



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 05:34 AM UTC

PDB ID : 8ETC / pdb_00008etc
EMDB ID : EMD-24398
Title : Fkbp39 associated nascent 60S ribosome State 4
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-16
Resolution : 3.10 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:

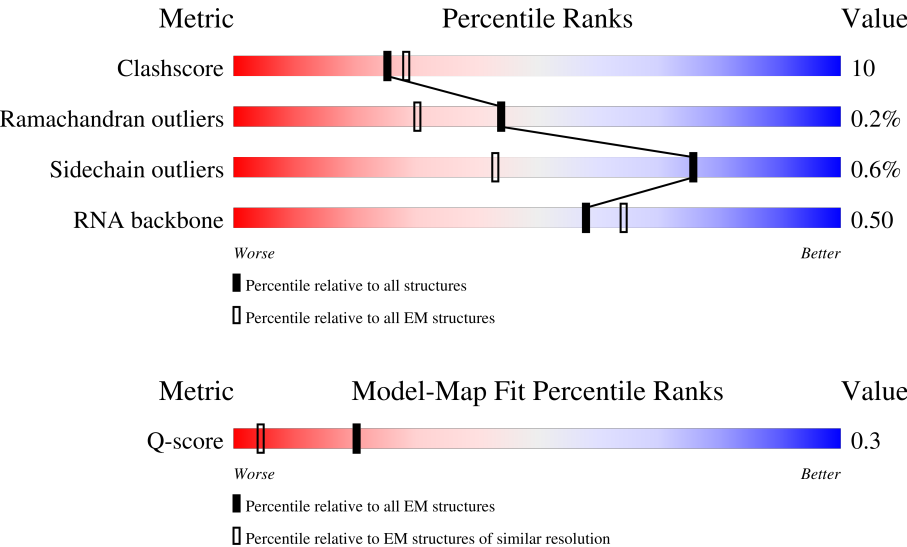
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	1	3497	11% 32% 23% 7% 39%
2	2	165	55% 27% 7% 11%
3	3	302	27% 16% 22% 62%

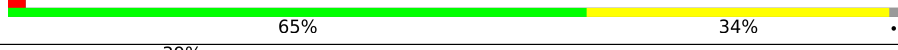
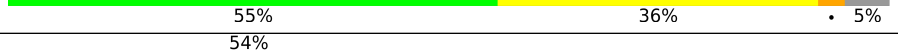
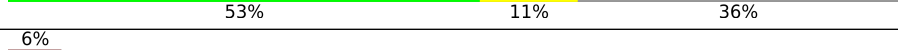
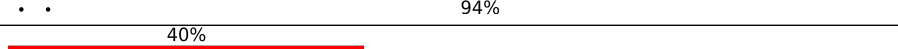
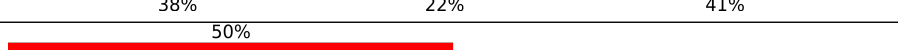
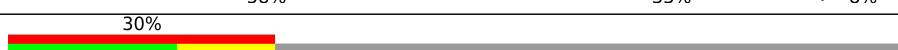
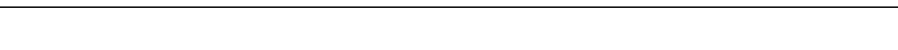
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Mol	Chain	Length	Quality of chain
4	8	51	
5	B	388	
6	C	363	
7	E	195	
8	F	250	
9	G	259	
10	H	190	
11	L	208	
12	M	134	
13	N	201	
14	O	197	
15	P	187	
16	Q	187	
17	R	193	
18	S	176	
19	U	117	
20	V	139	
21	W	241	
22	X	141	
23	Y	126	
24	Z	136	
25	a	148	
26	b	642	
27	c	117	
28	d	113	

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Mol	Chain	Length	Quality of chain
29	e	127	
30	f	108	
31	g	112	
32	h	122	
33	i	99	
34	j	91	
35	k	74	
36	r	260	
37	s	470	
38	u	192	
39	w	802	
40	y	244	
41	z	117	
42	T	160	

2 Entry composition

There are 43 unique types of molecules in this entry. The entry contains 95651 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 RNA (2151-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2140	Total	C	N	O	P	0	0
			45843	20476	8349	14878	2140		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (147-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	147	Total	C	N	O	P	0	0
			3131	1401	560	1023	147		

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	114	Total	C	N	O	S	0	0
			969	614	181	168	6		

- Molecule 4 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	49	Total	C	N	O	S	0	0
			428	267	97	63	1		

- Molecule 5 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	365	Total	C	N	O	S	0	0
			2903	1837	542	514	10		

- Molecule 6 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	359	Total	C	N	O	S	0	0
			2795	1765	536	491	3		

- Molecule 7 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	163	Total	C	N	O	S	0	0
			1260	807	232	218	3		

- Molecule 8 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	218	Total	C	N	O	S	0	0
			1770	1141	324	302	3		

- Molecule 9 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	182	Total	C	N	O	S	2	0
			1453	931	263	257	2		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	183	Total	C	N	O	S	0	0
			1451	914	266	265	6		

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	180	Total	C	N	O	S	0	0
			1427	891	284	251	1		

- Molecule 12 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	166	Total	C	N	O	S	0	0
			1406	883	291	229	3		

- Molecule 14 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	169	Total	C	N	O	S	0	0
			1339	848	252	236	3		

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	135	Total	C	N	O	S	0	0
			1047	658	202	186	1		

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	124	Total	C	N	O	S	0	0
			1038	651	217	165	5		

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	168	Total	C	N	O	S	0	0
			1408	909	263	231	5		

- Molecule 19 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	U	98	Total	C	N	O	0	0
			484	288	98	98		

- Molecule 20 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	138	Total	C	N	O	S	0	0
			1032	647	194	183	8		

- Molecule 21 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	215	Total	C	N	O	S	0	0
			1057	627	215	215			

- Molecule 22 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	114	Total	C	N	O	S	0	0
			914	584	167	162	1		

- Molecule 23 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 24 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	134	Total	C	N	O	S	0	0
			662	393	134	135			

- Molecule 25 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	94	Total	C	N	O	S	0	0
			747	474	142	131			

- Molecule 26 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	415	Total	C	N	O	S	0	0
			2837	1765	535	534	3		

- Molecule 27 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	c	97	Total	C	N	O	0	0
			477	282	97	98		

- Molecule 28 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	102	Total	C	N	O	S	0	0
			849	534	165	147	3		

- Molecule 29 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	118	Total	C	N	O	S	0	0
			944	591	191	157	5		

- Molecule 30 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 31 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	105	Total	C	N	O	S	0	0
			853	534	176	141	2		

- Molecule 32 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	h	121	Total	C	N	O	0	0
			999	629	194	176		

- Molecule 33 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	94	Total	C	N	O	S	0	0
			754	469	158	126	1		

- Molecule 34 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	75	Total	C	N	O	S	0	0
			600	367	131	95	7		

- Molecule 35 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	k	70	Total	C	N	O	S	0	0
			564	357	104	102	1		

- Molecule 36 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	r	166	Total	C	N	O	S	0	0
			1086	656	224	205	1		

- Molecule 37 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	s	30	Total	C	N	O	0	0
			253	154	58	41		

- Molecule 38 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	u	114	Total	C	N	O	S	0	0
			944	598	190	147	9		

- Molecule 39 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	w	420	Total	C	N	O	S	0	0
			3377	2152	589	621	15		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	y	225	Total	C	N	O	S	0	0
			1697	1058	293	341	5		

- Molecule 41 is a protein called UPF0642 protein C32H8.05.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	z	35	Total	C	N	O	0	0
			292	183	63	46		

- Molecule 42 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	T	21	Total	C	N	O	0	0
			159	101	28	30		

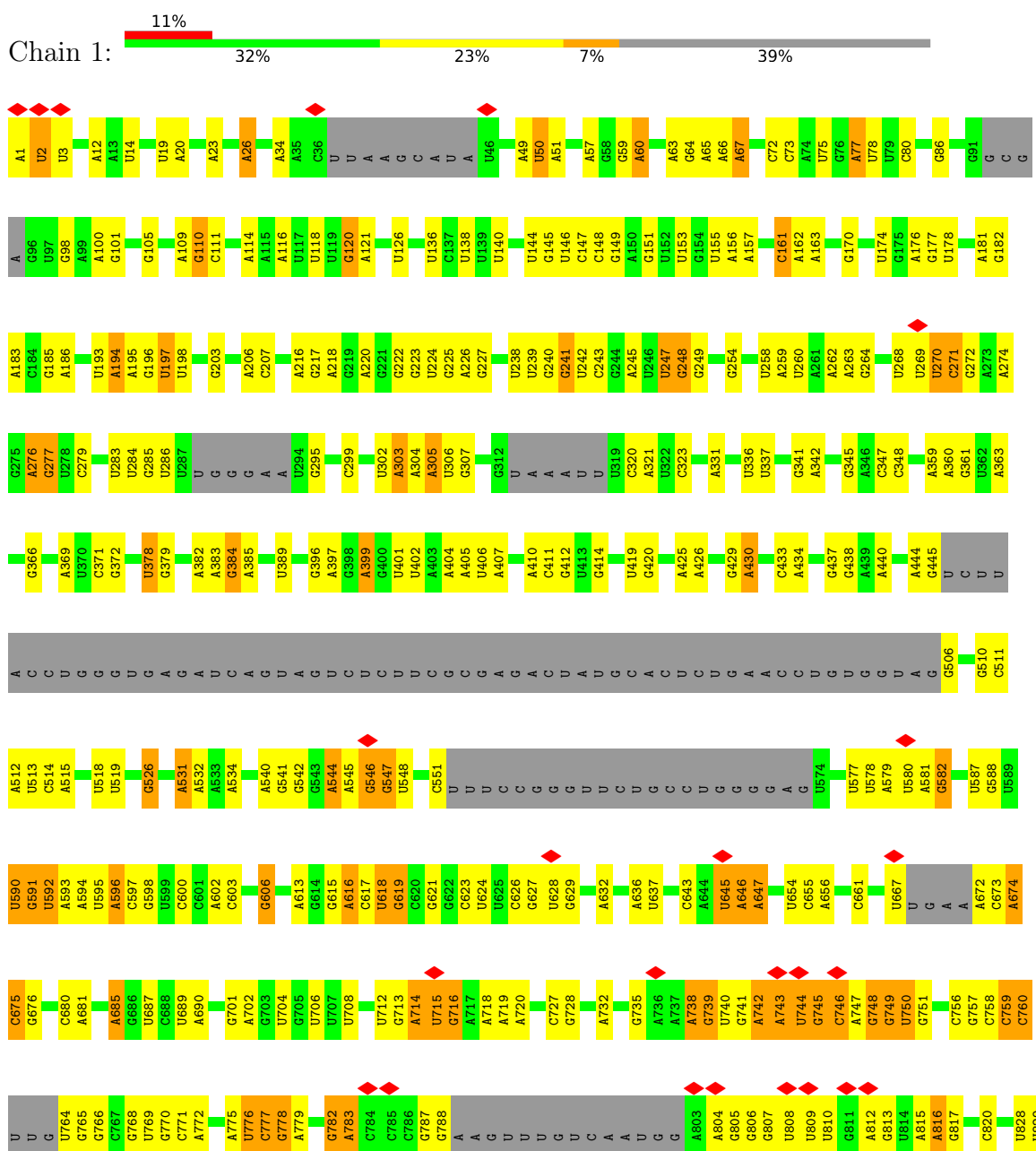
- Molecule 43 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
43	j	1	Total	Zn	0
			1	1	

3 Residue-property plots

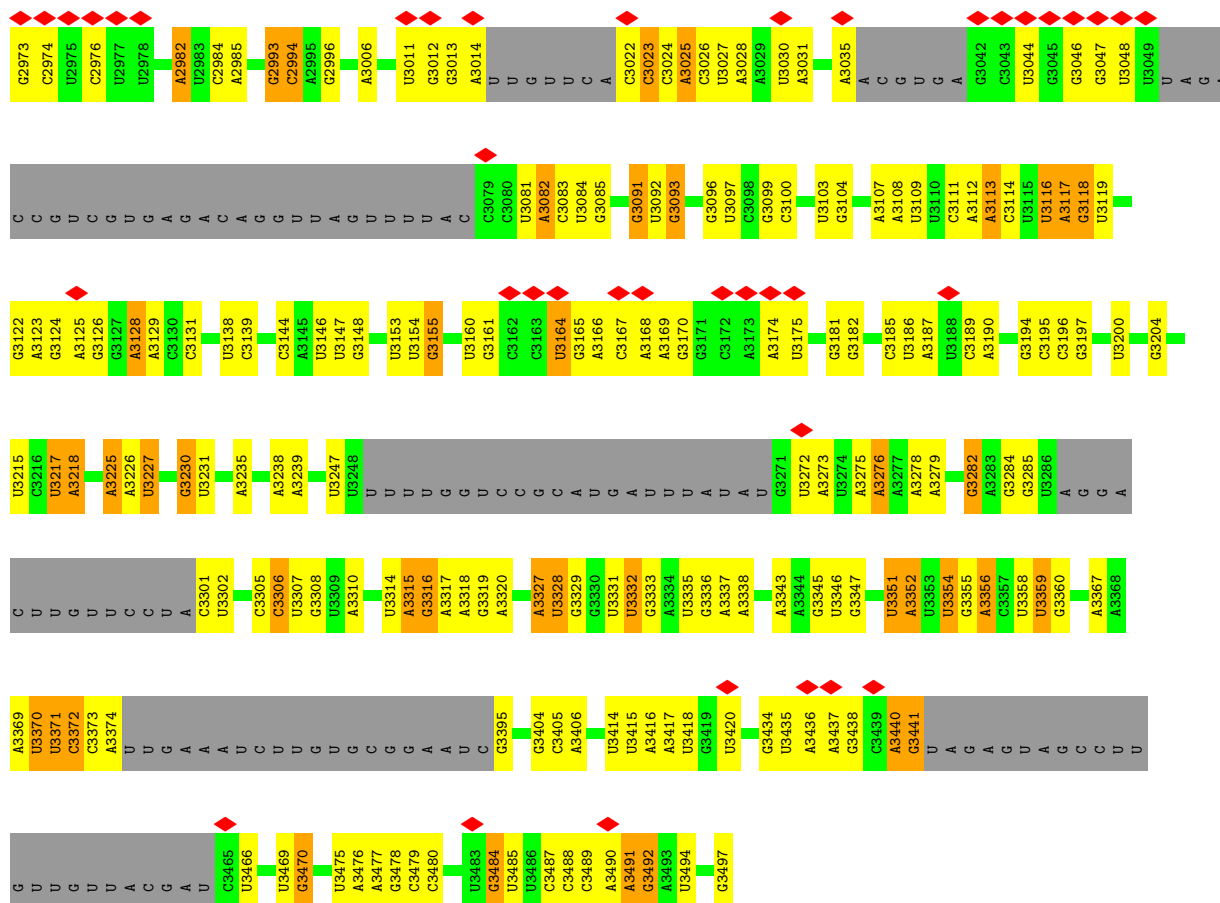
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: RNA (2151-MER)





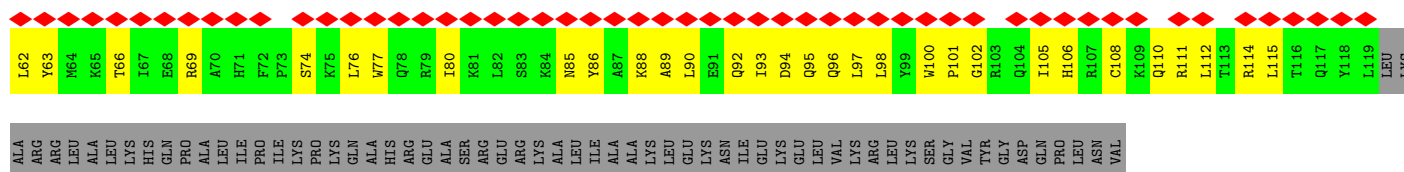
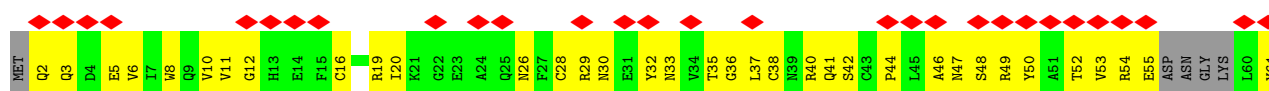


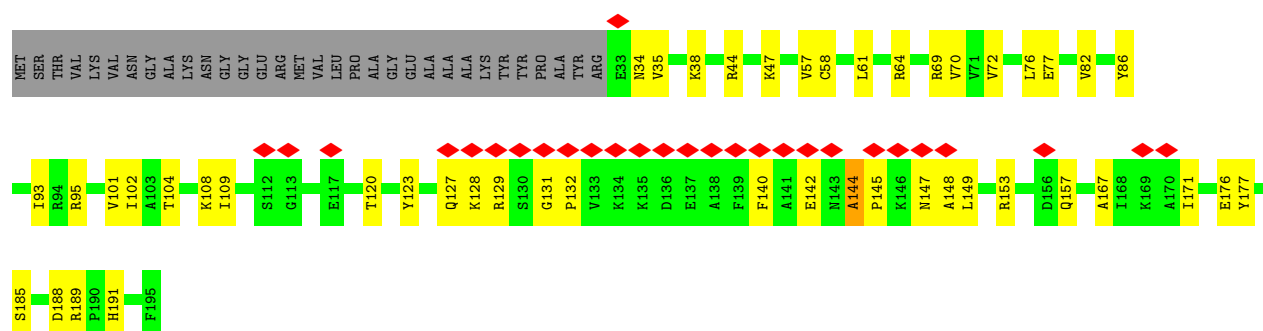


• Molecule 2: RNA (147-MER)

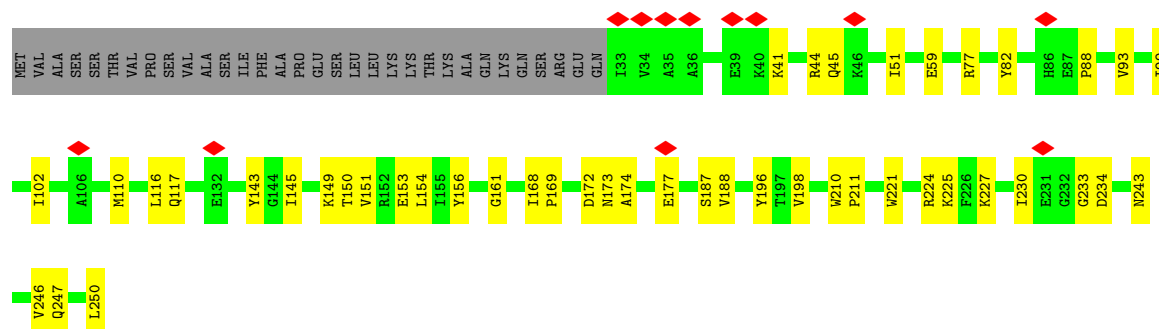


• Molecule 3: Protein mak16

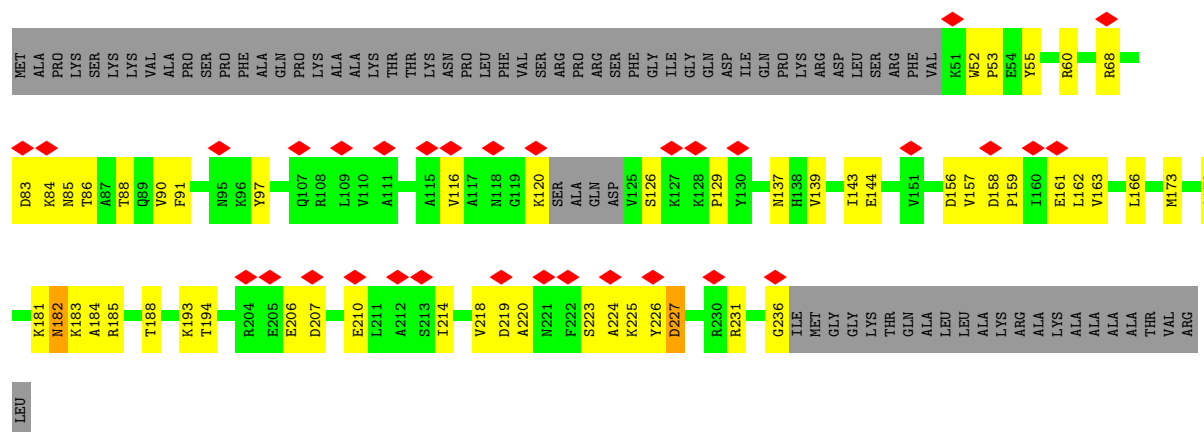




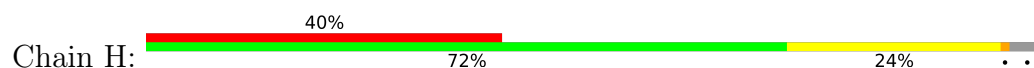
• Molecule 8: 60S ribosomal protein L7-B

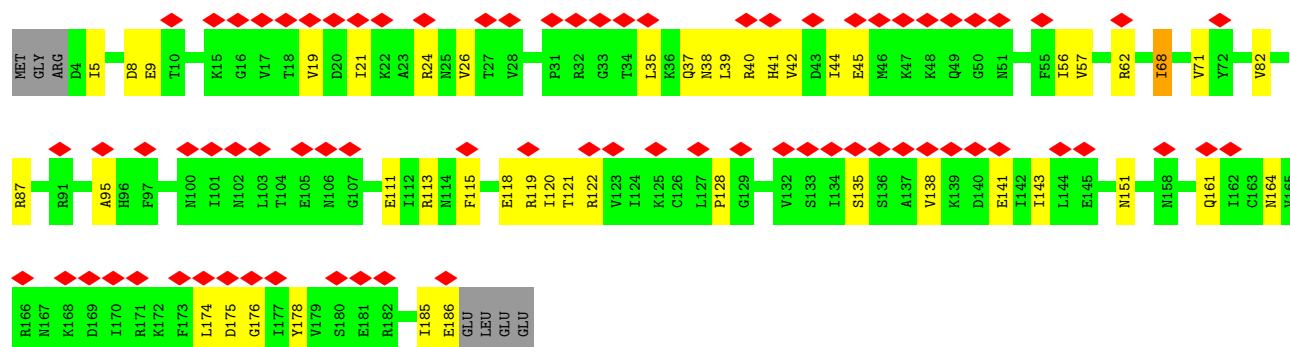


• Molecule 9: 60S ribosomal protein L8

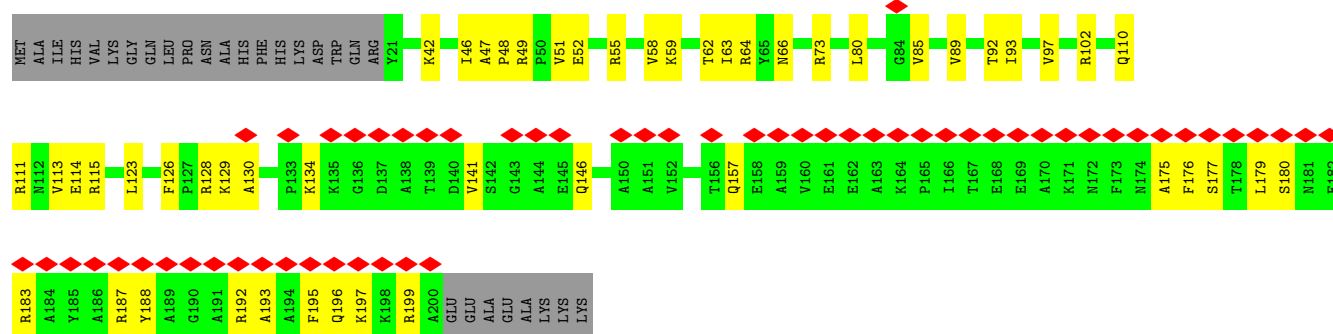


• Molecule 10: 60S ribosomal protein L9-A

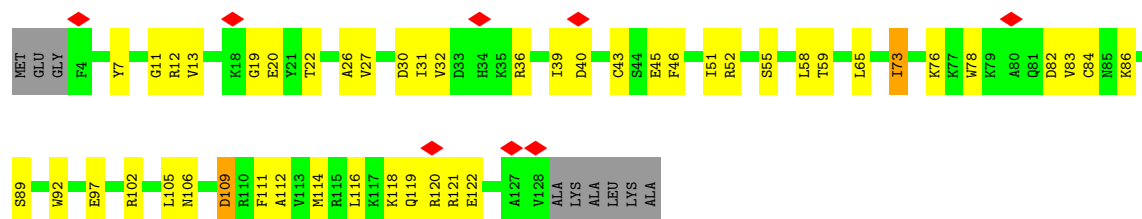




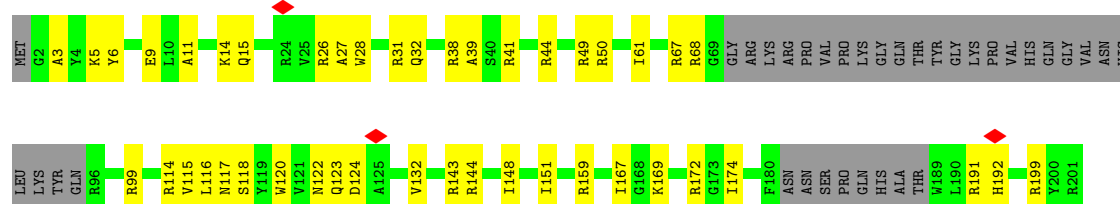
• Molecule 11: 60S ribosomal protein L13



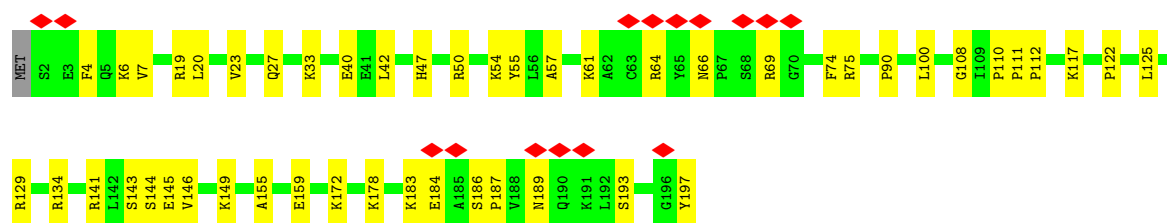
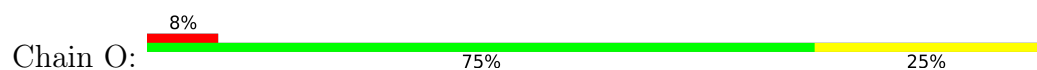
• Molecule 12: 60S ribosomal protein L14



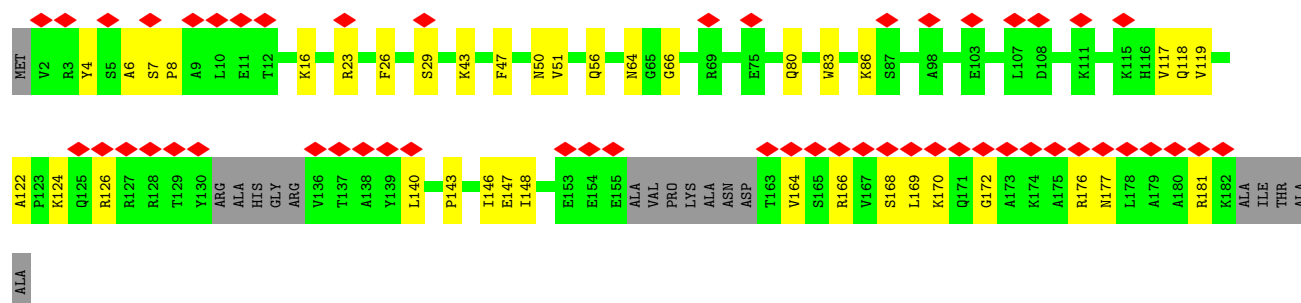
• Molecule 13: 60S ribosomal protein L15-A



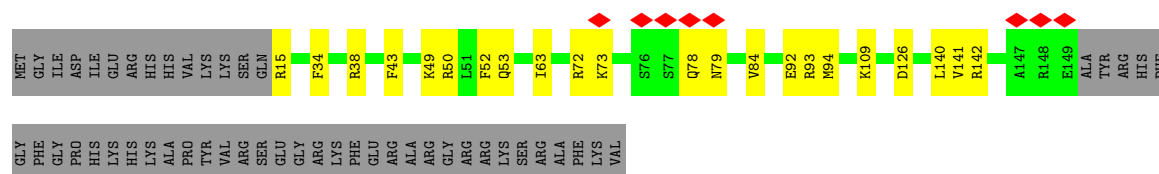
• Molecule 14: 60S ribosomal protein L16-B



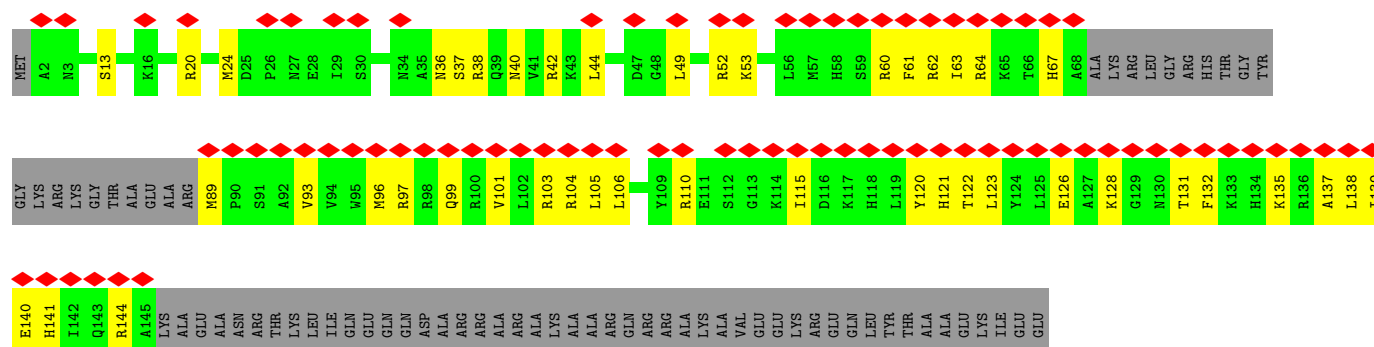
• Molecule 15: 60S ribosomal protein L17-A



• Molecule 16: 60S ribosomal protein L18-A

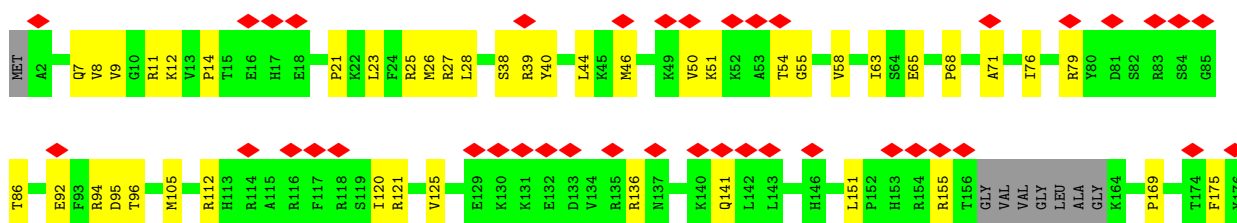


• Molecule 17: 60S ribosomal protein L19-A



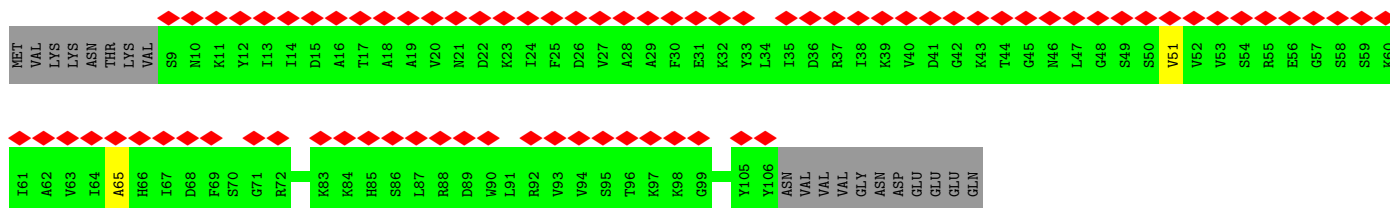
• Molecule 18: 60S ribosomal protein L20-A

Chain S: 23% 70% 25% 5%



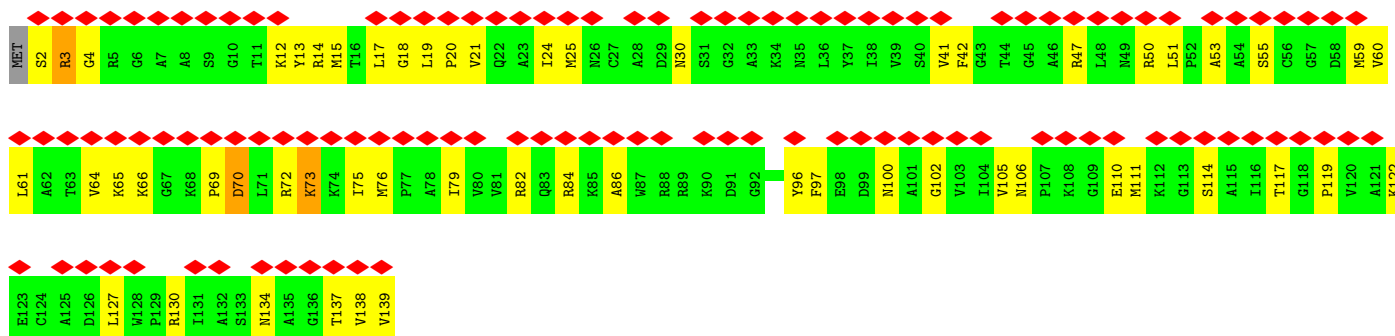
- Molecule 19: 60S ribosomal protein L22

Chain U: 68% 82% 16%



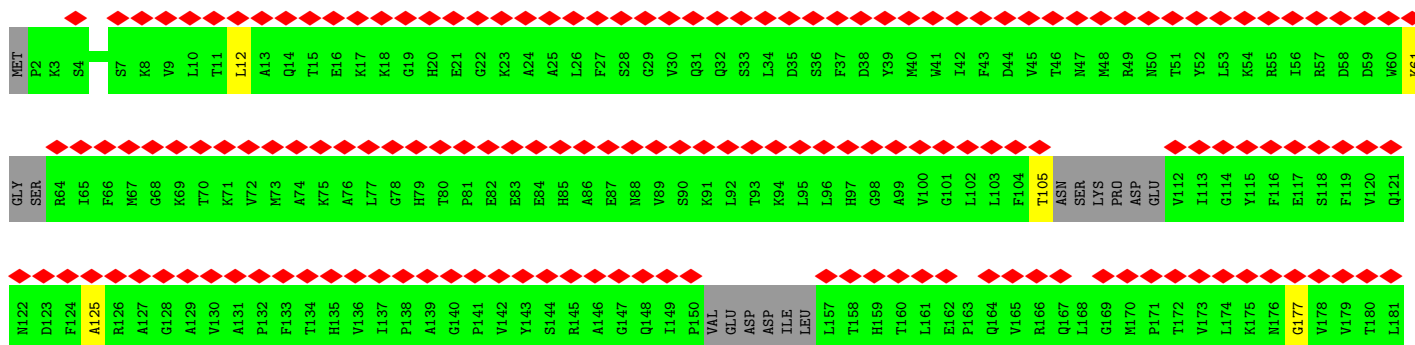
- Molecule 20: 60S ribosomal protein L23-A

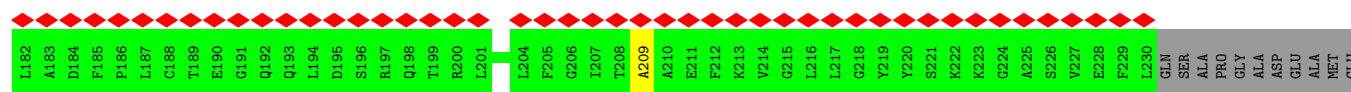
Chain V: 82% 59% 38% ..



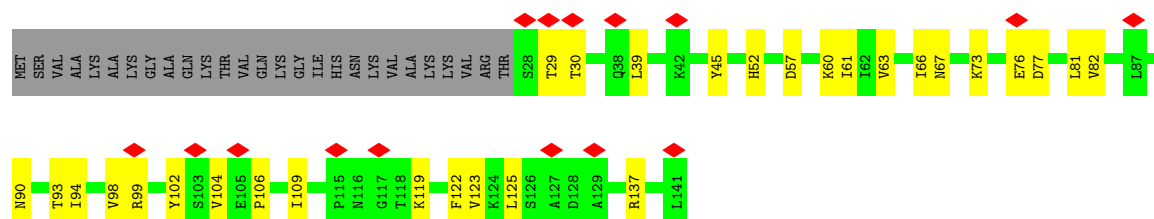
- Molecule 21: Ribosome assembly factor mrt4

Chain W: 86% 87% 11%

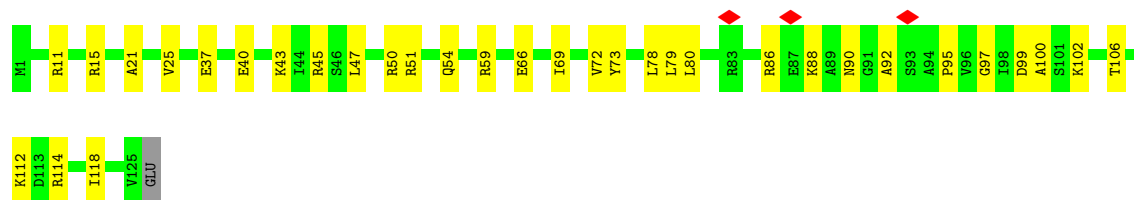
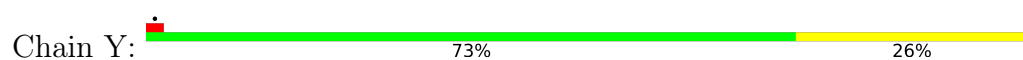




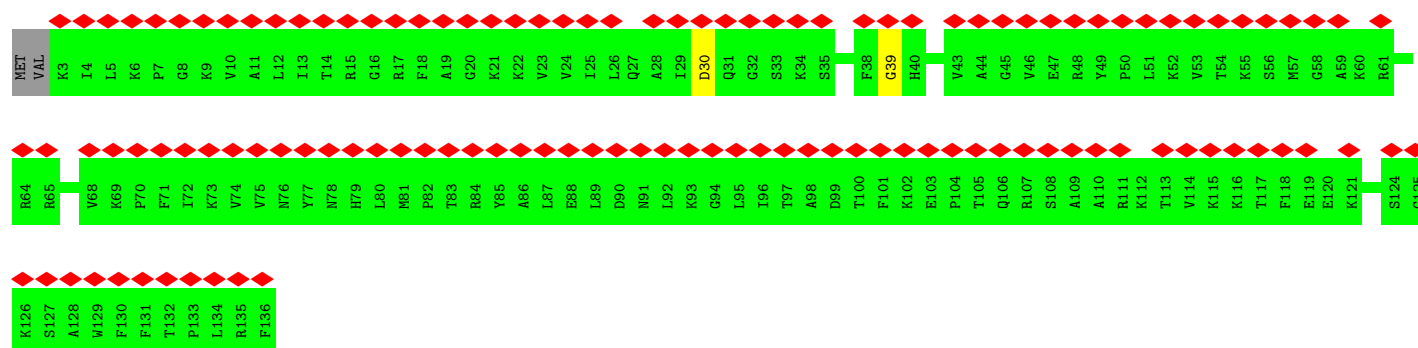
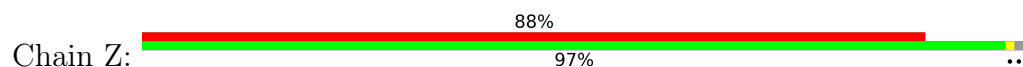
• Molecule 22: 60S ribosomal protein L25-A



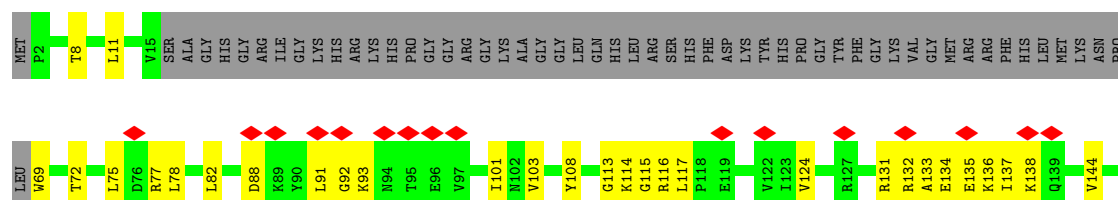
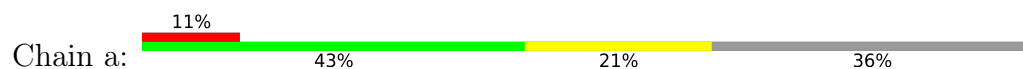
• Molecule 23: 60S ribosomal protein L26



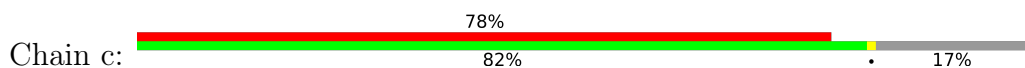
• Molecule 24: 60S ribosomal protein L27-A



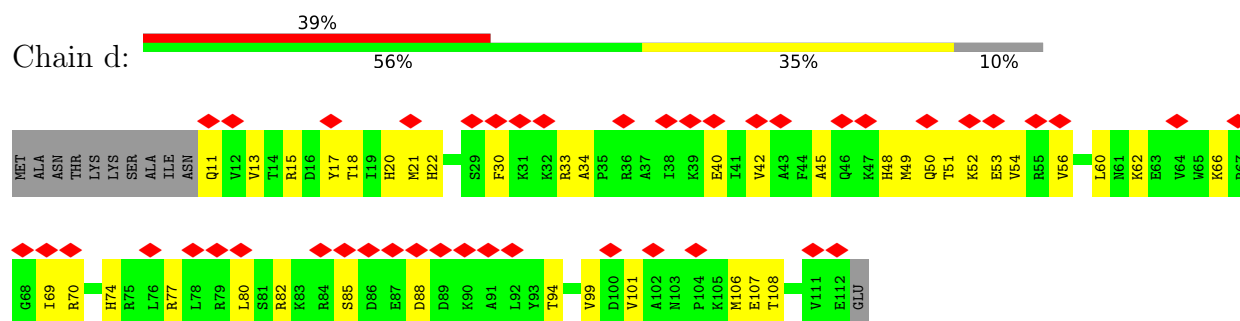
• Molecule 25: 60S ribosomal protein L28-A



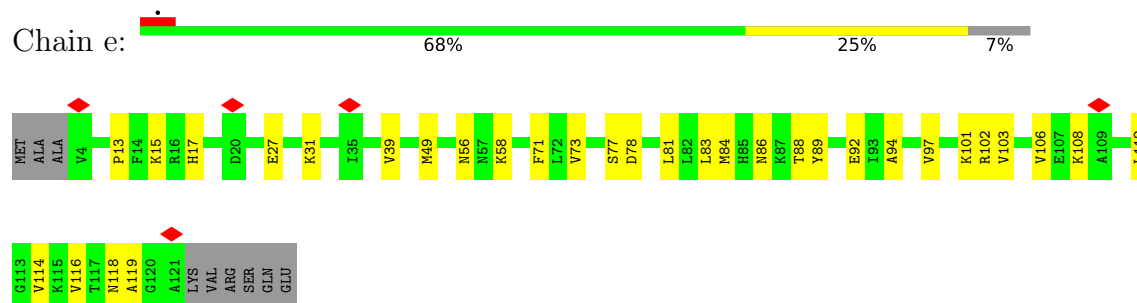
Chain b:



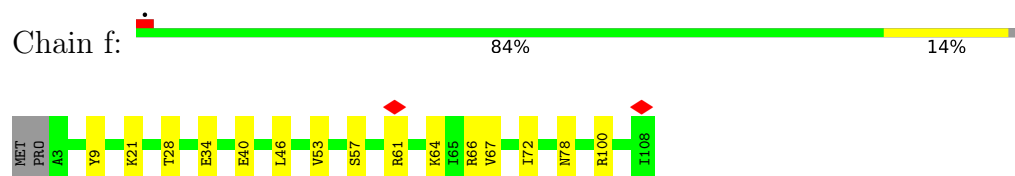
- Molecule 28: 60S ribosomal protein L31



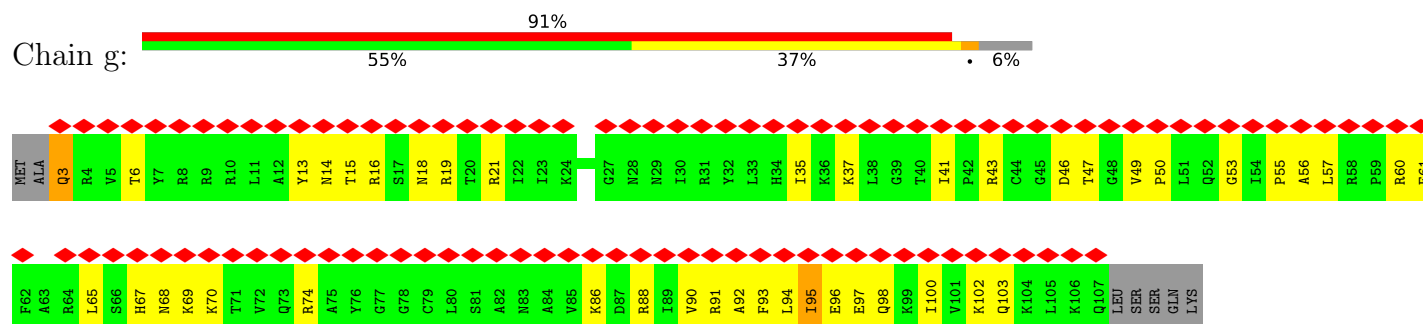
- Molecule 29: 60S ribosomal protein L32-A



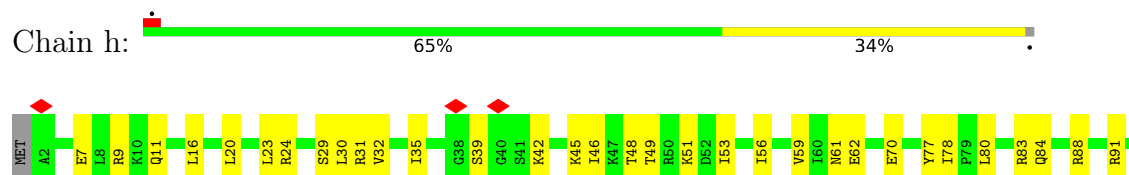
- Molecule 30: 60S ribosomal protein L33-B

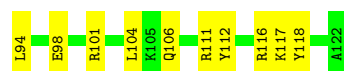


- Molecule 31: 60S ribosomal protein L34-A

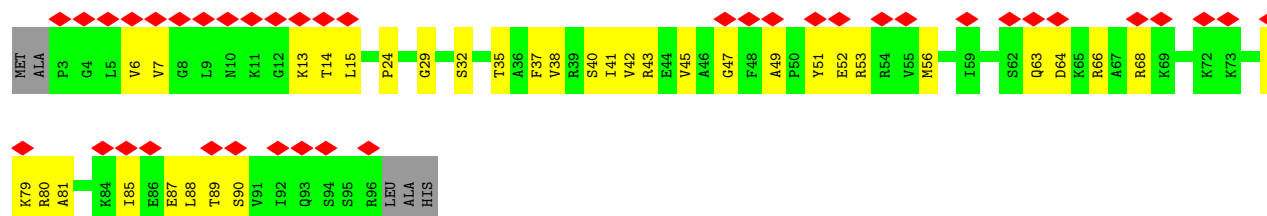
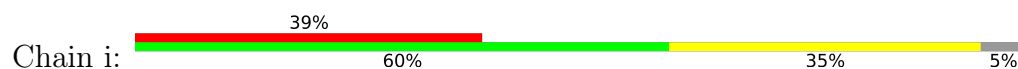


- Molecule 32: 60S ribosomal protein L35

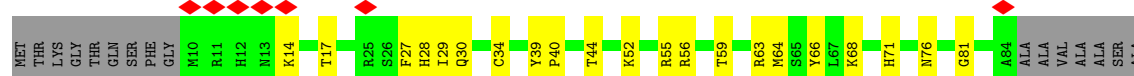




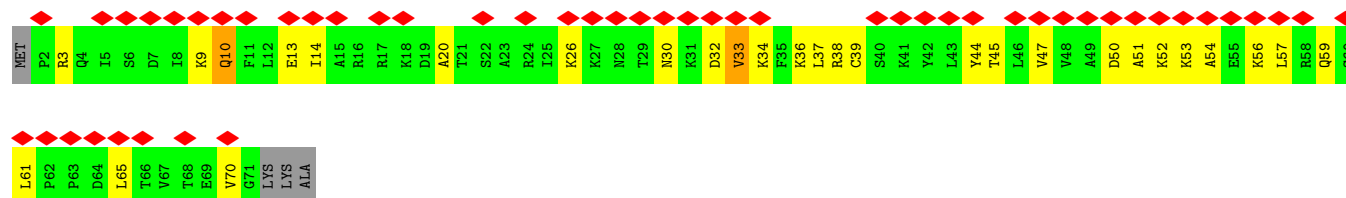
• Molecule 33: 60S ribosomal protein L36-B



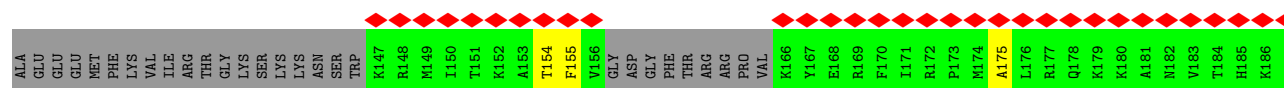
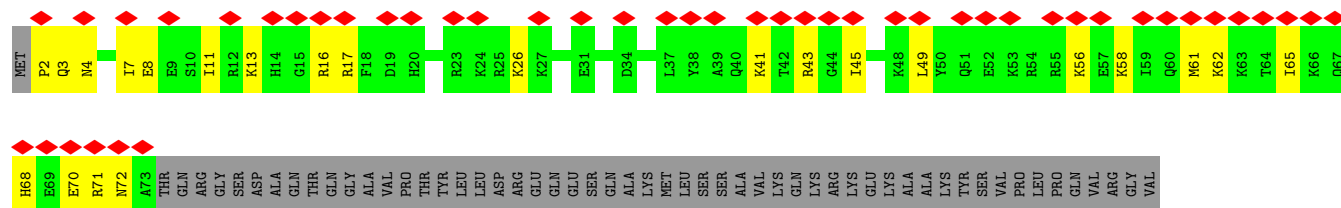
• Molecule 34: 60S ribosomal protein L37-B

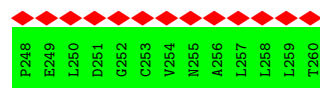


• Molecule 35: 60S ribosomal protein L38-1

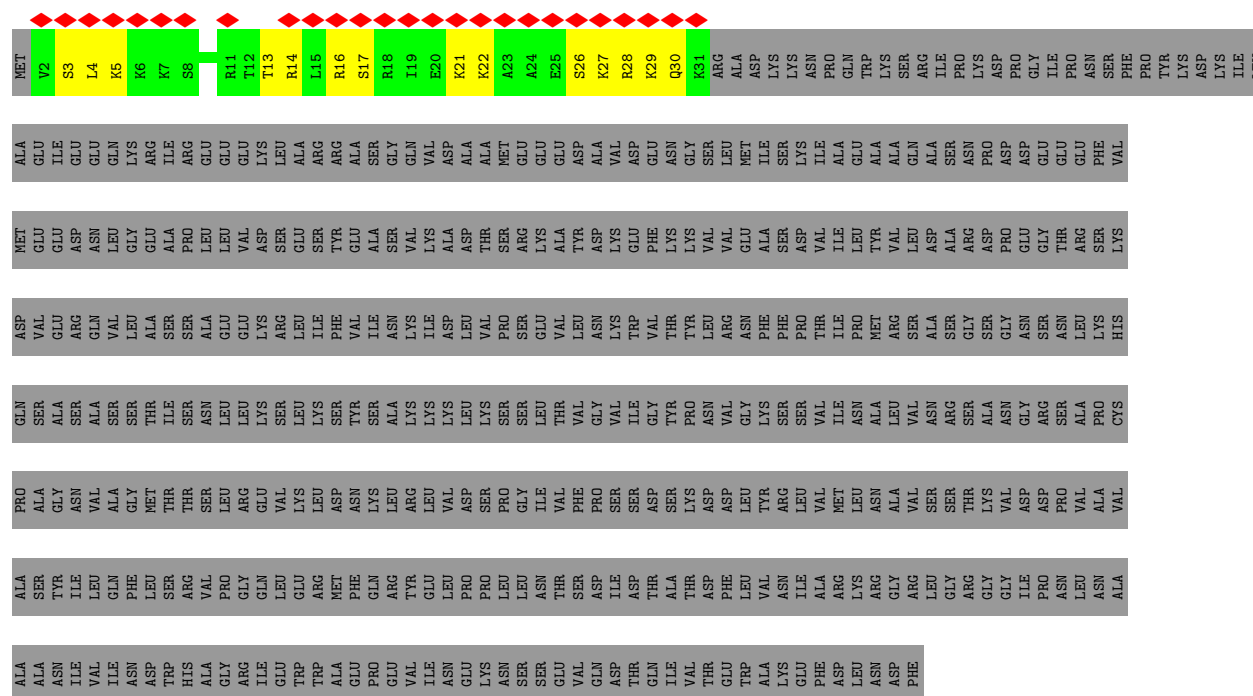


• Molecule 36: Ribosome biogenesis protein nsa2

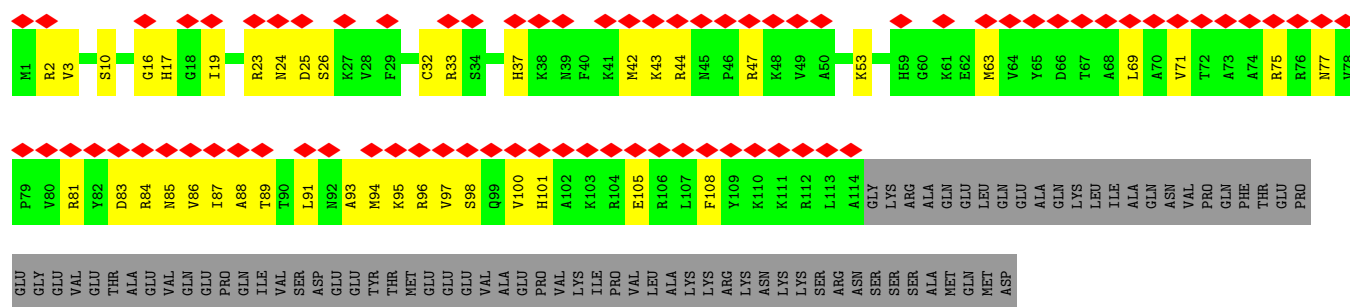




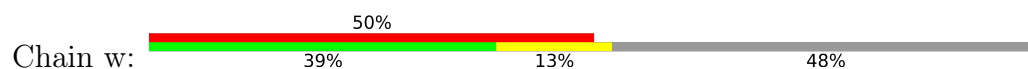
• Molecule 37: GTPase grn1



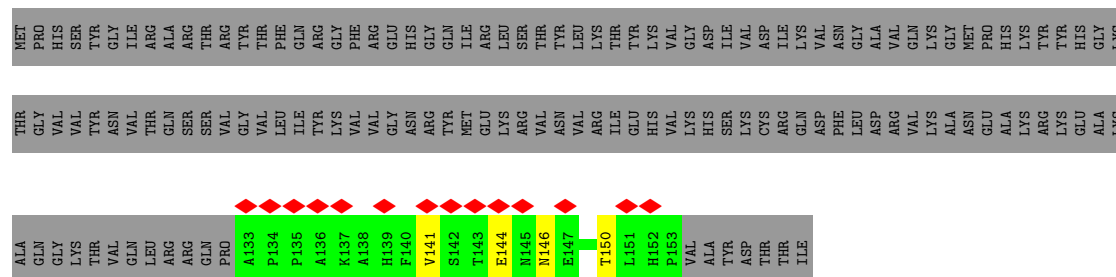
• Molecule 38: Ribosome biogenesis protein rlp24



• Molecule 39: AdoMet-dependent rRNA methyltransferase spb1







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.558	Depositor
Minimum map value	-0.297	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	0.09	0/51306	0.22	0/79930
2	2	0.10	0/3500	0.20	0/5446
3	3	0.16	0/990	0.44	0/1333
4	8	0.11	0/439	0.33	0/586
5	B	0.12	0/2965	0.33	0/3988
6	C	0.16	0/2848	0.37	1/3842 (0.0%)
7	E	0.15	0/1284	0.37	0/1731
8	F	0.11	0/1806	0.30	0/2424
9	G	0.14	0/1475	0.35	0/1988
10	H	0.13	0/1470	0.38	0/1982
11	L	0.15	0/1452	0.39	0/1955
12	M	0.15	0/1024	0.40	0/1375
13	N	0.10	0/1436	0.27	0/1920
14	O	0.13	0/1588	0.32	0/2128
15	P	0.12	0/1361	0.34	0/1823
16	Q	0.11	0/1057	0.32	0/1419
17	R	0.12	0/1054	0.36	0/1404
18	S	0.13	0/1444	0.35	0/1939
19	U	0.05	0/483	0.19	0/671
20	V	0.14	0/1048	0.40	0/1410
21	W	0.06	0/1053	0.28	0/1457
22	X	0.14	0/930	0.40	0/1251
23	Y	0.11	0/1008	0.31	0/1341
24	Z	0.06	0/661	0.17	0/917
25	a	0.15	0/760	0.42	0/1026
26	b	0.23	0/2868	0.48	1/3902 (0.0%)
27	c	0.06	0/476	0.16	0/658
28	d	0.11	0/864	0.31	0/1161
29	e	0.13	0/958	0.32	0/1278
30	f	0.10	0/859	0.26	0/1152
31	g	0.16	0/865	0.50	2/1159 (0.2%)
32	h	0.12	0/1008	0.35	0/1340

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	i	0.18	0/761	0.48	0/1009
34	j	0.10	0/613	0.31	0/811
35	k	0.22	0/570	0.57	0/762
36	r	0.13	0/1091	0.36	0/1464
37	s	0.15	0/252	0.40	0/325
38	u	0.20	0/966	0.49	0/1292
39	w	0.12	0/3444	0.37	0/4638
40	y	0.12	0/1720	0.34	0/2345
41	z	0.14	0/297	0.42	0/388
42	T	0.22	0/165	0.45	0/228
All	All	0.12	0/102219	0.29	4/149198 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	345	SER	N-CA-C	-6.50	104.40	112.72
26	b	162	PRO	CA-N-CD	-5.19	104.74	112.00
31	g	95	ILE	CA-C-N	-5.00	112.18	120.68
31	g	95	ILE	C-N-CA	-5.00	112.18	120.68

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	45843	0	23070	659	0
2	2	3131	0	1583	39	0
3	3	969	0	964	60	0
4	8	428	0	452	16	0
5	B	2903	0	2974	74	0
6	C	2795	0	2918	73	0
7	E	1260	0	1343	40	0
8	F	1770	0	1848	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	G	1453	0	1545	37	0
10	H	1451	0	1511	34	0
11	L	1427	0	1482	45	0
12	M	1007	0	1072	37	0
13	N	1406	0	1441	43	0
14	O	1557	0	1652	40	0
15	P	1339	0	1380	35	0
16	Q	1047	0	1143	18	0
17	R	1038	0	1113	39	0
18	S	1408	0	1462	33	0
19	U	484	0	222	1	0
20	V	1032	0	1081	53	0
21	W	1057	0	487	4	0
22	X	914	0	970	25	0
23	Y	998	0	1090	31	0
24	Z	662	0	305	1	0
25	a	747	0	790	37	0
26	b	2837	0	2413	90	0
27	c	477	0	233	1	0
28	d	849	0	885	29	0
29	e	944	0	1005	24	0
30	f	839	0	866	10	0
31	g	853	0	919	34	0
32	h	999	0	1092	36	0
33	i	754	0	836	28	0
34	j	600	0	613	17	0
35	k	564	0	611	31	0
36	r	1086	0	842	29	0
37	s	253	0	300	16	0
38	u	944	0	983	49	0
39	w	3377	0	3430	93	0
40	y	1697	0	1679	53	0
41	z	292	0	317	16	0
42	T	159	0	150	8	0
43	j	1	0	0	0	0
All	All	95651	0	71072	1692	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 10.

All (1692) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:b:117:LEU:HD13	26:b:129:LEU:HD22	1.50	0.94
36:r:71:ARG:NH1	36:r:71:ARG:O	2.07	0.88
25:a:75:LEU:HA	25:a:78:LEU:HD23	1.57	0.86
1:1:591:G:H1'	1:1:592:U:H3'	1.58	0.85
12:M:51:ILE:HD11	12:M:55:SER:HB3	1.58	0.84
26:b:162:PRO:HB3	36:r:3:GLN:HG3	1.60	0.83
41:z:104:ARG:HH12	41:z:108:SER:HB3	1.44	0.82
11:L:176:PHE:HD1	11:L:179:LEU:HD12	1.43	0.81
18:S:11:ARG:HE	42:T:141:VAL:HG23	1.45	0.81
26:b:427:TRP:HZ3	38:u:84:ARG:HH11	1.27	0.81
26:b:453:LEU:HD12	26:b:456:LEU:HD23	1.61	0.81
1:1:3112:A:HO2'	1:1:3113:A:H8	1.30	0.80
5:B:210:GLU:HB2	41:z:114:LEU:HD21	1.63	0.80
10:H:5:ILE:HB	18:S:141:GLN:HE21	1.46	0.80
5:B:212:ASN:O	5:B:212:ASN:ND2	2.15	0.80
6:C:140:ARG:HH21	6:C:242:PRO:HG2	1.48	0.78
18:S:58:VAL:HG21	42:T:141:VAL:HG21	1.64	0.78
11:L:176:PHE:HB3	25:a:131:ARG:NH1	1.98	0.78
35:k:53:LYS:HA	35:k:56:LYS:HE3	1.65	0.78
3:3:16:CYS:HB3	3:3:19:ARG:HG2	1.64	0.78
5:B:331:PRO:HD2	5:B:334:ARG:HE	1.48	0.78
36:r:58:LYS:HA	36:r:61:MET:HE2	1.66	0.77
20:V:12:LYS:HB2	20:V:127:LEU:HD21	1.67	0.77
1:1:2465:G:H5'	1:1:2466:C:H5	1.50	0.77
38:u:2:ARG:HD3	38:u:75:ARG:HH22	1.50	0.77
40:y:161:VAL:HG13	40:y:181:LEU:HD11	1.68	0.76
5:B:19:ARG:HB2	5:B:232:ARG:HH21	1.51	0.76
3:3:3:GLN:HG2	3:3:6:VAL:HG12	1.68	0.75
6:C:338:LYS:HE2	6:C:338:LYS:HA	1.68	0.75
1:1:616:A:O2'	7:E:38:LYS:NZ	2.20	0.75
1:1:3470:G:H1	5:B:381:GLY:H	1.32	0.74
3:3:20:ILE:HD11	3:3:29:ARG:HG3	1.69	0.74
35:k:56:LYS:HA	35:k:59:GLN:HE22	1.53	0.74
1:1:1790:A:OP1	35:k:36:LYS:NZ	2.21	0.74
3:3:19:ARG:NH2	3:3:28:CYS:SG	2.60	0.74
15:P:176:ARG:NH1	15:P:177:ASN:OD1	2.21	0.74
18:S:95:ASP:OD2	18:S:96:THR:N	2.20	0.73
33:i:64:ASP:OD1	33:i:68:ARG:NH1	2.20	0.73
39:w:253:HIS:ND1	39:w:253:HIS:O	2.21	0.73
12:M:82:ASP:OD1	12:M:82:ASP:O	2.07	0.73
34:j:39:TYR:CD1	34:j:40:PRO:HA	2.23	0.72
1:1:2933:A:N6	1:1:2945:G:O2'	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:35:THR:HG23	3:3:37:LEU:H	1.53	0.72
1:1:3336:G:H1	1:1:3351:U:H3	1.36	0.72
1:1:735:G:N2	1:1:738:A:OP2	2.23	0.72
26:b:419:LYS:NZ	40:y:35:TYR:OH	2.21	0.72
26:b:436:LEU:HD22	38:u:91:LEU:HD12	1.71	0.72
1:1:1762:U:OP2	17:R:103:ARG:NH1	2.23	0.71
15:P:50:ASN:HB3	15:P:56:GLN:HG3	1.72	0.71
28:d:56:VAL:HG13	28:d:60:LEU:HD23	1.73	0.71
12:M:11:GLY:HA2	12:M:65:LEU:HD23	1.72	0.71
18:S:12:LYS:HA	18:S:55:GLY:HA2	1.70	0.71
2:2:79:A:OP2	23:Y:50:ARG:NH1	2.24	0.71
6:C:101:MET:HE2	6:C:104:PRO:HA	1.72	0.71
1:1:787:G:H21	1:1:804:A:H62	1.37	0.70
26:b:444:PHE:CD1	38:u:94:MET:HE1	2.27	0.70
1:1:1242:U:O2'	18:S:112:ARG:NH1	2.24	0.70
1:1:1527:G:OP2	1:1:1527:G:N2	2.21	0.70
1:1:1439:U:OP2	29:e:56:ASN:ND2	2.24	0.70
3:3:32:TYR:HA	3:3:52:THR:HG21	1.74	0.70
2:2:71:G:O2'	32:h:51:LYS:NZ	2.25	0.70
26:b:144:GLN:OE1	26:b:144:GLN:N	2.25	0.69
40:y:28:LEU:HB3	40:y:52:THR:HG23	1.73	0.69
29:e:84:MET:N	29:e:84:MET:SD	2.65	0.69
1:1:216:A:N3	6:C:223:ASN:ND2	2.39	0.69
1:1:3027:U:OP2	20:V:3:ARG:NH1	2.25	0.69
23:Y:99:ASP:OD1	23:Y:100:ALA:N	2.26	0.69
39:w:475:VAL:HG23	39:w:476:LYS:H	1.58	0.69
26:b:446:ASP:HB3	26:b:449:ILE:HB	1.75	0.69
33:i:6:VAL:HG13	33:i:7:VAL:HG23	1.74	0.69
39:w:84:ILE:HB	39:w:87:CYS:SG	2.33	0.69
11:L:55:ARG:O	11:L:115:ARG:NH1	2.26	0.69
1:1:590:U:H3'	1:1:591:G:H5''	1.74	0.68
12:M:120:ARG:HH11	14:O:183:LYS:HD2	1.57	0.68
33:i:85:ILE:O	33:i:89:THR:HG23	1.93	0.68
17:R:89:MET:N	17:R:89:MET:SD	2.66	0.68
1:1:592:U:C4	6:C:347:LYS:HA	2.29	0.68
1:1:3139:C:OP2	20:V:47:ARG:NH1	2.27	0.68
5:B:212:ASN:C	5:B:212:ASN:HD22	2.01	0.68
10:H:21:ILE:HG22	10:H:26:VAL:HG12	1.74	0.68
11:L:55:ARG:NH1	11:L:73:ARG:O	2.26	0.68
40:y:107:ILE:HG13	40:y:108:VAL:HG23	1.75	0.68
39:w:114:VAL:HG22	39:w:154:THR:HB	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:29:ARG:HG2	29:e:81:LEU:HD21	1.74	0.67
1:1:34:A:N3	1:1:842:A:O2'	2.27	0.67
15:P:124:LYS:HB3	15:P:140:LEU:HD22	1.75	0.67
30:f:57:SER:O	30:f:64:LYS:NZ	2.27	0.67
1:1:3092:U:H3'	1:1:3093:G:H5'	1.76	0.67
1:1:277:G:H5''	13:N:14:LYS:HE3	1.77	0.67
5:B:301:THR:HG1	26:b:437:ASP:H	1.42	0.67
18:S:11:ARG:HD2	18:S:21:PRO:HG2	1.77	0.67
39:w:149:LEU:HD12	39:w:153:GLY:HA3	1.77	0.67
1:1:3082:A:H5'	14:O:69:ARG:HH22	1.58	0.67
1:1:110:G:OP2	11:L:73:ARG:NH2	2.28	0.66
1:1:2985:A:O2'	1:1:3028:A:N3	2.27	0.66
33:i:52:GLU:HG3	33:i:88:LEU:HD21	1.77	0.66
40:y:45:VAL:HG12	40:y:46:VAL:HG13	1.76	0.66
1:1:3276:A:OP2	14:O:172:LYS:NZ	2.28	0.66
39:w:106:TYR:O	39:w:108:LYS:NZ	2.28	0.66
1:1:3111:C:OP2	41:z:83:THR:N	2.29	0.66
1:1:1159:U:O4	37:s:29:LYS:NZ	2.26	0.66
13:N:44:ARG:NH1	13:N:120:TRP:O	2.29	0.66
1:1:420:G:H21	15:P:118:GLN:HE22	1.43	0.66
1:1:1734:A:O2'	35:k:3:ARG:NH1	2.28	0.66
9:G:227[B]:ASP:O	9:G:231:ARG:NH2	2.29	0.66
25:a:88:ASP:O	25:a:93:LYS:NZ	2.27	0.66
1:1:1438:G:N2	1:1:1441:A:OP2	2.26	0.66
18:S:76:ILE:HG23	18:S:125:VAL:HG22	1.76	0.66
1:1:1786:U:H2'	1:1:1787:G:H8	1.60	0.66
1:1:3014:A:H61	1:1:3022:C:H42	1.44	0.66
6:C:329:ARG:HG2	6:C:330:LEU:HD12	1.78	0.66
1:1:1755:A:H61	1:1:1768:G:H22	1.44	0.65
7:E:72:VAL:HA	7:E:82:VAL:HG23	1.78	0.65
26:b:424:ASP:O	26:b:427:TRP:NE1	2.30	0.65
1:1:2452:G:H1	1:1:2484:G:H1	1.43	0.65
3:3:69:ARG:NH2	3:3:76:LEU:O	2.29	0.65
1:1:1548:G:N2	1:1:1896:A:O2'	2.25	0.65
3:3:74:SER:HB3	6:C:148:PRO:HA	1.79	0.65
11:L:192:ARG:O	11:L:196:GLN:NE2	2.29	0.65
20:V:2:SER:O	20:V:4:GLY:N	2.29	0.65
1:1:361:G:O6	34:j:55:ARG:NH2	2.28	0.65
1:1:1758:G:OP2	17:R:121:HIS:ND1	2.27	0.65
1:1:1876:U:H1'	31:g:67:HIS:CD2	2.32	0.65
8:F:153:GLU:HG3	8:F:250:LEU:HD13	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:b:436:LEU:HD23	38:u:94:MET:HG3	1.78	0.65
1:1:3012:G:H1	1:1:3024:C:H5	1.43	0.65
20:V:61:LEU:HD12	20:V:75:ILE:HG22	1.78	0.65
20:V:72:ARG:O	20:V:73:LYS:HG2	1.96	0.65
26:b:102:ALA:O	26:b:106:VAL:HG23	1.96	0.65
1:1:772:A:H1'	16:Q:142:ARG:HH11	1.62	0.65
1:1:1424:A:N6	1:1:1452:A:O2'	2.30	0.65
11:L:176:PHE:HB3	25:a:131:ARG:HH12	1.60	0.65
1:1:701:G:OP1	16:Q:109:LYS:NZ	2.30	0.64
1:1:1143:A:N3	1:1:1404:G:O2'	2.30	0.64
5:B:119:TYR:O	5:B:175:LYS:NZ	2.30	0.64
5:B:346:THR:HG21	41:z:103:LYS:HB3	1.80	0.64
1:1:1224:A:OP1	14:O:50:ARG:NH1	2.30	0.64
1:1:2458:G:H5''	1:1:2459:G:H5'	1.80	0.64
1:1:3480:C:H4'	5:B:315:GLY:HA2	1.79	0.64
25:a:82:LEU:HD21	25:a:101:ILE:HG12	1.78	0.64
39:w:83:PRO:HA	39:w:89:THR:HG21	1.78	0.64
40:y:54:GLY:N	40:y:80:GLU:OE1	2.30	0.64
1:1:161:C:H1'	33:i:24:PRO:HB2	1.79	0.64
1:1:1639:U:O2	1:1:1639:U:H2'	1.95	0.64
1:1:744:U:H3'	1:1:745:G:C8	2.33	0.64
9:G:225:LYS:HD2	9:G:226:TYR:H	1.63	0.64
1:1:1790:A:O5'	35:k:26:LYS:NZ	2.31	0.64
1:1:2926:G:H1	1:1:2952:C:H42	1.44	0.64
20:V:106:ASN:ND2	20:V:110:GLU:O	2.31	0.64
36:r:154:THR:HA	36:r:213:VAL:HA	1.80	0.64
32:h:84:GLN:HE22	32:h:91:ARG:HG2	1.62	0.64
42:T:144:GLU:CD	42:T:144:GLU:H	2.06	0.64
1:1:1529:U:H4'	1:1:1548:G:H4'	1.79	0.64
1:1:3024:C:O2'	1:1:3025:A:O5'	2.16	0.64
1:1:3104:G:OP2	14:O:75:ARG:NH1	2.31	0.64
4:8:27:ILE:HD12	4:8:30:ARG:HD2	1.80	0.64
9:G:227[A]:ASP:O	9:G:231:ARG:NH2	2.31	0.64
1:1:1229:C:H3'	1:1:1230:C:H5'	1.79	0.64
5:B:92:TYR:HB3	5:B:99:LEU:HD12	1.79	0.64
26:b:128:GLN:OE1	26:b:131:ARG:HD3	1.98	0.64
13:N:28:TRP:O	13:N:32:GLN:NE2	2.31	0.63
22:X:102:TYR:HB2	22:X:104:VAL:HG22	1.81	0.63
14:O:141:ARG:NH1	14:O:145:GLU:OE2	2.31	0.63
32:h:80:LEU:HA	32:h:83:ARG:HD2	1.80	0.63
10:H:118:GLU:HG3	10:H:122:ARG:HH21	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1218:C:H5	1:1:1350:G:H1	1.45	0.63
1:1:513:U:O2'	7:E:44:ARG:NH1	2.32	0.63
22:X:63:VAL:O	32:h:31:ARG:NH1	2.32	0.63
39:w:39:LYS:HZ1	39:w:40:TYR:HD1	1.44	0.63
31:g:86:LYS:O	31:g:90:VAL:HG12	1.98	0.63
36:r:8:GLU:HA	36:r:11:ILE:HB	1.79	0.63
38:u:47:ARG:NH1	39:w:298:GLU:OE1	2.31	0.63
1:1:366:G:N2	1:1:369:A:OP2	2.27	0.63
1:1:372:G:OP2	34:j:52:LYS:NZ	2.31	0.62
1:1:1783:G:O2'	1:1:1784:U:O2	2.16	0.62
35:k:56:LYS:HA	35:k:59:GLN:NE2	2.14	0.62
1:1:420:G:N3	15:P:118:GLN:NE2	2.46	0.62
1:1:3035:A:OP2	5:B:2:SER:N	2.32	0.62
9:G:90:VAL:HG22	9:G:214:ILE:HD11	1.82	0.62
1:1:1379:U:OP1	16:Q:38:ARG:NH1	2.31	0.62
39:w:111:LYS:HB3	39:w:150:VAL:HB	1.80	0.62
1:1:621:G:OP2	8:F:44:ARG:NH2	2.31	0.62
1:1:743:A:N6	25:a:116:ARG:HD2	2.15	0.62
9:G:183:LYS:HD3	9:G:194:THR:HG23	1.81	0.62
39:w:59:TRP:NE1	39:w:118:ASP:OD2	2.33	0.62
20:V:82:ARG:HD3	20:V:119:PRO:HG2	1.81	0.62
26:b:15:VAL:HG21	26:b:142:LYS:HA	1.82	0.62
1:1:953:A:N6	1:1:1900:G:O3'	2.33	0.61
1:1:3469:U:H4'	1:1:3470:G:H5'	1.81	0.61
23:Y:40:GLU:O	23:Y:43:LYS:NZ	2.32	0.61
25:a:75:LEU:HD11	25:a:113:GLY:HA2	1.82	0.61
28:d:30:PHE:HB3	28:d:70:ARG:HE	1.66	0.61
1:1:1006:A:H2'	1:1:1007:C:C6	2.35	0.61
1:1:1538:A:P	15:P:23:ARG:HH21	2.23	0.61
1:1:816:A:O2'	16:Q:93:ARG:NH2	2.33	0.61
1:1:348:C:OP2	6:C:197:ARG:NH1	2.32	0.61
1:1:3230:G:OP1	14:O:75:ARG:NH2	2.34	0.61
36:r:68:HIS:O	36:r:72:ASN:ND2	2.34	0.61
3:3:55:GLU:HB2	3:3:115:LEU:HD21	1.82	0.61
11:L:176:PHE:HA	11:L:179:LEU:HG	1.81	0.61
20:V:122:LYS:NZ	20:V:139:VAL:OXT	2.34	0.61
26:b:156:GLN:HB3	26:b:160:ARG:HH21	1.64	0.60
1:1:402:U:H5'	23:Y:86:ARG:HH22	1.66	0.60
1:1:632:A:OP1	7:E:44:ARG:NH2	2.34	0.60
39:w:167:ASN:ND2	39:w:217:VAL:O	2.34	0.60
1:1:1486:A:OP1	1:1:1541:G:N1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1835:U:O2'	1:1:1837:G:N2	2.34	0.60
1:1:3332:U:H2'	1:1:3333:G:C8	2.37	0.60
1:1:3494:U:H5''	15:P:43:LYS:HE2	1.83	0.60
1:1:615:G:N2	1:1:637:U:OP1	2.28	0.60
1:1:1233:A:OP2	1:1:1234:A:O2'	2.19	0.60
1:1:3131:C:OP1	41:z:91:ARG:NH2	2.35	0.60
28:d:11:GLN:O	28:d:82:ARG:NH1	2.31	0.60
39:w:289:LEU:HD13	39:w:292:LEU:HD12	1.83	0.60
1:1:869:A:H61	1:1:888:G:H1'	1.65	0.60
1:1:1779:U:H4'	31:g:55:PRO:HA	1.82	0.60
1:1:3164:U:H5	17:R:62:ARG:HH22	1.48	0.60
3:3:10:VAL:HG13	6:C:34:PRO:HB3	1.83	0.60
7:E:86:TYR:HB2	7:E:157:GLN:NE2	2.16	0.60
12:M:78:TRP:NE1	12:M:84:CYS:SG	2.73	0.60
35:k:10:GLN:O	35:k:14:ILE:HG13	2.00	0.60
1:1:1284:U:H5''	1:1:1285:C:H5'	1.83	0.60
15:P:119:VAL:HG22	15:P:146:ILE:HG12	1.83	0.60
40:y:19:LEU:HD21	40:y:200:ASN:HD22	1.66	0.60
1:1:378:U:H4'	1:1:412:G:H5'	1.84	0.60
35:k:20:ALA:HB1	35:k:37:LEU:HD11	1.84	0.60
1:1:1696:G:H2'	1:1:1697:G:H8	1.65	0.60
4:8:27:ILE:O	4:8:33:ASN:ND2	2.33	0.60
10:H:113:ARG:HE	10:H:121:THR:HG23	1.67	0.60
26:b:9:ILE:HG12	26:b:68:GLU:HB3	1.82	0.60
32:h:98:GLU:HA	32:h:101:ARG:HG2	1.84	0.60
1:1:3285:G:H1	1:1:3302:U:H3	1.50	0.60
13:N:172:ARG:HG3	13:N:174:ILE:HG12	1.84	0.60
12:M:7:TYR:O	12:M:12:ARG:NE	2.35	0.59
32:h:16:LEU:HD12	32:h:56:ILE:HG23	1.84	0.59
20:V:25:MET:HE1	20:V:102:GLY:HA3	1.81	0.59
1:1:719:A:OP1	13:N:199:ARG:NH2	2.35	0.59
1:1:1696:G:H2'	1:1:1697:G:C8	2.38	0.59
20:V:42:PHE:CD2	20:V:59:MET:HG2	2.38	0.59
31:g:92:ALA:O	31:g:96:GLU:HG3	2.01	0.59
1:1:174:U:OP2	11:L:134:LYS:NZ	2.29	0.59
1:1:515:A:O2'	6:C:318:LYS:NZ	2.35	0.59
1:1:1207:C:H4'	14:O:90:PRO:HD3	1.83	0.59
1:1:3083:C:OP1	14:O:66:ASN:ND2	2.31	0.59
39:w:139:LEU:HD22	39:w:218:PHE:HE2	1.65	0.59
1:1:1156:U:H2'	1:1:1157:G:H8	1.67	0.59
1:1:1767:G:H4'	1:1:1770:G:H4'	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2480:C:O2'	5:B:266:ARG:NH1	2.36	0.59
1:1:531:A:OP2	8:F:77:ARG:NH1	2.36	0.59
1:1:1377:G:O2'	6:C:307:PRO:O	2.20	0.59
3:3:5:GLU:OE1	6:C:289:VAL:N	2.33	0.59
6:C:341:VAL:HG23	6:C:343:ILE:HD11	1.84	0.59
20:V:41:VAL:HG12	20:V:60:VAL:HG12	1.85	0.59
26:b:76:HIS:ND1	26:b:77:PRO:HD2	2.18	0.59
1:1:864:G:H1	1:1:894:U:H3	1.51	0.59
1:1:3315:A:OP2	12:M:118:LYS:NZ	2.31	0.59
5:B:80:GLU:OE2	5:B:319:ASN:ND2	2.36	0.59
40:y:18:ASN:ND2	40:y:63:THR:O	2.35	0.59
1:1:286:U:H3	1:1:295:G:H1	1.50	0.59
6:C:295:SER:OG	6:C:297:GLU:OE1	2.20	0.59
22:X:94:ILE:HD12	22:X:94:ILE:H	1.68	0.59
40:y:85:ARG:NH2	40:y:89:PRO:O	2.35	0.59
1:1:1787:G:OP1	35:k:34:LYS:NZ	2.34	0.59
3:3:33:ASN:ND2	3:3:42:SER:O	2.35	0.59
9:G:161:GLU:OE2	13:N:26:ARG:NH1	2.29	0.59
20:V:70:ASP:OD2	20:V:70:ASP:N	2.33	0.59
36:r:3:GLN:N	36:r:3:GLN:OE1	2.36	0.59
1:1:744:U:H3'	1:1:745:G:H8	1.67	0.58
9:G:156:ASP:O	9:G:183:LYS:NZ	2.35	0.58
13:N:68:ARG:NH1	13:N:124:ASP:O	2.36	0.58
39:w:73:ILE:HD13	39:w:86:ASN:HB2	1.83	0.58
1:1:2929:G:H1	1:1:2949:U:H3	1.50	0.58
9:G:210:GLU:O	9:G:214:ILE:HG22	2.02	0.58
14:O:122:PRO:HA	14:O:125:LEU:HD12	1.84	0.58
26:b:71:LYS:O	26:b:75:ILE:HG23	2.03	0.58
39:w:237:LYS:HB3	39:w:239:LYS:HE3	1.85	0.58
1:1:985:G:H1'	1:1:1147:G:C8	2.38	0.58
2:2:103:G:O2'	34:j:81:GLY:O	2.20	0.58
35:k:10:GLN:HA	35:k:13:GLU:HG3	1.84	0.58
1:1:138:U:N3	32:h:70:GLU:OE2	2.33	0.58
1:1:877:G:N2	1:1:880:A:OP2	2.31	0.58
38:u:85:ASN:OD1	38:u:86:VAL:N	2.36	0.58
1:1:1470:U:N3	39:w:783:ASP:OD2	2.36	0.58
1:1:1660:A:OP1	1:1:1678:A:N6	2.37	0.58
5:B:159:ARG:HG2	5:B:182:GLN:HA	1.86	0.58
7:E:127:GLN:CD	7:E:128:LYS:H	2.11	0.58
10:H:115:PHE:O	10:H:118:GLU:HG2	2.03	0.58
1:1:1308:C:O2'	1:1:1309:A:O5'	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1755:A:N1	1:1:1767:G:N2	2.51	0.58
5:B:212:ASN:ND2	5:B:212:ASN:C	2.61	0.58
9:G:163:VAL:HA	9:G:166:LEU:HD12	1.86	0.58
40:y:18:ASN:HB2	40:y:60:GLY:HA2	1.86	0.58
1:1:738:A:O2'	11:L:187:ARG:NH1	2.25	0.58
14:O:144:SER:OG	14:O:145:GLU:OE1	2.17	0.58
26:b:423:GLN:HG3	38:u:81:ARG:HH21	1.68	0.58
35:k:52:LYS:NZ	35:k:53:LYS:HZ3	2.01	0.58
1:1:1845:A:OP1	31:g:67:HIS:ND1	2.37	0.58
1:1:739:G:H5'	11:L:183:ARG:HH12	1.68	0.57
1:1:968:A:O2'	1:1:970:C:N4	2.37	0.57
1:1:3204:G:N3	10:H:161:GLN:NE2	2.52	0.57
11:L:176:PHE:CD1	11:L:179:LEU:HD12	2.33	0.57
6:C:207:PRO:HG2	6:C:227:VAL:HG22	1.84	0.57
20:V:119:PRO:HA	20:V:137:THR:HG23	1.87	0.57
40:y:21:ASN:HB2	40:y:67:ARG:HB3	1.86	0.57
1:1:1761:U:O4	17:R:128:LYS:NZ	2.35	0.57
1:1:3100:C:OP2	5:B:28:LYS:NZ	2.36	0.57
26:b:422:LEU:HD22	26:b:427:TRP:CZ2	2.40	0.57
26:b:427:TRP:CE3	38:u:84:ARG:HD2	2.40	0.57
38:u:23:ARG:NH2	38:u:25:ASP:OD1	2.32	0.57
40:y:193:ILE:H	40:y:193:ILE:HD12	1.69	0.57
1:1:63:A:N3	1:1:78:U:O2'	2.32	0.57
1:1:1578:G:H5'	13:N:67:ARG:HE	1.69	0.57
13:N:99:ARG:HB3	13:N:167:ILE:HG12	1.85	0.57
26:b:55:GLN:O	26:b:59:THR:HG22	2.04	0.57
1:1:401:U:O3'	23:Y:86:ARG:NH2	2.38	0.57
1:1:444:A:N1	1:1:647:A:N6	2.52	0.57
13:N:99:ARG:NH2	13:N:118:SER:O	2.37	0.57
20:V:117:THR:HG22	39:w:250:TYR:HA	1.86	0.57
1:1:3138:U:H5''	20:V:47:ARG:HD2	1.87	0.57
1:1:3235:A:OP2	5:B:30:LYS:NZ	2.26	0.57
31:g:46:ASP:OD1	31:g:88:ARG:NH2	2.32	0.57
1:1:2993:G:H22	36:r:7:ILE:H	1.53	0.57
1:1:3146:U:O2'	38:u:16:GLY:O	2.23	0.57
6:C:337:TYR:HE1	8:F:59:GLU:HG3	1.69	0.57
14:O:184:GLU:OE1	14:O:184:GLU:N	2.27	0.57
1:1:323:C:OP1	11:L:102:ARG:NH2	2.29	0.57
1:1:1536:G:N2	1:1:1547:G:N7	2.45	0.57
3:3:19:ARG:NH1	3:3:38:CYS:HB2	2.20	0.57
3:3:85:ASN:HB3	3:3:88:LYS:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3475:U:OP1	28:d:20:HIS:NE2	2.27	0.57
2:2:80:A:N6	2:2:87:A:H61	2.02	0.57
4:8:18:ARG:HG3	4:8:21:ARG:HH21	1.69	0.57
35:k:34:LYS:HG2	35:k:47:VAL:HG22	1.85	0.57
1:1:3327:A:H2'	1:1:3328:U:C6	2.40	0.57
31:g:65:LEU:HB2	31:g:70:LYS:HE3	1.86	0.57
1:1:727:C:H2'	1:1:728:G:H8	1.70	0.56
1:1:1632:C:H5'	1:1:1731:A:H1'	1.87	0.56
1:1:2925:G:H2'	1:1:2926:G:H8	1.70	0.56
8:F:221:TRP:HB3	8:F:234:ASP:OD2	2.05	0.56
1:1:742:A:OP1	25:a:132:ARG:NH2	2.37	0.56
14:O:55:TYR:OH	14:O:74:PHE:O	2.21	0.56
38:u:63:MET:HG2	38:u:108:PHE:CD1	2.40	0.56
40:y:15:VAL:HA	40:y:61:ARG:HG2	1.87	0.56
1:1:383:A:OP2	23:Y:88:LYS:NZ	2.38	0.56
1:1:385:A:O2'	1:1:399:A:N1	2.34	0.56
20:V:69:PRO:O	20:V:73:LYS:NZ	2.35	0.56
26:b:31:PRO:HD2	26:b:49:ARG:HD3	1.87	0.56
31:g:13:TYR:O	31:g:15:THR:HG23	2.05	0.56
1:1:746:C:N3	16:Q:73:LYS:HA	2.20	0.56
23:Y:80:LEU:HD22	23:Y:95:PRO:HB2	1.86	0.56
35:k:50:ASP:HB3	35:k:53:LYS:HD2	1.87	0.56
40:y:109:ALA:HB2	40:y:149:GLY:HA2	1.87	0.56
1:1:440:A:OP1	30:f:66:ARG:NH2	2.39	0.56
1:1:1460:C:H4'	6:C:42:THR:HG23	1.88	0.56
2:2:162:C:OP1	9:G:181:LYS:NZ	2.33	0.56
17:R:135:LYS:O	17:R:139:ILE:HG12	2.04	0.56
18:S:44:LEU:HG	18:S:50:VAL:HB	1.88	0.56
25:a:131:ARG:CZ	25:a:131:ARG:HA	2.35	0.56
17:R:52:ARG:NH1	17:R:53:LYS:O	2.38	0.56
1:1:238:U:H5'	1:1:240:G:H5'	1.88	0.56
22:X:102:TYR:HA	22:X:137:ARG:HH22	1.69	0.56
1:1:778:G:H1	1:1:815:A:H2	1.54	0.56
1:1:1636:U:OP2	17:R:42:ARG:NH2	2.39	0.56
7:E:144:ALA:HB2	15:P:176:ARG:CZ	2.36	0.56
12:M:19:GLY:O	12:M:22:THR:OG1	2.24	0.56
18:S:79:ARG:NH1	18:S:86:THR:OG1	2.33	0.56
1:1:740:U:H2'	1:1:741:G:O4'	2.04	0.56
1:1:1679:A:H5''	1:1:1680:U:H5''	1.87	0.56
3:3:30:ASN:O	3:3:54:ARG:NH2	2.38	0.56
6:C:293:ILE:HD11	16:Q:34:PHE:CG	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:w:214:PRO:HB2	39:w:215:ARG:NH2	2.21	0.56
1:1:749:G:H1	1:1:776:U:H3	1.53	0.55
3:3:6:VAL:O	3:3:10:VAL:HG23	2.06	0.55
5:B:281:LYS:HB2	5:B:325:ASN:HD22	1.71	0.55
9:G:137:ASN:HD22	13:N:3:ALA:H	1.52	0.55
26:b:388:TYR:CE2	26:b:398:LEU:HG	2.41	0.55
38:u:2:ARG:NH2	38:u:3:VAL:O	2.38	0.55
1:1:262:A:N3	32:h:112:TYR:OH	2.38	0.55
1:1:744:U:H5'	1:1:745:G:N7	2.22	0.55
8:F:116:LEU:HD12	8:F:117:GLN:HG3	1.86	0.55
17:R:110:ARG:HD3	17:R:120:TYR:HD2	1.71	0.55
20:V:82:ARG:NH1	20:V:119:PRO:O	2.32	0.55
25:a:135:GLU:HA	25:a:138:LYS:HG2	1.88	0.55
39:w:32:LYS:HB3	39:w:195:PHE:HE2	1.72	0.55
40:y:199:VAL:HG11	40:y:222:PHE:CE2	2.41	0.55
1:1:1160:A:C6	1:1:1161:A:C4	2.94	0.55
40:y:177:LEU:HB3	40:y:179:VAL:HG12	1.88	0.55
1:1:1825:U:H4'	31:g:19:ARG:HH12	1.70	0.55
26:b:426:SER:C	26:b:428:LYS:H	2.14	0.55
38:u:84:ARG:H	38:u:84:ARG:HD3	1.71	0.55
6:C:22:LEU:HD21	6:C:254:LYS:HD3	1.86	0.55
28:d:18:THR:OG1	28:d:77:ARG:NH1	2.36	0.55
29:e:13:PRO:HG2	29:e:15:LYS:HE2	1.88	0.55
29:e:86:ASN:HB3	29:e:114:VAL:HG22	1.87	0.55
35:k:30:ASN:OD1	35:k:32:ASP:HB2	2.06	0.55
1:1:756:C:H2'	1:1:757:G:C8	2.42	0.55
1:1:1827:G:H2'	1:1:1828:A:C8	2.41	0.55
7:E:76:LEU:HG	7:E:77:GLU:H	1.72	0.55
9:G:144:GLU:OE2	13:N:6:TYR:OH	2.23	0.55
29:e:116:VAL:HB	29:e:119:ALA:HB2	1.88	0.55
13:N:120:TRP:HZ2	13:N:123:GLN:HG2	1.72	0.55
31:g:57:LEU:HD22	31:g:61:GLU:HG3	1.89	0.55
33:i:49:ALA:HB3	33:i:52:GLU:OE1	2.07	0.55
40:y:97:VAL:HG13	40:y:128:ILE:HD11	1.89	0.55
1:1:263:A:H2'	1:1:264:G:H8	1.71	0.55
1:1:1566:C:O2'	1:1:1840:A:H1'	2.07	0.55
1:1:3314:U:C2	12:M:114:MET:HE1	2.42	0.55
23:Y:78:LEU:HD21	23:Y:97:GLY:HA3	1.89	0.55
14:O:110:PRO:HB2	14:O:112:PRO:HD2	1.89	0.55
20:V:84:ARG:HH21	39:w:238:ARG:HG3	1.71	0.55
29:e:77:SER:O	29:e:81:LEU:HD23	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1688:G:H2'	1:1:1689:A:C8	2.41	0.55
1:1:2994:C:O2'	1:1:2996:G:OP2	2.24	0.55
8:F:102:ILE:HD13	8:F:110:MET:HE1	1.89	0.55
1:1:1336:U:C2	14:O:64:ARG:HG3	2.41	0.54
1:1:1628:A:O5'	31:g:60:ARG:HG3	2.06	0.54
1:1:2982:A:N3	1:1:2982:A:H5'	2.21	0.54
15:P:126:ARG:HE	15:P:140:LEU:HD21	1.72	0.54
26:b:421:ILE:O	38:u:81:ARG:NH1	2.40	0.54
33:i:43:ARG:NH2	33:i:47:GLY:O	2.38	0.54
1:1:1180:G:OP1	30:f:21:LYS:NZ	2.40	0.54
1:1:1527:G:H2'	4:8:13:LEU:HD22	1.89	0.54
1:1:1668:C:H2'	1:1:1669:G:C8	2.43	0.54
1:1:1781:G:C6	1:1:1782:U:H1'	2.42	0.54
1:1:3354:U:H2'	1:1:3355:G:C8	2.42	0.54
2:2:98:U:O4	4:8:30:ARG:NH2	2.40	0.54
5:B:45:ALA:HB3	5:B:181:ILE:HG23	1.89	0.54
7:E:144:ALA:HB1	7:E:145:PRO:CD	2.37	0.54
38:u:42:MET:SD	38:u:44:ARG:NH2	2.80	0.54
38:u:83:ASP:O	38:u:87:ILE:HB	2.07	0.54
1:1:223:G:OP1	23:Y:15:ARG:NH1	2.40	0.54
5:B:123:PHE:CE2	5:B:124:LYS:HG3	2.42	0.54
6:C:216:GLY:HA2	6:C:219:LYS:HE3	1.89	0.54
23:Y:69:ILE:HD11	23:Y:79:LEU:HD13	1.90	0.54
33:i:56:MET:SD	33:i:88:LEU:HD23	2.47	0.54
39:w:111:LYS:NZ	39:w:149:LEU:O	2.35	0.54
1:1:222:G:H5''	23:Y:11:ARG:HG3	1.89	0.54
1:1:832:G:O6	6:C:106:LYS:NZ	2.40	0.54
1:1:1768:G:H1'	27:c:40:GLY:HA2	1.88	0.54
20:V:21:VAL:HG12	20:V:51:LEU:HD22	1.88	0.54
20:V:138:VAL:N	40:y:102:SER:OG	2.38	0.54
22:X:109:ILE:HG12	22:X:123:VAL:HG22	1.89	0.54
26:b:12:ILE:HD11	26:b:65:ILE:HG23	1.88	0.54
26:b:133:ALA:O	26:b:137:MET:HG3	2.07	0.54
1:1:194:A:N1	1:1:218:A:O2'	2.37	0.54
1:1:606:G:OP1	7:E:47:LYS:NZ	2.36	0.54
1:1:2925:G:H2'	1:1:2926:G:C8	2.43	0.54
2:2:49:A:O2'	34:j:59:THR:OG1	2.24	0.54
11:L:63:ILE:HD12	11:L:66:ASN:HD21	1.72	0.54
38:u:84:ARG:HA	38:u:87:ILE:HG22	1.90	0.54
39:w:93:ASP:HB3	39:w:96:SER:HB2	1.90	0.54
1:1:67:A:O2'	1:1:323:C:O2	2.24	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:590:U:H3'	1:1:591:G:C5'	2.38	0.54
12:M:51:ILE:HD12	12:M:52:ARG:H	1.73	0.54
23:Y:50:ARG:HB3	23:Y:114:ARG:NH2	2.22	0.54
1:1:1845:A:H2'	1:1:1846:A:H8	1.73	0.54
29:e:112:LEU:HB3	29:e:114:VAL:HG23	1.88	0.54
38:u:24:ASN:HB3	39:w:252:LEU:HD13	1.88	0.54
38:u:32:CYS:SG	38:u:33:ARG:HG2	2.47	0.54
40:y:2:ALA:HB1	40:y:215:LEU:HD22	1.90	0.54
2:2:151:U:OP1	13:N:38:ARG:NH2	2.29	0.54
18:S:11:ARG:NH1	18:S:14:PRO:HD3	2.22	0.54
26:b:98:GLN:HG3	26:b:144:GLN:HG3	1.89	0.54
39:w:39:LYS:NZ	39:w:40:TYR:HD1	2.05	0.54
1:1:1887:C:OP1	22:X:119:LYS:NZ	2.34	0.54
1:1:3314:U:OP2	12:M:121:ARG:NH2	2.40	0.54
10:H:37:GLN:NE2	10:H:38:ASN:O	2.41	0.54
20:V:110:GLU:HA	20:V:130:ARG:HG2	1.90	0.54
37:s:13:THR:HA	37:s:16:ARG:HG2	1.90	0.54
5:B:41:VAL:HG21	5:B:194:TRP:CG	2.43	0.54
7:E:61:LEU:HD11	7:E:102:ILE:HG12	1.90	0.54
13:N:32:GLN:H	13:N:32:GLN:CD	2.16	0.54
21:W:177:GLY:N	36:r:13:LYS:O	2.41	0.54
22:X:102:TYR:HA	22:X:137:ARG:NH2	2.23	0.54
1:1:64:G:OP2	13:N:169:LYS:NZ	2.41	0.53
1:1:1778:A:H4'	31:g:53:GLY:HA2	1.90	0.53
6:C:140:ARG:HG3	6:C:140:ARG:HH11	1.72	0.53
22:X:81:LEU:HD13	22:X:125:LEU:HD11	1.89	0.53
26:b:456:LEU:HD13	38:u:69:LEU:HD22	1.90	0.53
38:u:77:ASN:HB2	40:y:96:ARG:HB2	1.90	0.53
40:y:23:TYR:CE1	40:y:70:LEU:HD12	2.43	0.53
1:1:196:G:OP2	23:Y:45:ARG:NH2	2.35	0.53
1:1:1787:G:H4'	35:k:45:THR:HG21	1.90	0.53
16:Q:78:GLN:HG3	16:Q:79:ASN:H	1.73	0.53
26:b:7:LYS:NZ	36:r:2:PRO:HD2	2.23	0.53
26:b:87:TYR:CE1	26:b:154:VAL:HG13	2.42	0.53
26:b:423:GLN:N	26:b:427:TRP:HZ2	2.06	0.53
1:1:178:U:H3	1:1:254:G:H1	1.55	0.53
1:1:782:G:O2'	1:1:783:A:OP1	2.21	0.53
1:1:1393:U:H4'	6:C:309:ARG:HB2	1.91	0.53
1:1:1631:C:O2'	1:1:1731:A:N3	2.33	0.53
1:1:2918:G:OP1	37:s:14:ARG:NH2	2.41	0.53
2:2:118:C:O2'	2:2:120:U:OP2	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:140:PHE:HE2	15:P:172:GLY:HA3	1.73	0.53
17:R:60:ARG:HA	17:R:63:ILE:HB	1.89	0.53
28:d:51:THR:OG1	28:d:52:LYS:N	2.41	0.53
1:1:1648:A:HO2'	1:1:1733:C:HO2'	1.54	0.53
10:H:118:GLU:HB3	10:H:120:ILE:HG22	1.90	0.53
20:V:105:VAL:HA	20:V:111:MET:HA	1.90	0.53
32:h:30:LEU:HB3	32:h:46:ILE:HG12	1.90	0.53
39:w:84:ILE:HG22	39:w:85:PRO:HD2	1.91	0.53
1:1:371:C:OP2	34:j:56:ARG:NH1	2.42	0.53
14:O:6:LYS:HG3	14:O:7:VAL:HG23	1.89	0.53
1:1:2449:A:H61	1:1:2465:G:H1	1.56	0.53
31:g:21:ARG:HE	31:g:35:ILE:HG21	1.74	0.53
33:i:63:GLN:HG3	33:i:66:ARG:HB3	1.90	0.53
39:w:76:VAL:HG22	39:w:90:PHE:HB2	1.89	0.53
1:1:98:G:OP2	13:N:192:HIS:NE2	2.41	0.53
1:1:1498:G:N2	1:1:1501:A:OP2	2.41	0.53
1:1:1688:G:H2'	1:1:1689:A:H8	1.74	0.53
1:1:2931:C:H3'	1:1:2932:A:C8	2.44	0.53
3:3:53:VAL:HG11	3:3:112:LEU:HD22	1.91	0.53
10:H:186:GLU:OE1	10:H:186:GLU:N	2.42	0.53
17:R:137:ALA:HA	17:R:140:GLU:OE2	2.08	0.53
18:S:79:ARG:HE	18:S:121:ARG:NH2	2.07	0.53
33:i:32:SER:HB3	33:i:35:THR:HG22	1.90	0.53
35:k:53:LYS:CA	35:k:56:LYS:HE3	2.37	0.53
1:1:674:A:O2'	1:1:675:C:OP1	2.26	0.53
14:O:7:VAL:HG22	14:O:33:LYS:HG2	1.91	0.53
26:b:415:GLU:HB3	26:b:418:ASP:HB2	1.91	0.53
1:1:782:G:H1	1:1:810:U:H3	1.57	0.53
1:1:1309:A:HO2'	1:1:1310:C:H6	1.55	0.53
3:3:32:TYR:HB3	3:3:44:PRO:HG2	1.90	0.53
11:L:92:THR:HB	32:h:116:ARG:HG2	1.89	0.53
31:g:43:ARG:HA	31:g:50:PRO:HA	1.90	0.53
39:w:473:SER:O	39:w:476:LYS:NZ	2.42	0.53
1:1:1760:U:OP2	17:R:110:ARG:NH1	2.41	0.53
1:1:3107:A:N1	1:1:3139:C:O2'	2.37	0.53
13:N:39:ALA:HB3	13:N:61:ILE:HG22	1.90	0.53
18:S:21:PRO:O	42:T:146:ASN:ND2	2.42	0.53
26:b:39:LYS:HD2	26:b:39:LYS:H	1.73	0.53
1:1:715:U:H4'	1:1:716:G:OP1	2.08	0.52
1:1:1277:G:N3	1:1:1295:G:O2'	2.36	0.52
17:R:37:SER:OG	17:R:40:ASN:OD1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:s:17:SER:O	37:s:21:LYS:HG2	2.09	0.52
1:1:3190:A:OP1	20:V:14:ARG:NH2	2.43	0.52
7:E:167:ALA:O	7:E:171:ILE:HG22	2.09	0.52
11:L:110:GLN:HA	11:L:113:VAL:HB	1.90	0.52
17:R:105:LEU:HD11	17:R:138:LEU:HD23	1.91	0.52
20:V:20:PRO:HA	20:V:53:ALA:HA	1.90	0.52
26:b:105:LEU:O	26:b:109:VAL:HG23	2.08	0.52
1:1:1629:A:O2'	1:1:1649:C:O2	2.25	0.52
26:b:450:GLU:OE2	26:b:450:GLU:N	2.34	0.52
3:3:2:GLN:HB3	3:3:6:VAL:HG11	1.90	0.52
26:b:392:ASP:O	26:b:395:ARG:HG2	2.09	0.52
29:e:88:THR:HG23	29:e:89:TYR:HD1	1.73	0.52
39:w:32:LYS:HE2	39:w:187:SER:HA	1.91	0.52
40:y:88:LEU:HD12	40:y:94:ILE:HD11	1.92	0.52
1:1:379:G:N1	1:1:382:A:OP2	2.40	0.52
1:1:3225:A:N6	1:1:3227:U:O2	2.43	0.52
1:1:3485:U:H1'	28:d:107:GLU:OE1	2.10	0.52
16:Q:15:ARG:HD3	16:Q:52:PHE:HB3	1.91	0.52
1:1:984:A:O2'	1:1:1145:U:O2	2.21	0.52
1:1:1200:A:H4'	8:F:225:LYS:HD2	1.92	0.52
6:C:152:LEU:HD21	6:C:174:ILE:HG21	1.92	0.52
39:w:136:GLN:HA	39:w:139:LEU:HB3	1.92	0.52
40:y:182:VAL:HG23	40:y:221:ILE:HD13	1.91	0.52
1:1:832:G:H22	6:C:103:ALA:HA	1.74	0.52
1:1:1952:G:O2'	20:V:18:GLY:O	2.25	0.52
1:1:3194:G:OP1	5:B:279:ASN:ND2	2.43	0.52
7:E:57:VAL:O	7:E:104:THR:OG1	2.25	0.52
33:i:81:ALA:O	33:i:85:ILE:HG12	2.10	0.52
38:u:43:LYS:HD2	39:w:235:PRO:HB2	1.92	0.52
39:w:26:ARG:HH12	39:w:82:LYS:HB2	1.75	0.52
39:w:214:PRO:HD2	39:w:215:ARG:HH12	1.74	0.52
40:y:109:ALA:HB1	40:y:154:LEU:HD23	1.91	0.52
1:1:2:U:H2'	1:1:3:U:C6	2.45	0.52
1:1:1497:U:H3	1:1:1501:A:H62	1.58	0.52
1:1:1929:A:N7	17:R:20:ARG:NH1	2.57	0.52
1:1:3023:C:N4	1:1:3024:C:H42	2.08	0.52
10:H:5:ILE:HD12	18:S:141:GLN:HG3	1.92	0.52
11:L:46:ILE:HB	11:L:49:ARG:HH11	1.75	0.52
31:g:100:ILE:O	31:g:103:GLN:HG3	2.10	0.52
40:y:17:SER:HB2	40:y:34:PHE:HE2	1.74	0.52
3:3:20:ILE:O	3:3:26:ASN:HA	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:114:ARG:HE	29:e:83:LEU:HD23	1.73	0.52
6:C:76:ILE:HD12	6:C:77:PRO:HD2	1.90	0.52
6:C:254:LYS:HD2	6:C:254:LYS:C	2.35	0.52
1:1:545:A:N6	1:1:547:G:N3	2.58	0.52
1:1:689:U:H2'	1:1:690:A:C8	2.45	0.52
1:1:3415:U:H5''	5:B:174:LYS:HE2	1.90	0.52
5:B:85:VAL:HG22	5:B:202:THR:HG22	1.91	0.52
5:B:105:VAL:HG21	5:B:148:LEU:HD12	1.91	0.52
7:E:147:ASN:O	7:E:149:LEU:N	2.43	0.52
23:Y:21:ALA:HB1	23:Y:25:VAL:HB	1.92	0.52
39:w:158:LYS:HB2	39:w:195:PHE:HE1	1.75	0.52
1:1:114:A:N1	1:1:274:A:O2'	2.44	0.51
1:1:1891:C:O2'	1:1:1897:A:N1	2.39	0.51
10:H:35:LEU:HD13	10:H:82:VAL:HG12	1.92	0.51
13:N:9:GLU:HB3	33:i:42:VAL:HG11	1.91	0.51
25:a:148:ALA:HB3	33:i:13:LYS:HG2	1.91	0.51
1:1:2481:G:N2	1:1:2482:G:O6	2.41	0.51
1:1:3028:A:OP1	1:1:3111:C:H4'	2.10	0.51
16:Q:92:GLU:OE2	16:Q:92:GLU:N	2.24	0.51
39:w:253:HIS:O	39:w:253:HIS:CG	2.63	0.51
1:1:1654:A:H61	1:1:1880:A:H61	1.58	0.51
5:B:210:GLU:HB3	41:z:110:PHE:CE1	2.45	0.51
8:F:224:ARG:HH11	8:F:224:ARG:HG3	1.75	0.51
13:N:114:ARG:NH1	13:N:151:ILE:O	2.43	0.51
14:O:145:GLU:OE1	14:O:145:GLU:N	2.42	0.51
39:w:214:PRO:HB2	39:w:215:ARG:HH22	1.74	0.51
2:2:60:A:H62	4:8:27:ILE:HG12	1.75	0.51
6:C:231:ASN:HB3	6:C:234:ARG:HG2	1.92	0.51
9:G:158:ASP:HB3	9:G:159:PRO:HD3	1.93	0.51
18:S:26:MET:HG3	18:S:40:TYR:CE1	2.45	0.51
33:i:53:ARG:HA	33:i:56:MET:HG2	1.92	0.51
40:y:85:ARG:NH1	40:y:92:VAL:O	2.35	0.51
1:1:437:G:H2'	1:1:438:G:H8	1.75	0.51
1:1:511:C:H2'	1:1:512:A:H8	1.74	0.51
1:1:1271:A:N3	1:1:1280:G:N2	2.58	0.51
1:1:1673:A:H1'	1:1:1749:C:H1'	1.92	0.51
1:1:1844:C:H2'	1:1:1845:A:H8	1.76	0.51
5:B:105:VAL:HG11	5:B:148:LEU:HD11	1.92	0.51
26:b:427:TRP:HE3	38:u:84:ARG:HD2	1.75	0.51
38:u:10:SER:HB2	38:u:53:LYS:HB3	1.91	0.51
39:w:237:LYS:O	39:w:239:LYS:HG2	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:932:G:H1'	1:1:1624:A:N6	2.25	0.51
1:1:1786:U:H2'	1:1:1787:G:C8	2.43	0.51
5:B:360:ASP:OD2	38:u:17:HIS:NE2	2.43	0.51
8:F:230:ILE:HD12	18:S:38:SER:OG	2.10	0.51
22:X:57:ASP:O	22:X:61:ILE:HG12	2.10	0.51
38:u:84:ARG:O	38:u:87:ILE:HG22	2.11	0.51
1:1:203:G:N1	1:1:206:A:OP2	2.43	0.51
1:1:1766:C:N4	1:1:1767:G:O6	2.43	0.51
1:1:75:U:H5''	11:L:58:VAL:CG1	2.40	0.51
2:2:111:G:OP2	2:2:113:A:O2'	2.29	0.51
3:3:8:TRP:CE3	3:3:12:GLY:HA3	2.45	0.51
20:V:64:VAL:HB	20:V:72:ARG:HG2	1.93	0.51
31:g:91:ARG:O	31:g:95:ILE:HD12	2.10	0.51
39:w:59:TRP:HB3	39:w:116:LEU:HD21	1.92	0.51
1:1:26:A:N3	1:1:336:U:O2'	2.44	0.51
1:1:389:U:H3	1:1:396:G:H1	1.58	0.51
1:1:1013:U:O2'	1:1:1014:C:OP1	2.29	0.51
1:1:1231:A:O2'	1:1:1232:G:N2	2.41	0.51
1:1:1420:U:OP1	3:3:29:ARG:NH2	2.44	0.51
14:O:57:ALA:O	14:O:61:LYS:NZ	2.39	0.51
30:f:53:VAL:HG22	30:f:67:VAL:HG22	1.92	0.51
35:k:3:ARG:HB2	35:k:44:TYR:HD1	1.76	0.51
35:k:14:ILE:HG21	35:k:44:TYR:CD2	2.46	0.51
1:1:420:G:N2	15:P:118:GLN:HE22	2.08	0.51
1:1:1481:G:O2'	1:1:2443:G:O6	2.27	0.51
1:1:1757:C:H2'	1:1:1758:G:C8	2.46	0.51
6:C:94:ASN:HD22	6:C:102:PHE:HB2	1.75	0.51
7:E:142:GLU:HA	7:E:147:ASN:HD22	1.75	0.51
39:w:465:ASP:O	39:w:469:ARG:HG3	2.11	0.51
1:1:613:A:H1'	1:1:1368:A:H5''	1.93	0.50
1:1:742:A:C8	25:a:114:LYS:HD2	2.46	0.50
1:1:1525:A:H5''	34:j:14:LYS:HE3	1.92	0.50
25:a:131:ARG:HA	25:a:131:ARG:NE	2.26	0.50
26:b:115:ARG:HG2	36:r:175:ALA:HB1	1.93	0.50
1:1:1419:U:OP1	6:C:143:ARG:NH1	2.43	0.50
3:3:94:ASP:OD1	3:3:95:GLN:N	2.44	0.50
5:B:66:LYS:HB3	20:V:13:TYR:CE2	2.46	0.50
5:B:161:LEU:HB3	5:B:178:LEU:HD11	1.93	0.50
9:G:116:VAL:HG13	9:G:120:LYS:HD2	1.93	0.50
11:L:177:SER:O	11:L:180:SER:OG	2.23	0.50
12:M:86:LYS:O	12:M:89:SER:OG	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:47:ARG:HB3	20:V:50:ARG:HB3	1.93	0.50
1:1:80:C:P	13:N:191:ARG:HH21	2.34	0.50
1:1:1799:C:H2'	1:1:1800:G:H8	1.76	0.50
1:1:2932:A:O2'	1:1:2945:G:N2	2.43	0.50
2:2:159:U:H2'	39:w:455:LEU:HD11	1.94	0.50
18:S:39:ARG:HA	18:S:39:ARG:HE	1.76	0.50
1:1:181:A:H2'	1:1:182:G:C8	2.47	0.50
1:1:765:G:H2'	1:1:766:G:C8	2.46	0.50
7:E:58:CYS:HB3	7:E:101:VAL:HG13	1.92	0.50
7:E:93:ILE:HG12	7:E:157:GLN:OE1	2.11	0.50
11:L:51:VAL:HG23	11:L:52:GLU:HG2	1.93	0.50
14:O:143:SER:HA	14:O:146:VAL:HG12	1.92	0.50
22:X:94:ILE:O	22:X:98:VAL:HG22	2.12	0.50
29:e:31:LYS:HE3	29:e:49:MET:HE3	1.92	0.50
32:h:94:LEU:HD22	32:h:98:GLU:HG3	1.92	0.50
1:1:279:C:O2	33:i:80:ARG:NH2	2.43	0.50
1:1:1697:G:H1	1:1:1828:A:H61	1.59	0.50
1:1:1916:G:H2'	1:1:1917:U:C6	2.46	0.50
5:B:281:LYS:HB2	5:B:325:ASN:ND2	2.26	0.50
39:w:266:ASP:N	39:w:266:ASP:OD1	2.44	0.50
1:1:157:A:H4'	32:h:104:LEU:HD23	1.94	0.50
1:1:777:C:O2'	1:1:778:G:OP1	2.26	0.50
1:1:1480:A:N1	1:1:2444:A:H5''	2.27	0.50
1:1:2419:C:OP1	20:V:65:LYS:NZ	2.45	0.50
1:1:3491:A:O2'	1:1:3492:G:H8	1.95	0.50
7:E:86:TYR:HB2	7:E:157:GLN:HE21	1.77	0.50
10:H:24:ARG:HD2	10:H:40:ARG:HD3	1.93	0.50
16:Q:50:ARG:HA	16:Q:53:GLN:HG2	1.94	0.50
1:1:299:C:OP1	13:N:68:ARG:HB3	2.12	0.50
1:1:3360:G:O2'	12:M:122:GLU:OE2	2.21	0.50
1:1:3371:U:O2	7:E:153:ARG:NH2	2.40	0.50
28:d:49:MET:HE2	28:d:80:LEU:HB3	1.94	0.50
1:1:1289:U:H2'	1:1:1291:A:OP2	2.10	0.50
1:1:2439:U:H2'	1:1:2440:A:H8	1.76	0.50
2:2:104:A:O2'	32:h:62:GLU:OE1	2.29	0.50
9:G:206:GLU:HG2	9:G:207:ASP:OD1	2.12	0.50
14:O:117:LYS:NZ	18:S:169:PRO:O	2.44	0.50
25:a:75:LEU:CD1	25:a:113:GLY:HA2	2.42	0.50
12:M:111:PHE:O	12:M:114:MET:HB3	2.12	0.50
13:N:148:ILE:HG13	13:N:148:ILE:O	2.10	0.50
17:R:44:LEU:HD22	17:R:49:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:a:132:ARG:HD3	25:a:132:ARG:H	1.76	0.50
39:w:43:LEU:HD21	39:w:63:ALA:HA	1.93	0.50
39:w:108:LYS:HE2	39:w:110:TRP:CZ3	2.47	0.50
1:1:359:A:OP1	4:8:34:THR:OG1	2.22	0.49
1:1:1578:G:OP1	13:N:67:ARG:NH2	2.45	0.49
31:g:47:THR:HG23	31:g:49:VAL:HG12	1.94	0.49
1:1:100:A:H3'	1:1:101:G:H21	1.78	0.49
1:1:1160:A:H2'	1:1:1161:A:H5'	1.92	0.49
1:1:2459:G:OP1	1:1:2462:C:N4	2.45	0.49
1:1:2933:A:O2'	36:r:62:LYS:NZ	2.30	0.49
5:B:306:THR:HG21	5:B:316:VAL:HG13	1.93	0.49
9:G:184:ALA:O	9:G:188:THR:HG23	2.12	0.49
31:g:65:LEU:O	31:g:70:LYS:NZ	2.38	0.49
39:w:73:ILE:HG21	39:w:87:CYS:SG	2.53	0.49
40:y:186:ILE:O	40:y:190:SER:OG	2.26	0.49
1:1:247:U:H2'	1:1:248:G:C8	2.47	0.49
1:1:1001:C:N3	1:1:1144:G:N1	2.60	0.49
1:1:1284:U:O2'	1:1:1294:A:N3	2.38	0.49
1:1:1572:G:H21	1:1:1618:A:H62	1.61	0.49
1:1:1833:C:H4'	1:1:1835:U:C4	2.48	0.49
1:1:1844:C:H2'	1:1:1845:A:C8	2.46	0.49
11:L:89:VAL:O	11:L:93:ILE:HG12	2.12	0.49
14:O:19:ARG:HH12	14:O:129:ARG:NH2	2.10	0.49
26:b:285:ILE:HA	26:b:317:LYS:H	1.76	0.49
31:g:98:GLN:C	31:g:102:LYS:HZ2	2.20	0.49
1:1:1156:U:H2'	1:1:1157:G:C8	2.47	0.49
1:1:2432:U:H2'	1:1:2433:A:C8	2.46	0.49
1:1:3370:U:H2'	7:E:64:ARG:HD2	1.94	0.49
1:1:741:G:N1	25:a:72:THR:HG21	2.28	0.49
1:1:1564:U:O2'	2:2:122:G:O2'	2.23	0.49
1:1:2432:U:H2'	1:1:2433:A:H8	1.78	0.49
18:S:51:LYS:HB2	18:S:54:THR:HG22	1.93	0.49
23:Y:54:GLN:HE22	23:Y:66:GLU:HG2	1.76	0.49
26:b:160:ARG:HB3	36:r:4:ASN:O	2.11	0.49
26:b:416:LEU:HD11	40:y:50:HIS:O	2.12	0.49
26:b:441:VAL:HA	38:u:94:MET:HE3	1.95	0.49
1:1:1251:U:O2	1:1:1253:G:N1	2.45	0.49
1:1:1875:U:O2'	1:1:1877:C:OP2	2.31	0.49
11:L:188:TYR:HB2	11:L:192:ARG:HH22	1.76	0.49
12:M:12:ARG:NH1	12:M:59:THR:O	2.45	0.49
12:M:73:ILE:HA	12:M:76:LYS:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:110:ARG:HD3	17:R:120:TYR:CD2	2.48	0.49
29:e:94:ALA:HB3	29:e:97:VAL:HG23	1.95	0.49
1:1:23:A:OP1	34:j:44:THR:N	2.43	0.49
1:1:1639:U:O2	1:1:1639:U:C2'	2.61	0.49
1:1:2440:A:H5''	15:P:83:TRP:O	2.12	0.49
5:B:76:VAL:HB	5:B:323:MET:HG2	1.95	0.49
1:1:151:G:OP2	9:G:193:LYS:NZ	2.38	0.49
1:1:2976:C:OP1	5:B:8:GLN:NE2	2.45	0.49
5:B:301:THR:HG1	26:b:437:ASP:N	2.10	0.49
35:k:26:LYS:O	35:k:33:VAL:HA	2.12	0.49
40:y:106:ASN:HB3	40:y:147:LEU:HD22	1.95	0.49
1:1:3084:U:O2'	5:B:232:ARG:NH1	2.38	0.49
11:L:64:ARG:HG3	25:a:69:TRP:CD2	2.48	0.49
26:b:456:LEU:HD21	38:u:96:ARG:HG2	1.94	0.49
40:y:66:ASN:HD22	40:y:112:ASP:HA	1.76	0.49
1:1:1314:C:O2'	1:1:1315:C:OP1	2.29	0.49
1:1:3434:G:N2	1:1:3470:G:O2'	2.45	0.49
29:e:71:PHE:HB2	29:e:89:TYR:HD2	1.78	0.49
29:e:102:ARG:NH2	29:e:118:ASN:O	2.46	0.49
34:j:27:PHE:HA	34:j:34:CYS:HA	1.94	0.49
1:1:511:C:H2'	1:1:512:A:C8	2.48	0.48
1:1:764:U:H2'	1:1:765:G:O4'	2.13	0.48
1:1:1567:U:H2'	1:1:1568:A:H8	1.77	0.48
1:1:1698:C:H2'	1:1:1699:G:C8	2.48	0.48
1:1:3099:G:O2'	5:B:92:TYR:OH	2.27	0.48
3:3:110:GLN:HG3	3:3:114:ARG:NH1	2.28	0.48
5:B:29:VAL:HG22	5:B:218:ILE:HD11	1.95	0.48
9:G:220:ALA:HA	9:G:224:ALA:HB3	1.95	0.48
12:M:20:GLU:CD	12:M:20:GLU:H	2.21	0.48
15:P:126:ARG:NE	15:P:140:LEU:HD21	2.28	0.48
26:b:52:LYS:O	26:b:55:GLN:HG2	2.13	0.48
28:d:13:VAL:HG21	28:d:15:ARG:HH21	1.78	0.48
35:k:56:LYS:HD2	35:k:56:LYS:C	2.38	0.48
1:1:1235:A:H61	1:1:1331:G:H1'	1.77	0.48
1:1:1260:G:H2'	1:1:1261:G:H8	1.78	0.48
1:1:3301:C:H2'	1:1:3302:U:C6	2.48	0.48
2:2:60:A:N6	4:8:27:ILE:HG12	2.27	0.48
3:3:97:LEU:HD22	3:3:100:TRP:CE3	2.48	0.48
10:H:138:VAL:HB	10:H:141:GLU:HG2	1.95	0.48
13:N:5:LYS:HD2	33:i:38:VAL:HG21	1.94	0.48
33:i:56:MET:HA	33:i:56:MET:HE3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1143:A:O2'	1:1:1404:G:O3'	2.29	0.48
1:1:1884:G:H5''	1:1:1885:G:H5'	1.95	0.48
1:1:2478:A:N1	1:1:3084:U:H5	2.12	0.48
1:1:3284:G:H2'	1:1:3285:G:H8	1.78	0.48
10:H:95:ALA:N	10:H:175:ASP:OD1	2.46	0.48
26:b:7:LYS:HZ1	36:r:2:PRO:HD2	1.78	0.48
1:1:689:U:H2'	1:1:690:A:H8	1.78	0.48
1:1:1531:C:H2'	1:1:1532:A:C8	2.48	0.48
10:H:87:ARG:NH1	10:H:185:ILE:HA	2.29	0.48
10:H:115:PHE:HE1	10:H:176:GLY:HA2	1.78	0.48
1:1:544:A:H2	1:1:582:G:H22	1.61	0.48
1:1:1650:C:H2'	1:1:1651:A:C8	2.49	0.48
1:1:1755:A:H4'	1:1:1756:U:H2'	1.94	0.48
5:B:214:MET:HG3	5:B:279:ASN:HA	1.96	0.48
17:R:63:ILE:O	17:R:67:HIS:ND1	2.40	0.48
22:X:66:ILE:HD13	22:X:82:VAL:HG12	1.94	0.48
1:1:1162:G:H2'	1:1:1163:C:H5'	1.96	0.48
1:1:2459:G:O4'	37:s:13:THR:OG1	2.31	0.48
3:3:52:THR:HG22	3:3:63:TYR:HB2	1.96	0.48
5:B:71:GLU:OE1	5:B:71:GLU:N	2.47	0.48
5:B:331:PRO:HD2	5:B:334:ARG:NE	2.22	0.48
23:Y:47:LEU:HD11	23:Y:118:ILE:HD11	1.95	0.48
11:L:193:ALA:O	11:L:197:LYS:HG2	2.13	0.48
26:b:9:ILE:HD11	26:b:69:PHE:HA	1.95	0.48
26:b:422:LEU:HB3	26:b:427:TRP:HE1	1.78	0.48
28:d:42:VAL:HG23	28:d:54:VAL:HB	1.96	0.48
28:d:53:GLU:N	28:d:53:GLU:OE2	2.46	0.48
38:u:19:ILE:HG21	38:u:37:HIS:CE1	2.48	0.48
1:1:263:A:H2'	1:1:264:G:C8	2.48	0.48
1:1:1349:A:H62	14:O:19:ARG:HD3	1.79	0.48
1:1:1525:A:HO2'	1:1:1898:C:HO2'	1.58	0.48
1:1:2972:G:H1	1:1:3044:U:H3	1.62	0.48
1:1:3217:U:H1'	1:1:3218:A:H5''	1.96	0.48
22:X:90:ASN:O	22:X:93:THR:N	2.43	0.48
40:y:4:ARG:HB3	40:y:208:LEU:HA	1.95	0.48
1:1:126:U:OP1	13:N:144:ARG:NH1	2.33	0.48
1:1:270:U:O2'	1:1:271:C:OP1	2.25	0.48
1:1:1388:G:N3	1:1:1388:G:H2'	2.28	0.48
21:W:125:ALA:HB2	21:W:209:ALA:HB3	1.95	0.48
38:u:94:MET:O	38:u:97:VAL:HB	2.14	0.48
39:w:156:VAL:HG12	39:w:197:VAL:HG22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:y:126:GLU:HG3	40:y:137:VAL:HG11	1.96	0.48
1:1:401:U:O2'	23:Y:86:ARG:NH2	2.44	0.48
1:1:518:U:H2'	1:1:519:U:C6	2.49	0.48
1:1:1209:G:N3	1:1:1359:C:O2'	2.46	0.48
3:3:47:ASN:CG	3:3:48:SER:N	2.71	0.48
5:B:301:THR:O	5:B:301:THR:HG22	2.13	0.48
5:B:371:GLN:N	5:B:375:GLU:OE2	2.45	0.48
8:F:243:ASN:O	8:F:247:GLN:HG2	2.14	0.48
10:H:120:ILE:HD11	41:z:94:TRP:CZ3	2.49	0.48
12:M:97:GLU:OE1	12:M:97:GLU:HA	2.13	0.48
20:V:24:ILE:HG22	39:w:242:ARG:HD2	1.96	0.48
36:r:16:ARG:HG2	36:r:17:ARG:H	1.77	0.48
40:y:49:VAL:HG12	40:y:51:THR:HB	1.96	0.48
40:y:200:ASN:HD21	40:y:203:CYS:HB3	1.78	0.48
1:1:859:A:H5'	31:g:15:THR:HG22	1.95	0.47
1:1:1274:G:N3	1:1:1301:A:O2'	2.47	0.47
2:2:17:A:H2'	2:2:18:G:C8	2.48	0.47
17:R:132:PHE:CZ	17:R:141:HIS:HB2	2.49	0.47
1:1:86:G:O2'	1:1:98:G:O6	2.31	0.47
1:1:302:U:H5''	33:i:51:TYR:CE2	2.49	0.47
1:1:1627:G:OP2	31:g:37:LYS:NZ	2.36	0.47
1:1:1636:U:P	17:R:42:ARG:HH22	2.35	0.47
1:1:3414:U:H5'	5:B:175:LYS:HD3	1.95	0.47
14:O:193:SER:OG	14:O:197:TYR:OXT	2.31	0.47
23:Y:90:ASN:OD1	23:Y:92:ALA:N	2.44	0.47
38:u:63:MET:HG2	38:u:108:PHE:HD1	1.78	0.47
38:u:95:LYS:O	38:u:98:SER:N	2.47	0.47
2:2:67:A:O2'	22:X:60:LYS:NZ	2.33	0.47
4:8:27:ILE:HG13	4:8:33:ASN:HD21	1.79	0.47
11:L:192:ARG:HB2	11:L:196:GLN:HE22	1.77	0.47
32:h:49:THR:O	32:h:53:ILE:HG13	2.14	0.47
1:1:402:U:H5'	23:Y:86:ARG:NH2	2.29	0.47
1:1:1092:U:H2'	1:1:1093:A:H8	1.78	0.47
1:1:1590:G:H1	39:w:469:ARG:HD2	1.80	0.47
1:1:1670:G:N2	1:1:1673:A:OP2	2.47	0.47
11:L:128:ARG:O	11:L:129:LYS:HG2	2.14	0.47
12:M:13:VAL:HG11	12:M:83:VAL:HG11	1.97	0.47
17:R:97:ARG:O	17:R:101:VAL:HG13	2.13	0.47
23:Y:50:ARG:HG2	23:Y:51:ARG:N	2.28	0.47
1:1:3155:G:H5''	28:d:22:HIS:NE2	2.30	0.47
3:3:50:TYR:HA	3:3:100:TRP:HZ2	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:69:ARG:H	3:3:69:ARG:HD3	1.80	0.47
5:B:301:THR:OG1	26:b:437:ASP:N	2.29	0.47
6:C:284:ILE:HG13	16:Q:126:ASP:HB2	1.96	0.47
8:F:93:VAL:HG22	8:F:143:TYR:HB3	1.95	0.47
12:M:30:ASP:OD1	12:M:31:ILE:N	2.48	0.47
32:h:84:GLN:NE2	32:h:91:ARG:HG2	2.29	0.47
39:w:285:GLU:OE1	39:w:288:ARG:NH1	2.48	0.47
40:y:112:ASP:HB2	40:y:156:ASN:HD21	1.79	0.47
1:1:120:G:H22	9:G:126:SER:HB3	1.79	0.47
1:1:320:C:H2'	1:1:321:A:C8	2.49	0.47
1:1:3026:C:H5''	20:V:42:PHE:CD1	2.50	0.47
2:2:102:C:H5''	34:j:76:ASN:ND2	2.29	0.47
3:3:62:LEU:HD23	3:3:80:ILE:HD11	1.96	0.47
5:B:213:GLU:HB3	41:z:110:PHE:CE2	2.49	0.47
7:E:144:ALA:HB1	7:E:145:PRO:HD2	1.95	0.47
13:N:11:ALA:O	13:N:14:LYS:NZ	2.46	0.47
17:R:93:VAL:HA	17:R:96:MET:HB3	1.97	0.47
26:b:396:ARG:NH1	40:y:39:GLU:HG2	2.29	0.47
1:1:531:A:N1	6:C:349:PRO:HD2	2.30	0.47
1:1:680:C:H2'	1:1:681:A:C8	2.50	0.47
1:1:759:C:O2'	1:1:760:C:O5'	2.26	0.47
1:1:787:G:N2	1:1:804:A:H62	2.09	0.47
1:1:1236:A:N1	1:1:1330:U:H5	2.12	0.47
1:1:1799:C:H2'	1:1:1800:G:C8	2.50	0.47
1:1:2423:G:N2	1:1:2427:C:O2'	2.47	0.47
1:1:3316:G:H1	1:1:3359:U:H5''	1.79	0.47
7:E:140:PHE:HZ	15:P:169:LEU:HA	1.80	0.47
8:F:221:TRP:CE2	8:F:225:LYS:HE3	2.50	0.47
13:N:9:GLU:HA	13:N:9:GLU:OE2	2.15	0.47
13:N:115:VAL:O	13:N:159:ARG:NH1	2.48	0.47
23:Y:79:LEU:HD11	23:Y:100:ALA:HA	1.95	0.47
32:h:23:LEU:HB3	32:h:53:ILE:HG12	1.97	0.47
42:T:141:VAL:HG22	42:T:141:VAL:O	2.14	0.47
1:1:1845:A:H2'	1:1:1846:A:C8	2.50	0.47
8:F:172:ASP:OD1	8:F:173:ASN:N	2.48	0.47
21:W:61:LYS:H	21:W:105:THR:HA	1.79	0.47
39:w:95:THR:O	39:w:95:THR:OG1	2.30	0.47
1:1:176:A:OP2	32:h:111:ARG:NE	2.48	0.47
1:1:646:A:O2'	1:1:647:A:H8	1.97	0.47
1:1:3247:U:H4'	1:1:3395:G:H1'	1.96	0.47
5:B:256:HIS:CD2	5:B:258:ALA:HB2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:O:40:GLU:OE1	14:O:108:GLY:N	2.48	0.47
25:a:77:ARG:HH11	25:a:77:ARG:HG3	1.79	0.47
1:1:216:A:H4'	1:1:218:A:N7	2.30	0.47
1:1:506:G:H21	1:1:646:A:H62	1.62	0.47
1:1:595:U:H2'	1:1:596:A:C8	2.50	0.47
1:1:645:U:H3	15:P:166:ARG:HD2	1.79	0.47
1:1:778:G:H2'	1:1:779:A:H8	1.80	0.47
1:1:1001:C:N4	1:1:1144:G:O6	2.48	0.47
1:1:1284:U:H2'	1:1:1294:A:H5''	1.97	0.47
1:1:1308:C:O2'	1:1:1309:A:H8	1.97	0.47
1:1:1697:G:H1	1:1:1828:A:N6	2.13	0.47
1:1:3370:U:OP2	15:P:176:ARG:NH2	2.47	0.47
18:S:8:VAL:HG23	18:S:28:LEU:HD21	1.96	0.47
40:y:61:ARG:HB3	40:y:106:ASN:OD1	2.15	0.47
1:1:712:U:H3	1:1:720:A:H61	1.62	0.46
1:1:1309:A:O2'	1:1:1310:C:O5'	2.33	0.46
1:1:2931:C:H3'	1:1:2932:A:H8	1.79	0.46
10:H:174:LEU:O	10:H:178:TYR:OH	2.29	0.46
1:1:868:A:H2'	1:1:869:A:C8	2.50	0.46
1:1:1241:U:OP1	10:H:62:ARG:NH1	2.47	0.46
1:1:1648:A:OP2	35:k:38:ARG:NH1	2.35	0.46
1:1:3144:C:H5	1:1:3187:A:H62	1.61	0.46
1:1:3360:G:O3'	12:M:119:GLN:NE2	2.39	0.46
1:1:3437:A:H2'	1:1:3438:G:O4'	2.15	0.46
1:1:3477:A:H5'	1:1:3478:G:H5''	1.97	0.46
2:2:55:C:H1'	2:2:69:A:H2'	1.97	0.46
8:F:150:THR:HG23	8:F:246:VAL:HG11	1.96	0.46
9:G:85:ASN:OD1	9:G:86:THR:N	2.49	0.46
13:N:116:LEU:HD23	13:N:117:ASN:HB2	1.97	0.46
17:R:140:GLU:OE1	17:R:144:ARG:NH2	2.48	0.46
30:f:40:GLU:H	30:f:40:GLU:CD	2.23	0.46
40:y:82:GLN:O	40:y:86:ASN:ND2	2.44	0.46
1:1:3116:U:H3'	1:1:3117:A:C5'	2.45	0.46
1:1:3166:A:OP1	17:R:62:ARG:NH2	2.48	0.46
9:G:68:ARG:HH21	9:G:236:GLY:HA2	1.79	0.46
20:V:65:LYS:HG2	20:V:66:LYS:HD2	1.97	0.46
20:V:84:ARG:NH2	39:w:238:ARG:HG3	2.30	0.46
28:d:34:ALA:HB3	28:d:69:ILE:HG13	1.98	0.46
31:g:57:LEU:HB3	31:g:61:GLU:HG2	1.98	0.46
39:w:31:PHE:HA	39:w:34:VAL:HG12	1.97	0.46
39:w:289:LEU:HD11	39:w:324:ILE:HG21	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:z:104:ARG:NH1	41:z:104:ARG:O	2.48	0.46
1:1:359:A:N7	4:8:35:VAL:HG22	2.30	0.46
1:1:531:A:H2'	6:C:350:LYS:HD2	1.97	0.46
1:1:712:U:H2'	1:1:713:G:O4'	2.14	0.46
2:2:42:U:H3	34:j:71:HIS:CE1	2.34	0.46
5:B:179:MET:HE3	5:B:179:MET:HB2	1.79	0.46
5:B:284:ARG:NH1	5:B:293:ASN:O	2.49	0.46
6:C:259:LEU:HD12	6:C:262:SER:HB3	1.98	0.46
39:w:143:LYS:HA	39:w:143:LYS:HD3	1.73	0.46
1:1:382:A:H4'	1:1:383:A:H5'	1.97	0.46
1:1:397:A:H5''	15:P:16:LYS:HB2	1.97	0.46
1:1:618:U:H5'	1:1:619:G:C8	2.51	0.46
1:1:3097:U:OP1	5:B:120:LYS:NZ	2.37	0.46
1:1:3278:A:H2'	1:1:3279:A:C8	2.50	0.46
13:N:5:LYS:HG2	33:i:38:VAL:HG11	1.96	0.46
35:k:26:LYS:HB3	35:k:34:LYS:HB2	1.97	0.46
35:k:52:LYS:HZ2	35:k:53:LYS:HZ3	1.61	0.46
1:1:153:U:O4	9:G:183:LYS:HE2	2.15	0.46
1:1:741:G:H1	25:a:72:THR:HG21	1.81	0.46
1:1:1184:A:H2	1:1:2459:G:C5	2.33	0.46
3:3:40:ARG:HG2	3:3:41:GLN:N	2.30	0.46
6:C:330:LEU:HD23	8:F:188:VAL:HG21	1.97	0.46
26:b:75:ILE:HD12	26:b:79:HIS:HB2	1.98	0.46
28:d:62:LYS:O	28:d:66:LYS:HG3	2.16	0.46
39:w:277:ILE:HG13	39:w:306:LEU:HD11	1.97	0.46
1:1:1260:G:H2'	1:1:1261:G:C8	2.51	0.46
1:1:1466:C:O2'	1:1:1468:G:OP2	2.33	0.46
1:1:1874:U:H4'	1:1:1875:U:H6	1.80	0.46
1:1:1886:U:H2'	1:1:1887:C:C6	2.50	0.46
1:1:2416:U:H2'	1:1:2417:C:C6	2.51	0.46
1:1:2458:G:N2	1:1:2463:G:N7	2.64	0.46
1:1:3487:C:H4'	28:d:15:ARG:NH1	2.30	0.46
2:2:60:A:P	4:8:21:ARG:HH22	2.38	0.46
6:C:172:LYS:HE3	6:C:177:TYR:CE2	2.51	0.46
20:V:86:ALA:HA	20:V:96:TYR:HB3	1.98	0.46
38:u:2:ARG:HD3	38:u:75:ARG:NH2	2.25	0.46
38:u:87:ILE:HA	38:u:87:ILE:HD12	1.78	0.46
1:1:1:A:H3'	1:1:2:U:O4'	2.16	0.46
1:1:748:G:H2'	1:1:749:G:H8	1.81	0.46
1:1:749:G:P	16:Q:72:ARG:HH22	2.38	0.46
6:C:170:LEU:HD23	6:C:221:PHE:HZ	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:154:LEU:HD23	8:F:250:LEU:HD21	1.98	0.46
14:O:47:HIS:NE2	14:O:50:ARG:HB2	2.30	0.46
16:Q:78:GLN:HG3	16:Q:79:ASN:N	2.31	0.46
17:R:122:THR:O	17:R:126:GLU:HG3	2.16	0.46
18:S:92:GLU:HG3	18:S:136:ARG:HG2	1.97	0.46
26:b:456:LEU:O	26:b:457:ASP:C	2.59	0.46
39:w:311:LYS:NZ	39:w:315:ARG:HE	2.13	0.46
1:1:2993:G:N2	36:r:7:ILE:HB	2.31	0.46
10:H:45:GLU:HB2	10:H:56:ILE:HB	1.98	0.46
12:M:26:ALA:HB2	12:M:46:PHE:HE1	1.81	0.46
12:M:102:ARG:HA	12:M:105:LEU:HD12	1.97	0.46
17:R:132:PHE:HB3	17:R:137:ALA:HB3	1.96	0.46
19:U:51:VAL:HA	19:U:65:ALA:HA	1.98	0.46
28:d:99:VAL:HG12	28:d:101:VAL:HG13	1.98	0.46
33:i:42:VAL:HA	33:i:45:VAL:HG12	1.97	0.46
1:1:743:A:H61	25:a:116:ARG:HD2	1.81	0.46
1:1:1651:A:H2'	1:1:1652:G:C8	2.51	0.46
1:1:2947:C:O2'	36:r:56:LYS:HG2	2.16	0.46
1:1:3122:G:H4'	36:r:2:PRO:HG3	1.98	0.46
11:L:111:ARG:O	11:L:114:GLU:HG2	2.17	0.46
18:S:71:ALA:HA	18:S:96:THR:HG22	1.97	0.46
22:X:90:ASN:O	22:X:94:ILE:HD12	2.16	0.46
26:b:456:LEU:CD1	38:u:69:LEU:HD22	2.45	0.46
1:1:756:C:H2'	1:1:757:G:H8	1.81	0.45
1:1:1234:A:H4'	1:1:1235:A:O5'	2.16	0.45
1:1:2926:G:H1	1:1:2952:C:N4	2.11	0.45
1:1:3123:A:H2'	1:1:3124:G:O4'	2.16	0.45
3:3:33:ASN:OD1	3:3:36:GLY:N	2.47	0.45
3:3:89:ALA:O	3:3:93:ILE:HG12	2.16	0.45
22:X:73:LYS:O	22:X:77:ASP:HB3	2.16	0.45
26:b:18:PHE:C	26:b:18:PHE:CD1	2.94	0.45
29:e:103:VAL:HA	29:e:106:VAL:HG12	1.97	0.45
38:u:26:SER:HB3	40:y:100:ARG:HG3	1.98	0.45
1:1:197:U:H2'	23:Y:59:ARG:HH12	1.81	0.45
1:1:654:U:H2'	1:1:655:C:C6	2.51	0.45
1:1:748:G:H2'	1:1:749:G:C8	2.51	0.45
1:1:1289:U:O3'	1:1:1290:A:H8	1.99	0.45
1:1:1840:A:H2'	1:1:1841:A:C8	2.52	0.45
1:1:3153:U:OP1	1:1:3181:G:N2	2.43	0.45
2:2:107:C:OP1	22:X:52:HIS:NE2	2.48	0.45
6:C:78:ARG:NH1	6:C:90:ALA:HB2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:82:TYR:HB2	42:T:141:VAL:CG1	2.46	0.45
25:a:103:VAL:HB	25:a:108:TYR:HB2	1.99	0.45
40:y:111:ASN:HD21	40:y:114:VAL:HG13	1.81	0.45
41:z:109:ASN:OD1	41:z:110:PHE:N	2.49	0.45
1:1:946:A:O3'	1:1:948:G:N2	2.49	0.45
1:1:1520:G:H21	31:g:6:THR:HG22	1.81	0.45
1:1:1952:G:H5''	20:V:84:ARG:HG3	1.99	0.45
9:G:225:LYS:HG3	9:G:226:TYR:CD2	2.51	0.45
12:M:43:CYS:HB3	12:M:45:GLU:OE1	2.16	0.45
13:N:122:ASN:OD1	13:N:123:GLN:N	2.49	0.45
20:V:24:ILE:HB	39:w:242:ARG:HH11	1.81	0.45
25:a:75:LEU:H	25:a:75:LEU:HD12	1.81	0.45
38:u:69:LEU:C	38:u:71:VAL:H	2.24	0.45
1:1:1299:G:H21	1:1:1304:A:H62	1.64	0.45
6:C:133:VAL:HB	6:C:136:LEU:HD12	1.98	0.45
6:C:158:VAL:HG12	6:C:161:PHE:CZ	2.51	0.45
11:L:123:LEU:HD11	32:h:118:TYR:HB2	1.99	0.45
18:S:11:ARG:NE	42:T:141:VAL:HG23	2.23	0.45
18:S:46:MET:HE1	18:S:121:ARG:HD2	1.99	0.45
24:Z:30:ASP:HA	24:Z:39:GLY:HA2	1.98	0.45
25:a:134:GLU:O	25:a:138:LYS:HG2	2.16	0.45
26:b:113:TYR:HB3	26:b:129:LEU:HD21	1.98	0.45
26:b:160:ARG:O	36:r:4:ASN:N	2.42	0.45
1:1:853:U:H2'	1:1:854:G:H8	1.82	0.45
1:1:1017:U:H2'	1:1:1018:U:C6	2.52	0.45
1:1:1648:A:O2'	1:1:1733:C:O2'	2.26	0.45
1:1:1736:A:N6	1:1:1784:U:O4	2.50	0.45
1:1:3147:U:H2'	1:1:3148:G:H8	1.81	0.45
1:1:3215:U:H5''	36:r:26:LYS:HG2	1.99	0.45
1:1:3315:A:O2'	1:1:3316:G:O5'	2.35	0.45
7:E:144:ALA:HB2	15:P:176:ARG:NH1	2.32	0.45
11:L:49:ARG:O	11:L:146:GLN:NE2	2.49	0.45
11:L:111:ARG:O	11:L:115:ARG:HG3	2.17	0.45
23:Y:37:GLU:H	23:Y:37:GLU:CD	2.24	0.45
26:b:416:LEU:HD12	26:b:416:LEU:HA	1.65	0.45
31:g:14:ASN:HA	31:g:18:ASN:HB3	1.99	0.45
34:j:28:HIS:HE1	34:j:30:GLN:HB2	1.82	0.45
36:r:41:LYS:HA	36:r:41:LYS:HD3	1.82	0.45
41:z:88:ASP:OD1	41:z:90:ASN:N	2.43	0.45
1:1:50:U:H2'	1:1:51:A:H8	1.81	0.45
1:1:304:A:N3	1:1:307:G:O2'	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1232:G:H5'	37:s:22:LYS:HZ3	1.82	0.45
1:1:3437:A:H3'	1:1:3438:G:H8	1.81	0.45
8:F:224:ARG:HG3	8:F:224:ARG:NH1	2.32	0.45
14:O:20:LEU:HD23	14:O:42:LEU:HD21	1.98	0.45
25:a:133:ALA:O	25:a:137:ILE:HG12	2.16	0.45
26:b:412:TYR:CE1	26:b:414:VAL:HG22	2.51	0.45
32:h:7:GLU:O	32:h:11:GLN:NE2	2.50	0.45
34:j:17:THR:HB	34:j:29:ILE:HD11	1.99	0.45
37:s:27:LYS:HA	37:s:30:GLN:HG3	1.98	0.45
39:w:29:ALA:HB1	39:w:59:TRP:CZ2	2.52	0.45
39:w:320:TRP:HA	39:w:323:LYS:HE2	1.97	0.45
1:1:1531:C:H2'	1:1:1532:A:H8	1.82	0.45
1:1:1895:U:H4'	1:1:1896:A:H5''	1.99	0.45
10:H:128:PRO:O	10:H:151:ASN:ND2	2.45	0.45
14:O:111:PRO:N	14:O:112:PRO:HD2	2.31	0.45
17:R:115:ILE:HG21	17:R:123:LEU:HD12	1.97	0.45
40:y:33:ASN:O	40:y:37:VAL:HG23	2.17	0.45
1:1:778:G:H2'	1:1:779:A:C8	2.52	0.45
1:1:856:C:O2'	1:1:1568:A:N3	2.47	0.45
1:1:1164:A:H2'	1:1:1165:G:H8	1.81	0.45
1:1:1575:A:H1'	1:1:1591:A:C5	2.51	0.45
1:1:1712:A:H2'	1:1:1713:G:C8	2.51	0.45
1:1:2993:G:N7	26:b:160:ARG:NE	2.65	0.45
3:3:48:SER:OG	3:3:49:ARG:N	2.49	0.45
6:C:314:HIS:CE1	6:C:317:LYS:HA	2.52	0.45
6:C:320:PRO:HG3	6:C:326:VAL:HG12	1.98	0.45
10:H:44:ILE:HG22	10:H:57:VAL:HG22	1.99	0.45
13:N:167:ILE:HD12	13:N:167:ILE:HA	1.83	0.45
21:W:12:LEU:HA	36:r:68:HIS:CE1	2.52	0.45
26:b:128:GLN:O	26:b:132:ALA:N	2.30	0.45
32:h:78:ILE:HG13	32:h:83:ARG:HG3	1.99	0.45
35:k:51:ALA:O	35:k:54:ALA:HB3	2.17	0.45
38:u:85:ASN:O	38:u:89:THR:HG22	2.16	0.45
1:1:80:C:OP1	13:N:191:ARG:NH2	2.47	0.45
1:1:869:A:N6	1:1:888:G:H1'	2.30	0.45
1:1:1338:G:H5'	14:O:61:LYS:HE3	1.98	0.45
10:H:120:ILE:HD11	41:z:94:TRP:CH2	2.52	0.45
12:M:13:VAL:HA	12:M:27:VAL:HA	1.98	0.45
12:M:102:ARG:O	12:M:105:LEU:HB2	2.17	0.45
12:M:112:ALA:O	12:M:116:LEU:HG	2.16	0.45
28:d:85:SER:OG	28:d:88:ASP:O	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:g:3:GLN:HE21	31:g:3:GLN:N	2.14	0.45
1:1:155:U:OP2	13:N:49:ARG:NH2	2.45	0.45
1:1:718:A:N1	2:2:36:C:O2'	2.47	0.45
1:1:1270:C:H42	1:1:1280:G:H22	1.65	0.45
1:1:3091:G:H2'	1:1:3091:G:N3	2.32	0.45
1:1:3117:A:H2	1:1:3129:A:H62	1.64	0.45
11:L:80:LEU:HD11	11:L:97:VAL:HG22	1.99	0.45
18:S:7:GLN:HB3	18:S:63:ILE:HD11	1.99	0.45
20:V:19:LEU:HD11	20:V:100:ASN:HB3	1.98	0.45
26:b:102:ALA:HB2	26:b:144:GLN:NE2	2.32	0.45
26:b:425:PRO:HA	26:b:428:LYS:HD2	1.98	0.45
31:g:16:ARG:NE	31:g:16:ARG:HA	2.31	0.45
1:1:590:U:O5'	1:1:591:G:H5''	2.17	0.44
1:1:1190:A:H2'	8:F:99:ILE:HD11	1.98	0.44
1:1:1701:G:H2'	1:1:1702:A:C8	2.51	0.44
1:1:3351:U:H2'	1:1:3352:A:C8	2.53	0.44
5:B:346:THR:O	5:B:346:THR:HG22	2.17	0.44
8:F:51:ILE:HD12	8:F:187:SER:HB3	1.98	0.44
15:P:47:PHE:O	15:P:51:VAL:HG23	2.17	0.44
15:P:64:ASN:O	15:P:80:GLN:NE2	2.50	0.44
20:V:84:ARG:HA	20:V:97:PHE:O	2.17	0.44
22:X:99:ARG:NH1	22:X:99:ARG:HB2	2.32	0.44
25:a:77:ARG:HG3	25:a:77:ARG:NH1	2.32	0.44
39:w:479:VAL:O	39:w:479:VAL:HG13	2.18	0.44
1:1:1388:G:H8	3:3:38:CYS:HB3	1.82	0.44
2:2:28:U:H2'	2:2:29:C:O4'	2.18	0.44
3:3:50:TYR:HA	3:3:100:TRP:CZ2	2.51	0.44
3:3:94:ASP:O	3:3:98:LEU:HG	2.16	0.44
10:H:19:VAL:O	10:H:21:ILE:HG23	2.17	0.44
10:H:44:ILE:HD11	10:H:71:VAL:HG11	1.99	0.44
15:P:4:TYR:CD2	15:P:147:GLU:HG3	2.53	0.44
17:R:106:LEU:HB3	17:R:120:TYR:CE1	2.52	0.44
20:V:15:MET:HG2	20:V:55:SER:HB2	1.99	0.44
28:d:15:ARG:NH1	28:d:17:TYR:OH	2.46	0.44
39:w:171:VAL:HG21	39:w:217:VAL:HG13	1.98	0.44
39:w:653:PHE:CD2	39:w:653:PHE:O	2.70	0.44
1:1:276:A:OP1	13:N:50:ARG:NH1	2.49	0.44
1:1:414:G:H1'	2:2:24:G:N2	2.33	0.44
1:1:1370:C:OP1	29:e:58:LYS:HG3	2.18	0.44
12:M:58:LEU:HG	18:S:151:LEU:HD11	2.00	0.44
15:P:29:SER:HB2	15:P:119:VAL:HG11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:117:VAL:HG23	15:P:148:ILE:HG12	2.00	0.44
22:X:66:ILE:HD12	22:X:66:ILE:N	2.32	0.44
28:d:21:MET:N	28:d:74:HIS:O	2.50	0.44
32:h:106:GLN:OE1	32:h:106:GLN:HA	2.16	0.44
37:s:27:LYS:HA	37:s:27:LYS:HE3	1.98	0.44
40:y:25:LEU:HD11	40:y:70:LEU:HD11	1.99	0.44
1:1:587:U:H2'	1:1:588:G:H8	1.81	0.44
1:1:1394:C:H5''	6:C:312:ARG:HG2	2.00	0.44
1:1:1494:A:H5'	28:d:56:VAL:O	2.18	0.44
1:1:3013:G:H21	39:w:124:GLY:HA2	1.83	0.44
6:C:212:ASN:HD22	6:C:255:SER:HB3	1.82	0.44
9:G:83:ASP:CG	9:G:84:LYS:N	2.75	0.44
28:d:51:THR:HG21	28:d:94:THR:OG1	2.17	0.44
33:i:87:GLU:O	33:i:90:SER:OG	2.28	0.44
40:y:26:VAL:HG21	40:y:35:TYR:HD1	1.82	0.44
1:1:20:A:OP2	32:h:88:ARG:NH2	2.50	0.44
1:1:1223:C:H5''	36:r:43:ARG:HH22	1.82	0.44
1:1:1746:C:H5'	1:1:1828:A:O2'	2.17	0.44
2:2:155:U:H2'	2:2:156:G:O4'	2.18	0.44
3:3:62:LEU:HD21	3:3:96:GLN:NE2	2.32	0.44
5:B:10:ARG:NH2	5:B:263:THR:HB	2.32	0.44
6:C:314:HIS:NE2	8:F:169:PRO:HG2	2.33	0.44
10:H:8:ASP:OD1	10:H:9:GLU:N	2.50	0.44
11:L:89:VAL:O	11:L:92:THR:OG1	2.30	0.44
13:N:31:ARG:NH2	13:N:124:ASP:OD1	2.51	0.44
20:V:79:ILE:HG12	20:V:105:VAL:HG11	1.99	0.44
25:a:8:THR:HA	25:a:11:LEU:HB2	1.99	0.44
3:3:76:LEU:HD22	3:3:77:TRP:CE2	2.52	0.44
5:B:288:GLY:O	5:B:304:ARG:NH1	2.49	0.44
7:E:69:ARG:HD3	7:E:177:TYR:CE1	2.53	0.44
8:F:161:GLY:N	8:F:168:ILE:O	2.49	0.44
33:i:37:PHE:O	33:i:41:ILE:HG12	2.18	0.44
40:y:6:GLN:HG3	40:y:208:LEU:HB2	2.00	0.44
1:1:140:U:C5'	32:h:84:GLN:HG2	2.48	0.44
1:1:277:G:O6	13:N:15:GLN:NE2	2.48	0.44
1:1:1388:G:C8	3:3:38:CYS:HB3	2.53	0.44
1:1:1715:G:H1	1:1:1723:U:H3	1.66	0.44
1:1:1749:C:H2'	1:1:1750:C:C6	2.52	0.44
1:1:2464:G:O2'	1:1:2465:G:H5''	2.17	0.44
3:3:86:TYR:O	3:3:90:LEU:HD23	2.18	0.44
6:C:140:ARG:HG3	6:C:140:ARG:NH1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:26:ALA:HB2	12:M:46:PHE:CE1	2.53	0.44
14:O:40:GLU:CD	14:O:40:GLU:H	2.26	0.44
15:P:6:ALA:HB1	15:P:8:PRO:HD2	1.98	0.44
15:P:122:ALA:HB3	15:P:143:PRO:HB2	1.99	0.44
15:P:164:VAL:O	15:P:164:VAL:HG12	2.18	0.44
17:R:24:MET:HE2	17:R:24:MET:HB2	1.77	0.44
1:1:1668:C:H2'	1:1:1669:G:H8	1.82	0.44
1:1:1761:U:H3'	17:R:103:ARG:HH12	1.83	0.44
1:1:2445:A:H2'	1:1:2446:A:C8	2.53	0.44
1:1:3026:C:H5''	20:V:42:PHE:CE1	2.53	0.44
1:1:3372:C:OP2	7:E:95:ARG:NE	2.36	0.44
1:1:3416:A:C5	5:B:123:PHE:HE1	2.36	0.44
3:3:53:VAL:HG12	3:3:111:ARG:NH1	2.33	0.44
6:C:266:SER:OG	6:C:269:GLU:OE1	2.33	0.44
9:G:139:VAL:O	9:G:143:ILE:HG13	2.18	0.44
11:L:195:PHE:CE2	11:L:199:ARG:HD3	2.53	0.44
26:b:441:VAL:HG11	38:u:87:ILE:HD11	2.00	0.44
40:y:223:LYS:N	40:y:223:LYS:HD2	2.33	0.44
1:1:284:U:H2'	1:1:285:G:C8	2.53	0.44
1:1:305:A:N3	33:i:29:GLY:HA2	2.32	0.44
1:1:676:G:O2'	1:1:1469:A:OP1	2.35	0.44
1:1:954:U:H5''	39:w:771:ARG:HB2	2.00	0.44
1:1:1229:C:H42	37:s:27:LYS:NZ	2.16	0.44
1:1:1632:C:H2'	1:1:1633:G:C8	2.53	0.44
6:C:254:LYS:HD2	6:C:254:LYS:O	2.17	0.44
16:Q:63:ILE:HG23	16:Q:94:MET:CE	2.48	0.44
29:e:17:HIS:CG	29:e:39:VAL:HG21	2.53	0.44
39:w:279:PHE:HE2	39:w:289:LEU:HB3	1.82	0.44
1:1:77:A:N7	11:L:73:ARG:NH1	2.66	0.43
1:1:144:U:H2'	1:1:145:G:C8	2.53	0.43
1:1:241:G:H2'	1:1:242:U:O4'	2.18	0.43
1:1:743:A:H2	25:a:115:GLY:HA2	1.82	0.43
1:1:1232:G:H5'	37:s:22:LYS:NZ	2.33	0.43
1:1:1277:G:H1'	1:1:1295:G:H2'	2.00	0.43
2:2:80:A:H61	2:2:87:A:H61	1.64	0.43
6:C:337:TYR:CE1	8:F:59:GLU:HG3	2.52	0.43
13:N:118:SER:HB2	13:N:132:VAL:HG22	2.00	0.43
20:V:42:PHE:HD2	20:V:59:MET:HG2	1.81	0.43
26:b:109:VAL:HG21	26:b:140:ILE:HD11	1.98	0.43
39:w:51:ASP:HA	39:w:116:LEU:O	2.18	0.43
1:1:224:U:O2'	23:Y:99:ASP:OD2	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:742:A:H8	25:a:114:LYS:HD2	1.83	0.43
1:1:1314:C:HO2'	1:1:1315:C:P	2.41	0.43
1:1:3305:C:OP2	1:1:3306:C:N4	2.42	0.43
6:C:363:ASN:HD22	42:T:150:THR:HG21	1.83	0.43
9:G:84:LYS:O	9:G:88:THR:HG23	2.17	0.43
28:d:107:GLU:HG3	28:d:108:THR:N	2.33	0.43
1:1:363:A:N1	6:C:84:THR:OG1	2.48	0.43
1:1:1092:U:H2'	1:1:1093:A:C8	2.53	0.43
1:1:1396:G:H2'	1:1:1397:A:C8	2.53	0.43
1:1:1731:A:N6	1:1:1788:G:H2'	2.33	0.43
1:1:2439:U:H2'	1:1:2440:A:C8	2.54	0.43
1:1:3103:U:H2'	1:1:3104:G:C8	2.53	0.43
3:3:52:THR:O	3:3:62:LEU:HD12	2.18	0.43
4:8:15:LYS:O	4:8:19:GLN:HG2	2.19	0.43
9:G:157:VAL:HG21	9:G:163:VAL:HG11	2.00	0.43
10:H:57:VAL:HG21	10:H:68:ILE:HG12	1.99	0.43
17:R:99:GLN:OE1	17:R:103:ARG:HG3	2.19	0.43
31:g:93:PHE:HD2	31:g:94:LEU:HD12	1.83	0.43
32:h:45:LYS:HA	32:h:48:THR:HG22	2.00	0.43
16:Q:72:ARG:CZ	16:Q:73:LYS:HG3	2.48	0.43
17:R:13:SER:OG	17:R:38:ARG:NH2	2.48	0.43
18:S:155:ARG:O	18:S:155:ARG:HG2	2.17	0.43
20:V:30:ASN:HD21	20:V:114:SER:HB3	1.83	0.43
33:i:78:LEU:HD12	33:i:79:LYS:N	2.34	0.43
38:u:83:ASP:HB2	38:u:86:VAL:HB	2.00	0.43
38:u:84:ARG:HD3	38:u:84:ARG:N	2.34	0.43
39:w:107:LEU:HG	39:w:110:TRP:O	2.17	0.43
5:B:40:PRO:HG2	41:z:115:LYS:HE3	2.00	0.43
12:M:51:ILE:HD12	12:M:52:ARG:N	2.34	0.43
14:O:183:LYS:HG3	14:O:189:ASN:ND2	2.33	0.43
31:g:41:ILE:HG23	31:g:56:ALA:HB2	2.00	0.43
35:k:3:ARG:HB2	35:k:44:TYR:CD1	2.54	0.43
39:w:117:HIS:HB3	39:w:157:THR:HB	2.00	0.43
39:w:791:ARG:O	39:w:795:ARG:HG3	2.18	0.43
1:1:148:C:H2'	1:1:149:G:O4'	2.18	0.43
1:1:597:C:H2'	1:1:598:G:C8	2.53	0.43
1:1:623:C:C5	1:1:624:U:C4	3.07	0.43
1:1:750:U:H2'	1:1:751:G:C8	2.52	0.43
1:1:1153:U:OP2	37:s:28:ARG:NH2	2.52	0.43
1:1:1690:G:H3'	1:1:1691:A:H8	1.83	0.43
1:1:3186:U:H2'	1:1:3187:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3374:A:OP2	15:P:170:LYS:NZ	2.41	0.43
5:B:55:HIS:CD2	5:B:73:LEU:HD11	2.54	0.43
5:B:83:PRO:O	5:B:165:GLN:NE2	2.51	0.43
6:C:38:ARG:HH11	6:C:38:ARG:HG2	1.82	0.43
7:E:185:SER:O	7:E:188:ASP:HB2	2.18	0.43
9:G:60:ARG:HD3	39:w:455:LEU:HB3	1.99	0.43
16:Q:49:LYS:O	16:Q:53:GLN:HG2	2.19	0.43
39:w:16:TRP:CE2	39:w:186:SER:HA	2.54	0.43
39:w:82:LYS:HA	39:w:82:LYS:HD3	1.73	0.43
1:1:277:G:N2	1:1:302:U:H2'	2.34	0.43
1:1:713:G:H3'	1:1:714:A:H5''	2.01	0.43
1:1:1229:C:H3'	1:1:1230:C:C5'	2.47	0.43
1:1:1389:A:H4'	1:1:1390:A:O5'	2.17	0.43
1:1:1482:U:H2'	1:1:1483:A:H8	1.83	0.43
1:1:1587:U:H4'	1:1:1588:A:C8	2.53	0.43
1:1:2465:G:H5'	1:1:2466:C:C5	2.41	0.43
1:1:3160:U:H2'	1:1:3161:G:C8	2.54	0.43
1:1:3282:G:H1	1:1:3305:C:H42	1.65	0.43
3:3:100:TRP:CD1	3:3:101:PRO:HD2	2.53	0.43
3:3:102:GLY:O	3:3:105:ILE:HG12	2.18	0.43
7:E:120:THR:H	7:E:123:TYR:HB3	1.83	0.43
20:V:111:MET:HE2	20:V:134:ASN:HB2	2.01	0.43
23:Y:112:LYS:H	23:Y:112:LYS:HG2	1.57	0.43
26:b:396:ARG:HH12	40:y:39:GLU:HG2	1.82	0.43
26:b:400:ARG:NH2	40:y:33:ASN:OD1	2.52	0.43
1:1:121:A:C2	9:G:129:PRO:HB3	2.54	0.43
1:1:1016:G:N2	1:1:1170:G:OP1	2.52	0.43
5:B:294:ALA:HB3	5:B:303:LYS:HG3	2.00	0.43
10:H:38:ASN:OD1	10:H:40:ARG:HG2	2.18	0.43
12:M:39:ILE:HD13	12:M:51:ILE:HG21	1.99	0.43
26:b:448:GLU:HG2	26:b:451:ALA:HB3	2.00	0.43
29:e:73:VAL:HG13	29:e:78:ASP:HB2	1.99	0.43
1:1:283:U:H2'	1:1:284:U:C6	2.54	0.43
1:1:592:U:C2	6:C:346:GLU:O	2.72	0.43
1:1:1506:U:H2'	1:1:1507:G:C8	2.54	0.43
1:1:1800:G:N2	1:1:1805:A:O2'	2.52	0.43
1:1:3185:C:H2'	1:1:3186:U:O4'	2.18	0.43
1:1:3315:A:C2	7:E:176:GLU:HG3	2.53	0.43
2:2:83:G:OP2	23:Y:73:TYR:OH	2.34	0.43
5:B:222:ARG:CZ	5:B:331:PRO:HB3	2.49	0.43
6:C:66:SER:HA	6:C:77:PRO:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:151:VAL:HG21	8:F:196:TYR:HB2	2.01	0.43
14:O:4:PHE:CE2	30:f:34:GLU:HB2	2.54	0.43
14:O:54:LYS:HA	37:s:4:LEU:HD13	2.00	0.43
15:P:118:GLN:HB3	15:P:147:GLU:OE1	2.19	0.43
20:V:72:ARG:NH1	39:w:163:ARG:HH21	2.17	0.43
25:a:124:VAL:HB	25:a:144:VAL:HG22	2.01	0.43
26:b:54:THR:HG21	26:b:134:LEU:HD22	2.00	0.43
26:b:456:LEU:HG	26:b:457:ASP:N	2.33	0.43
35:k:9:LYS:HB3	35:k:9:LYS:HE2	1.77	0.43
35:k:26:LYS:HD2	35:k:70:VAL:HG23	2.01	0.43
40:y:7:PHE:HE2	40:y:57:ARG:NH1	2.17	0.43
41:z:104:ARG:NH1	41:z:108:SER:HB3	2.23	0.43
1:1:739:G:N2	1:1:783:A:O5'	2.52	0.43
1:1:1207:C:H2'	1:1:1208:G:N2	2.33	0.43
1:1:1841:A:H2'	1:1:1842:U:O4'	2.19	0.43
1:1:3231:U:OP1	14:O:149:LYS:NZ	2.35	0.43
5:B:39:LYS:O	5:B:186:GLY:N	2.51	0.43
10:H:135:SER:HB3	10:H:143:ILE:HD12	2.00	0.43
25:a:91:LEU:HD12	25:a:92:GLY:H	1.84	0.43
37:s:26:SER:OG	37:s:27:LYS:HD2	2.18	0.43
1:1:595:U:H2'	1:1:596:A:H8	1.83	0.42
1:1:745:G:C2	1:1:748:G:H1'	2.54	0.42
1:1:1188:G:O2'	1:1:1200:A:N3	2.48	0.42
1:1:1444:C:O2'	29:e:92:GLU:OE2	2.31	0.42
1:1:1628:A:H1'	31:g:60:ARG:HH21	1.83	0.42
1:1:2212:G:H2'	1:1:2213:A:C8	2.53	0.42
6:C:190:ARG:NE	6:C:199:ARG:HB3	2.33	0.42
11:L:47:ALA:N	11:L:48:PRO:HD2	2.34	0.42
17:R:101:VAL:HA	17:R:104:ARG:HG2	2.01	0.42
32:h:20:LEU:HD21	32:h:24:ARG:HE	1.84	0.42
37:s:3:SER:O	37:s:5:LYS:HG2	2.18	0.42
38:u:88:ALA:O	38:u:91:LEU:HB3	2.19	0.42
39:w:475:VAL:O	39:w:477:TYR:N	2.52	0.42
1:1:320:C:H2'	1:1:321:A:H8	1.84	0.42
1:1:541:G:H2'	1:1:542:G:H8	1.84	0.42
1:1:685:A:N1	1:1:973:G:O2'	2.48	0.42
1:1:2212:G:H2'	1:1:2213:A:H8	1.83	0.42
1:1:2452:G:H22	1:1:2484:G:N2	2.16	0.42
3:3:42:SER:O	3:3:44:PRO:HD3	2.18	0.42
5:B:189:ALA:O	5:B:193:GLU:HG2	2.18	0.42
5:B:301:THR:O	5:B:303:LYS:HG2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:73:LEU:CD1	6:C:78:ARG:HE	2.32	0.42
8:F:41:LYS:O	8:F:45:GLN:HG2	2.19	0.42
12:M:82:ASP:OD1	12:M:82:ASP:C	2.62	0.42
22:X:39:LEU:HD23	22:X:39:LEU:HA	1.85	0.42
28:d:33:ARG:HB2	28:d:69:ILE:O	2.19	0.42
1:1:1651:A:H2'	1:1:1652:G:H8	1.84	0.42
1:1:2482:G:O2'	5:B:258:ALA:O	2.29	0.42
1:1:3404:G:O2'	1:1:3406:A:N6	2.45	0.42
4:8:18:ARG:HG3	4:8:21:ARG:NH2	2.34	0.42
14:O:100:LEU:HD12	14:O:100:LEU:HA	1.83	0.42
25:a:135:GLU:HA	25:a:138:LYS:CG	2.48	0.42
36:r:45:ILE:O	36:r:49:LEU:HG	2.19	0.42
36:r:155:PHE:N	36:r:212:GLY:O	2.51	0.42
39:w:161:ARG:HH21	39:w:194:ILE:HD13	1.85	0.42
1:1:546:G:O6	18:S:94:ARG:NH2	2.53	0.42
1:1:1230:C:H4'	1:1:1231:A:N7	2.34	0.42
1:1:1231:A:H1'	37:s:22:LYS:NZ	2.35	0.42
1:1:1347:U:OP1	14:O:134:ARG:HG3	2.19	0.42
1:1:1423:G:OP2	29:e:101:LYS:HE2	2.20	0.42
1:1:1712:A:H2'	1:1:1713:G:H8	1.85	0.42
1:1:1802:C:C4	1:1:1803:U:H1'	2.54	0.42
1:1:3123:A:C8	26:b:208:GLY:HA2	2.54	0.42
5:B:382:THR:OG1	38:u:105:GLU:HG2	2.19	0.42
7:E:108:LYS:C	7:E:109:ILE:HD13	2.44	0.42
15:P:168:SER:HB3	30:f:61:ARG:HH21	1.84	0.42
18:S:175:PHE:HD2	18:S:175:PHE:HA	1.74	0.42
22:X:106:PRO:HA	22:X:125:LEU:HA	2.00	0.42
25:a:136:LYS:HB2	25:a:136:LYS:HE3	1.85	0.42
26:b:117:LEU:HD11	26:b:126:CYS:HB3	2.01	0.42
28:d:22:HIS:HB2	28:d:74:HIS:HB3	2.00	0.42
30:f:46:LEU:HD23	30:f:72:ILE:HG22	2.01	0.42
1:1:1507:G:H5'	17:R:24:MET:O	2.20	0.42
2:2:75:U:H2'	2:2:76:G:H8	1.85	0.42
9:G:137:ASN:ND2	13:N:3:ALA:H	2.17	0.42
23:Y:54:GLN:OE1	23:Y:106:THR:OG1	2.37	0.42
25:a:131:ARG:NH1	25:a:131:ARG:HA	2.34	0.42
28:d:40:GLU:HA	28:d:40:GLU:OE2	2.20	0.42
36:r:65:ILE:HD12	36:r:65:ILE:HA	1.94	0.42
1:1:382:A:O2'	1:1:384:G:H5'	2.19	0.42
1:1:1141:C:O2'	1:1:1142:U:H5'	2.20	0.42
1:1:1482:U:H5''	15:P:66:GLY:HA3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1911:C:H2'	1:1:1912:C:C6	2.55	0.42
1:1:2460:A:OP1	37:s:14:ARG:HD2	2.19	0.42
1:1:2982:A:N3	1:1:2982:A:H2'	2.34	0.42
2:2:44:G:OP1	34:j:66:TYR:OH	2.22	0.42
6:C:321:LEU:HD21	8:F:156:TYR:HD1	1.84	0.42
10:H:161:GLN:O	10:H:164:ASN:HB2	2.20	0.42
14:O:6:LYS:HB3	14:O:6:LYS:HE2	1.79	0.42
17:R:36:ASN:OD1	17:R:37:SER:N	2.53	0.42
20:V:70:ASP:HA	20:V:73:LYS:NZ	2.35	0.42
26:b:117:LEU:HD12	26:b:117:LEU:HA	1.88	0.42
26:b:160:ARG:HB3	36:r:4:ASN:HA	2.00	0.42
26:b:441:VAL:CG1	38:u:87:ILE:HD11	2.48	0.42
28:d:106:MET:HE2	28:d:106:MET:HB3	1.87	0.42
33:i:14:THR:C	33:i:15:LEU:HD12	2.45	0.42
39:w:73:ILE:HB	39:w:86:ASN:O	2.20	0.42
39:w:172:PHE:HB3	39:w:198:CYS:SG	2.59	0.42
40:y:175:SER:O	40:y:178:GLN:NE2	2.52	0.42
1:1:618:U:H3'	1:1:619:G:H8	1.85	0.42
1:1:1272:U:H3	1:1:1275:A:H5''	1.84	0.42
1:1:1283:A:H3'	1:1:1284:U:C6	2.54	0.42
1:1:1455:A:H2'	1:1:1456:G:H8	1.85	0.42
1:1:3370:U:H2'	7:E:64:ARG:HH11	1.84	0.42
5:B:218:ILE:HG13	5:B:337:THR:HB	2.01	0.42
11:L:179:LEU:O	11:L:183:ARG:HB2	2.20	0.42
20:V:24:ILE:HD13	20:V:65:LYS:NZ	2.35	0.42
39:w:28:ARG:HG3	39:w:32:LYS:HE3	2.00	0.42
39:w:145:ALA:C	39:w:149:LEU:HD23	2.45	0.42
1:1:359:A:C5	4:8:39:MET:HE3	2.55	0.42
1:1:617:C:H5'	7:E:38:LYS:NZ	2.35	0.42
1:1:881:C:HO2'	1:1:882:U:P	2.43	0.42
1:1:1720:C:N4	1:1:3165:G:H1	2.18	0.42
1:1:1783:G:O2'	1:1:1784:U:O5'	2.38	0.42
1:1:1825:U:H2'	1:1:1826:C:C6	2.55	0.42
1:1:2445:A:H2'	1:1:2446:A:H8	1.84	0.42
1:1:2453:C:H2'	1:1:2454:C:C6	2.55	0.42
1:1:3327:A:H2'	1:1:3328:U:H6	1.84	0.42
2:2:74:A:OP1	32:h:9:ARG:NH2	2.53	0.42
7:E:176:GLU:HG2	12:M:111:PHE:CE2	2.55	0.42
10:H:41:HIS:ND1	10:H:42:VAL:HG13	2.35	0.42
15:P:177:ASN:O	15:P:181:ARG:HG3	2.20	0.42
25:a:75:LEU:HB3	25:a:117:LEU:HD11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:d:45:ALA:HA	28:d:80:LEU:HD21	2.01	0.42
39:w:108:LYS:HE2	39:w:110:TRP:HZ3	1.84	0.42
39:w:142:MET:HA	39:w:145:ALA:HB3	2.01	0.42
39:w:160:PHE:CD1	39:w:160:PHE:N	2.87	0.42
39:w:162:SER:OG	39:w:164:ASP:OD1	2.38	0.42
40:y:160:LEU:HD11	40:y:221:ILE:HG21	2.01	0.42
1:1:144:U:H2'	1:1:145:G:H8	1.85	0.42
1:1:1008:U:N3	1:1:1009:C:O2	2.52	0.42
1:1:2923:G:C8	26:b:27:GLN:NE2	2.87	0.42
2:2:132:G:H1	2:2:137:A:N6	2.18	0.42
3:3:20:ILE:CD1	3:3:29:ARG:HG3	2.44	0.42
3:3:54:ARG:HB2	3:3:61:TYR:CE1	2.55	0.42
6:C:75:ARG:HH22	39:w:785:ARG:NH1	2.18	0.42
8:F:88:PRO:HG2	8:F:145:ILE:HG21	2.01	0.42
8:F:227:LYS:HB2	8:F:233:GLY:HA3	2.02	0.42
11:L:48:PRO:HG3	32:h:117:LYS:HE3	2.01	0.42
1:1:884:U:H2'	1:1:885:G:H8	1.84	0.42
1:1:1150:C:H2'	1:1:1151:A:C8	2.55	0.42
1:1:1233:A:P	1:1:1234:A:HO2'	2.39	0.42
1:1:1559:G:H5'	1:1:1885:G:OP2	2.20	0.42
1:1:1959:C:N4	1:1:1960:G:O6	2.53	0.42
1:1:3415:U:H2'	1:1:3416:A:O4'	2.20	0.42
3:3:100:TRP:CG	3:3:101:PRO:HD2	2.54	0.42
11:L:126:PHE:CE2	11:L:141:VAL:HB	2.54	0.42
11:L:128:ARG:C	11:L:130:ALA:H	2.28	0.42
18:S:9:VAL:HG12	18:S:23:LEU:HD12	2.02	0.42
20:V:17:LEU:HD23	20:V:55:SER:HB3	2.00	0.42
26:b:207:VAL:O	36:r:3:GLN:NE2	2.52	0.42
39:w:773:LYS:HD2	39:w:774:GLY:N	2.35	0.42
40:y:99:GLU:HG3	40:y:101:LEU:N	2.35	0.42
1:1:433:C:H2'	1:1:434:A:H8	1.84	0.41
1:1:655:C:H2'	1:1:656:A:C8	2.55	0.41
1:1:675:C:H2'	1:1:676:G:C8	2.55	0.41
1:1:1549:A:OP1	4:8:44:TRP:NE1	2.48	0.41
1:1:1826:C:H2'	1:1:1827:G:C8	2.55	0.41
1:1:1844:C:H4'	31:g:70:LYS:HE2	2.01	0.41
1:1:2417:C:H2'	1:1:2418:C:C6	2.55	0.41
1:1:3093:G:H21	1:1:3497:G:H5'	1.85	0.41
1:1:3168:A:H4'	1:1:3438:G:OP1	2.20	0.41
3:3:11:VAL:HG23	6:C:136:LEU:HD23	2.02	0.41
7:E:102:ILE:HD13	7:E:102:ILE:HA	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:210:TRP:CD1	8:F:211:PRO:HD2	2.55	0.41
13:N:143:ARG:O	32:h:98:GLU:HB2	2.20	0.41
20:V:47:ARG:HD3	20:V:50:ARG:HG2	2.01	0.41
22:X:67:ASN:ND2	32:h:35:ILE:HG22	2.35	0.41
1:1:140:U:H5'	32:h:84:GLN:HG2	2.01	0.41
1:1:704:U:O2'	1:1:820:C:O2	2.36	0.41
1:1:3367:A:H2'	7:E:86:TYR:OH	2.20	0.41
2:2:66:G:O6	34:j:63:ARG:NH1	2.53	0.41
3:3:66:THR:O	3:3:69:ARG:NH1	2.53	0.41
6:C:73:LEU:HD12	6:C:74:ALA:O	2.19	0.41
6:C:321:LEU:HD13	8:F:153:GLU:OE2	2.21	0.41
11:L:157:GLN:OE1	11:L:157:GLN:HA	2.20	0.41
20:V:17:LEU:HD13	20:V:53:ALA:HB3	2.00	0.41
26:b:395:ARG:O	26:b:395:ARG:HG3	2.19	0.41
26:b:421:ILE:C	38:u:81:ARG:HH12	2.29	0.41
32:h:30:LEU:HA	32:h:30:LEU:HD23	1.81	0.41
33:i:51:TYR:CD1	33:i:51:TYR:C	2.98	0.41
40:y:197:LEU:HD12	40:y:205:PHE:O	2.20	0.41
1:1:153:U:O2'	13:N:41:ARG:NH1	2.53	0.41
1:1:224:U:O2	23:Y:102:LYS:NZ	2.42	0.41
1:1:425:A:H2'	1:1:426:A:C8	2.56	0.41
1:1:743:A:C6	25:a:116:ARG:HD2	2.55	0.41
1:1:1253:G:H4'	1:1:1254:A:H5'	2.02	0.41
3:3:5:GLU:OE2	6:C:290:THR:N	2.53	0.41
4:8:24:PRO:O	4:8:27:ILE:HG22	2.20	0.41
5:B:211:GLN:HG2	5:B:284:ARG:HA	2.01	0.41
6:C:33:ARG:HG3	6:C:122:TYR:HE1	1.84	0.41
6:C:288:ASP:OD1	6:C:291:ARG:HG3	2.20	0.41
6:C:301:ILE:HG13	6:C:302:VAL:N	2.35	0.41
9:G:97:TYR:OH	9:G:207:ASP:OD2	2.34	0.41
9:G:159:PRO:HG2	9:G:162:LEU:HD13	2.01	0.41
9:G:178:ALA:HB2	9:G:218:VAL:HG21	2.01	0.41
11:L:42:LYS:O	11:L:46:ILE:HG12	2.20	0.41
12:M:106:ASN:ND2	12:M:109:ASP:OD2	2.53	0.41
1:1:183:A:H2	1:1:249:G:H22	1.69	0.41
1:1:862:A:H2'	1:1:863:G:O4'	2.20	0.41
1:1:1155:U:H5	1:1:1165:G:H1	1.68	0.41
3:3:8:TRP:O	3:3:12:GLY:N	2.54	0.41
5:B:205:ILE:HD11	5:B:209:PHE:CD2	2.56	0.41
8:F:174:ALA:HA	8:F:177:GLU:HG2	2.02	0.41
18:S:25:ARG:HH22	18:S:27:ARG:HD2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:70:ASP:HA	20:V:73:LYS:HZ1	1.85	0.41
23:Y:50:ARG:HD3	23:Y:114:ARG:HH21	1.84	0.41
26:b:121:ASP:OD2	26:b:122:SER:N	2.53	0.41
29:e:86:ASN:N	29:e:86:ASN:OD1	2.52	0.41
39:w:142:MET:HE1	39:w:143:LYS:HE2	2.02	0.41
1:1:19:U:H2'	1:1:20:A:C8	2.56	0.41
1:1:430:A:C2	1:1:2451:A:H4'	2.55	0.41
1:1:597:C:H2'	1:1:598:G:H8	1.84	0.41
1:1:1588:A:O2'	1:1:1589:U:P	2.79	0.41
1:1:1702:A:H2'	1:1:1703:G:C8	2.55	0.41
1:1:3331:U:H3	1:1:3356:A:H61	1.67	0.41
2:2:102:C:H5''	34:j:76:ASN:HD21	1.86	0.41
3:3:8:TRP:HB2	3:3:46:ALA:HB1	2.02	0.41
5:B:197:GLU:O	5:B:201:LYS:NZ	2.35	0.41
12:M:32:VAL:HB	12:M:36:ARG:HG3	2.02	0.41
23:Y:72:VAL:HG12	23:Y:79:LEU:HD22	2.02	0.41
26:b:113:TYR:CD2	26:b:133:ALA:HA	2.55	0.41
30:f:9:TYR:CE2	30:f:100:ARG:HG2	2.55	0.41
32:h:29:SER:O	32:h:32:VAL:HG12	2.21	0.41
35:k:38:ARG:NE	35:k:39:CYS:O	2.50	0.41
1:1:420:G:H5'	15:P:26:PHE:HZ	1.86	0.41
1:1:1177:C:H4'	1:1:1362:U:C4	2.56	0.41
1:1:1300:U:H1'	1:1:1303:C:H5	1.85	0.41
1:1:1800:G:N7	1:1:1801:C:N4	2.63	0.41
1:1:2932:A:C2	1:1:2945:G:H2'	2.55	0.41
1:1:3369:A:H4'	1:1:3370:U:H5'	2.01	0.41
1:1:3440:A:H2'	1:1:3441:G:C8	2.55	0.41
2:2:99:C:H2'	2:2:100:A:C8	2.55	0.41
12:M:73:ILE:H	12:M:73:ILE:HG12	1.68	0.41
13:N:27:ALA:HB2	13:N:122:ASN:OD1	2.21	0.41
20:V:51:LEU:HD23	20:V:51:LEU:HA	1.93	0.41
26:b:61:LYS:O	26:b:65:ILE:HG13	2.19	0.41
26:b:157:HIS:HA	26:b:160:ARG:NE	2.36	0.41
29:e:83:LEU:HD22	29:e:84:MET:HE3	2.03	0.41
32:h:116:ARG:HA	32:h:116:ARG:HD2	1.88	0.41
39:w:140:MET:SD	39:w:140:MET:C	3.04	0.41
1:1:594:A:H2'	1:1:595:U:O4'	2.20	0.41
1:1:828:U:H2'	1:1:829:U:C6	2.56	0.41
1:1:1500:G:N2	1:1:1544:G:H5''	2.35	0.41
1:1:1512:C:H2'	1:1:1513:U:C6	2.55	0.41
1:1:1713:G:H2'	1:1:1714:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:105:ILE:HG13	3:3:106:HIS:N	2.36	0.41
11:L:195:PHE:C	11:L:195:PHE:CD2	2.97	0.41
16:Q:43:PHE:HE1	16:Q:140:LEU:HD13	1.86	0.41
17:R:141:HIS:HA	17:R:144:ARG:HD2	2.03	0.41
33:i:38:VAL:O	33:i:42:VAL:HG12	2.21	0.41
41:z:101:LYS:HD2	41:z:103:LYS:HD3	2.02	0.41
1:1:59:G:H4'	1:1:60:A:H4'	2.02	0.41
1:1:146:U:H2'	1:1:147:C:C6	2.56	0.41
1:1:1449:U:H2'	1:1:1450:C:O4'	2.21	0.41
2:2:129:U:H2'	2:2:130:G:H8	1.86	0.41
5:B:115:LYS:HB3	5:B:122:TRP:CZ3	2.56	0.41
6:C:76:ILE:HG12	6:C:96:CYS:SG	2.61	0.41
6:C:221:PHE:HB3	6:C:229:ILE:HD11	2.02	0.41
7:E:131:GLY:HA2	7:E:132:PRO:HD3	1.87	0.41
14:O:155:ALA:O	14:O:159:GLU:HG2	2.20	0.41
25:a:116:ARG:C	25:a:117:LEU:HD12	2.45	0.41
26:b:382:VAL:O	26:b:385:ARG:NH1	2.53	0.41
29:e:108:LYS:O	29:e:112:LEU:HD23	2.20	0.41
34:j:64:MET:O	34:j:68:LYS:HG3	2.21	0.41
35:k:56:LYS:HD2	35:k:57:LEU:N	2.35	0.41
39:w:59:TRP:HE3	39:w:116:LEU:HD21	1.86	0.41
1:1:216:A:N7	6:C:165:LYS:HE3	2.35	0.41
1:1:379:G:H4'	1:1:404:A:N1	2.35	0.41
1:1:419:U:H2'	1:1:420:G:H8	1.85	0.41
1:1:765:G:H2'	1:1:766:G:H8	1.86	0.41
1:1:1282:A:H3'	1:1:1283:A:N3	2.36	0.41
1:1:1395:A:H2'	1:1:1396:G:C8	2.56	0.41
1:1:1840:A:H2'	1:1:1841:A:H8	1.85	0.41
1:1:1879:C:H2'	1:1:1880:A:H8	1.85	0.41
1:1:3014:A:H61	1:1:3022:C:N4	2.16	0.41
1:1:3112:A:O2'	1:1:3113:A:H8	1.95	0.41
1:1:3113:A:H2'	1:1:3114:C:C6	2.56	0.41
1:1:3116:U:H4'	10:H:119:ARG:HD2	2.02	0.41
1:1:3306:C:H2'	12:M:92:TRP:CZ2	2.56	0.41
1:1:3351:U:H2'	1:1:3352:A:H8	1.85	0.41
2:2:23:G:C6	2:2:24:G:N1	2.89	0.41
2:2:159:U:C2	39:w:455:LEU:HD21	2.56	0.41
6:C:321:LEU:HD21	8:F:156:TYR:CD1	2.56	0.41
7:E:189:ARG:HB3	7:E:191:HIS:CE1	2.56	0.41
8:F:156:TYR:CE2	8:F:188:VAL:HG11	2.56	0.41
10:H:38:ASN:OD1	10:H:39:LEU:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L:80:LEU:HD22	11:L:85:VAL:HG13	2.02	0.41
14:O:23:VAL:O	14:O:27:GLN:HG2	2.21	0.41
17:R:126:GLU:O	17:R:131:THR:HG23	2.21	0.41
18:S:105:MET:HE1	18:S:120:ILE:HG21	2.03	0.41
22:X:29:THR:HG22	22:X:30:THR:N	2.36	0.41
23:Y:102:LYS:HD3	23:Y:102:LYS:HA	1.83	0.41
31:g:68:ASN:OD1	31:g:69:LYS:HD3	2.20	0.41
31:g:93:PHE:HA	31:g:96:GLU:OE1	2.21	0.41
32:h:56:ILE:HA	32:h:59:VAL:HG12	2.02	0.41
33:i:37:PHE:O	33:i:40:SER:OG	2.27	0.41
35:k:50:ASP:OD2	35:k:52:LYS:HE3	2.20	0.41
38:u:96:ARG:NH1	38:u:100:VAL:HG23	2.36	0.41
39:w:43:LEU:HD12	39:w:43:LEU:O	2.20	0.41
1:1:1146:G:N2	1:1:1146:G:OP2	2.54	0.41
1:1:1320:G:H2'	1:1:1321:A:H8	1.86	0.41
1:1:1711:A:H2'	1:1:1712:A:C8	2.56	0.41
1:1:3165:G:HO2'	17:R:61:PHE:HZ	1.65	0.41
1:1:3470:G:H22	5:B:381:GLY:HA3	1.86	0.41
6:C:341:VAL:HG23	6:C:343:ILE:CD1	2.51	0.41
26:b:86:LEU:HD13	26:b:157:HIS:HE1	1.86	0.41
26:b:174:CYS:O	26:b:253:TYR:HA	2.21	0.41
31:g:93:PHE:O	31:g:97:GLU:HG2	2.21	0.41
38:u:93:ALA:O	38:u:97:VAL:HG23	2.21	0.41
39:w:95:THR:HB	39:w:140:MET:SD	2.61	0.41
1:1:596:A:H2'	1:1:597:C:C6	2.55	0.40
1:1:616:A:H5'	7:E:35:VAL:O	2.20	0.40
1:1:1211:A:H5''	30:f:78:ASN:HD22	1.86	0.40
1:1:1335:A:H4'	1:1:1336:U:H5'	2.03	0.40
1:1:2949:U:H2'	1:1:2950:U:C6	2.57	0.40
1:1:3147:U:H2'	1:1:3148:G:C8	2.56	0.40
1:1:3484:G:H2'	1:1:3485:U:C6	2.56	0.40
9:G:53:PRO:HB2	9:G:55:TYR:CD1	2.56	0.40
15:P:7:SER:N	15:P:8:PRO:HD2	2.37	0.40
22:X:45:TYR:CD2	32:h:77:TYR:HB3	2.56	0.40
39:w:759:VAL:O	39:w:781:MET:HA	2.21	0.40
1:1:1673:A:H5''	31:g:74:ARG:HH22	1.86	0.40
1:1:1806:U:H1'	1:1:1807:G:C8	2.57	0.40
1:1:3332:U:H2'	1:1:3333:G:H8	1.84	0.40
2:2:44:G:O2'	2:2:112:A:N1	2.48	0.40
3:3:92:GLN:O	3:3:96:GLN:HG3	2.21	0.40
5:B:218:ILE:CG1	5:B:337:THR:HB	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:285:SER:OG	6:C:286:ASN:N	2.55	0.40
9:G:143:ILE:HG22	9:G:173:MET:HG3	2.03	0.40
25:a:75:LEU:CB	25:a:117:LEU:HD11	2.51	0.40
26:b:423:GLN:HG3	38:u:81:ARG:NH2	2.35	0.40
32:h:39:SER:OG	32:h:42:LYS:NZ	2.42	0.40
40:y:21:ASN:OD1	40:y:201:ASP:N	2.53	0.40
1:1:73:C:C2	11:L:59:LYS:HE2	2.56	0.40
1:1:526:G:H4'	6:C:342:LYS:NZ	2.37	0.40
1:1:646:A:O2'	1:1:647:A:P	2.79	0.40
1:1:1397:A:H2'	1:1:1398:C:O4'	2.21	0.40
1:1:1415:A:H2'	1:1:1416:G:H8	1.86	0.40
1:1:1707:U:H5''	17:R:64:ARG:CZ	2.51	0.40
1:1:2922:U:OP1	26:b:47:TYR:OH	2.38	0.40
1:1:2931:C:N4	1:1:2947:C:H41	2.20	0.40
1:1:3154:U:C2	28:d:30:PHE:CZ	3.09	0.40
1:1:3437:A:H3'	1:1:3438:G:C8	2.55	0.40
3:3:97:LEU:HB3	3:3:105:ILE:HG22	2.02	0.40
18:S:65:GLU:O	18:S:68:PRO:HD3	2.21	0.40
28:d:48:HIS:O	28:d:50:GLN:NE2	2.54	0.40
41:z:104:ARG:O	41:z:104:ARG:HG2	2.20	0.40
1:1:303:A:H2'	1:1:304:A:C8	2.56	0.40
1:1:600:C:OP1	8:F:149:LYS:HD3	2.21	0.40
1:1:643:C:OP2	7:E:129:ARG:NH2	2.54	0.40
1:1:1326:G:H2'	1:1:1327:C:C6	2.56	0.40
1:1:1731:A:H2'	1:1:1732:A:C8	2.57	0.40
1:1:3487:C:H2'	1:1:3488:C:C6	2.56	0.40
3:3:108:CYS:O	3:3:112:LEU:HD23	2.22	0.40
5:B:144:ILE:H	5:B:144:ILE:HD12	1.86	0.40
6:C:152:LEU:HD23	6:C:251:ILE:HG12	2.03	0.40
7:E:57:VAL:HA	7:E:70:VAL:O	2.22	0.40
9:G:223:SER:O	9:G:227[B]:ASP:HB2	2.21	0.40
10:H:111:GLU:OE2	10:H:111:GLU:N	2.55	0.40
14:O:178:LYS:HE2	14:O:178:LYS:HB3	1.96	0.40
15:P:86:LYS:HE3	15:P:86:LYS:HB3	1.92	0.40
16:Q:84:VAL:HB	16:Q:141:VAL:HG23	2.03	0.40
22:X:29:THR:HG22	22:X:30:THR:HG23	2.04	0.40
35:k:61:LEU:HD12	35:k:65:LEU:HD22	2.03	0.40
1:1:147:C:H2'	1:1:148:C:C6	2.57	0.40
1:1:1334:A:C4	1:1:2982:A:C6	3.10	0.40
1:1:1554:G:O2'	1:1:1638:A:N1	2.49	0.40
1:1:1650:C:H2'	1:1:1651:A:H8	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2932:A:H2	1:1:2945:G:H2'	1.86	0.40
1:1:3118:G:N2	1:1:3128:A:OP2	2.48	0.40
5:B:10:ARG:HG2	5:B:12:GLY:O	2.22	0.40
9:G:91:PHE:CE2	9:G:185:ARG:HB3	2.56	0.40
11:L:62:THR:HG23	11:L:64:ARG:H	1.86	0.40
22:X:82:VAL:HG22	22:X:122:PHE:HD1	1.87	0.40
29:e:15:LYS:HD2	29:e:27:GLU:OE1	2.21	0.40
36:r:70:GLU:OE1	36:r:70:GLU:N	2.50	0.40
39:w:77:ASP:OD1	39:w:78:LEU:N	2.51	0.40
39:w:129:GLN:O	39:w:133:GLY:N	2.54	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	
3	3	110/302 (36%)	105 (96%)	5 (4%)	0	100	100
4	8	47/51 (92%)	44 (94%)	3 (6%)	0	100	100
5	B	361/388 (93%)	343 (95%)	18 (5%)	0	100	100
6	C	357/363 (98%)	338 (95%)	17 (5%)	2 (1%)	21	52
7	E	161/195 (83%)	148 (92%)	11 (7%)	2 (1%)	10	37
8	F	216/250 (86%)	210 (97%)	5 (2%)	1 (0%)	24	57
9	G	180/259 (70%)	169 (94%)	8 (4%)	3 (2%)	7	30
10	H	181/190 (95%)	173 (96%)	8 (4%)	0	100	100
11	L	178/208 (86%)	168 (94%)	9 (5%)	1 (1%)	21	52
12	M	123/134 (92%)	118 (96%)	5 (4%)	0	100	100
13	N	160/201 (80%)	156 (98%)	4 (2%)	0	100	100
14	O	194/197 (98%)	189 (97%)	4 (2%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	P	163/187 (87%)	157 (96%)	6 (4%)	0	100	100
16	Q	133/187 (71%)	128 (96%)	5 (4%)	0	100	100
17	R	120/193 (62%)	116 (97%)	4 (3%)	0	100	100
18	S	164/176 (93%)	156 (95%)	8 (5%)	0	100	100
19	U	96/117 (82%)	92 (96%)	4 (4%)	0	100	100
20	V	136/139 (98%)	132 (97%)	3 (2%)	1 (1%)	18	49
21	W	207/241 (86%)	195 (94%)	12 (6%)	0	100	100
22	X	112/141 (79%)	107 (96%)	5 (4%)	0	100	100
23	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100
24	Z	132/136 (97%)	129 (98%)	3 (2%)	0	100	100
25	a	90/148 (61%)	88 (98%)	2 (2%)	0	100	100
26	b	407/642 (63%)	399 (98%)	7 (2%)	1 (0%)	43	73
27	c	95/117 (81%)	95 (100%)	0	0	100	100
28	d	100/113 (88%)	99 (99%)	1 (1%)	0	100	100
29	e	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
30	f	104/108 (96%)	98 (94%)	6 (6%)	0	100	100
31	g	103/112 (92%)	98 (95%)	5 (5%)	0	100	100
32	h	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
33	i	92/99 (93%)	90 (98%)	2 (2%)	0	100	100
34	j	73/91 (80%)	71 (97%)	2 (3%)	0	100	100
35	k	68/74 (92%)	66 (97%)	2 (3%)	0	100	100
36	r	158/260 (61%)	156 (99%)	2 (1%)	0	100	100
37	s	28/470 (6%)	28 (100%)	0	0	100	100
38	u	112/192 (58%)	107 (96%)	5 (4%)	0	100	100
39	w	412/802 (51%)	378 (92%)	33 (8%)	1 (0%)	43	73
40	y	223/244 (91%)	214 (96%)	9 (4%)	0	100	100
41	z	33/117 (28%)	32 (97%)	1 (3%)	0	100	100
42	T	19/160 (12%)	17 (90%)	2 (10%)	0	100	100
All	All	6006/8379 (72%)	5757 (96%)	236 (4%)	13 (0%)	44	73

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	L	175	ALA
20	V	3	ARG
6	C	346	GLU
39	w	476	LYS
7	E	144	ALA
7	E	148	ALA
6	C	347	LYS
26	b	89	ARG
9	G	182[A]	ASN
9	G	182[B]	ASN
14	O	187	PRO
9	G	52	TRP
8	F	198	VAL

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	
3	3	104/271 (38%)	104 (100%)	0	100	100
4	8	45/47 (96%)	45 (100%)	0	100	100
5	B	308/326 (94%)	307 (100%)	1 (0%)	86	87
6	C	296/297 (100%)	296 (100%)	0	100	100
7	E	133/155 (86%)	132 (99%)	1 (1%)	73	81
8	F	182/210 (87%)	182 (100%)	0	100	100
9	G	154/212 (73%)	149 (97%)	5 (3%)	34	64
10	H	164/170 (96%)	163 (99%)	1 (1%)	78	83
11	L	144/167 (86%)	144 (100%)	0	100	100
12	M	108/113 (96%)	105 (97%)	3 (3%)	38	66
13	N	146/176 (83%)	146 (100%)	0	100	100
14	O	161/162 (99%)	160 (99%)	1 (1%)	78	83
15	P	138/149 (93%)	138 (100%)	0	100	100
16	Q	115/159 (72%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	R	111/162 (68%)	111 (100%)	0	100	100
18	S	150/154 (97%)	150 (100%)	0	100	100
20	V	106/107 (99%)	103 (97%)	3 (3%)	38	66
22	X	101/122 (83%)	100 (99%)	1 (1%)	68	79
23	Y	110/111 (99%)	110 (100%)	0	100	100
25	a	81/122 (66%)	81 (100%)	0	100	100
26	b	214/556 (38%)	212 (99%)	2 (1%)	70	80
28	d	93/102 (91%)	93 (100%)	0	100	100
29	e	100/107 (94%)	100 (100%)	0	100	100
30	f	89/91 (98%)	88 (99%)	1 (1%)	65	78
31	g	91/97 (94%)	90 (99%)	1 (1%)	65	78
32	h	106/107 (99%)	105 (99%)	1 (1%)	70	80
33	i	81/84 (96%)	81 (100%)	0	100	100
34	j	62/71 (87%)	62 (100%)	0	100	100
35	k	63/66 (96%)	61 (97%)	2 (3%)	34	64
36	r	63/224 (28%)	63 (100%)	0	100	100
37	s	28/409 (7%)	28 (100%)	0	100	100
38	u	99/168 (59%)	98 (99%)	1 (1%)	68	79
39	w	369/697 (53%)	366 (99%)	3 (1%)	73	81
40	y	189/206 (92%)	186 (98%)	3 (2%)	55	75
41	z	31/107 (29%)	31 (100%)	0	100	100
42	T	18/139 (13%)	18 (100%)	0	100	100
All	All	4553/6623 (69%)	4523 (99%)	30 (1%)	76	82

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	212	ASN
7	E	34	ASN
9	G	182[A]	ASN
9	G	182[B]	ASN
9	G	219	ASP
9	G	227[A]	ASP
9	G	227[B]	ASP

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Mol	Chain	Res	Type
10	H	68	ILE
12	M	40	ASP
12	M	73	ILE
12	M	109	ASP
14	O	186	SER
20	V	70	ASP
20	V	73	LYS
20	V	76	MET
22	X	76	GLU
26	b	456	LEU
26	b	458	GLU
30	f	28	THR
31	g	3	GLN
32	h	61	ASN
35	k	10	GLN
35	k	33	VAL
38	u	101	HIS
39	w	82	LYS
39	w	84	ILE
39	w	86	ASN
40	y	28	LEU
40	y	145	ASN
40	y	178	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
3	3	78	GLN
4	8	33	ASN
5	B	8	GLN
5	B	211	GLN
5	B	256	HIS
6	C	60	HIS
6	C	85	HIS
6	C	363	ASN
7	E	147	ASN
8	F	241	HIS
9	G	77	GLN
9	G	118	ASN
9	G	137	ASN
10	H	25	ASN
10	H	59	HIS

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Mol	Chain	Res	Type
10	H	77	ASN
10	H	96	HIS
10	H	100	ASN
10	H	158	ASN
11	L	28	GLN
11	L	112	ASN
11	L	172	ASN
12	M	125	ASN
13	N	34	ASN
14	O	82	GLN
14	O	116	GLN
15	P	80	GLN
15	P	118	GLN
29	e	17	HIS
31	g	3	GLN
31	g	73	GLN
32	h	11	GLN
32	h	15	ASN
32	h	61	ASN
33	i	61	ASN
34	j	48	ASN
35	k	59	GLN
36	r	40	GLN
36	r	68	HIS
36	r	72	ASN
38	u	92	ASN
39	w	86	ASN
39	w	88	HIS
39	w	134	GLN
39	w	291	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2109/3497 (60%)	502 (23%)	28 (1%)
2	2	144/165 (87%)	22 (15%)	1 (0%)
All	All	2253/3662 (61%)	524 (23%)	29 (1%)

All (524) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	12	A
1	1	14	U
1	1	26	A
1	1	49	A
1	1	50	U
1	1	57	A
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A
1	1	72	C
1	1	77	A
1	1	105	G
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	118	U
1	1	120	G
1	1	136	U
1	1	156	A
1	1	161	C
1	1	162	A
1	1	163	A
1	1	170	G
1	1	177	G
1	1	185	G
1	1	186	A
1	1	193	U
1	1	194	A
1	1	195	A
1	1	197	U
1	1	198	U
1	1	207	C
1	1	217	G
1	1	220	A
1	1	225	G
1	1	226	A
1	1	227	G
1	1	239	U
1	1	241	G
1	1	243	C

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Mol	Chain	Res	Type
1	1	245	A
1	1	247	U
1	1	248	G
1	1	258	U
1	1	259	A
1	1	260	U
1	1	268	U
1	1	269	U
1	1	270	U
1	1	271	C
1	1	272	G
1	1	276	A
1	1	277	G
1	1	303	A
1	1	305	A
1	1	306	U
1	1	331	A
1	1	337	U
1	1	341	G
1	1	342	A
1	1	345	G
1	1	347	C
1	1	360	A
1	1	378	U
1	1	384	G
1	1	399	A
1	1	405	A
1	1	406	U
1	1	407	A
1	1	410	A
1	1	411	C
1	1	429	G
1	1	430	A
1	1	445	G
1	1	510	G
1	1	514	C
1	1	526	G
1	1	531	A
1	1	532	A
1	1	534	A
1	1	540	A
1	1	544	A

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Mol	Chain	Res	Type
1	1	546	G
1	1	547	G
1	1	548	U
1	1	551	C
1	1	577	U
1	1	578	U
1	1	579	A
1	1	580	U
1	1	581	A
1	1	582	G
1	1	590	U
1	1	591	G
1	1	592	U
1	1	593	A
1	1	596	A
1	1	602	A
1	1	603	C
1	1	606	G
1	1	616	A
1	1	618	U
1	1	619	G
1	1	626	C
1	1	627	G
1	1	628	U
1	1	629	G
1	1	636	A
1	1	645	U
1	1	646	A
1	1	647	A
1	1	661	C
1	1	667	U
1	1	673	C
1	1	675	C
1	1	685	A
1	1	687	U
1	1	702	A
1	1	706	U
1	1	708	U
1	1	714	A
1	1	715	U
1	1	716	G
1	1	732	A

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Mol	Chain	Res	Type
1	1	738	A
1	1	739	G
1	1	742	A
1	1	743	A
1	1	744	U
1	1	745	G
1	1	746	C
1	1	747	A
1	1	748	G
1	1	749	G
1	1	750	U
1	1	758	C
1	1	759	C
1	1	760	C
1	1	768	G
1	1	769	U
1	1	771	C
1	1	775	A
1	1	776	U
1	1	778	G
1	1	782	G
1	1	783	A
1	1	788	G
1	1	806	G
1	1	807	G
1	1	808	U
1	1	809	U
1	1	812	A
1	1	813	G
1	1	816	A
1	1	817	G
1	1	849	A
1	1	862	A
1	1	868	A
1	1	879	A
1	1	882	U
1	1	887	U
1	1	889	G
1	1	893	C
1	1	939	G
1	1	940	G
1	1	941	G

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Mol	Chain	Res	Type
1	1	946	A
1	1	948	G
1	1	954	U
1	1	956	G
1	1	962	U
1	1	964	U
1	1	965	A
1	1	968	A
1	1	976	C
1	1	985	G
1	1	1002	A
1	1	1006	A
1	1	1007	C
1	1	1009	C
1	1	1010	A
1	1	1011	G
1	1	1012	A
1	1	1013	U
1	1	1014	C
1	1	1016	G
1	1	1017	U
1	1	1023	G
1	1	1094	A
1	1	1135	G
1	1	1138	U
1	1	1139	U
1	1	1142	U
1	1	1143	A
1	1	1147	G
1	1	1155	U
1	1	1158	G
1	1	1160	A
1	1	1161	A
1	1	1162	G
1	1	1163	C
1	1	1170	G
1	1	1173	G
1	1	1175	U
1	1	1176	G
1	1	1184	A
1	1	1185	A
1	1	1191	C

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Mol	Chain	Res	Type
1	1	1205	G
1	1	1211	A
1	1	1212	U
1	1	1223	C
1	1	1224	A
1	1	1227	C
1	1	1228	A
1	1	1229	C
1	1	1230	C
1	1	1231	A
1	1	1232	G
1	1	1235	A
1	1	1244	G
1	1	1249	U
1	1	1252	A
1	1	1253	G
1	1	1258	C
1	1	1259	A
1	1	1273	G
1	1	1276	A
1	1	1277	G
1	1	1282	A
1	1	1283	A
1	1	1284	U
1	1	1286	C
1	1	1287	G
1	1	1289	U
1	1	1290	A
1	1	1291	A
1	1	1292	G
1	1	1293	G
1	1	1294	A
1	1	1295	G
1	1	1296	U
1	1	1303	C
1	1	1308	C
1	1	1309	A
1	1	1310	C
1	1	1315	C
1	1	1316	G
1	1	1317	A
1	1	1318	A

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Mol	Chain	Res	Type
1	1	1333	A
1	1	1334	A
1	1	1335	A
1	1	1336	U
1	1	1337	G
1	1	1338	G
1	1	1339	A
1	1	1347	U
1	1	1361	A
1	1	1363	A
1	1	1379	U
1	1	1389	A
1	1	1390	A
1	1	1391	G
1	1	1420	U
1	1	1426	G
1	1	1433	U
1	1	1451	G
1	1	1452	A
1	1	1453	A
1	1	1468	G
1	1	1471	C
1	1	1477	G
1	1	1486	A
1	1	1487	A
1	1	1515	A
1	1	1517	G
1	1	1519	G
1	1	1521	G
1	1	1530	C
1	1	1537	A
1	1	1540	A
1	1	1541	G
1	1	1542	C
1	1	1588	A
1	1	1589	U
1	1	1590	G
1	1	1591	A
1	1	1593	A
1	1	1622	A
1	1	1624	A
1	1	1628	A

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Mol	Chain	Res	Type
1	1	1631	C
1	1	1640	A
1	1	1654	A
1	1	1655	G
1	1	1660	A
1	1	1661	A
1	1	1671	C
1	1	1672	A
1	1	1673	A
1	1	1674	C
1	1	1677	A
1	1	1678	A
1	1	1680	U
1	1	1681	G
1	1	1682	A
1	1	1691	A
1	1	1693	G
1	1	1720	C
1	1	1736	A
1	1	1737	C
1	1	1738	C
1	1	1739	A
1	1	1753	A
1	1	1754	A
1	1	1755	A
1	1	1756	U
1	1	1757	C
1	1	1759	G
1	1	1762	U
1	1	1764	U
1	1	1767	G
1	1	1771	C
1	1	1782	U
1	1	1783	G
1	1	1784	U
1	1	1789	A
1	1	1790	A
1	1	1791	G
1	1	1801	C
1	1	1804	C
1	1	1805	A
1	1	1806	U

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Mol	Chain	Res	Type
1	1	1811	A
1	1	1814	C
1	1	1821	G
1	1	1829	C
1	1	1833	C
1	1	1836	U
1	1	1837	G
1	1	1838	A
1	1	1849	G
1	1	1850	A
1	1	1852	G
1	1	1875	U
1	1	1876	U
1	1	1894	A
1	1	1897	A
1	1	1904	C
1	1	1905	A
1	1	1908	U
1	1	1917	U
1	1	1924	C
1	1	1926	U
1	1	1933	G
1	1	1934	A
1	1	1936	A
1	1	1939	A
1	1	1940	C
1	1	1941	A
1	1	1947	G
1	1	1948	A
1	1	1955	A
1	1	1960	G
1	1	1961	G
1	1	1964	A
1	1	1965	A
1	1	1967	U
1	1	2211	G
1	1	2212	G
1	1	2423	G
1	1	2424	U
1	1	2451	A
1	1	2453	C
1	1	2458	G

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Mol	Chain	Res	Type
1	1	2459	G
1	1	2460	A
1	1	2461	A
1	1	2462	C
1	1	2463	G
1	1	2464	G
1	1	2465	G
1	1	2476	U
1	1	2481	G
1	1	2482	G
1	1	2484	G
1	1	2918	G
1	1	2919	G
1	1	2920	C
1	1	2921	U
1	1	2931	C
1	1	2932	A
1	1	2933	A
1	1	2946	A
1	1	2949	U
1	1	2953	U
1	1	2973	G
1	1	2974	C
1	1	2982	A
1	1	2984	C
1	1	2993	G
1	1	2994	C
1	1	3006	A
1	1	3011	U
1	1	3023	C
1	1	3025	A
1	1	3030	U
1	1	3031	A
1	1	3046	G
1	1	3047	G
1	1	3048	U
1	1	3082	A
1	1	3085	G
1	1	3091	G
1	1	3093	G
1	1	3096	G
1	1	3108	A

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Mol	Chain	Res	Type
1	1	3109	U
1	1	3113	A
1	1	3116	U
1	1	3117	A
1	1	3118	G
1	1	3119	U
1	1	3125	A
1	1	3126	G
1	1	3128	A
1	1	3155	G
1	1	3164	U
1	1	3167	C
1	1	3169	A
1	1	3170	G
1	1	3174	A
1	1	3175	U
1	1	3182	G
1	1	3189	C
1	1	3195	C
1	1	3196	C
1	1	3197	G
1	1	3200	U
1	1	3218	A
1	1	3225	A
1	1	3226	A
1	1	3227	U
1	1	3230	G
1	1	3238	A
1	1	3239	A
1	1	3272	U
1	1	3273	A
1	1	3275	A
1	1	3276	A
1	1	3282	G
1	1	3306	C
1	1	3307	U
1	1	3308	G
1	1	3310	A
1	1	3315	A
1	1	3316	G
1	1	3317	A
1	1	3318	A

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Mol	Chain	Res	Type
1	1	3319	G
1	1	3320	A
1	1	3327	A
1	1	3329	G
1	1	3332	U
1	1	3335	U
1	1	3337	A
1	1	3338	A
1	1	3343	A
1	1	3345	G
1	1	3346	U
1	1	3347	G
1	1	3351	U
1	1	3352	A
1	1	3354	U
1	1	3356	A
1	1	3358	U
1	1	3359	U
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3373	C
1	1	3405	C
1	1	3417	A
1	1	3418	U
1	1	3420	U
1	1	3435	U
1	1	3436	A
1	1	3440	A
1	1	3441	G
1	1	3466	U
1	1	3470	G
1	1	3476	A
1	1	3479	C
1	1	3484	G
1	1	3489	C
1	1	3490	A
1	1	3491	A
1	1	3492	G
2	2	42	U
2	2	43	C
2	2	47	G

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Mol	Chain	Res	Type
2	2	48	A
2	2	59	G
2	2	67	A
2	2	70	C
2	2	71	G
2	2	79	A
2	2	87	A
2	2	98	U
2	2	103	G
2	2	112	A
2	2	114	C
2	2	121	U
2	2	122	G
2	2	124	G
2	2	132	G
2	2	157	A
2	2	159	U
2	2	160	G
2	2	162	C

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	258	U
1	1	270	U
1	1	672	A
1	1	674	A
1	1	715	U
1	1	743	A
1	1	770	G
1	1	777	C
1	1	782	G
1	1	805	G
1	1	881	C
1	1	1013	U
1	1	1159	U
1	1	1234	A
1	1	1272	U
1	1	1314	C
1	1	1333	A
1	1	1338	G
1	1	1389	A

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Mol	Chain	Res	Type
1	1	1540	A
1	1	1590	G
1	1	1874	U
1	1	1916	G
1	1	2993	G
1	1	3081	U
1	1	3217	U
1	1	3318	A
1	1	3328	U
2	2	131	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 [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

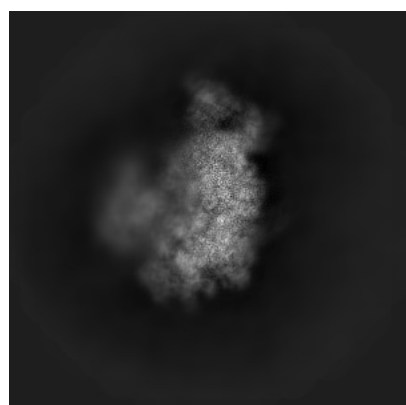
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24398. These allow visual inspection of the internal detail of the map and identification of artifacts.

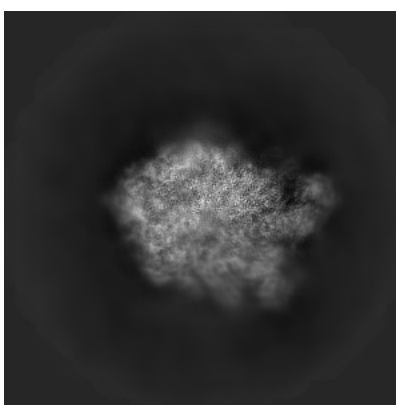
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

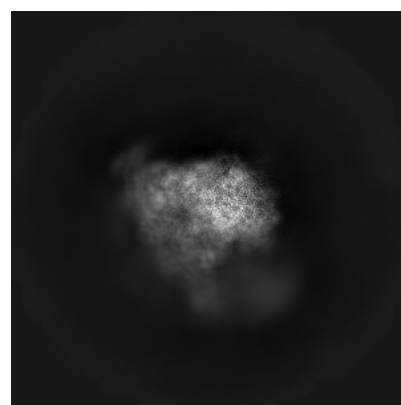
6.1.1 Primary map



X



Y

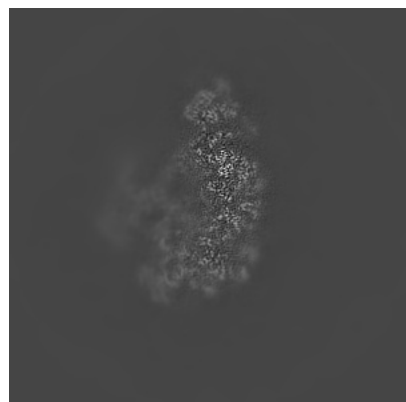


Z

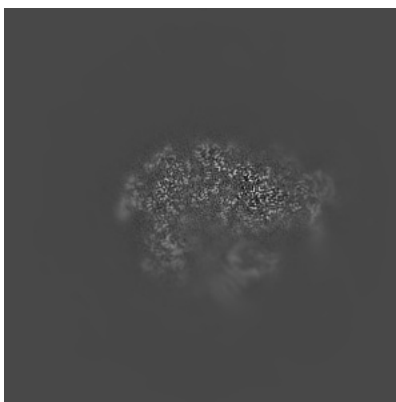
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

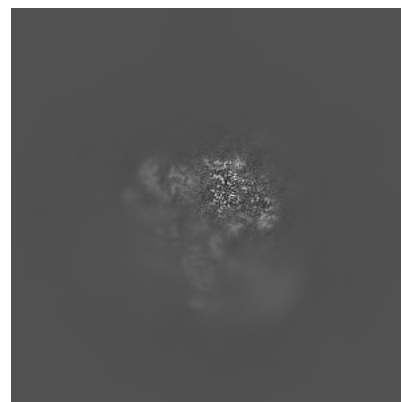
6.2.1 Primary map



X Index: 256



Y Index: 256

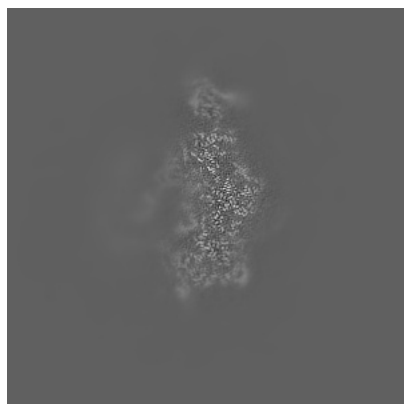


Z Index: 256

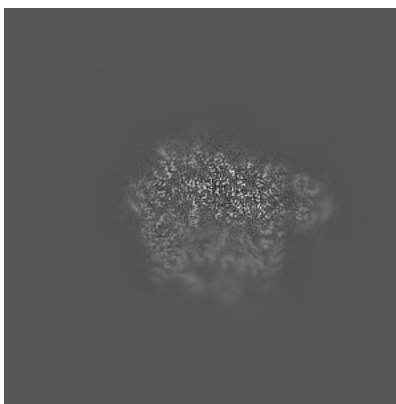
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

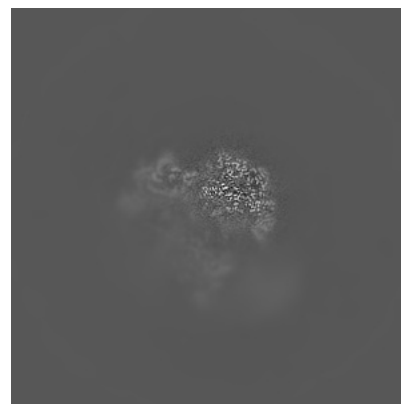
6.3.1 Primary map



X Index: 282



Y Index: 272

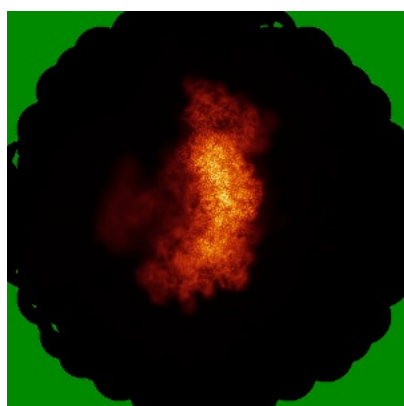


Z Index: 273

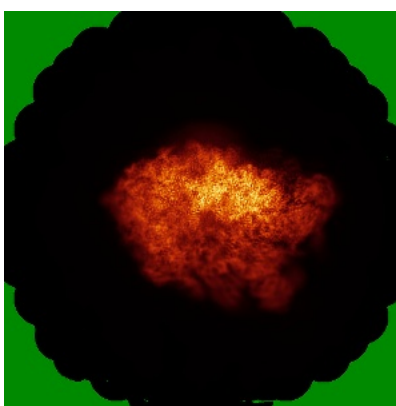
The images above show the largest variance slices of the map in three orthogonal directions.

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

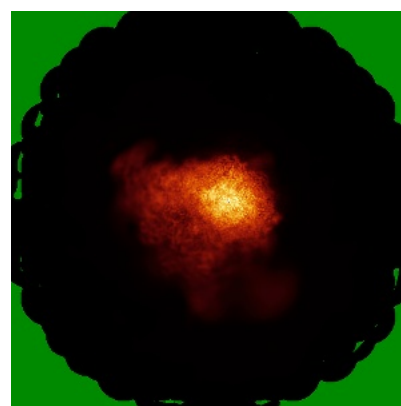
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

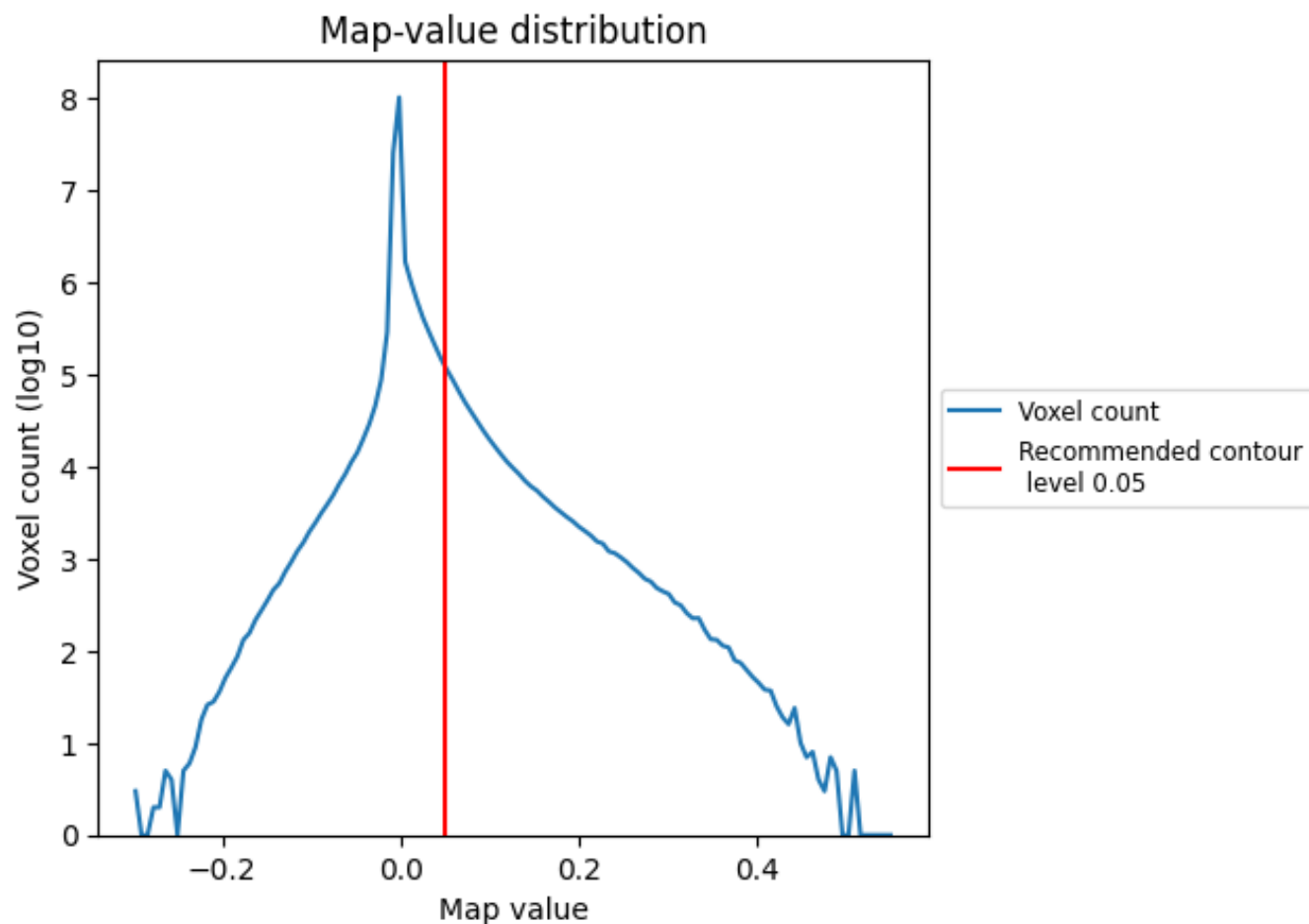
6.6 Mask visualisation

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

7 Map analysis [i](#)

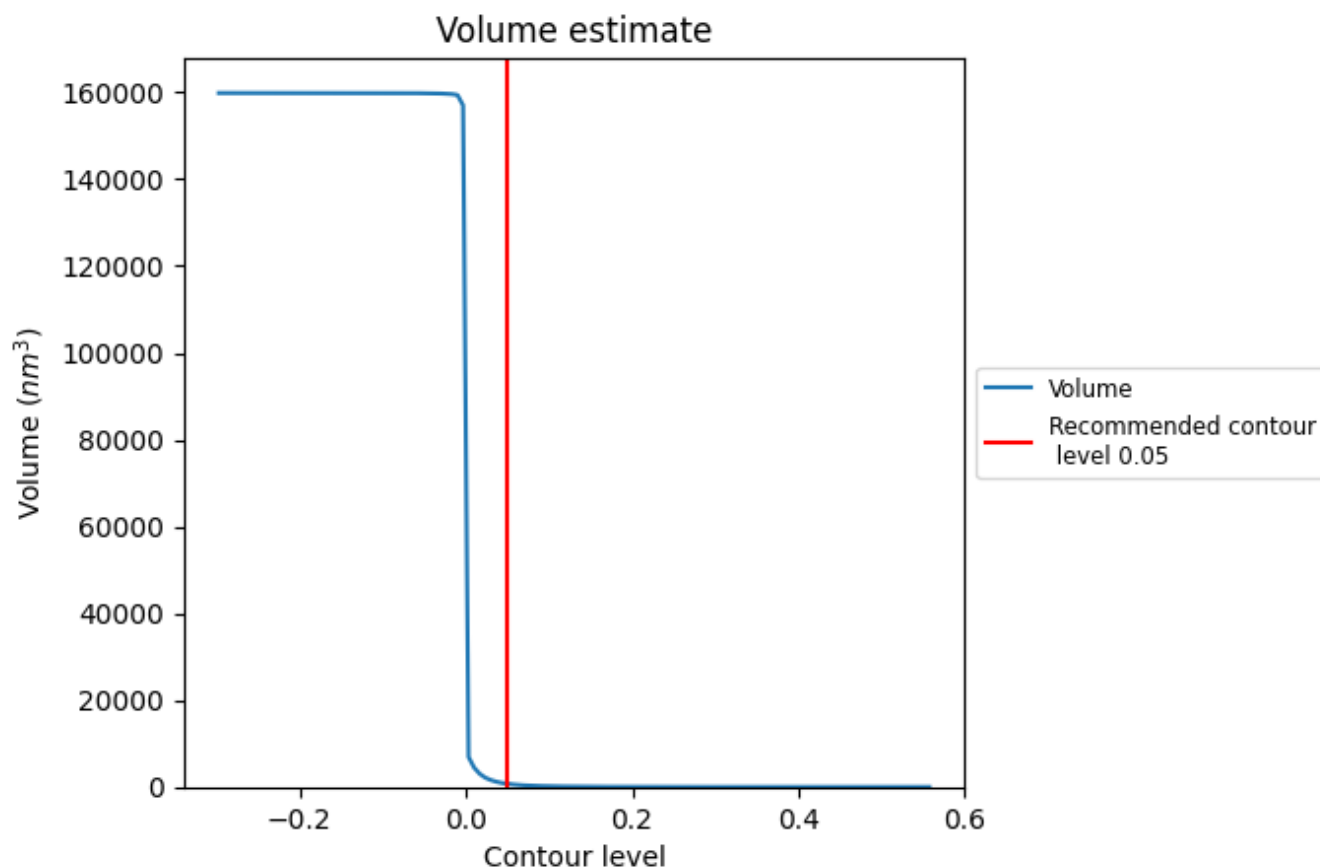
This section contains the results of statistical analysis of the map.

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.

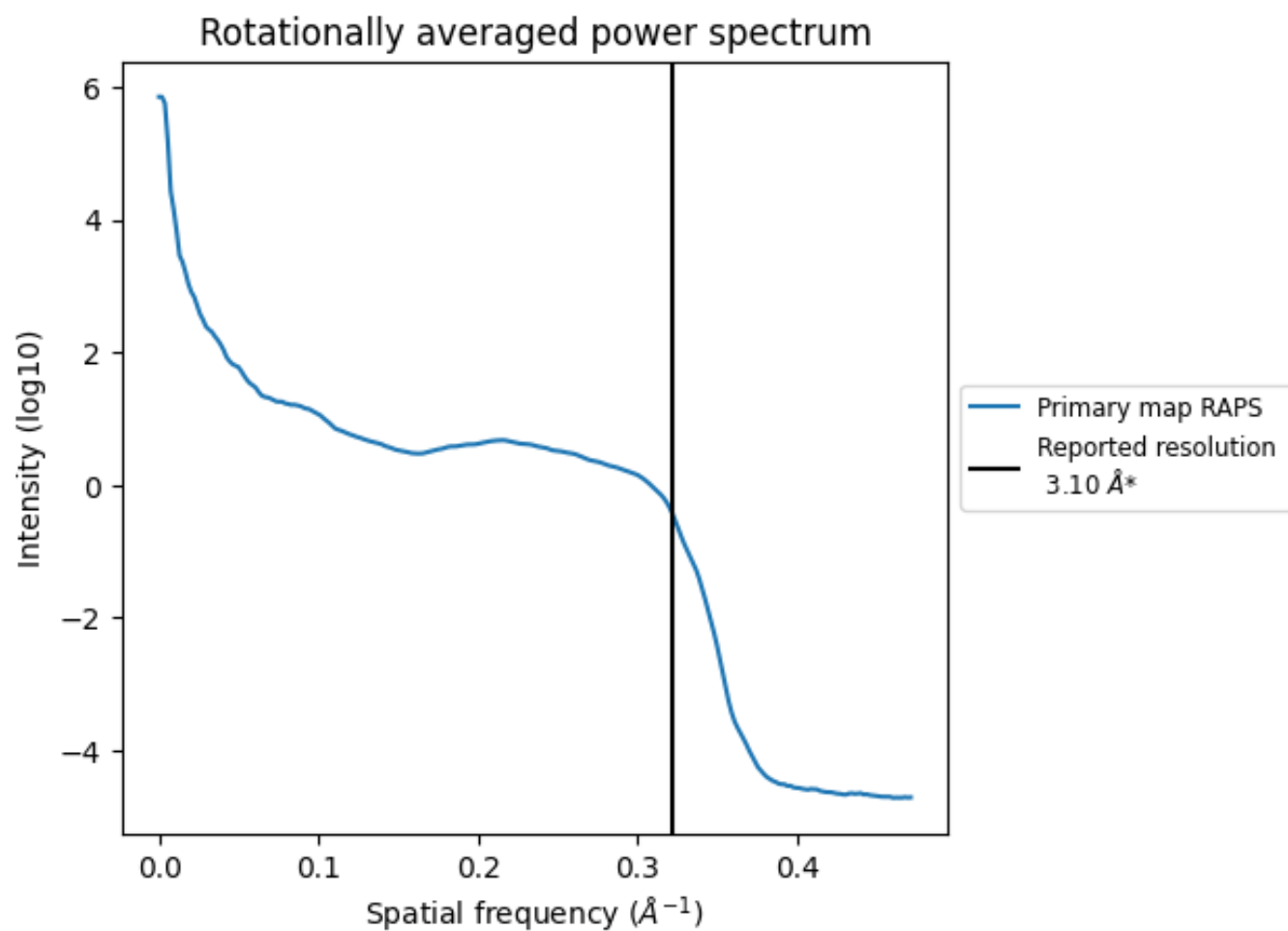
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 720 nm^3 ; this corresponds to an approximate mass of 650 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 0.323 Å⁻¹

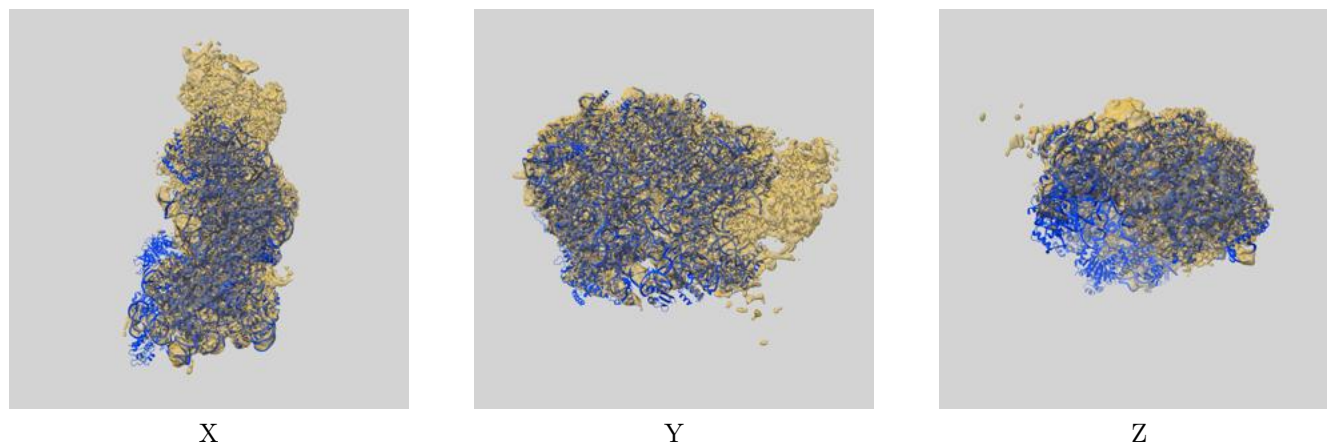
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

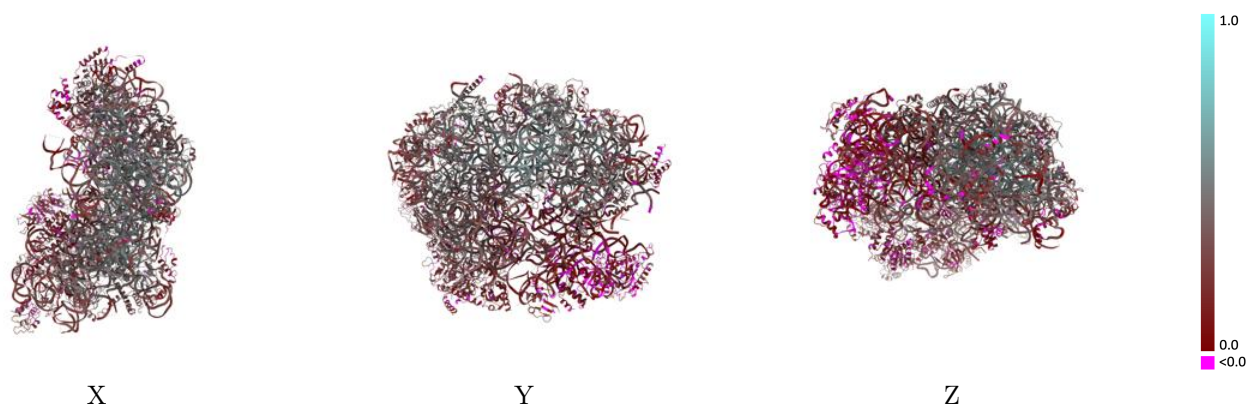
This section contains information regarding the fit between EMDB map EMD-24398 and PDB model 8ETC. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

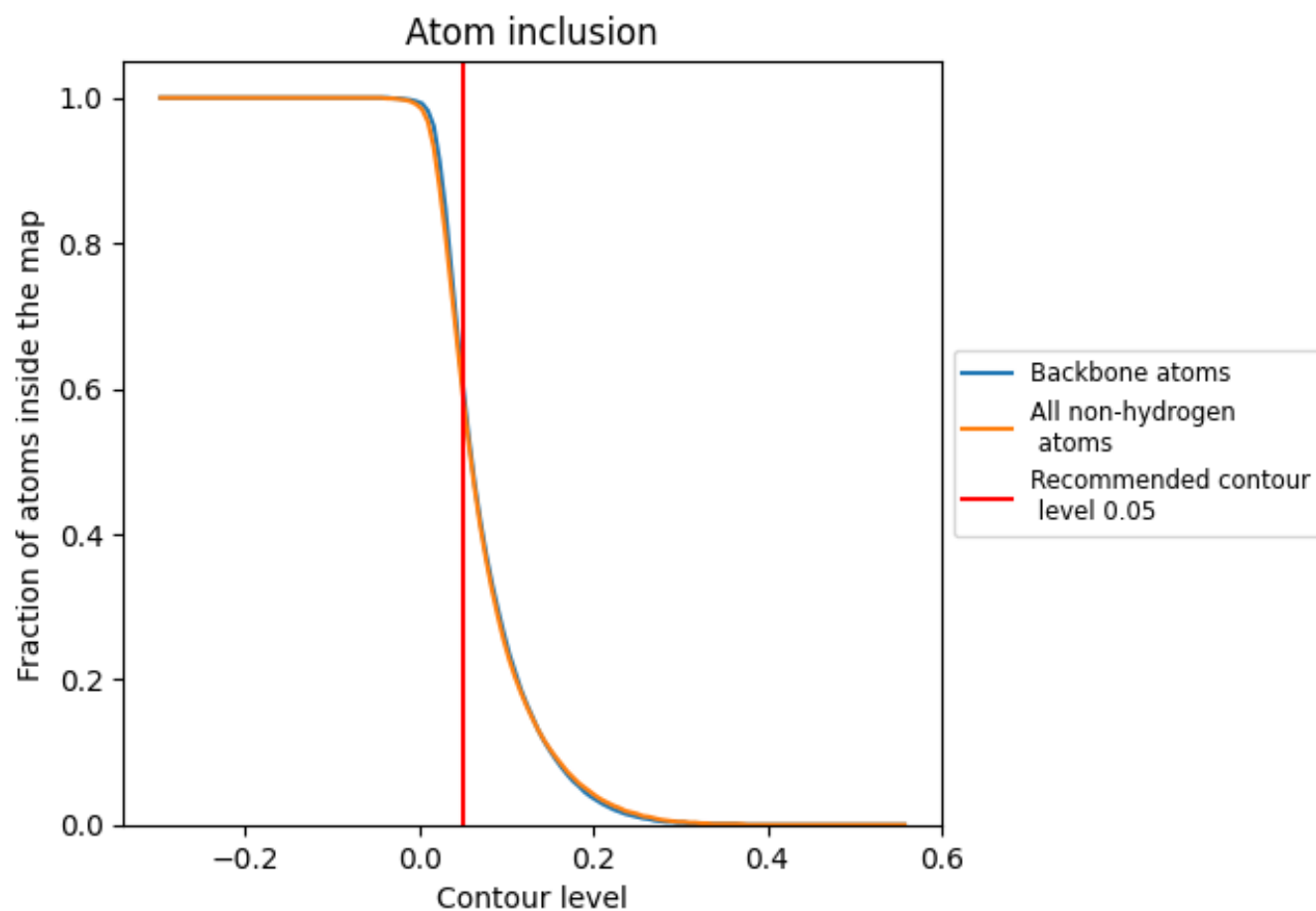


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 59% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5920	 0.3000
1	 0.7050	 0.3110
2	 0.8570	 0.4040
3	 0.2830	 0.2110
8	 0.1820	 0.1040
B	 0.5870	 0.3250
C	 0.7940	 0.4560
E	 0.5960	 0.3320
F	 0.7400	 0.3960
G	 0.6100	 0.2220
H	 0.4430	 0.2780
L	 0.5720	 0.3200
M	 0.7040	 0.3570
N	 0.8210	 0.4210
O	 0.6970	 0.4020
P	 0.5230	 0.2620
Q	 0.7530	 0.4250
R	 0.2560	 0.1580
S	 0.5840	 0.3140
T	 0.3520	 0.3050
U	 0.1690	 0.2040
V	 0.1950	 0.2250
W	 0.0440	 0.2350
X	 0.6450	 0.3210
Y	 0.7920	 0.4310
Z	 0.1220	 0.0450
a	 0.6120	 0.3680
b	 0.0950	 0.1760
c	 0.0690	 0.0840
d	 0.4690	 0.2520
e	 0.8050	 0.4590
f	 0.7930	 0.4660
g	 0.0560	 0.0230
h	 0.7480	 0.3690
i	 0.5090	 0.1890



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Chain	Atom inclusion	Q-score
j	 0.7880	 0.4290
k	 0.2560	 0.0370
r	 0.2040	 0.2060
s	 0.1620	 0.1830
u	 0.2910	 0.1950
w	 0.0500	 0.1440
y	 0.2130	 0.1980
z	 0.0810	 0.2270