



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 12:06 PM UTC

PDB ID : 4CE4 / pdb_00004ce4
EMDB ID : EMD-2490
Title : 39S large subunit of the porcine mitochondrial ribosome
Authors : Greber, B.J.; Boehringer, D.; Leitner, A.; Bieri, P.; Voigts-Hoffmann, F.;
Erzberger, J.P.; Leibundgut, M.; Aebersold, R.; Ban, N.
Deposited on : 2013-11-08
Resolution : 4.90 Å(reported)
Based on initial models : 2XZN, 2CW9, 1S3A, 1QF6, 1J26, 3V2D, 2QYQ, 1O0W, 1R73

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:

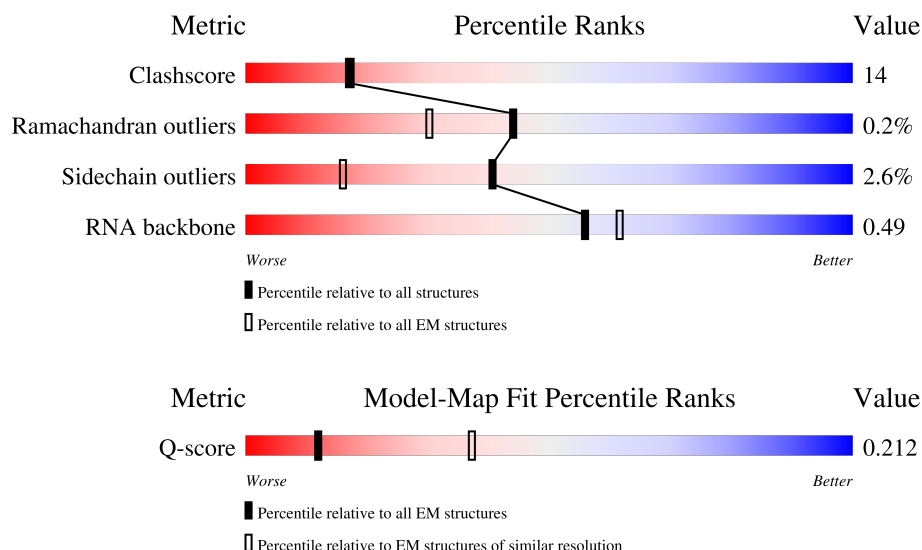
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.90 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	1274 (4.40 - 5.40)

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	0	148	
2	1	256	
3	2	252	

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Mol	Chain	Length	Quality of chain
4	3	161	
5	5	146	
6	6	65	
7	7	95	
8	8	188	
9	9	100	
10	A	1570	
11	B	29	
12	D	306	
13	E	399	
14	F	224	
15	I	268	
16	N	178	
17	O	145	
18	P	288	
19	Q	208	
20	R	169	
21	S	180	
22	T	292	
23	U	132	
24	V	207	
25	W	134	
26	X	87	
27	Y	216	
28	b	380	

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Mol	Chain	Length	Quality of chain
29	c	301	
30	h	298	
31	i	312	
32	l	166	
33	o	56	
34	u	205	
35	v	91	
35	w	91	
36	x	85	
37	z	426	

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 65473 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called MRPL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	76	Total	C	N	O	S	0	0
			607	392	114	99	2		

- Molecule 2 is a protein called MRPL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	58	Total	C	N	O	S	0	0
			489	312	90	85	2		

- Molecule 3 is a protein called MRPL47.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	76	Total	C	N	O	S	0	0
			633	394	116	119	4		

- Molecule 4 is a protein called MRPL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	59	Total	C	N	O	S	0	0
			491	321	95	74	1		

- Molecule 5 is a protein called MRPL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	68	Total	C	N	O	S	0	0
			508	317	103	83	5		

- Molecule 6 is a protein called MRPL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	48	Total	C	N	O	S	0	0
			391	253	70	66	2		

- Molecule 7 is a protein called MRPL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	43	Total	C	N	O	S	0	0
			362	224	82	55	1		

- Molecule 8 is a protein called MRPL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	60	Total	C	N	O	S	0	0
			520	338	106	74	2		

- Molecule 9 is a protein called MRPL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	36	Total	C	N	O	S	0	0
			316	200	68	45	3		

- Molecule 10 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	1444	Total	C	N	O	P	0	0
			30656	13760	5548	9904	1444		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127A	G	-	insertion	GB AJ002189

- Molecule 11 is a RNA chain called UNASSIGNED RNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	B	29	Total	C	O	P	0	0
			348	145	174	29		

- Molecule 12 is a protein called MRPL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	200	Total	C	N	O	S	0	0
			1531	944	309	269	9		

- Molecule 13 is a protein called MRPL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	208	Total	C	N	O	S	0	0
			1621	1040	300	274	7		

- Molecule 14 is a protein called MRPL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	224	Total	C	N	O	S	0	0
			1713	1101	310	298	4		

- Molecule 15 is a protein called MRPL9.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	I	57	Total	C	N	O	0	0
			447	282	79	86		

- Molecule 16 is a protein called MRPL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	147	Total	C	N	O	S	0	0
			1178	756	210	204	8		

- Molecule 17 is a protein called MRPL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	114	Total	C	N	O	S	0	0
			891	559	175	153	4		

- Molecule 18 is a protein called MRPL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	169	Total	C	N	O	S	0	0
			1309	816	258	233	2		

- Molecule 19 is a protein called MRPL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	154	Total	C	N	O	S	0	0
			1179	758	218	195	8		

- Molecule 20 is a protein called MRPL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	120	Total	C	N	O	S	0	0
			982	619	187	172	4		

- Molecule 21 is a protein called MRPL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	94	Total	C	N	O	S	0	0
			748	467	146	131	4		

- Molecule 22 is a protein called MRPL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	119	Total	C	N	O	S	0	0
			962	615	166	177	4		

- Molecule 23 is a protein called MRPL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	123	Total	C	N	O	S	0	0
			1018	647	212	156	3		

- Molecule 24 is a protein called MRPL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	109	Total	C	N	O	S	0	0
			877	565	156	154	2		

- Molecule 25 is a protein called MRPL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	134	Total	C	N	O	S	0	0
			1058	679	191	182	6		

- Molecule 26 is a protein called MRPL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	87	Total	C	N	O	S	0	0
			689	436	133	118	2		

- Molecule 27 is a protein called MRPL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	103	Total	C	N	O	S	0	0
			835	526	156	151	2		

- Molecule 28 is a protein called MRPL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	192	Total	C	N	O	S	0	0
			1562	1006	266	284	6		

- Molecule 29 is a protein called MRPL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	292	Total	C	N	O	S	0	0
			2310	1489	391	415	15		

- Molecule 30 is a protein called MRPL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	h	272	Total	C	N	O	S	0	0
			2075	1333	344	391	7		

- Molecule 31 is a protein called MRPL45.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	i	161	Total	C	N	O	S	0	0
			1335	845	243	239	8		

- Molecule 32 is a protein called MRPL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	l	76	Total	C	N	O	S	0	0
			619	398	108	111	2		

- Molecule 33 is a protein called MRPL52.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	o	56	Total	C	N	O	0	0
			336	224	56	56		

- Molecule 34 is a protein called ICT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	u	90	Total	C	N	O	S	0	0
			717	444	137	132	4		

- Molecule 35 is a protein called UNASSIGNED HELICES.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	v	91	Total	C	N	O	0	0
			546	364	91	91		
35	w	91	Total	C	N	O	0	0
			546	364	91	91		

- Molecule 36 is a protein called THIOREDOXIN FOLD.

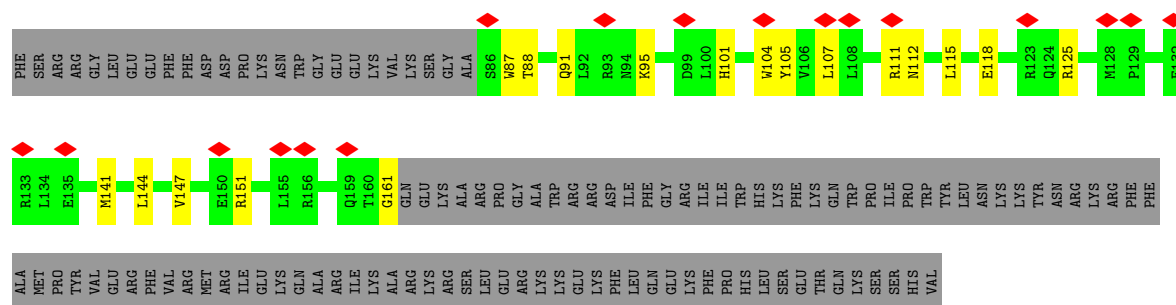
Mol	Chain	Residues	Atoms				AltConf	Trace
36	x	85	Total	C	N	O	0	0
			510	340	85	85		

- Molecule 37 is a protein called UNASSIGNED HELICES.

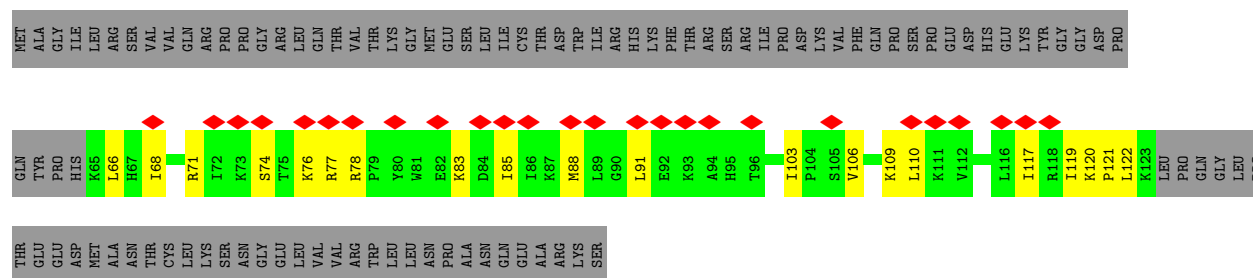
Mol	Chain	Residues	Atoms				AltConf	Trace
37	z	426	Total	C	N	O	0	0
			2556	1704	426	426		

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

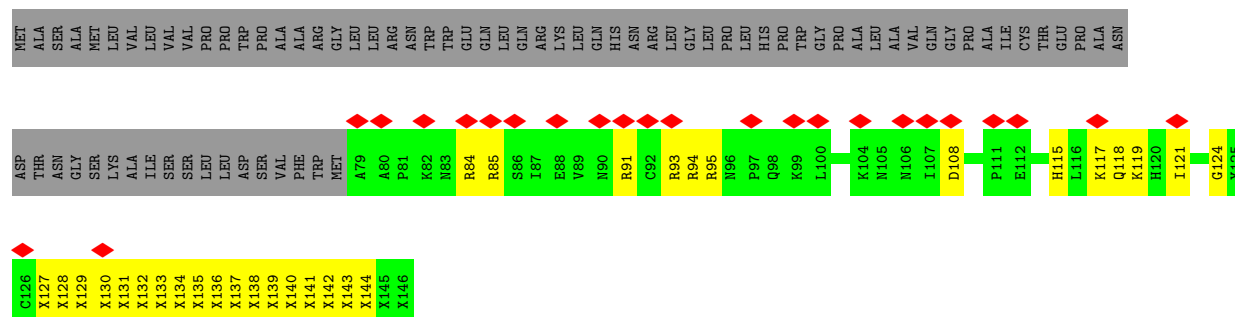
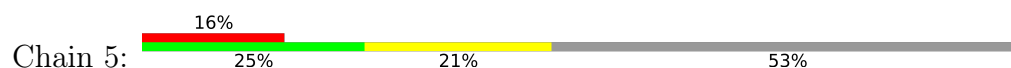
Mol	Chain	Residues	Atoms		AltConf
38	5	1	Total	Zn	0
			1	1	
38	9	1	Total	Zn	0
			1	1	



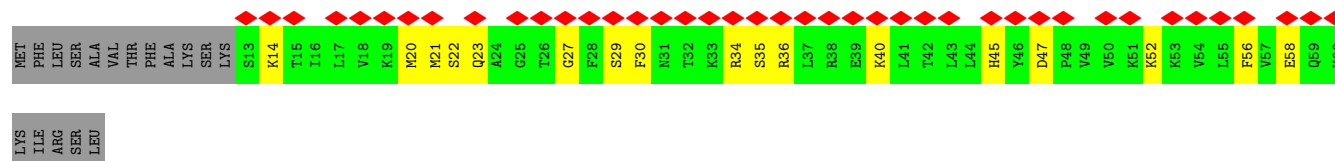
- Molecule 4: MRPL30



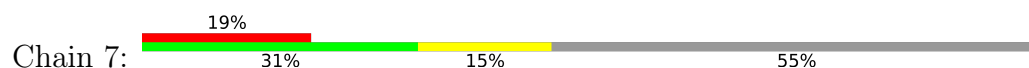
- Molecule 5: MRPL32

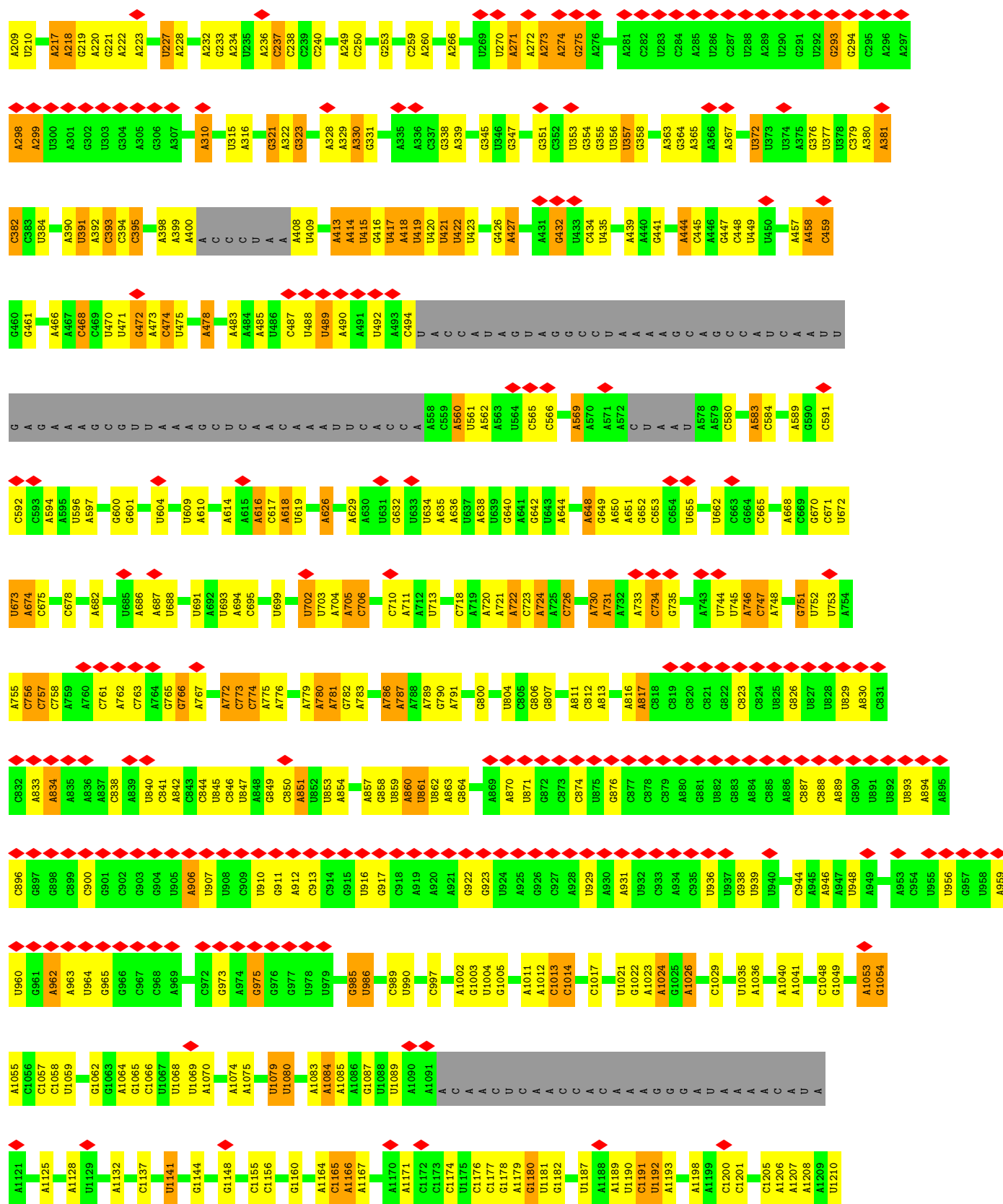


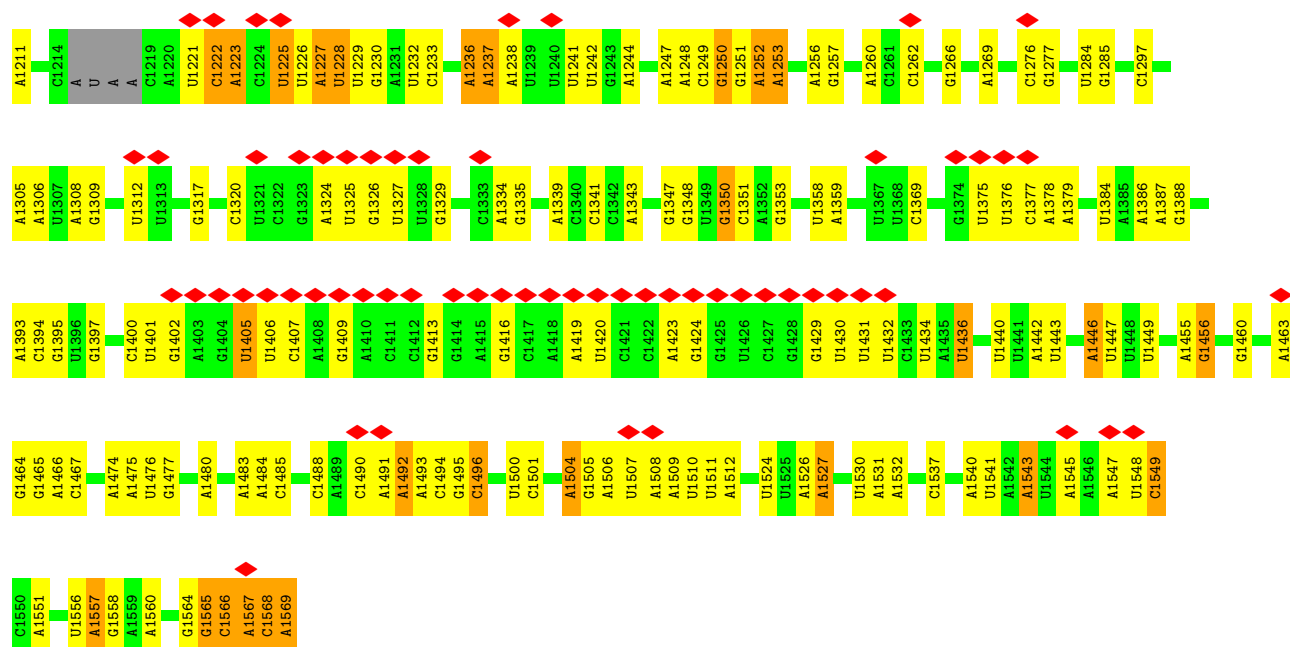
- Molecule 6: MRPL33



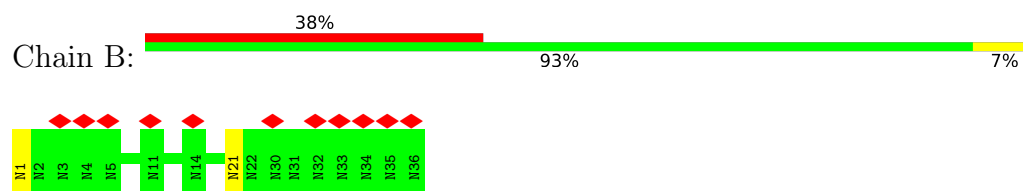
- Molecule 7: MRPL34



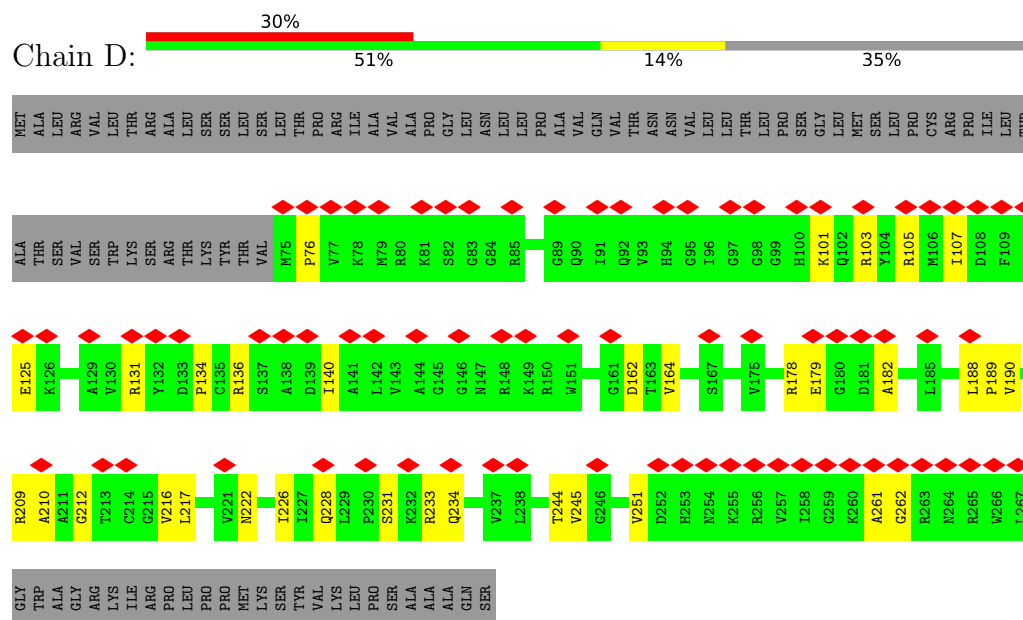




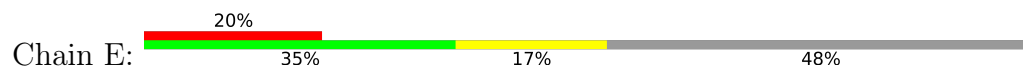
• Molecule 11: UNASSIGNED RNA



• Molecule 12: MRPL2



• Molecule 13: MRPL3

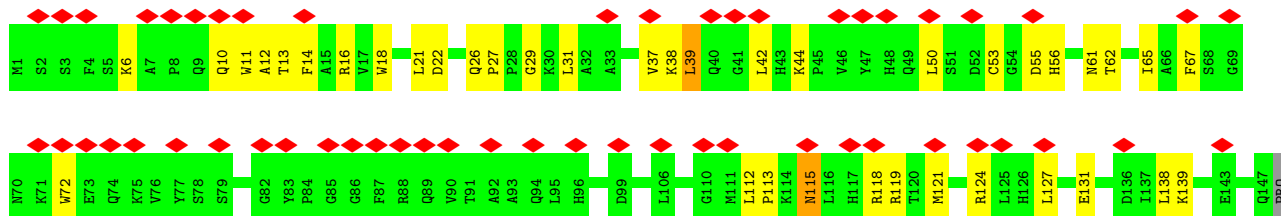




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THR
LYS
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TYR
LEU
ALA
GLN
GLN
ALA
LYS
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PRO
THR
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SER
GLN
MET
ILE

• Molecule 16: MRPL13

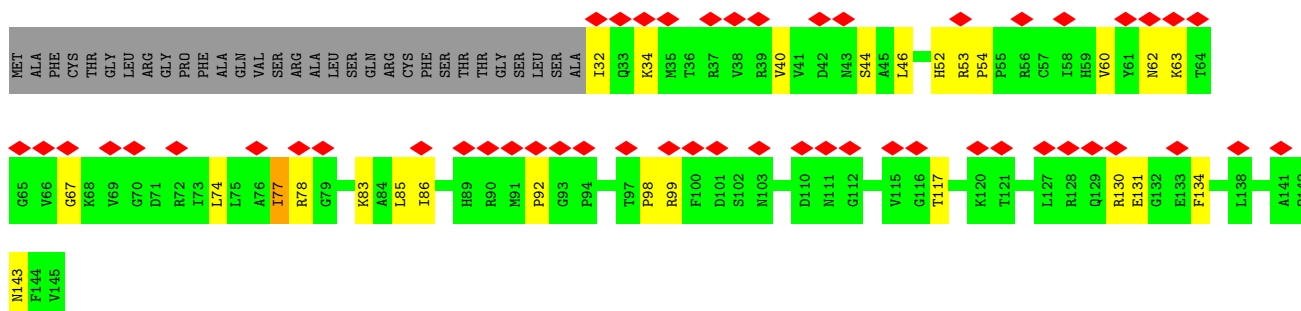
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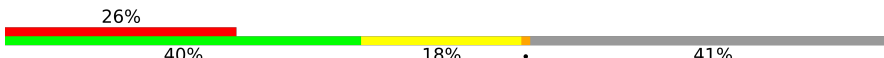
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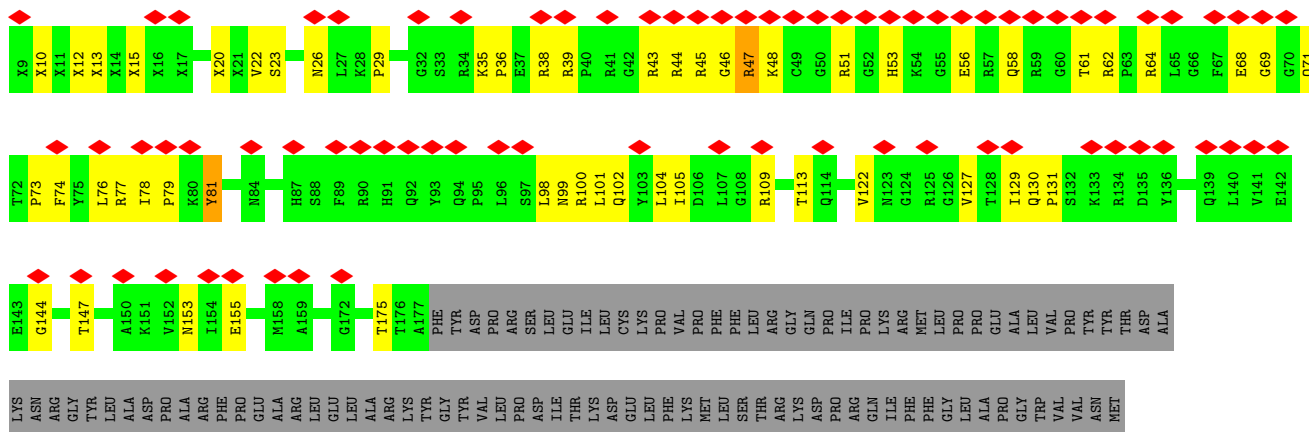
• Molecule 17: MRPL14

Chain O: 



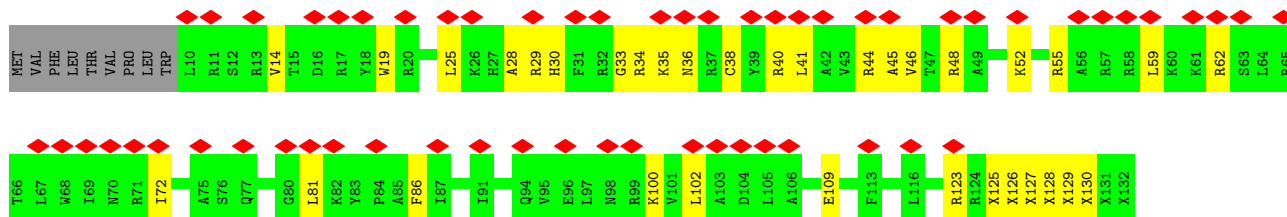
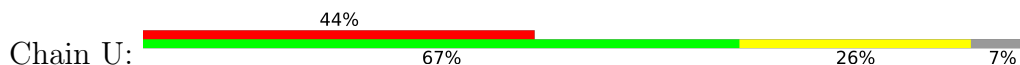
• Molecule 18: MRPL15

Chain P: 

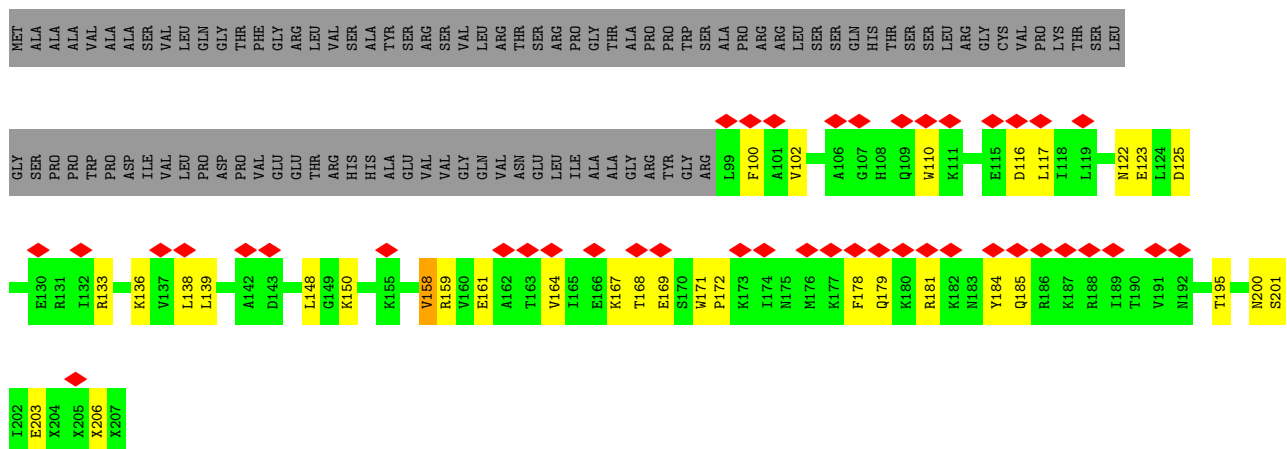
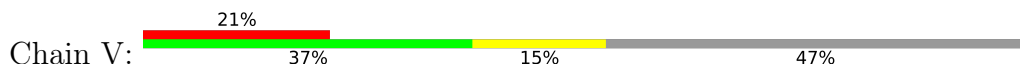


• Molecule 19: MRPL16

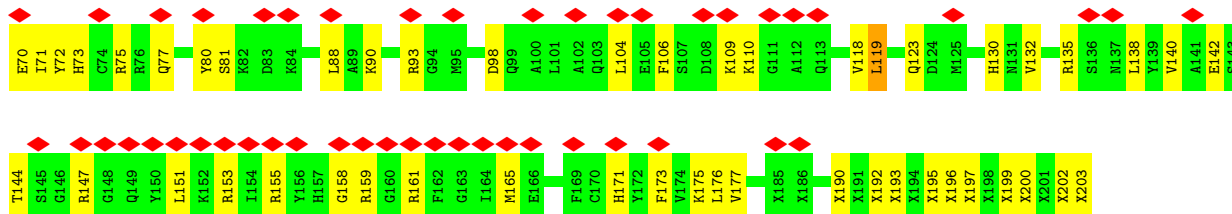
- Molecule 23: MRPL20



- Molecule 24: MRPL21

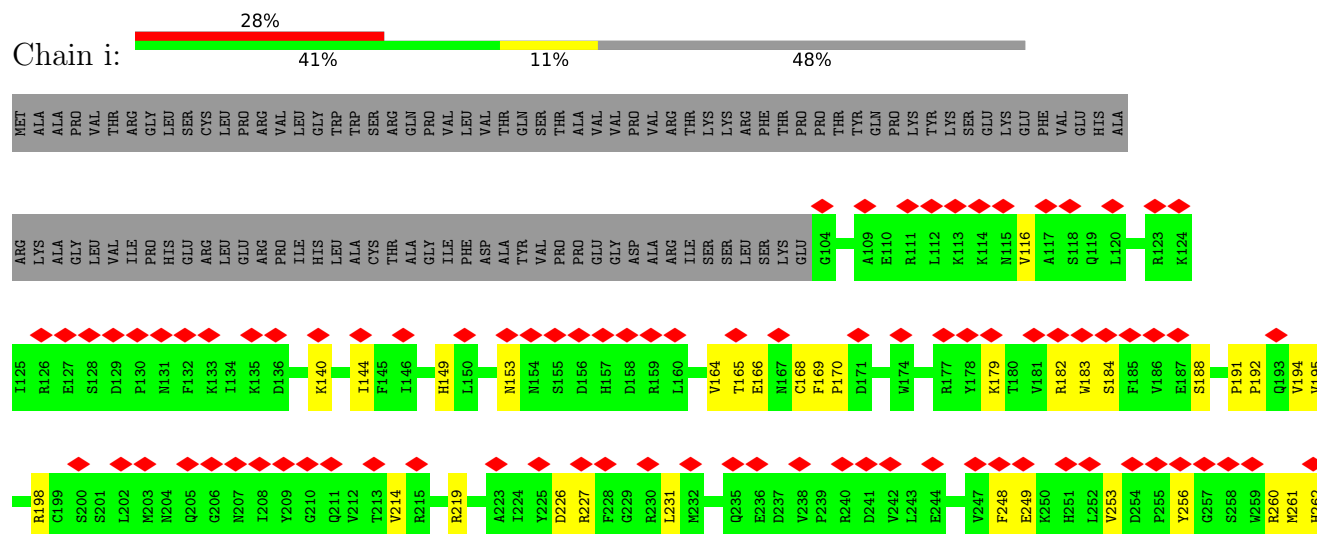


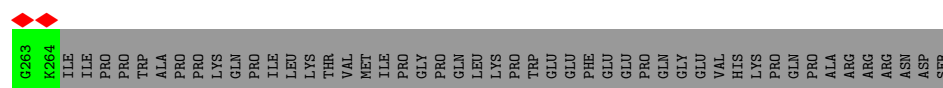
- Molecule 25: MRPL22



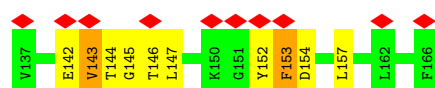
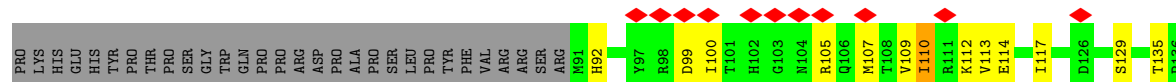
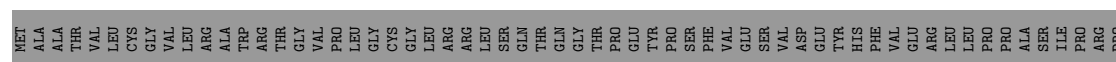
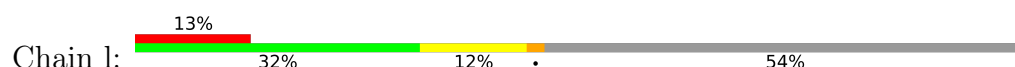
- Molecule 26: MRPL23

WORLDWIDE
PDB
PROTEIN DATA BANK

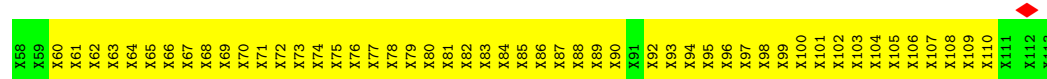




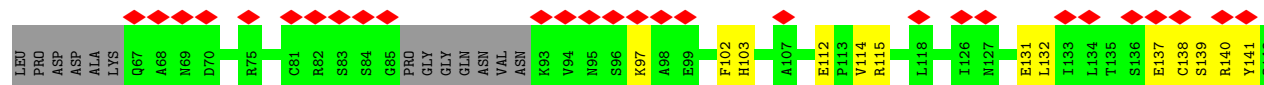
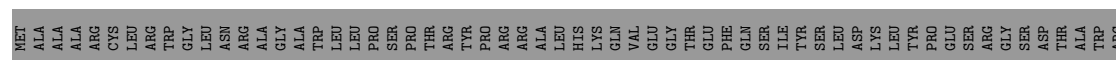
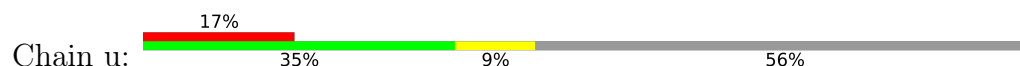
• Molecule 32: MRPL49



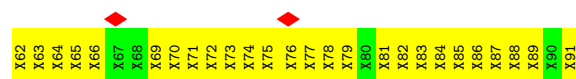
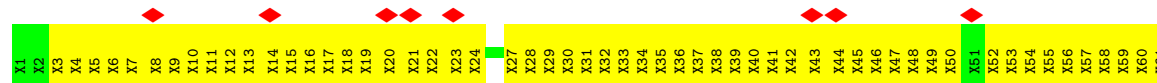
• Molecule 33: MRPL52



• Molecule 34: ICT1



• Molecule 35: UNASSIGNED HELICES



• Molecule 35: UNASSIGNED HELICES

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	232181	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PER DETECTOR FRAME	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3600	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	48.929	Depositor
Minimum map value	-45.891	Depositor
Average map value	-0.047	Depositor
Map value standard deviation	3.830	Depositor
Recommended contour level	11	Depositor
Map size ($\text{\AA}$)	360.96, 360.96, 360.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.41, 1.41, 1.41	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

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	0	0.22	0/624	0.64	0/836
2	1	0.23	0/498	0.78	1/670 (0.1%)
3	2	0.25	0/641	0.64	0/862
4	3	0.26	0/501	0.74	0/671
5	5	0.26	0/393	0.74	0/524
6	6	0.23	0/396	0.69	2/526 (0.4%)
7	7	0.24	0/370	0.74	0/492
8	8	0.23	0/529	0.64	0/698
9	9	0.22	0/322	0.60	0/424
10	A	0.09	0/34230	0.21	0/53284
12	D	0.26	0/1557	0.75	1/2093 (0.0%)
13	E	0.26	0/1662	0.68	0/2246
14	F	0.28	0/1582	0.78	2/2148 (0.1%)
15	I	0.26	0/450	0.72	0/603
16	N	0.27	0/1211	0.79	1/1639 (0.1%)
17	O	0.31	0/907	0.74	0/1224
18	P	0.28	0/1254	0.77	0/1686
19	Q	0.26	0/1104	0.75	0/1483
20	R	0.28	0/1000	0.72	2/1342 (0.1%)
21	S	0.25	0/763	0.70	0/1033
22	T	0.27	0/978	0.73	1/1318 (0.1%)
23	U	0.28	0/986	0.69	0/1319
24	V	0.24	0/866	0.76	0/1168
25	W	0.22	0/931	0.64	0/1241
26	X	0.24	0/585	0.69	0/788
27	Y	0.26	0/853	0.72	0/1155
28	b	0.27	0/1616	0.76	1/2205 (0.0%)
29	c	0.42	3/2171 (0.1%)	0.83	10/2937 (0.3%)
30	h	0.29	0/1918	0.77	2/2597 (0.1%)
31	i	0.30	0/1366	0.76	1/1844 (0.1%)
32	l	0.30	0/632	0.71	0/855
34	u	0.27	0/726	0.71	0/975

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.20	3/63622 (0.0%)	0.51	24/92886 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
29	c	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	c	141	ARG	C-N	10.31	1.48	1.33
29	c	100	SER	C-N	-7.59	1.23	1.33
29	c	122	ILE	C-N	6.47	1.42	1.33

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	F	154	GLY	CA-C-N	7.88	127.54	119.82
14	F	154	GLY	C-N-CA	7.88	127.54	119.82
29	c	100	SER	O-C-N	7.26	131.54	123.04
31	i	191	PRO	N-CA-C	6.32	118.41	110.70
16	N	115	ASN	CB-CA-C	-6.24	109.39	116.63
29	c	266	ILE	CA-C-N	5.96	125.44	119.24
29	c	266	ILE	C-N-CA	5.96	125.44	119.24
30	h	187	PRO	CA-C-N	5.92	126.48	120.38
30	h	187	PRO	C-N-CA	5.92	126.48	120.38
12	D	222	ASN	CB-CA-C	-5.73	109.98	116.63
29	c	118	LYS	CB-CA-C	-5.63	110.10	116.63
29	c	263	GLY	CA-C-N	5.56	125.87	119.92
29	c	263	GLY	C-N-CA	5.56	125.87	119.92
20	R	110	ILE	CA-C-N	5.49	124.95	119.24
20	R	110	ILE	C-N-CA	5.49	124.95	119.24
29	c	141	ARG	CA-C-N	5.46	128.05	120.29
29	c	141	ARG	C-N-CA	5.46	128.05	120.29
29	c	71	ASP	CA-C-N	-5.45	113.03	119.84
29	c	71	ASP	C-N-CA	-5.45	113.03	119.84
2	1	97	LEU	N-CA-C	-5.36	106.42	113.17
6	6	47	ASP	CA-C-N	5.26	124.87	119.56
6	6	47	ASP	C-N-CA	5.26	124.87	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	T	182	ARG	CB-CA-C	-5.25	108.96	115.89
28	b	240	ILE	N-CA-C	5.07	112.57	107.55

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	c	70	THR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	607	0	611	9	0
2	1	489	0	501	8	0
3	2	633	0	649	15	0
4	3	491	0	559	19	0
5	5	508	0	527	33	0
6	6	391	0	429	11	0
7	7	362	0	382	12	0
8	8	520	0	585	31	0
9	9	316	0	341	5	0
10	A	30656	0	15523	429	0
11	B	348	0	234	2	0
12	D	1531	0	1569	29	0
13	E	1621	0	1680	57	0
14	F	1713	0	1762	51	0
15	I	447	0	472	10	0
16	N	1178	0	1185	35	0
17	O	891	0	941	18	0
18	P	1309	0	1335	51	0
19	Q	1179	0	1211	34	0
20	R	982	0	995	15	0
21	S	748	0	752	13	0
22	T	962	0	987	32	0
23	U	1018	0	1099	31	0
24	V	877	0	925	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	W	1058	0	1069	40	0
26	X	689	0	708	20	0
27	Y	835	0	838	8	0
28	b	1562	0	1469	31	0
29	c	2310	0	2310	84	0
30	h	2075	0	2091	53	0
31	i	1335	0	1323	17	0
32	l	619	0	628	16	0
33	o	336	0	338	51	0
34	u	717	0	730	10	0
35	v	546	0	556	70	0
35	w	546	0	556	71	0
36	x	510	0	514	31	0
37	z	2556	0	2598	352	0
38	5	1	0	0	0	0
38	9	1	0	0	0	0
All	All	65473	0	50982	1588	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 14.

All (1588) 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)
30:h:226:LYS:NZ	30:h:302:ARG:HH12	1.63	0.95
13:E:258:THR:OG1	13:E:351:LYS:NZ	2.02	0.92
10:A:444:A:OP2	19:Q:67:LYS:NZ	2.03	0.89
10:A:1543:A:OP1	13:E:351:LYS:NZ	2.05	0.89
8:8:108:LYS:NZ	10:A:79:U:O4	2.06	0.89
10:A:83:A:OP2	10:A:1233:C:O2'	1.94	0.86
10:A:122:G:N2	10:A:125:A:OP2	2.09	0.85
10:A:1402:G:N2	10:A:1402:G:OP2	2.09	0.85
10:A:758:C:N4	10:A:765:G:O6	2.10	0.84
29:c:143:CYS:SG	29:c:176:PHE:CZ	2.70	0.84
10:A:240:C:OP1	14:F:117:ARG:NH1	2.11	0.84
19:Q:134:LYS:NZ	19:Q:143:GLY:O	2.11	0.83
4:3:78:ARG:O	4:3:83:LYS:NZ	2.11	0.83
10:A:1022:G:N1	10:A:1026:A:OP2	2.11	0.82
17:O:143:ASN:ND2	22:T:156:GLU:OE2	2.11	0.82
30:h:167:CYS:SG	30:h:171:ARG:NH1	2.52	0.82
35:w:28:UNK:HG1	37:z:786:UNK:HG1	1.59	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:i:226:ASP:HB2	31:i:231:LEU:HB3	1.61	0.82
1:0:50:ARG:NH1	10:A:1198:A:OP1	2.13	0.81
8:8:156:LYS:NZ	10:A:426:G:OP2	2.13	0.81
10:A:1180:G:H21	10:A:1229:U:H3	1.23	0.81
30:h:226:LYS:HZ3	30:h:302:ARG:HH12	1.25	0.80
10:A:134:G:N1	10:A:137:A:OP2	2.14	0.80
10:A:416:G:OP2	37:z:1208:UNK:HG1	1.79	0.80
22:T:182:ARG:HH12	22:T:190:LEU:HD11	1.46	0.79
5:5:94:ARG:NE	10:A:642:G:OP2	2.15	0.79
7:7:83:LEU:HD11	37:z:1409:UNK:HG1	1.63	0.79
10:A:1558:G:O2'	10:A:1560:A:OP2	1.98	0.79
29:c:132:PRO:CG	37:z:1814:UNK:HB2	2.13	0.79
10:A:259:C:H42	10:A:316:A:H61	1.26	0.79
33:o:89:UNK:HG2	37:z:1203:UNK:HB2	1.63	0.79
10:A:203:G:OP2	10:A:203:G:N2	2.14	0.78
8:8:141:LYS:NZ	10:A:1241:U:OP1	2.16	0.78
3:2:125:ARG:HH12	10:A:678:C:H1'	1.49	0.77
16:N:14:PHE:HE2	16:N:44:LYS:HZ2	1.31	0.77
10:A:1526:A:H3'	10:A:1527:A:H5''	1.66	0.77
10:A:182:U:OP1	18:P:47:ARG:NH1	2.17	0.77
12:D:162:ASP:OD1	12:D:178:ARG:NH1	2.18	0.77
8:8:142:ARG:NH2	10:A:1190:U:OP2	2.17	0.77
10:A:829:U:OP2	10:A:834:A:N6	2.17	0.77
8:8:130:LYS:NZ	10:A:1232:U:H5'	2.00	0.77
22:T:165:GLU:HB2	22:T:168:ASN:HB2	1.66	0.77
10:A:478:A:O2'	23:U:100:LYS:NZ	2.17	0.77
29:c:132:PRO:HG3	37:z:1814:UNK:HB2	1.67	0.76
10:A:1416:G:N2	10:A:1419:A:OP2	2.18	0.76
14:F:70:UNK:HG3	14:F:75:UNK:HG1	1.68	0.76
16:N:14:PHE:HB3	37:z:4008:UNK:HG2	1.66	0.76
24:V:123:GLU:HG2	24:V:125:ASP:H	1.51	0.75
6:6:23:GLN:HB2	37:z:1033:UNK:HG2	1.69	0.75
19:Q:64:ARG:HD2	19:Q:144:LYS:HD3	1.67	0.75
29:c:204:ARG:NH2	29:c:276:GLU:OE2	2.21	0.74
10:A:702:U:H5	26:X:33:UNK:HG1	1.53	0.74
10:A:1566:C:OP2	13:E:203:VAL:HG13	1.88	0.73
10:A:112:A:OP1	14:F:115:LYS:NZ	2.18	0.73
10:A:600:G:OP2	18:P:45:ARG:NH2	2.14	0.73
10:A:1369:C:O2'	17:O:34:LYS:NZ	2.21	0.73
31:i:166:GLU:OE1	31:i:260:ARG:NH1	2.20	0.73
3:2:111:ARG:HH11	3:2:141:MET:HB3	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:7:91:LYS:HD2	10:A:118:U:H5''	1.69	0.72
10:A:347:G:OP2	14:F:142:ARG:NH2	2.21	0.72
16:N:115:ASN:O	16:N:119:ARG:NH1	2.23	0.72
10:A:626:A:N7	18:P:39:ARG:NH2	2.37	0.72
13:E:199:GLY:HA2	13:E:225:GLN:H	1.54	0.72
10:A:589:A:O2'	24:V:122:ASN:ND2	2.22	0.72
10:A:800:G:N2	10:A:985:G:OP2	2.19	0.72
10:A:601:G:OP1	18:P:35:LYS:NZ	2.22	0.71
10:A:163:A:N1	10:A:1013:C:O2'	2.24	0.71
13:E:205:HIS:O	29:c:305:HIS:NE2	2.23	0.71
10:A:1164:A:N6	10:A:1171:A:OP2	2.23	0.71
10:A:441:G:H5''	19:Q:144:LYS:NZ	2.06	0.71
29:c:160:VAL:HG13	29:c:185:ARG:HH11	1.56	0.70
10:A:418:A:HO2'	10:A:419:U:C4'	2.03	0.70
10:A:1012:A:H5''	23:U:34:ARG:NH1	2.07	0.70
24:V:133:ARG:HG2	24:V:161:GLU:HG2	1.74	0.70
10:A:1066:C:O2	10:A:1419:A:O2'	2.10	0.70
29:c:299:PRO:HG3	37:z:1813:UNK:HA	1.72	0.70
2:1:90:ARG:NH1	10:A:1074:A:O3'	2.24	0.70
7:7:84:ARG:NH1	10:A:126:G:OP1	2.25	0.70
16:N:22:ASP:O	16:N:26:GLN:NE2	2.25	0.69
4:3:66:LEU:HD11	33:o:83:UNK:HG1	1.74	0.69
5:5:95:ARG:NH1	10:A:154:A:OP2	2.23	0.69
29:c:304:ALA:O	29:c:305:HIS:ND1	2.25	0.69
14:F:70:UNK:HG2	14:F:72:UNK:HG3	1.74	0.69
25:W:119:LEU:HD22	25:W:123:GLN:HE21	1.56	0.69
1:0:41:ASN:ND2	10:A:1176:C:OP2	2.25	0.69
8:8:130:LYS:HZ3	10:A:1232:U:H5'	1.55	0.69
17:O:85:LEU:HD21	17:O:130:ARG:HH12	1.57	0.69
33:o:90:UNK:HB1	37:z:1203:UNK:HG1	1.74	0.68
34:u:138:CYS:SG	34:u:139:SER:N	2.65	0.68
10:A:199:A:N3	14:F:147:ARG:NH2	2.41	0.68
10:A:419:U:H2'	10:A:420:U:C6	2.28	0.68
14:F:221:LEU:HG	14:F:223:HIS:H	1.55	0.68
28:b:186:PRO:HA	28:b:191:ASN:HD22	1.59	0.68
8:8:142:ARG:HH21	10:A:1190:U:H5''	1.57	0.68
9:9:93:PRO:HB2	10:A:1348:G:H5''	1.75	0.68
10:A:59:A:O2'	10:A:60:U:O2	2.10	0.68
10:A:1017:C:H5''	13:E:301:ARG:HG2	1.75	0.68
13:E:225:GLN:HG3	13:E:226:LYS:HG2	1.76	0.68
11:B:1:N:H5'	21:S:108:ARG:HD3	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:l:110:ILE:HD11	32:l:153:PHE:HZ	1.56	0.67
10:A:973:G:O2'	10:A:975:G:OP2	2.08	0.67
10:A:1241:U:H2'	10:A:1242:U:C6	2.30	0.67
10:A:761:C:OP2	10:A:763:C:N4	2.26	0.67
30:h:105:ARG:NH1	30:h:113:GLU:O	2.28	0.67
8:8:105:LYS:HG2	10:A:76:G:N7	2.09	0.67
10:A:1035:U:O4	16:N:119:ARG:NH2	2.28	0.67
31:i:164:VAL:O	31:i:261:MET:N	2.28	0.67
6:6:52:LYS:NZ	37:z:1034:UNK:HB2	2.09	0.67
17:O:46:LEU:HD11	17:O:77:ILE:HG21	1.77	0.67
29:c:162:SER:HB3	29:c:183:ASP:HB2	1.76	0.67
10:A:1068:U:H2'	10:A:1070:A:OP2	1.96	0.66
4:3:74:SER:HB2	10:A:471:U:H5''	1.77	0.66
10:A:1084:A:OP2	15:I:116:LYS:NZ	2.20	0.66
28:b:270:PHE:HB2	28:b:317:ALA:HB3	1.76	0.66
10:A:826:G:O6	10:A:838:C:N4	2.19	0.66
10:A:189:U:OP2	24:V:181:ARG:NH2	2.30	0.65
13:E:154:LYS:NZ	13:E:342:GLY:O	2.22	0.65
28:b:236:LEU:HB3	28:b:252:CYS:HB3	1.78	0.65
6:6:40:LYS:HB3	6:6:58:GLU:HB3	1.77	0.65
13:E:180:VAL:HB	13:E:242:THR:H	1.61	0.65
30:h:83:PHE:HB2	30:h:205:SER:HB2	1.78	0.65
28:b:169:PRO:HD3	28:b:316:LEU:HD12	1.78	0.65
10:A:11:G:O2'	10:A:112:A:N6	2.30	0.65
28:b:189:HIS:HB3	28:b:318:PHE:HB2	1.79	0.65
10:A:294:G:OP2	25:W:158:GLY:N	2.28	0.64
20:R:34:THR:HG23	20:R:85:LEU:HD11	1.79	0.64
29:c:139:TYR:OH	29:c:298:LEU:O	2.13	0.64
36:x:67:UNK:HG2	36:x:75:UNK:HG2	1.79	0.64
10:A:85:A:O2'	18:P:64:ARG:NH1	2.30	0.64
10:A:149:A:H2'	25:W:147:ARG:HH22	1.62	0.64
13:E:204:SER:HB2	13:E:223:PRO:HB3	1.78	0.64
27:Y:56:LEU:HD21	27:Y:76:VAL:HG21	1.79	0.64
10:A:1053:A:N7	14:F:137:ARG:NH2	2.42	0.64
12:D:212:GLY:HA2	12:D:251:VAL:HG12	1.79	0.64
30:h:229:PHE:O	30:h:233:THR:OG1	2.16	0.64
30:h:163:GLU:HG3	30:h:192:ARG:HD3	1.80	0.64
16:N:139:LYS:HD2	30:h:260:GLN:HG3	1.79	0.64
7:7:88:LYS:NZ	10:A:127:G:OP2	2.31	0.63
31:i:194:VAL:HG12	31:i:195:VAL:HG23	1.80	0.63
10:A:382:C:N3	10:A:427:A:N6	2.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:304:ALA:HB3	29:c:308:ILE:HG21	1.78	0.63
30:h:148:LEU:HD12	30:h:149:PRO:HD2	1.80	0.63
10:A:179:A:O2'	23:U:48:ARG:NH2	2.31	0.63
29:c:165:ARG:HA	29:c:180:VAL:HG12	1.81	0.63
36:x:69:UNK:HG1	36:x:99:UNK:HG2	1.80	0.62
10:A:137:A:HO2'	10:A:139:A:H8	1.47	0.62
10:A:441:G:H5''	19:Q:144:LYS:HZ3	1.64	0.62
10:A:1087:G:OP2	15:I:122:ARG:NH2	2.31	0.62
8:8:143:ARG:NH2	10:A:1206:A:N1	2.40	0.62
18:P:98:LEU:HD23	18:P:101:LEU:HD12	1.81	0.62
36:x:94:UNK:HA	36:x:98:UNK:HB1	1.81	0.62
29:c:145:MET:HE2	29:c:259:ASP:HB3	1.82	0.62
8:8:124:ARG:HH12	10:A:1201:C:H5''	1.65	0.62
10:A:109:U:O2	14:F:147:ARG:NH1	2.32	0.62
15:I:108:ARG:O	15:I:147:ARG:NH1	2.28	0.62
10:A:786:A:H3'	20:R:10:SER:HB3	1.80	0.62
10:A:1353:G:N2	10:A:1464:G:O2'	2.32	0.62
27:Y:146:VAL:HG12	27:Y:153:ILE:HA	1.82	0.62
23:U:29:ARG:O	23:U:30:HIS:ND1	2.32	0.62
10:A:911:G:O2'	10:A:913:C:N4	2.33	0.62
37:z:1036:UNK:HA	37:z:1039:UNK:HG3	1.81	0.62
28:b:217:LEU:HD23	28:b:271:LEU:HD12	1.81	0.61
16:N:39:LEU:HD23	16:N:112:LEU:HD11	1.83	0.61
8:8:104:ARG:NH1	10:A:207:A:H1'	2.15	0.61
10:A:1504:A:H2'	10:A:1505:G:H8	1.64	0.61
29:c:117:THR:HG22	29:c:118:LYS:HG3	1.82	0.61
10:A:50:A:N6	10:A:345:G:O2'	2.32	0.61
29:c:114:LYS:HD2	29:c:115:PRO:HD2	1.82	0.61
30:h:160:LEU:HD11	30:h:219:LEU:HB3	1.83	0.61
35:w:14:UNK:O	35:w:17:UNK:HG3	2.01	0.61
10:A:1506:A:H2'	10:A:1507:U:C6	2.35	0.61
13:E:264:LYS:HD2	13:E:312:LEU:HD23	1.81	0.61
10:A:1182:G:H1	10:A:1222:C:H42	1.49	0.61
2:1:90:ARG:HD2	2:1:103:LYS:HD2	1.82	0.61
10:A:104:C:N4	14:F:104:LYS:O	2.34	0.61
10:A:153:A:OP1	10:A:153:A:H8	1.83	0.61
10:A:569:A:H4'	16:N:29:GLY:HA3	1.83	0.61
10:A:906:A:H62	10:A:910:U:H3	1.47	0.61
24:V:167:LYS:H	36:x:97:UNK:HB2	1.66	0.61
4:3:85:ILE:HG23	4:3:109:LYS:HB3	1.81	0.61
29:c:278:SER:OG	29:c:294:GLN:O	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:88:THR:HG23	3:2:147:VAL:HG22	1.81	0.61
10:A:162:C:H42	10:A:1011:A:H61	1.48	0.61
16:N:67:PHE:O	16:N:72:TRP:NE1	2.33	0.60
21:S:160:ARG:HA	21:S:163:HIS:HB3	1.83	0.60
10:A:1227:A:O2'	10:A:1228:U:O4'	2.18	0.60
10:A:1250:G:N2	18:P:77:ARG:NH1	2.49	0.60
12:D:125:GLU:HB2	12:D:164:VAL:HB	1.83	0.60
32:l:109:VAL:HG13	32:l:146:THR:HG23	1.82	0.60
36:x:44:UNK:HA	36:x:47:UNK:HG3	1.83	0.60
10:A:339:A:OP2	10:A:1064:A:O2'	2.19	0.60
13:E:272:ARG:NH2	13:E:308:MET:O	2.34	0.60
23:U:33:GLY:O	23:U:36:ASN:ND2	2.34	0.60
10:A:160:A:OP2	10:A:1035:U:N3	2.32	0.60
16:N:21:LEU:HD13	16:N:31:LEU:HD11	1.83	0.60
29:c:114:LYS:HD3	29:c:250:LYS:HZ3	1.67	0.60
29:c:164:VAL:HB	29:c:181:VAL:HG23	1.84	0.60
31:i:168:CYS:SG	31:i:262:HIS:ND1	2.67	0.60
29:c:274:GLN:HB2	29:c:298:LEU:HD12	1.83	0.60
3:2:112:ASN:OD1	26:X:22:UNK:N	2.35	0.60
10:A:985:G:N2	10:A:989:C:O2'	2.35	0.60
14:F:120:VAL:HG12	14:F:122:GLY:H	1.66	0.60
14:F:143:SER:HB3	14:F:146:TRP:HD1	1.67	0.60
10:A:418:A:O2'	10:A:419:U:O4'	2.12	0.59
10:A:1569:A:H5'	37:z:1821:UNK:HB2	1.85	0.59
10:A:1564:G:H2'	10:A:1565:G:C8	2.38	0.59
10:A:858:G:H3'	12:D:209:ARG:HH21	1.68	0.59
14:F:273:LEU:HA	14:F:276:UNK:HG3	1.84	0.59
6:6:14:LYS:H	6:6:35:SER:HB3	1.67	0.59
10:A:1252:A:H2'	10:A:1252:A:N3	2.18	0.59
24:V:136:LYS:HD3	24:V:158:VAL:HB	1.84	0.59
30:h:223:MET:HG2	30:h:228:LEU:HD21	1.84	0.59
30:h:226:LYS:HZ2	30:h:302:ARG:HH12	1.48	0.59
8:8:139:ALA:HA	8:8:142:ARG:NH1	2.18	0.59
14:F:219:VAL:HG21	14:F:248:LEU:HD13	1.85	0.59
10:A:1013:C:O2'	10:A:1014:C:OP1	2.19	0.59
3:2:111:ARG:HE	3:2:115:LEU:HD11	1.68	0.58
10:A:1353:G:H21	10:A:1465:G:H5'	1.68	0.58
30:h:286:GLY:HA3	30:h:292:ALA:HB2	1.85	0.58
12:D:111:ARG:NH2	12:D:125:GLU:OE1	2.37	0.58
16:N:62:THR:HG21	16:N:127:LEU:HB3	1.86	0.58
28:b:151:LEU:HD22	28:b:168:VAL:HB	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:o:87:UNK:O	33:o:90:UNK:HG3	2.03	0.58
37:z:1044:UNK:HA	37:z:1047:UNK:HG3	1.85	0.58
10:A:840:U:H4'	12:D:261:ALA:HB2	1.85	0.58
17:O:53:ARG:HD3	17:O:54:PRO:HD2	1.85	0.58
29:c:104:LEU:HB2	29:c:123:LYS:HB3	1.84	0.58
30:h:48:UNK:O	30:h:52:UNK:HG3	2.03	0.58
15:I:123:LEU:HA	15:I:128:LEU:HB2	1.85	0.58
32:l:99:ASP:HB3	32:l:107:MET:HG3	1.86	0.58
10:A:789:A:H61	10:A:997:C:H42	1.52	0.58
10:A:1557:A:OP2	20:R:11:HIS:NE2	2.36	0.58
28:b:255:LEU:HD12	28:b:256:PRO:HD2	1.86	0.58
31:i:192:PRO:HG2	31:i:219:ARG:HB2	1.84	0.58
37:z:1210:UNK:O	37:z:1213:UNK:HG3	2.03	0.58
10:A:237:C:O2'	18:P:51:ARG:NH2	2.36	0.57
10:A:137:A:H4'	10:A:138:G:H5'	1.85	0.57
24:V:123:GLU:OE2	24:V:167:LYS:NZ	2.37	0.57
10:A:159:A:H5''	16:N:119:ARG:NH1	2.20	0.57
1:O:42:LEU:HD22	10:A:1155:C:H5''	1.86	0.57
10:A:1504:A:H2'	10:A:1505:G:C8	2.39	0.57
26:X:24:UNK:HG1	26:X:56:TYR:OH	2.04	0.57
33:o:89:UNK:HA	33:o:92:UNK:HG3	1.85	0.57
25:W:81:SER:H	25:W:110:LYS:NZ	2.03	0.57
25:W:90:LYS:HA	25:W:93:ARG:NH1	2.20	0.57
34:u:97:LYS:HA	34:u:137:GLU:HB3	1.87	0.57
32:l:153:PHE:HD1	32:l:153:PHE:H	1.51	0.57
3:2:111:ARG:NH1	3:2:141:MET:HB3	2.19	0.57
29:c:150:VAL:HG22	29:c:206:LEU:HD12	1.85	0.57
33:o:97:UNK:O	33:o:100:UNK:HG3	2.05	0.57
10:A:191:A:OP2	10:A:1320:C:O2'	2.21	0.57
37:z:1027:UNK:O	37:z:1030:UNK:HG3	2.05	0.57
4:3:110:LEU:HD11	4:3:119:ILE:HG12	1.86	0.57
15:I:98:LEU:HD21	15:I:105:LEU:HD12	1.86	0.57
17:O:99:ARG:NH2	22:T:161:GLU:OE1	2.34	0.57
5:5:93:ARG:NH2	10:A:640:G:OP1	2.38	0.56
6:6:21:MET:HA	6:6:27:GLY:HA2	1.87	0.56
10:A:859:U:OP2	12:D:209:ARG:NE	2.38	0.56
30:h:78:ARG:HH22	36:x:17:UNK:HA	1.70	0.56
37:z:1308:UNK:O	37:z:1311:UNK:HG3	2.04	0.56
4:3:106:VAL:HA	4:3:109:LYS:NZ	2.19	0.56
13:E:344:LYS:NZ	22:T:91:LYS:NZ	2.53	0.56
10:A:470:U:O2'	10:A:483:A:N3	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:485:A:N6	10:A:580:C:H42	2.04	0.56
37:z:1207:UNK:O	37:z:1210:UNK:HG3	2.05	0.56
10:A:205:A:N1	37:z:2303:UNK:HG1	2.20	0.56
10:A:1024:A:N3	10:A:1276:C:O2'	2.35	0.56
13:E:150:LEU:HD21	13:E:244:LEU:HD23	1.87	0.56
22:T:96:ARG:NE	37:z:2211:UNK:HG1	2.20	0.56
37:z:2309:UNK:HA	37:z:2312:UNK:HG3	1.88	0.56
1:0:57:GLU:HG3	1:0:98:ARG:HA	1.87	0.56
36:x:40:UNK:HA	36:x:43:UNK:HG3	1.88	0.56
10:A:458:A:H2'	10:A:459:C:H2'	1.88	0.56
10:A:1305:A:H2'	10:A:1306:A:H8	1.70	0.56
16:N:6:LYS:HG2	24:V:110:TRP:HH2	1.71	0.56
23:U:19:TRP:HH2	30:h:39:UNK:HG1	1.71	0.56
37:z:1211:UNK:O	37:z:1214:UNK:HG3	2.05	0.56
37:z:1407:UNK:O	37:z:1410:UNK:HG3	2.06	0.56
37:z:1841:UNK:O	37:z:1844:UNK:HG3	2.06	0.56
4:3:68:ILE:HD12	4:3:122:LEU:HD12	1.88	0.56
10:A:600:G:N7	18:P:44:ARG:NH2	2.54	0.56
10:A:634:U:H1'	14:F:147:ARG:NH1	2.21	0.56
13:E:344:LYS:HZ2	22:T:91:LYS:NZ	2.04	0.56
14:F:92:ARG:HG2	32:l:143:VAL:HG11	1.87	0.56
32:l:110:ILE:HD12	32:l:147:LEU:HD23	1.87	0.56
10:A:1003:G:H5''	25:W:110:LYS:HB3	1.87	0.56
19:Q:71:ASP:HA	19:Q:155:LYS:HE2	1.88	0.56
37:z:1031:UNK:O	37:z:1034:UNK:HG3	2.05	0.56
37:z:1034:UNK:O	37:z:1037:UNK:HG3	2.06	0.56
37:z:1811:UNK:O	37:z:1814:UNK:HG3	2.06	0.56
5:5:95:ARG:NH2	10:A:151:G:OP1	2.39	0.56
10:A:391:U:H2'	10:A:392:A:N3	2.21	0.56
10:A:422:U:O2	32:l:105:ARG:NH2	2.28	0.56
13:E:257:VAL:HG11	13:E:340:VAL:HG22	1.87	0.56
30:h:236:ASN:ND2	30:h:236:ASN:O	2.39	0.56
14:F:103:GLN:HA	14:F:106:PHE:CE2	2.41	0.55
10:A:461:G:O2'	10:A:485:A:O2'	2.22	0.55
13:E:303:TRP:O	13:E:306:THR:OG1	2.19	0.55
2:1:87:LEU:HD23	2:1:104:VAL:HG12	1.87	0.55
4:3:71:ARG:HH21	4:3:74:SER:HA	1.71	0.55
10:A:560:A:N6	10:A:1312:U:OP1	2.39	0.55
10:A:911:G:H21	10:A:912:A:N6	2.05	0.55
10:A:1460:G:N2	10:A:1463:A:OP2	2.39	0.55
17:O:44:SER:HB2	17:O:117:THR:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:179:GLN:HB2	24:V:184:TYR:HB3	1.89	0.55
34:u:112:GLU:OE1	34:u:115:ARG:NH2	2.37	0.55
12:D:198:GLU:HA	12:D:205:ALA:HA	1.88	0.55
19:Q:64:ARG:NH1	19:Q:132:THR:HB	2.22	0.55
10:A:1058:C:H2'	10:A:1059:U:H6	1.71	0.55
30:h:87:LEU:HD22	30:h:125:LEU:HD11	1.87	0.55
30:h:275:TYR:HB3	30:h:280:LEU:HD23	1.89	0.55
37:z:1409:UNK:HA	37:z:1412:UNK:HG3	1.87	0.55
8:8:124:ARG:NH2	10:A:1201:C:OP1	2.39	0.55
17:O:98:PRO:HB3	22:T:162:ILE:HG12	1.88	0.55
25:W:123:GLN:OE1	25:W:135:ARG:NH2	2.36	0.55
10:A:217:A:H5'	32:l:92:HIS:HD2	1.69	0.55
13:E:243:PRO:HG3	37:z:1843:UNK:HG2	1.88	0.55
14:F:66:UNK:HB1	14:F:80:THR:HB	1.88	0.55
29:c:104:LEU:HD12	29:c:123:LYS:HD3	1.88	0.55
33:o:103:UNK:HA	33:o:106:UNK:HG3	1.89	0.55
20:R:17:ARG:HA	20:R:25:ARG:HH21	1.72	0.55
23:U:34:ARG:O	23:U:38:CYS:N	2.40	0.55
10:A:1004:U:P	25:W:110:LYS:HZ3	2.31	0.54
10:A:1500:U:H2'	10:A:1501:C:C6	2.42	0.54
16:N:61:ASN:ND2	16:N:131:GLU:OE2	2.32	0.54
20:R:82:GLU:HG3	20:R:84:ASP:H	1.73	0.54
30:h:39:UNK:HA	30:h:42:UNK:HG3	1.88	0.54
30:h:101:GLU:OE2	30:h:105:ARG:NH2	2.40	0.54
10:A:618:A:H8	10:A:618:A:OP2	1.91	0.54
10:A:648:A:H2'	10:A:780:A:H2'	1.88	0.54
18:P:35:LYS:HD2	18:P:36:PRO:HD2	1.87	0.54
22:T:152:ARG:HG3	22:T:161:GLU:HG2	1.90	0.54
36:x:47:UNK:HG2	36:x:48:UNK:HG2	1.90	0.54
33:o:94:UNK:O	33:o:97:UNK:HG3	2.06	0.54
36:x:34:UNK:HA	36:x:37:UNK:HG3	1.89	0.54
36:x:35:UNK:O	36:x:39:UNK:HG3	2.06	0.54
37:z:1304:UNK:O	37:z:1307:UNK:HG3	2.08	0.54
10:A:187:C:H2'	24:V:181:ARG:HH12	1.71	0.54
10:A:367:A:N6	10:A:432:G:H5''	2.23	0.54
10:A:1494:C:H4'	13:E:271:ARG:NH1	2.23	0.54
32:l:142:GLU:C	32:l:144:THR:H	2.15	0.54
10:A:249:A:H2'	10:A:250:C:C6	2.43	0.54
10:A:1397:G:O2'	10:A:1400:C:OP2	2.22	0.54
19:Q:83:THR:OG1	19:Q:123:ARG:NH2	2.41	0.54
10:A:395:C:O2'	10:A:413:A:H2	1.91	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1384:U:H2'	10:A:1386:A:OP2	2.08	0.54
19:Q:98:HIS:HA	19:Q:151:VAL:HG12	1.88	0.54
28:b:240:ILE:HG12	28:b:248:GLY:HA3	1.90	0.54
10:A:108:A:O2'	10:A:109:U:OP2	2.18	0.54
10:A:260:A:OP2	12:D:101:LYS:NZ	2.41	0.54
10:A:420:U:H2'	10:A:421:U:O4'	2.08	0.54
28:b:194:THR:OG1	28:b:197:GLU:OE1	2.25	0.54
33:o:99:UNK:HA	33:o:102:UNK:HG3	1.89	0.54
10:A:119:A:H62	10:A:127(A):G:H21	1.56	0.54
16:N:16:ARG:HH11	16:N:124:ARG:HH11	1.55	0.54
31:i:165:THR:HB	31:i:169:PHE:HB3	1.90	0.54
5:5:108:ASP:OD1	5:5:119:LYS:HB3	2.08	0.54
5:5:132:UNK:O	5:5:135:UNK:HG3	2.08	0.54
10:A:160:A:H2	10:A:173:C:H5'	1.72	0.54
10:A:626:A:H62	18:P:39:ARG:HH21	1.54	0.54
34:u:143:PHE:HA	34:u:146:LEU:HB3	1.90	0.54
36:x:93:UNK:HA	36:x:97:UNK:HG3	1.88	0.54
37:z:1038:UNK:O	37:z:1041:UNK:HG3	2.08	0.54
3:2:101:HIS:HA	3:2:104:TRP:CD1	2.44	0.53
10:A:137:A:O2'	10:A:139:A:H8	1.91	0.53
28:b:173:LEU:HA	28:b:206:TYR:HB3	1.90	0.53
35:v:10:UNK:O	35:v:13:UNK:HG3	2.08	0.53
35:w:10:UNK:O	35:w:13:UNK:HG3	2.07	0.53
10:A:734:C:OP2	12:D:103:ARG:NH2	2.41	0.53
10:A:786:A:OP1	10:A:1558:G:N1	2.42	0.53
14:F:90:ALA:HB2	18:P:10:UNK:HG1	1.91	0.53
22:T:120:THR:HG23	22:T:130:THR:HG23	1.90	0.53
32:l:113:VAL:HG12	32:l:114:GLU:HG2	1.89	0.53
33:o:66:UNK:HA	33:o:69:UNK:HG3	1.91	0.53
10:A:604:U:H3	10:A:626:A:H61	1.56	0.53
18:P:99:ASN:HB2	18:P:144:GLY:HA3	1.90	0.53
31:i:183:TRP:HB3	31:i:227:ARG:HD2	1.90	0.53
4:3:120:LYS:HD2	4:3:121:PRO:HD2	1.89	0.53
10:A:217:A:H61	10:A:227:U:H4'	1.73	0.53
10:A:1053:A:H62	14:F:137:ARG:HH12	1.56	0.53
33:o:70:UNK:HA	33:o:73:UNK:HG3	1.91	0.53
37:z:2715:UNK:O	37:z:2718:UNK:HG3	2.09	0.53
10:A:780:A:H5''	10:A:781:A:OP2	2.08	0.53
13:E:203:VAL:HG21	13:E:225:GLN:OE1	2.08	0.53
13:E:344:LYS:NZ	22:T:91:LYS:HZ1	2.06	0.53
16:N:16:ARG:HD3	16:N:124:ARG:NH1	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:102:GLN:NE2	18:P:144:GLY:O	2.41	0.53
22:T:116:ILE:HD12	22:T:178:LYS:HD2	1.91	0.53
37:z:2713:UNK:O	37:z:2716:UNK:HG3	2.09	0.53
20:R:14:VAL:HG22	20:R:15:PHE:H	1.74	0.53
36:x:24:UNK:HB1	36:x:60:UNK:HA	1.91	0.53
10:A:182:U:O2'	10:A:355:G:OP2	2.20	0.53
10:A:644:A:N1	25:W:155:ARG:NH1	2.56	0.53
36:x:36:UNK:HA	36:x:40:UNK:HB1	1.90	0.53
9:9:89:CYS:SG	9:9:91:THR:OG1	2.66	0.53
10:A:1079:U:O2'	10:A:1080:U:OP1	2.22	0.53
15:I:116:LYS:HB2	15:I:120:ARG:NH1	2.24	0.53
33:o:107:UNK:HA	33:o:110:UNK:HG3	1.90	0.53
34:u:114:VAL:HG11	34:u:157:ILE:HG23	1.91	0.53
35:v:17:UNK:HA	35:v:20:UNK:HG3	1.90	0.53
37:z:1808:UNK:HA	37:z:1811:UNK:HG3	1.91	0.53
10:A:163:A:H2'	23:U:35:LYS:NZ	2.24	0.53
23:U:19:TRP:CH2	30:h:39:UNK:HG1	2.44	0.53
10:A:310:A:H5'	12:D:262:GLY:HA2	1.91	0.52
10:A:1070:A:H61	10:A:1141:U:H3	1.56	0.52
18:P:73:PRO:HD2	18:P:76:LEU:HD12	1.91	0.52
15:I:123:LEU:HB3	15:I:129:ALA:HB3	1.91	0.52
21:S:82:ARG:HG3	21:S:93:LEU:HB2	1.90	0.52
23:U:35:LYS:HD3	23:U:45:ALA:HB2	1.90	0.52
33:o:86:UNK:HA	33:o:89:UNK:HG3	1.90	0.52
10:A:177:C:H4'	23:U:55:ARG:NH1	2.24	0.52
10:A:911:G:H21	10:A:912:A:H62	1.55	0.52
13:E:239:LYS:NZ	13:E:244:LEU:HD13	2.24	0.52
18:P:122:VAL:HG22	18:P:127:VAL:HG11	1.91	0.52
37:z:1310:UNK:HA	37:z:1313:UNK:HG3	1.89	0.52
6:6:34:ARG:HG2	6:6:36:ARG:H	1.75	0.52
19:Q:121:LEU:HB2	19:Q:162:GLU:HG3	1.91	0.52
22:T:148:THR:HG22	22:T:165:GLU:HG3	1.90	0.52
8:8:125:ARG:HB3	18:P:79:PRO:HG2	1.92	0.52
10:A:271:A:H3'	10:A:271:A:N3	2.24	0.52
10:A:1329:G:H1	10:A:1401:U:H3	1.58	0.52
19:Q:64:ARG:NH1	19:Q:144:LYS:HB3	2.25	0.52
26:X:71:ARG:NH2	26:X:96:TYR:OH	2.42	0.52
35:w:17:UNK:HG1	35:w:56:UNK:HB1	1.91	0.52
37:z:1314:UNK:HA	37:z:1317:UNK:HG3	1.91	0.52
1:0:53:ILE:HG23	1:0:68:ALA:HB2	1.92	0.52
10:A:187:C:H5'	10:A:1023:A:H62	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:x:94:UNK:O	36:x:99:UNK:HG3	2.10	0.52
37:z:1418:UNK:HA	37:z:1421:UNK:HG3	1.92	0.52
10:A:372:U:C4	10:A:1248:A:H2	2.28	0.52
14:F:250:VAL:HA	14:F:253:MET:HE2	1.91	0.52
16:N:113:PRO:O	16:N:118:ARG:HB2	2.10	0.52
18:P:12:UNK:HA	18:P:15:UNK:HG3	1.92	0.52
23:U:86:PHE:HE2	23:U:102:LEU:HD21	1.74	0.52
27:Y:154:ILE:N	27:Y:155:PRO:HD2	2.25	0.52
35:v:14:UNK:HA	35:v:17:UNK:HG3	1.92	0.52
7:7:71:ARG:HD3	7:7:74:ARG:HH21	1.74	0.52
10:A:936:U:H1'	10:A:938:G:OP2	2.10	0.52
10:A:1557:A:OP1	13:E:343:HIS:NE2	2.41	0.52
14:F:89:THR:HG22	18:P:10:UNK:HG2	1.92	0.52
28:b:173:LEU:HD22	28:b:272:LEU:HD12	1.90	0.52
35:w:12:UNK:HA	35:w:15:UNK:HG3	1.91	0.52
35:w:30:UNK:HA	35:w:33:UNK:HG3	1.92	0.52
37:z:832:UNK:HA	37:z:835:UNK:HG3	1.92	0.52
37:z:1416:UNK:O	37:z:1419:UNK:HG3	2.10	0.52
5:5:128:UNK:O	5:5:131:UNK:HG3	2.10	0.52
8:8:124:ARG:HH11	18:P:78:ILE:HD11	1.75	0.52
37:z:3302:UNK:O	37:z:3305:UNK:HG3	2.10	0.51
10:A:63:A:N1	37:z:2309:UNK:HG1	2.25	0.51
10:A:724:A:O2'	10:A:726:C:N4	2.44	0.51
10:A:731:A:H5'	12:D:134:PRO:HB3	1.92	0.51
14:F:72:UNK:HG2	14:F:73:UNK:H	1.76	0.51
37:z:1201:UNK:HA	37:z:1204:UNK:HG3	1.92	0.51
5:5:85:ARG:NH2	10:A:1436:U:O3'	2.43	0.51
10:A:1164:A:H4'	10:A:1165:C:OP2	2.10	0.51
10:A:1250:G:C2	18:P:77:ARG:NH1	2.78	0.51
16:N:16:ARG:NH1	16:N:124:ARG:HG2	2.26	0.51
17:O:60:VAL:HG12	17:O:62:ASN:H	1.75	0.51
31:i:179:LYS:HA	31:i:182:ARG:HG2	1.92	0.51
36:x:20:UNK:HB2	36:x:66:UNK:HG2	1.91	0.51
37:z:1037:UNK:HA	37:z:1040:UNK:HG3	1.93	0.51
37:z:838:UNK:HA	37:z:841:UNK:HG3	1.93	0.51
10:A:1492:A:H8	10:A:1492:A:OP2	1.93	0.51
2:1:83:GLU:HB3	2:1:107:PRO:HB3	1.93	0.51
4:3:106:VAL:HA	4:3:109:LYS:HZ3	1.75	0.51
10:A:702:U:O4'	26:X:71:ARG:NH1	2.43	0.51
10:A:1248:A:H4'	10:A:1249:C:OP2	2.10	0.51
17:O:74:LEU:HD23	17:O:83:LYS:HG2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:z:1307:UNK:HA	37:z:1310:UNK:HG3	1.93	0.51
10:A:762:A:H4'	10:A:763:C:OP2	2.09	0.51
10:A:849:G:N7	12:D:231:SER:OG	2.43	0.51
23:U:72:ILE:HD13	23:U:102:LEU:HD23	1.93	0.51
30:h:92:PHE:HA	30:h:194:THR:HG23	1.93	0.51
35:w:31:UNK:O	35:w:34:UNK:HG3	2.11	0.51
37:z:1016:UNK:HA	37:z:1019:UNK:HG3	1.92	0.51
10:A:159:A:H2'	10:A:160:A:C8	2.46	0.51
17:O:92:PRO:HG3	17:O:99:ARG:HB2	1.91	0.51
29:c:38:UNK:HA	29:c:41:UNK:HG3	1.93	0.51
29:c:316:SER:O	29:c:320:VAL:HG23	2.11	0.51
33:o:73:UNK:HA	33:o:76:UNK:HG3	1.93	0.51
37:z:1020:UNK:HA	37:z:1023:UNK:HG3	1.93	0.51
37:z:1930:UNK:HA	37:z:1933:UNK:HG3	1.93	0.51
10:A:959:A:N3	10:A:1413:G:O2'	2.43	0.51
10:A:1506:A:H2'	10:A:1507:U:H6	1.75	0.51
35:v:55:UNK:HA	35:v:58:UNK:HG3	1.93	0.51
4:3:76:LYS:HE3	10:A:472:G:H21	1.76	0.50
10:A:422:U:H2'	10:A:423:U:C6	2.47	0.50
10:A:1128:A:OP2	10:A:1128:A:H2	1.93	0.50
13:E:150:LEU:HA	13:E:196:LEU:HD13	1.92	0.50
25:W:81:SER:CB	25:W:110:LYS:HZ1	2.23	0.50
28:b:252:CYS:SG	28:b:291:TYR:OH	2.68	0.50
29:c:183:ASP:OD1	29:c:184:LYS:N	2.44	0.50
37:z:1312:UNK:O	37:z:1315:UNK:HG3	2.11	0.50
27:Y:63:GLU:OE2	27:Y:73:GLN:HB2	2.10	0.50
30:h:45:UNK:O	30:h:48:UNK:HG3	2.11	0.50
35:w:37:UNK:HA	35:w:40:UNK:HG3	1.94	0.50
37:z:1005:UNK:HA	37:z:1008:UNK:HG3	1.94	0.50
1:O:72:HIS:CE1	10:A:1225:U:H1'	2.46	0.50
4:3:88:MET:SD	10:A:416:G:N2	2.72	0.50
10:A:196:U:OP1	23:U:40:ARG:NH2	2.44	0.50
10:A:775:A:H1'	37:z:838:UNK:HG2	1.93	0.50
29:c:51:UNK:O	29:c:54:UNK:HG3	2.11	0.50
35:v:29:UNK:HA	35:v:32:UNK:HG3	1.93	0.50
37:z:3304:UNK:HA	37:z:3307:UNK:HG3	1.94	0.50
10:A:86:U:H2'	10:A:87:A:H8	1.77	0.50
14:F:71:UNK:O	14:F:202:TYR:OH	2.29	0.50
16:N:12:ALA:O	16:N:13:THR:OG1	2.28	0.50
16:N:37:VAL:HG13	16:N:42:LEU:HB2	1.93	0.50
29:c:279:ALA:HB3	29:c:320:VAL:HG11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:z:1198:UNK:O	37:z:1201:UNK:HG3	2.12	0.50
37:z:1980:UNK:HA	37:z:1983:UNK:HG3	1.93	0.50
37:z:3303:UNK:O	37:z:3306:UNK:HG3	2.12	0.50
8:8:130:LYS:HZ2	10:A:1232:U:H5'	1.77	0.50
10:A:859:U:H5''	12:D:210:ALA:HB2	1.94	0.50
10:A:1227:A:H2'	10:A:1228:U:C6	2.47	0.50
13:E:301:ARG:NH1	13:E:304:PRO:HD3	2.26	0.50
23:U:127:UNK:HA	23:U:130:UNK:HG3	1.94	0.50
35:w:33:UNK:HA	35:w:36:UNK:HG3	1.92	0.50
37:z:1012:UNK:HA	37:z:1015:UNK:HG3	1.93	0.50
37:z:1048:UNK:HA	37:z:1051:UNK:HG3	1.92	0.50
37:z:1200:UNK:O	37:z:1203:UNK:HG3	2.11	0.50
37:z:3306:UNK:O	37:z:3309:UNK:HG3	2.11	0.50
5:5:91:ARG:NH2	10:A:151:G:OP2	2.45	0.50
10:A:1526:A:C3'	10:A:1527:A:H5''	2.38	0.50
21:S:122:VAL:HG13	21:S:157:SER:HA	1.93	0.50
22:T:116:ILE:HG12	22:T:136:ILE:HG12	1.94	0.50
28:b:215:THR:OG1	28:b:275:GLN:OE1	2.29	0.50
33:o:80:UNK:O	33:o:83:UNK:HG3	2.12	0.50
35:v:12:UNK:HA	35:v:15:UNK:HG3	1.92	0.50
35:w:29:UNK:HA	35:w:32:UNK:HG3	1.92	0.50
37:z:1010:UNK:O	37:z:1013:UNK:HG3	2.11	0.50
37:z:1033:UNK:O	37:z:1037:UNK:HB1	2.11	0.50
37:z:1413:UNK:HA	37:z:1416:UNK:HG3	1.93	0.50
29:c:45:UNK:HA	29:c:48:UNK:HG3	1.93	0.50
29:c:49:UNK:HA	29:c:52:UNK:HG3	1.94	0.50
35:w:72:UNK:HA	35:w:75:UNK:HG3	1.94	0.50
37:z:833:UNK:HA	37:z:836:UNK:HG3	1.92	0.50
37:z:2006:UNK:HA	37:z:2009:UNK:HG3	1.94	0.50
37:z:3008:UNK:HA	37:z:3011:UNK:HG3	1.93	0.50
6:6:52:LYS:HZ1	37:z:1034:UNK:HB2	1.75	0.50
10:A:929:U:H5	10:A:936:U:H3	1.58	0.50
13:E:173:LEU:HD22	13:E:348:VAL:HG21	1.94	0.50
13:E:183:TYR:OH	13:E:192:ARG:NH1	2.45	0.50
14:F:274:UNK:HA	14:F:277:UNK:HG3	1.93	0.50
35:w:8:UNK:HA	35:w:11:UNK:HG3	1.94	0.50
35:w:18:UNK:O	35:w:21:UNK:HG3	2.11	0.50
37:z:1008:UNK:HA	37:z:1011:UNK:HG3	1.94	0.50
37:z:1414:UNK:HA	37:z:1417:UNK:HG3	1.94	0.50
13:E:208:LYS:HD3	29:c:305:HIS:HE1	1.76	0.50
31:i:166:GLU:HB2	31:i:260:ARG:HD3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:o:60:UNK:HA	33:o:63:UNK:HG3	1.94	0.50
35:v:72:UNK:HA	35:v:75:UNK:HG3	1.94	0.50
36:x:95:UNK:HG2	36:x:96:UNK:HG2	1.93	0.50
37:z:783:UNK:HA	37:z:786:UNK:HG3	1.94	0.50
37:z:2017:UNK:HA	37:z:2020:UNK:HG3	1.94	0.50
10:A:119:A:O2'	26:X:84:ASN:ND2	2.45	0.49
10:A:842:A:O2'	10:A:871:U:OP1	2.30	0.49
37:z:1004:UNK:HA	37:z:1007:UNK:HG3	1.94	0.49
37:z:1422:UNK:HA	37:z:1425:UNK:HG3	1.93	0.49
5:5:117:LYS:HE3	5:5:124:GLY:H	1.77	0.49
10:A:249:A:H2'	10:A:250:C:H6	1.77	0.49
15:I:110:ASP:OD1	15:I:111:LEU:N	2.45	0.49
18:P:10:UNK:HA	18:P:13:UNK:HG3	1.94	0.49
31:i:153:ASN:ND2	31:i:188:SER:O	2.45	0.49
33:o:93:UNK:HA	33:o:96:UNK:HG3	1.94	0.49
37:z:2007:UNK:HA	37:z:2010:UNK:HG3	1.94	0.49
10:A:488:U:H2'	10:A:489:U:C6	2.47	0.49
10:A:1058:C:H2'	10:A:1059:U:C6	2.47	0.49
33:o:100:UNK:HA	33:o:103:UNK:HG3	1.94	0.49
35:v:33:UNK:HA	35:v:36:UNK:HG3	1.93	0.49
36:x:17:UNK:HB2	36:x:68:UNK:HG2	1.94	0.49
37:z:1021:UNK:HA	37:z:1024:UNK:HG3	1.94	0.49
37:z:2204:UNK:HA	37:z:2207:UNK:HG3	1.94	0.49
29:c:49:UNK:HB2	29:c:216:LEU:HD22	1.95	0.49
33:o:69:UNK:HA	33:o:72:UNK:HG3	1.93	0.49
35:v:3:UNK:O	35:v:6:UNK:HG3	2.13	0.49
37:z:1708:UNK:HA	37:z:1711:UNK:HG3	1.94	0.49
37:z:1840:UNK:O	37:z:1843:UNK:HG3	2.12	0.49
37:z:2604:UNK:HA	37:z:2607:UNK:HG3	1.94	0.49
37:z:2605:UNK:HA	37:z:2608:UNK:HG3	1.95	0.49
16:N:21:LEU:HD21	16:N:38:LYS:NZ	2.28	0.49
24:V:102:VAL:HB	24:V:138:LEU:HB3	1.93	0.49
28:b:191:ASN:O	28:b:320:GLN:N	2.41	0.49
30:h:47:UNK:O	30:h:50:UNK:HG3	2.11	0.49
35:w:56:UNK:HA	35:w:59:UNK:HG3	1.95	0.49
37:z:2205:UNK:HA	37:z:2208:UNK:HG3	1.93	0.49
3:2:95:LYS:HD3	3:2:151:ARG:HH21	1.76	0.49
8:8:109:ALA:HB1	8:8:113:ARG:HH21	1.78	0.49
10:A:874:C:O2'	10:A:962:A:N1	2.39	0.49
19:Q:191:SER:H	19:Q:194:UNK:HG3	1.78	0.49
29:c:65:UNK:HG2	29:c:77:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:o:79:UNK:HA	33:o:82:UNK:HG3	1.95	0.49
7:7:85:ARG:HG2	7:7:90:ARG:HG3	1.93	0.49
10:A:1053:A:H2'	14:F:131:LYS:HZ3	1.76	0.49
10:A:1057:C:H2'	10:A:1058:C:C6	2.48	0.49
13:E:344:LYS:HZ2	22:T:91:LYS:HZ1	1.61	0.49
25:W:88:LEU:HD11	25:W:109:LYS:HD3	1.95	0.49
35:v:20:UNK:HA	35:v:23:UNK:HG3	1.94	0.49
35:v:30:UNK:HA	35:v:33:UNK:HG3	1.93	0.49
37:z:1014:UNK:O	37:z:1017:UNK:HG3	2.11	0.49
37:z:1035:UNK:O	37:z:1038:UNK:HG3	2.13	0.49
37:z:1220:UNK:HA	37:z:1223:UNK:HG3	1.95	0.49
37:z:2405:UNK:HA	37:z:2408:UNK:HG3	1.94	0.49
4:3:71:ARG:HA	4:3:117:ILE:HG22	1.95	0.49
29:c:37:UNK:HA	29:c:40:UNK:HG3	1.95	0.49
30:h:226:LYS:HB2	37:z:4000:UNK:HG1	1.95	0.49
35:v:37:UNK:HA	35:v:40:UNK:HG3	1.94	0.49
35:w:27:UNK:O	35:w:30:UNK:HG3	2.13	0.49
35:w:54:UNK:HA	35:w:57:UNK:HG3	1.95	0.49
37:z:1028:UNK:O	37:z:1031:UNK:HG3	2.13	0.49
37:z:1199:UNK:O	37:z:1202:UNK:HG3	2.12	0.49
37:z:1204:UNK:O	37:z:1208:UNK:HG3	2.13	0.49
4:3:88:MET:O	10:A:416:G:O2'	2.31	0.49
10:A:846:C:H2'	10:A:847:U:H6	1.78	0.49
10:A:1511:U:H2'	10:A:1512:A:N3	2.28	0.49
10:A:1549:C:H2'	10:A:1549:C:O2	2.13	0.49
26:X:44:ILE:HD13	26:X:95:ALA:HB2	1.95	0.49
30:h:44:UNK:HA	30:h:47:UNK:HG3	1.95	0.49
33:o:83:UNK:O	33:o:86:UNK:HG3	2.12	0.49
37:z:2211:UNK:HA	37:z:2214:UNK:HG3	1.95	0.49
10:A:209:A:H2'	10:A:210:U:C6	2.48	0.48
10:A:731:A:H3'	12:D:134:PRO:HB3	1.95	0.48
10:A:1192:U:H3	10:A:1207:A:H62	1.61	0.48
22:T:121:THR:HG22	22:T:123:ASP:H	1.78	0.48
35:v:9:UNK:HA	35:v:12:UNK:HG3	1.95	0.48
35:v:75:UNK:HA	35:v:78:UNK:HG3	1.95	0.48
37:z:836:UNK:O	37:z:839:UNK:HG3	2.13	0.48
37:z:2011:UNK:HA	37:z:2014:UNK:HG3	1.95	0.48
37:z:2707:UNK:HA	37:z:2710:UNK:HG3	1.95	0.48
37:z:3007:UNK:HA	37:z:3010:UNK:HG3	1.95	0.48
29:c:165:ARG:HB2	29:c:233:LYS:HE3	1.95	0.48
35:v:31:UNK:O	35:v:34:UNK:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:v:71:UNK:HA	35:v:74:UNK:HG3	1.95	0.48
35:w:40:UNK:HA	35:w:43:UNK:HG3	1.96	0.48
37:z:1412:UNK:O	37:z:1415:UNK:HG3	2.13	0.48
37:z:1426:UNK:HA	37:z:1429:UNK:HG3	1.94	0.48
10:A:1350:G:OP2	10:A:1351:C:H5''	2.13	0.48
10:A:1567:A:C8	37:z:1829:UNK:HB2	2.48	0.48
33:o:74:UNK:HA	33:o:77:UNK:HG3	1.95	0.48
35:v:56:UNK:HA	35:v:59:UNK:HG3	1.95	0.48
35:v:58:UNK:HA	35:v:61:UNK:HG3	1.95	0.48
35:w:20:UNK:HA	35:w:23:UNK:HG3	1.95	0.48
37:z:1017:UNK:HA	37:z:1020:UNK:HG3	1.94	0.48
37:z:1026:UNK:HA	37:z:1029:UNK:HG3	1.95	0.48
37:z:1713:UNK:HA	37:z:1716:UNK:HG3	1.96	0.48
37:z:1799:UNK:HA	37:z:1802:UNK:HG3	1.96	0.48
37:z:2305:UNK:HA	37:z:2308:UNK:HG3	1.93	0.48
1:0:77:PRO:HB3	1:0:89:LEU:HD22	1.96	0.48
7:7:70:VAL:HG12	10:A:36:N:OP2	2.13	0.48
10:A:1449:U:H1'	17:O:63:LYS:NZ	2.29	0.48
20:R:53:ARG:HA	20:R:105:THR:HG21	1.95	0.48
25:W:144:THR:HG23	25:W:173:PHE:HB2	1.94	0.48
28:b:171:VAL:HG21	28:b:314:ALA:HB1	1.95	0.48
37:z:1042:UNK:O	37:z:1045:UNK:HG3	2.12	0.48
37:z:1206:UNK:O	37:z:1209:UNK:HG3	2.12	0.48
37:z:1430:UNK:HA	37:z:1433:UNK:HG3	1.95	0.48
37:z:1707:UNK:HA	37:z:1710:UNK:HG3	1.95	0.48
37:z:3305:UNK:HA	37:z:3308:UNK:HG3	1.94	0.48
37:z:4104:UNK:HA	37:z:4107:UNK:HG3	1.94	0.48
28:b:169:PRO:HG3	28:b:316:LEU:HB2	1.96	0.48
28:b:259:PRO:HG2	28:b:323:TRP:HA	1.94	0.48
33:o:77:UNK:HA	33:o:80:UNK:HG3	1.96	0.48
37:z:1931:UNK:HA	37:z:1934:UNK:HG3	1.95	0.48
37:z:2209:UNK:HA	37:z:2212:UNK:HG3	1.95	0.48
5:5:130:UNK:HA	5:5:133:UNK:HG3	1.94	0.48
5:5:141:UNK:HA	5:5:144:UNK:HG3	1.95	0.48
10:A:152:U:H3'	10:A:153:A:H5''	1.94	0.48
10:A:293:G:O2'	25:W:161:ARG:NH2	2.35	0.48
10:A:1393:A:OP1	10:A:1395:G:O2'	2.26	0.48
13:E:239:LYS:HZ3	13:E:244:LEU:HD13	1.78	0.48
23:U:125:UNK:HA	23:U:128:UNK:HG3	1.95	0.48
35:w:71:UNK:HA	35:w:74:UNK:HG3	1.95	0.48
36:x:15:UNK:N	36:x:96:UNK:HG3	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:z:1423:UNK:HA	37:z:1426:UNK:HG3	1.95	0.48
37:z:1427:UNK:HA	37:z:1430:UNK:HG3	1.95	0.48
37:z:2307:UNK:HA	37:z:2310:UNK:HG3	1.96	0.48
37:z:2312:UNK:HA	37:z:2315:UNK:HG3	1.96	0.48
37:z:3309:UNK:HA	37:z:3312:UNK:HG3	1.96	0.48
3:2:115:LEU:HD22	3:2:118:GLU:OE1	2.14	0.48
10:A:421:U:O2'	10:A:422:U:O5'	2.32	0.48
10:A:772:A:O2'	37:z:777:UNK:HG1	2.14	0.48
12:D:216:VAL:HG13	12:D:228:GLN:HB3	1.95	0.48
13:E:243:PRO:HG2	37:z:1847:UNK:HG1	1.95	0.48
29:c:41:UNK:HA	29:c:44:UNK:HG3	1.96	0.48
33:o:82:UNK:HA	33:o:85:UNK:HG3	1.96	0.48
35:v:84:UNK:HA	35:v:87:UNK:HG3	1.96	0.48
35:w:58:UNK:HA	35:w:61:UNK:HG3	1.96	0.48
37:z:1029:UNK:HA	37:z:1032:UNK:HG3	1.95	0.48
37:z:2311:UNK:HA	37:z:2314:UNK:HG3	1.95	0.48
5:5:127:UNK:HA	5:5:130:UNK:HG3	1.96	0.48
10:A:81:G:N2	10:A:85:A:OP2	2.41	0.48
10:A:746:A:OP2	10:A:747:C:OP2	2.32	0.48
10:A:773:C:O2'	10:A:774:C:O2	2.31	0.48
10:A:1495:G:H1'	10:A:1496:C:H2'	1.96	0.48
22:T:182:ARG:NH1	22:T:190:LEU:HD11	2.22	0.48
25:W:71:ILE:HD11	25:W:130:HIS:HB2	1.96	0.48
29:c:40:UNK:HA	29:c:43:UNK:HG3	1.95	0.48
37:z:837:UNK:HA	37:z:840:UNK:HG3	1.96	0.48
37:z:1710:UNK:HA	37:z:1713:UNK:HG3	1.96	0.48
37:z:1820:UNK:HA	37:z:1823:UNK:HG3	1.95	0.48
5:5:137:UNK:HA	5:5:140:UNK:HG3	1.96	0.48
10:A:1358:U:H2'	10:A:1359:A:C8	2.49	0.48
19:Q:64:ARG:NH2	19:Q:145:GLY:O	2.47	0.48
19:Q:197:UNK:HA	19:Q:200:UNK:HG3	1.95	0.48
24:V:178:PHE:HD1	24:V:185:GLN:HG2	1.77	0.48
35:w:16:UNK:HA	35:w:19:UNK:HG3	1.95	0.48
37:z:781:UNK:HA	37:z:784:UNK:HG3	1.96	0.48
37:z:2608:UNK:HA	37:z:2611:UNK:HG3	1.94	0.48
37:z:3308:UNK:HA	37:z:3311:UNK:HG3	1.96	0.48
2:1:123:PHE:HE2	2:1:125:VAL:HG13	1.79	0.48
5:5:138:UNK:HA	5:5:141:UNK:HG3	1.95	0.48
18:P:38:ARG:NH1	18:P:45:ARG:NH1	2.62	0.48
35:v:16:UNK:HA	35:v:19:UNK:HG3	1.96	0.48
37:z:1009:UNK:HA	37:z:1012:UNK:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:z:2212:UNK:HA	37:z:2215:UNK:HG3	1.94	0.48
10:A:86:U:H2'	10:A:87:A:C8	2.48	0.47
10:A:187:C:C2'	24:V:181:ARG:HH12	2.26	0.47
10:A:415:U:OP1	37:z:1205:UNK:HA	2.14	0.47
10:A:1276:C:H2'	10:A:1277:G:H8	1.79	0.47
26:X:45:PRO:HG2	26:X:48:MET:HB2	1.96	0.47
29:c:39:UNK:HA	29:c:42:UNK:HG3	1.96	0.47
29:c:273:PHE:HB2	29:c:301:HIS:HA	1.96	0.47
35:w:9:UNK:HA	35:w:12:UNK:HG3	1.95	0.47
37:z:1318:UNK:HA	37:z:1321:UNK:HG3	1.94	0.47
37:z:1929:UNK:HA	37:z:1932:UNK:HG3	1.96	0.47
12:D:107:ILE:HG13	12:D:136:ARG:NH1	2.28	0.47
26:X:79:ARG:HG2	26:X:86:ARG:HG2	1.96	0.47
32:l:144:THR:HG22	32:l:145:GLY:H	1.80	0.47
33:o:85:UNK:HA	33:o:88:UNK:HG3	1.96	0.47
35:v:86:UNK:HA	35:v:89:UNK:HG3	1.96	0.47
35:w:62:UNK:HA	35:w:65:UNK:HG3	1.96	0.47
37:z:1013:UNK:HA	37:z:1016:UNK:HG3	1.96	0.47
37:z:1801:UNK:HA	37:z:1804:UNK:HG3	1.96	0.47
37:z:2304:UNK:HA	37:z:2307:UNK:HG3	1.96	0.47
10:A:861:U:H4'	10:A:862:U:OP2	2.15	0.47
35:v:8:UNK:HA	35:v:11:UNK:HG3	1.95	0.47
35:v:62:UNK:HA	35:v:65:UNK:HG3	1.96	0.47
35:w:55:UNK:HA	35:w:58:UNK:HG3	1.95	0.47
35:w:84:UNK:HA	35:w:87:UNK:HG3	1.95	0.47
37:z:1209:UNK:HA	37:z:1212:UNK:HG3	1.95	0.47
37:z:3012:UNK:HA	37:z:3015:UNK:HG3	1.96	0.47
10:A:271:A:N6	10:A:273:A:N7	2.62	0.47
10:A:1475:A:H2'	10:A:1476:U:C6	2.50	0.47
25:W:151:LEU:HB3	25:W:153:ARG:NH1	2.29	0.47
29:c:50:UNK:HA	29:c:53:UNK:HG3	1.96	0.47
33:o:64:UNK:O	33:o:67:UNK:HG3	2.14	0.47
33:o:78:UNK:HA	33:o:81:UNK:HG3	1.96	0.47
35:v:27:UNK:O	35:v:30:UNK:HG3	2.15	0.47
35:w:75:UNK:HA	35:w:78:UNK:HG3	1.96	0.47
36:x:29:UNK:HG2	36:x:33:UNK:CG	2.44	0.47
37:z:1313:UNK:HA	37:z:1316:UNK:HG3	1.97	0.47
37:z:1709:UNK:HA	37:z:1712:UNK:HG3	1.96	0.47
37:z:2214:UNK:O	37:z:2217:UNK:HG3	2.14	0.47
37:z:2708:UNK:HA	37:z:2711:UNK:HG3	1.96	0.47
8:8:104:ARG:O	10:A:76:G:H8	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:417:U:H5'	10:A:418:A:OP2	2.14	0.47
12:D:226:ILE:HG21	12:D:234:GLN:HE21	1.80	0.47
16:N:16:ARG:HH11	16:N:124:ARG:NH1	2.12	0.47
22:T:89:PRO:HA	22:T:92:PHE:HD2	1.79	0.47
22:T:138:ILE:HA	22:T:187:LEU:HD12	1.96	0.47
23:U:25:LEU:HA	23:U:28:ALA:HB3	1.97	0.47
35:w:53:UNK:HA	35:w:56:UNK:HG3	1.97	0.47
37:z:1843:UNK:HA	37:z:1846:UNK:HG3	1.97	0.47
37:z:2313:UNK:HA	37:z:2316:UNK:HG3	1.96	0.47
37:z:4003:UNK:HA	37:z:4006:UNK:HG3	1.95	0.47
7:7:82:ILE:HG23	7:7:93:LEU:HD13	1.96	0.47
7:7:85:ARG:NH1	7:7:92:SER:O	2.48	0.47
10:A:66:U:H2'	10:A:67:A:C8	2.49	0.47
10:A:299:A:OP2	10:A:299:A:H8	1.96	0.47
10:A:1005:G:H4'	25:W:165:MET:HG3	1.96	0.47
10:A:1564:G:H2'	10:A:1565:G:H8	1.78	0.47
16:N:11:TRP:CD1	16:N:12:ALA:H	2.33	0.47
35:w:3:UNK:O	35:w:6:UNK:HG3	2.15	0.47
37:z:1809:UNK:HA	37:z:1812:UNK:HG3	1.96	0.47
8:8:154:GLN:NE2	10:A:1200:C:O2'	2.37	0.47
10:A:408:A:N1	10:A:1166:A:H2'	2.29	0.47
10:A:448:C:H4'	10:A:1317:G:O2'	2.15	0.47
10:A:597:A:H4'	18:P:53:HIS:CD2	2.50	0.47
10:A:1250:G:N2	18:P:77:ARG:HH11	2.12	0.47
14:F:186:ASP:HB3	14:F:258:THR:HA	1.96	0.47
15:I:95:GLU:HB3	15:I:111:LEU:HD11	1.97	0.47
28:b:158:TYR:HB2	28:b:161:LEU:HG	1.97	0.47
30:h:183:GLU:HG3	30:h:184:PHE:H	1.80	0.47
35:v:13:UNK:HA	35:v:16:UNK:HG3	1.97	0.47
35:w:45:UNK:HA	35:w:48:UNK:HG3	1.96	0.47
35:w:85:UNK:HA	35:w:88:UNK:HG3	1.96	0.47
37:z:835:UNK:HA	37:z:838:UNK:HG3	1.97	0.47
37:z:3009:UNK:HA	37:z:3012:UNK:HG3	1.97	0.47
37:z:3011:UNK:HA	37:z:3014:UNK:HG3	1.97	0.47
5:5:93:ARG:NH1	10:A:642:G:OP2	2.48	0.47
5:5:131:UNK:O	5:5:134:UNK:HG3	2.14	0.47
5:5:134:UNK:HA	5:5:137:UNK:HG3	1.97	0.47
16:N:138:LEU:HD21	30:h:263:SER:HA	1.97	0.47
29:c:228:GLN:HA	29:c:234:LEU:HD11	1.97	0.47
33:o:67:UNK:O	33:o:70:UNK:HG3	2.15	0.47
35:v:42:UNK:HA	35:v:45:UNK:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:w:7:UNK:HA	35:w:10:UNK:HG3	1.97	0.47
35:w:41:UNK:HA	35:w:44:UNK:HG3	1.96	0.47
35:w:60:UNK:HA	35:w:63:UNK:HG3	1.96	0.47
35:w:86:UNK:HA	35:w:89:UNK:HG3	1.96	0.47
37:z:1431:UNK:HA	37:z:1434:UNK:HG3	1.95	0.47
37:z:2012:UNK:HA	37:z:2015:UNK:HG3	1.96	0.47
37:z:2203:UNK:HA	37:z:2206:UNK:HG3	1.97	0.47
8:8:105:LYS:HE2	10:A:76:G:C6	2.49	0.47
13:E:325:TRP:CD1	13:E:337:ASN:HB2	2.50	0.47
37:z:1989:UNK:HA	37:z:1992:UNK:HG3	1.97	0.47
37:z:2316:UNK:HA	37:z:2319:UNK:HG3	1.95	0.47
37:z:2706:UNK:HA	37:z:2709:UNK:HG3	1.97	0.47
3:2:111:ARG:HH11	3:2:141:MET:CB	2.24	0.47
10:A:315:U:H2'	10:A:316:A:H8	1.78	0.47
10:A:786:A:C5	20:R:17:ARG:HD2	2.49	0.47
10:A:1222:C:H3'	10:A:1223:A:H5''	1.96	0.47
14:F:199:ASP:N	14:F:199:ASP:OD1	2.47	0.47
19:Q:89:ILE:HD12	19:Q:161:VAL:HB	1.97	0.47
21:S:126:GLU:HB3	21:S:130:ARG:NH1	2.29	0.47
25:W:130:HIS:HD2	25:W:132:VAL:HG22	1.80	0.47
29:c:71:ASP:HB3	29:c:72:PRO:HD2	1.96	0.47
33:o:104:UNK:HA	33:o:107:UNK:HG3	1.97	0.47
35:v:40:UNK:HA	35:v:43:UNK:HG3	1.96	0.47
35:v:45:UNK:HA	35:v:48:UNK:HG3	1.97	0.47
35:w:6:UNK:O	35:w:9:UNK:HG3	2.15	0.47
35:w:34:UNK:HA	35:w:37:UNK:HG3	1.98	0.47
37:z:1419:UNK:HA	37:z:1422:UNK:HG3	1.96	0.47
37:z:1434:UNK:HA	37:z:1437:UNK:HG3	1.96	0.47
37:z:1985:UNK:HA	37:z:1988:UNK:HG3	1.97	0.47
10:A:363:A:O2'	10:A:384:U:OP1	2.29	0.46
19:Q:200:UNK:HA	19:Q:203:UNK:HG3	1.97	0.46
23:U:126:UNK:HA	23:U:129:UNK:HG3	1.97	0.46
25:W:196:UNK:HA	25:W:199:UNK:HG3	1.96	0.46
29:c:211:LEU:O	29:c:269:THR:OG1	2.34	0.46
34:u:103:HIS:CD2	34:u:131:GLU:HG3	2.49	0.46
35:v:41:UNK:HA	35:v:44:UNK:HG3	1.96	0.46
37:z:1022:UNK:HA	37:z:1025:UNK:HG3	1.98	0.46
37:z:2207:UNK:HA	37:z:2210:UNK:HG3	1.96	0.46
10:A:161:G:N2	10:A:173:C:OP1	2.48	0.46
10:A:474:C:H2'	10:A:475:U:C6	2.50	0.46
10:A:1236:A:O2'	10:A:1237:A:OP1	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:171:VAL:HG12	29:c:173:ALA:H	1.80	0.46
37:z:2013:UNK:HA	37:z:2016:UNK:HG3	1.98	0.46
37:z:2408:UNK:HA	37:z:2411:UNK:HG3	1.95	0.46
10:A:163:A:H2'	23:U:35:LYS:HZ1	1.80	0.46
10:A:356:U:O4	18:P:58:GLN:NE2	2.48	0.46
10:A:787:A:O2'	13:E:266:PHE:O	2.33	0.46
12:D:131:ARG:O	12:D:140:ILE:N	2.46	0.46
23:U:59:LEU:HG	23:U:62:ARG:HD2	1.97	0.46
30:h:263:SER:HB2	30:h:267:LEU:O	2.15	0.46
35:v:36:UNK:HA	35:v:39:UNK:HG3	1.96	0.46
37:z:840:UNK:HA	37:z:843:UNK:HG3	1.98	0.46
37:z:1934:UNK:HA	37:z:1937:UNK:HG3	1.97	0.46
37:z:2010:UNK:HA	37:z:2013:UNK:HG3	1.96	0.46
37:z:2407:UNK:HA	37:z:2410:UNK:HG3	1.97	0.46
10:A:376:G:O2'	18:P:56:GLU:OE1	2.33	0.46
10:A:419:U:H2'	10:A:420:U:C5	2.51	0.46
13:E:222:PRO:HB3	37:z:1836:UNK:HB2	1.97	0.46
19:Q:194:UNK:HA	19:Q:197:UNK:HG3	1.96	0.46
26:X:56:TYR:HD1	26:X:60:ILE:HD12	1.81	0.46
29:c:48:UNK:HA	29:c:51:UNK:HG3	1.98	0.46
35:v:60:UNK:HA	35:v:63:UNK:HG3	1.96	0.46
35:v:85:UNK:HA	35:v:88:UNK:HG3	1.96	0.46
35:w:74:UNK:HA	35:w:77:UNK:HG3	1.97	0.46
37:z:1007:UNK:HA	37:z:1010:UNK:HG3	1.97	0.46
37:z:2015:UNK:HA	37:z:2018:UNK:HG3	1.98	0.46
37:z:2206:UNK:HA	37:z:2209:UNK:HG3	1.96	0.46
3:2:125:ARG:HH21	10:A:699:U:H1'	1.81	0.46
13:E:208:LYS:HD3	29:c:305:HIS:CE1	2.50	0.46
18:P:38:ARG:HH11	18:P:45:ARG:NH2	2.14	0.46
19:Q:195:UNK:HA	19:Q:198:UNK:HG3	1.98	0.46
19:Q:201:UNK:HA	19:Q:204:UNK:HG3	1.96	0.46
22:T:96:ARG:CZ	37:z:2211:UNK:HG1	2.45	0.46
30:h:41:UNK:HA	30:h:44:UNK:HG3	1.96	0.46
30:h:42:UNK:HA	30:h:45:UNK:HG3	1.96	0.46
37:z:1798:UNK:HA	37:z:1801:UNK:HG3	1.97	0.46
37:z:1802:UNK:HA	37:z:1805:UNK:HG3	1.98	0.46
37:z:1804:UNK:HA	37:z:1807:UNK:HG3	1.98	0.46
37:z:2711:UNK:HA	37:z:2714:UNK:HG3	1.96	0.46
37:z:3006:UNK:HA	37:z:3009:UNK:HG3	1.98	0.46
5:5:134:UNK:HG1	20:R:41:ARG:NH2	2.31	0.46
12:D:119:LYS:HA	12:D:120:PRO:HD3	1.82	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:U:123:ARG:HA	23:U:126:UNK:HG3	1.98	0.46
29:c:46:UNK:HA	29:c:49:UNK:HG3	1.98	0.46
29:c:268:ARG:HG2	29:c:269:THR:H	1.80	0.46
33:o:81:UNK:HA	33:o:84:UNK:HG3	1.97	0.46
35:w:73:UNK:HA	35:w:76:UNK:HG3	1.97	0.46
37:z:1838:UNK:HA	37:z:1841:UNK:HG3	1.97	0.46
37:z:1992:UNK:HA	37:z:1995:UNK:HG3	1.96	0.46
5:5:133:UNK:HA	5:5:136:UNK:HG3	1.98	0.46
10:A:72:U:O2'	10:A:73:A:OP1	2.31	0.46
13:E:165:GLY:O	22:T:170:ARG:NH2	2.48	0.46
24:V:136:LYS:NZ	24:V:139:LEU:HD23	2.31	0.46
24:V:206:UNK:HB2	37:z:1982:UNK:HG1	1.98	0.46
35:v:5:UNK:HA	35:v:8:UNK:HG3	1.97	0.46
37:z:1836:UNK:HA	37:z:1839:UNK:HG3	1.97	0.46
37:z:2404:UNK:HA	37:z:2407:UNK:HG3	1.96	0.46
37:z:3010:UNK:HA	37:z:3013:UNK:HG3	1.98	0.46
4:3:66:LEU:HD21	33:o:83:UNK:HG1	1.98	0.46
10:A:377:U:O2	18:P:69:GLY:HA3	2.15	0.46
10:A:816:A:H3'	10:A:817:A:H5''	1.98	0.46
12:D:190:VAL:HA	12:D:217:LEU:HD23	1.97	0.46
14:F:278:UNK:HA	14:F:281:UNK:HG3	1.97	0.46
23:U:35:LYS:HG2	23:U:41:LEU:HB3	1.97	0.46
25:W:104:LEU:HD12	25:W:119:LEU:HD12	1.98	0.46
35:v:38:UNK:HA	35:v:41:UNK:HG3	1.98	0.46
35:w:36:UNK:HA	35:w:39:UNK:HG3	1.96	0.46
37:z:1215:UNK:HA	37:z:1218:UNK:HG3	1.98	0.46
37:z:1410:UNK:HA	37:z:1413:UNK:HG3	1.98	0.46
37:z:2008:UNK:HA	37:z:2011:UNK:HG3	1.96	0.46
37:z:2208:UNK:HA	37:z:2211:UNK:HG3	1.97	0.46
37:z:2705:UNK:HA	37:z:2708:UNK:HG3	1.98	0.46
37:z:2712:UNK:HA	37:z:2715:UNK:HG3	1.97	0.46
10:A:103:A:C2	10:A:105:G:C8	3.04	0.46
30:h:63:UNK:HG2	36:x:20:UNK:HG1	1.97	0.46
35:v:7:UNK:HA	35:v:10:UNK:HG3	1.98	0.46
35:w:5:UNK:HA	35:w:8:UNK:HG3	1.97	0.46
35:w:70:UNK:HA	35:w:73:UNK:HG3	1.98	0.46
37:z:2603:UNK:HA	37:z:2606:UNK:HG3	1.98	0.46
37:z:3307:UNK:O	37:z:3310:UNK:HG3	2.15	0.46
9:9:69:LEU:HD22	9:9:97:GLN:HB3	1.98	0.46
10:A:321:G:OP1	10:A:323:G:O2'	2.27	0.46
10:A:944:C:OP1	17:O:52:HIS:NE2	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1476:U:H2'	10:A:1477:G:O4'	2.16	0.46
19:Q:66:ARG:O	19:Q:129:LYS:NZ	2.49	0.46
20:R:9:ILE:HG23	20:R:11:HIS:H	1.81	0.46
33:o:63:UNK:HA	33:o:66:UNK:HG3	1.98	0.46
35:v:34:UNK:HA	35:v:37:UNK:HG3	1.98	0.46
37:z:1217:UNK:HA	37:z:1220:UNK:HG3	1.97	0.46
37:z:1988:UNK:HA	37:z:1991:UNK:HG3	1.98	0.46
37:z:2005:UNK:HA	37:z:2008:UNK:HG3	1.98	0.46
37:z:2009:UNK:HA	37:z:2012:UNK:HG3	1.97	0.46
37:z:3013:UNK:HA	37:z:3016:UNK:HG3	1.98	0.46
8:8:151:ASN:HD22	10:A:1200:C:H5''	1.81	0.45
10:A:219:G:OP1	14:F:168:LYS:NZ	2.49	0.45
10:A:294:G:O6	25:W:159:ARG:NH1	2.48	0.45
10:A:367:A:H61	10:A:432:G:H5''	1.80	0.45
10:A:616:A:H4'	30:h:35:UNK:HG3	1.97	0.45
10:A:916:U:H2'	10:A:917:G:H8	1.81	0.45
10:A:1079:U:HO2'	10:A:1080:U:P	2.38	0.45
10:A:1284:U:H2'	10:A:1285:G:H8	1.81	0.45
12:D:199:SER:HB3	12:D:207:TYR:HE1	1.82	0.45
14:F:86:VAL:HG11	14:F:273:LEU:HD13	1.97	0.45
18:P:23:SER:H	18:P:26:ASN:HD22	1.64	0.45
25:W:81:SER:H	25:W:110:LYS:HZ2	1.62	0.45
25:W:142:GLU:HB3	25:W:175:LYS:HB2	1.98	0.45
26:X:68:VAL:HG22	26:X:97:VAL:HG12	1.98	0.45
29:c:84:THR:HG22	29:c:86:TYR:H	1.81	0.45
33:o:76:UNK:HA	33:o:79:UNK:HG3	1.97	0.45
35:v:39:UNK:HA	35:v:42:UNK:HG3	1.98	0.45
35:w:59:UNK:HA	35:w:62:UNK:HG3	1.97	0.45
37:z:1023:UNK:O	37:z:1026:UNK:HG3	2.16	0.45
37:z:1411:UNK:O	37:z:1414:UNK:HG3	2.17	0.45
37:z:1711:UNK:HA	37:z:1714:UNK:HG3	1.97	0.45
37:z:1806:UNK:HA	37:z:1809:UNK:HG3	1.98	0.45
37:z:2014:UNK:HA	37:z:2017:UNK:HG3	1.97	0.45
10:A:473:A:H4'	10:A:583:A:H2'	1.99	0.45
10:A:1156:C:O2'	10:A:1249:C:OP2	2.33	0.45
10:A:1484:A:H2'	10:A:1485:C:H6	1.81	0.45
18:P:68:GLU:OE2	18:P:74:PHE:N	2.49	0.45
29:c:36:UNK:HA	29:c:39:UNK:HG3	1.98	0.45
37:z:1818:UNK:O	37:z:1821:UNK:HG3	2.17	0.45
37:z:3311:UNK:HA	37:z:3314:UNK:HG3	1.99	0.45
10:A:1002:A:H2'	10:A:1003:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:136:LYS:HZ1	24:V:139:LEU:HD23	1.82	0.45
30:h:72:ILE:HD12	30:h:85:LEU:HD22	1.97	0.45
35:v:11:UNK:O	35:v:14:UNK:HG3	2.16	0.45
35:v:52:UNK:HA	35:v:55:UNK:HG3	1.97	0.45
35:w:13:UNK:HA	35:w:16:UNK:HG3	1.98	0.45
35:w:39:UNK:HA	35:w:42:UNK:HG3	1.99	0.45
37:z:1003:UNK:HA	37:z:1006:UNK:HG3	1.97	0.45
37:z:1803:UNK:HA	37:z:1806:UNK:HG3	1.98	0.45
37:z:1837:UNK:HA	37:z:1840:UNK:HG3	1.98	0.45
37:z:1986:UNK:HA	37:z:1989:UNK:HG3	1.97	0.45
37:z:2213:UNK:HA	37:z:2216:UNK:HG3	1.98	0.45
37:z:2314:UNK:HA	37:z:2317:UNK:HG3	1.97	0.45
10:A:188:A:OP2	24:V:181:ARG:NH2	2.49	0.45
10:A:851:A:N6	12:D:203:ARG:O	2.50	0.45
10:A:893:U:H3	10:A:896:C:H41	1.63	0.45
10:A:1566:C:H2'	13:E:206:PHE:CZ	2.51	0.45
13:E:193:MET:HG2	13:E:231:ASN:HD22	1.81	0.45
13:E:269:VAL:HG21	13:E:291:PRO:HB3	1.97	0.45
25:W:90:LYS:HG3	25:W:93:ARG:NH1	2.31	0.45
26:X:38:ASP:O	26:X:98:GLN:NE2	2.49	0.45
31:i:179:LYS:HB3	31:i:184:SER:OG	2.15	0.45
35:v:32:UNK:HA	35:v:35:UNK:HG3	1.98	0.45
35:v:43:UNK:HA	35:v:46:UNK:HG3	1.98	0.45
35:v:54:UNK:HA	35:v:57:UNK:HG3	1.98	0.45
35:v:73:UNK:HA	35:v:76:UNK:HG3	1.97	0.45
35:w:38:UNK:HA	35:w:41:UNK:HG3	1.98	0.45
35:w:43:UNK:HA	35:w:46:UNK:HG3	1.98	0.45
37:z:4102:UNK:HA	37:z:4105:UNK:HG3	1.98	0.45
10:A:478:A:HO2'	23:U:100:LYS:HZ2	1.56	0.45
10:A:1484:A:H2'	10:A:1485:C:C6	2.51	0.45
16:N:112:LEU:HD13	16:N:121:MET:HE3	1.98	0.45
29:c:53:UNK:O	29:c:57:UNK:HG3	2.17	0.45
35:v:44:UNK:HA	35:v:47:UNK:HG3	1.99	0.45
35:v:59:UNK:HA	35:v:62:UNK:HG3	1.98	0.45
36:x:34:UNK:O	36:x:37:UNK:HG3	2.16	0.45
37:z:1405:UNK:HA	37:z:1408:UNK:HG3	1.98	0.45
37:z:1706:UNK:HA	37:z:1709:UNK:HG3	1.98	0.45
37:z:1842:UNK:HA	37:z:1845:UNK:HG3	1.98	0.45
37:z:1981:UNK:HA	37:z:1984:UNK:HG3	1.98	0.45
37:z:1984:UNK:HA	37:z:1987:UNK:HG3	1.99	0.45
37:z:1990:UNK:HA	37:z:1993:UNK:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:z:2607:UNK:HA	37:z:2610:UNK:HG3	1.98	0.45
10:A:107:U:H1'	10:A:110:A:C2	2.52	0.45
10:A:609:U:H2'	10:A:610:A:H8	1.82	0.45
10:A:756:C:O2'	10:A:757:C:O4'	2.35	0.45
10:A:790:G:H2'	10:A:791:A:H8	1.81	0.45
24:V:159:ARG:HB2	24:V:203:GLU:HB2	1.99	0.45
35:v:70:UNK:HA	35:v:73:UNK:HG3	1.98	0.45
35:w:42:UNK:HA	35:w:45:UNK:HG3	1.98	0.45
35:w:69:UNK:HA	35:w:72:UNK:HG3	1.98	0.45
37:z:1006:UNK:HA	37:z:1009:UNK:HG3	1.99	0.45
37:z:1987:UNK:HA	37:z:1990:UNK:HG3	1.99	0.45
10:A:2:C:H42	10:A:149:A:N6	2.15	0.45
10:A:234:A:O2'	18:P:35:LYS:N	2.37	0.45
10:A:938:G:H2'	10:A:939:U:C6	2.51	0.45
34:u:143:PHE:CD2	37:z:2718:UNK:HB2	2.52	0.45
35:v:6:UNK:O	35:v:9:UNK:HG3	2.17	0.45
35:w:32:UNK:HA	35:w:35:UNK:HG3	1.99	0.45
37:z:1317:UNK:HA	37:z:1320:UNK:HG3	1.98	0.45
37:z:1421:UNK:HA	37:z:1424:UNK:HG3	1.99	0.45
37:z:2406:UNK:HA	37:z:2409:UNK:HG3	1.98	0.45
10:A:66:U:O2'	10:A:67:A:OP1	2.33	0.45
10:A:1506:A:OP2	10:A:1506:A:H2	2.00	0.45
20:R:37:VAL:HG13	20:R:85:LEU:HD22	1.99	0.45
23:U:123:ARG:HH22	24:V:150:LYS:NZ	2.14	0.45
29:c:44:UNK:HA	29:c:47:UNK:HG3	1.98	0.45
33:o:75:UNK:HA	33:o:78:UNK:HG3	1.98	0.45
35:w:35:UNK:O	35:w:38:UNK:HG3	2.17	0.45
37:z:1415:UNK:HA	37:z:1418:UNK:HG3	1.97	0.45
37:z:1800:UNK:HA	37:z:1803:UNK:HG3	1.98	0.45
5:5:84:ARG:NH2	10:A:638:A:O2'	2.38	0.45
9:9:81:ARG:NH1	10:A:1524:U:C4	2.85	0.45
10:A:298:A:H4'	10:A:299:A:H5'	1.98	0.45
10:A:705:A:OP2	10:A:706:C:H5	2.00	0.45
10:A:753:U:H2'	10:A:753:U:O2	2.16	0.45
10:A:1343:A:H2	10:A:1343:A:OP2	1.99	0.45
11:B:21:N:OP2	21:S:119:THR:HG21	2.17	0.45
14:F:73:UNK:HG2	14:F:74:UNK:HG3	1.98	0.45
22:T:161:GLU:OE1	22:T:191:ARG:NH2	2.50	0.45
26:X:64:PRO:HB2	26:X:100:ALA:HB2	1.98	0.45
35:w:15:UNK:O	35:w:18:UNK:HG3	2.17	0.45
35:w:44:UNK:HA	35:w:47:UNK:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:w:57:UNK:HA	35:w:60:UNK:HG3	1.97	0.45
35:w:61:UNK:HA	35:w:64:UNK:HG3	1.98	0.45
1:0:38:SER:OG	19:Q:142:GLY:O	2.34	0.45
10:A:860:A:C6	12:D:233:ARG:NH1	2.82	0.45
10:A:944:C:OP2	17:O:78:ARG:NH2	2.50	0.45
10:A:1241:U:H2'	10:A:1242:U:H6	1.78	0.45
28:b:288:SER:HB2	28:b:289:PRO:HD2	1.99	0.45
31:i:248:PHE:CD1	31:i:261:MET:HG2	2.52	0.45
33:o:86:UNK:O	37:z:1203:UNK:HG1	2.17	0.45
35:w:17:UNK:HG1	35:w:56:UNK:CB	2.46	0.45
36:x:85:UNK:O	36:x:88:UNK:HG3	2.18	0.45
37:z:1811:UNK:HB2	37:z:1820:UNK:HG1	1.98	0.45
37:z:1835:UNK:HA	37:z:1838:UNK:HG3	1.98	0.45
37:z:1983:UNK:HA	37:z:1986:UNK:HG3	1.98	0.45
3:2:101:HIS:O	3:2:105:TYR:HB2	2.18	0.44
4:3:71:ARG:HB2	4:3:91:LEU:HD13	1.99	0.44
13:E:351:LYS:HB2	13:E:351:LYS:HE3	1.71	0.44
20:R:22:PRO:HA	20:R:25:ARG:NH1	2.32	0.44
30:h:226:LYS:NZ	30:h:302:ARG:NH1	2.48	0.44
35:v:61:UNK:HA	35:v:64:UNK:HG3	1.99	0.44
35:v:83:UNK:HA	35:v:86:UNK:HG3	1.99	0.44
36:x:20:UNK:O	36:x:66:UNK:N	2.51	0.44
37:z:1811:UNK:HG1	37:z:1820:UNK:HB2	1.98	0.44
37:z:2210:UNK:HA	37:z:2213:UNK:HG3	1.99	0.44
10:A:380:A:H3'	10:A:381:A:C2	2.52	0.44
10:A:448:C:H2'	10:A:449:U:C6	2.52	0.44
10:A:1182:G:H1	10:A:1222:C:N4	2.15	0.44
10:A:1557:A:OP2	10:A:1558:G:OP2	2.34	0.44
30:h:147:ASP:O	30:h:248:ARG:NH2	2.51	0.44
35:v:69:UNK:HA	35:v:72:UNK:HG3	1.98	0.44
35:v:74:UNK:HA	35:v:77:UNK:HG3	1.97	0.44
36:x:34:UNK:O	36:x:38:UNK:HG3	2.17	0.44
37:z:1019:UNK:HA	37:z:1022:UNK:HG3	1.99	0.44
37:z:1024:UNK:HA	37:z:1027:UNK:HG3	1.99	0.44
37:z:1420:UNK:O	37:z:1423:UNK:HG3	2.17	0.44
37:z:1821:UNK:HA	37:z:1824:UNK:HG3	1.97	0.44
37:z:2310:UNK:HA	37:z:2313:UNK:HG3	1.99	0.44
37:z:2709:UNK:O	37:z:2712:UNK:HG3	2.17	0.44
6:6:30:PHE:CZ	10:A:1241:U:H4'	2.53	0.44
10:A:174:C:H2'	10:A:175:U:H6	1.82	0.44
10:A:609:U:O2	14:F:104:LYS:NZ	2.39	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:E:200:GLY:H	13:E:225:GLN:HB3	1.82	0.44
33:o:68:UNK:O	33:o:71:UNK:HG3	2.16	0.44
33:o:84:UNK:HA	33:o:87:UNK:HG3	1.99	0.44
35:w:52:UNK:HA	35:w:55:UNK:HG3	1.99	0.44
37:z:1041:UNK:HA	37:z:1044:UNK:HG3	1.98	0.44
37:z:1991:UNK:HA	37:z:1994:UNK:HG3	1.99	0.44
37:z:3014:UNK:HA	37:z:3017:UNK:HG3	1.98	0.44
37:z:3310:UNK:HA	37:z:3313:UNK:HG3	1.99	0.44
2:1:128:THR:HG22	2:1:131:THR:H	1.83	0.44
3:2:161:GLY:O	37:z:3004:UNK:N	2.48	0.44
10:A:434:C:H2'	10:A:435:U:C6	2.52	0.44
10:A:1566:C:H4'	10:A:1567:A:OP2	2.16	0.44
12:D:195:ASN:OD1	12:D:244:THR:OG1	2.24	0.44
14:F:263:LEU:HB3	14:F:264:PRO:HD3	1.99	0.44
17:O:32:ILE:N	17:O:67:GLY:O	2.51	0.44
18:P:56:GLU:HG2	18:P:62:ARG:HA	1.99	0.44
26:X:27:UNK:HB2	26:X:30:UNK:CG	2.47	0.44
35:w:19:UNK:O	35:w:22:UNK:HG3	2.18	0.44
37:z:1305:UNK:HA	37:z:1308:UNK:HG3	1.99	0.44
37:z:1311:UNK:O	37:z:1314:UNK:HG3	2.17	0.44
37:z:2315:UNK:HA	37:z:2318:UNK:HG3	1.98	0.44
10:A:357:U:H5'	18:P:43:ARG:HH12	1.83	0.44
10:A:367:A:H61	10:A:432:G:C5'	2.30	0.44
10:A:415:U:H3'	10:A:416:G:C8	2.51	0.44
10:A:804:U:H2'	10:A:806:G:OP2	2.17	0.44
13:E:344:LYS:CD	22:T:91:LYS:HZ1	2.31	0.44
16:N:21:LEU:HD21	16:N:38:LYS:HZ2	1.82	0.44
35:v:4:UNK:HA	35:v:7:UNK:HG3	1.98	0.44
37:z:1002:UNK:HA	37:z:1005:UNK:HG3	2.00	0.44
37:z:1928:UNK:HA	37:z:1931:UNK:HG3	1.99	0.44
5:5:139:UNK:HA	5:5:142:UNK:HG3	2.00	0.44
14:F:66:UNK:HG2	14:F:189:ILE:O	2.18	0.44
16:N:16:ARG:HH12	16:N:124:ARG:HG2	1.83	0.44
26:X:54:ARG:HG3	26:X:65:VAL:HB	1.99	0.44
33:o:72:UNK:HA	33:o:75:UNK:HG3	1.99	0.44
37:z:1432:UNK:HA	37:z:1435:UNK:HG3	1.99	0.44
37:z:1797:UNK:HA	37:z:1800:UNK:HG3	2.00	0.44
37:z:2606:UNK:HA	37:z:2609:UNK:HG3	1.99	0.44
37:z:2710:UNK:O	37:z:2713:UNK:HG3	2.17	0.44
21:S:126:GLU:HB3	21:S:130:ARG:HH12	1.82	0.44
28:b:148:LYS:HA	28:b:151:LEU:HG	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:43:UNK:HA	29:c:46:UNK:HG3	2.00	0.44
37:z:1047:UNK:HA	37:z:1050:UNK:HG3	1.99	0.44
5:5:115:HIS:ND1	5:5:117:LYS:HE2	2.33	0.44
10:A:706:C:H42	10:A:751:G:H1	1.66	0.44
10:A:861:U:H5''	10:A:862:U:H5	1.82	0.44
12:D:76:PRO:HB3	12:D:105:ARG:HH11	1.83	0.44
21:S:158:ILE:HA	21:S:161:LEU:HD12	1.99	0.44
25:W:75:ARG:HG3	25:W:118:VAL:HG22	1.99	0.44
29:c:132:PRO:CG	37:z:1814:UNK:CB	2.92	0.44
29:c:273:PHE:HD2	29:c:274:GLN:HG2	1.83	0.44
30:h:40:UNK:HA	30:h:43:UNK:HG3	1.99	0.44
33:o:62:UNK:HA	33:o:65:UNK:HG3	2.00	0.44
35:v:47:UNK:O	35:v:50:UNK:HG3	2.18	0.44
35:v:53:UNK:HA	35:v:56:UNK:HG3	2.00	0.44
35:w:21:UNK:HA	35:w:24:UNK:HG3	1.99	0.44
37:z:1219:UNK:HA	37:z:1222:UNK:HG3	2.00	0.44
37:z:2215:UNK:O	37:z:2218:UNK:HG3	2.17	0.44
37:z:2403:UNK:HA	37:z:2406:UNK:HG3	1.98	0.44
2:1:101:VAL:HG11	10:A:1074:A:H1'	2.00	0.44
9:9:75:ASP:OD2	9:9:91:THR:HG21	2.17	0.44
10:A:315:U:H2'	10:A:316:A:C8	2.52	0.44
13:E:273:TRP:HB3	13:E:307:LYS:HD3	1.98	0.44
14:F:109:ILE:H	14:F:109:ILE:HG13	1.52	0.44
14:F:277:UNK:HA	14:F:280:UNK:HG3	1.99	0.44
25:W:77:GLN:H	25:W:171:HIS:CE1	2.36	0.44
35:w:83:UNK:HA	35:w:86:UNK:HG3	1.99	0.44
37:z:831:UNK:O	37:z:834:UNK:HG3	2.18	0.44
37:z:1417:UNK:HA	37:z:1420:UNK:HG3	1.99	0.44
37:z:1712:UNK:HA	37:z:1715:UNK:HG3	1.98	0.44
37:z:1805:UNK:HA	37:z:1808:UNK:HG3	1.98	0.44
37:z:1932:UNK:HA	37:z:1935:UNK:HG3	2.00	0.44
37:z:1978:UNK:HA	37:z:1981:UNK:HG3	2.00	0.44
37:z:3005:UNK:HA	37:z:3008:UNK:HG3	2.00	0.44
5:5:140:UNK:HA	5:5:143:UNK:HG3	2.00	0.43
10:A:1347:G:H1	10:A:1358:U:H3	1.66	0.43
10:A:1476:U:C4	10:A:1477:G:C5	3.06	0.43
14:F:262:THR:HG23	14:F:264:PRO:HD2	2.00	0.43
14:F:276:UNK:HA	14:F:279:UNK:HG3	1.99	0.43
25:W:73:HIS:HD2	25:W:118:VAL:HG13	1.83	0.43
29:c:146:MET:HE3	29:c:146:MET:HB3	1.84	0.43
30:h:181:SER:HB2	30:h:190:VAL:HG11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:o:96:UNK:O	33:o:100:UNK:HB1	2.18	0.43
37:z:1218:UNK:HA	37:z:1221:UNK:HG3	2.00	0.43
37:z:1933:UNK:HA	37:z:1936:UNK:HG3	2.00	0.43
8:8:124:ARG:NH1	18:P:78:ILE:HD11	2.33	0.43
10:A:392:A:H2'	10:A:393:C:O4'	2.18	0.43
10:A:609:U:H2'	10:A:610:A:C8	2.53	0.43
12:D:179:GLU:HA	12:D:245:VAL:HG23	2.00	0.43
13:E:340:VAL:HA	13:E:341:PRO:HD3	1.91	0.43
24:V:116:ASP:OD1	24:V:117:LEU:N	2.51	0.43
24:V:206:UNK:CB	37:z:1982:UNK:HG1	2.49	0.43
29:c:47:UNK:O	29:c:50:UNK:HG3	2.18	0.43
30:h:202:LEU:O	30:h:206:SER:OG	2.28	0.43
33:o:106:UNK:HA	33:o:109:UNK:HG3	1.99	0.43
35:w:4:UNK:HA	35:w:7:UNK:HG3	1.99	0.43
37:z:834:UNK:O	37:z:837:UNK:HG3	2.17	0.43
37:z:1315:UNK:HA	37:z:1318:UNK:HG3	2.00	0.43
37:z:2303:UNK:O	37:z:2306:UNK:HG3	2.17	0.43
4:3:76:LYS:HD3	10:A:471:U:C4	2.53	0.43
5:5:136:UNK:HA	5:5:139:UNK:HG3	1.99	0.43
10:A:94:U:H2'	10:A:95:U:O4'	2.18	0.43
10:A:1308:A:H2'	10:A:1309:G:C8	2.52	0.43
14:F:276:UNK:O	14:F:279:UNK:HG3	2.17	0.43
28:b:205:THR:HG22	28:b:243:ASN:HD22	1.83	0.43
29:c:42:UNK:HA	29:c:45:UNK:HG3	1.99	0.43
29:c:59:UNK:O	29:c:81:ASN:ND2	2.44	0.43
30:h:281:ILE:O	30:h:303:LYS:NZ	2.49	0.43
32:l:152:TYR:CZ	32:l:154:ASP:HB3	2.53	0.43
37:z:1212:UNK:HA	37:z:1215:UNK:HG3	1.99	0.43
37:z:1406:UNK:HA	37:z:1409:UNK:HG3	2.00	0.43
37:z:2202:UNK:HA	37:z:2205:UNK:HG3	2.00	0.43
8:8:151:ASN:ND2	10:A:1200:C:H5''	2.34	0.43
10:A:1210:U:H2'	10:A:1211:A:H8	1.82	0.43
10:A:1284:U:H2'	10:A:1285:G:C8	2.53	0.43
16:N:6:LYS:HG2	24:V:110:TRP:CH2	2.52	0.43
16:N:14:PHE:CZ	16:N:53:CYS:HB2	2.53	0.43
25:W:80:TYR:HD1	25:W:110:LYS:HD2	1.83	0.43
35:v:57:UNK:HA	35:v:60:UNK:HG3	1.99	0.43
37:z:2709:UNK:HA	37:z:2712:UNK:HG3	2.01	0.43
2:1:102:ARG:HD2	10:A:48:U:C5	2.53	0.43
7:7:63:ARG:HH12	10:A:123:U:H4'	1.83	0.43
10:A:220:A:H2	10:A:223:A:N7	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:461:G:H1	10:A:468:C:N4	2.17	0.43
10:A:1003:G:H5''	25:W:110:LYS:HD3	2.00	0.43
10:A:1455:A:H4'	10:A:1456:G:H4'	2.01	0.43
14:F:97:HIS:CE1	18:P:29:PRO:HG3	2.53	0.43
14:F:275:UNK:HA	14:F:278:UNK:HG3	2.00	0.43
19:Q:202:UNK:HA	19:Q:205:UNK:HG3	1.99	0.43
29:c:35:UNK:HA	29:c:38:UNK:HG3	1.99	0.43
30:h:43:UNK:HA	30:h:46:UNK:HG3	1.98	0.43
30:h:187:PRO:HA	30:h:188:PRO:HD3	1.81	0.43
35:v:18:UNK:HA	35:v:21:UNK:HG3	2.00	0.43
37:z:778:UNK:HA	37:z:781:UNK:HG3	1.99	0.43
37:z:1319:UNK:HA	37:z:1322:UNK:HG3	2.00	0.43
37:z:1425:UNK:HA	37:z:1428:UNK:HG3	2.00	0.43
37:z:2402:UNK:HA	37:z:2405:UNK:HG3	2.01	0.43
37:z:4103:UNK:HA	37:z:4106:UNK:HG3	2.00	0.43
10:A:138:G:H1'	27:Y:94:HIS:CE1	2.54	0.43
10:A:372:U:N3	10:A:1248:A:H2	2.17	0.43
13:E:281:THR:OG1	13:E:282:HIS:N	2.44	0.43
19:Q:203:UNK:O	19:Q:206:UNK:HG3	2.18	0.43
28:b:158:TYR:HB3	28:b:267:ARG:NH1	2.33	0.43
29:c:45:UNK:HG1	29:c:258:ILE:HD11	2.00	0.43
32:l:112:LYS:HD2	32:l:117:ILE:HD11	2.01	0.43
37:z:834:UNK:HA	37:z:837:UNK:HG3	2.01	0.43
37:z:1202:UNK:O	37:z:1205:UNK:HG3	2.18	0.43
6:6:20:MET:HB2	6:6:29:SER:HB3	2.01	0.43
10:A:730:A:H4'	10:A:731:A:OP1	2.15	0.43
21:S:126:GLU:OE2	21:S:160:ARG:HD3	2.19	0.43
25:W:197:UNK:HA	25:W:200:UNK:HG3	2.00	0.43
29:c:43:UNK:O	29:c:46:UNK:HG3	2.19	0.43
35:v:19:UNK:HA	35:v:22:UNK:HG3	2.00	0.43
35:v:35:UNK:O	35:v:38:UNK:HG3	2.19	0.43
35:w:28:UNK:HA	35:w:31:UNK:HG3	2.01	0.43
35:w:81:UNK:HB2	35:w:84:UNK:HG3	2.01	0.43
37:z:1428:UNK:O	37:z:1431:UNK:HG3	2.19	0.43
37:z:1433:UNK:HA	37:z:1436:UNK:HG3	2.01	0.43
37:z:1705:UNK:HA	37:z:1708:UNK:HG3	2.00	0.43
3:2:107:LEU:HD12	3:2:144:LEU:HD22	2.00	0.43
10:A:49:A:H5'	10:A:50:A:OP2	2.19	0.43
10:A:589:A:P	33:o:61:UNK:HB1	2.58	0.43
10:A:1568:C:H5'	13:E:205:HIS:CD2	2.54	0.43
19:Q:198:UNK:HA	19:Q:201:UNK:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:168:THR:OG1	24:V:169:GLU:N	2.52	0.43
36:x:24:UNK:HB1	36:x:59:UNK:O	2.19	0.43
8:8:105:LYS:HG2	10:A:76:G:C8	2.53	0.43
13:E:273:TRP:CD1	13:E:307:LYS:HB3	2.53	0.43
16:N:26:GLN:HA	16:N:27:PRO:HD3	1.90	0.43
18:P:81:TYR:HD1	18:P:81:TYR:HA	1.73	0.43
33:o:71:UNK:O	33:o:74:UNK:HG3	2.19	0.43
34:u:103:HIS:HA	34:u:131:GLU:HB2	2.01	0.43
37:z:1320:UNK:HA	37:z:1323:UNK:HG3	2.01	0.43
37:z:2016:UNK:HA	37:z:2019:UNK:HG3	2.01	0.43
37:z:2308:UNK:HA	37:z:2311:UNK:HG3	2.00	0.43
10:A:357:U:H5'	18:P:43:ARG:NH1	2.34	0.43
10:A:413:A:C6	10:A:414:A:C8	3.07	0.43
10:A:1378:A:H2'	10:A:1379:A:C8	2.53	0.43
18:P:46:GLY:O	18:P:48:LYS:N	2.50	0.43
18:P:129:ILE:HG22	18:P:131:PRO:HD3	2.01	0.43
19:Q:199:UNK:O	19:Q:202:UNK:HG3	2.19	0.43
29:c:196:LEU:HD22	29:c:277:VAL:HG11	2.00	0.43
5:5:139:UNK:HB1	10:A:653:C:H5''	2.01	0.42
10:A:163:A:OP2	23:U:48:ARG:HD3	2.18	0.42
10:A:217:A:H4'	10:A:218:A:H5'	2.00	0.42
10:A:1334:A:H2'	10:A:1335:G:C8	2.54	0.42
12:D:188:LEU:HD12	12:D:189:PRO:HD2	2.00	0.42
13:E:222:PRO:O	13:E:224:LYS:HG2	2.18	0.42
18:P:101:LEU:O	18:P:105:ILE:HG13	2.18	0.42
22:T:153:ASN:HD21	22:T:155:ILE:HD11	1.84	0.42
31:i:198:ARG:HA	31:i:214:VAL:HG13	2.00	0.42
37:z:782:UNK:HA	37:z:785:UNK:HG3	2.01	0.42
10:A:1040:A:H2'	10:A:1041:A:C8	2.54	0.42
10:A:1205:C:H2'	10:A:1206:A:O4'	2.19	0.42
10:A:1405:U:OP2	10:A:1405:U:H6	2.02	0.42
14:F:207:ALA:HA	14:F:212:TRP:HD1	1.83	0.42
25:W:72:TYR:HD1	25:W:175:LYS:HG2	1.84	0.42
25:W:98:ASP:OD2	29:c:95:TRP:HB2	2.17	0.42
25:W:190:UNK:HA	25:W:193:UNK:HG3	2.00	0.42
33:o:90:UNK:HA	33:o:93:UNK:HG3	2.00	0.42
36:x:93:UNK:O	36:x:98:UNK:N	2.52	0.42
37:z:1018:UNK:HA	37:z:1021:UNK:HG3	2.00	0.42
37:z:1197:UNK:HA	37:z:1200:UNK:HG3	2.01	0.42
37:z:1201:UNK:O	37:z:1205:UNK:HB1	2.19	0.42
37:z:1216:UNK:O	37:z:1219:UNK:HG3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:z:1316:UNK:O	37:z:1319:UNK:HG3	2.19	0.42
37:z:1408:UNK:O	37:z:1411:UNK:HG3	2.19	0.42
5:5:129:UNK:O	5:5:132:UNK:HG3	2.19	0.42
10:A:217:A:N6	10:A:227:U:H4'	2.34	0.42
12:D:182:ALA:HB2	12:D:244:THR:HG22	2.01	0.42
17:O:99:ARG:N	22:T:161:GLU:O	2.45	0.42
24:V:171:TRP:HA	24:V:172:PRO:HD3	1.89	0.42
25:W:138:LEU:HD21	25:W:176:LEU:HD23	2.01	0.42
28:b:268:PHE:CE1	28:b:321:CYS:HB3	2.55	0.42
29:c:47:UNK:HA	29:c:50:UNK:HG3	2.02	0.42
29:c:259:ASP:OD1	29:c:260:VAL:N	2.53	0.42
37:z:1424:UNK:HA	37:z:1427:UNK:HG3	2.00	0.42
37:z:1982:UNK:O	37:z:1985:UNK:HG3	2.18	0.42
37:z:2602:UNK:HA	37:z:2605:UNK:HG3	2.00	0.42
5:5:84:ARG:HH11	23:U:34:ARG:CZ	2.32	0.42
21:S:89:HIS:HB3	21:S:107:THR:HB	2.00	0.42
22:T:98:ASP:OD2	22:T:145:LEU:HB2	2.19	0.42
24:V:139:LEU:HG	24:V:158:VAL:HG11	2.01	0.42
31:i:166:GLU:CD	31:i:260:ARG:HH11	2.27	0.42
35:v:15:UNK:HA	35:v:18:UNK:HG3	2.00	0.42
35:v:82:UNK:HA	35:v:85:UNK:HG3	2.00	0.42
35:w:17:UNK:HA	35:w:20:UNK:HG3	2.01	0.42
37:z:1037:UNK:O	37:z:1041:UNK:HB1	2.20	0.42
37:z:4001:UNK:HA	37:z:4004:UNK:HG3	2.01	0.42
8:8:135:LYS:NZ	10:A:1229:U:OP1	2.44	0.42
10:A:1191:C:H42	10:A:1208:A:H61	1.68	0.42
19:Q:203:UNK:HA	19:Q:206:UNK:HG3	2.01	0.42
25:W:140:VAL:HG22	25:W:176:LEU:HD11	2.01	0.42
29:c:139:TYR:HE2	29:c:297:SER:HB3	1.83	0.42
29:c:153:ARG:HD2	29:c:206:LEU:HD11	2.02	0.42
35:v:28:UNK:HA	35:v:31:UNK:HG3	2.00	0.42
6:6:22:SER:HB3	6:6:56:PHE:CZ	2.54	0.42
10:A:173:C:N3	16:N:50:LEU:HD11	2.35	0.42
10:A:1023:A:H4'	10:A:1024:A:C8	2.55	0.42
10:A:1252:A:H4'	10:A:1253:A:OP2	2.16	0.42
13:E:263:GLY:HA2	13:E:313:GLY:HA3	2.02	0.42
16:N:26:GLN:NE2	16:N:31:LEU:HD22	2.35	0.42
21:S:131:VAL:O	21:S:135:ARG:HG2	2.19	0.42
25:W:200:UNK:HA	25:W:203:UNK:HG3	2.02	0.42
29:c:135:VAL:O	29:c:139:TYR:HB2	2.20	0.42
30:h:171:ARG:NH2	30:h:186:VAL:O	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:o:96:UNK:HA	33:o:99:UNK:HG3	2.02	0.42
37:z:1411:UNK:HA	37:z:1414:UNK:HG3	2.02	0.42
37:z:1810:UNK:O	37:z:1813:UNK:HG3	2.20	0.42
37:z:1839:UNK:HA	37:z:1842:UNK:HG3	2.01	0.42
37:z:1839:UNK:O	37:z:1842:UNK:HG3	2.20	0.42
37:z:2302:UNK:HA	37:z:2305:UNK:HG3	2.00	0.42
10:A:329:A:H2'	10:A:330:A:H4'	2.01	0.42
10:A:833:A:H5'	10:A:1429:G:H4'	2.01	0.42
10:A:944:C:H2'	10:A:946:A:OP2	2.20	0.42
16:N:44:LYS:HE3	16:N:55:ASP:OD2	2.20	0.42
18:P:100:ARG:O	18:P:104:LEU:HG	2.20	0.42
22:T:114:GLY:HA2	22:T:187:LEU:HD11	2.00	0.42
28:b:214:TRP:CZ3	28:b:274:LYS:HG2	2.54	0.42
33:o:71:UNK:HA	33:o:74:UNK:HG3	2.02	0.42
33:o:101:UNK:O	33:o:104:UNK:HG3	2.19	0.42
37:z:1048:UNK:O	37:z:1052:UNK:HG3	2.19	0.42
37:z:2004:UNK:HA	37:z:2007:UNK:HG3	2.02	0.42
3:2:87:TRP:CD1	3:2:91:GLN:HE21	2.38	0.42
5:5:118:GLN:HB2	25:W:106:PHE:CE1	2.55	0.42
8:8:114:PHE:CZ	18:P:78:ILE:HG13	2.55	0.42
10:A:448:C:O2'	10:A:1317:G:H4'	2.20	0.42
10:A:720:A:H2'	10:A:721:A:C8	2.54	0.42
10:A:916:U:H2'	10:A:917:G:C8	2.54	0.42
18:P:104:LEU:HD22	18:P:109:ARG:CZ	2.49	0.42
21:S:113:LYS:HD3	28:b:146:TYR:CZ	2.55	0.42
25:W:70:GLU:HG3	25:W:177:VAL:HG22	2.01	0.42
28:b:303:PHE:HA	28:b:307:HIS:HD2	1.85	0.42
29:c:152:GLU:HG2	29:c:156:LYS:HE3	2.02	0.42
30:h:37:UNK:HA	30:h:40:UNK:HG3	2.01	0.42
37:z:1046:UNK:O	37:z:1049:UNK:HG3	2.20	0.42
37:z:1204:UNK:HA	37:z:1207:UNK:HG3	2.01	0.42
37:z:1927:UNK:HA	37:z:1930:UNK:HG3	2.00	0.42
37:z:2215:UNK:HA	37:z:2218:UNK:HG3	2.02	0.42
4:3:88:MET:HE3	4:3:88:MET:HB3	1.89	0.42
10:A:364:G:N1	10:A:596:U:OP2	2.36	0.42
18:P:47:ARG:HE	18:P:48:LYS:HE2	1.84	0.42
24:V:122:ASN:O	24:V:195:THR:OG1	2.26	0.42
25:W:81:SER:HB3	25:W:110:LYS:HZ1	1.85	0.42
26:X:80:ARG:HE	26:X:87:ILE:HD11	1.84	0.42
27:Y:56:LEU:HD11	27:Y:62:VAL:HG11	2.02	0.42
33:o:92:UNK:HA	33:o:95:UNK:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:v:81:UNK:HB2	35:v:84:UNK:HG3	2.01	0.42
37:z:1311:UNK:HA	37:z:1314:UNK:HG3	2.01	0.42
37:z:1429:UNK:HA	37:z:1432:UNK:HG3	2.02	0.42
37:z:1429:UNK:O	37:z:1432:UNK:HG3	2.19	0.42
10:A:164:A:H1'	23:U:52:LYS:HZ3	1.84	0.42
17:O:32:ILE:HG13	17:O:86:ILE:HD13	2.02	0.42
17:O:131:GLU:HB2	17:O:134:PHE:HD2	1.85	0.42
21:S:122:VAL:HG11	21:S:160:ARG:HD2	2.02	0.42
24:V:200:ASN:OD1	24:V:201:SER:N	2.53	0.42
29:c:155:PHE:CD2	29:c:163:LEU:HB2	2.55	0.42
30:h:38:UNK:HA	30:h:41:UNK:HG3	2.02	0.42
32:l:110:ILE:HD11	32:l:153:PHE:CZ	2.45	0.42
35:v:76:UNK:HA	35:v:79:UNK:HG3	2.02	0.42
35:w:6:UNK:HA	35:w:9:UNK:HG3	2.02	0.42
37:z:1424:UNK:O	37:z:1427:UNK:HG3	2.20	0.42
37:z:1979:UNK:O	37:z:1982:UNK:HG3	2.19	0.42
5:5:127:UNK:O	5:5:130:UNK:HG3	2.19	0.41
5:5:135:UNK:O	5:5:138:UNK:HG3	2.20	0.41
10:A:194:G:H21	23:U:44:ARG:HH22	1.68	0.41
10:A:220:A:H5''	14:F:166:PRO:HB3	2.02	0.41
10:A:236:A:H2'	10:A:237:C:H5''	2.02	0.41
10:A:1569:A:C8	29:c:302:LEU:HD21	2.54	0.41
14:F:125:ARG:HB3	14:F:125:ARG:NH1	2.35	0.41
16:N:16:ARG:HB2	16:N:55:ASP:HA	2.02	0.41
19:Q:204:UNK:O	19:Q:207:UNK:HG3	2.20	0.41
30:h:46:UNK:O	30:h:49:UNK:HG3	2.20	0.41
30:h:148:LEU:HD13	30:h:305:PHE:HE1	1.85	0.41
35:w:82:UNK:HA	35:w:85:UNK:HG3	2.01	0.41
10:A:353:U:O2'	10:A:1053:A:N1	2.53	0.41
10:A:844:C:H2'	10:A:845:U:C6	2.55	0.41
13:E:295:SER:OG	13:E:296:THR:N	2.54	0.41
19:Q:191:SER:H	19:Q:194:UNK:CG	2.33	0.41
19:Q:199:UNK:HA	19:Q:202:UNK:HG3	2.02	0.41
22:T:102:ARG:HG3	22:T:167:TYR:CG	2.55	0.41
37:z:1015:UNK:O	37:z:1018:UNK:HG3	2.20	0.41
37:z:1046:UNK:HA	37:z:1049:UNK:HG3	2.02	0.41
37:z:1796:UNK:HA	37:z:1799:UNK:HG3	2.02	0.41
1:0:52:GLY:N	1:0:69:THR:O	2.50	0.41
10:A:51:A:H2'	10:A:52:A:C8	2.55	0.41
10:A:195:U:O2'	10:A:1012:A:OP1	2.34	0.41
10:A:766:G:H2'	10:A:767:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:786:A:N6	20:R:19:GLY:H	2.19	0.41
10:A:863:A:H2'	10:A:864:G:C8	2.55	0.41
10:A:1306:A:H5''	19:Q:184:PRO:HB3	2.01	0.41
15:I:134:PRO:HA	15:I:137:LYS:HB3	2.02	0.41
19:Q:196:UNK:HA	19:Q:199:UNK:HG3	2.01	0.41
33:o:98:UNK:O	33:o:101:UNK:HG3	2.20	0.41
37:z:1023:UNK:HA	37:z:1026:UNK:HG3	2.02	0.41
37:z:1322:UNK:O	37:z:1325:UNK:HG3	2.19	0.41
37:z:1428:UNK:HA	37:z:1431:UNK:HG3	2.01	0.41
37:z:1433:UNK:O	37:z:1436:UNK:HG3	2.21	0.41
37:z:1834:UNK:HA	37:z:1837:UNK:HG3	2.02	0.41
37:z:2704:UNK:HA	37:z:2707:UNK:HG3	2.01	0.41
8:8:130:LYS:NZ	10:A:1233:C:P	2.94	0.41
8:8:132:LYS:NZ	10:A:1230:G:H2'	2.35	0.41
10:A:188:A:OP2	10:A:189:U:OP2	2.38	0.41
10:A:217:A:H5'	32:l:92:HIS:CD2	2.54	0.41
10:A:353:U:H2'	10:A:354:G:C8	2.55	0.41
10:A:1053:A:C2'	14:F:131:LYS:HZ3	2.32	0.41
19:Q:106:ARG:HG3	19:Q:122:TRP:CZ2	2.55	0.41
28:b:173:LEU:HD11	28:b:204:VAL:HG13	2.02	0.41
34:u:102:PHE:CZ	34:u:132:LEU:HD23	2.55	0.41
36:x:57:UNK:O	36:x:58:UNK:HG3	2.20	0.41
37:z:830:UNK:HA	37:z:833:UNK:HG3	2.02	0.41
37:z:1006:UNK:O	37:z:1009:UNK:HG3	2.21	0.41
37:z:1011:UNK:O	37:z:1014:UNK:HG3	2.20	0.41
37:z:1018:UNK:O	37:z:1021:UNK:HG3	2.20	0.41
37:z:1420:UNK:HA	37:z:1423:UNK:HG3	2.03	0.41
37:z:1807:UNK:HA	37:z:1810:UNK:HG3	2.02	0.41
10:A:298:A:C4'	10:A:299:A:OP2	2.68	0.41
10:A:461:G:H1	10:A:468:C:H42	1.67	0.41
18:P:20:UNK:HG2	18:P:22:VAL:H	1.85	0.41
22:T:119:VAL:HG22	22:T:174:ILE:HG12	2.02	0.41
26:X:56:TYR:CD1	26:X:60:ILE:HD12	2.56	0.41
30:h:238:MET:O	30:h:242:VAL:HG23	2.20	0.41
35:v:7:UNK:O	35:v:10:UNK:HG3	2.21	0.41
35:w:17:UNK:O	35:w:20:UNK:HG3	2.20	0.41
35:w:28:UNK:O	35:w:31:UNK:HG3	2.21	0.41
36:x:28:UNK:HB2	36:x:30:UNK:HG3	2.02	0.41
36:x:64:UNK:HB1	36:x:78:UNK:HB1	2.01	0.41
37:z:1043:UNK:HA	37:z:1046:UNK:HG3	2.03	0.41
37:z:1935:UNK:HA	37:z:1938:UNK:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:84:ARG:HH11	23:U:34:ARG:NH2	2.18	0.41
10:A:218:A:H2'	10:A:219:G:C8	2.55	0.41
10:A:271:A:C6	10:A:273:A:N7	2.88	0.41
10:A:416:G:P	10:A:416:G:H8	2.44	0.41
10:A:1070:A:N6	10:A:1141:U:H3	2.18	0.41
10:A:1440:U:H5''	13:E:304:PRO:HA	2.02	0.41
10:A:1543:A:OP1	13:E:258:THR:OG1	2.38	0.41
18:P:155:GLU:HA	18:P:175:THR:HB	2.02	0.41
22:T:117:LEU:HD22	22:T:176:VAL:HG22	2.02	0.41
29:c:34:UNK:HA	29:c:37:UNK:HG3	2.02	0.41
33:o:105:UNK:HA	33:o:108:UNK:HG3	2.02	0.41
35:v:6:UNK:HA	35:v:9:UNK:HG3	2.01	0.41
35:v:88:UNK:O	35:v:91:UNK:HG3	2.20	0.41
37:z:1032:UNK:HA	37:z:1035:UNK:HG3	2.03	0.41
37:z:1039:UNK:O	37:z:1042:UNK:HG3	2.20	0.41
37:z:1819:UNK:HA	37:z:1822:UNK:HG3	2.03	0.41
10:A:90:A:H2'	10:A:91:A:C8	2.56	0.41
10:A:1023:A:H4'	10:A:1024:A:H8	1.86	0.41
10:A:1160:G:H1	10:A:1176:C:H42	1.69	0.41
14:F:216:VAL:HG22	14:F:258:THR:HB	2.03	0.41
20:R:33:LEU:HD21	20:R:56:ALA:HA	2.02	0.41
29:c:143:CYS:SG	29:c:176:PHE:CE2	3.04	0.41
35:v:35:UNK:HA	35:v:38:UNK:HG3	2.02	0.41
37:z:783:UNK:CG	37:z:831:UNK:HG1	2.50	0.41
37:z:1221:UNK:HA	37:z:1224:UNK:HG3	2.03	0.41
37:z:1822:UNK:HA	37:z:1825:UNK:HG3	2.02	0.41
37:z:1833:UNK:HA	37:z:1836:UNK:HG3	2.02	0.41
37:z:1933:UNK:O	37:z:1936:UNK:HG3	2.21	0.41
37:z:2303:UNK:HA	37:z:2306:UNK:HG3	2.02	0.41
5:5:135:UNK:HA	5:5:138:UNK:HG3	2.03	0.41
6:6:45:HIS:HB3	6:6:56:PHE:CD1	2.55	0.41
7:7:53:GLY:HA2	10:A:765:G:H21	1.86	0.41
10:A:271:A:N6	10:A:275:G:N1	2.69	0.41
10:A:415:U:H5'	37:z:1204:UNK:CG	2.50	0.41
10:A:1002:A:H2'	10:A:1003:G:C8	2.56	0.41
10:A:1446:A:C6	10:A:1447:U:C4	3.08	0.41
14:F:217:LEU:HD23	14:F:259:LEU:HD21	2.03	0.41
22:T:182:ARG:HA	22:T:204:MET:SD	2.61	0.41
23:U:109:GLU:HG3	24:V:100:PHE:CZ	2.56	0.41
29:c:114:LYS:CD	29:c:250:LYS:HZ3	2.33	0.41
29:c:205:ALA:HA	29:c:208:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:w:11:UNK:HA	35:w:14:UNK:HG3	2.03	0.41
35:w:76:UNK:HA	35:w:79:UNK:HG3	2.02	0.41
37:z:2317:UNK:HA	37:z:2320:UNK:HG3	2.03	0.41
7:7:91:LYS:HE3	7:7:91:LYS:HB2	1.90	0.41
10:A:11:G:H5''	10:A:12:C:OP2	2.20	0.41
10:A:421:U:HO2'	10:A:422:U:H6	1.62	0.41
10:A:422:U:C4	10:A:423:U:C4	3.09	0.41
10:A:562:A:N6	10:A:1017:C:O2'	2.53	0.41
10:A:1021:U:H2'	10:A:1022:G:C8	2.56	0.41
10:A:1148:G:N2	19:Q:141:GLY:HA3	2.35	0.41
10:A:1257:G:O2'	10:A:1419:A:N1	2.47	0.41
13:E:251:PRO:HG3	13:E:326:ARG:HA	2.03	0.41
14:F:90:ALA:HA	14:F:91:PRO:HD3	1.93	0.41
14:F:113:LYS:NZ	14:F:158:PRO:HB3	2.36	0.41
26:X:27:UNK:HB2	26:X:30:UNK:HG1	2.03	0.41
27:Y:84:ASN:HB3	27:Y:117:HIS:CE1	2.56	0.41
28:b:218:LEU:HB3	28:b:235:TRP:HB3	2.03	0.41
28:b:256:PRO:HA	28:b:257:PRO:HD3	1.85	0.41
29:c:34:UNK:H2	29:c:159:TYR:HE1	1.68	0.41
29:c:204:ARG:HA	29:c:207:ILE:HB	2.02	0.41
29:c:281:HIS:CD2	29:c:320:VAL:HG12	2.56	0.41
29:c:313:LEU:O	29:c:316:SER:OG	2.26	0.41
30:h:81:GLU:OE2	30:h:210:ARG:NH2	2.54	0.41
31:i:169:PHE:N	31:i:170:PRO:HD2	2.36	0.41
35:v:21:UNK:HA	35:v:24:UNK:HG3	2.03	0.41
37:z:1832:UNK:HA	37:z:1835:UNK:HG3	2.03	0.41
10:A:274:A:N6	10:A:722:A:O2'	2.55	0.41
18:P:68:GLU:HB3	18:P:71:GLN:HE21	1.86	0.41
19:Q:205:UNK:O	19:Q:208:UNK:HG3	2.21	0.41
26:X:63:VAL:HA	26:X:64:PRO:HD3	1.94	0.41
34:u:114:VAL:HG13	34:u:160:ALA:HB3	2.03	0.41
35:w:88:UNK:O	35:w:91:UNK:HG3	2.20	0.41
8:8:124:ARG:HD2	18:P:78:ILE:HD12	2.03	0.40
8:8:130:LYS:HE3	18:P:79:PRO:HB3	2.03	0.40
10:A:137:A:O2'	10:A:139:A:C8	2.72	0.40
10:A:472:G:H2'	10:A:473:A:C2	2.56	0.40
10:A:650:A:H2'	10:A:651:A:C8	2.55	0.40
10:A:790:G:H2'	10:A:791:A:C8	2.56	0.40
10:A:985:G:H4'	10:A:986:U:O5'	2.22	0.40
14:F:92:ARG:NH1	32:l:144:THR:OG1	2.54	0.40
25:W:199:UNK:HA	25:W:202:UNK:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:i:140:LYS:O	31:i:144:ILE:HG13	2.22	0.40
37:z:1316:UNK:HA	37:z:1319:UNK:HG3	2.03	0.40
37:z:1983:UNK:O	37:z:1986:UNK:HG3	2.20	0.40
10:A:673:U:OP2	10:A:674:A:N6	2.52	0.40
13:E:256:ASP:OD2	13:E:353:SER:HA	2.21	0.40
22:T:194:LEU:HB2	22:T:197:TYR:HD2	1.85	0.40
29:c:53:UNK:HA	29:c:56:UNK:HG3	2.03	0.40
29:c:130:ASP:O	29:c:132:PRO:HD3	2.21	0.40
29:c:196:LEU:HA	29:c:199:PHE:HD2	1.86	0.40
35:v:63:UNK:HA	35:v:66:UNK:HG3	2.03	0.40
35:w:11:UNK:O	35:w:14:UNK:HG3	2.21	0.40
37:z:1926:UNK:O	37:z:1929:UNK:HG3	2.21	0.40
37:z:1982:UNK:HA	37:z:1985:UNK:HG3	2.03	0.40
8:8:107:VAL:O	8:8:111:ILE:HG12	2.21	0.40
10:A:485:A:H61	10:A:580:C:N4	2.18	0.40
10:A:648:A:H4'	10:A:783:A:OP2	2.21	0.40
18:P:113:THR:HG23	18:P:153:ASN:HD22	1.87	0.40
26:X:25:UNK:CG	26:X:43:ARG:HB2	2.51	0.40
30:h:148:LEU:HD13	30:h:305:PHE:CE1	2.56	0.40
33:o:67:UNK:HA	33:o:70:UNK:HG3	2.03	0.40
36:x:20:UNK:N	36:x:66:UNK:O	2.54	0.40
36:x:60:UNK:O	36:x:61:UNK:HG3	2.22	0.40
37:z:1404:UNK:HA	37:z:1407:UNK:HG3	2.02	0.40
37:z:1984:UNK:O	37:z:1987:UNK:HG3	2.21	0.40
10:A:72:U:HO2'	10:A:73:A:P	2.43	0.40
10:A:177:C:H4'	23:U:55:ARG:HH12	1.86	0.40
10:A:205:A:C2	37:z:2303:UNK:HG1	2.55	0.40
10:A:232:A:H2'	10:A:233:G:C8	2.57	0.40
10:A:339:A:OP2	10:A:1065:G:H5'	2.21	0.40
10:A:635:A:H2'	10:A:636:A:C8	2.56	0.40
10:A:1182:G:N2	10:A:1222:C:N3	2.59	0.40
10:A:1378:A:H2'	10:A:1379:A:H8	1.87	0.40
13:E:171:THR:HG21	13:E:340:VAL:HG23	2.04	0.40
13:E:259:ALA:HB3	13:E:341:PRO:HB2	2.04	0.40
16:N:18:TRP:CD1	16:N:56:HIS:HB3	2.56	0.40
20:R:48:ARG:O	20:R:52:LEU:HB2	2.21	0.40
25:W:192:UNK:HA	25:W:195:UNK:HG3	2.03	0.40
28:b:145:PRO:HB2	28:b:146:TYR:H	1.71	0.40
29:c:166:ALA:HB1	29:c:167:PRO:HD2	2.03	0.40
29:c:294:GLN:HB3	29:c:320:VAL:HG22	2.04	0.40
30:h:186:VAL:N	30:h:187:PRO:HD2	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:z:839:UNK:HA	37:z:842:UNK:HG3	2.04	0.40
37:z:1025:UNK:HA	37:z:1028:UNK:HG3	2.02	0.40
37:z:1987:UNK:O	37:z:1990:UNK:HG3	2.22	0.40
37:z:3312:UNK:HA	37:z:3315:UNK:HG3	2.04	0.40
4:3:77:ARG:NH2	10:A:470:U:O4	2.54	0.40
10:A:1054:G:H5"	10:A:1324:A:C2	2.57	0.40
13:E:280:ALA:HA	13:E:288:HIS:ND1	2.36	0.40
27:Y:124:ASP:HA	27:Y:125:PRO:HD3	1.93	0.40
30:h:41:UNK:O	30:h:44:UNK:HG3	2.21	0.40
35:v:46:UNK:HA	35:v:49:UNK:HG3	2.04	0.40
37:z:1015:UNK:HA	37:z:1018:UNK:HG3	2.03	0.40
37:z:2714:UNK:HA	37:z:2717:UNK:HG3	2.02	0.40
37:z:4002:UNK:HA	37:z:4005:UNK:HG3	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	
1	0	72/148 (49%)	69 (96%)	3 (4%)	0	100	100
2	1	56/256 (22%)	51 (91%)	5 (9%)	0	100	100
3	2	74/252 (29%)	73 (99%)	1 (1%)	0	100	100
4	3	57/161 (35%)	56 (98%)	1 (2%)	0	100	100
5	5	47/146 (32%)	44 (94%)	3 (6%)	0	100	100
6	6	46/65 (71%)	43 (94%)	3 (6%)	0	100	100
7	7	41/95 (43%)	41 (100%)	0	0	100	100
8	8	58/188 (31%)	58 (100%)	0	0	100	100
9	9	34/100 (34%)	34 (100%)	0	0	100	100
12	D	198/306 (65%)	188 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	E	206/399 (52%)	194 (94%)	12 (6%)	0	100	100
14	F	196/224 (88%)	188 (96%)	8 (4%)	0	100	100
15	I	55/268 (20%)	47 (86%)	8 (14%)	0	100	100
16	N	145/178 (82%)	132 (91%)	13 (9%)	0	100	100
17	O	112/145 (77%)	109 (97%)	3 (3%)	0	100	100
18	P	155/288 (54%)	144 (93%)	10 (6%)	1 (1%)	21	58
19	Q	136/208 (65%)	131 (96%)	5 (4%)	0	100	100
20	R	118/169 (70%)	107 (91%)	11 (9%)	0	100	100
21	S	92/180 (51%)	87 (95%)	5 (5%)	0	100	100
22	T	117/292 (40%)	113 (97%)	4 (3%)	0	100	100
23	U	114/132 (86%)	110 (96%)	3 (3%)	1 (1%)	14	49
24	V	104/207 (50%)	97 (93%)	7 (7%)	0	100	100
25	W	109/134 (81%)	106 (97%)	3 (3%)	0	100	100
26	X	68/87 (78%)	68 (100%)	0	0	100	100
27	Y	101/216 (47%)	95 (94%)	6 (6%)	0	100	100
28	b	190/380 (50%)	179 (94%)	10 (5%)	1 (0%)	24	63
29	c	259/301 (86%)	246 (95%)	12 (5%)	1 (0%)	30	67
30	h	239/298 (80%)	220 (92%)	18 (8%)	1 (0%)	30	67
31	i	159/312 (51%)	148 (93%)	11 (7%)	0	100	100
32	l	74/166 (45%)	70 (95%)	3 (4%)	1 (1%)	9	39
34	u	86/205 (42%)	77 (90%)	9 (10%)	0	100	100
All	All	3518/6506 (54%)	3325 (94%)	187 (5%)	6 (0%)	44	77

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	l	143	VAL
23	U	14	VAL
28	b	187	VAL
18	P	47	ARG
30	h	223	MET
29	c	71	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	62/115 (54%)	60 (97%)	2 (3%)	34	55
2	1	54/229 (24%)	51 (94%)	3 (6%)	19	41
3	2	72/228 (32%)	72 (100%)	0	100	100
4	3	56/147 (38%)	55 (98%)	1 (2%)	51	67
5	5	44/108 (41%)	43 (98%)	1 (2%)	44	63
6	6	45/60 (75%)	45 (100%)	0	100	100
7	7	39/78 (50%)	39 (100%)	0	100	100
8	8	54/162 (33%)	53 (98%)	1 (2%)	50	66
9	9	34/77 (44%)	34 (100%)	0	100	100
12	D	158/248 (64%)	158 (100%)	0	100	100
13	E	173/320 (54%)	169 (98%)	4 (2%)	44	63
14	F	166/166 (100%)	158 (95%)	8 (5%)	23	45
15	I	50/228 (22%)	48 (96%)	2 (4%)	28	49
16	N	127/157 (81%)	124 (98%)	3 (2%)	43	63
17	O	99/123 (80%)	97 (98%)	2 (2%)	48	66
18	P	129/235 (55%)	125 (97%)	4 (3%)	35	56
19	Q	111/155 (72%)	106 (96%)	5 (4%)	24	46
20	R	101/143 (71%)	97 (96%)	4 (4%)	28	49
21	S	80/153 (52%)	80 (100%)	0	100	100
22	T	107/258 (42%)	105 (98%)	2 (2%)	50	66
23	U	100/109 (92%)	98 (98%)	2 (2%)	48	66
24	V	94/173 (54%)	91 (97%)	3 (3%)	34	55
25	W	95/95 (100%)	94 (99%)	1 (1%)	65	74
26	X	62/62 (100%)	61 (98%)	1 (2%)	55	69
27	Y	91/192 (47%)	89 (98%)	2 (2%)	45	64
28	b	165/328 (50%)	158 (96%)	7 (4%)	26	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	c	236/244 (97%)	228 (97%)	8 (3%)	32	54
30	h	206/230 (90%)	204 (99%)	2 (1%)	68	76
31	i	148/281 (53%)	143 (97%)	5 (3%)	32	54
32	l	68/147 (46%)	62 (91%)	6 (9%)	9	29
34	u	79/177 (45%)	76 (96%)	3 (4%)	29	51
All	All	3105/5428 (57%)	3023 (97%)	82 (3%)	41	61

All (82) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	50	ARG
1	0	83	LEU
2	1	96	LYS
2	1	125	VAL
2	1	126	THR
4	3	103	ILE
5	5	121	ILE
8	8	129	TYR
13	E	203	VAL
13	E	237	VAL
13	E	287	THR
13	E	294	ILE
14	F	92	ARG
14	F	96	LEU
14	F	109	ILE
14	F	114	THR
14	F	159	THR
14	F	190	VAL
14	F	203	LEU
14	F	234	THR
15	I	130	VAL
15	I	136	ASN
16	N	10	GLN
16	N	39	LEU
16	N	65	ILE
17	O	40	VAL
17	O	77	ILE
18	P	61	THR
18	P	81	TYR
18	P	130	GLN

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Mol	Chain	Res	Type
18	P	147	THR
19	Q	77	THR
19	Q	83	THR
19	Q	90	LEU
19	Q	118	MET
19	Q	149	HIS
20	R	36	LEU
20	R	52	LEU
20	R	104	TYR
20	R	124	ILE
22	T	166	LEU
22	T	177	VAL
23	U	46	VAL
23	U	81	LEU
24	V	148	LEU
24	V	158	VAL
24	V	164	VAL
25	W	119	LEU
26	X	56	TYR
27	Y	138	THR
27	Y	153	ILE
28	b	179	VAL
28	b	187	VAL
28	b	206	TYR
28	b	258	PHE
28	b	297	THR
28	b	304	TYR
28	b	308	GLN
29	c	69	LYS
29	c	70	THR
29	c	126	THR
29	c	165	ARG
29	c	180	VAL
29	c	207	ILE
29	c	280	VAL
29	c	305	HIS
30	h	230	GLU
30	h	233	THR
31	i	116	VAL
31	i	149	HIS
31	i	249	GLU
31	i	253	VAL

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Mol	Chain	Res	Type
31	i	256	TYR
32	l	100	ILE
32	l	110	ILE
32	l	129	SER
32	l	135	THR
32	l	153	PHE
32	l	157	LEU
34	u	140	ARG
34	u	141	TYR
34	u	144	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	41	ASN
1	0	59	HIS
1	0	72	HIS
3	2	119	GLN
5	5	83	ASN
8	8	151	ASN
8	8	154	GLN
9	9	99	GLN
12	D	169	HIS
12	D	183	HIS
12	D	234	GLN
13	E	231	ASN
14	F	188	HIS
14	F	241	ASN
15	I	121	ASN
16	N	26	GLN
16	N	80	HIS
16	N	117	HIS
17	O	103	ASN
18	P	26	ASN
18	P	53	HIS
18	P	71	GLN
18	P	99	ASN
20	R	31	ASN
20	R	101	ASN
21	S	163	HIS
23	U	36	ASN
23	U	79	HIS

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Mol	Chain	Res	Type
23	U	89	ASN
23	U	94	GLN
24	V	122	ASN
25	W	73	HIS
25	W	130	HIS
25	W	157	HIS
25	W	171	HIS
26	X	84	ASN
26	X	98	GLN
28	b	147	HIS
28	b	191	ASN
28	b	307	HIS
28	b	320	GLN
29	c	79	ASN
30	h	80	GLN
31	i	251	HIS
32	l	92	HIS
34	u	103	HIS
34	u	124	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	1431/1570 (91%)	368 (25%)	25 (1%)
11	B	0/29	-	-
All	All	1431/1599 (89%)	368 (25%)	25 (1%)

All (368) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	A	2	C
10	A	5	A
10	A	7	G
10	A	8	C
10	A	46	A
10	A	48	U
10	A	49	A
10	A	50	A
10	A	56	A
10	A	59	A
10	A	64	C

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Mol	Chain	Res	Type
10	A	65	C
10	A	66	U
10	A	67	A
10	A	69	C
10	A	70	A
10	A	73	A
10	A	82	G
10	A	95	U
10	A	96	U
10	A	97	A
10	A	100	C
10	A	101	U
10	A	102	G
10	A	105	G
10	A	108	A
10	A	109	U
10	A	112	A
10	A	116	A
10	A	117	G
10	A	128	A
10	A	131	G
10	A	132	A
10	A	133	U
10	A	138	G
10	A	139	A
10	A	140	A
10	A	142	A
10	A	144	A
10	A	145	A
10	A	147	A
10	A	148	A
10	A	149	A
10	A	150	A
10	A	152	U
10	A	153	A
10	A	154	A
10	A	156	A
10	A	157	A
10	A	160	A
10	A	161	G
10	A	162	C
10	A	163	A

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Mol	Chain	Res	Type
10	A	164	A
10	A	169	U
10	A	171	C
10	A	172	C
10	A	174	C
10	A	179	A
10	A	188	A
10	A	189	U
10	A	191	A
10	A	203	G
10	A	204	A
10	A	205	A
10	A	206	A
10	A	217	A
10	A	218	A
10	A	221	G
10	A	222	A
10	A	227	U
10	A	228	A
10	A	237	C
10	A	238	C
10	A	253	G
10	A	266	A
10	A	270	U
10	A	271	A
10	A	272	A
10	A	273	A
10	A	274	A
10	A	275	G
10	A	293	G
10	A	299	A
10	A	310	A
10	A	321	G
10	A	322	A
10	A	323	G
10	A	328	A
10	A	330	A
10	A	331	G
10	A	338	G
10	A	351	G
10	A	357	U
10	A	358	G

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Mol	Chain	Res	Type
10	A	365	A
10	A	372	U
10	A	379	C
10	A	381	A
10	A	382	C
10	A	390	A
10	A	391	U
10	A	393	C
10	A	394	C
10	A	395	C
10	A	398	A
10	A	399	A
10	A	400	A
10	A	409	U
10	A	413	A
10	A	414	A
10	A	415	U
10	A	417	U
10	A	418	A
10	A	419	U
10	A	421	U
10	A	422	U
10	A	427	A
10	A	432	G
10	A	439	A
10	A	444	A
10	A	445	C
10	A	447	G
10	A	457	A
10	A	458	A
10	A	459	C
10	A	466	A
10	A	468	C
10	A	472	G
10	A	474	C
10	A	478	A
10	A	487	C
10	A	489	U
10	A	490	A
10	A	492	U
10	A	494	C
10	A	560	A

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Mol	Chain	Res	Type
10	A	561	U
10	A	565	C
10	A	566	C
10	A	569	A
10	A	583	A
10	A	584	C
10	A	591	C
10	A	592	C
10	A	594	A
10	A	614	A
10	A	616	A
10	A	617	C
10	A	618	A
10	A	619	U
10	A	626	A
10	A	629	A
10	A	632	G
10	A	648	A
10	A	649	G
10	A	652	G
10	A	655	U
10	A	662	U
10	A	665	C
10	A	668	A
10	A	670	G
10	A	671	C
10	A	673	U
10	A	674	A
10	A	675	C
10	A	682	A
10	A	686	A
10	A	687	A
10	A	688	U
10	A	691	U
10	A	693	U
10	A	694	A
10	A	695	C
10	A	702	U
10	A	703	U
10	A	704	A
10	A	705	A
10	A	706	C

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Mol	Chain	Res	Type
10	A	710	C
10	A	711	A
10	A	713	U
10	A	718	C
10	A	722	A
10	A	723	C
10	A	724	A
10	A	726	C
10	A	731	A
10	A	733	A
10	A	734	C
10	A	735	G
10	A	744	U
10	A	745	U
10	A	746	A
10	A	747	C
10	A	748	A
10	A	752	U
10	A	755	A
10	A	757	C
10	A	766	G
10	A	772	A
10	A	773	C
10	A	774	C
10	A	776	A
10	A	779	A
10	A	780	A
10	A	781	A
10	A	782	G
10	A	787	A
10	A	807	G
10	A	811	A
10	A	812	C
10	A	813	A
10	A	817	A
10	A	823	C
10	A	830	A
10	A	834	A
10	A	841	C
10	A	850	C
10	A	851	A
10	A	853	U

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Mol	Chain	Res	Type
10	A	854	A
10	A	857	A
10	A	861	U
10	A	870	A
10	A	876	G
10	A	887	C
10	A	888	C
10	A	889	A
10	A	894	A
10	A	900	C
10	A	906	A
10	A	907	U
10	A	922	G
10	A	923	G
10	A	931	A
10	A	948	U
10	A	956	U
10	A	960	U
10	A	962	A
10	A	963	A
10	A	964	U
10	A	965	G
10	A	975	G
10	A	985	G
10	A	986	U
10	A	990	U
10	A	1013	C
10	A	1014	C
10	A	1024	A
10	A	1026	A
10	A	1029	C
10	A	1036	A
10	A	1048	C
10	A	1049	G
10	A	1053	A
10	A	1054	G
10	A	1055	A
10	A	1062	G
10	A	1069	U
10	A	1075	A
10	A	1080	U
10	A	1083	A

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Mol	Chain	Res	Type
10	A	1084	A
10	A	1085	A
10	A	1089	U
10	A	1125	A
10	A	1132	A
10	A	1137	C
10	A	1141	U
10	A	1144	G
10	A	1165	C
10	A	1166	A
10	A	1167	A
10	A	1174	C
10	A	1177	C
10	A	1178	G
10	A	1179	A
10	A	1180	G
10	A	1181	U
10	A	1187	U
10	A	1189	A
10	A	1191	C
10	A	1192	U
10	A	1193	A
10	A	1221	U
10	A	1222	C
10	A	1223	A
10	A	1225	U
10	A	1226	U
10	A	1227	A
10	A	1228	U
10	A	1236	A
10	A	1237	A
10	A	1238	A
10	A	1244	A
10	A	1247	A
10	A	1250	G
10	A	1251	G
10	A	1252	A
10	A	1253	A
10	A	1256	A
10	A	1260	A
10	A	1262	C
10	A	1266	G

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Mol	Chain	Res	Type
10	A	1269	A
10	A	1297	C
10	A	1325	U
10	A	1326	G
10	A	1327	U
10	A	1339	A
10	A	1341	C
10	A	1350	G
10	A	1376	U
10	A	1377	C
10	A	1387	A
10	A	1388	G
10	A	1394	C
10	A	1405	U
10	A	1406	U
10	A	1407	C
10	A	1409	G
10	A	1420	U
10	A	1423	A
10	A	1424	G
10	A	1430	U
10	A	1431	U
10	A	1432	U
10	A	1434	U
10	A	1436	U
10	A	1442	A
10	A	1443	U
10	A	1446	A
10	A	1456	G
10	A	1466	A
10	A	1467	C
10	A	1474	A
10	A	1480	A
10	A	1483	A
10	A	1488	C
10	A	1490	C
10	A	1491	A
10	A	1492	A
10	A	1493	A
10	A	1496	C
10	A	1504	A
10	A	1508	A

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Mol	Chain	Res	Type
10	A	1509	A
10	A	1510	U
10	A	1527	A
10	A	1530	U
10	A	1531	A
10	A	1532	A
10	A	1537	C
10	A	1540	A
10	A	1541	U
10	A	1543	A
10	A	1545	A
10	A	1547	A
10	A	1548	U
10	A	1549	C
10	A	1551	A
10	A	1556	U
10	A	1557	A
10	A	1565	G
10	A	1567	A
10	A	1568	C
10	A	1569	A

All (25) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	1	A
10	A	66	U
10	A	72	U
10	A	115	U
10	A	273	A
10	A	298	A
10	A	418	A
10	A	618	A
10	A	672	U
10	A	702	U
10	A	730	A
10	A	746	A
10	A	751	G
10	A	756	C
10	A	786	A
10	A	860	A
10	A	985	G

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Mol	Chain	Res	Type
10	A	1013	C
10	A	1079	U
10	A	1166	A
10	A	1236	A
10	A	1252	A
10	A	1375	U
10	A	1566	C
10	A	1568	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
37	z	20
35	v	4
35	w	4
10	A	2
11	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	z	3019:UNK	C	3301:UNK	N	179.35
1	z	1718:UNK	C	1795:UNK	N	178.65
1	z	1325:UNK	C	1403:UNK	N	151.39
1	z	844:UNK	C	1001:UNK	N	141.39
1	z	2220:UNK	C	2301:UNK	N	132.08
1	z	4008:UNK	C	4101:UNK	N	128.55
1	z	2719:UNK	C	3004:UNK	N	119.93
1	z	1225:UNK	C	1302:UNK	N	101.25
1	z	2022:UNK	C	2201:UNK	N	100.33
1	z	1052:UNK	C	1196:UNK	N	80.72
1	z	3316:UNK	C	4000:UNK	N	74.67
1	z	2613:UNK	C	2703:UNK	N	73.14
1	z	1439:UNK	C	1704:UNK	N	68.39
1	z	1939:UNK	C	1977:UNK	N	49.60
1	v	25:UNK	C	26:UNK	N	44.67
1	z	1997:UNK	C	2003:UNK	N	44.67
1	w	25:UNK	C	26:UNK	N	43.96
1	z	1847:UNK	C	1926:UNK	N	43.50
1	z	2413:UNK	C	2601:UNK	N	40.26
1	A	37:N	O3'	45:A	P	29.60
1	v	80:UNK	C	81:UNK	N	27.95
1	w	50:UNK	C	51:UNK	N	27.75
1	w	80:UNK	C	81:UNK	N	26.67
1	v	50:UNK	C	51:UNK	N	25.67
1	z	2321:UNK	C	2401:UNK	N	25.50
1	w	67:UNK	C	68:UNK	N	13.96
1	A	27:N	O3'	35:N	P	12.68
1	v	67:UNK	C	68:UNK	N	12.57
1	B	22:N	O3'	30:N	P	11.59
1	z	1814:UNK	C	1816:UNK	N	8.48
1	z	787:UNK	C	829:UNK	N	8.09

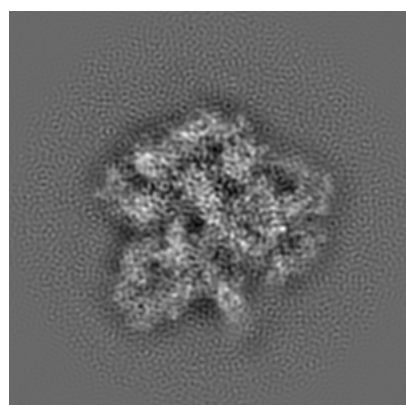
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2490. These allow visual inspection of the internal detail of the map and identification of artifacts.

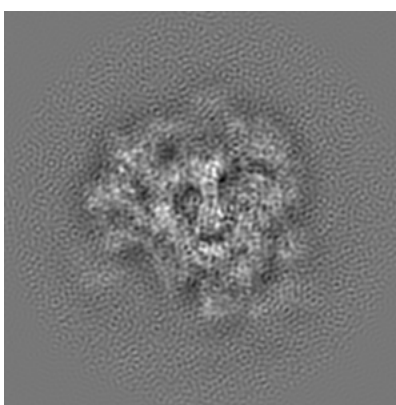
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

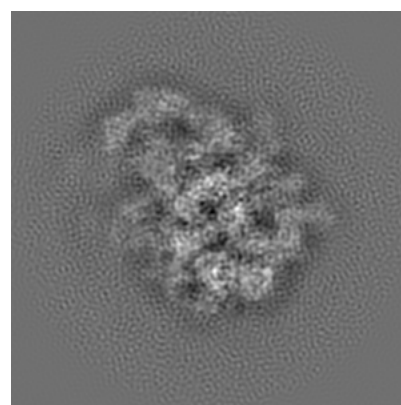
6.1.1 Primary map



X



Y

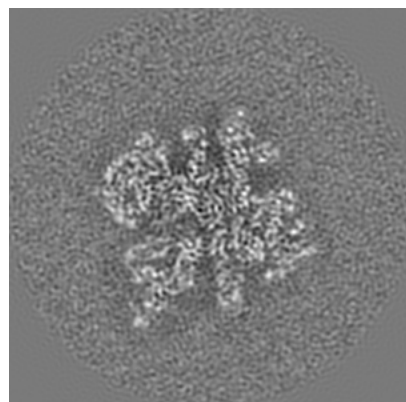


Z

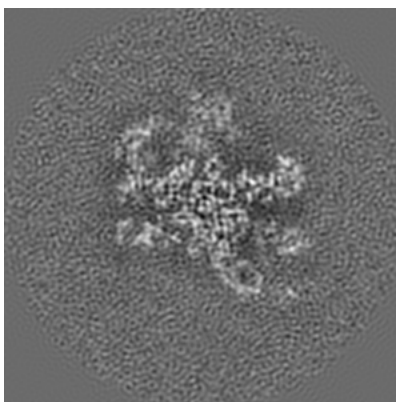
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

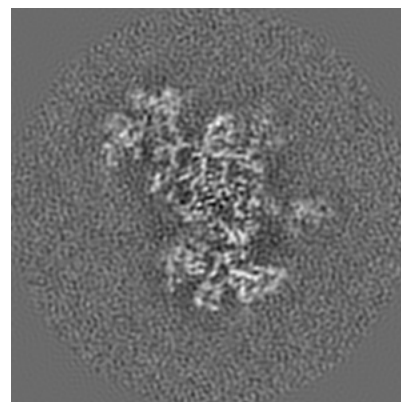
6.2.1 Primary map



X Index: 128



Y Index: 128

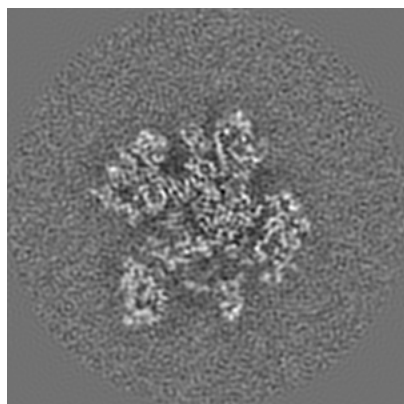


Z Index: 128

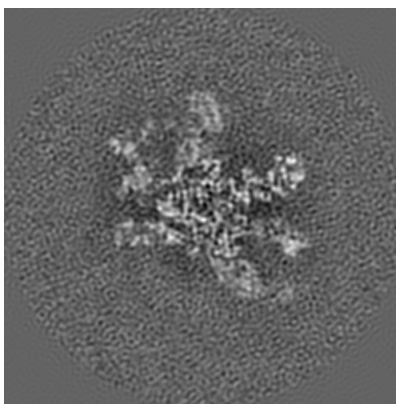
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

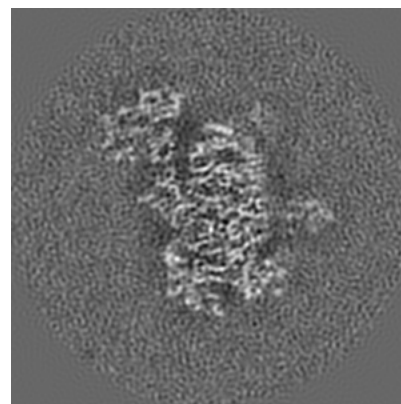
6.3.1 Primary map



X Index: 132



Y Index: 130

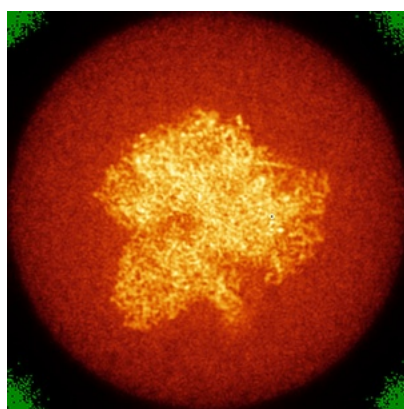


Z Index: 134

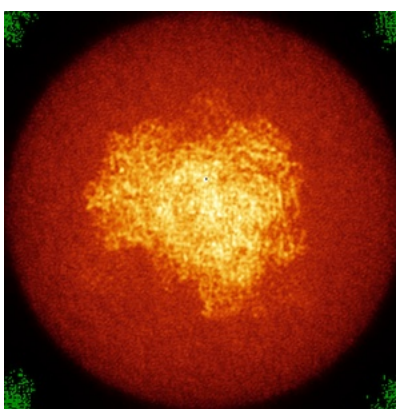
The images above show the largest variance slices of the map in three orthogonal directions.

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

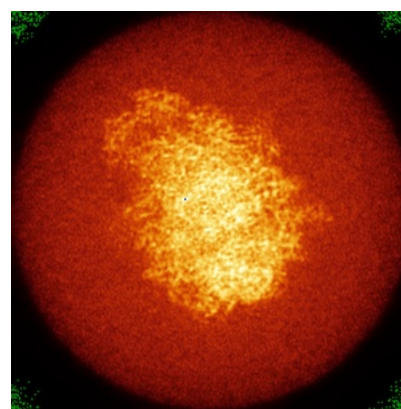
6.4.1 Primary map



X



Y

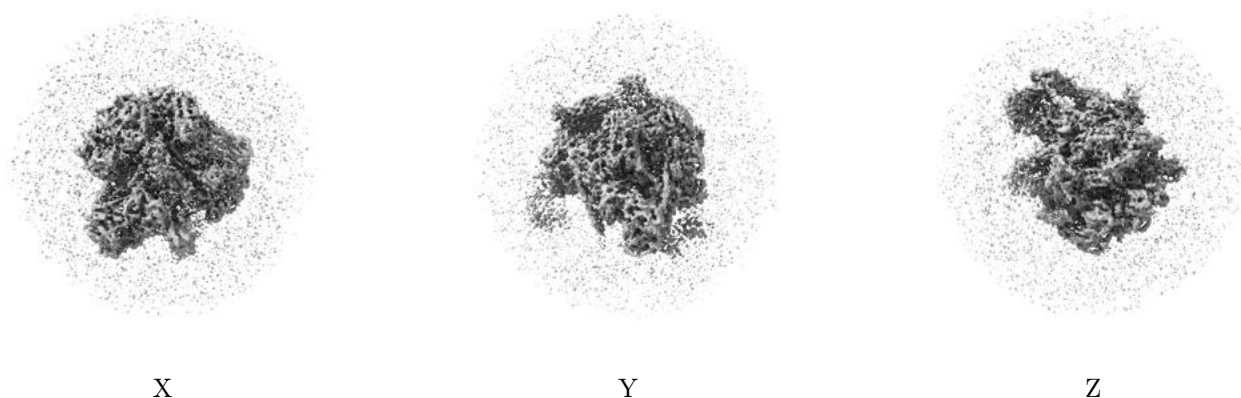


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 11.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

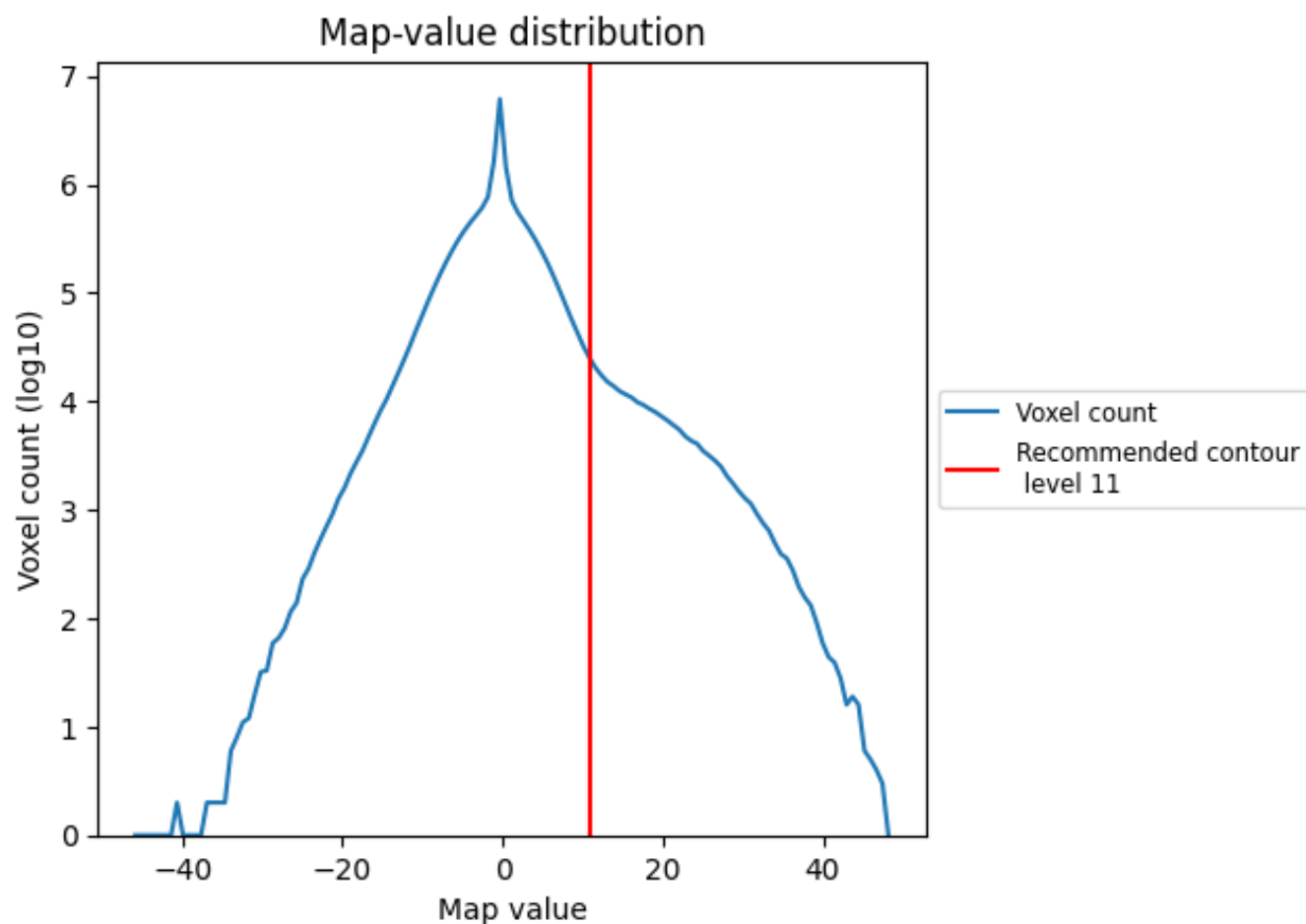
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

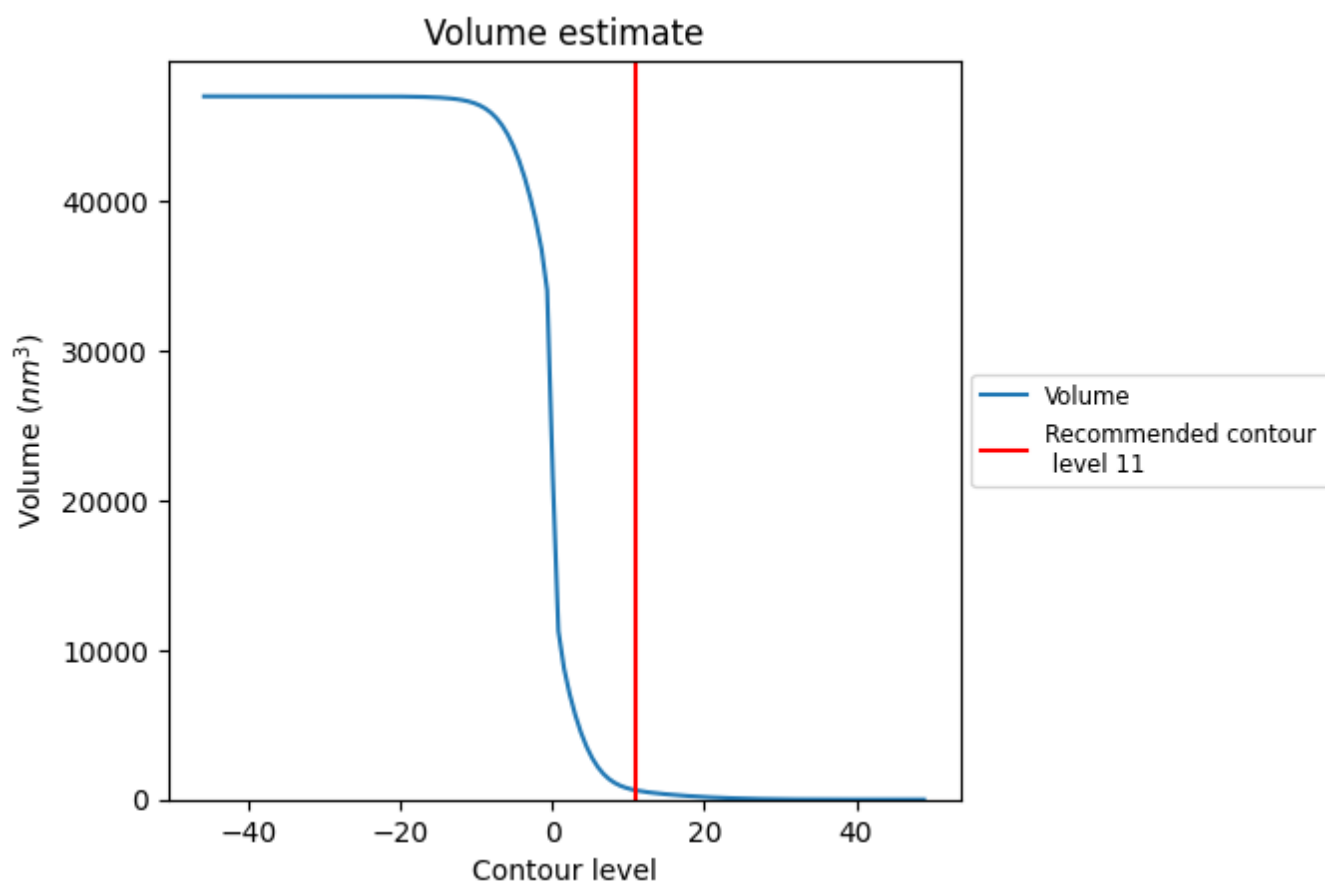
This section contains the results of statistical analysis of the map.

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.

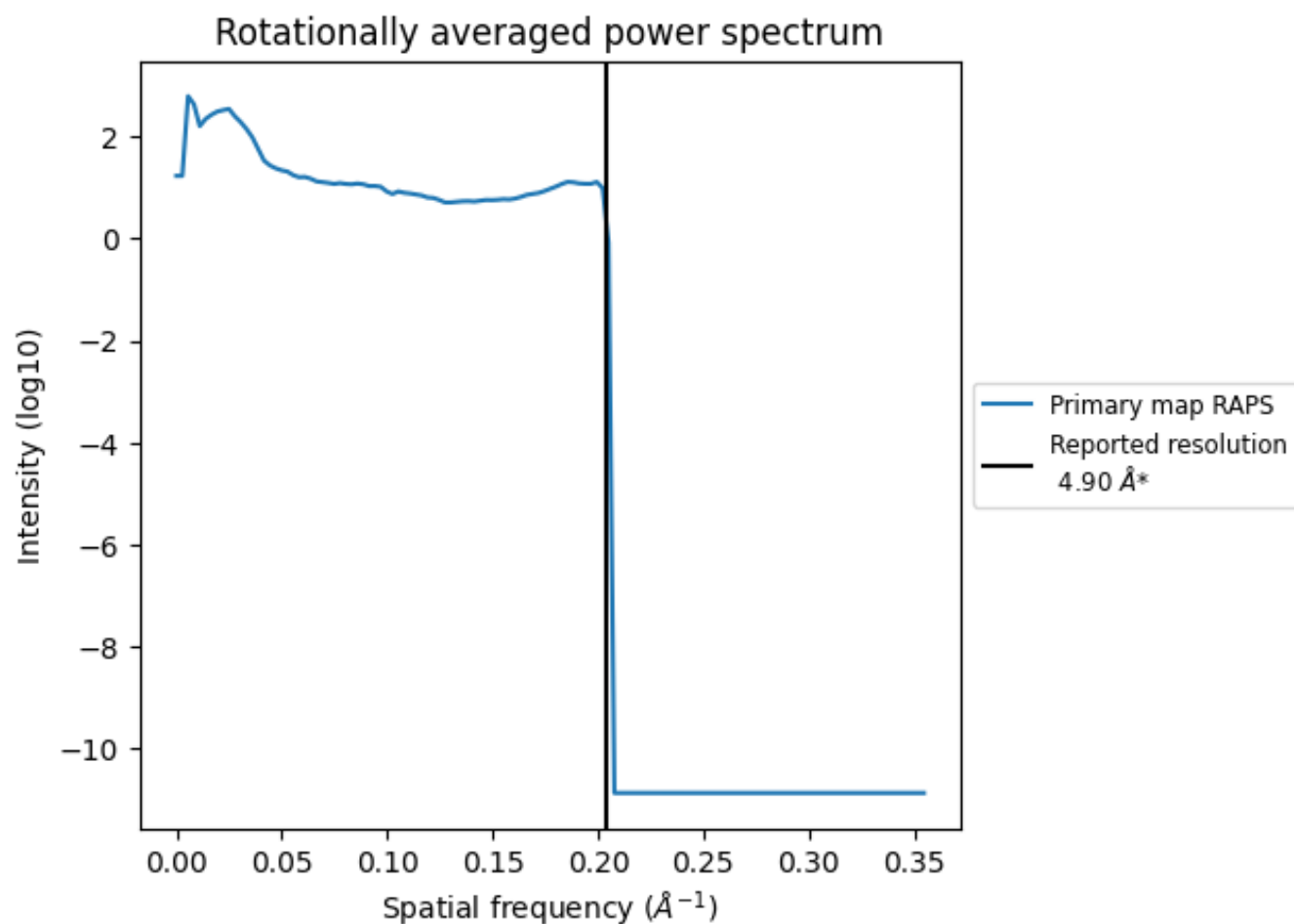
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 619 nm³; this corresponds to an approximate mass of 559 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 0.204 Å⁻¹

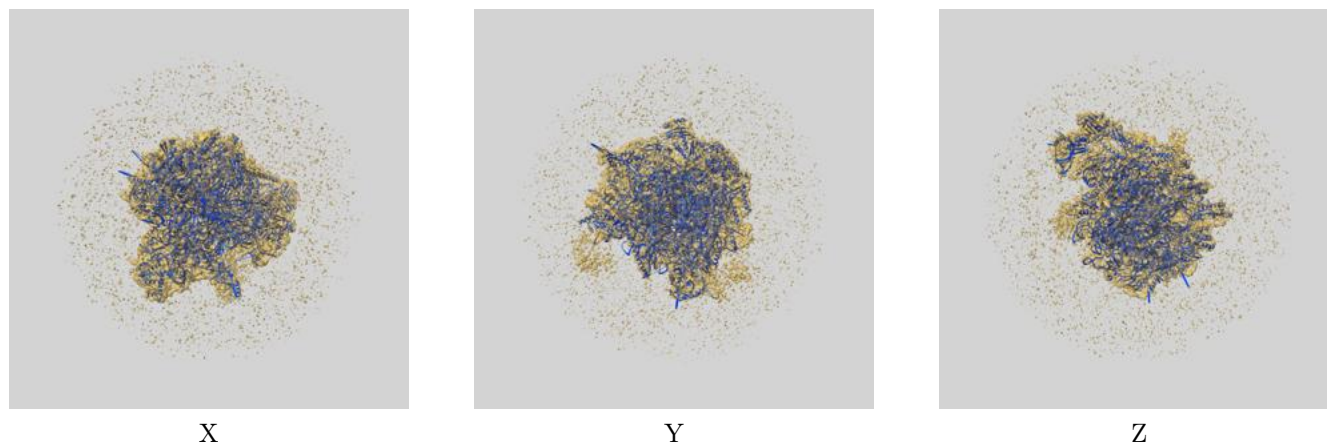
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

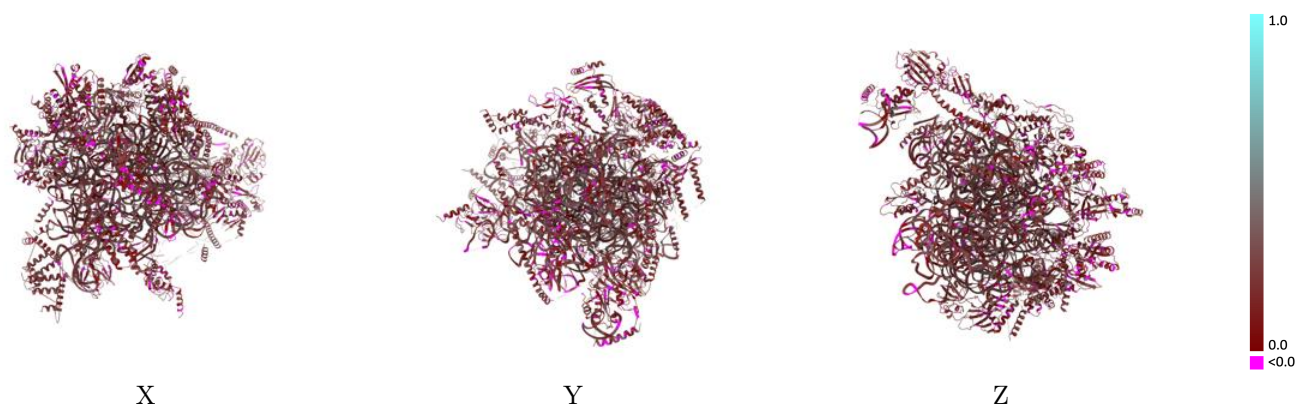
This section contains information regarding the fit between EMDB map EMD-2490 and PDB model 4CE4. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



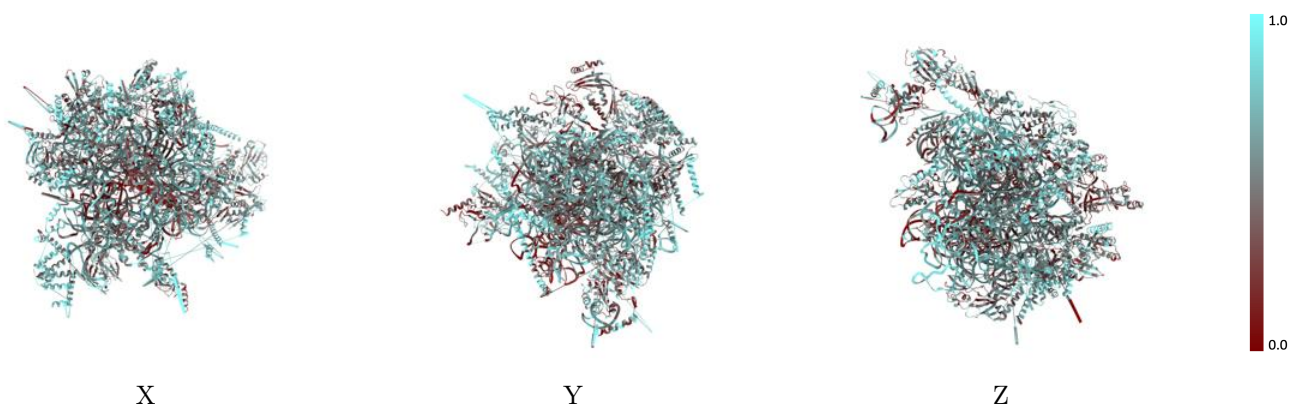
The images above show the 3D surface view of the map at the recommended contour level 11.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



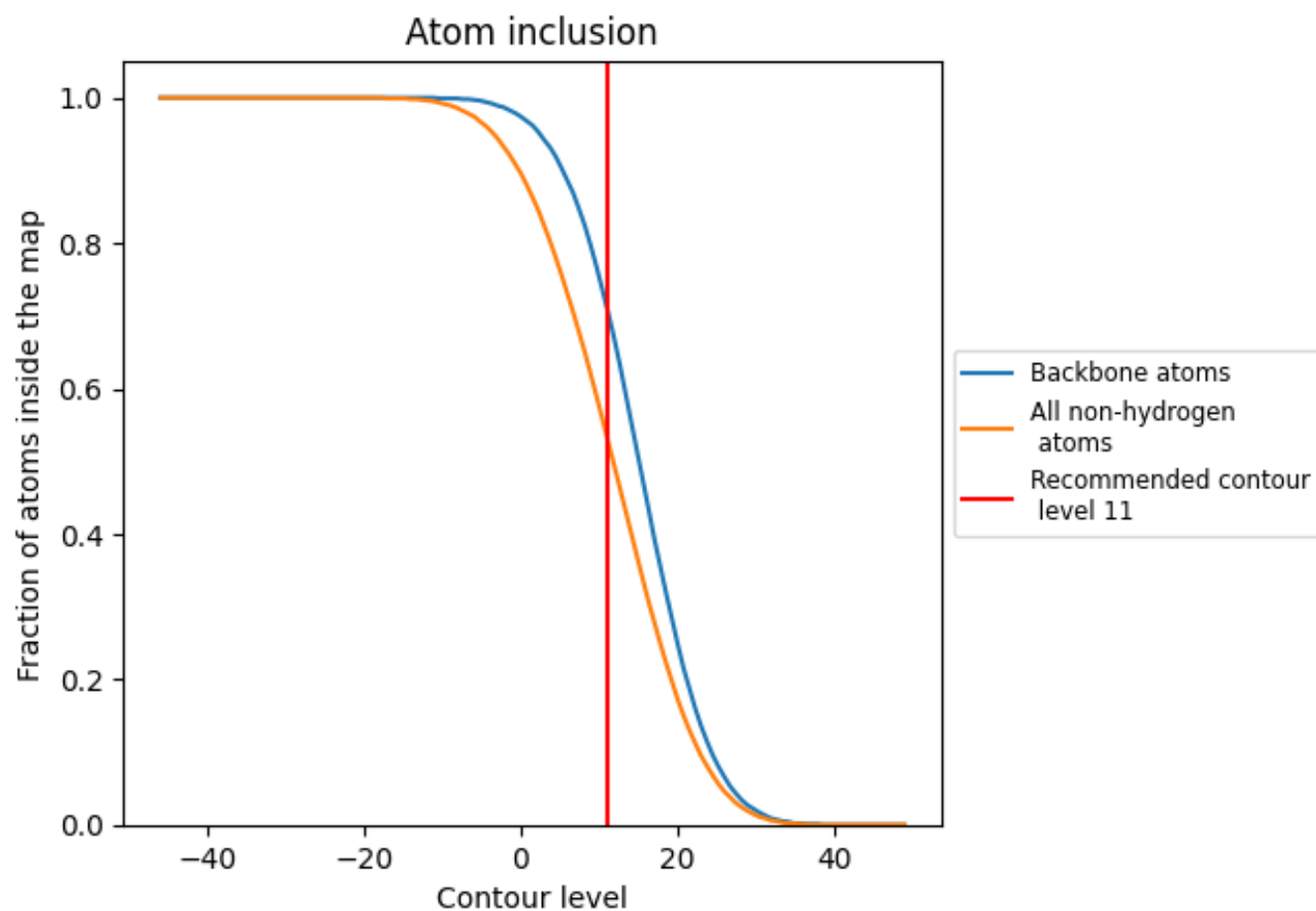
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 53% 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 (11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5340	 0.2120
0	 0.4130	 0.2170
1	 0.4630	 0.1570
2	 0.5700	 0.1350
3	 0.4600	 0.2130
5	 0.5340	 0.2220
6	 0.1930	 0.0790
7	 0.4280	 0.2160
8	 0.3730	 0.2070
9	 0.3480	 0.2100
A	 0.5760	 0.2430
B	 0.5090	 0.1790
D	 0.4180	 0.1520
E	 0.4690	 0.1920
F	 0.4790	 0.1970
I	 0.2420	 0.1430
N	 0.4870	 0.2170
O	 0.4280	 0.2010
P	 0.4140	 0.1780
Q	 0.5090	 0.2000
R	 0.5100	 0.1860
S	 0.4600	 0.1730
T	 0.5330	 0.1820
U	 0.4230	 0.2040
V	 0.4550	 0.2230
W	 0.4690	 0.2180
X	 0.4560	 0.2160
Y	 0.2770	 0.1180
b	 0.5410	 0.1730
c	 0.5260	 0.1590
h	 0.5850	 0.1590
i	 0.3650	 0.1510
l	 0.5350	 0.1460
o	 0.7620	 0.1880
u	 0.4640	 0.1450



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Chain	Atom inclusion	Q-score
v	 0.7160	 0.2320
w	 0.6830	 0.2250
x	 0.6430	 0.2130
z	 0.6840	 0.2170