



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 12:29 AM UTC

PDB ID : 8V83 / pdb_00008v83
EMDB ID : EMD-43017
Title : 60S ribosome biogenesis intermediate (Dbp10 pre-catalytic structure - Overall map)
Authors : Cruz, V.E.; Weirich, C.S.; Peddada, N.; Erzberger, J.P.
Deposited on : 2023-12-04
Resolution : 2.53 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

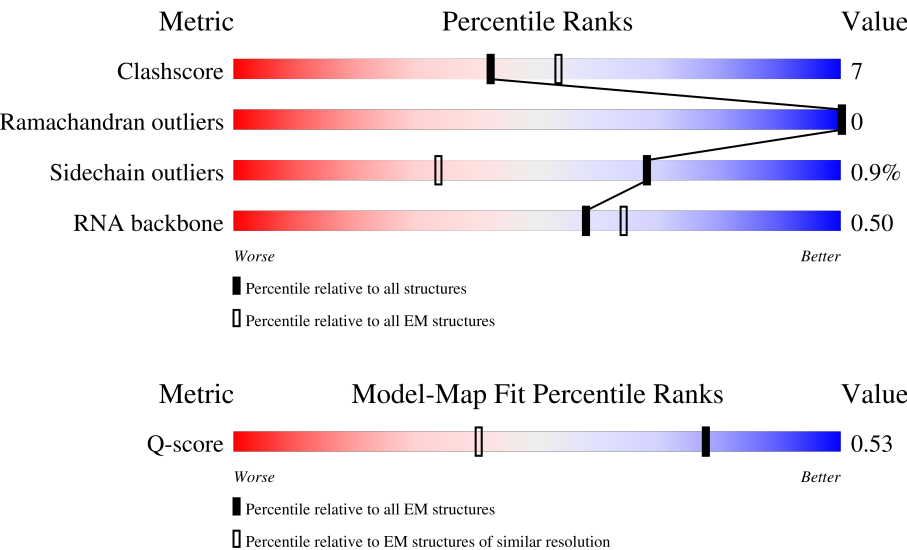
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.53 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	7309 (2.03 - 3.03)

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 <=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	1	3396	
2	2	158	
3	6	232	

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Mol	Chain	Length	Quality of chain
4	7	204	
5	8	434	
6	A	291	
7	B	387	
8	C	362	
9	D	505	
10	E	176	
11	F	244	
12	G	256	
13	H	191	
14	I	463	
15	J	427	
16	K	376	
17	L	199	
18	M	138	
19	N	204	
20	O	199	
21	P	184	
22	Q	186	
23	R	306	
24	S	172	
25	T	250	
26	V	137	
27	W	236	
28	Y	127	

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Mol	Chain	Length	Quality of chain
29	Z	453	
30	a	217	
31	b	647	
32	e	130	
33	f	107	
34	h	120	
35	i	100	
36	j	88	
37	l	181	
38	m	807	
39	n	605	
40	o	220	
41	q	618	
42	r	261	
43	t	322	
44	u	199	
45	v	231	
46	w	278	
47	x	295	
48	y	245	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 119224 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called *Saccharomyces cerevisiae* S288C 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2015	Total	C	N	O	P	0	0
			43147	19266	7811	14055	2015		

- Molecule 2 is a RNA chain called *Saccharomyces cerevisiae* S288C 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	150	Total	C	N	O	P	0	0
			3189	1426	563	1050	150		

- Molecule 3 is a RNA chain called *Saccharomyces cerevisiae* ITS-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	58	Total	C	N	O	P	0	0
			1227	550	210	409	58		

- Molecule 4 is a protein called 60S ribosomal subunit assembly/export protein LOC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	7	11	Total	C	N	O	0	0
			87	56	15	16		

- Molecule 5 is a protein called Ribosomal RNA-processing protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	8	143	Total	C	N	O	S	0	0
			1203	743	240	216	4		

- Molecule 6 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	255	Total	C	N	O	S	0	0
			2080	1326	372	376	6		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	331	Total	C	N	O	S	0	0
			2626	1669	484	467	6		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	343	Total	C	N	O	S	0	0
			2611	1643	499	466	3		

- Molecule 9 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	423	Total	C	N	O	S	0	0
			3377	2183	573	609	12		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	151	Total	C	N	O	S	0	0
			1205	780	215	209	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	241	Total	C	N	O	S	0	0
			1936	1246	351	338	1		

- Molecule 12 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	164	Total	C	N	O	S	0	0
			1272	818	217	235	2		

- Molecule 13 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	189	Total	C	N	O	S	0	0
			1502	952	272	275	3		

- Molecule 14 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	394	Total	C	N	O	S	0	0
			3126	1997	525	593	11		

- Molecule 15 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	151	Total	C	N	O	S	0	0
			1271	793	240	235	3		

- Molecule 16 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	268	Total	C	N	O	S	0	0
			2155	1387	355	409	4		

- Molecule 17 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	110	Total	C	N	O	S	0	0
			884	552	185	147			

- Molecule 18 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	134	Total	C	N	O	S	0	0
			1041	668	197	174	2		

- Molecule 19 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	177	Total	C	N	O	S	0	0
			1513	948	320	244	1		

- Molecule 20 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	188	Total	C	N	O	S	0	0
			1486	960	275	250	1		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	137	Total	C	N	O	0	0
			1062	666	198	198		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Q	144	Total	C	N	O	S	0
			1110	704	213	192	1	0

- Molecule 23 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	190	Total	C	N	O	S	0
			1578	996	297	275	10	0

- Molecule 24 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	S	170	Total	C	N	O	S	0
			1432	922	265	242	3	0

- Molecule 25 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	T	79	Total	C	N	O	0	0
			625	390	109	126		

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	V	114	Total	C	N	O	S	0
			845	535	154	149	7	0

- Molecule 27 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	W	232	Total	C	N	O	S	0
			1870	1184	321	360	5	0

- Molecule 28 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Y	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 29 is a protein called Ribosome biogenesis protein SSF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	253	Total	C	N	O	S	0	0
			2020	1280	361	370	9		

- Molecule 30 is a protein called Large ribosomal subunit protein uL1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	210	Total	C	N	O	S	0	0
			1668	1067	291	301	9		

- Molecule 31 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	423	Total	C	N	O	S	0	0
			3429	2193	586	632	18		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	126	Total	C	N	O	S	0	0
			1018	646	204	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 34 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 35 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	84	Total	C	N	O	S	0	0
			665	413	136	114	2		

- Molecule 36 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	72	Total	C	N	O	S	0	0
			571	347	124	95	5		

- Molecule 37 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	176	Total	C	N	O	S	0	0
			1394	896	244	247	7		

- Molecule 38 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	211	Total	C	N	O	S	0	0
			1759	1116	305	333	5		

- Molecule 39 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	337	Total	C	N	O	S	0	0
			2760	1804	462	486	8		

- Molecule 40 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 41 is a protein called 25S rRNA (cytosine(2870)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	358	Total	C	N	O	S	0	0
			2799	1779	490	518	12		

- Molecule 42 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	184	Total	C	N	O	S	0	0
			1489	937	286	261	5		

- Molecule 43 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	249	Total	C	N	O	S	0	0
			1973	1258	352	360	3		

- Molecule 44 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	112	Total	C	N	O	S	0	0
			944	594	191	150	9		

- Molecule 45 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	149	Total	C	N	O	S	0	0
			1242	778	242	219	3		

- Molecule 46 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	w	243	Total	C	N	O	S	0	0
			2058	1334	353	366	5		

- Molecule 47 is a protein called Ribosome production factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	279	Total	C	N	O	S	0	0
			2362	1500	427	431	4		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	225	Total	C	N	O	S	0	0
			1701	1056	295	343	7		

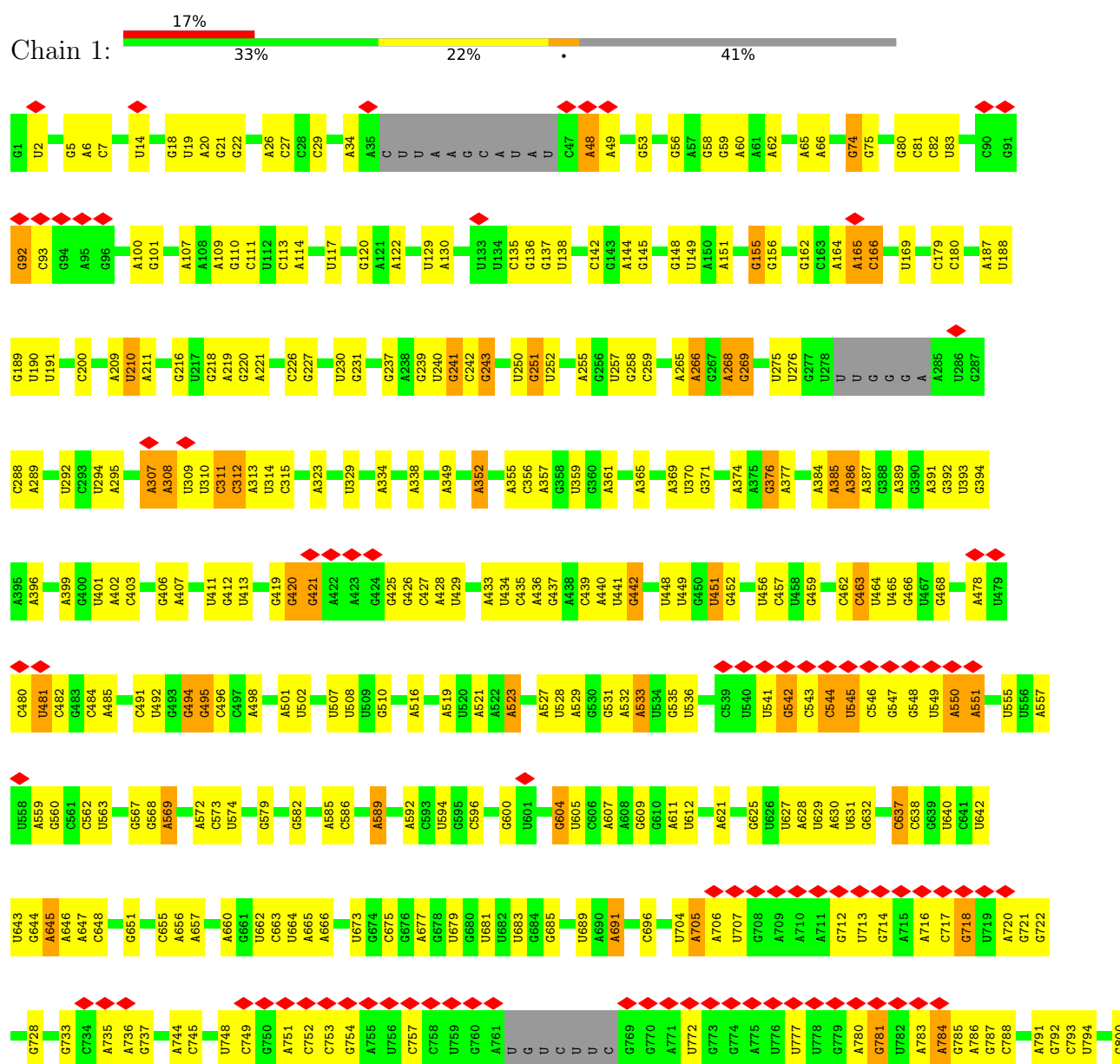
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

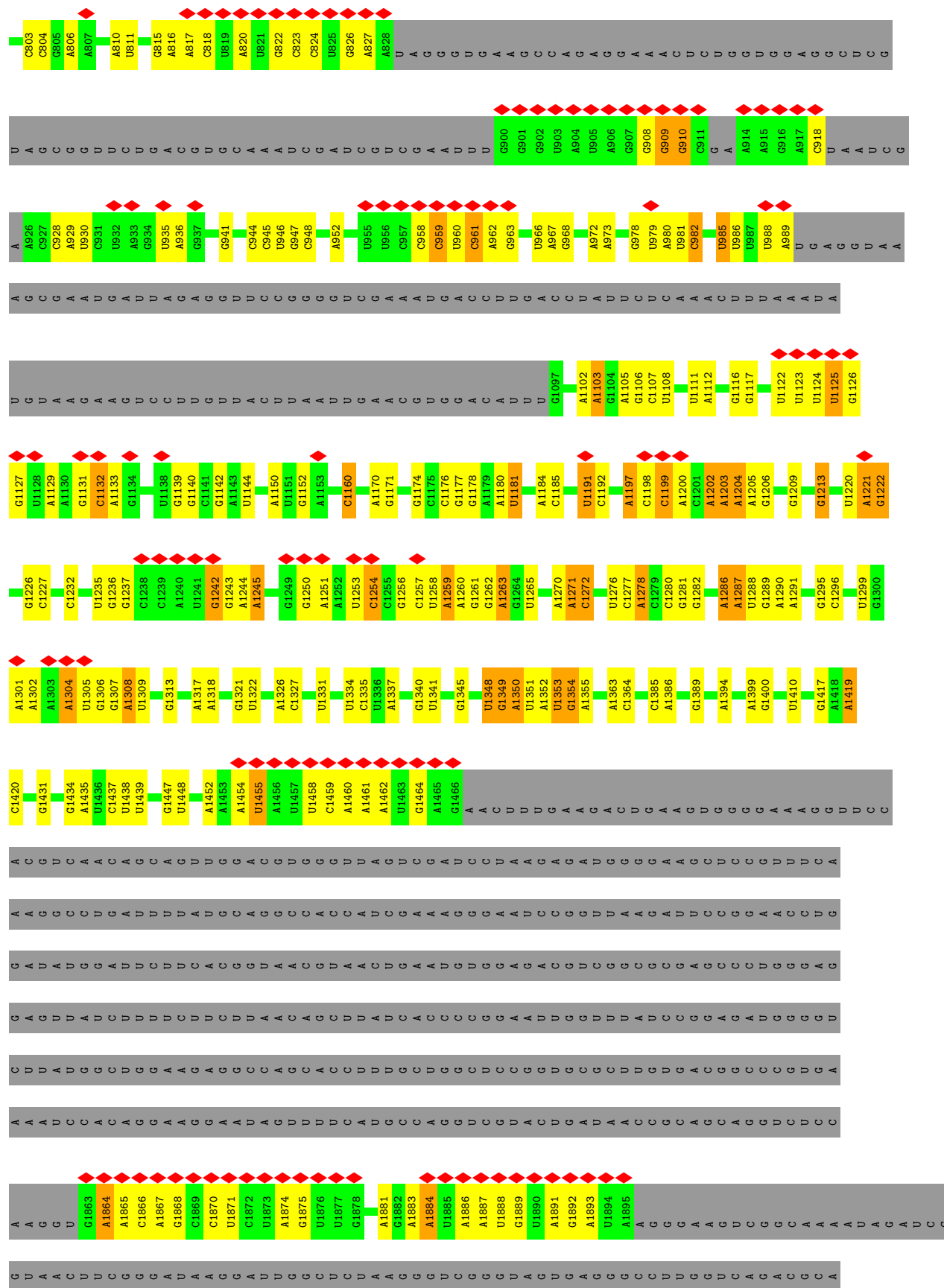
Mol	Chain	Residues	Atoms		AltConf
49	j	1	Total 1	Zn 1	0
49	u	1	Total 1	Zn 1	0

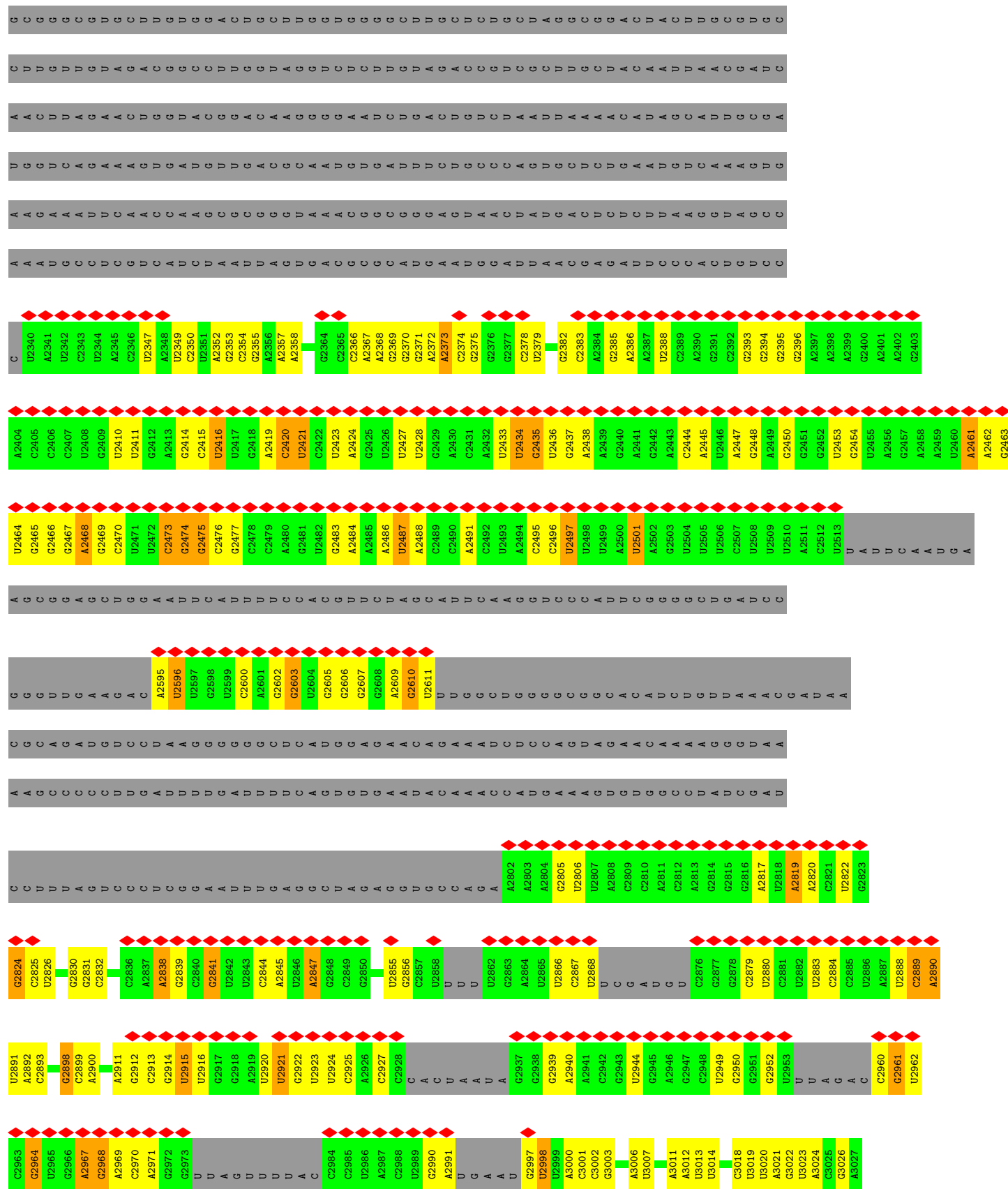
3 Residue-property plots

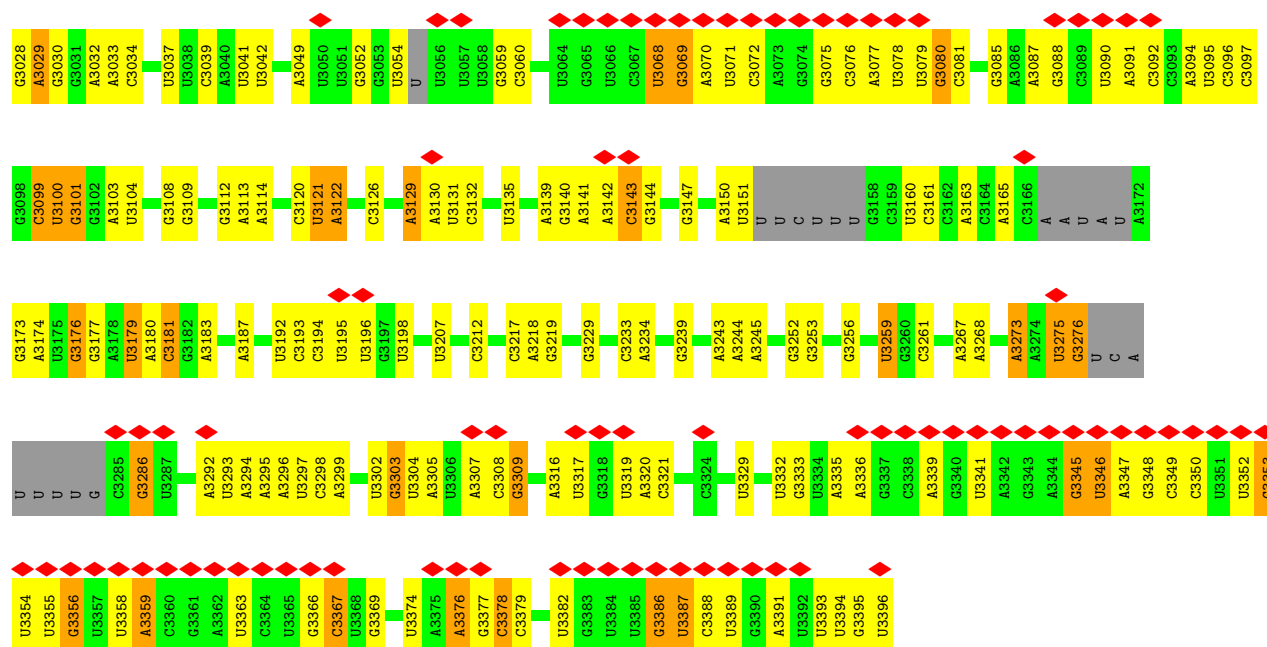
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: *Saccharomyces cerevisiae* S288C 25S ribosomal RNA

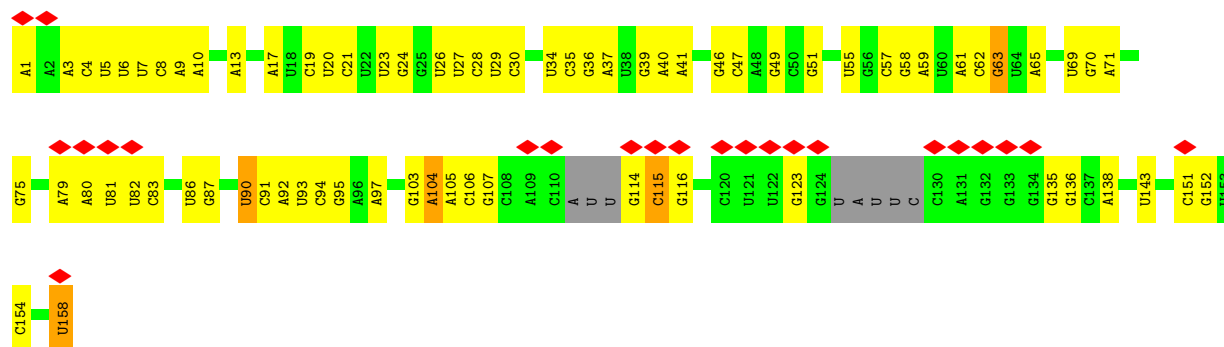




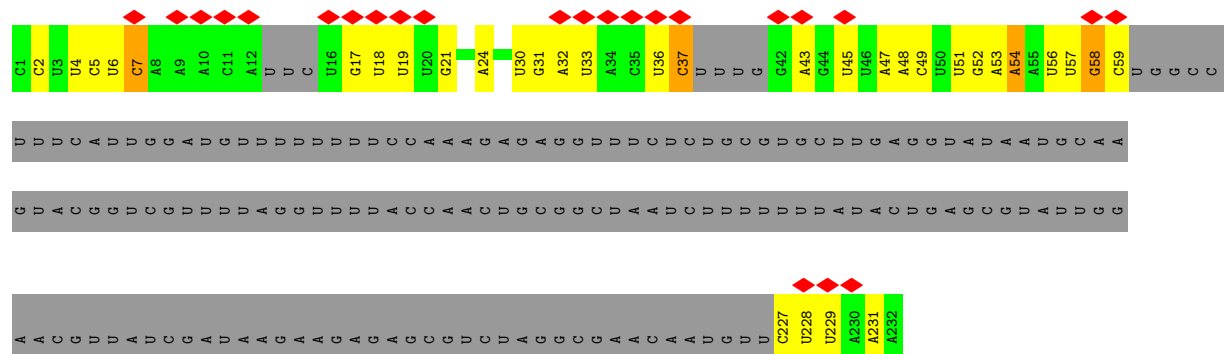




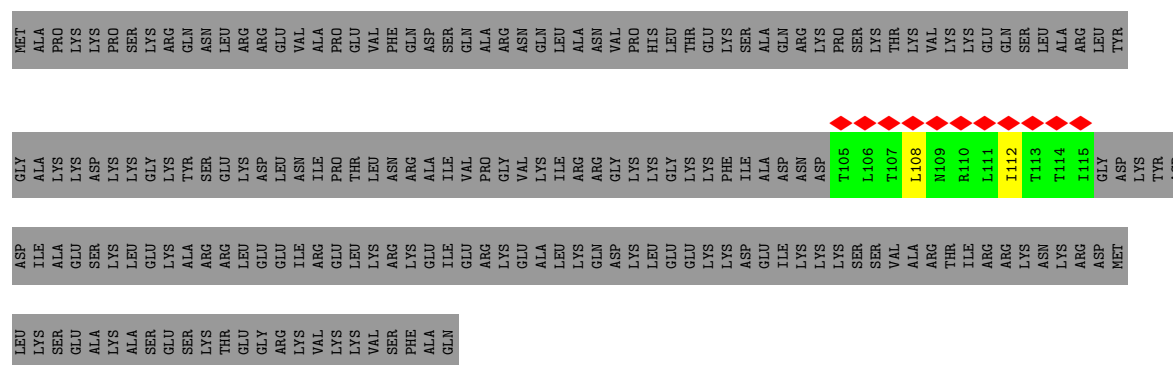
• Molecule 2: Saccharomyces cerevisiae S288C 5.8S ribosomal RNA



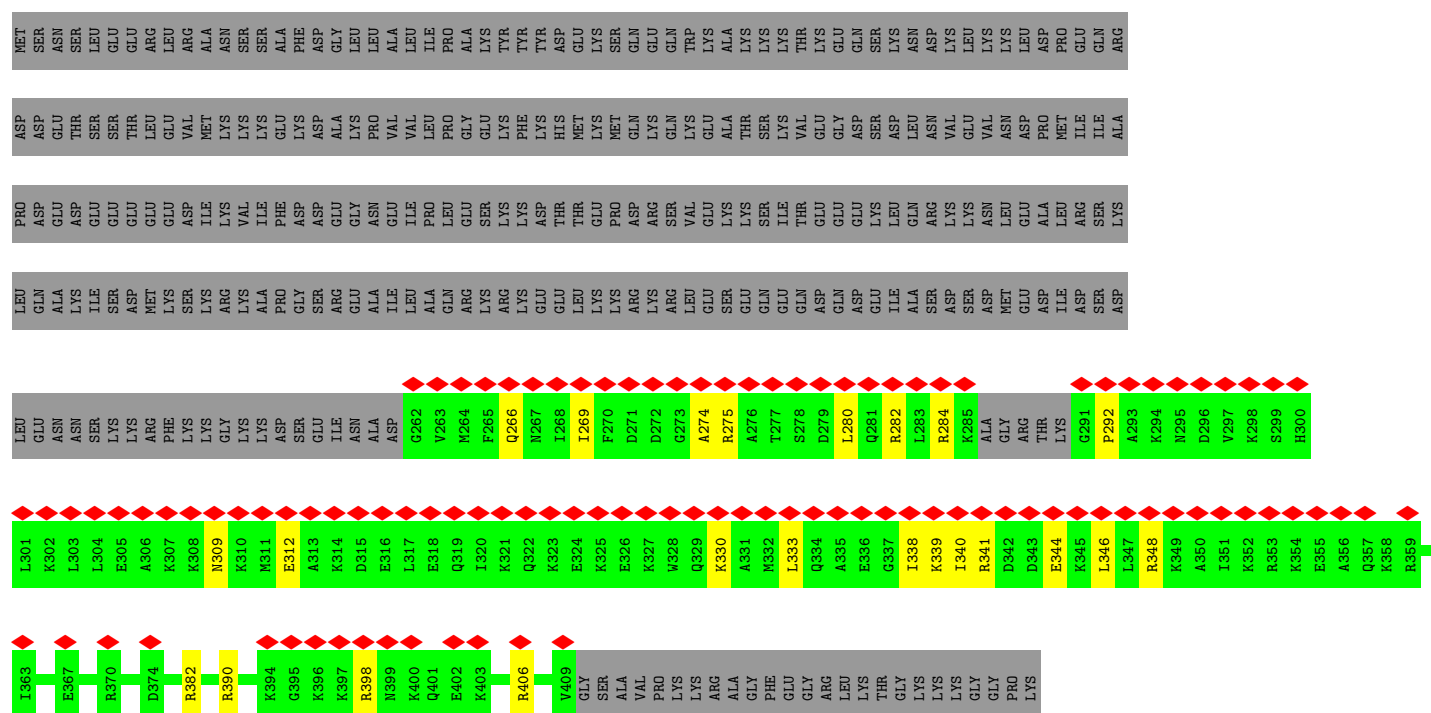
• Molecule 3: Saccharomyces cerevisiae ITS-2



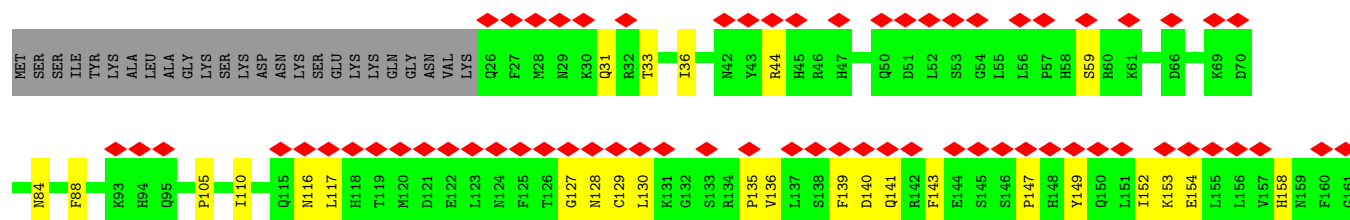
• Molecule 4: 60S ribosomal subunit assembly/export protein LOC1

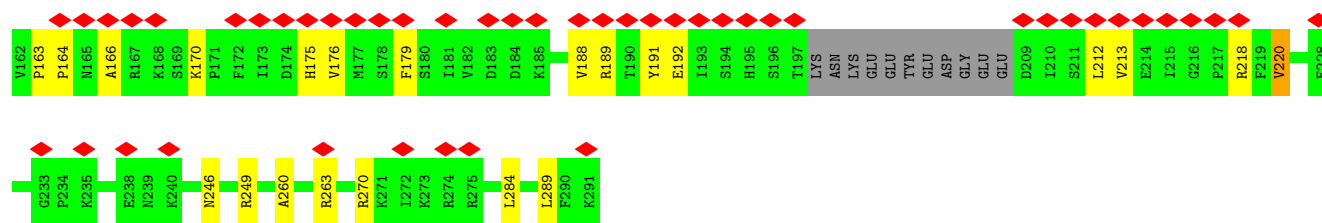


Chain 8: 25% 28% 5% 67%

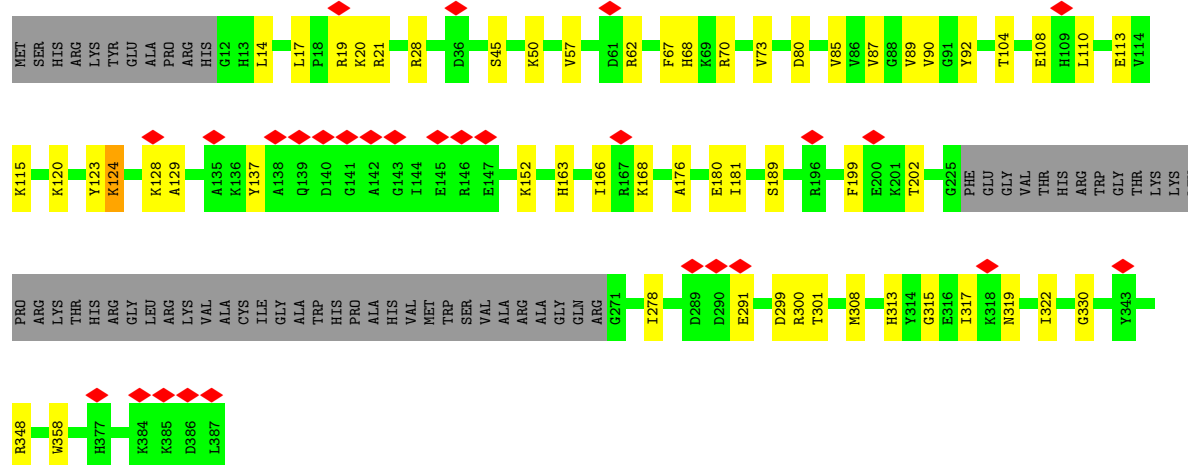


Chain A: 39% 71% 16% 12%

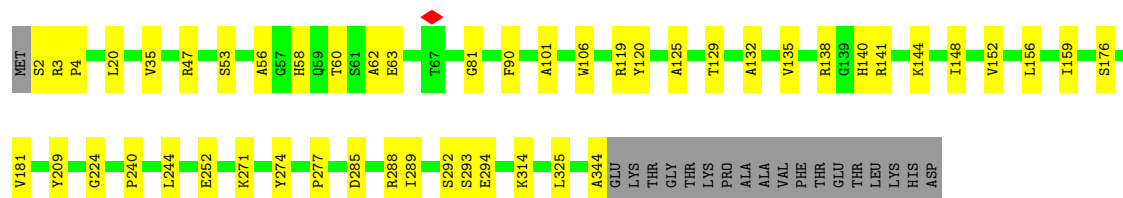
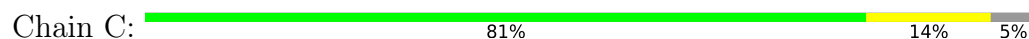




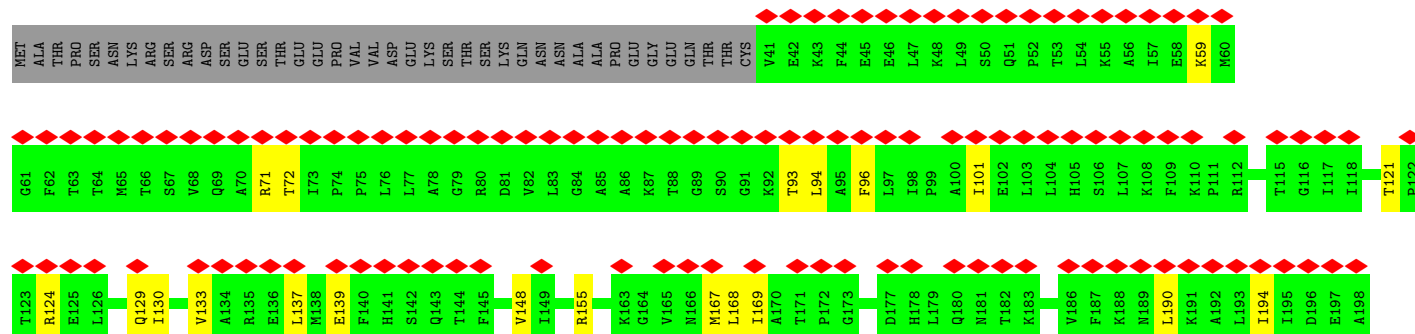
• Molecule 7: 60S ribosomal protein L3

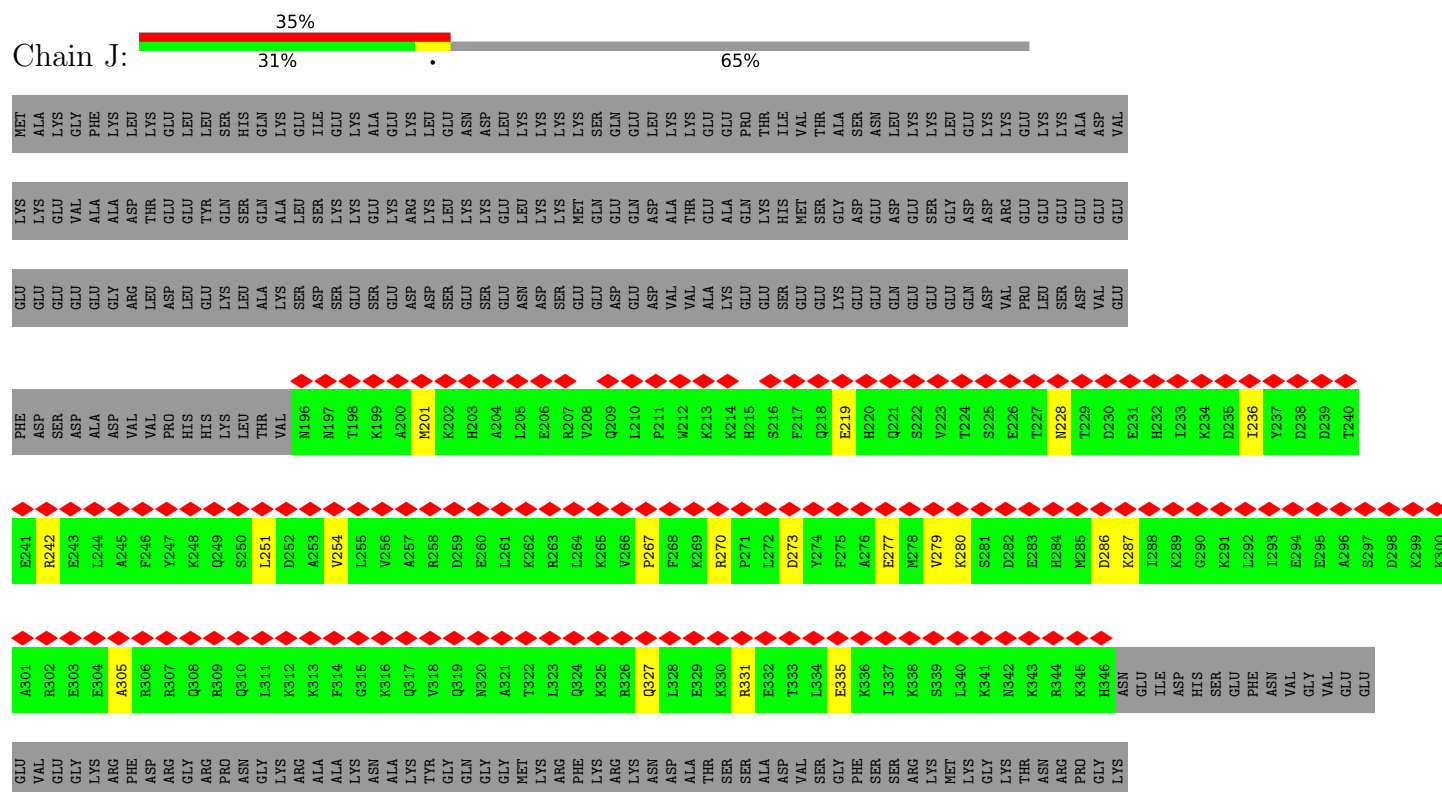


• Molecule 8: 60S ribosomal protein L4-A



• Molecule 9: ATP-dependent RNA helicase HAS1

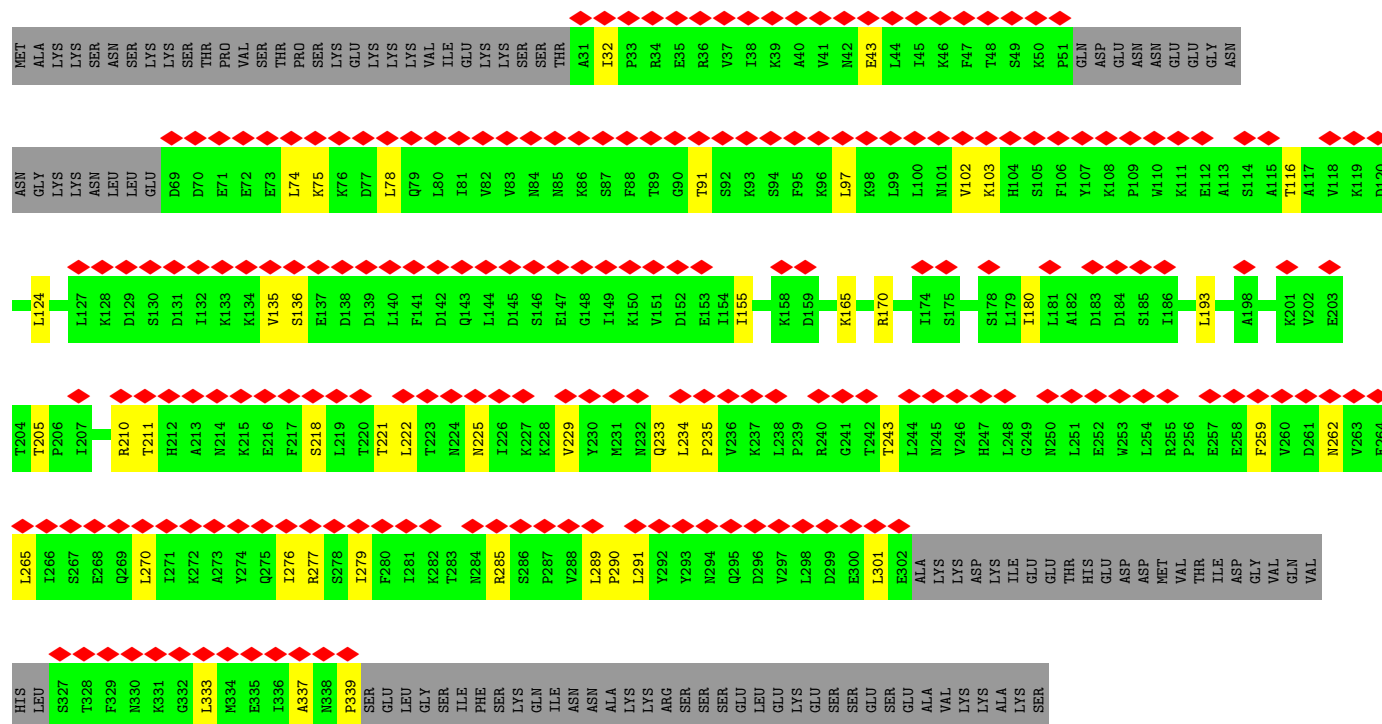




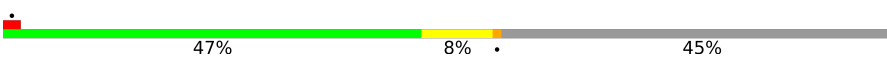
SER
ARG
LYS
ALA
SER
ARG
PHE

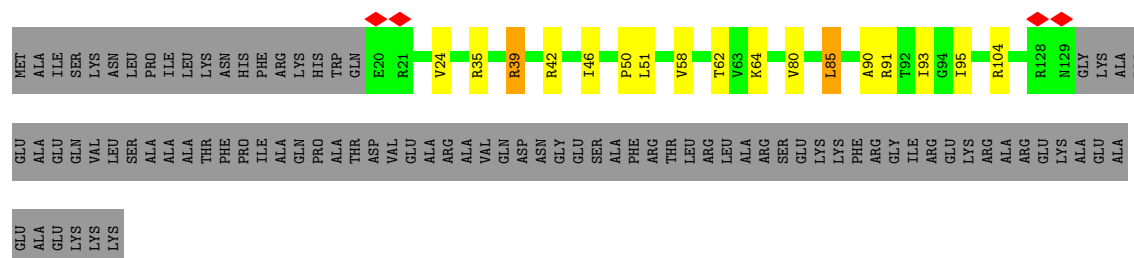
• Molecule 16: Proteasome-interacting protein CIC1

Chain K: 



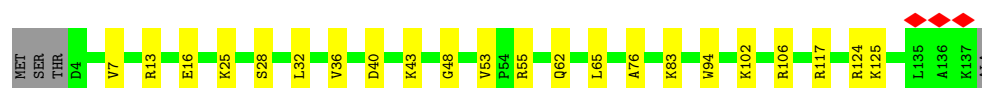
• Molecule 17: 60S ribosomal protein L13-A

Chain L: 

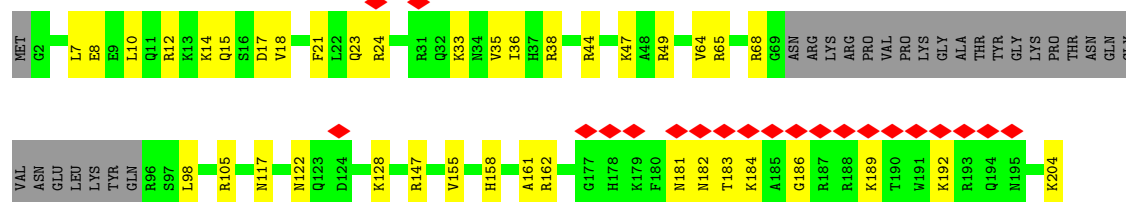


• Molecule 18: 60S ribosomal protein L14-A

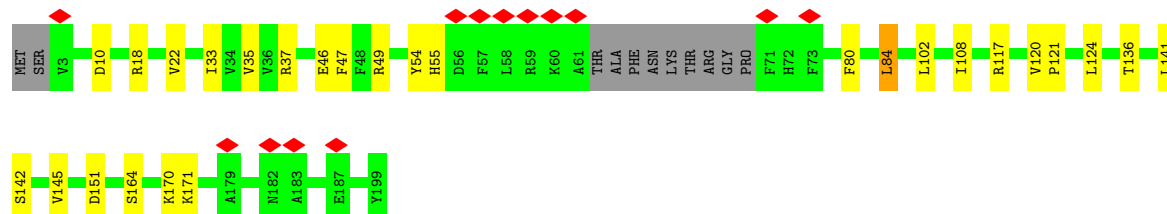
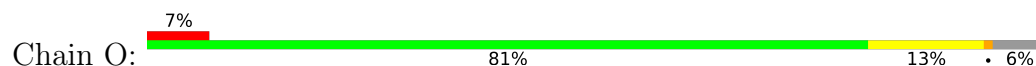
Chain M: 



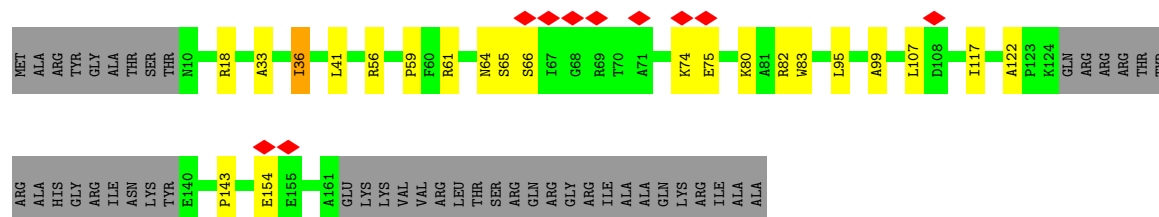
• Molecule 19: Large ribosomal subunit protein eL15A



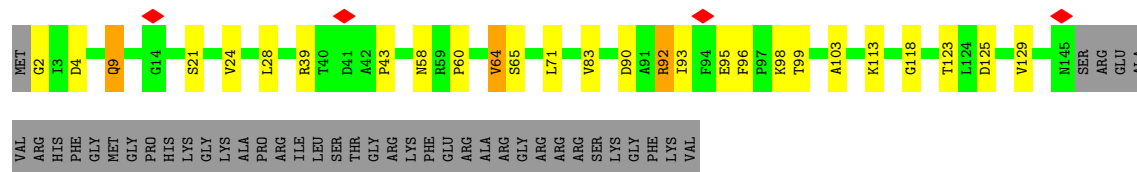
- Molecule 20: Large ribosomal subunit protein uL13A



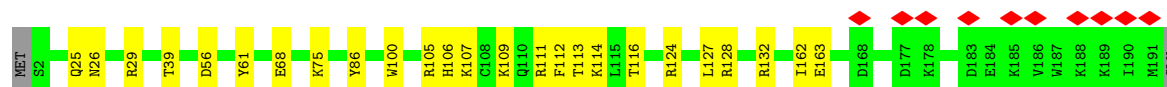
- Molecule 21: 60S ribosomal protein L17-A

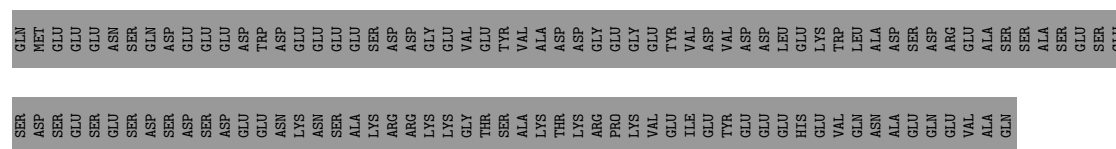


- Molecule 22: 60S ribosomal protein L18-A

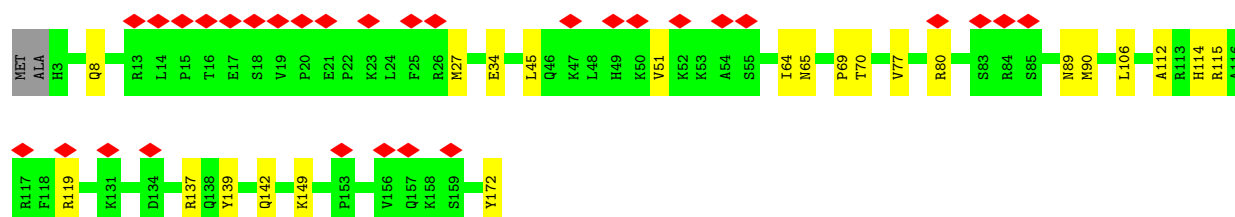
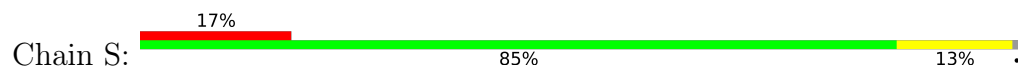


- Molecule 23: Protein MAK16

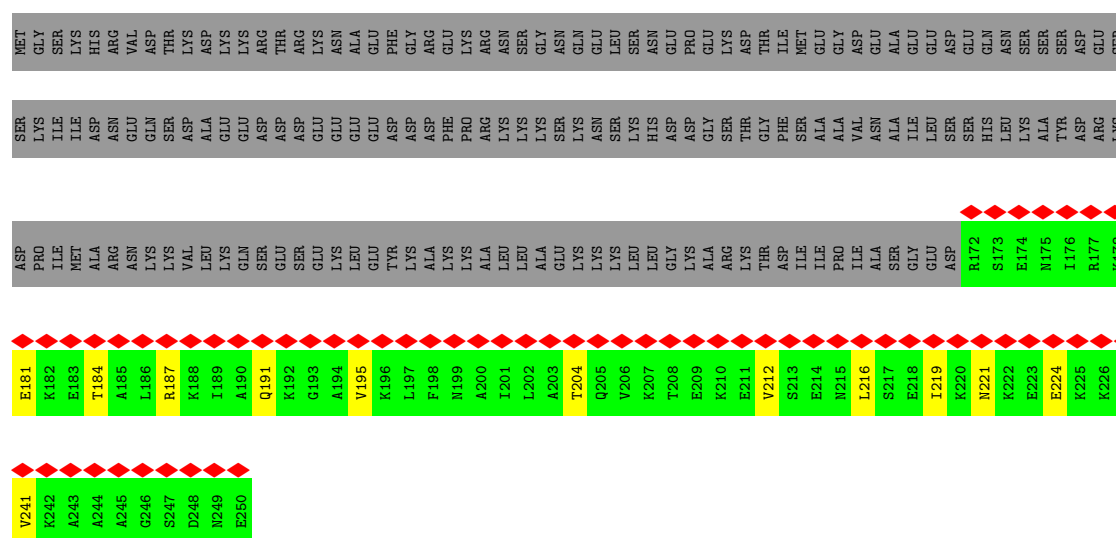




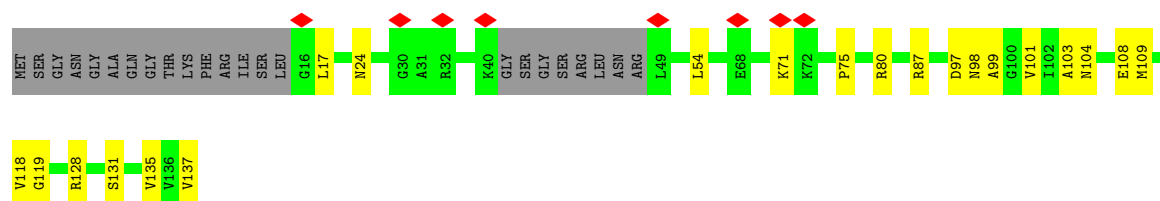
• Molecule 24: Large ribosomal subunit protein eL20A



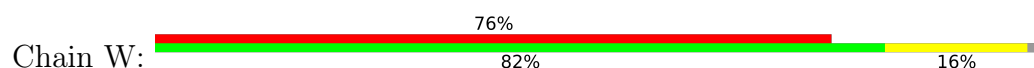
• Molecule 25: Ribosomal RNA-processing protein 15



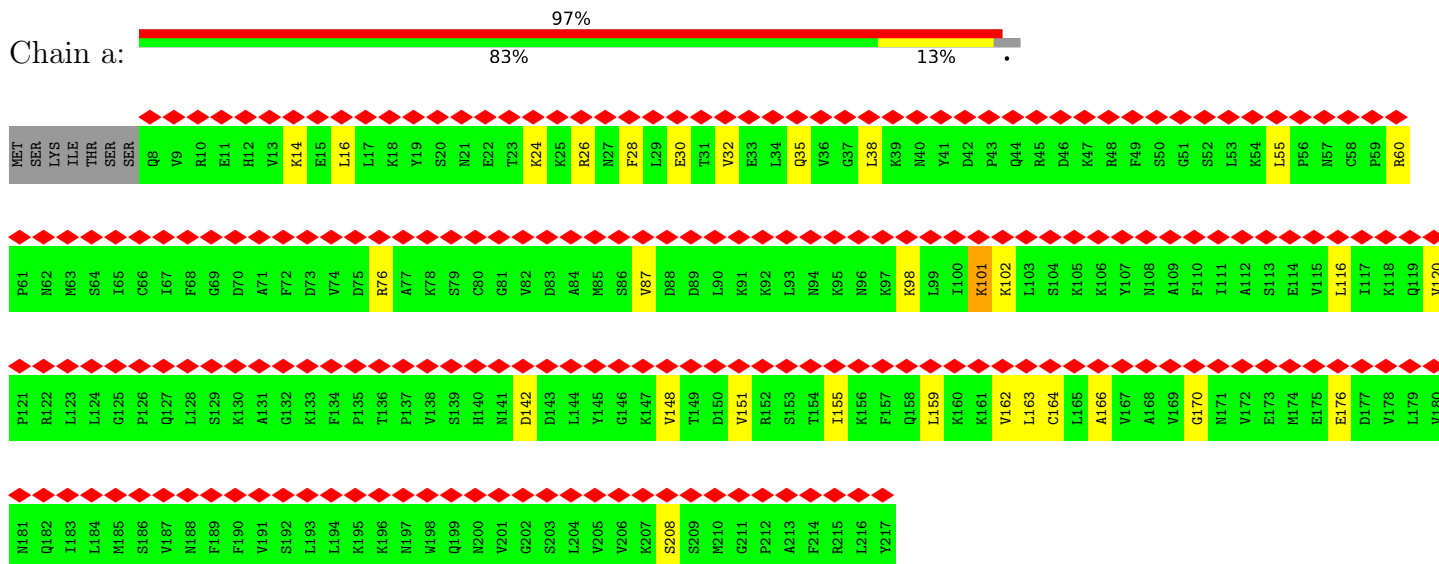
• Molecule 26: 60S ribosomal protein L23-A



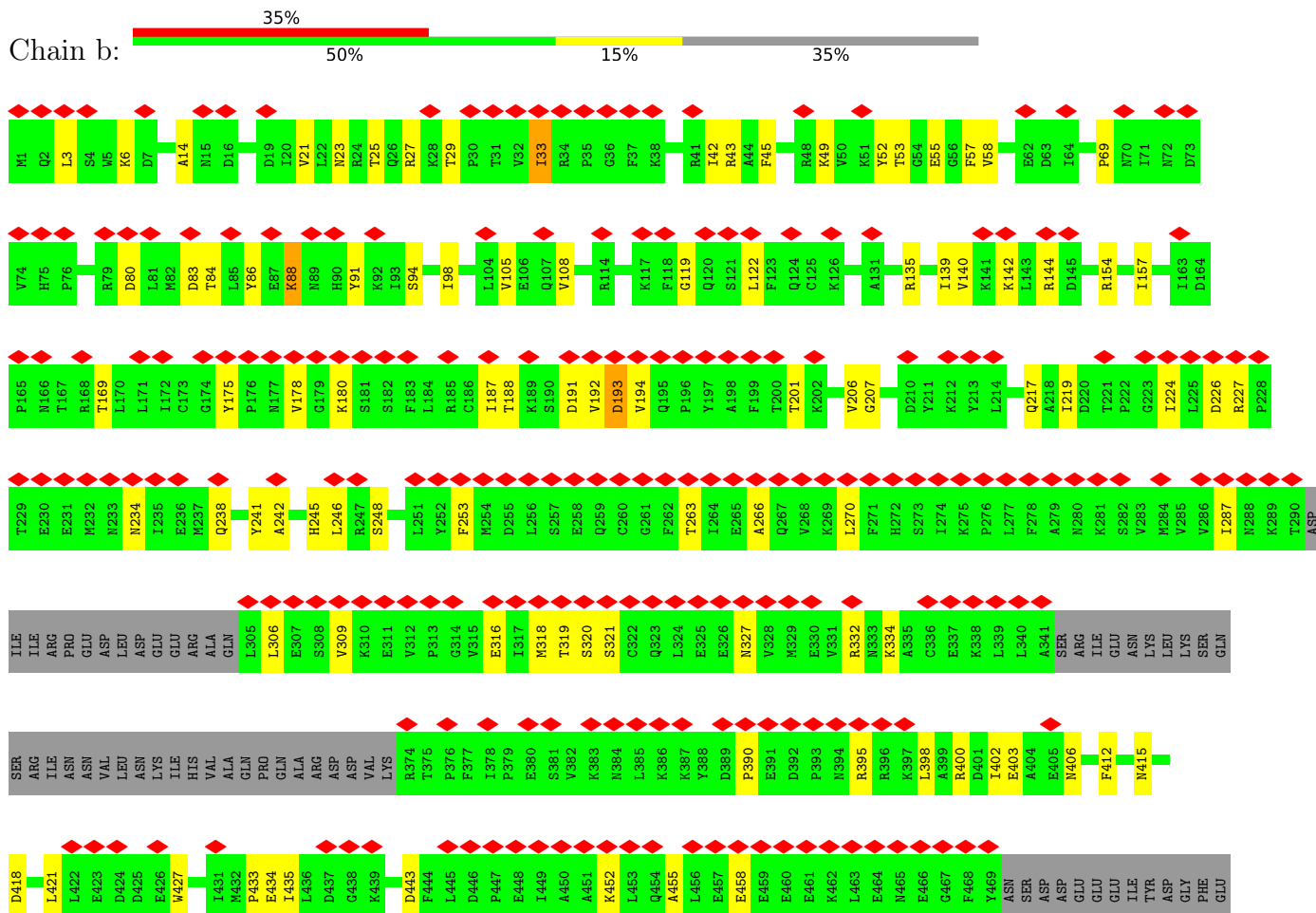
• Molecule 27: Ribosome assembly factor MRT4



Chain a:



Chain b:





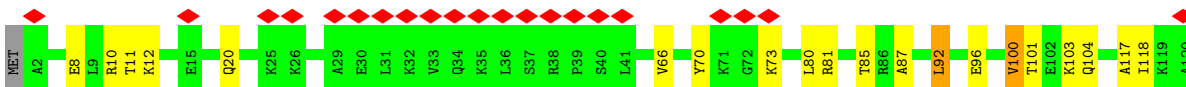
Chain e: 80% 16% ..



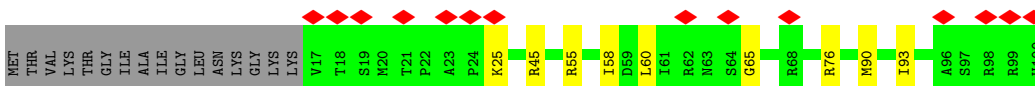
Chain f: 82% 16%



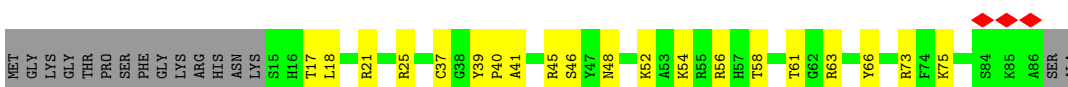
Chain h:



Chain i:



Chain j: 59% 23% 18%



Chain 1: 97% 80% 18%



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

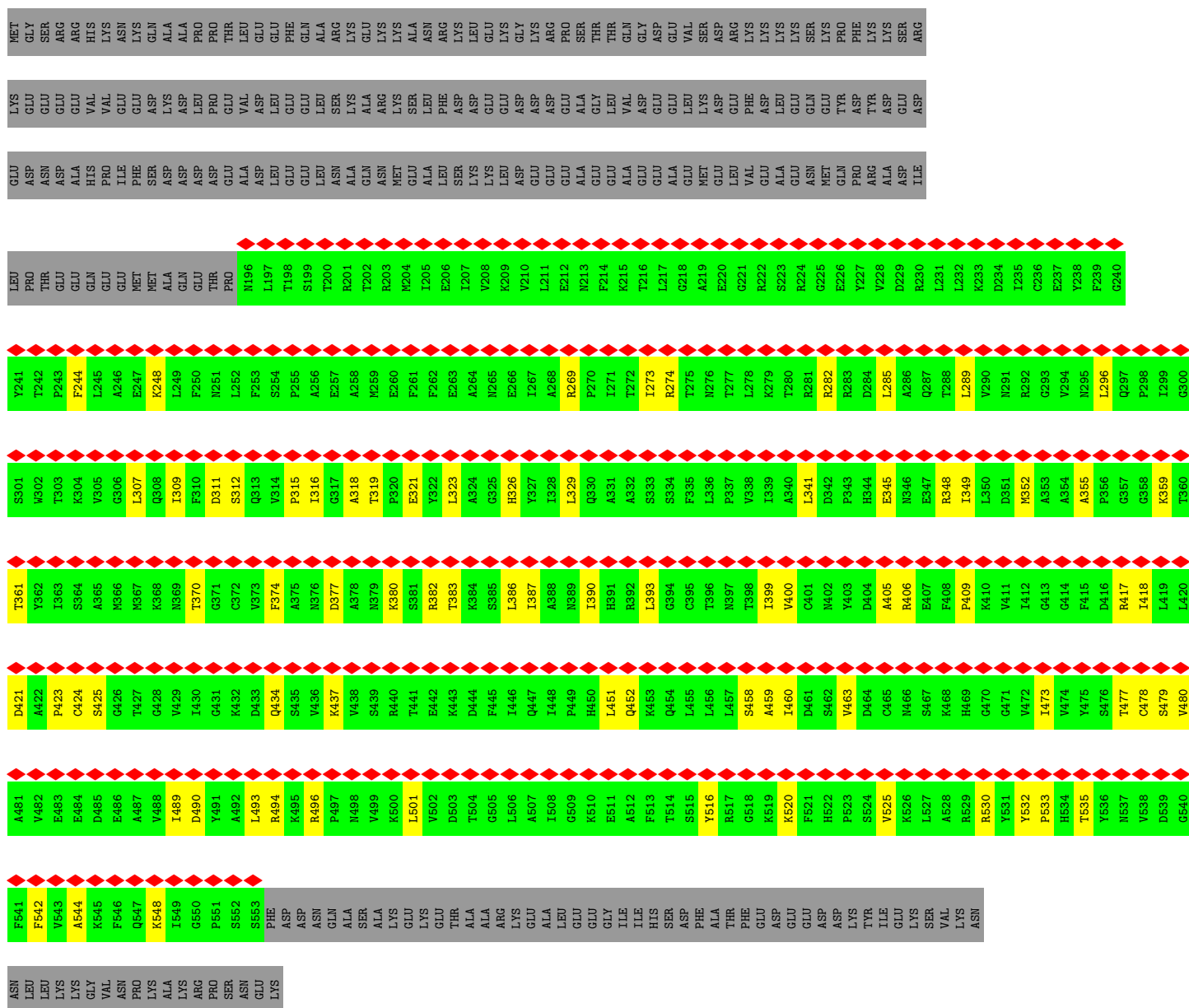
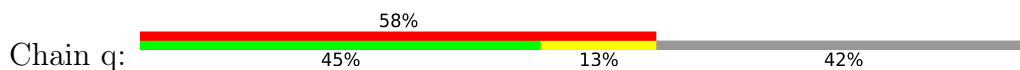
Chain n:

LYS	GLN	LYS	LYS	LEU	TYR	LYS	MET	LYS	TYR	SER	ASN	ALA	LYS	LYS	GLU	GLN	GLU	ASN	LEU	LYS	LYS	LYS	LYS	GLN	ILE	ALA	LYS	GLN	LYS	ALA	LYS	LEU	ASN	LYS	LEU	ASP	SER	LYS	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

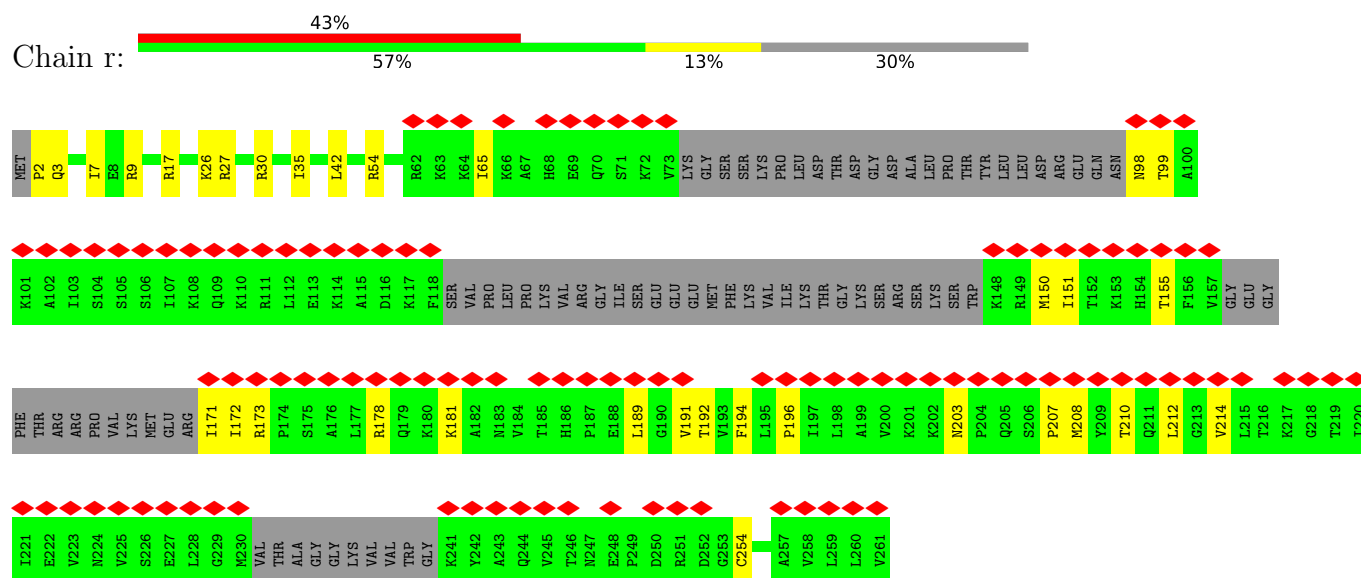
Chain o:

MET	VAL	LYS	THR	SER	THR	LYS	THR	GLU	THR	VAL	THR	LYS	GLN	PRO	THR	GLU	GLU	LYS	PRO	ILE	GLN	GLU	LEU	ALA	LEU	GLU	THR	SER	SER	SER	SER	ASP	GLU	GLU	ASP	GLU	ASP	GLU	ILE	GLU	GLY	LEU	ALA	ALA	SER	ASP	ASP	GLN
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

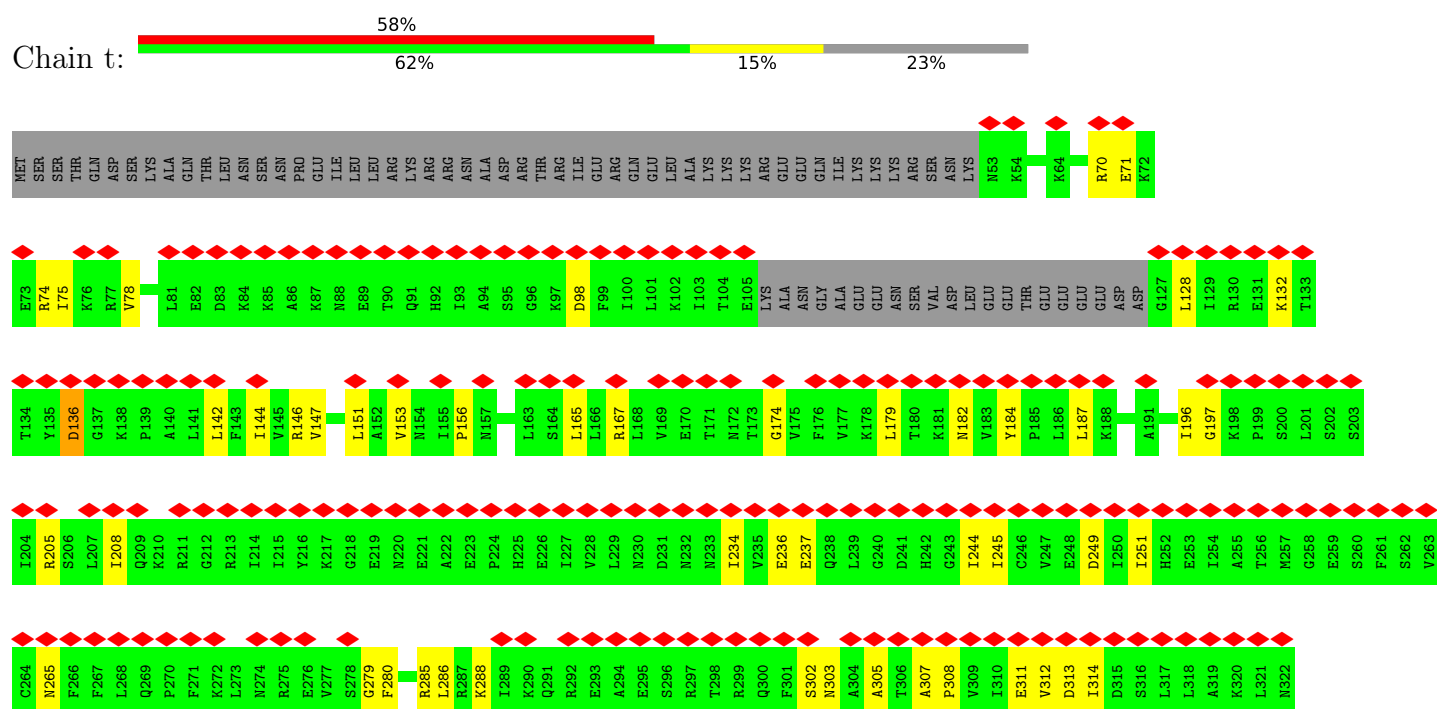
- Molecule 41: 25S rRNA (cytosine(2870)-C(5))-methyltransferase



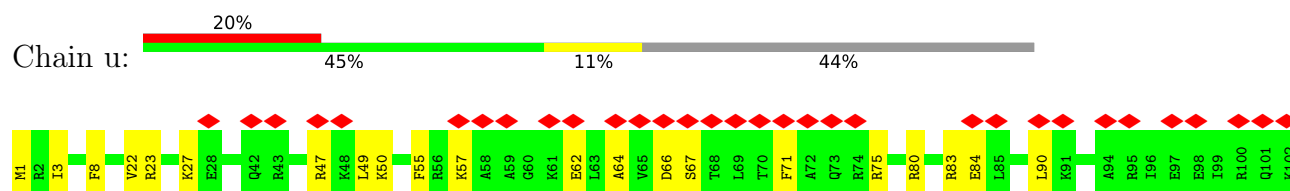
- Molecule 42: Ribosome biogenesis protein NSA2

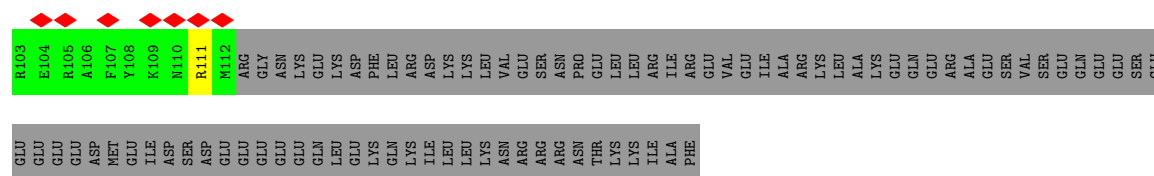


- Molecule 43: Ribosome biogenesis protein RLP7

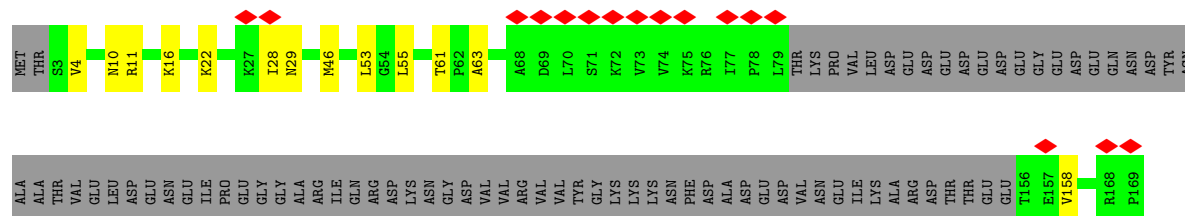


- Molecule 44: Ribosome biogenesis protein RLP24

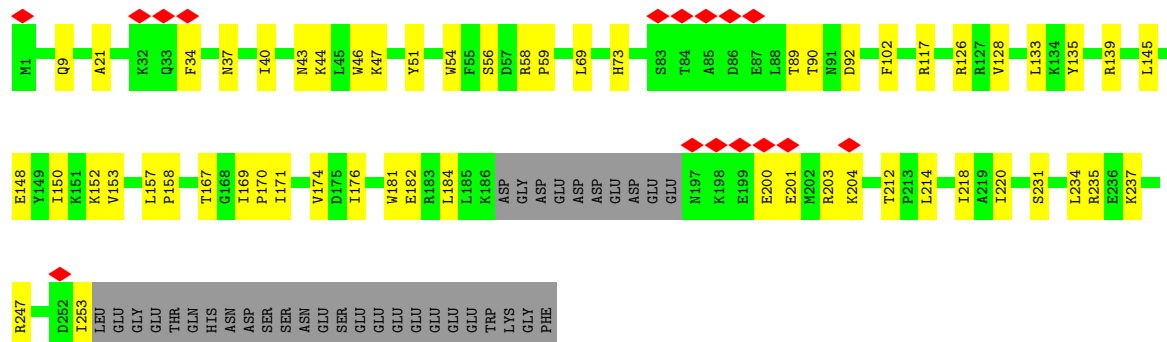




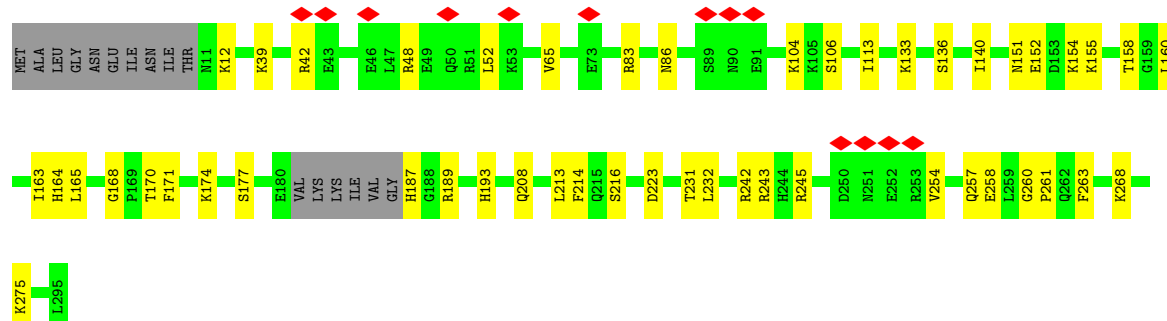
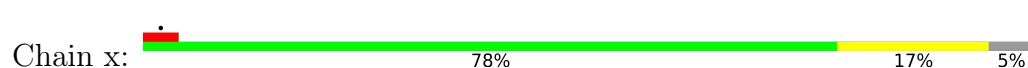
• Molecule 45: Nucleolar protein 16



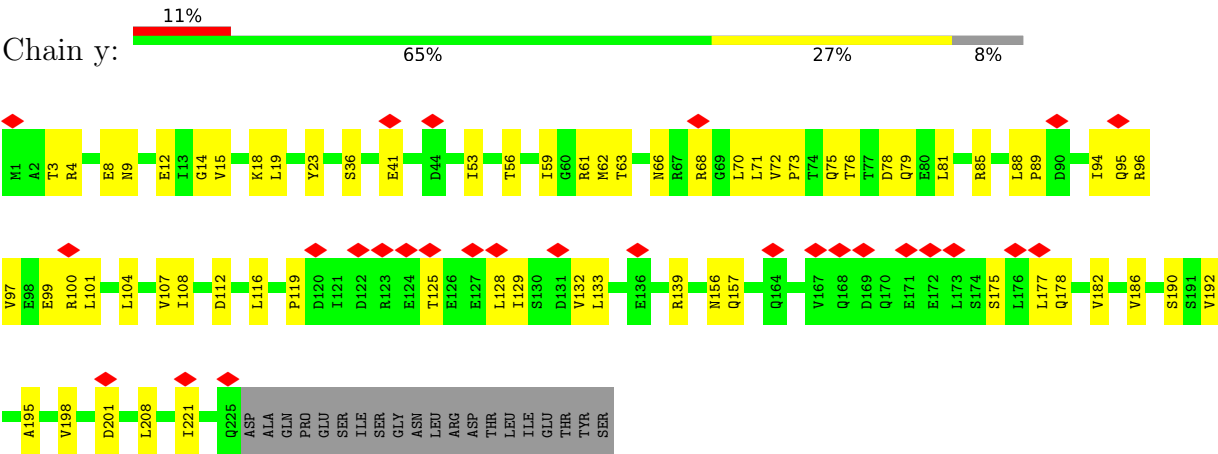
• Molecule 46: Ribosomal RNA-processing protein 1



• Molecule 47: Ribosome production factor 1



● Molecule 48: Eukaryotic translation initiation factor 6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	374572	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39.3	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.300	Depositor
Minimum map value	-0.185	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	444.78, 444.78, 444.78	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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	1	0.21	0/48286	0.29	1/75246 (0.0%)
2	2	0.23	0/3562	0.29	0/5542
3	6	0.13	0/1367	0.25	0/2118
4	7	0.09	0/86	0.17	0/117
5	8	0.11	0/1210	0.24	0/1590
6	A	0.13	0/2126	0.27	0/2868
7	B	0.18	0/2679	0.31	0/3600
8	C	0.21	0/2660	0.34	0/3601
9	D	0.13	0/3441	0.26	0/4642
10	E	0.19	0/1226	0.31	0/1648
11	F	0.20	0/1974	0.33	0/2654
12	G	0.18	0/1294	0.34	0/1751
13	H	0.18	0/1523	0.31	0/2052
14	I	0.18	0/3182	0.33	0/4288
15	J	0.10	0/1289	0.23	0/1715
16	K	0.12	0/2190	0.27	0/2955
17	L	0.22	0/897	0.35	0/1205
18	M	0.18	0/1056	0.30	0/1421
19	N	0.20	0/1544	0.32	0/2065
20	O	0.21	0/1513	0.31	0/2029
21	P	0.18	0/1080	0.32	0/1455
22	Q	0.20	0/1127	0.31	0/1521
23	R	0.22	0/1609	0.34	0/2157
24	S	0.17	0/1468	0.30	0/1973
25	T	0.10	0/626	0.21	0/831
26	V	0.16	0/858	0.28	0/1156
27	W	0.12	0/1902	0.26	0/2564
28	Y	0.21	0/995	0.33	0/1329
29	Z	0.09	0/2051	0.23	0/2758
30	a	0.10	0/1695	0.25	0/2276
31	b	0.14	0/3495	0.29	0/4714
32	e	0.22	0/1039	0.38	0/1391

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	f	0.24	0/868	0.33	0/1168
34	h	0.18	0/978	0.32	0/1301
35	i	0.15	0/672	0.28	0/894
36	j	0.21	0/583	0.35	0/774
37	l	0.09	0/1425	0.23	0/1922
38	m	0.12	0/1806	0.26	0/2443
39	n	0.11	0/2828	0.25	0/3825
40	o	0.13	0/1129	0.27	0/1502
41	q	0.10	0/2854	0.25	0/3860
42	r	0.13	0/1508	0.24	0/2007
43	t	0.12	0/1999	0.29	0/2690
44	u	0.13	0/964	0.27	0/1283
45	v	0.15	0/1258	0.28	0/1670
46	w	0.18	0/2104	0.31	0/2832
47	x	0.20	0/2408	0.35	0/3230
48	y	0.16	0/1722	0.33	0/2343
All	All	0.19	0/126156	0.29	1/180976 (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
17	L	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	406	G	O4'-C1'-N9	5.29	116.14	108.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	L	39	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	43147	0	21691	520	0
2	2	3189	0	1614	41	0
3	6	1227	0	622	19	0
4	7	87	0	101	2	0
5	8	1203	0	1291	16	0
6	A	2080	0	2100	31	0
7	B	2626	0	2705	42	0
8	C	2611	0	2724	38	0
9	D	3377	0	3500	38	0
10	E	1205	0	1291	15	0
11	F	1936	0	2032	21	0
12	G	1272	0	1331	20	0
13	H	1502	0	1564	21	0
14	I	3126	0	3178	41	0
15	J	1271	0	1310	16	0
16	K	2155	0	2230	29	0
17	L	884	0	936	16	0
18	M	1041	0	1137	17	0
19	N	1513	0	1564	30	0
20	O	1486	0	1588	19	0
21	P	1062	0	1075	15	0
22	Q	1110	0	1190	17	0
23	R	1578	0	1623	24	0
24	S	1432	0	1470	16	0
25	T	625	0	666	14	0
26	V	845	0	886	13	0
27	W	1870	0	1902	31	0
28	Y	984	0	1075	15	0
29	Z	2020	0	2105	42	0
30	a	1668	0	1753	21	0
31	b	3429	0	3484	65	0
32	e	1018	0	1086	19	0
33	f	850	0	880	11	0
34	h	969	0	1078	17	0
35	i	665	0	721	7	0
36	j	571	0	571	14	0
37	l	1394	0	1426	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	1759	0	1725	33	0
39	n	2760	0	2810	49	0
40	o	1107	0	1159	20	0
41	q	2799	0	2834	52	0
42	r	1489	0	1582	24	0
43	t	1973	0	2083	29	0
44	u	944	0	973	21	0
45	v	1242	0	1317	20	0
46	w	2058	0	2096	33	0
47	x	2362	0	2389	32	0
48	y	1701	0	1697	47	0
49	j	1	0	0	0	0
49	u	1	0	0	0	0
All	All	119224	0	98165	1437	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 7.

All (1437) 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)
27:W:45:LEU:HD13	27:W:48:VAL:CG1	1.71	1.19
41:q:460:ILE:O	41:q:463:VAL:HG12	1.46	1.14
31:b:192:VAL:CG2	31:b:201:THR:HG21	1.78	1.12
38:m:395:TYR:OH	39:n:33:ARG:HG2	1.46	1.12
27:W:45:LEU:O	27:W:45:LEU:HD12	1.49	1.10
31:b:192:VAL:HG22	31:b:201:THR:HG21	1.29	1.08
39:n:259:LEU:HD11	39:n:381:LEU:HD12	1.38	1.06
27:W:45:LEU:HD13	27:W:48:VAL:HG11	1.09	1.04
27:W:45:LEU:CD1	27:W:48:VAL:HG11	1.95	0.96
48:y:192:VAL:HG12	48:y:195:ALA:HB3	1.47	0.93
48:y:192:VAL:CG1	48:y:195:ALA:HB3	2.00	0.92
1:1:3018:C:H5"	48:y:8:GLU:HG3	1.55	0.89
6:A:289:LEU:CD1	46:w:47:LYS:HG2	2.05	0.87
27:W:45:LEU:CD1	27:W:48:VAL:CG1	2.56	0.82
31:b:192:VAL:HG22	31:b:201:THR:CG2	2.09	0.81
39:n:259:LEU:HD11	39:n:381:LEU:CD1	2.11	0.80
41:q:460:ILE:O	41:q:463:VAL:CG1	2.28	0.80
39:n:427:ILE:HG22	39:n:428:GLN:N	1.98	0.78
1:1:648:C:N3	5:8:390:ARG:NH2	2.32	0.77
41:q:480:VAL:O	41:q:530:ARG:NH2	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:b:135:ARG:NH1	42:r:254:CYS:SG	2.61	0.74
6:A:289:LEU:HD11	46:w:47:LYS:HG2	1.68	0.74
23:R:132:ARG:NH2	47:x:152:GLU:O	2.20	0.74
47:x:174:LYS:HE3	47:x:268:LYS:HG3	1.70	0.74
1:1:3140:G:N7	7:B:28:ARG:NH2	2.36	0.74
7:B:113:GLU:HG2	7:B:176:ALA:HB2	1.70	0.74
48:y:76:THR:O	48:y:96:ARG:NH2	2.20	0.73
7:B:115:LYS:HE3	7:B:129:ALA:HB3	1.70	0.73
21:P:122:ALA:HB3	21:P:143:PRO:HB2	1.69	0.73
17:L:80:VAL:HG13	17:L:85:LEU:HD12	1.67	0.73
1:1:704:U:H3'	1:1:705:A:H5''	1.71	0.72
19:N:33:LYS:O	19:N:65:ARG:NH2	2.21	0.72
8:C:20:LEU:HD11	8:C:252:GLU:HG3	1.72	0.71
41:q:463:VAL:HG13	41:q:548:LYS:HD2	1.70	0.71
1:1:3151:U:O2'	1:1:3395:G:N2	2.24	0.71
9:D:471:ALA:HA	9:D:482:PRO:HG3	1.73	0.71
3:6:2:C:O2	43:t:70:ARG:NH1	2.24	0.71
1:1:149:U:OP1	19:N:49:ARG:NH2	2.24	0.70
31:b:287:ILE:HD11	31:b:319:THR:HG23	1.73	0.70
1:1:250:U:H4'	1:1:251:G:H5'	1.72	0.70
1:1:156:G:H22	17:L:91:ARG:HH12	1.39	0.70
1:1:2353:G:OP2	21:P:82:ARG:NH2	2.22	0.70
29:Z:137:ASN:ND2	29:Z:185:SER:O	2.24	0.70
35:i:45:ARG:HD3	35:i:93:ILE:HD11	1.72	0.70
42:r:151:ILE:HD13	42:r:212:LEU:HD13	1.74	0.69
1:1:707:U:O2'	1:1:754:G:N3	2.26	0.69
27:W:45:LEU:O	27:W:45:LEU:CD1	2.36	0.69
43:t:71:GLU:OE2	43:t:74:ARG:NH2	2.26	0.69
1:1:3037:U:H5''	7:B:348:ARG:HD2	1.75	0.68
12:G:183:LYS:HG2	12:G:194:THR:HB	1.74	0.68
1:1:29:C:OP2	19:N:192:LYS:NZ	2.24	0.68
30:a:14:LYS:HE2	30:a:176:GLU:OE1	1.93	0.68
47:x:164:HIS:HB3	47:x:168:GLY:HA3	1.75	0.68
29:Z:29:ARG:HH21	29:Z:61:GLU:HB2	1.58	0.68
39:n:427:ILE:CG2	39:n:428:GLN:N	2.56	0.68
1:1:728:G:H5'	22:Q:43:PRO:HB2	1.74	0.68
41:q:341:LEU:O	41:q:417:ARG:NH1	2.26	0.67
27:W:74:GLN:NE2	27:W:96:CYS:O	2.27	0.67
1:1:3052:G:H1	1:1:3091:A:H2	1.40	0.67
6:A:105:PRO:HD3	38:m:140:ILE:HG13	1.76	0.67
11:F:224:ILE:O	24:S:119:ARG:NH2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:q:349:ILE:HG12	41:q:417:ARG:HB2	1.76	0.67
41:q:285:LEU:HD12	41:q:326:HIS:HB3	1.77	0.67
43:t:244:ILE:HD12	43:t:249:ASP:HB3	1.77	0.67
2:2:154:C:H5''	12:G:181:LYS:HD3	1.77	0.66
39:n:427:ILE:CG2	39:n:428:GLN:H	2.08	0.66
37:l:76:THR:HG22	37:l:76:THR:O	1.94	0.66
31:b:83:ASP:OD2	31:b:88:LYS:NZ	2.27	0.66
41:q:406:ARG:HH21	41:q:451:LEU:HD13	1.59	0.66
24:S:8:GLN:HB2	24:S:64:ILE:HD11	1.77	0.66
31:b:443:ASP:O	44:u:75:ARG:NH1	2.28	0.66
1:1:1236:G:N2	1:1:1244:A:OP1	2.29	0.66
48:y:53:ILE:HG12	48:y:59:ILE:HG22	1.77	0.66
9:D:457:HIS:O	9:D:460:LYS:NZ	2.26	0.65
1:1:292:U:OP2	19:N:68:ARG:NH2	2.29	0.65
1:1:1307:G:H4'	1:1:1308:A:H5'	1.78	0.65
30:a:76:ARG:NH2	30:a:142:ASP:OD1	2.30	0.65
1:1:2466:G:OP1	30:a:60:ARG:NH1	2.27	0.65
19:N:155:VAL:O	19:N:162:ARG:NH2	2.29	0.65
39:n:174:ARG:NH2	39:n:357:ALA:O	2.30	0.65
18:M:48:GLY:HA3	18:M:53:VAL:HB	1.78	0.65
41:q:341:LEU:HD11	41:q:417:ARG:HB3	1.79	0.65
1:1:251:G:O6	45:v:175:ARG:NE	2.28	0.65
7:B:85:VAL:HG22	7:B:202:THR:HG22	1.79	0.65
10:E:10:TYR:HB3	23:R:113:THR:HG21	1.79	0.65
29:Z:29:ARG:NH1	29:Z:41:ASN:OD1	2.30	0.64
1:1:662:U:H2'	1:1:663:C:C6	2.32	0.64
1:1:2470:C:H5''	30:a:26:ARG:HD2	1.78	0.64
1:1:751:A:N1	1:1:781:G:O6	2.31	0.64
48:y:12:GLU:HB3	48:y:15:VAL:HB	1.79	0.64
1:1:651:G:O2'	1:1:1435:A:OP1	2.16	0.64
5:8:344:GLU:OE2	5:8:348:ARG:NH2	2.31	0.64
42:r:3:GLN:O	42:r:9:ARG:NH2	2.31	0.64
43:t:75:ILE:HD12	43:t:156:PRO:HG2	1.80	0.63
1:1:269:G:OP2	19:N:44:ARG:NH1	2.30	0.63
14:I:336:THR:HG22	14:I:342:VAL:HG22	1.81	0.63
26:V:54:LEU:HD21	26:V:119:GLY:HA3	1.79	0.63
41:q:289:LEU:HD12	41:q:296:LEU:HD11	1.79	0.63
1:1:3183:A:OP1	20:O:37:ARG:NH2	2.31	0.63
41:q:463:VAL:CG1	41:q:548:LYS:HD2	2.28	0.63
48:y:112:ASP:OD2	48:y:156:ASN:ND2	2.31	0.63
2:2:57:C:H4'	2:2:63:G:N7	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:W:12:LEU:HD21	42:r:65:ILE:HD13	1.80	0.63
30:a:87:VAL:HB	30:a:116:LEU:HD21	1.79	0.63
3:6:36:U:O3'	16:K:277:ARG:NH1	2.31	0.63
8:C:314:LYS:HD2	11:F:162:PRO:HB3	1.79	0.63
16:K:43:GLU:OE2	40:o:217:GLU:N	2.24	0.63
31:b:175:TYR:O	31:b:180:LYS:NZ	2.27	0.63
43:t:208:ILE:HD12	43:t:251:ILE:HG12	1.81	0.63
21:P:36:ILE:HD11	21:P:95:LEU:HD11	1.81	0.62
34:h:85:THR:HG22	34:h:87:ALA:H	1.64	0.62
3:6:36:U:OP1	40:o:207:ARG:NH2	2.32	0.62
17:L:50:PRO:HG2	34:h:118:ILE:HD12	1.80	0.62
1:1:685:G:OP1	17:L:39:ARG:NH2	2.32	0.62
41:q:460:ILE:C	41:q:463:VAL:HG12	2.21	0.62
13:H:62:ARG:NH1	27:W:3:ARG:O	2.32	0.62
1:1:251:G:N2	45:v:181:GLU:OE1	2.33	0.62
8:C:288:ARG:NH1	8:C:292:SER:OG	2.33	0.62
26:V:135:VAL:HG22	48:y:101:LEU:HA	1.82	0.62
1:1:2473:C:O2	1:1:2474:G:N2	2.33	0.62
1:1:169:U:C4	45:v:175:ARG:HD2	2.35	0.62
39:n:242:LEU:HA	39:n:266:SER:HA	1.82	0.62
1:1:1253:U:H5''	1:1:1254:C:H5'	1.82	0.61
1:1:269:G:H5''	19:N:14:LYS:HE3	1.82	0.61
1:1:2428:U:OP1	41:q:348:ARG:NH1	2.32	0.61
1:1:1200:A:H62	1:1:2824:G:H1	1.48	0.61
41:q:463:VAL:HG11	41:q:473:ILE:HD11	1.82	0.61
1:1:2423:U:O2'	1:1:2605:G:N2	2.34	0.61
1:1:3126:C:H4'	13:H:129:ARG:HH22	1.66	0.61
1:1:3295:A:H2'	1:1:3296:A:C8	2.35	0.61
1:1:1290:A:H2'	1:1:1291:A:C8	2.36	0.61
6:A:136:VAL:HB	6:A:176:VAL:HG22	1.81	0.61
6:A:284:LEU:HD21	46:w:43:ASN:HB3	1.83	0.61
12:G:148:ALA:HA	12:G:201:THR:HG22	1.83	0.61
48:y:18:LYS:NZ	48:y:63:THR:O	2.33	0.61
48:y:78:ASP:OD1	48:y:96:ARG:NH1	2.30	0.61
1:1:53:G:OP2	36:j:48:ASN:ND2	2.33	0.61
10:E:175:LYS:O	18:M:117:ARG:NH2	2.33	0.61
1:1:532:A:HO2'	1:1:533:A:H8	1.48	0.60
8:C:2:SER:OG	8:C:3:ARG:N	2.33	0.60
48:y:66:ASN:HD22	48:y:112:ASP:HA	1.65	0.60
1:1:519:A:N6	24:S:65:ASN:O	2.34	0.60
13:H:57:VAL:HG23	13:H:68:LEU:HD13	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:f:14:LEU:HD11	33:f:31:LYS:HB2	1.83	0.60
1:1:3376:A:H5''	1:1:3377:G:H5''	1.84	0.60
20:O:37:ARG:HD2	20:O:108:ILE:HD11	1.83	0.60
1:1:959:C:N4	1:1:961:C:O4'	2.34	0.60
1:1:3374:U:OP1	1:1:3376:A:N6	2.30	0.60
18:M:36:VAL:HG11	18:M:55:ARG:HH21	1.65	0.60
19:N:36:ILE:HD11	19:N:105:ARG:HB3	1.84	0.60
43:t:146:ARG:NH1	43:t:147:VAL:O	2.35	0.60
17:L:62:THR:HG22	17:L:64:LYS:H	1.66	0.60
9:D:124:ARG:CZ	9:D:456:SER:HB2	2.32	0.60
1:1:113:C:OP1	19:N:147:ARG:NH1	2.34	0.60
1:1:3268:A:OP1	10:E:46:ARG:NH2	2.34	0.60
31:b:415:ASN:ND2	31:b:418:ASP:OD1	2.34	0.60
1:1:718:G:O2'	1:1:720:A:OP2	2.19	0.60
22:Q:98:LYS:HE2	22:Q:118:GLY:HA3	1.84	0.59
1:1:269:G:OP1	19:N:47:LYS:NZ	2.26	0.59
1:1:2369:G:H2'	1:1:2370:G:H8	1.67	0.59
12:G:140:VAL:HG22	12:G:166:LEU:HD21	1.83	0.59
12:G:172:LYS:NZ	38:m:247:PHE:O	2.31	0.59
39:n:427:ILE:HD13	39:n:431:TRP:CE3	2.37	0.59
1:1:2603:G:H21	37:l:57:SER:HA	1.67	0.59
1:1:3165:A:OP1	47:x:189:ARG:NE	2.32	0.59
12:G:231:LYS:HA	38:m:242:PRO:HB3	1.84	0.59
23:R:162:ILE:HD11	47:x:231:THR:HG21	1.84	0.59
41:q:316:ILE:HG21	41:q:329:LEU:HD21	1.84	0.59
43:t:197:GLY:HA3	43:t:314:ILE:HB	1.83	0.59
1:1:3180:A:OP1	20:O:171:LYS:NZ	2.31	0.59
26:V:24:ASN:ND2	26:V:97:ASP:OD2	2.36	0.59
37:l:38:ARG:HE	37:l:52:ALA:HB1	1.67	0.59
24:S:112:ALA:O	24:S:115:ARG:NH1	2.35	0.59
1:1:531:G:H2'	1:1:532:A:C8	2.38	0.59
1:1:947:G:H5''	32:e:55:ILE:HB	1.84	0.59
1:1:441:U:OP2	23:R:128:ARG:NH1	2.33	0.59
39:n:259:LEU:CD1	39:n:381:LEU:CD1	2.79	0.59
6:A:189:ARG:HG2	6:A:218:ARG:HG3	1.85	0.59
23:R:100:TRP:O	23:R:105:ARG:NH1	2.34	0.59
39:n:368:SER:HB2	39:n:412:VAL:HG12	1.85	0.59
43:t:98:ASP:HB3	43:t:184:TYR:CZ	2.38	0.59
47:x:136:SER:O	47:x:140:ILE:HG12	2.02	0.59
11:F:92:ILE:HD12	22:Q:4:ASP:HB2	1.85	0.58
16:K:211:THR:HG22	16:K:222:LEU:HD13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:t:280:PHE:O	43:t:285:ARG:NH1	2.36	0.58
1:1:2369:G:H2'	1:1:2370:G:C8	2.38	0.58
1:1:3386:G:O2'	1:1:3387:U:OP1	2.20	0.58
1:1:1454:A:H3'	1:1:1455:U:H5''	1.86	0.58
31:b:188:THR:HG21	31:b:207:GLY:HA3	1.84	0.58
39:n:144:ASN:ND2	39:n:207:GLU:OE2	2.34	0.58
9:D:71:ARG:NH1	9:D:251:ASN:O	2.36	0.58
14:I:275:ARG:HG2	14:I:275:ARG:O	2.02	0.58
16:K:170:ARG:NH1	16:K:193:LEU:O	2.36	0.58
46:w:150:ILE:HG23	46:w:220:ILE:HD11	1.84	0.58
1:1:1242:G:OP1	31:b:227:ARG:NH1	2.36	0.58
1:1:3163:A:N1	1:1:3286:G:O6	2.37	0.58
2:2:63:G:H22	2:2:97:A:H2	1.49	0.58
13:H:9:GLN:HB3	13:H:52:LEU:HD11	1.86	0.58
31:b:21:VAL:HG21	31:b:57:PHE:CE1	2.38	0.58
37:l:170:GLY:HA2	41:q:323:LEU:HD22	1.86	0.58
1:1:1864:A:N7	5:8:282:ARG:NH2	2.51	0.58
22:Q:64:VAL:HG11	22:Q:113:LYS:HD2	1.85	0.58
1:1:34:A:N3	1:1:810:A:O2'	2.32	0.58
12:G:81:THR:HG21	12:G:181:LYS:HG3	1.85	0.58
46:w:89:THR:N	46:w:92:ASP:OD2	2.37	0.58
1:1:2968:G:H2'	1:1:2969:A:H8	1.67	0.57
2:2:143:U:OP1	19:N:38:ARG:NH2	2.36	0.57
10:E:10:TYR:H	23:R:86:TYR:HH	1.52	0.57
20:O:22:VAL:HG21	20:O:120:VAL:HG11	1.86	0.57
25:T:212:VAL:HA	25:T:216:LEU:HB2	1.85	0.57
27:W:55:GLU:OE1	27:W:121:ARG:NH1	2.37	0.57
41:q:355:ALA:O	41:q:382:ARG:NH2	2.37	0.57
1:1:705:A:H4'	1:1:706:A:H5'	1.85	0.57
1:1:720:A:OP1	1:1:784:A:N6	2.38	0.57
46:w:135:TYR:OH	46:w:139:ARG:NH2	2.37	0.57
1:1:2467:G:H21	1:1:2488:A:H62	1.53	0.57
25:T:221:ASN:HD22	25:T:224:GLU:HG3	1.69	0.57
29:Z:176:LEU:HG	29:Z:181:THR:HG21	1.86	0.57
1:1:1389:G:OP1	32:e:104:ASN:ND2	2.34	0.57
6:A:135:PRO:HB3	6:A:175:HIS:CD2	2.39	0.57
1:1:294:U:OP2	19:N:15:GLN:NE2	2.26	0.57
14:I:275:ARG:NH1	14:I:338:TYR:CE2	2.73	0.57
48:y:99:GLU:HB2	48:y:125:THR:HG21	1.86	0.57
1:1:1304:A:H5'	1:1:1306:G:N7	2.20	0.57
1:1:179:C:OP1	45:v:29:ASN:ND2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:733:G:N2	1:1:736:A:OP2	2.36	0.57
1:1:1206:G:H4'	42:r:54:ARG:HB3	1.87	0.57
10:E:52:VAL:HG11	10:E:65:ILE:HD12	1.85	0.57
31:b:29:THR:OG1	31:b:49:LYS:NZ	2.37	0.57
12:G:75:ILE:HD11	19:N:18:VAL:HG13	1.87	0.56
1:1:753:C:H2'	1:1:754:G:C8	2.40	0.56
6:A:127:GLY:O	15:J:280:LYS:NZ	2.38	0.56
8:C:35:VAL:HG21	8:C:244:LEU:HD21	1.87	0.56
1:1:2998:U:OP1	1:1:3143:C:N4	2.38	0.56
7:B:67:PHE:HA	7:B:70:ARG:HD2	1.87	0.56
8:C:138:ARG:HH21	8:C:240:PRO:HG2	1.71	0.56
12:G:91:PHE:HD1	12:G:189:LEU:HD21	1.71	0.56
31:b:206:VAL:HG13	31:b:219:ILE:HG12	1.87	0.56
32:e:89:THR:HG22	32:e:117:ILE:HG12	1.87	0.56
39:n:127:ASP:OD1	39:n:130:ARG:NH2	2.37	0.56
40:o:120:VAL:HG13	40:o:137:LEU:HG	1.86	0.56
32:e:96:ILE:HG21	32:e:105:ARG:HG2	1.88	0.56
32:e:126:LEU:O	47:x:154:LYS:NZ	2.34	0.56
6:A:31:GLN:OE1	6:A:84:ASN:ND2	2.38	0.56
9:D:148:VAL:HG23	9:D:168:LEU:HD11	1.88	0.56
9:D:200:ARG:NH2	9:D:458:SER:OG	2.38	0.56
34:h:66:VAL:HG12	34:h:80:LEU:HD11	1.87	0.56
34:h:100:VAL:HG22	34:h:104:GLN:HB3	1.88	0.56
37:l:23:ASN:HA	37:l:26:PHE:HD1	1.71	0.56
1:1:2395:G:H2'	1:1:2396:G:H8	1.69	0.56
39:n:74:GLU:HG3	39:n:76:VAL:H	1.70	0.56
1:1:34:A:H3'	1:1:48:A:H61	1.70	0.56
1:1:428:A:H2'	1:1:429:U:C6	2.41	0.56
1:1:1256:G:H2'	1:1:1257:C:C6	2.41	0.56
1:1:2830:G:N2	42:r:254:CYS:SG	2.79	0.56
13:H:124:ARG:NH1	13:H:164:ILE:O	2.39	0.56
19:N:98:LEU:HD12	19:N:128:LYS:HD2	1.88	0.56
46:w:171:ILE:HG23	46:w:237:LYS:HE2	1.88	0.56
1:1:567:G:H2'	1:1:568:G:C8	2.40	0.56
41:q:463:VAL:CG1	41:q:473:ILE:HD11	2.36	0.56
1:1:1209:G:H5'	27:W:4:SER:HB2	1.87	0.56
27:W:224:ASP:OD1	27:W:225:SER:N	2.39	0.56
43:t:279:GLY:O	43:t:288:LYS:NZ	2.34	0.56
3:6:58:G:OP1	3:6:58:G:N2	2.27	0.55
17:L:42:ARG:NH2	17:L:51:LEU:O	2.39	0.55
41:q:273:ILE:HD13	41:q:309:ILE:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:w:126:ARG:HA	46:w:176:ILE:HD12	1.88	0.55
1:1:596:C:OP1	11:F:33:ARG:NH1	2.40	0.55
8:C:132:ALA:HB2	8:C:148:ILE:HG21	1.89	0.55
29:Z:343:GLU:HG2	29:Z:351:VAL:HG22	1.88	0.55
1:1:751:A:H2'	1:1:752:C:C6	2.41	0.55
19:N:17:ASP:OD2	35:i:55:ARG:NH2	2.39	0.55
31:b:84:THR:O	31:b:234:ASN:ND2	2.40	0.55
1:1:3233:C:H2'	1:1:3234:A:H8	1.71	0.55
6:A:163:PRO:HG2	6:A:166:ALA:HB2	1.89	0.55
27:W:152:GLU:OE1	27:W:152:GLU:N	2.38	0.55
32:e:86:THR:HG22	32:e:87:MET:HE2	1.89	0.55
1:1:441:U:OP1	23:R:124:ARG:NH1	2.40	0.55
2:2:40:A:H2'	2:2:41:A:C8	2.41	0.55
41:q:424:CYS:SG	41:q:478:CYS:N	2.77	0.55
1:1:361:A:O3'	36:j:45:ARG:NH2	2.39	0.55
1:1:498:A:O2'	1:1:3273:A:N1	2.37	0.55
1:1:314:U:H2'	1:1:315:C:C6	2.42	0.55
47:x:231:THR:HG22	47:x:242:ARG:HB2	1.89	0.55
30:a:26:ARG:NH2	30:a:30:GLU:OE2	2.39	0.55
1:1:2461:A:O2'	1:1:2463:G:OP1	2.24	0.55
1:1:2891:U:H2'	1:1:2892:A:H8	1.71	0.55
1:1:3013:U:H2'	1:1:3014:U:C6	2.42	0.55
3:6:7:C:H5	3:6:21:G:H1	1.55	0.55
9:D:418:PRO:HB2	9:D:421:LYS:HB2	1.89	0.55
37:l:20:ILE:HG21	37:l:89:LEU:HD22	1.89	0.55
1:1:2495:C:H2'	1:1:2496:C:C6	2.43	0.54
23:R:109:LYS:O	23:R:113:THR:HG23	2.07	0.54
39:n:434:ASP:OD2	39:n:447:TYR:OH	2.25	0.54
1:1:3177:G:O2'	1:1:3179:U:OP1	2.23	0.54
6:A:164:PRO:HG3	15:J:219:GLU:HB3	1.89	0.54
7:B:14:LEU:HD23	7:B:17:LEU:HD12	1.90	0.54
16:K:135:VAL:HG22	16:K:136:SER:N	2.23	0.54
27:W:45:LEU:HD13	27:W:48:VAL:HG12	1.78	0.54
33:f:49:ILE:HG23	33:f:100:ILE:HG13	1.88	0.54
38:m:354:TRP:O	38:m:357:THR:OG1	2.25	0.54
1:1:2830:G:H2'	1:1:2831:G:C8	2.42	0.54
13:H:28:VAL:HG13	13:H:33:THR:HG22	1.89	0.54
46:w:92:ASP:HB2	46:w:145:LEU:HD13	1.89	0.54
37:l:64:MET:HB3	41:q:387:ILE:HD11	1.89	0.54
1:1:1348:U:OP1	22:Q:39:ARG:NH1	2.41	0.54
1:1:1410:U:O2'	32:e:95:GLU:OE1	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:234:LEU:HD12	16:K:235:PRO:HD2	1.89	0.54
31:b:421:LEU:O	44:u:80:ARG:NH1	2.40	0.54
1:1:786:A:H4'	1:1:787:G:H5'	1.90	0.54
8:C:325:LEU:O	11:F:41:ARG:NH2	2.33	0.54
36:j:66:TYR:OH	36:j:73:ARG:NH2	2.41	0.54
1:1:3026:G:O2'	42:r:2:PRO:HG3	2.08	0.54
24:S:34:GLU:OE1	24:S:34:GLU:N	2.37	0.54
38:m:387:ARG:HH21	39:n:200:LEU:HD23	1.72	0.54
47:x:243:ARG:HH21	47:x:260:GLY:HA3	1.73	0.54
1:1:978:G:O2'	1:1:1103:A:N1	2.38	0.54
1:1:1142:G:OP1	1:1:1144:U:O2'	2.23	0.54
1:1:3147:G:O2'	7:B:104:THR:HG23	2.08	0.54
31:b:320:SER:OG	31:b:321:SER:N	2.41	0.54
46:w:170:PRO:O	46:w:174:VAL:HG13	2.08	0.54
1:1:3233:C:H2'	1:1:3234:A:C8	2.43	0.54
1:1:3367:C:OP1	44:u:111:ARG:NH1	2.41	0.54
14:I:247:TRP:CE3	14:I:275:ARG:HD3	2.43	0.54
48:y:119:PRO:O	48:y:139:ARG:NH1	2.40	0.54
11:F:89:ILE:HD11	11:F:229:PHE:HB3	1.91	0.53
43:t:142:LEU:HD11	43:t:179:LEU:HD22	1.89	0.53
1:1:18:G:OP1	34:h:81:ARG:NH1	2.41	0.53
48:y:192:VAL:HG11	48:y:195:ALA:HB3	1.88	0.53
1:1:679:U:OP2	6:A:270:ARG:NH2	2.38	0.53
15:J:236:ILE:O	15:J:242:ARG:NH2	2.42	0.53
47:x:193:HIS:HB3	47:x:223:ASP:HB2	1.89	0.53
48:y:129:ILE:HG23	48:y:133:LEU:HD22	1.90	0.53
1:1:542:G:H1	1:1:549:U:H3	1.57	0.53
1:1:2420:C:H2'	1:1:2421:U:C6	2.43	0.53
14:I:327:THR:HG22	14:I:329:ASN:H	1.74	0.53
27:W:136:THR:HG22	27:W:187:LEU:HG	1.91	0.53
47:x:170:THR:HG21	47:x:275:LYS:HG2	1.91	0.53
16:K:333:LEU:HD22	43:t:165:LEU:HD12	1.90	0.53
37:l:99:ILE:HG22	37:l:118:VAL:HG22	1.90	0.53
46:w:133:LEU:HB3	46:w:184:LEU:HD11	1.91	0.53
1:1:1385:C:OP1	8:C:141:ARG:NH1	2.22	0.53
1:1:3296:A:OP1	7:B:120:LYS:N	2.41	0.53
2:2:55:U:OP1	45:v:11:ARG:NH1	2.41	0.53
36:j:54:LYS:O	36:j:58:THR:HB	2.08	0.53
37:l:40:GLN:HB3	37:l:45:TYR:HE2	1.74	0.53
1:1:2357:A:H2'	1:1:2358:A:C8	2.44	0.53
39:n:168:ALA:HB1	39:n:264:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:n:431:TRP:NE1	39:n:442:VAL:O	2.41	0.53
48:y:175:SER:O	48:y:178:GLN:NE2	2.42	0.53
1:1:2424:A:N6	1:1:2605:G:O2'	2.42	0.53
13:H:4:ILE:N	24:S:142:GLN:OE1	2.41	0.53
25:T:195:VAL:HG11	29:Z:266:VAL:HG11	1.91	0.53
42:r:181:LYS:HG2	42:r:196:PRO:HA	1.91	0.53
1:1:411:U:H2'	1:1:412:G:H8	1.74	0.53
26:V:80:ARG:HB2	26:V:99:ALA:HB3	1.91	0.53
31:b:192:VAL:HG21	31:b:201:THR:HG21	1.82	0.53
1:1:420:G:H1	2:2:3:A:H61	1.56	0.52
1:1:628:A:H2'	1:1:629:U:O4'	2.10	0.52
14:I:201:ASP:HB3	14:I:221:SER:HB3	1.90	0.52
1:1:371:G:H4'	1:1:396:A:N1	2.25	0.52
1:1:485:A:H5''	23:R:127:LEU:HD11	1.90	0.52
1:1:585:A:H2'	1:1:586:C:C6	2.44	0.52
1:1:644:G:O6	5:8:398:ARG:NH2	2.41	0.52
1:1:2997:G:OP1	2:2:1:A:N6	2.42	0.52
1:1:3139:A:H4'	7:B:20:LYS:HD3	1.91	0.52
1:1:3345:G:H2'	1:1:3346:U:H4'	1.92	0.52
2:2:7:U:H2'	2:2:8:C:C6	2.44	0.52
2:2:9:A:H2'	2:2:10:A:C8	2.44	0.52
16:K:270:LEU:HG	16:K:276:ILE:HD13	1.91	0.52
20:O:10:ASP:OD1	20:O:37:ARG:HD3	2.09	0.52
25:T:184:THR:HA	25:T:187:ARG:HD2	1.90	0.52
1:1:155:G:H1	9:D:155:ARG:HH22	1.56	0.52
1:1:507:U:H2'	1:1:508:U:C6	2.45	0.52
1:1:1176:C:H2'	1:1:1177:G:N2	2.25	0.52
1:1:3020:U:H2'	1:1:3033:A:N6	2.24	0.52
1:1:3131:U:H2'	1:1:3132:C:C6	2.44	0.52
27:W:47:ASP:HB3	27:W:126:ARG:HH11	1.74	0.52
33:f:2:ALA:O	33:f:5:HIS:NE2	2.41	0.52
1:1:600:G:H22	1:1:605:U:H1'	1.75	0.52
14:I:5:VAL:HG21	14:I:384:VAL:HG21	1.92	0.52
14:I:363:SER:HB3	14:I:380:LEU:HD12	1.92	0.52
16:K:289:LEU:HD12	16:K:290:PRO:HD2	1.92	0.52
1:1:665:A:H2'	1:1:666:A:C8	2.45	0.52
1:1:945:C:H2'	1:1:946:U:C6	2.43	0.52
1:1:2464:U:H2'	1:1:2465:G:C8	2.44	0.52
33:f:51:TYR:HD2	33:f:67:MET:HE3	1.74	0.52
48:y:182:VAL:HG22	48:y:221:ILE:HG12	1.91	0.52
1:1:3121:U:H1'	1:1:3122:A:H5''	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:124:ARG:HH11	9:D:452:GLN:HB3	1.75	0.52
1:1:357:A:O4'	8:C:81:GLY:HA3	2.10	0.52
1:1:464:U:H5''	23:R:75:LYS:HD2	1.92	0.52
46:w:218:ILE:HD12	46:w:253:ILE:HG21	1.91	0.52
1:1:92:G:H5'	1:1:93:C:H5''	1.92	0.52
8:C:294:GLU:HG2	22:Q:129:VAL:HG13	1.91	0.52
20:O:46:GLU:OE1	20:O:49:ARG:NH2	2.43	0.52
41:q:463:VAL:HG13	41:q:548:LYS:CD	2.38	0.52
1:1:3002:C:O2'	7:B:180:GLU:OE2	2.27	0.52
1:1:1295:G:H2'	1:1:1296:C:C6	2.45	0.52
6:A:260:ALA:HA	6:A:263:ARG:HE	1.75	0.52
1:1:137:G:H2'	1:1:138:U:C6	2.45	0.51
1:1:3099:C:H5''	7:B:278:ILE:HD11	1.92	0.51
30:a:24:LYS:HG2	30:a:26:ARG:HE	1.75	0.51
31:b:187:ILE:HG22	31:b:332:ARG:HD2	1.90	0.51
1:1:411:U:H2'	1:1:412:G:C8	2.45	0.51
1:1:3295:A:H2'	1:1:3296:A:H8	1.73	0.51
2:2:37:A:H5''	2:2:39:G:O4'	2.11	0.51
2:2:69:U:H2'	2:2:70:G:O4'	2.09	0.51
9:D:392:MET:HE3	9:D:394:LEU:HD11	1.92	0.51
1:1:216:G:OP1	28:Y:16:ARG:NH1	2.42	0.51
8:C:125:ALA:O	8:C:129:THR:HG23	2.10	0.51
18:M:102:LYS:HE3	18:M:106:ARG:HH11	1.75	0.51
31:b:433:PRO:HG3	44:u:90:LEU:HD11	1.91	0.51
1:1:607:A:OP1	10:E:26:ARG:NH2	2.43	0.51
1:1:1126:G:O2'	15:J:327:GLN:OE1	2.27	0.51
1:1:3099:C:O2'	1:1:3100:U:O5'	2.27	0.51
9:D:272:ASP:OD1	9:D:273:SER:N	2.39	0.51
1:1:435:C:H2'	1:1:436:A:C8	2.46	0.51
1:1:696:C:OP2	8:C:119:ARG:NH2	2.40	0.51
1:1:2423:U:O2	1:1:2607:G:O6	2.28	0.51
3:6:17:G:H2'	3:6:18:U:C6	2.46	0.51
23:R:86:TYR:HE1	23:R:113:THR:HG22	1.76	0.51
42:r:203:ASN:ND2	42:r:214:VAL:O	2.43	0.51
1:1:145:G:OP2	12:G:193:LYS:NZ	2.43	0.51
38:m:354:TRP:NE1	38:m:364:ARG:O	2.41	0.51
41:q:490:ASP:OD2	41:q:494:ARG:NH2	2.44	0.51
48:y:128:LEU:O	48:y:132:VAL:HG22	2.11	0.51
1:1:642:U:H2'	1:1:643:U:O4'	2.11	0.51
1:1:1438:U:H2'	1:1:1439:U:C6	2.46	0.51
7:B:168:LYS:HB3	7:B:319:ASN:HD21	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:H:92:TYR:CZ	13:H:142:ASP:HA	2.45	0.51
24:S:45:LEU:HG	24:S:51:VAL:HB	1.91	0.51
39:n:427:ILE:HG22	39:n:428:GLN:H	1.67	0.51
44:u:66:ASP:OD1	44:u:67:SER:N	2.44	0.51
27:W:45:LEU:CD1	27:W:48:VAL:HG12	2.39	0.51
47:x:86:ASN:H	47:x:216:SER:HB2	1.75	0.51
48:y:129:ILE:O	48:y:133:LEU:HB2	2.11	0.51
1:1:655:C:H2'	1:1:656:A:H8	1.75	0.51
1:1:1202:A:H5'	1:1:1203:A:H5''	1.93	0.51
14:I:271:ALA:HB3	14:I:306:MET:HE1	1.94	0.51
42:r:150:MET:HB3	42:r:172:ILE:HB	1.93	0.51
1:1:627:U:H2'	1:1:628:A:C8	2.46	0.50
1:1:2911:A:H2'	1:1:2912:G:C8	2.46	0.50
19:N:158:HIS:HB3	19:N:161:ALA:HB3	1.93	0.50
39:n:418:LYS:HG2	39:n:419:ASN:H	1.77	0.50
41:q:532:TYR:O	41:q:535:THR:OG1	2.29	0.50
1:1:3018:C:OP1	48:y:9:ASN:ND2	2.33	0.50
18:M:55:ARG:NH2	18:M:76:ALA:O	2.45	0.50
36:j:39:TYR:CD1	36:j:40:PRO:HA	2.46	0.50
1:1:2420:C:O2'	1:1:2421:U:OP1	2.29	0.50
18:M:40:ASP:OD1	18:M:43:LYS:N	2.42	0.50
25:T:216:LEU:HD13	25:T:229:ILE:HG12	1.93	0.50
29:Z:50:ILE:HG23	29:Z:205:HIS:HD2	1.76	0.50
31:b:43:ARG:NH1	31:b:119:GLY:O	2.37	0.50
1:1:1870:C:H2'	1:1:1871:U:C6	2.46	0.50
1:1:2357:A:H2'	1:1:2358:A:H8	1.77	0.50
1:1:2477:G:H5''	1:1:2487:U:H2'	1.93	0.50
34:h:117:ALA:HB1	45:v:55:LEU:HD22	1.94	0.50
40:o:93:ILE:HG23	40:o:164:VAL:HG13	1.93	0.50
7:B:108:GLU:HG3	7:B:137:TYR:HB3	1.93	0.50
7:B:108:GLU:HB2	7:B:137:TYR:CG	2.46	0.50
46:w:153:VAL:O	46:w:158:PRO:HD2	2.11	0.50
33:f:59:VAL:HG12	33:f:60:ARG:HG2	1.94	0.50
37:l:121:MET:HE2	37:l:150:THR:HG23	1.94	0.50
1:1:307:A:H3'	1:1:308:A:H5''	1.94	0.50
1:1:494:G:O2'	1:1:495:G:H8	1.93	0.50
1:1:1865:A:C8	5:8:284:ARG:HD3	2.47	0.50
1:1:2892:A:H2'	1:1:2893:C:C6	2.46	0.50
8:C:120:TYR:CE2	8:C:277:PRO:HB3	2.46	0.50
14:I:130:SER:O	47:x:133:LYS:NZ	2.37	0.50
48:y:15:VAL:HA	48:y:61:ARG:HG2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:230:U:H2'	1:1:231:G:O4'	2.11	0.50
1:1:334:A:O2'	45:v:22:LYS:HE2	2.12	0.50
1:1:637:C:H2'	1:1:638:C:C6	2.47	0.50
1:1:656:A:H2'	1:1:657:A:C8	2.47	0.50
1:1:665:A:H2'	1:1:666:A:H8	1.76	0.50
1:1:2838:A:H2'	1:1:2839:G:O4'	2.12	0.50
1:1:3267:A:H2'	10:E:69:PHE:CZ	2.47	0.50
2:2:26:U:H2'	2:2:27:U:C6	2.46	0.50
14:I:386:ILE:HB	14:I:396:VAL:HB	1.94	0.50
19:N:35:VAL:HG13	19:N:65:ARG:HG2	1.94	0.50
23:R:86:TYR:CE1	23:R:113:THR:HG22	2.47	0.50
30:a:55:LEU:HD11	30:a:155:ILE:HG12	1.93	0.50
1:1:630:A:H2'	1:1:631:U:C6	2.46	0.50
1:1:1334:U:H2'	1:1:1335:C:C6	2.47	0.50
1:1:2990:G:O2'	1:1:3309:G:N7	2.42	0.50
1:1:3298:C:C2	1:1:3299:A:C8	3.00	0.50
1:1:3353:G:C6	1:1:3356:G:C6	3.00	0.50
3:6:18:U:H2'	3:6:19:U:C6	2.47	0.50
40:o:194:LYS:HD3	40:o:194:LYS:H	1.76	0.50
41:q:315:PRO:HG2	41:q:318:ALA:HB3	1.94	0.50
1:1:1277:C:C2	1:1:1278:A:C8	3.00	0.49
1:1:1299:U:O2'	42:r:42:LEU:O	2.29	0.49
1:1:2856:G:H21	42:r:192:THR:HG21	1.77	0.49
1:1:2889:C:O2'	1:1:2890:A:OP2	2.29	0.49
9:D:199:ASP:OD1	9:D:200:ARG:N	2.45	0.49
14:I:3:LEU:HD11	14:I:386:ILE:HD11	1.93	0.49
31:b:169:THR:HB	31:b:248:SER:HB2	1.94	0.49
31:b:306:LEU:HA	31:b:309:VAL:HG22	1.93	0.49
34:h:101:THR:HG22	34:h:103:LYS:H	1.76	0.49
39:n:250:LEU:HD12	39:n:250:LEU:H	1.76	0.49
1:1:435:C:H2'	1:1:436:A:H8	1.77	0.49
1:1:594:U:H2'	1:1:609:G:O6	2.12	0.49
6:A:179:PHE:HD1	6:A:188:VAL:HG22	1.76	0.49
18:M:28:SER:HB3	18:M:53:VAL:HG22	1.94	0.49
22:Q:123:THR:OG1	22:Q:125:ASP:OD1	2.22	0.49
48:y:14:GLY:HA2	48:y:198:VAL:HG13	1.93	0.49
48:y:70:LEU:HD21	48:y:94:ILE:HG12	1.93	0.49
1:1:2467:G:N1	1:1:2487:U:OP2	2.41	0.49
9:D:274:ASP:OD1	9:D:274:ASP:N	2.38	0.49
31:b:21:VAL:HG21	31:b:57:PHE:CZ	2.47	0.49
41:q:282:ARG:HD2	41:q:307:LEU:HD21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:288:ARG:O	8:C:292:SER:OG	2.23	0.49
21:P:64:ASN:HB2	21:P:80:LYS:HD3	1.93	0.49
41:q:409:PRO:HG2	41:q:458:SER:HB3	1.93	0.49
1:1:604:G:H2'	1:1:605:U:C6	2.48	0.49
1:1:791:A:H2'	1:1:792:G:C8	2.48	0.49
27:W:159:HIS:HA	27:W:180:ILE:HD11	1.94	0.49
1:1:3332:U:H2'	1:1:3333:G:O4'	2.12	0.49
9:D:59:LYS:NZ	9:D:139:GLU:OE2	2.42	0.49
31:b:455:ALA:O	31:b:458:GLU:HG2	2.12	0.49
6:A:140:ASP:OD1	6:A:141:GLN:N	2.46	0.49
6:A:192:GLU:N	6:A:213:VAL:O	2.34	0.49
7:B:68:HIS:O	7:B:70:ARG:NH1	2.45	0.49
11:F:87:VAL:HG11	11:F:243:MET:HE1	1.95	0.49
20:O:18:ARG:O	20:O:22:VAL:HG13	2.12	0.49
43:t:302:SER:HB2	43:t:307:ALA:HB2	1.93	0.49
47:x:106:SER:OG	47:x:152:GLU:OE2	2.30	0.49
1:1:3193:C:H2'	1:1:3194:C:C6	2.47	0.49
7:B:92:TYR:OH	7:B:180:GLU:OE1	2.26	0.49
21:P:41:LEU:HD21	21:P:99:ALA:HB2	1.94	0.49
1:1:1243:G:O6	1:1:1244:A:N6	2.46	0.49
7:B:90:VAL:HG13	7:B:104:THR:HG22	1.94	0.49
14:I:43:LEU:HD21	47:x:83:ARG:HD2	1.95	0.49
25:T:195:VAL:HG22	29:Z:326:ILE:HD12	1.95	0.49
1:1:675:C:O2'	1:1:679:U:OP1	2.28	0.49
1:1:2889:C:N4	1:1:2915:U:OP2	2.35	0.49
1:1:2891:U:H2'	1:1:2892:A:C8	2.48	0.49
1:1:3294:A:H2'	1:1:3295:A:O4'	2.13	0.49
9:D:309:LEU:HD22	9:D:314:LEU:HD23	1.93	0.49
11:F:130:ILE:HD12	11:F:134:VAL:HG11	1.95	0.49
48:y:107:VAL:HG23	48:y:108:ILE:HG12	1.94	0.49
1:1:640:U:O2'	1:1:941:G:OP2	2.26	0.48
5:8:266:GLN:HB3	29:Z:141:LEU:HB3	1.95	0.48
16:K:103:LYS:HG2	16:K:265:LEU:HD22	1.93	0.48
18:M:32:LEU:HD11	18:M:94:TRP:CG	2.48	0.48
48:y:71:LEU:HD23	48:y:95:GLN:HB3	1.94	0.48
1:1:26:A:H2'	1:1:27:C:H6	1.78	0.48
1:1:148:G:O6	12:G:135:GLY:HA3	2.13	0.48
1:1:481:U:H3	1:1:484:C:N4	2.11	0.48
1:1:2352:A:H5''	21:P:83:TRP:O	2.13	0.48
1:1:3028:G:H2'	1:1:3029:A:C8	2.48	0.48
11:F:222:HIS:ND1	11:F:224:ILE:HG12	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:331:ARG:NE	15:J:335:GLU:OE2	2.42	0.48
19:N:186:GLY:HA3	19:N:189:LYS:HB2	1.95	0.48
29:Z:50:ILE:HD11	29:Z:333:PRO:HD2	1.95	0.48
30:a:162:VAL:HG13	30:a:164:CYS:H	1.78	0.48
31:b:242:ALA:O	31:b:246:LEU:HB2	2.13	0.48
1:1:1281:G:H5''	27:W:69:LYS:HG2	1.96	0.48
1:1:1350:A:H2'	1:1:1351:U:C6	2.48	0.48
24:S:77:VAL:HG11	24:S:106:LEU:HD13	1.96	0.48
41:q:361:THR:HG21	41:q:393:LEU:HD12	1.96	0.48
1:1:80:G:H2'	1:1:81:C:C6	2.49	0.48
1:1:929:A:H2'	1:1:930:U:C6	2.48	0.48
1:1:1226:G:H2'	1:1:1227:C:C6	2.47	0.48
1:1:3006:A:H2'	1:1:3007:U:O4'	2.13	0.48
7:B:108:GLU:HB2	7:B:137:TYR:CD2	2.48	0.48
15:J:277:GLU:HB2	38:m:158:GLY:HA3	1.96	0.48
27:W:154:ASP:OD1	27:W:155:VAL:N	2.39	0.48
39:n:249:ASP:HB3	39:n:252:LYS:HB2	1.94	0.48
41:q:493:LEU:HD11	41:q:501:LEU:HG	1.95	0.48
1:1:162:G:OP1	38:m:263:LYS:NZ	2.45	0.48
1:1:1197:A:H3'	1:1:1199:C:H5'	1.95	0.48
1:1:1353:U:H5	23:R:25:GLN:OE1	1.96	0.48
1:1:2367:A:H2'	1:1:2368:A:H8	1.79	0.48
1:1:3018:C:H5''	48:y:8:GLU:CG	2.35	0.48
29:Z:27:VAL:HG12	29:Z:44:VAL:HG13	1.95	0.48
37:l:20:ILE:HD11	37:l:24:ILE:HB	1.96	0.48
39:n:189:GLN:HB2	39:n:198:ARG:HG2	1.95	0.48
1:1:374:A:N3	1:1:376:G:H5''	2.29	0.48
1:1:495:G:OP1	32:e:5:PRO:HD3	2.14	0.48
1:1:981:U:H2'	1:1:982:C:O4'	2.14	0.48
1:1:2961:G:H2'	1:1:2962:U:C6	2.48	0.48
6:A:44:ARG:NH2	6:A:117:LEU:O	2.44	0.48
9:D:130:ILE:HG22	9:D:169:ILE:HD13	1.95	0.48
12:G:185:ARG:O	12:G:188:THR:OG1	2.30	0.48
26:V:108:GLU:HA	26:V:128:ARG:HG3	1.94	0.48
1:1:166:C:OP2	45:v:217:ARG:NH2	2.35	0.48
1:1:3393:U:H2'	1:1:3394:U:C6	2.48	0.48
11:F:98:LYS:HB3	11:F:99:PRO:HD3	1.94	0.48
13:H:36:LYS:NZ	13:H:152:GLU:OE2	2.30	0.48
13:H:177:ASP:O	42:r:17:ARG:NH1	2.47	0.48
15:J:279:VAL:HG23	15:J:280:LYS:HG3	1.95	0.48
17:L:35:ARG:HB3	17:L:39:ARG:NH2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:35:GLN:HG3	30:a:166:ALA:HB2	1.96	0.48
37:l:47:VAL:HG11	37:l:66:LEU:HG	1.95	0.48
1:1:19:U:H2'	1:1:20:A:C8	2.49	0.48
1:1:560:G:OP1	18:M:83:LYS:NZ	2.33	0.48
1:1:981:U:H3	1:1:1102:A:H2	1.62	0.48
1:1:2484:A:H5''	30:a:101:LYS:HE3	1.95	0.48
7:B:50:LYS:NZ	7:B:330:GLY:O	2.35	0.48
9:D:72:THR:HG22	9:D:250:ILE:HD12	1.95	0.48
31:b:219:ILE:HD12	31:b:246:LEU:HD21	1.94	0.48
40:o:98:LEU:HD23	40:o:162:LEU:HD22	1.95	0.48
42:r:98:ASN:OD1	42:r:99:THR:N	2.45	0.48
1:1:20:A:H2'	1:1:21:G:C8	2.48	0.48
1:1:629:U:H2'	1:1:630:A:H8	1.79	0.48
1:1:1191:U:H4'	1:1:1192:C:H5''	1.95	0.48
7:B:358:TRP:HB2	44:u:1:MET:SD	2.54	0.48
29:Z:128:LYS:NZ	29:Z:209:ASP:OD1	2.38	0.48
30:a:148:VAL:HA	30:a:151:VAL:HG12	1.95	0.48
31:b:25:THR:HG22	31:b:52:TYR:HD2	1.79	0.48
38:m:349:GLU:OE1	38:m:349:GLU:N	2.43	0.48
39:n:366:TYR:HB2	39:n:407:VAL:HG11	1.96	0.48
44:u:27:LYS:HG2	48:y:100:ARG:HH11	1.78	0.48
1:1:664:U:H2'	1:1:665:A:H8	1.78	0.48
8:C:135:VAL:HG12	8:C:140:HIS:HB2	1.95	0.48
25:T:221:ASN:ND2	25:T:224:GLU:HG3	2.28	0.48
31:b:42:ILE:HD13	31:b:122:LEU:HB2	1.96	0.48
1:1:257:U:H2'	1:1:258:G:H8	1.79	0.47
1:1:664:U:H2'	1:1:665:A:C8	2.49	0.47
1:1:3259:U:H1'	18:M:125:LYS:NZ	2.29	0.47
28:Y:55:GLU:HB2	28:Y:108:LYS:HB3	1.96	0.47
28:Y:71:SER:N	28:Y:81:GLN:O	2.45	0.47
37:l:95:TYR:HB3	37:l:125:ILE:HD13	1.95	0.47
1:1:985:U:H2'	1:1:986:U:H6	1.78	0.47
1:1:2924:U:H2'	1:1:2925:C:C6	2.49	0.47
9:D:219:ASN:OD1	9:D:222:ARG:NH1	2.46	0.47
14:I:247:TRP:CZ3	14:I:275:ARG:HD3	2.49	0.47
17:L:50:PRO:CG	34:h:118:ILE:HD12	2.44	0.47
20:O:47:PHE:HD1	20:O:136:THR:HG23	1.79	0.47
29:Z:177:ASN:HB2	29:Z:180:ARG:HB3	1.95	0.47
45:v:208:TYR:O	45:v:210:GLN:N	2.46	0.47
46:w:182:GLU:CD	46:w:247:ARG:HH12	2.22	0.47
1:1:787:G:H2'	1:1:788:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1286:A:H8	1:1:1287:A:H1'	1.80	0.47
1:1:1448:U:H5''	21:P:66:SER:HB2	1.96	0.47
1:1:3080:G:H2'	1:1:3081:C:C6	2.49	0.47
1:1:3252:G:H2'	1:1:3253:G:C8	2.48	0.47
9:D:292:ILE:HG12	9:D:360:TRP:HB2	1.96	0.47
18:M:16:GLU:HB3	24:S:149:LYS:HG2	1.95	0.47
30:a:159:LEU:HD11	30:a:163:LEU:HA	1.96	0.47
41:q:352:MET:HE2	41:q:405:ALA:HB1	1.96	0.47
1:1:2349:U:H2'	1:1:2350:C:C6	2.49	0.47
1:1:2968:G:H2'	1:1:2969:A:C8	2.48	0.47
17:L:90:ALA:HB1	17:L:95:ILE:HB	1.96	0.47
20:O:142:SER:HA	20:O:145:VAL:HG22	1.96	0.47
29:Z:207:PHE:HB2	29:Z:331:LEU:HD11	1.97	0.47
37:l:16:LEU:O	37:l:20:ILE:HG12	2.14	0.47
39:n:30:ALA:O	39:n:34:ARG:HG3	2.14	0.47
39:n:77:LEU:HD21	39:n:81:ARG:HH21	1.79	0.47
1:1:501:A:H2'	1:1:502:U:C6	2.49	0.47
1:1:3329:U:H5''	7:B:308:MET:HE2	1.96	0.47
9:D:284:LEU:HD22	9:D:342:ILE:HD13	1.95	0.47
23:R:29:ARG:NH1	32:e:81:ASP:OD1	2.43	0.47
27:W:134:THR:OG1	27:W:191:GLU:N	2.43	0.47
31:b:105:VAL:HA	31:b:108:VAL:HG22	1.97	0.47
1:1:258:G:H2'	1:1:259:C:C6	2.49	0.47
1:1:3302:U:H2'	1:1:3303:G:C8	2.49	0.47
5:8:269:ILE:HG13	5:8:274:ALA:O	2.15	0.47
9:D:320:HIS:CE1	9:D:323:GLN:HG3	2.49	0.47
14:I:359:ASP:OD2	14:I:385:ARG:NE	2.37	0.47
1:1:2415:C:H2'	1:1:2416:U:O4'	2.15	0.47
6:A:110:ILE:HD13	6:A:152:ILE:HG12	1.97	0.47
6:A:147:PRO:HB2	15:J:201:MET:HE3	1.97	0.47
7:B:291:GLU:OE1	7:B:291:GLU:N	2.48	0.47
9:D:121:THR:HG21	9:D:130:ILE:HD12	1.97	0.47
16:K:337:ALA:HB1	16:K:339:PRO:HD2	1.96	0.47
20:O:35:VAL:HG21	20:O:80:PHE:HE2	1.80	0.47
28:Y:54:ASP:HB2	28:Y:70:ILE:HD13	1.96	0.47
36:j:21:ARG:NH1	36:j:41:ALA:O	2.36	0.47
37:l:76:THR:O	37:l:76:THR:CG2	2.61	0.47
38:m:399:ARG:NH2	39:n:42:TYR:OH	2.47	0.47
41:q:386:LEU:HD23	41:q:400:VAL:HG13	1.96	0.47
48:y:53:ILE:O	48:y:56:THR:OG1	2.32	0.47
48:y:186:VAL:O	48:y:190:SER:OG	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:y:192:VAL:CG1	48:y:195:ALA:CB	2.85	0.47
1:1:338:A:OP1	8:C:47:ARG:HA	2.15	0.47
1:1:544:C:H3'	1:1:545:U:H2'	1.97	0.47
1:1:1313:G:O2'	1:1:1318:A:N1	2.47	0.47
1:1:3087:A:H2'	1:1:3088:G:H8	1.79	0.47
11:F:84:VAL:HG23	11:F:117:VAL:HB	1.96	0.47
13:H:90:MET:HE1	13:H:161:LEU:HB3	1.97	0.47
47:x:113:ILE:HG21	47:x:261:PRO:HG3	1.97	0.47
1:1:3358:U:C4	1:1:3359:A:H1'	2.50	0.47
16:K:32:ILE:HG21	16:K:291:LEU:HD13	1.97	0.47
27:W:78:GLY:HA3	27:W:84:GLU:HA	1.96	0.47
30:a:32:VAL:N	30:a:170:GLY:O	2.41	0.47
47:x:245:ARG:NH1	47:x:257:GLN:OE1	2.48	0.47
1:1:419:G:H2'	1:1:420:G:C8	2.50	0.47
1:1:589:A:H1'	1:1:1337:A:H5''	1.96	0.47
1:1:2819:A:H2'	1:1:2820:A:C8	2.49	0.47
14:I:252:ARG:HB2	14:I:306:MET:HE2	1.97	0.47
29:Z:52:GLN:HB3	29:Z:135:VAL:HG13	1.97	0.47
34:h:85:THR:HG22	34:h:87:ALA:N	2.29	0.47
41:q:418:ILE:HG21	41:q:459:ALA:HB1	1.97	0.47
45:v:186:GLU:HG2	45:v:190:LYS:HE2	1.96	0.47
1:1:3113:A:H2'	1:1:3114:A:O4'	2.14	0.46
40:o:197:LYS:O	40:o:200:MET:HG2	2.15	0.46
1:1:412:G:H2'	1:1:413:U:C6	2.51	0.46
1:1:1253:U:O2'	1:1:1263:A:H5''	2.16	0.46
1:1:3059:G:H2'	1:1:3060:C:C6	2.50	0.46
1:1:3129:A:H2'	1:1:3129:A:N3	2.30	0.46
28:Y:118:LEU:HD11	28:Y:122:LYS:HE2	1.96	0.46
31:b:80:ASP:OD2	31:b:245:HIS:NE2	2.48	0.46
35:i:55:ARG:O	35:i:58:ILE:HG13	2.16	0.46
38:m:395:TYR:CD1	39:n:37:ILE:HG13	2.50	0.46
41:q:377:ASP:OD2	41:q:382:ARG:NH1	2.48	0.46
1:1:80:G:H2'	1:1:81:C:H6	1.80	0.46
1:1:683:U:OP1	19:N:204:LYS:NZ	2.36	0.46
1:1:1364:C:H4'	22:Q:9:GLN:NE2	2.31	0.46
1:1:3348:G:H2'	1:1:3349:C:C6	2.51	0.46
6:A:191:TYR:HB3	6:A:212:LEU:HB3	1.98	0.46
16:K:276:ILE:HD12	16:K:279:ILE:HD11	1.96	0.46
31:b:84:THR:HG21	31:b:238:GLN:HG3	1.96	0.46
44:u:80:ARG:NH2	48:y:88:LEU:O	2.48	0.46
1:1:630:A:H2'	1:1:631:U:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:806:A:H61	1:1:935:U:H3'	1.80	0.46
1:1:988:U:H2'	1:1:989:A:C8	2.50	0.46
1:1:1340:G:OP2	32:e:61:LYS:NZ	2.37	0.46
1:1:2949:U:H2'	1:1:2950:G:H8	1.80	0.46
1:1:3276:G:H3'	10:E:48:ARG:HH22	1.80	0.46
11:F:86:VAL:O	11:F:114:GLY:HA2	2.15	0.46
25:T:204:THR:HG21	25:T:237:PHE:HD1	1.80	0.46
28:Y:51:ARG:HB3	28:Y:115:ARG:HH22	1.81	0.46
29:Z:204:ARG:HG2	29:Z:334:ARG:HG2	1.97	0.46
1:1:1419:A:OP1	2:2:21:C:H5'	2.16	0.46
1:1:3298:C:H5'	21:P:74:LYS:HD3	1.98	0.46
19:N:181:ASN:HA	19:N:184:LYS:HE3	1.97	0.46
29:Z:48:ARG:HB3	29:Z:57:ILE:HG22	1.97	0.46
29:Z:192:ILE:HG12	29:Z:203:MET:HG2	1.97	0.46
38:m:392:LEU:HD11	38:m:396:LEU:HD12	1.97	0.46
47:x:163:ILE:HG12	47:x:170:THR:HG23	1.97	0.46
1:1:144:A:H2'	1:1:145:G:O4'	2.16	0.46
1:1:532:A:O2'	1:1:533:A:H8	1.97	0.46
1:1:1460:A:H4'	5:8:292:PRO:HG3	1.98	0.46
7:B:89:VAL:HG12	7:B:199:PHE:HZ	1.79	0.46
43:t:78:VAL:HG22	43:t:305:ALA:HA	1.97	0.46
1:1:2892:A:H2'	1:1:2893:C:H6	1.81	0.46
2:2:114:G:H2'	2:2:115:C:O4'	2.15	0.46
4:7:108:LEU:O	4:7:112:ILE:HG12	2.16	0.46
16:K:301:LEU:HD13	40:o:189:ILE:HD12	1.98	0.46
1:1:495:G:H2'	1:1:496:C:C6	2.51	0.46
1:1:523:A:O2'	24:S:69:PRO:HD2	2.15	0.46
1:1:744:A:H2'	1:1:745:C:O4'	2.15	0.46
1:1:3099:C:H42	1:1:3135:U:H3	1.63	0.46
3:6:58:G:O6	40:o:126:LYS:N	2.48	0.46
7:B:113:GLU:OE2	7:B:166:ILE:N	2.49	0.46
22:Q:64:VAL:HG22	22:Q:96:PHE:CE1	2.51	0.46
23:R:163:GLU:HG2	47:x:254:VAL:HB	1.98	0.46
25:T:191:GLN:NE2	29:Z:326:ILE:O	2.48	0.46
31:b:403:GLU:HG3	31:b:412:PHE:HB3	1.96	0.46
39:n:115:ASP:OD1	39:n:115:ASP:N	2.48	0.46
1:1:18:G:OP1	34:h:81:ARG:NH2	2.47	0.46
1:1:288:C:H2'	1:1:289:A:C8	2.51	0.46
1:1:451:U:H2'	1:1:452:G:C8	2.51	0.46
1:1:1276:U:O2'	1:1:1277:C:H5'	2.16	0.46
1:1:3041:U:H2'	1:1:3042:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:96:PHE:HB3	9:D:227:PHE:CE2	2.51	0.46
28:Y:50:ILE:HD11	28:Y:70:ILE:HD11	1.98	0.46
29:Z:29:ARG:HG2	29:Z:44:VAL:HG21	1.97	0.46
29:Z:67:LEU:HD21	29:Z:346:ILE:HG22	1.97	0.46
44:u:84:GLU:OE1	44:u:84:GLU:N	2.49	0.46
47:x:171:PHE:CG	47:x:213:LEU:HD22	2.51	0.46
1:1:528:U:H2'	1:1:529:A:C8	2.50	0.46
1:1:1105:A:H2'	1:1:1106:G:H8	1.81	0.46
1:1:3080:G:H2'	1:1:3081:C:H6	1.81	0.46
1:1:3376:A:N7	29:Z:62:ARG:NH2	2.64	0.46
6:A:130:LEU:HD11	15:J:270:ARG:HD2	1.98	0.46
31:b:57:PHE:CE1	31:b:140:VAL:HG21	2.50	0.46
34:h:101:THR:HG22	34:h:103:LYS:N	2.30	0.46
44:u:1:MET:HE2	44:u:1:MET:HB3	1.83	0.46
48:y:85:ARG:NH2	48:y:89:PRO:O	2.49	0.46
1:1:448:U:H2'	1:1:449:U:C6	2.51	0.45
1:1:791:A:H2'	1:1:792:G:H8	1.80	0.45
2:2:6:U:H2'	2:2:7:U:C6	2.51	0.45
9:D:447:TYR:CD2	9:D:483:PRO:HG2	2.51	0.45
14:I:17:LEU:HD13	14:I:34:HIS:HB3	1.96	0.45
19:N:21:PHE:O	19:N:24:ARG:HG2	2.15	0.45
28:Y:51:ARG:HD2	28:Y:115:ARG:NH2	2.31	0.45
37:l:122:SER:HB2	37:l:125:ILE:HD11	1.98	0.45
41:q:274:ARG:HH22	41:q:393:LEU:HD13	1.80	0.45
1:1:481:U:H3	1:1:484:C:H41	1.64	0.45
1:1:631:U:H2'	1:1:632:G:C8	2.52	0.45
2:2:65:A:O3'	34:h:10:ARG:NH2	2.45	0.45
2:2:107:G:H4'	2:2:138:A:H5'	1.96	0.45
3:6:36:U:H2'	3:6:37:C:C6	2.51	0.45
3:6:54:A:H5'	40:o:97:ARG:HG2	1.98	0.45
7:B:17:LEU:HD23	7:B:19:ARG:HG3	1.97	0.45
17:L:42:ARG:O	17:L:46:ILE:HG12	2.16	0.45
38:m:171:ILE:O	38:m:180:ILE:HB	2.16	0.45
42:r:207:PRO:O	42:r:210:THR:HG22	2.16	0.45
43:t:205:ARG:HG2	43:t:251:ILE:HG21	1.97	0.45
1:1:644:G:H2'	1:1:645:A:H5'	1.98	0.45
1:1:655:C:H2'	1:1:656:A:C8	2.50	0.45
1:1:748:U:H2'	1:1:749:C:C6	2.51	0.45
1:1:1191:U:OP2	20:O:49:ARG:NH1	2.36	0.45
1:1:3094:A:H2'	1:1:3095:U:C6	2.51	0.45
14:I:245:PRO:HB2	14:I:276:TRP:NE1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Z:213:VAL:HB	29:Z:323:LYS:HB2	1.99	0.45
38:m:387:ARG:HA	38:m:387:ARG:HD3	1.68	0.45
39:n:90:LEU:HD11	43:t:286:LEU:HD22	1.98	0.45
41:q:319:THR:OG1	41:q:321:GLU:OE1	2.34	0.45
46:w:148:GLU:OE2	46:w:152:LYS:HG3	2.17	0.45
47:x:214:PHE:CG	47:x:232:LEU:HD13	2.52	0.45
48:y:23:TYR:OH	48:y:70:LEU:HB3	2.16	0.45
1:1:151:A:OP1	19:N:147:ARG:NH2	2.50	0.45
2:2:71:A:H2'	28:Y:51:ARG:NH2	2.32	0.45
3:6:45:U:O2'	16:K:243:THR:O	2.33	0.45
8:C:60:THR:HB	8:C:90:PHE:CE1	2.51	0.45
36:j:52:LYS:O	36:j:56:ARG:HG3	2.17	0.45
42:r:171:ILE:HD13	42:r:212:LEU:HD11	1.99	0.45
47:x:151:ASN:ND2	47:x:158:THR:OG1	2.49	0.45
48:y:157:GLN:HE21	48:y:201:ASP:HB3	1.80	0.45
1:1:1883:A:H2'	1:1:1884:A:O4'	2.16	0.45
1:1:2444:C:N4	1:1:2501:U:O4	2.50	0.45
2:2:46:G:O2'	2:2:61:A:N1	2.44	0.45
2:2:63:G:OP1	2:2:90:U:H5''	2.16	0.45
16:K:75:LYS:HE3	16:K:285:ARG:HD2	1.98	0.45
31:b:25:THR:HG21	31:b:53:THR:HB	1.98	0.45
39:n:364:VAL:HG22	39:n:386:ASN:HB3	1.98	0.45
48:y:116:LEU:HD11	48:y:177:LEU:HD21	1.98	0.45
1:1:548:G:H2'	1:1:549:U:C6	2.51	0.45
1:1:2964:G:H2'	1:1:2967:A:N6	2.31	0.45
5:8:275:ARG:HB2	5:8:284:ARG:HB2	1.98	0.45
6:A:170:LYS:HZ3	15:J:277:GLU:H	1.63	0.45
6:A:176:VAL:HG21	15:J:254:VAL:HB	1.98	0.45
12:G:145:ASN:HA	38:m:255:PRO:HB3	1.98	0.45
22:Q:24:VAL:O	22:Q:28:LEU:HG	2.16	0.45
22:Q:58:ASN:C	22:Q:60:PRO:HD3	2.41	0.45
31:b:193:ASP:N	31:b:193:ASP:OD1	2.48	0.45
35:i:58:ILE:HG22	35:i:90:MET:HB3	1.99	0.45
40:o:207:ARG:O	40:o:211:LEU:HG	2.17	0.45
44:u:8:PHE:HE2	44:u:49:LEU:HD12	1.82	0.45
1:1:952:A:H4'	1:1:968:G:N2	2.31	0.45
1:1:1122:U:H2'	1:1:1123:U:C6	2.52	0.45
1:1:1317:A:O2'	1:1:1318:A:H3'	2.16	0.45
1:1:2354:C:H2'	1:1:2355:G:O4'	2.16	0.45
1:1:3275:U:H2'	1:1:3276:G:H5'	1.99	0.45
2:2:19:C:H2'	2:2:20:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7:112:ILE:HG21	37:l:25:SER:HB3	1.98	0.45
7:B:123:TYR:CZ	7:B:124:LYS:HG3	2.52	0.45
13:H:8:GLN:HB3	13:H:72:LYS:HD2	1.98	0.45
26:V:131:SER:HA	48:y:61:ARG:HD3	1.99	0.45
31:b:139:ILE:HA	31:b:142:LYS:HE3	1.99	0.45
31:b:154:ARG:HA	31:b:157:ILE:HG22	1.98	0.45
36:j:17:THR:OG1	36:j:18:LEU:N	2.49	0.45
46:w:200:GLU:HA	46:w:203:ARG:HG2	1.99	0.45
1:1:359:U:O3'	36:j:25:ARG:NH1	2.50	0.45
1:1:685:G:O2'	45:v:63:ALA:O	2.32	0.45
6:A:154:GLU:OE2	6:A:158:HIS:NE2	2.49	0.45
9:D:94:LEU:HD23	9:D:137:LEU:HD11	1.98	0.45
16:K:97:LEU:HD11	16:K:205:THR:HB	1.99	0.45
23:R:112:PHE:O	23:R:116:THR:HG23	2.16	0.45
25:T:187:ARG:NH1	29:Z:330:GLU:OE2	2.50	0.45
32:e:31:ASN:OD1	32:e:31:ASN:N	2.49	0.45
37:l:54:LEU:HD13	41:q:374:PHE:CZ	2.52	0.45
1:1:456:U:H2'	1:1:457:C:H6	1.82	0.45
7:B:300:ARG:HD2	31:b:433:PRO:HB3	1.99	0.45
23:R:114:LYS:HB3	32:e:87:MET:HE1	1.98	0.45
28:Y:51:ARG:HG3	28:Y:52:ARG:O	2.17	0.45
30:a:38:LEU:HB2	30:a:163:LEU:HB2	1.98	0.45
36:j:46:SER:HB3	36:j:54:LYS:NZ	2.32	0.45
38:m:334:ASN:OD1	39:n:458:SER:OG	2.27	0.45
40:o:149:GLN:HG3	40:o:166:VAL:HG23	1.99	0.45
44:u:57:LYS:HE3	44:u:64:ALA:HB1	1.99	0.45
48:y:4:ARG:HB3	48:y:208:LEU:HA	1.99	0.45
1:1:314:U:H2'	1:1:315:C:H6	1.80	0.45
1:1:713:U:H2'	1:1:714:G:O4'	2.17	0.45
1:1:1191:U:OP2	20:O:49:ARG:HD3	2.17	0.45
8:C:293:SER:HB3	46:w:171:ILE:HG21	1.98	0.45
37:l:12:VAL:HG22	37:l:79:PHE:CE2	2.52	0.45
45:v:170:VAL:HG12	45:v:172:ARG:HG3	1.99	0.45
46:w:9:GLN:HB3	46:w:21:ALA:HB2	1.98	0.45
1:1:275:U:H2'	1:1:276:U:C6	2.52	0.44
1:1:1213:G:H5'	24:S:137:ARG:HH21	1.82	0.44
1:1:2450:G:N1	1:1:2497:U:C2	2.85	0.44
3:6:57:U:H3	40:o:173:ILE:HG22	1.82	0.44
34:h:70:TYR:O	34:h:73:LYS:HG2	2.18	0.44
46:w:34:PHE:HA	46:w:37:ASN:ND2	2.33	0.44
1:1:1132:C:H2'	1:1:1133:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3087:A:H2'	1:1:3088:G:C8	2.52	0.44
1:1:3176:G:OP2	33:f:6:ARG:HB2	2.18	0.44
1:1:3305:A:O3'	7:B:21:ARG:NH2	2.39	0.44
2:2:7:U:H2'	2:2:8:C:H6	1.82	0.44
2:2:47:C:H1'	2:2:61:A:H2'	1.98	0.44
12:G:108:ARG:NH2	38:m:272:GLU:OE1	2.50	0.44
38:m:269:SER:HB3	38:m:272:GLU:HB2	1.99	0.44
1:1:1259:A:H2'	1:1:1260:A:C8	2.53	0.44
1:1:1326:A:H2'	1:1:1327:C:O4'	2.18	0.44
1:1:1865:A:H61	29:Z:170:GLN:HE22	1.64	0.44
1:1:1888:U:H2'	1:1:1889:G:C8	2.52	0.44
1:1:2378:C:C2	1:1:2379:U:C5	3.05	0.44
3:6:227:C:N4	43:t:153:VAL:O	2.39	0.44
7:B:57:VAL:HG22	7:B:73:VAL:HG22	2.00	0.44
8:C:156:LEU:HD12	8:C:159:ILE:HD12	1.99	0.44
11:F:126:LEU:O	11:F:130:ILE:HG12	2.17	0.44
13:H:27:VAL:HG12	13:H:82:VAL:HG21	1.99	0.44
14:I:309:PHE:CD1	14:I:334:ILE:HG13	2.52	0.44
16:K:124:LEU:HD11	16:K:155:ILE:HG12	1.98	0.44
41:q:460:ILE:HG21	41:q:496:ARG:HG3	1.98	0.44
46:w:54:TRP:O	46:w:117:ARG:NH1	2.50	0.44
48:y:99:GLU:HG3	48:y:101:LEU:N	2.33	0.44
1:1:491:C:H2'	1:1:492:U:O4'	2.18	0.44
1:1:909:G:H3'	1:1:910:G:C8	2.53	0.44
2:2:4:C:H2'	2:2:5:U:C6	2.52	0.44
9:D:296:LEU:HD21	9:D:305:TYR:CD2	2.52	0.44
41:q:542:PHE:HE2	41:q:544:ALA:HB2	1.82	0.44
48:y:3:THR:HG21	48:y:41:GLU:CD	2.42	0.44
1:1:752:C:H2'	1:1:753:C:C6	2.53	0.44
1:1:815:G:H2'	1:1:816:A:O4'	2.18	0.44
8:C:53:SER:HB3	8:C:56:ALA:HB2	2.00	0.44
18:M:55:ARG:HD3	24:S:70:THR:HB	1.99	0.44
20:O:151:ASP:OD1	20:O:151:ASP:N	2.50	0.44
29:Z:43:LEU:HD11	29:Z:335:LEU:HD21	1.99	0.44
1:1:516:A:H5''	8:C:344:ALA:HB2	1.99	0.44
1:1:947:G:C5'	32:e:55:ILE:HB	2.48	0.44
1:1:3000:A:H2'	1:1:3001:C:C6	2.53	0.44
2:2:158:U:H1'	43:t:151:LEU:HD21	2.00	0.44
6:A:128:ASN:OD1	6:A:129:CYS:N	2.50	0.44
14:I:48:ASP:N	14:I:61:ALA:O	2.48	0.44
14:I:130:SER:OG	14:I:132:LYS:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:251:LEU:HA	15:J:254:VAL:HG12	1.98	0.44
28:Y:56:VAL:HG12	28:Y:106:ILE:HA	1.99	0.44
1:1:1105:A:H2'	1:1:1106:G:C8	2.53	0.44
1:1:1178:G:O6	33:f:20:LYS:HE2	2.18	0.44
1:1:2921:U:H5	26:V:71:LYS:HG2	1.83	0.44
1:1:3113:A:OP1	13:H:73:SER:OG	2.33	0.44
1:1:3379:C:H4'	7:B:315:GLY:HA2	1.99	0.44
11:F:176:TYR:CZ	11:F:197:GLN:HG2	2.52	0.44
14:I:276:TRP:HB3	14:I:300:ARG:HD2	2.00	0.44
19:N:8:GLU:O	19:N:12:ARG:HG2	2.18	0.44
24:S:27:MET:HE2	24:S:27:MET:HB3	1.87	0.44
31:b:224:ILE:HG22	31:b:270:LEU:HD11	2.00	0.44
31:b:318:MET:HE3	31:b:334:LYS:HD3	2.00	0.44
32:e:79:VAL:HG13	32:e:111:ARG:HG2	1.99	0.44
36:j:21:ARG:NH2	36:j:37:CYS:O	2.50	0.44
39:n:25:LEU:O	39:n:81:ARG:NH2	2.50	0.44
39:n:180:PHE:CE2	39:n:182:SER:HB3	2.53	0.44
42:r:155:THR:HG22	42:r:214:VAL:HA	1.99	0.44
1:1:691:A:N1	2:2:28:C:O2'	2.49	0.44
1:1:947:G:H2'	1:1:948:C:C6	2.53	0.44
3:6:18:U:H2'	3:6:19:U:H6	1.82	0.44
7:B:108:GLU:O	7:B:108:GLU:HG2	2.17	0.44
14:I:61:ALA:HB1	14:I:140:PHE:CD2	2.52	0.44
26:V:104:ASN:OD1	26:V:108:GLU:N	2.47	0.44
33:f:31:LYS:NZ	33:f:78:SER:O	2.51	0.44
38:m:145:ASP:OD1	38:m:145:ASP:N	2.47	0.44
38:m:337:SER:HA	39:n:182:SER:HA	1.99	0.44
1:1:164:A:H5'	1:1:165:A:H4'	2.00	0.44
1:1:393:U:H2'	1:1:394:G:O4'	2.17	0.44
1:1:456:U:H2'	1:1:457:C:C6	2.52	0.44
1:1:573:C:H2'	1:1:574:U:C6	2.53	0.44
1:1:800:G:H22	8:C:101:ALA:HA	1.82	0.44
1:1:3150:A:H4'	7:B:128:LYS:O	2.18	0.44
2:2:58:G:O6	36:j:63:ARG:NH1	2.51	0.44
8:C:271:LYS:HB2	8:C:274:TYR:HB3	1.99	0.44
9:D:93:THR:HA	9:D:96:PHE:CZ	2.53	0.44
9:D:289:LYS:HE3	16:K:116:THR:HG21	2.00	0.44
9:D:369:ASP:HB3	9:D:372:ASP:HB3	2.00	0.44
14:I:399:TYR:CZ	14:I:401:GLY:HA2	2.52	0.44
24:S:80:ARG:HH11	24:S:89:ASN:HD21	1.65	0.44
41:q:423:PRO:O	41:q:452:GLN:NE2	2.39	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:t:236:GLU:HG3	43:t:245:ILE:HG23	2.00	0.44
1:1:385:A:H5'	1:1:386:A:OP2	2.18	0.43
1:1:1244:A:H5''	1:1:1271:A:H4'	1.99	0.43
1:1:2410:U:H2'	1:1:2411:U:C6	2.52	0.43
1:1:3160:U:H2'	1:1:3161:C:C6	2.53	0.43
2:2:29:U:H2'	2:2:30:C:C6	2.52	0.43
8:C:181:VAL:HG11	8:C:224:GLY:HA3	1.99	0.43
26:V:87:ARG:HH22	26:V:137:VAL:HG21	1.83	0.43
37:l:46:TYR:HB2	37:l:70:LEU:HD11	2.00	0.43
42:r:173:ARG:O	42:r:178:ARG:NH2	2.51	0.43
43:t:167:ARG:NH2	43:t:265:ASN:OD1	2.51	0.43
48:y:68:ARG:NH1	48:y:112:ASP:O	2.48	0.43
1:1:407:A:C2	2:2:17:A:H1'	2.53	0.43
1:1:1261:G:H4'	1:1:1278:A:H2	1.84	0.43
1:1:2462:A:H2'	1:1:2463:G:C8	2.53	0.43
5:8:382:ARG:NH1	5:8:406:ARG:O	2.41	0.43
11:F:178:ILE:HD11	11:F:187:GLU:HG3	1.99	0.43
12:G:99:PRO:HD3	12:G:132:VAL:HG22	1.99	0.43
23:R:56:ASP:HB3	23:R:61:TYR:CE1	2.53	0.43
43:t:136:ASP:N	43:t:136:ASP:OD1	2.50	0.43
46:w:201:GLU:HA	46:w:204:LYS:HG2	2.00	0.43
1:1:2367:A:H2'	1:1:2368:A:C8	2.53	0.43
1:1:2841:G:O2'	1:1:2847:A:N6	2.52	0.43
1:1:3039:C:OP1	7:B:62:ARG:NH1	2.39	0.43
1:1:3068:U:O2'	1:1:3069:G:O3'	2.35	0.43
1:1:3378:C:H2'	1:1:3379:C:H6	1.82	0.43
3:6:51:U:O2'	3:6:54:A:N7	2.38	0.43
30:a:16:LEU:HD21	30:a:208:SER:HB3	2.00	0.43
31:b:23:ASN:OD1	31:b:27:ARG:NE	2.44	0.43
40:o:149:GLN:HA	40:o:164:VAL:HG11	2.00	0.43
1:1:288:C:H2'	1:1:289:A:H8	1.83	0.43
1:1:2466:G:H5''	30:a:60:ARG:NH1	2.33	0.43
1:1:2483:G:N1	1:1:2486:A:OP2	2.51	0.43
14:I:124:GLU:OE1	14:I:135:LYS:HD2	2.17	0.43
27:W:139:GLU:HB3	27:W:185:PRO:HD3	1.98	0.43
30:a:98:LYS:O	30:a:102:LYS:HG2	2.18	0.43
1:1:258:G:H2'	1:1:259:C:H6	1.82	0.43
1:1:733:G:O2'	1:1:735:A:N7	2.35	0.43
1:1:1455:U:H4'	1:1:1455:U:OP1	2.18	0.43
1:1:2595:A:H3'	1:1:2596:U:C6	2.53	0.43
1:1:2939:G:H2'	1:1:2940:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:91:VAL:HG12	10:E:155:LEU:HD21	2.00	0.43
14:I:220:ASP:OD1	14:I:221:SER:N	2.52	0.43
27:W:69:LYS:HB2	27:W:72:VAL:HG12	2.00	0.43
39:n:148:THR:HG23	39:n:150:GLN:H	1.83	0.43
41:q:374:PHE:CE2	41:q:399:ILE:HD12	2.53	0.43
45:v:10:ASN:OD1	45:v:16:LYS:NZ	2.38	0.43
1:1:114:A:N1	1:1:266:A:O2'	2.38	0.43
7:B:85:VAL:HB	7:B:163:HIS:CE1	2.54	0.43
12:G:161:GLU:HA	12:G:164:VAL:HG22	2.00	0.43
22:Q:83:VAL:O	22:Q:103:ALA:HA	2.19	0.43
31:b:178:VAL:HG11	31:b:253:PHE:HB3	2.00	0.43
1:1:810:A:H2'	1:1:811:U:C6	2.53	0.43
1:1:823:C:H2'	1:1:824:C:C6	2.54	0.43
1:1:1184:A:H2'	1:1:1185:C:C6	2.53	0.43
1:1:1243:G:N2	1:1:1270:A:O2'	2.36	0.43
1:1:1340:G:H2'	1:1:1341:U:C6	2.53	0.43
1:1:2470:C:OP1	30:a:26:ARG:HB3	2.19	0.43
1:1:3052:G:N1	1:1:3091:A:H2	2.12	0.43
1:1:3095:U:H2'	1:1:3096:C:C6	2.54	0.43
3:6:37:C:P	16:K:277:ARG:HH12	2.40	0.43
5:8:309:ASN:HA	5:8:312:GLU:HG2	2.00	0.43
9:D:232:THR:H	9:D:235:VAL:HB	1.82	0.43
16:K:218:SER:HB2	16:K:221:THR:HB	2.00	0.43
41:q:269:ARG:HH12	41:q:533:PRO:HB3	1.84	0.43
1:1:433:A:H2'	1:1:434:U:O4'	2.19	0.43
1:1:1459:C:H2'	1:1:1460:A:H8	1.84	0.43
1:1:2468:A:H4'	1:1:2469:G:H5'	2.01	0.43
1:1:3294:A:OP1	7:B:128:LYS:NZ	2.46	0.43
1:1:3335:A:H2'	1:1:3336:A:C8	2.54	0.43
6:A:36:ILE:HG23	6:A:88:PHE:HD1	1.83	0.43
8:C:106:TRP:HA	17:L:24:VAL:HG21	2.01	0.43
13:H:53:ILE:HD12	18:M:7:VAL:HG21	2.01	0.43
23:R:111:ARG:HG3	32:e:87:MET:HE3	2.01	0.43
25:T:219:ILE:CG1	47:x:42:ARG:HD3	2.49	0.43
29:Z:48:ARG:HD3	29:Z:57:ILE:HA	2.01	0.43
34:h:73:LYS:HB3	34:h:73:LYS:HE2	1.78	0.43
41:q:311:ASP:OD1	41:q:312:SER:N	2.52	0.43
41:q:359:LYS:NZ	41:q:421:ASP:OD2	2.37	0.43
43:t:234:ILE:HA	43:t:237:GLU:HG2	2.00	0.43
43:t:244:ILE:HG23	43:t:249:ASP:HB2	2.01	0.43
1:1:425:G:H5'	32:e:23:ASP:OD2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:806:A:N6	1:1:935:U:H3'	2.34	0.43
1:1:1461:A:H2'	1:1:1462:A:C8	2.54	0.43
5:8:280:LEU:HB3	25:T:241:VAL:HG21	2.01	0.43
8:C:152:VAL:HG21	8:C:156:LEU:HD22	2.00	0.43
14:I:3:LEU:HD21	14:I:386:ILE:HD11	1.99	0.43
35:i:60:LEU:O	35:i:65:GLY:N	2.49	0.43
1:1:958:C:H2'	1:1:959:C:O3'	2.19	0.43
1:1:1139:G:H2'	1:1:1140:G:H8	1.84	0.43
1:1:1209:G:N7	27:W:3:ARG:NH1	2.67	0.43
1:1:3069:G:H22	29:Z:354:HIS:CE1	2.37	0.43
2:2:103:G:OP2	2:2:105:A:O2'	2.23	0.43
11:F:190:THR:O	11:F:190:THR:OG1	2.37	0.43
12:G:172:LYS:HG2	38:m:248:THR:HA	2.01	0.43
29:Z:26:MET:HB2	29:Z:79:VAL:HG11	2.01	0.43
1:1:156:G:H5'	35:i:25:LYS:HD3	2.01	0.42
1:1:1290:A:H2'	1:1:1291:A:H8	1.83	0.42
5:8:333:LEU:HD22	5:8:338:ILE:HD12	2.00	0.42
9:D:101:ILE:HG13	9:D:167:MET:HE1	2.01	0.42
27:W:57:ARG:NH1	27:W:65:LEU:O	2.45	0.42
31:b:169:THR:HG23	31:b:217:GLN:HG3	1.99	0.42
31:b:400:ARG:HB2	48:y:36:SER:CB	2.49	0.42
31:b:452:LYS:HB3	44:u:71:PHE:HE1	1.83	0.42
1:1:242:C:O2'	1:1:243:G:H8	2.01	0.42
1:1:352:A:N1	1:1:365:A:H5''	2.33	0.42
1:1:645:A:H1'	1:1:2373:A:N1	2.34	0.42
1:1:959:C:H41	15:J:305:ALA:HB1	1.84	0.42
1:1:1394:A:H4'	1:1:1420:C:H4'	2.00	0.42
1:1:3033:A:H2'	1:1:3034:C:H6	1.84	0.42
7:B:45:SER:HB3	7:B:181:ILE:HG23	2.00	0.42
8:C:4:PRO:HG3	46:w:51:TYR:CE2	2.54	0.42
16:K:124:LEU:HB3	16:K:180:ILE:HG12	2.00	0.42
21:P:59:PRO:O	21:P:61:ARG:HG3	2.18	0.42
26:V:101:VAL:HB	26:V:109:MET:HE1	2.01	0.42
29:Z:46:ASP:HB3	29:Z:333:PRO:HD3	2.00	0.42
38:m:395:TYR:CD1	39:n:37:ILE:CG1	3.02	0.42
40:o:206:GLU:O	40:o:210:LYS:HG2	2.18	0.42
1:1:355:A:H2'	1:1:356:C:O4'	2.18	0.42
1:1:3259:U:H5''	1:1:3261:C:H5	1.84	0.42
2:2:93:U:H2'	2:2:94:C:O4'	2.19	0.42
8:C:120:TYR:CE2	8:C:277:PRO:CB	3.02	0.42
9:D:190:LEU:HB3	9:D:218:PRO:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:138:GLN:HE21	10:E:142:ASP:CG	2.27	0.42
26:V:17:LEU:HD11	26:V:98:ASN:HB3	2.01	0.42
29:Z:206:TYR:HE1	29:Z:330:GLU:HG2	1.84	0.42
38:m:262:PRO:HB2	38:m:264:ARG:HG2	2.01	0.42
39:n:38:PHE:HB3	39:n:117:ILE:HD13	2.01	0.42
42:r:27:ARG:HG2	42:r:30:ARG:NH2	2.35	0.42
1:1:22:G:H1'	2:2:104:A:N3	2.34	0.42
1:1:311:C:H2'	1:1:312:C:O4'	2.19	0.42
1:1:437:G:OP2	47:x:155:LYS:NZ	2.52	0.42
1:1:441:U:H5''	1:1:442:G:H5'	2.01	0.42
1:1:549:U:H2'	1:1:550:A:C8	2.54	0.42
1:1:1321:G:H2'	1:1:1322:U:O4'	2.20	0.42
1:1:1354:G:N7	23:R:26:ASN:HB2	2.35	0.42
1:1:2913:C:O2	1:1:3042:U:O2'	2.32	0.42
1:1:3100:U:HO2'	1:1:3101:G:H8	1.66	0.42
2:2:4:C:H2'	2:2:5:U:H6	1.84	0.42
6:A:246:ASN:OD1	6:A:249:ARG:NH2	2.42	0.42
27:W:26:ILE:HA	27:W:29:GLU:HG2	2.01	0.42
31:b:320:SER:OG	31:b:327:ASN:HB3	2.19	0.42
39:n:180:PHE:HE2	39:n:182:SER:HB3	1.84	0.42
42:r:189:LEU:HB2	42:r:191:VAL:HG12	2.01	0.42
47:x:243:ARG:HH21	47:x:260:GLY:CA	2.32	0.42
1:1:349:A:C4	2:2:24:G:H1'	2.54	0.42
1:1:541:U:H2'	1:1:542:G:C8	2.54	0.42
1:1:629:U:H2'	1:1:630:A:C8	2.54	0.42
1:1:1160:C:OP1	22:Q:2:GLY:N	2.53	0.42
1:1:3192:U:H2'	1:1:3193:C:C6	2.55	0.42
10:E:10:TYR:OH	23:R:106:HIS:ND1	2.38	0.42
14:I:45:ALA:O	14:I:62:ARG:NH1	2.43	0.42
21:P:33:ALA:O	21:P:36:ILE:HG22	2.20	0.42
1:1:142:C:P	39:n:104:ARG:HH22	2.42	0.42
1:1:226:C:H2'	1:1:227:G:O4'	2.19	0.42
1:1:1245:A:N7	1:1:1271:A:O2'	2.43	0.42
9:D:366:PRO:HB3	9:D:463:TYR:CE1	2.55	0.42
11:F:98:LYS:O	11:F:102:VAL:HG23	2.19	0.42
14:I:9:ASP:OD1	14:I:9:ASP:N	2.52	0.42
14:I:355:VAL:HG11	14:I:375:LEU:HD23	2.00	0.42
31:b:191:ASP:OD1	31:b:192:VAL:N	2.52	0.42
31:b:226:ASP:OD1	31:b:270:LEU:HB2	2.19	0.42
38:m:306:TYR:O	39:n:230:HIS:NE2	2.41	0.42
48:y:104:LEU:HA	48:y:107:VAL:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:6:A:H2'	1:1:7:C:O4'	2.19	0.42
1:1:2461:A:N3	1:1:2461:A:H2'	2.35	0.42
1:1:2475:G:H2'	1:1:2476:C:C6	2.55	0.42
1:1:3112:G:O6	1:1:3120:C:H5''	2.20	0.42
10:E:43:LEU:HD11	10:E:85:ILE:HG13	2.01	0.42
11:F:184:LEU:O	11:F:188:ILE:HG12	2.19	0.42
20:O:84:LEU:HD13	20:O:102:LEU:HD21	2.01	0.42
28:Y:86:THR:HG22	28:Y:96:PRO:HA	2.01	0.42
29:Z:51:MET:HE3	29:Z:51:MET:HB3	1.94	0.42
32:e:20:HIS:CG	32:e:42:VAL:HG21	2.55	0.42
1:1:129:U:H2'	1:1:130:A:C8	2.54	0.42
1:1:1124:U:O2'	1:1:1125:U:H6	2.03	0.42
1:1:1237:G:H1'	1:1:1263:A:H62	1.84	0.42
1:1:1242:G:H2'	1:1:1243:G:C8	2.55	0.42
1:1:2434:U:H5''	1:1:2435:G:H8	1.84	0.42
1:1:3320:A:H2'	1:1:3321:C:C6	2.55	0.42
2:2:6:U:H2'	2:2:7:U:H6	1.84	0.42
9:D:129:GLN:O	9:D:133:VAL:HG23	2.19	0.42
14:I:306:MET:HE3	14:I:333:VAL:HG11	2.01	0.42
16:K:91:THR:HG22	40:o:184:LEU:HD11	2.01	0.42
18:M:13:ARG:NH1	18:M:65:LEU:O	2.53	0.42
23:R:107:LYS:HA	23:R:107:LYS:HD3	1.76	0.42
25:T:187:ARG:HE	29:Z:204:ARG:NH1	2.17	0.42
29:Z:147:SER:OG	29:Z:196:ARG:NH2	2.53	0.42
31:b:55:GLU:HA	31:b:58:VAL:HG22	2.02	0.42
31:b:427:TRP:HB3	44:u:83:ARG:HH21	1.84	0.42
33:f:13:HIS:HA	33:f:30:ILE:HD13	2.02	0.42
47:x:140:ILE:CD1	47:x:165:LEU:HB3	2.49	0.42
47:x:177:SER:O	47:x:263:PHE:HA	2.20	0.42
1:1:75:G:H5''	17:L:58:VAL:HB	2.02	0.42
1:1:1132:C:H2'	1:1:1133:A:H8	1.85	0.42
1:1:1250:G:H2'	1:1:1251:A:C8	2.54	0.42
1:1:1353:U:H1'	23:R:39:THR:HG21	2.02	0.42
7:B:152:LYS:HZ3	7:B:189:SER:HA	1.85	0.42
12:G:186:LEU:HD23	12:G:186:LEU:HA	1.88	0.42
16:K:210:ARG:O	16:K:225:ASN:ND2	2.53	0.42
24:S:90:MET:HE1	24:S:114:HIS:NE2	2.35	0.42
28:Y:39:LEU:HD22	28:Y:43:TYR:HE2	1.85	0.42
29:Z:25:SER:HB2	29:Z:55:THR:HG22	2.02	0.42
38:m:387:ARG:CZ	39:n:137:ASN:HB3	2.50	0.42
39:n:39:LYS:NZ	39:n:120:GLU:OE1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:t:187:LEU:HD13	43:t:196:ILE:HD13	2.01	0.42
1:1:600:G:N7	1:1:604:G:N2	2.67	0.42
1:1:1221:A:O2'	1:1:1222:G:OP1	2.35	0.42
1:1:1288:U:H2'	1:1:1289:G:H8	1.84	0.42
1:1:1363:A:H2'	1:1:1364:C:O4'	2.19	0.42
1:1:2855:U:H2'	1:1:2856:G:C8	2.54	0.42
14:I:296:LEU:HD22	14:I:345:PHE:CD1	2.55	0.42
28:Y:56:VAL:HG21	28:Y:104:LEU:HD13	2.01	0.42
32:e:128:LEU:HD23	32:e:128:LEU:HA	1.92	0.42
41:q:489:ILE:HD11	41:q:525:VAL:HG13	2.02	0.42
1:1:294:U:P	19:N:15:GLN:HE22	2.41	0.41
1:1:389:A:OP1	21:P:18:ARG:NH1	2.52	0.41
1:1:945:C:H2'	1:1:946:U:H6	1.83	0.41
1:1:985:U:H2'	1:1:986:U:C6	2.55	0.41
1:1:2366:C:H2'	1:1:2367:A:H8	1.84	0.41
1:1:2609:A:H2'	1:1:2610:G:C8	2.55	0.41
1:1:2879:C:H2'	1:1:2880:U:C6	2.55	0.41
1:1:3090:U:H2'	1:1:3091:A:O4'	2.19	0.41
6:A:33:THR:O	6:A:59:SER:HA	2.19	0.41
14:I:205:PHE:CZ	14:I:217:VAL:HB	2.55	0.41
15:J:267:PRO:HG2	38:m:177:GLY:HA3	2.02	0.41
20:O:46:GLU:OE1	20:O:46:GLU:N	2.53	0.41
27:W:214:LYS:HB3	27:W:214:LYS:HE3	1.87	0.41
39:n:145:LEU:HD23	39:n:145:LEU:HA	1.93	0.41
40:o:184:LEU:HD23	40:o:184:LEU:H	1.84	0.41
46:w:181:TRP:CE2	46:w:214:LEU:HD13	2.54	0.41
47:x:48:ARG:O	47:x:52:LEU:HG	2.20	0.41
1:1:1447:G:H5'	21:P:65:SER:H	1.85	0.41
1:1:3297:U:H2'	1:1:3298:C:H6	1.83	0.41
1:1:3378:C:H5''	7:B:313:HIS:NE2	2.35	0.41
2:2:91:C:H2'	2:2:92:A:C8	2.55	0.41
5:8:346:LEU:HD23	5:8:346:LEU:HA	1.95	0.41
7:B:299:ASP:OD1	7:B:301:THR:HG22	2.19	0.41
8:C:141:ARG:HB3	8:C:176:SER:HB3	2.02	0.41
15:J:286:ASP:OD1	15:J:287:LYS:N	2.53	0.41
22:Q:71:LEU:HD13	22:Q:99:THR:HG21	2.01	0.41
29:Z:94:VAL:HB	29:Z:111:VAL:HB	2.01	0.41
36:j:46:SER:HB3	36:j:54:LYS:HZ3	1.84	0.41
41:q:425:SER:H	41:q:479:SER:HB2	1.84	0.41
44:u:8:PHE:CE2	44:u:49:LEU:HD12	2.55	0.41
46:w:169:ILE:HB	46:w:170:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:74:G:OP1	17:L:104:ARG:HD3	2.19	0.41
1:1:562:C:H2'	1:1:563:U:C6	2.54	0.41
1:1:966:U:C2	1:1:967:A:C8	3.08	0.41
1:1:1458:U:H2'	1:1:1459:C:C6	2.55	0.41
1:1:2831:G:H2'	1:1:2832:C:C6	2.55	0.41
1:1:2898:G:N7	42:r:7:ILE:HB	2.34	0.41
1:1:3069:G:N3	1:1:3069:G:H2'	2.35	0.41
3:6:32:A:O2'	16:K:285:ARG:NE	2.54	0.41
27:W:22:ASN:O	27:W:26:ILE:HG12	2.20	0.41
31:b:435:ILE:HD12	44:u:3:ILE:HD11	2.02	0.41
36:j:61:THR:HG23	45:v:4:VAL:HG11	2.03	0.41
38:m:284:ARG:HH22	45:v:180:ARG:HH22	1.67	0.41
40:o:93:ILE:HD13	40:o:93:ILE:HA	1.92	0.41
40:o:103:HIS:HA	40:o:122:LEU:HD22	2.01	0.41
41:q:244:PHE:CZ	41:q:248:LYS:HE3	2.54	0.41
46:w:73:HIS:CE1	46:w:128:VAL:HG13	2.55	0.41
48:y:72:VAL:HG21	48:y:81:LEU:HD13	2.03	0.41
1:1:29:C:H4'	1:1:62:A:H4'	2.02	0.41
1:1:3029:A:H8	1:1:3029:A:OP2	2.04	0.41
1:1:3181:C:O2'	20:O:164:SER:OG	2.32	0.41
3:6:30:U:H2'	3:6:31:G:O4'	2.21	0.41
10:E:52:VAL:CG1	10:E:65:ILE:HB	2.51	0.41
21:P:154:GLU:CD	21:P:154:GLU:H	2.27	0.41
29:Z:30:VAL:HB	29:Z:86:THR:HG22	2.02	0.41
31:b:434:GLU:N	31:b:434:GLU:OE1	2.54	0.41
39:n:128:ALA:O	39:n:132:ILE:HG23	2.20	0.41
44:u:47:ARG:HB2	44:u:47:ARG:NH1	2.35	0.41
1:1:107:A:OP1	17:L:39:ARG:NE	2.53	0.41
1:1:369:A:P	47:x:12:LYS:HD3	2.61	0.41
1:1:426:G:H2'	1:1:427:C:C6	2.55	0.41
1:1:631:U:H2'	1:1:632:G:H8	1.86	0.41
1:1:1458:U:H2'	1:1:1459:C:H6	1.85	0.41
1:1:3069:G:H1	29:Z:354:HIS:CG	2.37	0.41
1:1:3259:U:H1'	18:M:125:LYS:HZ2	1.86	0.41
5:8:339:LYS:HE2	5:8:341:ARG:HD3	2.01	0.41
9:D:363:GLN:HG3	9:D:373:TYR:CE1	2.56	0.41
15:J:273:ASP:OD2	38:m:170:HIS:NE2	2.49	0.41
19:N:23:GLN:HG3	19:N:122:ASN:OD1	2.20	0.41
19:N:182:ASN:OD1	19:N:183:THR:HG23	2.20	0.41
31:b:94:SER:O	31:b:98:ILE:HG12	2.20	0.41
34:h:92:LEU:HG	34:h:96:GLU:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:o:193:VAL:HG12	40:o:197:LYS:NZ	2.36	0.41
45:v:207:ILE:HG13	45:v:208:TYR:H	1.86	0.41
46:w:181:TRP:HZ3	46:w:212:THR:HB	1.85	0.41
47:x:140:ILE:HD11	47:x:165:LEU:HB3	2.03	0.41
1:1:100:A:H2'	1:1:101:G:N3	2.36	0.41
1:1:712:G:H22	1:1:754:G:H5''	1.85	0.41
1:1:1259:A:H1'	1:1:1280:C:O2'	2.20	0.41
2:2:36:G:O2'	2:2:104:A:N1	2.50	0.41
5:8:330:LYS:HG3	5:8:340:ILE:HD11	2.03	0.41
6:A:143:PHE:HA	6:A:149:TYR:HB3	2.02	0.41
7:B:87:VAL:HB	7:B:110:LEU:HD22	2.02	0.41
14:I:296:LEU:HB3	14:I:345:PHE:CZ	2.56	0.41
20:O:121:PRO:HA	20:O:124:LEU:HD12	2.02	0.41
22:Q:90:ASP:OD1	22:Q:92:ARG:HB2	2.21	0.41
26:V:118:VAL:O	26:V:137:VAL:N	2.51	0.41
27:W:134:THR:HG23	27:W:190:THR:HA	2.03	0.41
31:b:402:ILE:O	31:b:406:ASN:ND2	2.30	0.41
34:h:8:GLU:O	34:h:11:THR:OG1	2.34	0.41
48:y:75:GLN:OE1	48:y:75:GLN:N	2.53	0.41
1:1:568:G:H2'	1:1:569:A:O4'	2.21	0.41
1:1:972:A:H2'	1:1:973:A:C8	2.55	0.41
1:1:1459:C:H2'	1:1:1460:A:C8	2.56	0.41
1:1:3002:C:H2'	1:1:3003:G:O4'	2.21	0.41
9:D:194:ILE:HG23	9:D:225:MET:HB2	2.02	0.41
10:E:46:ARG:HD3	10:E:47:PHE:CZ	2.55	0.41
13:H:45:PHE:CD1	13:H:55:VAL:HG12	2.55	0.41
14:I:412:ASP:OD1	14:I:412:ASP:N	2.54	0.41
17:L:90:ALA:HA	17:L:93:ILE:HG22	2.03	0.41
21:P:56:ARG:NH1	21:P:75:GLU:OE2	2.52	0.41
31:b:263:THR:O	31:b:266:ALA:N	2.53	0.41
31:b:390:PRO:O	31:b:395:ARG:NH1	2.53	0.41
31:b:421:LEU:O	44:u:80:ARG:HD2	2.21	0.41
38:m:275:ARG:O	38:m:279:ILE:HG13	2.21	0.41
39:n:428:GLN:HG3	39:n:453:LEU:HD11	2.03	0.41
41:q:434:GLN:O	41:q:437:LYS:HG2	2.21	0.41
48:y:19:LEU:HB3	48:y:198:VAL:HB	2.02	0.41
1:1:137:G:H2'	1:1:138:U:H6	1.86	0.41
1:1:179:C:H2'	1:1:180:C:H6	1.86	0.41
1:1:421:G:H5'	1:1:421:G:N3	2.36	0.41
1:1:1271:A:H3'	1:1:1272:C:H5''	2.03	0.41
1:1:1281:G:H2'	1:1:1282:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2454:G:C8	41:q:516:TYR:HA	2.56	0.41
8:C:62:ALA:HB3	8:C:90:PHE:CE2	2.55	0.41
9:D:286:ARG:HE	9:D:421:LYS:HE2	1.86	0.41
12:G:162:LEU:HA	19:N:7:LEU:HD21	2.03	0.41
17:L:93:ILE:HD12	17:L:93:ILE:HA	1.89	0.41
20:O:170:LYS:HE2	20:O:170:LYS:HB3	1.87	0.41
25:T:181:GLU:O	25:T:184:THR:OG1	2.38	0.41
38:m:310:LEU:HD13	39:n:119:LYS:HG2	2.03	0.41
46:w:58:ARG:HB3	46:w:59:PRO:HD2	2.03	0.41
46:w:157:LEU:HD12	46:w:157:LEU:HA	1.82	0.41
47:x:39:LYS:HG2	47:x:42:ARG:HH21	1.85	0.41
1:1:56:G:O3'	19:N:158:HIS:ND1	2.52	0.41
1:1:240:U:H4'	1:1:241:G:H5'	2.02	0.41
1:1:268:A:C5	19:N:12:ARG:HD2	2.55	0.41
1:1:294:U:OP1	35:i:76:ARG:NH1	2.53	0.41
1:1:377:A:H1'	1:1:392:G:N2	2.36	0.41
1:1:462:C:H2'	1:1:463:C:O4'	2.21	0.41
1:1:793:C:H2'	1:1:794:U:O4'	2.21	0.41
1:1:928:C:H2'	1:1:929:A:C8	2.56	0.41
1:1:1152:G:C6	1:1:1197:A:C4	3.09	0.41
1:1:1250:G:H2'	1:1:1251:A:H8	1.86	0.41
1:1:1349:G:H2'	11:F:15:LYS:HB2	2.02	0.41
1:1:3023:U:H2'	1:1:3024:A:H8	1.86	0.41
1:1:3041:U:H2'	1:1:3042:U:H6	1.86	0.41
1:1:3275:U:H5'	1:1:3276:G:C8	2.56	0.41
1:1:3307:A:C6	1:1:3308:C:H5	2.39	0.41
8:C:63:GLU:N	8:C:63:GLU:OE1	2.54	0.41
13:H:41:ILE:HG22	13:H:43:VAL:HG13	2.02	0.41
16:K:102:VAL:HB	16:K:262:ASN:ND2	2.36	0.41
18:M:25:LYS:HE3	18:M:62:GLN:HG2	2.03	0.41
26:V:75:PRO:HG2	26:V:103:ALA:O	2.21	0.41
27:W:69:LYS:O	27:W:73:LEU:HG	2.21	0.41
28:Y:34:PRO:HD2	28:Y:104:LEU:O	2.21	0.41
31:b:69:PRO:O	31:b:91:TYR:OH	2.35	0.41
34:h:12:LYS:NZ	34:h:20:GLN:OE1	2.50	0.41
37:l:42:ASP:HB3	37:l:73:PHE:HB2	2.02	0.41
38:m:133:ASP:OD1	38:m:133:ASP:O	2.39	0.41
41:q:380:LYS:O	41:q:383:THR:OG1	2.34	0.41
43:t:144:ILE:O	43:t:174:GLY:HA2	2.21	0.41
43:t:197:GLY:HA2	43:t:311:GLU:HG2	2.02	0.41
44:u:50:LYS:HG3	44:u:55:PHE:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:v:53:LEU:HD22	45:v:158:VAL:HG21	2.03	0.41
1:1:26:A:H2'	1:1:27:C:C6	2.56	0.41
1:1:120:G:C5	12:G:128:LYS:HB3	2.56	0.41
1:1:210:U:C2	1:1:230:U:H4'	2.56	0.41
1:1:239:G:H2'	1:1:240:U:C6	2.56	0.41
1:1:257:U:H2'	1:1:258:G:C8	2.56	0.41
1:1:527:A:H2'	1:1:528:U:C6	2.56	0.41
1:1:803:C:H2'	1:1:804:C:C6	2.56	0.41
1:1:3393:U:H2'	1:1:3394:U:H6	1.84	0.41
8:C:138:ARG:HH21	8:C:240:PRO:CG	2.32	0.41
8:C:144:LYS:HA	8:C:144:LYS:HD3	1.94	0.41
11:F:120:THR:O	11:F:124:LEU:HG	2.21	0.41
13:H:81:GLY:HA3	13:H:149:ASN:O	2.21	0.41
20:O:54:TYR:CD1	20:O:141:LEU:HD21	2.56	0.41
29:Z:52:GLN:NE2	29:Z:57:ILE:HD13	2.36	0.41
29:Z:134:ASP:HB3	29:Z:188:ARG:HD3	2.02	0.41
31:b:316:GLU:N	31:b:316:GLU:OE1	2.54	0.41
32:e:102:ALA:O	32:e:106:VAL:HG23	2.20	0.41
42:r:35:ILE:HG21	42:r:54:ARG:HH21	1.86	0.41
43:t:132:LYS:HE3	43:t:308:PRO:HG3	2.04	0.41
45:v:208:TYR:O	45:v:210:GLN:HG3	2.21	0.41
46:w:40:ILE:HG13	46:w:44:LYS:HE3	2.03	0.41
46:w:46:TRP:CE2	46:w:102:PHE:HB2	2.55	0.41
1:1:58:G:H4'	19:N:155:VAL:HG12	2.03	0.40
1:1:155:G:H22	9:D:155:ARG:NH2	2.20	0.40
1:1:981:U:O2'	1:1:1105:A:O2'	2.26	0.40
1:1:1170:A:H2'	1:1:1171:G:O4'	2.21	0.40
1:1:2923:U:H2'	1:1:2924:U:C6	2.56	0.40
2:2:9:A:H2'	2:2:10:A:H8	1.83	0.40
2:2:63:G:N3	2:2:63:G:H2'	2.36	0.40
3:6:53:A:N6	16:K:165:LYS:O	2.46	0.40
6:A:139:PHE:CD2	6:A:153:LYS:HG3	2.56	0.40
7:B:80:ASP:HB2	7:B:317:ILE:HD12	2.03	0.40
14:I:4:LEU:HB2	14:I:408:VAL:CG2	2.51	0.40
14:I:216:LEU:HG	14:I:230:TRP:CE3	2.56	0.40
16:K:229:VAL:HA	16:K:233:GLN:HB2	2.03	0.40
21:P:33:ALA:HB1	21:P:117:ILE:HG12	2.03	0.40
23:R:68:GLU:HG2	46:w:56:SER:O	2.20	0.40
30:a:28:PHE:HD2	30:a:30:GLU:HG2	1.86	0.40
31:b:14:ALA:HB2	31:b:144:ARG:HA	2.03	0.40
31:b:80:ASP:HB3	31:b:241:TYR:CG	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:m:384:ILE:H	38:m:384:ILE:HG12	1.67	0.40
39:n:135:ALA:HA	39:n:225:TYR:CD2	2.56	0.40
45:v:189:TYR:HB2	45:v:219:LEU:HD21	2.02	0.40
1:1:14:U:H3	2:2:136:G:H21	1.69	0.40
1:1:1213:G:OP1	24:S:139:TYR:OH	2.28	0.40
6:A:116:ASN:HB2	6:A:220:VAL:HG23	2.02	0.40
8:C:285:ASP:O	8:C:289:ILE:HG12	2.20	0.40
14:I:247:TRP:CD2	14:I:275:ARG:HD3	2.56	0.40
14:I:275:ARG:O	14:I:275:ARG:CG	2.68	0.40
29:Z:109:PHE:HB3	29:Z:337:LEU:HB3	2.03	0.40
30:a:116:LEU:HB3	30:a:120:VAL:HG23	2.03	0.40
31:b:421:LEU:HD13	31:b:421:LEU:HA	1.93	0.40
44:u:23:ARG:HH21	44:u:27:LYS:HD2	1.85	0.40
46:w:167:THR:HG23	46:w:234:LEU:HB2	2.03	0.40
1:1:550:A:H2'	1:1:551:A:C8	2.56	0.40
1:1:689:U:O4	8:C:209:TYR:OH	2.22	0.40
1:1:1107:C:H2'	1:1:1108:U:H6	1.86	0.40
1:1:1891:A:H2'	1:1:1892:G:C8	2.57	0.40
1:1:3103:A:H2'	1:1:3104:U:O4'	2.21	0.40
1:1:3120:C:OP1	42:r:26:LYS:HE2	2.21	0.40
13:H:70:THR:O	13:H:74:LEU:HG	2.22	0.40
14:I:138:ASP:OD1	14:I:139:GLY:N	2.54	0.40
14:I:212:ASN:OD1	14:I:215:LYS:NZ	2.38	0.40
16:K:78:LEU:HD23	16:K:259:PHE:CE1	2.55	0.40
22:Q:65:SER:HA	22:Q:93:ILE:HD13	2.03	0.40
31:b:33:ILE:HG12	31:b:45:PHE:CD1	2.56	0.40
41:q:345:GLU:HA	41:q:370:THR:HG21	2.03	0.40
41:q:390:ILE:HD13	41:q:390:ILE:HA	1.88	0.40
43:t:312:VAL:HG22	43:t:313:ASP:H	1.87	0.40
44:u:1:MET:N	48:y:79:GLN:OE1	2.55	0.40
1:1:209:A:H4'	1:1:211:A:N7	2.37	0.40
1:1:673:U:OP1	22:Q:21:SER:OG	2.34	0.40
1:1:1176:C:OP2	1:1:1177:G:O2'	2.32	0.40
1:1:1204:A:H2'	1:1:1205:A:O4'	2.22	0.40
1:1:2805:G:H2'	1:1:2806:U:O4'	2.20	0.40
1:1:2855:U:H2'	1:1:2856:G:H8	1.86	0.40
1:1:2949:U:H2'	1:1:2950:G:C8	2.56	0.40
1:1:2960:C:N4	1:1:2961:G:O6	2.54	0.40
1:1:3070:A:H5''	1:1:3072:C:N4	2.36	0.40
1:1:3096:C:H2'	1:1:3097:C:C6	2.57	0.40
8:C:285:ASP:HB3	8:C:288:ARG:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:84:VAL:O	33:f:105:SER:OG	2.32	0.40
11:F:189:ILE:HG23	11:F:190:THR:HG23	2.04	0.40
13:H:92:TYR:HB3	13:H:179:ILE:HG23	2.03	0.40
37:l:95:TYR:HD1	37:l:125:ILE:HG12	1.87	0.40
39:n:99:VAL:HG12	39:n:103:LYS:HE2	2.02	0.40
43:t:74:ARG:HG3	43:t:303:ASN:HA	2.03	0.40
46:w:231:SER:O	46:w:235:ARG:HG3	2.21	0.40
48:y:62:MET:O	48:y:73:PRO:HD3	2.22	0.40
1:1:82:C:H2'	1:1:83:U:O4'	2.21	0.40
1:1:313:A:H2'	1:1:314:U:O4'	2.21	0.40
1:1:1174:G:H1'	1:1:1181:U:N3	2.36	0.40
1:1:2382:G:H2'	1:1:2383:C:C6	2.56	0.40
1:1:2462:A:H4'	41:q:520:LYS:HE2	2.04	0.40
1:1:2495:C:H2'	1:1:2496:C:H6	1.83	0.40
1:1:2900:A:H62	31:b:6:LYS:NZ	2.20	0.40
1:1:3108:G:O2'	13:H:166:ARG:NH2	2.55	0.40
1:1:3212:C:OP2	18:M:124:ARG:NH2	2.55	0.40
8:C:138:ARG:HB2	8:C:244:LEU:O	2.20	0.40
29:Z:25:SER:OG	29:Z:81:HIS:HB2	2.22	0.40
33:f:16:TYR:CG	33:f:25:PRO:HA	2.57	0.40
42:r:208:MET:HE3	42:r:208:MET:HB3	1.91	0.40
45:v:46:MET:HE3	45:v:46:MET:HB2	1.82	0.40
47:x:104:LYS:HB2	47:x:152:GLU:OE2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	7	9/204 (4%)	9 (100%)	0	0	100	100
5	8	139/434 (32%)	137 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	251/291 (86%)	245 (98%)	6 (2%)	0	100	100
7	B	327/387 (84%)	320 (98%)	7 (2%)	0	100	100
8	C	341/362 (94%)	334 (98%)	7 (2%)	0	100	100
9	D	417/505 (83%)	408 (98%)	9 (2%)	0	100	100
10	E	147/176 (84%)	144 (98%)	3 (2%)	0	100	100
11	F	239/244 (98%)	236 (99%)	3 (1%)	0	100	100
12	G	162/256 (63%)	153 (94%)	9 (6%)	0	100	100
13	H	187/191 (98%)	184 (98%)	3 (2%)	0	100	100
14	I	390/463 (84%)	384 (98%)	6 (2%)	0	100	100
15	J	149/427 (35%)	147 (99%)	2 (1%)	0	100	100
16	K	262/376 (70%)	253 (97%)	9 (3%)	0	100	100
17	L	108/199 (54%)	106 (98%)	2 (2%)	0	100	100
18	M	132/138 (96%)	129 (98%)	3 (2%)	0	100	100
19	N	173/204 (85%)	172 (99%)	1 (1%)	0	100	100
20	O	184/199 (92%)	182 (99%)	2 (1%)	0	100	100
21	P	133/184 (72%)	129 (97%)	4 (3%)	0	100	100
22	Q	142/186 (76%)	142 (100%)	0	0	100	100
23	R	188/306 (61%)	186 (99%)	2 (1%)	0	100	100
24	S	168/172 (98%)	163 (97%)	5 (3%)	0	100	100
25	T	77/250 (31%)	76 (99%)	1 (1%)	0	100	100
26	V	110/137 (80%)	109 (99%)	1 (1%)	0	100	100
27	W	230/236 (98%)	221 (96%)	9 (4%)	0	100	100
28	Y	123/127 (97%)	121 (98%)	2 (2%)	0	100	100
29	Z	247/453 (54%)	243 (98%)	4 (2%)	0	100	100
30	a	208/217 (96%)	197 (95%)	11 (5%)	0	100	100
31	b	417/647 (64%)	404 (97%)	13 (3%)	0	100	100
32	e	124/130 (95%)	122 (98%)	2 (2%)	0	100	100
33	f	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
34	h	117/120 (98%)	116 (99%)	1 (1%)	0	100	100
35	i	82/100 (82%)	79 (96%)	3 (4%)	0	100	100
36	j	70/88 (80%)	67 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	l	174/181 (96%)	171 (98%)	3 (2%)	0	100	100
38	m	205/807 (25%)	201 (98%)	4 (2%)	0	100	100
39	n	329/605 (54%)	319 (97%)	10 (3%)	0	100	100
40	o	131/220 (60%)	126 (96%)	5 (4%)	0	100	100
41	q	356/618 (58%)	349 (98%)	7 (2%)	0	100	100
42	r	174/261 (67%)	171 (98%)	3 (2%)	0	100	100
43	t	245/322 (76%)	240 (98%)	5 (2%)	0	100	100
44	u	110/199 (55%)	108 (98%)	2 (2%)	0	100	100
45	v	145/231 (63%)	140 (97%)	5 (3%)	0	100	100
46	w	239/278 (86%)	232 (97%)	7 (3%)	0	100	100
47	x	275/295 (93%)	264 (96%)	11 (4%)	0	100	100
48	y	223/245 (91%)	211 (95%)	12 (5%)	0	100	100
All	All	8763/12778 (69%)	8552 (98%)	211 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	
4	7	11/181 (6%)	11 (100%)	0	100	100
5	8	128/388 (33%)	128 (100%)	0	100	100
6	A	232/263 (88%)	231 (100%)	1 (0%)	84	92
7	B	278/323 (86%)	276 (99%)	2 (1%)	76	89
8	C	273/289 (94%)	272 (100%)	1 (0%)	84	92
9	D	371/440 (84%)	371 (100%)	0	100	100
10	E	131/153 (86%)	130 (99%)	1 (1%)	73	88
11	F	204/205 (100%)	204 (100%)	0	100	100
12	G	133/208 (64%)	131 (98%)	2 (2%)	57	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	H	169/171 (99%)	169 (100%)	0	100	100
14	I	352/410 (86%)	352 (100%)	0	100	100
15	J	139/383 (36%)	138 (99%)	1 (1%)	76	89
16	K	247/346 (71%)	246 (100%)	1 (0%)	84	92
17	L	89/159 (56%)	88 (99%)	1 (1%)	65	83
18	M	106/109 (97%)	106 (100%)	0	100	100
19	N	153/176 (87%)	150 (98%)	3 (2%)	48	73
20	O	153/162 (94%)	149 (97%)	4 (3%)	40	66
21	P	109/146 (75%)	107 (98%)	2 (2%)	51	75
22	Q	118/151 (78%)	114 (97%)	4 (3%)	32	57
23	R	171/274 (62%)	171 (100%)	0	100	100
24	S	155/156 (99%)	154 (99%)	1 (1%)	78	90
25	T	69/219 (32%)	68 (99%)	1 (1%)	59	80
26	V	88/105 (84%)	88 (100%)	0	100	100
27	W	209/213 (98%)	207 (99%)	2 (1%)	68	85
28	Y	108/110 (98%)	106 (98%)	2 (2%)	50	74
29	Z	234/413 (57%)	233 (100%)	1 (0%)	84	92
30	a	191/198 (96%)	190 (100%)	1 (0%)	81	91
31	b	380/573 (66%)	373 (98%)	7 (2%)	51	75
32	e	109/111 (98%)	108 (99%)	1 (1%)	70	86
33	f	90/91 (99%)	89 (99%)	1 (1%)	65	83
34	h	104/105 (99%)	102 (98%)	2 (2%)	50	74
35	i	70/82 (85%)	70 (100%)	0	100	100
36	j	59/71 (83%)	58 (98%)	1 (2%)	53	77
37	l	151/156 (97%)	150 (99%)	1 (1%)	76	89
38	m	193/723 (27%)	191 (99%)	2 (1%)	68	85
39	n	305/548 (56%)	301 (99%)	4 (1%)	61	81
40	o	118/199 (59%)	116 (98%)	2 (2%)	53	77
41	q	304/535 (57%)	303 (100%)	1 (0%)	86	94
42	r	163/229 (71%)	162 (99%)	1 (1%)	78	90
43	t	220/287 (77%)	217 (99%)	3 (1%)	59	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	u	98/180 (54%)	96 (98%)	2 (2%)	48	73
45	v	134/205 (65%)	130 (97%)	4 (3%)	36	62
46	w	225/257 (88%)	223 (99%)	2 (1%)	70	86
47	x	263/276 (95%)	258 (98%)	5 (2%)	50	74
48	y	193/211 (92%)	192 (100%)	1 (0%)	81	91
All	All	7800/11190 (70%)	7729 (99%)	71 (1%)	68	86

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	A	220	VAL
7	B	124	LYS
7	B	322	ILE
8	C	58	HIS
10	E	26	ARG
12	G	190	VAL
12	G	215	VAL
15	J	228	ASN
16	K	74	LEU
17	L	85	LEU
19	N	10	LEU
19	N	64	VAL
19	N	117	ASN
20	O	33	ILE
20	O	55	HIS
20	O	84	LEU
20	O	117	ARG
21	P	36	ILE
21	P	107	LEU
22	Q	9	GLN
22	Q	64	VAL
22	Q	92	ARG
22	Q	95	GLU
24	S	172	TYR
25	T	232	VAL
27	W	173	THR
27	W	208	ILE
28	Y	70	ILE
28	Y	105	VAL
29	Z	339	LEU

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Mol	Chain	Res	Type
30	a	101	LYS
31	b	3	LEU
31	b	33	ILE
31	b	86	TYR
31	b	88	LYS
31	b	193	ASP
31	b	194	VAL
31	b	398	LEU
32	e	31	ASN
33	f	49	ILE
34	h	92	LEU
34	h	100	VAL
36	j	75	LYS
37	l	56	THR
38	m	309	ASP
38	m	384	ILE
39	n	115	ASP
39	n	141	LEU
39	n	179	VAL
39	n	387	VAL
40	o	102	PHE
40	o	167	LEU
41	q	477	THR
42	r	194	PHE
43	t	128	LEU
43	t	136	ASP
43	t	182	ASN
44	u	22	VAL
44	u	62	GLU
45	v	28	ILE
45	v	61	THR
45	v	175	ARG
45	v	219	LEU
46	w	69	LEU
46	w	90	THR
47	x	65	VAL
47	x	160	LEU
47	x	187	HIS
47	x	208	GLN
47	x	258	GLU
48	y	97	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29)

such sidechains are listed below:

Mol	Chain	Res	Type
5	8	309	ASN
5	8	393	ASN
7	B	182	GLN
7	B	211	GLN
7	B	319	ASN
9	D	320	HIS
11	F	112	ASN
11	F	146	GLN
11	F	209	ASN
13	H	157	ASN
15	J	197	ASN
15	J	221	GLN
19	N	138	GLN
22	Q	136	ASN
23	R	17	HIS
27	W	22	ASN
27	W	91	GLN
29	Z	171	ASN
30	a	27	ASN
31	b	124	GLN
31	b	267	GLN
32	e	49	ASN
37	l	117	HIS
39	n	386	ASN
42	r	13	GLN
45	v	31	GLN
48	y	6	GLN
48	y	11	ASN
48	y	111	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1993/3396 (58%)	396 (19%)	5 (0%)
2	2	147/158 (93%)	28 (19%)	0
3	6	54/232 (23%)	19 (35%)	0
All	All	2194/3786 (57%)	443 (20%)	5 (0%)

All (443) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	5	G
1	1	48	A
1	1	49	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	74	G
1	1	92	G
1	1	109	A
1	1	110	G
1	1	111	C
1	1	117	U
1	1	122	A
1	1	135	C
1	1	136	G
1	1	155	G
1	1	165	A
1	1	166	C
1	1	187	A
1	1	188	U
1	1	189	G
1	1	190	U
1	1	191	U
1	1	200	C
1	1	210	U
1	1	218	G
1	1	219	A
1	1	220	G
1	1	221	A
1	1	237	G
1	1	241	G
1	1	243	G
1	1	251	G
1	1	252	U
1	1	255	A
1	1	265	A
1	1	266	A
1	1	268	A
1	1	269	G
1	1	295	A
1	1	307	A

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Mol	Chain	Res	Type
1	1	308	A
1	1	309	U
1	1	310	U
1	1	311	C
1	1	312	C
1	1	323	A
1	1	329	U
1	1	352	A
1	1	370	U
1	1	376	G
1	1	384	A
1	1	385	A
1	1	386	A
1	1	387	A
1	1	391	A
1	1	399	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	420	G
1	1	421	G
1	1	439	C
1	1	440	A
1	1	442	G
1	1	451	U
1	1	459	G
1	1	463	C
1	1	465	U
1	1	466	G
1	1	468	G
1	1	478	A
1	1	480	C
1	1	481	U
1	1	482	C
1	1	494	G
1	1	495	G
1	1	510	G
1	1	521	A
1	1	523	A
1	1	533	A
1	1	535	G
1	1	536	U

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Mol	Chain	Res	Type
1	1	542	G
1	1	543	C
1	1	544	C
1	1	545	U
1	1	546	C
1	1	547	G
1	1	550	A
1	1	551	A
1	1	555	U
1	1	557	A
1	1	559	A
1	1	569	A
1	1	572	A
1	1	579	G
1	1	582	G
1	1	589	A
1	1	592	A
1	1	604	G
1	1	611	A
1	1	612	U
1	1	621	A
1	1	625	G
1	1	637	C
1	1	645	A
1	1	646	A
1	1	647	A
1	1	660	A
1	1	677	A
1	1	681	U
1	1	691	A
1	1	705	A
1	1	716	A
1	1	717	C
1	1	718	G
1	1	721	G
1	1	722	G
1	1	737	G
1	1	757	C
1	1	772	U
1	1	777	U
1	1	780	A
1	1	781	G

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Mol	Chain	Res	Type
1	1	783	A
1	1	784	A
1	1	785	G
1	1	817	A
1	1	818	C
1	1	820	A
1	1	822	G
1	1	826	G
1	1	827	A
1	1	908	G
1	1	909	G
1	1	910	G
1	1	918	C
1	1	936	A
1	1	944	C
1	1	959	C
1	1	960	U
1	1	961	C
1	1	962	A
1	1	963	G
1	1	979	U
1	1	980	A
1	1	982	C
1	1	985	U
1	1	1103	A
1	1	1111	U
1	1	1112	A
1	1	1116	G
1	1	1117	G
1	1	1125	U
1	1	1127	G
1	1	1129	A
1	1	1131	G
1	1	1132	C
1	1	1150	A
1	1	1160	C
1	1	1180	A
1	1	1181	U
1	1	1191	U
1	1	1197	A
1	1	1198	C
1	1	1199	C

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Mol	Chain	Res	Type
1	1	1202	A
1	1	1203	A
1	1	1204	A
1	1	1213	G
1	1	1220	U
1	1	1221	A
1	1	1222	G
1	1	1232	C
1	1	1235	U
1	1	1242	G
1	1	1245	A
1	1	1254	C
1	1	1258	U
1	1	1259	A
1	1	1262	G
1	1	1263	A
1	1	1265	U
1	1	1271	A
1	1	1272	C
1	1	1278	A
1	1	1286	A
1	1	1287	A
1	1	1301	A
1	1	1302	A
1	1	1304	A
1	1	1305	U
1	1	1308	A
1	1	1309	U
1	1	1331	U
1	1	1345	G
1	1	1348	U
1	1	1349	G
1	1	1350	A
1	1	1352	A
1	1	1353	U
1	1	1354	G
1	1	1355	A
1	1	1386	A
1	1	1399	A
1	1	1400	G
1	1	1417	G
1	1	1419	A

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Mol	Chain	Res	Type
1	1	1431	G
1	1	1434	G
1	1	1437	C
1	1	1452	A
1	1	1455	U
1	1	1464	G
1	1	1864	A
1	1	1866	C
1	1	1867	A
1	1	1868	G
1	1	1874	A
1	1	1875	G
1	1	1881	A
1	1	1884	A
1	1	1886	A
1	1	1887	A
1	1	1893	A
1	1	2347	U
1	1	2371	G
1	1	2372	A
1	1	2373	A
1	1	2374	C
1	1	2375	G
1	1	2385	G
1	1	2386	A
1	1	2388	U
1	1	2393	G
1	1	2394	G
1	1	2414	G
1	1	2416	U
1	1	2419	A
1	1	2420	C
1	1	2421	U
1	1	2427	U
1	1	2433	U
1	1	2434	U
1	1	2435	G
1	1	2436	U
1	1	2437	G
1	1	2438	A
1	1	2445	A
1	1	2447	A

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Mol	Chain	Res	Type
1	1	2448	G
1	1	2453	U
1	1	2461	A
1	1	2468	A
1	1	2473	C
1	1	2474	G
1	1	2475	G
1	1	2487	U
1	1	2491	A
1	1	2497	U
1	1	2501	U
1	1	2596	U
1	1	2600	C
1	1	2602	G
1	1	2603	G
1	1	2606	G
1	1	2610	G
1	1	2611	U
1	1	2817	A
1	1	2819	A
1	1	2822	U
1	1	2824	G
1	1	2825	C
1	1	2826	U
1	1	2838	A
1	1	2841	G
1	1	2844	C
1	1	2845	A
1	1	2847	A
1	1	2866	U
1	1	2867	C
1	1	2868	U
1	1	2883	U
1	1	2884	C
1	1	2888	U
1	1	2890	A
1	1	2898	G
1	1	2899	C
1	1	2914	G
1	1	2915	U
1	1	2916	U
1	1	2920	U

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Mol	Chain	Res	Type
1	1	2921	U
1	1	2922	G
1	1	2927	C
1	1	2944	U
1	1	2952	G
1	1	2961	G
1	1	2964	G
1	1	2967	A
1	1	2968	G
1	1	2970	C
1	1	2971	A
1	1	2991	A
1	1	2998	U
1	1	3011	A
1	1	3012	A
1	1	3019	U
1	1	3021	A
1	1	3022	G
1	1	3029	A
1	1	3030	G
1	1	3032	A
1	1	3049	A
1	1	3054	U
1	1	3068	U
1	1	3069	G
1	1	3071	U
1	1	3075	G
1	1	3076	C
1	1	3077	A
1	1	3078	U
1	1	3079	U
1	1	3080	G
1	1	3085	G
1	1	3092	C
1	1	3099	C
1	1	3100	U
1	1	3101	G
1	1	3109	G
1	1	3122	A
1	1	3129	A
1	1	3130	A
1	1	3141	A

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Mol	Chain	Res	Type
1	1	3142	A
1	1	3143	C
1	1	3144	G
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3179	U
1	1	3181	C
1	1	3187	A
1	1	3195	U
1	1	3196	U
1	1	3198	U
1	1	3207	U
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3229	G
1	1	3239	G
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3256	G
1	1	3259	U
1	1	3273	A
1	1	3275	U
1	1	3276	G
1	1	3286	G
1	1	3292	A
1	1	3293	U
1	1	3303	G
1	1	3304	U
1	1	3309	G
1	1	3316	A
1	1	3317	U
1	1	3319	U
1	1	3339	A
1	1	3341	U
1	1	3345	G
1	1	3346	U
1	1	3347	A
1	1	3350	C
1	1	3352	U

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Mol	Chain	Res	Type
1	1	3353	G
1	1	3354	U
1	1	3355	U
1	1	3356	G
1	1	3359	A
1	1	3363	U
1	1	3366	G
1	1	3367	C
1	1	3369	G
1	1	3376	A
1	1	3378	C
1	1	3382	U
1	1	3387	U
1	1	3388	C
1	1	3389	U
1	1	3391	A
1	1	3396	U
2	2	13	A
2	2	23	U
2	2	34	U
2	2	35	C
2	2	49	G
2	2	51	G
2	2	59	A
2	2	62	C
2	2	63	G
2	2	75	G
2	2	79	A
2	2	80	A
2	2	81	U
2	2	82	U
2	2	83	C
2	2	86	U
2	2	87	G
2	2	90	U
2	2	95	G
2	2	104	A
2	2	106	C
2	2	115	C
2	2	116	G
2	2	123	G
2	2	135	G

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Mol	Chain	Res	Type
2	2	151	C
2	2	152	G
2	2	158	U
3	6	4	U
3	6	5	C
3	6	6	U
3	6	7	C
3	6	24	A
3	6	33	U
3	6	37	C
3	6	43	A
3	6	47	A
3	6	48	A
3	6	49	C
3	6	52	G
3	6	54	A
3	6	56	U
3	6	58	G
3	6	59	C
3	6	228	U
3	6	229	U
3	6	231	A

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1886	A
1	1	2420	C
1	1	2889	C
1	1	3121	U
1	1	3386	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

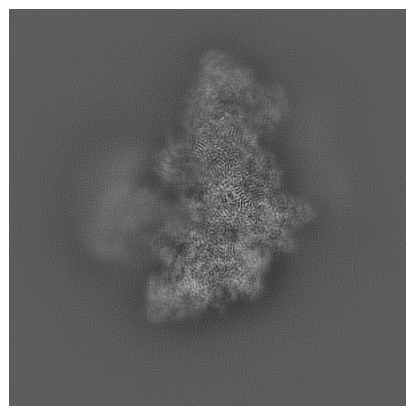
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43017. These allow visual inspection of the internal detail of the map and identification of artifacts.

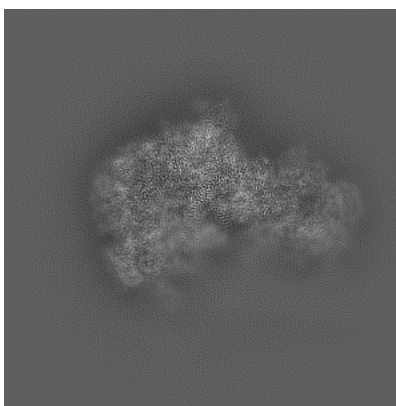
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

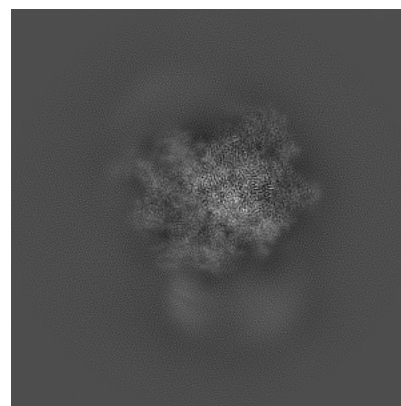
6.1.1 Primary map



X

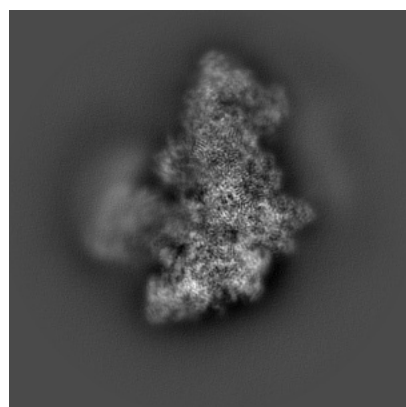


Y

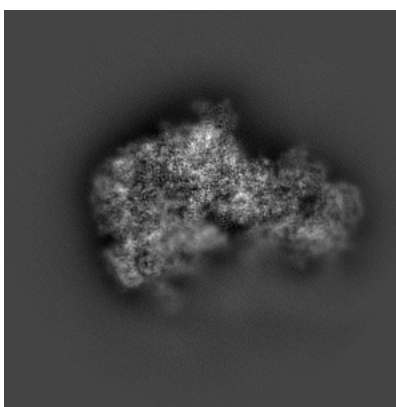


Z

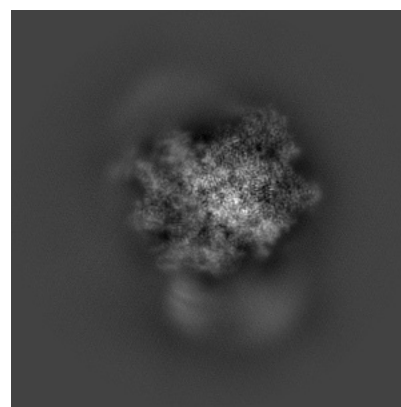
6.1.2 Raw map



X



Y

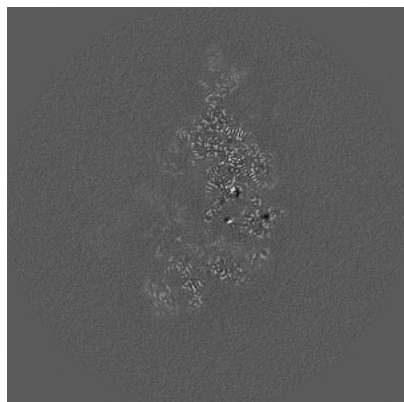


Z

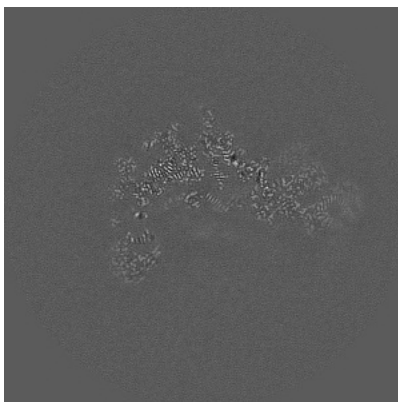
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

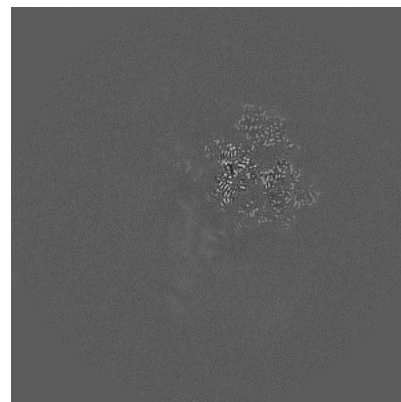
6.2.1 Primary map



X Index: 210

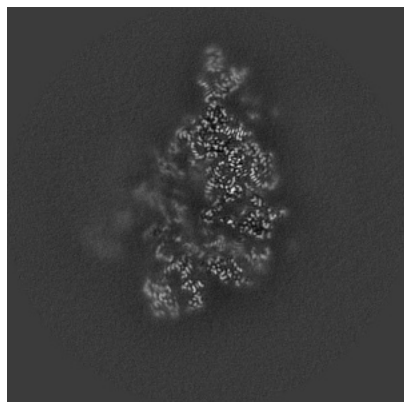


Y Index: 210

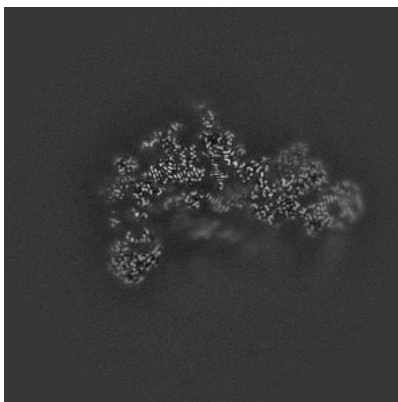


Z Index: 210

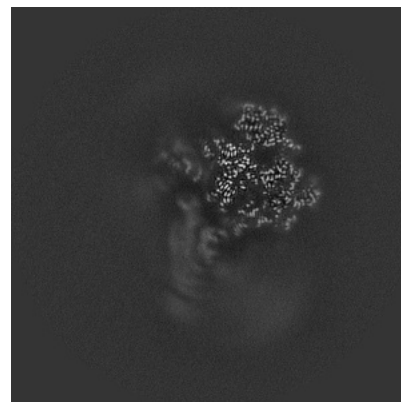
6.2.2 Raw map



X Index: 210



Y Index: 210

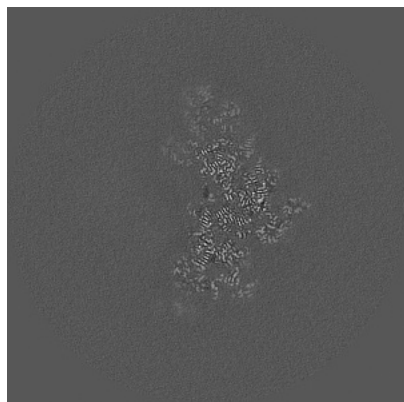


Z Index: 210

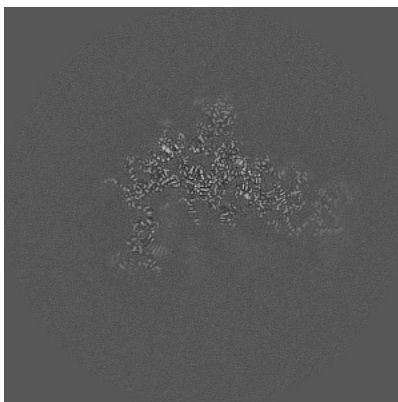
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

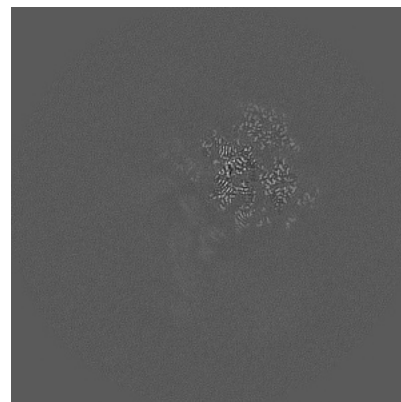
6.3.1 Primary map



X Index: 246

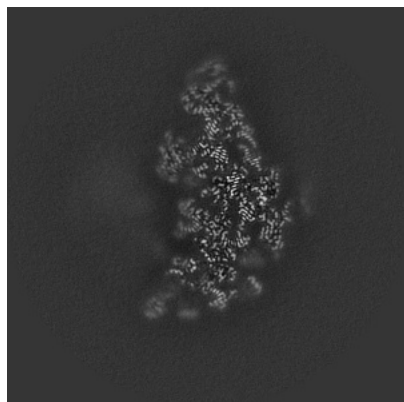


Y Index: 228

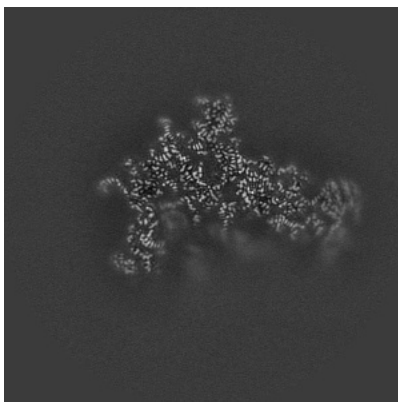


Z Index: 207

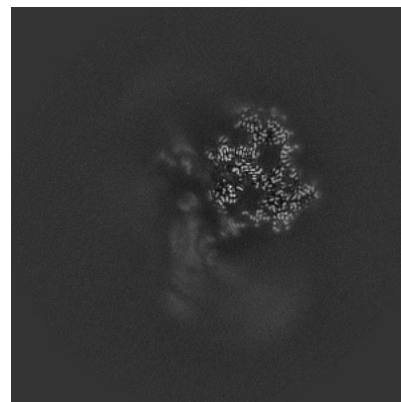
6.3.2 Raw map



X Index: 237



Y Index: 225

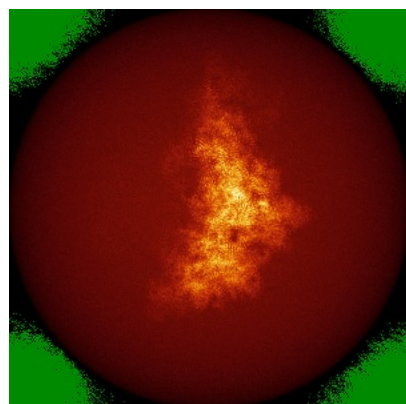


Z Index: 214

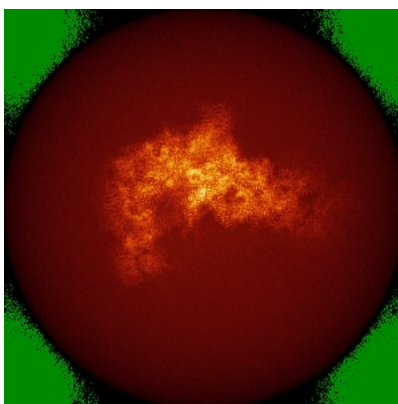
The images above show the largest variance slices of the map in three orthogonal directions.

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

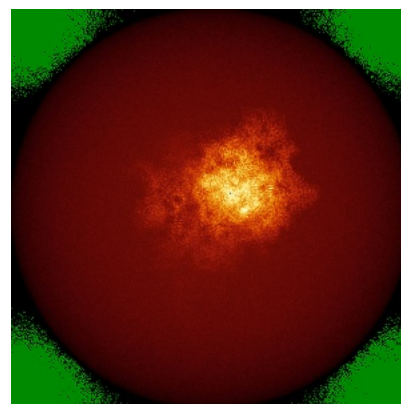
6.4.1 Primary map



X



Y



Z

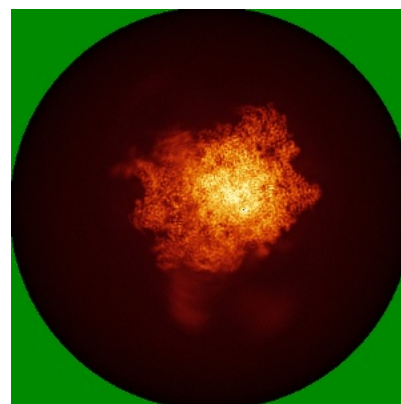
6.4.2 Raw map



X



Y

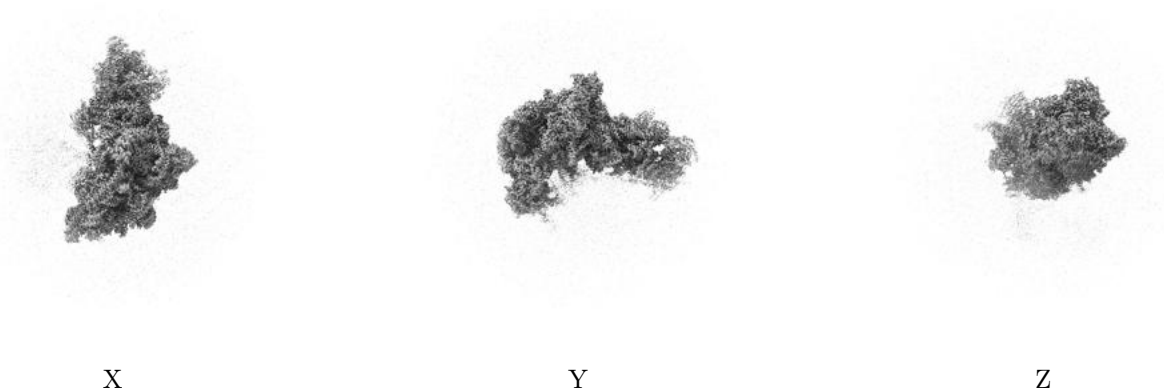


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

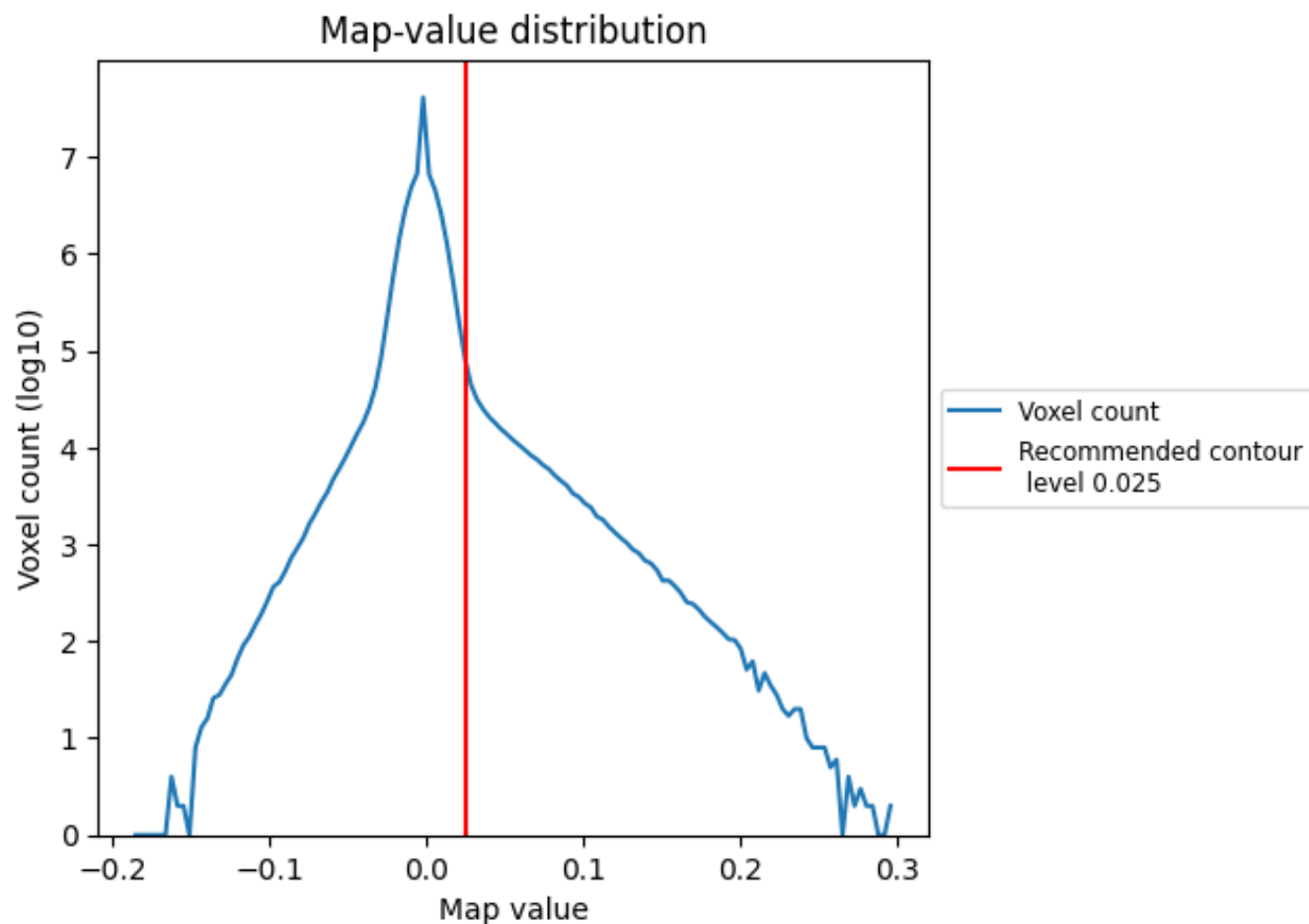
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

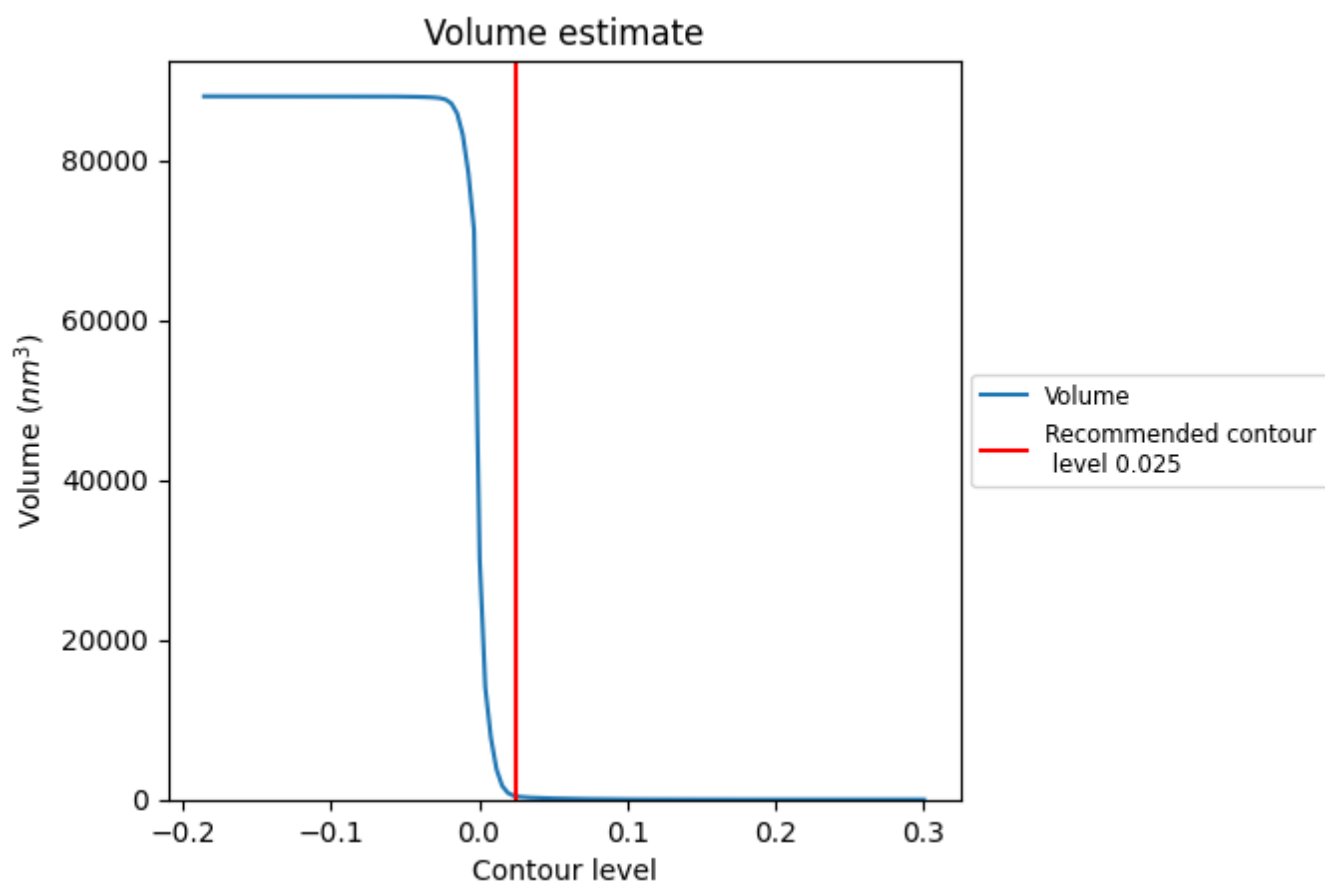
This section contains the results of statistical analysis of the map.

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.

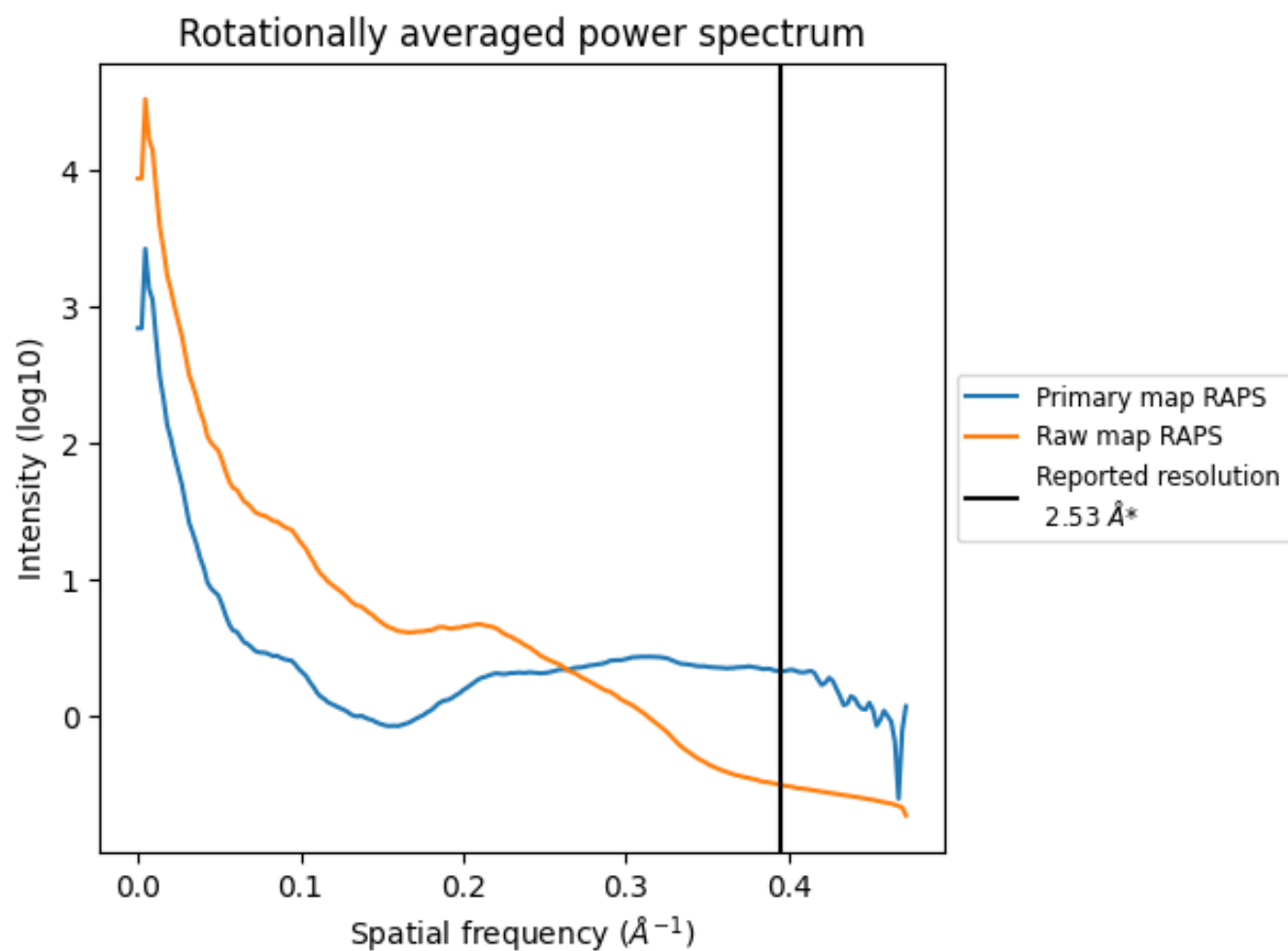
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 427 nm^3 ; this corresponds to an approximate mass of 386 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 ⓘ

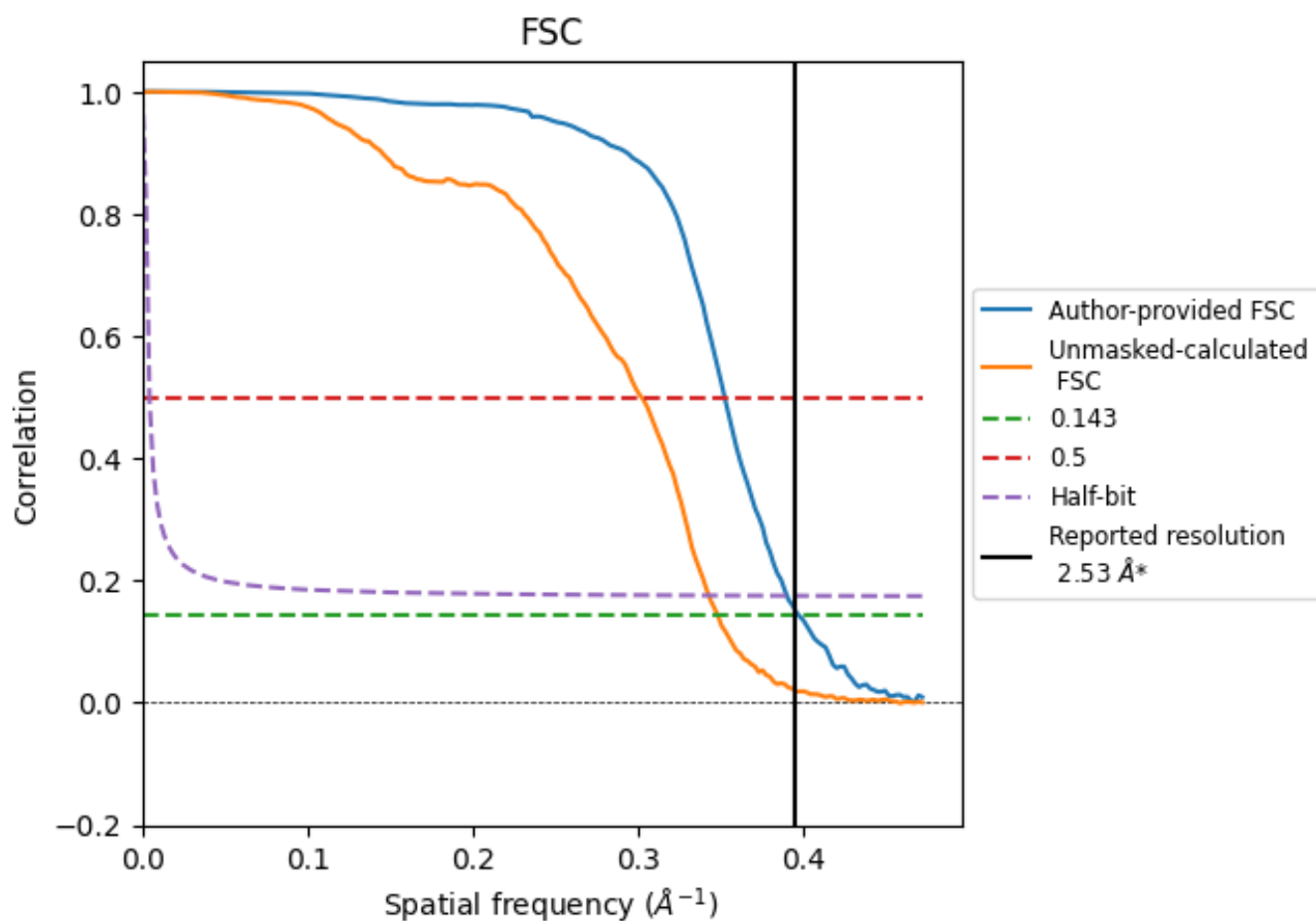


*Reported resolution corresponds to spatial frequency of 0.395 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.395 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.53	-	-
Author-provided FSC curve	2.52	2.84	2.56
Unmasked-calculated*	2.87	3.31	2.92

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.87 differs from the reported value 2.53 by more than 10 %

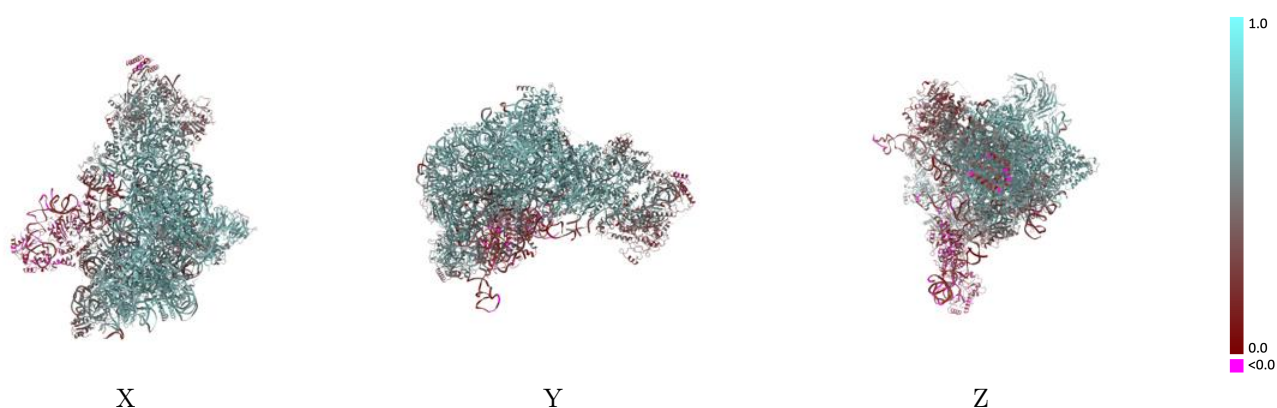
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43017 and PDB model 8V83. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)

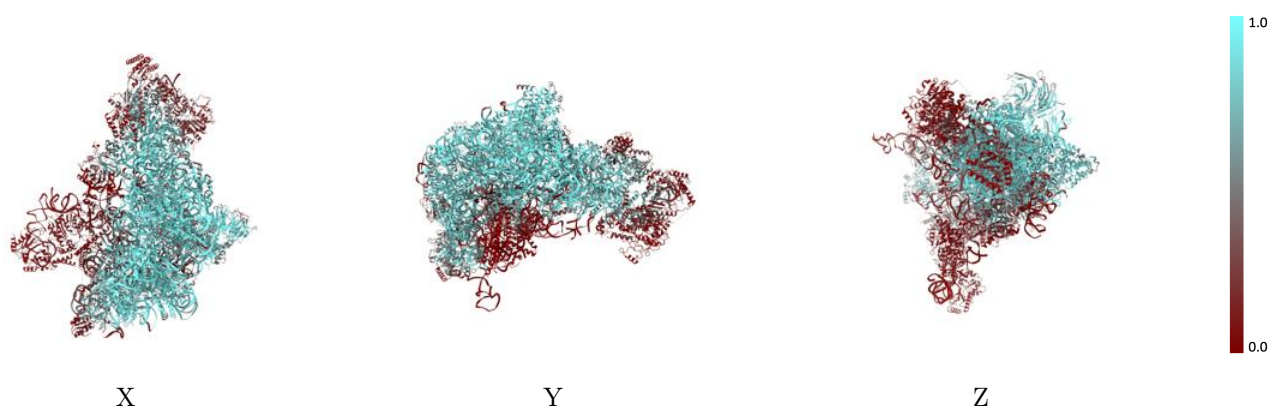
This section was not generated.

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



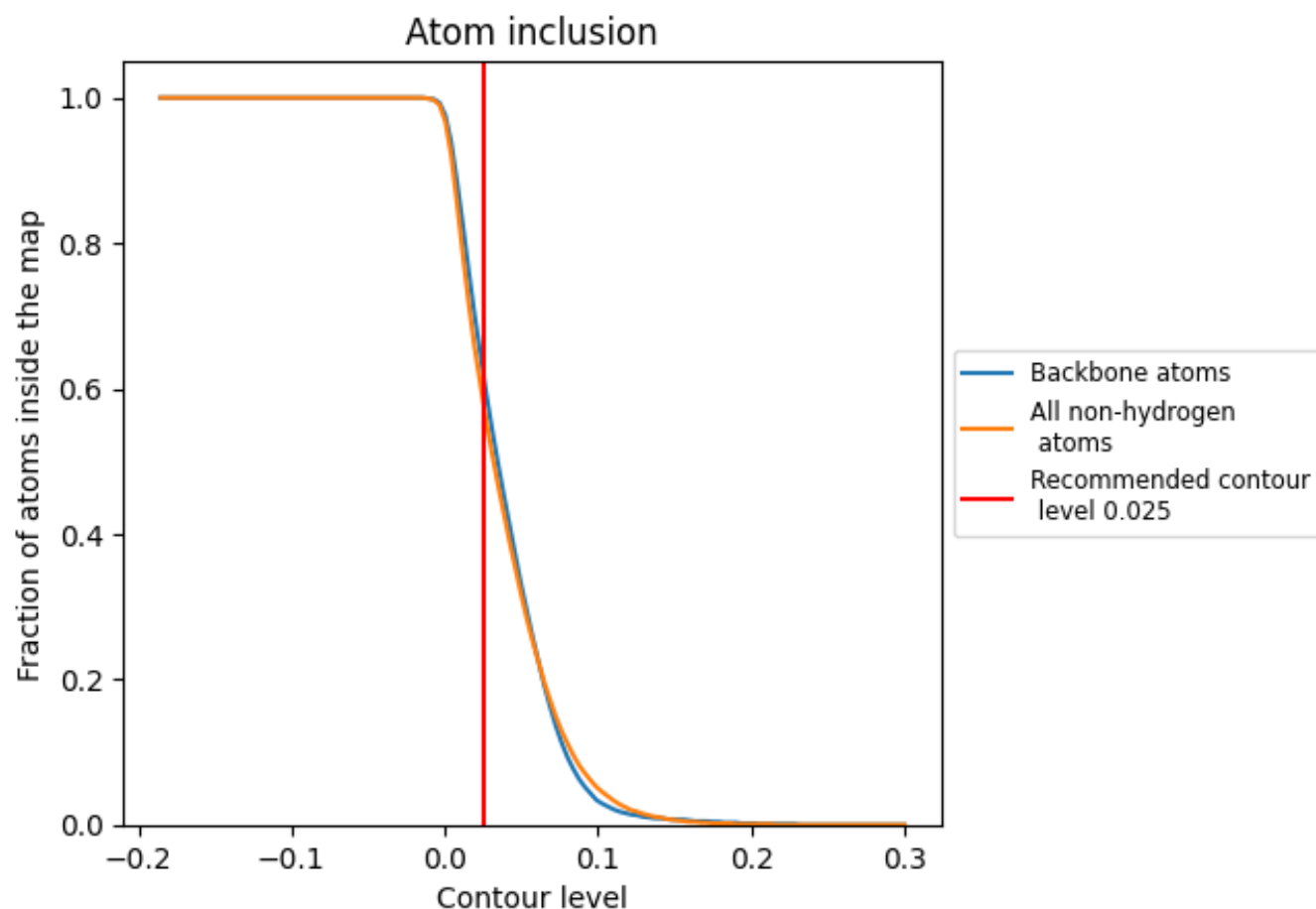
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5830	 0.5300
1	 0.6480	 0.5310
2	 0.7780	 0.6090
6	 0.4710	 0.4920
7	 0.0000	 0.1490
8	 0.2450	 0.4480
A	 0.4400	 0.5340
B	 0.7660	 0.6210
C	 0.9430	 0.7060
D	 0.3700	 0.5020
E	 0.8420	 0.6540
F	 0.8750	 0.6720
G	 0.8170	 0.6480
H	 0.7820	 0.6360
I	 0.7930	 0.6450
J	 0.0890	 0.3730
K	 0.2360	 0.4210
L	 0.8890	 0.6820
M	 0.8580	 0.6640
N	 0.8160	 0.6540
O	 0.8440	 0.6680
P	 0.7870	 0.6530
Q	 0.8930	 0.6820
R	 0.8700	 0.6810
S	 0.7080	 0.6190
T	 0.0020	 0.2290
V	 0.7060	 0.5970
W	 0.2570	 0.4550
Y	 0.8870	 0.6900
Z	 0.0070	 0.2720
a	 0.0000	 0.1330
b	 0.3790	 0.4920
e	 0.9260	 0.6990
f	 0.9290	 0.7010
h	 0.6650	 0.6070



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Chain	Atom inclusion	Q-score
i	 0.6680	 0.6010
j	 0.9140	 0.6930
l	 0.0010	 0.1510
m	 0.2710	 0.4340
n	 0.1620	 0.3940
o	 0.3630	 0.4340
q	 0.0020	 0.1470
r	 0.3540	 0.4950
t	 0.2530	 0.4450
u	 0.5420	 0.5320
v	 0.6850	 0.6060
w	 0.8080	 0.6390
x	 0.8300	 0.6550
y	 0.6770	 0.5810