



## Full wwPDB EM Validation Report ⓘ

Nov 17, 2025 – 05:27 PM JST

PDB ID : 9KN0 / pdb\_00009kn0  
EMDB ID : EMD-62451  
Title : Bat MERsSr-CoV NL140422 Nsp1 bound to the Human 40S Ribosomal subunit-State2  
Authors : Yuan, S.; Yan, R.; Wu, M.  
Deposited on : 2024-11-18  
Resolution : 2.65 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev129  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
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) : 2.46

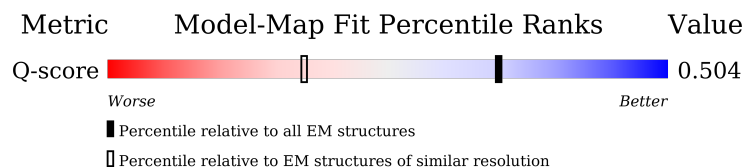
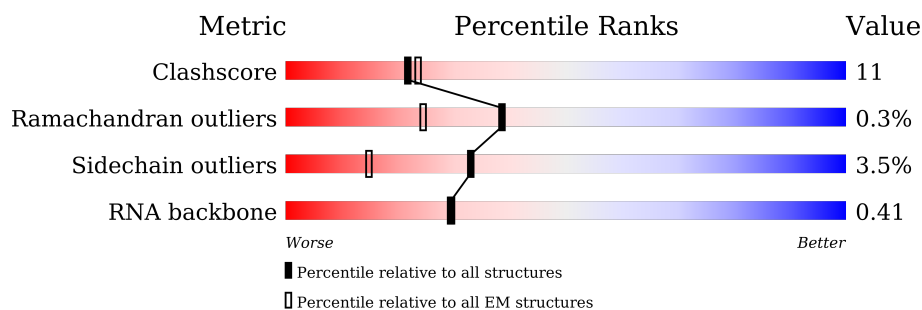
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.65 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.






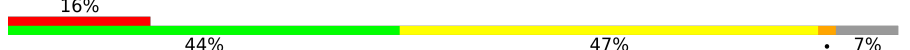

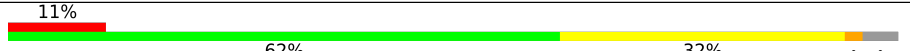
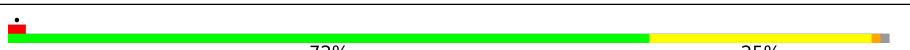

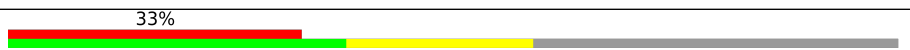

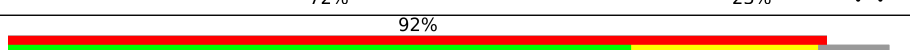
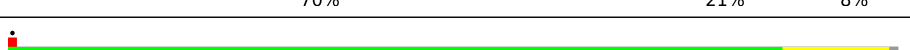


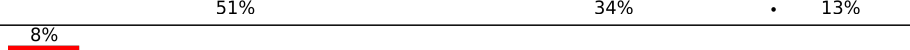






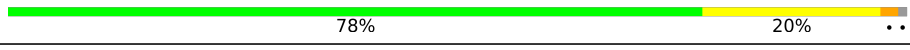
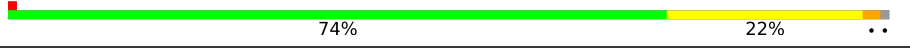

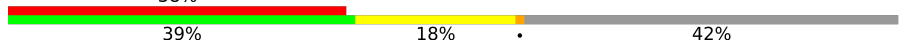
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	9050 ( 2.15 - 3.15 )

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  $\geq 3$ , 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	2	1869	<div> <div>5%</div> <div> <div></div> <div>39%</div> <div>36%</div> <div>13%</div> <div>11%</div> </div> </div>
2	A	295	<div> <div></div> <div> <div></div> <div>50%</div> <div>21%</div> <div>•</div> <div>28%</div> </div> </div>
3	B	264	<div> <div></div> <div> <div></div> <div>60%</div> <div>19%</div> <div>•</div> <div>19%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	130	
27	Z	125	
28	a	101	

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Mol	Chain	Length	Quality of chain
29	b	82	
30	c	62	
31	d	55	
32	e	56	
33	f	74	
34	g	315	
35	h	25	
36	n	196	

## 2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 74775 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1671	Total	C	N	O	P	0	0
			35647	15925	6406	11655	1661		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	213	Total	C	N	O	S	0	0
			1686	1072	295	311	8		

- Molecule 3 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 6 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 8 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	230	Total	C	N	O	S	0	0
			1864	1164	373	320	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	221	ARG	LYS	variant	UNP P62753

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

- Molecule 10 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 11 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 12 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	97	Total	C	N	O	S	0	0
			816	533	144	133	6		

- Molecule 13 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

- Molecule 14 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	121	Total	C	N	O	S	0	0
			935	586	165	175	9		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 17 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O	S	0	0
			1037	659	196	175	7		

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	138	Total	C	N	O	S	0	0
			1097	698	206	190	3		

- Molecule 19 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 21 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1123	703	217	200	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 24 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 25 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 26 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 27 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	99	Total	C	N	O	S	0	0
			794	494	165	130	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	78	VAL	ALA	conflict	UNP P62854

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	82	Total	C	N	O	S	0	0
			641	402	118	114	7		

- Molecule 30 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			489	297	97	93	2		

- Molecule 31 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 32 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	56	Total	C	N	O	S	0	0
			442	273	96	72	1		

- Molecule 33 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	74	Total	C	N	O	S	0	0
			611	385	117	102	7		

- Molecule 34 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2441	1537	425	467	12		

- Molecule 35 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	22	Total	C	N	O	S	0	0
			213	130	57	23	3		

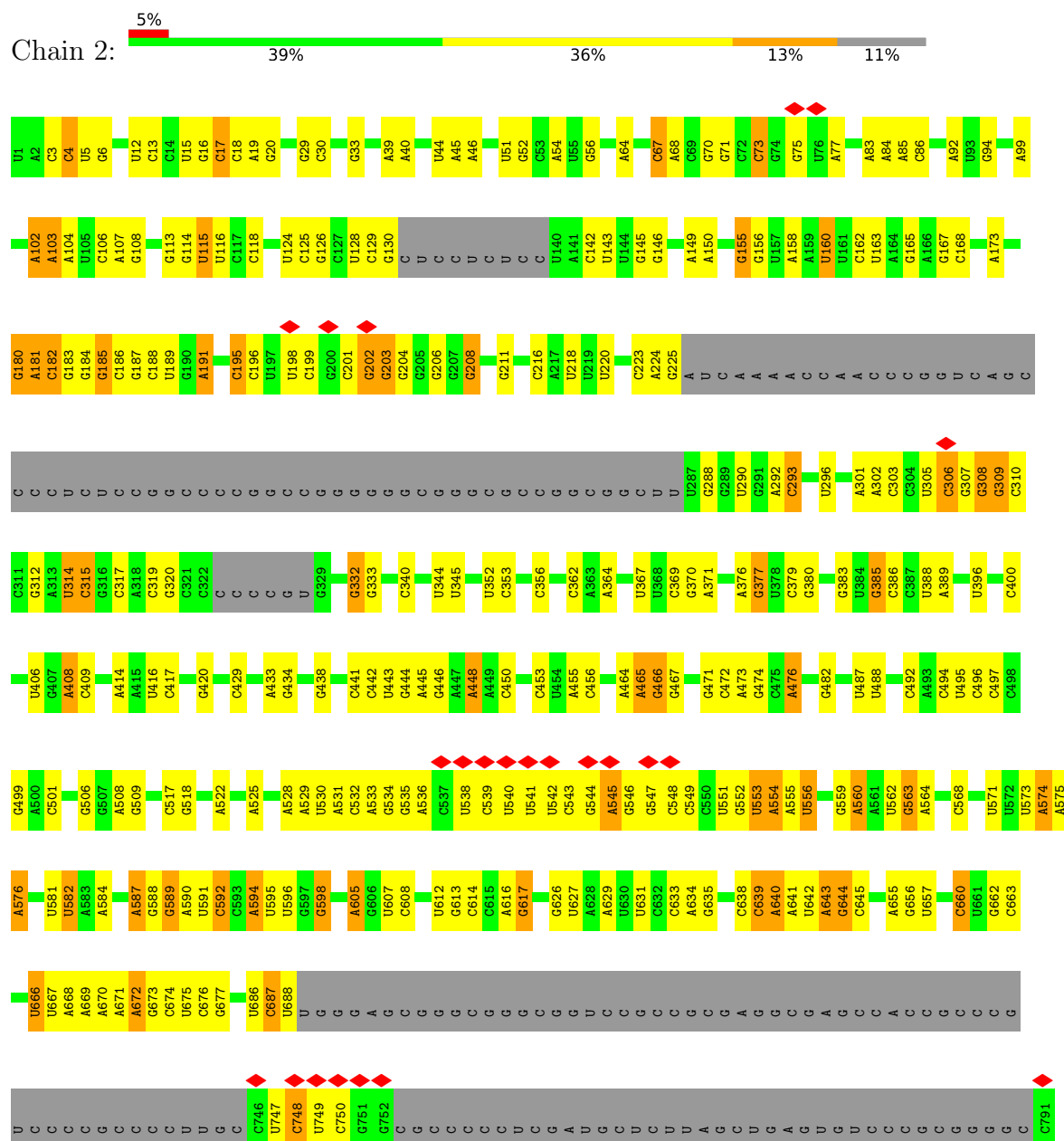
- Molecule 36 is a protein called ORF1ab polyprotein.

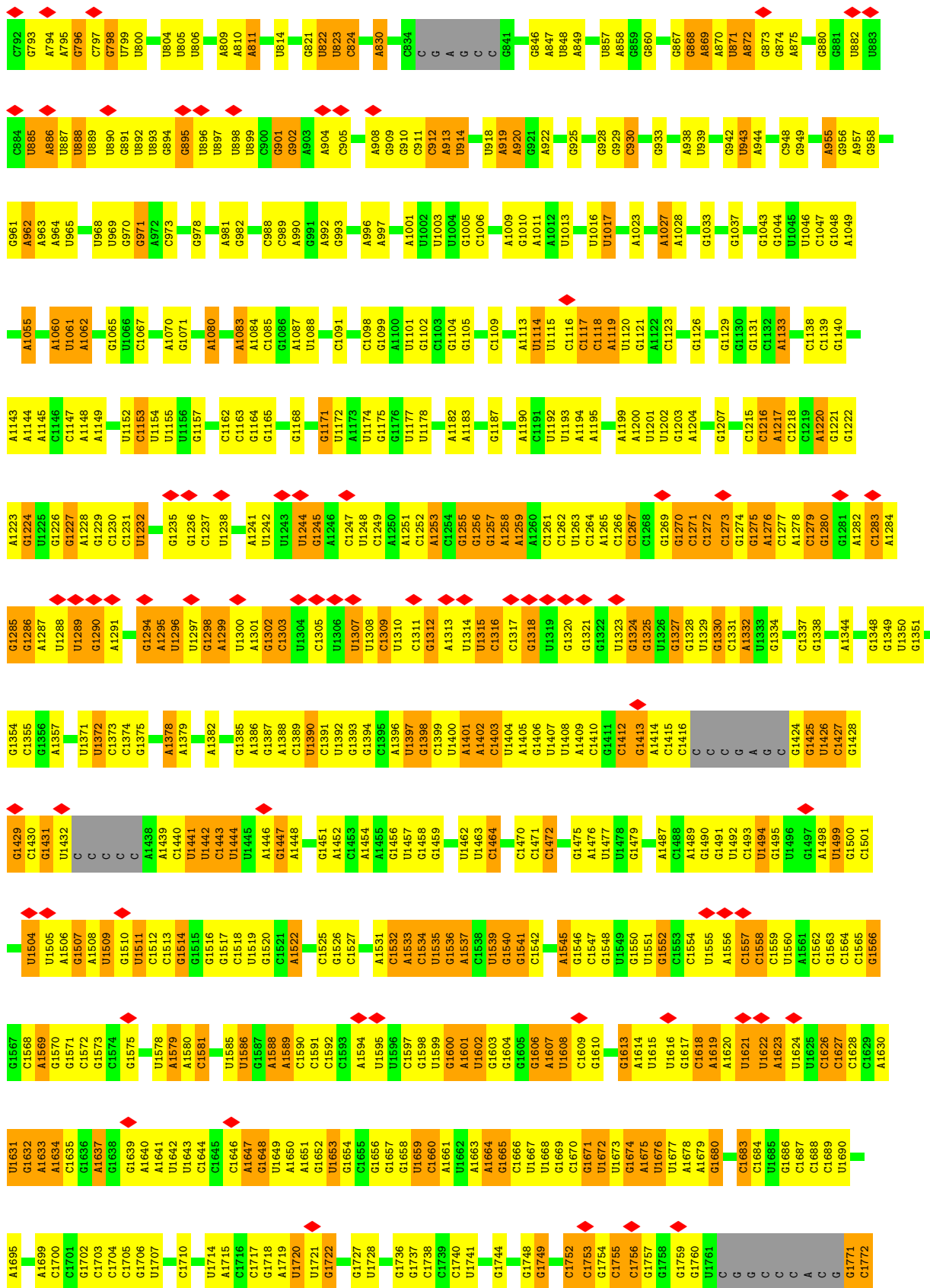
Mol	Chain	Residues	Atoms				AltConf	Trace
36	n	27	Total	C	N	O	0	0
			215	140	34	41		

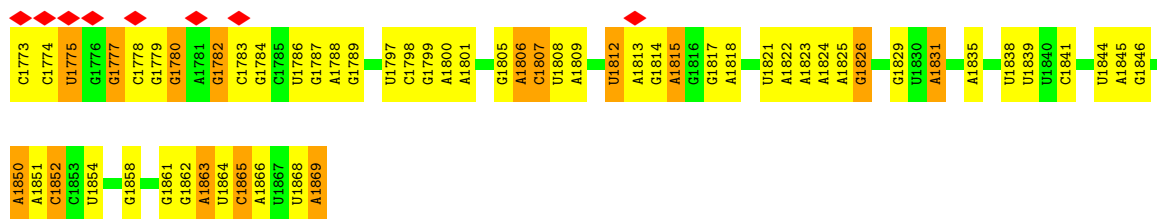
### 3 Residue-property plots

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.

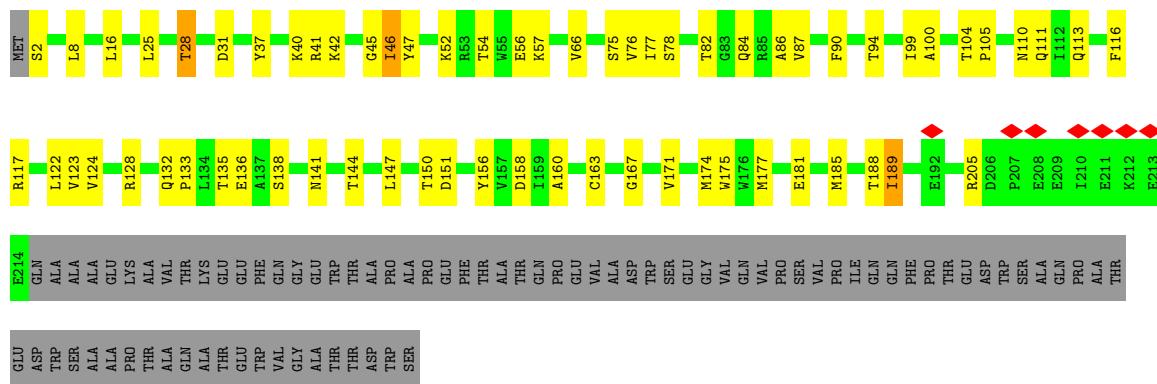
#### • Molecule 1: 18S ribosomal RNA



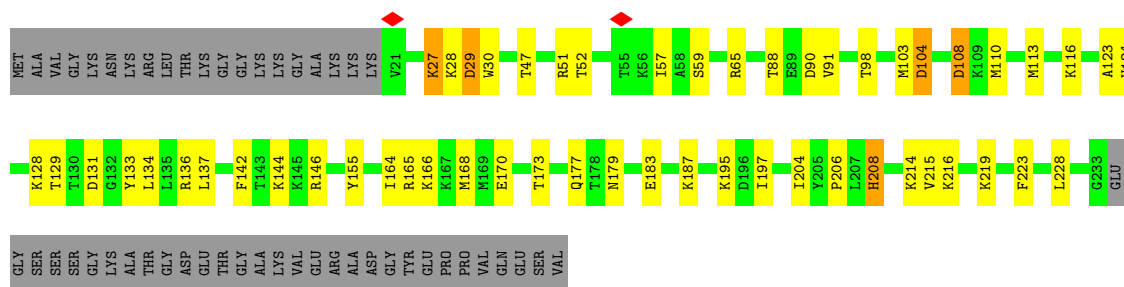




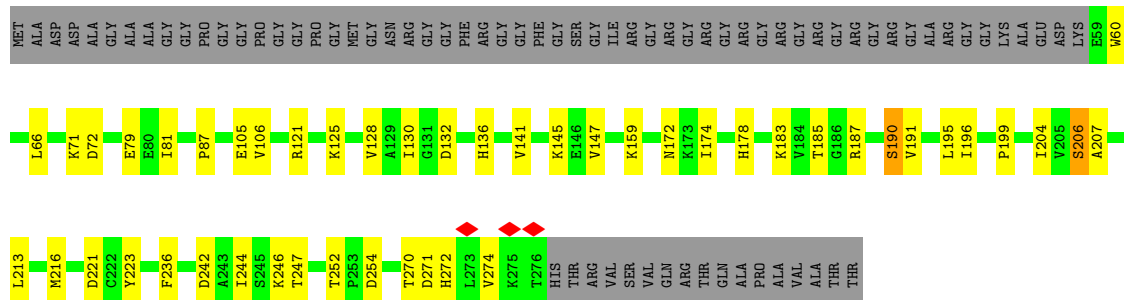
• Molecule 2: Small ribosomal subunit protein uS2



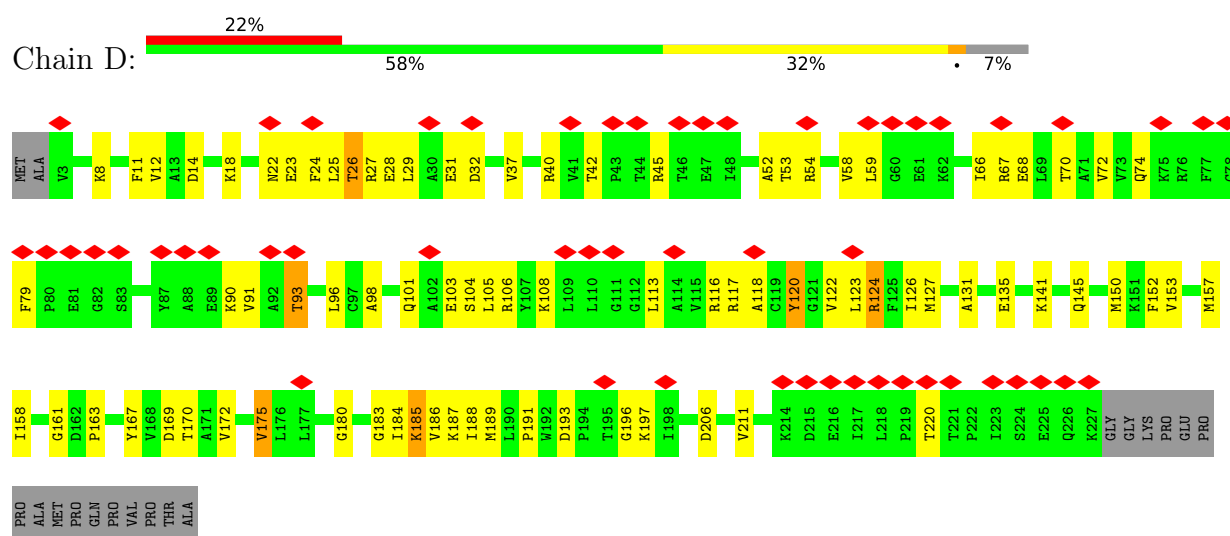
• Molecule 3: Small ribosomal subunit protein eS1



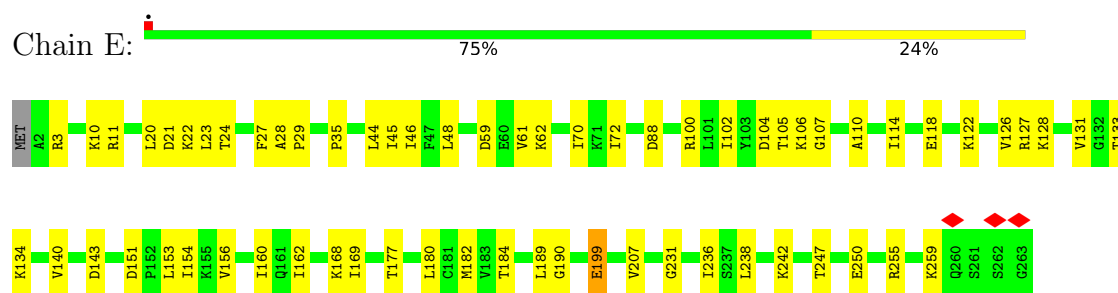
• Molecule 4: Small ribosomal subunit protein uS5



• Molecule 5: Small ribosomal subunit protein uS3



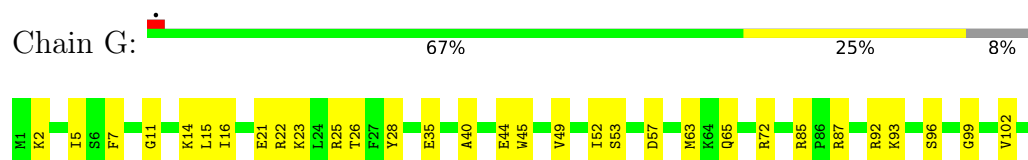
- Molecule 6: Small ribosomal subunit protein eS4, X isoform

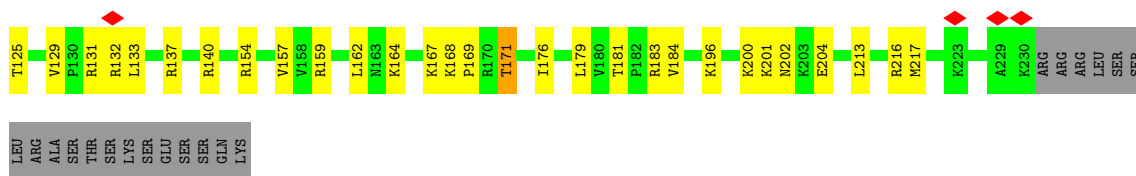


- Molecule 7: Small ribosomal subunit protein uS7

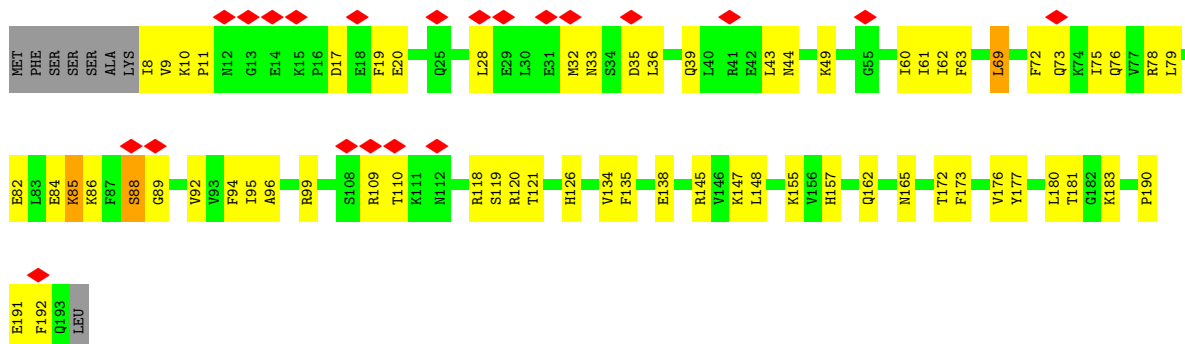


- Molecule 8: Small ribosomal subunit protein eS6

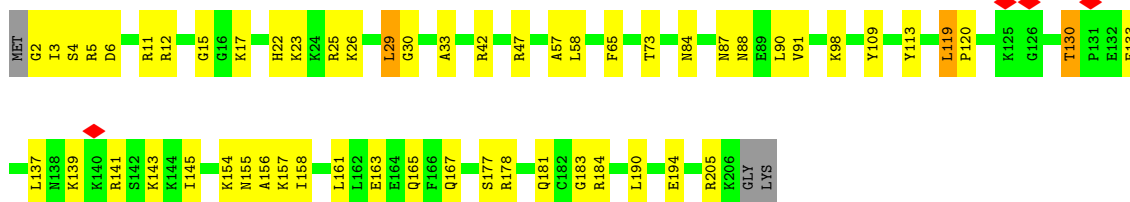




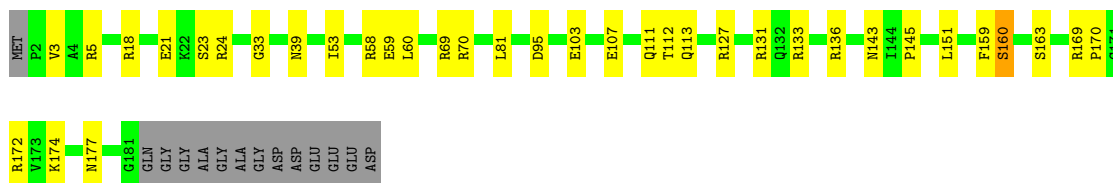
• Molecule 9: Small ribosomal subunit protein eS7



• Molecule 10: Small ribosomal subunit protein eS8

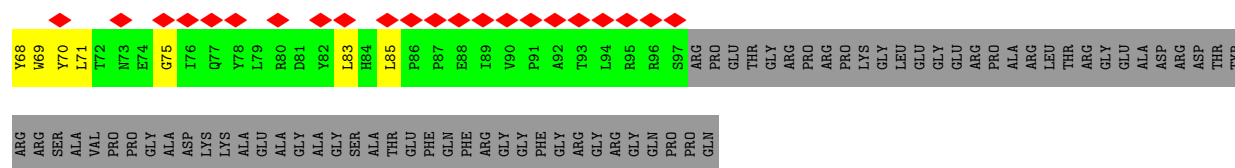


• Molecule 11: Small ribosomal subunit protein uS4

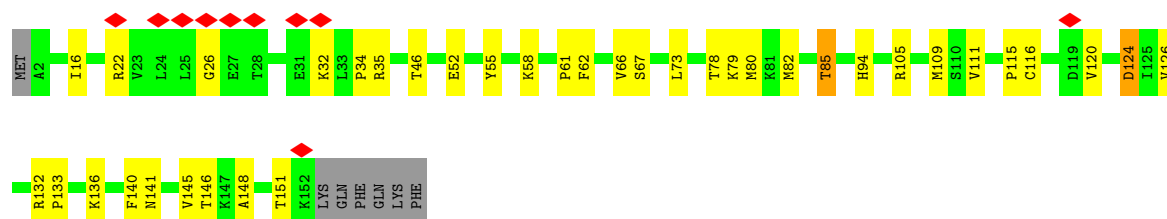


• Molecule 12: Small ribosomal subunit protein eS10

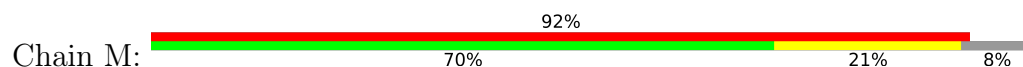




• Molecule 13: Small ribosomal subunit protein uS17



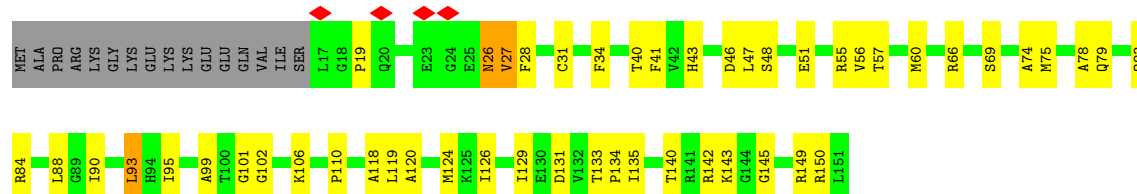
• Molecule 14: Small ribosomal subunit protein eS12



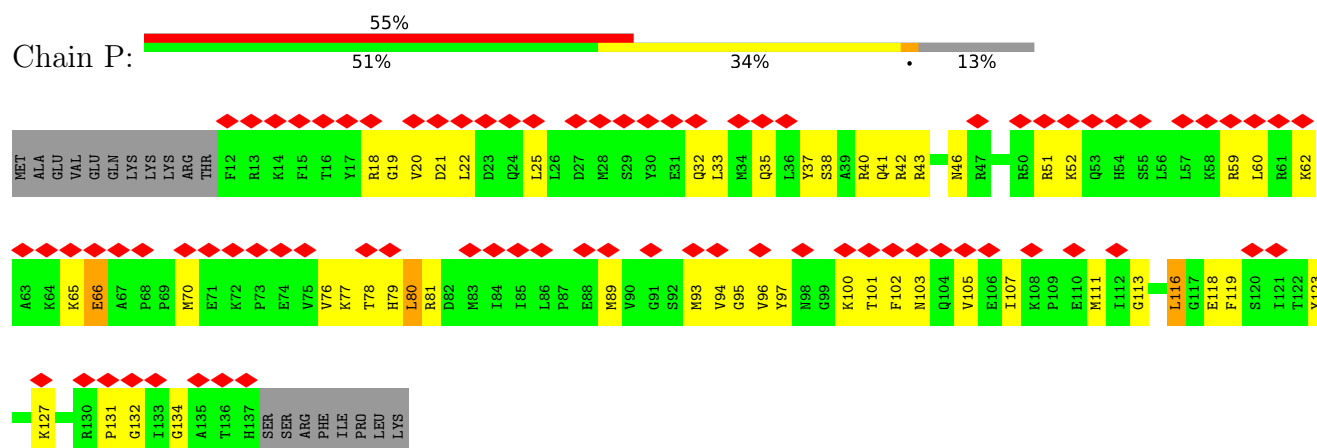
• Molecule 15: Small ribosomal subunit protein uS15



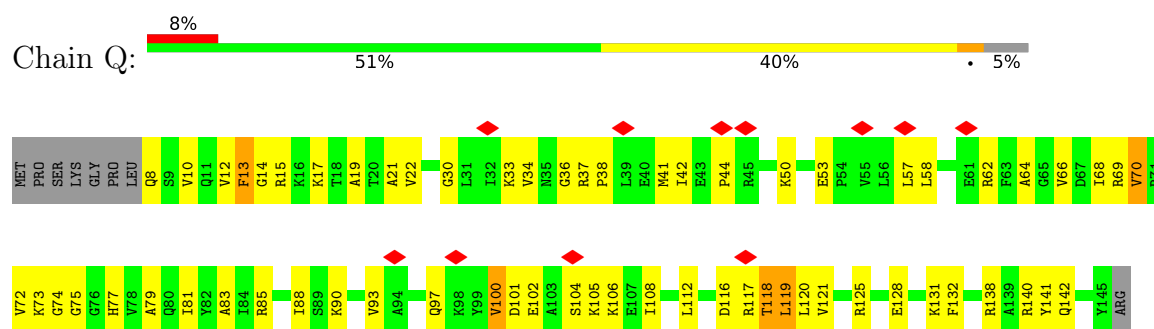
• Molecule 16: Small ribosomal subunit protein uS11



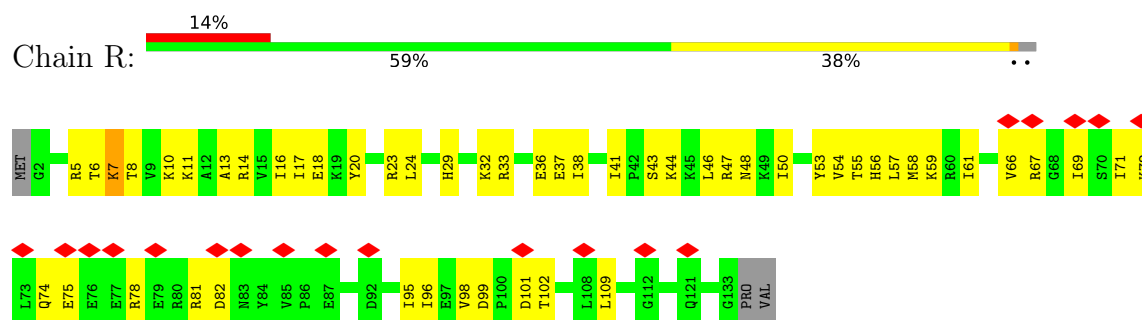
- Molecule 17: Small ribosomal subunit protein uS19



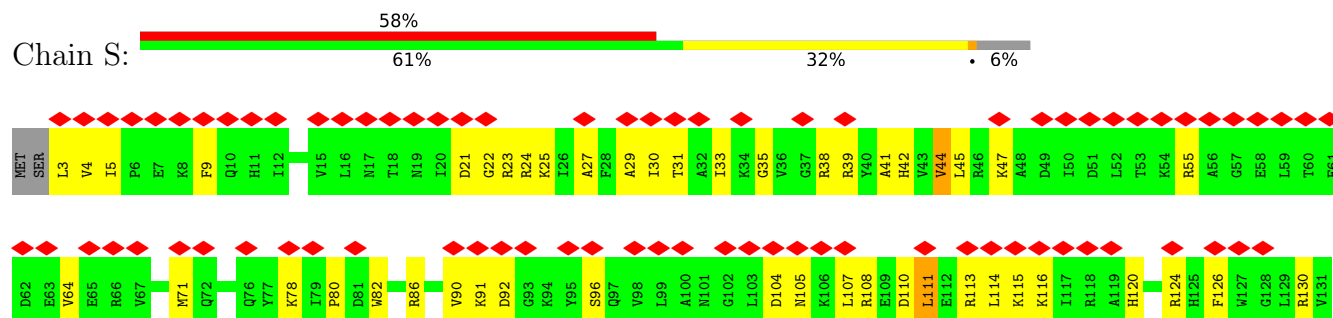
- Molecule 18: Small ribosomal subunit protein uS9



- Molecule 19: Small ribosomal subunit protein eS17

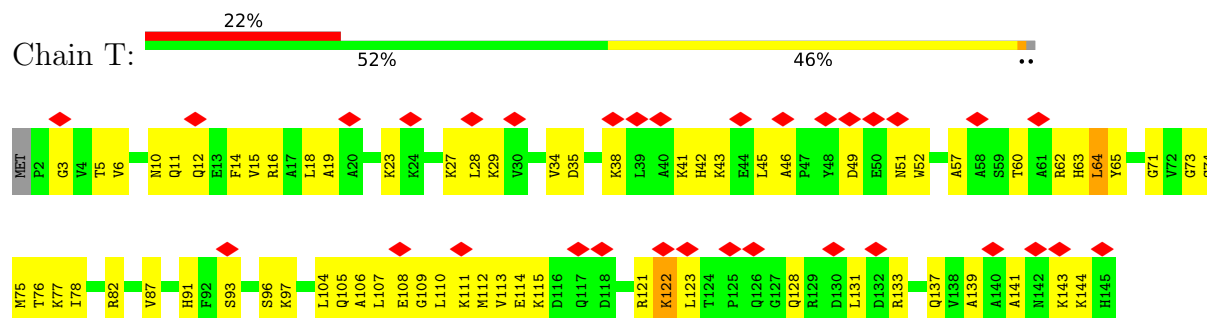


- Molecule 20: Small ribosomal subunit protein uS13

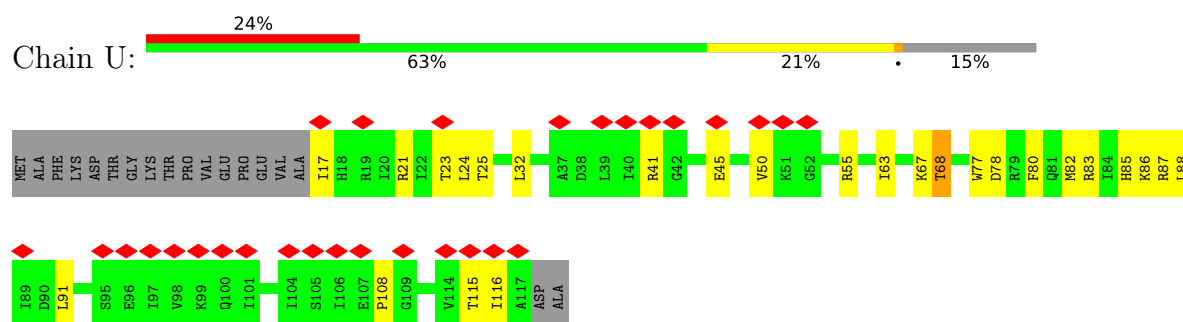




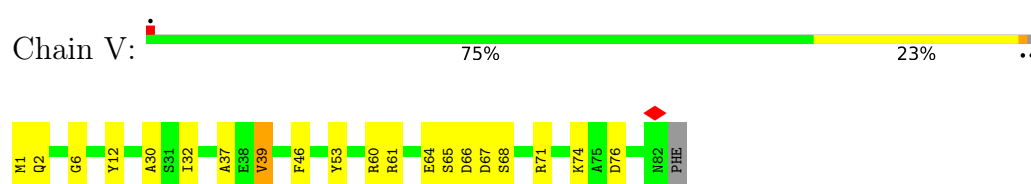
- Molecule 21: Small ribosomal subunit protein eS19



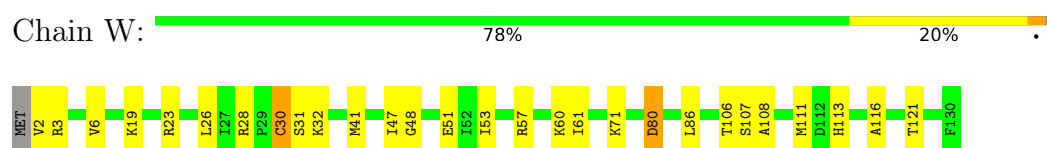
- Molecule 22: Small ribosomal subunit protein uS10



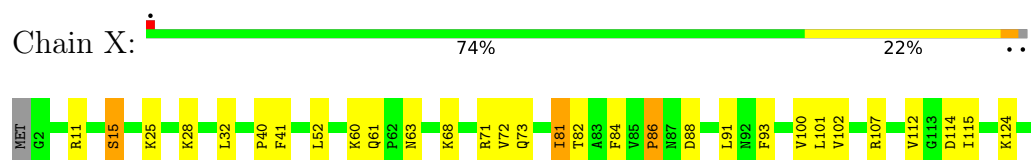
- Molecule 23: Small ribosomal subunit protein eS21

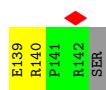


- Molecule 24: Small ribosomal subunit protein uS8

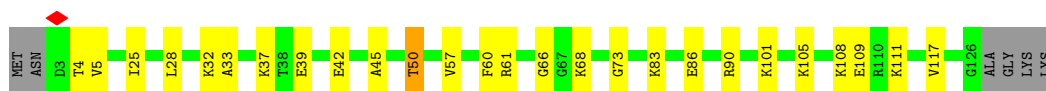
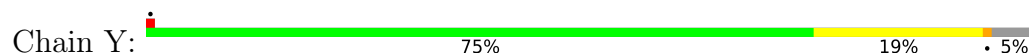


- Molecule 25: Small ribosomal subunit protein uS12

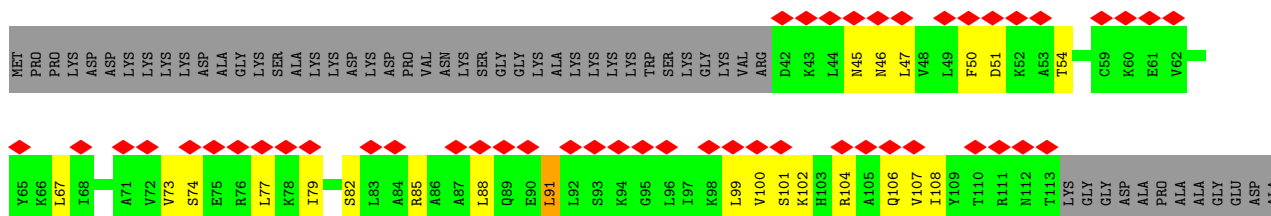




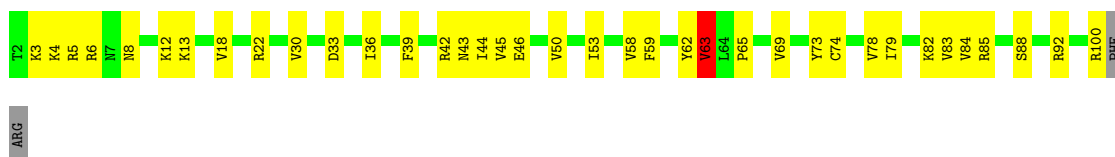
- Molecule 26: Small ribosomal subunit protein eS24



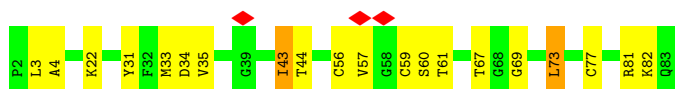
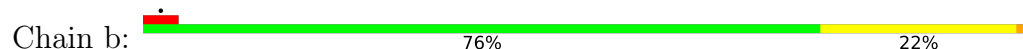
- Molecule 27: Small ribosomal subunit protein eS25



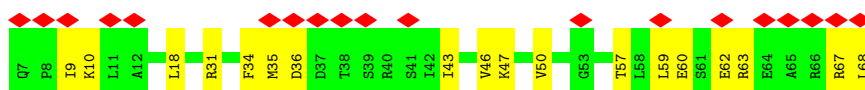
- Molecule 28: Small ribosomal subunit protein eS26



- Molecule 29: Small ribosomal subunit protein eS27

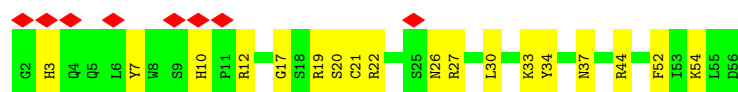


- Molecule 30: Small ribosomal subunit protein eS28

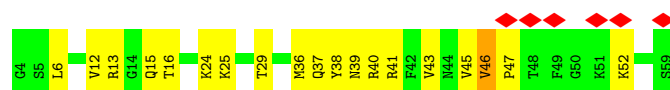


- Molecule 31: Small ribosomal subunit protein uS14

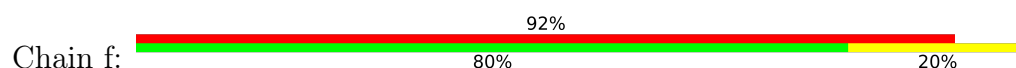




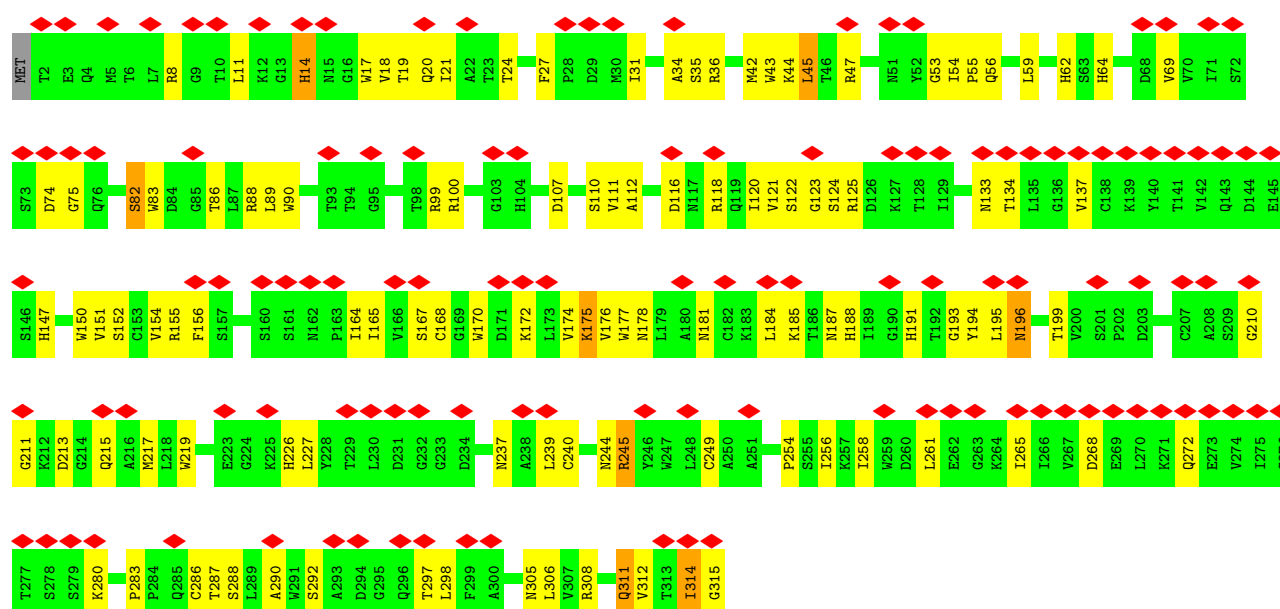
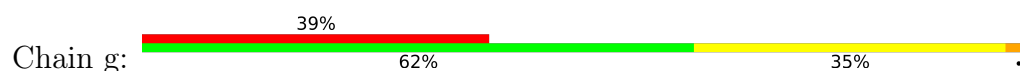
- Molecule 32: Small ribosomal subunit protein eS30



- Molecule 33: Small ribosomal subunit protein eS31



- Molecule 34: Small ribosomal subunit protein RACK1



- Molecule 35: Small ribosomal subunit protein eS32





● Molecule 36: ORF1ab polypeptide



MET	SER	VAL	ALA	GLY	VAL	VAL	ALA	GLN	GLY	ALA	ARG	ASN	ARG	TYR	ARG	ALA	ALA	LEU	ASN	ASN	GLU	LYS	ARG	PRO	ASP	HIS	VAL	SER	LEU	THR	VAL	PRO	CYS	CYS	GLY	THR	GLY	ASP	LEU	ALA	GLU	HIS	LEU	SER	PRO	TRP	PHE	ALA	ASP	GLY	THR	ALA	CYS	GLU	MET	VAL	ARG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ALA	ILE	LEU	LYS	LYS	GLU	LYS	ILE	LEU	PHE	LEU	PRO	LEU	ASN	VAL	GLY	TYR	ILE	LYS	HIS	LEU	PRO	GLY	PRO	ARG	VAL	TYR	LEU	VAL	GLU	ARG	LEU	THR	GLY	GLY	THR	TYR	SER	THR	PRO	PHE	MET	VAL	ASN	GLN	LEU	ALA	TYR	SER	SER	SER	ALA	SER	ASP	ALA	ILE	VAL	GLY
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THR	THR	LEU	GLN	GLY	LYS	PRO	VAL	GLY	PHE	PHE	PRO	TYR	ASP	PRO	LEU	LEU	GLU	THR	GLY	ASP	PHE	THR	PHE	LEU	LEU	ARG	LYS	ASN	GLY	ARG	GLY	GLY	ASN	HIS	PHE	ARG	HIS	PRO	LEU	GLU	GLU	ASP	ASP	ILE	VAL	TYR	F166	P167	Y168	E169	L174	D175	D176	L187	L190
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------

V191	G192	GLY
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	114202	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.624	Depositor
Minimum map value	-1.261	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.058	Depositor
Recommended contour level	0.167	Depositor
Map size (Å)	486.4, 486.4, 486.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	2	0.22	0/39865	0.29	0/62134
2	A	0.18	0/1723	0.31	0/2341
3	B	0.19	0/1756	0.33	0/2350
4	C	0.21	0/1726	0.33	0/2332
5	D	0.15	0/1780	0.35	0/2397
6	E	0.23	0/2118	0.34	0/2849
7	F	0.14	0/1516	0.38	0/2037
8	G	0.16	0/1887	0.29	0/2513
9	H	0.15	0/1524	0.35	1/2042 (0.0%)
10	I	0.18	0/1711	0.31	0/2282
11	J	0.22	0/1524	0.32	0/2035
12	K	0.11	0/840	0.30	0/1133
13	L	0.23	0/1250	0.31	0/1673
14	M	0.11	0/945	0.32	0/1269
15	N	0.18	0/1226	0.26	0/1649
16	O	0.19	0/1023	0.33	0/1372
17	P	0.13	0/1058	0.36	0/1414
18	Q	0.14	0/1114	0.38	0/1492
19	R	0.13	0/1082	0.32	0/1452
20	S	0.13	0/1202	0.37	0/1610
21	T	0.16	0/1143	0.43	0/1530
22	U	0.12	0/813	0.32	0/1092
23	V	0.19	0/631	0.31	0/844
24	W	0.24	0/1051	0.36	0/1406
25	X	0.22	0/1116	0.34	0/1490
26	Y	0.22	0/1031	0.35	0/1370
27	Z	0.16	0/580	0.37	0/780
28	a	0.22	0/807	0.40	0/1082
29	b	0.18	0/654	0.30	0/876
30	c	0.14	0/491	0.34	0/656
31	d	0.10	0/470	0.27	0/623
32	e	0.19	0/447	0.34	0/587
33	f	0.12	0/623	0.40	0/822
34	g	0.12	0/2498	0.36	0/3399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	h	0.16	0/214	0.25	0/272
36	n	0.13	0/219	0.23	0/293
All	All	0.20	0/79658	0.31	1/115498 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	H	88	SER	CB-CA-C	-5.51	109.73	117.23

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	35647	0	18022	606	0
2	A	1686	0	1688	40	0
3	B	1729	0	1803	42	0
4	C	1690	0	1777	31	0
5	D	1752	0	1848	64	0
6	E	2076	0	2177	38	0
7	F	1495	0	1549	86	0
8	G	1864	0	2018	44	0
9	H	1501	0	1593	47	0
10	I	1682	0	1769	41	0
11	J	1499	0	1618	27	0
12	K	816	0	841	29	0
13	L	1229	0	1302	25	0
14	M	935	0	964	14	0
15	N	1202	0	1289	11	0
16	O	1010	0	1034	39	0
17	P	1037	0	1082	44	0
18	Q	1097	0	1161	57	0
19	R	1068	0	1121	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	S	1184	0	1244	42	0
21	T	1123	0	1153	68	0
22	U	803	0	873	23	0
23	V	625	0	628	15	0
24	W	1034	0	1080	23	0
25	X	1098	0	1167	21	0
26	Y	1014	0	1082	18	0
27	Z	574	0	627	20	0
28	a	794	0	849	31	0
29	b	641	0	665	12	0
30	c	489	0	514	20	0
31	d	459	0	452	20	0
32	e	442	0	487	12	0
33	f	611	0	638	18	0
34	g	2441	0	2396	87	0
35	h	213	0	258	3	0
36	n	215	0	220	5	0
All	All	74775	0	58989	1493	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 11.

All (1493) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1718:G:N2	1:2:1815:A:H62	1.52	1.06
1:2:1718:G:H21	1:2:1815:A:N6	1.58	1.01
1:2:1589:A:HO2'	1:2:1653:U:HO2'	1.06	0.94
1:2:191:A:N6	1:2:208:G:H21	1.68	0.91
2:A:163:CYS:HB3	2:A:174:MET:HE3	1.52	0.91
1:2:191:A:H62	1:2:208:G:N2	1.69	0.90
1:2:191:A:H62	1:2:208:G:H21	1.19	0.87
28:a:36:ILE:HD13	28:a:78:VAL:HG21	1.59	0.85
21:T:6:VAL:HG23	21:T:14:PHE:HE2	1.42	0.84
34:g:176:VAL:HG12	34:g:185:LYS:HD3	1.61	0.82
24:W:106:THR:HG22	24:W:108:ALA:H	1.45	0.82
1:2:1091:C:HO2'	24:W:2:VAL:N	1.78	0.81
1:2:1718:G:H21	1:2:1815:A:H62	0.83	0.81
1:2:1658:G:OP2	1:2:1660:C:N4	2.13	0.80
1:2:568:C:N3	1:2:582:U:O4	2.15	0.80
1:2:216:C:O2	1:2:309:G:N2	2.11	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:928:G:H1	1:2:1013:U:H3	1.29	0.79
7:F:35:LEU:HD22	7:F:146:ARG:HD3	1.65	0.79
7:F:45:TYR:HB3	7:F:67:PRO:HG3	1.65	0.79
7:F:50:PRO:HG2	7:F:90:VAL:HG13	1.65	0.78
21:T:113:VAL:HG23	21:T:121:ARG:HE	1.49	0.77
1:2:103:A:OP2	1:2:356:C:N4	2.17	0.77
1:2:1337:C:H2'	1:2:1338:G:H8	1.50	0.77
5:D:170:THR:HG23	5:D:187:LYS:HG2	1.67	0.77
5:D:105:LEU:HD11	5:D:122:VAL:HG11	1.66	0.77
1:2:1659:U:O2	1:2:1664:A:N7	2.17	0.76
1:2:124:U:O2	1:2:340:C:N4	2.18	0.76
1:2:1547:C:N4	1:2:1586:U:O4	2.19	0.76
17:P:95:GLY:HA3	17:P:102:PHE:HB3	1.68	0.76
16:O:84:ARG:HH21	16:O:88:LEU:HD21	1.48	0.76
1:2:560:A:OP2	11:J:177:ASN:ND2	2.19	0.75
1:2:1649:U:H3	1:2:1675:A:H62	1.33	0.75
34:g:178:ASN:HD21	34:g:181:ASN:HB3	1.50	0.75
7:F:167:LYS:NZ	7:F:172:CYS:SG	2.57	0.75
21:T:34:VAL:O	21:T:52:TRP:NE1	2.21	0.74
7:F:123:GLU:HG2	7:F:140:ASP:HA	1.70	0.74
21:T:42:HIS:HB3	21:T:93:SER:HB3	1.69	0.74
5:D:12:VAL:HG11	31:d:34:TYR:HB3	1.67	0.74
7:F:145:ARG:HE	30:c:47:LYS:HE3	1.52	0.73
3:B:90:ASP:OD2	3:B:91:VAL:N	2.20	0.73
1:2:64:A:H2	1:2:83:A:H62	1.34	0.73
8:G:22:ARG:HA	8:G:25:ARG:HH12	1.53	0.73
1:2:913:A:H5''	9:H:120:ARG:HH21	1.54	0.73
1:2:1545:A:N6	1:2:1588:A:N1	2.37	0.73
1:2:1679:A:N7	7:F:60:ARG:NH1	2.37	0.73
28:a:82:LYS:HG2	28:a:85:ARG:HH12	1.51	0.72
1:2:1270:G:N2	1:2:1511:U:O4	2.22	0.72
1:2:1121:G:O2'	3:B:204:ILE:O	2.08	0.72
32:e:36:MET:HE3	32:e:40:ARG:HE	1.53	0.72
18:Q:58:LEU:O	18:Q:62:ARG:NH1	2.23	0.72
10:I:57:ALA:HB2	10:I:183:GLY:HA2	1.72	0.72
1:2:1661:A:OP1	31:d:19:ARG:NH1	2.22	0.72
20:S:115:LYS:HG2	20:S:126:PHE:HB2	1.70	0.72
1:2:1227:G:N2	1:2:1635:C:O2'	2.22	0.71
1:2:1622:U:OP1	20:S:124:ARG:NH2	2.22	0.71
30:c:9:ILE:HG12	30:c:59:LEU:HG	1.71	0.71
8:G:213:LEU:O	8:G:217:MET:HG2	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:33:LYS:HZ3	18:Q:36:GLY:H	1.36	0.71
19:R:72:LYS:HA	19:R:75:GLU:HB2	1.73	0.71
7:F:51:HIS:HA	7:F:86:LYS:HE2	1.72	0.71
7:F:140:ASP:HB3	30:c:46:VAL:HG12	1.72	0.71
21:T:27:LYS:HB3	21:T:110:LEU:HD21	1.73	0.71
17:P:81:ARG:HE	17:P:116:LEU:H	1.39	0.71
1:2:1554:C:H5'	1:2:1555:U:H5''	1.71	0.71
25:X:139:GLU:N	25:X:139:GLU:OE2	2.24	0.70
1:2:1550:G:H3'	1:2:1579:A:H61	1.56	0.70
1:2:1402:A:N6	1:2:1441:U:O2'	2.23	0.70
11:J:136:ARG:HD3	11:J:160:SER:HA	1.72	0.70
13:L:22:ARG:HD2	13:L:32:LYS:HE2	1.73	0.70
1:2:962:A:H5'	16:O:66:ARG:HB3	1.73	0.70
1:2:563:G:N7	11:J:172:ARG:NH2	2.40	0.70
1:2:1588:A:N6	1:2:1589:A:N1	2.39	0.70
24:W:111:MET:HE3	24:W:116:ALA:HA	1.74	0.69
1:2:1373:C:O2'	19:R:10:LYS:NZ	2.25	0.69
12:K:32:HIS:HB3	12:K:35:LEU:HB2	1.72	0.69
3:B:47:THR:OG1	3:B:65:ARG:NH1	2.25	0.69
27:Z:47:LEU:HB2	27:Z:79:ILE:HG22	1.74	0.69
34:g:237:ASN:ND2	34:g:286:CYS:O	2.25	0.69
1:2:17:C:O2'	1:2:1194:A:N1	2.24	0.69
1:2:1532:C:H3'	1:2:1637:A:H62	1.57	0.69
5:D:108:LYS:HB3	5:D:113:LEU:HD23	1.75	0.69
1:2:70:G:OP2	8:G:167:LYS:NZ	2.26	0.69
1:2:1540:G:N2	1:2:1541:G:O6	2.26	0.69
1:2:1665:G:H22	21:T:87:VAL:HG22	1.57	0.69
31:d:21:CYS:HB3	31:d:26:ASN:H	1.58	0.68
1:2:587:A:H5'	1:2:592:C:H41	1.59	0.68
11:J:143:ASN:O	11:J:143:ASN:ND2	2.27	0.68
30:c:35:MET:HE2	30:c:35:MET:H	1.57	0.68
1:2:125:C:OP1	8:G:202:ASN:ND2	2.25	0.68
1:2:1153:C:OP2	24:W:71:LYS:NZ	2.26	0.68
1:2:1621:U:H3'	1:2:1623:A:H1'	1.75	0.68
2:A:84:GLN:HG2	2:A:100:ALA:HB1	1.74	0.68
2:A:205:ARG:NH1	19:R:82:ASP:OD1	2.27	0.67
17:P:22:LEU:HA	17:P:25:LEU:HG	1.76	0.67
1:2:145:G:H2'	1:2:146:G:C8	2.30	0.67
5:D:74:GLN:NE2	5:D:79:PHE:O	2.27	0.67
1:2:1674:G:OP1	7:F:51:HIS:NE2	2.27	0.67
5:D:106:ARG:HD2	5:D:175:VAL:HG13	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1534:C:OP1	7:F:164:ARG:N	2.28	0.67
7:F:100:ILE:HG21	7:F:177:LEU:HD22	1.77	0.67
34:g:254:PRO:HB3	34:g:283:PRO:HB2	1.76	0.67
11:J:59:GLU:OE2	11:J:69:ARG:NH2	2.26	0.66
17:P:19:GLY:HA2	20:S:92:ASP:HA	1.77	0.66
9:H:79:LEU:HD12	9:H:94:PHE:HZ	1.58	0.66
1:2:1271:C:OP2	1:2:1512:C:O2'	2.14	0.66
16:O:99:ALA:H	16:O:133:THR:HB	1.60	0.66
16:O:26:ASN:OD1	16:O:26:ASN:N	2.28	0.66
3:B:65:ARG:NH2	16:O:51:GLU:OE1	2.29	0.66
5:D:53:THR:O	5:D:90:LYS:NZ	2.28	0.66
28:a:3:LYS:NZ	28:a:8:ASN:OD1	2.29	0.66
1:2:919:A:OP2	15:N:64:ARG:NH2	2.25	0.65
1:2:1722:G:N2	1:2:1812:U:O2	2.29	0.65
19:R:44:LYS:HG3	19:R:47:ARG:HH21	1.61	0.65
21:T:60:THR:O	21:T:64:LEU:HD12	1.95	0.65
1:2:1444:U:OP2	18:Q:15:ARG:NH2	2.29	0.65
1:2:1675:A:O2'	1:2:1676:U:OP1	2.13	0.65
1:2:1572:C:H2'	1:2:1573:G:C8	2.31	0.65
32:e:37:GLN:O	32:e:41:ARG:HG2	1.96	0.65
33:f:98:VAL:C	33:f:99:LYS:HE2	2.20	0.65
23:V:2:GLN:NE2	23:V:6:GLY:O	2.29	0.65
7:F:81:ARG:HH12	21:T:82:ARG:HH12	1.43	0.65
11:J:170:PRO:HB3	11:J:174:LYS:HD2	1.78	0.65
1:2:1527:C:OP1	18:Q:142:GLN:NE2	2.28	0.65
1:2:367:U:H4'	1:2:371:A:C8	2.32	0.65
1:2:1531:A:O2'	1:2:1604:G:N2	2.30	0.65
20:S:110:ASP:OD1	20:S:111:LEU:N	2.30	0.65
4:C:72:ASP:OD2	4:C:272:HIS:NE2	2.30	0.64
7:F:179:ASN:HA	7:F:182:LYS:HG2	1.78	0.64
1:2:920:A:OP1	24:W:57:ARG:NE	2.21	0.64
2:A:163:CYS:CB	2:A:174:MET:HE3	2.26	0.64
6:E:153:LEU:HD12	8:G:216:ARG:HH21	1.61	0.64
13:L:82:MET:HE3	13:L:85:THR:HB	1.79	0.64
3:B:27:LYS:H	3:B:27:LYS:HD2	1.62	0.64
19:R:78:ARG:HD2	19:R:81:ARG:HH21	1.62	0.64
1:2:54:A:OP1	26:Y:111:LYS:NZ	2.25	0.64
5:D:31:GLU:O	5:D:54:ARG:NH1	2.30	0.64
5:D:135:GLU:HG2	5:D:153:VAL:HG13	1.80	0.64
10:I:130:THR:HG22	10:I:133:GLU:HG2	1.80	0.64
11:J:103:GLU:O	11:J:107:GLU:HG2	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1513:C:O2'	1:2:1514:G:N7	2.31	0.64
2:A:128:ARG:NH2	2:A:151:ASP:O	2.31	0.64
20:S:113:ARG:HA	20:S:116:LYS:HD3	1.80	0.64
6:E:102:ILE:HG23	6:E:182:MET:HE1	1.80	0.64
22:U:24:LEU:HB2	22:U:87:ARG:HB2	1.78	0.64
1:2:107:A:H2'	1:2:108:G:C8	2.33	0.64
1:2:640:A:H2'	1:2:641:A:C8	2.32	0.64
1:2:617:G:H4'	25:X:88:ASP:HB3	1.78	0.63
5:D:22:ASN:O	5:D:26:THR:OG1	2.16	0.63
9:H:181:THR:HG22	9:H:183:LYS:HG3	1.79	0.63
28:a:85:ARG:HG2	28:a:85:ARG:HH11	1.63	0.63
1:2:1259:A:N6	1:2:1518:C:OP2	2.28	0.63
1:2:223:C:H2'	1:2:224:A:C8	2.33	0.63
1:2:943:U:OP1	3:B:214:LYS:NZ	2.31	0.63
1:2:1325:G:O2'	1:2:1327:G:OP1	2.16	0.63
7:F:179:ASN:HB2	7:F:187:SER:HB2	1.79	0.63
9:H:69:LEU:HD13	9:H:96:ALA:HB2	1.80	0.63
1:2:77:A:C8	8:G:154:ARG:HG2	2.34	0.63
1:2:981:A:H2'	1:2:982:G:C8	2.33	0.63
2:A:66:VAL:HG21	2:A:185:MET:HB3	1.81	0.63
1:2:943:U:O2'	16:O:135:ILE:O	2.16	0.63
1:2:1568:C:OP1	21:T:96:SER:OG	2.16	0.63
1:2:1598:G:N7	27:Z:85:ARG:NH2	2.46	0.63
24:W:3:ARG:HD3	24:W:6:VAL:HG12	1.80	0.63
1:2:455:A:H2'	1:2:456:C:C6	2.34	0.63
1:2:1263:U:OP2	1:2:1513:C:N4	2.32	0.63
1:2:1400:U:H3'	1:2:1401:A:H5''	1.81	0.63
9:H:157:HIS:HB3	9:H:190:PRO:HG3	1.79	0.63
1:2:1630:A:O2'	20:S:31:THR:O	2.13	0.63
1:2:1427:C:O2'	1:2:1429:G:OP1	2.16	0.63
1:2:677:G:N1	1:2:1027:A:OP2	2.28	0.62
7:F:179:ASN:HB3	7:F:184:SER:HB3	1.81	0.62
16:O:95:ILE:HD11	16:O:126:ILE:HD12	1.79	0.62
29:b:67:THR:HG22	29:b:69:GLY:H	1.64	0.62
20:S:80:PRO:HB2	20:S:82:TRP:HD1	1.63	0.62
25:X:68:LYS:HB3	25:X:91:LEU:HD22	1.81	0.62
2:A:8:LEU:HD11	23:V:39:VAL:HG11	1.81	0.62
1:2:1426:U:OP2	18:Q:69:ARG:NH2	2.32	0.62
21:T:104:LEU:HD21	21:T:115:LYS:HB2	1.80	0.62
1:2:1552:G:OP2	1:2:1578:U:N3	2.23	0.62
12:K:26:ASP:OD1	12:K:28:HIS:ND1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:925:G:H1	1:2:1017:U:H3	1.46	0.62
1:2:1665:G:N2	21:T:87:VAL:O	2.32	0.62
3:B:173:THR:O	3:B:177:GLN:HG2	1.99	0.62
10:I:141:ARG:HB3	10:I:145:ILE:HB	1.82	0.62
1:2:1291:A:N6	33:f:140:TYR:OH	2.27	0.62
20:S:44:VAL:HG12	20:S:45:LEU:HD12	1.81	0.62
20:S:21:ASP:HB3	20:S:24:ARG:HG2	1.81	0.62
1:2:1344:A:N1	1:2:1385:G:O2'	2.31	0.62
1:2:1715:A:H61	1:2:1818:A:H61	1.48	0.62
25:X:93:PHE:O	25:X:140:ARG:NH1	2.31	0.62
1:2:944:A:H5''	16:O:134:PRO:HB3	1.82	0.61
5:D:14:ASP:O	5:D:18:LYS:HG2	1.99	0.61
1:2:94:G:O2'	1:2:508:A:O2'	2.17	0.61
1:2:1374:C:O2'	1:2:1464:C:O2	2.17	0.61
22:U:80:PHE:HB3	31:d:52:PHE:HB3	1.83	0.61
1:2:536:A:H61	1:2:546:G:H4'	1.66	0.61
22:U:21:ARG:HH11	22:U:88:LEU:HD13	1.66	0.61
4:C:172:ASN:ND2	11:J:95:ASP:OD1	2.31	0.61
7:F:97:PHE:HA	7:F:100:ILE:HG12	1.81	0.61
14:M:111:VAL:HB	14:M:121:LYS:HE2	1.83	0.61
16:O:102:GLY:O	16:O:106:LYS:NZ	2.26	0.61
33:f:106:TYR:O	33:f:115:SER:OG	2.19	0.61
1:2:1252:C:H2'	1:2:1526:G:H1'	1.82	0.61
7:F:137:GLN:OE1	30:c:63:ARG:NH2	2.25	0.61
18:Q:33:LYS:HE3	18:Q:69:ARG:HG3	1.83	0.61
12:K:83:LEU:HD23	12:K:85:LEU:HD11	1.82	0.61
1:2:1060:A:O2'	1:2:1062:A:N7	2.28	0.61
7:F:137:GLN:HE22	30:c:63:ARG:HH12	1.48	0.61
9:H:19:PHE:HZ	9:H:60:ILE:HG23	1.65	0.61
16:O:56:VAL:HG13	16:O:60:MET:HE2	1.82	0.61
21:T:23:LYS:HZ1	21:T:51:ASN:HB3	1.65	0.61
8:G:22:ARG:HA	8:G:25:ARG:NH1	2.15	0.60
25:X:41:PHE:HZ	25:X:102:VAL:HG12	1.66	0.60
25:X:61:GLN:O	25:X:61:GLN:NE2	2.34	0.60
1:2:1388:A:H61	5:D:161:GLY:HA3	1.66	0.60
4:C:196:ILE:HB	4:C:223:TYR:HB2	1.83	0.60
9:H:49:LYS:HG2	9:H:61:ILE:HB	1.83	0.60
25:X:40:PRO:HB3	25:X:81:ILE:HD11	1.82	0.60
33:f:99:LYS:HE2	33:f:99:LYS:N	2.15	0.60
1:2:874:G:H2'	1:2:875:A:H8	1.65	0.60
1:2:1143:A:H5'	4:C:190:SER:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:643:A:OP1	11:J:39:ASN:ND2	2.34	0.60
1:2:1217:A:H2'	1:2:1218:C:C6	2.36	0.60
1:2:1275:G:H4'	1:2:1323:U:H3	1.66	0.60
1:2:1519:U:OP2	20:S:137:LYS:NZ	2.35	0.60
19:R:41:ILE:HD13	19:R:50:ILE:HD12	1.84	0.60
34:g:147:HIS:CE1	34:g:175:LYS:HG3	2.37	0.60
1:2:118:C:H1'	1:2:445:A:C5	2.37	0.60
1:2:928:G:H2'	1:2:929:G:C8	2.36	0.60
1:2:1113:A:C5	1:2:1114:U:H1'	2.36	0.60
1:2:1589:A:H4'	21:T:82:ARG:HD2	1.84	0.60
24:W:80:ASP:OD1	24:W:80:ASP:N	2.33	0.60
5:D:211:VAL:O	19:R:20:TYR:OH	2.19	0.60
21:T:6:VAL:HG23	21:T:14:PHE:CE2	2.31	0.60
34:g:191:HIS:ND1	34:g:213:ASP:OD2	2.30	0.60
1:2:1670:C:H2'	1:2:1671:G:C4	2.37	0.60
2:A:82:THR:HG22	2:A:171:VAL:HG11	1.84	0.60
5:D:68:GLU:O	5:D:72:VAL:HG23	2.01	0.60
10:I:119:LEU:HD13	10:I:120:PRO:HD2	1.84	0.60
1:2:1592:C:O2'	21:T:12:GLN:OE1	2.18	0.59
20:S:41:ALA:O	20:S:45:LEU:HD13	2.02	0.59
1:2:1863:A:H1'	28:a:79:ILE:HD13	1.84	0.59
4:C:66:LEU:HD11	4:C:81:ILE:HG12	1.83	0.59
7:F:124:ASP:HA	7:F:200:ALA:HB2	1.84	0.59
21:T:64:LEU:HD13	21:T:113:VAL:HG21	1.83	0.59
1:2:532:C:O2	1:2:552:G:N2	2.35	0.59
1:2:1756:C:O2'	1:2:1757:G:O4'	2.20	0.59
5:D:93:THR:HG22	5:D:96:LEU:HB2	1.84	0.59
28:a:74:CYS:O	28:a:78:VAL:HG23	2.02	0.59
1:2:1539:U:H5'	21:T:43:LYS:HE3	1.84	0.59
21:T:114:GLU:HG2	21:T:122:LYS:HD3	1.84	0.59
34:g:62:HIS:CE1	34:g:88:ARG:HD3	2.38	0.59
5:D:123:LEU:O	5:D:127:MET:HG2	2.01	0.59
7:F:137:GLN:NE2	7:F:138:ALA:O	2.35	0.59
9:H:10:LYS:HG3	9:H:10:LYS:O	2.03	0.59
2:A:37:TYR:OH	2:A:57:LYS:NZ	2.35	0.59
18:Q:53:GLU:O	18:Q:57:LEU:HB2	2.03	0.59
1:2:1139:C:H2'	1:2:1140:G:O4'	2.02	0.59
21:T:109:GLY:H	21:T:114:GLU:HB3	1.67	0.59
22:U:17:ILE:HG21	22:U:116:ILE:HG23	1.84	0.59
34:g:196:ASN:HB2	34:g:211:GLY:HA2	1.85	0.59
1:2:1354:G:N2	1:2:1357:A:OP2	2.30	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:136:ARG:HB3	3:B:216:LYS:HG3	1.82	0.59
6:E:127:ARG:N	6:E:140:VAL:O	2.34	0.59
17:P:20:VAL:HG13	17:P:25:LEU:HD23	1.85	0.59
1:2:125:C:OP2	8:G:201:LYS:NZ	2.35	0.58
3:B:128:LYS:HE2	3:B:134:LEU:HB2	1.84	0.58
7:F:142:SER:HB3	30:c:50:VAL:HG22	1.84	0.58
20:S:31:THR:HG22	20:S:38:ARG:H	1.68	0.58
18:Q:12:VAL:HG22	18:Q:90:LYS:HG2	1.84	0.58
20:S:138:THR:HA	20:S:141:ARG:HD3	1.84	0.58
31:d:10:HIS:O	31:d:12:ARG:NH1	2.37	0.58
10:I:11:ARG:NH1	10:I:15:GLY:O	2.35	0.58
1:2:867:G:H2'	1:2:868:G:C8	2.38	0.58
21:T:74:SER:O	21:T:78:ILE:HD12	2.03	0.58
1:2:895:G:OP2	1:2:895:G:N2	2.30	0.58
1:2:1570:G:H2'	1:2:1571:G:H8	1.68	0.58
1:2:1806:A:O2'	1:2:1807:C:OP1	2.19	0.58
5:D:104:SER:O	5:D:108:LYS:HG2	2.02	0.58
7:F:40:ALA:HB3	7:F:67:PRO:HA	1.85	0.58
13:L:124:ASP:OD1	13:L:124:ASP:N	2.32	0.58
21:T:16:ARG:HA	21:T:16:ARG:CZ	2.33	0.58
27:Z:74:SER:OG	27:Z:79:ILE:O	2.22	0.58
1:2:1258:A:N6	1:2:1660:C:O4'	2.37	0.58
1:2:1287:A:OP2	33:f:97:LYS:NZ	2.36	0.58
1:2:1447:G:OP2	22:U:85:HIS:ND1	2.36	0.58
11:J:107:GLU:O	11:J:113:GLN:NE2	2.32	0.58
14:M:30:GLY:HA2	14:M:106:CYS:HB2	1.84	0.58
18:Q:131:LYS:O	18:Q:140:ARG:NH2	2.37	0.58
16:O:131:ASP:OD1	16:O:133:THR:HG22	2.04	0.57
22:U:63:ILE:HG22	31:d:33:LYS:HD3	1.86	0.57
1:2:1506:A:OP2	33:f:80:ARG:NH2	2.37	0.57
1:2:1622:U:O4	17:P:123:TYR:OH	2.15	0.57
12:K:51:SER:HB2	12:K:55:ARG:HH21	1.68	0.57
14:M:26:LEU:HD21	14:M:31:LEU:HD13	1.86	0.57
1:2:848:U:H2'	1:2:849:A:H8	1.69	0.57
1:2:1337:C:H2'	1:2:1338:G:C8	2.35	0.57
1:2:1389:C:OP1	19:R:43:SER:OG	2.17	0.57
1:2:1565:C:N4	1:2:1566:G:O6	2.37	0.57
1:2:1649:U:O4	1:2:1675:A:N7	2.37	0.57
4:C:204:ILE:HG22	4:C:206:SER:HB3	1.86	0.57
1:2:73:C:N4	8:G:169:PRO:O	2.37	0.57
6:E:151:ASP:HB3	6:E:154:ILE:HG13	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:X:71:ARG:NH1	25:X:82:THR:OG1	2.32	0.57
30:c:60:GLU:OE2	30:c:62:GLU:N	2.36	0.57
19:R:57:LEU:O	19:R:61:ILE:HG13	2.04	0.57
27:Z:51:ASP:H	27:Z:54:THR:HB	1.69	0.57
1:2:94:G:HO2'	1:2:508:A:HO2'	1.49	0.57
1:2:641:A:O2'	1:2:645:C:OP1	2.23	0.57
1:2:1470:C:OP2	7:F:59:LYS:NZ	2.38	0.57
10:I:113:TYR:OH	10:I:156:ALA:O	2.22	0.57
17:P:18:ARG:HG3	20:S:90:VAL:HA	1.85	0.57
19:R:67:ARG:HD2	19:R:67:ARG:O	2.05	0.57
21:T:110:LEU:HB3	21:T:112:MET:HE1	1.87	0.57
34:g:170:TRP:HA	34:g:194:TYR:HB2	1.87	0.57
1:2:92:A:H1'	6:E:3:ARG:HB2	1.87	0.57
1:2:796:G:N3	1:2:798:G:N1	2.53	0.57
7:F:143:PRO:O	7:F:147:VAL:HG13	2.05	0.57
9:H:79:LEU:HD12	9:H:94:PHE:CZ	2.38	0.57
1:2:1272:C:OP2	33:f:90:LYS:NZ	2.32	0.57
2:A:122:LEU:HB3	2:A:144:THR:HG22	1.87	0.57
3:B:52:THR:HG23	3:B:57:ILE:HA	1.86	0.57
23:V:32:ILE:HG12	23:V:60:ARG:HD2	1.86	0.57
1:2:1276:A:H8	12:K:50:GLN:HE22	1.52	0.56
17:P:93:MET:HE3	17:P:105:VAL:H	1.69	0.56
34:g:110:SER:OG	34:g:155:ARG:NH2	2.38	0.56
1:2:1221:G:H2'	1:2:1222:G:C8	2.40	0.56
1:2:1330:G:H5''	1:2:1493:C:H41	1.69	0.56
1:2:957:A:H3'	1:2:958:G:H21	1.71	0.56
6:E:88:ASP:OD1	6:E:122:LYS:NZ	2.37	0.56
10:I:190:LEU:HD22	10:I:194:GLU:HG2	1.87	0.56
19:R:33:ARG:NH2	19:R:36:GLU:OE1	2.38	0.56
20:S:23:ARG:NH1	27:Z:45:ASN:OD1	2.31	0.56
1:2:1606:G:O2'	1:2:1608:U:OP2	2.24	0.56
5:D:8:LYS:O	5:D:12:VAL:HG12	2.05	0.56
1:2:495:U:O2'	6:E:27:PHE:O	2.22	0.56
1:2:506:G:OP1	26:Y:108:LYS:NZ	2.37	0.56
6:E:11:ARG:HA	6:E:28:ALA:HB2	1.87	0.56
12:K:83:LEU:HB3	12:K:85:LEU:HG	1.87	0.56
28:a:73:TYR:CB	28:a:78:VAL:HG22	2.35	0.56
1:2:552:G:OP1	32:e:39:ASN:ND2	2.31	0.56
1:2:1452:A:H5''	19:R:48:ASN:OD1	2.05	0.56
7:F:161:ALA:HB3	7:F:172:CYS:HB3	1.87	0.56
12:K:65:ARG:NH1	31:d:20:SER:OG	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:54:ILE:HG22	34:g:56:GLN:HE22	1.71	0.56
34:g:245:ARG:HG2	34:g:261:LEU:HD11	1.86	0.56
1:2:1556:A:N7	1:2:1557:C:O2'	2.37	0.56
7:F:198:ARG:HH12	7:F:199:VAL:HG22	1.71	0.56
14:M:75:ASN:HD21	14:M:129:LYS:HG3	1.70	0.56
4:C:105:GLU:HB2	4:C:216:MET:HE1	1.88	0.56
5:D:25:LEU:HA	5:D:28:GLU:HB3	1.88	0.56
20:S:23:ARG:NH2	27:Z:46:ASN:O	2.38	0.56
34:g:59:LEU:HG	34:g:90:TRP:CE3	2.41	0.56
1:2:218:U:O2	10:I:184:ARG:NH2	2.38	0.56
1:2:1223:A:H61	1:2:1642:U:H3	1.53	0.56
3:B:146:ARG:HE	3:B:206:PRO:HG2	1.71	0.56
8:G:35:GLU:HG2	8:G:114:VAL:HG21	1.87	0.56
18:Q:132:PHE:O	18:Q:140:ARG:NH1	2.38	0.55
21:T:35:ASP:OD1	21:T:35:ASP:N	2.38	0.55
25:X:107:ARG:HG3	25:X:112:VAL:HG22	1.87	0.55
34:g:165:ILE:HB	34:g:177:TRP:HB2	1.88	0.55
1:2:29:G:H2'	1:2:30:C:C6	2.41	0.55
7:F:86:LYS:O	7:F:90:VAL:HG23	2.05	0.55
9:H:162:GLN:OE1	9:H:165:ASN:ND2	2.39	0.55
19:R:41:ILE:HB	19:R:47:ARG:HG2	1.88	0.55
1:2:996:A:H2'	1:2:997:A:C8	2.41	0.55
1:2:1736:G:H2'	1:2:1737:G:C8	2.42	0.55
1:2:1797:U:H2'	1:2:1798:C:C6	2.40	0.55
1:2:379:C:H5'	10:I:33:ALA:HA	1.87	0.55
1:2:1451:G:OP1	19:R:32:LYS:NZ	2.39	0.55
1:2:1757:G:H22	1:2:1775:U:H1'	1.72	0.55
2:A:2:SER:N	2:A:56:GLU:OE2	2.40	0.55
1:2:1706:G:O2'	1:2:1850:A:O2'	2.21	0.55
2:A:54:THR:HG23	2:A:174:MET:HE1	1.87	0.55
11:J:18:ARG:O	11:J:24:ARG:NH2	2.39	0.55
1:2:1324:G:H21	1:2:1509:U:H5	1.55	0.55
4:C:242:ASP:OD1	4:C:246:LYS:NZ	2.34	0.55
7:F:195:GLU:OE2	7:F:198:ARG:NH1	2.40	0.55
1:2:1144:A:H2'	1:2:1145:A:C8	2.42	0.55
17:P:40:ARG:H	17:P:42:ARG:HH11	1.55	0.55
1:2:1280:G:O6	1:2:1316:C:N4	2.40	0.55
9:H:88:SER:OG	9:H:89:GLY:N	2.40	0.55
13:L:111:VAL:HG12	13:L:140:PHE:HB2	1.89	0.55
18:Q:117:ARG:HH12	18:Q:121:VAL:HG21	1.70	0.55
1:2:1566:G:H21	1:2:1568:C:H3'	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:32:ASP:C	7:F:34:SER:H	2.15	0.55
7:F:190:ILE:HD12	7:F:191:LYS:N	2.22	0.55
13:L:55:TYR:CD2	13:L:115:PRO:HG2	2.42	0.55
36:n:174:LEU:HD21	36:n:187:LEU:HD23	1.89	0.55
3:B:29:ASP:OD2	3:B:51:ARG:NH1	2.36	0.54
5:D:103:GLU:OE1	5:D:103:GLU:HA	2.07	0.54
6:E:238:LEU:HB2	6:E:242:LYS:HE3	1.88	0.54
7:F:152:TRP:HE3	7:F:153:LEU:HD22	1.70	0.54
7:F:195:GLU:O	7:F:199:VAL:HG23	2.06	0.54
1:2:1139:C:H5	1:2:1149:A:H62	1.54	0.54
1:2:1190:A:N3	1:2:1714:U:O2'	2.41	0.54
1:2:1294:G:O3'	17:P:62:LYS:NZ	2.40	0.54
21:T:18:LEU:HB2	21:T:62:ARG:NH2	2.22	0.54
21:T:73:GLY:H	21:T:76:THR:HG23	1.72	0.54
1:2:296:U:O2'	6:E:131:VAL:O	2.25	0.54
1:2:420:G:O2'	1:2:660:C:N3	2.37	0.54
11:J:53:ILE:HD13	11:J:81:LEU:HD21	1.88	0.54
13:L:22:ARG:NH2	13:L:26:GLY:O	2.40	0.54
18:Q:102:GLU:O	18:Q:106:LYS:N	2.30	0.54
21:T:29:LYS:HG3	21:T:106:ALA:HA	1.88	0.54
25:X:84:PHE:CE2	25:X:86:PRO:HA	2.42	0.54
1:2:1037:G:H4'	1:2:1845:A:H4'	1.88	0.54
7:F:98:GLU:HG2	27:Z:108:ILE:HD13	1.90	0.54
16:O:46:ASP:OD1	16:O:47:LEU:N	2.40	0.54
28:a:59:PHE:HB2	28:a:62:TYR:HB2	1.89	0.54
5:D:27:ARG:NH1	12:K:62:PHE:O	2.41	0.54
30:c:18:LEU:HD23	30:c:67:ARG:HE	1.73	0.54
1:2:1152:U:O2'	24:W:19:LYS:NZ	2.41	0.54
2:A:52:LYS:HG3	19:R:109:LEU:HG	1.88	0.54
17:P:116:LEU:HG	17:P:118:GLU:H	1.72	0.54
26:Y:39:GLU:HA	26:Y:42:GLU:OE1	2.07	0.54
1:2:3:C:O2	11:J:18:ARG:NH2	2.34	0.54
1:2:441:C:OP1	10:I:2:GLY:HA3	2.08	0.54
1:2:1256:G:N2	31:d:30:LEU:O	2.40	0.54
1:2:1720:U:H5	1:2:1722:G:H1'	1.73	0.54
6:E:255:ARG:HH11	6:E:259:LYS:HZ2	1.56	0.54
21:T:5:THR:OG1	21:T:6:VAL:N	2.40	0.54
26:Y:57:VAL:HB	26:Y:60:PHE:HE2	1.72	0.54
34:g:168:CYS:HB2	34:g:195:LEU:HD12	1.89	0.54
1:2:379:C:O2	10:I:5:ARG:NE	2.41	0.54
1:2:964:A:H2'	1:2:965:U:H6	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1329:U:H3	1:2:1500:G:H1	1.54	0.54
2:A:78:SER:HB2	2:A:87:VAL:HG21	1.90	0.54
7:F:49:LEU:HD12	7:F:50:PRO:HD2	1.89	0.54
7:F:112:LEU:HD13	7:F:177:LEU:HD12	1.89	0.54
9:H:155:LYS:NZ	24:W:51:GLU:OE1	2.41	0.54
18:Q:118:THR:HA	18:Q:121:VAL:HG22	1.89	0.54
1:2:1705:C:H2'	1:2:1706:G:C8	2.43	0.54
16:O:28:PHE:HZ	28:a:58:VAL:HG21	1.71	0.54
19:R:16:ILE:HG22	19:R:24:LEU:HD11	1.90	0.54
19:R:61:ILE:HG12	19:R:66:VAL:HG21	1.89	0.54
1:2:104:A:H62	1:2:356:C:H5	1.56	0.54
1:2:656:G:H5'	1:2:662:G:N2	2.23	0.54
1:2:1174:U:H2'	1:2:1175:G:C8	2.43	0.54
1:2:1223:A:H2'	1:2:1224:G:C8	2.43	0.54
1:2:1755:C:OP1	1:2:1778:C:N4	2.40	0.54
7:F:122:ARG:NH1	7:F:123:GLU:OE2	2.41	0.54
9:H:17:ASP:HB2	9:H:20:GLU:HG3	1.90	0.54
1:2:1615:U:OP2	17:P:43:ARG:NH1	2.41	0.53
7:F:100:ILE:HD11	7:F:108:PRO:HB3	1.90	0.53
9:H:73:GLN:NE2	9:H:76:GLN:OE1	2.40	0.53
27:Z:73:VAL:O	27:Z:77:LEU:HD23	2.08	0.53
1:2:29:G:H4'	25:X:129:SER:HB3	1.89	0.53
1:2:822:U:H2'	1:2:824:C:OP2	2.08	0.53
1:2:1392:U:OP1	22:U:83:ARG:NH1	2.39	0.53
10:I:163:GLU:O	10:I:167:GLN:HG2	2.08	0.53
15:N:34:LYS:HE2	15:N:67:THR:HB	1.91	0.53
16:O:75:MET:HE3	16:O:79:GLN:HE22	1.73	0.53
21:T:15:VAL:HG23	21:T:16:ARG:HH11	1.73	0.53
21:T:43:LYS:HD2	21:T:45:LEU:HB2	1.90	0.53
1:2:155:G:H4'	8:G:15:LEU:HD13	1.89	0.53
1:2:1401:A:HO2'	1:2:1402:A:H8	1.56	0.53
1:2:1601:A:H4'	1:2:1602:U:H5'	1.89	0.53
7:F:35:LEU:HD12	7:F:39:ILE:HD11	1.90	0.53
19:R:17:ILE:HD11	19:R:54:VAL:HG13	1.90	0.53
26:Y:28:LEU:HD23	26:Y:68:LYS:HB3	1.90	0.53
1:2:376:A:OP2	13:L:58:LYS:NZ	2.36	0.53
1:2:545:A:H5'	1:2:546:G:N1	2.23	0.53
1:2:1295:A:H4'	1:2:1305:C:H41	1.74	0.53
1:2:1660:C:H4'	1:2:1663:A:H62	1.72	0.53
5:D:23:GLU:HG2	12:K:64:TRP:CD1	2.43	0.53
16:O:101:GLY:HA3	16:O:134:PRO:HD2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:a:73:TYR:HB3	28:a:78:VAL:HG22	1.90	0.53
1:2:1259:A:H1'	1:2:1263:U:H3	1.74	0.53
18:Q:132:PHE:CD2	22:U:77:TRP:HB2	2.43	0.53
22:U:50:VAL:HG12	22:U:91:LEU:HD22	1.90	0.53
1:2:84:A:N3	1:2:150:A:O2'	2.41	0.53
1:2:1010:G:H2'	1:2:1011:A:C8	2.43	0.53
8:G:159:ARG:HE	8:G:171:THR:HB	1.74	0.53
9:H:28:LEU:O	9:H:32:MET:HG3	2.08	0.53
17:P:41:GLN:NE2	17:P:113:GLY:O	2.42	0.53
27:Z:50:PHE:HA	27:Z:54:THR:HG21	1.90	0.53
1:2:1060:A:H4'	1:2:1061:U:H5'	1.90	0.53
16:O:40:THR:HG21	16:O:74:ALA:HB2	1.89	0.53
34:g:152:SER:HG	34:g:168:CYS:HG	1.57	0.53
5:D:59:LEU:HD23	5:D:66:ILE:HG12	1.90	0.53
1:2:1589:A:OP1	21:T:82:ARG:N	2.42	0.52
1:2:1597:C:OP1	27:Z:85:ARG:NH2	2.42	0.52
1:2:1648:G:N7	18:Q:17:LYS:HE2	2.24	0.52
7:F:19:LEU:HG	7:F:23:TRP:HD1	1.75	0.52
21:T:38:LYS:HE2	21:T:41:LYS:HA	1.89	0.52
1:2:1618:C:H2'	31:d:10:HIS:HE1	1.73	0.52
2:A:135:THR:O	2:A:138:SER:OG	2.26	0.52
13:L:66:VAL:HG11	13:L:141:ASN:HD22	1.73	0.52
21:T:18:LEU:HD22	21:T:62:ARG:NH1	2.24	0.52
1:2:16:G:H2'	1:2:17:C:C6	2.44	0.52
1:2:115:U:H2'	1:2:116:U:C6	2.45	0.52
1:2:1194:A:OP1	25:X:60:LYS:NZ	2.36	0.52
1:2:1288:U:H4'	1:2:1289:U:H5	1.75	0.52
1:2:1736:G:H2'	1:2:1737:G:H8	1.73	0.52
19:R:71:ILE:HB	19:R:74:GLN:HG2	1.92	0.52
34:g:27:PHE:HE2	34:g:75:GLY:HA3	1.73	0.52
6:E:107:GLY:HA2	6:E:189:LEU:HG	1.91	0.52
18:Q:19:ALA:HA	18:Q:74:GLY:HA3	1.91	0.52
21:T:64:LEU:HD22	21:T:121:ARG:HG3	1.92	0.52
34:g:17:TRP:HB2	34:g:36:ARG:HG3	1.91	0.52
1:2:1494:U:H4'	1:2:1495:G:H5''	1.90	0.52
1:2:1845:A:H2'	1:2:1846:G:C8	2.44	0.52
4:C:174:ILE:HD12	4:C:174:ILE:H	1.73	0.52
8:G:57:ASP:HA	8:G:106:LEU:HA	1.92	0.52
10:I:4:SER:OG	10:I:6:ASP:OD1	2.26	0.52
20:S:25:LYS:HE3	20:S:55:ARG:HH11	1.75	0.52
1:2:522:A:H5''	11:J:145:PRO:HD2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:91:VAL:HG22	5:D:93:THR:H	1.75	0.52
20:S:24:ARG:HB2	20:S:29:ALA:HB2	1.91	0.52
21:T:139:ALA:O	21:T:144:LYS:N	2.42	0.52
24:W:30:CYS:HB2	24:W:61:ILE:HG13	1.90	0.52
1:2:1013:U:OP1	1:2:1129:G:O2'	2.26	0.52
19:R:13:ALA:HB3	19:R:53:TYR:HD2	1.74	0.52
32:e:46:VAL:HG23	32:e:47:PRO:HD3	1.92	0.52
34:g:215:GLN:HB3	34:g:217:MET:HG3	1.92	0.52
1:2:1660:C:H4'	1:2:1663:A:N6	2.25	0.52
16:O:34:PHE:HB3	16:O:41:PHE:HB2	1.92	0.52
18:Q:12:VAL:CG2	18:Q:90:LYS:HG2	2.39	0.52
1:2:51:U:H2'	1:2:52:G:C8	2.45	0.52
1:2:1398:G:H22	1:2:1448:A:H2	1.58	0.52
5:D:157:MET:HE1	5:D:187:LYS:HB3	1.92	0.52
13:L:55:TYR:OH	13:L:116:CYS:HB3	2.10	0.52
18:Q:85:ARG:NH2	18:Q:119:LEU:HD13	2.25	0.52
19:R:23:ARG:HB3	34:g:170:TRP:HZ3	1.75	0.52
34:g:64:HIS:HB3	34:g:83:TRP:HB2	1.92	0.52
1:2:747:U:H5''	1:2:748:C:H5''	1.91	0.52
1:2:1706:G:H2'	1:2:1707:U:H6	1.74	0.52
2:A:144:THR:OG1	2:A:156:TYR:O	2.27	0.52
5:D:141:LYS:HZ1	5:D:180:GLY:HA3	1.75	0.52
12:K:7:ASN:ND2	12:K:39:ASN:O	2.43	0.52
13:L:94:HIS:HB2	13:L:105:ARG:HD2	1.92	0.52
22:U:82:MET:HB2	31:d:52:PHE:CD1	2.45	0.52
1:2:352:U:H2'	1:2:353:C:C6	2.46	0.51
7:F:191:LYS:HG3	7:F:192:LYS:N	2.24	0.51
1:2:1374:C:H2'	1:2:1375:G:O4'	2.11	0.51
2:A:141:ASN:ND2	4:C:87:PRO:HD3	2.25	0.51
5:D:120:TYR:O	5:D:124:ARG:HD3	2.11	0.51
13:L:73:LEU:HD12	13:L:109:MET:HE1	1.92	0.51
19:R:7:LYS:O	19:R:11:LYS:HB2	2.10	0.51
34:g:133:ASN:HD21	34:g:137:VAL:H	1.57	0.51
34:g:217:MET:SD	34:g:226:HIS:NE2	2.83	0.51
1:2:12:U:H2'	1:2:13:C:C6	2.45	0.51
1:2:165:G:O2'	8:G:53:SER:OG	2.28	0.51
1:2:910:G:H2'	1:2:911:C:O4'	2.09	0.51
1:2:1647:A:OP1	18:Q:138:ARG:NH1	2.37	0.51
1:2:1649:U:H3	1:2:1675:A:N6	2.06	0.51
3:B:208:HIS:ND1	3:B:208:HIS:C	2.67	0.51
12:K:3:MET:HE3	12:K:8:ARG:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:56:HIS:HA	19:R:59:LYS:HE2	1.92	0.51
7:F:113:VAL:O	7:F:117:ILE:HG12	2.10	0.51
9:H:138:GLU:OE2	15:N:21:SER:OG	2.24	0.51
19:R:37:GLU:OE1	34:g:150:TRP:NE1	2.39	0.51
29:b:59:CYS:SG	29:b:60:SER:N	2.83	0.51
34:g:168:CYS:CB	34:g:195:LEU:HD12	2.41	0.51
1:2:588:G:H4'	1:2:589:G:H5'	1.92	0.51
1:2:1668:U:OP2	18:Q:141:TYR:OH	2.14	0.51
8:G:137:ARG:HB3	8:G:140:ARG:HG3	1.93	0.51
28:a:62:TYR:O	28:a:63:VAL:HG12	2.10	0.51
34:g:121:VAL:HG12	34:g:154:VAL:HG21	1.93	0.51
1:2:332:G:OP1	8:G:196:LYS:NZ	2.43	0.51
5:D:172:VAL:HG13	5:D:185:LYS:HG2	1.92	0.51
16:O:75:MET:HE3	16:O:79:GLN:NE2	2.25	0.51
18:Q:58:LEU:HB2	18:Q:62:ARG:HD2	1.91	0.51
20:S:111:LEU:HA	20:S:114:LEU:HD12	1.91	0.51
26:Y:4:THR:OG1	26:Y:32:LYS:NZ	2.44	0.51
33:f:107:LYS:HD2	33:f:114:ILE:HA	1.92	0.51
1:2:942:G:H2'	1:2:943:U:C6	2.46	0.51
1:2:1047:C:H5''	16:O:143:LYS:HA	1.93	0.51
5:D:123:LEU:HD21	5:D:152:PHE:HB3	1.92	0.51
7:F:122:ARG:HG2	7:F:123:GLU:HG3	1.93	0.51
1:2:167:G:O2'	8:G:131:ARG:NE	2.44	0.51
2:A:40:LYS:NZ	2:A:41:ARG:O	2.42	0.51
4:C:187:ARG:HH11	4:C:187:ARG:HB3	1.76	0.51
9:H:63:PHE:HA	9:H:95:ILE:O	2.11	0.51
4:C:199:PRO:HG2	11:J:58:ARG:NE	2.26	0.51
8:G:65:GLN:O	8:G:65:GLN:NE2	2.44	0.51
9:H:62:ILE:HB	9:H:94:PHE:HD1	1.76	0.51
10:I:98:LYS:HD3	10:I:178:ARG:HG3	1.92	0.51
12:K:49:MET:HA	12:K:69:TRP:HZ2	1.75	0.51
18:Q:14:GLY:N	18:Q:21:ALA:O	2.44	0.51
22:U:24:LEU:HB3	22:U:32:LEU:HD11	1.93	0.51
1:2:17:C:H2'	1:2:18:C:C6	2.45	0.51
1:2:1117:C:H2'	1:2:1118:C:C6	2.46	0.51
1:2:1216:C:O2'	1:2:1644:C:OP1	2.27	0.51
1:2:1217:A:H2'	1:2:1218:C:H6	1.76	0.51
34:g:164:ILE:HD11	34:g:176:VAL:HG13	1.93	0.51
1:2:528:A:H2'	1:2:529:A:C8	2.45	0.50
9:H:19:PHE:CZ	9:H:60:ILE:HD12	2.46	0.50
17:P:65:LYS:NZ	17:P:66:GLU:OE1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:X:134:TYR:O	32:e:13:ARG:NH2	2.41	0.50
34:g:62:HIS:ND1	34:g:82:SER:HB2	2.26	0.50
2:A:158:ASP:OD2	23:V:65:SER:OG	2.22	0.50
17:P:96:VAL:HG22	17:P:119:PHE:H	1.75	0.50
34:g:167:SER:OG	34:g:177:TRP:NE1	2.40	0.50
1:2:4:C:H4'	4:C:207:ALA:HB2	1.93	0.50
1:2:1285:G:N2	1:2:1286:G:O6	2.43	0.50
9:H:61:ILE:HD11	9:H:176:VAL:HG22	1.93	0.50
34:g:14:HIS:CE1	34:g:35:SER:HB2	2.46	0.50
1:2:1155:U:OP1	4:C:185:THR:OG1	2.24	0.50
1:2:1283:C:H41	14:M:94:ILE:HD11	1.75	0.50
1:2:1351:G:O2'	1:2:1378:A:N1	2.42	0.50
3:B:108:ASP:N	3:B:108:ASP:OD1	2.45	0.50
6:E:22:LYS:HG3	6:E:23:LEU:HD23	1.93	0.50
12:K:41:PRO:HD2	12:K:44:HIS:HB2	1.92	0.50
34:g:42:MET:SD	34:g:56:GLN:N	2.70	0.50
34:g:174:VAL:HB	34:g:188:HIS:HB2	1.93	0.50
20:S:105:ASN:HA	20:S:108:ARG:HG2	1.93	0.50
1:2:77:A:H1'	8:G:176:ILE:HG13	1.93	0.50
1:2:517:C:H2'	1:2:518:G:O4'	2.11	0.50
1:2:551:U:H5'	32:e:43:VAL:HG11	1.92	0.50
9:H:126:HIS:CE1	9:H:181:THR:HG23	2.47	0.50
10:I:12:ARG:NH2	10:I:17:LYS:O	2.44	0.50
18:Q:81:ILE:C	18:Q:83:ALA:H	2.18	0.50
1:2:581:U:H4'	26:Y:66:GLY:HA2	1.94	0.50
1:2:1290:G:H21	1:2:1311:C:H41	1.60	0.50
34:g:20:GLN:HG2	34:g:69:VAL:H	1.77	0.50
1:2:1270:G:N7	33:f:83:LYS:NZ	2.59	0.50
28:a:44:ILE:HD12	28:a:65:PRO:HG2	1.94	0.50
34:g:167:SER:OG	34:g:175:LYS:HB2	2.12	0.50
34:g:172:LYS:HB3	34:g:191:HIS:HB2	1.94	0.50
34:g:199:THR:HG21	34:g:239:LEU:O	2.12	0.50
1:2:1447:G:OP1	22:U:87:ARG:NH2	2.45	0.50
5:D:24:PHE:O	5:D:28:GLU:CB	2.59	0.50
8:G:181:THR:H	8:G:184:VAL:HG22	1.77	0.50
1:2:594:A:H61	1:2:643:A:H5''	1.75	0.49
1:2:1865:C:O2	28:a:92:ARG:HB3	2.12	0.49
3:B:110:MET:HA	3:B:113:MET:HE2	1.94	0.49
5:D:40:ARG:HD3	22:U:108:PRO:HB3	1.92	0.49
16:O:145:GLY:O	28:a:22:ARG:NH2	2.45	0.49
1:2:667:U:H5''	1:2:1087:A:C5	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1644:C:H4'	18:Q:140:ARG:HB2	1.94	0.49
3:B:223:PHE:HE1	3:B:228:LEU:HD12	1.77	0.49
34:g:99:ARG:O	34:g:99:ARG:NH1	2.45	0.49
1:2:314:U:H2'	1:2:315:C:C6	2.47	0.49
1:2:532:C:H2'	1:2:533:A:H8	1.77	0.49
5:D:163:PRO:O	5:D:167:TYR:HB2	2.13	0.49
7:F:204:ARG:HG3	30:c:63:ARG:HE	1.76	0.49
8:G:200:LYS:O	8:G:204:GLU:HG3	2.11	0.49
9:H:62:ILE:HB	9:H:94:PHE:CD1	2.48	0.49
20:S:30:ILE:HD11	20:S:41:ALA:HB1	1.94	0.49
21:T:15:VAL:HG12	21:T:62:ARG:HE	1.76	0.49
34:g:45:LEU:HD13	34:g:47:ARG:H	1.77	0.49
34:g:54:ILE:O	34:g:56:GLN:NE2	2.45	0.49
1:2:396:U:OP2	13:L:79:LYS:NZ	2.36	0.49
1:2:1373:C:OP1	19:R:7:LYS:HE3	2.12	0.49
11:J:60:LEU:HD22	11:J:70:ARG:HA	1.94	0.49
12:K:59:LYS:HB2	12:K:70:TYR:CD2	2.47	0.49
19:R:5:ARG:HB2	19:R:10:LYS:HE3	1.94	0.49
20:S:71:MET:HE3	20:S:71:MET:O	2.12	0.49
26:Y:37:LYS:HG2	26:Y:57:VAL:HG23	1.95	0.49
30:c:31:ARG:HH21	30:c:43:ILE:HD11	1.77	0.49
1:2:1055:A:N6	1:2:1061:U:OP2	2.46	0.49
1:2:1119:A:H3'	1:2:1120:U:H6	1.77	0.49
1:2:1447:G:H2'	1:2:1448:A:H8	1.78	0.49
1:2:1522:A:H2'	17:P:131:PRO:HG3	1.94	0.49
1:2:1863:A:OP2	28:a:4:LYS:NZ	2.45	0.49
4:C:79:GLU:HG2	23:V:12:TYR:HB3	1.95	0.49
1:2:186:C:H2'	1:2:187:G:H8	1.77	0.49
1:2:433:A:H5''	10:I:22:HIS:HB3	1.95	0.49
1:2:887:U:H2'	1:2:888:U:H4'	1.93	0.49
1:2:929:G:H2'	1:2:930:C:O4'	2.12	0.49
1:2:1098:C:H2'	1:2:1099:G:C8	2.47	0.49
1:2:1821:U:H2'	1:2:1822:A:C8	2.48	0.49
2:A:77:ILE:HG21	2:A:133:PRO:HG2	1.93	0.49
5:D:101:GLN:HA	5:D:104:SER:HB3	1.94	0.49
5:D:193:ASP:OD2	5:D:196:GLY:HA3	2.12	0.49
19:R:29:HIS:O	19:R:33:ARG:HG2	2.12	0.49
27:Z:51:ASP:N	27:Z:54:THR:HB	2.28	0.49
28:a:85:ARG:HG2	28:a:85:ARG:NH1	2.27	0.49
1:2:848:U:H2'	1:2:849:A:C8	2.48	0.49
1:2:964:A:H2'	1:2:965:U:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1230:C:OP2	20:S:138:THR:HG22	2.12	0.49
1:2:1674:G:O2'	1:2:1675:A:O5'	2.29	0.49
7:F:172:CYS:O	7:F:176:GLU:HB3	2.13	0.49
1:2:380:G:OP2	10:I:181:GLN:NE2	2.41	0.49
1:2:1540:G:N2	1:2:1592:C:N3	2.60	0.49
4:C:130:ILE:HD13	4:C:159:LYS:HG3	1.93	0.49
7:F:121:PRO:HA	7:F:193:LYS:HD2	1.94	0.49
17:P:60:LEU:HD13	17:P:89:MET:HE1	1.94	0.49
18:Q:75:GLY:O	18:Q:79:ALA:HB3	2.12	0.49
22:U:78:ASP:OD2	31:d:44:ARG:NH2	2.46	0.49
1:2:1424:G:O5'	1:2:1425:G:OP1	2.26	0.49
5:D:42:THR:OG1	5:D:45:ARG:HG3	2.11	0.49
21:T:16:ARG:HA	21:T:16:ARG:NH1	2.28	0.49
1:2:156:G:OP1	8:G:2:LYS:NZ	2.32	0.49
1:2:1272:C:N4	1:2:1273:C:N3	2.61	0.49
9:H:35:ASP:OD1	9:H:35:ASP:N	2.36	0.49
27:Z:54:THR:HA	27:Z:77:LEU:CD1	2.43	0.49
27:Z:77:LEU:HD11	27:Z:79:ILE:HD13	1.94	0.49
1:2:1010:G:H2'	1:2:1011:A:H8	1.78	0.48
1:2:1201:U:H2'	1:2:1202:U:C6	2.47	0.48
1:2:1271:C:N4	1:2:1511:U:O2'	2.45	0.48
3:B:103:MET:HE2	3:B:215:VAL:HG23	1.95	0.48
5:D:101:GLN:HG2	5:D:126:ILE:HD11	1.95	0.48
18:Q:90:LYS:NZ	18:Q:120:LEU:HB2	2.28	0.48
34:g:210:GLY:HA3	34:g:239:LEU:HD11	1.95	0.48
34:g:272:GLN:OE1	34:g:272:GLN:N	2.45	0.48
1:2:1753:C:OP2	1:2:1780:G:N2	2.46	0.48
5:D:118:ALA:O	5:D:122:VAL:HG12	2.13	0.48
25:X:52:LEU:HD11	25:X:73:GLN:HB2	1.94	0.48
30:c:67:ARG:HG3	30:c:68:LEU:HG	1.95	0.48
1:2:377:G:H5''	10:I:98:LYS:HB3	1.95	0.48
1:2:508:A:H3'	1:2:509:G:H8	1.79	0.48
3:B:123:ALA:HB2	3:B:165:ARG:HG3	1.95	0.48
5:D:186:VAL:HG12	5:D:188:ILE:HD11	1.95	0.48
18:Q:97:GLN:HB2	18:Q:105:LYS:HG3	1.94	0.48
1:2:1129:G:H5''	29:b:22:LYS:HE3	1.95	0.48
1:2:1174:U:H2'	1:2:1175:G:H8	1.78	0.48
1:2:1390:U:H2'	1:2:1391:C:C6	2.48	0.48
6:E:44:LEU:HD13	6:E:72:ILE:HD11	1.94	0.48
13:L:148:ALA:HB3	13:L:151:THR:HG23	1.94	0.48
16:O:120:ALA:HB2	28:a:53:ILE:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:d:17:GLY:HA2	31:d:27:ARG:HE	1.79	0.48
34:g:175:LYS:HD2	34:g:187:ASN:OD1	2.12	0.48
34:g:305:ASN:O	34:g:305:ASN:ND2	2.44	0.48
1:2:106:C:H2'	1:2:107:A:H8	1.79	0.48
1:2:1798:C:H5'	10:I:3:ILE:HG22	1.94	0.48
5:D:101:GLN:H	5:D:101:GLN:CD	2.22	0.48
6:E:48:LEU:HD11	6:E:70:ILE:HG13	1.95	0.48
9:H:33:ASN:OD1	9:H:33:ASN:N	2.44	0.48
9:H:73:GLN:HB3	9:H:135:PHE:CZ	2.48	0.48
1:2:303:C:O2	10:I:184:ARG:NH1	2.46	0.48
1:2:434:G:OP1	10:I:23:LYS:HG2	2.13	0.48
16:O:43:HIS:CG	16:O:55:ARG:HG3	2.49	0.48
17:P:33:LEU:O	17:P:37:TYR:HB2	2.13	0.48
31:d:22:ARG:HH11	31:d:37:ASN:HB2	1.79	0.48
1:2:639:C:OP1	32:e:40:ARG:NH1	2.46	0.48
1:2:1578:U:H5''	1:2:1579:A:O4'	2.14	0.48
1:2:1854:U:OP1	16:O:150:ARG:NH2	2.45	0.48
2:A:147:LEU:HB3	2:A:163:CYS:SG	2.53	0.48
6:E:133:THR:O	6:E:134:LYS:HG2	2.14	0.48
7:F:128:ILE:HA	7:F:137:GLN:HB3	1.94	0.48
7:F:204:ARG:HG3	30:c:63:ARG:NE	2.28	0.48
15:N:106:ARG:HB3	15:N:106:ARG:CZ	2.44	0.48
17:P:78:THR:HG22	17:P:80:LEU:H	1.79	0.48
23:V:53:TYR:OH	23:V:76:ASP:OD2	2.25	0.48
28:a:42:ARG:NH2	28:a:43:ASN:O	2.47	0.48
1:2:5:U:H2'	1:2:6:G:H8	1.78	0.48
1:2:476:A:N3	1:2:488:U:O2'	2.34	0.48
1:2:1164:G:O2'	1:2:1165:G:H5'	2.14	0.48
1:2:1334:G:O3'	5:D:183:GLY:HA3	2.13	0.48
1:2:1626:C:H2'	1:2:1627:C:H5	1.77	0.48
1:2:1752:C:H2'	1:2:1752:C:O2	2.14	0.48
7:F:122:ARG:HG3	30:c:57:THR:HG23	1.95	0.48
24:W:41:MET:HE3	24:W:47:ILE:HG21	1.95	0.48
1:2:383:G:H4'	13:L:132:ARG:HD2	1.95	0.48
1:2:563:G:O2'	1:2:564:A:H5''	2.13	0.48
1:2:872:A:O2'	1:2:874:G:OP2	2.28	0.48
5:D:23:GLU:HG2	12:K:64:TRP:NE1	2.28	0.48
18:Q:90:LYS:O	18:Q:93:VAL:HG12	2.14	0.48
20:S:27:ALA:HA	20:S:30:ILE:HG12	1.96	0.48
23:V:67:ASP:O	23:V:71:ARG:HG3	2.13	0.48
1:2:551:U:H2'	1:2:552:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1394:G:H21	1:2:1475:G:H1'	1.78	0.48
1:2:1533:A:OP1	1:2:1637:A:N6	2.47	0.48
10:I:42:ARG:HG2	10:I:58:LEU:HB2	1.95	0.48
26:Y:105:LYS:O	26:Y:109:GLU:HG3	2.14	0.48
1:2:1288:U:H5'	1:2:1312:G:H22	1.78	0.47
1:2:1298:G:P	17:P:59:ARG:HH21	2.36	0.47
1:2:1471:C:H5''	1:2:1472:C:C6	2.49	0.47
5:D:72:VAL:HG12	12:K:68:TYR:HD2	1.78	0.47
5:D:98:ALA:HB2	5:D:169:ASP:HB3	1.95	0.47
6:E:45:ILE:HA	6:E:61:VAL:HG11	1.95	0.47
6:E:128:LYS:HA	6:E:156:VAL:HG22	1.96	0.47
17:P:42:ARG:O	17:P:46:ASN:N	2.47	0.47
29:b:34:ASP:OD2	29:b:43:ILE:HD12	2.14	0.47
34:g:111:VAL:O	34:g:155:ARG:NH2	2.41	0.47
1:2:414:A:OP1	1:2:814:U:O2'	2.31	0.47
1:2:638:C:C2'	1:2:639:C:H5'	2.44	0.47
1:2:1033:G:N1	1:2:1080:A:O2'	2.36	0.47
1:2:1646:C:H3'	18:Q:138:ARG:NH1	2.29	0.47
1:2:1866:A:N6	28:a:84:VAL:HB	2.29	0.47
11:J:33:GLY:HA3	32:e:38:TYR:CG	2.49	0.47
17:P:97:TYR:HE1	17:P:100:LYS:HA	1.79	0.47
21:T:49:ASP:C	21:T:51:ASN:H	2.21	0.47
1:2:857:U:H2'	1:2:858:A:C8	2.49	0.47
1:2:868:G:O2'	1:2:869:A:OP1	2.25	0.47
3:B:30:TRP:CE2	16:O:19:PRO:HD3	2.49	0.47
6:E:160:ILE:HD12	6:E:169:ILE:HG12	1.95	0.47
7:F:38:TYR:CD1	7:F:144:LEU:HD23	2.49	0.47
9:H:39:GLN:HG3	9:H:75:ILE:HG21	1.96	0.47
1:2:494:C:N4	1:2:509:G:H21	2.12	0.47
18:Q:70:VAL:HG11	18:Q:88:ILE:HG13	1.96	0.47
18:Q:104:SER:O	18:Q:108:ILE:HG23	2.15	0.47
1:2:528:A:H2'	1:2:529:A:H8	1.78	0.47
1:2:1621:U:O4'	17:P:81:ARG:NH2	2.48	0.47
13:L:120:VAL:HG22	13:L:145:VAL:HG11	1.96	0.47
18:Q:38:PRO:HG2	18:Q:41:MET:HG2	1.95	0.47
34:g:154:VAL:O	34:g:155:ARG:NE	2.48	0.47
34:g:297:THR:HG23	34:g:311:GLN:HG3	1.96	0.47
1:2:180:G:H2'	1:2:181:A:C8	2.49	0.47
1:2:830:A:OP2	1:2:846:G:N2	2.48	0.47
1:2:962:A:N1	1:2:1055:A:O2'	2.47	0.47
1:2:970:G:H3'	1:2:971:G:H5''	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1413:G:N2	1:2:1425:G:N7	2.61	0.47
1:2:1648:G:C8	18:Q:125:ARG:HG3	2.50	0.47
6:E:134:LYS:HE2	6:E:134:LYS:HB3	1.73	0.47
6:E:168:LYS:HE2	6:E:168:LYS:HB3	1.56	0.47
7:F:47:LYS:NZ	7:F:50:PRO:HA	2.29	0.47
34:g:167:SER:HG	34:g:175:LYS:HB2	1.79	0.47
1:2:584:A:OP2	11:J:169:ARG:NH2	2.48	0.47
1:2:1286:G:N2	1:2:1287:A:O2'	2.48	0.47
1:2:1349:G:H2'	1:2:1350:U:C6	2.50	0.47
1:2:1403:C:OP2	1:2:1405:A:N6	2.37	0.47
1:2:1658:G:H2'	1:2:1659:U:O4'	2.15	0.47
1:2:1771:G:O2'	1:2:1772:C:OP1	2.25	0.47
4:C:191:VAL:HG11	4:C:236:PHE:HA	1.95	0.47
18:Q:30:GLY:HA3	18:Q:64:ALA:HA	1.97	0.47
34:g:290:ALA:O	34:g:298:LEU:HD12	2.14	0.47
34:g:314:ILE:HG13	34:g:315:GLY:H	1.78	0.47
1:2:860:G:H21	24:W:107:SER:HB3	1.79	0.47
1:2:1579:A:O2'	1:2:1581:C:OP2	2.22	0.47
1:2:1600:G:O2'	1:2:1601:A:O4'	2.22	0.47
2:A:28:THR:HA	2:A:45:GLY:O	2.15	0.47
9:H:43:LEU:HD13	9:H:72:PHE:HD2	1.80	0.47
11:J:3:VAL:HB	11:J:5:ARG:HG3	1.97	0.47
19:R:24:LEU:HD22	19:R:54:VAL:HG11	1.97	0.47
21:T:11:GLN:O	21:T:15:VAL:HG13	2.15	0.47
21:T:62:ARG:HH12	21:T:131:LEU:HD11	1.80	0.47
1:2:344:U:H2'	1:2:345:U:C6	2.50	0.47
1:2:496:C:OP1	6:E:29:PRO:HD3	2.14	0.47
13:L:126:VAL:HG12	13:L:145:VAL:HG22	1.97	0.47
5:D:106:ARG:HH11	5:D:175:VAL:HG13	1.79	0.47
6:E:114:ILE:HD12	6:E:118:GLU:HG2	1.97	0.47
6:E:199:GLU:HG3	6:E:207:VAL:HB	1.97	0.47
19:R:33:ARG:HE	19:R:33:ARG:HA	1.79	0.47
21:T:110:LEU:HD22	21:T:112:MET:HE1	1.97	0.47
21:T:122:LYS:H	21:T:122:LYS:HD2	1.80	0.47
1:2:301:A:H2'	1:2:302:A:O4'	2.14	0.46
1:2:465:A:H4'	1:2:466:G:O5'	2.14	0.46
1:2:495:U:H2'	1:2:496:C:O4'	2.15	0.46
1:2:993:G:OP1	1:2:1131:G:N2	2.43	0.46
1:2:1220:A:H4'	7:F:145:ARG:HH22	1.80	0.46
1:2:1387:G:H22	5:D:206:ASP:HB2	1.80	0.46
1:2:1546:G:H1'	1:2:1671:G:H1'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1618:C:H2'	31:d:10:HIS:CE1	2.50	0.46
1:2:1673:U:H2'	1:2:1674:G:C8	2.50	0.46
2:A:42:LYS:NZ	19:R:99:ASP:OD2	2.40	0.46
2:A:110:ASN:HD22	2:A:113:GLN:HE21	1.64	0.46
4:C:121:ARG:HD3	4:C:145:LYS:NZ	2.30	0.46
12:K:58:VAL:HG12	12:K:71:LEU:HA	1.96	0.46
17:P:111:MET:HE1	20:S:113:ARG:NH1	2.30	0.46
18:Q:93:VAL:HA	18:Q:108:ILE:HD11	1.97	0.46
21:T:104:LEU:O	21:T:108:GLU:N	2.48	0.46
1:2:1276:A:H1'	12:K:50:GLN:NE2	2.31	0.46
1:2:1786:U:H2'	1:2:1787:G:C8	2.50	0.46
7:F:188:TYR:HA	7:F:191:LYS:HG2	1.97	0.46
25:X:28:LYS:O	25:X:32:LEU:HB2	2.15	0.46
26:Y:57:VAL:HB	26:Y:60:PHE:CE2	2.50	0.46
1:2:317:C:OP2	8:G:183:ARG:NH2	2.44	0.46
1:2:676:C:H2'	1:2:677:G:O4'	2.16	0.46
1:2:1144:A:H5'	1:2:1355:C:H41	1.80	0.46
1:2:1302:G:N1	1:2:1307:U:O4	2.47	0.46
1:2:1844:U:H2'	1:2:1845:A:C8	2.50	0.46
1:2:533:A:H2'	1:2:534:G:C8	2.50	0.46
1:2:1312:G:N2	12:K:1:MET:SD	2.89	0.46
1:2:1683:C:H2'	1:2:1684:C:H6	1.81	0.46
2:A:77:ILE:HB	2:A:124:VAL:HG12	1.97	0.46
3:B:124:HIS:HA	3:B:137:LEU:O	2.16	0.46
5:D:66:ILE:HD12	5:D:67:ARG:N	2.31	0.46
5:D:131:ALA:HA	5:D:191:PRO:HD3	1.97	0.46
8:G:132:ARG:HH21	8:G:133:LEU:HD11	1.81	0.46
17:P:96:VAL:HB	17:P:103:ASN:HB2	1.96	0.46
17:P:132:GLY:O	17:P:134:GLY:N	2.48	0.46
1:2:988:C:H5''	3:B:116:LYS:HA	1.97	0.46
1:2:1016:U:C6	15:N:61:ALA:HB1	2.51	0.46
1:2:1677:U:P	7:F:63:LYS:HD2	2.56	0.46
1:2:1757:G:N2	1:2:1777:G:H22	2.13	0.46
3:B:27:LYS:HA	3:B:51:ARG:NH2	2.30	0.46
5:D:158:ILE:HG12	5:D:189:MET:HE3	1.97	0.46
9:H:8:ILE:HG23	9:H:44:ASN:HA	1.96	0.46
13:L:94:HIS:CB	13:L:105:ARG:HD2	2.46	0.46
34:g:112:ALA:N	34:g:121:VAL:O	2.45	0.46
1:2:1831:A:O2'	1:2:1852:C:H5'	2.16	0.46
5:D:25:LEU:HD13	5:D:37:VAL:HG21	1.97	0.46
7:F:22:LYS:HE2	7:F:23:TRP:CH2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:109:ARG:HG2	9:H:110:THR:H	1.81	0.46
11:J:21:GLU:OE1	11:J:23:SER:OG	2.32	0.46
20:S:47:LYS:NZ	20:S:78:LYS:O	2.44	0.46
24:W:30:CYS:SG	24:W:31:SER:N	2.88	0.46
1:2:441:C:H2'	1:2:442:C:C6	2.51	0.46
1:2:1043:G:H2'	1:2:1044:G:O4'	2.15	0.46
1:2:1798:C:H2'	1:2:1799:G:O4'	2.16	0.46
2:A:16:LEU:HD12	19:R:96:ILE:HD12	1.97	0.46
3:B:88:THR:HA	3:B:98:THR:HA	1.97	0.46
3:B:219:LYS:HE3	3:B:219:LYS:HB3	1.59	0.46
7:F:38:TYR:CD2	7:F:143:PRO:HB2	2.51	0.46
1:2:67:C:H41	8:G:164:LYS:H	1.63	0.46
1:2:443:U:H2'	1:2:444:G:O4'	2.15	0.46
1:2:1447:G:H2'	1:2:1448:A:C8	2.50	0.46
5:D:197:LYS:HB3	5:D:197:LYS:HE2	1.58	0.46
7:F:93:VAL:O	7:F:97:PHE:HB2	2.16	0.46
9:H:85:LYS:HB2	9:H:85:LYS:HE3	1.79	0.46
15:N:87:ASP:N	15:N:87:ASP:OD1	2.45	0.46
25:X:101:LEU:HB3	25:X:124:LYS:HB2	1.96	0.46
1:2:15:U:H2'	1:2:16:G:O4'	2.16	0.46
1:2:1171:G:O2'	1:2:1187:G:O6	2.33	0.46
1:2:1253:A:C8	1:2:1666:C:H4'	2.50	0.46
6:E:180:LEU:N	6:E:231:GLY:O	2.48	0.46
14:M:112:LYS:HG3	14:M:113:ASP:H	1.80	0.46
17:P:101:THR:OG1	17:P:102:PHE:N	2.49	0.46
1:2:5:U:H2'	1:2:6:G:C8	2.50	0.46
1:2:804:U:H2'	1:2:805:U:C6	2.51	0.46
1:2:1084:A:OP1	1:2:1858:G:O2'	2.24	0.46
1:2:1296:U:OP2	1:2:1305:C:N4	2.49	0.46
1:2:1782:G:H8	1:2:1782:G:OP2	1.98	0.46
1:2:1869:A:C5	28:a:39:PHE:HE2	2.33	0.46
17:P:19:GLY:N	20:S:91:LYS:O	2.41	0.46
21:T:28:LEU:HA	21:T:110:LEU:HD11	1.98	0.46
21:T:123:LEU:HD21	21:T:128:GLN:HB3	1.98	0.46
30:c:35:MET:SD	30:c:35:MET:N	2.89	0.46
1:2:106:C:H2'	1:2:107:A:C8	2.51	0.45
1:2:220:U:H5'	10:I:177:SER:HB3	1.97	0.45
1:2:314:U:H2'	1:2:315:C:H6	1.81	0.45
1:2:672:A:N6	1:2:1027:A:OP1	2.48	0.45
1:2:1083:A:N7	1:2:1841:C:O2'	2.47	0.45
16:O:46:ASP:OD2	16:O:48:SER:OG	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:3:GLY:HA2	21:T:133:ARG:HH22	1.81	0.45
21:T:6:VAL:HG11	21:T:65:TYR:CD1	2.51	0.45
33:f:97:LYS:HG3	33:f:99:LYS:NZ	2.32	0.45
1:2:573:U:H2'	1:2:574:A:H5''	1.98	0.45
1:2:612:U:H4'	32:e:15:GLN:OE1	2.17	0.45
1:2:633:C:O2'	32:e:16:THR:HG21	2.16	0.45
1:2:1009:A:O2'	15:N:114:ARG:HG3	2.16	0.45
1:2:1091:C:O2'	24:W:2:VAL:N	2.46	0.45
1:2:1133:A:H4'	28:a:13:LYS:HD3	1.97	0.45
8:G:5:ILE:HG21	8:G:45:TRP:HH2	1.81	0.45
21:T:115:LYS:HE3	21:T:115:LYS:HB3	1.71	0.45
1:2:416:U:H2'	1:2:417:C:O4'	2.17	0.45
1:2:1288:U:O4	33:f:95:ARG:N	2.47	0.45
1:2:1412:C:OP2	1:2:1431:G:N2	2.45	0.45
7:F:77:MET:HB2	7:F:82:ASN:O	2.15	0.45
11:J:131:ARG:HD2	11:J:131:ARG:HA	1.62	0.45
1:2:429:C:O2'	1:2:811:A:N1	2.47	0.45
1:2:809:A:H2'	1:2:810:A:O4'	2.17	0.45
1:2:901:G:O2'	1:2:902:G:OP1	2.27	0.45
1:2:1397:U:O4	18:Q:13:PHE:HD2	1.98	0.45
1:2:1676:U:H5''	7:F:71:ARG:HG2	1.98	0.45
5:D:116:ARG:HG2	5:D:150:MET:HE2	1.98	0.45
9:H:84:GLU:HG3	9:H:92:VAL:HG12	1.98	0.45
14:M:18:LEU:HA	14:M:21:VAL:HG12	1.99	0.45
14:M:101:ARG:NH1	14:M:103:VAL:HG12	2.32	0.45
15:N:64:ARG:HD3	15:N:70:LYS:HG3	1.98	0.45
23:V:30:ALA:O	23:V:60:ARG:HD3	2.16	0.45
34:g:133:ASN:HD21	34:g:137:VAL:HG23	1.81	0.45
1:2:29:G:H2'	1:2:30:C:H6	1.78	0.45
1:2:187:G:H2'	1:2:188:C:C6	2.51	0.45
1:2:1279:C:H5''	1:2:1280:G:C8	2.51	0.45
1:2:1471:C:H5''	1:2:1472:C:H6	1.81	0.45
1:2:1558:C:H2'	1:2:1559:C:C6	2.52	0.45
1:2:1569:A:OP1	21:T:97:LYS:NZ	2.34	0.45
4:C:244:ILE:O	4:C:247:THR:OG1	2.24	0.45
6:E:62:LYS:HE3	6:E:62:LYS:HB3	1.72	0.45
28:a:73:TYR:HB2	28:a:78:VAL:HG22	1.97	0.45
34:g:8:ARG:HH11	34:g:311:GLN:HB2	1.80	0.45
1:2:533:A:H2'	1:2:534:G:H8	1.81	0.45
1:2:1570:G:H2'	1:2:1571:G:C8	2.51	0.45
1:2:1669:G:C6	1:2:1670:C:C4	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:9:VAL:HG22	9:H:11:PRO:HD3	1.98	0.45
11:J:151:LEU:HD12	11:J:151:LEU:HA	1.83	0.45
34:g:19:THR:N	34:g:34:ALA:O	2.50	0.45
34:g:123:GLY:HA2	34:g:151:VAL:HG12	1.99	0.45
1:2:955:A:N1	1:2:968:U:O2'	2.49	0.45
1:2:956:G:O5'	16:O:60:MET:HG2	2.16	0.45
1:2:1545:A:H2'	1:2:1546:G:H8	1.81	0.45
2:A:160:ALA:HB3	23:V:66:ASP:OD2	2.17	0.45
5:D:11:PHE:HE2	22:U:25:THR:HG22	1.81	0.45
9:H:118:ARG:O	9:H:121:THR:OG1	2.30	0.45
18:Q:53:GLU:O	18:Q:57:LEU:CB	2.65	0.45
21:T:19:ALA:O	21:T:23:LYS:HD2	2.17	0.45
4:C:254:ASP:HB2	23:V:1:MET:HG2	1.98	0.45
9:H:82:GLU:O	9:H:86:LYS:HG2	2.17	0.45
17:P:79:HIS:HE1	17:P:102:PHE:HZ	1.63	0.45
23:V:74:LYS:HE3	23:V:74:LYS:HB2	1.65	0.45
24:W:106:THR:HG21	24:W:121:THR:HG21	1.99	0.45
1:2:913:A:H2	9:H:99:ARG:H	1.64	0.45
1:2:1323:U:O4'	12:K:50:GLN:NE2	2.49	0.45
1:2:1337:C:O2'	22:U:68:THR:HB	2.17	0.45
1:2:1537:A:N1	27:Z:104:ARG:HD2	2.32	0.45
1:2:1656:G:C6	1:2:1669:G:C6	3.05	0.45
7:F:156:THR:HA	7:F:159:ARG:HG2	1.98	0.45
12:K:8:ARG:HD3	12:K:9:ILE:HG13	1.99	0.45
18:Q:42:ILE:HG22	18:Q:44:PRO:HD2	1.99	0.45
19:R:78:ARG:HD2	19:R:81:ARG:NH2	2.30	0.45
24:W:23:ARG:HG3	29:b:4:ALA:HB2	1.99	0.45
1:2:102:A:OP2	1:2:408:A:N6	2.43	0.45
1:2:1244:U:H5'	1:2:1328:G:H5''	1.99	0.45
1:2:1456:G:H2'	1:2:1457:U:H6	1.81	0.45
1:2:1633:A:H5''	1:2:1634:A:H5''	1.99	0.45
1:2:1703:C:H2'	1:2:1704:C:O4'	2.17	0.45
5:D:24:PHE:O	5:D:28:GLU:HB2	2.17	0.45
8:G:72:ARG:HD3	8:G:96:SER:HB3	1.99	0.45
34:g:120:ILE:HD11	34:g:134:THR:HG22	1.97	0.45
1:2:202:G:H5'	1:2:203:G:C8	2.52	0.44
1:2:293:C:O2	1:2:293:C:H2'	2.16	0.44
1:2:380:G:O6	10:I:178:ARG:NH2	2.50	0.44
1:2:595:U:H2'	1:2:596:U:C6	2.52	0.44
1:2:656:G:N2	1:2:663:C:H5''	2.32	0.44
1:2:1258:A:C2	1:2:1663:A:H2'	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1270:G:H5''	1:2:1303:C:H42	1.82	0.44
1:2:1564:C:OP1	21:T:105:GLN:NE2	2.50	0.44
6:E:35:PRO:HB3	6:E:143:ASP:O	2.17	0.44
20:S:90:VAL:HG21	20:S:113:ARG:NH2	2.33	0.44
1:2:406:U:O2'	1:2:408:A:OP1	2.26	0.44
1:2:575:A:H2'	1:2:576:A:O4'	2.17	0.44
1:2:1600:G:H2'	1:2:1601:A:C4	2.53	0.44
3:B:208:HIS:C	3:B:208:HIS:HD1	2.24	0.44
7:F:95:HIS:C	7:F:97:PHE:H	2.25	0.44
7:F:193:LYS:HG3	7:F:197:GLU:OE2	2.17	0.44
16:O:78:ALA:HB1	16:O:119:LEU:HG	2.00	0.44
23:V:64:GLU:O	23:V:68:SER:OG	2.28	0.44
34:g:244:ASN:ND2	34:g:245:ARG:HH21	2.15	0.44
1:2:911:C:O2'	1:2:912:C:H5'	2.16	0.44
1:2:1065:G:OP1	16:O:149:ARG:HD2	2.17	0.44
1:2:1630:A:H2'	1:2:1631:U:O4'	2.17	0.44
2:A:54:THR:CG2	2:A:174:MET:HE1	2.46	0.44
7:F:49:LEU:HD23	18:Q:50:LYS:HB2	1.99	0.44
31:d:3:HIS:ND1	31:d:7:TYR:HB2	2.32	0.44
34:g:240:CYS:SG	34:g:249:CYS:HB2	2.57	0.44
1:2:388:U:H2'	1:2:389:A:C8	2.52	0.44
1:2:613:G:N2	1:2:626:G:OP1	2.46	0.44
1:2:1670:C:H2'	1:2:1671:G:N3	2.32	0.44
7:F:88:MET:O	7:F:92:ILE:HG13	2.17	0.44
8:G:52:ILE:HD13	8:G:102:VAL:HG21	2.00	0.44
10:I:139:LYS:HE3	10:I:141:ARG:HE	1.82	0.44
34:g:107:ASP:OD2	34:g:125:ARG:NE	2.44	0.44
1:2:1308:U:O2'	1:2:1309:C:H4'	2.18	0.44
1:2:1332:A:O2'	5:D:145:GLN:OE1	2.24	0.44
1:2:1535:U:H5'	1:2:1536:G:H8	1.81	0.44
1:2:1608:U:H4'	1:2:1632:G:O6	2.18	0.44
1:2:1740:C:H2'	1:2:1741:U:C6	2.51	0.44
5:D:29:LEU:HD12	5:D:32:ASP:HB2	1.99	0.44
7:F:102:LEU:HD12	7:F:103:LEU:N	2.33	0.44
13:L:66:VAL:HG11	13:L:141:ASN:ND2	2.33	0.44
14:M:75:ASN:HB3	14:M:128:PHE:HB3	1.99	0.44
1:2:306:C:H5'	1:2:308:G:H5'	1.99	0.44
1:2:385:G:H3'	13:L:136:LYS:HB2	1.99	0.44
1:2:943:U:H2'	1:2:944:A:H8	1.82	0.44
1:2:989:C:OP2	3:B:155:TYR:OH	2.19	0.44
1:2:1443:C:H5'	1:2:1444:U:OP2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1562:C:OP1	21:T:74:SER:N	2.51	0.44
2:A:105:PRO:HA	2:A:136:GLU:OE2	2.17	0.44
5:D:31:GLU:OE1	5:D:31:GLU:N	2.43	0.44
7:F:159:ARG:HG3	7:F:160:GLU:OE1	2.18	0.44
11:J:159:PHE:O	11:J:163:SER:OG	2.35	0.44
12:K:57:TYR:HB3	12:K:75:GLY:HA2	2.00	0.44
21:T:10:ASN:HB3	21:T:143:LYS:NZ	2.33	0.44
24:W:86:LEU:HD21	24:W:113:HIS:HB2	1.99	0.44
28:a:3:LYS:NZ	28:a:5:ARG:O	2.45	0.44
28:a:18:VAL:HG21	28:a:33:ASP:OD2	2.18	0.44
29:b:35:VAL:HG13	29:b:77:CYS:HB3	1.99	0.44
32:e:52:LYS:NZ	36:n:167:PRO:HG3	2.33	0.44
1:2:1148:A:H4'	1:2:1149:A:O4'	2.17	0.44
1:2:1221:G:H2'	1:2:1222:G:H8	1.81	0.44
1:2:1262:C:H5''	1:2:1513:C:N4	2.32	0.44
3:B:47:THR:OG1	16:O:46:ASP:OD2	2.28	0.44
3:B:142:PHE:O	3:B:208:HIS:N	2.49	0.44
5:D:105:LEU:HA	5:D:105:LEU:HD23	1.74	0.44
16:O:142:ARG:HG3	16:O:143:LYS:N	2.32	0.44
17:P:96:VAL:HG13	17:P:118:GLU:HA	2.00	0.44
21:T:62:ARG:NH1	21:T:131:LEU:HD11	2.33	0.44
21:T:74:SER:O	21:T:77:LYS:N	2.50	0.44
34:g:237:ASN:OD1	34:g:237:ASN:N	2.51	0.44
1:2:290:U:O2'	1:2:292:A:N7	2.44	0.44
1:2:1232:U:O4	1:2:1526:G:N1	2.50	0.44
16:O:119:LEU:O	16:O:124:MET:HB2	2.18	0.44
17:P:105:VAL:HG23	17:P:107:ILE:HG12	2.00	0.44
19:R:6:THR:HG22	19:R:8:THR:H	1.83	0.44
29:b:33:MET:HE3	29:b:73:LEU:HD11	1.99	0.44
34:g:172:LYS:HG2	34:g:193:GLY:C	2.43	0.44
1:2:1299:A:O2'	17:P:52:LYS:O	2.33	0.44
1:2:1666:C:H2'	1:2:1667:U:O4'	2.17	0.44
1:2:1825:A:H3'	1:2:1826:G:C5'	2.48	0.44
10:I:17:LYS:HB3	10:I:17:LYS:HE3	1.70	0.44
16:O:75:MET:HG2	16:O:118:ALA:HB2	2.00	0.44
19:R:24:LEU:HB3	19:R:58:MET:HE3	1.99	0.44
20:S:111:LEU:HD11	20:S:115:LYS:HE3	2.00	0.44
22:U:23:THR:HA	22:U:88:LEU:HD23	2.00	0.44
24:W:53:ILE:HB	24:W:60:LYS:HB2	2.00	0.44
1:2:376:A:H2'	1:2:377:G:O4'	2.18	0.43
1:2:973:C:O2	16:O:55:ARG:NH1	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1566:G:H1	21:T:97:LYS:HZ3	1.66	0.43
1:2:1674:G:H8	1:2:1674:G:O5'	2.01	0.43
3:B:28:LYS:NZ	16:O:51:GLU:OE2	2.51	0.43
4:C:147:VAL:HG11	36:n:190:LEU:HD13	2.00	0.43
4:C:270:THR:O	4:C:274:VAL:HG23	2.18	0.43
6:E:21:ASP:OD1	6:E:24:THR:OG1	2.33	0.43
16:O:31:CYS:HB2	16:O:93:LEU:HG	2.00	0.43
18:Q:77:HIS:O	18:Q:81:ILE:HG12	2.18	0.43
19:R:17:ILE:HG22	19:R:69:ILE:HD13	2.00	0.43
34:g:256:ILE:HD13	34:g:258:ILE:HG12	1.99	0.43
1:2:1318:G:O2'	1:2:1504:U:O2	2.19	0.43
1:2:1491:G:H2'	1:2:1492:U:C6	2.53	0.43
7:F:167:LYS:HB2	7:F:171:GLU:OE1	2.18	0.43
9:H:43:LEU:HD13	9:H:72:PHE:CD2	2.53	0.43
18:Q:13:PHE:H	18:Q:22:VAL:HG13	1.83	0.43
21:T:137:GLN:O	21:T:141:ALA:HB2	2.17	0.43
31:d:33:LYS:HG2	31:d:34:TYR:CD2	2.53	0.43
1:2:1257:G:H4'	1:2:1258:A:H5'	2.00	0.43
1:2:1458:G:H2'	1:2:1459:G:H8	1.83	0.43
1:2:1568:C:O3'	21:T:41:LYS:NZ	2.51	0.43
11:J:107:GLU:HA	11:J:112:THR:HG21	2.00	0.43
15:N:99:ARG:NH1	15:N:99:ARG:HG2	2.33	0.43
18:Q:58:LEU:HB2	18:Q:62:ARG:CD	2.48	0.43
1:2:674:C:H2'	1:2:675:U:C6	2.54	0.43
1:2:1162:C:H2'	1:2:1163:C:O4'	2.18	0.43
1:2:1382:A:OP2	19:R:11:LYS:NZ	2.52	0.43
2:A:111:GLN:HA	2:A:116:PHE:CG	2.53	0.43
7:F:44:LYS:HE2	7:F:45:TYR:CZ	2.53	0.43
13:L:148:ALA:O	13:L:151:THR:OG1	2.33	0.43
25:X:63:ASN:HD22	25:X:114:ASP:CG	2.26	0.43
34:g:116:ASP:OD1	34:g:118:ARG:HB2	2.18	0.43
1:2:530:U:H2'	1:2:531:A:C8	2.54	0.43
1:2:582:U:H1'	26:Y:33:ALA:HB2	2.00	0.43
1:2:1298:G:OP1	17:P:77:LYS:HB2	2.18	0.43
1:2:1546:G:H2'	1:2:1547:C:C6	2.54	0.43
1:2:1845:A:H2'	1:2:1846:G:H8	1.82	0.43
2:A:167:GLY:O	2:A:171:VAL:HG12	2.19	0.43
6:E:104:ASP:O	6:E:190:GLY:HA3	2.18	0.43
7:F:52:SER:O	7:F:52:SER:OG	2.34	0.43
7:F:96:ALA:HB2	7:F:170:ALA:HA	2.01	0.43
20:S:5:ILE:HD11	20:S:9:PHE:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:67:C:C5	8:G:162:LEU:HB3	2.53	0.43
1:2:145:G:H2'	1:2:146:G:H8	1.82	0.43
1:2:1105:G:O3'	29:b:69:GLY:HA3	2.18	0.43
1:2:1171:G:OP1	35:h:6:ARG:NH1	2.51	0.43
1:2:1613:G:H1'	1:2:1627:C:H42	1.83	0.43
1:2:1659:U:C2	1:2:1664:A:N7	2.86	0.43
1:2:1788:A:H2'	1:2:1789:G:O4'	2.18	0.43
17:P:51:ARG:HG3	17:P:52:LYS:HG2	2.01	0.43
19:R:14:ARG:HG3	19:R:69:ILE:HD12	2.00	0.43
25:X:60:LYS:HG3	25:X:114:ASP:O	2.19	0.43
1:2:184:G:H2'	1:2:185:G:H8	1.84	0.43
1:2:501:C:O2	1:2:501:C:H2'	2.18	0.43
1:2:1101:U:H2'	1:2:1102:G:C8	2.54	0.43
1:2:1479:G:H4'	18:Q:128:GLU:OE2	2.19	0.43
1:2:1499:U:H2'	1:2:1500:G:N7	2.34	0.43
1:2:1651:A:H62	1:2:1673:U:H3	1.65	0.43
2:A:40:LYS:NZ	19:R:101:ASP:OD2	2.51	0.43
7:F:182:LYS:HD2	7:F:184:SER:HB2	2.00	0.43
10:I:3:ILE:HD11	10:I:30:GLY:HA3	2.01	0.43
21:T:63:HIS:HB2	21:T:75:MET:HE1	2.01	0.43
33:f:114:ILE:HD12	33:f:114:ILE:N	2.34	0.43
34:g:306:LEU:HD23	34:g:306:LEU:HA	1.70	0.43
1:2:186:C:H2'	1:2:187:G:C8	2.53	0.43
1:2:686:U:OP1	24:W:32:LYS:N	2.46	0.43
1:2:1397:U:N3	1:2:1442:U:H4'	2.32	0.43
4:C:252:THR:OG1	4:C:254:ASP:OD2	2.34	0.43
6:E:20:LEU:HD21	6:E:46:ILE:HD12	2.01	0.43
9:H:145:ARG:HG3	9:H:147:LYS:HD2	2.01	0.43
20:S:21:ASP:OD1	20:S:22:GLY:N	2.52	0.43
24:W:47:ILE:HG13	24:W:48:GLY:N	2.34	0.43
1:2:406:U:H2'	1:2:408:A:H5''	2.01	0.43
1:2:638:C:O2'	1:2:639:C:H5'	2.18	0.43
1:2:1687:C:H2'	1:2:1688:C:H6	1.84	0.43
7:F:153:LEU:HB3	7:F:189:ALA:HA	2.01	0.43
14:M:82:ASN:HA	14:M:85:LEU:HB3	2.00	0.43
25:X:11:ARG:O	25:X:15:SER:OG	2.29	0.43
27:Z:99:LEU:HD23	27:Z:99:LEU:HA	1.81	0.43
34:g:43:TRP:CE3	34:g:53:GLY:HA3	2.54	0.43
1:2:1182:A:C5	1:2:1183:A:H1'	2.54	0.43
1:2:1378:A:H4'	1:2:1379:A:O5'	2.19	0.43
1:2:1509:U:H4'	1:2:1511:U:C5	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1667:U:H2'	1:2:1668:U:C6	2.54	0.43
2:A:99:ILE:HD11	2:A:117:ARG:HD2	2.01	0.43
3:B:168:MET:HG2	3:B:197:ILE:CG2	2.49	0.43
10:I:84:ASN:HB2	10:I:91:VAL:HG23	2.01	0.43
12:K:43:LEU:O	12:K:47:LYS:HG2	2.19	0.43
17:P:37:TYR:CG	17:P:38:SER:N	2.87	0.43
18:Q:33:LYS:HA	18:Q:38:PRO:HA	2.01	0.43
28:a:88:SER:O	28:a:92:ARG:HG3	2.19	0.43
34:g:178:ASN:HB3	34:g:185:LYS:HD2	2.00	0.43
1:2:553:U:H5'	1:2:554:A:H5''	2.01	0.42
1:2:639:C:HO2'	1:2:640:A:H8	1.63	0.42
1:2:1138:C:O2'	23:V:61:ARG:HG2	2.19	0.42
1:2:1172:U:H5'	35:h:10:MET:HE3	2.00	0.42
1:2:1245:G:N2	1:2:1255:G:N3	2.66	0.42
1:2:1271:C:C4	31:d:3:HIS:HD2	2.37	0.42
1:2:1456:G:H2'	1:2:1457:U:C6	2.54	0.42
1:2:1646:C:H3'	18:Q:138:ARG:HH12	1.84	0.42
1:2:1650:A:H3'	1:2:1651:A:C2	2.54	0.42
1:2:1672:U:H5''	1:2:1673:U:OP2	2.17	0.42
15:N:94:LYS:O	15:N:98:VAL:HG23	2.19	0.42
18:Q:37:ARG:HG2	18:Q:41:MET:HB2	2.00	0.42
22:U:55:ARG:HG2	22:U:87:ARG:NE	2.34	0.42
34:g:244:ASN:HD21	34:g:245:ARG:HH21	1.67	0.42
1:2:223:C:H2'	1:2:224:A:H8	1.81	0.42
1:2:383:G:O2'	13:L:133:PRO:O	2.28	0.42
1:2:434:G:H5''	10:I:23:LYS:HE3	2.00	0.42
1:2:938:A:H2'	1:2:939:U:O4'	2.19	0.42
1:2:1236:G:H2'	1:2:1237:C:H4'	2.01	0.42
1:2:1525:C:H2'	1:2:1526:G:C8	2.53	0.42
1:2:1547:C:H2'	1:2:1548:G:O4'	2.19	0.42
10:I:65:PHE:HB2	10:I:109:TYR:OH	2.19	0.42
13:L:32:LYS:HG3	13:L:34:PRO:HD3	2.00	0.42
17:P:40:ARG:H	17:P:42:ARG:NH1	2.18	0.42
19:R:46:LEU:O	19:R:50:ILE:HG13	2.18	0.42
22:U:80:PHE:CE1	31:d:54:LYS:HG3	2.54	0.42
29:b:82:LYS:HA	29:b:82:LYS:HD2	1.87	0.42
34:g:268:ASP:OD1	34:g:268:ASP:N	2.52	0.42
1:2:571:U:O2'	26:Y:60:PHE:O	2.34	0.42
1:2:1046:U:H1'	16:O:140:THR:HB	2.00	0.42
1:2:1665:G:P	21:T:91:HIS:HE2	2.40	0.42
1:2:1817:G:H2'	1:2:1818:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:179:ASN:O	7:F:183:GLY:N	2.43	0.42
10:I:26:LYS:O	10:I:29:LEU:HB3	2.19	0.42
16:O:75:MET:HE2	16:O:75:MET:HB3	1.97	0.42
20:S:111:LEU:CD1	20:S:115:LYS:HE3	2.49	0.42
26:Y:86:GLU:OE1	26:Y:90:ARG:HD2	2.19	0.42
1:2:1298:G:H3'	17:P:59:ARG:NH2	2.35	0.42
1:2:1679:A:H4'	1:2:1680:G:H5''	2.01	0.42
2:A:90:PHE:O	2:A:94:THR:OG1	2.32	0.42
3:B:103:MET:HG2	3:B:104:ASP:N	2.33	0.42
3:B:137:LEU:HG	3:B:215:VAL:HG13	2.02	0.42
6:E:247:THR:OG1	6:E:250:GLU:HG3	2.20	0.42
8:G:49:VAL:HG13	8:G:114:VAL:HG23	2.01	0.42
9:H:8:ILE:O	9:H:44:ASN:HB2	2.19	0.42
9:H:78:ARG:O	9:H:82:GLU:HG2	2.19	0.42
14:M:87:GLU:HG2	14:M:99:LYS:HG3	2.01	0.42
1:2:446:G:P	10:I:47:ARG:HH12	2.42	0.42
1:2:453:C:H5''	8:G:93:LYS:HE3	2.02	0.42
1:2:1203:G:H2'	1:2:1204:A:C8	2.54	0.42
3:B:166:LYS:O	3:B:170:GLU:HG2	2.19	0.42
4:C:60:TRP:O	4:C:71:LYS:NZ	2.36	0.42
4:C:183:LYS:HA	4:C:195:LEU:O	2.20	0.42
5:D:126:ILE:HD12	5:D:188:ILE:HG12	2.02	0.42
6:E:100:ARG:HG2	6:E:102:ILE:HG12	2.00	0.42
8:G:176:ILE:HG22	8:G:179:LEU:HB2	2.01	0.42
9:H:177:TYR:O	9:H:181:THR:HB	2.20	0.42
17:P:18:ARG:CZ	20:S:90:VAL:HG12	2.50	0.42
20:S:38:ARG:HB3	20:S:39:ARG:H	1.70	0.42
20:S:104:ASP:HA	20:S:107:LEU:HG	2.01	0.42
34:g:11:LEU:HD11	34:g:43:TRP:HZ3	1.84	0.42
34:g:88:ARG:HA	34:g:99:ARG:HH12	1.84	0.42
1:2:1177:U:H2'	1:2:1178:U:C6	2.55	0.42
1:2:1652:G:H4'	7:F:81:ARG:HA	2.02	0.42
2:A:177:MET:O	2:A:181:GLU:HG2	2.19	0.42
3:B:179:ASN:HB3	3:B:183:GLU:HB2	2.00	0.42
18:Q:100:VAL:HG13	18:Q:101:ASP:H	1.85	0.42
22:U:88:LEU:HD23	22:U:88:LEU:HA	1.73	0.42
34:g:17:TRP:HB2	34:g:36:ARG:CG	2.50	0.42
1:2:195:C:H2'	1:2:196:C:C6	2.54	0.42
1:2:455:A:H2'	1:2:456:C:H6	1.78	0.42
1:2:1619:A:H3'	1:2:1619:A:N3	2.35	0.42
5:D:105:LEU:HD13	5:D:184:ILE:HD11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:61:ARG:HA	26:Y:61:ARG:HD2	1.90	0.42
34:g:175:LYS:HE3	34:g:184:LEU:HD13	2.02	0.42
35:h:2:ARG:HD3	35:h:5:TRP:NE1	2.34	0.42
1:2:823:U:C5	11:J:143:ASN:HB3	2.55	0.42
1:2:1609:C:N4	20:S:107:LEU:HD11	2.34	0.42
1:2:1613:G:H1'	1:2:1627:C:N4	2.35	0.42
3:B:168:MET:HG2	3:B:197:ILE:HG21	2.02	0.42
9:H:69:LEU:O	9:H:73:GLN:N	2.53	0.42
12:K:32:HIS:O	12:K:36:ALA:N	2.53	0.42
20:S:33:ILE:HG22	20:S:35:GLY:H	1.85	0.42
22:U:41:ARG:NH1	22:U:45:GLU:OE2	2.53	0.42
22:U:67:LYS:HE3	22:U:78:ASP:OD1	2.19	0.42
34:g:31:ILE:HB	34:g:43:TRP:HB2	2.01	0.42
34:g:280:LYS:NZ	34:g:280:LYS:HB3	2.34	0.42
1:2:1241:A:O5'	1:2:1267:C:O2'	2.38	0.42
1:2:1566:G:H1	21:T:97:LYS:NZ	2.17	0.42
2:A:76:VAL:HG12	2:A:123:VAL:HB	2.01	0.42
10:I:88:ASN:CG	10:I:205:ARG:HE	2.24	0.42
15:N:91:LEU:HB3	15:N:122:ILE:HG12	2.00	0.42
19:R:44:LYS:HE3	19:R:44:LYS:HB2	1.66	0.42
30:c:10:LYS:HE2	30:c:36:ASP:HB3	2.01	0.42
34:g:44:LYS:HE2	34:g:44:LYS:HB2	1.82	0.42
34:g:195:LEU:HD21	34:g:210:GLY:N	2.35	0.42
1:2:555:A:OP2	1:2:556:U:H5'	2.20	0.42
1:2:616:A:N3	32:e:12:VAL:HG21	2.35	0.42
1:2:666:U:H2'	1:2:667:U:C6	2.55	0.42
1:2:1192:U:H2'	1:2:1193:U:C6	2.55	0.42
1:2:1199:A:H2'	1:2:1200:A:C8	2.54	0.42
1:2:1607:A:H1'	20:S:130:ARG:HG2	2.01	0.42
1:2:1738:C:OP1	8:G:92:ARG:NH1	2.31	0.42
5:D:116:ARG:NH1	5:D:150:MET:HE2	2.34	0.42
7:F:44:LYS:H	7:F:44:LYS:HD3	1.85	0.42
12:K:3:MET:HA	12:K:4:PRO:HD3	1.92	0.42
18:Q:57:LEU:HD23	18:Q:112:LEU:HD23	2.00	0.42
20:S:130:ARG:HA	20:S:130:ARG:HD3	1.83	0.42
26:Y:83:LYS:HZ2	26:Y:83:LYS:HG3	1.73	0.42
29:b:31:TYR:CD1	29:b:81:ARG:HG3	2.55	0.42
31:d:54:LYS:HB3	31:d:54:LYS:HE3	1.91	0.42
33:f:96:LYS:HD2	33:f:96:LYS:N	2.35	0.42
34:g:164:ILE:HD12	34:g:177:TRP:O	2.20	0.42
1:2:67:C:N4	8:G:164:LYS:H	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:532:C:H2'	1:2:533:A:C8	2.55	0.41
1:2:1314:U:N3	1:2:1315:U:H1'	2.34	0.41
1:2:1546:G:H2'	1:2:1547:C:H6	1.85	0.41
1:2:1656:G:C2	1:2:1657:G:C8	3.08	0.41
3:B:144:LYS:HB2	3:B:208:HIS:HB2	2.01	0.41
6:E:143:ASP:O	6:E:143:ASP:OD1	2.38	0.41
7:F:59:LYS:HD3	7:F:62:ARG:HG3	2.01	0.41
7:F:184:SER:O	7:F:190:ILE:HD11	2.20	0.41
10:I:23:LYS:HE2	10:I:23:LYS:HB3	1.65	0.41
17:P:70:MET:HE3	17:P:70:MET:HB3	1.86	0.41
21:T:71:GLY:O	21:T:75:MET:N	2.38	0.41
25:X:107:ARG:HE	25:X:107:ARG:HB3	1.74	0.41
26:Y:45:ALA:HB1	26:Y:50:THR:O	2.20	0.41
29:b:34:ASP:OD1	29:b:82:LYS:NZ	2.52	0.41
1:2:929:G:N2	1:2:1104:G:H4'	2.35	0.41
1:2:1275:G:H4'	1:2:1323:U:N3	2.34	0.41
1:2:1545:A:H1'	18:Q:75:GLY:HA2	2.02	0.41
1:2:1568:C:H2'	1:2:1569:A:C4	2.55	0.41
4:C:125:LYS:HE2	4:C:141:VAL:HG11	2.01	0.41
4:C:132:ASP:OD1	4:C:136:HIS:HB2	2.20	0.41
4:C:187:ARG:HH22	4:C:190:SER:HA	1.84	0.41
14:M:44:LYS:HB3	14:M:46:GLN:HG3	2.02	0.41
18:Q:120:LEU:HD12	18:Q:121:VAL:HG13	2.01	0.41
23:V:37:ALA:HB1	23:V:46:PHE:CD1	2.55	0.41
26:Y:25:ILE:HD11	26:Y:73:GLY:HA3	2.00	0.41
1:2:39:A:H2'	1:2:40:A:O4'	2.21	0.41
1:2:216:C:N3	1:2:309:G:N1	2.45	0.41
1:2:1204:A:O2'	1:2:1700:C:OP2	2.29	0.41
1:2:1406:G:H2'	1:2:1407:U:C6	2.55	0.41
1:2:1540:G:H4'	1:2:1541:G:OP1	2.20	0.41
1:2:1706:G:H2'	1:2:1707:U:C6	2.53	0.41
7:F:158:ALA:HB1	7:F:173:LEU:HD12	2.02	0.41
8:G:57:ASP:O	8:G:107:SER:OG	2.29	0.41
10:I:157:LYS:HD2	10:I:157:LYS:HA	1.63	0.41
30:c:35:MET:H	30:c:35:MET:CE	2.30	0.41
34:g:88:ARG:HD2	34:g:100:ARG:NH1	2.35	0.41
1:2:1566:G:H22	21:T:97:LYS:NZ	2.18	0.41
1:2:1672:U:OP2	18:Q:17:LYS:HD3	2.21	0.41
1:2:1702:G:H2'	1:2:1703:C:O4'	2.21	0.41
3:B:164:ILE:O	3:B:168:MET:HG3	2.20	0.41
4:C:145:LYS:HA	4:C:145:LYS:HD3	1.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:52:ALA:O	5:D:90:LYS:HA	2.20	0.41
7:F:202:SER:C	7:F:203:ASN:HD22	2.28	0.41
8:G:14:LYS:HG2	8:G:16:ILE:HG23	2.02	0.41
12:K:47:LYS:HA	12:K:47:LYS:HD2	1.84	0.41
28:a:12:LYS:HB3	28:a:12:LYS:HE3	1.86	0.41
34:g:24:THR:OG1	34:g:74:ASP:O	2.21	0.41
1:2:51:U:H2'	1:2:52:G:H8	1.84	0.41
1:2:562:U:H2'	1:2:563:G:C8	2.55	0.41
1:2:563:G:H8	1:2:563:G:OP2	2.03	0.41
1:2:642:U:H4'	1:2:644:G:H4'	2.01	0.41
1:2:1070:A:H2'	1:2:1071:G:O4'	2.21	0.41
1:2:1287:A:N6	33:f:98:VAL:H	2.19	0.41
1:2:1387:G:H2'	1:2:1388:A:O4'	2.20	0.41
8:G:7:PHE:O	8:G:11:GLY:N	2.54	0.41
8:G:63:MET:HG2	8:G:99:GLY:O	2.20	0.41
8:G:85:ARG:O	8:G:87:ARG:NH1	2.54	0.41
9:H:148:LEU:HD21	24:W:48:GLY:HA2	2.02	0.41
12:K:36:ALA:O	12:K:38:LYS:HG2	2.21	0.41
28:a:78:VAL:HG12	28:a:84:VAL:HG22	2.02	0.41
34:g:111:VAL:HG23	34:g:122:SER:OG	2.20	0.41
34:g:188:HIS:HB3	34:g:219:TRP:CZ3	2.55	0.41
1:2:85:A:H2'	1:2:86:C:H6	1.84	0.41
1:2:948:C:H2'	1:2:949:G:C8	2.56	0.41
1:2:1258:A:C6	1:2:1659:U:H2'	2.55	0.41
1:2:1507:G:C6	33:f:83:LYS:HB2	2.55	0.41
1:2:1676:U:OP1	7:F:74:ASN:HB3	2.21	0.41
1:2:1717:C:H2'	1:2:1718:G:O4'	2.20	0.41
3:B:183:GLU:O	3:B:187:LYS:HG2	2.21	0.41
7:F:103:LEU:HD11	27:Z:67:LEU:HB2	2.02	0.41
10:I:143:LYS:H	10:I:143:LYS:CD	2.33	0.41
10:I:161:LEU:O	10:I:165:GLN:HG3	2.20	0.41
17:P:93:MET:HE1	17:P:95:GLY:HA2	2.03	0.41
18:Q:116:ASP:HB3	18:Q:119:LEU:HD22	2.01	0.41
27:Z:102:LYS:HA	27:Z:106:GLN:O	2.19	0.41
28:a:45:VAL:HG11	28:a:53:ILE:HG13	2.02	0.41
1:2:448:A:H5''	10:I:25:ARG:HA	2.02	0.41
1:2:1003:U:O2'	3:B:165:ARG:HD3	2.20	0.41
5:D:117:ARG:NE	36:n:169:GLU:HG2	2.35	0.41
7:F:99:ILE:HA	7:F:102:LEU:HG	2.03	0.41
19:R:18:GLU:HB2	19:R:69:ILE:HD11	2.02	0.41
19:R:95:ILE:HD13	19:R:95:ILE:HA	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:121:ARG:CZ	21:T:123:LEU:HB2	2.50	0.41
23:V:71:ARG:HH11	23:V:71:ARG:HB3	1.86	0.41
27:Z:88:LEU:HA	27:Z:91:LEU:HD22	2.03	0.41
30:c:10:LYS:HG3	30:c:34:PHE:HD2	1.86	0.41
1:2:581:U:OP1	11:J:133:ARG:NH1	2.40	0.41
1:2:1271:C:N3	31:d:3:HIS:HD2	2.19	0.41
3:B:129:THR:OG1	3:B:133:TYR:HB2	2.21	0.41
4:C:106:VAL:HG22	4:C:128:VAL:HG22	2.02	0.41
6:E:162:ILE:HD13	6:E:162:ILE:HA	1.89	0.41
20:S:3:LEU:N	27:Z:50:PHE:HB2	2.36	0.41
21:T:57:ALA:HB1	21:T:107:LEU:HD21	2.02	0.41
34:g:88:ARG:HD2	34:g:100:ARG:CZ	2.51	0.41
1:2:182:C:H4'	1:2:183:G:O5'	2.21	0.41
1:2:433:A:H2'	1:2:434:G:C8	2.56	0.41
1:2:568:C:C4	1:2:582:U:O4	2.73	0.41
1:2:598:G:O2'	1:2:605:A:N1	2.42	0.41
1:2:687:C:OP1	24:W:32:LYS:HD2	2.21	0.41
1:2:885:U:H4'	1:2:886:A:C2	2.56	0.41
1:2:904:A:H5''	1:2:905:C:C5	2.56	0.41
1:2:913:A:H61	9:H:119:SER:HB2	1.86	0.41
1:2:1397:U:H4'	1:2:1398:G:H5''	2.02	0.41
1:2:1399:C:H2'	1:2:1400:U:H6	1.84	0.41
1:2:1399:C:H2'	1:2:1400:U:C6	2.55	0.41
1:2:1535:U:H5'	1:2:1536:G:C8	2.55	0.41
1:2:1771:G:HO2'	1:2:1772:C:P	2.40	0.41
1:2:1868:U:N3	28:a:100:ARG:HB2	2.35	0.41
3:B:131:ASP:OD1	3:B:131:ASP:N	2.45	0.41
4:C:178:HIS:ND1	4:C:221:ASP:OD2	2.41	0.41
6:E:184:THR:C	6:E:189:LEU:HD13	2.46	0.41
8:G:21:GLU:OE1	8:G:28:TYR:OH	2.28	0.41
8:G:217:MET:HG2	8:G:217:MET:H	1.72	0.41
9:H:134:VAL:HG12	9:H:173:PHE:CD2	2.56	0.41
9:H:191:GLU:HG3	9:H:192:PHE:N	2.36	0.41
11:J:111:GLN:NE2	11:J:127:ARG:HB2	2.36	0.41
12:K:8:ARG:NH2	12:K:83:LEU:HD13	2.35	0.41
14:M:15:ASN:O	14:M:19:GLN:HG3	2.21	0.41
16:O:27:VAL:HG13	16:O:90:ILE:HA	2.03	0.41
18:Q:102:GLU:HB2	34:g:55:PRO:O	2.20	0.41
22:U:86:LYS:HA	22:U:86:LYS:HD2	1.76	0.41
25:X:40:PRO:CB	25:X:81:ILE:HD11	2.50	0.41
26:Y:5:VAL:HA	26:Y:28:LEU:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:a:46:GLU:O	28:a:50:VAL:HG23	2.19	0.41
29:b:56:CYS:N	29:b:61:THR:O	2.54	0.41
1:2:19:A:H2'	1:2:20:G:O4'	2.21	0.41
1:2:301:A:N3	10:I:73:THR:OG1	2.44	0.41
1:2:1147:C:OP1	28:a:6:ARG:NH1	2.46	0.41
1:2:1288:U:C5	33:f:94:LYS:HA	2.56	0.41
1:2:1298:G:C2'	1:2:1301:A:H62	2.33	0.41
1:2:1372:U:H5''	1:2:1386:A:N3	2.37	0.41
1:2:1628:C:H5''	21:T:38:LYS:HD3	2.03	0.41
1:2:1643:U:H6	1:2:1643:U:H2'	1.76	0.41
1:2:1704:C:H2'	1:2:1705:C:C6	2.56	0.41
2:A:47:TYR:HB2	2:A:150:THR:HG21	2.03	0.41
6:E:104:ASP:OD1	6:E:110:ALA:HB2	2.21	0.41
7:F:119:SER:C	7:F:193:LYS:HD3	2.46	0.41
10:I:154:LYS:H	10:I:154:LYS:HG2	1.70	0.41
13:L:61:PRO:HG2	13:L:62:PHE:CE2	2.56	0.41
17:P:127:LYS:HE2	17:P:127:LYS:HB2	1.85	0.41
21:T:143:LYS:HE3	21:T:143:LYS:HB2	1.89	0.41
24:W:28:ARG:HB3	24:W:60:LYS:HG2	2.03	0.41
27:Z:100:VAL:HB	27:Z:108:ILE:HB	2.03	0.41
30:c:10:LYS:HD2	30:c:10:LYS:HA	1.81	0.41
1:2:160:U:O2'	1:2:162:C:OP2	2.26	0.40
1:2:180:G:H4'	1:2:181:A:OP1	2.21	0.40
1:2:380:G:N1	1:2:383:G:OP2	2.44	0.40
1:2:499:G:C2	1:2:501:C:H1'	2.56	0.40
1:2:912:C:C2	1:2:914:U:H1'	2.56	0.40
1:2:1047:C:H2'	1:2:1048:G:O4'	2.20	0.40
2:A:25:LEU:HD12	2:A:46:ILE:HG21	2.01	0.40
3:B:28:LYS:HZ2	3:B:28:LYS:HG2	1.72	0.40
17:P:21:ASP:O	17:P:25:LEU:N	2.48	0.40
18:Q:90:LYS:HA	18:Q:93:VAL:HG12	2.03	0.40
34:g:89:LEU:HD12	34:g:89:LEU:O	2.21	0.40
34:g:292:SER:HB2	34:g:297:THR:HB	2.03	0.40
1:2:496:C:H2'	1:2:497:C:H6	1.86	0.40
1:2:545:A:H5'	1:2:546:G:H1	1.87	0.40
1:2:634:A:H2'	1:2:635:G:C8	2.57	0.40
1:2:1348:G:C8	1:2:1349:G:C8	3.09	0.40
1:2:1408:U:H4'	18:Q:8:GLN:N	2.36	0.40
1:2:1545:A:OP1	18:Q:73:LYS:HA	2.21	0.40
1:2:1599:U:O4	7:F:166:ILE:HA	2.21	0.40
1:2:1748:G:H2'	1:2:1749:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:86:ALA:HB1	2:A:175:TRP:HB2	2.03	0.40
13:L:16:ILE:HD13	13:L:16:ILE:HA	1.93	0.40
13:L:35:ARG:NH1	13:L:55:TYR:O	2.43	0.40
16:O:69:SER:O	16:O:110:PRO:HG2	2.21	0.40
18:Q:33:LYS:HE3	18:Q:33:LYS:HB3	1.86	0.40
19:R:17:ILE:HG13	19:R:58:MET:HE1	2.03	0.40
19:R:20:TYR:CG	19:R:38:ILE:HD12	2.56	0.40
20:S:42:HIS:CD2	21:T:46:ALA:HB1	2.56	0.40
36:n:174:LEU:HD21	36:n:187:LEU:CD2	2.51	0.40
1:2:529:A:H2'	1:2:530:U:C6	2.56	0.40
1:2:871:U:O2'	1:2:872:A:H4'	2.21	0.40
1:2:918:U:H2'	1:2:919:A:O4'	2.21	0.40
1:2:1005:G:H2'	1:2:1006:C:H6	1.87	0.40
1:2:1822:A:H2'	1:2:1823:A:C8	2.57	0.40
5:D:58:VAL:O	5:D:66:ILE:HG23	2.21	0.40
5:D:72:VAL:HA	12:K:20:VAL:HG11	2.04	0.40
8:G:23:LYS:HG2	8:G:40:ALA:O	2.21	0.40
10:I:87:ASN:HB3	10:I:90:LEU:HG	2.03	0.40
20:S:86:ARG:O	20:S:86:ARG:HG2	2.21	0.40
21:T:111:LYS:HD3	21:T:111:LYS:HA	1.87	0.40
33:f:107:LYS:HB3	33:f:113:LYS:O	2.21	0.40
33:f:114:ILE:HD12	33:f:114:ILE:H	1.84	0.40
34:g:107:ASP:O	34:g:124:SER:OG	2.34	0.40
1:2:1298:G:H5'	17:P:78:THR:HA	2.03	0.40
1:2:1599:U:C4	7:F:166:ILE:HA	2.56	0.40
6:E:10:LYS:HD3	6:E:10:LYS:HA	1.89	0.40
6:E:133:THR:C	6:E:134:LYS:HG2	2.46	0.40
8:G:44:GLU:OE1	8:G:44:GLU:N	2.44	0.40
8:G:168:LYS:H	8:G:168:LYS:HG2	1.64	0.40
9:H:73:GLN:HA	9:H:76:GLN:HB2	2.03	0.40
14:M:56:CYS:SG	14:M:57:ASP:N	2.95	0.40
1:2:955:A:C8	1:2:969:U:C4	3.10	0.40
1:2:1391:C:H2'	1:2:1392:U:O4'	2.22	0.40
1:2:1509:U:H4'	1:2:1511:U:C4	2.56	0.40
1:2:1689:C:H2'	1:2:1690:U:C6	2.57	0.40
2:A:132:GLN:HB3	2:A:133:PRO:HD3	2.04	0.40
7:F:175:ASP:OD1	7:F:176:GLU:N	2.54	0.40
9:H:36:LEU:HD12	9:H:36:LEU:O	2.22	0.40
17:P:32:GLN:HA	17:P:35:GLN:HG2	2.04	0.40
30:c:67:ARG:HD2	30:c:68:LEU:H	1.86	0.40
34:g:21:ILE:HG13	34:g:288:SER:OG	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:244:ASN:OD1	34:g:245:ARG:NE	2.43	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	211/295 (72%)	204 (97%)	6 (3%)	1 (0%)	25	40
3	B	211/264 (80%)	209 (99%)	2 (1%)	0	100	100
4	C	216/293 (74%)	211 (98%)	5 (2%)	0	100	100
5	D	223/243 (92%)	218 (98%)	5 (2%)	0	100	100
6	E	260/263 (99%)	254 (98%)	6 (2%)	0	100	100
7	F	187/204 (92%)	168 (90%)	17 (9%)	2 (1%)	12	19
8	G	228/249 (92%)	221 (97%)	7 (3%)	0	100	100
9	H	184/194 (95%)	177 (96%)	7 (4%)	0	100	100
10	I	203/208 (98%)	198 (98%)	5 (2%)	0	100	100
11	J	178/194 (92%)	168 (94%)	9 (5%)	1 (1%)	22	35
12	K	95/165 (58%)	88 (93%)	7 (7%)	0	100	100
13	L	149/158 (94%)	144 (97%)	5 (3%)	0	100	100
14	M	119/132 (90%)	108 (91%)	9 (8%)	2 (2%)	7	12
15	N	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
16	O	133/151 (88%)	127 (96%)	6 (4%)	0	100	100
17	P	124/145 (86%)	110 (89%)	13 (10%)	1 (1%)	16	28
18	Q	136/146 (93%)	123 (90%)	12 (9%)	1 (1%)	19	31
19	R	130/135 (96%)	129 (99%)	1 (1%)	0	100	100
20	S	141/152 (93%)	119 (84%)	21 (15%)	1 (1%)	19	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	T	142/145 (98%)	130 (92%)	12 (8%)	0	100	100
22	U	99/119 (83%)	93 (94%)	6 (6%)	0	100	100
23	V	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
24	W	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
25	X	139/143 (97%)	135 (97%)	3 (2%)	1 (1%)	19	31
26	Y	122/130 (94%)	119 (98%)	3 (2%)	0	100	100
27	Z	70/125 (56%)	64 (91%)	6 (9%)	0	100	100
28	a	97/101 (96%)	96 (99%)	0	1 (1%)	13	21
29	b	80/82 (98%)	78 (98%)	1 (1%)	1 (1%)	10	16
30	c	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
31	d	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
32	e	54/56 (96%)	48 (89%)	6 (11%)	0	100	100
33	f	72/74 (97%)	63 (88%)	9 (12%)	0	100	100
34	g	312/315 (99%)	291 (93%)	20 (6%)	1 (0%)	37	53
35	h	20/25 (80%)	20 (100%)	0	0	100	100
36	n	25/196 (13%)	25 (100%)	0	0	100	100
All	All	4827/5583 (86%)	4596 (95%)	218 (4%)	13 (0%)	38	53

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	189	ILE
7	F	33	ILE
18	Q	13	PHE
34	g	314	ILE
14	M	110	VAL
28	a	63	VAL
14	M	95	ASP
29	b	3	LEU
7	F	79	HIS
11	J	160	SER
20	S	96	SER
17	P	116	LEU
25	X	86	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	179/243 (74%)	172 (96%)	7 (4%)	27	45
3	B	194/231 (84%)	187 (96%)	7 (4%)	30	48
4	C	184/225 (82%)	180 (98%)	4 (2%)	47	68
5	D	189/202 (94%)	181 (96%)	8 (4%)	25	42
6	E	224/225 (100%)	217 (97%)	7 (3%)	35	55
7	F	159/170 (94%)	151 (95%)	8 (5%)	20	35
8	G	200/218 (92%)	195 (98%)	5 (2%)	42	64
9	H	167/174 (96%)	163 (98%)	4 (2%)	44	65
10	I	178/180 (99%)	172 (97%)	6 (3%)	32	51
11	J	160/168 (95%)	160 (100%)	0	100	100
12	K	88/136 (65%)	88 (100%)	0	100	100
13	L	135/142 (95%)	127 (94%)	8 (6%)	16	28
14	M	102/108 (94%)	102 (100%)	0	100	100
15	N	130/131 (99%)	126 (97%)	4 (3%)	35	55
16	O	105/119 (88%)	99 (94%)	6 (6%)	17	29
17	P	112/130 (86%)	108 (96%)	4 (4%)	30	48
18	Q	114/121 (94%)	105 (92%)	9 (8%)	10	17
19	R	119/122 (98%)	115 (97%)	4 (3%)	32	51
20	S	124/132 (94%)	119 (96%)	5 (4%)	27	44
21	T	114/115 (99%)	112 (98%)	2 (2%)	54	73
22	U	93/107 (87%)	91 (98%)	2 (2%)	47	68
23	V	66/67 (98%)	65 (98%)	1 (2%)	60	77
24	W	112/113 (99%)	109 (97%)	3 (3%)	40	61
25	X	113/115 (98%)	106 (94%)	7 (6%)	15	26
26	Y	108/112 (96%)	105 (97%)	3 (3%)	38	60
27	Z	64/103 (62%)	60 (94%)	4 (6%)	15	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	a	87/89 (98%)	83 (95%)	4 (5%)	23	38
29	b	74/74 (100%)	70 (95%)	4 (5%)	18	32
30	c	55/55 (100%)	55 (100%)	0	100	100
31	d	48/48 (100%)	48 (100%)	0	100	100
32	e	45/45 (100%)	39 (87%)	6 (13%)	3	4
33	f	67/67 (100%)	67 (100%)	0	100	100
34	g	272/273 (100%)	257 (94%)	15 (6%)	18	31
35	h	21/24 (88%)	21 (100%)	0	100	100
36	n	24/162 (15%)	24 (100%)	0	100	100
All	All	4226/4746 (89%)	4079 (96%)	147 (4%)	33	50

All (147) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	28	THR
2	A	31	ASP
2	A	46	ILE
2	A	75	SER
2	A	104	THR
2	A	188	THR
2	A	189	ILE
3	B	27	LYS
3	B	29	ASP
3	B	59	SER
3	B	104	ASP
3	B	108	ASP
3	B	195	LYS
3	B	208	HIS
4	C	190	SER
4	C	206	SER
4	C	213	LEU
4	C	271	ASP
5	D	26	THR
5	D	70	THR
5	D	93	THR
5	D	120	TYR
5	D	124	ARG
5	D	175	VAL
5	D	185	LYS

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Mol	Chain	Res	Type
5	D	220	THR
6	E	59	ASP
6	E	105	THR
6	E	106	LYS
6	E	126	VAL
6	E	177	THR
6	E	199	GLU
6	E	236	ILE
7	F	69	VAL
7	F	77	MET
7	F	103	LEU
7	F	107	ASN
7	F	111	VAL
7	F	122	ARG
7	F	125	SER
7	F	177	LEU
8	G	26	THR
8	G	125	THR
8	G	129	VAL
8	G	157	VAL
8	G	171	THR
9	H	69	LEU
9	H	85	LYS
9	H	172	THR
9	H	180	LEU
10	I	29	LEU
10	I	119	LEU
10	I	130	THR
10	I	137	LEU
10	I	155	ASN
10	I	158	ILE
13	L	46	THR
13	L	52	GLU
13	L	67	SER
13	L	78	THR
13	L	80	MET
13	L	85	THR
13	L	124	ASP
13	L	146	THR
15	N	9	LYS
15	N	63	VAL
15	N	140	LYS

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Mol	Chain	Res	Type
15	N	145	THR
16	O	26	ASN
16	O	27	VAL
16	O	57	THR
16	O	83	GLN
16	O	93	LEU
16	O	129	ILE
17	P	66	GLU
17	P	76	VAL
17	P	80	LEU
17	P	94	VAL
18	Q	10	VAL
18	Q	34	VAL
18	Q	66	VAL
18	Q	68	ILE
18	Q	70	VAL
18	Q	72	VAL
18	Q	100	VAL
18	Q	118	THR
18	Q	119	LEU
19	R	7	LYS
19	R	55	THR
19	R	98	VAL
19	R	102	THR
20	S	4	VAL
20	S	44	VAL
20	S	64	VAL
20	S	111	LEU
20	S	120	HIS
21	T	64	LEU
21	T	122	LYS
22	U	68	THR
22	U	115	THR
23	V	39	VAL
24	W	26	LEU
24	W	30	CYS
24	W	80	ASP
25	X	15	SER
25	X	25	LYS
25	X	72	VAL
25	X	81	ILE
25	X	100	VAL

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Mol	Chain	Res	Type
25	X	115	ILE
25	X	128	VAL
26	Y	50	THR
26	Y	101	LYS
26	Y	117	VAL
27	Z	82	SER
27	Z	91	LEU
27	Z	101	SER
27	Z	107	VAL
28	a	30	VAL
28	a	63	VAL
28	a	69	VAL
28	a	83	VAL
29	b	43	ILE
29	b	44	THR
29	b	57	VAL
29	b	73	LEU
32	e	6	LEU
32	e	24	LYS
32	e	25	LYS
32	e	29	THR
32	e	45	VAL
32	e	46	VAL
34	g	14	HIS
34	g	18	VAL
34	g	45	LEU
34	g	82	SER
34	g	86	THR
34	g	156	PHE
34	g	175	LYS
34	g	196	ASN
34	g	227	LEU
34	g	245	ARG
34	g	265	ILE
34	g	287	THR
34	g	308	ARG
34	g	311	GLN
34	g	312	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	50	ASN
2	A	84	GLN
2	A	110	ASN
2	A	141	ASN
3	B	75	GLN
3	B	101	HIS
3	B	149	GLN
6	E	138	HIS
6	E	142	HIS
6	E	214	ASN
6	E	216	ASN
7	F	165	ASN
9	H	73	GLN
10	I	52	ASN
10	I	111	GLN
11	J	143	ASN
12	K	7	ASN
12	K	50	GLN
12	K	84	HIS
14	M	75	ASN
15	N	13	GLN
15	N	62	GLN
17	P	98	ASN
17	P	103	ASN
18	Q	97	GLN
19	R	56	HIS
20	S	10	GLN
20	S	72	GLN
21	T	105	GLN
22	U	100	GLN
26	Y	89	HIS
27	Z	103	HIS
29	b	65	GLN
30	c	7	GLN
31	d	3	HIS
31	d	4	GLN
34	g	56	GLN
34	g	188	HIS
34	g	285	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1662/1869 (88%)	499 (30%)	14 (0%)

All (499) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	4	C
1	2	17	C
1	2	33	G
1	2	44	U
1	2	45	A
1	2	46	A
1	2	56	G
1	2	67	C
1	2	68	A
1	2	71	G
1	2	73	C
1	2	75	G
1	2	99	A
1	2	102	A
1	2	103	A
1	2	113	G
1	2	114	G
1	2	115	U
1	2	126	G
1	2	128	U
1	2	129	C
1	2	130	G
1	2	142	C
1	2	143	U
1	2	149	A
1	2	155	G
1	2	158	A
1	2	160	U
1	2	163	U
1	2	168	C
1	2	173	A
1	2	181	A
1	2	182	C
1	2	185	G
1	2	189	U
1	2	191	A
1	2	195	C
1	2	198	U

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Mol	Chain	Res	Type
1	2	199	C
1	2	201	C
1	2	202	G
1	2	203	G
1	2	204	G
1	2	206	G
1	2	208	G
1	2	211	G
1	2	225	G
1	2	288	G
1	2	293	C
1	2	305	U
1	2	306	C
1	2	307	G
1	2	308	G
1	2	309	G
1	2	310	C
1	2	312	G
1	2	315	C
1	2	319	C
1	2	320	G
1	2	333	G
1	2	362	C
1	2	364	A
1	2	369	C
1	2	370	G
1	2	377	G
1	2	385	G
1	2	386	C
1	2	400	C
1	2	408	A
1	2	409	C
1	2	438	G
1	2	448	A
1	2	450	C
1	2	464	A
1	2	465	A
1	2	466	G
1	2	467	G
1	2	471	G
1	2	472	C
1	2	473	A

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Mol	Chain	Res	Type
1	2	474	G
1	2	476	A
1	2	482	G
1	2	487	U
1	2	492	C
1	2	525	A
1	2	535	G
1	2	538	U
1	2	539	C
1	2	540	U
1	2	541	U
1	2	542	U
1	2	543	C
1	2	544	G
1	2	545	A
1	2	547	G
1	2	548	C
1	2	549	C
1	2	553	U
1	2	554	A
1	2	556	U
1	2	559	G
1	2	560	A
1	2	563	G
1	2	574	A
1	2	576	A
1	2	582	U
1	2	587	A
1	2	589	G
1	2	590	A
1	2	591	U
1	2	592	C
1	2	594	A
1	2	598	G
1	2	605	A
1	2	607	U
1	2	608	C
1	2	614	C
1	2	617	G
1	2	627	U
1	2	629	A
1	2	631	U

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Mol	Chain	Res	Type
1	2	639	C
1	2	640	A
1	2	643	A
1	2	644	G
1	2	655	A
1	2	657	U
1	2	660	C
1	2	666	U
1	2	668	A
1	2	669	A
1	2	670	A
1	2	671	A
1	2	672	A
1	2	673	G
1	2	687	C
1	2	688	U
1	2	748	C
1	2	749	U
1	2	750	C
1	2	793	G
1	2	794	A
1	2	795	A
1	2	796	G
1	2	797	C
1	2	798	G
1	2	799	U
1	2	800	U
1	2	806	U
1	2	811	A
1	2	821	G
1	2	822	U
1	2	823	U
1	2	824	C
1	2	830	A
1	2	847	A
1	2	869	A
1	2	870	A
1	2	871	U
1	2	872	A
1	2	873	G
1	2	880	G
1	2	882	U

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Mol	Chain	Res	Type
1	2	885	U
1	2	886	A
1	2	888	U
1	2	889	U
1	2	890	U
1	2	891	G
1	2	892	U
1	2	893	U
1	2	894	G
1	2	895	G
1	2	896	U
1	2	897	U
1	2	898	U
1	2	899	U
1	2	901	G
1	2	902	G
1	2	908	A
1	2	909	G
1	2	912	C
1	2	913	A
1	2	914	U
1	2	919	A
1	2	920	A
1	2	922	A
1	2	930	C
1	2	933	G
1	2	943	U
1	2	955	A
1	2	961	G
1	2	962	A
1	2	963	A
1	2	971	G
1	2	978	G
1	2	990	A
1	2	992	A
1	2	1001	A
1	2	1017	U
1	2	1023	A
1	2	1027	A
1	2	1028	A
1	2	1049	A
1	2	1055	A

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Mol	Chain	Res	Type
1	2	1060	A
1	2	1061	U
1	2	1062	A
1	2	1067	C
1	2	1080	A
1	2	1083	A
1	2	1085	C
1	2	1088	U
1	2	1109	C
1	2	1114	U
1	2	1115	U
1	2	1116	C
1	2	1117	C
1	2	1118	C
1	2	1119	A
1	2	1123	C
1	2	1126	G
1	2	1133	A
1	2	1153	C
1	2	1154	U
1	2	1157	G
1	2	1168	G
1	2	1171	G
1	2	1195	A
1	2	1207	G
1	2	1215	C
1	2	1216	C
1	2	1217	A
1	2	1220	A
1	2	1224	G
1	2	1226	G
1	2	1227	G
1	2	1228	A
1	2	1229	G
1	2	1231	C
1	2	1232	U
1	2	1235	G
1	2	1238	U
1	2	1242	U
1	2	1244	U
1	2	1245	G
1	2	1247	C

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Mol	Chain	Res	Type
1	2	1248	U
1	2	1249	C
1	2	1251	A
1	2	1253	A
1	2	1255	G
1	2	1256	G
1	2	1257	G
1	2	1258	A
1	2	1259	A
1	2	1261	C
1	2	1264	C
1	2	1265	A
1	2	1266	C
1	2	1267	C
1	2	1269	G
1	2	1270	G
1	2	1271	C
1	2	1272	C
1	2	1273	C
1	2	1274	G
1	2	1275	G
1	2	1276	A
1	2	1277	C
1	2	1278	A
1	2	1279	C
1	2	1280	G
1	2	1282	A
1	2	1283	C
1	2	1284	A
1	2	1285	G
1	2	1286	G
1	2	1289	U
1	2	1290	G
1	2	1294	G
1	2	1295	A
1	2	1296	U
1	2	1297	U
1	2	1298	G
1	2	1299	A
1	2	1300	U
1	2	1302	G
1	2	1303	C

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Mol	Chain	Res	Type
1	2	1307	U
1	2	1309	C
1	2	1310	U
1	2	1312	G
1	2	1313	A
1	2	1315	U
1	2	1316	C
1	2	1317	C
1	2	1318	G
1	2	1320	G
1	2	1321	G
1	2	1324	G
1	2	1325	G
1	2	1327	G
1	2	1330	G
1	2	1331	C
1	2	1332	A
1	2	1371	U
1	2	1372	U
1	2	1378	A
1	2	1390	U
1	2	1393	G
1	2	1396	A
1	2	1397	U
1	2	1398	G
1	2	1401	A
1	2	1402	A
1	2	1403	C
1	2	1404	U
1	2	1409	A
1	2	1410	C
1	2	1412	C
1	2	1413	G
1	2	1414	A
1	2	1415	C
1	2	1416	C
1	2	1425	G
1	2	1426	U
1	2	1427	C
1	2	1428	G
1	2	1429	G
1	2	1430	C

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Mol	Chain	Res	Type
1	2	1431	G
1	2	1432	U
1	2	1439	A
1	2	1440	C
1	2	1441	U
1	2	1442	U
1	2	1443	C
1	2	1444	U
1	2	1446	A
1	2	1447	G
1	2	1454	A
1	2	1462	U
1	2	1463	U
1	2	1464	C
1	2	1472	C
1	2	1476	A
1	2	1477	U
1	2	1487	A
1	2	1489	A
1	2	1490	G
1	2	1494	U
1	2	1498	A
1	2	1499	U
1	2	1501	C
1	2	1504	U
1	2	1505	U
1	2	1507	G
1	2	1508	A
1	2	1509	U
1	2	1510	G
1	2	1511	U
1	2	1514	G
1	2	1516	G
1	2	1517	G
1	2	1520	G
1	2	1522	A
1	2	1532	C
1	2	1533	A
1	2	1534	C
1	2	1535	U
1	2	1536	G
1	2	1537	A

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Mol	Chain	Res	Type
1	2	1539	U
1	2	1540	G
1	2	1541	G
1	2	1542	C
1	2	1545	A
1	2	1551	U
1	2	1552	G
1	2	1557	C
1	2	1558	C
1	2	1560	U
1	2	1563	G
1	2	1566	G
1	2	1569	A
1	2	1575	G
1	2	1579	A
1	2	1580	A
1	2	1581	C
1	2	1585	U
1	2	1586	U
1	2	1588	A
1	2	1589	A
1	2	1590	C
1	2	1591	C
1	2	1594	A
1	2	1595	U
1	2	1600	G
1	2	1601	A
1	2	1602	U
1	2	1603	G
1	2	1606	G
1	2	1607	A
1	2	1608	U
1	2	1610	G
1	2	1613	G
1	2	1614	A
1	2	1616	U
1	2	1617	G
1	2	1618	C
1	2	1619	A
1	2	1620	A
1	2	1621	U
1	2	1622	U

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Mol	Chain	Res	Type
1	2	1623	A
1	2	1624	U
1	2	1626	C
1	2	1627	C
1	2	1631	U
1	2	1632	G
1	2	1633	A
1	2	1634	A
1	2	1637	A
1	2	1639	G
1	2	1640	A
1	2	1641	A
1	2	1647	A
1	2	1648	G
1	2	1653	U
1	2	1654	G
1	2	1659	U
1	2	1660	C
1	2	1664	A
1	2	1665	G
1	2	1671	G
1	2	1672	U
1	2	1675	A
1	2	1676	U
1	2	1678	A
1	2	1680	G
1	2	1683	C
1	2	1686	G
1	2	1695	A
1	2	1699	A
1	2	1710	C
1	2	1719	A
1	2	1720	U
1	2	1721	U
1	2	1722	G
1	2	1727	G
1	2	1728	U
1	2	1744	G
1	2	1749	G
1	2	1752	C
1	2	1753	C
1	2	1754	G

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Mol	Chain	Res	Type
1	2	1755	C
1	2	1756	C
1	2	1759	G
1	2	1760	G
1	2	1772	C
1	2	1773	C
1	2	1774	C
1	2	1775	U
1	2	1777	G
1	2	1779	G
1	2	1780	G
1	2	1782	G
1	2	1783	C
1	2	1784	G
1	2	1800	A
1	2	1801	A
1	2	1805	G
1	2	1806	A
1	2	1807	C
1	2	1808	U
1	2	1809	A
1	2	1812	U
1	2	1813	A
1	2	1814	G
1	2	1815	A
1	2	1824	A
1	2	1826	G
1	2	1829	G
1	2	1831	A
1	2	1835	A
1	2	1838	U
1	2	1839	U
1	2	1850	A
1	2	1851	A
1	2	1852	C
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1864	U
1	2	1865	C
1	2	1869	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	102	A
1	2	180	G
1	2	314	U
1	2	332	G
1	2	465	A
1	2	868	G
1	2	901	G
1	2	1425	G
1	2	1540	G
1	2	1674	G
1	2	1675	A
1	2	1771	G
1	2	1806	A
1	2	1812	U

## 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](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

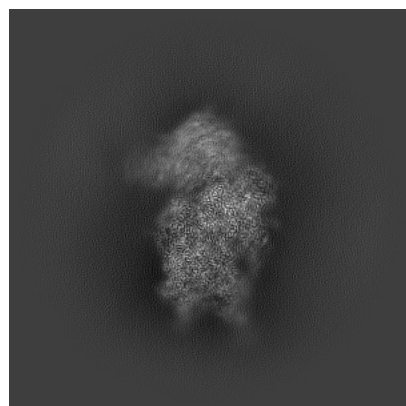
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62451. These allow visual inspection of the internal detail of the map and identification of artifacts.

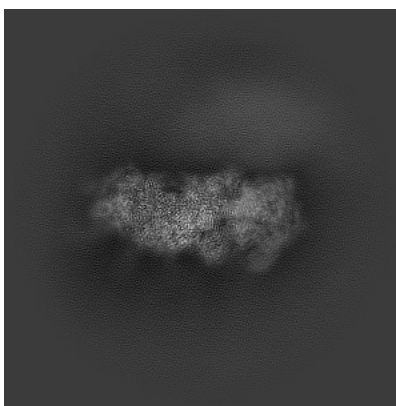
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

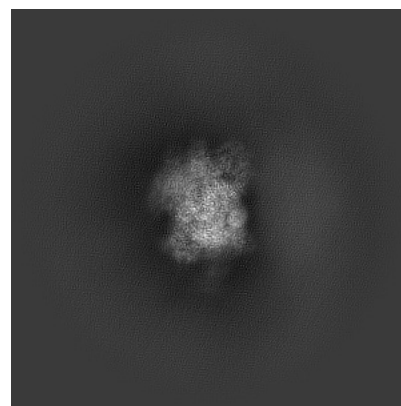
#### 6.1.1 Primary map



X

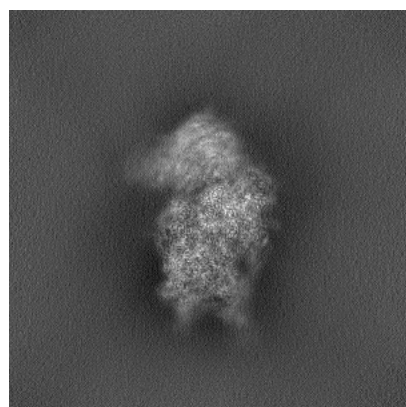


Y

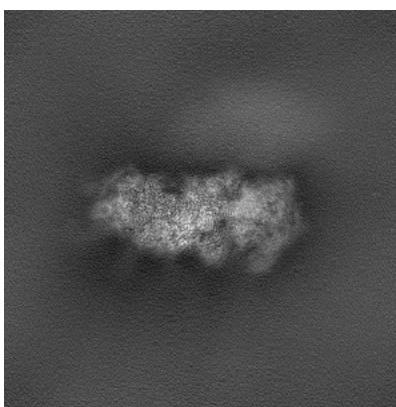


Z

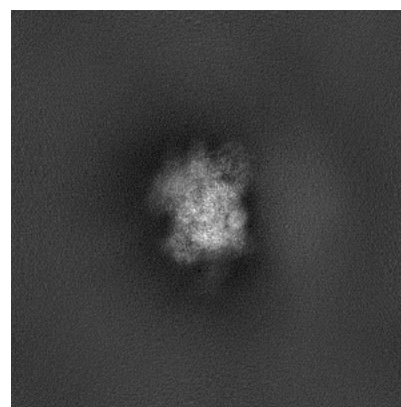
#### 6.1.2 Raw map



X



Y

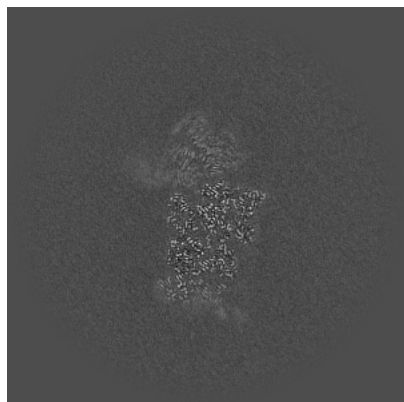


Z

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

## 6.2 Central slices [i](#)

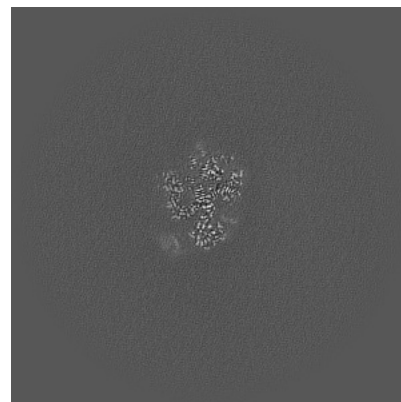
### 6.2.1 Primary map



X Index: 256

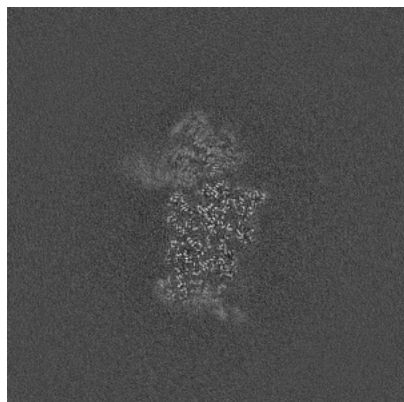


Y Index: 256

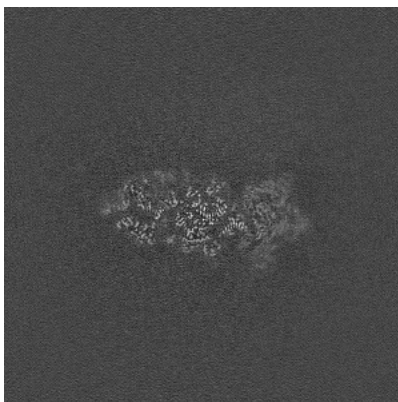


Z Index: 256

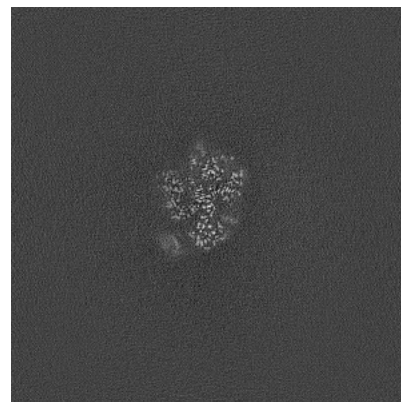
### 6.2.2 Raw map



X Index: 256



Y Index: 256

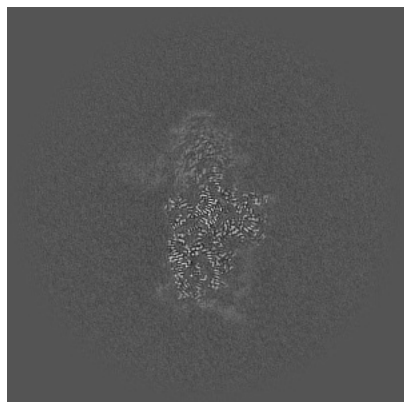


Z Index: 256

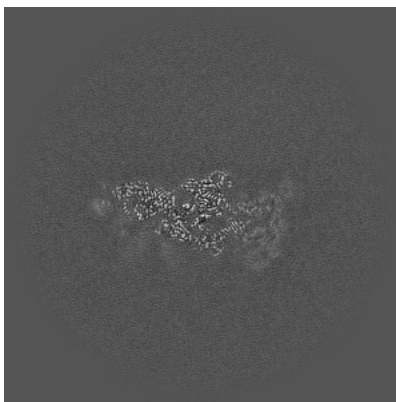
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

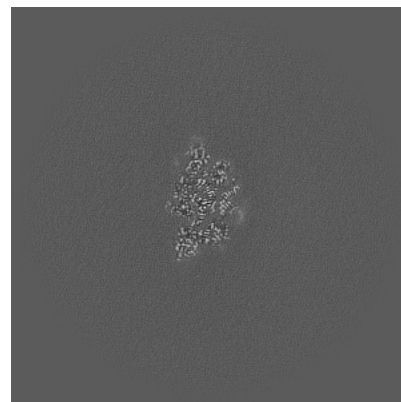
### 6.3.1 Primary map



X Index: 248



Y Index: 275

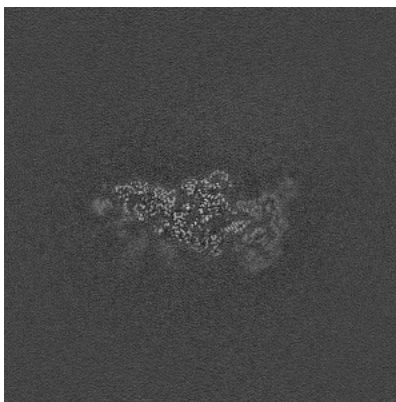


Z Index: 235

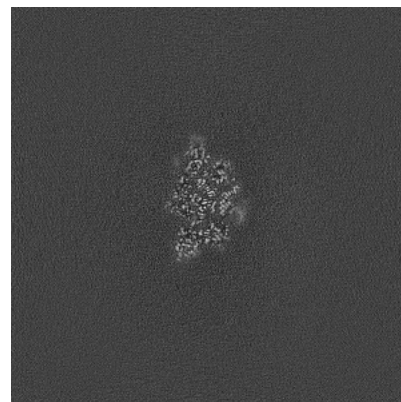
### 6.3.2 Raw map



X Index: 251



Y Index: 274

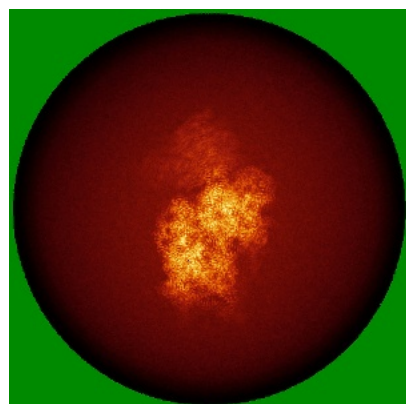


Z Index: 235

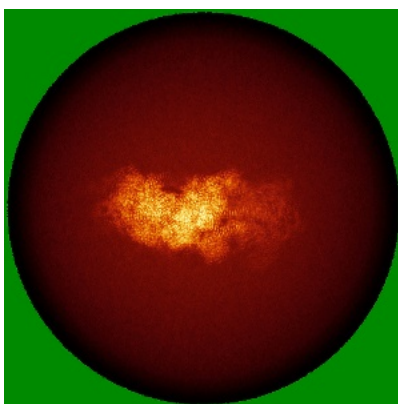
The images above show the largest variance slices of the map in three orthogonal directions.

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

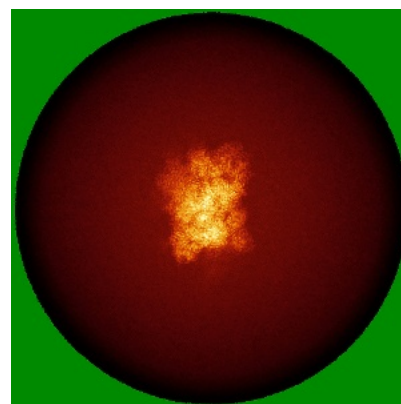
### 6.4.1 Primary map



X

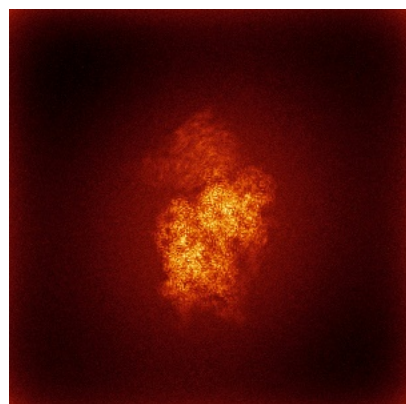


Y

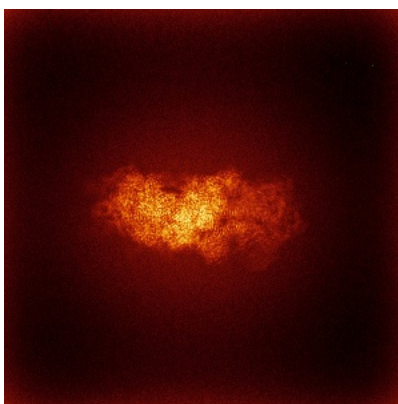


Z

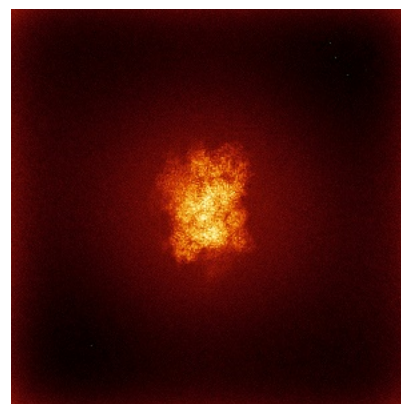
### 6.4.2 Raw map



X



Y

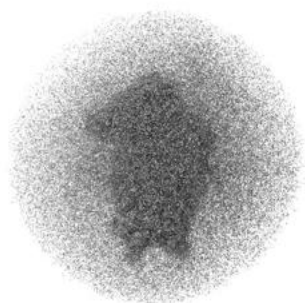


Z

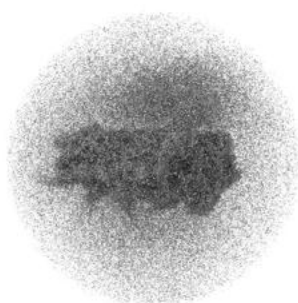
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

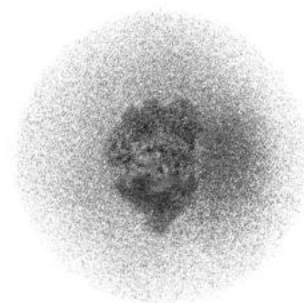
### 6.5.1 Primary map



X



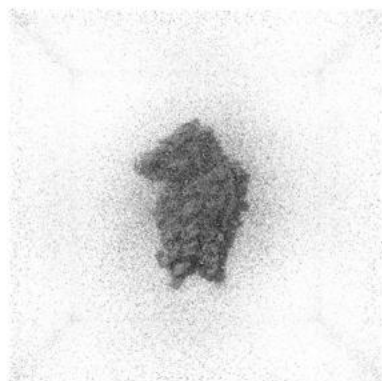
Y



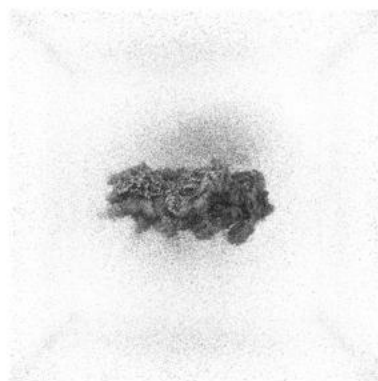
Z

The images above show the 3D surface view of the map at the recommended contour level 0.167. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

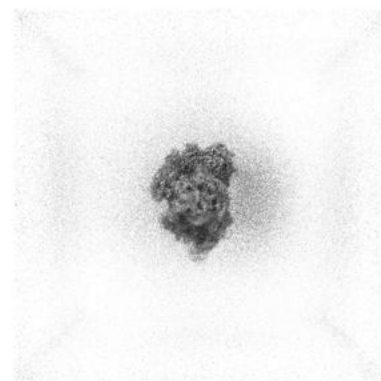
### 6.5.2 Raw map



X



Y



Z

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

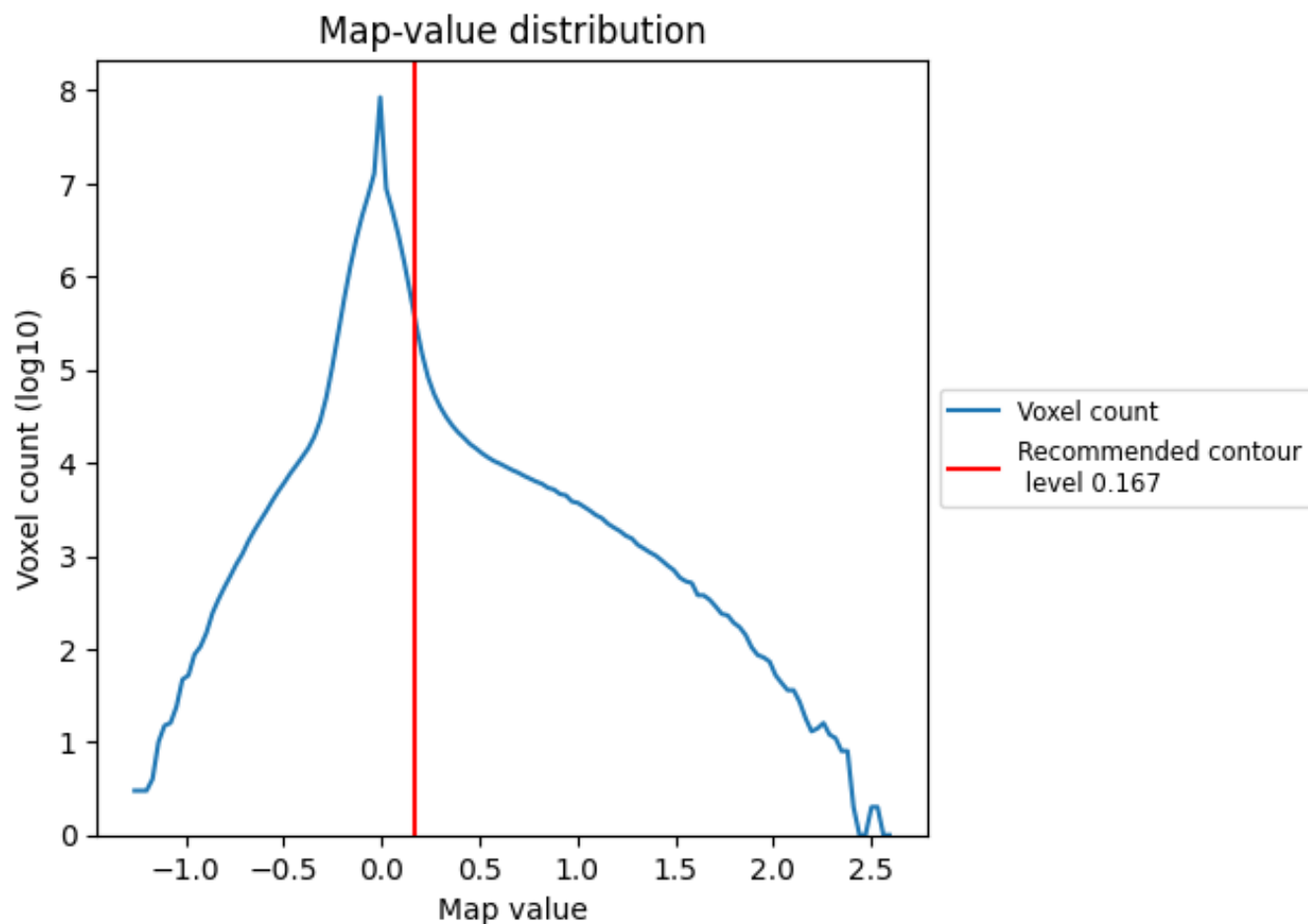
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

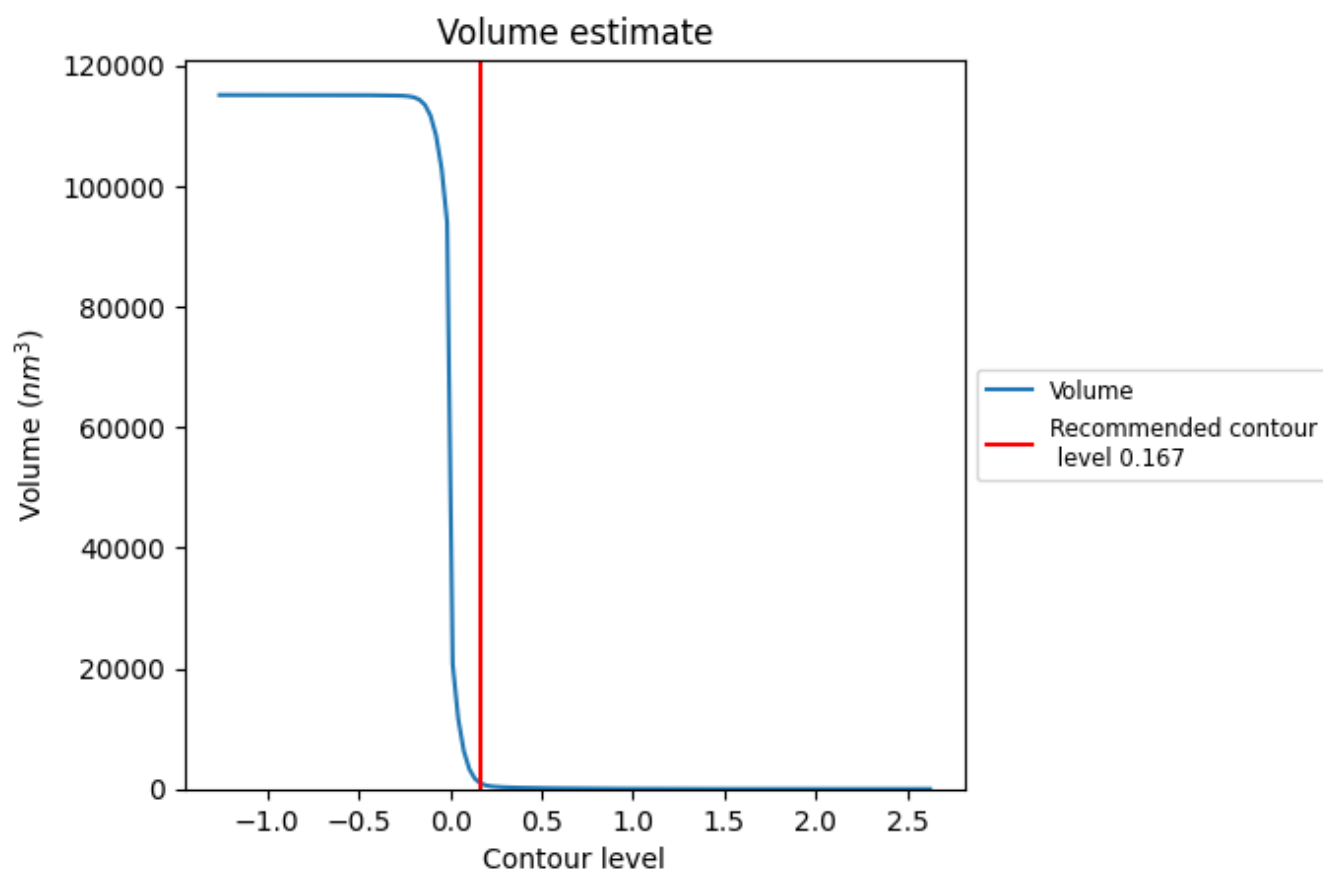
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

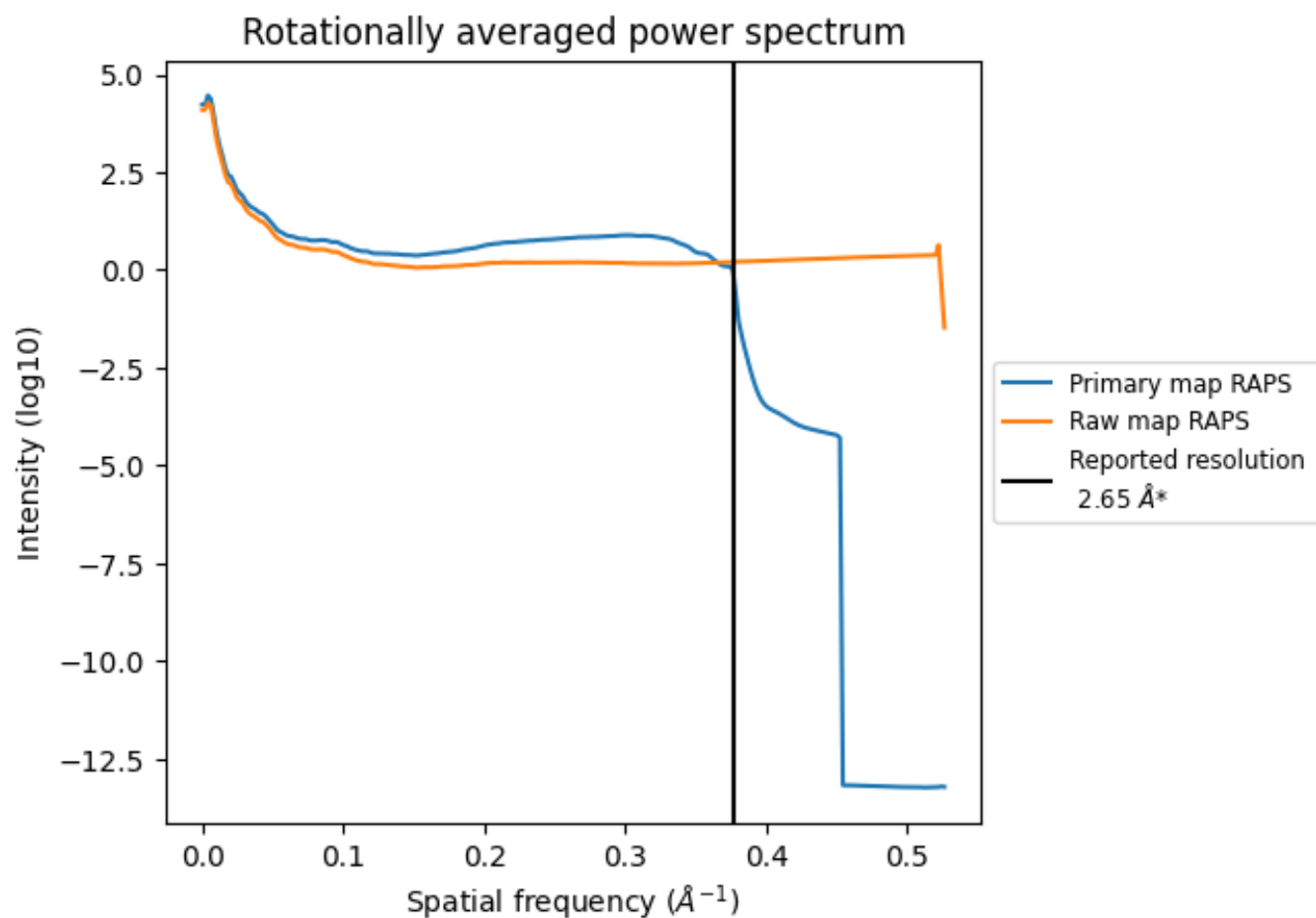
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 925  $\text{nm}^3$ ; this corresponds to an approximate mass of 836 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 ⓘ

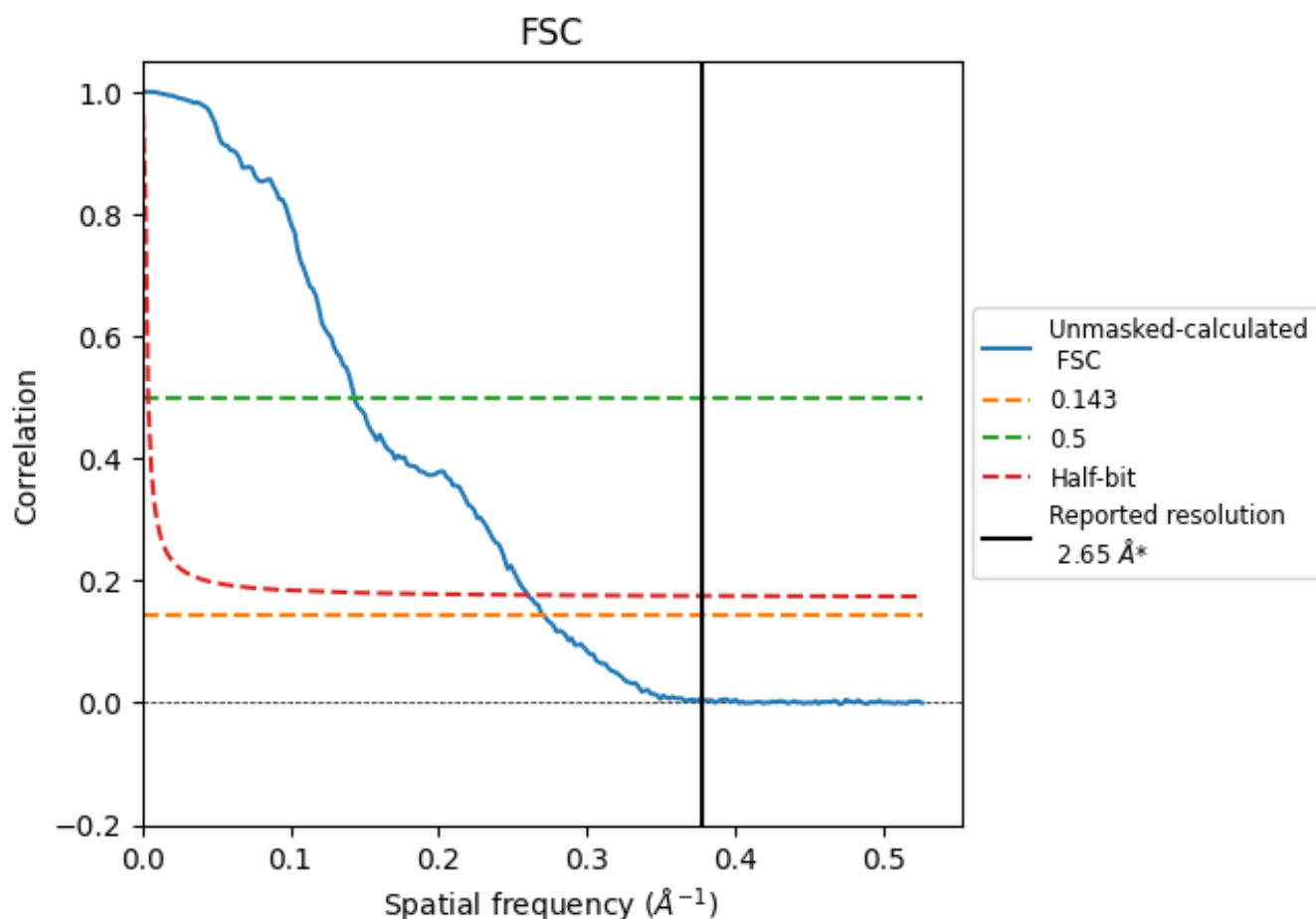


\*Reported resolution corresponds to spatial frequency of 0.377  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.377 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

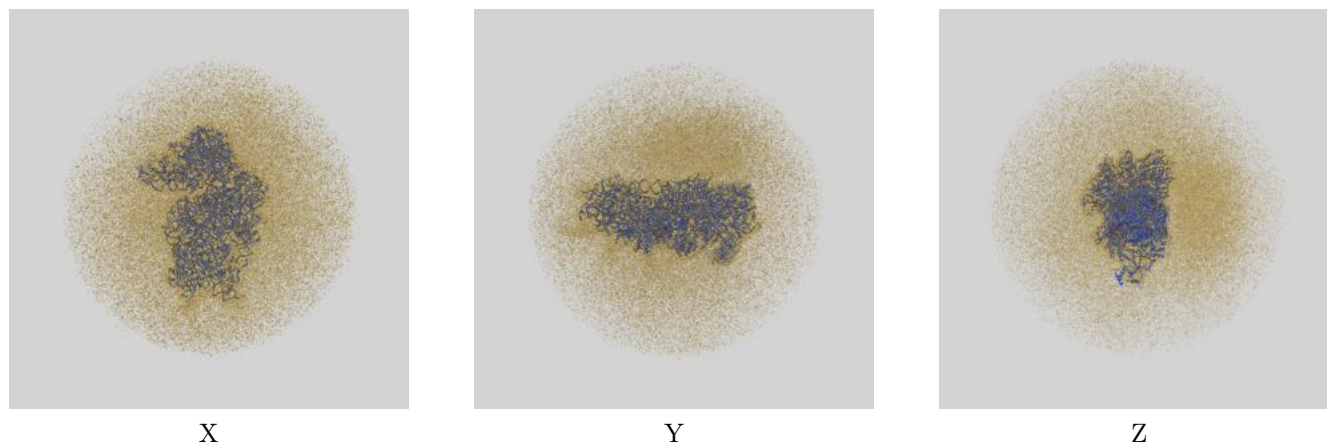
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.65	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.69	6.98	3.84

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.69 differs from the reported value 2.65 by more than 10 %

## 9 Map-model fit [i](#)

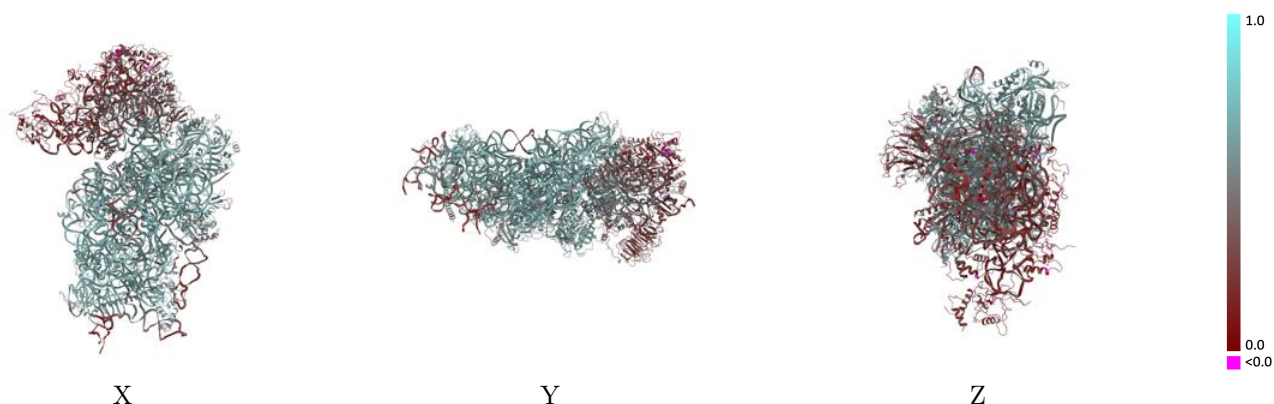
This section contains information regarding the fit between EMDB map EMD-62451 and PDB model 9KN0. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlay [i](#)



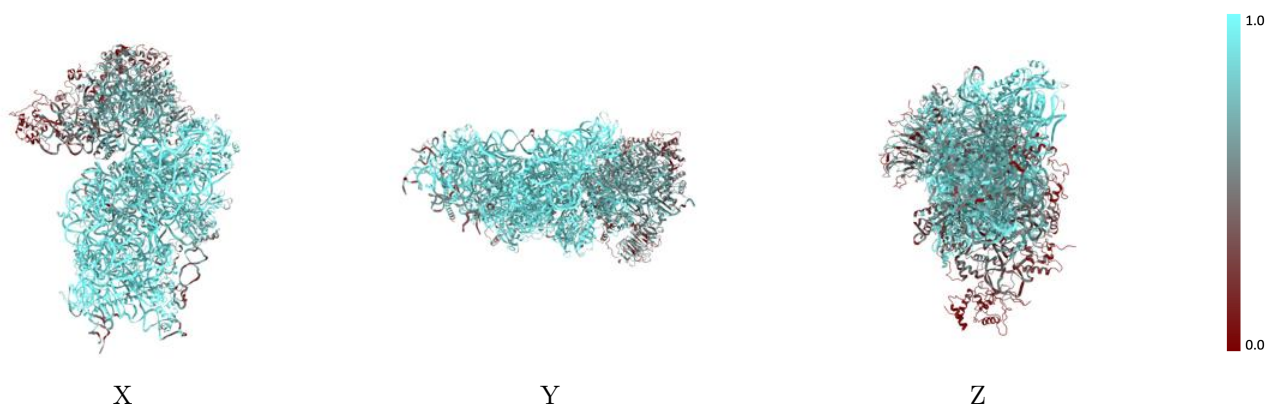
The images above show the 3D surface view of the map at the recommended contour level 0.167 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



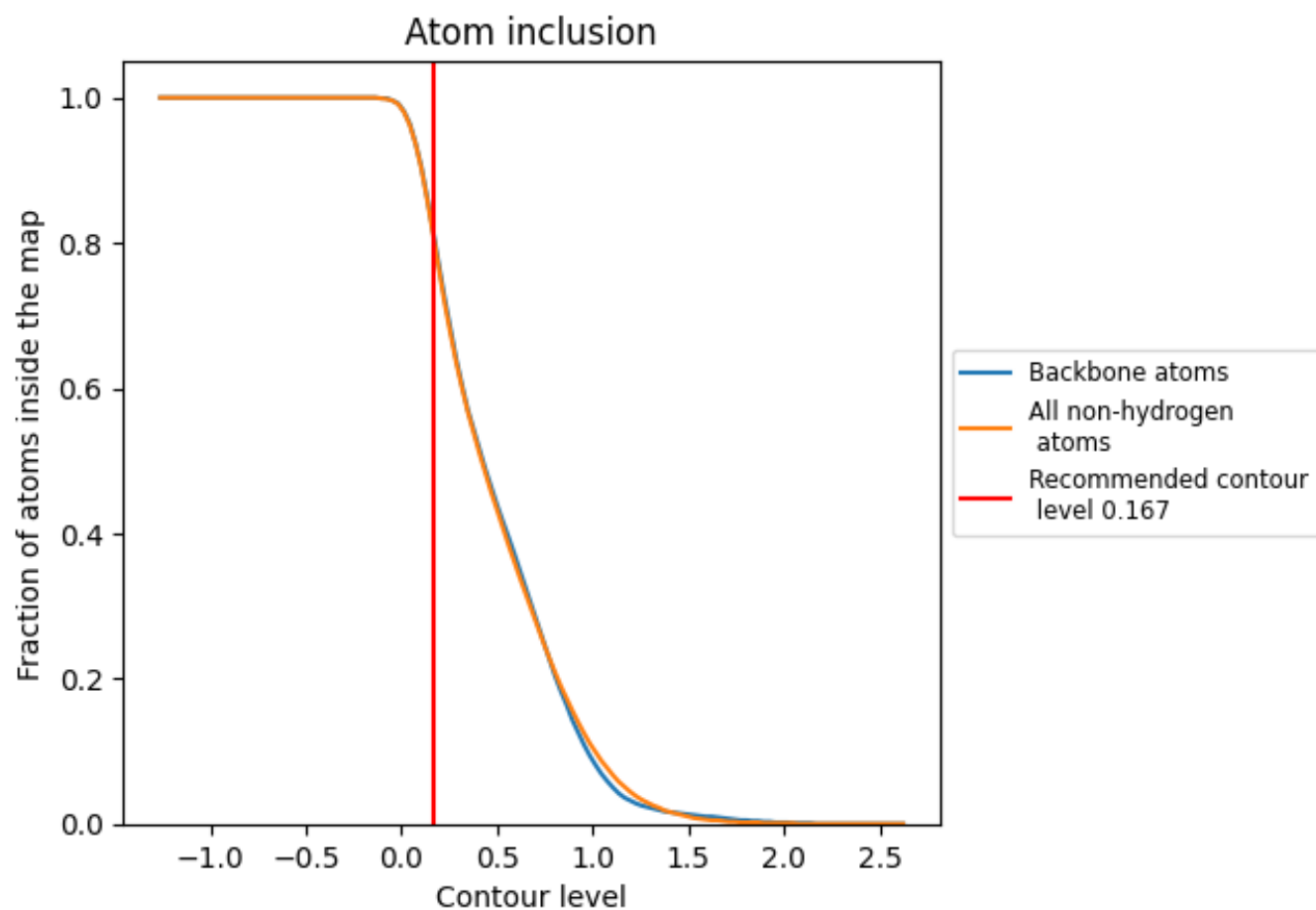
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.167).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% 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 (0.167) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8100	 0.5040
2	 0.8720	 0.5160
A	 0.9350	 0.6060
B	 0.9360	 0.5980
C	 0.9540	 0.6340
D	 0.6010	 0.3810
E	 0.9700	 0.6400
F	 0.6280	 0.3700
G	 0.9160	 0.5810
H	 0.7810	 0.5190
I	 0.9220	 0.6010
J	 0.9760	 0.6390
K	 0.4010	 0.2530
L	 0.9120	 0.6130
M	 0.1030	 0.2100
N	 0.9550	 0.6190
O	 0.9230	 0.5920
P	 0.3090	 0.2240
Q	 0.6910	 0.3910
R	 0.7180	 0.4780
S	 0.3760	 0.2660
T	 0.5830	 0.2980
U	 0.5720	 0.3860
V	 0.9430	 0.6160
W	 0.9800	 0.6410
X	 0.9710	 0.6350
Y	 0.9640	 0.6300
Z	 0.3120	 0.2250
a	 0.9520	 0.6160
b	 0.8890	 0.5650
c	 0.5540	 0.3760
d	 0.6850	 0.3890
e	 0.8500	 0.5620
f	 0.1360	 0.2530
g	 0.4690	 0.3190



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Chain	Atom inclusion	Q-score
h	 0.9170	 0.5980
n	 0.8550	 0.5710