



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 10:32 PM UTC

PDB ID : 8WI9 / pdb_00008wi9
EMDB ID : EMD-37561
Title : Cryo- EM structure of Mycobacterium smegmatis 30S ribosomal subunit (body 2) of 70S ribosome, bS1 and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 3.50 Å(reported)
Based on initial model : 8WHX

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:

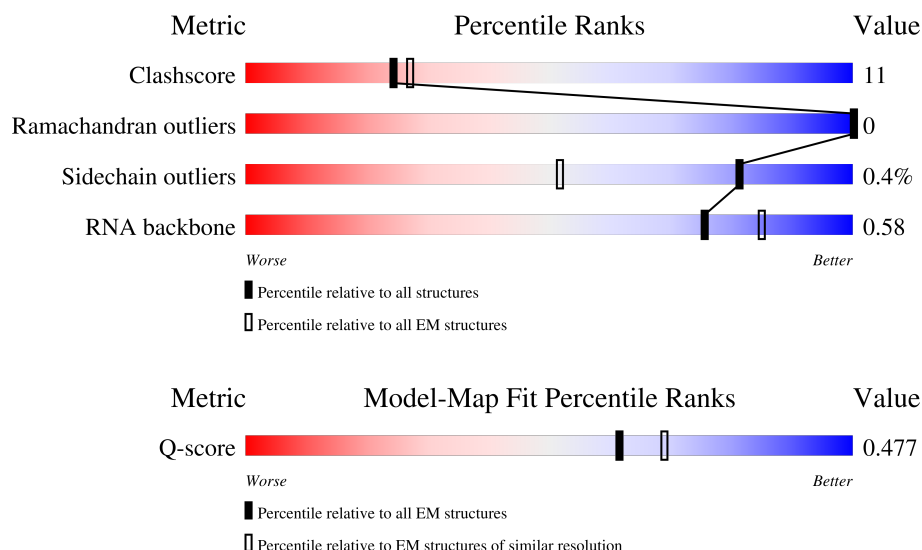
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.50 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.



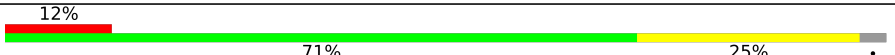
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	a	1528	
2	b	479	
3	v	33	

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Mol	Chain	Length	Quality of chain
4	d	275	
5	e	201	
6	f	214	
7	g	96	
8	h	156	
9	i	132	
10	j	150	
11	k	101	
12	l	138	
13	m	124	
14	n	124	
15	o	61	
16	p	89	
17	q	156	
18	r	98	
19	s	84	
20	t	93	
21	u	86	
22	c	277	
23	x	11	
24	w	264	

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 54459 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1515	Total	C	N	O	P	0	0
			32521	14485	5945	10576	1515		

- Molecule 2 is a protein called 30S ribosomal protein bS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	b	154	Total	C	N	O	0	0
			1193	758	198	237		

- Molecule 3 is a protein called 30S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	v	31	Total	C	N	O	S	0	0
			271	166	69	35	1		

- Molecule 4 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	207	Total	C	N	O	S	0	0
			1656	1034	321	297	4		

- Molecule 5 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 6 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	168	Total	C	N	O	S	0	0
			1223	769	230	220	4		

- Molecule 7 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 8 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	153	Total	C	N	O	S	0	0
			1207	751	235	219	2		

- Molecule 9 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 10 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	j	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 11 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	80	Total	C	N	O	S	0	0
			645	409	119	115	2		

- Molecule 12 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 13 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	121	Total	C	N	O	S	0	0
			949	588	195	164	2		

- Molecule 14 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 15 is a protein called 30S ribosomal protein S14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 16 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	88	Total	C	N	O		0	0
			720	449	147	124			

- Molecule 17 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	113	Total	C	N	O		0	0
			891	570	162	159			

- Molecule 18 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 19 is a protein called 30S ribosomal protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 20 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 21 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	u	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 22 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	c	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 23 is a protein called 50S ribosomal protein L31.

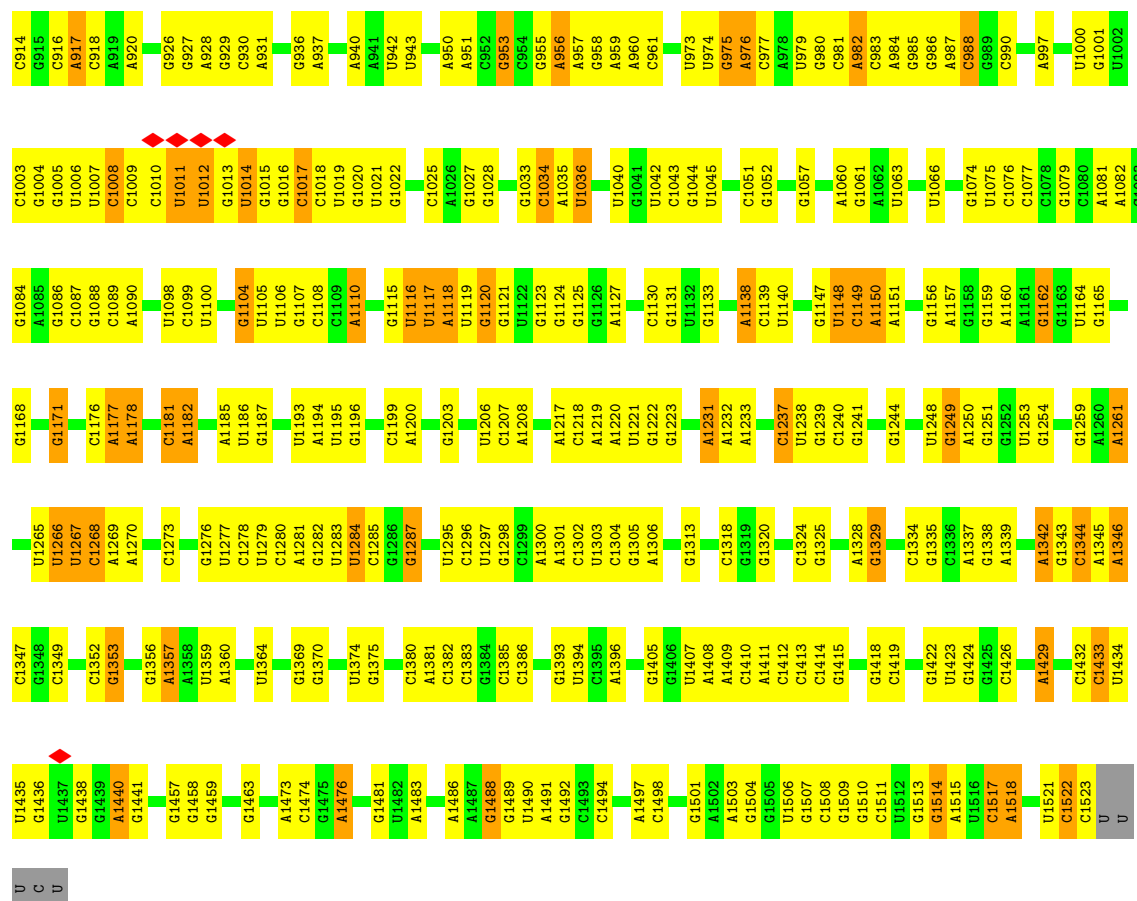
Mol	Chain	Residues	Atoms				AltConf	Trace
23	x	11	Total	C	N	O	0	0
			94	59	21	14		

- Molecule 24 is a protein called Ribosome hibernation promotion factor RafH.

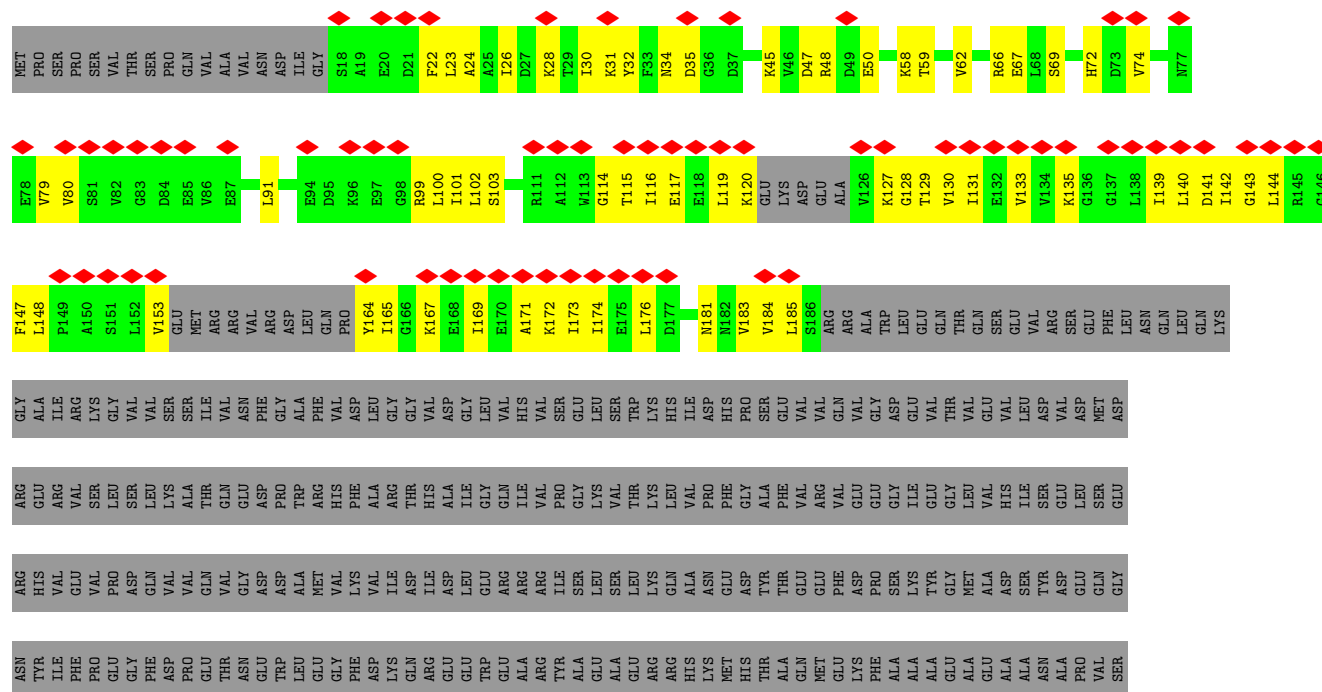
Mol	Chain	Residues	Atoms					AltConf	Trace
24	w	255	Total	C	N	O	S	0	0
			2030	1273	387	364	6		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	259	HIS	-	expression tag	UNP A0QZ86
w	260	HIS	-	expression tag	UNP A0QZ86
w	261	HIS	-	expression tag	UNP A0QZ86
w	262	HIS	-	expression tag	UNP A0QZ86
w	263	HIS	-	expression tag	UNP A0QZ86
w	264	HIS	-	expression tag	UNP A0QZ86



• Molecule 2: 30S ribosomal protein bS1

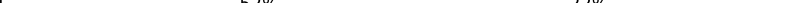


- Molecule 3: 30S ribosomal protein S22

Chain v: 79% 15% 6%

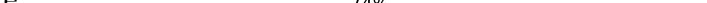
MET G2 R8 R11 R22 Q27 K30 L31 G32 LYS

- Molecule 4: 30S ribosomal protein S3

Chain d: 

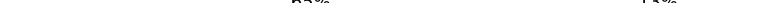
SER	T177	A180	E188	A189	K190	R195	V200	I207	V208	GLY	GLY	LYS	ARG	GLU	LEU	ALA	ALA	ALA	ALA	PRO	ALA	SER	ASP	PRO	ALA	THR	ALA	ALA	ALA	ALA	GLU	ALA	PRO	ALA																			
ASP	G2	N6	P7	H8	S20	R21	W22	Y23	A24	D25	K26	Q27	G	K33	E34	A37	I38	R39	K40	L41	L42	A43	T44	G45	E47	R48	A49	G50	I51	A52	D53	V54	E55	R58	T59	R60	D61	R62	V63	R64	V65	D66	I67	H68	T69	A70	R71	P72	G73	I74	V75	I76	G77

- Molecule 5: 30S ribosomal protein S4

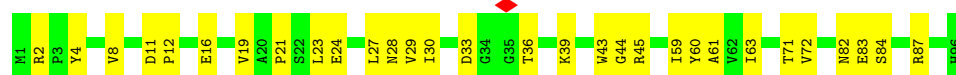
Chain e:  74% 25%

L145	L148	L152	L153	L154	G158	E159	R160	P163	S164	V165	L166	L175	L176	V177	E182	Q185	I186	D187	V188	P189	L190	E197	L198	K201	MET	A2	P7	R10	R13	D23	Q24	S25		P47	Q48	Q49	L50	Q51	E52	K53		E64	K65	Q66	E73	R76	R87	E90	S91		D94	N95		Y98	R99		R104	T105		M108	A109	R110		H115		L119		G122	V132	Y135		I138	D139
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	----	----	-----	-----	-----	-----	-----	--	-----	-----	-----	-----	-----	-----	-----	--	-----	-----	-----	-----	-----	-----	-----	-----	--	-----	-----	--	-----	-----	--	------	------	--	------	------	------	--	------	--	------	--	------	------	------	--	------	------

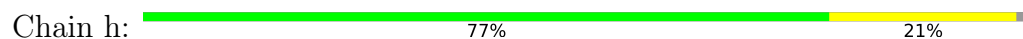
- Molecule 6: 30S ribosomal protein S5

Chain f:  65% 13% 21%

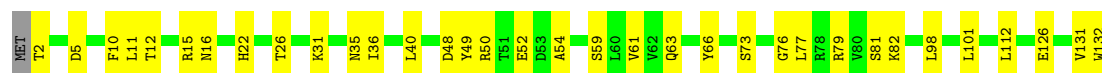
- Molecule 7: 30S ribosomal protein S6



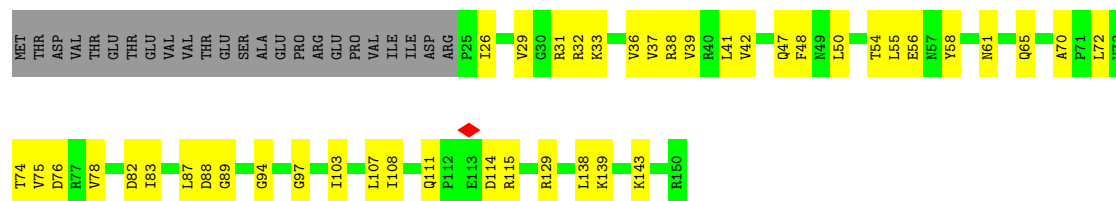
- Molecule 8: 30S ribosomal protein S7



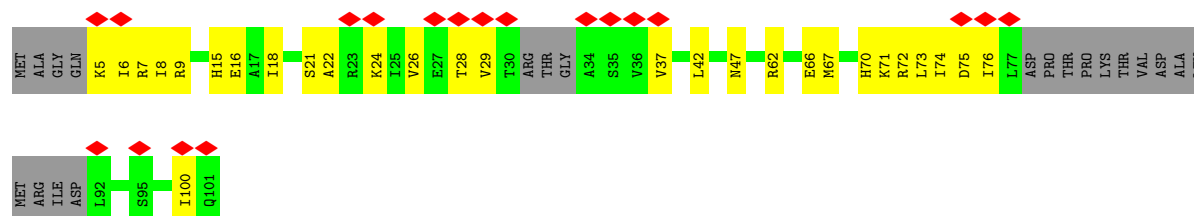
- Molecule 9: 30S ribosomal protein S8



- Molecule 10: 30S ribosomal protein S9

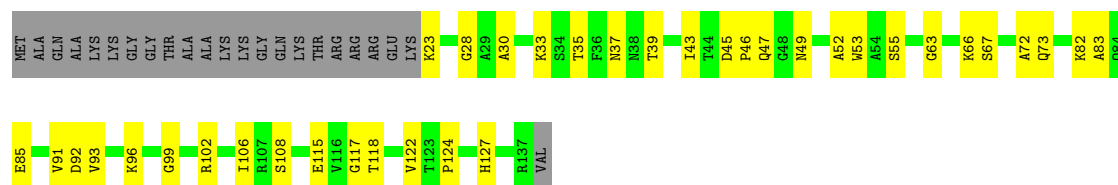


- Molecule 11: 30S ribosomal protein S10



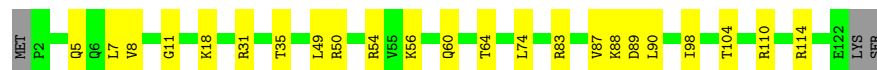
- Molecule 12: 30S ribosomal protein S11





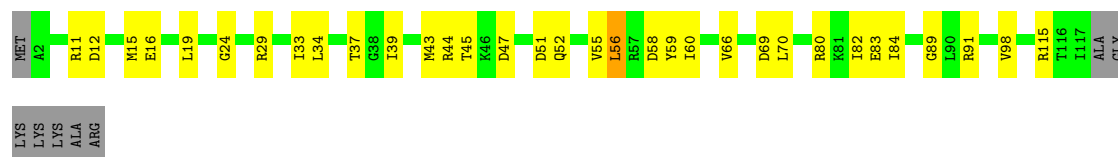
- Molecule 13: 30S ribosomal protein S12

Chain m: 79% 19% .



- Molecule 14: 30S ribosomal protein S13

Chain n: 67% 26% 6% .



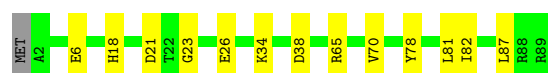
- Molecule 15: 30S ribosomal protein S14A

Chain o: 67% 31% .



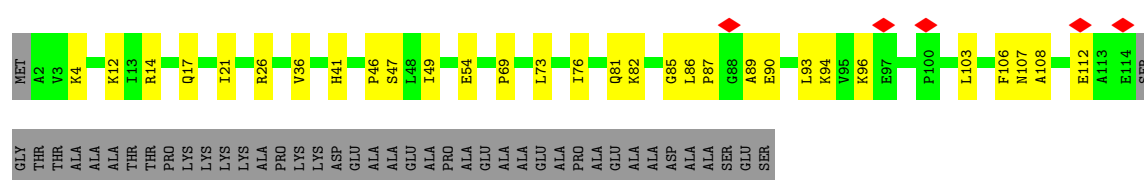
- Molecule 16: 30S ribosomal protein S15

Chain p: 84% 15% .

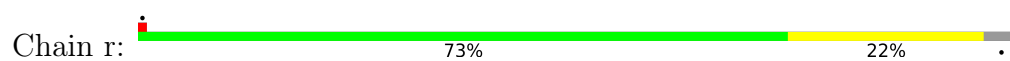


- Molecule 17: 30S ribosomal protein S16

Chain q: 53% 19% 28% .



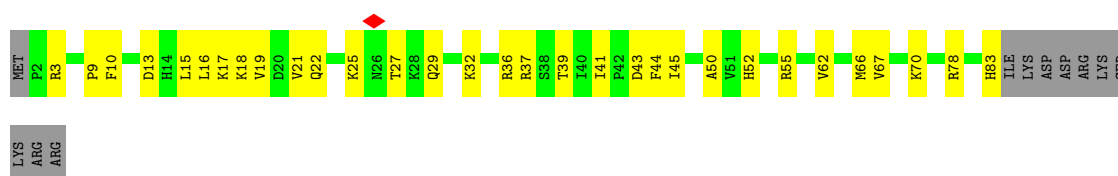
- Molecule 18: 30S ribosomal protein S17



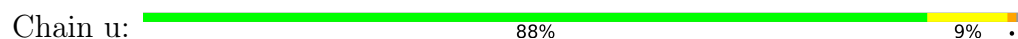
• Molecule 19: 30S ribosomal protein S18B



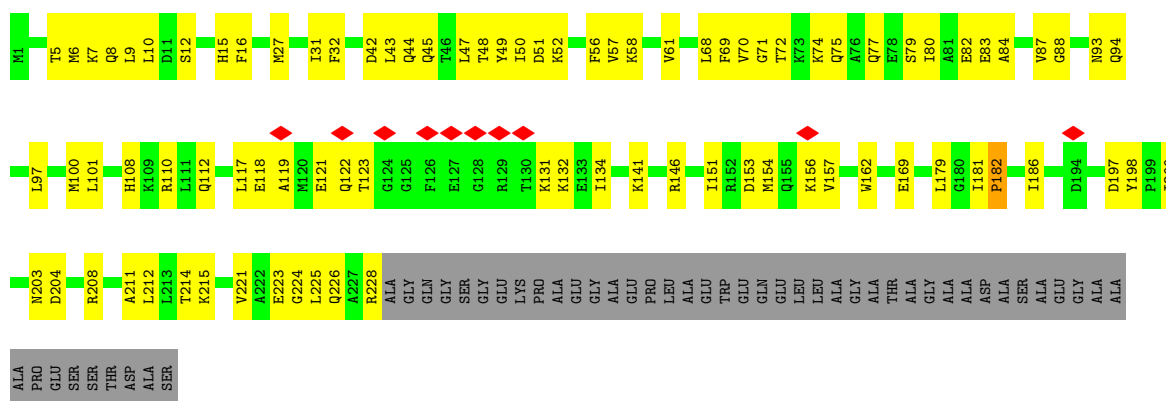
• Molecule 20: 30S ribosomal protein S19



• Molecule 21: 30S ribosomal protein S20



• Molecule 22: 30S ribosomal protein S2

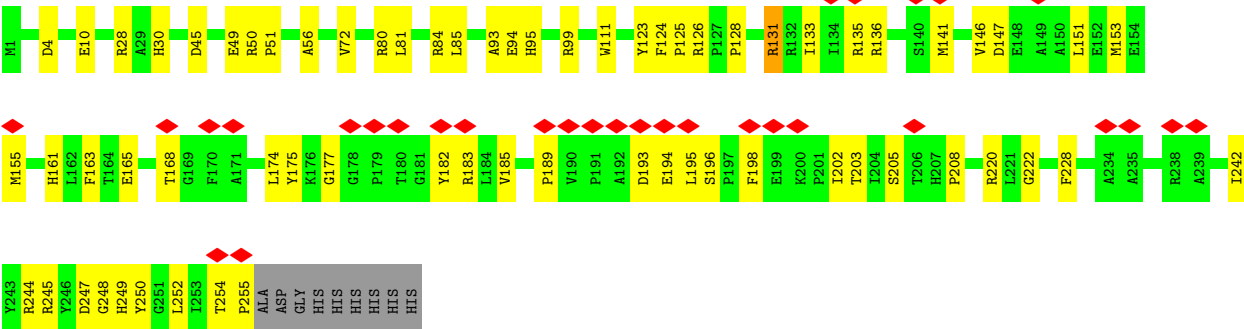


• Molecule 23: 50S ribosomal protein L31





● Molecule 24: Ribosome hibernation promotion factor RafH



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110934	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	NONE; CTF correction in RELION 3.1.4	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.196	Depositor
Minimum map value	-0.034	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.12	0/36400	0.26	0/56798
2	b	0.16	0/1201	0.48	0/1615
3	v	0.11	0/271	0.25	0/348
4	d	0.15	0/1680	0.37	1/2256 (0.0%)
5	e	0.12	0/1672	0.29	0/2251
6	f	0.12	0/1239	0.29	0/1673
7	g	0.14	0/782	0.36	0/1059
8	h	0.13	0/1225	0.36	1/1653 (0.1%)
9	i	0.12	0/1025	0.29	0/1385
10	j	0.16	0/1012	0.41	0/1362
11	k	0.15	0/655	0.44	0/883
12	l	0.15	0/873	0.38	0/1180
13	m	0.12	0/960	0.31	0/1283
14	n	0.14	0/942	0.40	0/1260
15	o	0.15	0/488	0.37	0/650
16	p	0.12	0/729	0.27	0/977
17	q	0.14	0/908	0.36	0/1226
18	r	0.12	0/759	0.32	0/1016
19	s	0.12	0/518	0.28	0/693
20	t	0.14	0/680	0.37	0/915
21	u	0.16	0/663	0.40	0/882
22	c	0.14	0/1822	0.40	1/2457 (0.0%)
23	x	0.16	0/95	0.44	0/123
24	w	0.14	0/2078	0.33	0/2816
All	All	0.13	0/58677	0.30	3/86761 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	c	182	PRO	CA-N-CD	-8.07	100.70	112.00
8	h	58	PRO	CA-N-CD	-8.05	100.73	112.00
4	d	108	PRO	CA-N-CD	-6.87	102.38	112.00

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	a	32521	0	16366	481	0
2	b	1193	0	1238	48	0
3	v	271	0	329	5	0
4	d	1656	0	1704	44	0
5	e	1641	0	1668	40	0
6	f	1223	0	1287	22	0
7	g	771	0	797	21	0
8	h	1207	0	1259	22	0
9	i	1010	0	1046	26	0
10	j	994	0	1050	35	0
11	k	645	0	672	23	0
12	l	855	0	863	26	0
13	m	949	0	1032	16	0
14	n	935	0	986	27	0
15	o	477	0	503	18	0
16	p	720	0	760	9	0
17	q	891	0	935	26	0
18	r	748	0	795	15	0
19	s	513	0	540	9	0
20	t	662	0	677	25	0
21	u	660	0	712	6	0
22	c	1793	0	1839	66	0
23	x	94	0	95	8	0
24	w	2030	0	2023	66	0
All	All	54459	0	39176	977	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 11.

All (977) 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)
24:w:124:PHE:CD2	24:w:126:ARG:HG2	1.76	1.20
1:a:1232:A:H62	1:a:1268:C:N4	1.44	1.15
1:a:1232:A:N6	1:a:1268:C:H42	1.46	1.12
24:w:124:PHE:HD2	24:w:126:ARG:HG2	1.14	0.96
24:w:126:ARG:HG3	24:w:247:ASP:O	1.66	0.95
1:a:82:U:H3	1:a:87:G:H1	0.92	0.91
1:a:728:A:O2'	1:a:729:A:N7	2.07	0.86
1:a:745:G:H1	1:a:792:G:HO2'	1.25	0.84
1:a:83:U:O2	1:a:86:G:O6	1.96	0.84
2:b:128:GLY:HA3	2:b:142:ILE:HG22	1.61	0.83
1:a:644:G:H22	1:a:721:G:H1	1.28	0.81
24:w:124:PHE:HD2	24:w:126:ARG:CG	1.93	0.81
24:w:124:PHE:CD2	24:w:126:ARG:CG	2.63	0.78
24:w:128:PRO:HA	24:w:131:ARG:HG3	1.65	0.78
1:a:149:A:N6	1:a:166:C:O2	2.19	0.76
1:a:936:G:H21	1:a:1208:A:H62	1.34	0.75
1:a:1338:G:H2'	1:a:1339:A:H8	1.52	0.75
2:b:34:ASN:OD1	2:b:35:ASP:N	2.19	0.75
18:r:64:GLU:OE1	18:r:64:GLU:N	2.19	0.75
4:d:86:ILE:HD13	4:d:100:LEU:HD13	1.67	0.75
10:j:37:VAL:HG22	10:j:87:LEU:HD22	1.69	0.74
4:d:62:ARG:HH12	4:d:64:ARG:HB2	1.52	0.74
24:w:124:PHE:HE2	24:w:126:ARG:CD	2.00	0.74
2:b:66:ARG:HH22	2:b:72:HIS:HA	1.50	0.74
24:w:124:PHE:CE2	24:w:126:ARG:HG2	2.23	0.74
1:a:772:A:O2'	1:a:774:A:N7	2.20	0.73
11:k:21:SER:HA	11:k:24:LYS:NZ	2.04	0.73
1:a:1106:U:OP1	11:k:7:ARG:NH2	2.23	0.72
2:b:120:LYS:HZ2	2:b:176:LEU:HD22	1.54	0.72
14:n:39:ILE:HG12	14:n:52:GLN:HG2	1.72	0.72
2:b:135:LYS:HB2	24:w:155:MET:HG2	1.71	0.71
1:a:437:U:HO2'	5:e:115:HIS:HD1	1.36	0.71
2:b:79:VAL:HG12	2:b:80:VAL:HG23	1.71	0.71
4:d:139:SER:OG	4:d:142:ARG:NH2	2.24	0.71
2:b:22:PHE:CE1	2:b:26:ILE:HD11	2.25	0.71
1:a:11:G:H1	6:f:122:ARG:HH11	1.39	0.71
2:b:130:VAL:HA	2:b:140:LEU:HA	1.73	0.71
24:w:245:ARG:HE	24:w:249:HIS:HB2	1.55	0.71
22:c:8:GLN:HG3	22:c:212:LEU:HD11	1.73	0.70
22:c:6:MET:SD	22:c:7:LYS:NZ	2.64	0.70
24:w:124:PHE:CE2	24:w:126:ARG:CD	2.75	0.70
1:a:598:C:O2	17:q:12:LYS:NZ	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:654:G:H2'	1:a:655:A:H8	1.56	0.70
6:f:63:ILE:HD12	6:f:73:VAL:HG22	1.73	0.70
11:k:67:MET:HE1	15:o:36:LYS:HD3	1.73	0.70
1:a:693:G:H2'	1:a:694:G:C8	2.26	0.70
1:a:666:U:H1'	12:l:53:TRP:HE1	1.56	0.69
1:a:481:G:OP1	13:m:114:ARG:NH2	2.25	0.69
1:a:1349:C:O2'	11:k:62:ARG:NH2	2.25	0.69
17:q:103:LEU:O	17:q:107:ASN:ND2	2.26	0.69
1:a:653:G:H2'	1:a:654:G:C8	2.27	0.69
20:t:41:ILE:HG22	20:t:43:ASP:H	1.57	0.69
1:a:297:G:N2	1:a:300:A:OP2	2.24	0.68
1:a:452:A:H62	17:q:94:LYS:H	1.39	0.68
8:h:12:LEU:O	8:h:21:GLN:NE2	2.26	0.68
1:a:1231:A:H2'	1:a:1232:A:C8	2.30	0.67
2:b:100:LEU:HD12	2:b:102:LEU:HD21	1.77	0.67
1:a:83:U:O2	1:a:86:G:C6	2.47	0.67
9:i:50:ARG:HH12	9:i:63:GLN:HE22	1.41	0.67
2:b:115:THR:O	2:b:119:LEU:HG	1.94	0.67
18:r:21:LYS:HB2	18:r:78:GLU:HG3	1.75	0.66
1:a:985:G:H2'	1:a:986:G:C8	2.30	0.66
1:a:1018:C:H2'	1:a:1019:U:C6	2.31	0.66
7:g:28:ASN:OD1	7:g:29:VAL:N	2.29	0.66
21:u:45:ASP:N	21:u:45:ASP:OD1	2.28	0.66
1:a:1199:C:H2'	1:a:1200:A:H8	1.58	0.66
1:a:1338:G:H2'	1:a:1339:A:C8	2.31	0.66
1:a:517:G:OP1	13:m:110:ARG:NH2	2.28	0.66
1:a:1017:C:H2'	1:a:1018:C:C6	2.30	0.66
1:a:485:G:H2'	1:a:486:G:C8	2.31	0.66
1:a:1057:G:N2	1:a:1060:A:OP2	2.25	0.66
1:a:1199:C:H2'	1:a:1200:A:C8	2.31	0.66
1:a:25:G:H2'	1:a:26:G:C8	2.31	0.65
20:t:25:LYS:HE2	20:t:27:THR:HB	1.77	0.65
2:b:129:THR:O	2:b:141:ASP:N	2.30	0.65
1:a:1014:U:H2'	1:a:1015:G:C8	2.31	0.65
1:a:1051:C:H2'	1:a:1052:G:H8	1.62	0.65
1:a:1015:G:H2'	1:a:1016:G:H8	1.59	0.65
8:h:116:MET:HE2	8:h:116:MET:HA	1.78	0.65
1:a:593:C:OP1	5:e:76:ARG:NH1	2.27	0.65
5:e:49:GLN:HB3	5:e:198:LEU:HB2	1.78	0.65
24:w:131:ARG:HD2	24:w:250:TYR:CZ	2.31	0.65
1:a:427:U:OP1	5:e:13:ARG:NH2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:940:A:OP1	20:t:55:ARG:NH1	2.29	0.65
1:a:1010:C:N4	1:a:1014:U:H3	1.94	0.65
1:a:203:U:H2'	1:a:204:A:H8	1.62	0.64
1:a:1027:G:HO2'	1:a:1196:G:HO2'	1.45	0.64
1:a:489:A:H8	1:a:523:U:HO2'	1.45	0.64
15:o:26:LYS:HD3	15:o:27:CYS:HB3	1.78	0.64
9:i:40:LEU:HD21	9:i:131:VAL:HG11	1.80	0.64
24:w:131:ARG:O	24:w:249:HIS:ND1	2.29	0.64
1:a:694:G:H2'	1:a:695:A:C8	2.32	0.64
2:b:117:GLU:HA	2:b:120:LYS:HG2	1.80	0.64
17:q:86:LEU:HB2	17:q:87:PRO:HD3	1.80	0.64
22:c:32:PHE:HB2	22:c:42:ASP:HB2	1.79	0.63
1:a:1261:A:OP1	11:k:9:ARG:NH1	2.24	0.63
17:q:46:PRO:HG3	17:q:96:LYS:HD3	1.80	0.63
10:j:72:LEU:HD23	10:j:107:LEU:HD11	1.81	0.63
24:w:161:HIS:HE1	24:w:163:PHE:HB3	1.62	0.63
1:a:1303:U:O2'	20:t:78:ARG:NH2	2.32	0.63
1:a:1410:C:H2'	1:a:1411:A:H8	1.63	0.63
4:d:99:GLN:NE2	4:d:101:ASN:OD1	2.31	0.63
17:q:90:GLU:N	17:q:90:GLU:OE2	2.30	0.63
1:a:873:U:H2'	1:a:874:A:H8	1.64	0.63
24:w:153:MET:HE3	24:w:161:HIS:HB3	1.80	0.63
1:a:411:A:C4	1:a:413:G:H1'	2.34	0.63
10:j:26:ILE:HD11	10:j:41:LEU:HB3	1.81	0.63
14:n:33:ILE:O	14:n:37:THR:HG22	1.99	0.63
1:a:1506:U:H2'	1:a:1507:G:H8	1.63	0.62
1:a:209:A:N3	1:a:222:U:O2'	2.29	0.62
2:b:143:GLY:O	2:b:144:LEU:HD23	2.00	0.62
1:a:312:C:H2'	1:a:313:A:H8	1.64	0.62
5:e:197:GLU:OE1	6:f:137:ARG:NH2	2.25	0.62
1:a:401:C:O2'	1:a:601:A:N3	2.30	0.62
1:a:1407:U:H2'	1:a:1408:A:C8	2.35	0.62
1:a:1522:C:H2'	1:a:1523:C:O4'	2.00	0.62
1:a:144:G:H2'	1:a:145:G:C8	2.35	0.62
1:a:803:G:HO2'	9:i:2:THR:N	1.96	0.62
1:a:402:G:OP1	5:e:66:GLN:NE2	2.33	0.62
1:a:872:G:O2'	1:a:888:A:N6	2.32	0.62
22:c:6:MET:SD	22:c:6:MET:N	2.73	0.62
11:k:6:ILE:HG13	11:k:76:ILE:HD11	1.81	0.62
14:n:51:ASP:OD1	14:n:52:GLN:N	2.33	0.62
15:o:16:PHE:HD1	15:o:19:ARG:HG3	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:c:186:ILE:HG22	22:c:200:ILE:HB	1.82	0.62
1:a:362:G:N2	1:a:365:U:OP2	2.33	0.61
18:r:73:ARG:HB2	18:r:95:GLU:HG3	1.81	0.61
11:k:21:SER:HA	11:k:24:LYS:HZ2	1.62	0.61
11:k:42:LEU:HB2	11:k:71:LYS:HB2	1.83	0.61
1:a:38:C:H2'	1:a:39:G:H8	1.66	0.61
1:a:692:A:H2'	1:a:693:G:C8	2.35	0.61
1:a:485:G:H2'	1:a:486:G:H8	1.64	0.61
1:a:983:C:H2'	1:a:984:A:C8	2.35	0.61
4:d:39:ARG:NH1	4:d:54:VAL:O	2.34	0.61
14:n:58:ASP:OD1	14:n:59:TYR:N	2.33	0.61
1:a:1219:A:H5'	1:a:1318:C:H41	1.66	0.61
1:a:961:C:O2	15:o:19:ARG:HD2	2.00	0.61
1:a:1231:A:N3	1:a:1353:G:O2'	2.31	0.61
1:a:1410:C:H2'	1:a:1411:A:C8	2.36	0.61
17:q:54:GLU:OE2	17:q:54:GLU:N	2.24	0.61
19:s:46:GLY:O	19:s:72:ARG:NH2	2.34	0.60
1:a:880:G:N2	1:a:883:A:OP2	2.34	0.60
1:a:928:A:H2'	1:a:929:G:C8	2.36	0.60
1:a:669:C:OP1	12:l:55:SER:OG	2.19	0.60
20:t:19:VAL:HG21	20:t:44:PHE:HE1	1.64	0.60
1:a:826:U:H4'	19:s:19:LYS:HE2	1.83	0.60
4:d:20:SER:OG	4:d:22:TRP:NE1	2.35	0.60
19:s:57:CYS:SG	19:s:60:HIS:ND1	2.74	0.60
1:a:21:U:H2'	1:a:22:C:C6	2.36	0.60
24:w:49:GLU:HG2	24:w:50:ARG:HG3	1.84	0.60
1:a:561:G:OP1	16:p:65:ARG:NH1	2.29	0.60
20:t:29:GLN:OE1	20:t:29:GLN:N	2.35	0.60
10:j:54:THR:HG23	10:j:56:GLU:H	1.67	0.59
18:r:72:ASP:OD2	18:r:96:LYS:NZ	2.33	0.59
9:i:48:ASP:OD1	9:i:49:TYR:N	2.35	0.59
24:w:126:ARG:HB2	24:w:248:GLY:HA3	1.83	0.59
11:k:8:ILE:HD13	11:k:100:ILE:HG12	1.84	0.59
2:b:140:LEU:HD21	2:b:169:ILE:HG22	1.85	0.59
9:i:10:PHE:HD2	9:i:36:ILE:HD11	1.68	0.59
22:c:47:LEU:HA	22:c:50:ILE:HG22	1.83	0.59
1:a:1149:C:O2'	1:a:1150:A:OP2	2.20	0.59
7:g:83:GLU:OE2	7:g:83:GLU:N	2.26	0.59
1:a:269:U:H2'	1:a:270:A:C8	2.38	0.58
4:d:27:GLN:N	4:d:27:GLN:OE1	2.35	0.58
13:m:74:LEU:HD21	13:m:104:THR:HB	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:u:46:LYS:HA	21:u:49:GLU:OE1	2.02	0.58
22:c:72:THR:N	22:c:169:GLU:OE2	2.31	0.58
1:a:1040:U:OP1	15:o:45:ARG:NH2	2.32	0.58
1:a:826:U:H2'	1:a:828:G:H5'	1.85	0.58
7:g:12:PRO:O	7:g:45:ARG:NH2	2.35	0.58
7:g:44:GLY:HA2	7:g:60:TYR:H	1.68	0.58
1:a:1324:C:H2'	1:a:1325:G:H8	1.68	0.58
9:i:26:THR:HG23	9:i:61:VAL:HG22	1.85	0.58
1:a:1359:U:O4	8:h:10:ARG:NH1	2.35	0.58
6:f:83:ALA:O	6:f:87:LYS:HG3	2.03	0.58
6:f:130:VAL:O	6:f:137:ARG:NH2	2.36	0.58
10:j:114:ASP:OD1	10:j:114:ASP:N	2.30	0.58
1:a:748:A:H4'	1:a:1507:G:N2	2.18	0.58
1:a:1342:A:OP2	15:o:35:ARG:NH2	2.37	0.58
1:a:1517:C:H5'	1:a:1518:A:H5'	1.86	0.58
1:a:1521:U:H3	24:w:124:PHE:HA	1.67	0.58
1:a:21:U:H2'	1:a:22:C:H6	1.69	0.58
24:w:56:ALA:HB2	24:w:81:LEU:HD21	1.86	0.58
1:a:525:C:OP1	5:e:53:LYS:NZ	2.32	0.58
1:a:1383:C:H1'	24:w:84:ARG:HD3	1.86	0.58
1:a:92:A:O2'	1:a:93:C:O5'	2.22	0.58
1:a:380:G:N2	1:a:383:A:OP2	2.33	0.58
1:a:654:G:H2'	1:a:655:A:C8	2.38	0.58
1:a:688:C:H2'	1:a:689:A:H8	1.68	0.58
1:a:953:G:N2	1:a:1346:A:OP1	2.28	0.58
14:n:39:ILE:HD12	14:n:39:ILE:H	1.69	0.58
20:t:13:ASP:O	20:t:17:LYS:HG3	2.03	0.58
1:a:1329:G:O6	10:j:32:ARG:NH2	2.36	0.57
20:t:32:LYS:HA	20:t:50:ALA:HB3	1.85	0.57
1:a:1130:C:H2'	1:a:1131:G:C8	2.38	0.57
1:a:312:C:H2'	1:a:313:A:C8	2.39	0.57
5:e:73:GLU:OE1	5:e:76:ARG:NH2	2.35	0.57
5:e:104:ARG:H	5:e:108:MET:HE2	1.69	0.57
1:a:1061:G:N7	6:f:77:LYS:NZ	2.52	0.57
1:a:642:C:H2'	1:a:643:A:C8	2.39	0.57
1:a:1159:G:OP1	10:j:115:ARG:NH1	2.37	0.57
5:e:94:ASP:OD1	5:e:95:ASN:N	2.38	0.57
1:a:49:U:H2'	1:a:50:G:C8	2.39	0.57
20:t:39:THR:HG22	20:t:70:LYS:HE2	1.84	0.57
1:a:82:U:O2	1:a:87:G:N2	2.28	0.57
1:a:461:G:O2'	1:a:463:C:N4	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:127:LYS:HD3	2:b:128:GLY:N	2.20	0.57
11:k:8:ILE:HB	11:k:74:ILE:HB	1.87	0.57
24:w:185:VAL:HG22	24:w:205:SER:HB2	1.87	0.57
1:a:1324:C:H2'	1:a:1325:G:C8	2.39	0.56
1:a:1120:G:H4'	1:a:1121:G:H5'	1.87	0.56
1:a:272:C:H2'	1:a:273:A:H8	1.68	0.56
1:a:890:A:H2'	1:a:891:A:H8	1.71	0.56
1:a:920:A:N3	1:a:1359:U:O2'	2.31	0.56
1:a:1418:G:H2'	1:a:1419:C:C6	2.41	0.56
17:q:81:GLN:O	17:q:85:GLY:N	2.37	0.56
1:a:92:A:H1'	1:a:93:C:H5	1.69	0.56
1:a:226:G:H5''	18:r:12:ALA:HB2	1.88	0.56
1:a:1491:A:H2'	1:a:1492:G:C8	2.41	0.56
4:d:58:ARG:HG3	4:d:63:VAL:HG22	1.87	0.56
1:a:1508:C:H2'	1:a:1509:G:H8	1.69	0.56
22:c:58:LYS:HG2	22:c:223:GLU:OE1	2.06	0.56
24:w:124:PHE:CE2	24:w:126:ARG:CG	2.89	0.56
1:a:695:A:H2'	1:a:696:A:C8	2.41	0.56
4:d:137:ILE:O	4:d:141:MET:HG2	2.05	0.56
5:e:87:ARG:O	5:e:91:SER:OG	2.24	0.56
15:o:16:PHE:CD1	15:o:19:ARG:HG3	2.41	0.56
22:c:83:GLU:HG3	22:c:214:THR:HB	1.88	0.56
4:d:69:THR:HG22	4:d:102:ILE:HD11	1.87	0.56
24:w:123:TYR:HD1	24:w:124:PHE:O	1.88	0.56
24:w:124:PHE:CE2	24:w:126:ARG:HD3	2.40	0.56
1:a:804:U:H2'	1:a:805:A:H8	1.69	0.56
1:a:884:G:H2'	1:a:885:G:H8	1.70	0.56
1:a:975:G:O2'	1:a:976:A:N7	2.37	0.56
22:c:45:GLN:HA	22:c:48:THR:HG22	1.86	0.56
1:a:1159:G:N2	1:a:1162:G:OP2	2.38	0.56
4:d:109:GLU:OE1	4:d:139:SER:OG	2.19	0.56
7:g:27:LEU:O	7:g:30:ILE:HG13	2.06	0.56
2:b:173:ILE:HD12	2:b:183:VAL:HG22	1.88	0.55
1:a:806:C:O2	9:i:16:ASN:ND2	2.39	0.55
22:c:121:GLU:OE1	22:c:122:GLN:NE2	2.39	0.55
1:a:1138:A:H62	1:a:1159:G:H21	1.55	0.55
1:a:1380:C:OP2	6:f:54:ARG:NH2	2.39	0.55
12:l:52:ALA:HB1	12:l:82:LYS:HB3	1.88	0.55
20:t:15:LEU:HA	20:t:18:LYS:HB2	1.86	0.55
24:w:124:PHE:HE2	24:w:126:ARG:HD2	1.69	0.55
1:a:1349:C:HO2'	11:k:62:ARG:HH22	1.52	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:69:SER:HB3	2:b:74:VAL:HG21	1.89	0.55
12:l:47:GLN:N	12:l:47:GLN:OE1	2.38	0.55
1:a:819:U:H3	1:a:829:G:H1	1.54	0.55
12:l:99:GLY:HA2	12:l:102:ARG:HD3	1.87	0.55
22:c:156:LYS:HD2	22:c:157:VAL:HG12	1.88	0.55
1:a:632:U:O4	1:a:732:G:O2'	2.22	0.55
1:a:1034:C:O2'	24:w:45:ASP:OD2	2.25	0.55
2:b:66:ARG:NH2	2:b:72:HIS:HA	2.21	0.55
7:g:21:PRO:O	7:g:24:GLU:HB3	2.06	0.55
1:a:859:C:OP1	9:i:82:LYS:NZ	2.30	0.55
5:e:132:VAL:HG11	5:e:177:VAL:HG21	1.88	0.55
5:e:145:LEU:O	5:e:154:ARG:NH2	2.40	0.55
22:c:57:VAL:O	22:c:61:VAL:HG12	2.06	0.55
24:w:182:TYR:HB2	24:w:202:ILE:HG22	1.88	0.55
1:a:1010:C:H42	1:a:1014:U:H3	1.49	0.55
4:d:87:ARG:O	4:d:91:GLU:HG2	2.06	0.55
5:e:197:GLU:OE2	6:f:130:VAL:N	2.39	0.55
1:a:87:G:H2'	1:a:88:G:H8	1.72	0.54
1:a:928:A:H2'	1:a:929:G:H8	1.71	0.54
1:a:1160:A:OP2	10:j:115:ARG:NH2	2.39	0.54
1:a:1266:U:O2'	1:a:1267:U:OP1	2.25	0.54
1:a:49:U:H2'	1:a:50:G:H8	1.71	0.54
1:a:1375:G:N2	1:a:1486:A:H8	2.06	0.54
5:e:7:PRO:HB2	5:e:10:ARG:HG3	1.88	0.54
8:h:138:ARG:NH1	8:h:139:GLU:OE2	2.39	0.54
1:a:10:G:OP2	1:a:10:G:N2	2.41	0.54
1:a:1300:A:OP1	20:t:3:ARG:NH2	2.34	0.54
1:a:1517:C:C5'	1:a:1518:A:H5'	2.36	0.54
22:c:79:SER:O	22:c:82:GLU:HG3	2.07	0.54
24:w:189:PRO:HD3	24:w:208:PRO:HB3	1.88	0.54
1:a:1044:G:O2'	1:a:1171:G:N2	2.39	0.54
1:a:404:G:OP2	5:e:110:ARG:NH1	2.40	0.54
1:a:858:A:H1'	9:i:12:THR:HG21	1.90	0.54
2:b:23:LEU:HA	2:b:26:ILE:HD12	1.90	0.54
14:n:19:LEU:HD13	14:n:33:ILE:HD11	1.90	0.54
24:w:136:ARG:HH21	24:w:254:THR:HG21	1.72	0.54
1:a:82:U:O4	1:a:87:G:O6	2.25	0.54
1:a:294:C:OP1	1:a:590:A:O2'	2.23	0.54
1:a:358:U:H2'	1:a:359:G:H8	1.73	0.54
1:a:936:G:H21	1:a:1208:A:N6	2.03	0.54
1:a:1457:G:H2'	1:a:1458:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:53:ASP:OD1	4:d:54:VAL:N	2.40	0.54
6:f:190:ALA:HB1	6:f:194:MET:HE2	1.90	0.54
7:g:44:GLY:HA3	7:g:59:ILE:HG23	1.90	0.54
12:l:43:ILE:HG13	12:l:83:ALA:HB2	1.89	0.54
1:a:13:G:H5'	6:f:133:GLY:HA3	1.89	0.54
1:a:1232:A:H62	1:a:1268:C:H42	0.69	0.54
1:a:1407:U:H2'	1:a:1408:A:H8	1.73	0.54
16:p:6:GLU:CD	16:p:6:GLU:H	2.15	0.54
1:a:1305:G:H2'	1:a:1306:A:C8	2.43	0.54
22:c:118:GLU:O	22:c:122:GLN:HG2	2.07	0.54
22:c:182:PRO:HD2	22:c:182:PRO:O	2.08	0.54
8:h:69:VAL:HG23	8:h:100:ALA:HB1	1.89	0.54
1:a:544:C:C4	18:r:48:LEU:HD11	2.43	0.54
1:a:1296:C:H2'	1:a:1297:U:C6	2.44	0.54
2:b:174:ILE:HD12	2:b:184:VAL:HG12	1.90	0.54
4:d:62:ARG:NH1	4:d:64:ARG:HB2	2.22	0.54
1:a:390:U:H2'	1:a:391:G:C8	2.43	0.53
1:a:1220:A:H62	1:a:1281:A:N6	2.06	0.53
1:a:1269:A:H2	1:a:1335:G:H1'	1.73	0.53
2:b:58:LYS:HD3	2:b:59:THR:HB	1.90	0.53
7:g:8:VAL:HG22	7:g:61:ALA:HB3	1.89	0.53
19:s:17:THR:OG1	19:s:18:ARG:N	2.39	0.53
5:e:135:TYR:HB3	17:q:106:PHE:HB2	1.90	0.53
22:c:51:ASP:OD1	22:c:52:LYS:N	2.41	0.53
22:c:156:LYS:HD2	22:c:157:VAL:N	2.23	0.53
1:a:32:G:O2'	1:a:296:U:OP1	2.26	0.53
1:a:725:A:OP1	1:a:833:C:O2'	2.24	0.53
1:a:407:A:H2'	1:a:408:G:H8	1.72	0.53
1:a:1508:C:H2'	1:a:1509:G:C8	2.43	0.53
10:j:33:LYS:HG3	10:j:33:LYS:O	2.08	0.53
12:l:37:ASN:HA	12:l:67:SER:HB3	1.90	0.53
22:c:117:LEU:HB3	22:c:141:LYS:HE2	1.91	0.53
1:a:163:G:H2'	1:a:164:G:H8	1.73	0.53
1:a:452:A:N6	17:q:94:LYS:H	2.07	0.53
1:a:1244:G:O6	1:a:1254:G:N2	2.41	0.53
1:a:1497:A:H2'	1:a:1498:C:C6	2.43	0.53
5:e:189:PRO:O	5:e:190:LEU:HG	2.09	0.53
10:j:82:ASP:C	10:j:83:ILE:HD13	2.33	0.53
24:w:133:ILE:HG22	24:w:250:TYR:HB2	1.91	0.53
1:a:895:A:H4'	1:a:896:A:O5'	2.09	0.53
1:a:1458:G:H2'	1:a:1459:G:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:45:LYS:HZ1	22:c:75:GLN:HA	1.74	0.53
11:k:15:HIS:O	11:k:18:ILE:HG22	2.09	0.53
22:c:44:GLN:OE1	22:c:44:GLN:N	2.40	0.53
1:a:99:U:OP1	21:u:12:ARG:NH1	2.42	0.53
1:a:1265:U:OP2	1:a:1266:U:O2'	2.17	0.53
1:a:604:U:O2'	17:q:17:GLN:OE1	2.24	0.52
2:b:91:LEU:HB2	2:b:101:ILE:HG22	1.91	0.52
24:w:10:GLU:N	24:w:10:GLU:OE1	2.42	0.52
1:a:481:G:H2'	1:a:482:A:C8	2.44	0.52
1:a:498:C:H4'	1:a:499:C:O5'	2.10	0.52
1:a:504:G:H2'	1:a:505:C:C6	2.44	0.52
10:j:42:VAL:HG23	10:j:82:ASP:HB3	1.92	0.52
10:j:88:ASP:N	10:j:88:ASP:OD1	2.41	0.52
24:w:126:ARG:HH21	24:w:249:HIS:CE1	2.27	0.52
1:a:45:G:H2'	1:a:46:G:H8	1.73	0.52
1:a:337:G:H2'	1:a:338:A:H8	1.74	0.52
1:a:979:U:H2'	1:a:980:G:H8	1.75	0.52
13:m:35:THR:N	13:m:54:ARG:O	2.43	0.52
24:w:161:HIS:CE1	24:w:163:PHE:HB3	2.42	0.52
2:b:26:ILE:HG21	22:c:10:LEU:HD22	1.92	0.52
20:t:22:GLN:HA	20:t:25:LYS:HZ2	1.75	0.52
1:a:145:G:O2'	1:a:1429:A:N3	2.39	0.52
1:a:1296:C:H2'	1:a:1297:U:H6	1.74	0.52
6:f:68:LYS:O	6:f:98:ARG:NH2	2.43	0.52
24:w:4:ASP:OD1	24:w:4:ASP:N	2.38	0.52
1:a:60:U:H2'	1:a:61:G:H8	1.75	0.52
1:a:570:U:OP1	9:i:31:LYS:HG3	2.10	0.52
1:a:489:A:H8	1:a:523:U:O2'	1.93	0.52
1:a:1440:A:H3'	1:a:1441:G:H8	1.75	0.52
6:f:135:ALA:HB1	6:f:162:VAL:HG23	1.92	0.52
1:a:819:U:H3	1:a:829:G:H22	1.57	0.52
1:a:930:C:H2'	1:a:931:A:H8	1.75	0.52
1:a:1414:C:H2'	1:a:1415:G:O4'	2.10	0.52
22:c:211:ALA:O	22:c:215:LYS:HG2	2.09	0.52
6:f:64:VAL:HG11	6:f:93:ARG:HG3	1.91	0.51
1:a:654:G:H21	12:l:127:HIS:HB2	1.75	0.51
12:l:85:GLU:N	12:l:85:GLU:OE1	2.43	0.51
22:c:56:PHE:CG	22:c:198:TYR:HE2	2.29	0.51
1:a:926:G:N1	1:a:1320:G:OP2	2.43	0.51
1:a:1273:C:OP1	8:h:41:ARG:NH1	2.44	0.51
1:a:1337:A:H2'	1:a:1338:G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1374:U:H2'	1:a:1375:G:C8	2.45	0.51
8:h:70:LYS:HG2	8:h:96:SER:HB2	1.93	0.51
8:h:113:GLU:HB2	8:h:119:ARG:HG2	1.93	0.51
14:n:16:GLU:N	14:n:16:GLU:OE1	2.43	0.51
17:q:49:ILE:HB	17:q:93:LEU:HD11	1.92	0.51
22:c:108:HIS:O	22:c:112:GLN:HG2	2.10	0.51
1:a:890:A:H2'	1:a:891:A:C8	2.46	0.51
1:a:1486:A:H2	1:a:1489:G:H1	1.59	0.51
6:f:178:VAL:HG21	9:i:101:LEU:HD13	1.93	0.51
1:a:322:C:H2'	1:a:323:U:C6	2.46	0.51
1:a:571:U:H2'	1:a:572:G:H8	1.75	0.51
18:r:74:VAL:HG12	18:r:93:ILE:HG23	1.92	0.51
1:a:83:U:C2	1:a:86:G:O6	2.62	0.51
1:a:494:C:H2'	1:a:495:G:H8	1.75	0.51
22:c:97:LEU:H	22:c:100:MET:HE3	1.75	0.51
1:a:413:G:O2'	1:a:428:G:N2	2.42	0.51
1:a:1003:C:H2'	1:a:1004:G:C8	2.45	0.51
2:b:59:THR:HG21	2:b:99:ARG:HA	1.92	0.51
8:h:79:ARG:HG2	8:h:84:THR:HG23	1.93	0.51
1:a:987:A:H2'	1:a:988:C:C6	2.46	0.51
8:h:109:ARG:HA	8:h:116:MET:HE1	1.93	0.51
11:k:18:ILE:HG12	11:k:72:ARG:HG2	1.93	0.51
1:a:399:G:H2'	1:a:400:C:C6	2.46	0.50
1:a:481:G:H2'	1:a:482:A:H8	1.75	0.50
1:a:1305:G:HO2'	1:a:1344:C:HO2'	1.54	0.50
8:h:116:MET:HE2	8:h:119:ARG:HE	1.76	0.50
22:c:44:GLN:HA	22:c:47:LEU:HD12	1.92	0.50
1:a:444:A:H2'	1:a:445:C:C6	2.45	0.50
1:a:832:U:H2'	1:a:833:C:C6	2.46	0.50
1:a:1168:G:N2	15:o:60:SER:OG	2.44	0.50
1:a:1066:U:H3	1:a:1079:G:H22	1.58	0.50
22:c:42:ASP:HB3	22:c:45:GLN:OE1	2.11	0.50
23:x:57:ARG:O	23:x:57:ARG:HD3	2.11	0.50
1:a:507:G:O2'	1:a:515:A:N1	2.37	0.50
1:a:804:U:H2'	1:a:805:A:C8	2.46	0.50
4:d:64:ARG:NH2	4:d:66:ASP:OD2	2.43	0.50
24:w:242:ILE:HG12	24:w:252:LEU:HD13	1.92	0.50
1:a:424:G:H2'	1:a:425:G:H8	1.77	0.50
1:a:298:A:H2'	1:a:299:G:C8	2.47	0.50
3:v:8:ARG:HA	3:v:11:ARG:HG2	1.94	0.50
12:l:91:VAL:O	12:l:117:GLY:N	2.31	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:w:146:VAL:HB	24:w:198:PHE:HB3	1.93	0.50
1:a:407:A:H2'	1:a:408:G:C8	2.47	0.50
4:d:34:GLU:OE2	4:d:58:ARG:NE	2.45	0.50
5:e:166:LEU:HD23	5:e:177:VAL:HG22	1.94	0.50
22:c:132:LYS:H	22:c:132:LYS:HD2	1.77	0.50
24:w:51:PRO:HD2	24:w:72:VAL:HA	1.92	0.50
24:w:245:ARG:NE	24:w:249:HIS:HB2	2.26	0.50
1:a:472:C:H2'	1:a:473:A:C8	2.47	0.49
1:a:1063:U:O2'	1:a:1082:A:OP2	2.25	0.49
1:a:1337:A:H2'	1:a:1338:G:H8	1.76	0.49
10:j:70:ALA:O	10:j:74:THR:HG22	2.12	0.49
13:m:50:ARG:NH1	13:m:89:ASP:OD2	2.43	0.49
18:r:67:GLU:OE1	18:r:67:GLU:N	2.38	0.49
1:a:724:C:H2'	1:a:725:A:H8	1.77	0.49
1:a:1110:A:H61	1:a:1125:G:H1'	1.78	0.49
1:a:1278:C:H4'	1:a:1284:U:O4	2.11	0.49
1:a:1298:G:N1	1:a:1301:A:OP2	2.42	0.49
22:c:87:VAL:HG11	22:c:221:VAL:HG13	1.93	0.49
1:a:25:G:H2'	1:a:26:G:H8	1.74	0.49
1:a:587:A:OP1	1:a:611:G:N2	2.40	0.49
7:g:30:ILE:HG22	7:g:71:THR:HG22	1.94	0.49
1:a:320:G:H2'	1:a:321:A:C8	2.47	0.49
12:l:63:GLY:O	12:l:66:LYS:HG2	2.12	0.49
15:o:22:THR:HB	15:o:33:VAL:HG11	1.94	0.49
22:c:77:GLN:O	22:c:80:ILE:HG12	2.11	0.49
1:a:30:A:H61	1:a:538:G:H1'	1.78	0.49
1:a:128:U:O2'	1:a:262:G:N3	2.45	0.49
2:b:30:ILE:HG12	22:c:16:PHE:HZ	1.78	0.49
8:h:23:VAL:O	8:h:27:VAL:HG13	2.12	0.49
11:k:26:VAL:HA	11:k:29:VAL:HG22	1.93	0.49
1:a:203:U:H2'	1:a:204:A:C8	2.46	0.49
9:i:10:PHE:CD2	9:i:36:ILE:HD11	2.48	0.49
24:w:177:GLY:H	24:w:182:TYR:HA	1.78	0.49
1:a:254:G:OP1	18:r:85:THR:OG1	2.30	0.49
1:a:501:G:N7	13:m:50:ARG:NH2	2.60	0.49
8:h:57:ASP:OD1	8:h:59:VAL:N	2.44	0.49
22:c:5:THR:OG1	22:c:6:MET:SD	2.69	0.49
1:a:1295:U:H2'	1:a:1296:C:C6	2.47	0.49
5:e:176:LEU:HB3	17:q:106:PHE:HE1	1.78	0.49
1:a:636:G:N2	16:p:23:GLY:HA3	2.27	0.49
19:s:51:ARG:NH1	19:s:56:ASN:O	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:859:C:H2'	1:a:860:C:H6	1.78	0.48
12:l:28:GLY:HA2	12:l:46:PRO:HD3	1.94	0.48
12:l:73:GLN:HG3	12:l:108:SER:OG	2.13	0.48
20:t:62:VAL:HA	20:t:66:MET:SD	2.53	0.48
1:a:522:G:H2'	1:a:523:U:C6	2.48	0.48
1:a:525:C:H5'	5:e:64:GLU:HB2	1.96	0.48
1:a:805:A:H2'	1:a:806:C:C6	2.49	0.48
1:a:891:A:N3	1:a:1396:A:O2'	2.45	0.48
1:a:1522:C:H5'	1:a:1522:C:H6	1.78	0.48
5:e:148:LEU:O	5:e:152:ILE:HG22	2.14	0.48
9:i:12:THR:HG22	9:i:15:ARG:HH12	1.78	0.48
12:l:117:GLY:O	24:w:220:ARG:NH2	2.40	0.48
14:n:43:MET:HE2	14:n:47:ASP:HB2	1.96	0.48
1:a:252:U:H2'	1:a:253:U:C6	2.49	0.48
1:a:498:C:H5''	1:a:499:C:C6	2.48	0.48
17:q:54:GLU:H	17:q:54:GLU:CD	2.16	0.48
1:a:299:G:H2'	1:a:300:A:C8	2.48	0.48
2:b:164:TYR:HD1	2:b:167:LYS:HE2	1.78	0.48
2:b:172:LYS:O	2:b:185:LEU:HD22	2.13	0.48
4:d:33:LYS:HG2	15:o:25:ASN:HD22	1.79	0.48
1:a:674:G:H22	1:a:768:U:H5'	1.78	0.48
1:a:1295:U:H2'	1:a:1296:C:H6	1.79	0.48
18:r:77:MET:SD	18:r:89:ARG:NH2	2.86	0.48
1:a:252:U:H2'	1:a:253:U:H6	1.78	0.48
1:a:1265:U:H5''	1:a:1266:U:H4'	1.95	0.48
1:a:1281:A:H2'	1:a:1281:A:N3	2.29	0.48
2:b:148:LEU:HD22	2:b:153:VAL:HG22	1.96	0.48
1:a:527:A:OP2	5:e:2:ALA:N	2.47	0.48
1:a:534:U:H2'	1:a:535:C:H6	1.79	0.48
1:a:1521:U:H3	24:w:125:PRO:HD3	1.79	0.48
3:v:27:GLN:HA	3:v:30:LYS:HD3	1.95	0.48
4:d:129:PHE:HD2	4:d:133:MET:HE1	1.78	0.48
7:g:27:LEU:HD11	7:g:63:ILE:HD13	1.94	0.48
20:t:9:PRO:HD3	23:x:65:TYR:CD1	2.49	0.48
1:a:81:C:H3'	1:a:82:U:H5''	1.95	0.48
1:a:122:G:OP1	1:a:585:U:O2'	2.19	0.48
1:a:269:U:H2'	1:a:270:A:H8	1.79	0.48
14:n:12:ASP:OD1	14:n:44:ARG:NE	2.36	0.48
22:c:79:SER:O	22:c:83:GLU:HG2	2.14	0.48
1:a:23:C:H5''	6:f:116:ALA:HB3	1.94	0.48
1:a:422:C:H4'	1:a:423:G:O5'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:425:G:H2'	1:a:426:U:C6	2.49	0.48
1:a:263:A:H2'	1:a:264:U:C6	2.49	0.47
1:a:707:G:N2	1:a:710:G:OP2	2.40	0.47
1:a:1287:G:H22	1:a:1313:G:H1'	1.79	0.47
5:e:182:GLU:HB2	5:e:185:GLN:HE21	1.78	0.47
14:n:80:ARG:HA	14:n:83:GLU:HG3	1.96	0.47
1:a:1203:G:OP2	1:a:1304:C:N4	2.43	0.47
18:r:83:SER:O	18:r:87:ARG:NH1	2.47	0.47
1:a:54:A:O2'	1:a:360:G:N2	2.47	0.47
9:i:76:GLY:HA3	9:i:132:TRP:CE2	2.49	0.47
12:l:102:ARG:O	12:l:106:ILE:HG13	2.14	0.47
14:n:52:GLN:O	14:n:56:LEU:HD22	2.13	0.47
1:a:324:G:N1	1:a:327:A:OP2	2.48	0.47
5:e:47:ARG:NH1	5:e:51:GLN:OE1	2.47	0.47
6:f:87:LYS:O	6:f:90:GLU:HG3	2.13	0.47
7:g:87:ARG:NH1	19:s:73:GLU:O	2.48	0.47
13:m:56:LYS:HE3	13:m:60:GLN:HA	1.96	0.47
5:e:98:TYR:O	5:e:160:ARG:NH2	2.47	0.47
1:a:106:C:O2'	17:q:26:ARG:O	2.31	0.47
1:a:518:U:H2'	1:a:519:A:H8	1.79	0.47
1:a:805:A:H2'	1:a:806:C:H6	1.80	0.47
1:a:1138:A:H1'	1:a:1162:G:N2	2.29	0.47
1:a:1208:A:C8	20:t:83:HIS:CD2	3.02	0.47
4:d:25:ASP:OD1	4:d:25:ASP:N	2.48	0.47
4:d:177:THR:HG22	4:d:180:ALA:H	1.79	0.47
9:i:31:LYS:HB2	9:i:31:LYS:HE3	1.73	0.47
10:j:75:VAL:HG11	10:j:107:LEU:HD13	1.97	0.47
1:a:1222:G:H2'	1:a:1223:G:H8	1.79	0.47
4:d:6:ASN:OD1	4:d:8:HIS:N	2.47	0.47
7:g:4:TYR:CD2	7:g:72:VAL:HG21	2.49	0.47
1:a:1409:A:H2'	1:a:1410:C:H6	1.80	0.47
2:b:120:LYS:HE2	2:b:173:ILE:HG21	1.97	0.47
18:r:63:ASP:OD1	18:r:63:ASP:N	2.48	0.47
1:a:688:C:C2	1:a:689:A:C8	3.03	0.47
1:a:986:G:N2	1:a:987:A:N3	2.62	0.47
1:a:1086:G:H5''	4:d:172:ARG:HG2	1.97	0.47
11:k:72:ARG:HA	11:k:72:ARG:HD3	1.63	0.47
1:a:997:A:C2	1:a:1200:A:H1'	2.50	0.46
5:e:164:SER:OG	5:e:185:GLN:OE1	2.33	0.46
5:e:176:LEU:HB3	17:q:106:PHE:CE1	2.51	0.46
11:k:7:ARG:HD2	11:k:73:LEU:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:n:52:GLN:HA	14:n:55:VAL:HG12	1.97	0.46
14:n:91:ARG:HB3	14:n:98:VAL:HG12	1.95	0.46
1:a:582:U:H2'	1:a:583:C:C6	2.50	0.46
1:a:719:C:P	7:g:2:ARG:HH22	2.38	0.46
1:a:905:A:O2'	1:a:1382:C:OP2	2.31	0.46
1:a:956:A:OP1	15:o:29:ARG:NH2	2.48	0.46
1:a:1125:G:N2	1:a:1127:A:H62	2.13	0.46
9:i:50:ARG:NE	9:i:52:GLU:OE2	2.48	0.46
10:j:61:ASN:O	10:j:65:GLN:HG3	2.15	0.46
20:t:22:GLN:HA	20:t:25:LYS:NZ	2.30	0.46
1:a:230:G:H2'	1:a:231:G:O4'	2.15	0.46
1:a:858:A:H2'	1:a:859:C:C6	2.51	0.46
12:l:45:ASP:OD2	12:l:49:ASN:ND2	2.41	0.46
1:a:191:C:H2'	1:a:192:G:O4'	2.15	0.46
1:a:382:A:H2'	1:a:383:A:C8	2.51	0.46
1:a:481:G:H1'	1:a:529:C:H1'	1.96	0.46
1:a:927:G:C2	1:a:928:A:C8	3.02	0.46
1:a:1301:A:C8	1:a:1305:G:C6	3.04	0.46
8:h:136:LYS:HB3	8:h:136:LYS:HE3	1.68	0.46
11:k:47:ASN:O	11:k:66:GLU:HA	2.15	0.46
1:a:12:A:N6	5:e:197:GLU:O	2.49	0.46
12:l:39:THR:HG21	12:l:72:ALA:HB2	1.98	0.46
14:n:82:ILE:HA	14:n:89:GLY:HA2	1.98	0.46
17:q:82:LYS:HB2	17:q:89:ALA:HB2	1.97	0.46
24:w:183:ARG:HG3	24:w:203:THR:HG23	1.97	0.46
1:a:36:A:H2'	1:a:37:A:C8	2.50	0.46
1:a:384:G:H2'	1:a:385:C:C6	2.51	0.46
1:a:1042:U:H2'	1:a:1043:C:C6	2.51	0.46
1:a:1237:C:H2'	1:a:1259:G:N7	2.30	0.46
4:d:151:VAL:HG22	4:d:200:VAL:HG22	1.96	0.46
19:s:70:ASN:O	19:s:74:VAL:HG22	2.15	0.46
1:a:741:G:H2'	1:a:742:A:H8	1.81	0.46
1:a:1139:C:O3'	22:c:132:LYS:NZ	2.48	0.46
10:j:76:ASP:O	10:j:76:ASP:OD1	2.33	0.46
18:r:65:ASN:HB2	18:r:67:GLU:CD	2.40	0.46
20:t:67:VAL:O	23:x:57:ARG:NH1	2.47	0.46
1:a:667:A:C2	1:a:684:A:C5	3.04	0.46
1:a:741:G:H2'	1:a:742:A:C8	2.51	0.46
5:e:119:LEU:HD21	5:e:122:GLY:HA2	1.98	0.46
14:n:33:ILE:HG13	14:n:34:LEU:N	2.30	0.46
22:c:225:LEU:O	22:c:228:ARG:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:337:G:H2'	1:a:338:A:C8	2.51	0.46
1:a:936:G:H2'	1:a:937:A:C8	2.51	0.46
4:d:139:SER:O	4:d:142:ARG:NE	2.46	0.46
12:l:122:VAL:HG23	12:l:122:VAL:O	2.16	0.46
9:i:22:HIS:O	9:i:66:TYR:OH	2.27	0.46
22:c:9:LEU:O	22:c:12:SER:OG	2.34	0.46
1:a:360:G:H2'	1:a:361:G:C8	2.50	0.45
1:a:436:C:H2'	1:a:437:U:C6	2.52	0.45
1:a:823:U:O4	1:a:826:U:N3	2.44	0.45
1:a:1207:C:OP1	14:n:91:ARG:NH2	2.36	0.45
1:a:1359:U:H2'	1:a:1360:A:C8	2.51	0.45
1:a:1432:C:H2'	1:a:1433:C:C6	2.51	0.45
13:m:5:GLN:HA	13:m:8:VAL:HG22	1.98	0.45
14:n:24:GLY:HA3	14:n:66:VAL:HG12	1.97	0.45
15:o:43:CYS:O	15:o:47:MET:HG3	2.17	0.45
1:a:246:A:C2	1:a:282:A:C5	3.05	0.45
1:a:431:A:C4	1:a:432:A:C8	3.04	0.45
1:a:493:A:H2'	1:a:494:C:C6	2.50	0.45
1:a:1003:C:H2'	1:a:1004:G:H8	1.81	0.45
1:a:1043:C:OP2	1:a:1044:G:O2'	2.25	0.45
1:a:1218:C:O3'	1:a:1282:G:N2	2.47	0.45
10:j:26:ILE:HD12	10:j:26:ILE:O	2.17	0.45
1:a:335:C:H2'	1:a:336:A:H8	1.81	0.45
1:a:449:C:H2'	1:a:450:G:O4'	2.17	0.45
22:c:203:ASN:OD1	22:c:204:ASP:N	2.50	0.45
1:a:1076:C:H2'	1:a:1077:C:H6	1.82	0.45
1:a:1232:A:H2'	1:a:1233:A:C8	2.52	0.45
1:a:1494:C:OP1	3:v:11:ARG:HB3	2.16	0.45
7:g:33:ASP:OD2	7:g:71:THR:OG1	2.31	0.45
20:t:17:LYS:O	20:t:21:VAL:HG13	2.16	0.45
22:c:223:GLU:O	22:c:226:GLN:HG2	2.16	0.45
1:a:270:A:H2'	1:a:271:C:C6	2.51	0.45
2:b:133:VAL:HG21	2:b:165:ILE:HG12	1.98	0.45
9:i:11:LEU:HD22	9:i:77:LEU:HD22	1.98	0.45
20:t:16:LEU:O	20:t:19:VAL:HG22	2.17	0.45
22:c:119:ALA:O	22:c:123:THR:HG23	2.16	0.45
24:w:195:LEU:HD12	24:w:196:SER:H	1.81	0.45
1:a:384:G:H2'	1:a:385:C:H6	1.81	0.45
1:a:581:U:H2'	1:a:582:U:C6	2.51	0.45
1:a:749:G:H4'	1:a:1497:A:H4'	1.97	0.45
2:b:47:ASP:OD1	2:b:48:ARG:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:131:ILE:HB	2:b:141:ASP:HB2	1.99	0.45
10:j:72:LEU:HA	10:j:75:VAL:HG12	1.98	0.45
12:l:92:ASP:HB2	12:l:118:THR:HG22	1.98	0.45
17:q:108:ALA:O	17:q:112:GLU:HG3	2.17	0.45
1:a:279:A:OP1	1:a:280:C:O2'	2.32	0.45
1:a:636:G:H21	16:p:23:GLY:HA3	1.81	0.45
1:a:1177:A:OP1	1:a:1178:A:H5''	2.16	0.45
2:b:30:ILE:HG12	22:c:16:PHE:CZ	2.51	0.45
6:f:181:ARG:NH1	9:i:73:SER:O	2.49	0.45
8:h:17:VAL:HG23	8:h:18:TYR:CD1	2.51	0.45
1:a:23:C:H2'	1:a:24:U:C6	2.52	0.45
1:a:770:A:OP1	24:w:30:HIS:ND1	2.39	0.45
1:a:902:U:H2'	1:a:903:U:C6	2.52	0.45
1:a:977:C:O2'	15:o:8:HIS:NE2	2.50	0.45
1:a:1248:U:O2'	1:a:1249:G:O5'	2.34	0.45
1:a:321:A:H2'	1:a:322:C:H6	1.81	0.45
1:a:419:C:N3	1:a:425:G:N1	2.65	0.45
1:a:492:U:H2'	1:a:493:A:H8	1.81	0.45
1:a:522:G:H2'	1:a:523:U:H6	1.82	0.45
1:a:620:A:H2'	1:a:621:U:C6	2.51	0.45
1:a:1171:G:H5''	4:d:176:HIS:CE1	2.52	0.45
1:a:1206:U:O2	1:a:1206:U:H2'	2.17	0.45
2:b:139:ILE:HG12	2:b:147:PHE:CD1	2.52	0.45
5:e:104:ARG:H	5:e:108:MET:CE	2.28	0.45
9:i:50:ARG:HH12	9:i:63:GLN:NE2	2.12	0.45
9:i:101:LEU:HD23	9:i:101:LEU:HA	1.83	0.45
13:m:54:ARG:HH11	13:m:64:THR:HB	1.82	0.45
13:m:87:VAL:HG11	13:m:90:LEU:HD12	1.99	0.45
23:x:58:VAL:O	23:x:62:GLU:HG2	2.17	0.45
1:a:24:U:H2'	1:a:25:G:O4'	2.17	0.44
1:a:725:A:H2'	1:a:726:G:C8	2.52	0.44
1:a:907:G:O2'	1:a:909:G:OP1	2.30	0.44
1:a:1249:G:H2'	1:a:1250:A:C8	2.52	0.44
1:a:1413:C:H2'	1:a:1414:C:C6	2.52	0.44
1:a:64:A:N7	1:a:104:A:H4'	2.31	0.44
1:a:534:U:H2'	1:a:535:C:C6	2.52	0.44
1:a:1393:G:H2'	1:a:1394:U:C6	2.52	0.44
2:b:172:LYS:HA	2:b:172:LYS:HD3	1.69	0.44
6:f:36:TYR:HD2	6:f:93:ARG:HH21	1.64	0.44
24:w:131:ARG:HD3	24:w:248:GLY:O	2.17	0.44
24:w:175:TYR:CE1	24:w:183:ARG:HB3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:438:U:O2'	1:a:439:U:O2	2.14	0.44
1:a:463:C:OP2	1:a:464:G:O2'	2.34	0.44
1:a:542:U:H5''	1:a:543:A:C5	2.53	0.44
1:a:543:A:H2'	1:a:547:G:C8	2.53	0.44
1:a:1334:C:H2'	1:a:1335:G:C8	2.51	0.44
4:d:55:GLU:OE1	4:d:55:GLU:N	2.50	0.44
15:o:10:ALA:HB2	15:o:23:ARG:HD2	2.00	0.44
22:c:131:LYS:O	22:c:134:ILE:HG13	2.16	0.44
24:w:126:ARG:HH21	24:w:249:HIS:HE1	1.65	0.44
1:a:688:C:H2'	1:a:689:A:C8	2.51	0.44
1:a:826:U:H5'	1:a:827:U:OP1	2.16	0.44
1:a:1329:G:C8	10:j:129:ARG:HB3	2.52	0.44
7:g:82:ASN:OD1	7:g:84:SER:OG	2.26	0.44
11:k:15:HIS:ND1	11:k:16:GLU:OE2	2.46	0.44
22:c:68:LEU:HD22	22:c:70:VAL:HG23	2.00	0.44
5:e:185:GLN:H	5:e:185:GLN:HG2	1.60	0.44
18:r:81:PRO:HB3	18:r:87:ARG:CZ	2.47	0.44
20:t:19:VAL:HG21	20:t:44:PHE:CE1	2.50	0.44
1:a:12:A:C6	5:e:201:LYS:HG3	2.52	0.44
1:a:26:G:H4'	1:a:867:G:C8	2.53	0.44
1:a:156:G:N2	1:a:159:A:OP2	2.44	0.44
1:a:1051:C:H2'	1:a:1052:G:C8	2.48	0.44
1:a:1276:G:H2'	1:a:1277:U:C6	2.53	0.44
11:k:37:VAL:HG12	11:k:75:ASP:H	1.82	0.44
12:l:96:LYS:HD2	12:l:124:PRO:HD3	1.99	0.44
23:x:56:GLY:O	23:x:60:ARG:HG3	2.17	0.44
24:w:93:ALA:HB1	24:w:95:HIS:CD2	2.53	0.44
1:a:26:G:H2'	1:a:27:C:H6	1.83	0.44
1:a:109:G:H2'	1:a:110:U:C6	2.53	0.44
1:a:1232:A:N3	1:a:1352:C:O2'	2.36	0.44
1:a:1239:G:H2'	1:a:1240:C:C6	2.53	0.44
2:b:114:GLY:HA2	2:b:117:GLU:OE1	2.18	0.44
14:n:29:ARG:HA	14:n:29:ARG:HD3	1.59	0.44
22:c:71:GLY:O	22:c:93:ASN:HA	2.18	0.44
24:w:147:ASP:O	24:w:151:LEU:HG	2.17	0.44
24:w:222:GLY:HA2	24:w:244:ARG:NH2	2.33	0.44
1:a:452:A:O2'	17:q:76:ILE:HD11	2.18	0.44
1:a:532:U:H2'	1:a:533:G:H8	1.83	0.44
1:a:653:G:H2'	1:a:654:G:H8	1.78	0.44
1:a:1181:C:H4'	1:a:1182:A:H5'	2.00	0.44
22:c:61:VAL:HG13	22:c:224:GLY:HA3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:96:G:C4	1:a:97:A:C8	3.06	0.44
1:a:375:U:H2'	1:a:376:G:H8	1.83	0.44
1:a:390:U:H2'	1:a:391:G:H8	1.82	0.44
1:a:1488:G:OP1	1:a:1491:A:H4'	2.18	0.44
1:a:1514:G:H2'	1:a:1515:A:C8	2.53	0.44
9:i:98:LEU:HD23	9:i:98:LEU:HA	1.85	0.44
22:c:131:LYS:HD3	22:c:134:ILE:HD11	2.00	0.44
16:p:82:ILE:HD12	16:p:87:LEU:HB2	2.00	0.43
23:x:60:ARG:HA	23:x:63:LYS:HG2	2.00	0.43
1:a:493:A:H2'	1:a:494:C:H6	1.83	0.43
1:a:1133:G:OP1	11:k:70:HIS:ND1	2.43	0.43
4:d:33:LYS:HE3	4:d:33:LYS:HB3	1.84	0.43
4:d:90:LEU:HB3	4:d:98:VAL:HG11	2.00	0.43
5:e:163:PRO:HG2	5:e:166:LEU:HD12	2.00	0.43
8:h:74:GLU:O	8:h:88:PRO:HA	2.18	0.43
16:p:26:GLU:HG3	16:p:81:LEU:HD22	2.00	0.43
24:w:126:ARG:CG	24:w:247:ASP:O	2.53	0.43
1:a:45:G:H2'	1:a:46:G:C8	2.52	0.43
1:a:119:C:H2'	1:a:120:G:H8	1.83	0.43
1:a:550:G:H2'	1:a:551:U:C6	2.53	0.43
1:a:748:A:H4'	1:a:1507:G:H22	1.83	0.43
5:e:23:ASP:OD1	5:e:25:SER:N	2.52	0.43
8:h:111:ARG:NH2	8:h:113:GLU:OE2	2.52	0.43
10:j:47:GLN:NE2	10:j:48:PHE:O	2.51	0.43
12:l:118:THR:HA	24:w:220:ARG:NH2	2.32	0.43
13:m:18:LYS:HA	13:m:18:LYS:HD3	1.76	0.43
14:n:33:ILE:HD13	14:n:60:ILE:HD11	2.00	0.43
1:a:39:G:H2'	1:a:40:C:C6	2.54	0.43
1:a:323:U:H2'	1:a:324:G:O4'	2.17	0.43
1:a:444:A:H2'	1:a:445:C:H6	1.82	0.43
1:a:658:U:H2'	1:a:659:C:H6	1.83	0.43
1:a:905:A:H2'	1:a:906:C:C6	2.53	0.43
1:a:953:G:H22	1:a:1346:A:P	2.40	0.43
1:a:1011:U:O2'	1:a:1012:U:O5'	2.34	0.43
10:j:47:GLN:HB3	10:j:82:ASP:OD2	2.19	0.43
12:l:30:ALA:HB3	12:l:93:VAL:HG22	2.01	0.43
1:a:500:A:N6	1:a:509:G:H1'	2.33	0.43
1:a:573:U:C2	1:a:574:C:C5	3.07	0.43
1:a:1099:C:H2'	1:a:1100:U:H6	1.83	0.43
5:e:90:GLU:O	5:e:95:ASN:ND2	2.52	0.43
7:g:39:LYS:HE2	7:g:39:LYS:HB2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:h:22:LEU:HD22	8:h:62:LEU:HD21	2.00	0.43
10:j:32:ARG:HD3	10:j:97:GLY:HA3	2.01	0.43
20:t:10:PHE:HE2	20:t:37:ARG:HG3	1.83	0.43
1:a:657:U:O2	1:a:757:A:O2'	2.36	0.43
7:g:11:ASP:OD1	7:g:11:ASP:N	2.41	0.43
7:g:30:ILE:O	7:g:36:THR:OG1	2.31	0.43
13:m:31:ARG:HE	13:m:31:ARG:HB3	1.61	0.43
21:u:5:LYS:HB3	21:u:5:LYS:HE2	1.79	0.43
22:c:84:ALA:O	22:c:88:GLY:N	2.48	0.43
1:a:109:G:H1'	1:a:354:G:H5'	2.01	0.43
1:a:1117:U:H4'	1:a:1118:A:OP1	2.18	0.43
1:a:1231:A:H4'	10:j:89:GLY:HA2	2.01	0.43
1:a:1357:A:OP1	8:h:36:LYS:NZ	2.46	0.43
1:a:1369:G:H2'	1:a:1370:G:H8	1.83	0.43
10:j:29:VAL:HG12	10:j:38:ARG:HG2	2.01	0.43
10:j:111:GLN:HG3	10:j:114:ASP:OD1	2.18	0.43
16:p:18:HIS:NE2	16:p:21:ASP:HB3	2.33	0.43
22:c:56:PHE:CD1	22:c:198:TYR:HE2	2.36	0.43
1:a:1036:U:H5'	4:d:163:SER:HB2	1.99	0.43
1:a:1098:U:H2'	1:a:1099:C:H6	1.84	0.43
1:a:1098:U:H2'	1:a:1099:C:C6	2.54	0.43
1:a:1219:A:H2	1:a:1222:G:N3	2.16	0.43
1:a:1269:A:H2'	1:a:1270:A:C8	2.53	0.43
4:d:104:GLU:O	4:d:106:LYS:NZ	2.52	0.43
4:d:190:LYS:HG2	4:d:195:ARG:CZ	2.48	0.43
6:f:36:TYR:HE1	6:f:66:ASP:HB3	1.84	0.43
22:c:74:LYS:HA	22:c:77:GLN:HB2	2.01	0.43
24:w:28:ARG:HD3	24:w:28:ARG:HA	1.88	0.43
1:a:571:U:H2'	1:a:572:G:C8	2.54	0.43
1:a:725:A:H2'	1:a:726:G:H8	1.83	0.43
1:a:846:A:H2'	1:a:847:A:C8	2.54	0.43
6:f:50:VAL:HG22	6:f:51:LYS:H	1.84	0.43
9:i:5:ASP:OD2	9:i:79:ARG:NE	2.39	0.43
9:i:35:ASN:HB3	9:i:112:LEU:HD12	2.01	0.43
10:j:48:PHE:CD2	10:j:55:LEU:HD22	2.53	0.43
14:n:51:ASP:OD1	14:n:51:ASP:C	2.62	0.43
17:q:47:SER:O	17:q:49:ILE:HG13	2.18	0.43
1:a:492:U:H2'	1:a:493:A:C8	2.54	0.43
1:a:708:A:H2'	1:a:709:A:C8	2.54	0.43
2:b:24:ALA:O	2:b:28:LYS:HG2	2.19	0.43
21:u:35:PHE:CE1	21:u:51:LEU:HB2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:w:175:TYR:CD2	24:w:228:PHE:HZ	2.37	0.43
1:a:105:A:H5'	1:a:106:C:H5	1.83	0.42
1:a:580:G:C6	1:a:619:G:C6	3.07	0.42
1:a:982:A:H2'	1:a:983:C:C6	2.55	0.42
9:i:81:SER:OG	9:i:126:GLU:OE2	2.30	0.42
10:j:50:LEU:HD12	10:j:58:TYR:HB3	2.01	0.42
24:w:135:ARG:HB2	24:w:245:ARG:HD2	2.00	0.42
1:a:60:U:H2'	1:a:61:G:C8	2.53	0.42
1:a:320:G:HO2'	1:a:1418:G:HO2'	1.64	0.42
1:a:426:U:H2'	1:a:427:U:C6	2.55	0.42
1:a:832:U:H2'	1:a:833:C:H6	1.83	0.42
11:k:24:LYS:O	11:k:28:THR:HG22	2.19	0.42
14:n:11:ARG:O	14:n:45:THR:OG1	2.36	0.42
22:c:197:ASP:C	22:c:198:TYR:HD1	2.27	0.42
24:w:85:LEU:HD23	24:w:85:LEU:HA	1.86	0.42
24:w:131:ARG:HD2	24:w:250:TYR:OH	2.18	0.42
24:w:193:ASP:OD1	24:w:194:GLU:N	2.52	0.42
1:a:424:G:H2'	1:a:425:G:C8	2.54	0.42
1:a:737:U:OP1	1:a:802:G:O2'	2.37	0.42
1:a:1476:A:O2'	24:w:80:ARG:NH2	2.51	0.42
2:b:116:ILE:HA	2:b:119:LEU:HD12	2.01	0.42
2:b:144:LEU:HD13	2:b:181:ASN:HB3	2.00	0.42
1:a:1008:C:H2'	1:a:1009:C:C6	2.54	0.42
1:a:1104:G:N2	1:a:1105:U:O4	2.50	0.42
1:a:1116:U:O2'	1:a:1117:U:H5''	2.19	0.42
1:a:1148:U:H1'	2:b:48:ARG:HH21	1.83	0.42
2:b:167:LYS:HD2	2:b:167:LYS:C	2.44	0.42
4:d:41:LEU:HD21	4:d:89:ASP:OD1	2.20	0.42
12:l:106:ILE:HG13	12:l:106:ILE:H	1.70	0.42
18:r:69:GLY:H	18:r:96:LYS:NZ	2.18	0.42
24:w:94:GLU:O	24:w:99:ARG:NH1	2.52	0.42
1:a:30:A:N6	1:a:538:G:H1'	2.34	0.42
1:a:188:G:H2'	1:a:189:G:C8	2.55	0.42
1:a:1035:A:C6	1:a:1187:G:C5	3.08	0.42
1:a:1382:C:C2	1:a:1486:A:N6	2.88	0.42
14:n:15:MET:HE3	14:n:43:MET:SD	2.60	0.42
20:t:45:ILE:HD13	20:t:45:ILE:HA	1.88	0.42
1:a:232:G:H1'	1:a:262:G:H1	1.84	0.42
1:a:751:G:H2'	1:a:752:U:C6	2.54	0.42
1:a:800:U:H4'	1:a:801:G:OP2	2.20	0.42
1:a:988:C:O2'	1:a:1017:C:O2'	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1086:G:H2'	1:a:1087:C:C6	2.54	0.42
2:b:67:GLU:HB3	2:b:103:SER:HB2	2.02	0.42
4:d:106:LYS:HA	4:d:106:LYS:HD3	1.89	0.42
10:j:39:VAL:HG21	10:j:103:ILE:HD13	2.02	0.42
1:a:144:G:H2'	1:a:145:G:H8	1.83	0.42
1:a:264:U:H2'	1:a:265:G:O4'	2.19	0.42
1:a:1249:G:O2'	1:a:1250:A:O4'	2.34	0.42
2:b:173:ILE:HD12	2:b:183:VAL:CG2	2.50	0.42
4:d:134:ARG:O	4:d:138:GLN:HG2	2.19	0.42
12:l:115:GLU:OE1	12:l:115:GLU:HA	2.20	0.42
19:s:18:ARG:C	19:s:19:LYS:HD2	2.45	0.42
22:c:181:ILE:HD13	22:c:181:ILE:HA	1.91	0.42
1:a:940:A:C5	20:t:55:ARG:HG3	2.55	0.42
10:j:138:LEU:HB3	10:j:143:LYS:O	2.19	0.42
16:p:34:LYS:NZ	16:p:38:ASP:OD1	2.53	0.42
22:c:12:SER:HB3	22:c:208:ARG:HG2	2.01	0.42
1:a:136:G:C6	1:a:225:G:C5	3.07	0.42
1:a:163:G:H2'	1:a:164:G:C8	2.55	0.42
1:a:824:C:O2'	1:a:826:U:O4	2.38	0.42
24:w:124:PHE:CD1	24:w:125:PRO:HD2	2.55	0.42
24:w:222:GLY:HA2	24:w:244:ARG:HH21	1.84	0.42
1:a:581:U:H2'	1:a:582:U:H6	1.84	0.42
1:a:1123:G:C2	1:a:1124:G:H1'	2.55	0.42
1:a:1279:U:H1'	1:a:1280:C:H5	1.85	0.42
1:a:1510:G:H2'	1:a:1511:C:C6	2.55	0.42
14:n:15:MET:HE2	14:n:15:MET:HA	2.01	0.42
22:c:5:THR:HG23	22:c:7:LYS:H	1.85	0.42
23:x:59:ALA:O	23:x:63:LYS:HG2	2.20	0.42
1:a:487:C:H3'	1:a:488:C:H2'	2.02	0.41
1:a:1084:G:OP1	22:c:110:ARG:NH1	2.50	0.41
1:a:1208:A:H5''	14:n:115:ARG:HH21	1.85	0.41
13:m:49:LEU:HD23	13:m:49:LEU:HA	1.85	0.41
23:x:60:ARG:O	23:x:64:ARG:HB2	2.19	0.41
1:a:523:U:H2'	1:a:524:C:C6	2.56	0.41
1:a:1156:G:H2'	1:a:1157:A:H8	1.85	0.41
5:e:186:ILE:HG22	5:e:188:VAL:HB	2.01	0.41
10:j:72:LEU:HB3	10:j:78:VAL:HG12	2.02	0.41
22:c:186:ILE:HG13	22:c:186:ILE:O	2.20	0.41
1:a:560:C:H2'	1:a:561:G:O4'	2.20	0.41
1:a:955:G:H2'	1:a:956:A:C2	2.56	0.41
1:a:1005:G:C6	1:a:1006:U:O4	2.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1329:G:O2'	1:a:1356:G:O6	2.31	0.41
4:d:130:ARG:O	4:d:134:ARG:HG2	2.20	0.41
11:k:5:LYS:HE3	11:k:7:ARG:HH12	1.85	0.41
20:t:36:ARG:NH1	20:t:52:HIS:O	2.53	0.41
22:c:101:LEU:HB3	22:c:179:LEU:HD12	2.02	0.41
22:c:151:ILE:HG23	22:c:154:MET:HG3	2.03	0.41
1:a:309:G:H2'	1:a:310:G:H8	1.85	0.41
1:a:452:A:H2	17:q:47:SER:HB3	1.85	0.41
1:a:535:C:H2'	1:a:536:C:H6	1.86	0.41
1:a:1253:U:H2'	1:a:1254:G:O4'	2.20	0.41
17:q:17:GLN:HE21	17:q:41:HIS:CD2	2.39	0.41
1:a:771:G:O6	1:a:772:A:N6	2.53	0.41
1:a:831:A:C6	1:a:832:U:C4	3.09	0.41
1:a:1498:C:P	3:v:22:ARG:HH21	2.42	0.41
4:d:188:GLU:HB3	4:d:195:ARG:HD2	2.02	0.41
5:e:105:THR:HG23	5:e:108:MET:H	1.85	0.41
17:q:21:ILE:HG22	17:q:36:VAL:HG22	2.03	0.41
20:t:17:LYS:HB2	20:t:17:LYS:HE3	1.78	0.41
22:c:15:HIS:HB3	22:c:43:LEU:HD21	2.02	0.41
1:a:215:U:H4'	1:a:216:U:H5'	2.01	0.41
1:a:588:A:C2	1:a:589:A:H1'	2.55	0.41
2:b:31:LYS:HD2	2:b:31:LYS:C	2.46	0.41
4:d:37:ALA:O	4:d:40:LYS:HG2	2.21	0.41
15:o:47:MET:HE3	15:o:47:MET:HB3	1.87	0.41
16:p:70:VAL:HG12	16:p:78:TYR:HB2	2.02	0.41
1:a:437:U:H2'	1:a:438:U:O4'	2.21	0.41
1:a:589:A:C5	1:a:590:A:C8	3.08	0.41
1:a:689:A:H2'	1:a:690:G:H8	1.85	0.41
1:a:1028:G:OP1	15:o:4:LYS:N	2.38	0.41
1:a:1409:A:H2'	1:a:1410:C:C6	2.54	0.41
3:v:27:GLN:O	3:v:30:LYS:HG2	2.21	0.41
4:d:83:ALA:O	4:d:86:ILE:HG13	2.20	0.41
4:d:120:ALA:HB1	4:d:189:ALA:HB2	2.03	0.41
11:k:22:ALA:O	11:k:26:VAL:HG12	2.20	0.41
1:a:448:A:OP2	1:a:465:G:N2	2.36	0.41
1:a:788:C:H2'	1:a:789:G:O4'	2.20	0.41
1:a:1422:G:H2'	1:a:1423:U:C6	2.56	0.41
7:g:23:LEU:HD23	7:g:23:LEU:HA	1.91	0.41
14:n:69:ASP:OD1	14:n:70:LEU:N	2.53	0.41
1:a:148:A:C5	1:a:149:A:C8	3.09	0.41
1:a:149:A:C5	1:a:150:G:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:231:G:H22	1:a:262:G:N2	2.18	0.41
1:a:397:A:H5'	1:a:398:C:OP1	2.20	0.41
1:a:731:U:H2'	1:a:732:G:O4'	2.20	0.41
1:a:821:C:C5	1:a:822:U:C2	3.09	0.41
1:a:960:A:C8	1:a:961:C:H5	2.38	0.41
1:a:1105:U:C2	1:a:1107:G:C8	3.09	0.41
1:a:1221:U:C5	8:h:116:MET:HG2	2.56	0.41
2:b:171:ALA:HB3	2:b:185:LEU:HD11	2.02	0.41
4:d:24:ALA:HB1	4:d:27:GLN:HG2	2.03	0.41
4:d:68:HIS:CD2	4:d:103:LEU:HB2	2.56	0.41
6:f:36:TYR:CE1	6:f:66:ASP:HB3	2.56	0.41
9:i:54:ALA:HB2	9:i:59:SER:OG	2.21	0.41
12:l:23:LYS:HB3	12:l:23:LYS:HE2	1.88	0.41
12:l:33:LYS:HE2	12:l:35:THR:HG22	2.02	0.41
14:n:15:MET:HE1	14:n:45:THR:HA	2.03	0.41
22:c:27:MET:O	22:c:31:ILE:HG12	2.21	0.41
22:c:208:ARG:HE	22:c:208:ARG:HB2	1.58	0.41
24:w:141:MET:HE3	24:w:255:PRO:HA	2.02	0.41
24:w:174:LEU:HD23	24:w:175:TYR:N	2.36	0.41
1:a:1089:C:C2	1:a:1090:A:C8	3.09	0.41
2:b:50:GLU:OE2	2:b:62:VAL:HB	2.21	0.41
5:e:138:ILE:HB	5:e:175:ILE:HB	2.03	0.41
6:f:101:LEU:HD11	6:f:145:VAL:HG22	2.03	0.41
10:j:108:ILE:HD11	10:j:115:ARG:HB2	2.02	0.41
19:s:56:ASN:OD1	19:s:56:ASN:N	2.54	0.41
22:c:45:GLN:O	22:c:49:TYR:CD2	2.73	0.41
1:a:500:A:N1	1:a:516:C:H1'	2.36	0.40
1:a:743:G:H2'	1:a:744:C:C6	2.55	0.40
1:a:1517:C:H1'	24:w:111:TRP:HB3	2.02	0.40
2:b:116:ILE:HG22	2:b:120:LYS:HE3	2.03	0.40
15:o:4:LYS:HB2	15:o:4:LYS:HE3	1.87	0.40
15:o:46:GLU:OE1	15:o:47:MET:HG2	2.21	0.40
17:q:69:PRO:O	17:q:73:LEU:HG	2.22	0.40
22:c:69:PHE:HA	22:c:162:TRP:HD1	1.86	0.40
22:c:94:GLN:OE1	22:c:146:ARG:NE	2.47	0.40
1:a:535:C:H2'	1:a:536:C:C6	2.56	0.40
1:a:849:G:H2'	1:a:850:C:C6	2.56	0.40
1:a:1185:A:H2'	1:a:1186:U:O4'	2.21	0.40
1:a:1329:G:H5''	10:j:129:ARG:HG2	2.03	0.40
1:a:1385:C:H2'	1:a:1386:C:O4'	2.21	0.40
1:a:1411:A:H2'	1:a:1412:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:16:GLU:HA	7:g:19:VAL:HG23	2.03	0.40
10:j:32:ARG:HG2	10:j:94:GLY:HA2	2.03	0.40
10:j:139:LYS:H	10:j:139:LYS:HG2	1.67	0.40
14:n:80:ARG:O	14:n:84:ILE:HG23	2.22	0.40
24:w:165:GLU:HB3	24:w:168:THR:OG1	2.22	0.40
8:h:86:GLN:HB2	8:h:148:ASN:HD22	1.86	0.40
8:h:113:GLU:HB3	8:h:118:GLU:HG2	2.02	0.40
13:m:83:ARG:HB3	13:m:98:ILE:HD11	2.04	0.40
1:a:120:G:H2'	1:a:121:U:C6	2.56	0.40
1:a:212:G:H2'	1:a:213:C:H6	1.86	0.40
1:a:313:A:H2'	1:a:314:C:C6	2.56	0.40
1:a:335:C:H2'	1:a:336:A:C8	2.56	0.40
1:a:503:A:C2	13:m:88:LYS:HB3	2.56	0.40
1:a:619:G:C2	1:a:620:A:C8	3.10	0.40
1:a:1000:U:H2'	1:a:1001:G:C8	2.56	0.40
1:a:1473:A:H2'	1:a:1474:C:C6	2.57	0.40
1:a:1486:A:H2	1:a:1489:G:N1	2.20	0.40
4:d:95:GLY:C	4:d:96:LYS:HG3	2.46	0.40
5:e:99:ARG:HA	5:e:99:ARG:HD3	1.74	0.40
17:q:14:ARG:HD3	17:q:14:ARG:HA	1.91	0.40
21:u:39:VAL:HG13	21:u:86:LEU:HD13	2.02	0.40
22:c:131:LYS:HB2	22:c:131:LYS:HE2	1.87	0.40
22:c:153:ASP:OD1	22:c:153:ASP:N	2.54	0.40
1:a:106:C:H2'	1:a:107:G:O4'	2.22	0.40
1:a:377:G:OP1	17:q:4:LYS:HD3	2.22	0.40
1:a:737:U:H2'	1:a:738:G:O4'	2.22	0.40
1:a:917:A:H2'	1:a:918:C:O4'	2.21	0.40
4:d:6:ASN:OD1	4:d:6:ASN:C	2.63	0.40
4:d:100:LEU:HD21	4:d:102:ILE:HB	2.03	0.40
7:g:43:TRP:O	7:g:60:TYR:HB2	2.21	0.40
10:j:31:ARG:HG2	10:j:36:VAL:HG22	2.04	0.40
13:m:7:LEU:O	13:m:11:GLY:N	2.54	0.40
22:c:97:LEU:N	22:c:100:MET:HE3	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	148/479 (31%)	143 (97%)	5 (3%)	0	100	100
3	v	29/33 (88%)	29 (100%)	0	0	100	100
4	d	205/275 (74%)	195 (95%)	10 (5%)	0	100	100
5	e	198/201 (98%)	189 (96%)	9 (4%)	0	100	100
6	f	166/214 (78%)	162 (98%)	4 (2%)	0	100	100
7	g	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
8	h	151/156 (97%)	148 (98%)	3 (2%)	0	100	100
9	i	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
10	j	124/150 (83%)	116 (94%)	8 (6%)	0	100	100
11	k	74/101 (73%)	71 (96%)	3 (4%)	0	100	100
12	l	113/138 (82%)	107 (95%)	6 (5%)	0	100	100
13	m	119/124 (96%)	112 (94%)	7 (6%)	0	100	100
14	n	114/124 (92%)	110 (96%)	4 (4%)	0	100	100
15	o	58/61 (95%)	52 (90%)	6 (10%)	0	100	100
16	p	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
17	q	111/156 (71%)	105 (95%)	6 (5%)	0	100	100
18	r	92/98 (94%)	89 (97%)	3 (3%)	0	100	100
19	s	63/84 (75%)	61 (97%)	2 (3%)	0	100	100
20	t	80/93 (86%)	77 (96%)	3 (4%)	0	100	100
21	u	83/86 (96%)	83 (100%)	0	0	100	100
22	c	226/277 (82%)	211 (93%)	15 (7%)	0	100	100
23	x	9/11 (82%)	9 (100%)	0	0	100	100
24	w	253/264 (96%)	240 (95%)	13 (5%)	0	100	100
All	All	2725/3442 (79%)	2610 (96%)	115 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	132/407 (32%)	131 (99%)	1 (1%)	73	77
3	v	29/31 (94%)	29 (100%)	0	100	100
4	d	170/212 (80%)	167 (98%)	3 (2%)	51	69
5	e	175/176 (99%)	173 (99%)	2 (1%)	65	74
6	f	123/147 (84%)	123 (100%)	0	100	100
7	g	85/85 (100%)	85 (100%)	0	100	100
8	h	129/132 (98%)	129 (100%)	0	100	100
9	i	107/108 (99%)	107 (100%)	0	100	100
10	j	102/125 (82%)	102 (100%)	0	100	100
11	k	73/90 (81%)	73 (100%)	0	100	100
12	l	89/105 (85%)	89 (100%)	0	100	100
13	m	102/105 (97%)	102 (100%)	0	100	100
14	n	99/104 (95%)	98 (99%)	1 (1%)	68	75
15	o	49/50 (98%)	49 (100%)	0	100	100
16	p	76/77 (99%)	76 (100%)	0	100	100
17	q	92/118 (78%)	92 (100%)	0	100	100
18	r	80/83 (96%)	79 (99%)	1 (1%)	61	72
19	s	55/72 (76%)	55 (100%)	0	100	100
20	t	73/84 (87%)	73 (100%)	0	100	100
21	u	69/70 (99%)	68 (99%)	1 (1%)	59	71
22	c	191/218 (88%)	191 (100%)	0	100	100
23	x	8/8 (100%)	8 (100%)	0	100	100
24	w	208/215 (97%)	207 (100%)	1 (0%)	81	80
All	All	2316/2822 (82%)	2306 (100%)	10 (0%)	81	81

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	b	32	TYR
4	d	66	ASP
4	d	125	ASN
4	d	142	ARG
5	e	108	MET
5	e	139	ASP
14	n	56	LEU
18	r	94	LEU
21	u	45	ASP
24	w	131	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
5	e	151	GLN
5	e	173	GLN
6	f	146	HIS
9	i	63	GLN
10	j	47	GLN
12	l	86	HIS
13	m	105	GLN
15	o	57	GLN
17	q	107	ASN
21	u	7	GLN
22	c	19	GLN
22	c	112	GLN
24	w	161	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1514/1528 (99%)	266 (17%)	0

All (266) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	12	A
1	a	13	G
1	a	36	A

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Mol	Chain	Res	Type
1	a	43	G
1	a	51	C
1	a	52	U
1	a	55	A
1	a	58	C
1	a	59	A
1	a	82	U
1	a	86	G
1	a	87	G
1	a	93	C
1	a	116	A
1	a	117	C
1	a	126	G
1	a	128	U
1	a	146	A
1	a	160	C
1	a	192	G
1	a	193	C
1	a	200	U
1	a	210	A
1	a	211	A
1	a	216	U
1	a	217	U
1	a	220	G
1	a	231	G
1	a	243	A
1	a	245	C
1	a	247	G
1	a	251	G
1	a	252	U
1	a	266	G
1	a	267	C
1	a	279	A
1	a	280	C
1	a	281	G
1	a	289	G
1	a	329	A
1	a	330	C
1	a	332	G
1	a	344	A
1	a	345	C
1	a	347	G

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Mol	Chain	Res	Type
1	a	351	G
1	a	352	C
1	a	353	A
1	a	354	G
1	a	367	U
1	a	372	C
1	a	373	A
1	a	390	U
1	a	392	C
1	a	397	A
1	a	398	C
1	a	406	G
1	a	414	A
1	a	421	U
1	a	422	C
1	a	423	G
1	a	424	G
1	a	426	U
1	a	428	G
1	a	429	U
1	a	430	A
1	a	433	C
1	a	434	C
1	a	452	A
1	a	453	G
1	a	456	C
1	a	457	A
1	a	458	A
1	a	459	G
1	a	461	G
1	a	465	G
1	a	466	U
1	a	475	A
1	a	476	A
1	a	477	G
1	a	478	A
1	a	485	G
1	a	486	G
1	a	491	C
1	a	497	G
1	a	498	C
1	a	499	C

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Mol	Chain	Res	Type
1	a	501	G
1	a	507	G
1	a	509	G
1	a	511	U
1	a	512	A
1	a	513	A
1	a	515	A
1	a	519	A
1	a	520	G
1	a	527	A
1	a	539	A
1	a	542	U
1	a	544	C
1	a	552	A
1	a	553	A
1	a	556	A
1	a	557	G
1	a	576	C
1	a	612	U
1	a	613	G
1	a	629	G
1	a	633	A
1	a	645	G
1	a	666	U
1	a	668	G
1	a	683	G
1	a	701	G
1	a	702	G
1	a	703	U
1	a	711	G
1	a	729	A
1	a	735	G
1	a	761	A
1	a	765	G
1	a	772	A
1	a	773	U
1	a	774	A
1	a	789	G
1	a	793	U
1	a	794	A
1	a	795	A
1	a	796	A

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Mol	Chain	Res	Type
1	a	797	C
1	a	808	A
1	a	818	U
1	a	821	C
1	a	822	U
1	a	823	U
1	a	824	C
1	a	826	U
1	a	827	U
1	a	828	G
1	a	829	G
1	a	841	U
1	a	871	A
1	a	884	G
1	a	896	A
1	a	908	G
1	a	909	G
1	a	913	C
1	a	914	C
1	a	916	C
1	a	917	A
1	a	942	U
1	a	943	U
1	a	950	A
1	a	951	A
1	a	953	G
1	a	956	A
1	a	957	A
1	a	958	G
1	a	959	A
1	a	973	U
1	a	974	U
1	a	975	G
1	a	976	A
1	a	981	C
1	a	982	A
1	a	988	C
1	a	990	C
1	a	1007	U
1	a	1008	C
1	a	1011	U
1	a	1012	U

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Mol	Chain	Res	Type
1	a	1013	G
1	a	1014	U
1	a	1017	C
1	a	1020	G
1	a	1021	U
1	a	1022	G
1	a	1025	C
1	a	1033	G
1	a	1034	C
1	a	1036	U
1	a	1045	U
1	a	1074	G
1	a	1075	U
1	a	1081	A
1	a	1088	G
1	a	1104	G
1	a	1108	C
1	a	1110	A
1	a	1115	G
1	a	1116	U
1	a	1117	U
1	a	1118	A
1	a	1119	U
1	a	1120	G
1	a	1138	A
1	a	1140	U
1	a	1147	G
1	a	1148	U
1	a	1149	C
1	a	1150	A
1	a	1151	A
1	a	1162	G
1	a	1164	U
1	a	1165	G
1	a	1171	G
1	a	1176	C
1	a	1177	A
1	a	1178	A
1	a	1181	C
1	a	1182	A
1	a	1193	U
1	a	1194	A

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Mol	Chain	Res	Type
1	a	1195	U
1	a	1217	A
1	a	1231	A
1	a	1237	C
1	a	1238	U
1	a	1241	G
1	a	1249	G
1	a	1251	G
1	a	1261	A
1	a	1266	U
1	a	1267	U
1	a	1268	C
1	a	1283	U
1	a	1284	U
1	a	1285	C
1	a	1287	G
1	a	1302	C
1	a	1328	A
1	a	1329	G
1	a	1342	A
1	a	1343	G
1	a	1344	C
1	a	1345	A
1	a	1346	A
1	a	1347	C
1	a	1353	G
1	a	1357	A
1	a	1364	U
1	a	1381	A
1	a	1405	G
1	a	1424	G
1	a	1426	C
1	a	1429	A
1	a	1433	C
1	a	1434	U
1	a	1435	U
1	a	1436	G
1	a	1438	G
1	a	1440	A
1	a	1463	G
1	a	1476	A
1	a	1481	G

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Mol	Chain	Res	Type
1	a	1483	A
1	a	1488	G
1	a	1490	U
1	a	1501	G
1	a	1503	A
1	a	1504	G
1	a	1513	G
1	a	1514	G
1	a	1517	C
1	a	1518	A
1	a	1522	C

There are no RNA pucker outliers to report.

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

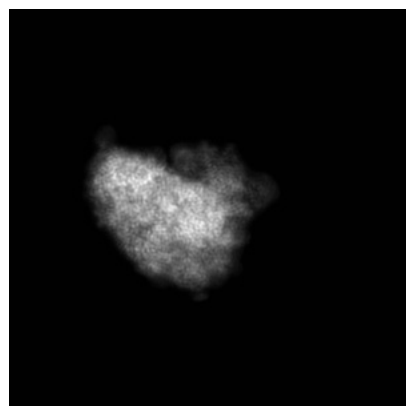
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37561. These allow visual inspection of the internal detail of the map and identification of artifacts.

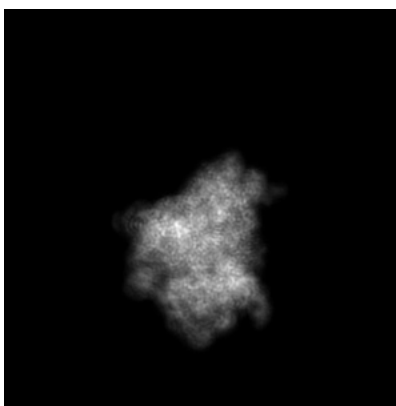
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

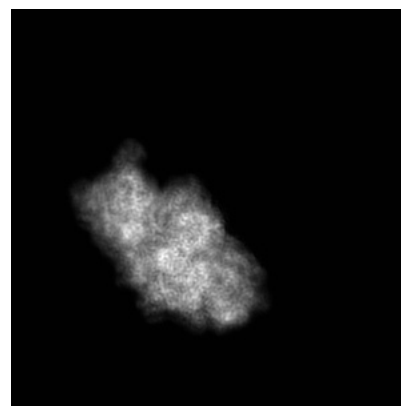
6.1.1 Primary map



X

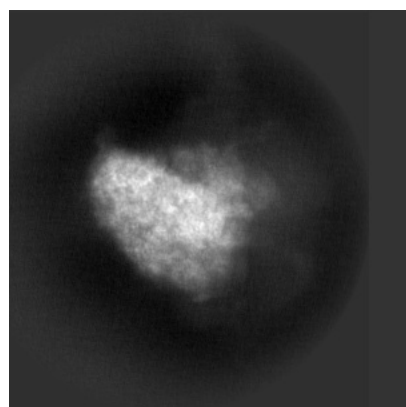


Y

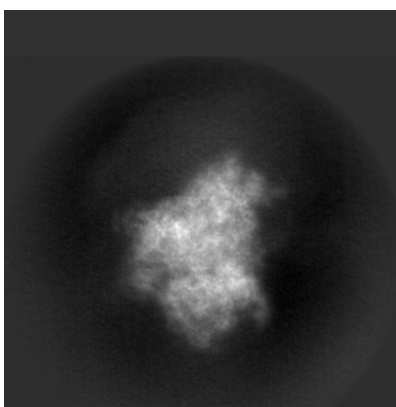


Z

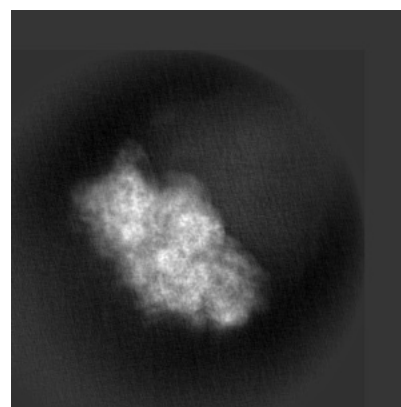
6.1.2 Raw map



X



Y

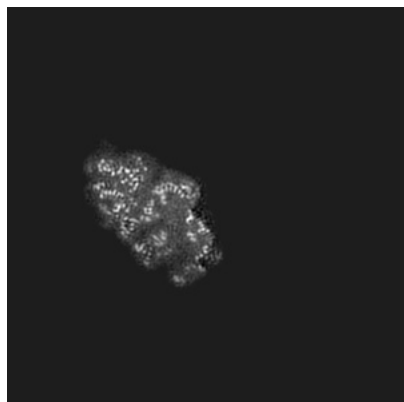


Z

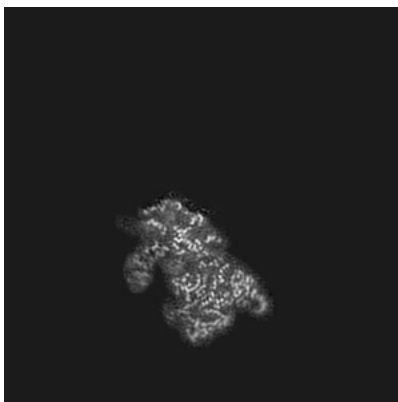
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

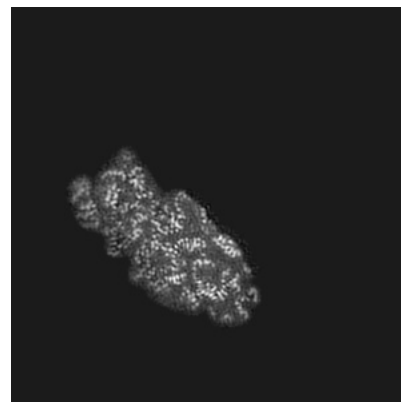
6.2.1 Primary map



X Index: 190

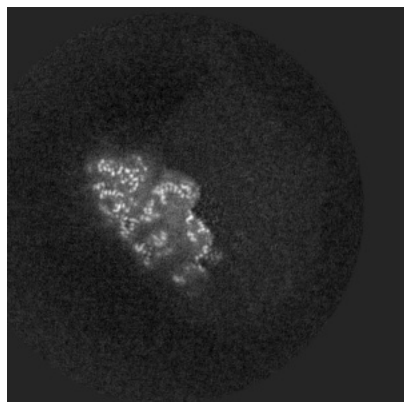


Y Index: 190

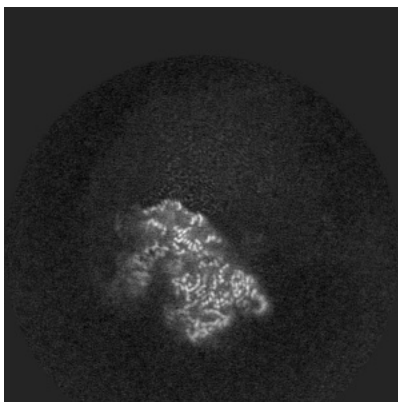


Z Index: 190

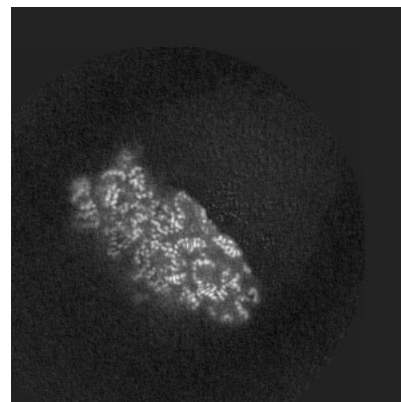
6.2.2 Raw map



X Index: 190



Y Index: 190

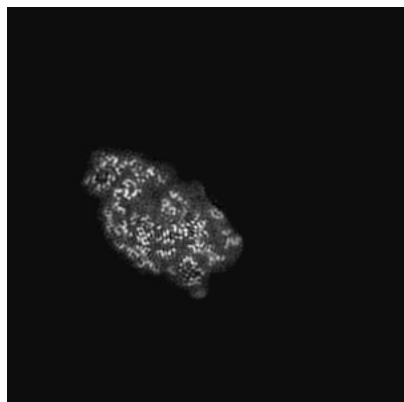


Z Index: 190

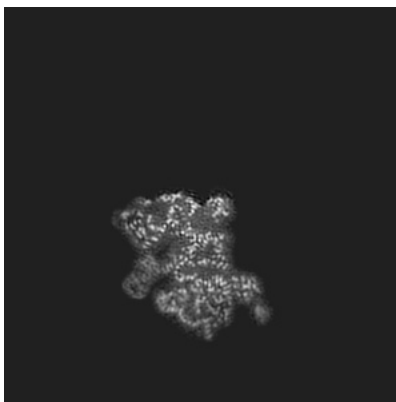
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

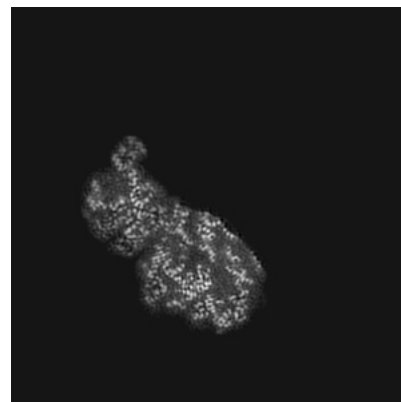
6.3.1 Primary map



X Index: 171

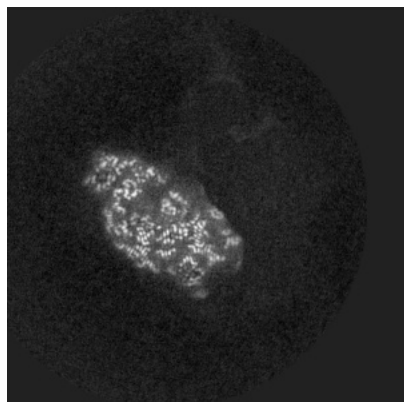


Y Index: 174

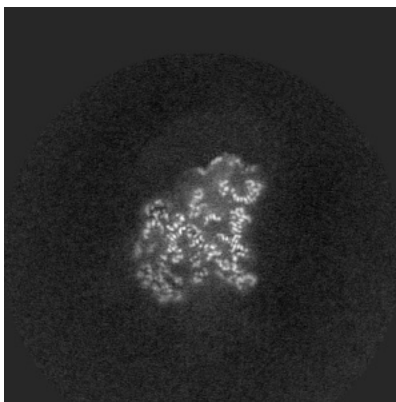


Z Index: 204

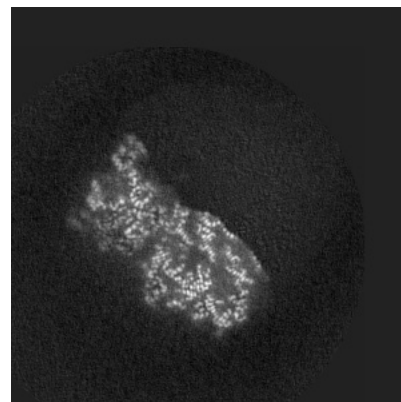
6.3.2 Raw map



X Index: 171



Y Index: 133

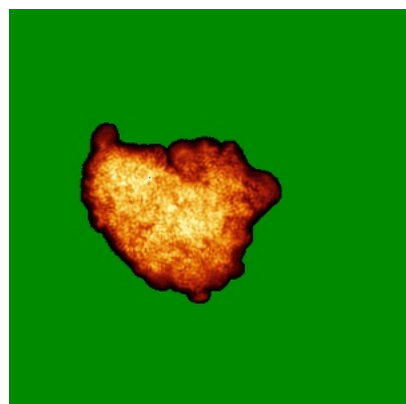


Z Index: 204

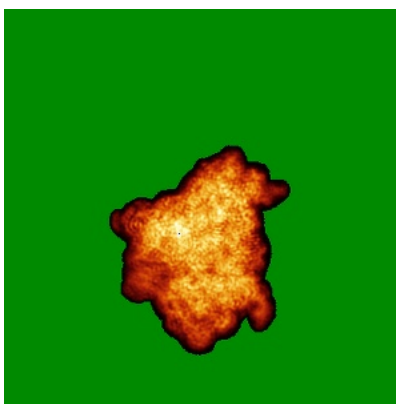
The images above show the largest variance slices of the map in three orthogonal directions.

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

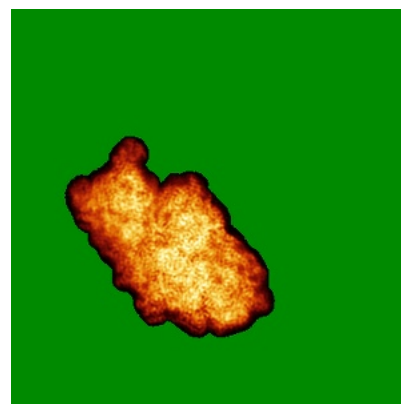
6.4.1 Primary map



X

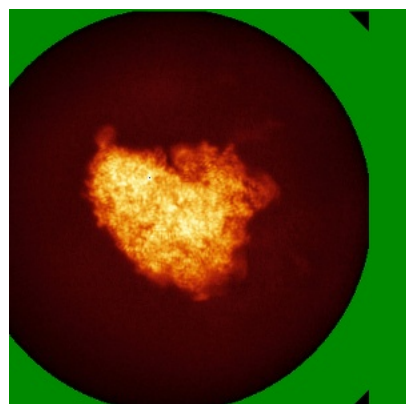


Y

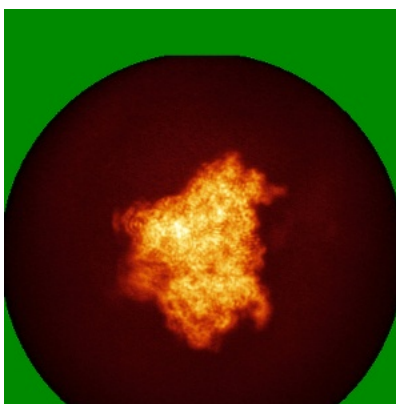


Z

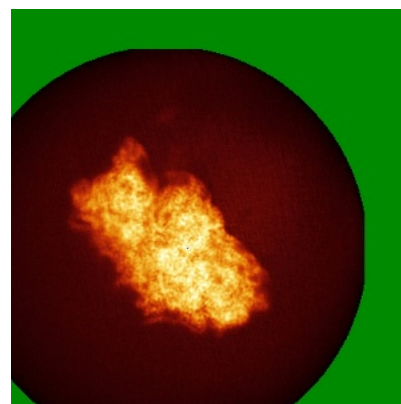
6.4.2 Raw map



X



Y

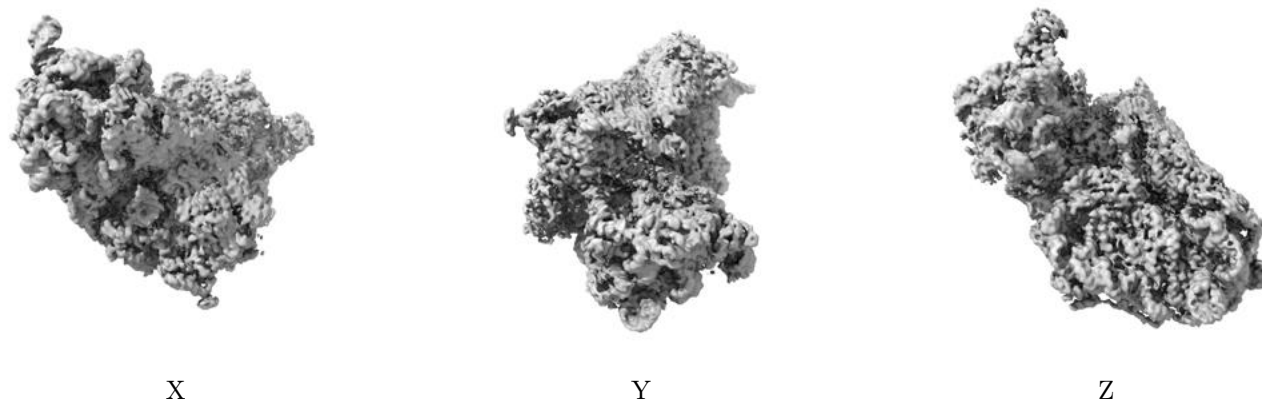


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

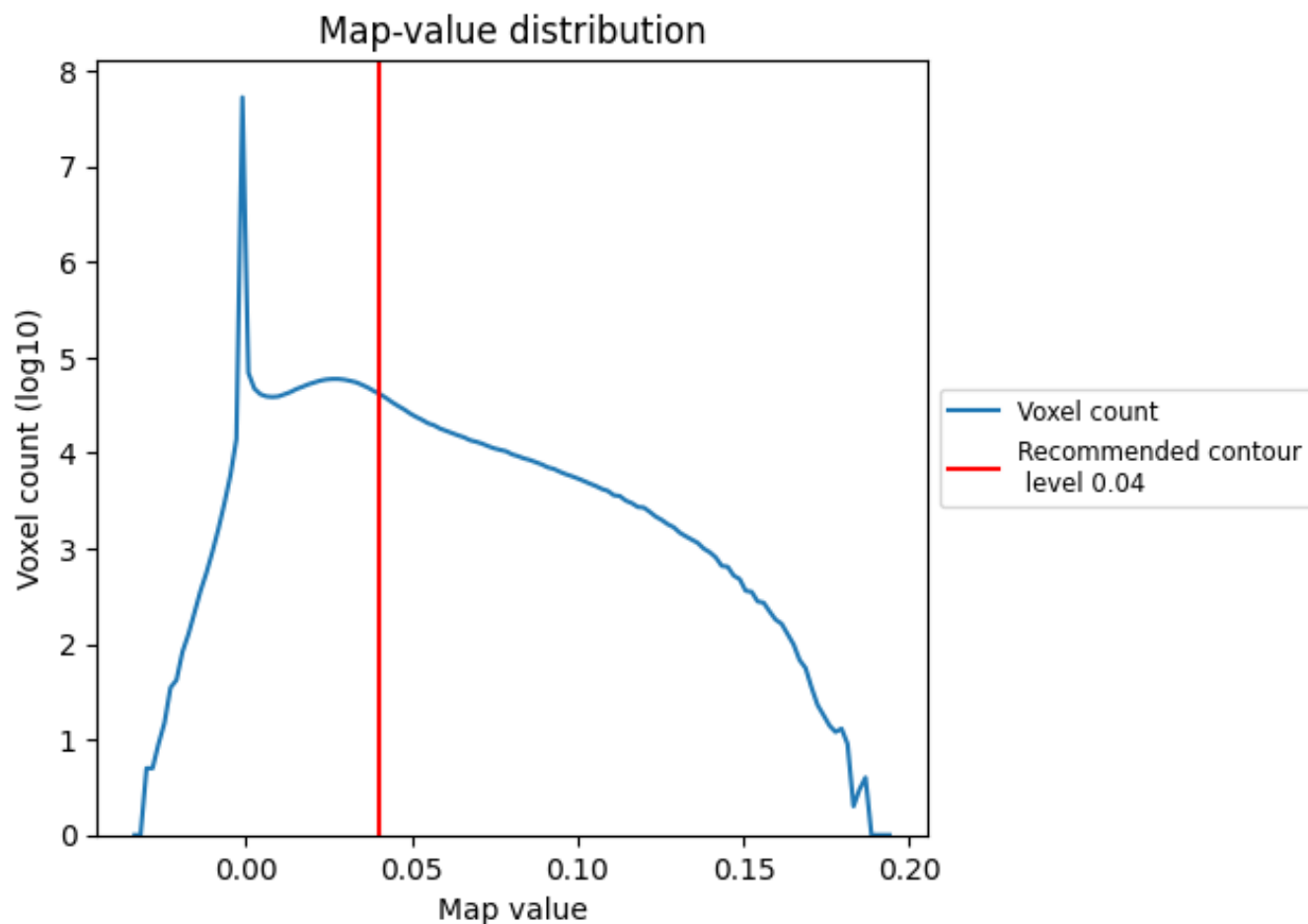
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

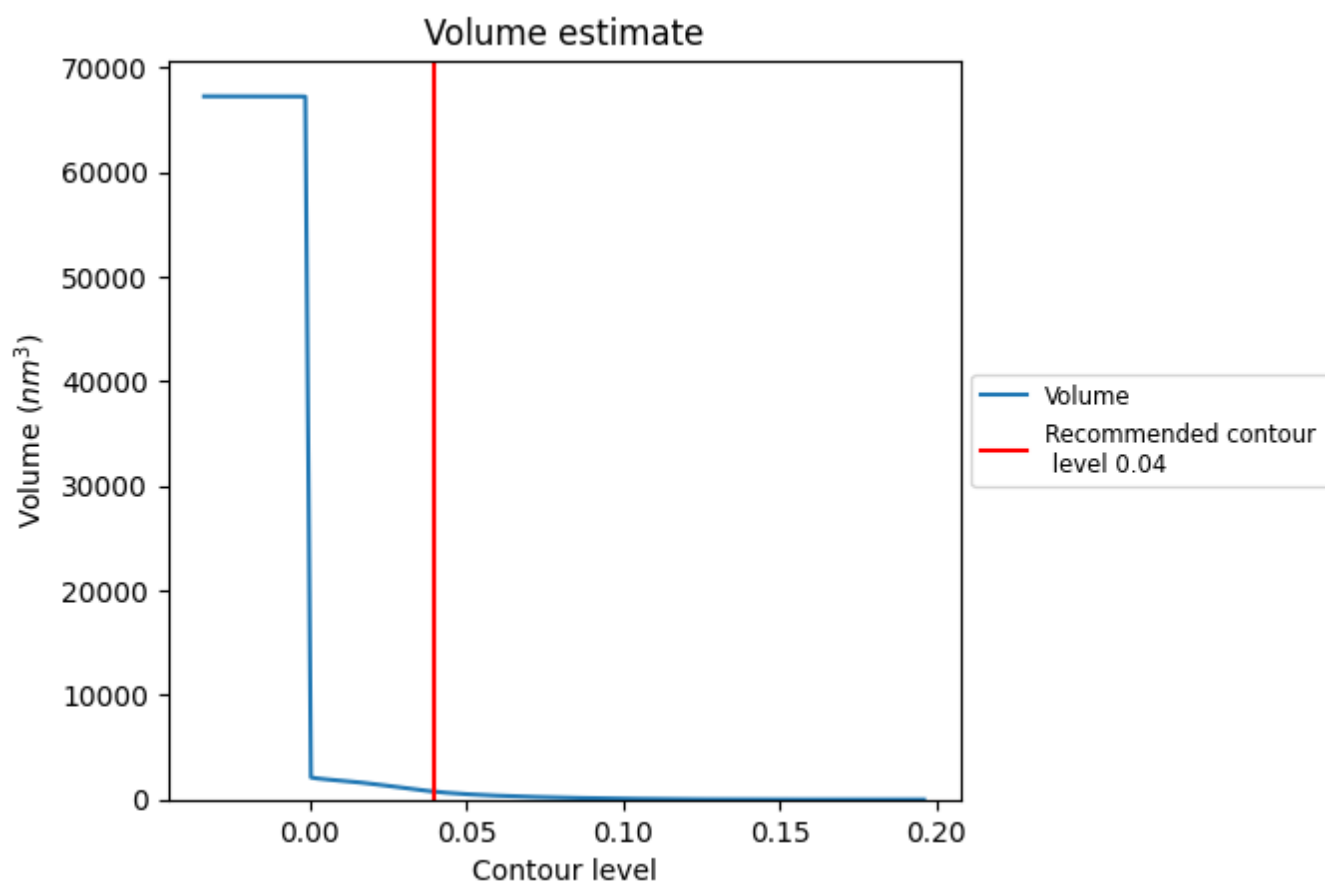
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

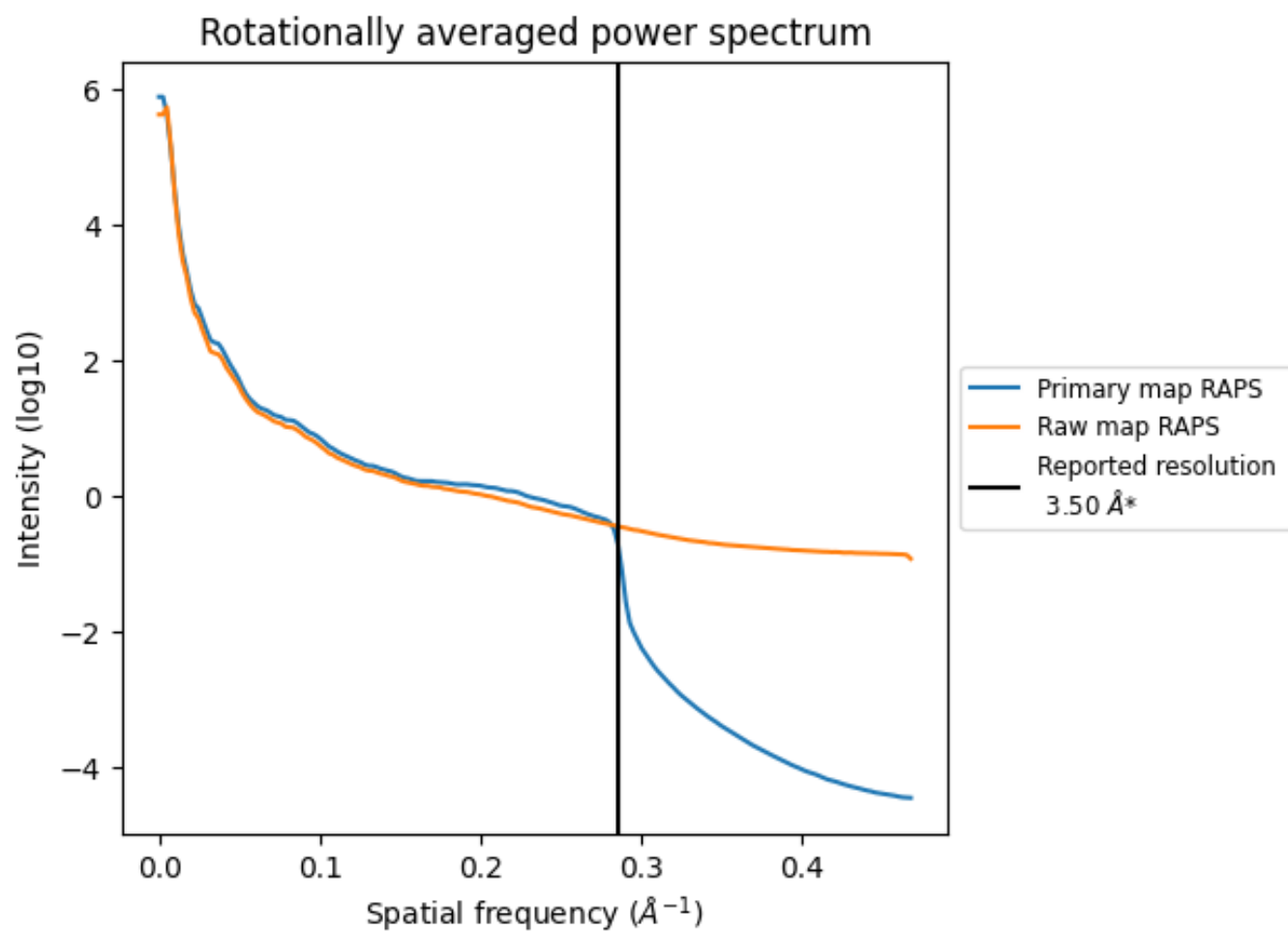
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 753 nm^3 ; this corresponds to an approximate mass of 681 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 ⓘ

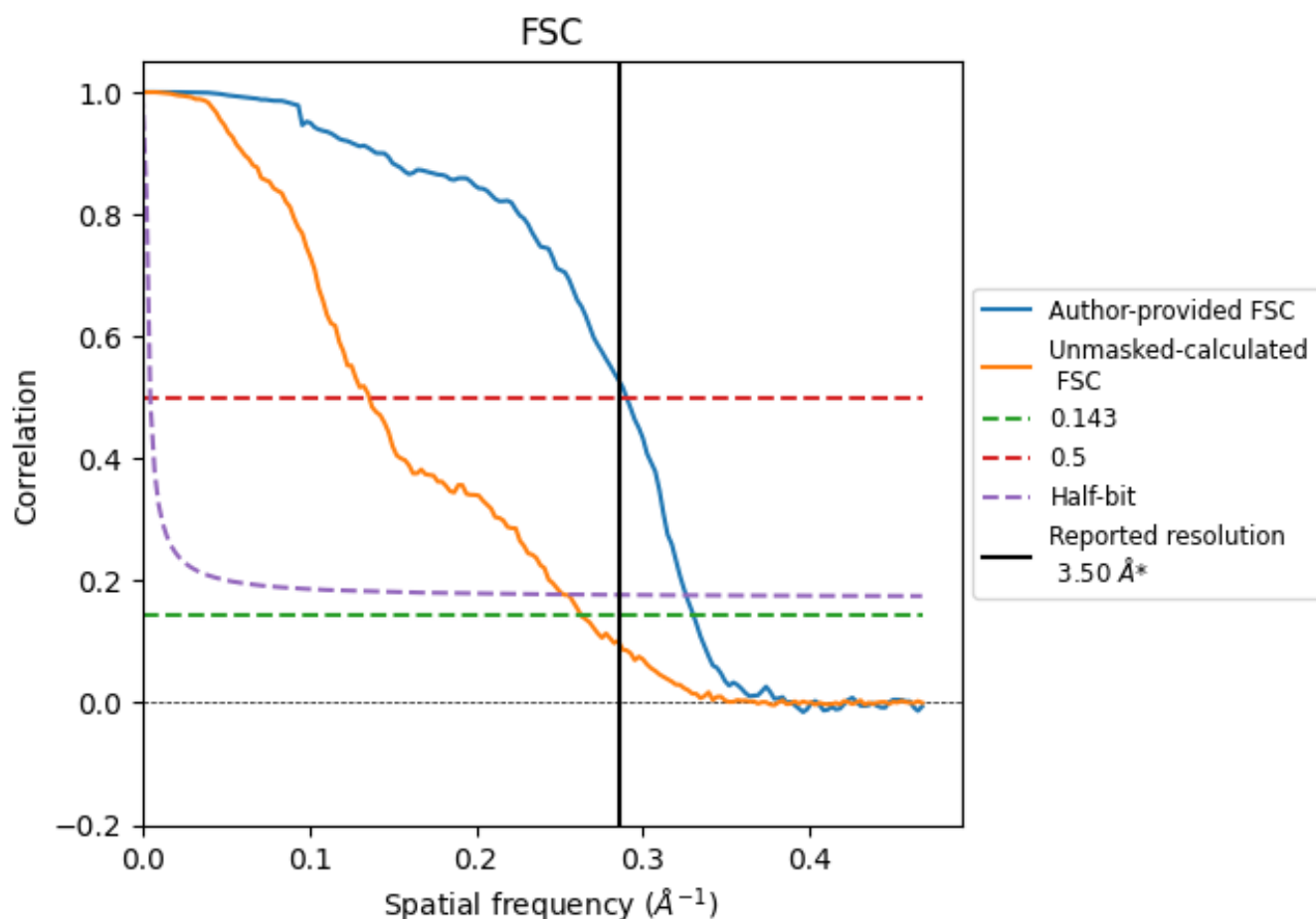


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

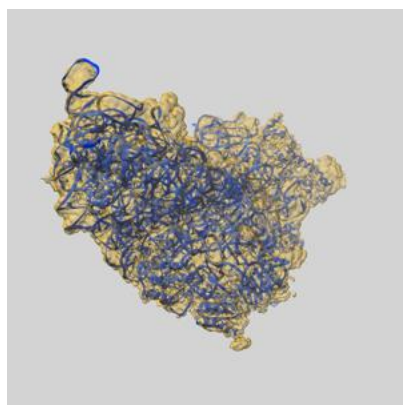
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	3.50
Author-provided FSC curve	3.03	3.45	3.07	-
Unmasked-calculated*	3.80	7.35	3.96	-

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

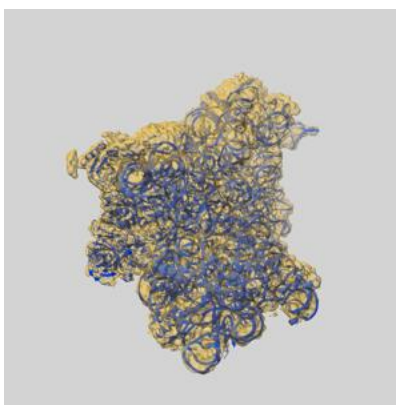
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37561 and PDB model 8WI9. Per-residue inclusion information can be found in section [3](#) on page [8](#).

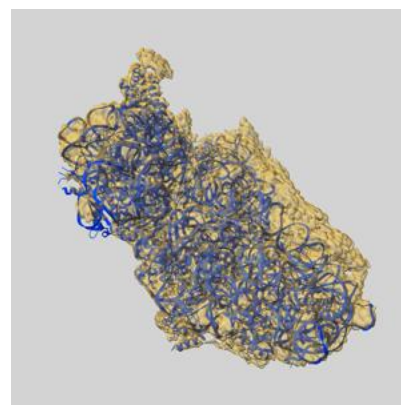
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



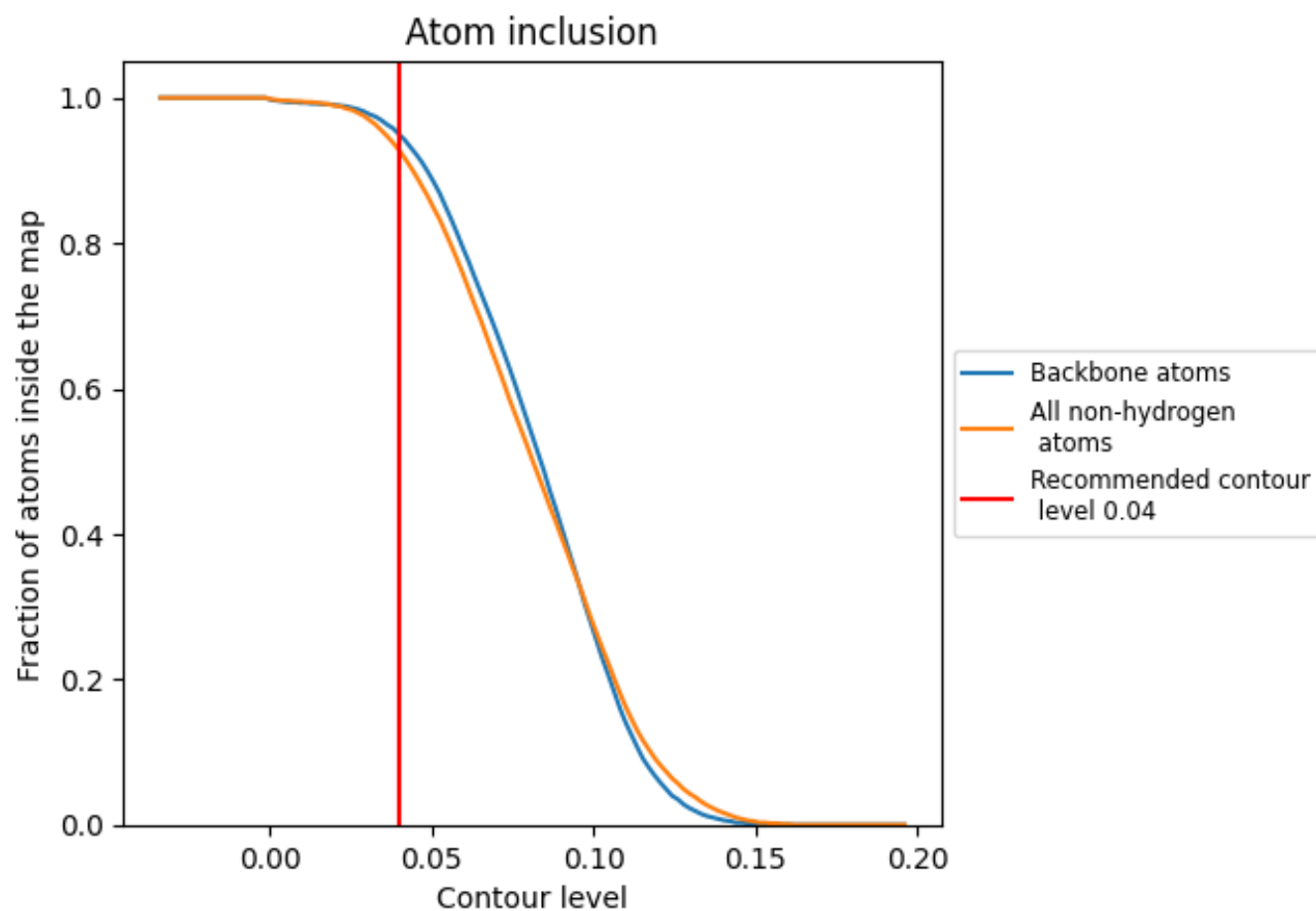
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion ⓘ



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9280	 0.4770
a	 0.9830	 0.4880
b	 0.4490	 0.2600
c	 0.8170	 0.4180
d	 0.5850	 0.3930
e	 0.9080	 0.4940
f	 0.9170	 0.5110
g	 0.9000	 0.4860
h	 0.9090	 0.4780
i	 0.9610	 0.5240
j	 0.8870	 0.4630
k	 0.6900	 0.4280
l	 0.9510	 0.5100
m	 0.9610	 0.5300
n	 0.9360	 0.4660
o	 0.8750	 0.4840
p	 0.9450	 0.5040
q	 0.9040	 0.5030
r	 0.9590	 0.5180
s	 0.9290	 0.4890
t	 0.9020	 0.4800
u	 0.9580	 0.5090
v	 0.9920	 0.5000
w	 0.7770	 0.4190
x	 0.7700	 0.3980

