476	G
34	2	1481	A
34	2	1484	G
34	2	1485	A
34	2	1487	U
34	2	1488	A
34	2	1489	C
34	2	1490	A
34	2	1491	A
34	2	1492	C
34	2	1494	U
34	2	1495	U
34	2	1498	C
34	2	1502	G
34	2	1506	U
34	2	1507	C
34	2	1508	U
34	2	1509	G
34	2	1512	U
34	2	1513	A
34	2	1514	A
34	2	1519	G
34	2	1521	G
34	2	1522	A
34	2	1523	A
34	2	1527	C
34	2	1531	C
34	2	1532	G
34	2	1533	U

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Mol	Chain	Res	Type
34	2	1534	G
34	2	1535	C
34	2	1537	G
34	2	1538	G
34	2	1540	G
34	2	1543	A
34	2	1552	U
34	2	1555	U
34	2	1556	U
34	2	1557	A
34	2	1565	U
34	2	1566	C
34	2	1569	C
34	2	1570	G
34	2	1571	A
34	2	1580	U
34	2	1583	U
34	2	1588	G
34	2	1589	C
34	2	1594	C
34	2	1595	A
34	2	1597	C
34	2	1598	A
34	2	1599	G
34	2	1602	U
34	2	1603	G
34	2	1605	G
34	2	1612	A
34	2	1614	G
34	2	1616	C
34	2	1623	C
34	2	1626	U
34	2	1629	A
34	2	1633	A
34	2	1635	C
34	2	1640	G
34	2	1643	G
34	2	1655	U
34	2	1656	G
34	2	1667	U
34	2	1676	A
34	2	1679	A

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Mol	Chain	Res	Type
34	2	1682	U
34	2	1685	U
34	2	1686	U
34	2	1687	A
34	2	1688	G
34	2	1692	A
34	2	1693	G
34	2	1694	G
34	2	1696	G
34	2	1697	G
34	2	1698	C
34	2	1699	A
34	2	1700	A
34	2	1701	C
34	2	1702	U
34	2	1703	C
34	2	1706	U
34	2	1707	C
34	2	1708	U
34	2	1709	C
34	2	1710	A
34	2	1711	G
34	2	1712	A
34	2	1725	G
34	2	1730	A
34	2	1740	U
34	2	1743	G
34	2	1748	A
34	2	1753	A
34	2	1754	A
34	2	1755	G
34	2	1756	U
34	2	1758	G
34	2	1759	U
34	2	1763	A
34	2	1764	A
34	2	1766	G
34	2	1767	U
34	2	1770	C
34	2	1774	A
34	2	1776	G
34	2	1777	U

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Mol	Chain	Res	Type
34	2	1778	G
34	2	1779	A
34	2	1780	A
34	2	1781	C
34	2	1784	G
34	2	1789	A
34	2	1790	G
34	2	1791	G
34	2	1792	A
34	2	1793	U
34	2	1794	C
34	2	1796	U
34	2	1798	A
35	i	6033	A
35	i	6034	A
35	i	6037	U
35	i	6039	A
35	i	6044	G
35	i	6046	U
35	i	6049	U
35	i	6052	A
35	i	6053	U
35	i	6056	A
35	i	6058	U
35	i	6061	U
35	i	6062	G
35	i	6063	A
35	i	6067	G
35	i	6068	U
35	i	6075	A
35	i	6076	U
35	i	6077	U
35	i	6079	C
35	i	6080	A
35	i	6081	A
35	i	6084	A
35	i	6086	U
35	i	6087	G
35	i	6088	C
35	i	6090	A
35	i	6094	U
35	i	6098	A

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Mol	Chain	Res	Type
35	i	6099	U
35	i	6101	U
35	i	6102	A
35	i	6104	G
35	i	6105	U
35	i	6106	U
35	i	6107	A
35	i	6108	G
35	i	6109	C
35	i	6110	U
35	i	6112	U
35	i	6114	U
35	i	6118	U
35	i	6119	U
35	i	6121	A
35	i	6122	C
35	i	6123	G
35	i	6124	U
35	i	6128	A
35	i	6129	G
35	i	6130	G
35	i	6132	U
35	i	6133	G
35	i	6135	C
35	i	6136	U
35	i	6137	A
35	i	6138	G
35	i	6139	U
35	i	6140	G
35	i	6142	C
35	i	6143	A
35	i	6144	G
35	i	6145	C
35	i	6146	C
35	i	6147	C
35	i	6148	C
35	i	6149	A
35	i	6153	U
35	i	6154	A
35	i	6155	U
35	i	6157	C
35	i	6158	A

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Mol	Chain	Res	Type
35	i	6159	G
35	i	6160	G
35	i	6162	A
35	i	6163	G
35	i	6165	C
35	i	6166	C
35	i	6168	C
35	i	6169	U
35	i	6170	C
35	i	6171	U
35	i	6172	G
35	i	6173	C
35	i	6174	G
35	i	6176	C
35	i	6178	U
35	i	6179	U
35	i	6180	U
35	i	6181	C
35	i	6183	G
35	i	6184	A
35	i	6186	U
35	i	6187	A
35	i	6192	G
35	i	6197	A
35	i	6198	A
35	i	6199	A
35	i	6200	A
35	i	6202	C
35	i	6211	U
35	i	6212	U
35	i	6213	A
35	i	6218	C
35	i	6219	U
35	i	6220	A
35	i	6221	C

All (111) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	2	3	U
34	2	44	U
34	2	59	C

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Mol	Chain	Res	Type
34	2	63	G
34	2	65	A
34	2	66	U
34	2	70	C
34	2	71	A
34	2	72	A
34	2	73	U
34	2	129	U
34	2	130	C
34	2	137	U
34	2	139	C
34	2	148	C
34	2	149	U
34	2	157	U
34	2	169	U
34	2	177	U
34	2	186	G
34	2	216	A
34	2	217	A
34	2	239	C
34	2	248	U
34	2	258	U
34	2	262	C
34	2	263	G
34	2	264	A
34	2	265	A
34	2	269	C
34	2	271	U
34	2	277	U
34	2	279	U
34	2	321	G
34	2	399	A
34	2	454	C
34	2	497	G
34	2	509	G
34	2	513	G
34	2	532	U
34	2	537	A
34	2	542	C
34	2	556	G
34	2	557	U
34	2	563	G

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Mol	Chain	Res	Type
34	2	564	C
34	2	576	G
34	2	577	U
34	2	578	A
34	2	579	A
34	2	605	A
34	2	621	A
34	2	638	U
34	2	695	U
34	2	700	C
34	2	704	C
34	2	708	C
34	2	710	U
34	2	721	U
34	2	740	A
34	2	766	U
34	2	779	A
34	2	792	A
34	2	794	U
34	2	809	G
34	2	811	A
34	2	826	C
34	2	828	A
34	2	854	A
34	2	862	A
34	2	884	G
34	2	909	C
34	2	911	U
34	2	912	G
34	2	913	G
34	2	927	U
34	2	963	U
34	2	1003	U
34	2	1010	G
34	2	1027	C
34	2	1044	C
34	2	1060	U
34	2	1073	G
34	2	1080	A
34	2	1083	A
34	2	1107	G
34	2	1184	U

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Mol	Chain	Res	Type
34	2	1189	C
34	2	1195	A
34	2	1217	G
34	2	1230	U
34	2	1243	A
34	2	1264	G
34	2	1343	A
34	2	1429	C
34	2	1455	C
34	2	1470	C
34	2	1491	A
34	2	1501	A
34	2	1532	G
34	2	1534	G
34	2	1556	U
34	2	1598	A
34	2	1613	C
34	2	1628	U
34	2	1634	C
34	2	1655	U
34	2	1678	G
34	2	1763	A
34	2	1765	G
34	2	1791	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 83 ligands modelled in this entry, 83 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	657:C	O3'	676:G	P	17.80

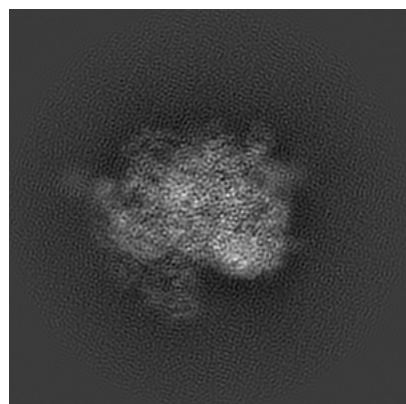
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8124. These allow visual inspection of the internal detail of the map and identification of artifacts.

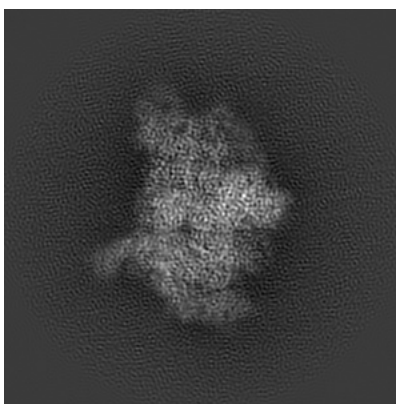
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

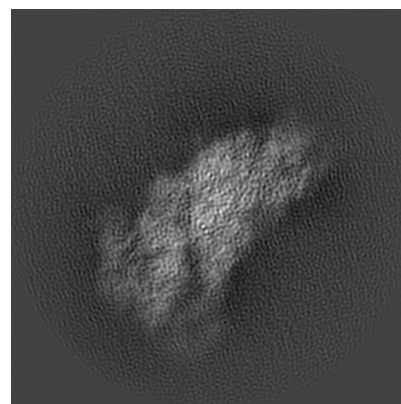
6.1.1 Primary map



X

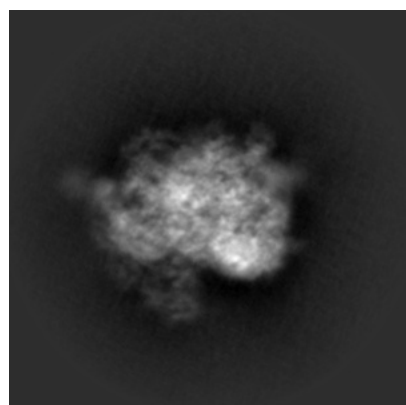


Y

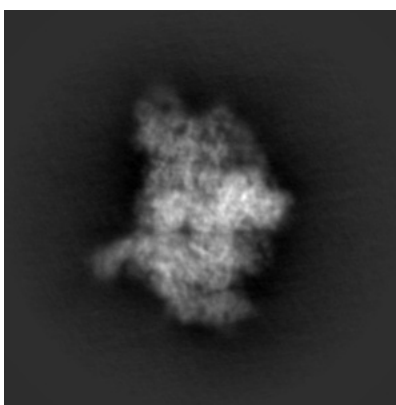


Z

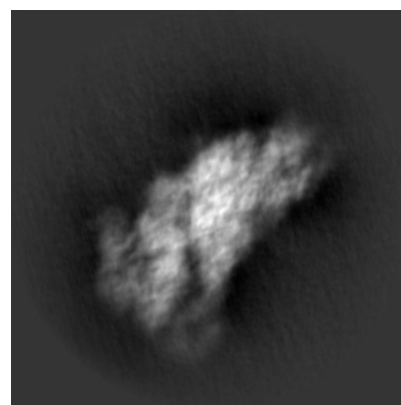
6.1.2 Raw map



X



Y

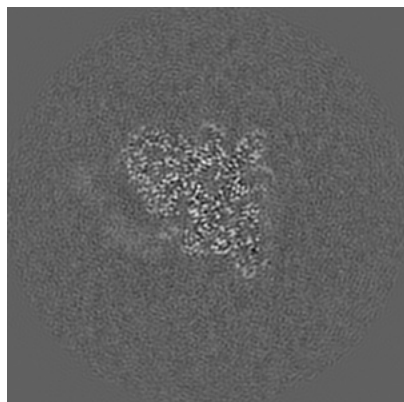


Z

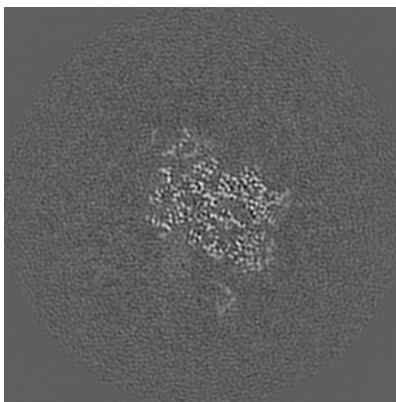
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

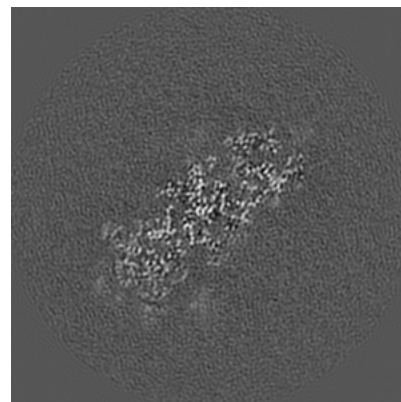
6.2.1 Primary map



X Index: 140

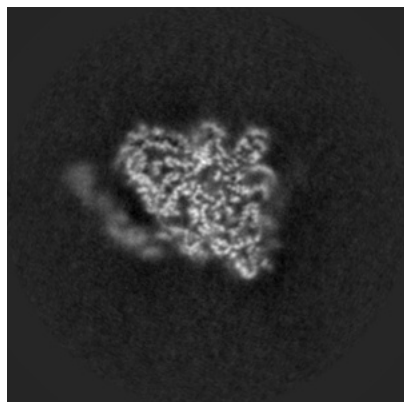


Y Index: 140

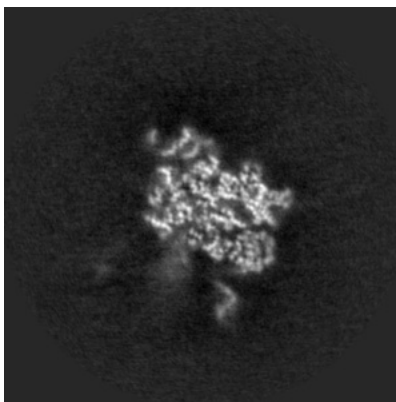


Z Index: 140

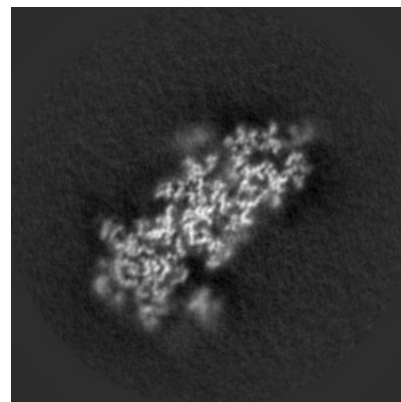
6.2.2 Raw map



X Index: 140



Y Index: 140

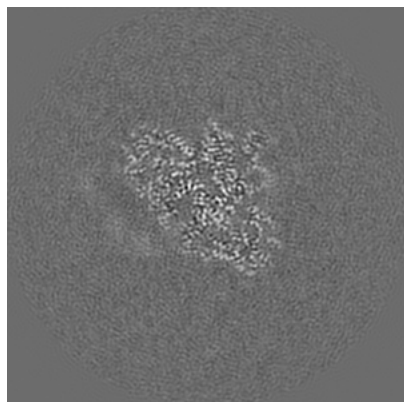


Z Index: 140

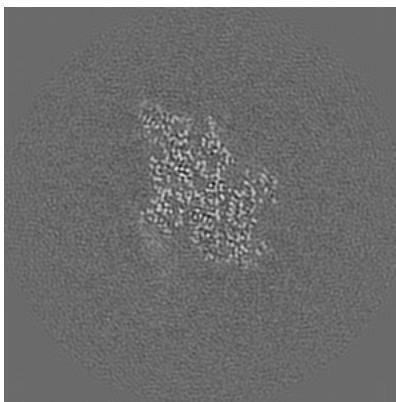
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

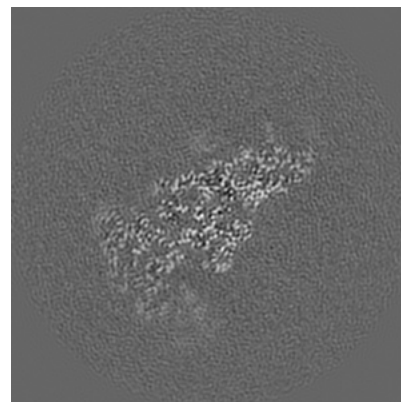
6.3.1 Primary map



X Index: 143

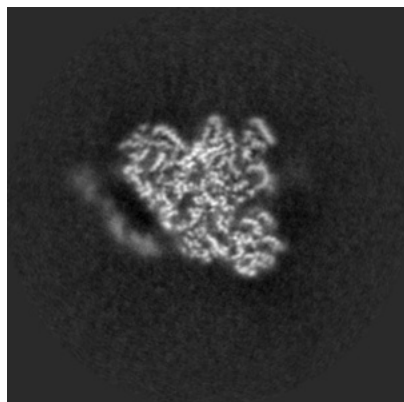


Y Index: 153

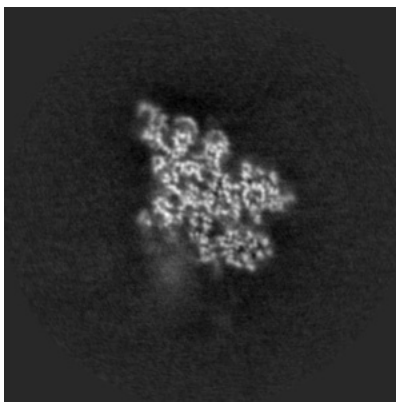


Z Index: 149

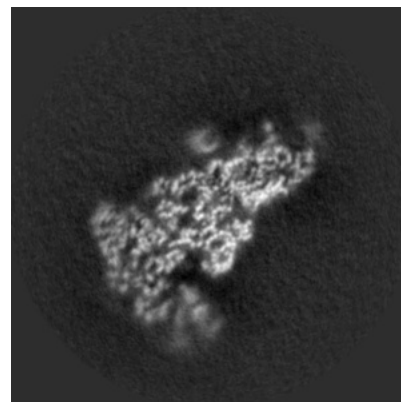
6.3.2 Raw map



X Index: 145



Y Index: 148

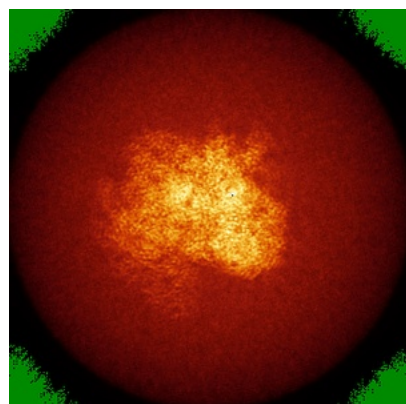


Z Index: 149

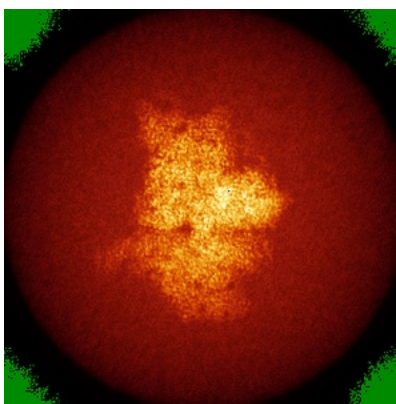
The images above show the largest variance slices of the map in three orthogonal directions.

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

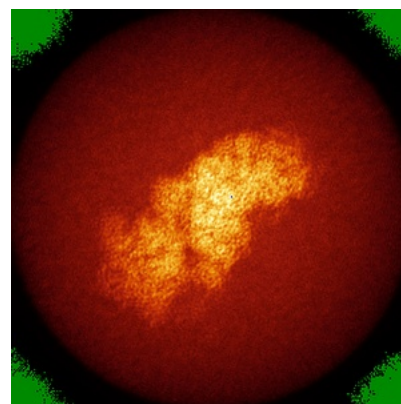
6.4.1 Primary map



X

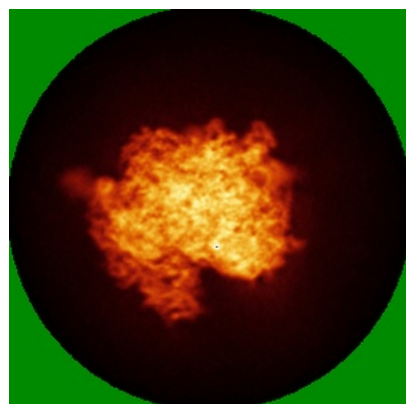


Y

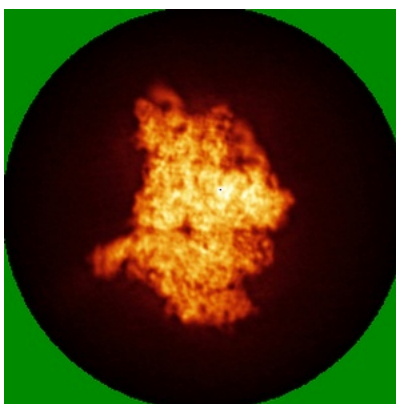


Z

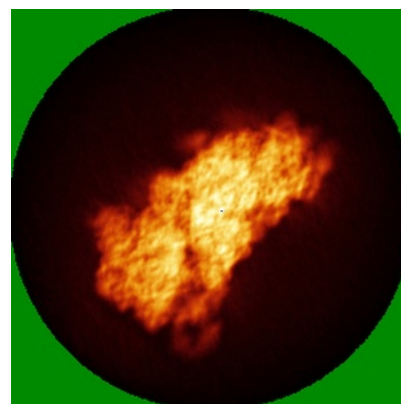
6.4.2 Raw map



X



Y

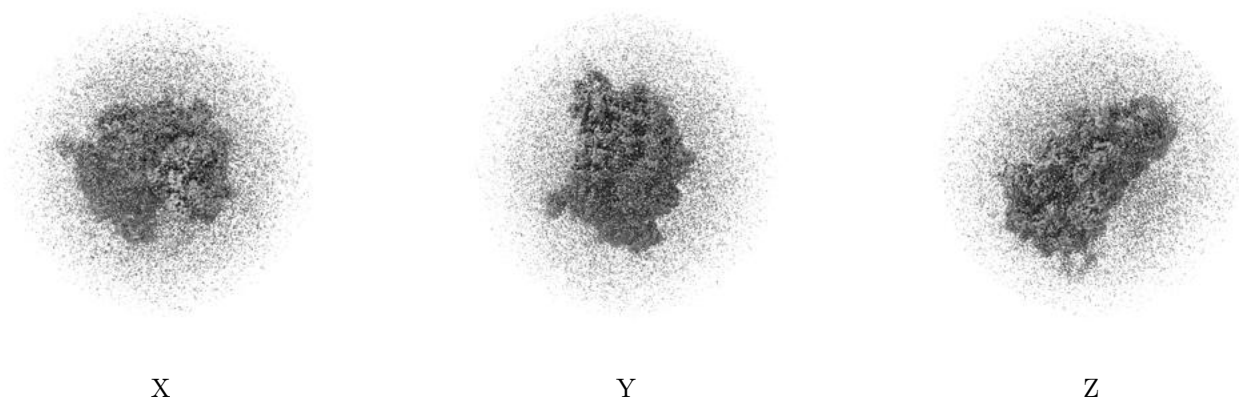


Z

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.

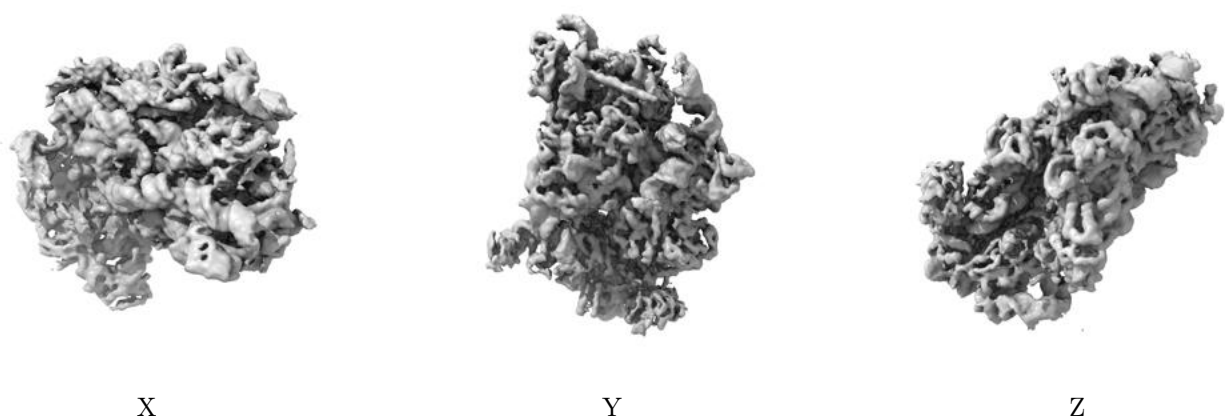
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

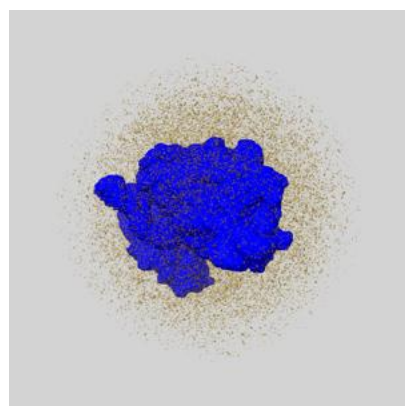
6.6 Mask visualisation [i](#)

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

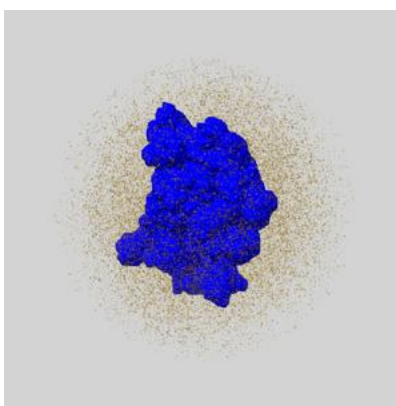
A mask typically either:

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

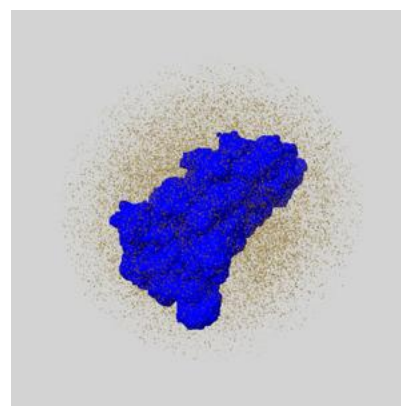
6.6.1 emd_8124_msk_1.map [i](#)



X



Y

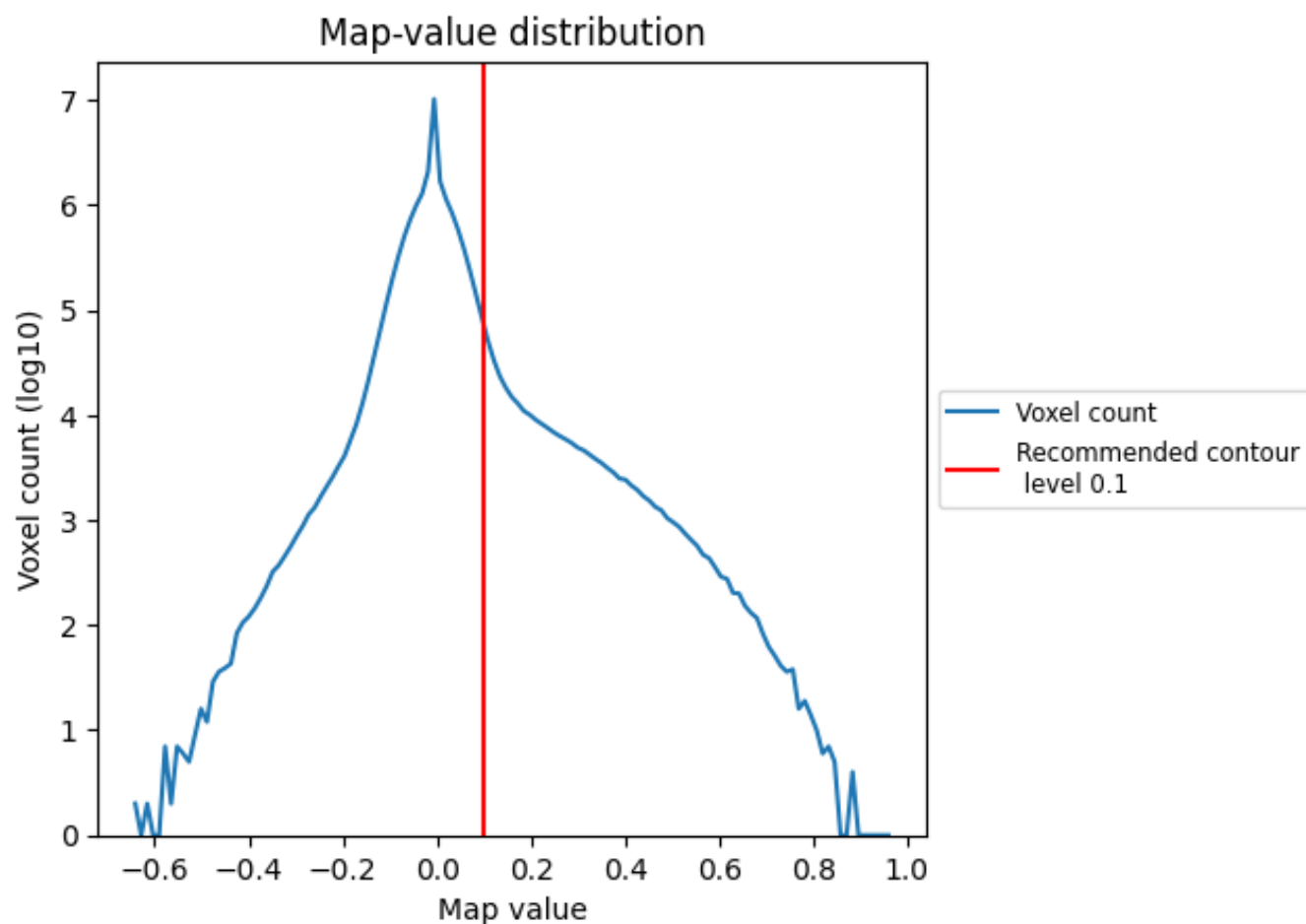


Z

7 Map analysis [i](#)

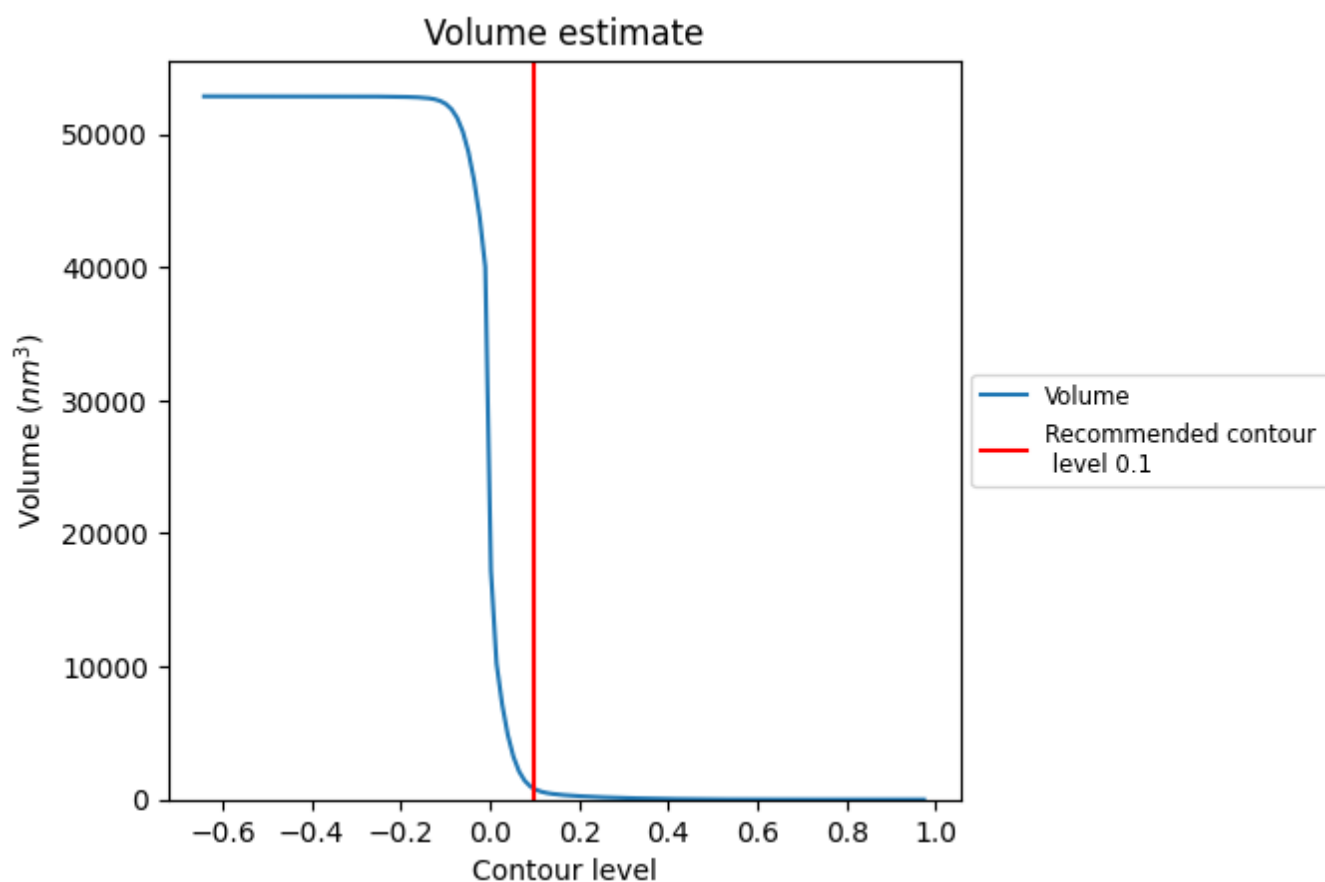
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

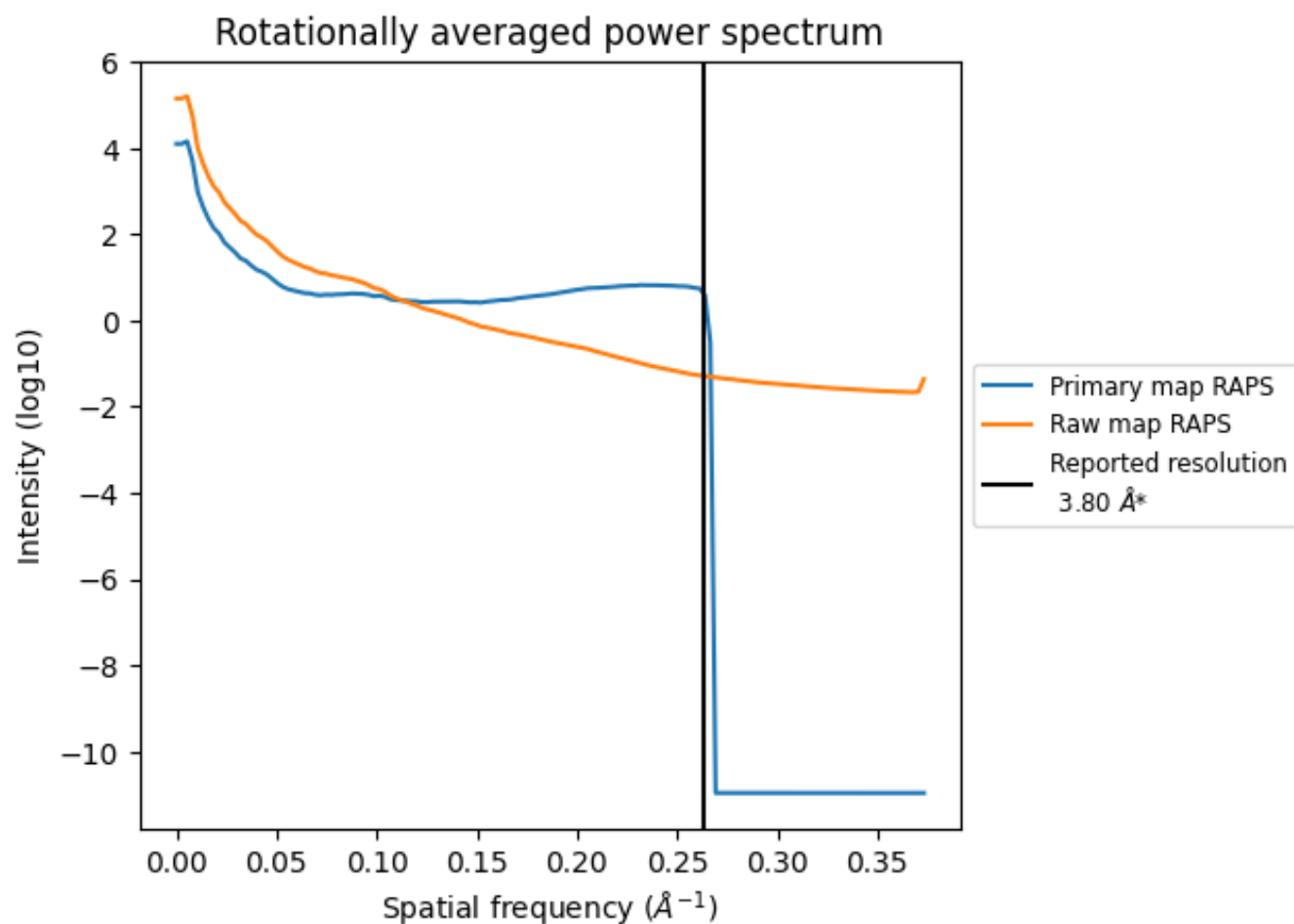
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 800 nm³; this corresponds to an approximate mass of 722 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 ⓘ

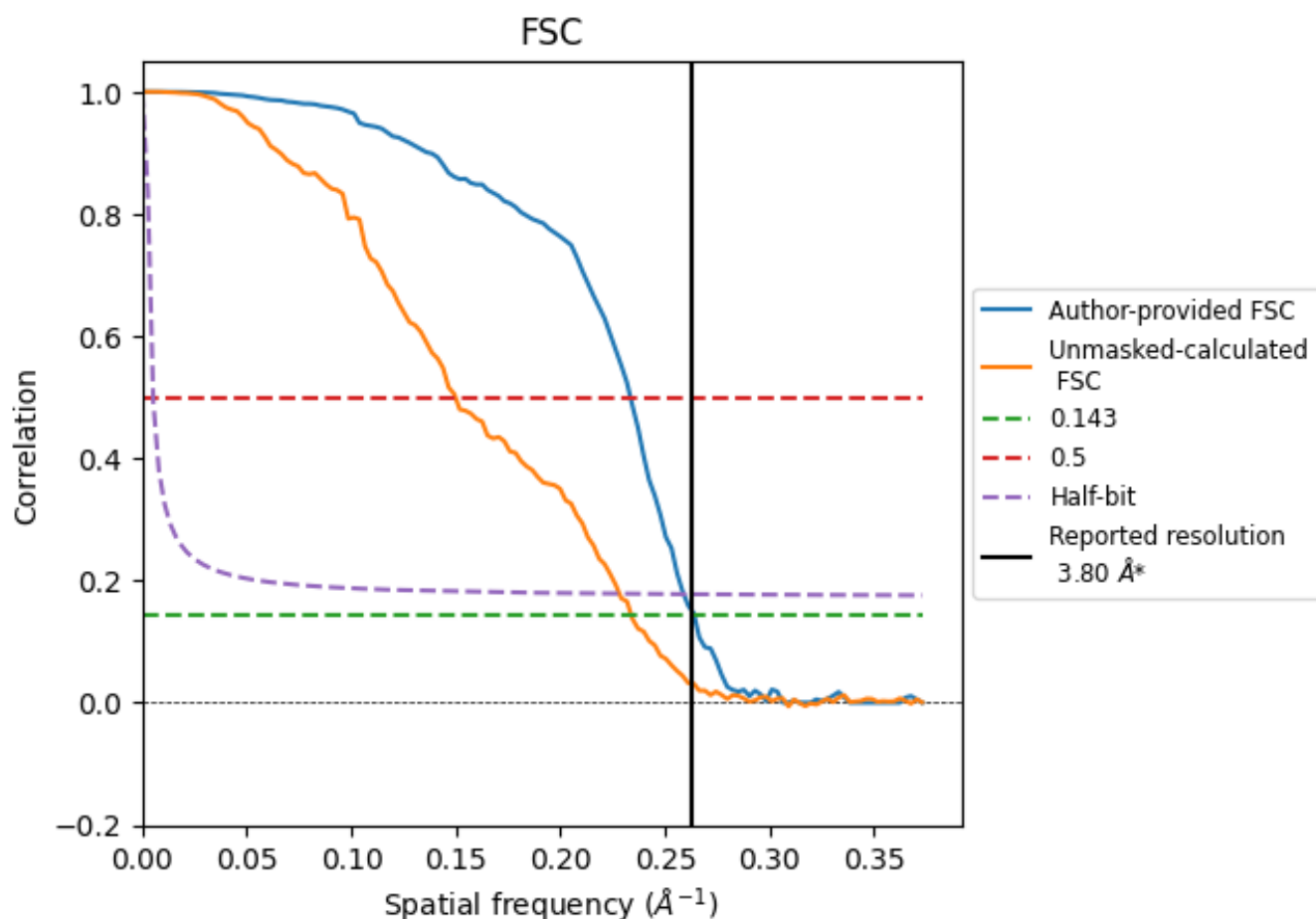


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

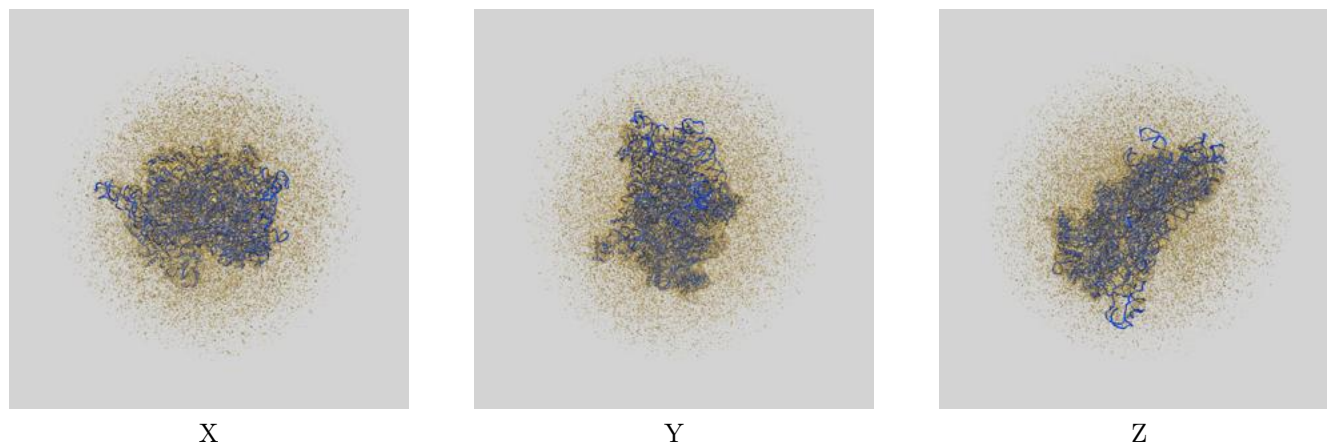
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.79	4.28	3.86
Unmasked-calculated*	4.27	6.68	4.38

*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 4.27 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

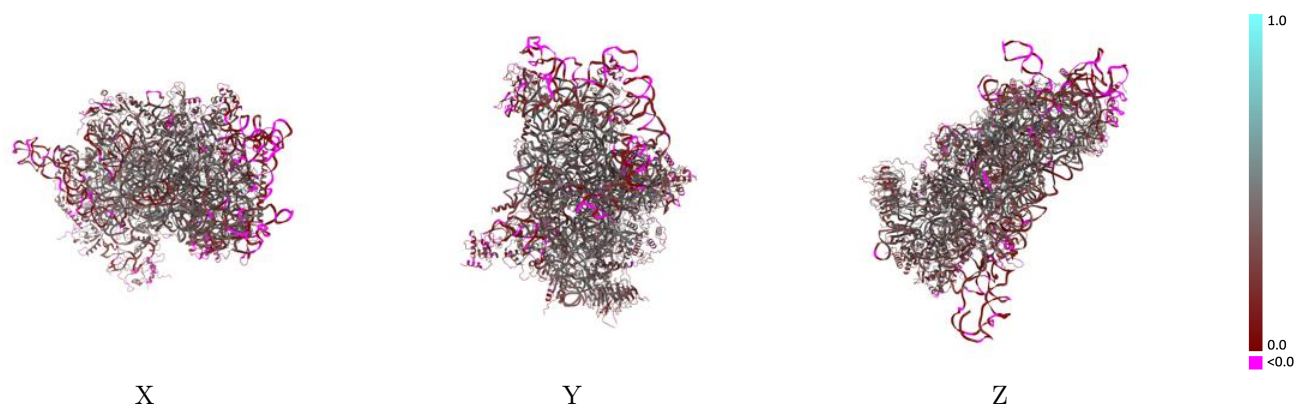
This section contains information regarding the fit between EMDB map EMD-8124 and PDB model 5IT9. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



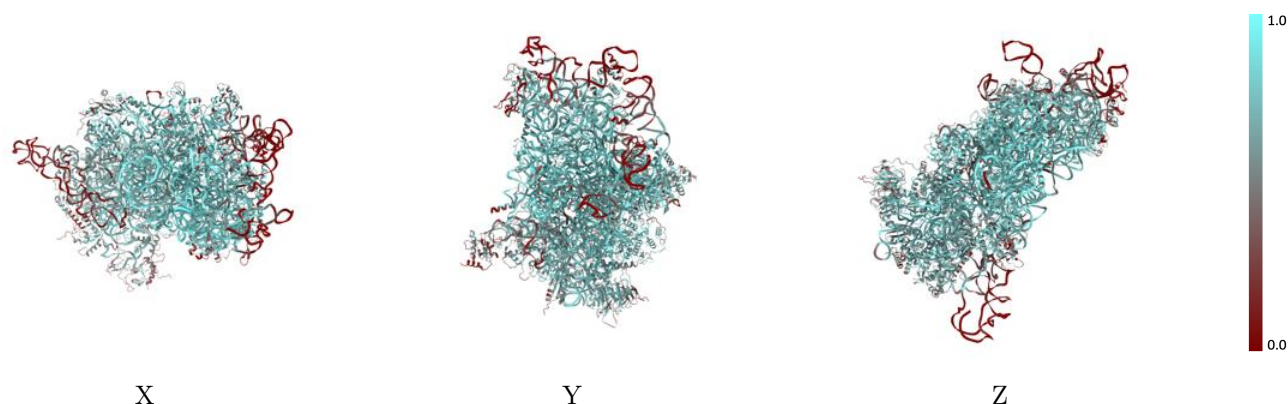
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



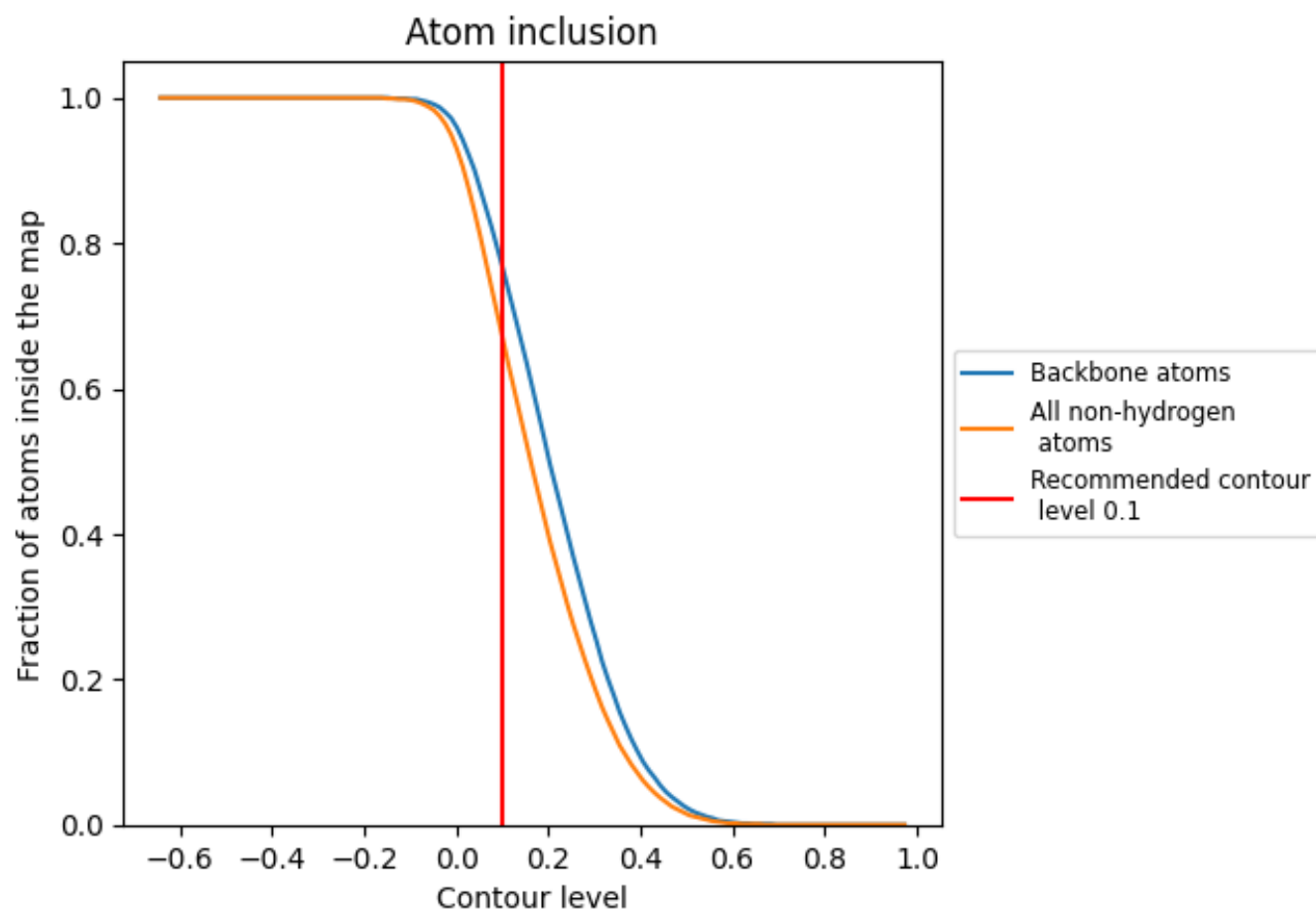
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 67% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6730	 0.3140
2	 0.7330	 0.3170
A	 0.7340	 0.3460
B	 0.6390	 0.2850
C	 0.7760	 0.4200
D	 0.6470	 0.3370
E	 0.7460	 0.4160
F	 0.6270	 0.3370
G	 0.5480	 0.2380
H	 0.6770	 0.3140
I	 0.6050	 0.2830
J	 0.7470	 0.3750
K	 0.5850	 0.2920
L	 0.7020	 0.3730
M	 0.3190	 0.1150
N	 0.7500	 0.3290
O	 0.7370	 0.3850
P	 0.5350	 0.2530
Q	 0.6930	 0.3620
R	 0.6370	 0.3090
S	 0.3880	 0.1730
T	 0.6580	 0.3360
U	 0.5890	 0.3210
V	 0.7540	 0.3810
W	 0.8200	 0.4430
X	 0.8040	 0.4260
Y	 0.6690	 0.3120
Z	 0.5230	 0.2640
a	 0.7460	 0.3880
b	 0.7020	 0.3450
c	 0.6010	 0.3480
d	 0.7520	 0.4040
e	 0.6290	 0.3100
f	 0.3500	 0.1300
g	 0.5950	 0.3310
i	 0.2960	 0.1530

