



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 09:13 PM UTC

PDB ID : 6EML / pdb_00006eml
EMDB ID : EMD-3886
Title : Cryo-EM structure of a late pre-40S ribosomal subunit from *Saccharomyces cerevisiae*
Authors : Heuer, A.; Thomson, E.; Schmidt, C.; Berninghausen, O.; Becker, T.; Hurt, E.; Beckmann, R.
Deposited on : 2017-10-02
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

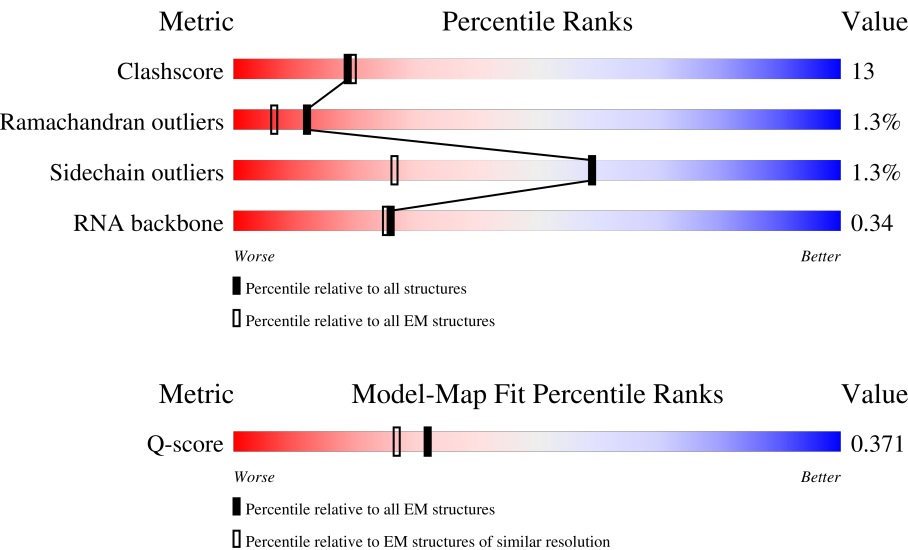
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	2	1800	
2	D	143	
3	B	225	

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Mol	Chain	Length	Quality of chain
4	C	136	
5	E	142	
6	F	143	
7	H	146	
8	I	144	
9	K	108	
10	L	67	
11	N	152	
12	P	252	
13	Q	255	
14	R	254	
15	S	261	
16	T	236	
17	U	190	
18	V	200	
19	W	197	
20	X	156	
21	Y	151	
22	Z	137	
23	a	87	
24	b	130	
25	c	145	
26	d	135	
27	f	82	
28	t	788	

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Mol	Chain	Length	Quality of chain
29	g	63	51%67%22%6%5%
30	p	274	27%44%22%32%
31	r	425	58%21%39%38%
32	e	483	44%49%46%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 75886 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 pre-18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1675	Total	C	N	O	P	0	0
			35695	15958	6312	11750	1675		

- Molecule 2 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	124	Total	C	N	O	S	0	0
			892	561	156	173	2		

- Molecule 3 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	202	Total	C	N	O	S	0	0
			1592	998	296	295	3		

- Molecule 4 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	114	Total	C	N	O	S	0	0
			871	541	169	159	2		

- Molecule 5 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	117	Total	C	N	O	S	0	0
			928	590	172	159	7		

- Molecule 6 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 7 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	122	Total	C	N	O	S	0	0
			1009	636	193	178	2		

- Molecule 8 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 9 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	K	64	Total	C	N	O	0	0
			519	332	95	92		

- Molecule 10 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	62	Total	C	N	O	S	0	0
			486	300	95	90	1		

- Molecule 11 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 12 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 13 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 14 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	220	Total	C	N	O	S	0	0
			1662	1065	295	300	2		

- Molecule 15 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 16 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 17 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	U	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 18 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 19 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 20 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 21 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 22 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Z	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	c	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	d	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 27 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 28 is a protein called Ribosome biogenesis protein TSR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	t	633	Total	C	N	O	S	0	0
			5037	3220	875	929	13		

- Molecule 29 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 30 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	p	185	Total	C	N	O	S	0	0
			1473	942	267	260	4		

- Molecule 31 is a protein called Serine/threonine-protein kinase RIO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	r	264	Total	C	N	O	S	0	0
			2166	1379	384	387	16		

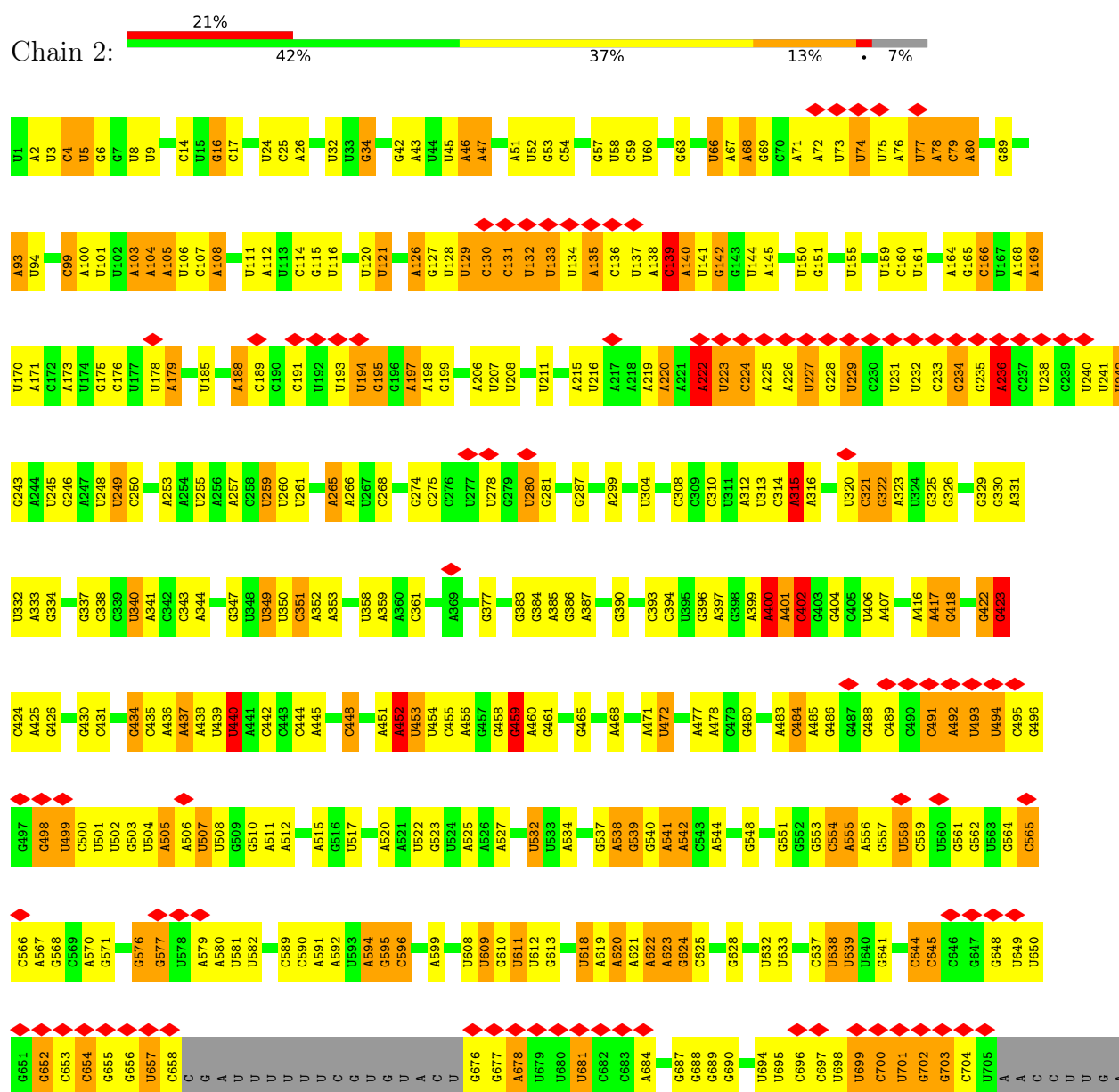
- Molecule 32 is a protein called Essential nuclear protein 1.

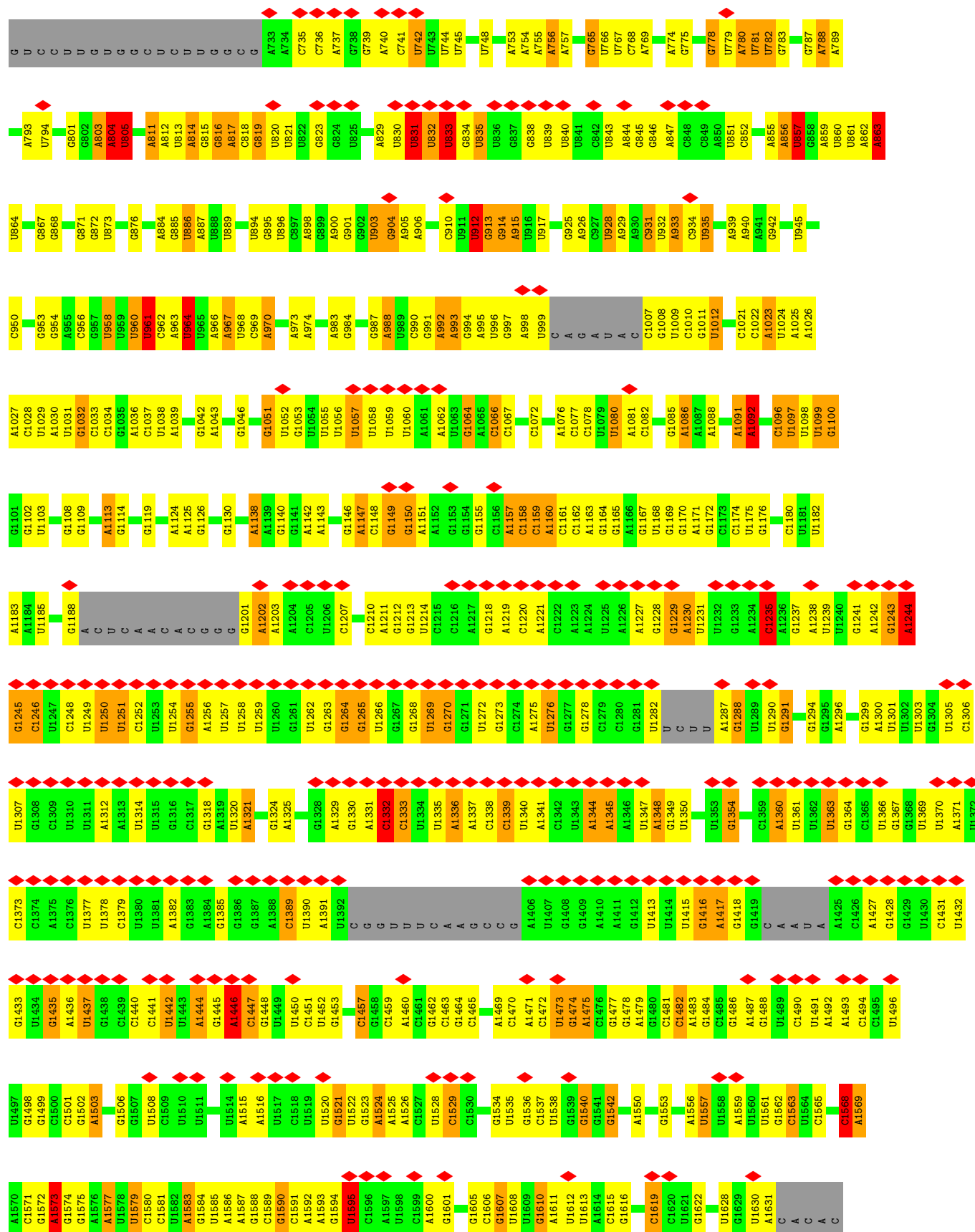
Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	261	Total	C	N	O		0	0
			1045	523	261	261			

3 Residue-property plots

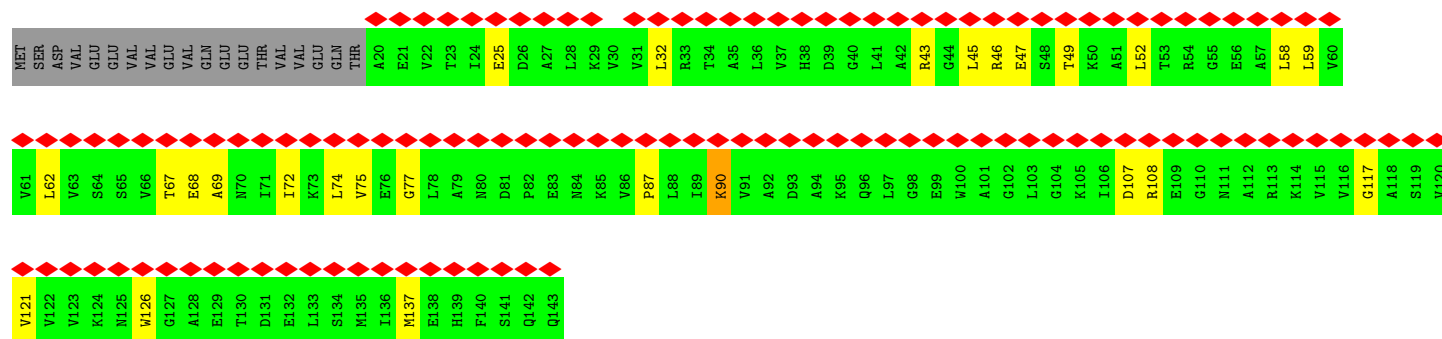
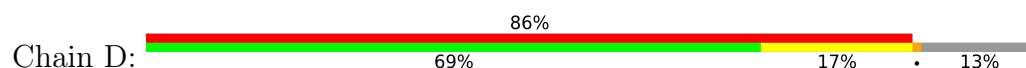
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: pre-18S ribosomal RNA

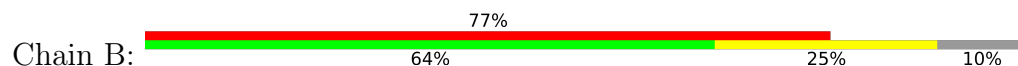




- Molecule 2: 40S ribosomal protein S12

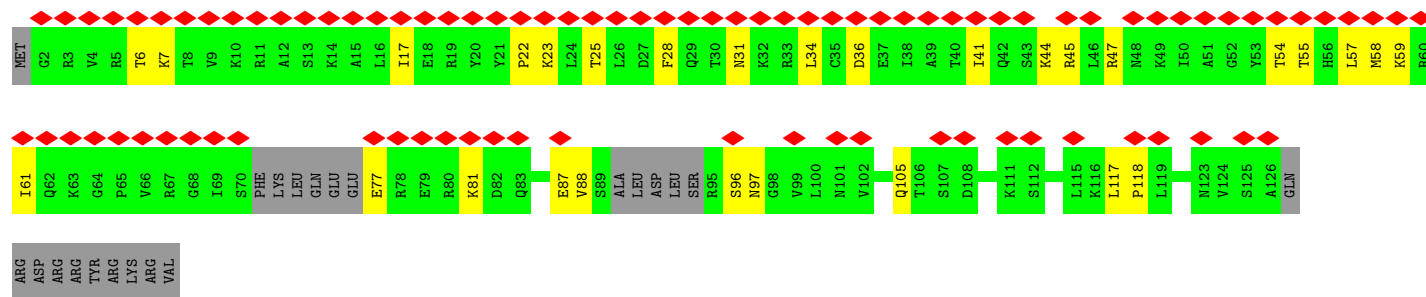


- Molecule 3: 40S ribosomal protein S5

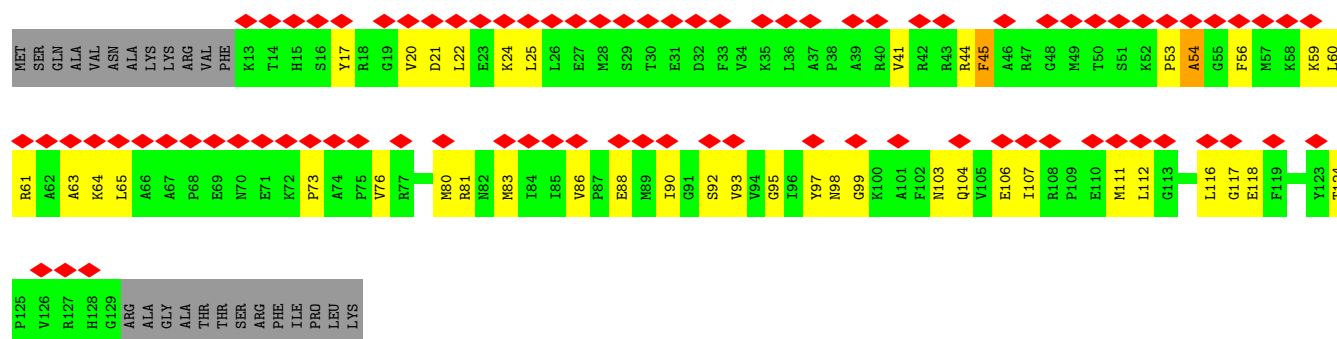


- Molecule 4: 40S ribosomal protein S17-A

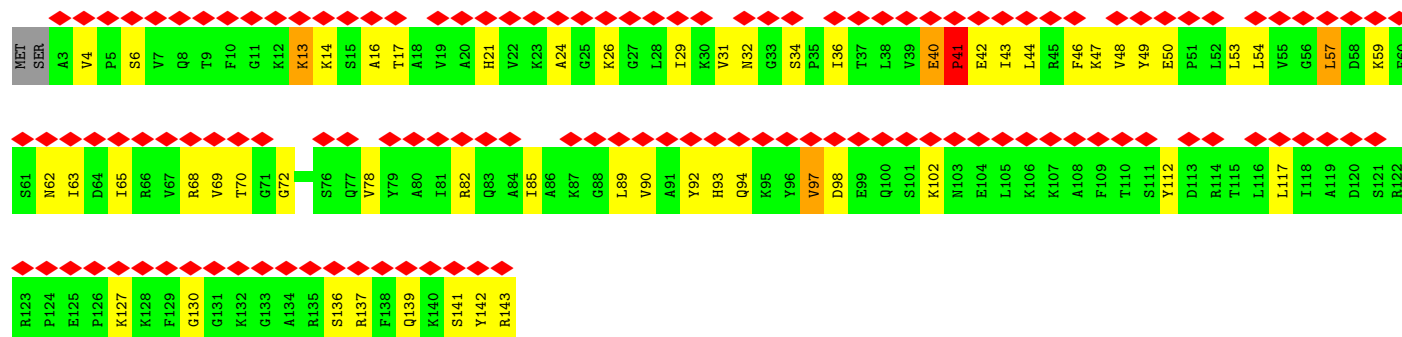
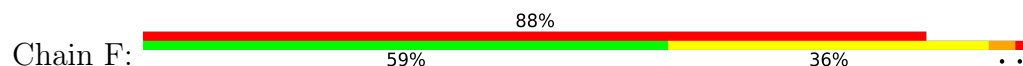




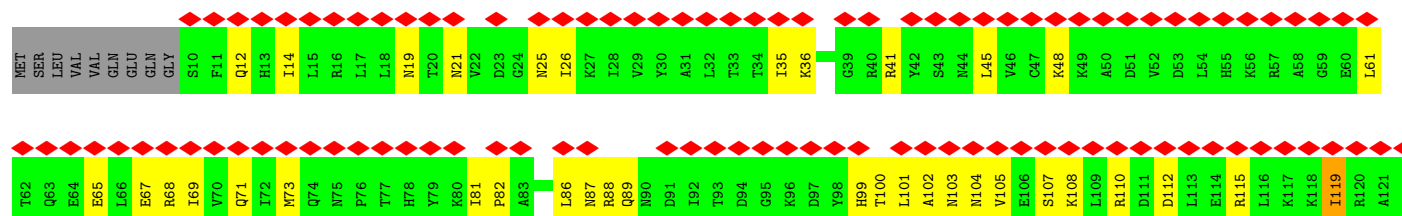
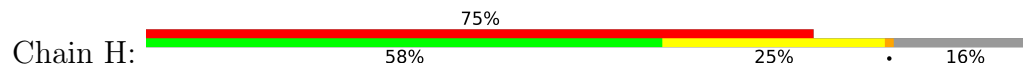
• Molecule 5: 40S ribosomal protein S15

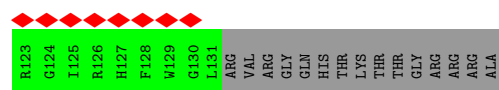


• Molecule 6: 40S ribosomal protein S16-A

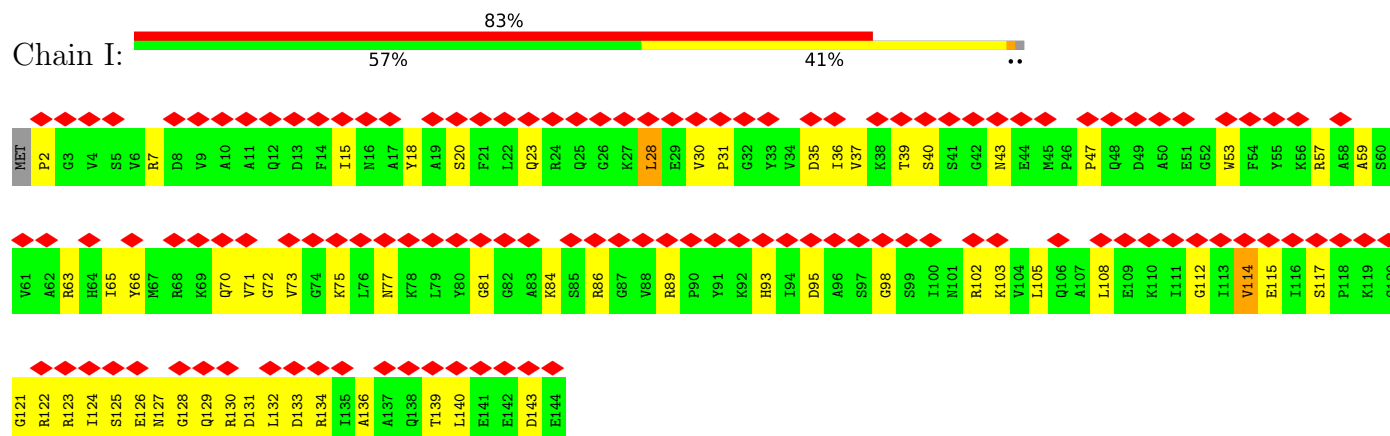


• Molecule 7: 40S ribosomal protein S18-A

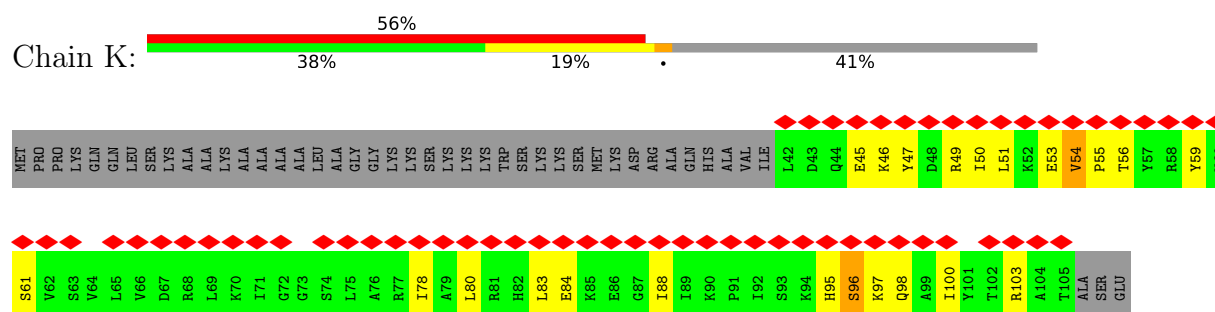




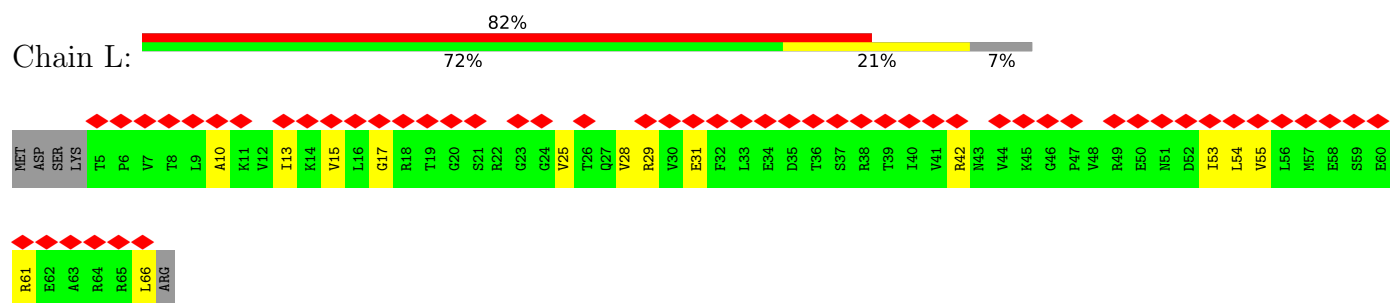
• Molecule 8: 40S ribosomal protein S19-A



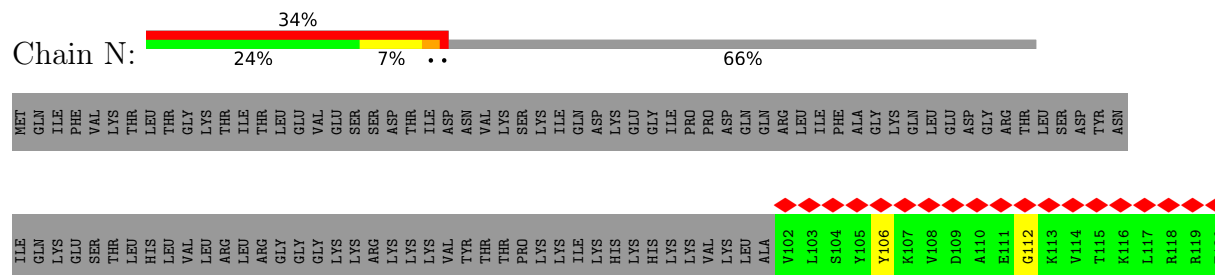
• Molecule 9: 40S ribosomal protein S25-A



• Molecule 10: 40S ribosomal protein S28-B

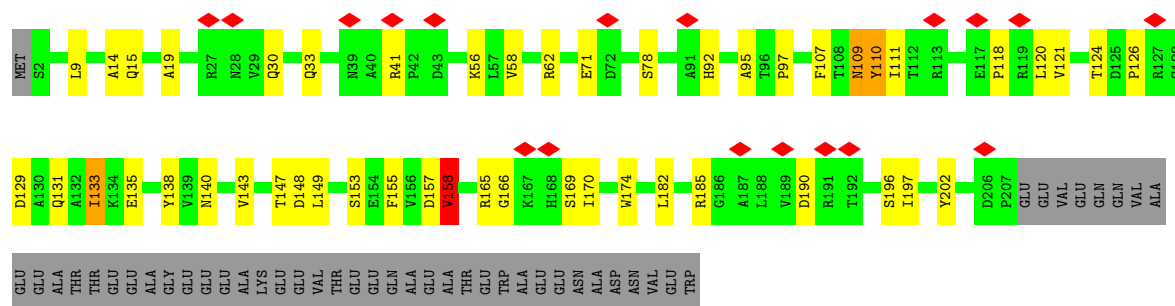


• Molecule 11: Ubiquitin-40S ribosomal protein S31

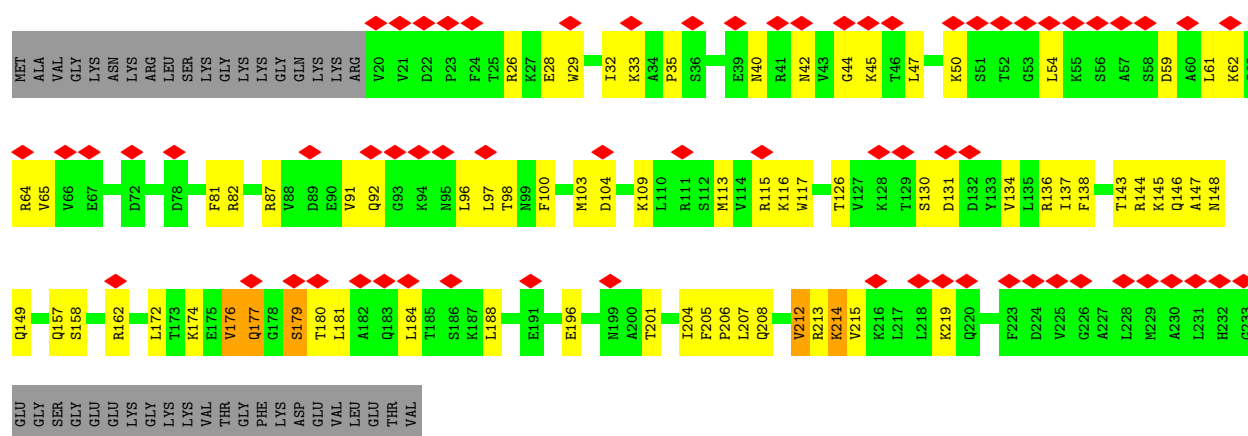




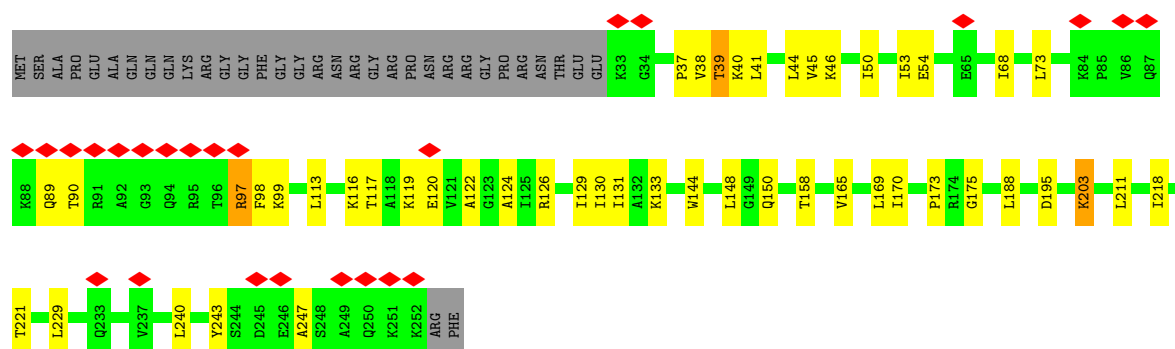
• Molecule 12: 40S ribosomal protein S0-A



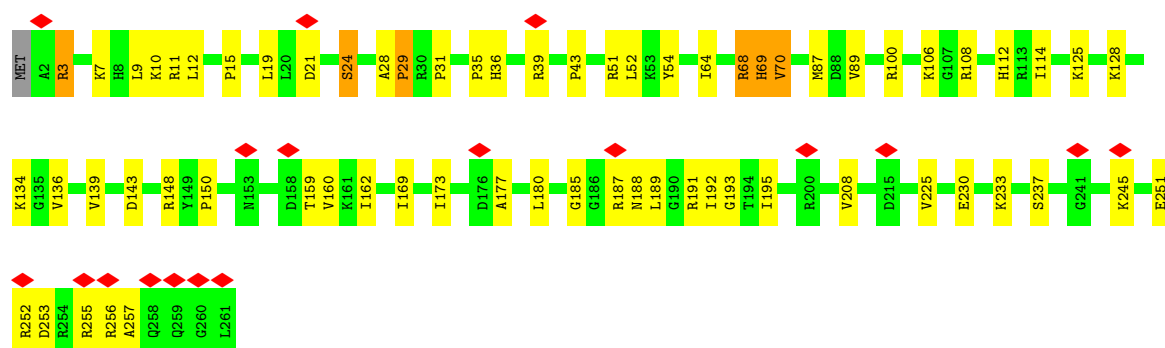
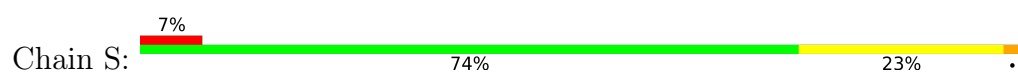
• Molecule 13: 40S ribosomal protein S1-A



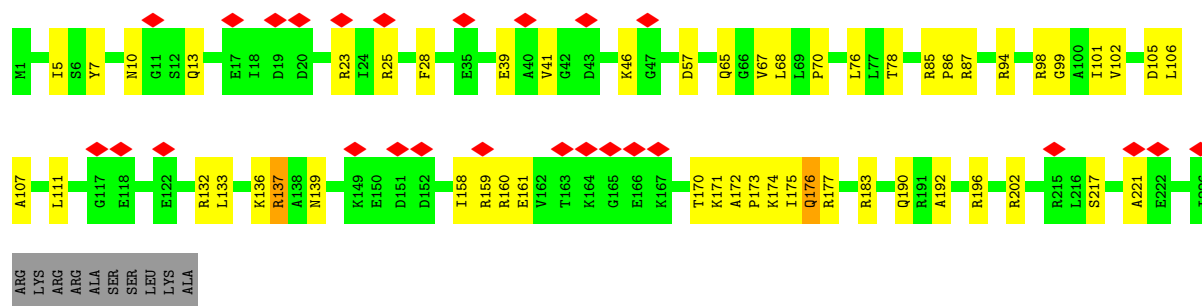
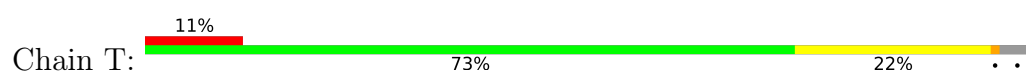
• Molecule 14: 40S ribosomal protein S2



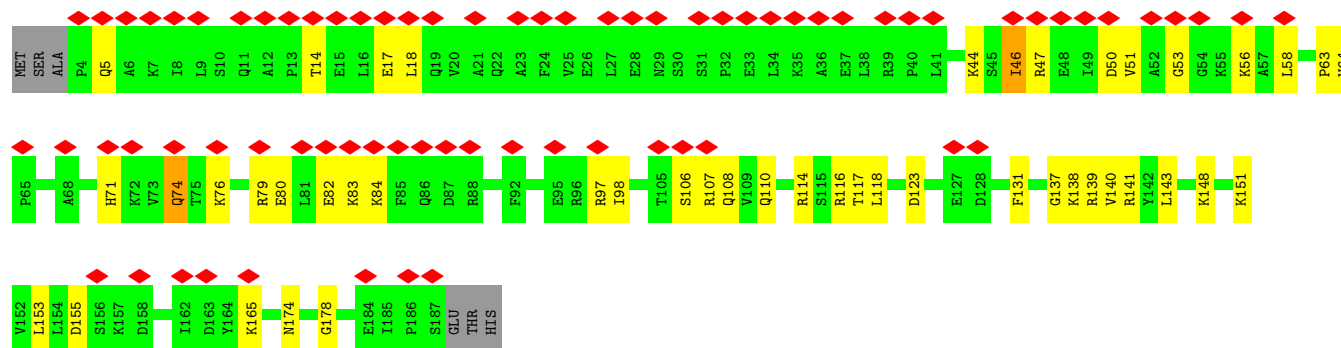
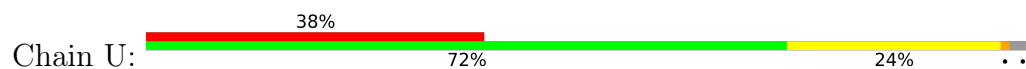
• Molecule 15: 40S ribosomal protein S4-A



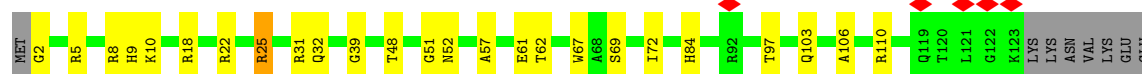
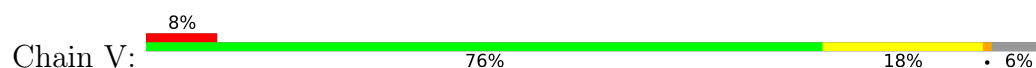
• Molecule 16: 40S ribosomal protein S6-A

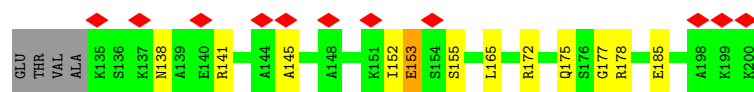


• Molecule 17: 40S ribosomal protein S7-A

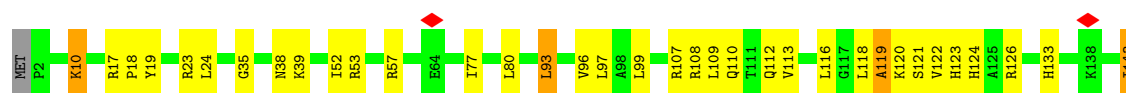


• Molecule 18: 40S ribosomal protein S8-A

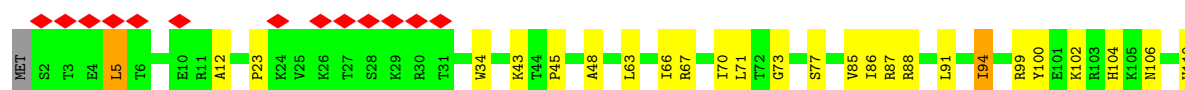
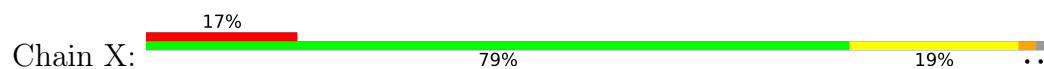




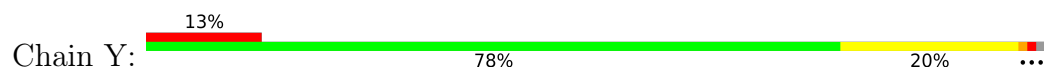
- Molecule 19: 40S ribosomal protein S9-A



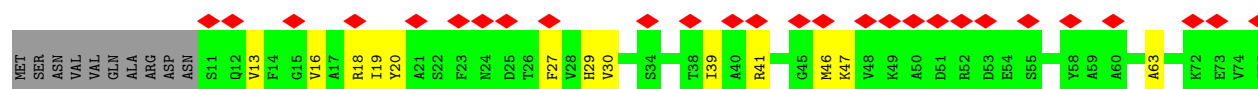
- Molecule 20: 40S ribosomal protein S11-A



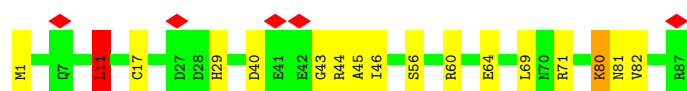
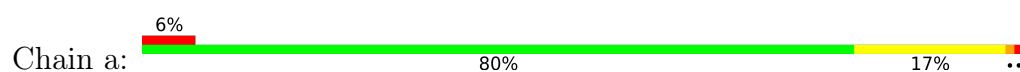
- Molecule 21: 40S ribosomal protein S13



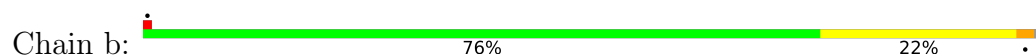
- Molecule 22: 40S ribosomal protein S14-A



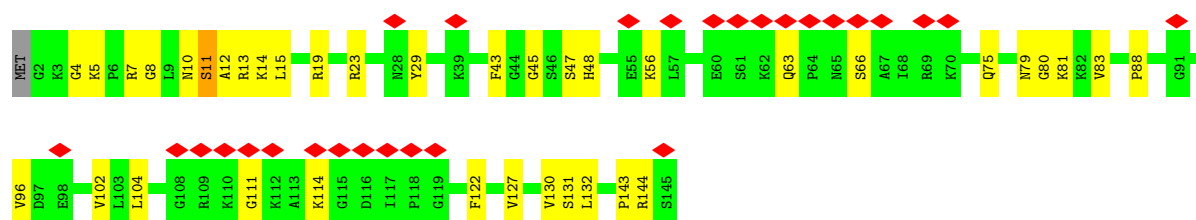
- Molecule 23: 40S ribosomal protein S21-A



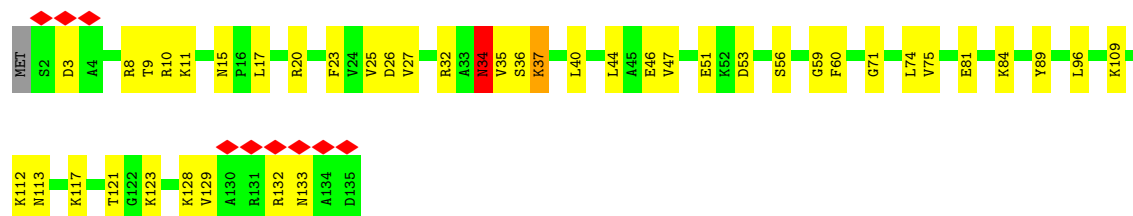
- Molecule 24: 40S ribosomal protein S22-A



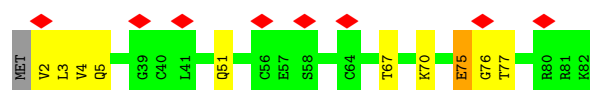
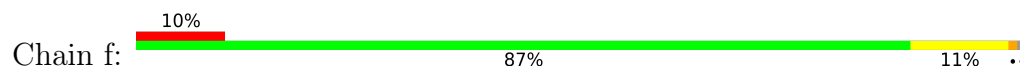
- Molecule 25: 40S ribosomal protein S23-A



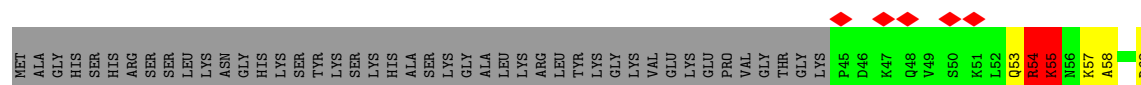
- Molecule 26: 40S ribosomal protein S24-A

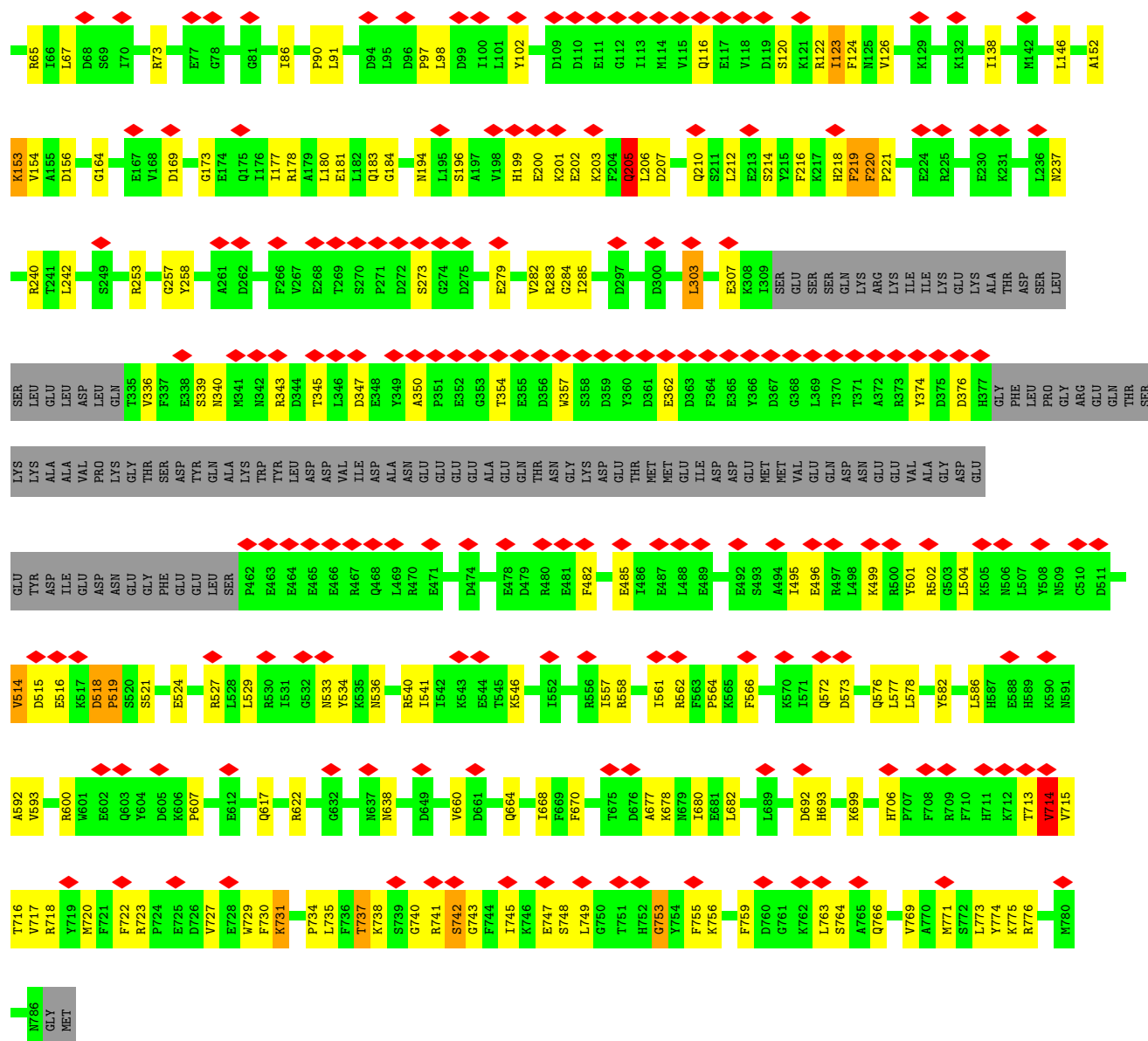


- Molecule 27: 40S ribosomal protein S27-A



- Molecule 28: Ribosome biogenesis protein TSR1

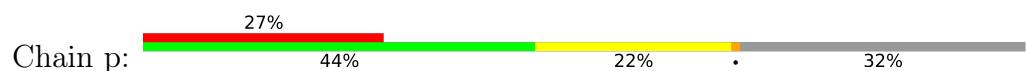




- Molecule 29: 40S ribosomal protein S30-A



- Molecule 30: Pre-rRNA-processing protein PNO1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84100	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.523	Depositor
Minimum map value	-0.262	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.0722	Depositor
Map size ($\text{\AA}$)	416.25598, 416.25598, 416.25598	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	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	0.79	38/39917 (0.1%)	0.84	74/62179 (0.1%)
2	D	0.62	0/900	0.98	1/1223 (0.1%)
3	B	0.54	0/1611	0.81	1/2177 (0.0%)
4	C	0.61	0/878	0.92	1/1177 (0.1%)
5	E	0.57	0/948	0.88	0/1273
6	F	0.56	0/1125	0.78	0/1510
7	H	0.52	0/1027	0.80	1/1383 (0.1%)
8	I	0.56	0/1130	0.85	0/1517
9	K	0.53	0/526	0.89	0/706
10	L	0.51	0/488	0.74	0/656
11	N	0.54	0/404	0.93	0/542
12	P	1.18	3/1617 (0.2%)	1.05	4/2215 (0.2%)
13	Q	0.84	1/1735 (0.1%)	0.96	0/2335
14	R	1.25	5/1692 (0.3%)	1.03	0/2296
15	S	1.36	6/2109 (0.3%)	1.13	4/2839 (0.1%)
16	T	0.98	1/1823 (0.1%)	0.94	1/2439 (0.0%)
17	U	0.85	0/1506	0.99	1/2028 (0.0%)
18	V	1.22	2/1514 (0.1%)	1.09	1/2021 (0.0%)
19	W	1.32	7/1519 (0.5%)	1.15	2/2035 (0.1%)
20	X	1.49	11/1239 (0.9%)	1.18	1/1673 (0.1%)
21	Y	1.18	2/1215 (0.2%)	1.08	4/1638 (0.2%)
22	Z	0.78	0/901	0.90	1/1217 (0.1%)
23	a	1.19	0/693	1.13	0/935
24	b	1.65	8/1038 (0.8%)	1.24	1/1395 (0.1%)
25	c	1.42	8/1139 (0.7%)	1.28	2/1518 (0.1%)
26	d	1.14	2/1087 (0.2%)	1.04	1/1449 (0.1%)
27	f	1.02	0/620	1.00	0/838
28	t	0.85	3/5150 (0.1%)	0.91	5/6972 (0.1%)
29	g	1.07	2/483 (0.4%)	1.17	2/643 (0.3%)
30	p	0.81	1/1500 (0.1%)	0.86	0/2020
31	r	0.25	0/2209	0.66	1/2965 (0.0%)
32	e	0.29	0/1044	0.82	3/1304 (0.2%)
All	All	0.89	100/80787 (0.1%)	0.91	112/117118 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	2	0	11
2	D	0	1
3	B	0	1
4	C	0	2
5	E	0	2
6	F	0	2
9	K	0	3
12	P	0	3
13	Q	0	5
14	R	0	1
15	S	0	1
17	U	0	3
18	V	0	1
19	W	0	2
20	X	0	1
21	Y	0	1
22	Z	0	1
23	a	0	3
24	b	0	1
25	c	0	1
28	t	0	8
29	g	0	1
31	r	0	2
All	All	0	57

All (100) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	220	A	C6-N1	-16.34	1.02	1.35
1	2	222	A	C6-N1	-15.35	1.04	1.35
1	2	1235	C	C1'-N1	13.44	1.68	1.48
1	2	831	U	C2-N3	11.90	1.61	1.37
1	2	833	U	C2-N3	11.42	1.60	1.37
1	2	401	A	O3'-P	11.29	1.78	1.61
1	2	863	A	C6-N1	-9.69	1.16	1.35
1	2	236	A	C6-N6	-9.53	1.14	1.33
1	2	833	U	N3-C4	8.93	1.56	1.38
15	S	24	SER	CA-C	-8.89	1.45	1.53
1	2	831	U	C4-O4	-8.06	1.07	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	857	U	N3-C4	-7.88	1.22	1.38
20	X	110	HIS	CA-C	-7.79	1.42	1.52
14	R	169	LEU	C-O	-7.78	1.14	1.24
24	b	126	LEU	CA-C	-7.50	1.45	1.53
1	2	831	U	N1-C2	7.45	1.53	1.38
1	2	440	U	N3-C4	-7.45	1.23	1.38
1	2	964	U	N3-C4	7.37	1.53	1.38
1	2	595	G	O3'-P	-7.37	1.50	1.61
1	2	229	U	N3-C4	7.34	1.53	1.38
1	2	1235	C	N1-C2	7.10	1.54	1.40
1	2	967	A	O3'-P	-6.88	1.50	1.61
16	T	176	GLN	C-O	-6.87	1.15	1.23
12	P	158	VAL	C-O	-6.80	1.16	1.24
21	Y	13	SER	C-O	-6.79	1.19	1.24
1	2	1595	U	N3-C4	-6.76	1.25	1.38
24	b	102	VAL	CA-C	-6.74	1.45	1.52
14	R	165	VAL	CA-C	-6.70	1.45	1.52
1	2	805	U	O3'-P	-6.66	1.51	1.61
19	W	143	ILE	CA-CB	-6.61	1.48	1.54
14	R	203	LYS	CA-C	-6.53	1.44	1.53
29	g	33	ARG	CA-C	-6.46	1.44	1.52
25	c	10	ASN	CA-C	-6.40	1.45	1.53
24	b	105	THR	CA-C	-6.28	1.45	1.52
1	2	1057	U	C4-O4	-6.23	1.11	1.23
26	d	11	LYS	N-CA	6.23	1.55	1.46
15	S	125	LYS	CA-C	-6.22	1.44	1.52
20	X	85	VAL	CA-C	-6.19	1.44	1.52
1	2	106	U	O3'-P	-6.19	1.51	1.61
20	X	100	TYR	CG-CD1	-6.18	1.26	1.39
1	2	831	U	N3-C4	6.16	1.50	1.38
29	g	35	TYR	C-O	-6.11	1.16	1.24
25	c	104	LEU	C-O	-6.06	1.16	1.23
25	c	12	ALA	CA-C	-6.05	1.44	1.52
20	X	94	ILE	N-CA	-6.05	1.40	1.46
12	P	97	PRO	N-CA	-6.04	1.39	1.47
20	X	99	ARG	NE-CZ	-6.00	1.26	1.33
1	2	633	U	O3'-P	-5.91	1.52	1.61
1	2	472	U	O3'-P	-5.90	1.52	1.61
19	W	163	PRO	C-O	5.87	1.31	1.24
19	W	10	LYS	C-O	-5.78	1.16	1.23
1	2	423	G	O3'-P	5.76	1.69	1.61
1	2	596	C	O3'-P	-5.71	1.52	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	P	121	VAL	C-O	-5.70	1.18	1.24
14	R	170	ILE	CA-CB	-5.62	1.47	1.54
1	2	863	A	C5-C6	-5.60	1.29	1.41
20	X	91	LEU	CA-C	-5.59	1.45	1.52
15	S	10	LYS	C-O	-5.57	1.16	1.23
1	2	1731	A	O3'-P	-5.56	1.52	1.61
1	2	385	A	O3'-P	-5.54	1.52	1.61
1	2	1086	A	N1-C2	5.54	1.45	1.34
28	t	220	PHE	C-O	-5.52	1.20	1.25
1	2	1130	G	O3'-P	-5.52	1.52	1.61
21	Y	10	GLY	CA-C	-5.51	1.46	1.52
19	W	93	LEU	N-CA	5.49	1.53	1.46
1	2	377	G	O3'-P	-5.47	1.52	1.61
24	b	104	LEU	N-CA	-5.46	1.39	1.45
1	2	1142	A	O3'-P	-5.42	1.53	1.61
25	c	14	LYS	N-CA	-5.40	1.39	1.46
20	X	131	ILE	C-O	-5.40	1.18	1.24
20	X	136	ARG	CA-C	-5.38	1.45	1.52
13	Q	206	PRO	C-O	-5.36	1.17	1.24
24	b	127	GLY	C-O	-5.36	1.16	1.23
26	d	11	LYS	C-O	-5.33	1.16	1.23
15	S	162	ILE	C-O	-5.32	1.18	1.24
25	c	11	SER	C-O	-5.32	1.17	1.24
15	S	188	ASN	N-CA	-5.29	1.40	1.46
25	c	19	ARG	CZ-NH2	5.29	1.40	1.33
24	b	123	GLY	C-O	-5.22	1.16	1.23
19	W	146	PHE	CG-CD1	-5.22	1.27	1.38
24	b	129	VAL	CA-C	-5.22	1.46	1.52
1	2	108	A	O3'-P	-5.22	1.53	1.61
1	2	347	G	O3'-P	-5.21	1.53	1.61
19	W	133	HIS	C-O	-5.19	1.18	1.24
20	X	99	ARG	C-O	-5.18	1.19	1.24
19	W	168	ARG	C-O	-5.16	1.19	1.24
24	b	111	MET	N-CA	-5.16	1.39	1.46
30	p	187	VAL	C-O	-5.16	1.18	1.24
14	R	203	LYS	C-O	-5.11	1.17	1.23
15	S	128	LYS	CA-C	-5.10	1.46	1.52
18	V	9	HIS	CA-C	-5.08	1.46	1.52
28	t	219	PHE	CA-C	-5.07	1.47	1.53
28	t	58	ALA	CA-C	5.06	1.59	1.52
1	2	612	U	O3'-P	-5.06	1.53	1.61
25	c	29	TYR	CE2-CZ	-5.05	1.26	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	X	12	ALA	CA-C	-5.02	1.46	1.52
20	X	100	TYR	CG-CD2	-5.02	1.28	1.39
18	V	2	GLY	N-CA	5.02	1.53	1.45
25	c	7	ARG	C-O	-5.01	1.17	1.24
1	2	961	U	O3'-P	-5.01	1.53	1.61

All (112) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1023	A	C4'-C3'-O3'	9.21	123.21	109.40
1	2	452	A	C1'-C2'-O2'	-8.97	98.34	111.80
1	2	400	A	C4'-C3'-O3'	8.80	122.60	109.40
1	2	322	G	C2'-C3'-O3'	8.24	121.85	109.50
21	Y	10	GLY	CA-C-O	-7.90	114.47	121.58
1	2	459	G	C4'-C3'-O3'	-7.88	101.18	113.00
1	2	139	C	C2'-C3'-O3'	7.84	121.27	109.50
1	2	99	C	C2'-C3'-O3'	7.79	121.18	109.50
4	C	117	LEU	N-CA-C	-7.76	101.14	108.13
1	2	863	A	N9-C1'-C2'	-7.55	102.68	114.00
1	2	609	U	C2'-C3'-O3'	7.53	120.79	109.50
15	S	29	PRO	CB-CA-C	-7.51	102.37	111.46
1	2	1446	A	C2'-C3'-O3'	7.42	120.63	109.50
1	2	963	A	C4'-C3'-O3'	-7.30	102.05	113.00
25	c	19	ARG	NE-CZ-NH1	-7.25	114.25	121.50
32	e	211	ILE	CA-C-N	7.12	134.52	121.70
32	e	211	ILE	C-N-CA	7.12	134.52	121.70
1	2	315	A	C4'-C3'-O3'	7.04	119.96	109.40
1	2	958	U	P-O5'-C5'	-7.00	110.40	120.90
1	2	242	U	C4'-C3'-O3'	6.99	123.49	113.00
1	2	1389	C	N1-C1'-C2'	6.93	122.40	112.00
32	e	405	ASN	N-CA-C	6.84	119.27	110.65
1	2	452	A	C2'-C3'-O3'	6.83	119.75	109.50
28	t	202	GLU	N-CA-C	-6.79	104.74	113.16
12	P	109	ASN	O-C-N	6.69	131.49	122.59
21	Y	29	SER	N-CA-C	6.66	117.37	108.38
17	U	155	ASP	N-CA-C	6.63	119.43	108.48
1	2	452	A	C4'-C3'-O3'	-6.62	99.48	109.40
1	2	831	U	C2-N3-C4	-6.62	107.15	127.00
19	W	166	GLY	N-CA-C	6.58	119.20	111.63
1	2	1100	G	P-O5'-C5'	-6.54	111.09	120.90
12	P	169	SER	N-CA-C	-6.54	107.17	114.62
22	Z	124	ASP	N-CA-C	6.54	119.50	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	401	A	C1'-C2'-O2'	-6.52	102.02	111.80
1	2	104	A	C2'-C3'-O3'	6.38	123.27	113.70
20	X	77	SER	N-CA-C	6.27	119.58	110.42
1	2	803	A	C4'-C3'-O3'	6.22	118.72	109.40
1	2	532	U	P-O5'-C5'	-6.21	111.58	120.90
1	2	121	U	P-O5'-C5'	-6.20	111.60	120.90
1	2	422	G	C4'-C3'-O3'	-6.20	103.70	113.00
28	t	514	VAL	N-CA-C	6.15	116.82	110.36
18	V	22	ARG	NE-CZ-NH1	-6.14	115.36	121.50
1	2	505	A	C4'-C3'-O3'	-6.13	103.80	113.00
1	2	132	U	C2'-C3'-O3'	6.12	118.68	109.50
25	c	23	ARG	NE-CZ-NH2	-6.07	113.73	119.20
1	2	555	A	C4'-C3'-O3'	6.05	118.47	109.40
1	2	1034	C	P-O5'-C5'	-5.99	111.91	120.90
1	2	384	G	P-O5'-C5'	-5.99	111.92	120.90
1	2	459	G	C1'-C2'-O2'	-5.95	99.48	108.40
31	r	71	ASP	N-CA-C	5.93	118.90	109.24
1	2	1244	A	C2'-C3'-O3'	5.91	122.57	113.70
1	2	1096	C	C4'-C3'-O3'	-5.91	104.13	113.00
26	d	34	ASN	N-CA-CB	-5.90	100.52	110.49
1	2	699	U	C2'-C3'-O3'	5.90	122.54	113.70
1	2	1793	G	C4'-C3'-O3'	5.87	118.20	109.40
19	W	151	ASP	N-CA-C	-5.85	106.68	113.88
1	2	1113	A	C4'-C3'-O3'	-5.84	104.25	113.00
1	2	452	A	O4'-C1'-C2'	5.80	111.60	105.80
21	Y	22	ALA	CA-C-N	-5.75	112.58	118.85
21	Y	22	ALA	C-N-CA	-5.75	112.58	118.85
1	2	220	A	C5-C6-N6	5.74	140.91	123.70
1	2	1092	A	C4'-C3'-O3'	-5.74	104.40	113.00
1	2	1097	U	C2'-C3'-O3'	5.73	118.09	109.50
1	2	652	G	C2'-C3'-O3'	5.63	122.15	113.70
1	2	833	U	C2-N3-C4	-5.61	110.18	127.00
1	2	539	G	C4'-C3'-O3'	-5.60	104.60	113.00
16	T	137	ARG	NE-CZ-NH2	5.59	124.23	119.20
1	2	1573	A	C2'-C3'-O3'	5.55	117.83	109.50
7	H	25	ASN	N-CA-C	5.51	119.31	112.47
28	t	55	LYS	N-CA-C	-5.51	104.66	111.33
29	g	8	LEU	CA-CB-CG	5.49	135.51	116.30
1	2	1051	G	N9-C1'-C2'	5.47	120.21	112.00
3	B	126	ASP	N-CA-C	5.47	119.45	112.34
15	S	69	HIS	N-CA-C	5.46	122.44	110.80
1	2	126	A	C4'-C3'-O3'	5.45	117.58	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	S	193	GLY	N-CA-C	5.45	126.09	113.18
1	2	121	U	C5'-C4'-C3'	-5.44	107.84	116.00
1	2	804	A	C4'-C3'-O3'	5.44	117.56	109.40
28	t	519	PRO	N-CA-C	5.42	123.64	112.47
1	2	1086	A	N9-C1'-C2'	5.39	120.09	112.00
1	2	321	C	N1-C1'-C2'	5.39	120.08	112.00
1	2	1251	U	N1-C1'-C2'	5.36	122.04	114.00
1	2	912	U	C2'-C3'-O3'	5.35	121.72	113.70
1	2	804	A	C1'-C2'-O2'	5.34	119.81	111.80
1	2	1658	G	N9-C1'-C2'	5.31	119.97	112.00
1	2	220	A	N1-C6-N6	-5.30	102.71	118.60
1	2	383	G	C2'-C3'-O3'	-5.29	105.77	113.70
1	2	1092	A	N9-C1'-C2'	5.27	119.90	112.00
1	2	831	U	N1-C1'-C2'	5.26	119.89	112.00
24	b	28	ARG	C-N-CD	-5.26	109.04	120.60
1	2	103	A	C4'-C3'-O3'	-5.25	105.12	113.00
1	2	310	C	P-O5'-C5'	-5.25	113.02	120.90
1	2	831	U	O4'-C1'-C2'	-5.25	102.35	107.60
1	2	402	C	C2'-C3'-O3'	-5.25	105.83	113.70
1	2	224	C	C2'-C3'-O3'	5.24	121.56	113.70
29	g	43	ARG	CG-CD-NE	-5.23	100.50	112.00
1	2	351	C	P-O5'-C5'	-5.17	113.14	120.90
1	2	99	C	C4'-C3'-O3'	5.16	117.14	109.40
12	P	109	ASN	CA-C-N	5.16	131.40	121.54
12	P	109	ASN	C-N-CA	5.16	131.40	121.54
1	2	863	A	O3'-P-O5'	-5.15	96.27	104.00
1	2	618	U	C2'-C3'-O3'	-5.14	105.98	113.70
1	2	280	U	C4'-C3'-O3'	5.13	117.10	109.40
1	2	493	U	C4'-C3'-O3'	5.11	117.06	109.40
2	D	117	GLY	N-CA-C	5.11	118.73	112.14
1	2	804	A	C2'-C3'-O3'	5.10	117.15	109.50
1	2	1332	C	C2'-C3'-O3'	5.09	117.13	109.50
1	2	1568	C	C4'-C3'-O3'	5.07	117.01	109.40
15	S	3	ARG	N-CA-C	5.06	116.83	110.91
1	2	400	A	C2'-C3'-O3'	5.06	117.09	109.50
28	t	205	GLN	N-CA-C	5.06	121.57	110.80
1	2	819	G	C4'-C3'-O3'	5.02	116.92	109.40

There are no chirality outliers.

All (57) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2	1086	A	Sidechain
1	2	1143	A	Sidechain
1	2	1595	U	Sidechain
1	2	222	A	Sidechain
1	2	236	A	Sidechain
1	2	440	U	Sidechain
1	2	507	U	Sidechain
1	2	618	U	Sidechain
1	2	857	U	Sidechain
1	2	863	A	Sidechain
1	2	964	U	Sidechain
3	B	57	SER	Peptide
4	C	22	PRO	Peptide
4	C	87	GLU	Peptide
2	D	107	ASP	Peptide
5	E	21	ASP	Peptide
5	E	45	PHE	Peptide
6	F	13	LYS	Peptide
6	F	41	PRO	Peptide
9	K	103	ARG	Peptide
9	K	54	VAL	Peptide
9	K	96	SER	Peptide
12	P	110	TYR	Peptide
12	P	166	GLY	Peptide
12	P	190	ASP	Peptide
13	Q	176	VAL	Peptide
13	Q	177	GLN	Peptide
13	Q	179	SER	Peptide
13	Q	214	LYS	Peptide
13	Q	54	LEU	Peptide
14	R	39	THR	Peptide
15	S	68	ARG	Peptide
17	U	47	ARG	Peptide
17	U	64	VAL	Peptide
17	U	97	ARG	Peptide
18	V	25	ARG	Sidechain
19	W	119	ALA	Peptide
19	W	163	PRO	Peptide
20	X	5	LEU	Peptide
21	Y	22	ALA	Peptide
22	Z	123	SER	Peptide
23	a	43	GLY	Peptide
23	a	45	ALA	Peptide

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Mol	Chain	Res	Type	Group
23	a	80	LYS	Peptide
24	b	54	ASP	Peptide
25	c	111	GLY	Peptide
29	g	46	ASN	Peptide
31	r	152	MET	Peptide
31	r	91	ARG	Peptide
28	t	350	ALA	Peptide
28	t	518	ASP	Peptide
28	t	713	THR	Peptide
28	t	714	VAL	Peptide
28	t	731	LYS	Peptide
28	t	737	THR	Peptide
28	t	742	SER	Peptide
28	t	753	GLY	Peptide

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	35695	0	17919	699	0
2	D	892	0	892	16	0
3	B	1592	0	1660	45	0
4	C	871	0	876	18	0
5	E	928	0	960	33	0
6	F	1105	0	1164	57	0
7	H	1009	0	1029	24	0
8	I	1112	0	1124	48	0
9	K	519	0	558	15	0
10	L	486	0	522	9	0
11	N	397	0	398	45	0
12	P	1577	0	1567	33	0
13	Q	1709	0	1784	53	0
14	R	1662	0	1762	30	0
15	S	2068	0	2154	56	0
16	T	1799	0	1879	50	0
17	U	1481	0	1572	40	0
18	V	1489	0	1525	28	0
19	W	1494	0	1573	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	X	1213	0	1257	16	0
21	Y	1192	0	1255	24	0
22	Z	891	0	883	26	0
23	a	684	0	672	10	0
24	b	1021	0	1060	15	0
25	c	1121	0	1196	28	0
26	d	1073	0	1132	32	0
27	f	610	0	633	9	0
28	t	5037	0	4895	134	0
29	g	475	0	525	23	0
30	p	1473	0	1554	42	0
31	r	2166	0	2176	377	0
32	e	1045	0	266	39	0
All	All	75886	0	58422	1672	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 13.

All (1672) 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)
1:2:565:C:H5''	31:r:47:SER:CB	1.18	1.62
31:r:198:ARG:HG3	31:r:233:PHE:CD2	1.17	1.60
1:2:1235:C:N1	1:2:1235:C:C1'	1.68	1.56
1:2:1269:U:H3	32:e:296:ASP:C	1.08	1.56
11:N:121:CYS:SG	11:N:145:HIS:CD2	2.02	1.53
31:r:198:ARG:HG3	31:r:233:PHE:CE2	1.42	1.52
1:2:577:G:C6	31:r:49:THR:N	1.74	1.46
31:r:198:ARG:CG	31:r:233:PHE:CE2	1.98	1.45
1:2:1269:U:C2	32:e:296:ASP:O	1.70	1.43
11:N:123:ASN:ND2	11:N:145:HIS:CA	1.82	1.39
1:2:565:C:C5'	31:r:47:SER:HB2	1.58	1.34
1:2:565:C:C5'	31:r:47:SER:CB	2.06	1.34
31:r:198:ARG:CG	31:r:233:PHE:CD2	2.08	1.34
31:r:235:ILE:CG1	31:r:250:VAL:C	2.01	1.33
1:2:1269:U:C4	32:e:296:ASP:O	1.84	1.31
11:N:143:LYS:HB3	11:N:145:HIS:CE1	1.65	1.31
31:r:235:ILE:HG13	31:r:251:VAL:N	1.40	1.31
31:r:195:TYR:C	31:r:236:MET:HG2	1.62	1.24
31:r:235:ILE:HG13	31:r:251:VAL:CA	1.62	1.23
31:r:235:ILE:HA	31:r:250:VAL:O	1.29	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:576:G:C6	31:r:46:GLN:HG2	1.75	1.21
28:t:734:PRO:HB3	31:r:9:ARG:NH1	1.55	1.20
1:2:1244:A:OP1	32:e:226:HIS:O	1.60	1.20
31:r:235:ILE:HG12	31:r:250:VAL:C	1.63	1.20
1:2:451:A:C6	1:2:453:U:O2	1.94	1.19
11:N:123:ASN:ND2	11:N:145:HIS:HA	0.87	1.19
1:2:1263:G:C2	1:2:1264:G:H1'	1.77	1.19
28:t:734:PRO:HD3	31:r:9:ARG:NH2	1.58	1.18
1:2:1435:G:H5'	32:e:331:ASN:CA	1.73	1.18
28:t:734:PRO:CD	31:r:9:ARG:HH22	1.56	1.18
1:2:1221:A:C6	1:2:1263:G:C2	2.32	1.17
31:r:2:LYS:O	31:r:141:TYR:CZ	1.97	1.17
31:r:235:ILE:CA	31:r:250:VAL:O	1.92	1.17
31:r:235:ILE:HG13	31:r:250:VAL:C	1.64	1.16
1:2:577:G:C1'	31:r:51:ARG:N	2.10	1.13
6:F:143:ARG:HH12	31:r:129:ARG:HB2	0.99	1.13
1:2:577:G:O2'	31:r:51:ARG:HA	1.46	1.12
6:F:143:ARG:HH12	31:r:129:ARG:CB	1.60	1.13
1:2:66:U:OP1	16:T:136:LYS:NZ	1.81	1.12
1:2:577:G:C5	31:r:49:THR:N	2.17	1.12
1:2:1622:G:H5''	31:r:144:LYS:CB	1.78	1.12
1:2:577:G:C1'	31:r:51:ARG:H	1.63	1.12
1:2:1080:U:O4	1:2:1091:A:N1	1.81	1.12
1:2:1269:U:O2	32:e:296:ASP:CA	1.99	1.11
11:N:123:ASN:CB	11:N:145:HIS:HB3	1.80	1.10
1:2:577:G:H1'	31:r:51:ARG:CB	1.81	1.10
11:N:121:CYS:SG	11:N:145:HIS:CG	2.44	1.10
28:t:734:PRO:HD3	31:r:9:ARG:HH22	0.99	1.10
1:2:565:C:H5''	31:r:47:SER:OG	1.52	1.09
1:2:1622:G:C5'	31:r:144:LYS:HD2	1.82	1.09
1:2:1575:G:N2	31:r:233:PHE:HB3	1.67	1.08
31:r:65:MET:HE2	31:r:65:MET:HA	1.33	1.08
1:2:1220:C:N4	1:2:1264:G:N2	1.99	1.08
1:2:1575:G:C2	31:r:233:PHE:CG	2.42	1.08
6:F:143:ARG:NH1	31:r:129:ARG:HB2	1.68	1.07
11:N:123:ASN:HD22	11:N:145:HIS:CA	1.56	1.07
1:2:577:G:H1'	31:r:51:ARG:HB3	1.28	1.06
31:r:229:ASP:O	31:r:234:ASN:ND2	1.88	1.06
11:N:143:LYS:CB	11:N:145:HIS:CE1	2.39	1.05
31:r:196:PRO:N	31:r:236:MET:HG2	1.68	1.04
1:2:1622:G:H5'	31:r:144:LYS:HD2	1.39	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:235:ILE:HD13	31:r:249:PHE:HB3	1.40	1.04
1:2:565:C:H5''	31:r:47:SER:HB2	1.09	1.04
11:N:143:LYS:HD3	11:N:144:CYS:H	1.22	1.04
28:t:734:PRO:CB	31:r:9:ARG:HH12	1.70	1.04
1:2:220:A:N7	1:2:831:U:N3	2.04	1.03
1:2:1575:G:N2	31:r:233:PHE:CB	2.23	1.02
31:r:235:ILE:CD1	31:r:249:PHE:HB3	1.90	1.02
1:2:1220:C:N4	1:2:1264:G:H21	1.57	1.01
1:2:1257:U:O2'	32:e:312:TYR:O	1.77	1.01
1:2:565:C:H5''	31:r:47:SER:HB3	1.38	1.01
31:r:235:ILE:CG1	31:r:250:VAL:O	2.08	1.01
1:2:1057:U:O2	1:2:1062:A:N6	1.94	1.01
11:N:123:ASN:HB2	11:N:145:HIS:HB3	1.01	1.00
1:2:1066:C:H4'	13:Q:149:GLN:HE22	1.23	1.00
1:2:1622:G:H5''	31:r:144:LYS:HB2	1.41	1.00
1:2:565:C:H2'	31:r:45:SER:HB3	1.43	1.00
1:2:577:G:O2'	31:r:51:ARG:CA	2.10	1.00
1:2:1263:G:N3	1:2:1264:G:H1'	1.76	1.00
1:2:1263:G:N1	1:2:1264:G:N3	2.10	0.99
11:N:123:ASN:CG	11:N:145:HIS:HA	1.87	0.98
11:N:123:ASN:HD21	11:N:145:HIS:HA	1.21	0.98
1:2:1219:A:C8	1:2:1265:G:N2	2.30	0.98
1:2:577:G:C2'	31:r:51:ARG:N	2.26	0.98
1:2:1335:U:H3	1:2:1416:G:H1	1.03	0.98
1:2:565:C:C4'	31:r:47:SER:HB2	1.95	0.97
1:2:565:C:H3'	31:r:47:SER:HB3	1.44	0.97
1:2:577:G:N1	31:r:49:THR:N	1.91	0.96
31:r:2:LYS:O	31:r:141:TYR:OH	1.81	0.96
28:t:742:SER:OG	31:r:10:TYR:CG	2.18	0.96
1:2:1221:A:N6	1:2:1263:G:N1	2.13	0.96
1:2:1221:A:C5	1:2:1263:G:N2	2.34	0.96
1:2:1575:G:C2	31:r:233:PHE:CD2	2.54	0.96
1:2:577:G:C6	31:r:49:THR:CA	2.39	0.96
31:r:198:ARG:NE	31:r:233:PHE:CE2	2.33	0.96
1:2:1263:G:N2	1:2:1264:G:H1'	1.81	0.95
11:N:123:ASN:HB2	11:N:145:HIS:CB	1.97	0.95
1:2:577:G:N9	31:r:51:ARG:N	2.09	0.95
11:N:123:ASN:OD1	11:N:124:PRO:HD2	1.68	0.93
1:2:1229:G:N2	1:2:1256:A:H62	1.66	0.93
1:2:657:U:H3	1:2:676:G:H1	1.01	0.93
1:2:1265:G:O2'	1:2:1266:U:C6	2.19	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:198:ARG:HG2	31:r:233:PHE:CZ	2.04	0.92
1:2:993:A:H62	1:2:1011:G:H21	1.01	0.92
31:r:198:ARG:HG2	31:r:233:PHE:CE2	2.00	0.92
1:2:486:G:H1	1:2:501:U:H3	0.96	0.91
1:2:742:U:O2'	17:U:106:SER:O	1.86	0.91
1:2:1220:C:H42	1:2:1264:G:N2	1.60	0.91
1:2:1269:U:N3	32:e:296:ASP:C	1.86	0.90
30:p:107:THR:O	30:p:111:ASN:HB2	1.71	0.90
11:N:147:VAL:O	11:N:148:TYR:HB2	1.68	0.90
1:2:229:U:H3	1:2:236:A:N6	1.68	0.90
28:t:53:GLN:HB3	28:t:54:ARG:HH21	1.34	0.89
31:r:195:TYR:C	31:r:236:MET:CG	2.45	0.89
31:r:198:ARG:CD	31:r:233:PHE:CE2	2.56	0.89
1:2:1263:G:N3	1:2:1264:G:C1'	2.37	0.88
1:2:24:U:OP1	19:W:10:LYS:NZ	2.07	0.88
1:2:993:A:H62	1:2:1011:G:N2	1.72	0.88
1:2:223:U:H3	1:2:838:G:H1	0.94	0.88
1:2:1221:A:C6	1:2:1263:G:N1	2.42	0.88
1:2:885:G:OP1	13:Q:136:ARG:NH2	2.06	0.88
1:2:1038:U:O4	1:2:1092:A:N1	2.07	0.87
1:2:1575:G:N1	31:r:233:PHE:CD2	2.42	0.87
1:2:1622:G:C5'	31:r:144:LYS:CD	2.53	0.87
1:2:451:A:C5	1:2:453:U:O2	2.27	0.87
31:r:236:MET:N	31:r:250:VAL:O	2.07	0.87
1:2:1149:G:N3	31:r:146:ASN:HB2	1.90	0.86
1:2:1243:G:C8	32:e:230:PRO:CA	2.58	0.86
31:r:2:LYS:HB3	31:r:141:TYR:CE1	2.10	0.86
31:r:198:ARG:CG	31:r:233:PHE:CZ	2.59	0.86
1:2:814:A:N1	1:2:857:U:O4	2.08	0.85
1:2:577:G:C1'	31:r:51:ARG:HB3	2.06	0.85
11:N:143:LYS:CB	11:N:145:HIS:HE1	1.89	0.85
1:2:51:A:N1	1:2:440:U:O4	2.09	0.85
1:2:1294:G:H4'	12:P:109:ASN:CG	2.02	0.85
1:2:1221:A:C5	1:2:1263:G:C2	2.65	0.84
31:r:2:LYS:HB3	31:r:141:TYR:CD1	2.12	0.84
1:2:577:G:H1'	31:r:51:ARG:N	1.91	0.84
31:r:198:ARG:NE	31:r:233:PHE:HE2	1.74	0.84
1:2:1294:G:O6	1:2:1303:U:N3	2.10	0.84
1:2:1263:G:C2	1:2:1264:G:C1'	2.60	0.83
1:2:1150:G:H1	1:2:1628:U:H3	1.23	0.83
1:2:1263:G:C6	1:2:1264:G:C2	2.67	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:235:ILE:CG1	31:r:251:VAL:CA	2.54	0.83
8:I:128:GLY:O	8:I:132:LEU:HB2	1.79	0.82
31:r:235:ILE:CG1	31:r:251:VAL:N	2.26	0.82
1:2:1654:G:H21	1:2:1746:A:H62	1.22	0.82
1:2:1654:G:N2	1:2:1746:A:H62	1.77	0.82
1:2:577:G:C2'	31:r:51:ARG:CA	2.58	0.82
1:2:1622:G:H5'	31:r:144:LYS:CD	2.09	0.82
15:S:253:ASP:O	15:S:257:ALA:HB3	1.78	0.82
1:2:1263:G:H2'	1:2:1264:G:C8	2.14	0.82
11:N:147:VAL:HG12	11:N:148:TYR:N	1.95	0.82
31:r:103:VAL:HG13	31:r:129:ARG:HH22	1.45	0.82
1:2:590:C:P	29:g:43:ARG:HH21	2.02	0.81
1:2:863:A:N7	1:2:964:U:O4	2.13	0.81
1:2:358:U:OP2	28:t:53:GLN:NE2	2.14	0.81
31:r:77:TYR:HD1	31:r:152:MET:HG3	1.45	0.81
1:2:229:U:N3	1:2:236:A:N6	2.28	0.81
1:2:1257:U:O2'	32:e:312:TYR:C	2.23	0.81
1:2:1269:U:N3	32:e:296:ASP:O	0.66	0.81
1:2:1257:U:O2'	32:e:312:TYR:CA	2.28	0.81
1:2:1219:A:C8	1:2:1265:G:C2	2.69	0.81
1:2:1269:U:C2	32:e:296:ASP:C	2.45	0.81
31:r:235:ILE:HG12	31:r:250:VAL:N	1.95	0.81
1:2:577:G:H2'	31:r:50:ASN:C	2.06	0.81
31:r:235:ILE:HG12	31:r:250:VAL:O	1.71	0.81
11:N:147:VAL:O	11:N:148:TYR:CB	2.29	0.80
3:B:198:LEU:O	3:B:202:ALA:HB2	1.80	0.80
25:c:66:SER:HB3	31:r:45:SER:HA	1.62	0.80
31:r:198:ARG:HB2	31:r:233:PHE:HA	1.64	0.80
19:W:178:ALA:O	19:W:182:GLU:HB3	1.80	0.80
1:2:1588:G:H1	1:2:1608:U:H3	1.29	0.79
31:r:5:THR:HA	31:r:8:MET:HE3	1.64	0.79
1:2:1575:G:N2	31:r:233:PHE:CG	2.48	0.79
1:2:1057:U:C2	1:2:1062:A:N6	2.49	0.79
1:2:1654:G:H21	1:2:1746:A:N6	1.81	0.79
1:2:577:G:C5	31:r:49:THR:CA	2.61	0.79
28:t:734:PRO:HB3	31:r:9:ARG:HH12	0.74	0.79
1:2:1577:A:H1'	31:r:105:LYS:NZ	1.97	0.79
1:2:577:G:N2	31:r:47:SER:N	2.22	0.78
1:2:222:A:N6	1:2:833:U:H3	1.81	0.78
1:2:742:U:H1'	17:U:107:ARG:HA	1.64	0.78
1:2:1442:U:H1'	28:t:766:GLN:NE2	1.99	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:235:ILE:HG13	31:r:251:VAL:HA	1.62	0.78
1:2:1572:G:OP1	31:r:282:LYS:NZ	2.17	0.78
6:F:85:ILE:O	6:F:89:LEU:HB2	1.84	0.78
1:2:577:G:C2	31:r:49:THR:N	2.51	0.77
31:r:212:ASP:O	31:r:216:PHE:N	2.17	0.77
1:2:703:G:N2	1:2:735:C:C2	2.53	0.77
19:W:112:GLN:O	19:W:116:LEU:HB2	1.84	0.77
28:t:742:SER:O	31:r:10:TYR:CZ	2.37	0.77
28:t:734:PRO:CG	31:r:9:ARG:HH22	1.98	0.76
1:2:332:U:O2'	18:V:5:ARG:NH1	2.18	0.76
11:N:143:LYS:HD3	11:N:144:CYS:N	2.00	0.76
11:N:123:ASN:HD22	11:N:145:HIS:HA	0.94	0.76
1:2:577:G:H1'	31:r:51:ARG:H	1.44	0.76
31:r:230:PHE:HA	31:r:234:ASN:HD21	1.50	0.76
1:2:1057:U:N3	1:2:1062:A:N6	2.33	0.76
6:F:143:ARG:NH1	31:r:129:ARG:CB	2.37	0.76
30:p:118:PRO:O	30:p:122:GLU:HB2	1.86	0.75
1:2:1235:C:C1'	1:2:1235:C:C6	2.69	0.75
4:C:77:GLU:O	4:C:81:LYS:HB2	1.85	0.75
1:2:1149:G:H1'	31:r:146:ASN:HB2	1.68	0.75
31:r:227:HIS:O	31:r:256:GLN:NE2	2.18	0.75
1:2:1575:G:C6	31:r:233:PHE:CE2	2.75	0.75
1:2:577:G:H1'	31:r:51:ARG:CA	2.17	0.75
30:p:259:VAL:O	30:p:263:LEU:HB2	1.86	0.75
1:2:1229:G:H21	1:2:1256:A:H62	1.35	0.74
32:e:301:TYR:O	32:e:304:TYR:N	2.20	0.74
1:2:1265:G:O2'	1:2:1266:U:H6	1.68	0.74
1:2:1622:G:H5''	31:r:144:LYS:HB3	1.68	0.74
1:2:993:A:N6	1:2:1011:G:H21	1.82	0.74
7:H:67:GLU:O	7:H:71:GLN:HB2	1.88	0.74
31:r:124:ILE:HG13	31:r:186:ILE:HG12	1.69	0.74
31:r:235:ILE:C	31:r:250:VAL:O	2.29	0.74
31:r:65:MET:HE2	31:r:65:MET:CA	2.15	0.74
17:U:79:ARG:O	17:U:83:LYS:HB2	1.88	0.73
31:r:12:THR:HG21	31:r:51:ARG:HH22	1.51	0.73
31:r:230:PHE:CA	31:r:234:ASN:HD21	2.01	0.73
1:2:811:A:C4	17:U:110:GLN:NE2	2.56	0.73
18:V:57:ALA:HB2	18:V:177:GLY:HA2	1.70	0.73
25:c:66:SER:O	31:r:45:SER:HB2	1.88	0.73
11:N:147:VAL:HG12	11:N:148:TYR:H	1.52	0.73
31:r:32:VAL:HG13	31:r:36:LEU:HD23	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1229:G:H21	1:2:1256:A:N6	1.86	0.73
1:2:1435:G:H5'	32:e:332:VAL:N	2.04	0.73
31:r:198:ARG:HE	31:r:233:PHE:HE2	1.25	0.73
31:r:220:LEU:HD13	31:r:227:HIS:HB2	1.69	0.73
14:R:38:VAL:HG13	14:R:39:THR:HG23	1.71	0.73
1:2:349:U:OP2	20:X:106:ASN:ND2	2.21	0.73
1:2:1263:G:C2	1:2:1264:G:N3	2.56	0.73
31:r:2:LYS:O	31:r:141:TYR:CE2	2.42	0.73
1:2:577:G:H2'	31:r:51:ARG:N	2.02	0.72
1:2:1221:A:N6	1:2:1263:G:C6	2.56	0.72
31:r:232:GLU:HG3	31:r:233:PHE:CD1	2.24	0.72
1:2:565:C:H2'	31:r:45:SER:CB	2.18	0.72
1:2:565:C:C2'	31:r:45:SER:HB3	2.18	0.72
1:2:1291:G:H1	1:2:1324:G:H22	1.35	0.72
1:2:522:U:C1'	26:d:34:ASN:HD21	2.03	0.72
1:2:1435:G:C5'	32:e:331:ASN:CA	2.60	0.72
5:E:56:PHE:O	5:E:60:LEU:HB2	1.89	0.72
31:r:95:TYR:N	31:r:113:SER:O	2.20	0.72
31:r:196:PRO:N	31:r:236:MET:CG	2.51	0.72
29:g:43:ARG:NH1	29:g:56:MET:SD	2.63	0.71
1:2:1622:G:H5''	31:r:144:LYS:CD	2.17	0.71
1:2:1605:G:OP2	6:F:127:LYS:NZ	2.22	0.71
31:r:93:THR:HG23	31:r:94:VAL:HG22	1.72	0.71
1:2:222:A:N6	1:2:833:U:N3	2.38	0.71
1:2:151:G:N3	16:T:13:GLN:NE2	2.37	0.71
1:2:331:A:OP2	18:V:175:GLN:NE2	2.21	0.71
1:2:565:C:C4'	31:r:47:SER:CB	2.62	0.71
1:2:179:A:N1	16:T:202:ARG:NH2	2.37	0.71
1:2:1473:U:O2'	3:B:103:ASN:ND2	2.23	0.71
1:2:1339:C:O2'	1:2:1341:A:N7	2.24	0.70
11:N:121:CYS:SG	11:N:145:HIS:NE2	2.64	0.70
1:2:220:A:N7	1:2:831:U:C2	2.58	0.70
12:P:30:GLN:HE22	12:P:149:LEU:HB3	1.55	0.70
1:2:68:A:OP1	16:T:160:ARG:NH2	2.24	0.70
1:2:478:A:O2'	19:W:124:HIS:ND1	2.23	0.70
1:2:1080:U:O4	1:2:1091:A:C2	2.44	0.70
31:r:198:ARG:C	31:r:198:ARG:HD3	2.16	0.70
1:2:868:G:H1	1:2:960:U:H3	1.38	0.70
1:2:1575:G:H21	31:r:233:PHE:CB	2.03	0.70
1:2:1294:G:OP1	12:P:109:ASN:ND2	2.24	0.70
1:2:1263:G:C6	1:2:1264:G:C4	2.80	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:565:C:C3'	31:r:47:SER:HB3	2.21	0.70
1:2:895:G:H1	1:2:917:U:H3	1.37	0.70
1:2:577:G:O2'	31:r:51:ARG:CB	2.40	0.70
1:2:1263:G:C2	1:2:1264:G:C4	2.79	0.70
1:2:1575:G:N1	31:r:233:PHE:CE2	2.60	0.70
1:2:1435:G:C5'	32:e:332:VAL:H	2.04	0.69
1:2:1474:G:OP1	3:B:109:LYS:NZ	2.21	0.69
28:t:53:GLN:C	28:t:55:LYS:H	1.98	0.69
31:r:114:ASP:OD1	31:r:115:LYS:N	2.25	0.69
1:2:1269:U:C2	32:e:296:ASP:CA	2.74	0.69
19:W:77:ILE:HD11	19:W:93:LEU:HB2	1.75	0.69
1:2:1263:G:H2'	1:2:1264:G:O4'	1.92	0.69
1:2:1435:G:H5'	32:e:332:VAL:H	1.56	0.69
31:r:142:LEU:HD23	31:r:144:LYS:HE3	1.74	0.69
25:c:66:SER:O	31:r:45:SER:CB	2.40	0.69
28:t:727:VAL:HG11	28:t:747:GLU:HG2	1.74	0.69
1:2:565:C:H3'	31:r:47:SER:CB	2.22	0.69
1:2:789:A:O2'	15:S:106:LYS:NZ	2.25	0.69
28:t:54:ARG:HE	28:t:54:ARG:N	1.91	0.69
1:2:229:U:C4	1:2:236:A:N6	2.61	0.69
13:Q:32:ILE:HB	13:Q:44:GLY:HA3	1.75	0.69
11:N:143:LYS:CD	11:N:144:CYS:H	2.04	0.68
31:r:235:ILE:CB	31:r:250:VAL:O	2.41	0.68
1:2:46:A:O4'	28:t:62:ARG:NH2	2.26	0.68
1:2:1442:U:O2'	28:t:766:GLN:NE2	2.26	0.68
12:P:15:GLN:O	12:P:19:ALA:HB2	1.93	0.68
15:S:191:ARG:HH11	15:S:245:LYS:HB3	1.58	0.68
31:r:149:ALA:O	31:r:153:HIS:N	2.25	0.68
1:2:950:C:O2'	21:Y:104:ARG:NH1	2.27	0.68
1:2:1263:G:C6	1:2:1264:G:N3	2.62	0.68
31:r:65:MET:HA	31:r:65:MET:CE	2.18	0.68
31:r:198:ARG:HD3	31:r:198:ARG:O	1.94	0.68
1:2:1577:A:H1'	31:r:105:LYS:HZ1	1.56	0.68
31:r:198:ARG:CG	31:r:233:PHE:CG	2.74	0.68
1:2:1244:A:OP1	32:e:227:GLY:HA3	1.62	0.68
1:2:1250:U:H1'	11:N:140:TYR:HB3	1.76	0.67
1:2:1263:G:N1	1:2:1264:G:C2	2.61	0.67
1:2:1263:G:H2'	1:2:1264:G:H8	1.57	0.67
2:D:67:THR:HG22	2:D:68:GLU:HG3	1.76	0.67
25:c:66:SER:HB3	31:r:45:SER:CA	2.24	0.67
31:r:235:ILE:HG12	31:r:250:VAL:CA	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:142:G:H22	1:2:173:A:H2	1.42	0.67
12:P:131:GLN:O	12:P:135:GLU:HB3	1.94	0.67
9:K:46:LYS:HA	9:K:49:ARG:HB3	1.76	0.67
1:2:703:G:C2	1:2:735:C:N3	2.62	0.67
1:2:1159:C:HO2'	6:F:142:TYR:HH	1.40	0.66
1:2:1243:G:H8	32:e:230:PRO:CA	2.04	0.66
22:Z:102:LEU:HB3	30:p:153:GLN:HE22	1.59	0.66
31:r:2:LYS:HE3	31:r:151:TRP:CH2	2.29	0.66
1:2:222:A:N7	1:2:833:U:O2	2.29	0.66
31:r:206:ILE:HD13	31:r:286:TYR:HB3	1.77	0.66
8:I:114:VAL:HG22	8:I:122:ARG:HG2	1.78	0.66
28:t:54:ARG:O	28:t:57:LYS:N	2.28	0.66
31:r:8:MET:HG2	31:r:82:TYR:CE1	2.30	0.66
31:r:64:LYS:O	31:r:65:MET:CE	2.43	0.66
31:r:230:PHE:HA	31:r:234:ASN:ND2	2.11	0.66
31:r:77:TYR:CD1	31:r:152:MET:HG3	2.30	0.66
28:t:212:LEU:O	28:t:216:PHE:HB2	1.96	0.66
1:2:208:U:H1'	18:V:178:ARG:HD2	1.77	0.65
5:E:111:MET:HG2	7:H:119:ILE:HG23	1.78	0.65
31:r:197:MET:HA	31:r:200:LEU:HB2	1.78	0.65
31:r:235:ILE:HD11	31:r:249:PHE:HB3	1.73	0.65
1:2:1446:A:N7	28:t:718:ARG:NH2	2.44	0.65
28:t:742:SER:OG	31:r:10:TYR:CD1	2.44	0.65
30:p:191:LYS:NZ	30:p:193:LEU:O	2.29	0.65
31:r:227:HIS:CE1	31:r:229:ASP:HB3	2.32	0.65
1:2:222:A:N7	1:2:833:U:C2	2.64	0.65
1:2:1235:C:N1	1:2:1235:C:H1'	2.04	0.65
1:2:1257:U:H1'	32:e:312:TYR:O	1.96	0.65
31:r:190:GLU:HG2	31:r:192:ILE:H	1.62	0.65
1:2:1435:G:H5'	32:e:331:ASN:C	2.21	0.65
18:V:61:GLU:HG3	18:V:62:THR:HG23	1.78	0.65
28:t:742:SER:OG	31:r:10:TYR:CD2	2.48	0.65
1:2:925:G:H21	1:2:988:A:H1'	1.62	0.65
28:t:279:GLU:HG2	28:t:558:ARG:HG2	1.77	0.65
1:2:491:C:N4	1:2:494:U:O2'	2.28	0.65
1:2:1149:G:N3	31:r:146:ASN:CB	2.43	0.65
1:2:1656:U:H2'	1:2:1658:G:H1'	1.77	0.65
6:F:143:ARG:CZ	31:r:129:ARG:HB2	2.26	0.65
15:S:185:GLY:H	15:S:189:LEU:HD13	1.62	0.65
31:r:232:GLU:O	31:r:233:PHE:HB2	1.96	0.65
1:2:1257:U:C2'	32:e:312:TYR:O	2.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1499:G:H1	1:2:1508:U:H3	1.45	0.65
25:c:66:SER:HB3	31:r:45:SER:CB	2.26	0.65
28:t:273:SER:HA	28:t:564:PRO:HA	1.79	0.65
31:r:50:ASN:O	31:r:54:SER:N	2.20	0.65
1:2:188:A:H62	1:2:197:A:H8	1.43	0.65
1:2:565:C:O4'	31:r:47:SER:HB2	1.96	0.65
1:2:1622:G:C5'	31:r:144:LYS:HB2	2.23	0.64
15:S:68:ARG:O	15:S:70:VAL:N	2.27	0.64
28:t:196:SER:HB3	28:t:200:GLU:HG3	1.78	0.64
31:r:199:ARG:O	31:r:201:ARG:NH1	2.30	0.64
1:2:141:U:H2'	16:T:183:ARG:HH22	1.61	0.64
1:2:576:G:N1	31:r:46:GLN:HG2	2.12	0.64
19:W:113:VAL:HG12	19:W:119:ALA:HB2	1.80	0.64
31:r:196:PRO:CA	31:r:236:MET:HG2	2.26	0.64
1:2:1307:U:H3	1:2:1318:G:H21	1.44	0.64
16:T:39:GLU:HG3	16:T:46:LYS:HG3	1.80	0.64
1:2:577:G:C4	31:r:49:THR:N	2.65	0.64
28:t:727:VAL:HG13	28:t:731:LYS:HD2	1.80	0.64
30:p:101:VAL:HG12	30:p:163:THR:HG22	1.80	0.64
32:e:305:ARG:O	32:e:307:VAL:N	2.30	0.64
1:2:1245:G:N1	1:2:1250:U:C4	2.66	0.64
2:D:49:THR:HA	2:D:52:LEU:HB2	1.79	0.63
31:r:104:GLY:O	31:r:129:ARG:NH1	2.31	0.63
1:2:451:A:C5	1:2:453:U:C2	2.86	0.63
1:2:961:U:H5''	21:Y:71:ILE:HD13	1.79	0.63
10:L:10:ALA:HB3	10:L:54:LEU:HB2	1.80	0.63
1:2:1022:C:O2'	1:2:1125:A:N1	2.31	0.63
8:I:93:HIS:NE2	8:I:95:ASP:OD1	2.32	0.63
28:t:177:ILE:O	28:t:181:GLU:HB2	1.99	0.63
31:r:198:ARG:HB2	31:r:233:PHE:CA	2.28	0.63
1:2:1221:A:N1	1:2:1263:G:C4	2.67	0.62
1:2:1366:U:O2'	8:I:7:ARG:NH1	2.32	0.62
31:r:100:THR:HB	31:r:111:LYS:HG3	1.81	0.62
1:2:1488:G:H3'	1:2:1515:A:H61	1.64	0.62
1:2:1583:A:N6	1:2:1612:U:OP2	2.32	0.62
5:E:59:LYS:O	5:E:63:ALA:HB3	1.99	0.62
15:S:11:ARG:O	15:S:12:LEU:HB2	1.98	0.62
31:r:2:LYS:CB	31:r:141:TYR:CD1	2.82	0.62
25:c:102:VAL:HG12	25:c:127:VAL:HG12	1.82	0.62
1:2:1213:G:N2	1:2:1450:U:O2	2.31	0.62
31:r:85:LEU:HA	31:r:88:MET:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1066:C:H4'	13:Q:149:GLN:NE2	2.06	0.62
1:2:1263:G:N1	1:2:1264:G:C4	2.68	0.62
1:2:1335:U:O2	1:2:1416:G:N2	2.23	0.62
1:2:967:A:OP2	21:Y:124:ARG:NH2	2.30	0.62
31:r:196:PRO:HD2	31:r:199:ARG:NE	2.14	0.62
1:2:703:G:C2	1:2:735:C:C2	2.87	0.62
31:r:218:VAL:HA	31:r:221:ALA:HB3	1.81	0.62
1:2:811:A:C6	17:U:110:GLN:HG3	2.35	0.62
31:r:3:LEU:HD23	31:r:110:TYR:OH	2.00	0.62
1:2:222:A:N7	1:2:833:U:N3	2.47	0.61
32:e:404:SER:C	32:e:406:GLY:HA2	2.25	0.61
1:2:1163:A:N3	1:2:1613:U:O2'	2.31	0.61
1:2:1269:U:O2	32:e:296:ASP:C	2.41	0.61
11:N:143:LYS:HB2	11:N:145:HIS:HE1	1.64	0.61
31:r:80:ILE:HG23	31:r:184:ARG:HD2	1.81	0.61
1:2:332:U:OP1	18:V:31:ARG:NH1	2.29	0.61
1:2:1446:A:C8	28:t:718:ARG:NH2	2.68	0.61
5:E:61:ARG:O	5:E:65:LEU:HB2	2.00	0.61
22:Z:85:ALA:H	22:Z:119:THR:HG22	1.65	0.61
25:c:143:PRO:HG3	28:t:220:PHE:HB3	1.83	0.61
1:2:1221:A:C2	1:2:1263:G:N3	2.68	0.61
1:2:1575:G:H21	31:r:233:PHE:HB3	1.55	0.61
31:r:2:LYS:HA	31:r:141:TYR:CD2	2.35	0.61
1:2:1066:C:C4'	13:Q:149:GLN:HE22	2.05	0.61
1:2:1219:A:C5	1:2:1265:G:N3	2.69	0.61
1:2:1542:G:N2	1:2:1569:A:OP2	2.33	0.61
1:2:1577:A:C1'	31:r:105:LYS:NZ	2.63	0.61
28:t:741:ARG:HH12	28:t:764:SER:HB3	1.65	0.61
1:2:511:A:OP2	19:W:176:ASN:ND2	2.25	0.61
1:2:1235:C:C1'	1:2:1235:C:C2	2.81	0.61
1:2:268:C:OP1	16:T:176:GLN:NE2	2.34	0.61
1:2:334:G:O6	18:V:5:ARG:NH2	2.34	0.61
1:2:861:U:OP1	21:Y:64:ARG:NH2	2.33	0.61
1:2:1221:A:N1	1:2:1263:G:C2	2.68	0.61
1:2:150:U:H4'	16:T:132:ARG:NH1	2.16	0.61
1:2:1294:G:O6	1:2:1303:U:C4	2.53	0.61
2:D:62:LEU:HD11	2:D:90:LYS:HD2	1.82	0.61
12:P:33:GLN:HG2	23:a:64:GLU:OE2	2.01	0.61
13:Q:126:THR:HA	13:Q:136:ARG:HG2	1.83	0.61
29:g:50:VAL:HG12	29:g:51:ASN:N	2.16	0.61
1:2:1442:U:C1'	28:t:766:GLN:NE2	2.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:t:354:THR:HA	28:t:357:TRP:HD1	1.65	0.60
31:r:195:TYR:N	31:r:236:MET:HB3	2.16	0.60
22:Z:30:VAL:HG13	22:Z:39:ILE:HG13	1.83	0.60
13:Q:134:VAL:HB	13:Q:219:LYS:HB3	1.81	0.60
1:2:522:U:O2'	26:d:60:PHE:O	2.18	0.60
31:r:208:LYS:HA	31:r:211:SER:HB2	1.81	0.60
1:2:330:G:OP2	18:V:172:ARG:NH1	2.33	0.60
2:D:69:ALA:HA	2:D:72:ILE:HD12	1.82	0.60
28:t:237:ASN:OD1	28:t:240:ARG:NH2	2.35	0.60
1:2:451:A:N6	1:2:453:U:O2	2.34	0.60
1:2:1046:G:OP1	13:Q:157:GLN:NE2	2.35	0.60
14:R:113:LEU:HD11	14:R:211:LEU:HB3	1.82	0.60
31:r:2:LYS:CE	31:r:142:LEU:HD13	2.31	0.60
31:r:18:VAL:HG13	31:r:37:ILE:HG21	1.83	0.60
1:2:522:U:H1'	26:d:34:ASN:HD21	1.65	0.60
1:2:590:C:H5'	29:g:43:ARG:NH2	2.17	0.60
2:D:43:ARG:HD3	2:D:121:VAL:HG12	1.82	0.60
16:T:23:ARG:NH2	16:T:41:VAL:O	2.34	0.60
1:2:1577:A:C1'	31:r:105:LYS:HZ3	2.14	0.60
3:B:92:ARG:NH2	3:B:169:ASN:OD1	2.35	0.60
1:2:93:A:O4'	15:S:3:ARG:NH1	2.35	0.60
28:t:374:TYR:OH	31:r:9:ARG:NH2	2.35	0.60
31:r:103:VAL:HG13	31:r:129:ARG:NH2	2.13	0.60
3:B:129:PRO:HA	3:B:132:VAL:HB	1.83	0.59
11:N:123:ASN:ND2	11:N:145:HIS:CB	2.64	0.59
28:t:86:ILE:HG12	28:t:242:LEU:HD22	1.83	0.59
6:F:130:GLY:O	6:F:137:ARG:NH1	2.35	0.59
16:T:5:ILE:HG12	16:T:111:LEU:HB2	1.84	0.59
22:Z:16:VAL:HG12	22:Z:80:HIS:HB2	1.84	0.59
31:r:225:LEU:HB3	31:r:257:CYS:SG	2.42	0.59
5:E:41:VAL:O	5:E:45:PHE:HB2	2.02	0.59
31:r:194:GLY:O	31:r:236:MET:SD	2.61	0.59
28:t:362:GLU:HB3	28:t:516:GLU:HA	1.85	0.59
1:2:386:G:OP2	18:V:25:ARG:NH2	2.35	0.59
1:2:565:C:C3'	31:r:47:SER:CB	2.81	0.59
1:2:1229:G:N2	1:2:1256:A:N6	2.40	0.59
28:t:734:PRO:HB3	31:r:9:ARG:CZ	2.30	0.59
1:2:139:C:H4'	1:2:140:A:H5'	1.85	0.59
1:2:1213:G:H1	1:2:1450:U:H3	1.48	0.59
1:2:1553:G:H1	5:E:44:ARG:HH12	1.50	0.59
2:D:43:ARG:HG2	2:D:121:VAL:HA	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:Q:81:PHE:HD2	13:Q:82:ARG:HG3	1.68	0.59
16:T:174:LYS:NZ	16:T:176:GLN:OE1	2.35	0.59
16:T:217:SER:O	16:T:221:ALA:HB3	2.02	0.59
1:2:223:U:O4	1:2:838:G:O6	2.20	0.59
1:2:639:U:O2'	17:U:118:LEU:HD13	2.02	0.59
11:N:121:CYS:SG	11:N:145:HIS:HD2	2.08	0.59
1:2:105:A:OP1	18:V:18:ARG:NH2	2.35	0.59
1:2:1262:U:H2'	1:2:1263:G:H8	1.67	0.59
1:2:68:A:OP2	16:T:171:LYS:NZ	2.33	0.59
31:r:110:TYR:HB2	31:r:122:MET:HB3	1.85	0.59
15:S:136:VAL:HG11	15:S:148:ARG:HE	1.67	0.58
2:D:32:LEU:HD21	2:D:121:VAL:HG21	1.85	0.58
12:P:143:VAL:N	12:P:157:ASP:OD2	2.35	0.58
13:Q:33:LYS:NZ	13:Q:42:ASN:OD1	2.36	0.58
31:r:74:ARG:HH11	31:r:147:GLN:HG2	1.67	0.58
1:2:1210:C:H5''	28:t:749:LEU:HD22	1.85	0.58
23:a:71:ARG:HE	27:f:4:VAL:HG11	1.68	0.58
31:r:230:PHE:C	31:r:234:ASN:HD21	2.11	0.58
1:2:265:A:N7	16:T:190:GLN:NE2	2.51	0.58
1:2:961:U:O2'	21:Y:86:GLU:OE2	2.19	0.58
1:2:1579:U:O2'	6:F:139:GLN:HA	2.04	0.58
1:2:1655:A:N1	1:2:1745:G:O2'	2.35	0.58
1:2:194:U:H2'	1:2:195:G:H4'	1.86	0.58
1:2:1556:A:OP2	5:E:44:ARG:NH2	2.36	0.58
31:r:81:ASP:OD1	31:r:126:ARG:NH2	2.36	0.58
1:2:1379:C:O2	6:F:68:ARG:NH2	2.37	0.58
2:D:87:PRO:HB3	2:D:137:MET:HE1	1.85	0.58
6:F:50:GLU:OE1	6:F:82:ARG:NH2	2.37	0.58
22:Z:112:ILE:HG21	30:p:97:ARG:HH22	1.68	0.58
28:t:98:LEU:O	28:t:116:GLN:NE2	2.36	0.58
1:2:58:U:O2'	1:2:451:A:N3	2.36	0.58
1:2:577:G:C4	31:r:48:GLY:C	2.82	0.58
1:2:1263:G:C5	1:2:1264:G:C4	2.92	0.58
30:p:242:MET:HE1	30:p:270:LEU:HD22	1.85	0.58
31:r:195:TYR:HA	31:r:236:MET:SD	2.43	0.58
1:2:804:A:O2'	1:2:805:U:O5'	2.18	0.58
1:2:856:A:H2'	17:U:116:ARG:HH21	1.68	0.58
1:2:1171:A:H2'	1:2:1172:G:C8	2.38	0.58
11:N:143:LYS:HB2	11:N:145:HIS:CE1	2.36	0.58
30:p:118:PRO:HA	30:p:121:VAL:HG22	1.86	0.58
1:2:66:U:C6	16:T:173:PRO:HG3	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:t:529:LEU:HD11	28:t:660:VAL:HG21	1.86	0.58
1:2:540:G:OP1	1:2:541:A:N6	2.36	0.57
1:2:856:A:C6	17:U:116:ARG:HG2	2.39	0.57
31:r:156:ARG:CZ	31:r:184:ARG:HA	2.34	0.57
1:2:538:A:O2'	1:2:540:G:N2	2.36	0.57
14:R:122:ALA:O	14:R:126:ARG:HB3	2.03	0.57
17:U:17:GLU:HG2	17:U:46:ILE:HG23	1.87	0.57
28:t:514:VAL:O	28:t:776:ARG:NH1	2.38	0.57
31:r:61:LEU:HD22	31:r:79:GLY:HA2	1.86	0.57
8:I:73:VAL:HG22	8:I:105:LEU:HD11	1.87	0.57
31:r:198:ARG:HG2	31:r:233:PHE:CE1	2.39	0.57
31:r:235:ILE:HA	31:r:251:VAL:HA	1.86	0.57
1:2:1484:G:N2	1:2:1606:C:O2	2.37	0.57
1:2:565:C:C5'	31:r:47:SER:OG	2.38	0.57
1:2:814:A:C2	1:2:857:U:O4	2.56	0.57
7:H:48:LYS:NZ	8:I:35:ASP:O	2.35	0.57
8:I:126:GLU:O	8:I:130:ARG:CB	2.53	0.57
11:N:123:ASN:CG	11:N:145:HIS:HB3	2.29	0.57
28:t:303:LEU:HA	28:t:561:ILE:HA	1.85	0.57
1:2:657:U:O2	1:2:676:G:N2	2.35	0.57
1:2:1482:C:OP2	1:2:1521:G:N2	2.38	0.57
8:I:28:LEU:HD13	8:I:30:VAL:HG13	1.87	0.57
13:Q:137:ILE:HD11	13:Q:172:LEU:HB3	1.86	0.57
1:2:590:C:OP1	29:g:43:ARG:NH2	2.37	0.57
1:2:1263:G:N3	1:2:1264:G:N9	2.52	0.57
1:2:1662:G:H1'	28:t:57:LYS:HD3	1.86	0.57
31:r:206:ILE:HA	31:r:209:LEU:HB3	1.87	0.57
1:2:1650:U:H2'	1:2:1651:A:C8	2.40	0.57
28:t:572:GLN:HG3	28:t:577:LEU:HB2	1.87	0.57
28:t:210:GLN:O	28:t:214:SER:HB3	2.04	0.56
1:2:1264:G:H8	1:2:1264:G:O5'	1.88	0.56
6:F:29:ILE:HG23	6:F:65:ILE:HB	1.87	0.56
19:W:123:HIS:ND1	29:g:37:ARG:NE	2.53	0.56
31:r:19:LEU:HD13	31:r:56:LEU:HD22	1.87	0.56
31:r:231:ASN:O	31:r:234:ASN:OD1	2.21	0.56
1:2:1654:G:H2'	1:2:1655:A:C8	2.41	0.56
6:F:143:ARG:HH12	31:r:129:ARG:HB3	1.60	0.56
15:S:89:VAL:HG22	15:S:100:ARG:HE	1.70	0.56
28:t:183:GLN:HB3	28:t:668:ILE:HD11	1.87	0.56
28:t:339:SER:O	28:t:343:ARG:NH1	2.38	0.56
29:g:50:VAL:CG1	29:g:51:ASN:H	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:258:ILE:HD13	31:r:268:TYR:HD2	1.71	0.56
1:2:77:U:H3	16:T:159:ARG:HB3	1.70	0.56
4:C:28:PHE:HA	4:C:31:ASN:HB2	1.86	0.56
5:E:90:ILE:HD11	5:E:112:LEU:HD11	1.86	0.56
6:F:63:ILE:HD12	6:F:65:ILE:HD11	1.88	0.56
15:S:54:TYR:O	26:d:15:ASN:ND2	2.37	0.56
1:2:1149:G:H1'	31:r:146:ASN:CB	2.35	0.56
7:H:45:LEU:HD11	8:I:36:ILE:HG22	1.88	0.56
18:V:48:THR:OG1	18:V:51:GLY:O	2.24	0.56
21:Y:55:ARG:NH2	27:f:51:GLN:NE2	2.53	0.56
31:r:32:VAL:N	31:r:73:TYR:O	2.24	0.56
1:2:540:G:N2	1:2:542:A:N7	2.53	0.56
1:2:570:A:N7	25:c:114:LYS:NZ	2.54	0.56
1:2:1575:G:N2	31:r:233:PHE:CD2	2.73	0.56
8:I:108:LEU:HB3	8:I:114:VAL:HG13	1.88	0.56
13:Q:176:VAL:HG13	13:Q:184:LEU:HD11	1.87	0.56
30:p:179:ASP:HB2	30:p:180:LEU:HD12	1.87	0.56
1:2:1586:A:H5''	6:F:136:SER:HB2	1.88	0.56
8:I:127:ASN:O	8:I:131:ASP:HB3	2.06	0.56
25:c:56:LYS:HE2	25:c:96:VAL:HG23	1.88	0.56
31:r:2:LYS:HE3	31:r:151:TRP:CZ2	2.40	0.56
1:2:576:G:C5	31:r:46:GLN:HG2	2.37	0.56
1:2:1610:G:H5'	3:B:107:LYS:HB2	1.86	0.56
31:r:23:GLU:O	31:r:26:SER:OG	2.19	0.56
1:2:900:A:H3'	1:2:901:G:H21	1.70	0.56
5:E:20:VAL:HG13	5:E:24:LYS:HG3	1.88	0.56
15:S:11:ARG:NH2	15:S:21:ASP:O	2.39	0.56
28:t:53:GLN:C	28:t:55:LYS:N	2.62	0.56
31:r:280:PHE:O	31:r:285:LYS:N	2.38	0.56
1:2:768:C:C2	19:W:143:ILE:HD13	2.42	0.55
1:2:1038:U:N3	1:2:1092:A:N6	2.53	0.55
13:Q:174:LYS:NZ	13:Q:196:GLU:OE2	2.36	0.55
31:r:214:MET:HA	31:r:217:ILE:HD12	1.87	0.55
1:2:1349:G:N2	1:2:1378:U:O4	2.39	0.55
1:2:1482:C:O2'	6:F:72:GLY:O	2.25	0.55
4:C:77:GLU:O	4:C:81:LYS:CB	2.52	0.55
5:E:81:ARG:NH2	5:E:117:GLY:O	2.40	0.55
13:Q:35:PRO:HA	13:Q:97:LEU:HD11	1.88	0.55
15:S:143:ASP:OD1	15:S:143:ASP:N	2.38	0.55
18:V:39:GLY:HA2	18:V:61:GLU:HB3	1.89	0.55
28:t:741:ARG:NH1	28:t:763:LEU:O	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:811:A:N9	17:U:110:GLN:NE2	2.54	0.55
1:2:1007:C:H2'	1:2:1008:G:H8	1.72	0.55
1:2:1180:C:H5'	31:r:99:ASN:HB3	1.88	0.55
1:2:1262:U:H2'	1:2:1263:G:C8	2.41	0.55
1:2:1344:A:N6	1:2:1377:U:O2'	2.40	0.55
3:B:219:ARG:HA	3:B:222:LYS:HB3	1.88	0.55
4:C:25:THR:O	4:C:31:ASN:ND2	2.37	0.55
29:g:50:VAL:HG12	29:g:51:ASN:H	1.71	0.55
31:r:194:GLY:C	31:r:236:MET:SD	2.89	0.55
1:2:577:G:C2'	31:r:51:ARG:HA	2.26	0.55
1:2:856:A:N6	17:U:116:ARG:HG2	2.22	0.55
1:2:565:C:N4	31:r:46:GLN:OE1	2.30	0.55
1:2:1263:G:C4	1:2:1264:G:N9	2.75	0.55
3:B:167:ARG:O	3:B:171:ALA:HB2	2.06	0.55
19:W:109:LEU:HB2	19:W:146:PHE:HB3	1.89	0.55
28:t:638:ASN:ND2	28:t:692:ASP:OD2	2.39	0.55
31:r:64:LYS:O	31:r:65:MET:HE2	2.07	0.55
1:2:992:A:O2'	1:2:1785:U:O2	2.22	0.55
31:r:64:LYS:O	31:r:65:MET:HE3	2.07	0.55
1:2:525:A:H5''	26:d:89:TYR:CE2	2.42	0.55
1:2:590:C:C5'	29:g:43:ARG:NH2	2.70	0.55
1:2:1389:C:OP2	4:C:45:ARG:NH1	2.39	0.55
15:S:230:GLU:HB2	15:S:233:LYS:HD2	1.88	0.55
1:2:592:A:OP1	19:W:39:LYS:NZ	2.31	0.54
1:2:1321:A:N6	12:P:135:GLU:OE1	2.41	0.54
1:2:1622:G:H5''	31:r:144:LYS:CG	2.35	0.54
3:B:214:LYS:NZ	3:B:218:GLU:OE2	2.40	0.54
25:c:47:SER:HG	25:c:48:HIS:HD1	1.51	0.54
14:R:41:LEU:HA	14:R:44:LEU:HD12	1.89	0.54
30:p:91:LYS:NZ	30:p:141:THR:O	2.40	0.54
30:p:269:ARG:O	30:p:273:ARG:NE	2.40	0.54
31:r:114:ASP:HB3	31:r:118:ASN:HB2	1.88	0.54
12:P:58:VAL:O	12:P:62:ARG:HB2	2.07	0.54
1:2:1595:U:O4	1:2:1600:A:N1	2.40	0.54
5:E:93:VAL:HG11	5:E:104:GLN:HE21	1.71	0.54
31:r:231:ASN:HA	31:r:276:ILE:HD11	1.87	0.54
1:2:93:A:C4'	15:S:3:ARG:NH1	2.71	0.54
1:2:964:U:H5'	21:Y:128:TYR:OH	2.07	0.54
1:2:1027:A:OP1	1:2:1789:G:O2'	2.25	0.54
30:p:205:ILE:HG22	30:p:250:LEU:HB3	1.89	0.54
1:2:1221:A:N1	1:2:1263:G:N3	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:235:ILE:HG12	31:r:250:VAL:H	1.70	0.54
1:2:448:C:OP1	15:S:29:PRO:HD3	2.08	0.54
1:2:1294:G:H4'	12:P:109:ASN:CB	2.38	0.54
3:B:45:LYS:NZ	3:B:115:LYS:O	2.35	0.54
24:b:112:ASP:N	24:b:112:ASP:OD1	2.40	0.54
1:2:742:U:O2	17:U:107:ARG:HG2	2.07	0.54
1:2:1147:A:OP1	14:R:89:GLN:NE2	2.40	0.54
1:2:1479:A:OP1	8:I:57:ARG:NH1	2.40	0.54
1:2:1672:G:H2'	1:2:1673:G:C8	2.43	0.54
6:F:59:LYS:HB3	6:F:92:TYR:HE2	1.73	0.54
31:r:142:LEU:HB2	31:r:151:TRP:HZ2	1.73	0.54
31:r:225:LEU:HD23	31:r:259:SER:HA	1.90	0.54
31:r:227:HIS:HE1	31:r:229:ASP:HB3	1.72	0.54
1:2:141:U:O2'	1:2:266:A:N3	2.41	0.54
8:I:37:VAL:HG22	8:I:39:THR:H	1.73	0.54
8:I:70:GLN:HB2	8:I:121:GLY:HA3	1.89	0.54
31:r:121:VAL:HG23	31:r:191:LEU:HA	1.88	0.54
1:2:207:U:O2	18:V:178:ARG:NH2	2.41	0.54
1:2:442:C:O2'	1:2:525:A:N1	2.41	0.54
1:2:1689:A:O2'	1:2:1712:A:N6	2.40	0.54
6:F:143:ARG:NH2	31:r:129:ARG:CB	2.66	0.54
8:I:86:ARG:HE	8:I:89:ARG:HE	1.56	0.54
25:c:66:SER:O	31:r:45:SER:OG	2.26	0.54
31:r:181:ASP:OD1	31:r:182:ASN:N	2.40	0.54
31:r:232:GLU:HG3	31:r:233:PHE:CE1	2.41	0.54
1:2:886:U:O2'	22:Z:121:VAL:O	2.24	0.53
9:K:46:LYS:HG2	9:K:49:ARG:HD2	1.89	0.53
31:r:2:LYS:C	31:r:141:TYR:CZ	2.80	0.53
1:2:654:C:N4	1:2:677:G:O6	2.41	0.53
1:2:1230:A:H62	1:2:1255:G:H21	1.54	0.53
2:D:46:ARG:NH1	2:D:47:GLU:OE2	2.41	0.53
4:C:17:ILE:HD11	4:C:54:THR:HA	1.91	0.53
19:W:19:TYR:HA	19:W:24:LEU:HD11	1.90	0.53
31:r:235:ILE:CB	31:r:251:VAL:HA	2.38	0.53
1:2:150:U:OP1	26:d:123:LYS:NZ	2.40	0.53
1:2:245:U:N3	1:2:248:U:OP2	2.38	0.53
1:2:577:G:O2'	31:r:51:ARG:HB3	2.08	0.53
1:2:748:U:O2	1:2:801:G:O6	2.26	0.53
2:D:58:LEU:HD21	2:D:126:TRP:HB3	1.89	0.53
12:P:71:GLU:HA	12:P:95:ALA:H	1.74	0.53
28:t:253:ARG:NH2	28:t:258:TYR:OH	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:33:PRO:HA	31:r:72:GLY:HA2	1.91	0.53
31:r:195:TYR:CA	31:r:236:MET:SD	2.97	0.53
1:2:1711:C:H5'	1:2:1712:A:H5''	1.89	0.53
17:U:143:LEU:O	24:b:42:GLN:NE2	2.41	0.53
31:r:52:ALA:O	31:r:56:LEU:HG	2.07	0.53
1:2:1211:A:N3	5:E:97:TYR:OH	2.36	0.53
3:B:37:GLN:HB3	6:F:53:LEU:HD22	1.91	0.53
6:F:41:PRO:O	6:F:43:ILE:N	2.39	0.53
11:N:123:ASN:HD22	11:N:145:HIS:N	2.06	0.53
31:r:236:MET:O	31:r:250:VAL:N	2.42	0.53
1:2:1477:G:H2'	1:2:1478:G:H8	1.72	0.53
1:2:1591:C:H2'	1:2:1592:A:H8	1.74	0.53
3:B:119:ASP:HB3	9:K:100:ILE:HG12	1.90	0.53
6:F:143:ARG:NH2	31:r:129:ARG:HB2	2.24	0.53
22:Z:18:ARG:HG2	22:Z:82:LYS:HB2	1.91	0.53
1:2:1647:U:H2'	1:2:1648:A:C8	2.43	0.53
1:2:1649:G:H22	1:2:1751:C:H2'	1.73	0.53
13:Q:103:MET:HE1	13:Q:212:VAL:HG23	1.90	0.53
16:T:161:GLU:HG2	16:T:170:THR:HB	1.90	0.53
22:Z:82:LYS:NZ	22:Z:116:GLU:OE2	2.41	0.53
25:c:43:PHE:O	25:c:45:GLY:N	2.36	0.53
31:r:2:LYS:HA	31:r:141:TYR:CE2	2.43	0.53
31:r:108:ASP:O	31:r:123:LYS:HA	2.09	0.53
1:2:1183:A:N3	1:2:1210:C:O2'	2.39	0.53
1:2:1575:G:N3	31:r:233:PHE:CD1	2.77	0.53
4:C:28:PHE:HB2	4:C:55:THR:HG21	1.90	0.53
5:E:53:PRO:O	5:E:54:ALA:C	2.52	0.53
9:K:59:TYR:OH	9:K:98:GLN:NE2	2.41	0.53
21:Y:99:ARG:NH2	21:Y:119:GLU:OE2	2.39	0.53
25:c:144:ARG:HB2	28:t:184:GLY:HA2	1.90	0.53
31:r:82:TYR:O	31:r:86:LYS:N	2.41	0.53
1:2:472:U:O2'	1:2:769:A:N3	2.33	0.53
1:2:637:C:OP1	24:b:32:LYS:N	2.39	0.53
1:2:871:G:O2'	27:f:67:THR:O	2.23	0.53
1:2:884:A:O3'	13:Q:136:ARG:NH1	2.25	0.53
1:2:1263:G:C4	1:2:1264:G:C4	2.96	0.53
1:2:1364:G:N2	8:I:2:PRO:O	2.42	0.53
1:2:333:A:H5'	18:V:48:THR:HB	1.91	0.53
1:2:553:G:H3'	1:2:554:C:H2'	1.91	0.53
1:2:1263:G:O6	1:2:1264:G:C2	2.61	0.53
7:H:112:ASP:HA	7:H:115:ARG:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:U:76:LYS:HA	17:U:79:ARG:HB2	1.91	0.53
31:r:210:TYR:HA	31:r:213:LEU:HB2	1.91	0.53
31:r:235:ILE:CA	31:r:251:VAL:HA	2.38	0.53
1:2:577:G:C1'	31:r:47:SER:O	2.56	0.52
1:2:1363:U:H3'	1:2:1364:G:H8	1.74	0.52
7:H:87:ASN:H	7:H:99:HIS:HD1	1.57	0.52
11:N:146:SER:O	11:N:147:VAL:C	2.52	0.52
1:2:1585:U:H2'	1:2:1586:A:H8	1.74	0.52
12:P:92:HIS:ND1	12:P:202:TYR:OH	2.37	0.52
31:r:196:PRO:HD2	31:r:199:ARG:HE	1.71	0.52
31:r:226:ILE:HB	31:r:258:ILE:HD11	1.91	0.52
1:2:438:A:O2'	1:2:465:G:N2	2.42	0.52
1:2:628:G:N1	1:2:970:A:OP2	2.33	0.52
7:H:45:LEU:HD12	7:H:48:LYS:HD2	1.91	0.52
31:r:32:VAL:O	31:r:73:TYR:N	2.27	0.52
32:e:404:SER:O	32:e:406:GLY:HA2	2.09	0.52
1:2:77:U:H3	16:T:159:ARG:CB	2.22	0.52
7:H:107:SER:HA	7:H:110:ARG:HB3	1.92	0.52
9:K:80:LEU:O	9:K:84:GLU:CB	2.58	0.52
18:V:185:GLU:HG2	20:X:23:PRO:HG2	1.92	0.52
19:W:107:ARG:NH2	19:W:153:GLU:OE2	2.42	0.52
1:2:788:A:C4	15:S:19:LEU:HD13	2.45	0.52
1:2:793:A:H5''	1:2:794:U:H5'	1.92	0.52
4:C:41:ILE:HD13	4:C:47:ARG:HA	1.92	0.52
5:E:93:VAL:HA	5:E:106:GLU:HA	1.92	0.52
1:2:74:U:O2'	1:2:76:A:OP2	2.28	0.52
1:2:107:C:H2'	1:2:108:A:H8	1.74	0.52
1:2:407:A:OP1	16:T:94:ARG:HD2	2.09	0.52
1:2:781:U:OP2	26:d:9:THR:OG1	2.27	0.52
8:I:105:LEU:HD22	8:I:122:ARG:HH12	1.74	0.52
11:N:123:ASN:CB	11:N:145:HIS:CB	2.70	0.52
30:p:222:THR:OG1	30:p:234:LEU:O	2.27	0.52
31:r:7:HIS:CD2	31:r:59:LEU:HD22	2.45	0.52
1:2:522:U:H5''	26:d:37:LYS:HG3	1.92	0.52
4:C:36:ASP:OD2	4:C:47:ARG:NH1	2.43	0.52
28:t:743:GLY:HA3	31:r:10:TYR:CE1	2.45	0.52
1:2:912:U:H4'	1:2:913:G:H3'	1.92	0.52
1:2:1228:G:N2	2:D:67:THR:O	2.43	0.52
1:2:1244:A:OP1	32:e:227:GLY:CA	2.48	0.52
3:B:64:VAL:HG12	3:B:65:ARG:HG2	1.91	0.52
5:E:59:LYS:O	5:E:63:ALA:CB	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:39:GLU:HA	16:T:46:LYS:HA	1.91	0.52
20:X:123:VAL:HG23	20:X:142:VAL:HG22	1.92	0.52
31:r:232:GLU:O	31:r:233:PHE:CB	2.58	0.52
1:2:577:G:C1'	31:r:51:ARG:CA	2.73	0.52
1:2:577:G:HO2'	31:r:51:ARG:HA	1.68	0.52
1:2:590:C:OP1	29:g:43:ARG:NE	2.43	0.52
1:2:1168:U:H1'	6:F:139:GLN:HE22	1.75	0.52
1:2:1524:A:H2'	1:2:1525:A:C8	2.45	0.52
1:2:1654:G:H2'	1:2:1655:A:H8	1.75	0.52
8:I:115:GLU:O	8:I:123:ARG:N	2.43	0.52
15:S:139:VAL:HG13	15:S:150:PRO:HG3	1.91	0.52
31:r:80:ILE:HG12	31:r:152:MET:HE2	1.91	0.52
1:2:903:U:H1'	1:2:906:A:H62	1.75	0.52
1:2:1291:G:H1	1:2:1324:G:N2	2.06	0.52
4:C:31:ASN:HA	4:C:34:LEU:HB3	1.91	0.52
12:P:92:HIS:HB3	12:P:182:LEU:HD11	1.92	0.52
17:U:50:ASP:HB3	17:U:56:LYS:HG2	1.91	0.52
28:t:152:ALA:HB3	28:t:180:LEU:HD22	1.92	0.52
31:r:160:ASN:HA	31:r:163:TYR:HB3	1.91	0.52
1:2:220:A:N6	1:2:831:U:C4	2.79	0.51
1:2:517:U:O2'	28:t:203:LYS:NZ	2.41	0.51
1:2:742:U:H4'	17:U:108:GLN:H	1.75	0.51
1:2:742:U:C1'	17:U:107:ARG:HA	2.38	0.51
3:B:142:PRO:HD2	3:B:167:ARG:HA	1.93	0.51
8:I:131:ASP:HA	8:I:134:ARG:HG2	1.92	0.51
28:t:496:GLU:HA	28:t:499:LYS:HE3	1.90	0.51
1:2:748:U:C2	1:2:801:G:O6	2.64	0.51
1:2:1171:A:H2'	1:2:1172:G:H8	1.75	0.51
1:2:1673:G:OP1	16:T:94:ARG:NH2	2.42	0.51
12:P:33:GLN:OE1	12:P:153:SER:OG	2.26	0.51
21:Y:119:GLU:O	21:Y:123:HIS:ND1	2.35	0.51
31:r:65:MET:CA	31:r:65:MET:CE	2.85	0.51
1:2:491:C:N4	1:2:492:A:N3	2.58	0.51
1:2:1202:A:N6	1:2:1457:C:OP1	2.40	0.51
1:2:1263:G:C5	1:2:1264:G:C5	2.99	0.51
1:2:1360:A:HO2'	8:I:2:PRO:N	2.08	0.51
6:F:17:THR:OG1	6:F:70:THR:OG1	2.27	0.51
9:K:83:LEU:HD22	9:K:88:ILE:HD12	1.92	0.51
1:2:867:G:OP2	21:Y:3:ARG:NH1	2.44	0.51
13:Q:158:SER:O	13:Q:162:ARG:NH1	2.43	0.51
26:d:27:VAL:HG11	26:d:35:VAL:HG11	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:d:113:ASN:O	26:d:117:LYS:NZ	2.40	0.51
28:t:218:HIS:CD2	29:g:4:VAL:HG21	2.45	0.51
30:p:263:LEU:HA	30:p:266:VAL:HG12	1.93	0.51
1:2:1263:G:C2'	1:2:1264:G:C8	2.89	0.51
5:E:95:GLY:HA2	5:E:104:GLN:HA	1.92	0.51
10:L:15:VAL:HG22	10:L:17:GLY:H	1.75	0.51
15:S:87:MET:SD	15:S:100:ARG:NH1	2.83	0.51
16:T:70:PRO:HA	16:T:99:GLY:HA3	1.92	0.51
28:t:120:SER:O	28:t:576:GLN:NE2	2.43	0.51
29:g:50:VAL:CG1	29:g:51:ASN:N	2.72	0.51
31:r:110:TYR:HE2	31:r:124:ILE:HD13	1.76	0.51
15:S:15:PRO:HB3	15:S:39:ARG:HD3	1.92	0.51
17:U:14:THR:HG22	17:U:17:GLU:HG3	1.93	0.51
31:r:195:TYR:HA	31:r:199:ARG:HH21	1.75	0.51
1:2:787:G:H2'	1:2:788:A:C8	2.46	0.51
5:E:17:TYR:HB3	5:E:20:VAL:HB	1.93	0.51
8:I:127:ASN:O	8:I:131:ASP:CB	2.58	0.51
13:Q:103:MET:HB3	13:Q:215:VAL:HG12	1.92	0.51
17:U:140:VAL:HB	24:b:52:TYR:HB3	1.92	0.51
21:Y:101:HIS:CE1	21:Y:105:ASN:HD22	2.29	0.51
27:f:75:GLU:O	27:f:77:THR:N	2.37	0.51
28:t:730:PHE:HB3	28:t:771:MET:HE1	1.93	0.51
30:p:108:PRO:O	30:p:112:SER:N	2.43	0.51
1:2:1484:G:H21	1:2:1606:C:H1'	1.75	0.51
12:P:15:GLN:O	12:P:19:ALA:CB	2.59	0.51
1:2:130:C:H2'	1:2:133:U:H5'	1.93	0.51
1:2:557:G:H5''	29:g:57:ASN:HB3	1.93	0.51
1:2:811:A:C8	17:U:110:GLN:NE2	2.76	0.51
1:2:1180:C:H5''	31:r:99:ASN:ND2	2.26	0.51
16:T:67:VAL:HG23	16:T:99:GLY:HA2	1.93	0.51
16:T:137:ARG:HD2	16:T:177:ARG:NE	2.26	0.51
28:t:54:ARG:NE	28:t:54:ARG:CA	2.73	0.51
28:t:154:VAL:O	28:t:253:ARG:NH2	2.44	0.51
31:r:235:ILE:CG1	31:r:251:VAL:HA	2.31	0.51
1:2:89:G:H21	1:2:452:A:H5'	1.75	0.51
20:X:128:CYS:SG	20:X:129:ARG:N	2.84	0.51
21:Y:99:ARG:NH2	21:Y:141:TYR:OH	2.44	0.51
1:2:222:A:N6	1:2:833:U:C4	2.79	0.50
1:2:489:C:O2	1:2:498:G:N2	2.44	0.50
1:2:623:A:H5'	1:2:624:G:H5''	1.92	0.50
1:2:1263:G:H21	1:2:1264:G:H1'	1.72	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:V:84:HIS:NE2	18:V:97:THR:OG1	2.35	0.50
26:d:8:ARG:NH2	26:d:26:ASP:OD2	2.44	0.50
28:t:164:GLY:H	28:t:194:ASN:HD22	1.58	0.50
31:r:217:ILE:HD13	31:r:273:VAL:HG22	1.93	0.50
1:2:259:U:H1'	18:V:178:ARG:NH1	2.26	0.50
7:H:69:ILE:HG22	7:H:73:MET:HE2	1.92	0.50
13:Q:115:ARG:NH1	30:p:103:PRO:HD2	2.26	0.50
14:R:37:PRO:HG3	14:R:46:LYS:HD2	1.92	0.50
14:R:99:LYS:HA	14:R:117:THR:HA	1.93	0.50
30:p:103:PRO:HA	30:p:106:MET:HB2	1.92	0.50
31:r:53:ILE:HD13	31:r:73:TYR:HE2	1.76	0.50
1:2:227:U:O4	1:2:234:G:N2	2.44	0.50
1:2:765:G:N1	19:W:149:ARG:HG3	2.27	0.50
1:2:993:A:OP1	1:2:1777:G:N2	2.44	0.50
1:2:1250:U:C2	11:N:140:TYR:HD2	2.29	0.50
1:2:1265:G:O6	1:2:1444:A:N6	2.45	0.50
1:2:1622:G:H5''	31:r:144:LYS:HD2	1.76	0.50
1:2:1622:G:P	31:r:144:LYS:HD2	2.51	0.50
15:S:9:LEU:HD23	15:S:28:ALA:HB3	1.94	0.50
24:b:15:ASN:HD21	24:b:72:CYS:H	1.58	0.50
25:c:96:VAL:HG12	25:c:127:VAL:HG11	1.92	0.50
1:2:486:G:O6	1:2:501:U:O4	2.29	0.50
1:2:1462:G:O2'	31:r:103:VAL:HB	2.11	0.50
3:B:142:PRO:HA	3:B:214:LYS:HG3	1.92	0.50
6:F:143:ARG:NH2	31:r:129:ARG:N	2.50	0.50
21:Y:42:ARG:HE	21:Y:80:LEU:HD11	1.76	0.50
26:d:23:PHE:HE1	26:d:75:VAL:HG12	1.76	0.50
28:t:748:SER:HB3	28:t:749:LEU:HD23	1.92	0.50
1:2:523:G:H5'	26:d:59:GLY:O	2.12	0.50
21:Y:87:ASP:OD1	21:Y:87:ASP:N	2.41	0.50
25:c:66:SER:N	31:r:45:SER:OG	2.44	0.50
1:2:678:A:N6	1:2:681:U:O4	2.44	0.50
1:2:753:A:OP1	15:S:187:ARG:N	2.43	0.50
1:2:788:A:OP2	15:S:108:ARG:NH1	2.38	0.50
1:2:903:U:O2'	1:2:905:A:N7	2.36	0.50
1:2:904:G:H1	1:2:998:A:H61	1.60	0.50
1:2:1221:A:C4	1:2:1263:G:N2	2.79	0.50
6:F:94:GLN:HB2	6:F:102:LYS:HD3	1.92	0.50
15:S:24:SER:O	15:S:24:SER:OG	2.26	0.50
19:W:96:VAL:HA	19:W:99:LEU:HD13	1.94	0.50
22:Z:84:ARG:HB2	22:Z:118:VAL:HG23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:b:30:SER:HA	24:b:34:ILE:HD12	1.93	0.50
28:t:573:ASP:N	28:t:573:ASP:OD1	2.45	0.50
31:r:165:PHE:O	31:r:169:LEU:N	2.40	0.50
1:2:57:G:OP1	26:d:112:LYS:NZ	2.45	0.50
1:2:565:C:C5'	31:r:47:SER:HB3	2.10	0.50
1:2:1182:U:H4'	5:E:124:THR:OG1	2.11	0.50
1:2:1294:G:O6	1:2:1303:U:O4	2.29	0.50
11:N:147:VAL:O	11:N:148:TYR:CG	2.64	0.50
17:U:79:ARG:O	17:U:83:LYS:CB	2.56	0.50
1:2:5:U:H2'	1:2:6:G:H8	1.75	0.50
1:2:565:C:H2'	31:r:46:GLN:H	1.76	0.50
1:2:1335:U:H2'	1:2:1336:A:C8	2.47	0.50
1:2:1483:A:N3	1:2:1607:G:O2'	2.40	0.50
8:I:112:GLY:O	8:I:125:SER:OG	2.30	0.50
17:U:80:GLU:OE1	17:U:84:LYS:NZ	2.38	0.50
28:t:53:GLN:O	28:t:55:LYS:N	2.45	0.50
1:2:740:A:OP1	20:X:43:LYS:HD3	2.12	0.50
1:2:748:U:O2	1:2:801:G:C6	2.65	0.50
1:2:1501:C:OP2	8:I:102:ARG:NH1	2.44	0.50
5:E:80:MET:HE1	5:E:83:MET:HE3	1.94	0.50
29:g:49:LEU:HD22	29:g:55:ARG:HB2	1.92	0.50
30:p:160:LYS:O	30:p:163:THR:OG1	2.26	0.50
31:r:109:ILE:HG23	31:r:121:VAL:HG13	1.94	0.50
3:B:143:ARG:HB2	10:L:55:VAL:HG11	1.93	0.49
18:V:48:THR:OG1	18:V:52:ASN:O	2.29	0.49
20:X:102:LYS:O	25:c:13:ARG:NH2	2.35	0.49
31:r:210:TYR:HA	31:r:213:LEU:HD12	1.93	0.49
1:2:1175:U:H2'	1:2:1176:G:H8	1.77	0.49
1:2:1250:U:O2'	11:N:135:HIS:NE2	2.42	0.49
6:F:50:GLU:O	6:F:54:LEU:HB3	2.12	0.49
7:H:101:LEU:O	7:H:105:VAL:N	2.41	0.49
12:P:124:THR:HG22	12:P:174:TRP:HE1	1.77	0.49
12:P:131:GLN:O	12:P:135:GLU:CB	2.60	0.49
31:r:232:GLU:O	31:r:233:PHE:HD1	1.95	0.49
1:2:594:A:P	19:W:38:ASN:HD21	2.35	0.49
1:2:1447:C:O5'	1:2:1447:C:H6	1.94	0.49
6:F:16:ALA:HB2	6:F:72:GLY:HA3	1.93	0.49
6:F:44:LEU:HB3	6:F:78:VAL:HG11	1.93	0.49
28:t:495:ILE:HD12	28:t:729:TRP:CD1	2.48	0.49
31:r:94:VAL:HG12	31:r:112:VAL:HG21	1.94	0.49
1:2:703:G:C2	1:2:735:C:O2	2.65	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1263:G:C2	1:2:1264:G:N9	2.80	0.49
3:B:57:SER:HB3	10:L:53:ILE:HB	1.94	0.49
5:E:64:LYS:NZ	5:E:90:ILE:O	2.46	0.49
8:I:126:GLU:O	8:I:130:ARG:HB2	2.13	0.49
12:P:148:ASP:OD2	12:P:165:ARG:NH1	2.44	0.49
1:2:590:C:H2'	1:2:591:A:C8	2.47	0.49
1:2:645:C:H42	1:2:689:G:H1	1.59	0.49
1:2:742:U:H4'	17:U:108:GLN:HB3	1.94	0.49
1:2:1219:A:C8	1:2:1265:G:N3	2.80	0.49
1:2:1528:U:H2'	1:2:1529:C:C6	2.48	0.49
7:H:100:THR:HG21	7:H:108:LYS:HG2	1.94	0.49
19:W:53:ARG:O	19:W:57:ARG:HB2	2.12	0.49
19:W:123:HIS:HE1	29:g:37:ARG:HG3	1.75	0.49
1:2:1157:A:H2'	1:2:1160:A:N7	2.28	0.49
1:2:1473:U:O4	3:B:180:ARG:NE	2.40	0.49
13:Q:65:VAL:HG12	13:Q:87:ARG:HA	1.94	0.49
31:r:221:ALA:HA	31:r:225:LEU:O	2.13	0.49
16:T:102:VAL:HG13	16:T:106:LEU:HD12	1.95	0.49
24:b:41:MET:HG2	24:b:129:VAL:HG21	1.93	0.49
28:t:735:LEU:HD21	28:t:769:VAL:HG13	1.95	0.49
29:g:49:LEU:HG	29:g:50:VAL:H	1.78	0.49
1:2:611:U:OP2	25:c:5:LYS:HD3	2.13	0.49
1:2:1170:G:N2	1:2:1571:C:O2'	2.44	0.49
6:F:32:ASN:HD21	6:F:69:VAL:HG13	1.77	0.49
10:L:15:VAL:HG23	10:L:28:VAL:HG22	1.94	0.49
13:Q:91:VAL:HA	13:Q:96:LEU:HB3	1.93	0.49
28:t:54:ARG:HE	28:t:54:ARG:CA	2.26	0.49
1:2:872:G:N2	1:2:956:C:O2	2.46	0.49
1:2:1648:A:OP1	28:t:540:ARG:NH2	2.43	0.49
3:B:71:ALA:HB1	3:B:91:GLU:HB2	1.94	0.49
10:L:42:ARG:NH1	10:L:61:ARG:O	2.46	0.49
22:Z:19:ILE:HB	22:Z:83:ILE:HD12	1.95	0.49
31:r:2:LYS:HG2	31:r:141:TYR:CG	2.45	0.49
31:r:166:MET:HE2	31:r:254:PHE:CE2	2.47	0.49
1:2:577:G:H1'	31:r:51:ARG:CG	2.41	0.49
1:2:1175:U:H3	1:2:1464:G:H1	1.59	0.49
3:B:221:ALA:O	3:B:225:ARG:N	2.44	0.49
15:S:180:LEU:HD22	15:S:192:ILE:HG22	1.94	0.49
17:U:123:ASP:OD1	17:U:138:LYS:NZ	2.45	0.49
26:d:44:LEU:HA	26:d:47:VAL:HG22	1.95	0.49
1:2:702:G:O6	1:2:737:A:N6	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:90:VAL:HG11	6:F:117:LEU:HD21	1.95	0.48
13:Q:126:THR:HG22	13:Q:136:ARG:HD3	1.94	0.48
31:r:117:GLY:O	31:r:119:PRO:HD3	2.13	0.48
1:2:400:A:H5''	18:V:25:ARG:HA	1.95	0.48
1:2:1219:A:H61	1:2:1264:G:H2'	1.78	0.48
1:2:1294:G:O2'	12:P:109:ASN:HB3	2.12	0.48
7:H:14:ILE:HD11	7:H:21:ASN:HB3	1.95	0.48
8:I:70:GLN:HB2	8:I:122:ARG:H	1.79	0.48
22:Z:80:HIS:HD2	22:Z:113:GLY:HA3	1.77	0.48
28:t:533:ASN:ND2	28:t:536:ASN:OD1	2.46	0.48
1:2:46:A:H4'	1:2:47:A:H5'	1.95	0.48
1:2:169:A:H5'	16:T:176:GLN:HG2	1.95	0.48
1:2:1502:G:N7	8:I:102:ARG:NH2	2.60	0.48
1:2:1561:U:H2'	1:2:1562:G:H8	1.78	0.48
8:I:126:GLU:O	8:I:130:ARG:HB3	2.14	0.48
13:Q:180:THR:OG1	13:Q:181:LEU:N	2.46	0.48
25:c:63:GLN:OE1	31:r:38:HIS:HB3	2.13	0.48
28:t:169:ASP:HB3	28:t:173:GLY:H	1.77	0.48
30:p:200:ARG:O	30:p:204:ARG:HB2	2.13	0.48
31:r:206:ILE:HD13	31:r:286:TYR:CB	2.43	0.48
1:2:558:U:OP1	29:g:55:ARG:HD3	2.14	0.48
1:2:1354:G:O6	1:2:1369:U:O4	2.32	0.48
5:E:41:VAL:HA	5:E:45:PHE:HD2	1.78	0.48
28:t:178:ARG:HE	28:t:219:PHE:HE1	1.59	0.48
28:t:345:THR:OG1	28:t:347:ASP:OD1	2.29	0.48
1:2:1169:G:N1	1:2:1575:G:OP2	2.42	0.48
1:2:1265:G:O6	1:2:1444:A:N7	2.46	0.48
1:2:1296:A:OP1	12:P:138:TYR:OH	2.29	0.48
1:2:1483:A:H2'	1:2:1484:G:C8	2.49	0.48
18:V:67:TRP:NE1	18:V:69:SER:OG	2.46	0.48
1:2:1170:G:O3'	31:r:198:ARG:NH1	2.46	0.48
1:2:1287:A:N6	1:2:1329:A:O2'	2.47	0.48
6:F:31:VAL:N	6:F:34:SER:O	2.47	0.48
26:d:20:ARG:HD2	26:d:74:LEU:HD22	1.95	0.48
28:t:340:ASN:O	28:t:343:ARG:NH1	2.46	0.48
31:r:156:ARG:NE	31:r:184:ARG:HG2	2.27	0.48
1:2:1477:G:H2'	1:2:1478:G:C8	2.49	0.48
1:2:1728:A:H1'	18:V:32:GLN:NE2	2.28	0.48
9:K:45:GLU:OE1	9:K:49:ARG:NH1	2.43	0.48
9:K:47:TYR:O	9:K:51:LEU:HB2	2.14	0.48
26:d:46:GLU:HG3	26:d:47:VAL:HG13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:t:257:GLY:HA2	28:t:284:GLY:HA3	1.95	0.48
28:t:482:PHE:HD2	28:t:485:GLU:HB2	1.77	0.48
31:r:163:TYR:CD1	31:r:182:ASN:HB2	2.49	0.48
12:P:107:PHE:HB2	12:P:135:GLU:HG3	1.96	0.48
30:p:90:ASN:HA	30:p:143:PRO:HB3	1.96	0.48
1:2:512:A:OP1	19:W:169:PRO:O	2.32	0.48
1:2:1257:U:C1'	32:e:312:TYR:O	2.61	0.48
1:2:1469:A:O2'	1:2:1540:G:N2	2.43	0.48
8:I:77:ASN:O	8:I:81:GLY:N	2.47	0.48
8:I:139:THR:O	8:I:143:ASP:N	2.44	0.48
17:U:141:ARG:NH1	24:b:51:GLU:OE1	2.47	0.48
17:U:174:ASN:O	17:U:178:GLY:N	2.47	0.48
1:2:567:A:H62	1:2:576:G:H21	1.62	0.48
1:2:1064:G:O2'	13:Q:204:ILE:O	2.32	0.48
17:U:137:GLY:H	17:U:153:LEU:HB2	1.79	0.48
22:Z:20:TYR:HB3	22:Z:27:PHE:HB2	1.96	0.48
3:B:26:ALA:HB2	6:F:26:LYS:HG3	1.96	0.47
4:C:96:SER:HA	4:C:97:ASN:HA	1.62	0.47
26:d:53:ASP:HB3	26:d:96:LEU:HD11	1.95	0.47
1:2:639:U:H3	1:2:695:U:H1'	1.79	0.47
1:2:1575:G:C6	31:r:233:PHE:CZ	3.02	0.47
13:Q:28:GLU:OE1	13:Q:50:LYS:NZ	2.38	0.47
15:S:112:HIS:NE2	15:S:237:SER:OG	2.39	0.47
17:U:139:ARG:HB2	17:U:151:LYS:HB2	1.96	0.47
22:Z:81:VAL:HG21	22:Z:102:LEU:HD21	1.96	0.47
1:2:859:A:C4	21:Y:73:ARG:CZ	2.98	0.47
1:2:1160:A:H2'	1:2:1161:C:C6	2.48	0.47
6:F:24:ALA:HA	6:F:63:ILE:HA	1.96	0.47
7:H:36:LYS:HB2	7:H:102:ALA:HA	1.95	0.47
18:V:103:GLN:NE2	18:V:165:LEU:O	2.47	0.47
28:t:201:LYS:HG2	28:t:205:GLN:HA	1.96	0.47
31:r:3:LEU:HD12	31:r:4:ASP:H	1.79	0.47
31:r:206:ILE:HB	31:r:284:LEU:HD22	1.97	0.47
1:2:235:G:H8	1:2:834:G:H21	1.62	0.47
5:E:98:ASN:OD1	5:E:103:ASN:ND2	2.48	0.47
11:N:147:VAL:HG11	11:N:149:LYS:NZ	2.30	0.47
13:Q:26:ARG:O	13:Q:50:LYS:N	2.46	0.47
13:Q:59:ASP:N	13:Q:59:ASP:OD1	2.46	0.47
15:S:100:ARG:HB2	15:S:114:ILE:HD13	1.97	0.47
30:p:219:ALA:HB1	30:p:267:ALA:HB2	1.97	0.47
1:2:103:A:O2'	1:2:308:C:N4	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:246:G:N2	20:X:66:ILE:O	2.37	0.47
1:2:1085:G:N2	1:2:1088:A:OP2	2.46	0.47
1:2:1231:U:H3	1:2:1254:U:H3	1.62	0.47
1:2:1591:C:H2'	1:2:1592:A:C8	2.50	0.47
3:B:23:VAL:HG11	6:F:57:LEU:HD13	1.95	0.47
12:P:78:SER:OG	12:P:129:ASP:OD1	2.26	0.47
14:R:97:ARG:HB3	14:R:119:LYS:HA	1.96	0.47
19:W:121:SER:OG	19:W:122:VAL:N	2.45	0.47
21:Y:95:ALA:O	21:Y:99:ARG:HB2	2.14	0.47
22:Z:47:LYS:HE2	22:Z:63:ALA:HA	1.96	0.47
25:c:66:SER:HB3	31:r:45:SER:HB2	1.94	0.47
28:t:54:ARG:NE	28:t:54:ARG:HA	2.26	0.47
28:t:153:LYS:O	28:t:582:TYR:OH	2.31	0.47
1:2:1575:G:C2	31:r:233:PHE:CD1	2.98	0.47
3:B:37:GLN:HG2	6:F:53:LEU:HD13	1.96	0.47
23:a:40:ASP:HB3	23:a:46:ILE:HD11	1.97	0.47
28:t:210:GLN:O	28:t:214:SER:CB	2.62	0.47
1:2:4:C:H1'	19:W:17:ARG:HH11	1.80	0.47
1:2:226:A:N1	1:2:835:U:C4	2.83	0.47
3:B:41:LYS:HG3	3:B:67:PRO:HB2	1.97	0.47
14:R:122:ALA:O	14:R:126:ARG:CB	2.62	0.47
18:V:106:ALA:O	18:V:110:ARG:N	2.44	0.47
26:d:37:LYS:HA	26:d:40:LEU:HD12	1.96	0.47
28:t:734:PRO:CB	31:r:9:ARG:HH22	2.28	0.47
31:r:152:MET:O	31:r:156:ARG:N	2.47	0.47
1:2:51:A:C2	1:2:440:U:O4	2.68	0.47
1:2:458:G:OP1	26:d:109:LYS:HE3	2.15	0.47
13:Q:45:LYS:HB3	22:Z:13:VAL:HG23	1.97	0.47
26:d:129:VAL:HG13	26:d:133:ASN:HD22	1.80	0.47
28:t:699:LYS:N	28:t:775:LYS:O	2.40	0.47
30:p:130:MET:HE2	30:p:132:LEU:HD12	1.97	0.47
31:r:258:ILE:HD13	31:r:268:TYR:CD2	2.49	0.47
1:2:76:A:N6	1:2:80:A:O2'	2.46	0.47
1:2:939:A:H2'	1:2:940:A:C8	2.49	0.47
1:2:1474:G:H2'	1:2:1475:A:C8	2.50	0.47
6:F:46:PHE:HA	6:F:49:TYR:HB2	1.95	0.47
14:R:53:ILE:HD11	14:R:73:LEU:HB2	1.97	0.47
15:S:252:ARG:HB2	15:S:256:ARG:HD3	1.95	0.47
16:T:85:ARG:HB3	16:T:87:ARG:HH12	1.79	0.47
32:e:335:ALA:O	32:e:339:GLY:HA3	2.15	0.47
1:2:1161:C:H1'	1:2:1619:C:H42	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:Q:148:ASN:OD1	13:Q:148:ASN:N	2.48	0.47
28:t:102:TYR:HB2	28:t:116:GLN:HE22	1.79	0.47
1:2:343:C:H2'	1:2:344:A:H8	1.79	0.46
1:2:431:C:O3'	28:t:73:ARG:NH1	2.48	0.46
1:2:434:G:OP2	28:t:65:ARG:NH1	2.48	0.46
1:2:885:G:N2	1:2:928:U:O2	2.47	0.46
1:2:968:U:OP1	1:2:1033:C:O2'	2.33	0.46
1:2:1268:G:H2'	1:2:1270:G:H8	1.80	0.46
7:H:104:ASN:O	7:H:108:LYS:HB2	2.15	0.46
1:2:577:G:N7	31:r:49:THR:HG23	2.29	0.46
1:2:768:C:N3	19:W:143:ILE:HD13	2.30	0.46
1:2:1150:G:N2	1:2:1628:U:O2	2.36	0.46
4:C:17:ILE:HG23	4:C:58:MET:HE2	1.98	0.46
5:E:64:LYS:HA	5:E:73:PRO:HB3	1.96	0.46
8:I:77:ASN:HD21	8:I:98:GLY:HA2	1.80	0.46
13:Q:145:LYS:HG2	13:Q:149:GLN:HG3	1.96	0.46
23:a:71:ARG:NE	27:f:4:VAL:HG11	2.30	0.46
28:t:122:ARG:HD2	28:t:576:GLN:HA	1.97	0.46
31:r:119:PRO:O	31:r:120:ARG:NH1	2.43	0.46
31:r:206:ILE:HG21	31:r:286:TYR:HB2	1.95	0.46
1:2:434:G:N1	1:2:437:A:OP2	2.43	0.46
1:2:1158:C:O2'	1:2:1581:C:OP2	2.27	0.46
8:I:65:ILE:HG12	8:I:71:VAL:HG11	1.97	0.46
30:p:220:THR:HB	30:p:222:THR:HG22	1.95	0.46
31:r:16:PHE:CD1	31:r:86:LYS:HD3	2.50	0.46
1:2:1067:C:OP1	13:Q:149:GLN:HA	2.15	0.46
9:K:59:TYR:CE1	9:K:100:ILE:HD12	2.50	0.46
11:N:143:LYS:HB3	11:N:145:HIS:ND1	2.19	0.46
18:V:153:GLU:HG2	18:V:155:SER:H	1.79	0.46
28:t:722:PHE:HD2	28:t:723:ARG:HG3	1.80	0.46
31:r:203:HIS:CE1	31:r:205:ASN:H	2.33	0.46
1:2:135:A:O2'	1:2:137:U:OP2	2.26	0.46
1:2:577:G:C1'	31:r:51:ARG:CB	2.69	0.46
4:C:57:LEU:O	4:C:61:ILE:N	2.47	0.46
16:T:98:ARG:NH2	16:T:99:GLY:O	2.49	0.46
19:W:53:ARG:NH2	19:W:97:LEU:O	2.48	0.46
1:2:54:C:O2'	1:2:459:G:N7	2.41	0.46
1:2:142:G:H5''	16:T:139:ASN:HD21	1.81	0.46
1:2:1099:U:OP1	24:b:71:LYS:NZ	2.37	0.46
1:2:1170:G:O3'	31:r:198:ARG:CZ	2.63	0.46
1:2:1220:C:H2'	1:2:1221:A:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1542:G:N2	1:2:1568:C:O2'	2.48	0.46
3:B:45:LYS:HB3	3:B:46:TRP:HE3	1.80	0.46
12:P:157:ASP:OD1	23:a:60:ARG:NH2	2.48	0.46
13:Q:61:LEU:HD13	13:Q:64:ARG:HB2	1.97	0.46
22:Z:29:HIS:HB3	22:Z:41:ARG:HG3	1.97	0.46
28:t:156:ASP:OD2	28:t:283:ARG:NH1	2.48	0.46
30:p:266:VAL:HA	30:p:269:ARG:HG2	1.98	0.46
1:2:592:A:P	19:W:39:LYS:HZ2	2.37	0.46
1:2:851:U:H2'	1:2:852:C:C2	2.50	0.46
5:E:22:LEU:HD23	5:E:25:LEU:HD12	1.98	0.46
13:Q:144:ARG:HB3	13:Q:208:GLN:HB3	1.98	0.46
19:W:35:GLY:O	19:W:110:GLN:NE2	2.38	0.46
31:r:15:ASP:O	31:r:19:LEU:N	2.27	0.46
31:r:198:ARG:CD	31:r:198:ARG:C	2.86	0.46
31:r:206:ILE:O	31:r:209:LEU:HB3	2.15	0.46
1:2:700:C:H2'	1:2:701:U:C6	2.51	0.46
1:2:787:G:H2'	1:2:788:A:H8	1.79	0.46
10:L:13:ILE:HG21	10:L:31:GLU:HB3	1.97	0.46
11:N:123:ASN:HD22	11:N:145:HIS:CB	2.25	0.46
31:r:195:TYR:O	31:r:236:MET:HG2	2.04	0.46
1:2:325:G:H2'	1:2:326:G:H8	1.80	0.46
1:2:1658:G:H5''	1:2:1659:A:H8	1.79	0.46
16:T:217:SER:O	16:T:221:ALA:CB	2.64	0.46
25:c:130:VAL:HG12	28:t:221:PRO:HD2	1.98	0.46
1:2:197:A:H2'	1:2:198:A:H8	1.81	0.46
14:R:54:GLU:OE1	23:a:11:LEU:HB2	2.16	0.46
20:X:87:ARG:HE	20:X:104:HIS:CD2	2.34	0.46
22:Z:102:LEU:O	22:Z:106:ALA:HB2	2.16	0.46
31:r:275:CYS:O	31:r:278:ARG:HB3	2.16	0.46
1:2:220:A:C6	1:2:831:U:N3	2.79	0.45
1:2:340:U:H2'	1:2:341:A:H8	1.81	0.45
1:2:406:U:H2'	1:2:407:A:C8	2.51	0.45
1:2:657:U:O4	1:2:676:G:O6	2.33	0.45
1:2:756:A:H3'	1:2:757:A:H8	1.81	0.45
1:2:931:C:H5'	13:Q:116:LYS:HG2	1.98	0.45
1:2:1159:C:O2'	6:F:142:TYR:OH	2.16	0.45
4:C:55:THR:O	4:C:59:LYS:HB2	2.16	0.45
12:P:92:HIS:HE1	12:P:197:ILE:HG21	1.81	0.45
13:Q:100:PHE:HB3	13:Q:181:LEU:HD23	1.98	0.45
17:U:50:ASP:HA	17:U:56:LYS:HA	1.98	0.45
30:p:127:GLN:N	30:p:140:ARG:O	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:r:172:LYS:NZ	31:r:222:ASN:HD22	2.15	0.45
32:e:305:ARG:C	32:e:307:VAL:N	2.74	0.45
1:2:1417:A:H2'	1:2:1418:G:C8	2.51	0.45
1:2:1791:A:H2'	30:p:200:ARG:NH1	2.32	0.45
1:2:166:C:O2'	16:T:133:LEU:O	2.35	0.45
1:2:1452:U:H2'	1:2:1453:G:C8	2.51	0.45
4:C:6:THR:OG1	4:C:7:LYS:N	2.47	0.45
13:Q:29:TRP:HA	13:Q:47:LEU:HG	1.98	0.45
29:g:23:LYS:HD2	29:g:27:PRO:HA	1.96	0.45
31:r:229:ASP:C	31:r:234:ASN:ND2	2.68	0.45
1:2:79:C:H5'	16:T:172:ALA:HB3	1.97	0.45
1:2:94:U:H1'	15:S:7:LYS:CG	2.46	0.45
6:F:59:LYS:HE2	6:F:97:VAL:HG11	1.98	0.45
8:I:31:PRO:HB3	8:I:103:LYS:HG3	1.99	0.45
11:N:123:ASN:CG	11:N:145:HIS:CB	2.90	0.45
28:t:524:GLU:HG3	28:t:527:ARG:HD3	1.98	0.45
28:t:617:GLN:HG2	28:t:622:ARG:HB3	1.97	0.45
30:p:217:GLU:OE2	30:p:224:ILE:N	2.46	0.45
1:2:164:A:H2'	1:2:165:G:H8	1.81	0.45
1:2:702:G:H2'	1:2:703:G:C8	2.51	0.45
1:2:768:C:O2	19:W:143:ILE:HG21	2.17	0.45
1:2:1294:G:H4'	12:P:109:ASN:ND2	2.29	0.45
1:2:1332:C:O2'	1:2:1333:C:O5'	2.31	0.45
1:2:1344:A:H62	1:2:1377:U:HO2'	1.61	0.45
1:2:1416:G:H2'	1:2:1417:A:C8	2.51	0.45
1:2:1498:G:OP1	8:I:75:LYS:HG2	2.16	0.45
10:L:25:VAL:HG11	10:L:66:LEU:HD11	1.98	0.45
14:R:98:PHE:O	14:R:117:THR:OG1	2.28	0.45
15:S:160:VAL:HG13	15:S:169:ILE:HG23	1.98	0.45
16:T:70:PRO:HB3	16:T:101:ILE:HB	1.99	0.45
17:U:71:HIS:HA	17:U:74:GLN:HG2	1.98	0.45
28:t:90:PRO:HG3	28:t:97:PRO:HB3	1.98	0.45
31:r:232:GLU:O	31:r:233:PHE:CD1	2.70	0.45
1:2:66:U:O4	16:T:158:ILE:HG21	2.17	0.45
1:2:94:U:H1'	15:S:7:LYS:HG3	1.98	0.45
1:2:887:A:H1'	22:Z:122:PRO:HB3	1.99	0.45
1:2:1042:G:H2'	1:2:1043:A:H8	1.81	0.45
5:E:56:PHE:O	5:E:60:LEU:CB	2.62	0.45
7:H:104:ASN:O	7:H:108:LYS:CB	2.64	0.45
17:U:74:GLN:HG3	17:U:131:PHE:CD2	2.51	0.45
28:t:670:PHE:HB3	28:t:682:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:t:743:GLY:HA3	31:r:10:TYR:HE1	1.82	0.45
31:r:74:ARG:NH1	31:r:147:GLN:HG2	2.31	0.45
31:r:232:GLU:C	31:r:233:PHE:CD1	2.95	0.45
1:2:589:C:H5''	29:g:42:ARG:HH12	1.81	0.45
1:2:591:A:H2'	1:2:592:A:C8	2.52	0.45
3:B:69:PHE:CD2	6:F:46:PHE:HB3	2.51	0.45
8:I:15:ILE:HD11	8:I:63:ARG:HH21	1.82	0.45
16:T:25:ARG:HA	16:T:28:PHE:HD2	1.82	0.45
25:c:127:VAL:O	25:c:130:VAL:N	2.37	0.45
28:t:533:ASN:HB3	28:t:536:ASN:HB2	1.97	0.45
31:r:232:GLU:HG3	31:r:233:PHE:HD1	1.77	0.45
1:2:1263:G:C4	1:2:1264:G:C8	3.05	0.45
8:I:114:VAL:HB	8:I:124:ILE:HD12	1.99	0.45
24:b:81:VAL:O	24:b:122:SER:OG	2.30	0.45
31:r:274:ASP:O	31:r:278:ARG:N	2.49	0.45
1:2:220:A:H3'	1:2:832:U:H1'	1.98	0.45
1:2:480:G:H1	1:2:508:U:H3	1.64	0.45
1:2:637:C:O2	17:U:114:ARG:NH1	2.46	0.45
9:K:80:LEU:O	9:K:84:GLU:HB2	2.17	0.45
24:b:103:ILE:HA	24:b:112:ASP:HA	1.98	0.45
28:t:307:GLU:HA	28:t:336:VAL:HG22	1.99	0.45
12:P:9:LEU:HD21	12:P:14:ALA:HB2	1.99	0.45
13:Q:201:THR:HG21	13:Q:207:LEU:HD22	1.98	0.45
21:Y:3:ARG:HD3	21:Y:3:ARG:HA	1.83	0.45
1:2:115:G:O2'	1:2:334:G:O2'	2.35	0.44
1:2:142:G:H5''	16:T:139:ASN:ND2	2.32	0.44
1:2:1244:A:OP1	32:e:226:HIS:C	2.50	0.44
1:2:1287:A:H4'	1:2:1288:G:H5'	2.00	0.44
1:2:1575:G:N3	31:r:233:PHE:CG	2.81	0.44
5:E:83:MET:HB3	5:E:116:LEU:HD12	1.99	0.44
13:Q:138:PHE:CD2	13:Q:214:LYS:HB2	2.52	0.44
15:S:191:ARG:NH1	15:S:245:LYS:HB3	2.29	0.44
16:T:76:LEU:HD23	16:T:76:LEU:HA	1.86	0.44
22:Z:125:SER:OG	22:Z:126:THR:N	2.40	0.44
28:t:518:ASP:OD2	28:t:521:SER:N	2.50	0.44
31:r:80:ILE:HD13	31:r:83:LEU:HD12	1.99	0.44
31:r:108:ASP:HB3	31:r:110:TYR:CZ	2.51	0.44
31:r:127:LEU:O	31:r:151:TRP:HZ3	1.99	0.44
31:r:231:ASN:O	31:r:234:ASN:CG	2.60	0.44
1:2:781:U:O2'	1:2:782:U:OP2	2.34	0.44
1:2:1563:C:OP1	8:I:84:LYS:NZ	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:58:LEU:HD12	2:D:59:LEU:HB2	1.98	0.44
14:R:158:THR:HG21	14:R:221:THR:HG22	2.00	0.44
14:R:175:GLY:N	14:R:195:ASP:OD2	2.49	0.44
15:S:112:HIS:NE2	15:S:237:SER:O	2.50	0.44
31:r:92:ASP:O	31:r:93:THR:HB	2.18	0.44
31:r:94:VAL:HA	31:r:112:VAL:HG22	1.99	0.44
31:r:165:PHE:O	31:r:169:LEU:HG	2.17	0.44
1:2:219:A:H2'	1:2:220:A:C8	2.52	0.44
1:2:402:C:OP1	15:S:3:ARG:NH2	2.49	0.44
1:2:1239:U:H3	1:2:1244:A:H2	1.64	0.44
3:B:116:HIS:HE1	9:K:95:HIS:NE2	2.15	0.44
14:R:126:ARG:O	14:R:130:ILE:HG12	2.18	0.44
17:U:44:LYS:HD3	17:U:63:PRO:HG3	1.98	0.44
25:c:131:SER:O	25:c:131:SER:OG	2.33	0.44
28:t:55:LYS:HB3	28:t:55:LYS:HE3	1.71	0.44
28:t:501:TYR:HB3	28:t:773:LEU:HB3	1.99	0.44
31:r:2:LYS:CE	31:r:142:LEU:CD1	2.95	0.44
31:r:2:LYS:NZ	31:r:142:LEU:HD12	2.33	0.44
1:2:220:A:N6	1:2:831:U:N3	2.65	0.44
8:I:129:GLN:O	8:I:133:ASP:HB2	2.17	0.44
14:R:188:LEU:HA	14:R:188:LEU:HD23	1.82	0.44
28:t:502:ARG:HH21	28:t:776:ARG:HB2	1.82	0.44
31:r:263:GLN:H	31:r:263:GLN:CD	2.25	0.44
1:2:1248:C:H2'	1:2:1249:U:C6	2.52	0.44
5:E:22:LEU:HA	5:E:25:LEU:HD12	1.99	0.44
14:R:116:LYS:HB2	14:R:131:ILE:HD12	2.00	0.44
14:R:229:LEU:HD11	23:a:1:MET:CE	2.48	0.44
17:U:51:VAL:HG23	17:U:53:GLY:H	1.82	0.44
1:2:577:G:N7	31:r:49:THR:CG2	2.80	0.44
1:2:1228:G:H4'	2:D:45:LEU:HB2	1.99	0.44
3:B:51:VAL:HB	3:B:64:VAL:HG13	2.00	0.44
3:B:55:ASP:HB2	3:B:138:THR:HG22	2.00	0.44
6:F:4:VAL:HG23	6:F:6:SER:HB3	1.99	0.44
8:I:40:SER:HB3	8:I:43:ASN:HB2	2.00	0.44
15:S:208:VAL:HG21	15:S:225:VAL:HG21	2.00	0.44
17:U:5:GLN:HB3	17:U:18:LEU:HD22	1.99	0.44
21:Y:23:PRO:HB2	21:Y:26:PHE:HB2	1.98	0.44
28:t:54:ARG:HA	28:t:54:ARG:HD3	1.83	0.44
30:p:119:PRO:HA	30:p:122:GLU:HB3	1.98	0.44
31:r:53:ILE:HA	31:r:56:LEU:HB2	1.99	0.44
32:e:305:ARG:O	32:e:306:ALA:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1219:A:N7	1:2:1265:G:C2	2.86	0.44
1:2:1221:A:N7	1:2:1263:G:N2	2.64	0.44
4:C:44:LYS:HG3	4:C:47:ARG:HH21	1.83	0.44
8:I:66:TYR:HE1	8:I:129:GLN:HG2	1.82	0.44
11:N:147:VAL:CG1	11:N:148:TYR:H	2.17	0.44
28:t:91:LEU:HD13	28:t:177:ILE:HD11	1.98	0.44
31:r:254:PHE:N	31:r:255:PRO:HD3	2.33	0.44
1:2:78:A:H1'	16:T:175:ILE:CD1	2.47	0.44
1:2:486:G:N2	1:2:501:U:O2	2.36	0.44
1:2:489:C:O2'	1:2:499:U:N3	2.51	0.44
1:2:638:U:O3'	17:U:117:THR:OG1	2.36	0.44
1:2:1147:A:O5'	1:2:1147:A:H8	2.01	0.44
1:2:1344:A:H2'	1:2:1345:A:C8	2.53	0.44
1:2:1682:U:H4'	16:T:65:GLN:NE2	2.33	0.44
6:F:13:LYS:O	6:F:16:ALA:N	2.51	0.44
9:K:80:LEU:O	9:K:84:GLU:HB3	2.18	0.44
12:P:140:ASN:ND2	23:a:29:HIS:O	2.51	0.44
24:b:81:VAL:HG13	24:b:85:ASP:HB2	2.00	0.44
28:t:717:VAL:HG13	28:t:720:MET:HB3	1.99	0.44
31:r:25:GLY:O	31:r:29:HIS:N	2.50	0.44
31:r:274:ASP:HA	31:r:277:ARG:HB3	1.99	0.44
1:2:1219:A:N6	1:2:1264:G:H2'	2.32	0.44
3:B:57:SER:HA	3:B:59:VAL:H	1.83	0.44
3:B:95:ASN:OD1	3:B:107:LYS:NZ	2.51	0.44
12:P:133:ILE:HG23	12:P:155:PHE:HB2	2.00	0.44
28:t:376:ASP:CB	31:r:95:TYR:OH	2.66	0.44
31:r:21:ALA:HB3	31:r:37:ILE:HG23	2.00	0.44
31:r:34:THR:HB	31:r:35:PRO:HD3	1.99	0.44
31:r:64:LYS:C	31:r:65:MET:HE3	2.43	0.44
31:r:87:THR:O	31:r:91:ARG:HG2	2.17	0.44
31:r:110:TYR:CE2	31:r:124:ILE:HD13	2.53	0.44
31:r:156:ARG:NE	31:r:184:ARG:HA	2.33	0.44
1:2:206:A:H2'	1:2:207:U:H6	1.83	0.43
1:2:489:C:HO2'	1:2:499:U:H3	1.64	0.43
3:B:192:GLU:OE2	9:K:61:SER:OG	2.32	0.43
7:H:67:GLU:O	7:H:71:GLN:CB	2.61	0.43
15:S:11:ARG:NH2	15:S:21:ASP:OD1	2.51	0.43
26:d:51:GLU:OE1	26:d:53:ASP:N	2.39	0.43
28:t:714:VAL:HG21	28:t:759:PHE:HB2	1.99	0.43
31:r:166:MET:O	31:r:170:TYR:N	2.32	0.43
1:2:129:U:H5'	1:2:131:C:C4	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:788:A:OP1	15:S:106:LYS:HE3	2.18	0.43
1:2:1219:A:N7	1:2:1265:G:N3	2.66	0.43
1:2:1250:U:C2	11:N:140:TYR:CD2	3.06	0.43
1:2:1464:G:O3'	6:F:141:SER:OG	2.31	0.43
1:2:1681:A:H2	1:2:1720:G:H21	1.66	0.43
14:R:44:LEU:HD13	14:R:50:ILE:HD12	2.00	0.43
16:T:192:ALA:HB1	16:T:196:ARG:HH22	1.81	0.43
17:U:82:GLU:OE2	17:U:165:LYS:NZ	2.38	0.43
19:W:108:ARG:HH21	19:W:145:SER:HB2	1.84	0.43
31:r:77:TYR:CE2	31:r:151:TRP:HD1	2.36	0.43
32:e:301:TYR:O	32:e:304:TYR:CA	2.66	0.43
1:2:565:C:H5''	31:r:47:SER:HG	1.72	0.43
1:2:953:G:H2'	1:2:954:G:C8	2.54	0.43
1:2:1348:A:H2'	1:2:1349:G:C8	2.53	0.43
1:2:1592:A:H2'	1:2:1593:A:H8	1.83	0.43
7:H:86:LEU:HB2	7:H:89:GLN:HE21	1.84	0.43
14:R:129:ILE:O	14:R:133:LYS:HG2	2.18	0.43
27:f:2:VAL:HG22	27:f:3:LEU:H	1.82	0.43
28:t:343:ARG:HE	28:t:562:ARG:HH12	1.67	0.43
31:r:198:ARG:CB	31:r:233:PHE:CD2	2.96	0.43
1:2:93:A:H4'	15:S:3:ARG:NH1	2.32	0.43
1:2:620:A:H2'	1:2:621:A:C8	2.53	0.43
1:2:898:A:H4'	22:Z:46:MET:HE3	2.00	0.43
1:2:1585:U:H3	1:2:1611:A:H2	1.65	0.43
14:R:243:TYR:HE2	14:R:247:ALA:HB3	1.83	0.43
28:t:282:VAL:HG21	28:t:557:ILE:HD12	2.00	0.43
31:r:52:ALA:O	31:r:55:ASP:HB2	2.19	0.43
1:2:565:C:C2'	31:r:47:SER:H	2.30	0.43
1:2:788:A:C2	15:S:19:LEU:HD13	2.54	0.43
1:2:896:U:O2	22:Z:41:ARG:NH1	2.52	0.43
3:B:69:PHE:CG	6:F:46:PHE:HB3	2.53	0.43
6:F:36:ILE:HD11	6:F:48:VAL:HG13	2.01	0.43
6:F:44:LEU:HD13	6:F:78:VAL:HG21	2.00	0.43
6:F:47:LYS:O	6:F:82:ARG:NE	2.39	0.43
13:Q:143:THR:HB	13:Q:205:PHE:HE2	1.82	0.43
14:R:45:VAL:HG21	14:R:68:ILE:HG23	2.00	0.43
22:Z:88:GLY:HA2	22:Z:122:PRO:HD3	1.98	0.43
26:d:3:ASP:H	26:d:32:ARG:HD2	1.82	0.43
28:t:745:ILE:HD13	28:t:745:ILE:HG21	1.79	0.43
31:r:151:TRP:O	31:r:155:SER:HB2	2.18	0.43
1:2:34:G:O2'	1:2:515:A:O2'	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:778:G:C6	1:2:780:A:H1'	2.54	0.43
1:2:1243:G:H1'	32:e:228:LYS:O	2.18	0.43
3:B:68:ILE:HA	6:F:112:TYR:HE1	1.82	0.43
3:B:188:LYS:HE3	3:B:192:GLU:HB3	2.01	0.43
8:I:132:LEU:O	8:I:136:ALA:HB2	2.19	0.43
11:N:145:HIS:HB2	11:N:146:SER:H	1.61	0.43
21:Y:108:ASP:OD2	21:Y:111:ALA:N	2.48	0.43
26:d:25:VAL:N	26:d:71:GLY:O	2.46	0.43
28:t:54:ARG:C	28:t:57:LYS:H	2.23	0.43
28:t:122:ARG:NH1	28:t:576:GLN:O	2.51	0.43
28:t:177:ILE:O	28:t:181:GLU:CB	2.65	0.43
28:t:593:VAL:HB	28:t:693:HIS:HA	1.99	0.43
1:2:340:U:H2'	1:2:341:A:C8	2.54	0.43
5:E:59:LYS:HD3	5:E:76:VAL:HG13	2.00	0.43
6:F:143:ARG:CZ	31:r:129:ARG:CB	2.91	0.43
31:r:45:SER:OG	31:r:46:GLN:N	2.51	0.43
31:r:105:LYS:O	31:r:129:ARG:HD3	2.18	0.43
1:2:112:A:O2'	20:X:67:ARG:NH1	2.52	0.43
1:2:249:U:N3	20:X:63:LEU:HD21	2.34	0.43
1:2:894:U:H2'	1:2:895:G:C8	2.54	0.43
1:2:1557:U:H4'	5:E:118:GLU:OE2	2.19	0.43
15:S:64:ILE:CG2	26:d:17:LEU:HD13	2.48	0.43
25:c:130:VAL:HG12	28:t:221:PRO:HG2	2.00	0.43
31:r:6:SER:HG	31:r:7:HIS:HD1	1.61	0.43
31:r:210:TYR:CD1	31:r:280:PHE:HE2	2.37	0.43
1:2:622:A:O2'	1:2:1032:G:OP2	2.36	0.43
1:2:933:A:N6	1:2:935:U:O2	2.52	0.43
1:2:1354:G:O6	1:2:1369:U:C4	2.72	0.43
1:2:1463:C:H5'	31:r:103:VAL:O	2.19	0.43
1:2:1487:A:H2'	1:2:1488:G:C8	2.54	0.43
1:2:1525:A:N3	1:2:1589:C:O2'	2.45	0.43
11:N:123:ASN:CG	11:N:145:HIS:CA	2.66	0.43
14:R:44:LEU:HD21	14:R:243:TYR:CD1	2.54	0.43
15:S:112:HIS:HE2	15:S:237:SER:HG	1.63	0.43
22:Z:107:ARG:HA	30:p:149:PRO:HB2	2.01	0.43
31:r:228:CYS:HA	31:r:272:ASP:OD1	2.19	0.43
1:2:208:U:C1'	18:V:178:ARG:HD2	2.48	0.43
1:2:315:A:H8	1:2:315:A:H2'	1.73	0.43
1:2:811:A:C5	17:U:110:GLN:HG3	2.53	0.43
1:2:1453:G:H21	5:E:99:GLY:HA2	1.84	0.43
3:B:136:ALA:O	3:B:140:THR:OG1	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:57:ASP:HA	16:T:107:ALA:H	1.84	0.43
21:Y:99:ARG:NH1	21:Y:143:SER:O	2.52	0.43
28:t:717:VAL:HB	28:t:755:PHE:H	1.82	0.43
1:2:480:G:N2	1:2:508:U:O2	2.41	0.42
1:2:1470:C:H3'	1:2:1573:A:H62	1.84	0.42
1:2:1594:G:C6	1:2:1595:U:O4	2.72	0.42
2:D:74:LEU:HD11	11:N:106:TYR:CD2	2.54	0.42
2:D:77:GLY:HA3	11:N:112:GLY:O	2.19	0.42
15:S:19:LEU:HD12	15:S:51:ARG:HH12	1.84	0.42
25:c:83:VAL:HG11	25:c:122:PHE:CE2	2.53	0.42
28:t:67:LEU:HD12	28:t:67:LEU:HA	1.87	0.42
30:p:182:ILE:HG23	30:p:232:HIS:CE1	2.54	0.42
31:r:229:ASP:HB2	31:r:256:GLN:CD	2.44	0.42
1:2:253:A:OP1	15:S:134:LYS:N	2.48	0.42
1:2:914:G:O2'	1:2:915:A:N7	2.47	0.42
1:2:1066:C:O2'	13:Q:148:ASN:O	2.30	0.42
1:2:1269:U:O4	32:e:297:HIS:O	2.37	0.42
3:B:132:VAL:HG13	3:B:202:ALA:HB2	2.00	0.42
6:F:62:ASN:ND2	6:F:92:TYR:OH	2.52	0.42
13:Q:116:LYS:HB2	13:Q:117:TRP:CD1	2.54	0.42
13:Q:130:SER:HB3	13:Q:179:SER:HA	2.01	0.42
13:Q:131:ASP:N	13:Q:131:ASP:OD1	2.46	0.42
28:t:678:LYS:O	28:t:680:ILE:N	2.53	0.42
31:r:61:LEU:HD21	31:r:82:TYR:CE2	2.53	0.42
1:2:512:A:OP2	19:W:172:VAL:HG12	2.20	0.42
1:2:590:C:C5'	29:g:43:ARG:HH21	2.32	0.42
1:2:816:G:H2'	1:2:817:A:H8	1.84	0.42
1:2:958:U:C6	21:Y:13:SER:O	2.72	0.42
1:2:1528:U:O2'	6:F:41:PRO:HB3	2.19	0.42
8:I:114:VAL:HG23	8:I:123:ARG:C	2.44	0.42
14:R:243:TYR:CE2	14:R:247:ALA:HB3	2.55	0.42
19:W:52:ILE:HG21	19:W:80:LEU:HD11	2.00	0.42
28:t:504:LEU:HD12	28:t:774:TYR:HD2	1.83	0.42
30:p:153:GLN:HA	30:p:156:ALA:HB3	2.00	0.42
1:2:54:C:O3'	26:d:109:LYS:HD3	2.19	0.42
6:F:59:LYS:HB2	6:F:93:HIS:CE1	2.53	0.42
9:K:54:VAL:HA	9:K:56:THR:HG23	2.01	0.42
12:P:56:LYS:HE3	12:P:158:VAL:HG23	2.01	0.42
30:p:117:TYR:HB2	30:p:118:PRO:HD3	2.00	0.42
30:p:194:THR:HA	30:p:198:LEU:HB2	2.01	0.42
15:S:251:GLU:O	15:S:255:ARG:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:d:10:ARG:HH11	26:d:10:ARG:HD3	1.64	0.42
31:r:2:LYS:NZ	31:r:142:LEU:CD1	2.83	0.42
31:r:14:ASP:O	31:r:18:VAL:N	2.32	0.42
1:2:74:U:HO2'	1:2:76:A:P	2.42	0.42
1:2:144:U:H5	16:T:137:ARG:HH12	1.67	0.42
1:2:1201:G:H22	1:2:1600:A:H5''	1.85	0.42
1:2:1472:C:O2'	1:2:1534:G:N2	2.53	0.42
14:R:144:TRP:CE2	14:R:173:PRO:HG3	2.55	0.42
23:a:80:LYS:O	23:a:82:VAL:N	2.51	0.42
28:t:541:ILE:HG12	28:t:586:LEU:HD12	2.00	0.42
31:r:217:ILE:O	31:r:221:ALA:N	2.53	0.42
1:2:451:A:H61	1:2:456:A:N6	2.18	0.42
1:2:953:G:H2'	1:2:954:G:H8	1.85	0.42
3:B:216:GLU:HA	3:B:219:ARG:HG2	2.00	0.42
7:H:19:ASN:HD22	7:H:103:ASN:HD22	1.67	0.42
13:Q:104:ASP:HA	13:Q:214:LYS:HD2	2.02	0.42
14:R:211:LEU:HD23	14:R:211:LEU:HA	1.90	0.42
24:b:27:ILE:HG21	24:b:27:ILE:HD13	1.70	0.42
25:c:79:ASN:HB3	25:c:81:LYS:HG3	2.02	0.42
26:d:81:GLU:HA	26:d:84:LYS:HG2	2.01	0.42
27:f:67:THR:OG1	27:f:70:LYS:O	2.37	0.42
30:p:101:VAL:HG11	30:p:109:LEU:HD11	2.02	0.42
30:p:148:ASP:N	30:p:148:ASP:OD1	2.52	0.42
31:r:209:LEU:HD12	31:r:249:PHE:HE1	1.85	0.42
1:2:990:C:H2'	1:2:991:G:O4'	2.19	0.42
1:2:1243:G:O3'	32:e:228:LYS:O	2.38	0.42
1:2:1336:A:H2'	1:2:1337:A:C8	2.54	0.42
1:2:1503:A:O2'	8:I:37:VAL:HG23	2.19	0.42
1:2:1592:A:H2'	1:2:1593:A:C8	2.55	0.42
14:R:240:LEU:HD12	14:R:243:TYR:HE1	1.85	0.42
15:S:136:VAL:HG11	15:S:148:ARG:HH11	1.85	0.42
19:W:144:PRO:O	19:W:146:PHE:N	2.53	0.42
1:2:644:C:H2'	1:2:645:C:C6	2.55	0.42
3:B:34:GLN:HA	3:B:37:GLN:HB2	2.02	0.42
3:B:68:ILE:HA	6:F:112:TYR:CE1	2.55	0.42
5:E:61:ARG:O	5:E:65:LEU:CB	2.67	0.42
10:L:13:ILE:HD11	10:L:29:ARG:HB3	2.02	0.42
15:S:21:ASP:OD1	15:S:21:ASP:N	2.51	0.42
16:T:85:ARG:HA	16:T:86:PRO:HD3	1.93	0.42
22:Z:18:ARG:HE	22:Z:82:LYS:HD3	1.84	0.42
28:t:138:ILE:HG21	28:t:578:LEU:HD11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:422:G:H2'	1:2:423:G:C8	2.55	0.42
1:2:632:U:O2'	1:2:1103:U:OP1	2.36	0.42
1:2:787:G:H5''	15:S:255:ARG:HD3	2.01	0.42
1:2:1221:A:C2	1:2:1263:G:C4	3.07	0.42
1:2:1237:G:H2'	1:2:1238:A:H8	1.85	0.42
3:B:147:THR:HG23	3:B:158:GLN:HB3	2.02	0.42
7:H:88:ARG:NH1	7:H:112:ASP:OD2	2.53	0.42
13:Q:40:ASN:OD1	13:Q:40:ASN:N	2.52	0.42
13:Q:92:GLN:HG2	13:Q:96:LEU:HA	2.02	0.42
15:S:159:THR:HG22	15:S:173:ILE:HB	2.01	0.42
28:t:515:ASP:HA	28:t:776:ARG:HH12	1.85	0.42
28:t:737:THR:O	28:t:740:GLY:N	2.53	0.42
29:g:51:ASN:O	29:g:53:LYS:N	2.53	0.42
1:2:52:U:H2'	1:2:53:G:C8	2.55	0.41
1:2:141:U:H2'	16:T:183:ARG:NH2	2.33	0.41
1:2:393:C:H2'	1:2:394:C:C6	2.55	0.41
1:2:399:A:H4'	15:S:3:ARG:HG2	2.02	0.41
1:2:484:C:H2'	1:2:485:A:C8	2.54	0.41
1:2:1244:A:O2'	1:2:1246:C:OP1	2.38	0.41
1:2:1529:C:OP1	3:B:112:ARG:NH1	2.53	0.41
8:I:117:SER:HB2	8:I:123:ARG:HB3	2.02	0.41
12:P:126:PRO:HG3	12:P:147:THR:HG22	2.02	0.41
20:X:73:GLY:HA3	20:X:86:ILE:HD12	2.01	0.41
28:t:529:LEU:HG	28:t:592:ALA:HB2	2.01	0.41
28:t:706:HIS:HB2	28:t:718:ARG:HB3	2.02	0.41
28:t:742:SER:CB	31:r:10:TYR:CD1	3.03	0.41
1:2:220:A:N6	1:2:831:U:H3	2.17	0.41
1:2:973:A:H2'	1:2:974:A:H8	1.84	0.41
3:B:167:ARG:O	3:B:171:ALA:CB	2.67	0.41
30:p:107:THR:O	30:p:111:ASN:CB	2.56	0.41
31:r:196:PRO:HA	31:r:235:ILE:O	2.20	0.41
31:r:284:LEU:O	31:r:284:LEU:HD23	2.20	0.41
1:2:478:A:HO2'	19:W:124:HIS:HD1	1.59	0.41
1:2:512:A:OP2	19:W:172:VAL:CG1	2.67	0.41
1:2:1161:C:H2'	1:2:1162:C:C6	2.55	0.41
6:F:40:GLU:HA	6:F:41:PRO:HA	1.78	0.41
13:Q:109:LYS:HG3	13:Q:113:MET:HE3	2.03	0.41
16:T:105:ASP:OD1	16:T:105:ASP:N	2.50	0.41
18:V:141:ARG:O	18:V:145:ALA:N	2.51	0.41
26:d:8:ARG:HB2	26:d:26:ASP:HB3	2.02	0.41
28:t:534:TYR:HE2	28:t:664:GLN:HE21	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:164:A:H2'	1:2:165:G:C8	2.54	0.41
1:2:1219:A:H61	1:2:1265:G:H5'	1.85	0.41
1:2:1263:G:H2'	1:2:1264:G:O5'	2.21	0.41
2:D:62:LEU:HD13	2:D:75:VAL:HG11	2.03	0.41
3:B:113:ILE:HD13	3:B:190:ILE:HG21	2.02	0.41
6:F:97:VAL:HG12	6:F:98:ASP:H	1.86	0.41
16:T:25:ARG:HA	16:T:28:PHE:CD2	2.56	0.41
19:W:110:GLN:OE1	19:W:126:ARG:NH1	2.50	0.41
1:2:105:A:O2'	18:V:8:ARG:NH2	2.52	0.41
1:2:400:A:H8	1:2:400:A:H2'	1.81	0.41
1:2:765:G:C6	19:W:149:ARG:HG3	2.55	0.41
1:2:1036:A:H2'	1:2:1037:C:C6	2.56	0.41
1:2:1149:G:N2	31:r:77:TYR:OH	2.54	0.41
1:2:1263:G:C2'	1:2:1264:G:H8	2.28	0.41
1:2:1587:A:H2'	1:2:1588:G:H8	1.86	0.41
15:S:35:PRO:HB2	15:S:36:HIS:CD2	2.56	0.41
15:S:177:ALA:HA	15:S:195:ILE:HB	2.03	0.41
21:Y:55:ARG:HH22	27:f:51:GLN:NE2	2.18	0.41
30:p:169:ASP:OD1	30:p:169:ASP:N	2.53	0.41
31:r:197:MET:SD	31:r:280:PHE:HE1	2.42	0.41
1:2:93:A:O3'	15:S:3:ARG:O	2.38	0.41
1:2:175:G:H22	1:2:266:A:P	2.44	0.41
1:2:329:G:H2'	1:2:330:G:H8	1.85	0.41
1:2:962:C:OP2	21:Y:70:LYS:HD2	2.21	0.41
1:2:1575:G:H22	31:r:233:PHE:HB3	1.72	0.41
4:C:118:PRO:HD2	12:P:15:GLN:NE2	2.36	0.41
6:F:50:GLU:O	6:F:54:LEU:CB	2.69	0.41
28:t:196:SER:HA	28:t:199:HIS:HB2	2.02	0.41
28:t:564:PRO:HB2	28:t:566:PHE:HD2	1.86	0.41
28:t:600:ARG:HH12	28:t:607:PRO:HA	1.86	0.41
30:p:169:ASP:HA	30:p:172:ILE:HD12	2.02	0.41
1:2:565:C:OP2	31:r:47:SER:OG	2.39	0.41
1:2:1575:G:C2	31:r:233:PHE:CB	2.89	0.41
1:2:1622:G:OP1	31:r:144:LYS:NZ	2.32	0.41
4:C:105:GLN:NE2	12:P:41:ARG:HG3	2.36	0.41
8:I:18:TYR:HD2	8:I:59:ALA:HA	1.84	0.41
9:K:50:ILE:HA	9:K:53:GLU:HB2	2.02	0.41
13:Q:35:PRO:HD3	13:Q:98:THR:HG23	2.02	0.41
13:Q:176:VAL:HG12	13:Q:177:GLN:H	1.84	0.41
17:U:46:ILE:HD11	17:U:58:LEU:HB3	2.02	0.41
21:Y:125:LEU:HD23	21:Y:125:LEU:HA	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:c:75:GLN:HE21	25:c:80:GLY:HA2	1.86	0.41
31:r:74:ARG:NH1	31:r:147:GLN:O	2.39	0.41
1:2:554:C:N4	1:2:571:G:O6	2.53	0.41
1:2:886:U:O2	22:Z:123:SER:N	2.53	0.41
1:2:1265:G:C6	1:2:1444:A:N6	2.87	0.41
7:H:12:GLN:NE2	7:H:61:LEU:O	2.54	0.41
8:I:140:LEU:HA	8:I:143:ASP:HB2	2.02	0.41
15:S:52:LEU:HD23	15:S:52:LEU:HA	1.89	0.41
20:X:71:LEU:HD22	20:X:88:ARG:HH21	1.85	0.41
25:c:15:LEU:HD23	25:c:15:LEU:HA	1.86	0.41
28:t:285:ILE:HD11	28:t:546:LYS:HD3	2.03	0.41
31:r:50:ASN:HA	31:r:53:ILE:HB	2.02	0.41
32:e:305:ARG:C	32:e:307:VAL:H	2.29	0.41
1:2:249:U:C5	20:X:34:TRP:CE3	3.09	0.41
1:2:1174:C:H42	1:2:1465:C:H42	1.69	0.41
1:2:1450:U:H2'	1:2:1451:C:H6	1.86	0.41
1:2:1590:G:H2'	1:2:1591:C:H6	1.86	0.41
1:2:1688:U:OP2	1:2:1689:A:N6	2.54	0.41
3:B:100:ASN:HD22	3:B:180:ARG:HD2	1.86	0.41
7:H:35:ILE:HG23	7:H:102:ALA:HB2	2.03	0.41
12:P:118:PRO:HB2	12:P:120:LEU:H	1.85	0.41
13:Q:82:ARG:HG2	13:Q:103:MET:HE3	2.03	0.41
14:R:144:TRP:CH2	24:b:97:ARG:NH1	2.88	0.41
14:R:148:LEU:HD23	14:R:148:LEU:HA	1.96	0.41
15:S:31:PRO:HG3	15:S:43:PRO:HG3	2.03	0.41
15:S:51:ARG:HA	15:S:51:ARG:HD3	1.93	0.41
16:T:7:TYR:HD2	16:T:10:ASN:H	1.69	0.41
19:W:123:HIS:CD2	29:g:33:ARG:HH22	2.38	0.41
23:a:17:CYS:HB2	23:a:56:SER:HB3	2.03	0.41
28:t:146:LEU:HD23	28:t:146:LEU:HA	1.91	0.41
28:t:716:THR:HG22	28:t:756:LYS:HG3	2.03	0.41
28:t:727:VAL:HA	28:t:731:LYS:HE3	2.02	0.41
30:p:183:GLU:HG3	30:p:240:ILE:HG21	2.02	0.41
31:r:101:ILE:HA	31:r:102:GLY:HA3	1.67	0.41
31:r:206:ILE:N	31:r:207:PRO:HD2	2.36	0.41
31:r:216:PHE:CZ	31:r:251:VAL:HG21	2.56	0.41
1:2:304:U:H5''	20:X:136:ARG:HG3	2.02	0.41
1:2:417:A:H1'	1:2:418:G:C2	2.56	0.41
1:2:765:G:N1	19:W:146:PHE:CE2	2.89	0.41
1:2:1583:A:H62	1:2:1612:U:H5	1.69	0.41
28:t:124:PHE:HB3	28:t:126:VAL:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:141:U:O4	16:T:183:ARG:HB3	2.21	0.40
1:2:590:C:H2'	1:2:591:A:H8	1.86	0.40
1:2:1221:A:N6	1:2:1263:G:H1	2.11	0.40
1:2:1299:G:H2'	1:2:1300:A:C8	2.55	0.40
1:2:1350:U:O2'	6:F:21:HIS:NE2	2.54	0.40
1:2:1477:G:H4'	8:I:47:PRO:HA	2.02	0.40
1:2:1710:U:H2'	1:2:1711:C:H4'	2.03	0.40
8:I:20:SER:HA	8:I:23:GLN:HB3	2.03	0.40
24:b:24:GLN:NE2	27:f:5:GLN:HG2	2.36	0.40
26:d:128:LYS:HE2	26:d:132:ARG:HD3	2.02	0.40
31:r:93:THR:HA	31:r:114:ASP:OD1	2.21	0.40
31:r:203:HIS:HE1	31:r:205:ASN:HB3	1.86	0.40
31:r:216:PHE:CE2	31:r:220:LEU:HD11	2.57	0.40
1:2:565:C:H2'	31:r:46:GLN:N	2.36	0.40
1:2:1276:U:N3	1:2:1437:U:O2	2.54	0.40
1:2:1791:A:H2'	30:p:200:ARG:HH11	1.87	0.40
7:H:65:GLU:HG2	7:H:68:ARG:HH22	1.86	0.40
13:Q:61:LEU:HD22	13:Q:64:ARG:HD2	2.02	0.40
13:Q:82:ARG:HH22	13:Q:188:LEU:C	2.28	0.40
15:S:237:SER:OG	15:S:237:SER:O	2.35	0.40
19:W:123:HIS:CE1	29:g:37:ARG:HG3	2.56	0.40
26:d:56:SER:HB3	26:d:74:LEU:HB2	2.03	0.40
31:r:77:TYR:CZ	31:r:151:TRP:HB2	2.57	0.40
31:r:218:VAL:O	31:r:222:ASN:N	2.54	0.40
1:2:16:G:H21	1:2:1138:A:H62	1.69	0.40
1:2:179:A:H2	16:T:202:ARG:HH12	1.68	0.40
1:2:522:U:H5'	26:d:36:SER:HA	2.03	0.40
1:2:993:A:N6	1:2:1012:U:C4	2.90	0.40
1:2:1158:C:H42	1:2:1163:A:H61	1.69	0.40
1:2:1498:G:H5''	8:I:72:GLY:HA3	2.04	0.40
1:2:1565:C:OP1	7:H:41:ARG:HG3	2.21	0.40
5:E:86:VAL:HG13	5:E:88:GLU:H	1.86	0.40
5:E:92:SER:H	5:E:107:ILE:HB	1.86	0.40
7:H:81:ILE:HA	7:H:82:PRO:HD3	1.89	0.40
17:U:80:GLU:O	17:U:84:LYS:HB2	2.21	0.40
18:V:138:ASN:HD22	18:V:141:ARG:HD2	1.87	0.40
19:W:18:PRO:O	19:W:23:ARG:NH2	2.54	0.40
20:X:45:PRO:HG2	20:X:48:ALA:HB2	2.03	0.40
25:c:8:GLY:O	25:c:11:SER:OG	2.35	0.40
31:r:216:PHE:O	31:r:220:LEU:HG	2.22	0.40
1:2:107:C:H2'	1:2:108:A:C8	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1501:C:H2'	1:2:1502:G:C8	2.56	0.40
1:2:1579:U:H2'	1:2:1580:C:C6	2.57	0.40
14:R:120:GLU:O	14:R:124:ALA:N	2.50	0.40
15:S:11:ARG:O	15:S:12:LEU:CB	2.66	0.40
16:T:137:ARG:HD2	16:T:177:ARG:HE	1.85	0.40
20:X:66:ILE:HG21	20:X:66:ILE:HD13	1.78	0.40
28:t:123:ILE:HG13	28:t:138:ILE:HG12	2.02	0.40
13:Q:146:GLN:HG2	13:Q:147:ALA:H	1.87	0.40
22:Z:77:THR:O	22:Z:111:ARG:N	2.54	0.40
30:p:202:ILE:HA	30:p:205:ILE:HG12	2.03	0.40
31:r:195:TYR:HE1	31:r:200:LEU:HG	1.87	0.40
31:r:235:ILE:HB	31:r:251:VAL:HG22	1.58	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	D	122/143 (85%)	89 (73%)	30 (25%)	3 (2%)	4	28
3	B	198/225 (88%)	168 (85%)	28 (14%)	2 (1%)	12	45
4	C	108/136 (79%)	92 (85%)	14 (13%)	2 (2%)	6	33
5	E	115/142 (81%)	93 (81%)	21 (18%)	1 (1%)	14	46
6	F	139/143 (97%)	121 (87%)	14 (10%)	4 (3%)	3	26
7	H	120/146 (82%)	107 (89%)	13 (11%)	0	100	100
8	I	141/144 (98%)	129 (92%)	11 (8%)	1 (1%)	18	51
9	K	62/108 (57%)	49 (79%)	10 (16%)	3 (5%)	2	16
10	L	60/67 (90%)	54 (90%)	6 (10%)	0	100	100
11	N	49/152 (32%)	32 (65%)	12 (24%)	5 (10%)	0	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	P	204/252 (81%)	168 (82%)	32 (16%)	4 (2%)	6	32
13	Q	212/255 (83%)	172 (81%)	38 (18%)	2 (1%)	14	46
14	R	218/254 (86%)	186 (85%)	29 (13%)	3 (1%)	9	38
15	S	258/261 (99%)	226 (88%)	31 (12%)	1 (0%)	30	61
16	T	224/236 (95%)	206 (92%)	17 (8%)	1 (0%)	30	61
17	U	182/190 (96%)	158 (87%)	22 (12%)	2 (1%)	11	43
18	V	184/200 (92%)	160 (87%)	21 (11%)	3 (2%)	7	36
19	W	183/197 (93%)	156 (85%)	24 (13%)	3 (2%)	7	36
20	X	153/156 (98%)	133 (87%)	19 (12%)	1 (1%)	18	51
21	Y	148/151 (98%)	130 (88%)	17 (12%)	1 (1%)	18	51
22	Z	125/137 (91%)	110 (88%)	15 (12%)	0	100	100
23	a	85/87 (98%)	66 (78%)	16 (19%)	3 (4%)	3	23
24	b	127/130 (98%)	118 (93%)	8 (6%)	1 (1%)	16	49
25	c	142/145 (98%)	116 (82%)	23 (16%)	3 (2%)	5	31
26	d	132/135 (98%)	121 (92%)	9 (7%)	2 (2%)	8	37
27	f	79/82 (96%)	60 (76%)	17 (22%)	2 (2%)	4	28
28	t	627/788 (80%)	542 (86%)	78 (12%)	7 (1%)	11	43
29	g	58/63 (92%)	42 (72%)	14 (24%)	2 (3%)	3	23
30	p	183/274 (67%)	168 (92%)	15 (8%)	0	100	100
31	r	256/425 (60%)	227 (89%)	26 (10%)	3 (1%)	10	41
32	e	259/483 (54%)	242 (93%)	14 (5%)	3 (1%)	10	41
All	All	5153/6307 (82%)	4441 (86%)	644 (12%)	68 (1%)	12	39

All (68) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	K	97	LYS
11	N	148	TYR
12	P	110	TYR
12	P	111	ILE
15	S	69	HIS
17	U	98	ILE
19	W	120	LYS
23	a	11	LEU
28	t	677	ALA

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Mol	Chain	Res	Type
29	g	52	GLY
31	r	235	ILE
32	e	306	ALA
2	D	90	LYS
3	B	56	ALA
4	C	88	VAL
11	N	142	GLY
11	N	147	VAL
14	R	40	LYS
14	R	97	ARG
18	V	10	LYS
23	a	81	ASN
26	d	34	ASN
28	t	54	ARG
28	t	205	GLN
28	t	519	PRO
31	r	93	THR
32	e	206	LEU
32	e	402	ASP
4	C	23	LYS
6	F	14	LYS
6	F	42	GLU
12	P	185	ARG
13	Q	213	ARG
25	c	4	GLY
25	c	132	LEU
26	d	37	LYS
27	f	75	GLU
27	f	76	GLY
2	D	25	GLU
2	D	108	ARG
3	B	58	LEU
5	E	54	ALA
9	K	55	PRO
9	K	96	SER
11	N	143	LYS
11	N	145	HIS
13	Q	62	LYS
16	T	68	LEU
18	V	152	ILE
18	V	153	GLU
25	c	88	PRO

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Mol	Chain	Res	Type
28	t	207	ASP
28	t	738	LYS
6	F	40	GLU
12	P	196	SER
17	U	74	GLN
20	X	5	LEU
23	a	44	ARG
8	I	53	TRP
14	R	150	GLN
19	W	162	SER
21	Y	22	ALA
29	g	51	ASN
19	W	163	PRO
28	t	753	GLY
31	r	192	ILE
6	F	41	PRO
24	b	29	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	D	89/119 (75%)	89 (100%)	0	100	100
3	B	173/191 (91%)	173 (100%)	0	100	100
4	C	88/124 (71%)	88 (100%)	0	100	100
5	E	98/118 (83%)	98 (100%)	0	100	100
6	F	117/119 (98%)	115 (98%)	2 (2%)	53	69
7	H	109/129 (84%)	107 (98%)	2 (2%)	51	68
8	I	115/116 (99%)	113 (98%)	2 (2%)	53	69
9	K	57/89 (64%)	56 (98%)	1 (2%)	51	68
10	L	55/60 (92%)	55 (100%)	0	100	100
11	N	43/135 (32%)	40 (93%)	3 (7%)	14	41
12	P	164/210 (78%)	161 (98%)	3 (2%)	51	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	Q	191/224 (85%)	190 (100%)	1 (0%)	81	80
14	R	179/205 (87%)	176 (98%)	3 (2%)	53	69
15	S	221/222 (100%)	220 (100%)	1 (0%)	81	80
16	T	188/201 (94%)	187 (100%)	1 (0%)	81	80
17	U	165/170 (97%)	163 (99%)	2 (1%)	63	73
18	V	150/161 (93%)	149 (99%)	1 (1%)	76	78
19	W	158/166 (95%)	157 (99%)	1 (1%)	78	79
20	X	129/137 (94%)	127 (98%)	2 (2%)	55	69
21	Y	127/128 (99%)	125 (98%)	2 (2%)	55	69
22	Z	81/105 (77%)	80 (99%)	1 (1%)	63	73
23	a	74/74 (100%)	72 (97%)	2 (3%)	39	61
24	b	110/111 (99%)	108 (98%)	2 (2%)	51	68
25	c	119/120 (99%)	119 (100%)	0	100	100
26	d	112/113 (99%)	111 (99%)	1 (1%)	70	76
27	f	70/71 (99%)	70 (100%)	0	100	100
28	t	533/703 (76%)	525 (98%)	8 (2%)	57	70
29	g	51/54 (94%)	50 (98%)	1 (2%)	48	66
30	p	162/238 (68%)	154 (95%)	8 (5%)	22	49
31	r	242/384 (63%)	239 (99%)	3 (1%)	63	73
All	All	4170/4997 (84%)	4117 (99%)	53 (1%)	59	72

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	57	LEU
6	F	97	VAL
7	H	26	ILE
7	H	119	ILE
8	I	28	LEU
8	I	114	VAL
9	K	78	ILE
11	N	143	LYS
11	N	145	HIS
11	N	146	SER
12	P	133	ILE

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Mol	Chain	Res	Type
12	P	158	VAL
12	P	170	ILE
13	Q	212	VAL
14	R	90	THR
14	R	203	LYS
14	R	218	ILE
15	S	70	VAL
16	T	78	THR
17	U	46	ILE
17	U	148	LYS
18	V	72	ILE
19	W	118	LEU
20	X	70	ILE
20	X	94	ILE
21	Y	16	ILE
21	Y	83	GLU
22	Z	137	LEU
23	a	11	LEU
23	a	69	LEU
24	b	93	LEU
24	b	103	ILE
26	d	121	THR
28	t	54	ARG
28	t	55	LYS
28	t	123	ILE
28	t	153	LYS
28	t	206	LEU
28	t	303	LEU
28	t	714	VAL
28	t	715	VAL
29	g	8	LEU
30	p	90	ASN
30	p	164	LEU
30	p	193	LEU
30	p	198	LEU
30	p	220	THR
30	p	231	ILE
30	p	258	LYS
30	p	262	ASN
31	r	65	MET
31	r	124	ILE
31	r	235	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (75) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	44	ASN
3	B	100	ASN
3	B	103	ASN
3	B	116	HIS
3	B	139	ASN
3	B	224	ASN
4	C	83	GLN
4	C	105	GLN
5	E	98	ASN
5	E	103	ASN
5	E	104	GLN
6	F	32	ASN
6	F	62	ASN
6	F	139	GLN
7	H	13	HIS
7	H	19	ASN
7	H	55	HIS
7	H	75	ASN
7	H	78	HIS
7	H	89	GLN
8	I	12	GLN
8	I	23	GLN
8	I	64	HIS
9	K	98	GLN
11	N	145	HIS
12	P	15	GLN
12	P	30	GLN
13	Q	74	GLN
13	Q	149	GLN
14	R	110	HIS
14	R	233	GLN
15	S	8	HIS
15	S	69	HIS
15	S	98	ASN
15	S	157	ASN
16	T	65	GLN
16	T	119	GLN
16	T	139	ASN
17	U	5	GLN
17	U	108	GLN
17	U	161	GLN

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Mol	Chain	Res	Type
17	U	180	GLN
18	V	20	GLN
18	V	32	GLN
18	V	44	HIS
18	V	103	GLN
19	W	155	HIS
20	X	14	GLN
20	X	104	HIS
21	Y	101	HIS
22	Z	80	HIS
24	b	15	ASN
24	b	44	HIS
24	b	80	ASN
25	c	18	HIS
25	c	65	ASN
25	c	75	GLN
26	d	133	ASN
28	t	53	GLN
28	t	116	GLN
28	t	166	GLN
28	t	194	ASN
28	t	255	ASN
28	t	509	ASN
28	t	631	GLN
28	t	706	HIS
28	t	766	GLN
30	p	90	ASN
30	p	111	ASN
30	p	131	ASN
31	r	24	GLN
31	r	146	ASN
31	r	182	ASN
31	r	222	ASN
31	r	234	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1664/1800 (92%)	592 (35%)	68 (4%)

All (592) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	U
1	2	4	C
1	2	5	U
1	2	8	U
1	2	9	U
1	2	14	C
1	2	16	G
1	2	17	C
1	2	25	C
1	2	26	A
1	2	32	U
1	2	34	G
1	2	42	G
1	2	43	A
1	2	45	U
1	2	46	A
1	2	47	A
1	2	59	C
1	2	60	U
1	2	63	G
1	2	66	U
1	2	67	A
1	2	68	A
1	2	69	G
1	2	71	A
1	2	72	A
1	2	73	U
1	2	74	U
1	2	75	U
1	2	77	U
1	2	78	A
1	2	79	C
1	2	80	A
1	2	93	A
1	2	99	C
1	2	100	A
1	2	101	U
1	2	104	A
1	2	105	A
1	2	111	U
1	2	114	C
1	2	116	U
1	2	120	U

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Mol	Chain	Res	Type
1	2	121	U
1	2	126	A
1	2	127	G
1	2	128	U
1	2	129	U
1	2	130	C
1	2	131	C
1	2	132	U
1	2	133	U
1	2	134	U
1	2	135	A
1	2	136	C
1	2	138	A
1	2	139	C
1	2	140	A
1	2	142	G
1	2	145	A
1	2	155	U
1	2	159	U
1	2	160	C
1	2	161	U
1	2	166	C
1	2	168	A
1	2	170	U
1	2	171	A
1	2	176	C
1	2	178	U
1	2	179	A
1	2	185	U
1	2	188	A
1	2	189	C
1	2	191	C
1	2	193	U
1	2	194	U
1	2	195	G
1	2	197	A
1	2	199	G
1	2	211	U
1	2	215	A
1	2	216	U
1	2	222	A
1	2	223	U

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Mol	Chain	Res	Type
1	2	225	A
1	2	227	U
1	2	228	G
1	2	231	U
1	2	233	C
1	2	234	G
1	2	238	U
1	2	240	U
1	2	241	U
1	2	243	G
1	2	249	U
1	2	250	C
1	2	255	U
1	2	257	A
1	2	259	U
1	2	260	U
1	2	261	U
1	2	265	A
1	2	274	G
1	2	275	C
1	2	278	U
1	2	280	U
1	2	281	G
1	2	287	G
1	2	299	A
1	2	313	U
1	2	314	C
1	2	315	A
1	2	316	A
1	2	320	U
1	2	321	C
1	2	322	G
1	2	323	A
1	2	337	G
1	2	338	C
1	2	340	U
1	2	349	U
1	2	350	U
1	2	351	C
1	2	352	A
1	2	353	A
1	2	359	A

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Mol	Chain	Res	Type
1	2	361	C
1	2	387	A
1	2	390	G
1	2	396	G
1	2	397	A
1	2	400	A
1	2	401	A
1	2	402	C
1	2	404	G
1	2	416	A
1	2	417	A
1	2	418	G
1	2	424	C
1	2	425	A
1	2	426	G
1	2	430	G
1	2	434	G
1	2	435	C
1	2	436	A
1	2	437	A
1	2	439	U
1	2	444	C
1	2	445	A
1	2	448	C
1	2	452	A
1	2	453	U
1	2	454	U
1	2	455	C
1	2	459	G
1	2	460	A
1	2	461	G
1	2	468	A
1	2	471	A
1	2	477	A
1	2	483	A
1	2	484	C
1	2	488	G
1	2	491	C
1	2	492	A
1	2	493	U
1	2	494	U
1	2	495	C

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Mol	Chain	Res	Type
1	2	496	G
1	2	498	G
1	2	499	U
1	2	500	C
1	2	502	U
1	2	503	G
1	2	504	U
1	2	505	A
1	2	506	A
1	2	507	U
1	2	510	G
1	2	520	A
1	2	527	A
1	2	532	U
1	2	534	A
1	2	537	G
1	2	538	A
1	2	539	G
1	2	541	A
1	2	542	A
1	2	544	A
1	2	548	G
1	2	551	G
1	2	554	C
1	2	555	A
1	2	556	A
1	2	558	U
1	2	559	C
1	2	561	G
1	2	562	G
1	2	564	G
1	2	565	C
1	2	566	C
1	2	568	G
1	2	576	G
1	2	577	G
1	2	579	A
1	2	580	A
1	2	581	U
1	2	582	U
1	2	594	A
1	2	595	G

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Mol	Chain	Res	Type
1	2	596	C
1	2	599	A
1	2	608	U
1	2	609	U
1	2	610	G
1	2	611	U
1	2	613	G
1	2	619	A
1	2	620	A
1	2	622	A
1	2	623	A
1	2	624	G
1	2	625	C
1	2	638	U
1	2	639	U
1	2	641	G
1	2	644	C
1	2	645	C
1	2	648	G
1	2	650	U
1	2	652	G
1	2	653	C
1	2	654	C
1	2	655	G
1	2	656	G
1	2	657	U
1	2	658	C
1	2	678	A
1	2	681	U
1	2	684	A
1	2	687	G
1	2	688	G
1	2	690	G
1	2	694	U
1	2	696	C
1	2	697	C
1	2	698	U
1	2	700	C
1	2	701	U
1	2	702	G
1	2	703	G
1	2	704	C

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Mol	Chain	Res	Type
1	2	736	C
1	2	739	G
1	2	741	C
1	2	742	U
1	2	744	U
1	2	745	U
1	2	754	A
1	2	755	A
1	2	756	A
1	2	765	G
1	2	766	U
1	2	767	U
1	2	774	A
1	2	775	G
1	2	778	G
1	2	779	U
1	2	780	A
1	2	781	U
1	2	782	U
1	2	783	G
1	2	788	A
1	2	803	A
1	2	804	A
1	2	805	U
1	2	811	A
1	2	812	A
1	2	813	U
1	2	814	A
1	2	815	G
1	2	816	G
1	2	817	A
1	2	818	C
1	2	819	G
1	2	820	U
1	2	821	U
1	2	823	G
1	2	829	A
1	2	830	U
1	2	831	U
1	2	832	U
1	2	833	U
1	2	835	U

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Mol	Chain	Res	Type
1	2	839	U
1	2	840	U
1	2	843	U
1	2	844	A
1	2	845	G
1	2	846	G
1	2	847	A
1	2	855	A
1	2	856	A
1	2	857	U
1	2	860	U
1	2	862	A
1	2	863	A
1	2	864	U
1	2	873	U
1	2	876	G
1	2	886	U
1	2	889	U
1	2	903	U
1	2	904	G
1	2	910	C
1	2	913	G
1	2	914	G
1	2	915	A
1	2	926	A
1	2	928	U
1	2	929	A
1	2	931	C
1	2	932	U
1	2	933	A
1	2	934	C
1	2	935	U
1	2	942	G
1	2	945	U
1	2	960	U
1	2	961	U
1	2	964	U
1	2	966	A
1	2	969	C
1	2	970	A
1	2	983	A
1	2	984	G

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Mol	Chain	Res	Type
1	2	987	G
1	2	988	A
1	2	992	A
1	2	993	A
1	2	994	G
1	2	995	A
1	2	996	U
1	2	997	G
1	2	999	U
1	2	1009	U
1	2	1010	C
1	2	1012	U
1	2	1021	C
1	2	1023	A
1	2	1024	U
1	2	1025	A
1	2	1026	A
1	2	1028	C
1	2	1029	U
1	2	1030	A
1	2	1031	U
1	2	1032	G
1	2	1039	A
1	2	1051	G
1	2	1052	U
1	2	1053	G
1	2	1055	U
1	2	1056	U
1	2	1058	U
1	2	1059	U
1	2	1060	U
1	2	1064	G
1	2	1066	C
1	2	1072	C
1	2	1076	A
1	2	1077	C
1	2	1078	C
1	2	1080	U
1	2	1081	A
1	2	1082	C
1	2	1091	A
1	2	1092	A

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Mol	Chain	Res	Type
1	2	1096	C
1	2	1097	U
1	2	1098	U
1	2	1099	U
1	2	1100	G
1	2	1102	G
1	2	1109	G
1	2	1113	A
1	2	1114	G
1	2	1119	G
1	2	1124	A
1	2	1126	G
1	2	1138	A
1	2	1140	G
1	2	1146	G
1	2	1147	A
1	2	1148	C
1	2	1149	G
1	2	1150	G
1	2	1151	A
1	2	1155	G
1	2	1158	C
1	2	1159	C
1	2	1160	A
1	2	1164	G
1	2	1165	G
1	2	1167	G
1	2	1185	U
1	2	1188	G
1	2	1202	A
1	2	1203	A
1	2	1207	C
1	2	1212	G
1	2	1214	U
1	2	1218	G
1	2	1227	A
1	2	1229	G
1	2	1230	A
1	2	1235	C
1	2	1241	G
1	2	1242	A
1	2	1243	G

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Mol	Chain	Res	Type
1	2	1244	A
1	2	1245	G
1	2	1246	C
1	2	1250	U
1	2	1251	U
1	2	1252	C
1	2	1255	G
1	2	1258	U
1	2	1259	U
1	2	1264	G
1	2	1265	G
1	2	1269	U
1	2	1270	G
1	2	1272	U
1	2	1273	G
1	2	1275	A
1	2	1276	U
1	2	1278	G
1	2	1282	U
1	2	1288	G
1	2	1290	U
1	2	1291	G
1	2	1301	U
1	2	1305	U
1	2	1306	C
1	2	1312	A
1	2	1314	U
1	2	1320	U
1	2	1321	A
1	2	1325	A
1	2	1330	G
1	2	1331	A
1	2	1333	C
1	2	1336	A
1	2	1338	C
1	2	1339	C
1	2	1340	U
1	2	1344	A
1	2	1345	A
1	2	1347	U
1	2	1348	A
1	2	1354	G

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Mol	Chain	Res	Type
1	2	1360	A
1	2	1361	U
1	2	1363	U
1	2	1367	G
1	2	1370	U
1	2	1371	A
1	2	1373	C
1	2	1382	A
1	2	1385	G
1	2	1390	U
1	2	1391	A
1	2	1413	U
1	2	1415	U
1	2	1416	G
1	2	1417	A
1	2	1427	A
1	2	1428	G
1	2	1431	C
1	2	1432	U
1	2	1433	G
1	2	1435	G
1	2	1436	A
1	2	1437	U
1	2	1440	C
1	2	1441	C
1	2	1442	U
1	2	1444	A
1	2	1445	G
1	2	1446	A
1	2	1447	C
1	2	1448	G
1	2	1457	C
1	2	1459	C
1	2	1460	A
1	2	1471	A
1	2	1473	U
1	2	1474	G
1	2	1475	A
1	2	1482	C
1	2	1486	G
1	2	1490	C
1	2	1491	U

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Mol	Chain	Res	Type
1	2	1492	A
1	2	1493	A
1	2	1494	C
1	2	1496	U
1	2	1503	A
1	2	1506	G
1	2	1516	A
1	2	1520	U
1	2	1521	G
1	2	1522	U
1	2	1523	G
1	2	1524	A
1	2	1526	A
1	2	1529	C
1	2	1535	U
1	2	1536	G
1	2	1537	C
1	2	1538	U
1	2	1540	G
1	2	1542	G
1	2	1550	A
1	2	1557	U
1	2	1559	A
1	2	1563	C
1	2	1568	C
1	2	1569	A
1	2	1573	A
1	2	1574	G
1	2	1577	A
1	2	1579	U
1	2	1583	A
1	2	1584	G
1	2	1590	G
1	2	1601	G
1	2	1607	G
1	2	1610	G
1	2	1616	G
1	2	1619	C
1	2	1630	U
1	2	1631	A
1	2	1648	A
1	2	1650	U

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Mol	Chain	Res	Type
1	2	1651	A
1	2	1652	C
1	2	1653	C
1	2	1656	U
1	2	1657	U
1	2	1658	G
1	2	1659	A
1	2	1660	A
1	2	1662	G
1	2	1673	G
1	2	1681	A
1	2	1686	C
1	2	1688	U
1	2	1689	A
1	2	1692	G
1	2	1693	A
1	2	1709	C
1	2	1710	U
1	2	1711	C
1	2	1712	A
1	2	1713	G
1	2	1717	G
1	2	1728	A
1	2	1730	A
1	2	1731	A
1	2	1732	A
1	2	1736	G
1	2	1744	A
1	2	1746	A
1	2	1750	A
1	2	1754	A
1	2	1770	U
1	2	1771	U
1	2	1772	C
1	2	1780	G
1	2	1781	A
1	2	1782	A
1	2	1783	C
1	2	1792	G
1	2	1794	A
1	2	1795	U
1	2	1796	C

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Mol	Chain	Res	Type
1	2	1797	A
1	2	1798	U
1	2	1800	A

All (68) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	47	A
1	2	68	A
1	2	79	C
1	2	99	C
1	2	104	A
1	2	126	A
1	2	128	U
1	2	129	U
1	2	132	U
1	2	138	A
1	2	139	C
1	2	159	U
1	2	169	A
1	2	215	A
1	2	224	C
1	2	232	U
1	2	242	U
1	2	280	U
1	2	312	A
1	2	315	A
1	2	322	G
1	2	352	A
1	2	400	A
1	2	401	A
1	2	417	A
1	2	423	G
1	2	452	A
1	2	493	U
1	2	555	A
1	2	565	C
1	2	609	U
1	2	649	U
1	2	652	G
1	2	696	C

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Mol	Chain	Res	Type
1	2	699	U
1	2	754	A
1	2	781	U
1	2	803	A
1	2	804	A
1	2	819	G
1	2	846	G
1	2	863	A
1	2	912	U
1	2	913	G
1	2	1023	A
1	2	1058	U
1	2	1081	A
1	2	1097	U
1	2	1099	U
1	2	1108	G
1	2	1157	A
1	2	1244	A
1	2	1250	U
1	2	1332	C
1	2	1339	C
1	2	1344	A
1	2	1441	C
1	2	1446	A
1	2	1481	C
1	2	1568	C
1	2	1573	A
1	2	1615	C
1	2	1649	G
1	2	1656	U
1	2	1680	G
1	2	1793	G
1	2	1795	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	401:A	O3'	402:C	P	1.78

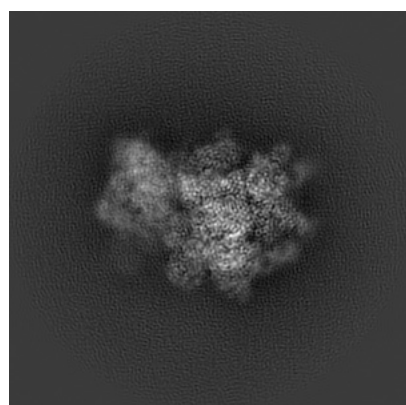
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3886. These allow visual inspection of the internal detail of the map and identification of artifacts.

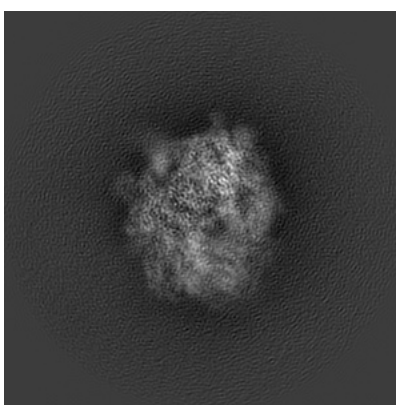
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

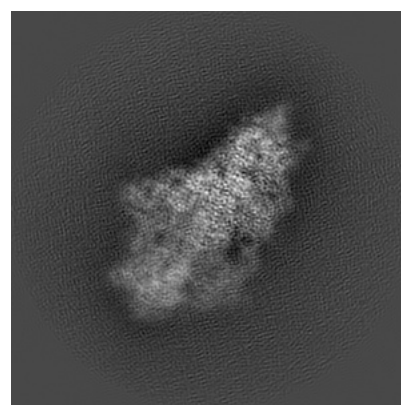
6.1.1 Primary map



X



Y

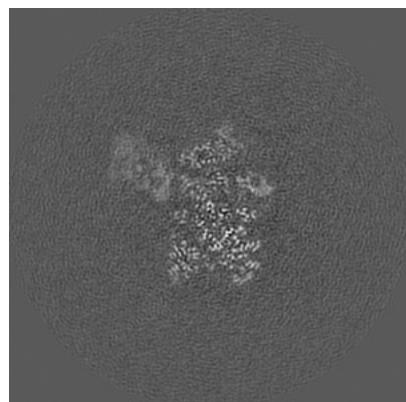


Z

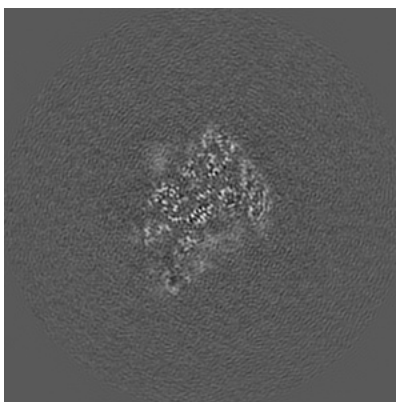
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

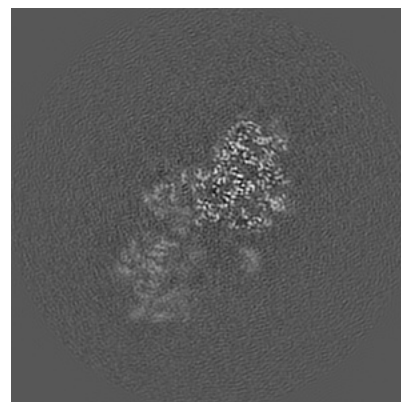
6.2.1 Primary map



X Index: 192



Y Index: 192

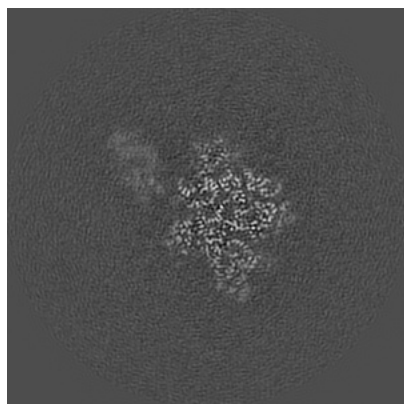


Z Index: 192

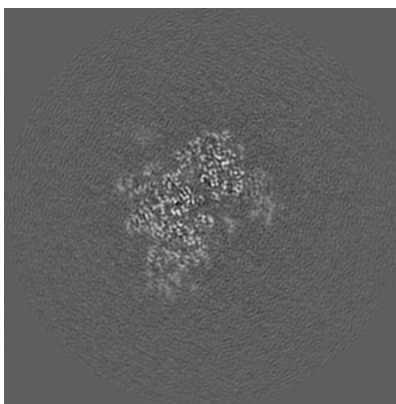
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

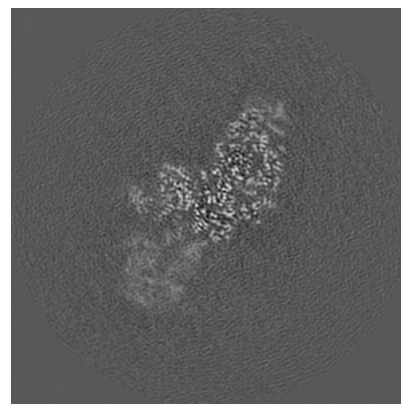
6.3.1 Primary map



X Index: 209



Y Index: 214

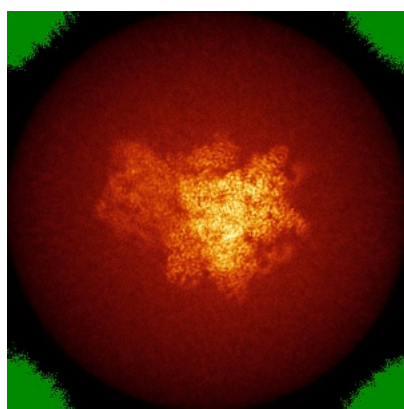


Z Index: 178

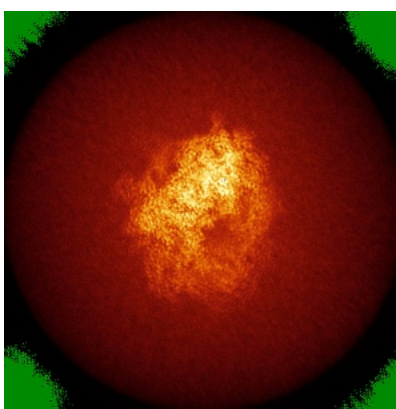
The images above show the largest variance slices of the map in three orthogonal directions.

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

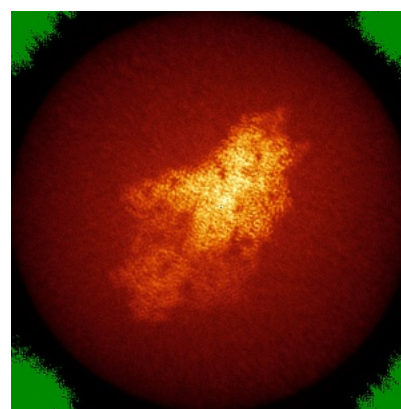
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0722. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

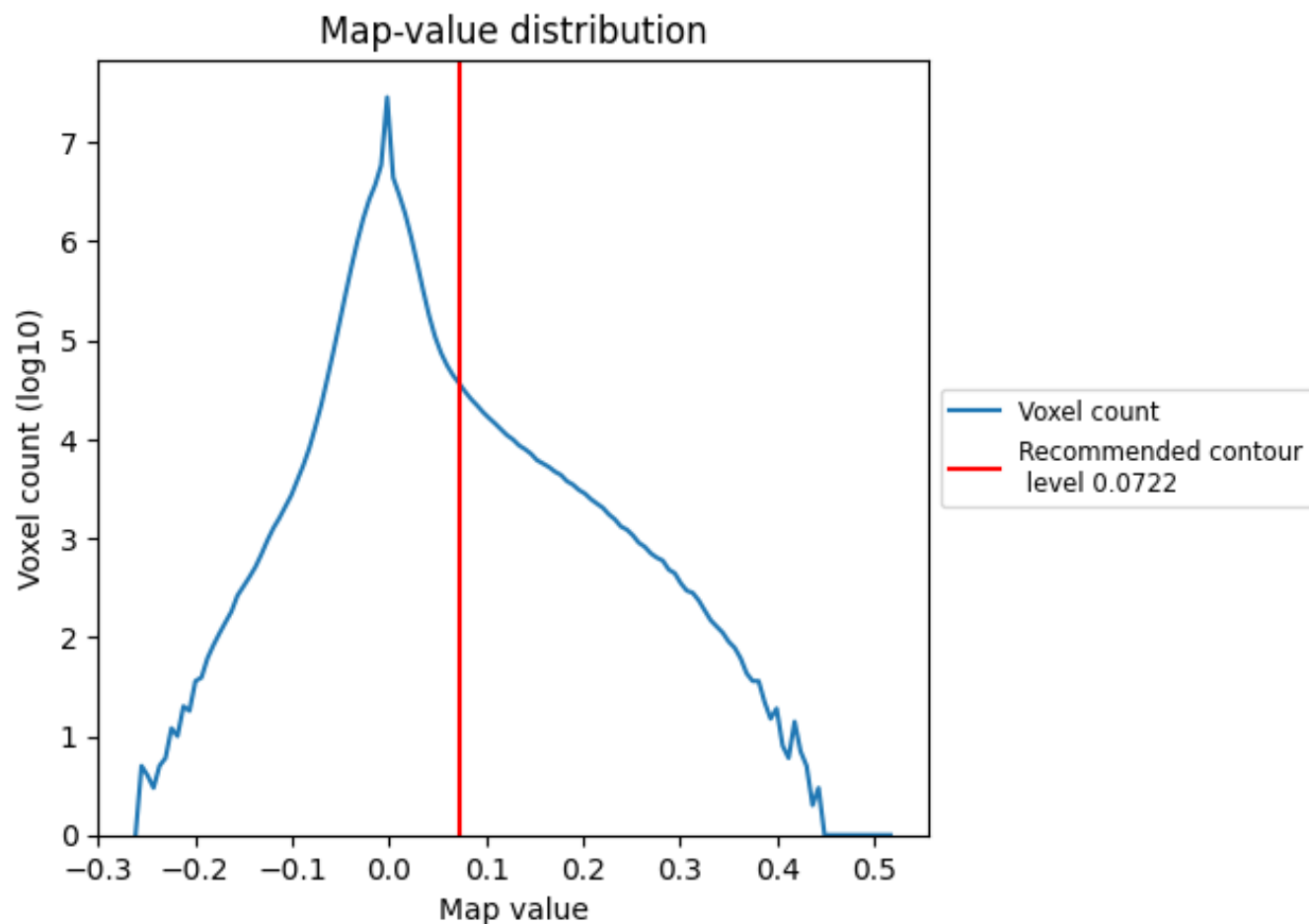
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

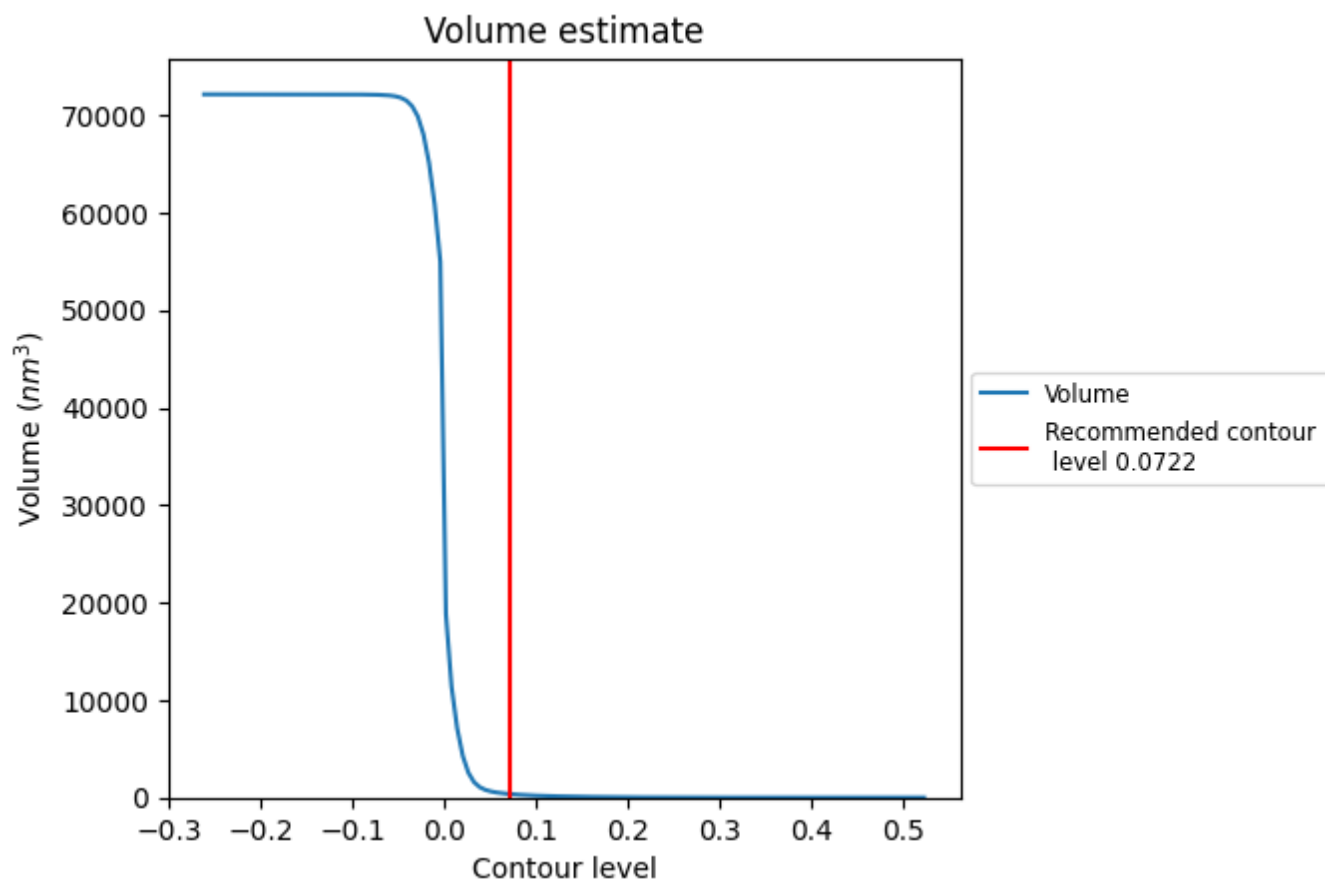
This section contains the results of statistical analysis of the map.

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.

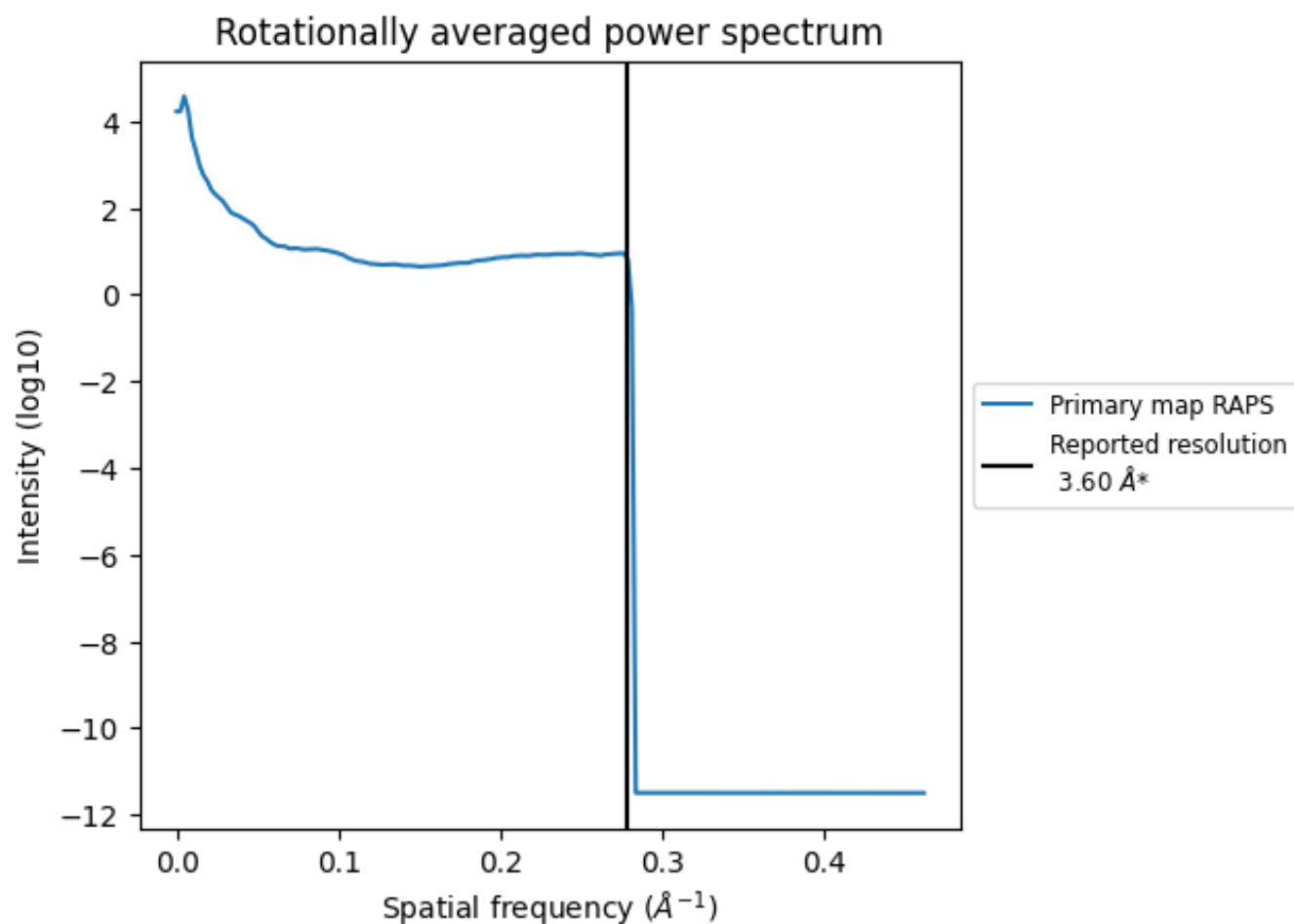
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 359 nm³; this corresponds to an approximate mass of 324 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 ⓘ

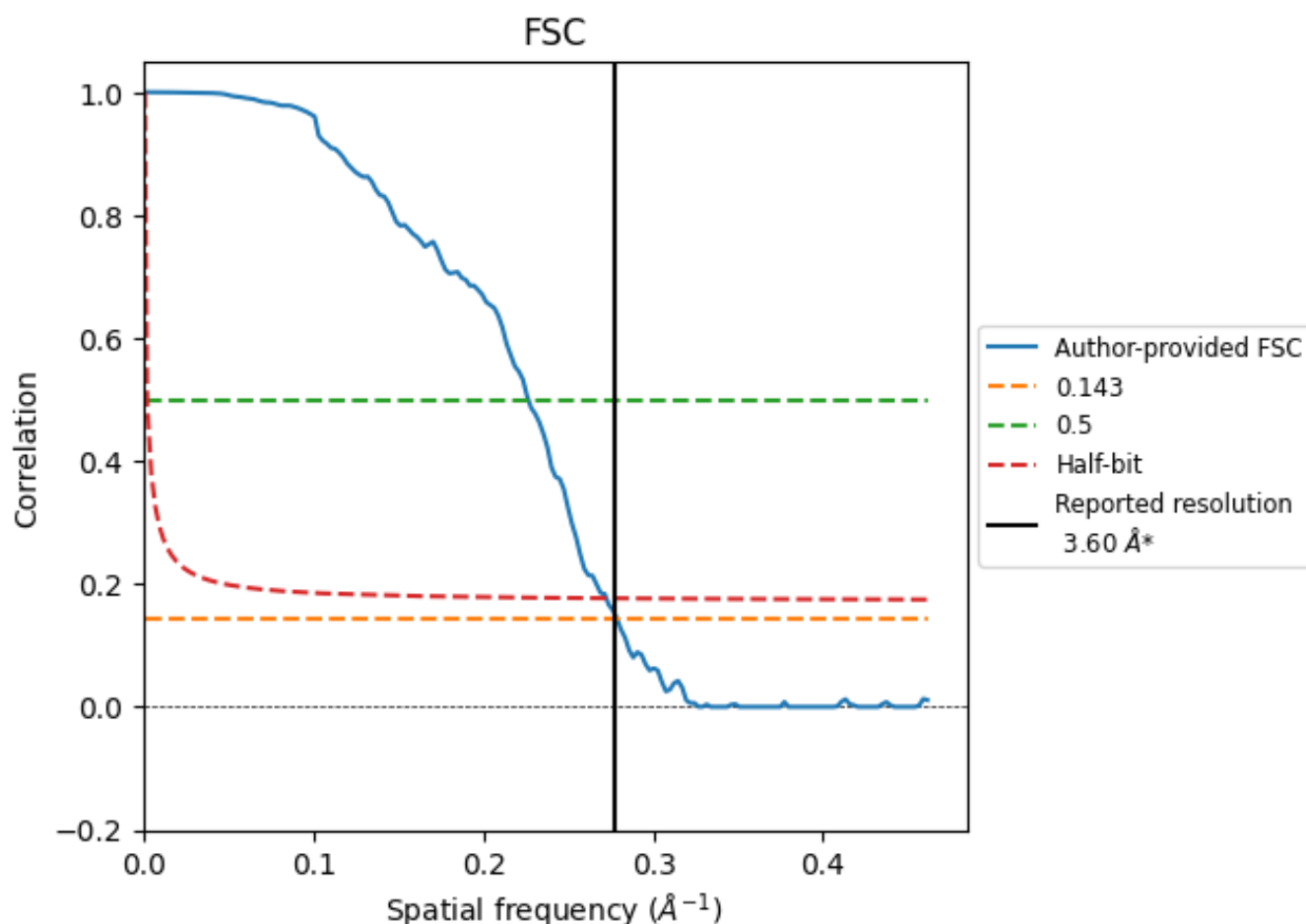


*Reported resolution corresponds to spatial frequency of 0.278 $\text{\AA}^{-1}$

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

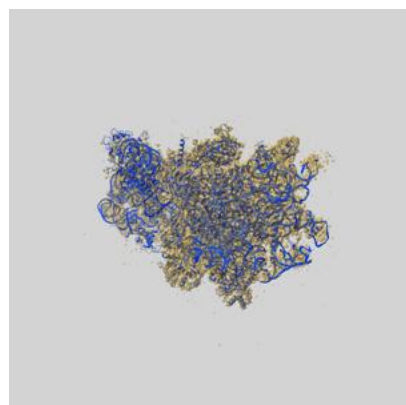
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	4.41	3.67
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

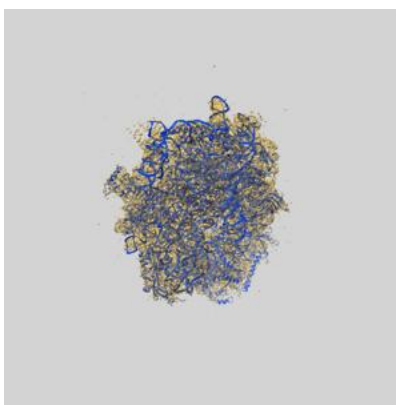
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3886 and PDB model 6EML. Per-residue inclusion information can be found in section [3](#) on page [10](#).

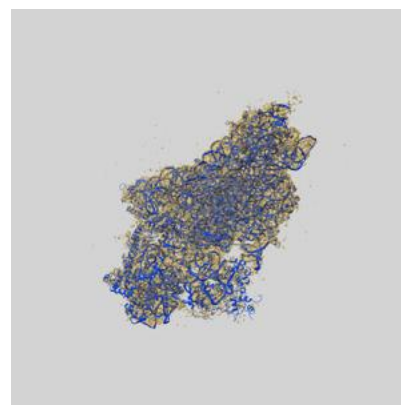
9.1 Map-model overlay [i](#)



X



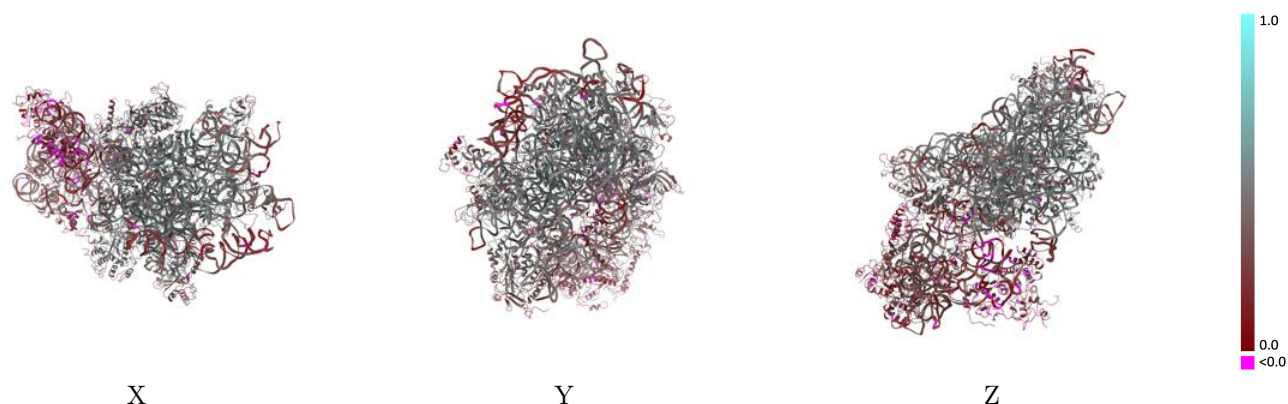
Y



Z

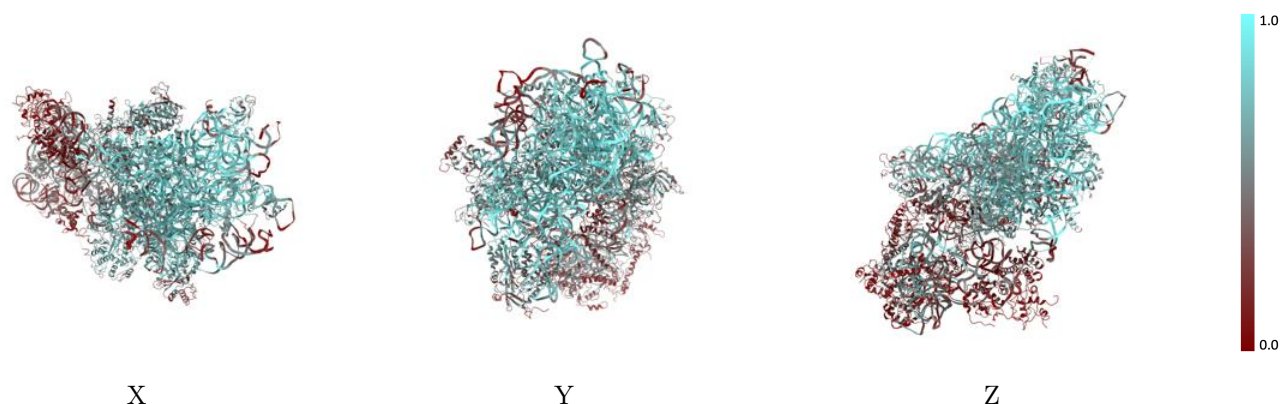
The images above show the 3D surface view of the map at the recommended contour level 0.0722 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



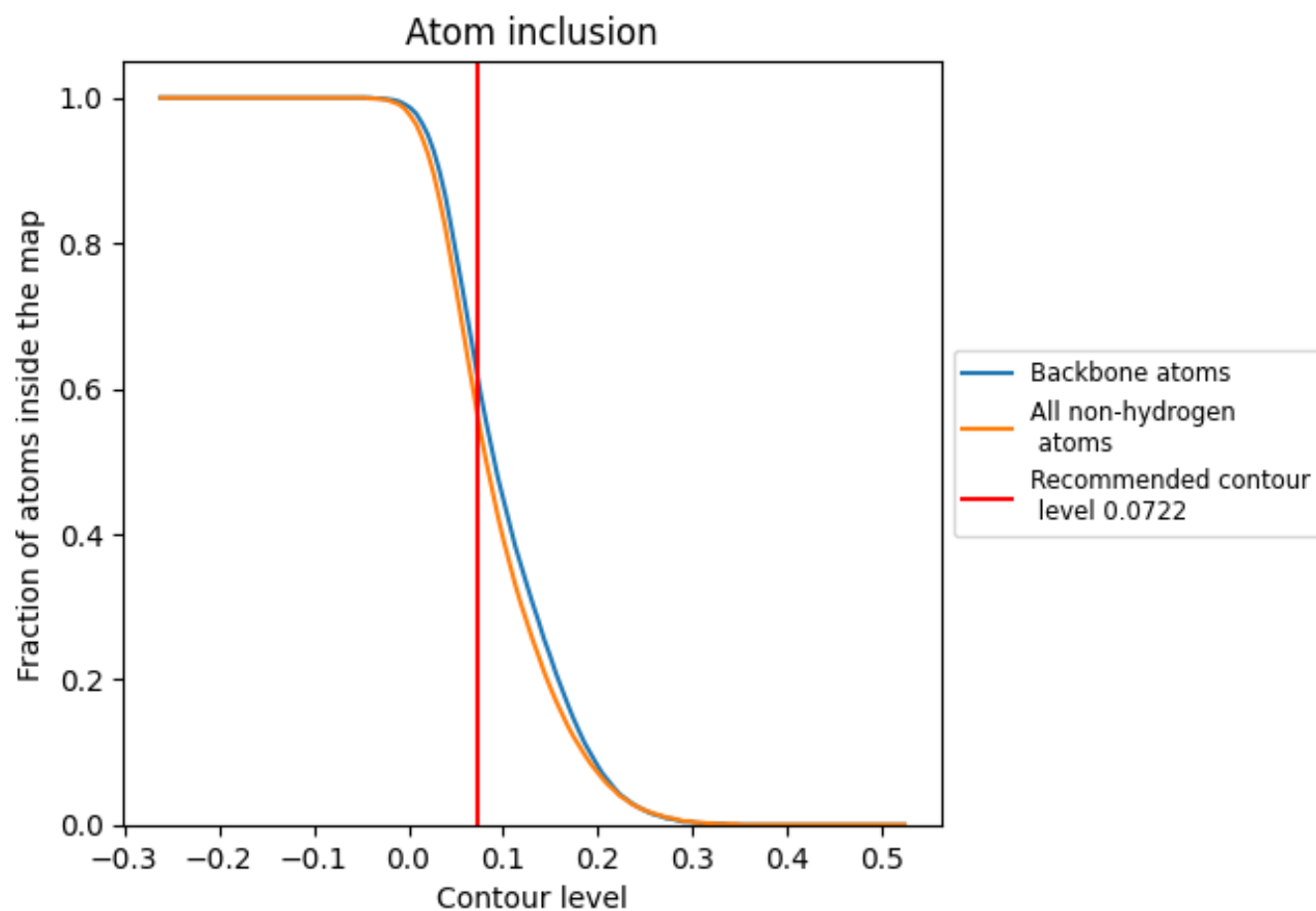
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0722).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 57% 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 (0.0722) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5680	 0.3710
2	 0.6670	 0.3790
B	 0.2300	 0.2400
C	 0.1810	 0.2180
D	 0.0450	 0.1680
E	 0.2590	 0.2530
F	 0.1600	 0.2270
H	 0.1810	 0.2510
I	 0.2110	 0.2440
K	 0.1050	 0.2120
L	 0.1750	 0.2370
N	 0.0310	 0.1090
P	 0.6650	 0.4400
Q	 0.5110	 0.3880
R	 0.6510	 0.4630
S	 0.7200	 0.4930
T	 0.6590	 0.4410
U	 0.4790	 0.3780
V	 0.7080	 0.4540
W	 0.7100	 0.4740
X	 0.6810	 0.4750
Y	 0.7000	 0.4510
Z	 0.4870	 0.3840
a	 0.6760	 0.4490
b	 0.7710	 0.5160
c	 0.6170	 0.4600
d	 0.6960	 0.4720
e	 0.1670	 0.1520
f	 0.6750	 0.4590
g	 0.3860	 0.3360
p	 0.4150	 0.3700
r	 0.1450	 0.1400
t	 0.5280	 0.4020

