



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:28 AM UTC

PDB ID : 8T4S / pdb_00008t4s
EMDB ID : EMD-41039
Title : MERS-CoV Nsp1 protein bound to the Human 40S Ribosomal subunit
Authors : Devarkar, S.C.; Xiong, Y.
Deposited on : 2023-06-09
Resolution : 2.60 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

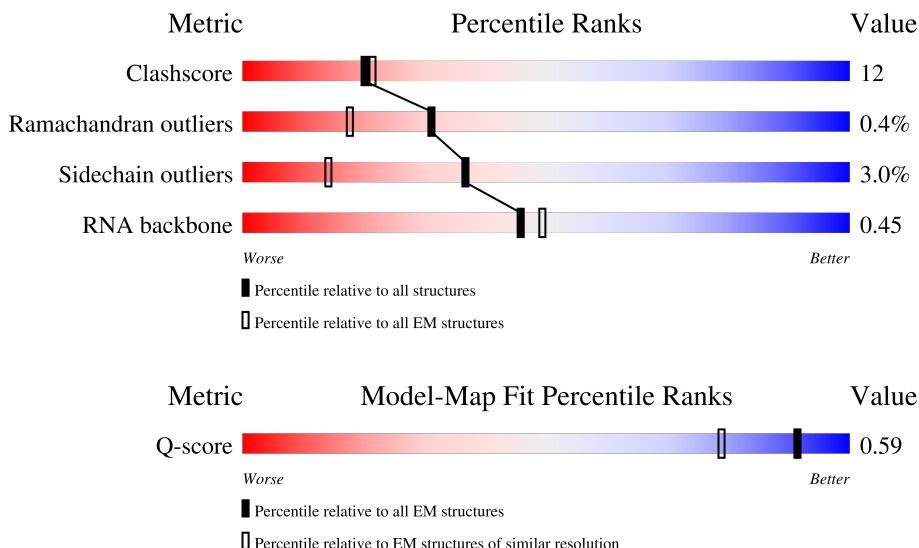
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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	8728 (2.10 - 3.10)

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	1869	
2	A	295	
3	B	264	

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Mol	Chain	Length	Quality of chain
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	133	
27	Z	125	
28	a	115	

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Mol	Chain	Length	Quality of chain
29	b	84	7%80%17%..
30	c	69	54%36%10%
31	d	56	84%12%..
32	e	133	28%14%.58%
33	f	156	24%19%..53%
34	g	317	70%28%.
35	h	25	56%32%12%
36	n	193	10%.87%

2 Entry composition

There are 39 unique types of molecules in this entry. The entry contains 74894 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1671	Total	C	N	O	P	0	0
			35677	15925	6406	11675	1671		

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

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

- Molecule 3 is a protein called 40S ribosomal protein S3a.

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

- Molecule 4 is a protein called 40S ribosomal protein S2.

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

- Molecule 5 is a protein called 40S ribosomal protein S3.

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

- Molecule 6 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 7 is a protein called 40S ribosomal protein S5.

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

- Molecule 8 is a protein called 40S ribosomal protein S6.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 9 is a protein called 40S ribosomal protein S7.

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

- Molecule 10 is a protein called 40S ribosomal protein S8.

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

- Molecule 11 is a protein called 40S ribosomal protein S9.

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

- Molecule 12 is a protein called 40S ribosomal protein S10.

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

- Molecule 13 is a protein called 40S ribosomal protein S11.

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

- Molecule 14 is a protein called 40S ribosomal protein S12.

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

- Molecule 15 is a protein called 40S ribosomal protein S13.

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

- Molecule 16 is a protein called 40S ribosomal protein S14.

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

- Molecule 17 is a protein called 40S ribosomal protein S15.

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

- Molecule 18 is a protein called 40S ribosomal protein S16.

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

- Molecule 19 is a protein called 40S ribosomal protein S17.

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

- Molecule 20 is a protein called 40S ribosomal protein S18.

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

- Molecule 21 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1122	703	217	199	3		

- Molecule 22 is a protein called 40S ribosomal protein S20.

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

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

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

- Molecule 24 is a protein called 40S ribosomal protein S15a.

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

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

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

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

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

- Molecule 27 is a protein called 40S ribosomal protein S25.

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

- Molecule 28 is a protein called 40S ribosomal protein S26.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 29 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 30 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 31 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	55	Total	C	N	O	S	0	0
			458	286	94	73	5		

- Molecule 32 is a protein called FAU ubiquitin-like and ribosomal protein S30.

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

- Molecule 33 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	74	Total	C	N	O	S	0	0
			610	385	117	101	7		

- Molecule 34 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 35 is a protein called 60S ribosomal protein L41.

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

- Molecule 36 is a protein called Replicase polypeptide 1ab.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	25	Total	C	N	O	S	0	0
			206	134	32	38	2		

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

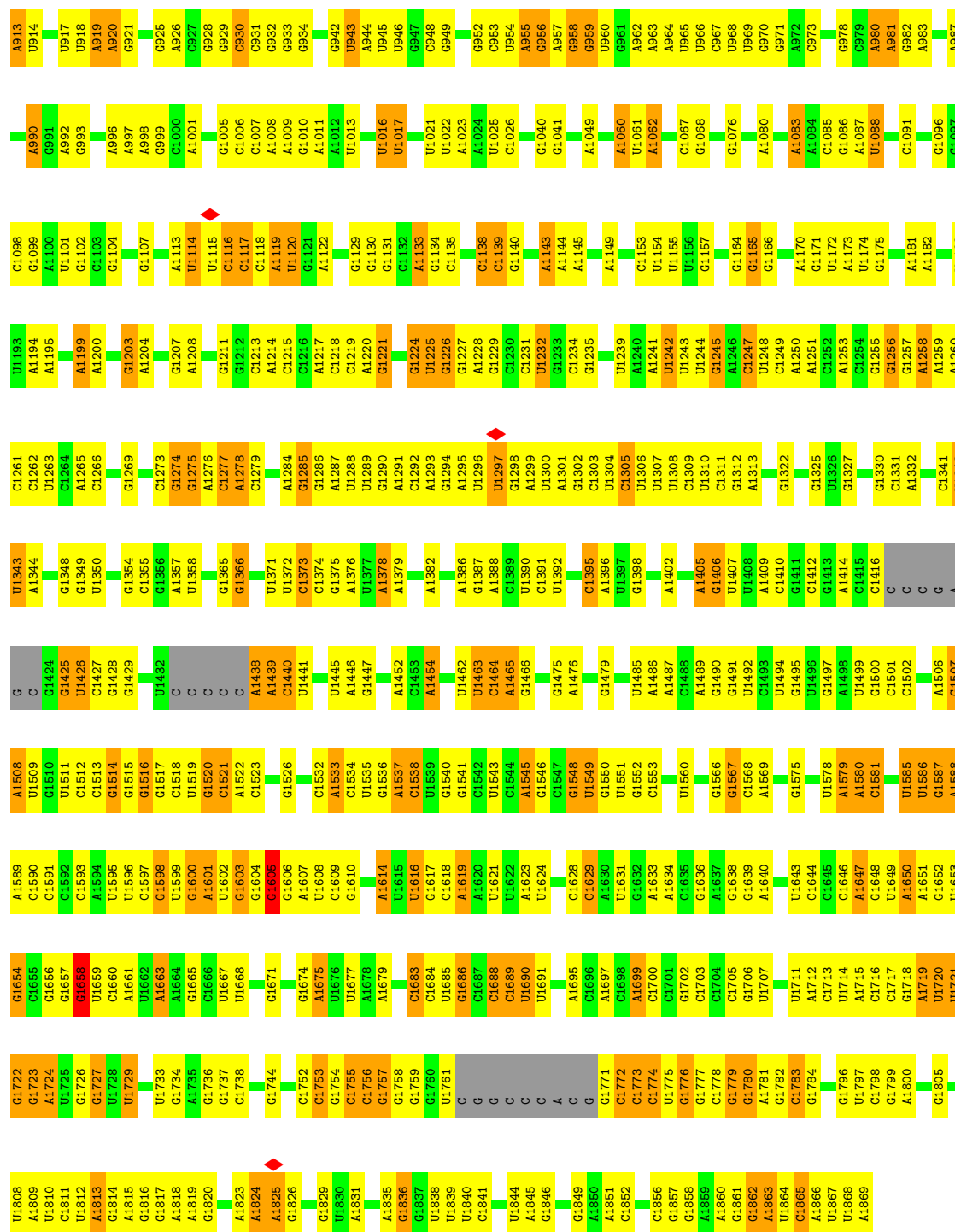
Mol	Chain	Residues	Atoms		AltConf
37	2	96	Total	Mg	0
			96	96	
37	I	1	Total	Mg	0
			1	1	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	a	1	Total	Zn	0
			1	1	
38	d	1	Total	Zn	0
			1	1	
38	f	1	Total	Zn	0
			1	1	

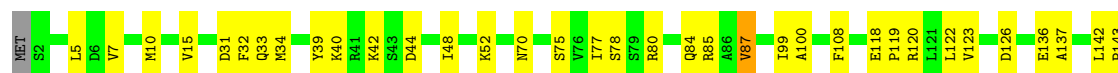
- Molecule 39 is water.

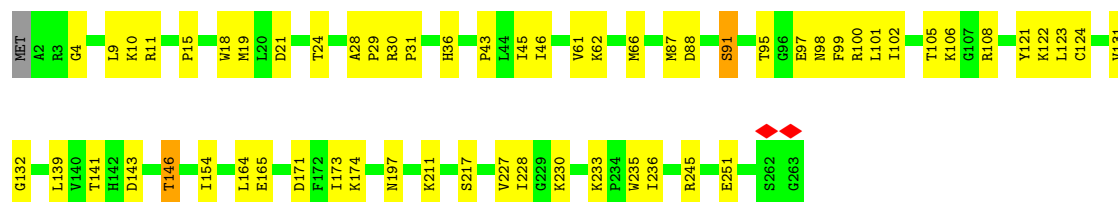
Mol	Chain	Residues	Atoms		AltConf
39	2	4	Total	O	0
			4	4	



• Molecule 2: 40S ribosomal protein SA

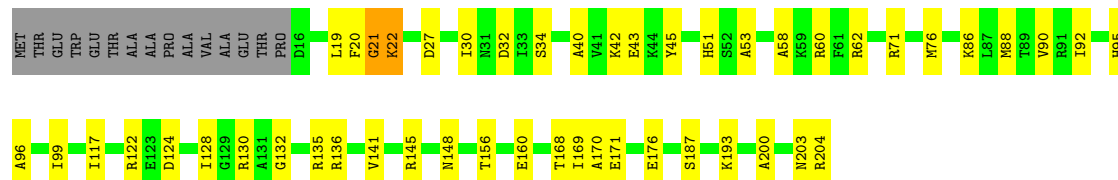
Chain A:





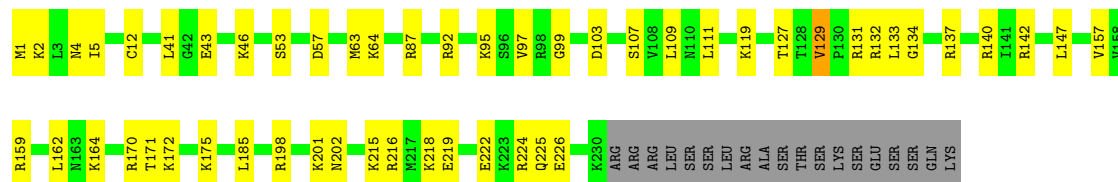
• Molecule 7: 40S ribosomal protein S5

Chain F: 69% 23% 7%



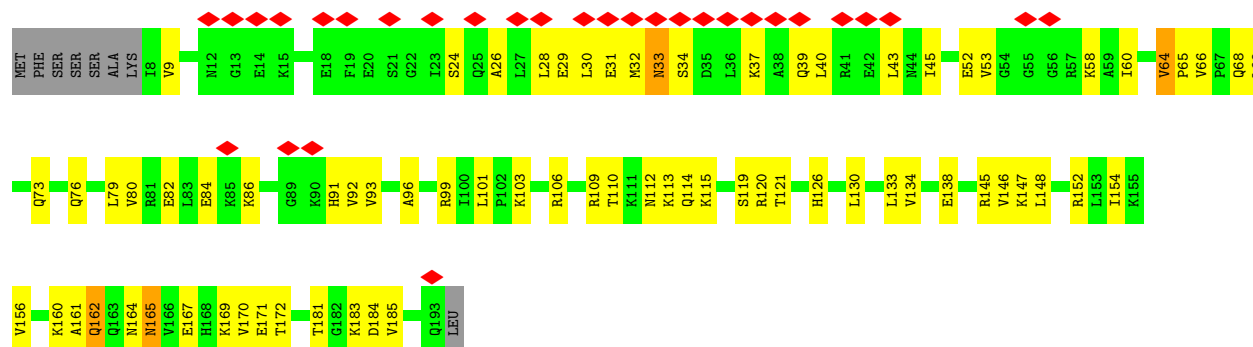
• Molecule 8: 40S ribosomal protein S6

Chain G: 71% 20% 8%



• Molecule 9: 40S ribosomal protein S7

Chain H: 15% 58% 36%



• Molecule 10: 40S ribosomal protein S8

Chain I: 74% 24% 2%

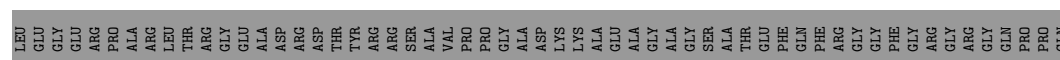




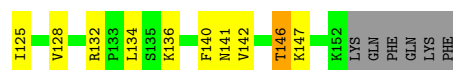
- Molecule 11: 40S ribosomal protein S9



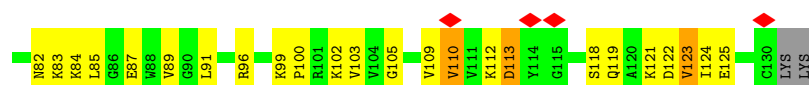
- Molecule 12: 40S ribosomal protein S10



- Molecule 13: 40S ribosomal protein S11

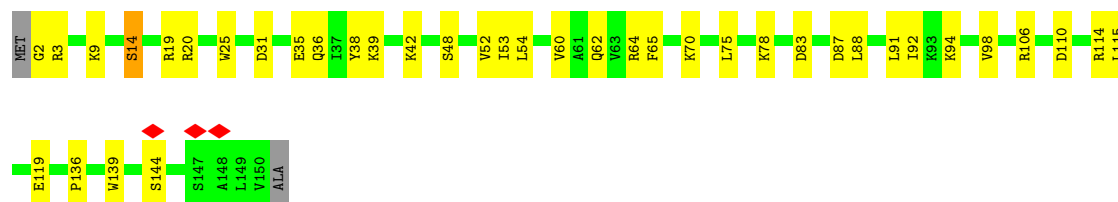


- Molecule 14: 40S ribosomal protein S12

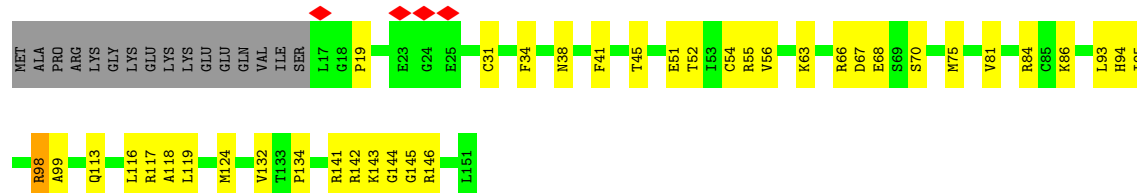


- Molecule 15: 40S ribosomal protein S13

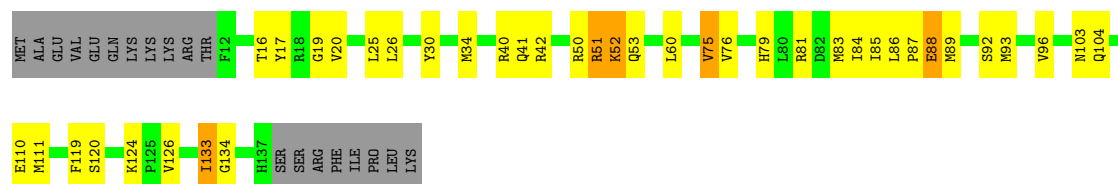




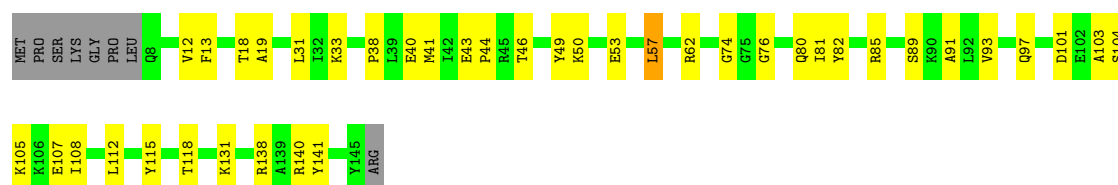
- Molecule 16: 40S ribosomal protein S14



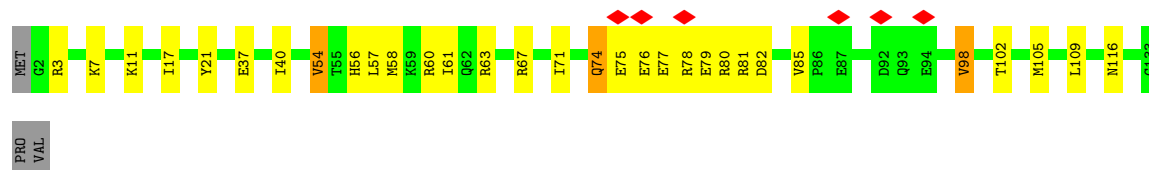
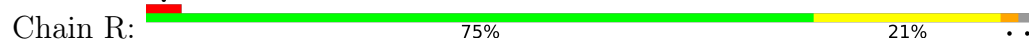
- Molecule 17: 40S ribosomal protein S15



- Molecule 18: 40S ribosomal protein S16

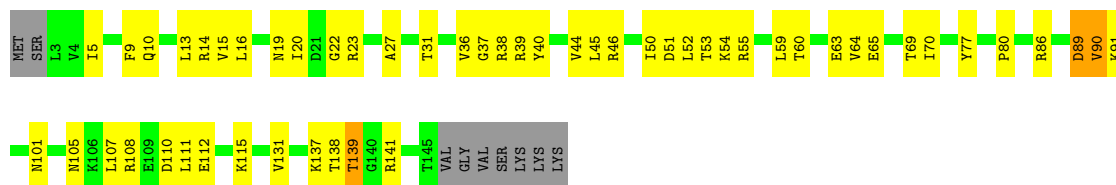


- Molecule 19: 40S ribosomal protein S17



- Molecule 20: 40S ribosomal protein S18

Chain S:  59% 33% 6%



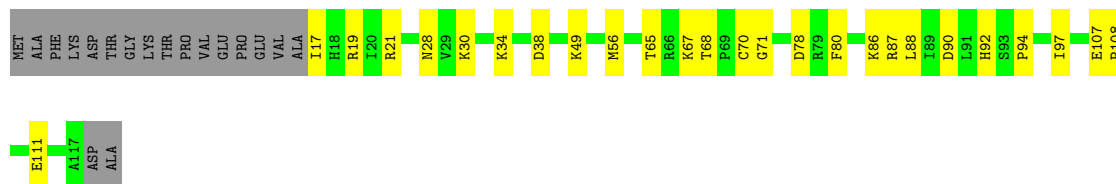
- Molecule 21: 40S ribosomal protein S19

Chain T:  74% 23%



- Molecule 22: 40S ribosomal protein S20

Chain U:  63% 22% 15%



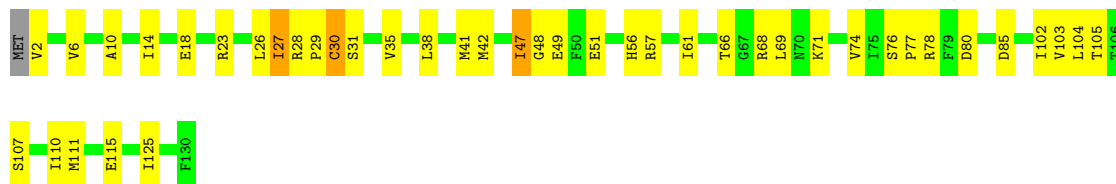
- Molecule 23: 40S ribosomal protein S21

Chain V:  76% 22%



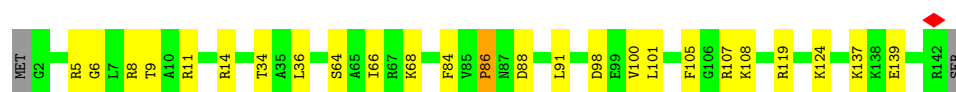
- Molecule 24: 40S ribosomal protein S15a

Chain W:  67% 30%

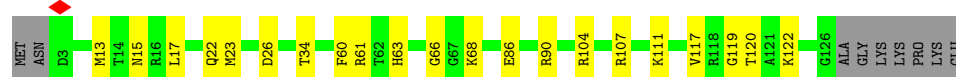
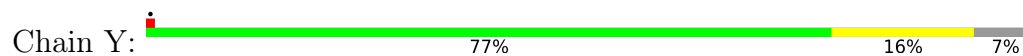


- Molecule 25: 40S ribosomal protein S23

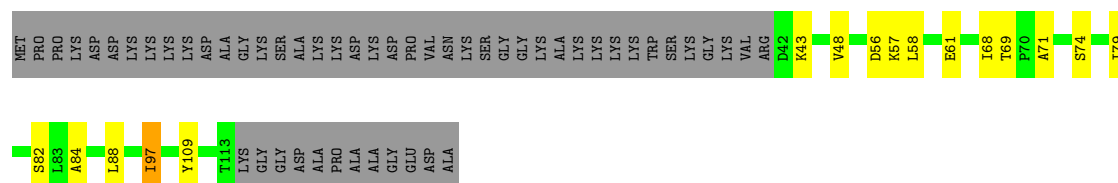
Chain X:  81% 17%



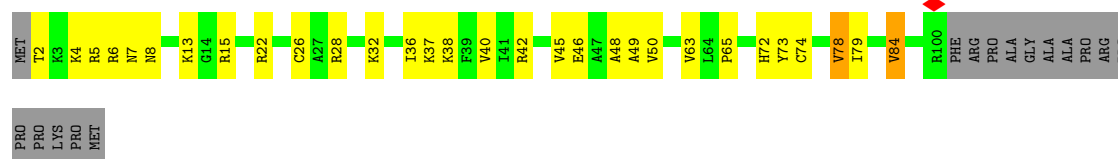
- Molecule 26: 40S ribosomal protein S24



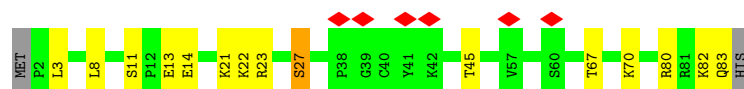
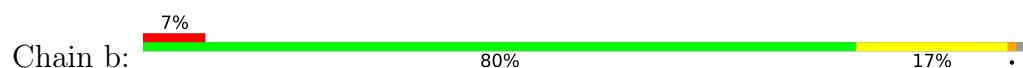
- Molecule 27: 40S ribosomal protein S25



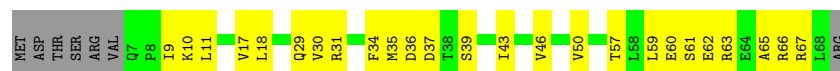
- Molecule 28: 40S ribosomal protein S26



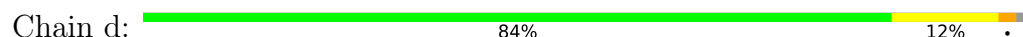
- Molecule 29: 40S ribosomal protein S27



- Molecule 30: 40S ribosomal protein S28



- Molecule 31: 40S ribosomal protein S29



MET	ALA	LEU
SER	MET	GLN
PHE	LEU	GLY
VAL	LEU	LYS
ALA	PRO	PRO
GLY	LYS	ILE
VAL	GLU	GLY
THR	PRO	MET
GLN	LEU	PHE
GLY	LEU	PHE
TYR	PRO	PRO
ALA	VAL	TYR
ARG	PRO	ASP
GLY	ILE	ILE
THR	ARG	GLU
TYR	LEU	LEU
ARG	ALA	VAL
ALA	THR	THR
ALA	GLY	GLY
LEU	HIS	LYS
ASN	THR	GLN
SER	ARG	GLN
GLU	ASN	ASN
LYS	HIS	ILE
HIS	PRO	LEU
GLN	GLY	LEU
ASP	PRO	ARG
HIS	ARG	LYS
VAL	VAL	TYR
LEU	TYR	GLY
THR	VAL	ARG
GLY	GLU	GLY
VAL	ARG	TYR
PRO	LEU	HIS
CYS	ILE	TYR
GLY	ALA	THR
SER	CYS	PRO
GLY	GLU	PHE
ASN	ASN	HIS
ASN	PRO	TYR
LEU	PHE	GLU
VAL	MET	ARG
GLU	VAL	ASP
LYS	ASN	ASN
LEU	GLN	THR
SER	LEU	SER
PRO	ALA	C167
THR	TYR	P168
PHE	THR	E169
MET	SER	M170
ASP	SER	M171
GLY	ALA	D172
ASN	ASN	D173
ALA	GLY	F174
TYR	SER	+
LEU	LEU	L187
VAL	VAL	+
GLY	GLY	F191
THR	THR	GLY
LYS	THR	GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	267551	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.809	Depositor
Minimum map value	-0.270	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2	0.30	0/39895	0.42	6/62174 (0.0%)
2	A	0.24	0/1723	0.38	1/2341 (0.0%)
3	B	0.23	0/1756	0.35	0/2350
4	C	0.23	0/1726	0.33	0/2332
5	D	0.25	0/1780	0.39	0/2397
6	E	0.27	0/2118	0.35	0/2849
7	F	0.39	0/1516	0.58	0/2037
8	G	0.20	0/1887	0.33	0/2513
9	H	0.22	0/1524	0.44	0/2042
10	I	0.23	0/1711	0.35	0/2282
11	J	0.30	0/1524	0.40	0/2035
12	K	0.25	0/840	0.47	0/1133
13	L	0.26	0/1250	0.37	0/1673
14	M	0.19	0/945	0.48	0/1269
15	N	0.21	0/1226	0.34	0/1649
16	O	0.21	0/1023	0.36	0/1372
17	P	0.34	0/1058	0.52	1/1414 (0.1%)
18	Q	0.27	0/1114	0.47	0/1492
19	R	0.20	0/1082	0.37	0/1452
20	S	0.23	0/1202	0.40	0/1610
21	T	0.25	0/1142	0.37	0/1530
22	U	0.22	0/813	0.38	0/1092
23	V	0.23	0/631	0.43	0/844
24	W	0.45	0/1051	0.48	0/1406
25	X	0.27	0/1116	0.41	0/1490
26	Y	0.29	0/1031	0.40	0/1370
27	Z	0.21	0/580	0.43	0/780
28	a	0.20	0/807	0.33	0/1082
29	b	0.16	0/653	0.35	0/876
30	c	0.30	0/490	0.60	0/656
31	d	0.36	0/469	0.41	0/623
32	e	0.54	0/447	0.47	0/587

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.49	0/622	0.62	1/822 (0.1%)
34	g	0.31	0/2497	0.42	0/3399
35	h	0.16	0/214	0.47	0/272
36	n	0.14	0/211	0.26	0/283
All	All	0.29	0/79674	0.42	9/115528 (0.0%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1658	G	C2'-C3'-O3'	7.01	124.21	113.70
1	2	1537	A	C4'-C3'-O3'	-6.94	102.59	113.00
1	2	1585	U	C2'-C3'-O3'	6.65	119.47	109.50
33	f	109	ASP	N-CA-C	-6.24	105.31	113.17
1	2	1605	G	C4'-C3'-O3'	-5.79	104.32	113.00
1	2	1658	G	C4'-C3'-O3'	-5.68	104.48	113.00
17	P	81	ARG	N-CA-C	-5.39	97.84	107.98
2	A	44	ASP	N-CA-C	-5.24	106.57	113.17
1	2	1440	C	C2'-C3'-O3'	5.14	121.41	113.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	35677	0	18011	701	0
2	A	1686	0	1688	37	0
3	B	1729	0	1803	72	0
4	C	1690	0	1777	36	0
5	D	1752	0	1848	64	0
6	E	2076	0	2177	46	0
7	F	1495	0	1549	37	0
8	G	1864	0	2018	41	0
9	H	1501	0	1593	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	I	1682	0	1769	43	0
11	J	1499	0	1618	45	0
12	K	816	0	841	29	0
13	L	1229	0	1302	34	0
14	M	935	0	964	54	0
15	N	1202	0	1289	27	0
16	O	1010	0	1034	35	0
17	P	1037	0	1082	32	0
18	Q	1097	0	1161	32	0
19	R	1068	0	1121	26	0
20	S	1184	0	1244	50	0
21	T	1122	0	1153	32	0
22	U	803	0	873	23	0
23	V	625	0	628	16	0
24	W	1034	0	1080	36	0
25	X	1098	0	1167	16	0
26	Y	1014	0	1082	35	0
27	Z	574	0	627	11	0
28	a	794	0	845	43	0
29	b	640	0	665	12	0
30	c	488	0	514	18	0
31	d	458	0	448	6	0
32	e	442	0	487	23	0
33	f	610	0	634	58	0
34	g	2440	0	2396	65	0
35	h	213	0	258	10	0
36	n	206	0	202	10	0
37	2	96	0	0	0	0
37	I	1	0	0	0	0
38	a	1	0	0	0	0
38	d	1	0	0	0	0
38	f	1	0	0	0	0
39	2	4	0	0	0	0
All	All	74894	0	58948	1625	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 12.

All (1625) 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)
26:Y:63:HIS:CE1	26:Y:68:LYS:HE3	1.40	1.51
33:f:81:LYS:CD	33:f:83:LYS:HE3	1.39	1.49
9:H:31:GLU:O	9:H:37:LYS:CD	1.74	1.35
33:f:81:LYS:HD2	33:f:83:LYS:CE	1.56	1.35
3:B:79:VAL:HG11	3:B:81:PHE:CE2	1.62	1.34
9:H:31:GLU:O	9:H:37:LYS:HD2	1.19	1.33
20:S:59:LEU:HD13	20:S:64:VAL:CG1	1.64	1.27
34:g:51:ASN:HD21	34:g:54:ILE:CG2	1.48	1.26
24:W:111:MET:SD	24:W:115:GLU:HG2	1.75	1.26
3:B:98:THR:O	3:B:232:HIS:NE2	1.65	1.25
34:g:257:LYS:HG2	34:g:269:GLU:OE1	1.34	1.23
3:B:36:PRO:HB3	3:B:231:LEU:HD21	1.25	1.14
26:Y:63:HIS:ND1	26:Y:68:LYS:HE3	1.62	1.14
5:D:117:ARG:HD2	36:n:169:GLU:OE2	1.49	1.13
26:Y:63:HIS:CE1	26:Y:68:LYS:CE	2.32	1.13
20:S:59:LEU:CD1	20:S:64:VAL:CG1	2.25	1.12
13:L:24:LEU:CD1	13:L:27:GLU:OE1	1.99	1.10
16:O:117:ARG:HD2	28:a:49:ALA:HB2	1.30	1.10
3:B:88:THR:HG22	3:B:98:THR:HG22	1.33	1.09
3:B:36:PRO:HB3	3:B:231:LEU:CD2	1.83	1.09
16:O:117:ARG:CD	28:a:49:ALA:HB2	1.83	1.08
33:f:81:LYS:CG	33:f:83:LYS:HE3	1.84	1.07
33:f:81:LYS:HG3	33:f:83:LYS:HG3	1.09	1.05
20:S:59:LEU:HD13	20:S:64:VAL:HG13	1.04	1.04
6:E:95:THR:HG23	26:Y:17:LEU:CD1	1.89	1.03
34:g:299:PHE:HD1	34:g:309:VAL:HG22	1.19	1.02
17:P:133:ILE:HG22	17:P:134:GLY:H	0.89	1.02
6:E:95:THR:HG23	26:Y:17:LEU:HD11	1.38	1.02
26:Y:63:HIS:ND1	26:Y:68:LYS:CE	2.23	1.01
1:2:1540:G:H1	1:2:1593:C:H5	1.01	1.01
17:P:133:ILE:HG22	17:P:134:GLY:N	1.64	1.01
28:a:37:LYS:HE2	28:a:72:HIS:CE1	1.96	1.00
3:B:108:ASP:OD2	28:a:65:PRO:HB3	1.61	1.00
6:E:95:THR:CG2	26:Y:17:LEU:CD1	2.40	0.99
33:f:81:LYS:HG3	33:f:83:LYS:CG	1.92	0.99
17:P:133:ILE:CG2	17:P:134:GLY:H	1.73	0.99
33:f:81:LYS:CG	33:f:83:LYS:HG3	1.93	0.99
34:g:51:ASN:ND2	34:g:54:ILE:CG2	2.26	0.99
22:U:21:ARG:HG3	22:U:90:ASP:OD1	1.61	0.98
3:B:79:VAL:CG1	3:B:81:PHE:CE2	2.46	0.98
34:g:299:PHE:CD1	34:g:309:VAL:HG22	1.97	0.98
34:g:51:ASN:HD21	34:g:54:ILE:HG22	1.26	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1532:C:H5	1:2:1638:G:H1	1.06	0.97
20:S:59:LEU:CD1	20:S:64:VAL:HG13	1.91	0.96
1:2:1172:U:C5'	35:h:10:MET:SD	2.54	0.95
3:B:88:THR:CG2	3:B:98:THR:HG22	1.97	0.95
26:Y:63:HIS:ND1	26:Y:68:LYS:HG3	1.81	0.95
1:2:1269:G:H1	1:2:1513:C:H5	1.13	0.95
34:g:51:ASN:ND2	34:g:54:ILE:HG22	1.81	0.93
1:2:1172:U:H5''	35:h:10:MET:SD	2.07	0.93
1:2:1235:G:H1	1:2:1523:C:H5	1.08	0.92
33:f:108:VAL:HG12	33:f:108:VAL:O	1.67	0.92
3:B:88:THR:HG22	3:B:98:THR:CG2	2.00	0.90
5:D:113:LEU:HD11	5:D:117:ARG:HD3	1.56	0.88
16:O:113:GLN:HE22	28:a:45:VAL:HA	1.37	0.88
34:g:51:ASN:HD21	34:g:54:ILE:HG23	1.34	0.88
26:Y:63:HIS:ND1	26:Y:68:LYS:CG	2.37	0.88
10:I:205:ARG:HH11	10:I:206:LYS:NZ	1.71	0.88
14:M:63:LYS:HE3	33:f:108:VAL:HG22	1.56	0.88
26:Y:63:HIS:HE1	26:Y:68:LYS:HE3	1.35	0.87
1:2:1172:U:H5'	35:h:10:MET:SD	2.15	0.86
5:D:117:ARG:CD	36:n:169:GLU:OE2	2.23	0.86
3:B:36:PRO:CB	3:B:231:LEU:HD21	2.05	0.85
33:f:81:LYS:CD	33:f:83:LYS:CE	2.34	0.85
13:L:24:LEU:HD12	13:L:27:GLU:OE1	1.75	0.85
16:O:117:ARG:HG2	28:a:49:ALA:HB1	1.59	0.84
1:2:1274:G:H5'	12:K:1:MET:HE3	1.60	0.84
1:2:890:U:H3	1:2:895:G:H1	1.19	0.83
1:2:878:G:H1	1:2:908:A:H61	1.26	0.83
13:L:24:LEU:HD13	13:L:27:GLU:OE1	1.76	0.83
16:O:117:ARG:HG2	28:a:49:ALA:CB	2.11	0.81
9:H:31:GLU:O	9:H:37:LYS:CG	2.28	0.80
5:D:117:ARG:HD2	36:n:169:GLU:CD	2.06	0.80
22:U:68:THR:HG23	22:U:70:CYS:O	1.79	0.80
1:2:893:U:H3'	1:2:894:G:H8	1.46	0.80
33:f:81:LYS:CG	33:f:83:LYS:CE	2.58	0.80
34:g:72:SER:OG	34:g:74:ASP:O	1.99	0.79
20:S:46:ARG:NH1	20:S:52:LEU:CD1	2.45	0.79
3:B:79:VAL:HG11	3:B:81:PHE:CZ	2.18	0.79
19:R:60:ARG:HA	19:R:63:ARG:HH21	1.48	0.79
1:2:1294:G:H1	1:2:1304:U:H3	1.31	0.78
3:B:79:VAL:CG1	3:B:81:PHE:CD2	2.66	0.78
14:M:63:LYS:HZ1	33:f:108:VAL:HG23	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1513:C:H2'	1:2:1514:G:H5''	1.66	0.78
5:D:117:ARG:NH1	36:n:169:GLU:OE2	2.16	0.78
28:a:36:ILE:HD13	28:a:78:VAL:HG21	1.64	0.77
3:B:228:LEU:HD12	3:B:232:HIS:CE1	2.19	0.77
16:O:117:ARG:CG	28:a:49:ALA:HB2	2.14	0.77
1:2:537:C:H42	1:2:546:G:H21	1.29	0.77
3:B:198:GLU:HB2	3:B:210:VAL:HG11	1.66	0.77
1:2:1438:A:H3'	1:2:1439:A:H5''	1.66	0.77
1:2:1579:A:O2'	1:2:1581:C:OP2	2.02	0.76
33:f:107:LYS:HA	33:f:114:ILE:HA	1.67	0.76
9:H:162:GLN:HB3	9:H:165:ASN:HD21	1.50	0.76
34:g:257:LYS:CG	34:g:269:GLU:OE1	2.26	0.76
1:2:201:C:H3'	1:2:202:G:H8	1.50	0.76
1:2:199:C:H3'	1:2:200:G:H8	1.51	0.76
3:B:228:LEU:CD1	3:B:232:HIS:CE1	2.69	0.76
1:2:981:A:H2'	1:2:982:G:C8	2.21	0.76
9:H:93:VAL:HG11	9:H:133:LEU:HD12	1.67	0.76
1:2:1604:G:H2'	1:2:1605:G:H5'	1.68	0.76
1:2:532:C:H2'	1:2:533:A:N7	2.01	0.75
1:2:1341:C:N4	1:2:1485:U:O4	2.19	0.75
3:B:108:ASP:OD2	28:a:65:PRO:CB	2.33	0.75
4:C:200:ARG:O	11:J:54:ARG:NH2	2.19	0.75
28:a:73:TYR:HB3	28:a:78:VAL:HG22	1.68	0.75
14:M:37:GLU:HA	14:M:40:LYS:HB2	1.68	0.75
5:D:56:GLN:OE1	5:D:56:GLN:N	2.19	0.74
1:2:560:A:H5'	11:J:174:LYS:CG	2.18	0.74
24:W:111:MET:SD	24:W:115:GLU:CG	2.68	0.74
28:a:37:LYS:HE2	28:a:72:HIS:ND1	2.03	0.74
10:I:205:ARG:HH11	10:I:206:LYS:HZ2	1.36	0.74
1:2:1862:G:O2'	28:a:5:ARG:NH2	2.21	0.73
10:I:205:ARG:NH1	10:I:206:LYS:NZ	2.36	0.73
1:2:64:A:H2	1:2:83:A:H62	1.36	0.73
20:S:46:ARG:NH1	20:S:52:LEU:HD12	2.02	0.73
5:D:193:ASP:HB2	5:D:198:ILE:HG22	1.70	0.73
1:2:587:A:H5'	1:2:592:C:H41	1.54	0.73
24:W:102:ILE:HG22	24:W:104:LEU:CD1	2.18	0.73
19:R:98:VAL:HG13	19:R:102:THR:HG23	1.71	0.73
30:c:11:LEU:HB2	30:c:35:MET:HG3	1.70	0.73
1:2:1224:G:H2'	1:2:1225:U:H5'	1.70	0.73
8:G:64:LYS:HB2	8:G:97:VAL:HG11	1.71	0.73
33:f:81:LYS:HD2	33:f:83:LYS:HE3	0.75	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:543:C:H3'	1:2:544:G:H8	1.54	0.72
5:D:67:ARG:NH1	12:K:93:THR:O	2.21	0.72
33:f:81:LYS:CG	33:f:83:LYS:CD	2.67	0.72
24:W:105:THR:HG22	24:W:110:ILE:HG12	1.71	0.72
1:2:591:U:H5''	1:2:591:U:H6	1.54	0.72
1:2:1729:U:H3	1:2:1805:G:H1	1.35	0.72
14:M:112:LYS:HB2	14:M:121:LYS:HD2	1.72	0.72
17:P:133:ILE:CG2	17:P:134:GLY:N	2.39	0.72
28:a:40:VAL:HG12	28:a:42:ARG:HG3	1.72	0.72
1:2:199:C:H3'	1:2:200:G:C8	2.24	0.72
20:S:59:LEU:HD11	20:S:64:VAL:CG1	2.15	0.72
1:2:126:G:OP1	8:G:198:ARG:NH1	2.22	0.72
1:2:640:A:H2'	1:2:641:A:C8	2.25	0.72
16:O:117:ARG:CG	28:a:49:ALA:CB	2.67	0.72
16:O:144:GLY:O	28:a:22:ARG:NH2	2.20	0.72
4:C:199:PRO:HG2	11:J:58:ARG:HD3	1.72	0.71
10:I:4:SER:OG	10:I:6:ASP:OD2	2.08	0.71
1:2:1016:U:H5''	15:N:14:SER:HB3	1.72	0.71
13:L:49:GLU:HG3	13:L:116:CYS:HA	1.71	0.71
10:I:97:VAL:O	10:I:100:CYS:SG	2.43	0.71
1:2:1277:C:H2'	1:2:1278:A:H8	1.55	0.71
1:2:65:C:N4	8:G:134:GLY:O	2.24	0.71
10:I:205:ARG:NH1	10:I:206:LYS:HZ2	1.87	0.71
28:a:46:GLU:HG2	28:a:48:ALA:H	1.56	0.71
33:f:81:LYS:HG2	33:f:83:LYS:CD	2.21	0.71
1:2:387:C:OP2	10:I:10:LYS:NZ	2.22	0.71
1:2:1228:A:H2'	1:2:1229:G:C8	2.26	0.71
1:2:560:A:H5'	11:J:174:LYS:HG2	1.73	0.70
20:S:15:VAL:HG12	20:S:16:LEU:HG	1.72	0.70
20:S:59:LEU:CD1	20:S:64:VAL:HG12	2.19	0.70
25:X:68:LYS:HB3	25:X:91:LEU:HD22	1.74	0.70
6:E:122:LYS:NZ	6:E:143:ASP:OD2	2.23	0.70
33:f:121:CYS:HB3	33:f:126:CYS:HB3	1.73	0.70
9:H:9:VAL:HG23	9:H:24:SER:HB3	1.73	0.69
25:X:101:LEU:HB3	25:X:124:LYS:HB2	1.74	0.69
1:2:1604:G:C2'	1:2:1605:G:H5'	2.21	0.69
1:2:1722:G:O6	1:2:1812:U:O2	2.11	0.69
3:B:137:LEU:HG	3:B:215:VAL:HG22	1.75	0.69
5:D:4:GLN:N	5:D:4:GLN:OE1	2.25	0.69
7:F:204:ARG:HG2	30:c:63:ARG:HH12	1.55	0.69
2:A:120:ARG:HH12	4:C:267:GLN:HB2	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:71:G:N7	8:G:170:ARG:NH1	2.39	0.69
1:2:560:A:OP2	11:J:177:ASN:ND2	2.24	0.69
1:2:1290:G:H21	33:f:140:TYR:HE2	1.39	0.69
1:2:1447:G:OP1	22:U:87:ARG:NH2	2.26	0.69
24:W:27:ILE:HG23	24:W:61:ILE:HB	1.75	0.69
1:2:1601:A:H5''	1:2:1636:G:H22	1.58	0.69
1:2:201:C:H3'	1:2:202:G:C8	2.28	0.69
34:g:257:LYS:HG2	34:g:269:GLU:CD	2.18	0.69
1:2:823:U:H5	11:J:143:ASN:HB3	1.59	0.68
9:H:31:GLU:HA	9:H:37:LYS:HG2	1.74	0.68
9:H:138:GLU:HG2	15:N:19:ARG:HD2	1.75	0.68
9:H:152:ARG:HH22	24:W:35:VAL:HG11	1.57	0.68
12:K:1:MET:HE1	12:K:43:LEU:HD21	1.75	0.68
14:M:89:VAL:HG21	14:M:102:LYS:HD3	1.76	0.68
3:B:98:THR:C	3:B:232:HIS:NE2	2.51	0.68
1:2:1532:C:H5	1:2:1638:G:N1	1.87	0.68
1:2:1757:G:H2'	1:2:1758:G:C8	2.29	0.68
9:H:31:GLU:C	9:H:37:LYS:HG2	2.18	0.68
33:f:81:LYS:CG	33:f:83:LYS:CG	2.64	0.68
1:2:892:U:H3'	1:2:893:U:H6	1.58	0.68
14:M:63:LYS:HE3	33:f:108:VAL:CG2	2.23	0.68
1:2:797:C:O2'	1:2:798:G:N7	2.26	0.68
27:Z:61:GLU:OE1	27:Z:61:GLU:N	2.27	0.68
9:H:31:GLU:O	9:H:37:LYS:HD3	1.86	0.68
18:Q:38:PRO:HG2	18:Q:41:MET:HG3	1.75	0.68
34:g:163:PRO:HB2	34:g:179:LEU:HB2	1.75	0.68
1:2:71:G:H3'	1:2:72:C:H5''	1.76	0.67
1:2:1753:C:H2'	1:2:1754:G:C8	2.29	0.67
1:2:373:G:H4'	13:L:85:THR:HG21	1.77	0.67
23:V:49:GLN:OE1	23:V:49:GLN:N	2.21	0.67
34:g:42:MET:HE3	34:g:57:ARG:HB3	1.76	0.67
7:F:128:ILE:HD11	7:F:135:ARG:HB3	1.77	0.67
17:P:86:LEU:O	17:P:88:GLU:N	2.27	0.67
17:P:110:GLU:OE1	17:P:110:GLU:N	2.23	0.67
2:A:42:LYS:HD3	2:A:48:ILE:HD11	1.77	0.67
1:2:883:U:H2'	1:2:884:C:C6	2.30	0.67
1:2:1608:U:O4	1:2:1631:U:H5	1.77	0.67
1:2:1614:A:OP2	17:P:42:ARG:NH1	2.27	0.67
13:L:69:ARG:HH12	13:L:132:ARG:HB3	1.60	0.67
1:2:925:G:H1	1:2:1017:U:H3	1.43	0.67
1:2:1273:C:H5	1:2:1508:A:H62	1.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1550:G:H3'	1:2:1579:A:H61	1.58	0.67
1:2:1374:C:O2'	1:2:1464:C:O2	2.13	0.66
22:U:70:CYS:SG	22:U:71:GLY:N	2.68	0.66
13:L:22:ARG:HD2	13:L:31:GLU:HG3	1.77	0.66
33:f:81:LYS:HG2	33:f:83:LYS:HD2	1.77	0.66
1:2:952:G:H21	16:O:52:THR:HG21	1.60	0.66
11:J:65:GLU:N	11:J:65:GLU:OE2	2.28	0.66
10:I:205:ARG:HH11	10:I:206:LYS:HZ3	1.44	0.66
1:2:1277:C:OP1	12:K:51:SER:OG	2.13	0.66
23:V:38:GLU:N	23:V:38:GLU:OE2	2.28	0.66
1:2:878:G:H1	1:2:908:A:N6	1.94	0.65
5:D:135:GLU:HG3	5:D:153:VAL:HG12	1.78	0.65
23:V:7:GLU:OE2	23:V:7:GLU:N	2.23	0.65
1:2:1856:C:OP1	16:O:141:ARG:NH1	2.26	0.65
1:2:501:C:O2	1:2:501:C:H2'	1.97	0.65
4:C:146:GLU:OE1	4:C:146:GLU:N	2.29	0.65
24:W:104:LEU:HG	24:W:125:ILE:HA	1.78	0.65
26:Y:63:HIS:CE1	26:Y:68:LYS:HG3	2.31	0.65
1:2:1588:A:H2'	1:2:1589:A:C8	2.31	0.65
3:B:36:PRO:HB3	3:B:231:LEU:HD23	1.76	0.65
1:2:1290:G:H1	1:2:1308:U:H3	1.45	0.65
1:2:77:A:H2	8:G:175:LYS:HG3	1.61	0.65
2:A:78:SER:HB2	2:A:87:VAL:HG21	1.78	0.65
34:g:2:THR:OG1	34:g:3:GLU:N	2.29	0.65
1:2:1274:G:H5'	12:K:1:MET:CE	2.27	0.65
30:c:60:GLU:OE1	30:c:63:ARG:N	2.30	0.64
34:g:133:ASN:HD21	34:g:137:VAL:HB	1.60	0.64
1:2:76:U:H3'	1:2:77:A:H5'	1.79	0.64
1:2:1546:G:H5'	18:Q:18:THR:HG21	1.79	0.64
2:A:164:ASN:O	2:A:170:SER:OG	2.12	0.64
1:2:107:A:H2'	1:2:108:G:C8	2.32	0.64
1:2:554:A:OP1	32:e:25:LYS:NZ	2.25	0.64
12:K:9:ILE:O	12:K:13:GLU:HG2	1.98	0.64
1:2:1293:A:H61	1:2:1305:C:H42	1.44	0.64
1:2:879:C:H3'	1:2:880:G:H8	1.63	0.64
1:2:880:G:H1	1:2:906:U:H3	1.45	0.64
1:2:1598:G:H4'	1:2:1600:G:H1	1.61	0.64
1:2:1648:G:N2	1:2:1675:A:OP2	2.25	0.64
17:P:83:MET:HE2	17:P:83:MET:HA	1.80	0.64
19:R:7:LYS:O	19:R:11:LYS:HG3	1.97	0.64
33:f:109:ASP:C	33:f:111:ASN:H	2.06	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:51:ASN:ND2	34:g:54:ILE:HG23	2.02	0.64
1:2:1277:C:H2'	1:2:1278:A:C8	2.32	0.64
9:H:31:GLU:C	9:H:37:LYS:CD	2.67	0.64
1:2:1780:G:H2'	1:2:1781:A:C8	2.33	0.64
5:D:74:GLN:OE1	5:D:79:PHE:HB2	1.97	0.64
32:e:45:VAL:HG23	32:e:45:VAL:O	1.97	0.64
1:2:1514:G:H8	17:P:79:HIS:CE1	2.16	0.64
14:M:52:LEU:HD13	14:M:65:VAL:HG11	1.79	0.64
6:E:95:THR:CG2	26:Y:17:LEU:HD12	2.27	0.63
2:A:34:MET:HE3	2:A:154:LEU:HD21	1.79	0.63
4:C:102:LEU:HD22	4:C:130:ILE:HG12	1.80	0.63
28:a:37:LYS:HE2	28:a:72:HIS:HE1	1.60	0.63
33:f:132:MET:HG2	33:f:141:CYS:HA	1.79	0.63
24:W:103:VAL:O	24:W:104:LEU:HD12	1.98	0.63
1:2:71:G:H4'	1:2:72:C:OP2	1.98	0.63
1:2:1291:A:H2	33:f:138:ARG:HE	1.46	0.63
20:S:46:ARG:NH1	20:S:52:LEU:HD11	2.12	0.63
3:B:98:THR:O	3:B:232:HIS:CE1	2.49	0.63
5:D:62:LYS:O	5:D:67:ARG:NH2	2.31	0.63
11:J:29:LEU:HD23	32:e:42:PHE:HE2	1.64	0.63
1:2:94:G:O2'	1:2:508:A:O2'	2.17	0.63
6:E:87:MET:HE2	6:E:123:LEU:HB2	1.80	0.63
1:2:1866:A:N6	28:a:84:VAL:HG22	2.14	0.63
6:E:100:ARG:NH2	6:E:121:TYR:O	2.31	0.62
34:g:181:ASN:HB2	34:g:183:LYS:HE2	1.81	0.62
1:2:1269:G:N1	1:2:1513:C:H5	1.92	0.62
9:H:52:GLU:HG3	9:H:58:LYS:HE2	1.81	0.62
5:D:143:ARG:HA	5:D:143:ARG:NH1	2.14	0.62
24:W:103:VAL:C	24:W:104:LEU:HD12	2.24	0.62
1:2:860:G:N2	24:W:107:SER:OG	2.33	0.62
3:B:53:GLN:OE1	3:B:53:GLN:N	2.32	0.62
20:S:46:ARG:HH12	20:S:52:LEU:HD12	1.61	0.62
5:D:106:ARG:HG3	5:D:175:VAL:HG22	1.82	0.62
14:M:85:LEU:HG	14:M:102:LYS:HE2	1.82	0.62
14:M:84:LYS:HA	14:M:87:GLU:HG2	1.82	0.62
33:f:107:LYS:HE3	33:f:112:GLY:HA2	1.82	0.62
1:2:643:A:OP1	11:J:41:ARG:NH2	2.32	0.62
1:2:913:A:H2	9:H:99:ARG:H	1.47	0.62
3:B:222:LYS:NZ	3:B:223:PHE:O	2.33	0.61
10:I:57:ALA:HB2	10:I:183:GLY:HA2	1.82	0.61
17:P:19:GLY:N	20:S:91:LYS:O	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:139:LEU:HD11	6:E:154:ILE:HG21	1.82	0.61
16:O:54:CYS:SG	16:O:84:ARG:HD3	2.40	0.61
1:2:885:U:H2'	1:2:886:A:H8	1.64	0.61
34:g:107:ASP:OD2	34:g:125:ARG:NH1	2.33	0.61
1:2:893:U:H3'	1:2:894:G:C8	2.30	0.61
1:2:1533:A:N7	1:2:1602:U:H5	1.98	0.61
3:B:23:ASP:O	3:B:27:LYS:NZ	2.33	0.61
9:H:148:LEU:HA	24:W:42:MET:HE2	1.81	0.61
1:2:145:G:H2'	1:2:146:G:C8	2.35	0.61
34:g:5:MET:HB2	34:g:270:LEU:HD21	1.81	0.61
34:g:87:LEU:HB2	34:g:101:PHE:HB2	1.83	0.61
1:2:196:C:H2'	1:2:197:U:C6	2.35	0.61
1:2:1139:C:H5	1:2:1149:A:H62	1.48	0.61
8:G:43:GLU:O	8:G:46:LYS:HG3	2.01	0.61
1:2:1599:U:H4'	1:2:1600:G:H5'	1.83	0.61
1:2:1241:A:H2	1:2:1516:G:C8	2.17	0.61
1:2:1657:G:C2'	1:2:1658:G:H5'	2.31	0.61
18:Q:19:ALA:HA	18:Q:74:GLY:HA3	1.83	0.61
13:L:33:LEU:HD12	13:L:34:PRO:HD2	1.83	0.61
30:c:9:ILE:HG13	30:c:59:LEU:HD22	1.83	0.61
1:2:747:U:H1'	9:H:109:ARG:HD2	1.83	0.60
9:H:162:GLN:HB3	9:H:165:ASN:ND2	2.15	0.60
17:P:34:MET:HB3	17:P:42:ARG:HG3	1.83	0.60
1:2:1076:G:OP1	15:N:106:ARG:NH2	2.33	0.60
1:2:1243:U:H2'	1:2:1244:U:H5'	1.82	0.60
5:D:116:ARG:HB2	36:n:172:ASP:HB3	1.82	0.60
7:F:135:ARG:NH1	7:F:136:ARG:O	2.35	0.60
21:T:40:ALA:HB3	21:T:43:LYS:HD3	1.83	0.60
1:2:1091:C:HO2'	24:W:2:VAL:N	1.99	0.60
2:A:108:PHE:HB2	2:A:136:GLU:HG2	1.83	0.60
3:B:88:THR:HA	3:B:98:THR:HA	1.83	0.60
1:2:530:U:H3'	1:2:531:A:C8	2.36	0.60
13:L:104:LYS:O	25:X:11:ARG:NH2	2.31	0.60
1:2:1858:G:OP2	16:O:146:ARG:NH2	2.34	0.60
9:H:34:SER:O	9:H:37:LYS:HG3	2.01	0.60
14:M:12:MET:HG2	14:M:123:VAL:HG11	1.84	0.60
1:2:1644:C:H4'	18:Q:140:ARG:HB2	1.83	0.60
4:C:271:ASP:OD1	4:C:271:ASP:N	2.34	0.60
1:2:617:G:H4'	25:X:88:ASP:HB3	1.83	0.59
1:2:980:A:H2'	1:2:981:A:C8	2.37	0.59
7:F:42:LYS:HB3	7:F:43:GLU:OE2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:507:G:OP2	26:Y:104:ARG:NH2	2.36	0.59
1:2:816:A:OP2	11:J:10:ARG:NH2	2.29	0.59
1:2:928:G:H1	1:2:1013:U:H3	1.50	0.59
1:2:1647:A:OP1	18:Q:138:ARG:NH1	2.35	0.59
2:A:77:ILE:HG12	2:A:99:ILE:HB	1.83	0.59
20:S:86:ARG:HG3	20:S:89:ASP:HB2	1.84	0.59
1:2:163:U:OP2	8:G:87:ARG:NH2	2.35	0.59
1:2:367:U:H4'	1:2:371:A:C8	2.37	0.59
7:F:124:ASP:OD1	7:F:124:ASP:N	2.34	0.59
34:g:201:SER:OG	34:g:203:ASP:OD1	2.18	0.59
1:2:1653:U:H2'	1:2:1654:G:C8	2.38	0.59
28:a:37:LYS:CE	28:a:72:HIS:CE1	2.79	0.59
1:2:881:G:N2	1:2:906:U:H1'	2.16	0.59
1:2:1224:G:C2'	1:2:1225:U:H5'	2.31	0.59
7:F:96:ALA:HA	7:F:99:ILE:HB	1.84	0.59
9:H:31:GLU:CA	9:H:37:LYS:HG2	2.32	0.59
22:U:67:LYS:HG2	22:U:78:ASP:OD1	2.02	0.59
1:2:382:C:H2'	1:2:383:G:H8	1.68	0.59
1:2:891:G:H3'	1:2:892:U:H6	1.68	0.59
9:H:152:ARG:HH22	24:W:35:VAL:CG1	2.16	0.59
1:2:1010:G:H2'	1:2:1011:A:C8	2.37	0.59
1:2:1617:G:H2'	1:2:1619:A:H2	1.68	0.59
1:2:1722:G:O6	1:2:1812:U:C2	2.55	0.59
24:W:42:MET:HE1	24:W:49:GLU:HA	1.84	0.59
1:2:1144:A:H5'	1:2:1355:C:H41	1.68	0.59
14:M:113:ASP:N	14:M:113:ASP:OD1	2.36	0.59
1:2:643:A:OP1	11:J:39:ASN:ND2	2.36	0.59
1:2:882:U:H2'	1:2:883:U:C6	2.37	0.59
3:B:228:LEU:HD11	3:B:232:HIS:CE1	2.38	0.59
33:f:125:GLU:N	33:f:125:GLU:OE2	2.34	0.59
10:I:125:LYS:HE2	10:I:125:LYS:HA	1.84	0.58
36:n:168:PRO:HA	36:n:171:MET:HE3	1.85	0.58
1:2:928:G:H2'	1:2:929:G:C8	2.38	0.58
1:2:1396:A:O2'	1:2:1398:G:N7	2.36	0.58
17:P:51:ARG:C	17:P:53:GLN:H	2.11	0.58
17:P:75:VAL:HA	17:P:93:MET:O	2.03	0.58
33:f:123:SER:HB2	33:f:126:CYS:HB2	1.85	0.58
1:2:381:C:OP2	10:I:54:LYS:NZ	2.35	0.58
1:2:1587:G:H4'	1:2:1588:A:OP2	2.03	0.58
2:A:85:ARG:NH2	19:R:82:ASP:O	2.36	0.58
4:C:79:GLU:N	4:C:79:GLU:OE1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:143:ARG:HA	5:D:143:ARG:CZ	2.33	0.58
22:U:68:THR:CG2	22:U:70:CYS:O	2.49	0.58
1:2:1235:G:N1	1:2:1523:C:H5	1.91	0.58
3:B:171:ILE:HD13	3:B:174:ARG:HH21	1.68	0.58
11:J:89:GLU:OE2	11:J:89:GLU:N	2.25	0.58
33:f:107:LYS:O	33:f:108:VAL:C	2.46	0.58
16:O:56:VAL:HG12	16:O:81:VAL:HG23	1.85	0.58
1:2:199:C:H5''	1:2:199:C:C6	2.39	0.58
1:2:588:G:H4'	1:2:589:G:H5'	1.85	0.58
1:2:957:A:H2'	1:2:958:G:H5'	1.86	0.58
1:2:962:A:H5''	16:O:66:ARG:HG2	1.85	0.58
1:2:1332:A:O2'	5:D:145:GLN:OE1	2.17	0.58
1:2:1537:A:H3'	1:2:1538:C:H5''	1.85	0.58
1:2:1845:A:H2'	1:2:1846:G:C8	2.39	0.58
18:Q:82:TYR:HA	18:Q:85:ARG:HD3	1.86	0.58
1:2:560:A:H5'	11:J:174:LYS:HG3	1.84	0.58
33:f:103:LEU:HD12	33:f:118:ARG:HH21	1.69	0.58
16:O:34:PHE:HB3	16:O:41:PHE:HB2	1.85	0.58
28:a:32:LYS:CE	28:a:37:LYS:NZ	2.67	0.58
1:2:1738:C:OP1	8:G:92:ARG:NH2	2.37	0.58
18:Q:97:GLN:HB2	18:Q:105:LYS:HG3	1.85	0.58
1:2:533:A:C2	1:2:534:G:H1'	2.39	0.57
1:2:957:A:C2'	1:2:958:G:H5'	2.34	0.57
1:2:1454:A:C8	19:R:3:ARG:HG3	2.39	0.57
15:N:38:TYR:CE1	15:N:78:LYS:HD2	2.39	0.57
1:2:72:C:O2'	1:2:73:C:H2'	2.03	0.57
8:G:5:ILE:HD13	8:G:111:LEU:HB2	1.87	0.57
33:f:103:LEU:HD23	33:f:103:LEU:H	1.69	0.57
1:2:581:U:OP1	11:J:133:ARG:NH2	2.30	0.57
1:2:1218:C:H2'	1:2:1219:C:C6	2.40	0.57
1:2:496:C:H5'	6:E:29:PRO:HA	1.85	0.57
3:B:35:ALA:O	3:B:42:ARG:NH1	2.38	0.57
2:A:176:TRP:HE3	2:A:177:MET:HG2	1.69	0.57
3:B:92:GLN:HE22	3:B:229:MET:HE1	1.70	0.57
20:S:31:THR:HG23	20:S:37:GLY:HA2	1.87	0.57
26:Y:15:ASN:ND2	26:Y:22:GLN:OE1	2.38	0.57
1:2:1781:A:H2'	1:2:1782:G:C8	2.40	0.57
8:G:142:ARG:HG2	8:G:147:LEU:HB2	1.86	0.57
17:P:86:LEU:HD12	17:P:88:GLU:HB3	1.85	0.57
19:R:71:ILE:HB	19:R:74:GLN:HB2	1.86	0.57
34:g:37:ASP:OD1	34:g:39:THR:OG1	2.23	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1241:A:C2	1:2:1516:G:H2'	2.40	0.57
1:2:1499:U:H4'	5:D:176:LEU:HD11	1.87	0.57
3:B:168:MET:O	3:B:172:MET:HG3	2.05	0.57
7:F:32:ASP:O	7:F:34:SER:N	2.35	0.57
34:g:29:ASP:OD1	34:g:47:ARG:NH1	2.37	0.57
1:2:1650:A:OP1	18:Q:138:ARG:HB2	2.05	0.57
1:2:492:C:OP2	26:Y:107:ARG:NH2	2.37	0.57
5:D:206:ASP:OD1	5:D:206:ASP:N	2.38	0.57
33:f:107:LYS:O	33:f:109:ASP:N	2.37	0.57
1:2:1376:A:P	19:R:67:ARG:HH12	2.28	0.56
1:2:1445:U:H1'	1:2:1580:A:N6	2.20	0.56
4:C:196:ILE:HB	4:C:223:TYR:HB2	1.86	0.56
9:H:60:ILE:HB	9:H:92:VAL:HG22	1.87	0.56
12:K:80:ARG:NH1	12:K:89:ILE:O	2.36	0.56
26:Y:63:HIS:CE1	26:Y:68:LYS:CD	2.88	0.56
7:F:135:ARG:HG2	7:F:136:ARG:H	1.70	0.56
24:W:6:VAL:CG1	24:W:29:PRO:HG2	2.36	0.56
30:c:37:ASP:OD1	30:c:39:SER:OG	2.21	0.56
1:2:852:G:H2'	1:2:853:C:H5'	1.87	0.56
1:2:1296:U:H3'	1:2:1297:U:H4'	1.87	0.56
1:2:1426:U:OP1	18:Q:33:LYS:NZ	2.24	0.56
1:2:1566:G:N7	21:T:101:ARG:NH2	2.53	0.56
1:2:1808:U:H2'	1:2:1809:A:C8	2.40	0.56
4:C:252:THR:OG1	4:C:254:ASP:OD1	2.20	0.56
1:2:874:G:H2'	1:2:875:A:H8	1.71	0.56
1:2:543:C:C4	1:2:544:G:H1'	2.41	0.56
1:2:1241:A:C2	1:2:1516:G:H8	2.23	0.56
1:2:1296:U:H5''	1:2:1297:U:H4'	1.86	0.56
2:A:77:ILE:HD12	2:A:122:LEU:HD11	1.87	0.56
7:F:122:ARG:HG2	30:c:57:THR:OG1	2.05	0.56
8:G:57:ASP:O	8:G:107:SER:OG	2.21	0.56
15:N:94:LYS:O	15:N:98:VAL:HG23	2.05	0.56
2:A:176:TRP:CE3	2:A:177:MET:HG2	2.41	0.56
9:H:29:GLU:OE1	9:H:30:LEU:HD22	2.05	0.56
13:L:49:GLU:HG2	13:L:118:ARG:NH1	2.19	0.56
6:E:211:LYS:NZ	6:E:217:SER:OG	2.38	0.56
21:T:117:GLN:CD	21:T:117:GLN:H	2.13	0.56
1:2:1773:C:H4'	1:2:1774:C:OP2	2.05	0.56
7:F:176:GLU:OE2	7:F:187:SER:OG	2.24	0.56
1:2:552:G:N2	1:2:553:U:O4	2.39	0.56
1:2:942:G:H2'	1:2:943:U:C6	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1597:C:H4'	1:2:1603:G:C6	2.41	0.56
28:a:32:LYS:HG2	28:a:37:LYS:NZ	2.21	0.56
29:b:67:THR:OG1	29:b:70:LYS:O	2.23	0.56
1:2:1060:A:O2'	1:2:1062:A:N7	2.31	0.56
1:2:1241:A:H2	1:2:1516:G:H8	1.54	0.56
1:2:1355:C:O2'	4:C:238:LYS:NZ	2.39	0.56
6:E:87:MET:HE1	6:E:236:ILE:HG21	1.88	0.56
7:F:76:MET:HA	7:F:76:MET:HE2	1.88	0.56
1:2:1287:A:H2	1:2:1311:C:O2	1.89	0.55
5:D:126:ILE:HG21	5:D:188:ILE:HD12	1.87	0.55
30:c:17:VAL:HA	30:c:30:VAL:HG23	1.88	0.55
1:2:913:A:H1'	9:H:66:VAL:HB	1.88	0.55
25:X:84:PHE:CE2	25:X:86:PRO:HA	2.41	0.55
1:2:860:G:N2	24:W:107:SER:HG	2.05	0.55
12:K:49:MET:HG3	12:K:69:TRP:CE3	2.42	0.55
15:N:115:LEU:O	15:N:119:GLU:HG2	2.06	0.55
1:2:1244:U:O2'	1:2:1245:G:H8	1.89	0.55
1:2:1754:G:C6	1:2:1779:G:N1	2.74	0.55
14:M:23:LYS:O	14:M:27:ILE:HD12	2.05	0.55
15:N:62:GLN:HB2	15:N:65:PHE:HB2	1.89	0.55
1:2:543:C:H3'	1:2:544:G:C8	2.37	0.55
1:2:1139:C:H2'	1:2:1140:G:O4'	2.07	0.55
1:2:1164:G:O2'	1:2:1165:G:H5'	2.07	0.55
20:S:13:LEU:HB3	20:S:20:ILE:HG12	1.89	0.55
30:c:36:ASP:OD1	30:c:37:ASP:N	2.39	0.55
1:2:103:A:OP2	1:2:356:C:N4	2.40	0.55
1:2:889:U:H2'	1:2:890:U:C2	2.42	0.55
5:D:74:GLN:NE2	5:D:80:PRO:O	2.40	0.55
21:T:85:ASN:HB2	21:T:88:MET:HB2	1.89	0.55
1:2:913:A:H62	9:H:119:SER:HB2	1.72	0.55
33:f:108:VAL:O	33:f:108:VAL:CG1	2.41	0.55
34:g:68:ASP:HB3	34:g:111:VAL:HG12	1.89	0.55
1:2:1225:U:H2'	1:2:1225:U:OP2	2.07	0.55
2:A:163:CYS:HB3	2:A:174:MET:HE2	1.87	0.55
28:a:32:LYS:HE2	28:a:37:LYS:NZ	2.22	0.55
34:g:255:SER:HB3	34:g:271:LYS:HE3	1.89	0.55
34:g:297:THR:CG2	34:g:309:VAL:HG13	2.37	0.55
1:2:533:A:C4	1:2:534:G:H1'	2.42	0.55
1:2:958:G:H2'	1:2:959:G:O4'	2.06	0.55
9:H:146:VAL:HG22	9:H:152:ARG:NH1	2.22	0.55
1:2:1705:C:H2'	1:2:1706:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:116:ARG:HG2	5:D:150:MET:HE1	1.88	0.55
14:M:26:LEU:HD13	14:M:31:LEU:HD23	1.88	0.55
3:B:144:LYS:HD2	3:B:146:ARG:HH22	1.72	0.54
7:F:40:ALA:HB1	7:F:45:TYR:CG	2.43	0.54
20:S:5:ILE:HG13	20:S:9:PHE:HB2	1.90	0.54
1:2:547:G:N3	1:2:547:G:H2'	2.22	0.54
1:2:953:C:H2'	1:2:954:U:O4'	2.06	0.54
1:2:1225:U:O2'	1:2:1226:G:C8	2.58	0.54
1:2:1521:C:N4	20:S:137:LYS:HG2	2.22	0.54
1:2:1679:A:H2'	7:F:60:ARG:HD2	1.90	0.54
9:H:154:ILE:HB	9:H:185:VAL:HG22	1.89	0.54
10:I:88:ASN:OD1	10:I:205:ARG:NH2	2.39	0.54
16:O:142:ARG:HG3	16:O:143:LYS:N	2.23	0.54
20:S:59:LEU:HD11	20:S:64:VAL:HG12	1.87	0.54
1:2:894:G:H2'	1:2:895:G:C8	2.43	0.54
1:2:1373:C:OP1	19:R:7:LYS:N	2.39	0.54
1:2:1810:U:H2'	1:2:1811:C:C6	2.41	0.54
11:J:29:LEU:CD2	32:e:41:ARG:HD2	2.37	0.54
20:S:44:VAL:HG13	20:S:70:ILE:HG23	1.88	0.54
1:2:29:G:H2'	1:2:30:C:C6	2.42	0.54
1:2:293:C:O2'	1:2:294:U:H3'	2.07	0.54
1:2:1310:U:H2'	1:2:1311:C:C6	2.43	0.54
2:A:39:TYR:CE1	2:A:40:LYS:HD2	2.42	0.54
19:R:57:LEU:O	19:R:61:ILE:HG13	2.06	0.54
28:a:74:CYS:O	28:a:78:VAL:HG23	2.06	0.54
3:B:229:MET:O	3:B:230:GLU:C	2.51	0.54
10:I:62:VAL:HG11	10:I:75:LYS:HE2	1.89	0.54
24:W:30:CYS:HB2	24:W:61:ILE:HG13	1.88	0.54
32:e:11:LYS:O	32:e:15:GLN:HG2	2.08	0.54
15:N:48:SER:O	15:N:52:VAL:HG23	2.08	0.54
20:S:39:ARG:NH2	21:T:36:THR:O	2.34	0.54
34:g:7:LEU:HD22	34:g:272:GLN:HG2	1.88	0.54
34:g:44:LYS:HE2	34:g:46:THR:HG22	1.88	0.54
1:2:792:C:H2'	1:2:793:G:C8	2.43	0.54
2:A:84:GLN:HG2	2:A:100:ALA:HB1	1.90	0.54
6:E:95:THR:HG21	26:Y:17:LEU:CD1	2.31	0.54
12:K:90:VAL:HG22	12:K:94:LEU:HD12	1.89	0.54
18:Q:104:SER:O	18:Q:108:ILE:HG12	2.08	0.54
7:F:19:LEU:O	7:F:21:GLY:N	2.41	0.54
9:H:80:VAL:O	9:H:84:GLU:HG2	2.08	0.54
29:b:11:SER:N	29:b:14:GLU:OE2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1218:C:H2'	1:2:1219:C:H6	1.73	0.54
18:Q:49:TYR:O	18:Q:53:GLU:HG3	2.07	0.54
20:S:138:THR:HA	20:S:141:ARG:HH11	1.72	0.54
1:2:1520:G:N3	1:2:1520:G:H2'	2.22	0.54
14:M:62:VAL:O	14:M:66:GLU:HG2	2.08	0.54
24:W:42:MET:CE	24:W:49:GLU:HA	2.38	0.54
1:2:537:C:H42	1:2:546:G:N2	2.00	0.53
1:2:792:C:H2'	1:2:793:G:H8	1.73	0.53
1:2:822:U:H2'	1:2:824:C:OP2	2.08	0.53
1:2:1232:U:H5	1:2:1526:G:O6	1.90	0.53
4:C:176:LYS:O	4:C:200:ARG:NH2	2.41	0.53
7:F:128:ILE:HB	7:F:132:GLY:HA3	1.88	0.53
21:T:96:SER:HB3	21:T:99:VAL:HG22	1.91	0.53
1:2:1101:U:H2'	1:2:1102:G:C8	2.43	0.53
1:2:1657:G:H2'	1:2:1658:G:H5'	1.90	0.53
11:J:45:ARG:O	11:J:49:THR:HG23	2.07	0.53
17:P:60:LEU:HD22	17:P:92:SER:HB3	1.89	0.53
21:T:50:GLU:O	21:T:50:GLU:HG2	2.08	0.53
6:E:21:ASP:OD2	6:E:24:THR:OG1	2.25	0.53
8:G:137:ARG:HB3	8:G:140:ARG:HG3	1.90	0.53
12:K:37:ASP:OD1	12:K:37:ASP:O	2.27	0.53
14:M:35:ILE:HD13	14:M:61:TYR:CE1	2.43	0.53
14:M:63:LYS:NZ	33:f:108:VAL:HG23	2.20	0.53
28:a:32:LYS:CE	28:a:37:LYS:HZ1	2.22	0.53
1:2:154:U:O2'	8:G:4:ASN:OD1	2.22	0.53
7:F:130:ARG:HH11	30:c:66:ARG:HB2	1.72	0.53
34:g:31:ILE:HD12	34:g:45:LEU:HD21	1.91	0.53
1:2:889:U:H5''	1:2:890:U:C6	2.44	0.53
1:2:1593:C:H1'	21:T:12:GLN:HE22	1.74	0.53
1:2:1610:G:H1'	20:S:108:ARG:HH12	1.74	0.53
21:T:124:THR:HG22	21:T:126:GLN:H	1.74	0.53
1:2:993:G:OP1	1:2:1131:G:N2	2.39	0.53
1:2:1758:G:H2'	1:2:1759:G:H8	1.72	0.53
1:2:1845:A:H2'	1:2:1846:G:H8	1.72	0.53
3:B:125:VAL:HB	3:B:127:VAL:HG13	1.91	0.53
15:N:83:ASP:N	15:N:83:ASP:OD1	2.41	0.53
18:Q:89:SER:HB3	18:Q:112:LEU:HD13	1.91	0.53
20:S:101:ASN:HA	20:S:105:ASN:HD21	1.72	0.53
31:d:22:ARG:HG2	31:d:38:MET:HG2	1.90	0.53
1:2:534:G:H2'	1:2:535:G:C8	2.43	0.53
1:2:1244:U:HO2'	1:2:1245:G:H8	1.54	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:156:THR:O	7:F:160:GLU:HG2	2.09	0.53
16:O:67:ASP:O	16:O:70:SER:OG	2.24	0.53
34:g:104:HIS:CE1	34:g:130:LYS:HG3	2.44	0.53
1:2:66:G:OP1	8:G:172:LYS:NZ	2.33	0.53
1:2:1860:A:H5''	28:a:8:ASN:HD22	1.73	0.53
9:H:169:LYS:O	9:H:172:THR:OG1	2.18	0.53
5:D:74:GLN:OE1	5:D:74:GLN:HA	2.09	0.53
1:2:1225:U:O2'	1:2:1226:G:H8	1.91	0.53
1:2:1243:U:C2'	1:2:1244:U:H5'	2.39	0.53
1:2:1388:A:H61	5:D:161:GLY:HA3	1.73	0.53
1:2:1844:U:P	35:h:11:ARG:HH12	2.31	0.53
5:D:221:THR:HG23	5:D:222:PRO:HD2	1.90	0.53
22:U:21:ARG:CG	22:U:90:ASP:OD1	2.45	0.53
33:f:81:LYS:HD2	33:f:83:LYS:NZ	2.18	0.53
1:2:379:C:O2	10:I:5:ARG:NE	2.39	0.52
12:K:16:PHE:HE2	12:K:89:ILE:HG22	1.74	0.52
36:n:174:PHE:CZ	36:n:187:LEU:HD21	2.44	0.52
1:2:687:C:H4'	9:H:121:THR:HG21	1.90	0.52
1:2:891:G:H3'	1:2:892:U:C6	2.44	0.52
1:2:897:U:H2'	1:2:898:U:H6	1.74	0.52
1:2:1293:A:N6	1:2:1305:C:H42	2.08	0.52
1:2:1667:U:H2'	1:2:1668:U:C6	2.44	0.52
20:S:80:PRO:HG2	21:T:36:THR:HG21	1.90	0.52
27:Z:57:LYS:HA	27:Z:61:GLU:OE1	2.09	0.52
1:2:72:C:N4	1:2:79:A:C8	2.76	0.52
1:2:685:A:H62	1:2:917:U:H3	1.57	0.52
1:2:1130:G:OP2	1:2:1130:G:N2	2.33	0.52
13:L:10:TYR:HE2	13:L:18:GLN:HE22	1.55	0.52
14:M:45:ARG:HH21	14:M:72:HIS:HA	1.74	0.52
34:g:269:GLU:OE1	34:g:269:GLU:HA	2.08	0.52
1:2:751:G:H2'	1:2:752:G:C8	2.45	0.52
1:2:1155:U:OP1	4:C:185:THR:OG1	2.24	0.52
1:2:1289:U:H2'	1:2:1290:G:O4'	2.10	0.52
1:2:1464:C:O2'	1:2:1465:A:OP1	2.24	0.52
15:N:20:ARG:HA	15:N:65:PHE:CE2	2.45	0.52
1:2:398:A:OP1	1:2:399:C:O2'	2.23	0.52
1:2:538:U:O2	1:2:546:G:H1'	2.08	0.52
1:2:631:U:H6	1:2:631:U:H5'	1.73	0.52
5:D:195:THR:HA	5:D:201:LYS:HE3	1.91	0.52
21:T:76:THR:HG22	21:T:94:ARG:HB3	1.90	0.52
30:c:43:ILE:HG22	30:c:65:ALA:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:144:U:OP2	1:2:144:U:H6	1.93	0.52
1:2:161:U:O2'	8:G:87:ARG:NH1	2.43	0.52
1:2:563:G:O2'	1:2:564:A:H8	1.92	0.52
2:A:143:PRO:HB3	23:V:34:MET:HE3	1.91	0.52
4:C:116:THR:HG22	4:C:117:ARG:H	1.75	0.52
11:J:95:ASP:OD1	11:J:96:TYR:N	2.43	0.52
1:2:544:G:H3'	1:2:545:A:C8	2.45	0.52
10:I:106:SER:HB3	10:I:171:LEU:HG	1.91	0.52
22:U:56:MET:HE3	22:U:88:LEU:HD12	1.91	0.52
1:2:1685:U:H2'	1:2:1686:G:O4'	2.09	0.52
34:g:32:LEU:HD22	34:g:71:ILE:HG12	1.92	0.52
1:2:5:U:OP2	4:C:230:THR:OG1	2.23	0.52
1:2:71:G:H22	1:2:73:C:H41	1.56	0.52
1:2:380:G:OP2	10:I:181:GLN:NE2	2.43	0.52
1:2:955:A:N1	1:2:968:U:O2'	2.37	0.52
1:2:1714:U:H2'	1:2:1715:A:C8	2.45	0.52
3:B:63:LYS:O	3:B:88:THR:OG1	2.27	0.52
14:M:121:LYS:HA	14:M:124:ILE:HD12	1.91	0.52
9:H:31:GLU:C	9:H:37:LYS:CG	2.80	0.52
23:V:64:GLU:HG3	29:b:3:LEU:HG	1.90	0.52
1:2:180:G:O2'	1:2:181:A:OP1	2.27	0.51
1:2:199:C:H5''	1:2:199:C:H6	1.73	0.51
1:2:551:U:H2'	1:2:552:G:C8	2.45	0.51
1:2:811:A:O2'	1:2:812:A:OP1	2.26	0.51
1:2:913:A:N6	9:H:119:SER:HB2	2.25	0.51
1:2:1589:A:H2'	1:2:1590:C:C6	2.44	0.51
1:2:1712:A:H2'	1:2:1713:C:C6	2.45	0.51
5:D:42:THR:HG23	5:D:45:ARG:HB2	1.92	0.51
8:G:132:ARG:HG3	8:G:133:LEU:HG	1.90	0.51
12:K:74:GLU:CD	12:K:74:GLU:H	2.19	0.51
15:N:88:LEU:O	15:N:92:ILE:HG12	2.09	0.51
1:2:433:A:H5''	10:I:22:HIS:HB3	1.92	0.51
1:2:434:G:OP2	10:I:25:ARG:NH2	2.43	0.51
1:2:955:A:N3	1:2:956:G:H1'	2.25	0.51
1:2:1586:U:O2	1:2:1586:U:H5''	2.10	0.51
3:B:136:ARG:HB2	3:B:218:LEU:HD11	1.92	0.51
6:E:165:GLU:OE2	6:E:165:GLU:N	2.43	0.51
20:S:60:THR:OG1	20:S:63:GLU:HG3	2.11	0.51
1:2:115:U:H2'	1:2:116:U:C6	2.45	0.51
1:2:591:U:H5''	1:2:591:U:C6	2.42	0.51
1:2:878:G:H3'	1:2:879:C:H5''	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:65:GLU:O	20:S:69:THR:HG23	2.09	0.51
1:2:1719:A:H3'	1:2:1720:U:H5''	1.91	0.51
14:M:42:LEU:HD13	14:M:68:LEU:HB3	1.91	0.51
32:e:51:LYS:HZ1	36:n:168:PRO:HD3	1.75	0.51
1:2:189:U:H5''	1:2:189:U:H6	1.75	0.51
1:2:533:A:H61	1:2:551:U:H3	1.58	0.51
1:2:883:U:H2'	1:2:884:C:H6	1.74	0.51
1:2:1256:G:O6	22:U:65:THR:HG22	2.09	0.51
1:2:1865:C:H1'	28:a:7:ASN:HD21	1.75	0.51
15:N:31:ASP:O	15:N:35:GLU:HG2	2.11	0.51
1:2:952:G:H2'	1:2:953:C:C6	2.46	0.51
1:2:1172:U:H2'	1:2:1173:A:H8	1.76	0.51
3:B:228:LEU:HD12	3:B:232:HIS:HE1	1.69	0.51
4:C:189:GLY:O	4:C:190:SER:OG	2.24	0.51
11:J:160:SER:O	11:J:162:ARG:N	2.43	0.51
17:P:93:MET:HE1	17:P:104:GLN:CD	2.36	0.51
1:2:377:G:H5''	10:I:98:LYS:HB3	1.92	0.51
6:E:95:THR:CG2	26:Y:17:LEU:HD13	2.39	0.51
11:J:29:LEU:HD23	32:e:42:PHE:CE2	2.45	0.51
33:f:109:ASP:C	33:f:111:ASN:N	2.69	0.51
1:2:1365:G:H2'	1:2:1366:G:H8	1.76	0.51
1:2:1552:G:OP1	1:2:1578:U:H5	1.94	0.51
4:C:165:VAL:HG21	4:C:217:ALA:HB1	1.92	0.51
9:H:147:LYS:HA	9:H:147:LYS:HE2	1.92	0.51
28:a:73:TYR:CB	28:a:78:VAL:HG22	2.40	0.51
1:2:885:U:H3	1:2:901:G:H1	1.58	0.51
1:2:895:G:H2'	1:2:896:U:C6	2.45	0.51
1:2:1229:G:H21	21:T:87:VAL:CG2	2.24	0.51
1:2:1721:U:H4'	1:2:1722:G:O5'	2.10	0.51
5:D:142:LEU:HD12	5:D:148:LYS:HG3	1.91	0.51
12:K:86:PRO:HG2	12:K:89:ILE:HG12	1.93	0.51
13:L:111:VAL:HG12	13:L:140:PHE:HB2	1.92	0.51
14:M:24:THR:HG22	14:M:113:ASP:OD1	2.11	0.51
15:N:136:PRO:HG2	15:N:139:TRP:HB2	1.93	0.51
18:Q:53:GLU:OE2	18:Q:85:ARG:NH2	2.41	0.51
26:Y:63:HIS:ND1	26:Y:68:LYS:CD	2.73	0.51
34:g:110:SER:HB3	34:g:154:VAL:HG22	1.93	0.51
1:2:223:C:H2'	1:2:224:A:C8	2.46	0.51
11:J:30:LYS:HE3	32:e:42:PHE:CE1	2.46	0.51
19:R:77:GLU:O	19:R:81:ARG:HG3	2.11	0.51
33:f:109:ASP:CG	33:f:113:LYS:HB2	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:50:ILE:HD11	5:D:86:LEU:HD23	1.93	0.50
10:I:88:ASN:OD1	10:I:205:ARG:NE	2.42	0.50
14:M:87:GLU:OE2	14:M:99:LYS:HG3	2.11	0.50
16:O:98:ARG:HG3	16:O:99:ALA:O	2.11	0.50
29:b:80:ARG:HH21	29:b:82:LYS:HA	1.76	0.50
1:2:17:C:O2'	1:2:1194:A:N1	2.34	0.50
1:2:1342:U:H4'	1:2:1343:U:O5'	2.11	0.50
1:2:1628:C:H2'	1:2:1629:C:C6	2.46	0.50
1:2:1715:A:H2'	1:2:1716:C:H6	1.76	0.50
1:2:1545:A:H2'	1:2:1546:G:C8	2.47	0.50
6:E:95:THR:HG21	26:Y:17:LEU:HD13	1.92	0.50
7:F:168:THR:OG1	7:F:171:GLU:OE1	2.27	0.50
9:H:30:LEU:HD11	9:H:82:GLU:HB3	1.93	0.50
14:M:112:LYS:HD3	14:M:121:LYS:HB2	1.92	0.50
19:R:75:GLU:OE2	19:R:78:ARG:NH1	2.44	0.50
21:T:8:ASP:OD1	21:T:8:ASP:N	2.44	0.50
1:2:1354:G:N2	1:2:1357:A:OP2	2.43	0.50
1:2:1374:C:H2'	1:2:1375:G:O4'	2.11	0.50
1:2:1598:G:H4'	1:2:1600:G:N1	2.25	0.50
5:D:221:THR:CG2	5:D:222:PRO:HD2	2.42	0.50
13:L:27:GLU:O	13:L:27:GLU:HG2	2.11	0.50
20:S:13:LEU:HD23	20:S:20:ILE:HD11	1.94	0.50
1:2:74:G:C2'	1:2:75:G:H5'	2.41	0.50
1:2:987:A:C6	3:B:120:MET:HE1	2.46	0.50
1:2:1711:U:H2'	1:2:1712:A:C8	2.47	0.50
1:2:1711:U:H2'	1:2:1712:A:H8	1.75	0.50
2:A:137:ALA:HB1	2:A:142:LEU:HB3	1.94	0.50
6:E:100:ARG:HG2	6:E:102:ILE:HG12	1.93	0.50
9:H:112:ASN:OD1	9:H:112:ASN:N	2.45	0.50
14:M:36:ARG:O	14:M:37:GLU:HG2	2.11	0.50
23:V:81:LYS:HA	23:V:81:LYS:HE2	1.92	0.50
29:b:45:THR:OG1	29:b:82:LYS:NZ	2.45	0.50
1:2:382:C:H2'	1:2:383:G:C8	2.46	0.50
1:2:465:A:H4'	1:2:466:G:O5'	2.11	0.50
1:2:1600:G:H3'	27:Z:43:LYS:HZ2	1.77	0.50
34:g:302:TYR:HE1	34:g:308:ARG:HB2	1.76	0.50
1:2:547:G:O5'	1:2:548:C:H5	1.94	0.50
1:2:1797:U:H2'	1:2:1798:C:C6	2.46	0.50
23:V:64:GLU:O	23:V:68:SER:OG	2.26	0.50
30:c:10:LYS:HD2	30:c:34:PHE:CD2	2.47	0.50
1:2:527:C:H2'	1:2:528:A:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:628:A:N6	5:D:144:GLY:H	2.10	0.50
1:2:1332:A:O2'	5:D:145:GLN:O	2.30	0.50
1:2:1633:A:H2'	1:2:1634:A:C8	2.46	0.50
10:I:155:ASN:OD1	10:I:155:ASN:N	2.44	0.50
20:S:59:LEU:CD1	20:S:64:VAL:HG11	2.31	0.50
1:2:750:C:O2'	1:2:751:G:OP1	2.28	0.50
1:2:799:U:H2'	1:2:800:U:C6	2.47	0.50
12:K:49:MET:HE2	12:K:49:MET:HA	1.94	0.50
1:2:51:U:H2'	1:2:52:G:C8	2.47	0.49
1:2:1306:U:H2'	1:2:1307:U:O4'	2.12	0.49
1:2:1856:C:H2'	1:2:1857:G:C8	2.47	0.49
2:A:118:GLU:HB2	4:C:65:LYS:HD2	1.94	0.49
3:B:147:ASN:OD1	3:B:148:ASN:N	2.45	0.49
6:E:15:PRO:HG2	6:E:18:TRP:CE2	2.46	0.49
6:E:95:THR:CG2	26:Y:17:LEU:HD11	2.15	0.49
1:2:1269:G:O5'	33:f:86:THR:HG21	2.12	0.49
1:2:1598:G:OP1	20:S:55:ARG:NH2	2.44	0.49
1:2:1752:C:H2'	1:2:1753:C:C6	2.47	0.49
1:2:1774:C:H1'	1:2:1775:U:O4'	2.12	0.49
7:F:27:ASP:OD1	7:F:27:ASP:N	2.43	0.49
11:J:69:ARG:HG2	11:J:73:GLU:OE2	2.12	0.49
8:G:170:ARG:HG2	8:G:171:THR:H	1.78	0.49
8:G:215:LYS:O	8:G:219:GLU:HG2	2.12	0.49
11:J:18:ARG:O	11:J:24:ARG:NH1	2.45	0.49
18:Q:43:GLU:N	18:Q:43:GLU:OE1	2.45	0.49
30:c:18:LEU:HB2	30:c:29:GLN:O	2.13	0.49
1:2:889:U:H2'	1:2:890:U:N3	2.26	0.49
9:H:28:LEU:O	9:H:32:MET:HG3	2.11	0.49
11:J:42:GLU:HG2	11:J:45:ARG:NH2	2.28	0.49
14:M:52:LEU:HD23	14:M:78:LYS:HD2	1.94	0.49
1:2:920:A:O5'	24:W:57:ARG:HG2	2.12	0.49
1:2:963:A:H2'	1:2:964:A:C8	2.48	0.49
1:2:1296:U:O2'	1:2:1299:A:H2	1.95	0.49
2:A:52:LYS:HB2	19:R:109:LEU:HD22	1.95	0.49
6:E:95:THR:HG23	26:Y:17:LEU:HD12	1.87	0.49
14:M:102:LYS:HZ1	14:M:105:GLY:HA3	1.76	0.49
1:2:538:U:H2'	1:2:539:C:C6	2.48	0.49
1:2:931:C:H2'	1:2:932:G:C8	2.48	0.49
1:2:1143:A:H5'	4:C:190:SER:HB3	1.93	0.49
1:2:1521:C:H5'	17:P:126:VAL:HB	1.93	0.49
5:D:209:SER:OG	19:R:40:ILE:HB	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:57:ALA:O	11:J:61:LEU:HD23	2.13	0.49
33:f:109:ASP:CB	33:f:113:LYS:HB2	2.42	0.49
1:2:74:G:O2'	1:2:75:G:H5'	2.12	0.49
2:A:80:ARG:NH1	2:A:126:ASP:OD2	2.46	0.49
2:A:198:MET:HE2	19:R:85:VAL:HG13	1.95	0.49
10:I:11:ARG:O	13:L:136:LYS:NZ	2.43	0.49
33:f:119:ARG:HD2	33:f:132:MET:HE3	1.93	0.49
1:2:1214:A:H2'	1:2:1217:A:N7	2.28	0.49
1:2:1567:G:N3	1:2:1567:G:H5''	2.26	0.49
16:O:98:ARG:HD2	16:O:134:PRO:HD3	1.94	0.49
20:S:86:ARG:CZ	20:S:107:LEU:HD12	2.42	0.49
1:2:561:A:OP1	11:J:174:LYS:HD3	2.12	0.49
1:2:1660:C:H6	1:2:1660:C:O5'	1.96	0.49
5:D:137:VAL:HG22	5:D:151:LYS:HG3	1.94	0.49
22:U:19:ARG:HG3	22:U:19:ARG:HH11	1.78	0.49
1:2:929:G:H2'	1:2:930:C:O4'	2.13	0.49
1:2:1856:C:H2'	1:2:1857:G:H8	1.78	0.49
7:F:124:ASP:HA	7:F:200:ALA:HB2	1.94	0.49
21:T:49:ASP:O	21:T:50:GLU:HB3	2.13	0.49
1:2:396:U:OP2	13:L:79:LYS:NZ	2.46	0.48
11:J:29:LEU:HD21	32:e:41:ARG:HD2	1.95	0.48
20:S:27:ALA:HB2	20:S:45:LEU:HD12	1.95	0.48
1:2:1010:G:H2'	1:2:1011:A:H8	1.79	0.48
1:2:4:C:H4'	4:C:207:ALA:HB2	1.95	0.48
1:2:12:U:H2'	1:2:13:C:C6	2.48	0.48
1:2:71:G:C5	8:G:170:ARG:NH1	2.82	0.48
1:2:1395:C:O2'	1:2:1396:A:H5'	2.14	0.48
3:B:33:VAL:HA	3:B:96:CYS:HB2	1.95	0.48
6:E:122:LYS:HD2	6:E:164:LEU:HD21	1.95	0.48
14:M:48:HIS:CD2	14:M:110:VAL:H	2.31	0.48
21:T:10:ASN:H	21:T:143:LYS:HE3	1.78	0.48
25:X:6:GLY:O	25:X:9:THR:OG1	2.29	0.48
34:g:223:GLU:OE2	34:g:225:LYS:HG2	2.12	0.48
21:T:60:THR:HG23	21:T:75:MET:SD	2.52	0.48
1:2:198:U:H3'	1:2:199:C:H5'	1.94	0.48
1:2:384:U:O4	10:I:5:ARG:NH2	2.33	0.48
1:2:547:G:P	1:2:547:G:H3'	2.53	0.48
1:2:656:G:H5'	1:2:662:G:N2	2.29	0.48
1:2:996:A:H2'	1:2:997:A:C8	2.49	0.48
1:2:1677:U:OP1	7:F:71:ARG:NH2	2.46	0.48
2:A:149:ASN:ND2	2:A:165:ASN:OD1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:139:CYS:HB3	3:B:168:MET:HE3	1.96	0.48
9:H:126:HIS:CE1	9:H:181:THR:HG23	2.48	0.48
24:W:6:VAL:HG13	24:W:29:PRO:HG2	1.96	0.48
1:2:455:A:H2'	1:2:456:C:C6	2.48	0.48
1:2:527:C:H4'	11:J:121:LYS:HE3	1.96	0.48
1:2:823:U:C5	11:J:143:ASN:HB3	2.44	0.48
1:2:881:G:N3	1:2:881:G:H2'	2.28	0.48
1:2:1086:G:O2'	1:2:1088:U:OP2	2.29	0.48
1:2:1098:C:H2'	1:2:1099:G:C8	2.48	0.48
1:2:1204:A:O2'	1:2:1700:C:OP2	2.31	0.48
1:2:1226:G:N1	1:2:1639:G:OP2	2.43	0.48
1:2:1247:C:H6	1:2:1247:C:OP1	1.96	0.48
1:2:1757:G:N1	1:2:1776:G:C8	2.81	0.48
3:B:180:ASP:OD1	3:B:180:ASP:N	2.36	0.48
14:M:63:LYS:CE	33:f:108:VAL:CG2	2.91	0.48
7:F:58:ALA:HB3	7:F:62:ARG:NH2	2.29	0.48
14:M:96:ARG:HG2	14:M:96:ARG:O	2.13	0.48
25:X:66:ILE:HD12	32:e:4:GLY:HA3	1.94	0.48
1:2:857:U:H2'	1:2:858:A:C8	2.48	0.48
1:2:1174:U:H2'	1:2:1175:G:C8	2.47	0.48
1:2:1491:G:H2'	1:2:1492:U:C6	2.48	0.48
3:B:88:THR:HG23	3:B:98:THR:HG22	1.92	0.48
3:B:232:HIS:O	3:B:233:GLY:C	2.56	0.48
6:E:105:THR:HG21	6:E:245:ARG:HA	1.96	0.48
12:K:84:HIS:CG	14:M:27:ILE:HG23	2.48	0.48
13:L:99:TYR:O	13:L:101:ARG:HG3	2.13	0.48
21:T:69:GLY:HA2	21:T:116:ASP:OD2	2.13	0.48
27:Z:56:ASP:C	27:Z:58:LEU:H	2.21	0.48
28:a:32:LYS:HE3	28:a:37:LYS:HZ1	1.78	0.48
34:g:115:SER:C	34:g:117:ASN:H	2.20	0.48
1:2:71:G:C3'	1:2:72:C:H5''	2.40	0.48
2:A:5:LEU:HD13	23:V:41:LYS:HA	1.94	0.48
5:D:193:ASP:OD2	5:D:197:LYS:N	2.47	0.48
14:M:44:LYS:HG2	14:M:46:GLN:HG3	1.96	0.48
1:2:750:C:H2'	1:2:751:G:C8	2.49	0.48
1:2:882:U:H2'	1:2:883:U:H6	1.79	0.48
1:2:1266:C:O2	1:2:1266:C:O4'	2.32	0.48
25:X:139:GLU:HA	25:X:139:GLU:OE2	2.14	0.48
34:g:199:THR:HG21	34:g:240:CYS:HA	1.96	0.48
1:2:71:G:N2	1:2:73:C:H41	2.11	0.47
1:2:113:G:O6	1:2:290:U:H1'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:165:G:OP2	1:2:165:G:N2	2.37	0.47
1:2:1736:G:H2'	1:2:1737:G:C8	2.49	0.47
1:2:1776:G:H2'	1:2:1777:G:O4'	2.13	0.47
1:2:197:U:H3	1:2:202:G:H1	1.62	0.47
1:2:293:C:O2	1:2:293:C:H2'	2.15	0.47
1:2:544:G:H3'	1:2:545:A:H8	1.78	0.47
1:2:1239:U:H5''	17:P:124:LYS:HD2	1.95	0.47
1:2:1713:C:H2'	1:2:1714:U:C6	2.48	0.47
1:2:1723:G:H2'	1:2:1724:A:C8	2.50	0.47
13:L:76:VAL:HG12	13:L:125:ILE:HD13	1.96	0.47
21:T:116:ASP:OD1	21:T:119:GLY:N	2.47	0.47
24:W:41:MET:HE2	24:W:47:ILE:HB	1.96	0.47
32:e:53:LYS:HA	32:e:53:LYS:HD3	1.65	0.47
1:2:201:C:H2'	1:2:202:G:O4'	2.15	0.47
1:2:581:U:H4'	26:Y:66:GLY:HA2	1.97	0.47
1:2:1021:U:H4'	1:2:1022:U:O4'	2.15	0.47
1:2:1067:C:H2'	1:2:1068:G:O4'	2.13	0.47
4:C:103:LYS:O	4:C:130:ILE:HG13	2.14	0.47
5:D:170:THR:HG23	5:D:187:LYS:HG2	1.95	0.47
14:M:122:ASP:O	14:M:125:GLU:HG2	2.13	0.47
26:Y:13:MET:HG2	26:Y:22:GLN:HG2	1.97	0.47
1:2:122:G:H21	6:E:146:THR:HG21	1.79	0.47
1:2:180:G:H2'	1:2:181:A:C8	2.49	0.47
1:2:1798:C:H2'	1:2:1799:G:O4'	2.14	0.47
12:K:84:HIS:CD2	14:M:27:ILE:HG23	2.50	0.47
23:V:40:ASP:OD1	23:V:41:LYS:N	2.47	0.47
29:b:13:GLU:OE2	29:b:13:GLU:N	2.35	0.47
1:2:1083:A:N7	1:2:1841:C:O2'	2.38	0.47
1:2:1726:G:H1	1:2:1808:U:H3	1.62	0.47
3:B:29:ASP:OD2	3:B:94:LYS:NZ	2.35	0.47
8:G:63:MET:HG2	8:G:99:GLY:O	2.14	0.47
9:H:29:GLU:OE1	9:H:86:LYS:NZ	2.47	0.47
19:R:58:MET:HE2	19:R:58:MET:HA	1.96	0.47
20:S:51:ASP:HB3	20:S:54:LYS:HE3	1.97	0.47
26:Y:63:HIS:CE1	26:Y:68:LYS:CG	2.96	0.47
1:2:554:A:H2'	1:2:556:U:C6	2.50	0.47
1:2:896:U:H2'	1:2:897:U:C5	2.49	0.47
1:2:1365:G:H2'	1:2:1366:G:C8	2.49	0.47
1:2:1548:G:H4'	1:2:1549:U:OP1	2.14	0.47
1:2:1722:G:H2'	1:2:1723:G:C8	2.50	0.47
3:B:92:GLN:HG2	3:B:97:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:60:A:O2'	1:2:61:A:OP1	2.25	0.47
1:2:1172:U:H2'	1:2:1173:A:C8	2.50	0.47
1:2:1275:G:O4'	1:2:1506:A:N6	2.48	0.47
1:2:1865:C:H5	28:a:6:ARG:H	1.59	0.47
2:A:163:CYS:CB	2:A:174:MET:HE2	2.45	0.47
3:B:79:VAL:HG12	3:B:81:PHE:CD2	2.48	0.47
4:C:121:ARG:NH2	4:C:123:ARG:HH11	2.12	0.47
5:D:154:ASP:OD1	5:D:155:GLY:N	2.48	0.47
6:E:19:MET:SD	6:E:108:ARG:HD2	2.55	0.47
12:K:1:MET:HG2	12:K:2:LEU:N	2.30	0.47
17:P:103:ASN:HB2	17:P:120:SER:OG	2.15	0.47
22:U:56:MET:HB2	22:U:86:LYS:HB3	1.97	0.47
27:Z:68:ILE:HB	27:Z:109:TYR:HB2	1.96	0.47
34:g:8:ARG:HG3	34:g:311:GLN:HB2	1.97	0.47
1:2:107:A:H2'	1:2:108:G:H8	1.78	0.47
1:2:145:G:H2'	1:2:146:G:H8	1.79	0.47
1:2:197:U:H3'	1:2:198:U:H6	1.80	0.47
1:2:1013:U:OP1	1:2:1129:G:O2'	2.32	0.47
1:2:1144:A:H2'	1:2:1145:A:C8	2.49	0.47
1:2:1464:C:HO2'	1:2:1465:A:P	2.38	0.47
1:2:1688:C:H5''	1:2:1688:C:H6	1.79	0.47
9:H:65:PRO:HG2	9:H:68:GLN:HB2	1.96	0.47
13:L:59:LYS:HG2	13:L:134:LEU:HD22	1.97	0.47
1:2:200:G:H2'	1:2:201:C:O4'	2.14	0.47
1:2:533:A:N6	1:2:551:U:H3	2.13	0.47
1:2:1278:A:H2'	1:2:1279:C:C6	2.50	0.47
9:H:146:VAL:CG2	9:H:152:ARG:NH1	2.78	0.47
11:J:34:GLU:HG3	11:J:35:TYR:CD2	2.49	0.47
28:a:26:CYS:SG	28:a:28:ARG:HB2	2.55	0.47
34:g:17:TRP:HB2	34:g:36:ARG:HD3	1.96	0.47
34:g:299:PHE:CD1	34:g:309:VAL:CG2	2.86	0.47
1:2:76:U:OP1	8:G:159:ARG:NH2	2.48	0.47
1:2:1138:C:H2'	2:A:155:ARG:HH12	1.79	0.47
1:2:1587:G:O6	21:T:67:ARG:HD2	2.14	0.47
1:2:593:C:H5''	1:2:594:A:OP2	2.15	0.46
1:2:1479:G:N2	31:d:56:ASP:OD1	2.48	0.46
1:2:1548:G:O2'	1:2:1549:U:H5'	2.15	0.46
5:D:215:ASP:N	5:D:215:ASP:OD1	2.39	0.46
7:F:130:ARG:NH1	30:c:66:ARG:HB2	2.30	0.46
9:H:160:LYS:O	9:H:161:ALA:C	2.58	0.46
20:S:36:VAL:HG13	20:S:40:TYR:HD2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:c:60:GLU:CD	30:c:62:GLU:H	2.23	0.46
34:g:162:ASN:O	34:g:164:ILE:HD13	2.16	0.46
3:B:136:ARG:HB3	3:B:216:LYS:HG3	1.98	0.46
5:D:67:ARG:NH2	12:K:97:SER:HB3	2.29	0.46
5:D:142:LEU:O	5:D:143:ARG:NH1	2.44	0.46
26:Y:86:GLU:OE1	26:Y:90:ARG:HD2	2.14	0.46
1:2:73:C:OP2	1:2:73:C:H3'	2.16	0.46
1:2:292:A:H4'	13:L:39:ASN:O	2.15	0.46
1:2:1005:G:OP2	3:B:162:ARG:NH2	2.46	0.46
1:2:1290:G:H22	1:2:1308:U:H3	1.63	0.46
1:2:1863:A:H1'	28:a:79:ILE:HD13	1.97	0.46
4:C:236:PHE:O	4:C:240:THR:HG22	2.14	0.46
8:G:129:VAL:HG12	8:G:131:ARG:H	1.81	0.46
9:H:130:LEU:HD21	9:H:156:VAL:HG21	1.97	0.46
10:I:48:VAL:HG11	10:I:54:LYS:HD2	1.97	0.46
14:M:91:LEU:HD13	14:M:100:PRO:HG2	1.97	0.46
17:P:85:ILE:HG22	17:P:89:MET:HG3	1.97	0.46
1:2:500:A:H3'	1:2:501:C:C5	2.51	0.46
5:D:59:LEU:HD23	5:D:66:ILE:HD13	1.97	0.46
20:S:108:ARG:HA	20:S:108:ARG:HD3	1.67	0.46
1:2:54:A:OP1	26:Y:111:LYS:NZ	2.42	0.46
1:2:536:A:H61	1:2:548:C:N4	2.13	0.46
1:2:554:A:H2'	1:2:556:U:C5	2.51	0.46
1:2:801:U:O4	9:H:106:ARG:NH2	2.48	0.46
1:2:1244:U:H5	1:2:1255:G:H1	1.62	0.46
1:2:1285:G:O6	14:M:36:ARG:HB2	2.16	0.46
1:2:1514:G:H8	17:P:79:HIS:HE1	1.61	0.46
1:2:1706:G:H2'	1:2:1707:U:H6	1.79	0.46
1:2:1825:A:H2'	1:2:1825:A:N3	2.29	0.46
10:I:101:ILE:HD12	10:I:190:LEU:HD11	1.98	0.46
10:I:170:LYS:HE2	10:I:170:LYS:HB2	1.77	0.46
13:L:118:ARG:HG3	13:L:118:ARG:HH11	1.80	0.46
17:P:41:GLN:HG2	17:P:83:MET:SD	2.56	0.46
19:R:37:GLU:OE1	34:g:150:TRP:NE1	2.48	0.46
19:R:77:GLU:OE1	19:R:80:ARG:NH2	2.40	0.46
20:S:101:ASN:HA	20:S:105:ASN:ND2	2.31	0.46
1:2:530:U:H3'	1:2:531:A:H8	1.79	0.46
1:2:816:A:P	11:J:10:ARG:HH22	2.36	0.46
1:2:880:G:H5'	1:2:881:G:OP2	2.16	0.46
1:2:1517:G:H2'	1:2:1518:C:O4'	2.15	0.46
1:2:1782:G:H5''	1:2:1783:C:OP2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:212:LYS:HE2	2:A:212:LYS:HB2	1.59	0.46
9:H:170:VAL:O	9:H:171:GLU:HB3	2.16	0.46
1:2:165:G:H4'	8:G:53:SER:OG	2.15	0.46
1:2:545:A:H3'	1:2:546:G:C8	2.50	0.46
1:2:875:A:O4'	9:H:114:GLN:NE2	2.49	0.46
1:2:990:A:O5'	3:B:116:LYS:NZ	2.44	0.46
1:2:1278:A:H2'	1:2:1279:C:H6	1.81	0.46
3:B:142:PHE:O	3:B:208:HIS:N	2.43	0.46
6:E:31:PRO:HG3	6:E:43:PRO:HG3	1.98	0.46
9:H:130:LEU:O	9:H:134:VAL:HG22	2.16	0.46
13:L:128:VAL:HG12	13:L:142:VAL:HA	1.98	0.46
14:M:60:MET:HE1	33:f:108:VAL:CG2	2.46	0.46
34:g:20:GLN:HG3	34:g:68:ASP:HA	1.97	0.46
34:g:174:VAL:HB	34:g:188:HIS:HB2	1.97	0.46
1:2:1269:G:C5'	33:f:86:THR:HG21	2.46	0.46
1:2:1541:G:H21	21:T:12:GLN:NE2	2.14	0.46
1:2:1607:A:H1'	1:2:1633:A:C2	2.51	0.46
3:B:83:LYS:HB2	3:B:83:LYS:HE2	1.70	0.46
3:B:100:PHE:HB3	3:B:181:LEU:HD21	1.98	0.46
5:D:7:LYS:HA	5:D:7:LYS:HD3	1.67	0.46
5:D:116:ARG:HG2	5:D:150:MET:CE	2.45	0.46
6:E:97:GLU:HG3	6:E:99:PHE:CZ	2.51	0.46
9:H:181:THR:HG22	9:H:183:LYS:HG3	1.97	0.46
18:Q:41:MET:HE1	21:T:10:ASN:HA	1.98	0.46
18:Q:93:VAL:HG13	18:Q:105:LYS:HD3	1.98	0.46
27:Z:74:SER:OG	27:Z:79:ILE:O	2.27	0.46
1:2:15:U:H2'	1:2:16:G:O4'	2.15	0.46
1:2:70:G:N1	1:2:71:G:N7	2.64	0.46
1:2:158:A:H2'	1:2:159:A:O4'	2.15	0.46
1:2:1462:U:H3'	1:2:1463:U:H6	1.81	0.46
1:2:1485:U:H2'	1:2:1486:A:O4'	2.16	0.46
1:2:1650:A:H2'	1:2:1651:A:O4'	2.15	0.46
11:J:79:ARG:HG3	11:J:80:ARG:N	2.31	0.46
14:M:52:LEU:HD22	14:M:66:GLU:OE1	2.16	0.46
18:Q:62:ARG:NH1	18:Q:107:GLU:OE2	2.49	0.46
33:f:137:ASP:O	33:f:138:ARG:HG2	2.15	0.46
1:2:650:A:OP2	25:X:108:LYS:HD2	2.15	0.46
1:2:1231:C:OP2	20:S:139:THR:HG21	2.16	0.46
1:2:1261:C:O2	1:2:1261:C:O4'	2.32	0.46
1:2:1465:A:OP2	19:R:56:HIS:NE2	2.48	0.46
1:2:1754:G:C5	1:2:1755:C:C5	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1823:A:C4	1:2:1824:A:H1'	2.50	0.46
11:J:170:PRO:HB3	11:J:174:LYS:HE2	1.97	0.46
18:Q:44:PRO:C	18:Q:46:THR:H	2.23	0.46
23:V:58:ALA:O	23:V:62:MET:HG3	2.16	0.46
33:f:80:ARG:HH21	33:f:82:LYS:HA	1.79	0.46
1:2:71:G:H1'	1:2:72:C:C5	2.51	0.45
1:2:867:G:H2'	1:2:868:G:C8	2.51	0.45
1:2:921:G:OP2	29:b:21:LYS:NZ	2.45	0.45
1:2:1608:U:H2'	1:2:1609:C:C6	2.51	0.45
3:B:65:ARG:HH22	16:O:51:GLU:HG2	1.81	0.45
4:C:134:ASN:HA	4:C:167:ARG:HH12	1.80	0.45
7:F:22:LYS:HB2	7:F:22:LYS:HE3	1.56	0.45
1:2:385:G:H3'	13:L:136:LYS:HB2	1.97	0.45
1:2:563:G:N7	11:J:172:ARG:NH2	2.63	0.45
1:2:1736:G:H2'	1:2:1737:G:H8	1.81	0.45
17:P:17:TYR:HB3	17:P:25:LEU:HD11	1.96	0.45
17:P:51:ARG:HG3	17:P:52:LYS:N	2.28	0.45
1:2:441:C:H2'	1:2:442:C:C6	2.52	0.45
1:2:1287:A:N1	1:2:1311:C:N3	2.65	0.45
1:2:1568:C:H2'	1:2:1569:A:C8	2.51	0.45
1:2:1839:U:H2'	1:2:1840:U:C6	2.51	0.45
8:G:119:LYS:HE2	8:G:119:LYS:HB2	1.78	0.45
14:M:54:SER:N	14:M:79:VAL:O	2.48	0.45
17:P:93:MET:HE3	17:P:93:MET:HB3	1.60	0.45
1:2:379:C:H5'	10:I:33:ALA:HA	1.98	0.45
1:2:639:C:HO2'	1:2:640:A:H8	1.62	0.45
1:2:897:U:H2'	1:2:898:U:C6	2.52	0.45
1:2:1242:U:H1'	1:2:1517:G:O2'	2.17	0.45
1:2:1846:G:O6	35:h:8:LYS:NZ	2.48	0.45
5:D:116:ARG:HD3	36:n:172:ASP:O	2.17	0.45
5:D:140:GLY:HA3	5:D:182:LEU:HD23	1.96	0.45
5:D:195:THR:H	5:D:201:LYS:HG3	1.81	0.45
14:M:83:LYS:HB3	14:M:99:LYS:HD3	1.97	0.45
16:O:38:ASN:O	16:O:68:GLU:HB3	2.16	0.45
1:2:156:G:OP1	8:G:2:LYS:NZ	2.39	0.45
1:2:688:U:H2'	9:H:103:LYS:HD2	1.98	0.45
1:2:1173:A:OP1	35:h:17:ARG:NH1	2.50	0.45
4:C:187:ARG:HH22	4:C:190:SER:HA	1.82	0.45
9:H:164:ASN:HA	9:H:167:GLU:HB2	1.98	0.45
10:I:163:GLU:O	10:I:167:GLN:HG2	2.17	0.45
21:T:24:LYS:HE3	21:T:24:LYS:HB3	1.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:107:GLU:HG3	22:U:108:PRO:HD2	1.97	0.45
1:2:1265:A:H8	1:2:1266:C:O2	2.00	0.45
1:2:1523:C:C2	20:S:141:ARG:NH2	2.84	0.45
3:B:124:HIS:HA	3:B:137:LEU:O	2.17	0.45
9:H:40:LEU:HD21	9:H:79:LEU:HD21	1.99	0.45
20:S:46:ARG:CZ	20:S:52:LEU:CD1	2.95	0.45
1:2:1648:G:O2'	1:2:1674:G:O6	2.29	0.45
1:2:1668:U:OP2	18:Q:141:TYR:OH	2.30	0.45
1:2:1865:C:C2	28:a:5:ARG:HG2	2.52	0.45
2:A:163:CYS:SG	2:A:174:MET:HE2	2.56	0.45
7:F:30:ILE:HG22	7:F:32:ASP:H	1.82	0.45
7:F:88:MET:O	7:F:92:ILE:HG13	2.17	0.45
7:F:141:VAL:HG13	7:F:145:ARG:HG2	1.99	0.45
17:P:51:ARG:O	17:P:52:LYS:HG2	2.16	0.45
1:2:532:C:H2'	1:2:533:A:C8	2.52	0.45
1:2:1241:A:H2	1:2:1516:G:H2'	1.81	0.45
1:2:1487:A:H4'	4:C:118:ALA:HB1	1.99	0.45
1:2:1863:A:OP2	28:a:4:LYS:NZ	2.45	0.45
2:A:75:SER:OG	2:A:119:PRO:HB3	2.17	0.45
5:D:70:THR:HG23	5:D:86:LEU:HD13	1.98	0.45
6:E:62:LYS:O	6:E:66:MET:HG2	2.17	0.45
24:W:27:ILE:HG12	24:W:28:ARG:N	2.28	0.45
28:a:32:LYS:CG	28:a:37:LYS:HZ1	2.30	0.45
1:2:606:G:H1'	32:e:58:ASN:ND2	2.32	0.45
3:B:127:VAL:HG23	3:B:176:VAL:HG11	1.99	0.45
11:J:95:ASP:OD1	11:J:95:ASP:C	2.60	0.45
1:2:370:G:O2'	10:I:10:LYS:NZ	2.46	0.45
1:2:919:A:OP2	15:N:64:ARG:NH2	2.45	0.45
1:2:1213:C:H2'	1:2:1214:A:C8	2.52	0.45
3:B:106:THR:HG23	3:B:109:LYS:H	1.82	0.45
1:2:500:A:O2'	1:2:501:C:H5'	2.17	0.44
1:2:604:A:H2'	1:2:605:A:C8	2.52	0.44
1:2:892:U:H3'	1:2:893:U:C6	2.46	0.44
1:2:1261:C:H3'	1:2:1262:C:O2	2.16	0.44
1:2:1269:G:H5'	33:f:86:THR:HG21	1.99	0.44
1:2:1722:G:H2'	1:2:1723:G:H8	1.82	0.44
1:2:1808:U:H2'	1:2:1809:A:H8	1.80	0.44
2:A:31:ASP:OD1	2:A:33:GLN:N	2.37	0.44
3:B:121:ILE:HG21	3:B:164:ILE:HG22	1.98	0.44
5:D:218:LEU:HD13	34:g:192:THR:HG23	1.98	0.44
9:H:53:VAL:HG11	9:H:172:THR:HA	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:18:GLN:HB3	13:L:33:LEU:HD11	1.99	0.44
34:g:115:SER:C	34:g:117:ASN:N	2.76	0.44
1:2:84:A:O3'	26:Y:119:GLY:HA2	2.17	0.44
1:2:125:C:OP2	8:G:201:LYS:NZ	2.50	0.44
1:2:594:A:H61	1:2:643:A:H5''	1.81	0.44
1:2:853:C:O2	1:2:853:C:O4'	2.36	0.44
3:B:227:LYS:HA	3:B:230:GLU:CD	2.42	0.44
6:E:10:LYS:HD3	6:E:10:LYS:HA	1.80	0.44
14:M:89:VAL:HG11	14:M:102:LYS:NZ	2.32	0.44
18:Q:43:GLU:HB2	18:Q:44:PRO:HD3	1.98	0.44
20:S:90:VAL:O	20:S:91:LYS:HB2	2.18	0.44
1:2:943:U:C2	1:2:944:A:C8	3.06	0.44
1:2:1101:U:H2'	1:2:1102:G:H8	1.82	0.44
1:2:1234:C:N4	20:S:137:LYS:NZ	2.66	0.44
1:2:1775:U:H2'	1:2:1776:G:H5''	1.99	0.44
1:2:1809:A:H2'	1:2:1810:U:C6	2.53	0.44
2:A:70:ASN:HB2	4:C:270:THR:CG2	2.47	0.44
10:I:104:ILE:HD11	10:I:189:VAL:HG22	1.98	0.44
11:J:32:ILE:HG21	32:e:34:ARG:HG2	1.99	0.44
15:N:25:TRP:HZ3	29:b:83:GLN:HB2	1.83	0.44
34:g:121:VAL:HG23	34:g:156:PHE:CZ	2.52	0.44
34:g:304:ASP:CG	34:g:306:LEU:HD12	2.42	0.44
1:2:70:G:C2	1:2:71:G:N7	2.86	0.44
1:2:1258:A:N1	1:2:1663:A:H2'	2.33	0.44
1:2:1755:C:H2'	1:2:1756:C:O4'	2.17	0.44
1:2:1817:G:H2'	1:2:1818:A:C8	2.53	0.44
9:H:29:GLU:CD	9:H:33:ASN:HD21	2.24	0.44
10:I:130:THR:HG23	10:I:133:GLU:OE2	2.17	0.44
13:L:103:GLU:OE2	25:X:14:ARG:NH2	2.50	0.44
15:N:54:LEU:HB3	15:N:60:VAL:HG22	2.00	0.44
17:P:111:MET:HE3	17:P:119:PHE:CE2	2.52	0.44
19:R:76:GLU:O	19:R:79:GLU:HG3	2.16	0.44
20:S:46:ARG:CZ	20:S:52:LEU:HD11	2.46	0.44
22:U:19:ARG:HE	22:U:92:HIS:HE2	1.65	0.44
24:W:6:VAL:HG11	24:W:29:PRO:HG2	1.99	0.44
27:Z:69:THR:HG22	27:Z:71:ALA:H	1.81	0.44
1:2:197:U:H3'	1:2:198:U:C6	2.52	0.44
1:2:297:A:H5'	6:E:132:GLY:HA2	1.98	0.44
1:2:376:A:H2'	1:2:377:G:O4'	2.18	0.44
1:2:539:C:N4	1:2:545:A:C2	2.86	0.44
1:2:1543:U:H4'	18:Q:43:GLU:CG	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:128:ILE:HG12	7:F:135:ARG:O	2.18	0.44
13:L:147:LYS:HA	13:L:147:LYS:HD3	1.73	0.44
16:O:45:THR:HG1	16:O:51:GLU:C	2.18	0.44
22:U:19:ARG:HG3	22:U:19:ARG:NH1	2.32	0.44
1:2:60:A:HO2'	1:2:61:A:P	2.39	0.44
1:2:151:C:OP1	26:Y:120:THR:OG1	2.20	0.44
1:2:544:G:C4	1:2:545:A:C8	3.06	0.44
1:2:808:A:H2'	1:2:809:A:C8	2.53	0.44
1:2:1388:A:C2	5:D:205:PRO:HG2	2.52	0.44
20:S:110:ASP:C	20:S:110:ASP:OD1	2.60	0.44
1:2:1241:A:C2	1:2:1516:G:C8	2.99	0.44
1:2:1515:G:H5''	1:2:1515:G:H8	1.83	0.44
1:2:1726:G:H2'	1:2:1727:G:C8	2.53	0.44
1:2:1771:G:H2'	1:2:1772:C:C2	2.52	0.44
5:D:14:ASP:OD1	5:D:15:GLY:N	2.51	0.44
1:2:891:G:H2'	1:2:892:U:O4'	2.17	0.44
1:2:1293:A:H61	1:2:1305:C:N4	2.14	0.44
2:A:143:PRO:HG3	23:V:32:ILE:HB	2.00	0.44
3:B:123:ALA:HB2	3:B:165:ARG:HG3	2.00	0.44
4:C:172:ASN:HB3	4:C:174:ILE:HD12	2.00	0.44
6:E:11:ARG:HA	6:E:28:ALA:HB2	2.00	0.44
22:U:30:LYS:HB2	22:U:30:LYS:HE2	1.54	0.44
24:W:10:ALA:O	24:W:14:ILE:HG22	2.18	0.44
1:2:495:U:H2'	1:2:496:C:O4'	2.18	0.44
1:2:535:G:O3'	32:e:46:VAL:HG21	2.17	0.44
1:2:545:A:H2'	1:2:546:G:C8	2.53	0.44
1:2:1217:A:H2'	1:2:1218:C:C6	2.53	0.44
1:2:1515:G:H5''	1:2:1515:G:C8	2.53	0.44
5:D:168:VAL:HA	5:D:188:ILE:O	2.17	0.44
8:G:1:MET:HE3	8:G:109:LEU:HB2	1.99	0.44
11:J:61:LEU:HD22	11:J:94:LEU:HD23	2.00	0.44
18:Q:76:GLY:O	18:Q:80:GLN:HG3	2.18	0.44
18:Q:103:ALA:O	18:Q:107:GLU:HG2	2.18	0.44
24:W:18:GLU:HG2	24:W:69:LEU:HB3	1.99	0.44
25:X:8:ARG:NH1	25:X:8:ARG:HG3	2.33	0.44
28:a:38:LYS:HE2	28:a:38:LYS:HB2	1.65	0.44
1:2:114:G:OP1	13:L:69:ARG:NH1	2.50	0.43
1:2:202:G:H2'	1:2:203:G:H8	1.83	0.43
1:2:533:A:H3'	1:2:534:G:C4'	2.48	0.43
1:2:964:A:H2'	1:2:965:U:H6	1.83	0.43
1:2:1507:G:N2	33:f:87:THR:OG1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:39:TYR:CD2	19:R:105:MET:HG3	2.52	0.43
2:A:206:ASP:OD1	2:A:208:GLU:HG2	2.18	0.43
3:B:103:MET:HE2	3:B:188:LEU:HD22	1.99	0.43
13:L:61:PRO:HA	13:L:66:VAL:HG23	1.99	0.43
31:d:29:GLY:O	31:d:40:ARG:HG2	2.18	0.43
32:e:36:MET:HE3	32:e:40:ARG:HH12	1.83	0.43
34:g:156:PHE:CE1	34:g:179:LEU:HD11	2.53	0.43
34:g:164:ILE:CG2	34:g:176:VAL:HG13	2.47	0.43
1:2:433:A:H2'	1:2:434:G:C8	2.53	0.43
1:2:1114:U:H2'	1:2:1115:U:O4'	2.18	0.43
1:2:1409:A:H2'	1:2:1410:C:C6	2.53	0.43
1:2:1595:U:H2'	1:2:1596:U:C6	2.53	0.43
4:C:65:LYS:HG2	4:C:273:LEU:HD13	2.01	0.43
11:J:84:ILE:HG13	11:J:86:VAL:HG23	1.99	0.43
14:M:18:LEU:HD12	14:M:18:LEU:HA	1.84	0.43
16:O:145:GLY:O	28:a:22:ARG:NH1	2.36	0.43
20:S:14:ARG:HH21	20:S:19:ASN:CG	2.27	0.43
27:Z:84:ALA:O	27:Z:88:LEU:HG	2.18	0.43
34:g:168:CYS:HB3	34:g:198:VAL:CG1	2.48	0.43
1:2:545:A:H3'	1:2:546:G:H8	1.84	0.43
1:2:548:C:O5'	1:2:548:C:H6	2.01	0.43
1:2:1192:U:P	25:X:119:ARG:HH22	2.41	0.43
1:2:1290:G:HO2'	33:f:145:CYS:HG	1.65	0.43
1:2:1535:U:O2	1:2:1535:U:H2'	2.17	0.43
1:2:1714:U:H2'	1:2:1715:A:H8	1.82	0.43
3:B:36:PRO:CG	3:B:231:LEU:HD21	2.47	0.43
9:H:184:ASP:OD1	9:H:184:ASP:N	2.51	0.43
10:I:193:LYS:HE3	10:I:193:LYS:HB3	1.88	0.43
24:W:47:ILE:HG23	24:W:48:GLY:H	1.82	0.43
33:f:106:TYR:HB2	33:f:117:LEU:HD11	1.99	0.43
33:f:136:PHE:HD1	33:f:136:PHE:H	1.66	0.43
1:2:561:A:P	11:J:174:LYS:HG3	2.57	0.43
1:2:881:G:C2	1:2:906:U:H1'	2.54	0.43
1:2:1378:A:H4'	1:2:1379:A:O5'	2.19	0.43
1:2:1690:U:H2'	1:2:1691:U:C6	2.54	0.43
10:I:79:ILE:HD12	10:I:170:LYS:HG2	2.00	0.43
11:J:152:ASP:OD1	11:J:153:SER:N	2.51	0.43
14:M:65:VAL:HG13	14:M:66:GLU:OE1	2.18	0.43
17:P:96:VAL:HB	17:P:120:SER:OG	2.19	0.43
18:Q:57:LEU:HD21	18:Q:115:TYR:CG	2.53	0.43
23:V:71:ARG:HH22	24:W:23:ARG:NH1	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:c:61:SER:O	30:c:61:SER:OG	2.26	0.43
34:g:36:ARG:HG2	34:g:65:PHE:CD2	2.54	0.43
1:2:30:C:O2'	25:X:137:LYS:NZ	2.51	0.43
1:2:84:A:N3	1:2:150:A:O2'	2.44	0.43
1:2:965:U:H2'	1:2:966:U:H5'	2.01	0.43
1:2:1866:A:O5'	1:2:1866:A:H8	2.01	0.43
7:F:136:ARG:HB2	7:F:203:ASN:ND2	2.33	0.43
12:K:27:VAL:HG12	12:K:46:MET:HE1	2.00	0.43
13:L:104:LYS:HE3	13:L:104:LYS:HB2	1.68	0.43
15:N:20:ARG:HH21	24:W:56:HIS:HB3	1.84	0.43
20:S:70:ILE:HG13	20:S:77:TYR:CD2	2.54	0.43
1:2:116:U:O5'	1:2:116:U:H6	2.01	0.43
1:2:921:G:C2	29:b:22:LYS:HG2	2.54	0.43
1:2:982:G:H2'	1:2:983:A:C8	2.54	0.43
1:2:1007:C:H2'	1:2:1008:A:C8	2.54	0.43
1:2:1119:A:H3'	1:2:1120:U:C6	2.54	0.43
1:2:1199:A:H2'	1:2:1200:A:O4'	2.19	0.43
3:B:103:MET:HB3	3:B:103:MET:HE3	1.76	0.43
5:D:63:GLY:O	5:D:66:ILE:HG22	2.18	0.43
9:H:69:LEU:HD22	9:H:96:ALA:HB2	1.99	0.43
10:I:78:ILE:HG23	10:I:102:VAL:HG21	2.00	0.43
15:N:3:ARG:HA	15:N:3:ARG:HD3	1.71	0.43
17:P:30:TYR:O	17:P:34:MET:HG3	2.19	0.43
18:Q:81:ILE:O	18:Q:82:TYR:HB2	2.17	0.43
20:S:37:GLY:O	20:S:39:ARG:N	2.51	0.43
33:f:109:ASP:O	33:f:110:GLU:HB2	2.18	0.43
1:2:544:G:C3'	1:2:545:A:H8	2.30	0.43
1:2:588:G:O3'	1:2:589:G:H4'	2.19	0.43
1:2:639:C:O2'	1:2:640:A:H8	2.01	0.43
1:2:896:U:H2'	1:2:897:U:C6	2.54	0.43
1:2:1249:C:H2'	1:2:1250:A:C2	2.54	0.43
1:2:1292:C:H2'	1:2:1293:A:C8	2.54	0.43
1:2:1405:A:H2'	1:2:1406:G:O4'	2.19	0.43
3:B:48:LEU:O	16:O:51:GLU:HG3	2.19	0.43
5:D:31:GLU:HG3	5:D:107:TYR:OH	2.19	0.43
7:F:86:LYS:O	7:F:90:VAL:HG13	2.18	0.43
16:O:93:LEU:HD12	16:O:93:LEU:HA	1.89	0.43
21:T:29:LYS:HE2	21:T:29:LYS:HB2	1.76	0.43
33:f:88:PRO:O	33:f:89:LYS:HB3	2.18	0.43
1:2:634:A:H2'	1:2:635:G:H8	1.82	0.43
1:2:804:U:H2'	1:2:805:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1133:A:H4'	28:a:13:LYS:HD2	2.00	0.43
1:2:1294:G:H3'	1:2:1295:A:H8	1.82	0.43
1:2:1536:G:H2'	1:2:1537:A:C8	2.54	0.43
5:D:196:GLY:H	5:D:201:LYS:NZ	2.16	0.43
6:E:124:CYS:HB3	6:E:141:THR:HB	2.01	0.43
22:U:34:LYS:HZ2	22:U:34:LYS:HG2	1.62	0.43
25:X:8:ARG:HG3	25:X:8:ARG:HH11	1.84	0.43
33:f:132:MET:HG2	33:f:141:CYS:CA	2.49	0.43
34:g:197:THR:HG21	34:g:238:ALA:HA	2.00	0.43
1:2:1170:A:C5'	35:h:10:MET:HE1	2.49	0.43
1:2:1771:G:H2'	1:2:1772:C:O2	2.19	0.43
6:E:106:LYS:NZ	6:E:251:GLU:OE2	2.30	0.43
11:J:107:GLU:C	11:J:112:THR:HG21	2.44	0.43
15:N:70:LYS:HE2	15:N:70:LYS:HB2	1.87	0.43
1:2:893:U:C4	1:2:894:G:C5	3.07	0.43
1:2:1239:U:O2'	1:2:1241:A:N7	2.47	0.43
1:2:1587:G:H3'	21:T:77:LYS:HD3	2.00	0.43
2:A:207:PRO:HA	2:A:210:ILE:HD12	2.01	0.43
10:I:92:ARG:HG2	10:I:92:ARG:HH11	1.82	0.43
12:K:17:LYS:HE2	12:K:17:LYS:HB3	1.80	0.43
24:W:38:LEU:HD22	24:W:47:ILE:HD12	2.01	0.43
24:W:51:GLU:HG2	29:b:8:LEU:HD11	2.01	0.43
32:e:51:LYS:NZ	36:n:168:PRO:HD3	2.33	0.43
34:g:257:LYS:HE2	34:g:269:GLU:OE2	2.19	0.43
1:2:634:A:H2'	1:2:635:G:C8	2.54	0.42
1:2:1113:A:H3'	1:2:1114:U:O4'	2.18	0.42
1:2:1387:G:H2'	1:2:1388:A:O4'	2.19	0.42
1:2:1513:C:C2'	1:2:1514:G:H5''	2.45	0.42
3:B:228:LEU:O	3:B:229:MET:C	2.61	0.42
5:D:67:ARG:HH21	12:K:97:SER:HB3	1.83	0.42
6:E:233:LYS:HB3	6:E:233:LYS:HE3	1.88	0.42
21:T:124:THR:HG22	21:T:126:GLN:N	2.33	0.42
24:W:76:SER:HA	24:W:77:PRO:C	2.44	0.42
28:a:32:LYS:HG2	28:a:37:LYS:HZ2	1.82	0.42
34:g:124:SER:OG	34:g:125:ARG:N	2.52	0.42
34:g:168:CYS:HB3	34:g:198:VAL:HG13	1.99	0.42
1:2:68:A:OP2	8:G:164:LYS:NZ	2.52	0.42
1:2:96:C:H2'	1:2:97:U:C6	2.54	0.42
1:2:160:U:O2'	1:2:161:U:H3'	2.19	0.42
1:2:191:A:H62	1:2:208:G:H21	1.67	0.42
1:2:1354:G:H5'	1:2:1355:C:OP2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1454:A:H5''	19:R:3:ARG:HD2	2.01	0.42
9:H:73:GLN:HA	9:H:76:GLN:HG2	2.01	0.42
13:L:125:ILE:HB	13:L:146:THR:HG23	2.01	0.42
14:M:13:ASP:OD1	14:M:13:ASP:N	2.52	0.42
14:M:102:LYS:NZ	14:M:105:GLY:HA3	2.33	0.42
21:T:21:PHE:CG	21:T:134:ILE:HD11	2.54	0.42
34:g:8:ARG:HG3	34:g:8:ARG:HH11	1.83	0.42
1:2:1129:G:H2'	1:2:1130:G:N3	2.33	0.42
1:2:1610:G:C1'	20:S:108:ARG:HH12	2.31	0.42
3:B:174:ARG:NH1	3:B:175:GLU:OE1	2.52	0.42
4:C:259:THR:HG21	23:V:16:LYS:H	1.84	0.42
11:J:46:VAL:HG21	11:J:106:LEU:CD2	2.49	0.42
12:K:36:ALA:C	12:K:38:LYS:H	2.28	0.42
13:L:49:GLU:O	13:L:53:GLY:N	2.53	0.42
14:M:119:GLN:OE1	14:M:119:GLN:N	2.48	0.42
15:N:36:GLN:HG3	15:N:39:LYS:HE3	2.00	0.42
15:N:87:ASP:OD1	15:N:88:LEU:N	2.52	0.42
21:T:76:THR:CG2	21:T:94:ARG:HB3	2.49	0.42
22:U:49:LYS:HE2	22:U:49:LYS:HB2	1.91	0.42
30:c:29:GLN:HE21	30:c:67:ARG:NH2	2.17	0.42
30:c:31:ARG:CZ	30:c:43:ILE:HD11	2.49	0.42
34:g:249:CYS:SG	34:g:291:TRP:NE1	2.86	0.42
1:2:92:A:O2'	6:E:4:GLY:HA3	2.20	0.42
1:2:189:U:H5''	1:2:189:U:C6	2.55	0.42
1:2:198:U:H3'	1:2:199:C:C5'	2.49	0.42
1:2:535:G:H3'	1:2:536:A:H8	1.84	0.42
1:2:566:U:H2'	1:2:567:C:O4'	2.20	0.42
1:2:641:A:H2'	1:2:642:U:O4'	2.19	0.42
1:2:948:C:H2'	1:2:949:G:H8	1.84	0.42
1:2:1291:A:H2	33:f:138:ARG:HH21	1.67	0.42
1:2:1309:C:O2	1:2:1309:C:O4'	2.35	0.42
7:F:51:HIS:O	18:Q:50:LYS:HE3	2.19	0.42
14:M:62:VAL:HA	14:M:65:VAL:HG12	2.02	0.42
26:Y:23:MET:HE2	26:Y:23:MET:HB3	1.95	0.42
34:g:181:ASN:OD1	34:g:181:ASN:N	2.50	0.42
1:2:218:U:O2	10:I:184:ARG:NH2	2.50	0.42
1:2:608:C:OP1	32:e:59:SER:OG	2.30	0.42
1:2:891:G:N3	1:2:891:G:H5'	2.34	0.42
1:2:1116:C:H2'	1:2:1117:C:C6	2.55	0.42
1:2:1203:G:N3	1:2:1699:A:H2	2.18	0.42
1:2:1262:C:O2	1:2:1262:C:O4'	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1604:G:C3'	1:2:1605:G:H5'	2.49	0.42
1:2:1712:A:H2'	1:2:1713:C:H6	1.82	0.42
14:M:12:MET:HG3	14:M:17:ALA:HB2	2.02	0.42
21:T:30:VAL:HG12	21:T:53:PHE:CD2	2.54	0.42
34:g:297:THR:CG2	34:g:309:VAL:CG1	2.97	0.42
1:2:531:A:H2'	1:2:532:C:O4'	2.20	0.42
1:2:1288:U:H4'	12:K:2:LEU:HD21	2.02	0.42
1:2:1836:G:OP1	1:2:1839:U:H4'	2.19	0.42
5:D:136:VAL:HG13	5:D:186:VAL:HG22	2.02	0.42
6:E:139:LEU:O	6:E:146:THR:HA	2.20	0.42
12:K:1:MET:HE1	12:K:43:LEU:CD2	2.48	0.42
25:X:98:ASP:C	25:X:98:ASP:OD1	2.63	0.42
1:2:51:U:H2'	1:2:52:G:H8	1.85	0.42
1:2:70:G:H21	1:2:79:A:H62	1.68	0.42
1:2:386:C:H2'	1:2:387:C:C6	2.55	0.42
1:2:612:U:H4'	32:e:15:GLN:OE1	2.20	0.42
1:2:1005:G:H2'	1:2:1006:C:C6	2.55	0.42
1:2:1390:U:H2'	1:2:1391:C:C6	2.55	0.42
3:B:68:GLU:OE2	3:B:85:LYS:HG2	2.19	0.42
3:B:229:MET:SD	3:B:229:MET:N	2.93	0.42
9:H:69:LEU:O	9:H:73:GLN:HG2	2.19	0.42
11:J:171:GLY:O	11:J:175:ARG:HG3	2.20	0.42
12:K:65:ARG:NH1	31:d:20:SER:OG	2.42	0.42
20:S:23:ARG:HB3	27:Z:48:VAL:HG11	2.01	0.42
1:2:194:C:H2'	1:2:195:C:H6	1.84	0.42
1:2:1546:G:C5'	18:Q:18:THR:HG21	2.48	0.42
1:2:1589:A:H2'	1:2:1590:C:O4'	2.20	0.42
1:2:1616:U:H2'	1:2:1617:G:O4'	2.19	0.42
9:H:113:LYS:HD3	9:H:113:LYS:HA	1.65	0.42
14:M:67:ALA:HB2	33:f:107:LYS:HG3	2.02	0.42
14:M:91:LEU:HB3	14:M:100:PRO:HD2	2.02	0.42
15:N:25:TRP:CZ3	29:b:83:GLN:HB2	2.54	0.42
16:O:119:LEU:O	16:O:124:MET:HB2	2.18	0.42
1:2:67:C:H41	8:G:164:LYS:H	1.66	0.42
1:2:383:G:H4'	13:L:132:ARG:HD2	2.01	0.42
1:2:1262:C:H2'	1:2:1263:U:O4'	2.20	0.42
1:2:1427:C:H2'	1:2:1429:G:C8	2.55	0.42
12:K:49:MET:HB3	12:K:69:TRP:CE2	2.55	0.42
15:N:110:ASP:O	15:N:114:ARG:HG2	2.19	0.42
1:2:896:U:H2'	1:2:897:U:C4	2.55	0.42
1:2:1232:U:O2	1:2:1232:U:O4'	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1291:A:H2	33:f:138:ARG:NE	2.13	0.42
4:C:204:ILE:HD12	4:C:215:MET:HG2	2.02	0.42
8:G:162:LEU:HD13	8:G:172:LYS:HB2	2.02	0.42
9:H:39:GLN:O	9:H:43:LEU:HD13	2.19	0.42
16:O:113:GLN:OE1	28:a:46:GLU:HB3	2.20	0.42
1:2:67:C:N4	8:G:164:LYS:H	2.17	0.41
1:2:407:G:H2'	1:2:407:G:N3	2.35	0.41
1:2:900:C:H2'	1:2:901:G:H8	1.85	0.41
1:2:1516:G:H5''	1:2:1516:G:N3	2.35	0.41
1:2:1683:C:H2'	1:2:1684:C:H6	1.85	0.41
1:2:1688:C:H5''	1:2:1688:C:C6	2.55	0.41
1:2:1689:C:C6	1:2:1689:C:H5''	2.55	0.41
1:2:1733:U:H2'	1:2:1734:G:O4'	2.20	0.41
10:I:17:LYS:HE3	10:I:17:LYS:HB3	1.86	0.41
16:O:63:LYS:HA	16:O:63:LYS:HD3	1.85	0.41
18:Q:12:VAL:HG21	18:Q:91:ALA:HA	2.02	0.41
18:Q:40:GLU:CD	18:Q:40:GLU:H	2.27	0.41
27:Z:97:ILE:HG23	27:Z:109:TYR:HB3	2.01	0.41
1:2:751:G:H2'	1:2:752:G:H8	1.83	0.41
1:2:1344:A:N6	1:2:1386:A:H5'	2.35	0.41
1:2:1416:C:OP1	21:T:129:ARG:HG3	2.19	0.41
1:2:1590:C:H3'	1:2:1591:C:H6	1.84	0.41
1:2:1608:U:O2	1:2:1608:U:O4'	2.37	0.41
3:B:30:TRP:CE2	16:O:19:PRO:HG3	2.55	0.41
4:C:173:LYS:HB3	23:V:3:ASN:HA	2.02	0.41
5:D:221:THR:CG2	5:D:222:PRO:CD	2.98	0.41
6:E:36:HIS:NE2	6:E:88:ASP:OD2	2.53	0.41
9:H:26:ALA:HA	9:H:86:LYS:HZ1	1.86	0.41
9:H:64:VAL:O	9:H:96:ALA:HA	2.20	0.41
9:H:101:LEU:HG	9:H:120:ARG:HB3	2.02	0.41
15:N:2:GLY:HA3	15:N:9:LYS:HG2	2.03	0.41
21:T:88:MET:HE3	21:T:88:MET:HB3	1.90	0.41
22:U:21:ARG:HD3	22:U:88:LEU:HD22	2.02	0.41
1:2:530:U:H5''	1:2:530:U:H6	1.85	0.41
1:2:1406:G:H2'	1:2:1407:U:C6	2.55	0.41
1:2:1706:G:H2'	1:2:1707:U:C6	2.55	0.41
4:C:73:MET:HE2	4:C:73:MET:HA	2.02	0.41
4:C:183:LYS:HA	4:C:195:LEU:O	2.20	0.41
10:I:26:LYS:O	10:I:29:LEU:HD23	2.21	0.41
19:R:21:TYR:HD1	19:R:58:MET:HE1	1.84	0.41
24:W:18:GLU:OE2	24:W:18:GLU:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:125:C:OP1	8:G:202:ASN:ND2	2.40	0.41
1:2:388:U:H2'	1:2:389:A:C8	2.55	0.41
1:2:534:G:C3'	1:2:535:G:H8	2.33	0.41
1:2:572:U:H5'	26:Y:60:PHE:O	2.19	0.41
5:D:169:ASP:OD1	5:D:169:ASP:C	2.63	0.41
6:E:45:ILE:HA	6:E:61:VAL:HG11	2.03	0.41
6:E:171:ASP:OD1	6:E:171:ASP:N	2.51	0.41
16:O:31:CYS:N	16:O:94:HIS:O	2.45	0.41
18:Q:40:GLU:CD	18:Q:40:GLU:N	2.79	0.41
1:2:1590:C:H3'	1:2:1591:C:C6	2.56	0.41
1:2:1643:U:H2'	1:2:1644:C:C6	2.54	0.41
1:2:1757:G:OP1	1:2:1776:G:N2	2.52	0.41
3:B:125:VAL:HG13	3:B:169:MET:HG2	2.01	0.41
10:I:202:ILE:O	10:I:206:LYS:HG2	2.20	0.41
16:O:75:MET:HG3	16:O:118:ALA:HB2	2.03	0.41
19:R:116:ASN:OD1	19:R:116:ASN:N	2.53	0.41
1:2:563:G:O2'	1:2:564:A:H5''	2.20	0.41
1:2:849:A:H2'	1:2:850:C:C6	2.55	0.41
1:2:929:G:N2	1:2:1104:G:H4'	2.35	0.41
1:2:958:G:H2'	1:2:959:G:C8	2.55	0.41
1:2:993:G:N7	28:a:15:ARG:NH1	2.67	0.41
1:2:1025:U:H2'	1:2:1026:C:O4'	2.21	0.41
1:2:1155:U:O2	24:W:71:LYS:HB2	2.21	0.41
1:2:1243:U:O2	1:2:1243:U:O4'	2.38	0.41
1:2:1866:A:C6	28:a:84:VAL:HG22	2.55	0.41
2:A:31:ASP:OD1	2:A:31:ASP:C	2.63	0.41
6:E:9:LEU:HB2	6:E:30:ARG:HD2	2.01	0.41
6:E:91:SER:OG	6:E:98:ASN:OD1	2.36	0.41
14:M:84:LYS:HE2	14:M:84:LYS:HB3	1.89	0.41
24:W:66:THR:C	24:W:68:ARG:H	2.29	0.41
1:2:71:G:O3'	1:2:72:C:C6	2.74	0.41
1:2:416:U:H2'	1:2:417:C:O4'	2.21	0.41
1:2:571:U:O2'	26:Y:60:PHE:O	2.33	0.41
1:2:595:U:H2'	1:2:596:U:C6	2.55	0.41
1:2:641:A:OP2	32:e:34:ARG:NH1	2.54	0.41
1:2:1349:G:H2'	1:2:1350:U:C6	2.55	0.41
4:C:263:LYS:HE3	4:C:263:LYS:HB3	1.74	0.41
5:D:116:ARG:HE	5:D:116:ARG:HB3	1.76	0.41
14:M:44:LYS:HB2	14:M:44:LYS:HE2	1.71	0.41
14:M:112:LYS:HE2	14:M:118:SER:HB3	2.02	0.41
16:O:98:ARG:HB2	16:O:132:VAL:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:93:MET:HE1	17:P:104:GLN:OE1	2.21	0.41
20:S:51:ASP:OD1	20:S:53:THR:N	2.52	0.41
33:f:121:CYS:CB	33:f:126:CYS:HB3	2.48	0.41
1:2:118:C:H1'	1:2:445:A:C5	2.56	0.41
1:2:215:G:H2'	1:2:216:C:C6	2.55	0.41
1:2:533:A:H3'	1:2:534:G:C5'	2.51	0.41
1:2:887:U:H2'	1:2:888:U:H5''	2.01	0.41
1:2:894:G:C2	1:2:895:G:C5	3.09	0.41
1:2:1425:G:H2'	1:2:1426:U:C6	2.56	0.41
1:2:1479:G:O2'	18:Q:131:LYS:HE2	2.20	0.41
1:2:1600:G:H3'	27:Z:43:LYS:NZ	2.35	0.41
1:2:1796:G:H2'	1:2:1797:U:C6	2.56	0.41
4:C:254:ASP:OD1	4:C:254:ASP:N	2.53	0.41
6:E:29:PRO:HG2	6:E:46:ILE:HD11	2.03	0.41
7:F:204:ARG:HA	30:c:63:ARG:HH22	1.86	0.41
8:G:222:GLU:O	8:G:226:GLU:HG2	2.21	0.41
10:I:131:PRO:O	10:I:132:GLU:HB2	2.20	0.41
17:P:111:MET:HE3	17:P:119:PHE:CZ	2.55	0.41
18:Q:101:ASP:OD1	18:Q:101:ASP:N	2.52	0.41
21:T:107:LEU:HD23	21:T:107:LEU:HA	1.95	0.41
1:2:197:U:C4	1:2:198:U:C4	3.09	0.41
1:2:534:G:H3'	1:2:535:G:H8	1.86	0.41
1:2:536:A:N1	1:2:548:C:N3	2.69	0.41
1:2:616:A:N3	32:e:12:VAL:HG21	2.35	0.41
1:2:800:U:H2'	1:2:801:U:O4'	2.21	0.41
1:2:885:U:H2'	1:2:886:A:C8	2.51	0.41
1:2:945:U:H2'	1:2:946:U:C6	2.56	0.41
1:2:1617:G:H2'	1:2:1619:A:C2	2.53	0.41
1:2:1661:A:C8	31:d:14:PHE:HB2	2.55	0.41
1:2:1702:G:H2'	1:2:1703:C:O4'	2.21	0.41
1:2:1716:C:H2'	1:2:1717:C:C6	2.56	0.41
1:2:1729:U:O4	1:2:1805:G:O6	2.39	0.41
3:B:214:LYS:HE3	3:B:214:LYS:HB2	1.84	0.41
6:E:230:LYS:HB2	6:E:230:LYS:HE2	1.69	0.41
7:F:95:HIS:O	7:F:96:ALA:HB3	2.21	0.41
8:G:216:ARG:HD3	8:G:216:ARG:HA	1.83	0.41
9:H:115:LYS:HB2	9:H:115:LYS:HE2	1.86	0.41
10:I:161:LEU:O	10:I:165:GLN:HG3	2.21	0.41
12:K:60:GLU:HB2	12:K:69:TRP:CD1	2.55	0.41
13:L:75:GLY:HA3	13:L:88:ILE:HD12	2.03	0.41
14:M:82:ASN:CB	14:M:103:VAL:HG12	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:85:LEU:HD12	14:M:85:LEU:HA	1.89	0.41
19:R:17:ILE:HG13	19:R:54:VAL:HG22	2.02	0.41
21:T:85:ASN:ND2	21:T:89:PRO:O	2.46	0.41
22:U:17:ILE:HG23	22:U:19:ARG:H	1.84	0.41
22:U:111:GLU:N	22:U:111:GLU:CD	2.79	0.41
24:W:77:PRO:HD3	25:X:5:ARG:O	2.21	0.41
34:g:11:LEU:HB2	34:g:307:VAL:HB	2.01	0.41
34:g:302:TYR:CE1	34:g:308:ARG:HB2	2.54	0.41
1:2:104:A:H62	1:2:356:C:H5	1.62	0.41
1:2:871:U:OP2	1:2:871:U:H4'	2.21	0.41
1:2:878:G:C2	1:2:909:G:C2	3.09	0.41
1:2:1519:U:H5''	1:2:1519:U:H6	1.86	0.41
5:D:31:GLU:CD	5:D:31:GLU:H	2.29	0.41
6:E:173:ILE:HD11	6:E:235:TRP:CD2	2.56	0.41
7:F:136:ARG:HB2	7:F:203:ASN:HD22	1.86	0.41
8:G:131:ARG:HD3	8:G:131:ARG:HA	1.90	0.41
9:H:109:ARG:HG2	9:H:110:THR:H	1.86	0.41
15:N:75:LEU:HA	15:N:75:LEU:HD13	1.87	0.41
23:V:37:ALA:HB1	23:V:46:PHE:CD1	2.55	0.41
28:a:40:VAL:CG1	28:a:42:ARG:NE	2.84	0.41
33:f:119:ARG:HD2	33:f:132:MET:CE	2.51	0.41
1:2:16:G:H2'	1:2:17:C:C6	2.56	0.40
1:2:180:G:HO2'	1:2:181:A:P	2.43	0.40
1:2:481:C:H2'	1:2:482:G:O4'	2.21	0.40
1:2:530:U:H5''	1:2:530:U:C6	2.56	0.40
1:2:547:G:N3	1:2:547:G:C2'	2.83	0.40
1:2:846:G:H2'	6:E:19:MET:HG2	2.02	0.40
1:2:1227:G:N3	1:2:1227:G:H2'	2.35	0.40
1:2:1507:G:N2	33:f:86:THR:O	2.54	0.40
1:2:1781:A:H2'	1:2:1782:G:H8	1.85	0.40
1:2:1819:A:H2'	1:2:1820:G:C8	2.56	0.40
3:B:31:TYR:CD2	3:B:94:LYS:HA	2.55	0.40
8:G:41:LEU:HD23	8:G:41:LEU:HA	1.91	0.40
10:I:177:SER:OG	10:I:178:ARG:N	2.54	0.40
13:L:124:ASP:OD1	13:L:124:ASP:N	2.54	0.40
19:R:77:GLU:HG3	19:R:81:ARG:HE	1.85	0.40
20:S:111:LEU:O	20:S:115:LYS:HD2	2.21	0.40
22:U:28:ASN:OD1	22:U:30:LYS:N	2.54	0.40
23:V:71:ARG:HH12	24:W:23:ARG:NH1	2.19	0.40
26:Y:117:VAL:HG23	26:Y:122:LYS:HG2	2.02	0.40
29:b:23:ARG:NH1	29:b:27:SER:O	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:263:GLY:O	34:g:265:ILE:HG23	2.21	0.40
1:2:84:A:H4'	26:Y:119:GLY:O	2.20	0.40
1:2:570:C:O2'	26:Y:34:THR:O	2.27	0.40
1:2:1296:U:H3'	1:2:1297:U:O3'	2.21	0.40
1:2:1523:C:O2	1:2:1523:C:O4'	2.37	0.40
1:2:1813:A:H2'	1:2:1814:G:O4'	2.20	0.40
2:A:10:MET:HE3	2:A:15:VAL:HG22	2.02	0.40
3:B:79:VAL:HG12	3:B:81:PHE:H	1.85	0.40
3:B:179:ASN:OD1	3:B:179:ASN:N	2.54	0.40
8:G:218:LYS:HE3	8:G:218:LYS:HB3	1.94	0.40
13:L:79:LYS:HB2	13:L:79:LYS:HE3	1.82	0.40
14:M:67:ALA:HB1	33:f:114:ILE:HG23	2.04	0.40
15:N:38:TYR:O	15:N:42:LYS:HG2	2.20	0.40
17:P:51:ARG:C	17:P:53:GLN:N	2.74	0.40
22:U:94:PRO:HG2	22:U:97:ILE:HG13	2.02	0.40
32:e:46:VAL:N	32:e:47:PRO:HD2	2.36	0.40
1:2:438:G:H5''	1:2:438:G:N3	2.36	0.40
1:2:973:C:N3	16:O:55:ARG:NH1	2.67	0.40
1:2:1174:U:OP1	35:h:21:ARG:NH1	2.55	0.40
1:2:1181:A:H2'	1:2:1182:A:C8	2.56	0.40
1:2:1305:C:C4	1:2:1306:U:C4	3.09	0.40
1:2:1391:C:H2'	1:2:1392:U:O4'	2.20	0.40
1:2:1779:G:C2	1:2:1780:G:C5	3.09	0.40
2:A:31:ASP:OD1	2:A:32:PHE:N	2.54	0.40
5:D:74:GLN:HE21	5:D:82:GLY:H	1.68	0.40
5:D:125:PHE:O	5:D:129:SER:OG	2.35	0.40
7:F:42:LYS:HA	7:F:42:LYS:HD2	1.91	0.40
7:F:71:ARG:NH2	7:F:148:ASN:OD1	2.47	0.40
11:J:33:GLY:HA3	32:e:38:TYR:CG	2.56	0.40
22:U:80:PHE:HB3	31:d:52:PHE:HB3	2.04	0.40
32:e:47:PRO:C	32:e:48:THR:HG23	2.45	0.40
35:h:2:ARG:HB3	35:h:5:TRP:CD1	2.57	0.40
1:2:296:U:O2'	6:E:131:VAL:O	2.37	0.40
1:2:878:G:N2	1:2:879:C:H1'	2.37	0.40
1:2:1134:G:H2'	1:2:1135:C:H6	1.86	0.40
1:2:1520:G:N3	1:2:1520:G:C2'	2.84	0.40
1:2:1713:C:H2'	1:2:1714:U:H6	1.86	0.40
8:G:12:CYS:HG	8:G:127:THR:HG1	1.68	0.40
8:G:103:ASP:OD1	8:G:103:ASP:C	2.63	0.40
10:I:105:ASP:OD1	10:I:106:SER:N	2.54	0.40
11:J:22:LYS:HD2	11:J:22:LYS:HA	1.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:88:ASP:HB3	11:J:91:LYS:HG2	2.03	0.40
12:K:59:LYS:HE3	12:K:59:LYS:HB2	1.96	0.40
16:O:86:LYS:HB2	16:O:86:LYS:HE2	1.90	0.40
16:O:95:ILE:HG13	16:O:116:LEU:HD11	2.02	0.40
20:S:10:GLN:O	20:S:22:GLY:HA3	2.21	0.40
34:g:79:LEU:HD13	34:g:89:LEU:HD13	2.02	0.40
1:2:77:A:C2	8:G:175:LYS:HG3	2.50	0.40
1:2:443:U:H2'	1:2:444:G:O4'	2.21	0.40
1:2:674:C:H2'	1:2:675:U:C6	2.56	0.40
1:2:1220:A:N6	1:2:1221:G:C6	2.90	0.40
1:2:1388:A:N6	5:D:161:GLY:HA3	2.35	0.40
1:2:1593:C:O2	1:2:1593:C:O4'	2.40	0.40
1:2:1631:U:O2	1:2:1631:U:O4'	2.39	0.40
1:2:1844:U:OP1	35:h:11:ARG:NH2	2.49	0.40
2:A:183:LEU:HB3	2:A:189:ILE:HD12	2.04	0.40
4:C:194:ARG:HD3	4:C:196:ILE:HD11	2.02	0.40
5:D:166:TYR:O	5:D:200:PRO:HG3	2.22	0.40
6:E:101:LEU:HD23	6:E:101:LEU:HA	1.91	0.40
7:F:169:ILE:O	7:F:170:ALA:HB3	2.20	0.40
8:G:224:ARG:NH2	8:G:225:GLN:HB2	2.36	0.40
9:H:84:GLU:OE2	9:H:91:HIS:HA	2.20	0.40
12:K:14:LEU:HD12	12:K:14:LEU:HA	1.88	0.40
15:N:91:LEU:HD23	15:N:91:LEU:HA	1.94	0.40
19:R:21:TYR:CD1	19:R:58:MET:HE1	2.56	0.40
34:g:57:ARG:HD3	34:g:95:GLY:HA3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	A	211/295 (72%)	202 (96%)	8 (4%)	1 (0%)	24 46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	211/264 (80%)	205 (97%)	6 (3%)	0	100	100
4	C	216/293 (74%)	210 (97%)	6 (3%)	0	100	100
5	D	223/243 (92%)	217 (97%)	5 (2%)	1 (0%)	30	51
6	E	260/263 (99%)	256 (98%)	4 (2%)	0	100	100
7	F	187/204 (92%)	169 (90%)	15 (8%)	3 (2%)	7	16
8	G	228/249 (92%)	221 (97%)	7 (3%)	0	100	100
9	H	184/194 (95%)	169 (92%)	15 (8%)	0	100	100
10	I	203/208 (98%)	198 (98%)	5 (2%)	0	100	100
11	J	178/194 (92%)	170 (96%)	7 (4%)	1 (1%)	21	42
12	K	95/165 (58%)	91 (96%)	4 (4%)	0	100	100
13	L	149/158 (94%)	142 (95%)	7 (5%)	0	100	100
14	M	119/132 (90%)	99 (83%)	18 (15%)	2 (2%)	7	15
15	N	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
16	O	133/151 (88%)	128 (96%)	5 (4%)	0	100	100
17	P	124/145 (86%)	113 (91%)	8 (6%)	3 (2%)	4	9
18	Q	136/146 (93%)	125 (92%)	11 (8%)	0	100	100
19	R	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
20	S	141/152 (93%)	129 (92%)	11 (8%)	1 (1%)	18	38
21	T	142/145 (98%)	134 (94%)	8 (6%)	0	100	100
22	U	99/119 (83%)	94 (95%)	5 (5%)	0	100	100
23	V	80/83 (96%)	77 (96%)	3 (4%)	0	100	100
24	W	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
25	X	139/143 (97%)	135 (97%)	3 (2%)	1 (1%)	18	38
26	Y	122/133 (92%)	116 (95%)	6 (5%)	0	100	100
27	Z	70/125 (56%)	69 (99%)	1 (1%)	0	100	100
28	a	97/115 (84%)	95 (98%)	1 (1%)	1 (1%)	12	28
29	b	80/84 (95%)	75 (94%)	5 (6%)	0	100	100
30	c	60/69 (87%)	56 (93%)	4 (7%)	0	100	100
31	d	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
32	e	54/133 (41%)	50 (93%)	4 (7%)	0	100	100
33	f	72/156 (46%)	61 (85%)	8 (11%)	3 (4%)	2	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	g	312/317 (98%)	293 (94%)	18 (6%)	1 (0%)	36	58
35	h	20/25 (80%)	19 (95%)	1 (5%)	0	100	100
36	n	23/193 (12%)	23 (100%)	0	0	100	100
All	All	4825/5768 (84%)	4588 (95%)	219 (4%)	18 (0%)	31	51

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	M	110	VAL
33	f	88	PRO
2	A	189	ILE
11	J	161	LEU
20	S	38	ARG
7	F	20	PHE
17	P	40	ARG
33	f	108	VAL
34	g	314	ILE
7	F	53	ALA
14	M	109	VAL
17	P	133	ILE
33	f	107	LYS
17	P	87	PRO
28	a	63	VAL
7	F	21	GLY
5	D	196	GLY
25	X	86	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	179/243 (74%)	176 (98%)	3 (2%)	53	78
3	B	194/231 (84%)	189 (97%)	5 (3%)	40	68
4	C	184/225 (82%)	182 (99%)	2 (1%)	65	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	D	189/202 (94%)	180 (95%)	9 (5%)	23	47
6	E	224/225 (100%)	218 (97%)	6 (3%)	39	67
7	F	159/170 (94%)	156 (98%)	3 (2%)	50	75
8	G	200/218 (92%)	196 (98%)	4 (2%)	48	74
9	H	167/174 (96%)	161 (96%)	6 (4%)	31	58
10	I	178/180 (99%)	176 (99%)	2 (1%)	65	84
11	J	160/168 (95%)	157 (98%)	3 (2%)	50	75
12	K	88/136 (65%)	85 (97%)	3 (3%)	32	60
13	L	135/142 (95%)	132 (98%)	3 (2%)	45	72
14	M	102/108 (94%)	98 (96%)	4 (4%)	28	55
15	N	130/131 (99%)	127 (98%)	3 (2%)	44	71
16	O	105/119 (88%)	104 (99%)	1 (1%)	68	86
17	P	112/130 (86%)	102 (91%)	10 (9%)	9	20
18	Q	114/121 (94%)	110 (96%)	4 (4%)	32	59
19	R	119/122 (98%)	116 (98%)	3 (2%)	42	69
20	S	124/132 (94%)	118 (95%)	6 (5%)	23	47
21	T	114/115 (99%)	112 (98%)	2 (2%)	51	76
22	U	93/107 (87%)	92 (99%)	1 (1%)	65	84
23	V	66/67 (98%)	63 (96%)	3 (4%)	24	50
24	W	112/113 (99%)	103 (92%)	9 (8%)	11	25
25	X	113/115 (98%)	107 (95%)	6 (5%)	20	43
26	Y	108/115 (94%)	106 (98%)	2 (2%)	50	75
27	Z	64/103 (62%)	62 (97%)	2 (3%)	35	63
28	a	87/99 (88%)	83 (95%)	4 (5%)	24	49
29	b	74/76 (97%)	73 (99%)	1 (1%)	59	81
30	c	55/62 (89%)	53 (96%)	2 (4%)	31	58
31	d	48/49 (98%)	47 (98%)	1 (2%)	47	73
32	e	45/104 (43%)	44 (98%)	1 (2%)	45	72
33	f	67/140 (48%)	59 (88%)	8 (12%)	5	10
34	g	272/275 (99%)	267 (98%)	5 (2%)	51	76
35	h	21/24 (88%)	20 (95%)	1 (5%)	23	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	n	22/161 (14%)	22 (100%)	0	100	100
All	All	4224/4902 (86%)	4096 (97%)	128 (3%)	37	64

All (128) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	7	VAL
2	A	87	VAL
2	A	123	VAL
3	B	59	SER
3	B	129	THR
3	B	166	LYS
3	B	173	THR
3	B	228	LEU
4	C	161	SER
4	C	259	THR
5	D	3	VAL
5	D	66	ILE
5	D	72	VAL
5	D	94	ARG
5	D	110	LEU
5	D	139	SER
5	D	150	MET
5	D	168	VAL
5	D	198	ILE
6	E	91	SER
6	E	146	THR
6	E	174	LYS
6	E	197	ASN
6	E	227	VAL
6	E	228	ILE
7	F	22	LYS
7	F	117	ILE
7	F	193	LYS
8	G	95	LYS
8	G	129	VAL
8	G	157	VAL
8	G	185	LEU
9	H	33	ASN
9	H	45	ILE
9	H	64	VAL
9	H	145	ARG

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Mol	Chain	Res	Type
9	H	162	GLN
9	H	165	ASN
10	I	62	VAL
10	I	130	THR
11	J	79	ARG
11	J	129	LEU
11	J	159	PHE
12	K	6	LYS
12	K	38	LYS
12	K	90	VAL
13	L	107	LYS
13	L	141	ASN
13	L	146	THR
14	M	51	VAL
14	M	75	ASN
14	M	113	ASP
14	M	123	VAL
15	N	14	SER
15	N	53	ILE
15	N	144	SER
16	O	98	ARG
17	P	16	THR
17	P	20	VAL
17	P	26	LEU
17	P	50	ARG
17	P	51	ARG
17	P	52	LYS
17	P	75	VAL
17	P	76	VAL
17	P	84	ILE
17	P	88	GLU
18	Q	13	PHE
18	Q	31	LEU
18	Q	57	LEU
18	Q	118	THR
19	R	54	VAL
19	R	74	GLN
19	R	98	VAL
20	S	50	ILE
20	S	89	ASP
20	S	90	VAL
20	S	112	GLU

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Mol	Chain	Res	Type
20	S	131	VAL
20	S	139	THR
21	T	8	ASP
21	T	124	THR
22	U	38	ASP
23	V	13	VAL
23	V	52	THR
23	V	68	SER
24	W	26	LEU
24	W	27	ILE
24	W	30	CYS
24	W	31	SER
24	W	47	ILE
24	W	74	VAL
24	W	78	ARG
24	W	80	ASP
24	W	85	ASP
25	X	34	THR
25	X	36	LEU
25	X	64	SER
25	X	100	VAL
25	X	105	PHE
25	X	107	ARG
26	Y	26	ASP
26	Y	61	ARG
27	Z	82	SER
27	Z	97	ILE
28	a	2	THR
28	a	50	VAL
28	a	78	VAL
28	a	84	VAL
29	b	27	SER
30	c	46	VAL
30	c	50	VAL
31	d	40	ARG
32	e	34	ARG
33	f	90	LYS
33	f	92	LYS
33	f	107	LYS
33	f	109	ASP
33	f	111	ASN
33	f	114	ILE

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Mol	Chain	Res	Type
33	f	120	GLU
33	f	130	VAL
34	g	2	THR
34	g	113	PHE
34	g	186	THR
34	g	209	SER
34	g	303	THR
35	h	13	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	84	GLN
2	A	193	HIS
3	B	75	GLN
3	B	92	GLN
3	B	95	ASN
3	B	101	HIS
4	C	267	GLN
5	D	101	GLN
6	E	50	ASN
6	E	112	HIS
6	E	142	HIS
6	E	214	ASN
6	E	232	ASN
7	F	82	ASN
9	H	68	GLN
9	H	76	GLN
9	H	114	GLN
9	H	168	HIS
10	I	52	ASN
10	I	167	GLN
12	K	61	GLN
12	K	77	GLN
12	K	84	HIS
13	L	94	HIS
13	L	121	GLN
14	M	73	GLN
15	N	49	GLN
18	Q	80	GLN
19	R	118	GLN
20	S	73	ASN

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Mol	Chain	Res	Type
21	T	12	GLN
22	U	81	GLN
24	W	90	GLN
25	X	16	HIS
27	Z	64	ASN
28	a	25	ASN
29	b	51	GLN
29	b	65	GLN
30	c	7	GLN
30	c	29	GLN
31	d	3	HIS
32	e	15	GLN
34	g	51	ASN
34	g	187	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1663/1869 (88%)	437 (26%)	53 (3%)

All (437) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	C
1	2	17	C
1	2	26	U
1	2	33	G
1	2	44	U
1	2	46	A
1	2	56	G
1	2	58	C
1	2	59	U
1	2	60	A
1	2	61	A
1	2	65	C
1	2	66	G
1	2	67	C
1	2	68	A
1	2	71	G
1	2	72	C
1	2	73	C

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Mol	Chain	Res	Type
1	2	74	G
1	2	75	G
1	2	76	U
1	2	77	A
1	2	79	A
1	2	103	A
1	2	113	G
1	2	114	G
1	2	115	U
1	2	116	U
1	2	126	G
1	2	129	C
1	2	130	G
1	2	143	U
1	2	144	U
1	2	147	A
1	2	154	U
1	2	155	G
1	2	163	U
1	2	168	C
1	2	174	C
1	2	175	A
1	2	179	C
1	2	181	A
1	2	184	G
1	2	187	G
1	2	188	C
1	2	189	U
1	2	190	G
1	2	191	A
1	2	192	C
1	2	198	U
1	2	199	C
1	2	200	G
1	2	215	G
1	2	290	U
1	2	291	G
1	2	292	A
1	2	293	C
1	2	294	U
1	2	307	G
1	2	308	G

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Mol	Chain	Res	Type
1	2	309	G
1	2	310	C
1	2	315	C
1	2	319	C
1	2	321	C
1	2	330	G
1	2	332	G
1	2	333	G
1	2	335	G
1	2	360	A
1	2	362	C
1	2	364	A
1	2	368	U
1	2	369	C
1	2	370	G
1	2	377	G
1	2	383	G
1	2	385	G
1	2	386	C
1	2	399	C
1	2	400	C
1	2	408	A
1	2	409	C
1	2	418	A
1	2	438	G
1	2	448	A
1	2	450	C
1	2	464	A
1	2	465	A
1	2	466	G
1	2	471	G
1	2	472	C
1	2	473	A
1	2	474	G
1	2	482	G
1	2	483	C
1	2	487	U
1	2	492	C
1	2	501	C
1	2	502	C
1	2	530	U
1	2	532	C

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Mol	Chain	Res	Type
1	2	533	A
1	2	534	G
1	2	536	A
1	2	542	U
1	2	546	G
1	2	547	G
1	2	548	C
1	2	549	C
1	2	550	C
1	2	552	G
1	2	554	A
1	2	555	A
1	2	556	U
1	2	559	G
1	2	563	G
1	2	568	C
1	2	570	C
1	2	576	A
1	2	583	A
1	2	587	A
1	2	588	G
1	2	589	G
1	2	590	A
1	2	591	U
1	2	598	G
1	2	604	A
1	2	605	A
1	2	607	U
1	2	608	C
1	2	614	C
1	2	617	G
1	2	629	A
1	2	631	U
1	2	632	C
1	2	640	A
1	2	643	A
1	2	644	G
1	2	655	A
1	2	659	G
1	2	660	C
1	2	669	A
1	2	671	A

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Mol	Chain	Res	Type
1	2	672	A
1	2	673	G
1	2	685	A
1	2	687	C
1	2	688	U
1	2	747	U
1	2	749	U
1	2	750	C
1	2	751	G
1	2	792	C
1	2	794	A
1	2	796	G
1	2	797	C
1	2	798	G
1	2	799	U
1	2	809	A
1	2	810	A
1	2	811	A
1	2	812	A
1	2	821	G
1	2	822	U
1	2	823	U
1	2	824	C
1	2	830	A
1	2	845	G
1	2	847	A
1	2	869	A
1	2	870	A
1	2	871	U
1	2	872	A
1	2	873	G
1	2	874	G
1	2	877	C
1	2	878	G
1	2	879	C
1	2	880	G
1	2	881	G
1	2	882	U
1	2	887	U
1	2	888	U
1	2	890	U
1	2	891	G

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Mol	Chain	Res	Type
1	2	893	U
1	2	894	G
1	2	895	G
1	2	903	A
1	2	906	U
1	2	913	A
1	2	914	U
1	2	918	U
1	2	919	A
1	2	920	A
1	2	926	A
1	2	930	C
1	2	933	G
1	2	934	G
1	2	943	U
1	2	955	A
1	2	956	G
1	2	959	G
1	2	960	U
1	2	967	C
1	2	969	U
1	2	970	G
1	2	971	G
1	2	978	G
1	2	981	A
1	2	990	A
1	2	992	A
1	2	998	A
1	2	999	G
1	2	1001	A
1	2	1009	A
1	2	1017	U
1	2	1023	A
1	2	1040	G
1	2	1041	G
1	2	1049	A
1	2	1060	A
1	2	1061	U
1	2	1062	A
1	2	1080	A
1	2	1083	A
1	2	1085	C

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Mol	Chain	Res	Type
1	2	1087	A
1	2	1088	U
1	2	1096	G
1	2	1107	G
1	2	1114	U
1	2	1116	C
1	2	1117	C
1	2	1118	C
1	2	1119	A
1	2	1120	U
1	2	1122	A
1	2	1133	A
1	2	1138	C
1	2	1139	C
1	2	1143	A
1	2	1153	C
1	2	1154	U
1	2	1157	G
1	2	1165	G
1	2	1166	G
1	2	1171	G
1	2	1195	A
1	2	1199	A
1	2	1203	G
1	2	1207	G
1	2	1208	A
1	2	1211	G
1	2	1215	C
1	2	1221	G
1	2	1224	G
1	2	1225	U
1	2	1226	G
1	2	1232	U
1	2	1242	U
1	2	1245	G
1	2	1247	C
1	2	1248	U
1	2	1251	A
1	2	1253	A
1	2	1256	G
1	2	1257	G
1	2	1258	A

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Mol	Chain	Res	Type
1	2	1259	A
1	2	1260	A
1	2	1274	G
1	2	1275	G
1	2	1276	A
1	2	1278	A
1	2	1284	A
1	2	1285	G
1	2	1286	G
1	2	1297	U
1	2	1298	G
1	2	1300	U
1	2	1301	A
1	2	1302	G
1	2	1303	C
1	2	1305	C
1	2	1312	G
1	2	1313	A
1	2	1322	G
1	2	1325	G
1	2	1327	G
1	2	1331	C
1	2	1342	U
1	2	1343	U
1	2	1348	G
1	2	1358	U
1	2	1366	G
1	2	1371	U
1	2	1372	U
1	2	1373	C
1	2	1378	A
1	2	1382	A
1	2	1395	C
1	2	1402	A
1	2	1405	A
1	2	1406	G
1	2	1412	C
1	2	1414	A
1	2	1426	U
1	2	1428	G
1	2	1438	A
1	2	1439	A

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Mol	Chain	Res	Type
1	2	1441	U
1	2	1446	A
1	2	1452	A
1	2	1454	A
1	2	1463	U
1	2	1465	A
1	2	1466	G
1	2	1475	G
1	2	1476	A
1	2	1489	A
1	2	1490	G
1	2	1494	U
1	2	1495	G
1	2	1497	G
1	2	1500	G
1	2	1501	C
1	2	1502	C
1	2	1507	G
1	2	1508	A
1	2	1509	U
1	2	1511	U
1	2	1512	C
1	2	1514	G
1	2	1516	G
1	2	1520	G
1	2	1521	C
1	2	1522	A
1	2	1533	A
1	2	1534	C
1	2	1538	C
1	2	1545	A
1	2	1549	U
1	2	1551	U
1	2	1553	C
1	2	1560	U
1	2	1567	G
1	2	1575	G
1	2	1579	A
1	2	1580	A
1	2	1581	C
1	2	1585	U
1	2	1586	U

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Mol	Chain	Res	Type
1	2	1588	A
1	2	1598	G
1	2	1600	G
1	2	1601	A
1	2	1603	G
1	2	1605	G
1	2	1606	G
1	2	1614	A
1	2	1616	U
1	2	1618	C
1	2	1619	A
1	2	1621	U
1	2	1623	A
1	2	1624	U
1	2	1629	C
1	2	1640	A
1	2	1646	C
1	2	1647	A
1	2	1649	U
1	2	1650	A
1	2	1652	G
1	2	1654	G
1	2	1656	G
1	2	1658	G
1	2	1659	U
1	2	1663	A
1	2	1665	G
1	2	1671	G
1	2	1675	A
1	2	1683	C
1	2	1686	G
1	2	1688	C
1	2	1689	C
1	2	1690	U
1	2	1695	A
1	2	1697	A
1	2	1699	A
1	2	1719	A
1	2	1720	U
1	2	1721	U
1	2	1722	G
1	2	1723	G

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Mol	Chain	Res	Type
1	2	1724	A
1	2	1727	G
1	2	1729	U
1	2	1744	G
1	2	1753	C
1	2	1755	C
1	2	1756	C
1	2	1757	G
1	2	1761	U
1	2	1772	C
1	2	1773	C
1	2	1774	C
1	2	1776	G
1	2	1778	C
1	2	1779	G
1	2	1780	G
1	2	1783	C
1	2	1784	G
1	2	1800	A
1	2	1813	A
1	2	1815	A
1	2	1816	G
1	2	1824	A
1	2	1825	A
1	2	1826	G
1	2	1829	G
1	2	1831	A
1	2	1835	A
1	2	1836	G
1	2	1838	U
1	2	1849	G
1	2	1851	A
1	2	1852	C
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1864	U
1	2	1865	C
1	2	1867	U
1	2	1868	U
1	2	1869	A

All (53) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	60	A
1	2	65	C
1	2	71	G
1	2	102	A
1	2	114	G
1	2	143	U
1	2	180	G
1	2	189	U
1	2	291	G
1	2	293	C
1	2	306	C
1	2	314	U
1	2	332	G
1	2	368	U
1	2	382	C
1	2	465	A
1	2	500	A
1	2	554	A
1	2	589	G
1	2	591	U
1	2	604	A
1	2	748	C
1	2	750	C
1	2	791	C
1	2	797	C
1	2	811	A
1	2	821	G
1	2	893	U
1	2	958	G
1	2	980	A
1	2	1016	U
1	2	1138	C
1	2	1165	G
1	2	1277	C
1	2	1312	G
1	2	1330	G
1	2	1342	U
1	2	1425	G
1	2	1438	A
1	2	1440	C
1	2	1464	C
1	2	1494	U
1	2	1548	G

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Mol	Chain	Res	Type
1	2	1585	U
1	2	1587	G
1	2	1603	G
1	2	1618	C
1	2	1649	U
1	2	1658	G
1	2	1718	G
1	2	1721	U
1	2	1773	C
1	2	1825	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 100 ligands modelled in this entry, 100 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

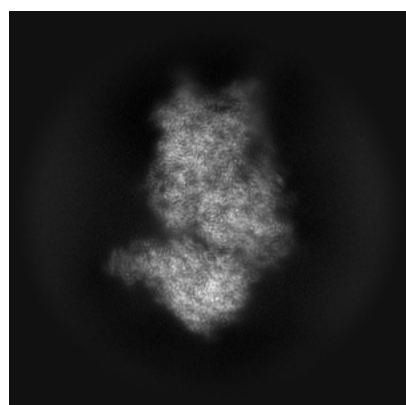
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41039. These allow visual inspection of the internal detail of the map and identification of artifacts.

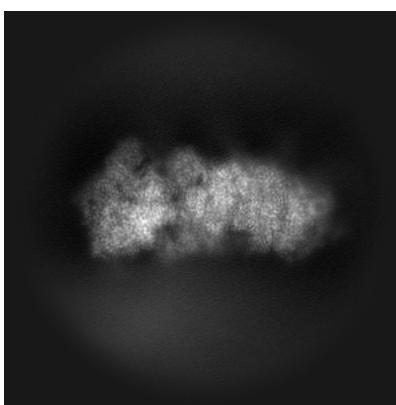
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

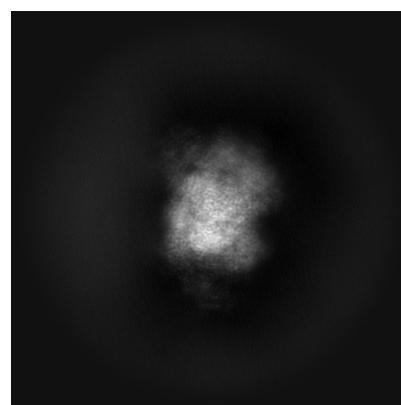
6.1.1 Primary map



X



Y

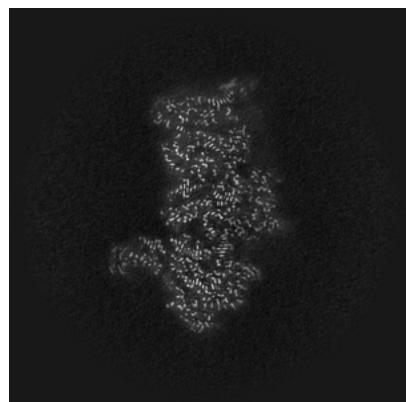


Z

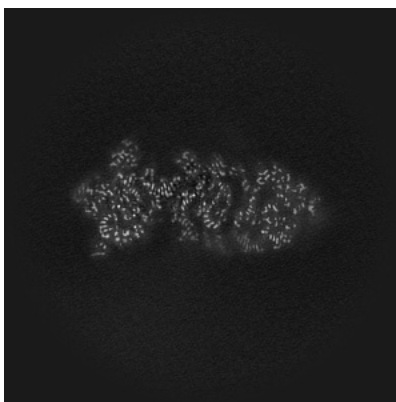
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

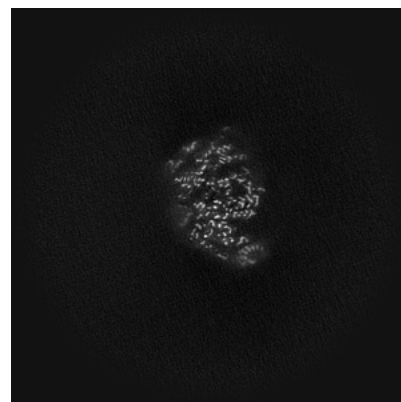
6.2.1 Primary map



X Index: 190



Y Index: 190

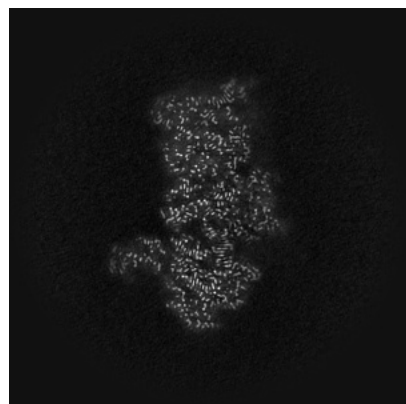


Z Index: 190

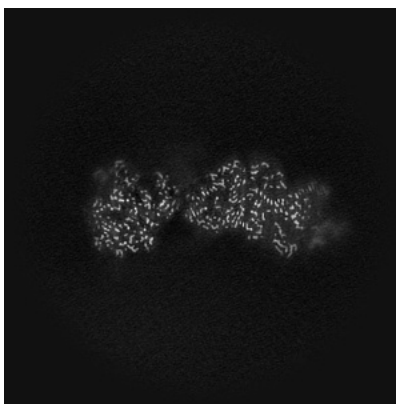
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

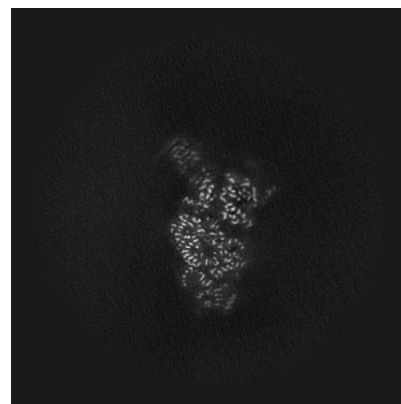
6.3.1 Primary map



X Index: 189



Y Index: 165

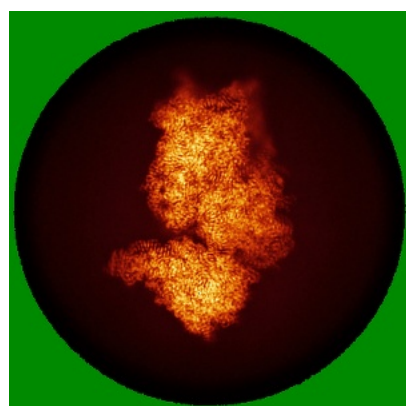


Z Index: 138

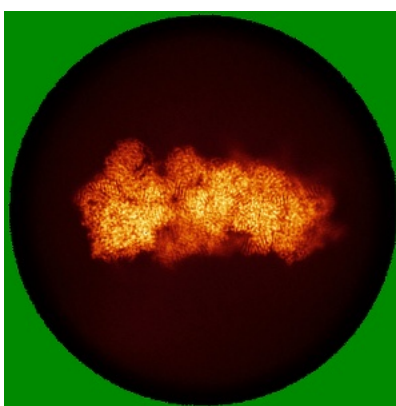
The images above show the largest variance slices of the map in three orthogonal directions.

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

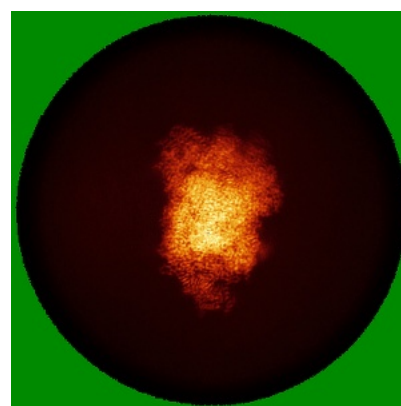
6.4.1 Primary map



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](#)

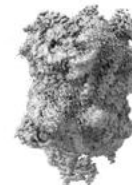
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.14. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

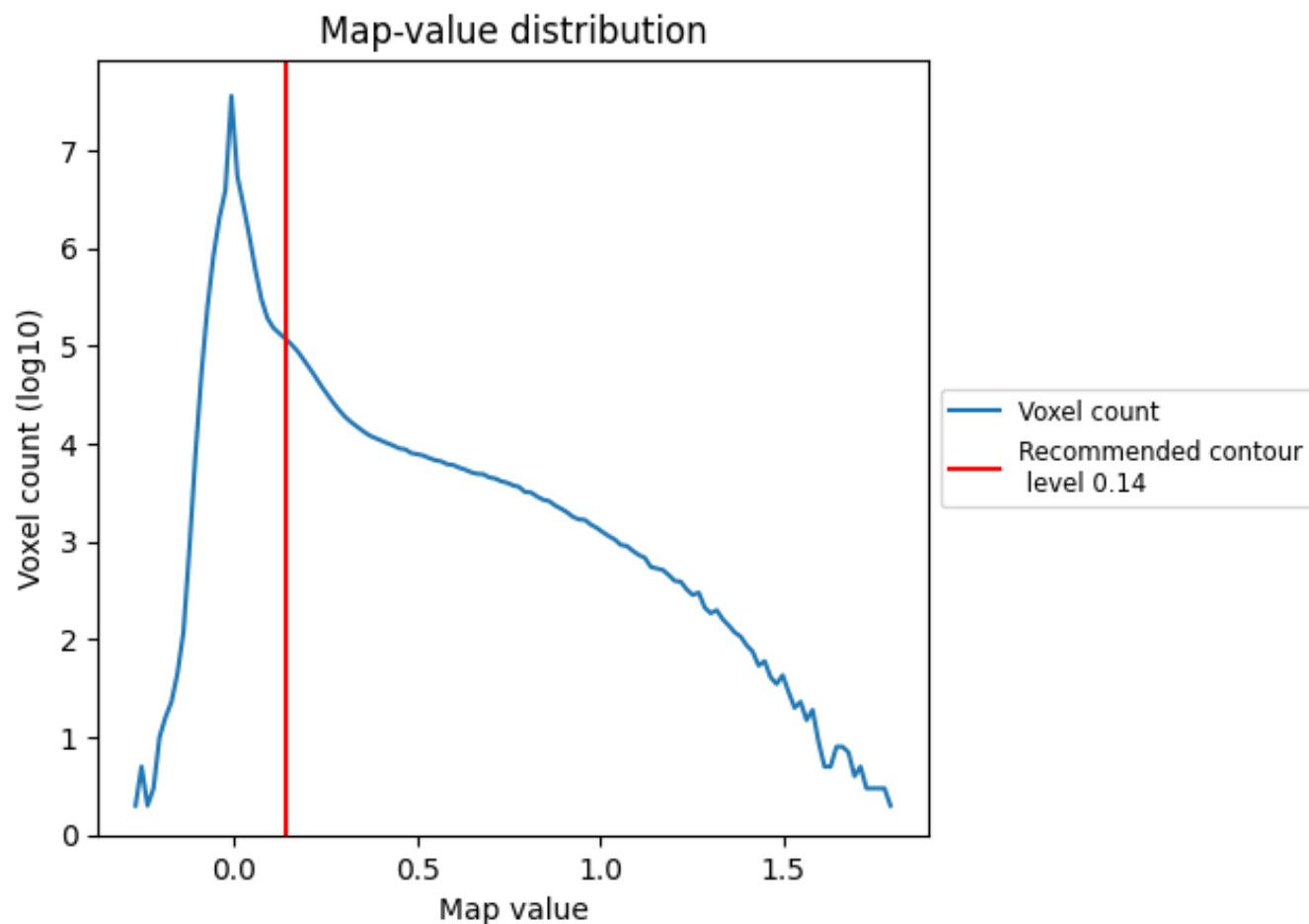
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

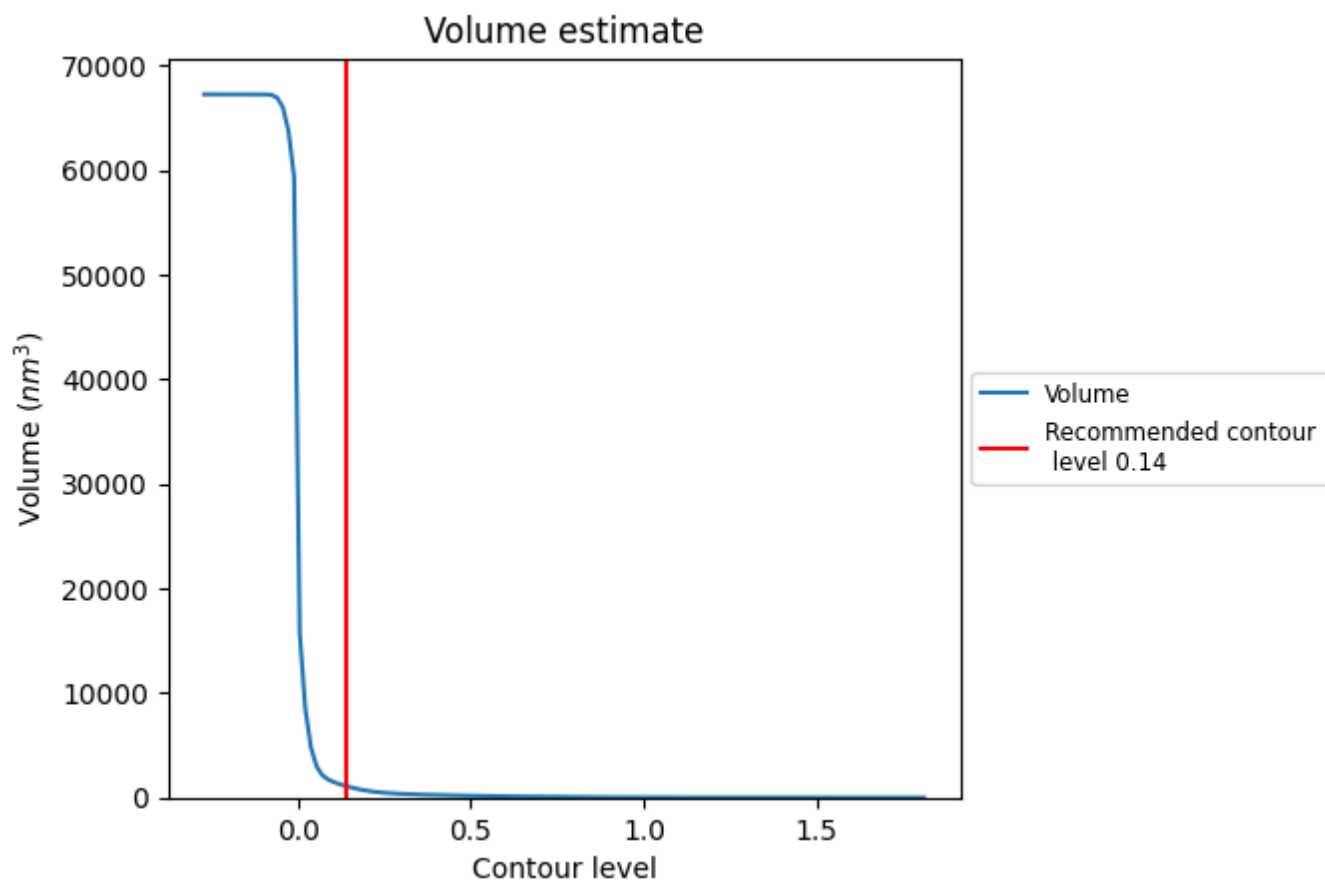
This section contains the results of statistical analysis of the map.

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.

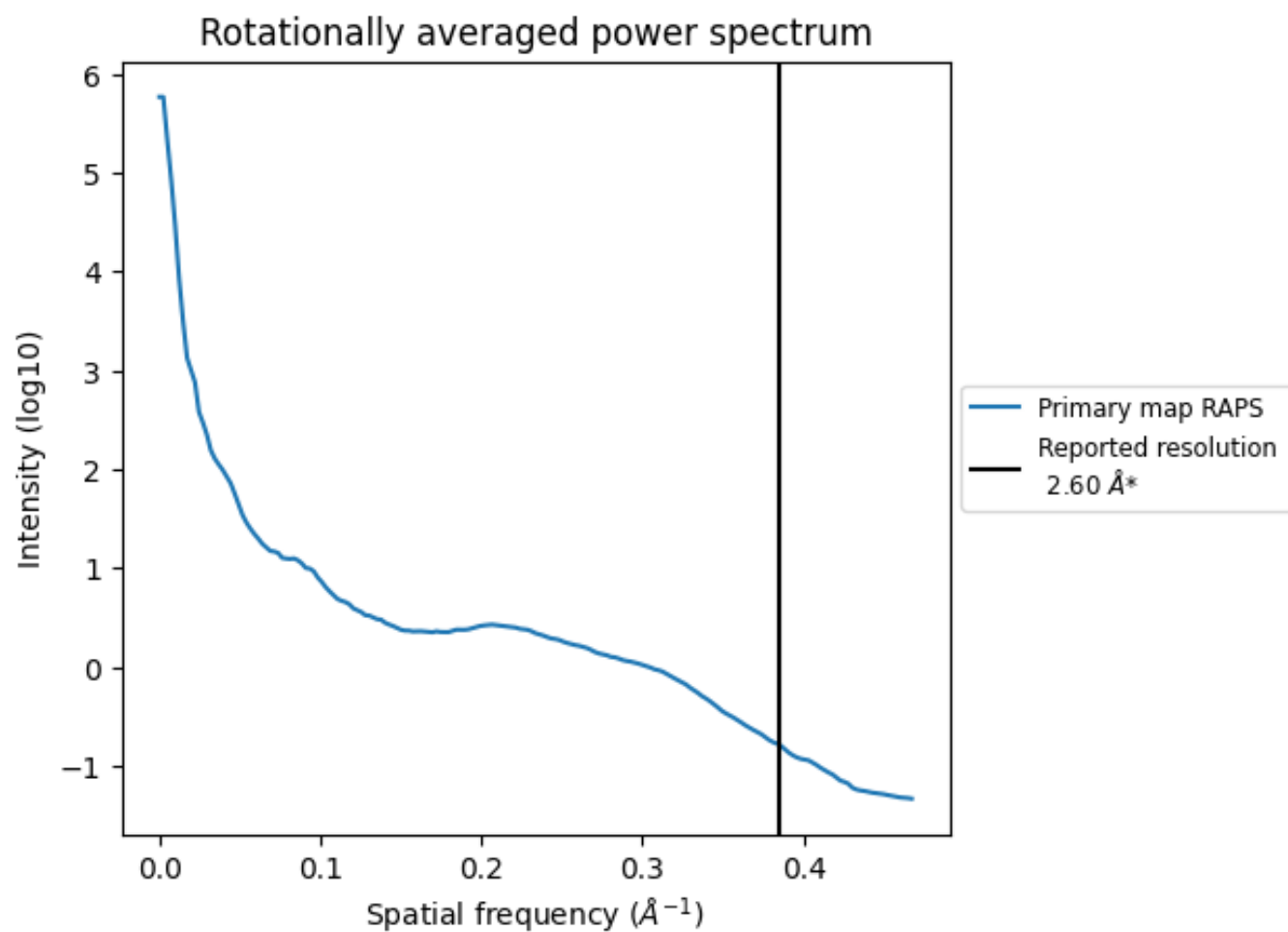
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1093 nm³; this corresponds to an approximate mass of 987 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 ⓘ

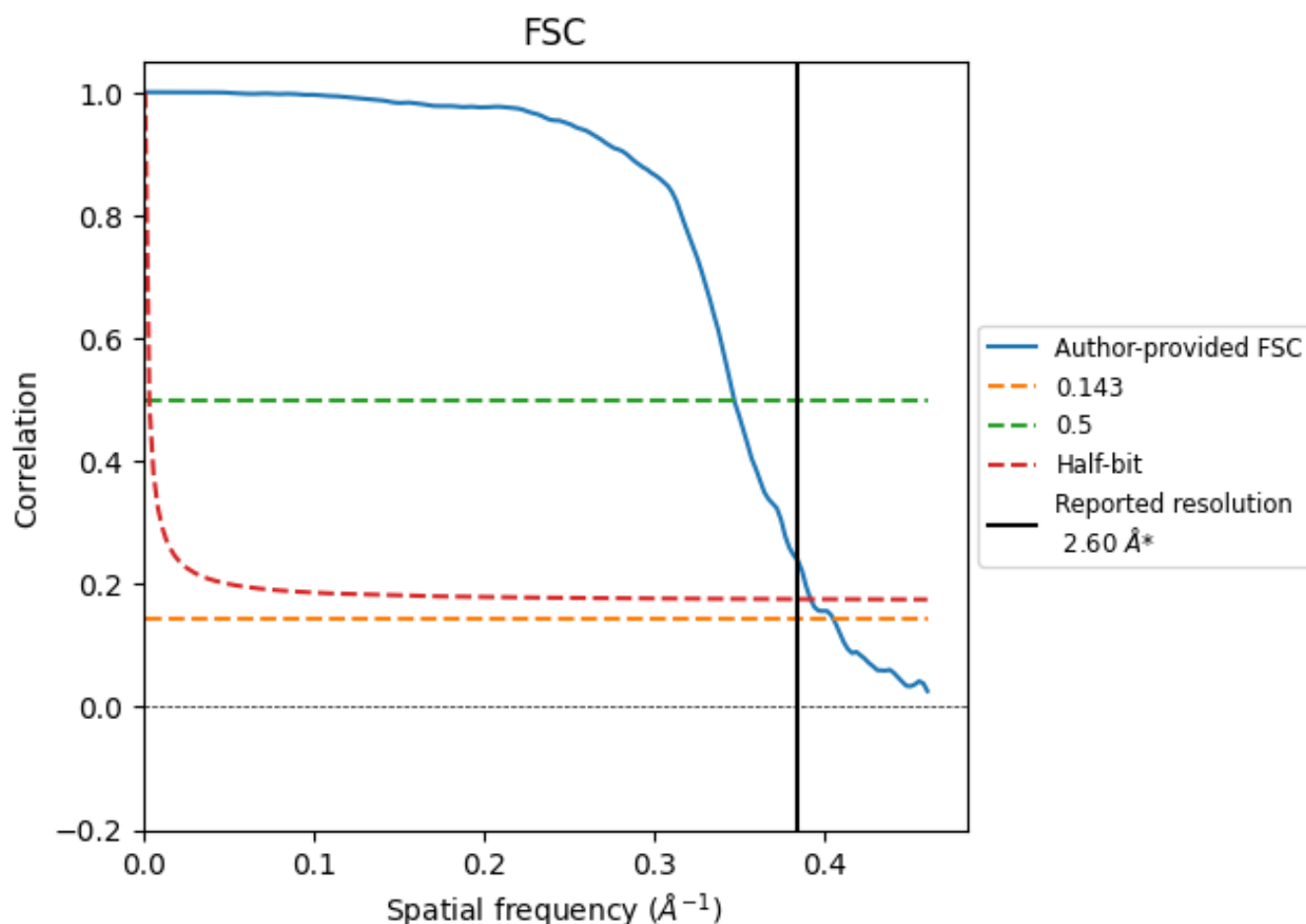


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

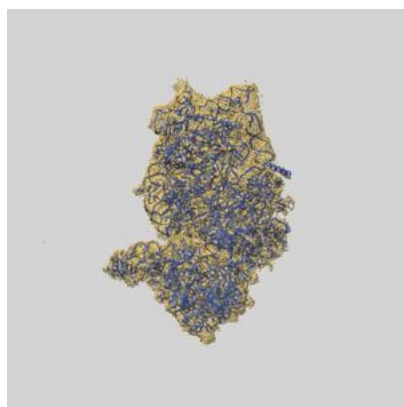
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.46	2.88	2.55
Unmasked-calculated*	-	-	-

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

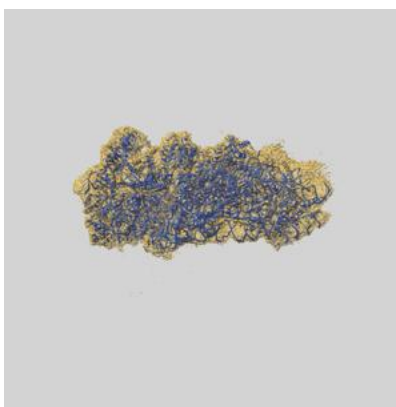
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41039 and PDB model 8T4S. Per-residue inclusion information can be found in section [3](#) on page [12](#).

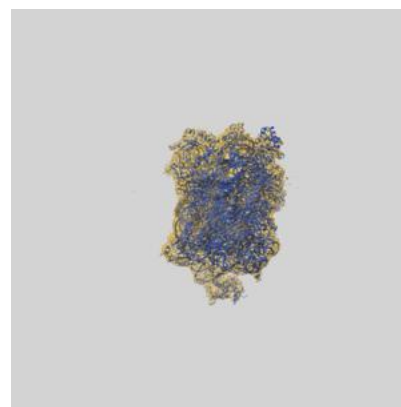
9.1 Map-model overlay [i](#)



X



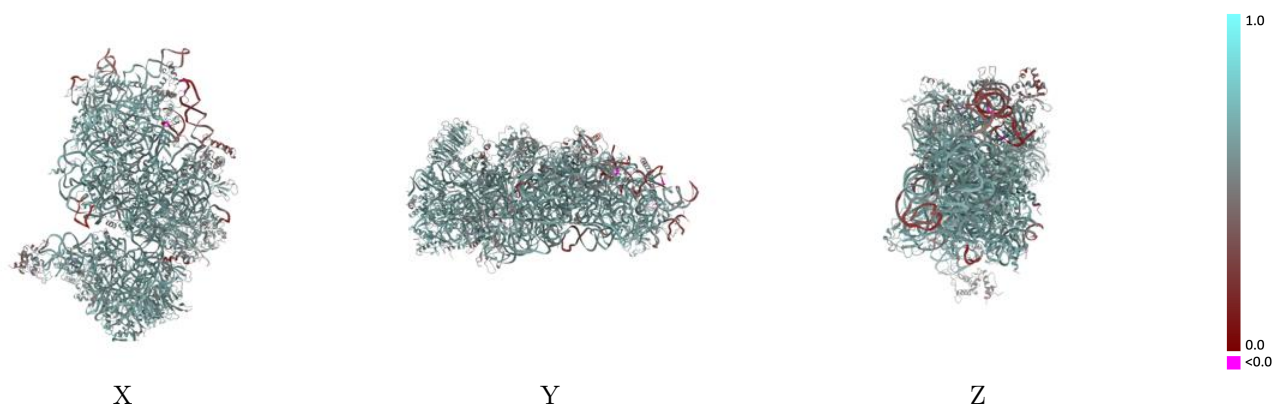
Y



Z

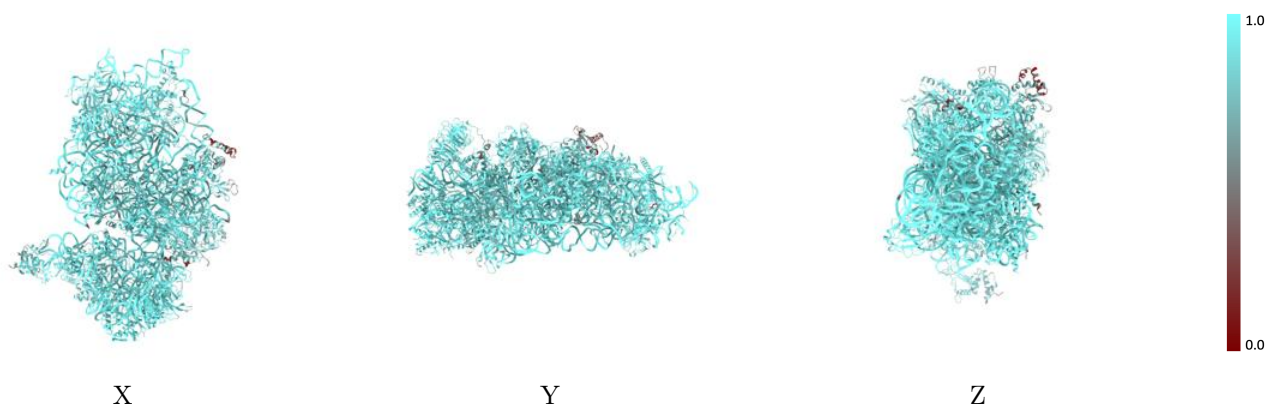
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



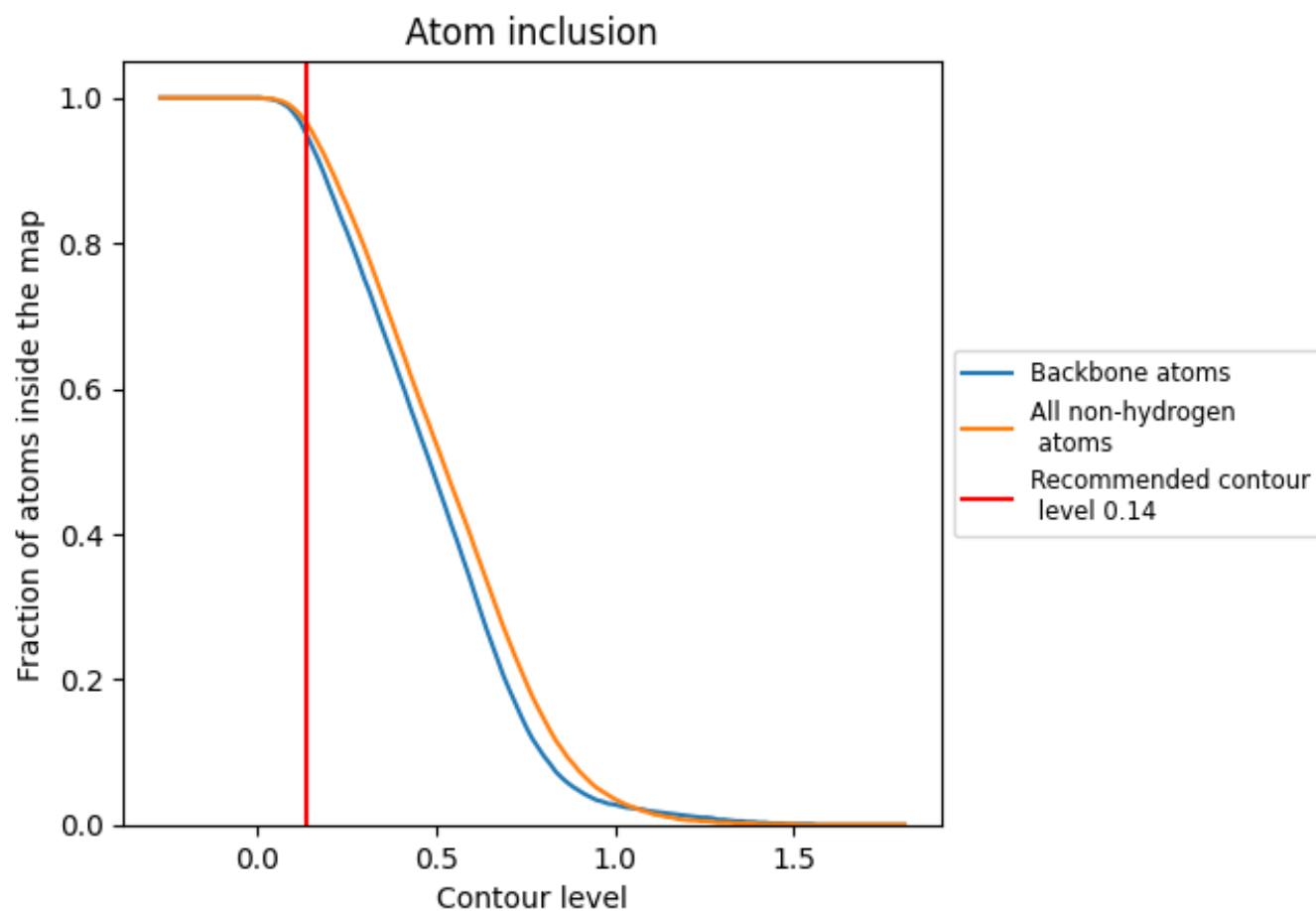
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.14).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 96% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.5900
2	 0.9880	 0.5930
A	 0.9560	 0.5880
B	 0.9130	 0.5600
C	 0.9840	 0.6260
D	 0.9610	 0.5890
E	 0.9830	 0.6260
F	 0.9820	 0.6110
G	 0.9690	 0.5790
H	 0.7250	 0.4640
I	 0.9720	 0.6090
J	 0.9760	 0.6220
K	 0.9850	 0.6190
L	 0.9620	 0.6240
M	 0.7820	 0.4390
N	 0.9360	 0.5760
O	 0.9130	 0.5350
P	 0.9550	 0.6060
Q	 0.9980	 0.6410
R	 0.8580	 0.5380
S	 0.9640	 0.5910
T	 0.9840	 0.6230
U	 0.9540	 0.5830
V	 0.9710	 0.5890
W	 0.9810	 0.6230
X	 0.9800	 0.6220
Y	 0.9750	 0.6110
Z	 0.9720	 0.6090
a	 0.9230	 0.5900
b	 0.8380	 0.5630
c	 0.9470	 0.5570
d	 0.9840	 0.6520
e	 0.9180	 0.5820
f	 0.8490	 0.5060
g	 0.9520	 0.5840



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Chain	Atom inclusion	Q-score
h	 0.9170	 0.5610
n	 0.9360	 0.5800