



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 05:32 AM UTC

PDB ID : 5X8R / pdb_00005x8r
EMDB ID : EMD-6710
Title : Structure of the 30S small subunit of chloroplast ribosome from spinach
Authors : Ahmed, T.; Shi, J.; Bhushan, S.
Deposited on : 2017-03-03
Resolution : 3.70 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:

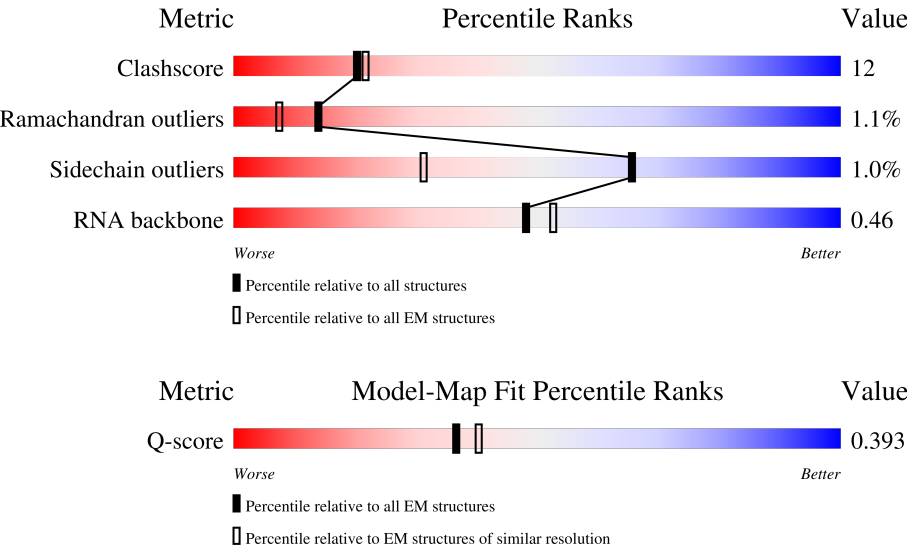
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	b	236	63% 67% 26% . .
2	c	218	13% 70% 27% . .
3	e	253	6% 43% 23% . 32%

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Mol	Chain	Length	Quality of chain
4	f	146	
5	g	155	
6	h	134	
7	i	157	
8	j	122	
9	k	138	
10	l	123	
11	m	126	
12	o	90	
13	p	88	
14	q	108	
15	r	101	
16	s	92	
17	t	108	
18	u	137	
19	y	236	
20	a	1491	
21	w	121	
22	d	201	
23	v	198	
24	n	100	
25	x	47	
26	8	370	

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 55412 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 30S ribosomal protein S2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	227	Total	C	N	O	S	0	0
			1787	1127	326	321	13		

- Molecule 2 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	213	Total	C	N	O	S	0	0
			1719	1099	310	304	6		

- Molecule 3 is a protein called 30S ribosomal protein S5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	e	171	Total	C	N	O	S	0	0
			1292	806	250	230	6		

- Molecule 4 is a protein called 30S ribosomal protein S6 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	f	111	Total	C	N	O	S	0	0
			886	566	145	171	4		

- Molecule 5 is a protein called 30S ribosomal protein S7, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	g	149	Total	C	N	O	S	0	0
			1161	723	231	204	3		

- Molecule 6 is a protein called 30S ribosomal protein S8, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	h	134	Total	C	N	O	S	0	0
			1088	684	211	187	6		

- Molecule 7 is a protein called 30S ribosomal protein S9, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	i	133	Total	C	N	O	S	0	0
			1020	650	191	178	1		

- Molecule 8 is a protein called protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	j	98	Total	C	N	O	S	0	0
			796	512	142	137	5		

- Molecule 9 is a protein called 30S ribosomal protein S11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	k	118	Total	C	N	O	S	0	0
			887	549	182	151	5		

- Molecule 10 is a protein called 30S ribosomal protein S12, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	l	123	Total	C	N	O	S	0	0
			967	604	198	162	3		

- Molecule 11 is a protein called 30S ribosomal protein S13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	m	110	Total	C	N	O	S	0	0
			898	559	183	153	3		

- Molecule 12 is a protein called 30S ribosomal protein S15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	o	62	Total	C	N	O	S	0	0
			525	339	100	85	1		

- Molecule 13 is a protein called 30S ribosomal protein S16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	p	80	Total	C	N	O	S	0	0
			664	425	123	114	2		

- Molecule 14 is a protein called protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	q	78	Total	C	N	O	S	0	0
			635	399	124	108	4		

- Molecule 15 is a protein called 30S ribosomal protein S18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	r	64	Total	C	N	O	S	0	0
			518	326	101	90	1		

- Molecule 16 is a protein called 30S ribosomal protein S19 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	s	78	Total	C	N	O	S	0	0
			627	403	118	104	2		

- Molecule 17 is a protein called protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	t	105	Total	C	N	O	S	0	0
			832	514	169	148	1		

- Molecule 18 is a protein called protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	u	44	Total	C	N	O	S	0	0
			393	238	87	66	2		

- Molecule 19 is a protein called protein plastid pY.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	y	108	Total	C	N	O	S	0	0
			845	521	164	159	1		

- Molecule 20 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	a	1480	Total	C	N	O	P	0	0
			31777	14168	5863	10266	1480		

- Molecule 21 is a protein called protein cS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	w	84	Total	C	N	O	S	0	0
			689	454	115	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	199	Total	C	N	O	S	0	0
			1633	1032	319	278	4		

- Molecule 23 is a protein called protein cS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	v	190	Total	C	N	O	S	0	0
			1464	908	255	298	3		

- Molecule 24 is a protein called 30S ribosomal protein S14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	n	99	Total	C	N	O	S	0	0
			819	507	174	135	3		

- Molecule 25 is a protein called protein bTHXc.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	x	37	Total	C	N	O	0	0
			289	179	65	45		

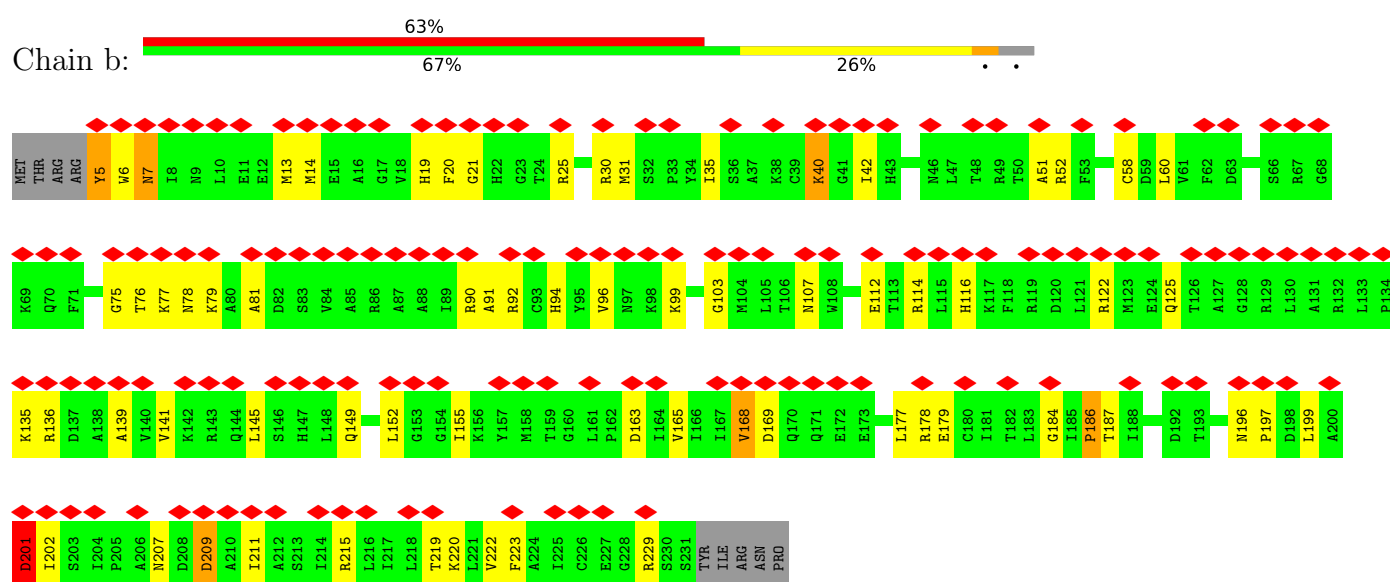
- Molecule 26 is a protein called 30S ribosomal protein S1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	8	154	Total	C	N	O	S	0	0
			1201	744	222	227	8		

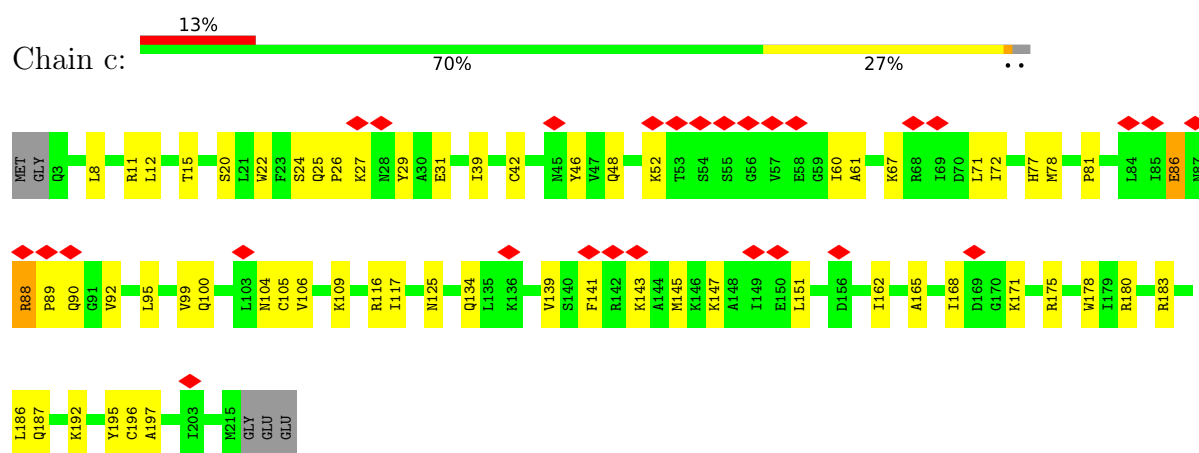
3 Residue-property plots

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: 30S ribosomal protein S2, chloroplastic

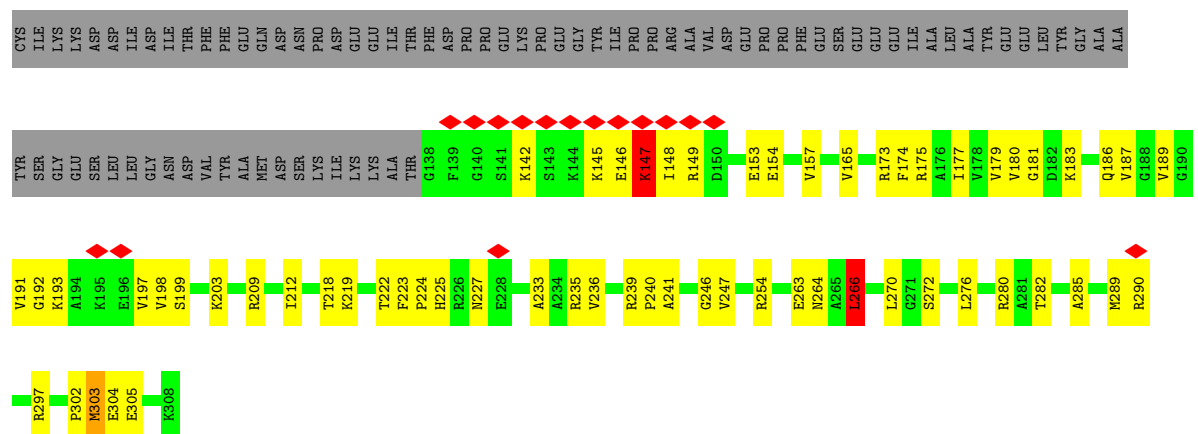


- Molecule 2: 30S ribosomal protein S3, chloroplastic

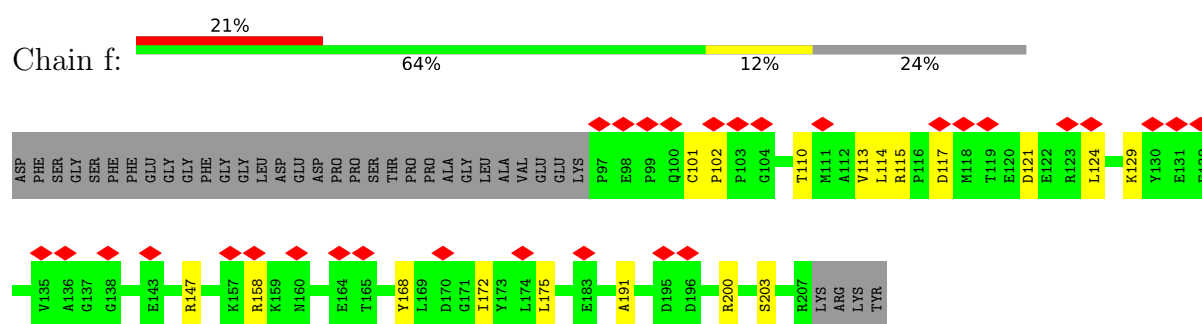


- Molecule 3: 30S ribosomal protein S5, chloroplastic

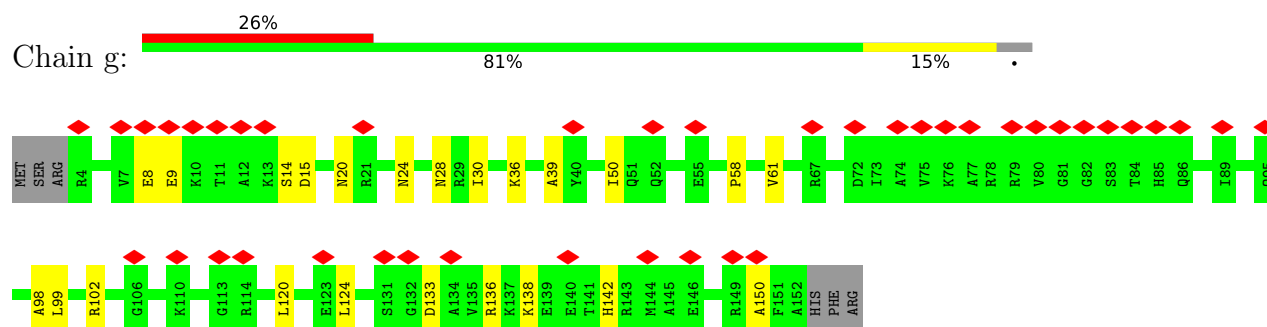




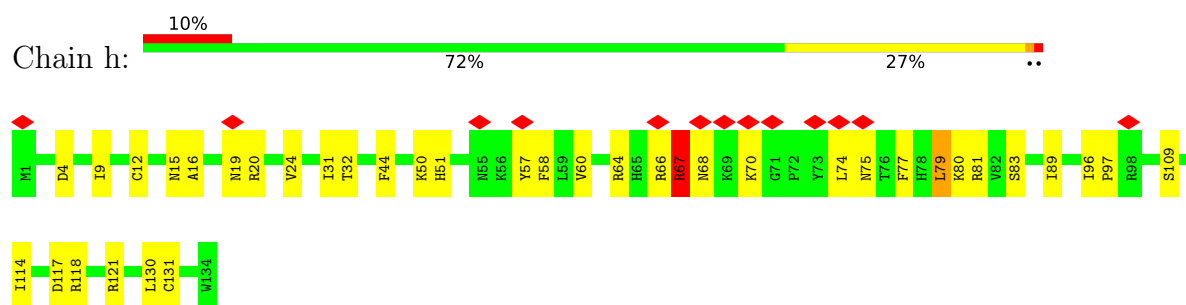
- Molecule 4: 30S ribosomal protein S6 alpha, chloroplastic



- Molecule 5: 30S ribosomal protein S7, chloroplastic

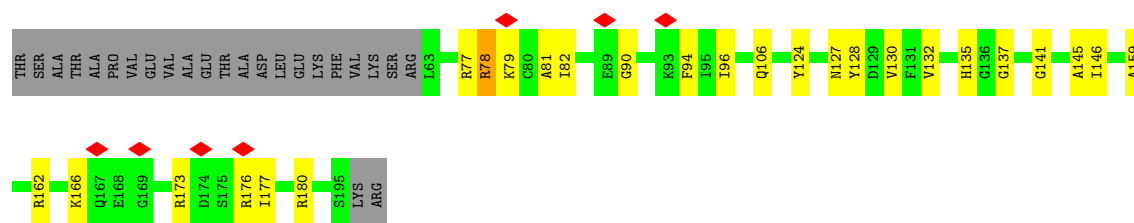


- Molecule 6: 30S ribosomal protein S8, chloroplastic

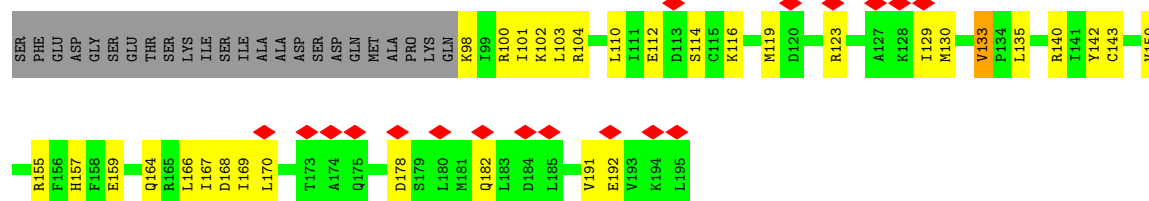


- Molecule 7: 30S ribosomal protein S9, chloroplastic

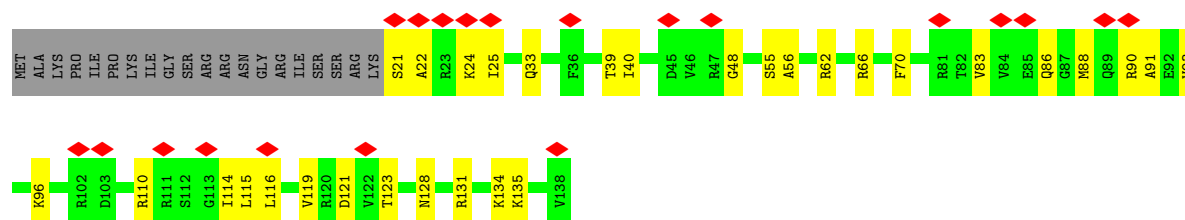




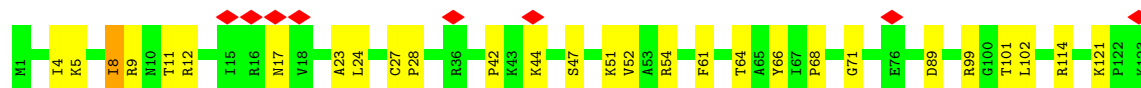
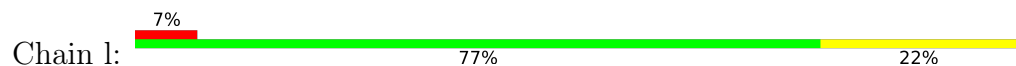
• Molecule 8: protein S10



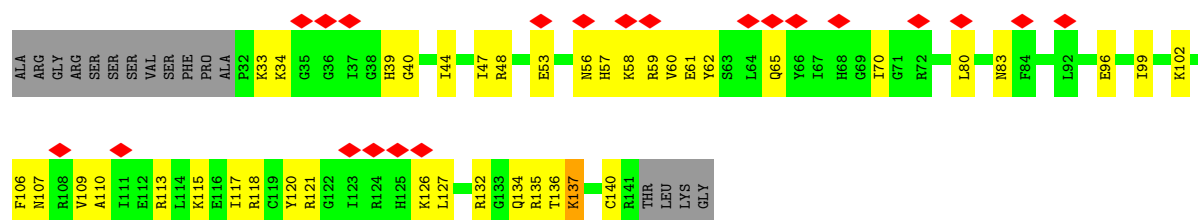
• Molecule 9: 30S ribosomal protein S11, chloroplastic



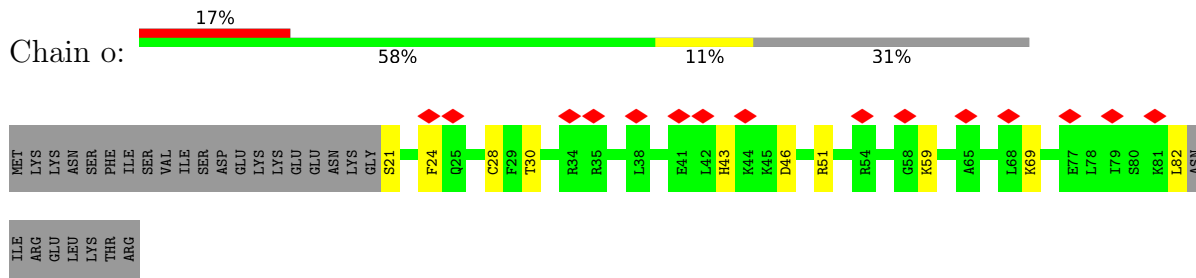
• Molecule 10: 30S ribosomal protein S12, chloroplastic



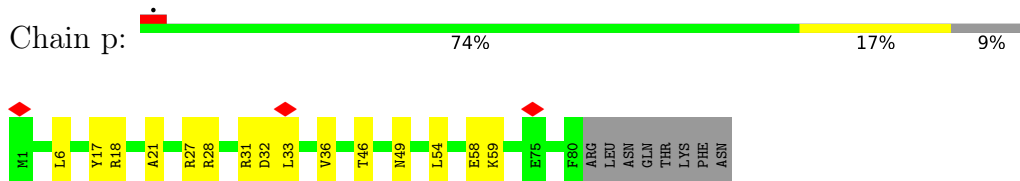
• Molecule 11: 30S ribosomal protein S13, chloroplastic



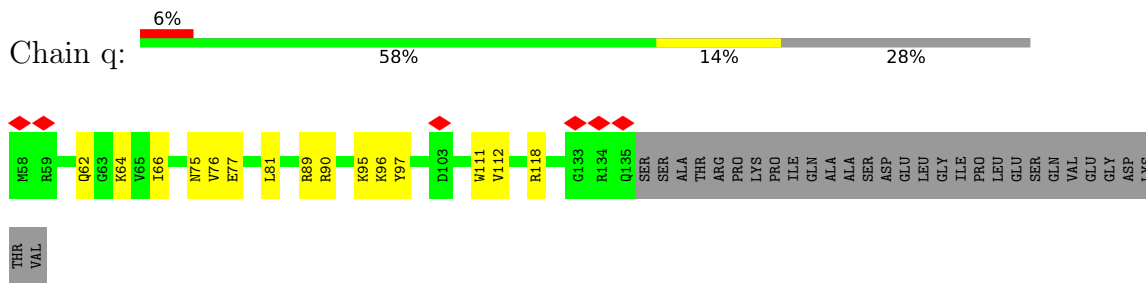
• Molecule 12: 30S ribosomal protein S15, chloroplastic



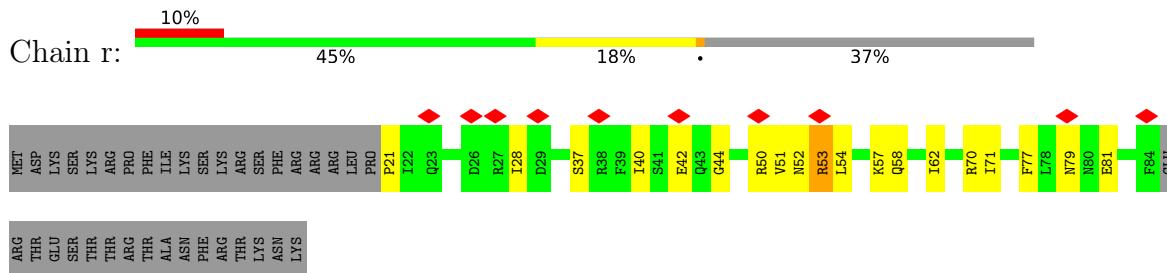
- Molecule 13: 30S ribosomal protein S16, chloroplastic



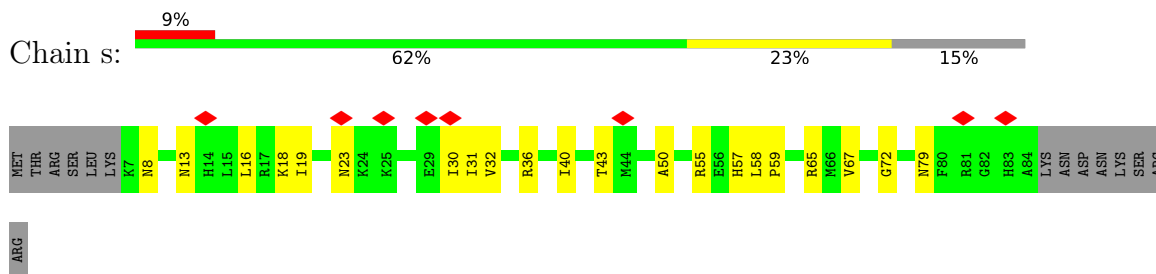
- Molecule 14: protein S17



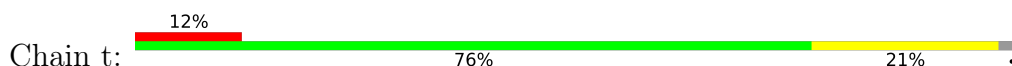
- Molecule 15: 30S ribosomal protein S18, chloroplastic

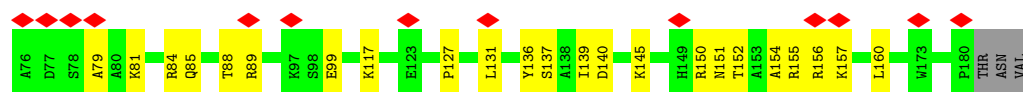


- Molecule 16: 30S ribosomal protein S19 alpha, chloroplastic

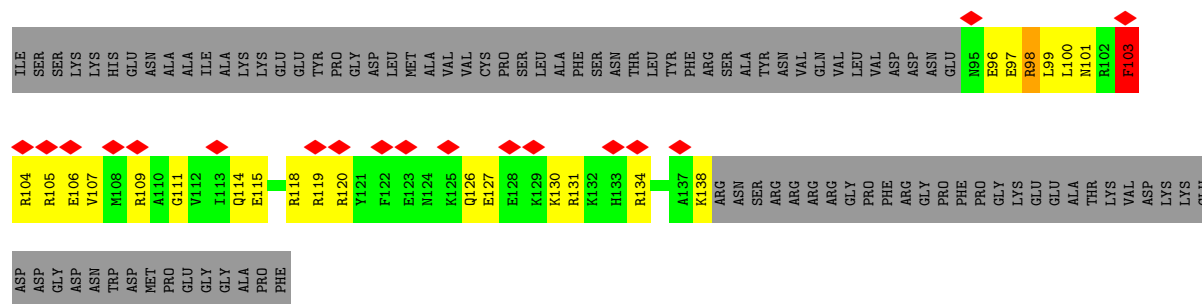


- Molecule 17: protein S20

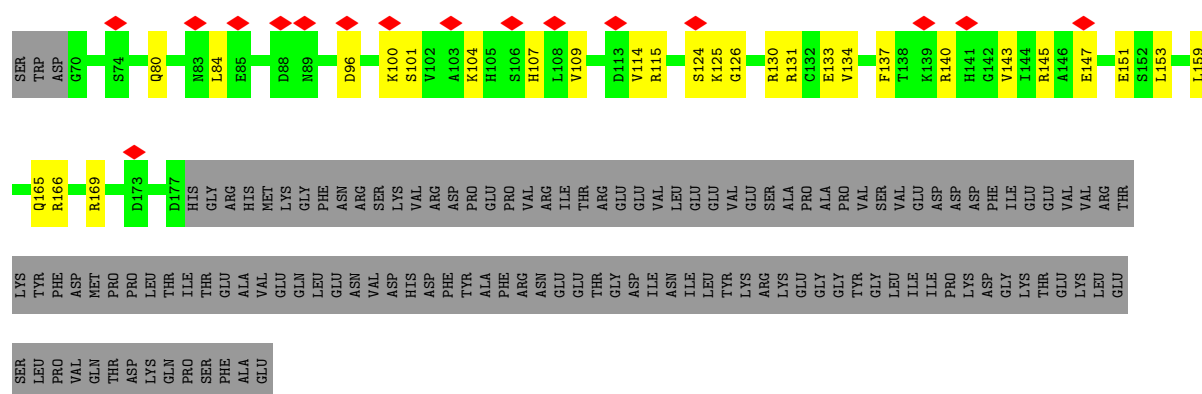
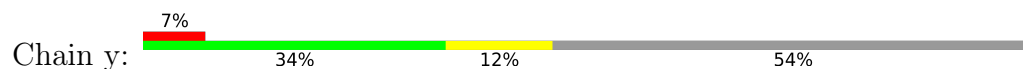




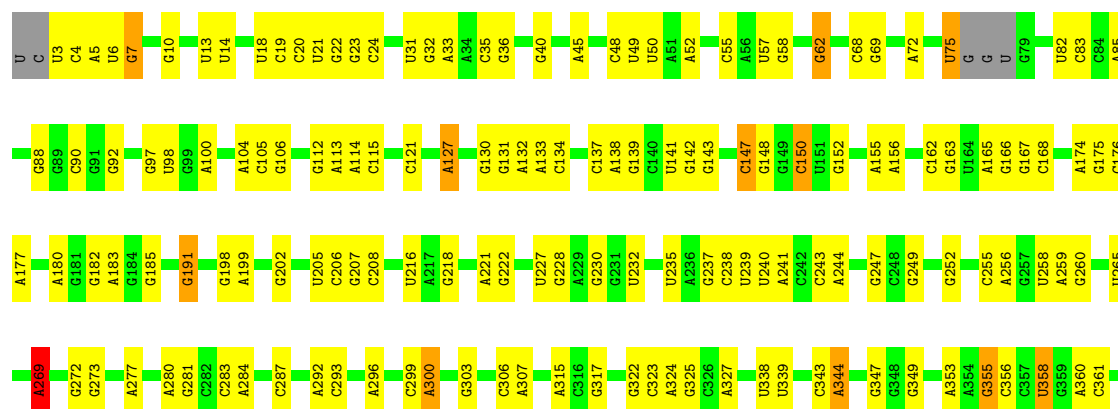
• Molecule 18: protein S21

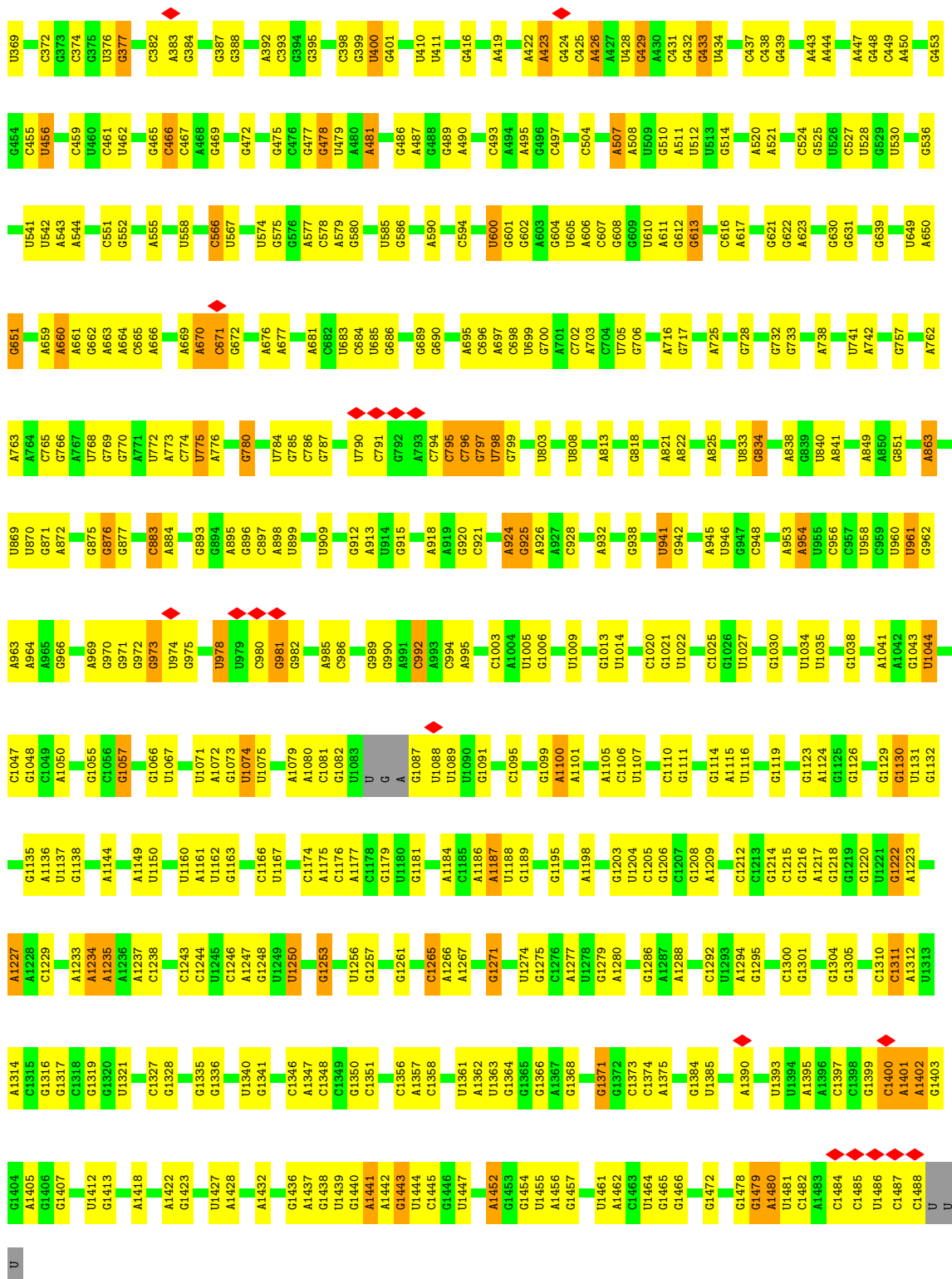


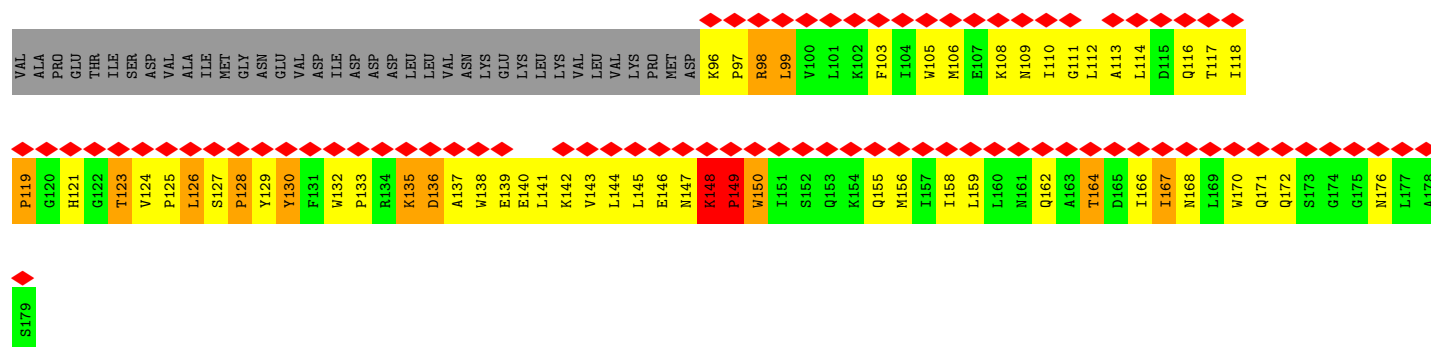
• Molecule 19: protein plastid pY



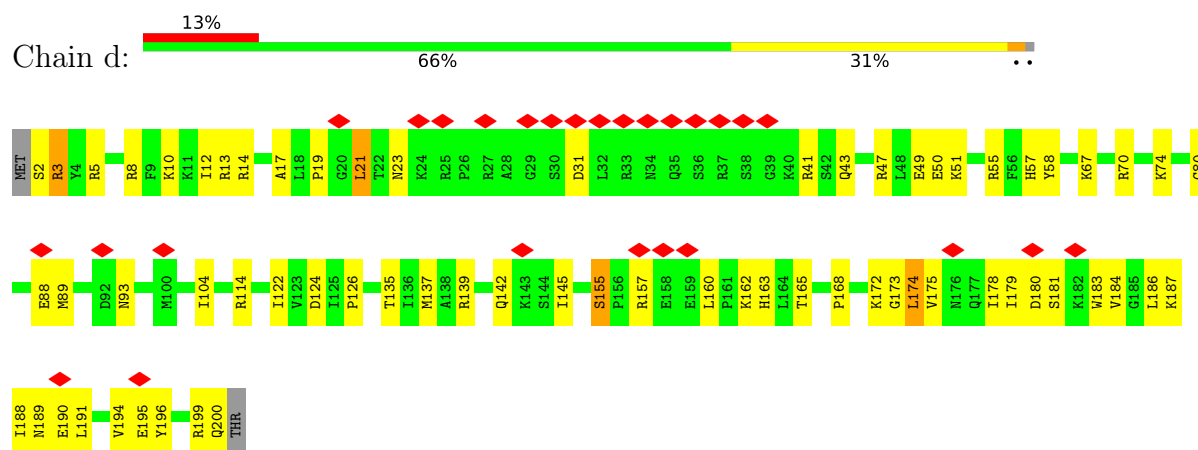
• Molecule 20: 16S rRNA



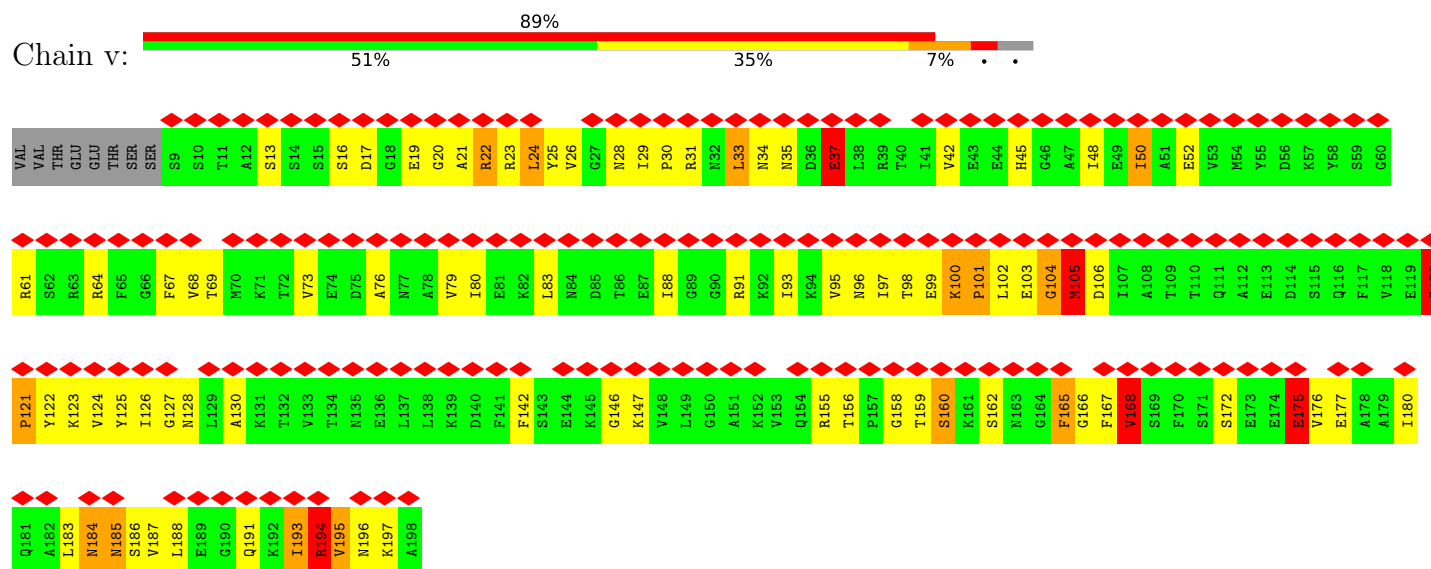




- Molecule 22: 30S ribosomal protein S4, chloroplastic



- Molecule 23: protein cS22



- Molecule 24: 30S ribosomal protein S14, chloroplastic



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81305	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3700	Depositor
Magnification	133333	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.316	Depositor
Minimum map value	-0.172	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	403.19998, 403.19998, 403.19998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.05, 1.05, 1.05	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	b	0.74	8/1819 (0.4%)	0.92	8/2458 (0.3%)
2	c	0.45	0/1746	0.71	0/2348
3	e	0.59	1/1307 (0.1%)	0.82	5/1754 (0.3%)
4	f	0.37	0/904	0.71	1/1225 (0.1%)
5	g	0.32	0/1175	0.65	0/1574
6	h	0.87	6/1103 (0.5%)	1.18	6/1477 (0.4%)
7	i	0.40	0/1038	0.75	0/1397
8	j	0.45	0/813	0.72	0/1099
9	k	0.37	0/901	0.64	0/1214
10	l	0.60	0/983	0.85	1/1323 (0.1%)
11	m	0.44	0/909	0.81	0/1209
12	o	0.34	0/532	0.66	0/707
13	p	0.48	0/674	0.74	0/902
14	q	0.44	0/647	0.70	0/867
15	r	0.49	0/522	0.78	2/697 (0.3%)
16	s	0.36	0/642	0.74	0/866
17	t	0.46	0/842	0.80	0/1127
18	u	0.85	3/396 (0.8%)	0.96	2/518 (0.4%)
19	y	0.42	0/852	0.72	0/1139
20	a	0.52	0/35582	0.50	1/55510 (0.0%)
21	w	0.92	2/709 (0.3%)	1.39	14/965 (1.5%)
22	d	0.39	0/1661	0.84	2/2230 (0.1%)
23	v	1.19	13/1481 (0.9%)	1.40	14/1991 (0.7%)
24	n	0.36	0/835	0.75	1/1116 (0.1%)
25	x	0.55	0/296	0.89	0/390
26	8	0.94	0/1216	1.86	41/1631 (2.5%)
All	All	0.56	33/59585 (0.1%)	0.70	98/87734 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	b	0	2
2	c	0	3
3	e	0	1
4	f	0	1
5	g	0	1
7	i	0	2
8	j	0	1
10	l	0	3
11	m	0	2
18	u	0	1
21	w	0	7
22	d	0	2
23	v	0	15
26	8	0	17
All	All	0	58

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	h	67	ARG	CZ-NH2	-15.64	1.13	1.33
6	h	67	ARG	CB-CG	-13.10	1.13	1.52
23	v	142	PHE	CE1-CZ	-12.45	1.01	1.38
23	v	142	PHE	CE2-CZ	-11.74	1.03	1.38
1	b	7	ASN	CG-ND2	-11.62	1.08	1.33
23	v	142	PHE	CG-CD2	-11.40	1.15	1.38
23	v	194	ARG	CG-CD	-10.85	1.19	1.52
23	v	142	PHE	CG-CD1	-10.60	1.16	1.38
23	v	165	PHE	CE2-CZ	-9.90	1.08	1.38
23	v	168	VAL	CB-CG1	-9.03	1.22	1.52
1	b	209	ASP	CG-OD2	-8.71	1.08	1.25
23	v	195	VAL	CB-CG2	-8.44	1.24	1.52
6	h	67	ARG	CA-CB	-7.92	1.40	1.53
23	v	165	PHE	CG-CD2	-7.80	1.22	1.38
18	u	103	PHE	CD1-CE1	-7.64	1.15	1.38
21	w	149	PRO	CG-CD	-7.51	1.25	1.50
1	b	201	ASP	CB-CG	7.47	1.70	1.52
21	w	164	THR	CB-CG2	-6.88	1.29	1.52
18	u	103	PHE	CD2-CE2	-6.87	1.18	1.38
6	h	67	ARG	CZ-NH1	-6.76	1.23	1.32
18	u	103	PHE	CB-CG	-6.44	1.35	1.50
23	v	26	VAL	CB-CG1	-6.24	1.31	1.52
23	v	193	ILE	CB-CG2	-6.17	1.32	1.52
1	b	201	ASP	CG-OD1	-5.62	1.14	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	b	201	ASP	CG-OD2	5.58	1.35	1.25
3	e	303	MET	CB-CG	-5.57	1.35	1.52
23	v	142	PHE	CD2-CE2	5.53	1.55	1.38
1	b	186	PRO	CA-CB	-5.47	1.46	1.53
6	h	67	ARG	CD-NE	-5.44	1.38	1.46
23	v	142	PHE	CD1-CE1	5.35	1.54	1.38
6	h	67	ARG	CG-CD	-5.31	1.36	1.52
1	b	7	ASN	CG-OD1	-5.14	1.13	1.23
1	b	7	ASN	CB-CG	-5.09	1.39	1.52

All (98) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	h	67	ARG	NE-CZ-NH1	24.07	145.57	121.50
1	b	201	ASP	CA-CB-CG	14.19	126.79	112.60
6	h	67	ARG	NH1-CZ-NH2	-13.91	101.21	119.30
6	h	67	ARG	CD-NE-CZ	13.84	143.78	124.40
6	h	67	ARG	CB-CG-CD	13.80	143.04	111.30
26	8	72	MET	N-CA-C	-11.99	85.27	110.80
26	8	316	SER	CA-C-N	11.08	138.64	122.36
26	8	316	SER	C-N-CA	11.08	138.64	122.36
26	8	73	GLU	N-CA-C	-10.99	87.39	110.80
26	8	299	ASP	N-CA-C	-10.18	89.11	110.80
26	8	362	GLN	N-CA-C	10.02	122.28	111.36
1	b	201	ASP	N-CA-CB	9.44	123.14	110.59
26	8	360	ILE	N-CA-C	-9.09	90.42	109.34
26	8	368	ARG	CB-CG-CD	9.05	132.11	111.30
26	8	69	ASN	N-CA-C	8.61	127.73	114.64
23	v	160	SER	N-CA-C	8.24	123.45	112.25
26	8	367	ALA	CA-C-N	8.08	136.97	121.54
26	8	367	ALA	C-N-CA	8.08	136.97	121.54
1	b	201	ASP	CB-CG-OD2	8.04	136.90	118.40
1	b	201	ASP	N-CA-C	-7.77	104.33	113.88
26	8	303	VAL	N-CA-C	7.63	125.21	109.34
23	v	185	ASN	CB-CA-C	-7.50	102.40	109.83
26	8	73	GLU	CB-CA-C	7.49	125.33	110.42
6	h	67	ARG	NE-CZ-NH2	-7.31	112.62	119.20
23	v	142	PHE	CD1-CG-CD2	-7.26	107.71	118.60
21	w	133	PRO	CA-N-CD	-7.04	102.15	112.00
26	8	280	ILE	CB-CA-C	7.00	122.77	111.29
15	r	53	ARG	CA-CB-CG	-6.96	100.19	114.10
26	8	304	LEU	CA-CB-CG	6.83	140.21	116.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	r	21	PRO	N-CA-CB	6.77	110.44	103.00
1	b	201	ASP	OD1-CG-OD2	-6.72	106.77	122.90
23	v	96	ASN	N-CA-C	-6.71	99.63	109.63
21	w	124	VAL	N-CA-C	6.56	114.64	108.15
26	8	273	PRO	CA-C-N	6.50	133.96	121.54
26	8	273	PRO	C-N-CA	6.50	133.96	121.54
26	8	367	ALA	N-CA-CB	6.47	121.43	110.49
26	8	300	ILE	N-CA-C	-6.44	95.94	109.34
21	w	99	LEU	N-CA-C	6.27	119.41	109.81
21	w	148	LYS	CA-C-N	6.26	127.67	119.84
21	w	148	LYS	C-N-CA	6.26	127.67	119.84
21	w	149	PRO	N-CA-C	6.16	125.17	112.47
23	v	22	ARG	CA-C-N	6.14	129.84	121.05
23	v	22	ARG	C-N-CA	6.14	129.84	121.05
21	w	149	PRO	CB-CA-C	-6.13	101.45	111.56
18	u	98	ARG	CA-CB-CG	6.12	126.34	114.10
1	b	5	TYR	CA-C-N	6.11	133.21	121.54
1	b	5	TYR	C-N-CA	6.11	133.21	121.54
1	b	40	LYS	CD-CE-NZ	-6.10	92.39	111.90
26	8	330	LYS	N-CA-CB	6.10	120.79	110.49
26	8	65	GLU	CA-C-N	6.10	133.07	122.95
26	8	65	GLU	C-N-CA	6.10	133.07	122.95
26	8	73	GLU	CB-CG-CD	6.05	122.89	112.60
26	8	344	LEU	CB-CG-CD2	-6.04	92.59	110.70
6	h	67	ARG	N-CA-CB	-5.97	99.27	110.07
3	e	157	VAL	N-CA-C	-5.95	108.06	113.71
21	w	123	THR	CA-C-N	-5.92	116.74	123.25
21	w	123	THR	C-N-CA	-5.92	116.74	123.25
21	w	135	LYS	CA-C-N	5.89	129.12	120.82
21	w	135	LYS	C-N-CA	5.89	129.12	120.82
4	f	101	CYS	N-CA-C	5.88	122.81	109.81
23	v	99	GLU	CA-CB-CG	-5.87	102.36	114.10
22	d	3	ARG	CA-C-N	5.86	132.74	121.54
22	d	3	ARG	C-N-CA	5.86	132.74	121.54
10	l	28	PRO	N-CA-C	5.83	121.52	113.65
23	v	177	GLU	CA-CB-CG	-5.82	102.47	114.10
26	8	73	GLU	CA-CB-CG	5.76	125.63	114.10
26	8	346	PHE	N-CA-CB	5.75	119.19	110.28
21	w	128	PRO	N-CA-C	5.73	120.23	110.95
26	8	262	SER	N-CA-C	5.72	122.99	110.80
23	v	37	GLU	CB-CG-CD	5.47	121.90	112.60
26	8	280	ILE	CA-CB-CG1	5.41	119.59	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	8	317	HIS	N-CA-C	5.41	119.29	111.56
26	8	363	ALA	N-CA-C	5.40	117.89	109.52
3	e	266	LEU	CA-CB-CG	5.37	135.08	116.30
26	8	70	ALA	N-CA-CB	5.36	119.92	110.37
26	8	328	THR	CA-C-N	5.36	131.77	121.54
26	8	328	THR	C-N-CA	5.36	131.77	121.54
21	w	148	LYS	C-N-CD	-5.34	103.10	125.00
21	w	136	ASP	N-CA-CB	-5.34	101.52	109.69
23	v	105	MET	N-CA-C	5.32	122.12	110.80
26	8	303	VAL	CB-CA-C	-5.32	102.57	111.29
26	8	370	ASP	CA-C-N	5.31	131.68	121.54
26	8	370	ASP	C-N-CA	5.31	131.68	121.54
3	e	303	MET	CB-CG-SD	5.30	128.59	112.70
26	8	283	ILE	CA-CB-CG1	5.30	119.41	110.40
26	8	298	SER	CA-C-N	5.30	131.66	121.54
26	8	298	SER	C-N-CA	5.30	131.66	121.54
20	a	269	A	N9-C1'-C2'	5.27	119.90	112.00
24	n	39	ASP	N-CA-C	5.23	116.98	111.28
26	8	368	ARG	N-CA-CB	-5.21	101.68	110.49
3	e	147	LYS	CA-C-N	5.21	131.34	121.97
3	e	147	LYS	C-N-CA	5.21	131.34	121.97
26	8	291	GLN	CG-CD-NE2	-5.21	108.59	116.40
23	v	175	GLU	CA-CB-CG	-5.19	103.72	114.10
23	v	50	ILE	N-CA-C	5.09	114.98	107.75
18	u	98	ARG	N-CA-CB	-5.08	102.50	109.97
23	v	165	PHE	CA-C-N	-5.08	112.64	120.86
23	v	165	PHE	C-N-CA	-5.08	112.64	120.86

There are no chirality outliers.

All (58) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
26	8	273	PRO	Peptide
26	8	277	PHE	Peptide
26	8	298	SER	Peptide
26	8	299	ASP	Peptide
26	8	302	THR	Peptide
26	8	303	VAL	Peptide
26	8	304	LEU	Peptide
26	8	315	LEU	Peptide
26	8	329	LYS	Peptide
26	8	346	PHE	Sidechain

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Mol	Chain	Res	Type	Group
26	8	359	ARG	Peptide
26	8	366	MET	Mainchain
26	8	369	ALA	Peptide
26	8	370	ASP	Peptide
26	8	69	ASN	Peptide
26	8	71	PRO	Peptide
26	8	72	MET	Peptide
1	b	168	VAL	Peptide
1	b	201	ASP	Sidechain
2	c	168	ILE	Peptide
2	c	86	GLU	Peptide
2	c	88	ARG	Peptide
22	d	155	SER	Peptide
22	d	23	ASN	Peptide
3	e	147	LYS	Peptide
4	f	102	PRO	Peptide
5	g	8	GLU	Peptide
7	i	78	ARG	Peptide
7	i	96	ILE	Peptide
8	j	135	LEU	Peptide
10	l	24	LEU	Peptide
10	l	27	CYS	Peptide
10	l	8	ILE	Peptide
11	m	137	LYS	Peptide
11	m	34	LYS	Peptide
18	u	103	PHE	Sidechain
23	v	100	LYS	Peptide
23	v	101	PRO	Peptide
23	v	104	GLY	Peptide
23	v	120	SER	Mainchain
23	v	147	LYS	Peptide
23	v	158	GLY	Peptide
23	v	159	THR	Peptide
23	v	165	PHE	Sidechain
23	v	168	VAL	Peptide
23	v	184	ASN	Peptide
23	v	185	ASN	Peptide
23	v	187	VAL	Peptide
23	v	188	LEU	Peptide
23	v	194	ARG	Sidechain
23	v	33	LEU	Peptide
21	w	108	LYS	Peptide

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Mol	Chain	Res	Type	Group
21	w	110	ILE	Peptide
21	w	126	LEU	Peptide
21	w	130	TYR	Peptide
21	w	148	LYS	Peptide
21	w	176	ASN	Peptide
21	w	98	ARG	Peptide

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	b	1787	0	1828	107	0
2	c	1719	0	1807	34	0
3	e	1292	0	1355	52	0
4	f	886	0	888	9	0
5	g	1161	0	1237	13	0
6	h	1088	0	1149	59	0
7	i	1020	0	1072	17	0
8	j	796	0	841	25	0
9	k	887	0	933	25	0
10	l	967	0	1046	17	0
11	m	898	0	950	41	0
12	o	525	0	572	10	0
13	p	664	0	703	12	0
14	q	635	0	667	13	0
15	r	518	0	544	36	0
16	s	627	0	653	17	0
17	t	832	0	883	20	0
18	u	393	0	406	91	0
19	y	845	0	892	17	0
20	a	31777	0	16007	325	0
21	w	689	0	706	152	0
22	d	1633	0	1727	117	0
23	v	1464	0	1456	93	0
24	n	819	0	858	41	0
25	x	289	0	301	20	0
26	8	1201	0	1220	147	0
All	All	55412	0	40701	1157	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (1157) 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)
22:d:162:LYS:HB2	22:d:183:TRP:CH2	1.20	1.62
22:d:162:LYS:HB2	22:d:183:TRP:CZ2	1.41	1.54
22:d:137:MET:SD	22:d:172:LYS:HE3	1.48	1.52
18:u:103:PHE:CD1	21:w:138:TRP:CD1	1.98	1.52
22:d:162:LYS:CB	22:d:183:TRP:CH2	1.92	1.51
22:d:89:MET:CE	22:d:178:ILE:HA	1.42	1.46
15:r:51:VAL:O	21:w:149:PRO:CD	1.64	1.43
3:e:247:VAL:N	22:d:195:GLU:OE1	1.60	1.34
23:v:123:LYS:HE2	23:v:167:PHE:CD2	1.72	1.24
18:u:103:PHE:CZ	21:w:138:TRP:HB3	1.74	1.20
22:d:50:GLU:OE1	22:d:188:ILE:CG2	1.90	1.20
6:h:67:ARG:HH11	26:8:68:ARG:N	1.39	1.20
18:u:106:GLU:HB2	21:w:138:TRP:CZ2	1.78	1.19
18:u:103:PHE:CE1	21:w:138:TRP:HB3	1.80	1.17
11:m:65:GLN:NE2	25:x:86:PRO:HD2	1.58	1.15
18:u:106:GLU:N	21:w:138:TRP:CH2	2.14	1.15
6:h:67:ARG:NH1	26:8:68:ARG:H	1.43	1.14
6:h:67:ARG:CD	26:8:71:PRO:HD2	1.77	1.13
21:w:136:ASP:CB	21:w:139:GLU:OE2	1.95	1.13
22:d:137:MET:SD	22:d:172:LYS:CE	2.36	1.12
16:s:8:ASN:OD1	24:n:42:GLU:OE2	1.65	1.11
18:u:100:LEU:HD11	21:w:168:ASN:ND2	1.63	1.11
18:u:103:PHE:HA	21:w:138:TRP:NE1	1.51	1.11
1:b:201:ASP:CB	26:8:66:ARG:HD3	1.82	1.10
6:h:67:ARG:HD2	26:8:71:PRO:HD2	1.27	1.10
15:r:51:VAL:O	21:w:149:PRO:HD3	0.92	1.10
22:d:137:MET:HG2	22:d:172:LYS:HG2	1.30	1.10
23:v:128:ASN:HB3	23:v:193:ILE:HA	1.23	1.10
18:u:106:GLU:HB3	21:w:139:GLU:OE1	1.53	1.09
18:u:107:VAL:HG23	21:w:138:TRP:HZ3	1.14	1.08
22:d:89:MET:HE1	22:d:178:ILE:HA	1.34	1.08
22:d:50:GLU:OE1	22:d:188:ILE:HG23	1.51	1.07
22:d:162:LYS:CB	22:d:183:TRP:CZ2	2.24	1.07
22:d:89:MET:HE3	22:d:178:ILE:HA	1.12	1.07
15:r:51:VAL:O	21:w:149:PRO:CG	2.04	1.06
18:u:107:VAL:HG23	21:w:138:TRP:CZ3	1.89	1.06
22:d:162:LYS:C	22:d:183:TRP:CZ3	2.35	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:w:136:ASP:HB2	21:w:139:GLU:OE2	1.56	1.04
18:u:103:PHE:CD1	21:w:138:TRP:HD1	1.54	1.04
20:a:75:U:H5''	23:v:194:ARG:CD	1.87	1.04
21:w:136:ASP:HB3	21:w:139:GLU:HG2	1.37	1.04
22:d:190:GLU:N	22:d:190:GLU:OE1	1.90	1.04
16:s:8:ASN:OD1	24:n:42:GLU:CD	2.00	1.03
25:x:90:ILE:HG22	25:x:91:PHE:H	1.15	1.03
18:u:106:GLU:N	21:w:138:TRP:CZ2	2.27	1.02
22:d:163:HIS:CB	22:d:175:VAL:HG13	1.86	1.02
22:d:89:MET:CE	22:d:178:ILE:CA	2.36	1.02
21:w:136:ASP:CG	21:w:139:GLU:OE2	2.00	1.02
22:d:19:PRO:CG	22:d:186:LEU:HD13	1.89	1.01
22:d:163:HIS:O	22:d:175:VAL:HA	1.59	1.01
18:u:100:LEU:HD11	21:w:168:ASN:HD21	0.85	1.01
21:w:136:ASP:OD1	21:w:139:GLU:OE2	1.79	1.00
22:d:181:SER:O	22:d:184:VAL:HG22	1.59	1.00
20:a:75:U:H5''	23:v:194:ARG:HD3	1.44	1.00
22:d:163:HIS:HB2	22:d:175:VAL:CG1	1.90	0.99
18:u:100:LEU:HD21	21:w:164:THR:HG21	1.44	0.98
18:u:103:PHE:CE1	21:w:138:TRP:CD1	2.51	0.98
1:b:201:ASP:HB2	26:8:66:ARG:HD3	1.45	0.98
25:x:90:ILE:HG22	25:x:91:PHE:N	1.79	0.97
15:r:51:VAL:HG13	21:w:146:GLU:C	1.90	0.97
18:u:106:GLU:N	21:w:138:TRP:HH2	1.59	0.97
20:a:611:A:H61	20:a:690:G:H1	1.02	0.96
22:d:162:LYS:HB2	22:d:183:TRP:CZ3	1.99	0.96
18:u:107:VAL:CG2	21:w:138:TRP:HZ3	1.77	0.96
18:u:106:GLU:CB	21:w:138:TRP:CZ2	2.48	0.95
15:r:51:VAL:HG22	21:w:147:ASN:OD1	1.64	0.95
18:u:106:GLU:H	21:w:138:TRP:HZ2	1.10	0.95
26:8:317:HIS:HA	26:8:324:VAL:HA	1.47	0.94
18:u:103:PHE:HD1	21:w:138:TRP:CD1	1.83	0.94
22:d:51:LYS:HD2	22:d:196:TYR:CE1	2.03	0.94
15:r:51:VAL:HG13	21:w:146:GLU:O	1.68	0.93
22:d:173:GLY:C	22:d:174:LEU:HD12	1.92	0.92
24:n:36:SER:C	24:n:37:LEU:HD12	1.95	0.92
18:u:107:VAL:N	21:w:138:TRP:CH2	2.38	0.92
22:d:162:LYS:HB3	22:d:183:TRP:CH2	2.01	0.92
18:u:103:PHE:CE1	21:w:167:ILE:HD12	2.05	0.91
15:r:51:VAL:O	21:w:149:PRO:HG3	1.68	0.91
15:r:51:VAL:HA	21:w:147:ASN:HA	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:u:103:PHE:CG	21:w:138:TRP:CD1	2.58	0.91
11:m:65:GLN:NE2	25:x:86:PRO:CD	2.33	0.91
15:r:53:ARG:NH2	21:w:150:TRP:CH2	2.39	0.91
15:r:53:ARG:HG3	21:w:149:PRO:HD2	1.52	0.90
18:u:106:GLU:CA	21:w:138:TRP:CH2	2.55	0.90
22:d:163:HIS:HB2	22:d:175:VAL:HG13	0.94	0.90
1:b:77:LYS:HE3	1:b:79:LYS:HD2	1.54	0.90
18:u:103:PHE:CA	21:w:138:TRP:NE1	2.35	0.90
23:v:124:VAL:CG1	23:v:195:VAL:CG2	2.50	0.90
22:d:163:HIS:N	22:d:183:TRP:HZ3	1.70	0.89
18:u:98:ARG:HE	21:w:168:ASN:HB3	1.35	0.88
18:u:103:PHE:CD1	21:w:138:TRP:CG	2.60	0.88
22:d:89:MET:HE3	22:d:178:ILE:CA	2.00	0.88
22:d:50:GLU:OE1	22:d:188:ILE:HG21	1.71	0.87
19:y:96:ASP:O	19:y:100:LYS:HB2	1.74	0.87
21:w:136:ASP:HB3	21:w:139:GLU:CG	2.04	0.87
18:u:103:PHE:CE1	21:w:138:TRP:CB	2.58	0.86
18:u:100:LEU:CD2	21:w:164:THR:HG21	2.06	0.86
1:b:201:ASP:CG	26:8:66:ARG:HD3	2.00	0.85
3:e:263:GLU:HB3	22:d:191:LEU:CD1	2.06	0.85
22:d:89:MET:HE1	22:d:178:ILE:CA	2.02	0.85
18:u:107:VAL:N	21:w:138:TRP:HH2	1.75	0.85
24:n:43:ILE:O	24:n:46:LYS:HB3	1.76	0.84
20:a:611:A:N6	20:a:690:G:H1	1.75	0.84
22:d:137:MET:CG	22:d:172:LYS:HG2	2.06	0.84
16:s:50:ALA:HA	16:s:58:LEU:O	1.78	0.84
18:u:100:LEU:CD1	21:w:168:ASN:HD21	1.81	0.84
22:d:19:PRO:HG3	22:d:186:LEU:HD13	1.60	0.84
1:b:7:ASN:ND2	26:8:345:VAL:O	2.11	0.83
22:d:19:PRO:HG3	22:d:186:LEU:CD1	2.07	0.83
11:m:65:GLN:CD	25:x:86:PRO:HD2	2.03	0.83
21:w:136:ASP:CB	21:w:139:GLU:CD	2.51	0.83
22:d:163:HIS:N	22:d:183:TRP:CZ3	2.45	0.83
18:u:126:GLN:O	18:u:130:LYS:HB2	1.78	0.83
26:8:63:ALA:O	26:8:66:ARG:C	2.22	0.83
26:8:291:GLN:HB3	26:8:327:SER:HA	1.60	0.83
26:8:342:PRO:HA	26:8:345:VAL:HB	1.61	0.83
18:u:107:VAL:H	21:w:138:TRP:HH2	1.26	0.82
20:a:954:A:N6	20:a:973:G:H21	1.78	0.82
24:n:34:VAL:HG12	24:n:41:TRP:HZ3	1.45	0.81
22:d:57:HIS:CD2	22:d:186:LEU:HD22	2.16	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:d:180:ASP:OD1	22:d:181:SER:N	2.14	0.81
24:n:34:VAL:HG12	24:n:41:TRP:CZ3	2.15	0.81
18:u:103:PHE:HA	21:w:138:TRP:HE1	1.45	0.80
3:e:246:GLY:HA3	22:d:195:GLU:HG3	1.60	0.80
6:h:67:ARG:CZ	26:8:69:ASN:H	1.94	0.80
2:c:71:LEU:HA	2:c:109:LYS:O	1.81	0.80
20:a:75:U:H5''	23:v:194:ARG:HD2	1.60	0.80
1:b:60:LEU:HD13	26:8:65:GLU:HB3	1.63	0.80
6:h:67:ARG:CG	26:8:71:PRO:HD2	2.11	0.80
18:u:103:PHE:CE1	21:w:138:TRP:HD1	1.97	0.80
3:e:263:GLU:HB3	22:d:191:LEU:HD11	1.62	0.79
22:d:162:LYS:C	22:d:183:TRP:HZ3	1.89	0.79
1:b:201:ASP:HB2	26:8:66:ARG:CD	2.12	0.79
20:a:612:G:H22	20:a:689:G:H1	1.28	0.79
21:w:136:ASP:OD1	21:w:139:GLU:CD	2.24	0.79
24:n:43:ILE:O	24:n:46:LYS:CB	2.31	0.78
3:e:174:PHE:O	3:e:193:LYS:HA	1.82	0.78
6:h:24:VAL:O	6:h:60:VAL:HA	1.83	0.78
23:v:128:ASN:HB3	23:v:193:ILE:CA	2.11	0.77
2:c:26:PRO:HG3	8:j:140:ARG:HH22	1.48	0.77
22:d:19:PRO:CG	22:d:186:LEU:CD1	2.63	0.77
18:u:98:ARG:HB2	21:w:168:ASN:CG	2.10	0.77
1:b:14:MET:SD	26:8:334:THR:OG1	2.43	0.77
21:w:130:TYR:CD2	21:w:140:GLU:OE2	2.37	0.77
18:u:106:GLU:C	21:w:138:TRP:CH2	2.62	0.76
24:n:37:LEU:HB2	24:n:41:TRP:CZ2	2.20	0.76
20:a:1358:C:O2	20:a:1440:G:N2	2.17	0.76
24:n:43:ILE:O	24:n:46:LYS:N	2.18	0.76
18:u:98:ARG:HD3	21:w:168:ASN:ND2	1.99	0.76
21:w:106:MET:HE3	21:w:109:ASN:HD21	1.50	0.76
1:b:7:ASN:HD22	26:8:345:VAL:HA	1.49	0.76
6:h:67:ARG:HD2	26:8:71:PRO:CD	2.11	0.75
18:u:100:LEU:HD21	21:w:164:THR:CG2	2.16	0.75
22:d:162:LYS:CA	22:d:183:TRP:CH2	2.69	0.75
15:r:53:ARG:NH2	21:w:150:TRP:CZ2	2.54	0.75
15:r:53:ARG:NH2	21:w:150:TRP:CZ3	2.55	0.75
23:v:50:ILE:HG22	23:v:69:THR:HB	1.68	0.75
17:t:84:ARG:NH1	20:a:88:G:N7	2.35	0.74
23:v:30:PRO:HG3	23:v:91:ARG:HB2	1.68	0.74
24:n:36:SER:O	24:n:37:LEU:HD12	1.86	0.74
26:8:365:ALA:O	26:8:366:MET:O	2.03	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:d:162:LYS:C	22:d:183:TRP:CH2	2.63	0.74
1:b:211:ILE:HG13	26:8:317:HIS:CE1	2.23	0.73
26:8:354:GLN:OE1	26:8:357:ARG:NH1	2.18	0.73
20:a:75:U:O3'	23:v:196:ASN:ND2	2.22	0.73
1:b:90:ARG:HH22	26:8:359:ARG:HB2	1.53	0.73
1:b:79:LYS:HD3	26:8:317:HIS:HB2	1.69	0.73
8:j:101:ILE:HA	8:j:192:GLU:O	1.87	0.73
6:h:67:ARG:HG2	26:8:67:CYS:HA	1.69	0.72
20:a:75:U:C5'	23:v:194:ARG:HD2	2.18	0.72
23:v:21:ALA:HA	23:v:23:ARG:HG2	1.71	0.72
23:v:123:LYS:HE2	23:v:167:PHE:CG	2.24	0.72
26:8:64:TYR:HA	26:8:67:CYS:HB2	1.72	0.72
21:w:98:ARG:HG2	21:w:155:GLN:HE21	1.54	0.72
20:a:954:A:H62	20:a:973:G:N2	1.88	0.72
1:b:52:ARG:HD2	26:8:73:GLU:HG3	1.71	0.72
7:i:79:LYS:HE2	7:i:177:ILE:HG13	1.71	0.72
18:u:98:ARG:NE	21:w:168:ASN:HB3	2.03	0.71
21:w:135:LYS:HG2	21:w:140:GLU:OE1	1.89	0.71
18:u:103:PHE:HA	21:w:138:TRP:CD1	2.25	0.71
20:a:954:A:H62	20:a:973:G:H21	1.37	0.71
1:b:79:LYS:HZ3	26:8:317:HIS:C	1.98	0.71
22:d:89:MET:HE1	22:d:178:ILE:HG12	1.73	0.71
14:q:64:LYS:HD3	14:q:111:TRP:HB3	1.73	0.71
18:u:96:GLU:HB3	21:w:172:GLN:CD	2.16	0.71
23:v:127:GLY:O	23:v:193:ILE:HA	1.91	0.71
22:d:162:LYS:CA	22:d:183:TRP:CZ3	2.73	0.70
22:d:162:LYS:CB	22:d:183:TRP:HH2	1.97	0.70
21:w:112:LEU:HD11	21:w:167:ILE:HD11	1.73	0.70
22:d:179:ILE:HG23	22:d:183:TRP:HB3	1.73	0.70
19:y:166:ARG:NH1	20:a:1350:G:OP2	2.25	0.70
23:v:67:PHE:HB3	23:v:101:PRO:HB3	1.73	0.69
11:m:56:ASN:HD22	11:m:59:ARG:HD2	1.57	0.69
23:v:146:GLY:HA3	23:v:175:GLU:HG2	1.74	0.69
22:d:174:LEU:HD12	22:d:174:LEU:N	2.06	0.69
21:w:136:ASP:CB	21:w:139:GLU:CG	2.70	0.69
20:a:75:U:C5'	23:v:194:ARG:CD	2.68	0.69
1:b:58:CYS:SG	1:b:220:LYS:NZ	2.66	0.69
23:v:13:SER:HB3	23:v:103:GLU:HG3	1.75	0.69
21:w:136:ASP:O	21:w:140:GLU:CD	2.36	0.69
11:m:126:LYS:O	11:m:132:ARG:NH2	2.26	0.68
20:a:1442:A:H2'	20:a:1443:G:H5'	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:162:ILE:O	2:c:178:TRP:HA	1.93	0.68
18:u:103:PHE:CE1	21:w:138:TRP:CG	2.78	0.68
21:w:126:LEU:HB2	21:w:128:PRO:HD3	1.76	0.68
23:v:42:VAL:HA	23:v:45:HIS:HD2	1.57	0.68
26:8:318:ASP:HB3	26:8:323:ARG:HB2	1.74	0.68
3:e:247:VAL:CA	22:d:195:GLU:OE1	2.42	0.68
23:v:124:VAL:CG1	23:v:195:VAL:HG21	2.22	0.68
26:8:359:ARG:HG3	26:8:360:ILE:HG13	1.75	0.68
18:u:106:GLU:CD	21:w:136:ASP:OD1	2.37	0.67
23:v:124:VAL:HB	23:v:168:VAL:CG1	2.24	0.67
1:b:75:GLY:H	1:b:96:VAL:HB	1.59	0.67
23:v:123:LYS:CE	23:v:167:PHE:CD2	2.66	0.67
26:8:257:GLN:HE22	26:8:283:ILE:HA	1.60	0.67
23:v:124:VAL:HG11	23:v:195:VAL:HG21	1.75	0.67
18:u:106:GLU:CA	21:w:138:TRP:CZ2	2.77	0.67
22:d:51:LYS:HD2	22:d:196:TYR:CZ	2.29	0.67
18:u:103:PHE:CZ	21:w:138:TRP:CB	2.66	0.67
6:h:67:ARG:NH1	26:8:68:ARG:N	2.16	0.66
6:h:67:ARG:NE	26:8:69:ASN:H	1.92	0.66
18:u:101:ASN:O	18:u:105:ARG:HB2	1.96	0.66
11:m:109:VAL:O	11:m:118:ARG:NH1	2.23	0.66
23:v:29:ILE:HG23	23:v:33:LEU:HD23	1.78	0.66
15:r:53:ARG:HG3	21:w:149:PRO:CD	2.25	0.66
23:v:20:GLY:HA2	23:v:100:LYS:HE2	1.78	0.66
1:b:145:LEU:O	1:b:149:GLN:HB2	1.96	0.65
25:x:90:ILE:CG2	25:x:91:PHE:N	2.52	0.65
21:w:136:ASP:HB3	21:w:139:GLU:CD	2.20	0.65
15:r:53:ARG:HG3	21:w:149:PRO:HG2	1.79	0.65
11:m:65:GLN:HE22	25:x:86:PRO:CD	2.09	0.65
15:r:51:VAL:HG22	21:w:147:ASN:HA	1.80	0.64
20:a:956:C:N3	20:a:972:G:N2	2.45	0.64
23:v:124:VAL:CG1	23:v:195:VAL:HG22	2.28	0.64
16:s:19:ILE:HG23	16:s:23:ASN:HD22	1.62	0.64
22:d:19:PRO:CD	22:d:186:LEU:HD13	2.27	0.64
9:k:90:ARG:HG2	9:k:115:LEU:HD23	1.80	0.64
23:v:42:VAL:HG13	23:v:79:VAL:HG21	1.78	0.64
20:a:1356:C:H2'	20:a:1357:A:H8	1.63	0.64
15:r:51:VAL:CG2	21:w:147:ASN:OD1	2.42	0.64
22:d:162:LYS:HB2	22:d:183:TRP:CE2	2.23	0.64
3:e:246:GLY:HA3	22:d:195:GLU:CG	2.26	0.63
8:j:101:ILE:HG13	8:j:167:ILE:HG23	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:u:109:ARG:HG2	18:u:111:GLY:H	1.62	0.63
1:b:201:ASP:HB2	26:8:66:ARG:CG	2.28	0.63
2:c:180:ARG:NH2	20:a:1055:G:O2'	2.31	0.63
6:h:20:ARG:NH1	6:h:70:LYS:O	2.31	0.63
5:g:138:LYS:O	5:g:142:HIS:HB2	1.99	0.63
6:h:67:ARG:HB3	26:8:67:CYS:HA	1.81	0.63
23:v:124:VAL:HG13	23:v:195:VAL:HG22	1.81	0.63
6:h:51:HIS:O	6:h:57:TYR:HA	1.99	0.63
10:l:114:ARG:NH1	20:a:449:C:OP1	2.32	0.63
18:u:106:GLU:HB2	21:w:138:TRP:CH2	2.30	0.63
1:b:114:ARG:HE	1:b:152:LEU:HD11	1.64	0.63
9:k:93:VAL:HB	9:k:119:VAL:HG12	1.80	0.63
22:d:89:MET:HE1	22:d:178:ILE:CG1	2.28	0.63
22:d:199:ARG:O	22:d:200:GLN:HB2	1.99	0.63
23:v:19:GLU:HG2	23:v:22:ARG:HG3	1.80	0.63
3:e:246:GLY:HA2	22:d:191:LEU:HD22	1.79	0.62
17:t:156:ARG:HH22	20:a:168:C:H1'	1.64	0.62
18:u:99:LEU:HB2	21:w:171:GLN:HE22	1.63	0.62
14:q:76:VAL:O	14:q:96:LYS:HA	1.99	0.62
20:a:670:A:H61	20:a:681:A:H61	1.46	0.62
20:a:840:U:H2'	20:a:841:A:H8	1.64	0.62
20:a:1013:G:O2'	20:a:1138:G:N2	2.32	0.62
1:b:184:GLY:O	26:8:59:LEU:HD22	2.00	0.62
11:m:65:GLN:HE22	25:x:86:PRO:N	1.97	0.62
15:r:37:SER:HA	15:r:40:ILE:HG12	1.81	0.62
21:w:96:LYS:HG2	21:w:119:PRO:HA	1.82	0.62
9:k:135:LYS:HG2	18:u:118:ARG:HB3	1.81	0.62
17:t:81:LYS:HE2	20:a:62:G:H8	1.64	0.62
20:a:344:A:O2'	20:a:422:A:N7	2.33	0.62
20:a:1438:G:H2'	20:a:1439:U:C6	2.34	0.62
23:v:25:TYR:HB2	23:v:98:THR:HB	1.81	0.62
23:v:183:LEU:HD21	23:v:193:ILE:HG22	1.81	0.62
17:t:139:ILE:HG12	17:t:160:LEU:HD22	1.81	0.61
20:a:1135:G:HO2'	24:n:99:SER:HG	1.41	0.61
6:h:4:ASP:OD2	6:h:81:ARG:NH1	2.34	0.61
11:m:56:ASN:HB2	11:m:59:ARG:HB2	1.82	0.61
15:r:28:ILE:HG21	15:r:62:ILE:HG22	1.82	0.61
20:a:401:G:OP2	22:d:8:ARG:NH1	2.32	0.61
21:w:103:PHE:HB2	21:w:166:ILE:HG21	1.81	0.61
20:a:1020:C:H2'	20:a:1021:G:H8	1.65	0.61
5:g:30:ILE:HG23	5:g:39:ALA:HB1	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:s:8:ASN:OD1	24:n:42:GLU:OE1	2.18	0.61
18:u:103:PHE:CG	21:w:138:TRP:CG	2.85	0.61
16:s:32:VAL:HA	16:s:50:ALA:HB3	1.83	0.61
22:d:179:ILE:HG23	22:d:183:TRP:CB	2.29	0.61
22:d:21:LEU:HG	22:d:57:HIS:HA	1.83	0.61
23:v:123:LYS:HG3	23:v:168:VAL:O	2.00	0.61
23:v:180:ILE:HA	23:v:195:VAL:HG13	1.83	0.61
1:b:52:ARG:NE	26:8:74:GLY:H	1.97	0.61
11:m:134:GLN:HG2	11:m:135:ARG:HB2	1.83	0.61
18:u:103:PHE:HE1	21:w:167:ILE:HD12	1.63	0.61
24:n:17:GLU:HG3	24:n:59:LEU:HD22	1.83	0.61
20:a:780:G:H1	20:a:803:U:H3	1.48	0.61
14:q:75:ASN:ND2	20:a:247:G:OP1	2.33	0.61
18:u:100:LEU:CD2	21:w:164:THR:CG2	2.76	0.61
2:c:20:SER:OG	2:c:22:TRP:NE1	2.32	0.60
3:e:235:ARG:HB3	3:e:270:LEU:O	2.01	0.60
15:r:42:GLU:O	15:r:79:ASN:ND2	2.34	0.60
22:d:137:MET:HG2	22:d:172:LYS:CG	2.18	0.60
23:v:33:LEU:HD13	23:v:88:ILE:HG21	1.82	0.60
22:d:162:LYS:HB3	22:d:183:TRP:HH2	1.62	0.60
18:u:106:GLU:CB	21:w:138:TRP:CH2	2.85	0.60
20:a:465:G:N1	20:a:481:A:OP2	2.33	0.60
1:b:6:TRP:HB3	1:b:220:LYS:HZ1	1.66	0.60
23:v:42:VAL:HG11	23:v:68:VAL:HG11	1.83	0.60
3:e:276:LEU:HD11	3:e:280:ARG:HH11	1.67	0.60
8:j:103:LEU:O	8:j:164:GLN:HA	2.01	0.60
2:c:67:LYS:HG2	2:c:72:ILE:HG12	1.82	0.60
18:u:98:ARG:HB2	21:w:168:ASN:CB	2.31	0.60
20:a:1209:A:N6	20:a:1222:G:O2'	2.35	0.60
18:u:107:VAL:N	21:w:138:TRP:CZ3	2.70	0.60
26:8:304:LEU:HD13	26:8:306:PRO:HD3	1.82	0.60
20:a:306:C:H2'	20:a:307:A:H8	1.66	0.60
10:l:68:PRO:O	10:l:99:ARG:NH2	2.35	0.59
11:m:56:ASN:O	11:m:60:VAL:N	2.35	0.59
15:r:51:VAL:CG1	21:w:146:GLU:O	2.47	0.59
3:e:263:GLU:OE1	22:d:191:LEU:HD12	2.02	0.59
26:8:268:VAL:HG21	26:8:305:GLN:HB3	1.84	0.59
10:l:5:LYS:O	10:l:9:ARG:NH1	2.35	0.59
20:a:141:U:H2'	20:a:142:G:H8	1.67	0.59
21:w:136:ASP:CB	21:w:139:GLU:HG2	2.20	0.59
11:m:135:ARG:NH2	20:a:898:A:N7	2.39	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:i:166:LYS:NZ	20:a:1126:G:OP2	2.32	0.59
20:a:437:C:OP1	22:d:114:ARG:NH1	2.35	0.59
22:d:89:MET:CE	22:d:178:ILE:HG12	2.33	0.59
22:d:188:ILE:HG22	22:d:189:ASN:N	2.18	0.59
3:e:239:ARG:HD3	3:e:240:PRO:HD2	1.83	0.59
21:w:114:LEU:HD22	21:w:141:LEU:HG	1.83	0.59
1:b:79:LYS:HE2	26:8:317:HIS:O	2.03	0.59
2:c:25:GLN:O	2:c:29:TYR:N	2.35	0.59
8:j:155:ARG:NH2	20:a:924:A:N1	2.51	0.59
10:l:17:ASN:ND2	20:a:504:C:OP2	2.36	0.59
3:e:225:HIS:HE1	3:e:290:ARG:H	1.50	0.59
10:l:71:GLY:O	10:l:99:ARG:NH1	2.36	0.59
14:q:62:GLN:HA	14:q:112:VAL:O	2.03	0.59
20:a:1203:G:H2'	20:a:1227:A:H61	1.68	0.59
1:b:202:ILE:HD11	6:h:67:ARG:HH21	1.67	0.58
11:m:121:ARG:NH2	20:a:1256:U:O3'	2.36	0.58
6:h:81:ARG:NH2	6:h:83:SER:O	2.31	0.58
8:j:102:LYS:O	8:j:191:VAL:HA	2.03	0.58
14:q:66:ILE:HD12	14:q:75:ASN:HB3	1.86	0.58
17:t:99:GLU:OE1	17:t:145:LYS:NZ	2.35	0.58
18:u:98:ARG:HB2	21:w:168:ASN:OD1	2.04	0.58
23:v:155:ARG:HG2	23:v:162:SER:HA	1.84	0.58
5:g:28:ASN:OD1	5:g:36:LYS:NZ	2.36	0.58
11:m:58:LYS:NZ	20:a:1215:C:O2	2.37	0.58
22:d:19:PRO:CD	22:d:186:LEU:CD1	2.81	0.58
25:x:90:ILE:CG2	25:x:91:PHE:H	1.91	0.58
1:b:20:PHE:HZ	26:8:291:GLN:HE22	1.52	0.58
3:e:246:GLY:CA	22:d:191:LEU:HD22	2.32	0.58
18:u:99:LEU:N	21:w:171:GLN:OE1	2.24	0.58
21:w:158:ILE:HG22	21:w:162:GLN:HE21	1.67	0.58
23:v:83:LEU:HD23	23:v:95:VAL:HG21	1.85	0.58
1:b:77:LYS:O	26:8:319:ARG:NH1	2.37	0.58
3:e:246:GLY:C	22:d:195:GLU:OE1	2.42	0.58
23:v:123:LYS:HE2	23:v:167:PHE:HD2	1.55	0.58
23:v:125:TYR:HD2	23:v:167:PHE:CE2	2.21	0.58
20:a:127:A:N1	20:a:191:G:O6	2.36	0.58
7:i:176:ARG:NH1	20:a:1321:U:OP2	2.35	0.58
7:i:106:GLN:NE2	20:a:1238:C:O2	2.35	0.57
8:j:98:LYS:N	8:j:170:LEU:O	2.37	0.57
20:a:455:C:H3'	20:a:456:U:H2'	1.85	0.57
24:n:17:GLU:O	24:n:21:HIS:HB2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:w:119:PRO:HG2	21:w:121:HIS:H	1.69	0.57
7:i:173:ARG:NH2	20:a:1067:U:OP1	2.37	0.57
18:u:103:PHE:CE2	21:w:138:TRP:HB3	2.32	0.57
22:d:165:THR:O	22:d:173:GLY:HA2	2.04	0.57
26:8:316:SER:HB3	26:8:325:SER:HB2	1.86	0.57
11:m:61:GLU:HB3	25:x:85:PRO:HB2	1.85	0.57
17:t:89:ARG:NH2	20:a:293:C:O2	2.36	0.57
20:a:542:U:N3	20:a:594:C:O2	2.38	0.57
4:f:121:ASP:HA	4:f:124:LEU:HB2	1.86	0.57
18:u:106:GLU:C	21:w:138:TRP:HH2	2.10	0.57
20:a:605:U:H2'	20:a:606:A:H8	1.69	0.57
15:r:50:ARG:HH22	18:u:138:LYS:HD3	1.69	0.57
18:u:119:ARG:NH1	18:u:120:ARG:O	2.37	0.57
20:a:600:U:O4	20:a:700:G:O2'	2.21	0.57
22:d:190:GLU:O	22:d:194:VAL:HG23	2.04	0.57
8:j:142:TYR:O	8:j:157:HIS:HA	2.05	0.57
20:a:400:U:OP2	22:d:13:ARG:NH1	2.38	0.57
20:a:895:A:H2'	20:a:896:G:H8	1.69	0.57
21:w:142:LYS:O	21:w:146:GLU:HG3	2.05	0.57
18:u:104:ARG:C	21:w:138:TRP:CH2	2.83	0.57
6:h:67:ARG:HD3	26:8:67:CYS:C	2.30	0.56
1:b:25:ARG:NH1	20:a:798:U:OP1	2.38	0.56
2:c:48:GLN:O	2:c:52:LYS:HB2	2.05	0.56
9:k:131:ARG:HH21	18:u:120:ARG:HH11	1.53	0.56
11:m:80:LEU:HD23	11:m:83:ASN:HD22	1.70	0.56
19:y:131:ARG:NH1	19:y:147:GLU:OE1	2.39	0.56
22:d:50:GLU:CD	22:d:188:ILE:HG23	2.30	0.56
6:h:83:SER:HB2	6:h:89:ILE:HG22	1.87	0.56
10:l:54:ARG:HA	10:l:64:THR:HA	1.85	0.56
20:a:989:G:H2'	20:a:990:G:H8	1.70	0.56
20:a:1187:A:H61	20:a:1244:C:H2'	1.71	0.56
20:a:1427:U:H2'	20:a:1428:A:H8	1.71	0.56
21:w:105:TRP:HD1	21:w:170:TRP:HD1	1.52	0.56
23:v:121:PRO:HB3	23:v:197:LYS:HD2	1.87	0.56
23:v:124:VAL:HG12	23:v:195:VAL:CG2	2.33	0.56
26:8:262:SER:OG	26:8:281:GLY:O	2.22	0.56
1:b:122:ARG:NH2	1:b:125:GLN:OE1	2.39	0.56
2:c:39:ILE:HD12	2:c:99:VAL:HG13	1.88	0.56
4:f:200:ARG:NH1	20:a:622:G:OP1	2.37	0.56
18:u:103:PHE:HD1	21:w:138:TRP:HD1	1.20	0.56
2:c:134:GLN:HE21	2:c:139:VAL:HG11	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:h:50:LYS:HA	6:h:58:PHE:O	2.05	0.56
16:s:40:ILE:HG21	16:s:67:VAL:HA	1.86	0.56
26:8:366:MET:SD	26:8:366:MET:N	2.78	0.56
16:s:18:LYS:HE3	16:s:31:ILE:HB	1.88	0.56
20:a:877:G:O2'	20:a:1482:C:OP1	2.24	0.56
20:a:1237:A:H5''	20:a:1238:C:H5	1.70	0.56
22:d:114:ARG:HB3	22:d:122:ILE:HD11	1.87	0.56
26:8:320:GLU:OE1	26:8:323:ARG:NH2	2.35	0.56
11:m:113:ARG:HH21	16:s:65:ARG:HG3	1.71	0.56
20:a:490:A:OP1	22:d:10:LYS:NZ	2.37	0.56
1:b:202:ILE:HG12	26:8:66:ARG:HG2	1.88	0.56
2:c:105:CYS:SG	2:c:106:VAL:N	2.79	0.56
3:e:154:GLU:OE2	3:e:209:ARG:NH2	2.39	0.56
22:d:162:LYS:CG	22:d:183:TRP:CZ2	2.88	0.56
8:j:112:GLU:O	8:j:116:LYS:HB2	2.06	0.56
1:b:178:ARG:NH1	20:a:1025:C:OP1	2.39	0.56
1:b:76:THR:H	1:b:168:VAL:HG21	1.71	0.55
3:e:177:ILE:HG12	3:e:191:VAL:HG12	1.87	0.55
3:e:233:ALA:HB2	20:a:813:A:H5'	1.87	0.55
13:p:54:LEU:O	13:p:58:GLU:HB2	2.06	0.55
19:y:80:GLN:HB2	19:y:115:ARG:HA	1.87	0.55
20:a:1412:U:H2'	20:a:1413:G:H8	1.71	0.55
21:w:114:LEU:HD21	21:w:145:LEU:HD21	1.88	0.55
22:d:180:ASP:O	22:d:183:TRP:HB2	2.05	0.55
15:r:51:VAL:CA	21:w:147:ASN:HA	2.32	0.55
20:a:243:C:H2'	20:a:244:A:H8	1.72	0.55
1:b:7:ASN:HB2	26:8:345:VAL:HG13	1.86	0.55
6:h:68:ASN:CG	26:8:70:ALA:HB2	2.31	0.55
20:a:1362:A:N1	20:a:1436:G:O6	2.39	0.55
21:w:105:TRP:CD1	21:w:170:TRP:HD1	2.24	0.55
3:e:246:GLY:C	22:d:195:GLU:HG2	2.31	0.55
6:h:67:ARG:CG	26:8:67:CYS:HA	2.36	0.55
20:a:1486:U:H2'	20:a:1487:C:C6	2.42	0.55
21:w:113:ALA:HA	21:w:128:PRO:O	2.06	0.55
1:b:6:TRP:H	26:8:348:LYS:HG2	1.70	0.55
12:o:51:ARG:NH2	20:a:676:A:N7	2.53	0.55
17:t:154:ALA:HA	17:t:157:LYS:HB2	1.88	0.55
20:a:347:G:H1	20:a:358:U:H3	1.55	0.55
22:d:137:MET:SD	22:d:172:LYS:NZ	2.80	0.55
1:b:99:LYS:NZ	20:a:1048:G:OP1	2.40	0.55
20:a:1363:U:H2'	20:a:1364:G:H8	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:a:1393:U:H3	20:a:1407:G:H1	1.53	0.55
22:d:2:SER:OG	22:d:3:ARG:N	2.40	0.55
26:8:291:GLN:CD	26:8:327:SER:HB2	2.31	0.55
6:h:67:ARG:CZ	26:8:68:ARG:N	2.68	0.55
20:a:962:G:N7	20:a:966:G:N1	2.55	0.55
21:w:130:TYR:HD2	21:w:140:GLU:OE2	1.88	0.55
2:c:143:LYS:O	2:c:147:LYS:HB2	2.07	0.55
13:p:6:LEU:HA	13:p:18:ARG:O	2.06	0.55
16:s:36:ARG:HD3	16:s:72:GLY:HA3	1.88	0.55
19:y:169:ARG:NH1	20:a:1447:U:OP2	2.39	0.55
20:a:376:U:OP2	22:d:3:ARG:NE	2.38	0.55
23:v:125:TYR:HD2	23:v:167:PHE:CZ	2.25	0.55
1:b:20:PHE:CE1	26:8:329:LYS:HG2	2.42	0.55
22:d:139:ARG:HB3	22:d:142:GLN:HG2	1.88	0.55
22:d:180:ASP:HB3	22:d:183:TRP:CD1	2.42	0.55
23:v:31:ARG:HB2	23:v:61:ARG:HG2	1.89	0.55
23:v:183:LEU:O	23:v:186:SER:HB2	2.06	0.55
1:b:40:LYS:HD3	26:8:290:SER:HA	1.89	0.54
11:m:107:ASN:HA	11:m:110:ALA:HB3	1.88	0.54
14:q:81:LEU:HD13	14:q:90:ARG:HD2	1.88	0.54
22:d:19:PRO:HG2	22:d:186:LEU:HD13	1.83	0.54
26:8:365:ALA:C	26:8:366:MET:O	2.50	0.54
1:b:165:VAL:HB	1:b:187:THR:HG22	1.89	0.54
23:v:124:VAL:HB	23:v:168:VAL:HG12	1.87	0.54
3:e:175:ARG:HA	3:e:192:GLY:O	2.07	0.54
12:o:69:LYS:NZ	20:a:702:C:OP1	2.40	0.54
20:a:833:U:H4'	20:a:834:G:H5''	1.89	0.54
20:a:960:U:C4	20:a:961:U:O4	2.60	0.54
6:h:109:SER:OG	20:a:590:A:N3	2.37	0.54
23:v:127:GLY:O	23:v:194:ARG:N	2.36	0.54
1:b:79:LYS:HZ2	26:8:316:SER:C	2.15	0.54
9:k:33:GLN:HB3	9:k:40:ILE:HB	1.88	0.54
11:m:99:ILE:HA	11:m:102:LYS:HG2	1.88	0.54
19:y:101:SER:O	19:y:165:GLN:NE2	2.41	0.54
20:a:1479:G:H2'	20:a:1480:A:C8	2.42	0.54
26:8:280:ILE:HG23	26:8:283:ILE:HG12	1.90	0.54
1:b:201:ASP:CG	26:8:66:ARG:CD	2.78	0.54
3:e:227:ASN:ND2	3:e:285:ALA:O	2.40	0.54
6:h:12:CYS:O	6:h:16:ALA:HB2	2.08	0.54
23:v:64:ARG:HH11	23:v:91:ARG:HH22	1.54	0.54
24:n:34:VAL:HA	24:n:41:TRP:CH2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:f:115:ARG:HE	4:f:117:ASP:HB2	1.72	0.54
11:m:106:PHE:HA	11:m:109:VAL:HB	1.90	0.54
22:d:135:THR:HA	22:d:174:LEU:HG	1.90	0.54
1:b:187:THR:N	26:8:66:ARG:HH22	2.04	0.54
20:a:327:A:N3	20:a:339:U:O2'	2.35	0.54
3:e:304:GLU:OE2	6:h:118:ARG:NE	2.30	0.54
2:c:42:CYS:O	2:c:46:TYR:HB2	2.09	0.53
20:a:932:A:OP1	24:n:3:ARG:NH2	2.41	0.53
21:w:111:GLY:HA3	21:w:129:TYR:CE1	2.43	0.53
1:b:107:ASN:ND2	20:a:1022:U:O2	2.40	0.53
3:e:153:GLU:OE1	3:e:183:LYS:NZ	2.41	0.53
18:u:96:GLU:HB3	21:w:172:GLN:OE1	2.07	0.53
20:a:347:G:O6	20:a:358:U:O4	2.26	0.53
21:w:123:THR:HG22	21:w:125:PRO:HD3	1.90	0.53
1:b:20:PHE:HB2	26:8:329:LYS:HE3	1.91	0.53
1:b:90:ARG:HH12	26:8:359:ARG:HA	1.73	0.53
2:c:8:LEU:HD13	2:c:195:TYR:HD1	1.73	0.53
2:c:171:LYS:HE3	2:c:175:ARG:HH22	1.74	0.53
14:q:75:ASN:HA	14:q:97:TYR:O	2.08	0.53
1:b:5:TYR:CZ	26:8:344:LEU:HD11	2.43	0.53
1:b:7:ASN:HD22	26:8:345:VAL:CA	2.21	0.53
6:h:68:ASN:ND2	26:8:70:ALA:HB2	2.23	0.53
15:r:57:LYS:HZ1	20:a:611:A:H5''	1.73	0.53
16:s:18:LYS:NZ	16:s:31:ILE:O	2.38	0.53
18:u:106:GLU:CA	21:w:138:TRP:HH2	2.08	0.53
19:y:115:ARG:NH1	19:y:133:GLU:OE1	2.41	0.53
20:a:35:C:H2'	20:a:36:G:H8	1.73	0.53
1:b:91:ALA:HB2	1:b:222:VAL:HG13	1.89	0.53
3:e:173:ARG:NH2	20:a:1030:G:OP2	2.42	0.53
6:h:67:ARG:HG3	6:h:68:ASN:N	2.23	0.53
10:l:101:THR:OG1	10:l:102:LEU:N	2.42	0.53
11:m:135:ARG:NH1	20:a:898:A:OP2	2.39	0.53
18:u:127:GLU:O	18:u:131:ARG:CB	2.56	0.53
23:v:28:ASN:HA	23:v:64:ARG:HB3	1.90	0.53
23:v:121:PRO:O	23:v:176:VAL:HG11	2.08	0.53
6:h:67:ARG:HH12	26:8:65:GLU:C	2.16	0.53
11:m:57:HIS:N	20:a:1277:A:OP1	2.31	0.53
20:a:1234:A:H2'	20:a:1235:A:H4'	1.90	0.53
5:g:15:ASP:H	5:g:20:ASN:H	1.57	0.53
8:j:100:ARG:HH12	20:a:1074:U:H4'	1.74	0.53
18:u:115:GLU:OE2	18:u:130:LYS:NZ	2.35	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:v:23:ARG:HB2	23:v:98:THR:HG23	1.90	0.53
1:b:60:LEU:HD22	26:8:65:GLU:CD	2.34	0.53
3:e:236:VAL:HG11	3:e:282:THR:HG22	1.91	0.53
20:a:567:U:H3	22:d:124:ASP:HB2	1.74	0.53
3:e:222:THR:HB	3:e:264:ASN:HB2	1.90	0.53
4:f:129:LYS:NZ	4:f:191:ALA:O	2.41	0.53
16:s:55:ARG:NH1	16:s:79:ASN:OD1	2.42	0.53
20:a:493:C:OP2	22:d:55:ARG:NH1	2.37	0.53
21:w:119:PRO:HD3	21:w:150:TRP:HB3	1.90	0.53
11:m:65:GLN:NE2	25:x:86:PRO:N	2.56	0.52
18:u:103:PHE:CA	21:w:138:TRP:CD1	2.90	0.52
20:a:685:U:H2'	20:a:686:G:H8	1.74	0.52
23:v:180:ILE:HD11	23:v:197:LYS:HB3	1.90	0.52
9:k:96:LYS:HG3	9:k:123:THR:HA	1.91	0.52
20:a:928:C:H42	24:n:57:ALA:HB1	1.74	0.52
24:n:40:LYS:C	24:n:41:TRP:CG	2.87	0.52
1:b:13:MET:HE1	1:b:51:ALA:HB2	1.90	0.52
2:c:86:GLU:HB3	2:c:90:GLN:HB2	1.91	0.52
6:h:67:ARG:HG3	6:h:68:ASN:H	1.73	0.52
20:a:1444:U:H2'	20:a:1445:C:C6	2.45	0.52
1:b:94:HIS:HB2	1:b:155:ILE:HG22	1.91	0.52
1:b:211:ILE:HG13	26:8:317:HIS:NE2	2.23	0.52
9:k:134:LYS:HD2	20:a:728:G:H5''	1.92	0.52
20:a:7:G:O2'	20:a:269:A:O4'	2.27	0.52
20:a:772:U:H2'	20:a:773:A:H8	1.74	0.52
20:a:1437:A:H2'	20:a:1438:G:C8	2.44	0.52
2:c:81:PRO:HG3	2:c:116:ARG:HG2	1.92	0.52
9:k:48:GLY:O	20:a:631:G:N2	2.43	0.52
12:o:21:SER:HB2	12:o:24:PHE:HD2	1.75	0.52
13:p:28:ARG:NH1	20:a:361:C:O3'	2.43	0.52
20:a:876:G:O2'	20:a:1452:A:N7	2.43	0.52
5:g:58:PRO:HA	5:g:61:VAL:HG12	1.92	0.52
13:p:28:ARG:NH2	20:a:361:C:O2'	2.36	0.52
18:u:97:GLU:HB2	21:w:172:GLN:HG2	1.90	0.52
20:a:1253:G:OP2	25:x:55:GLY:N	2.43	0.52
24:n:37:LEU:HB2	24:n:41:TRP:HZ2	1.68	0.52
3:e:181:GLY:HA2	3:e:186:GLN:O	2.10	0.52
18:u:111:GLY:HA2	18:u:114:GLN:HG2	1.91	0.52
20:a:1274:U:OP1	25:x:65:LYS:NZ	2.42	0.52
12:o:30:THR:HG21	12:o:82:LEU:HD13	1.91	0.52
13:p:27:ARG:NH2	20:a:280:A:OP1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:8:363:ALA:O	26:8:364:GLU:HB3	2.09	0.52
1:b:201:ASP:CG	26:8:66:ARG:HH11	2.18	0.52
13:p:54:LEU:O	13:p:58:GLU:CB	2.57	0.52
23:v:23:ARG:HD2	23:v:98:THR:O	2.10	0.52
26:8:285:GLY:HA2	26:8:324:VAL:O	2.09	0.52
1:b:103:GLY:N	1:b:179:GLU:OE2	2.42	0.52
15:r:81:GLU:OE1	18:u:104:ARG:NH2	2.39	0.52
18:u:107:VAL:CG2	21:w:138:TRP:CZ3	2.67	0.52
20:a:622:G:H2'	20:a:623:A:H8	1.74	0.52
20:a:1136:A:O2'	24:n:97:ARG:NH2	2.31	0.52
23:v:21:ALA:HB3	23:v:73:VAL:HG22	1.92	0.52
3:e:154:GLU:HG3	3:e:180:VAL:HG12	1.91	0.51
17:t:151:ASN:HA	17:t:155:ARG:HH11	1.76	0.51
20:a:808:U:OP2	20:a:818:G:N1	2.43	0.51
22:d:21:LEU:HD23	22:d:104:ILE:HB	1.92	0.51
23:v:88:ILE:HD12	23:v:93:ILE:HD12	1.91	0.51
13:p:32:ASP:OD1	13:p:33:LEU:N	2.43	0.51
23:v:104:GLY:O	23:v:106:ASP:N	2.44	0.51
1:b:78:ASN:HA	1:b:81:ALA:HB2	1.91	0.51
1:b:223:PHE:HZ	26:8:359:ARG:HB3	1.76	0.51
15:r:51:VAL:HA	21:w:147:ASN:CA	2.32	0.51
20:a:280:A:H2'	20:a:281:G:H8	1.76	0.51
20:a:1253:G:N2	20:a:1279:G:O2'	2.40	0.51
1:b:79:LYS:CD	26:8:317:HIS:HB2	2.38	0.51
5:g:133:ASP:OD1	5:g:136:ARG:NH2	2.44	0.51
11:m:117:ILE:HG23	11:m:127:LEU:HD13	1.91	0.51
20:a:1166:C:OP1	24:n:9:ARG:NH1	2.43	0.51
20:a:1371:G:H1	20:a:1427:U:H3	1.59	0.51
3:e:218:THR:HG23	3:e:224:PRO:HG3	1.92	0.51
11:m:65:GLN:NE2	25:x:86:PRO:O	2.38	0.51
12:o:21:SER:N	20:a:698:C:HO2'	2.07	0.51
13:p:21:ALA:N	13:p:32:ASP:OD2	2.41	0.51
23:v:67:PHE:CZ	23:v:102:LEU:HD12	2.46	0.51
18:u:127:GLU:O	18:u:131:ARG:HB3	2.11	0.51
20:a:1399:G:H21	20:a:1402:A:H2	1.59	0.51
26:8:342:PRO:O	26:8:346:PHE:N	2.40	0.51
1:b:6:TRP:CG	26:8:348:LYS:HZ3	2.29	0.51
1:b:201:ASP:OD2	26:8:66:ARG:CD	2.58	0.51
1:b:209:ASP:OD1	26:8:316:SER:N	2.44	0.51
14:q:96:LYS:NZ	20:a:249:G:OP2	2.33	0.51
20:a:1484:C:H2'	20:a:1485:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:w:109:ASN:HD22	21:w:132:TRP:NE1	2.09	0.51
6:h:31:ILE:HD11	6:h:130:LEU:HD21	1.92	0.51
15:r:53:ARG:HG3	21:w:149:PRO:CG	2.39	0.51
16:s:50:ALA:HB1	16:s:57:HIS:HB3	1.92	0.51
20:a:419:A:OP2	20:a:433:G:N2	2.43	0.51
26:8:257:GLN:NE2	26:8:283:ILE:HA	2.25	0.51
6:h:67:ARG:HD3	26:8:67:CYS:O	2.11	0.51
18:u:106:GLU:CD	21:w:136:ASP:CG	2.79	0.51
19:y:84:LEU:HD11	19:y:153:LEU:HD11	1.93	0.51
26:8:317:HIS:HB3	26:8:324:VAL:HG12	1.93	0.51
1:b:21:GLY:O	1:b:207:ASN:ND2	2.44	0.50
9:k:21:SER:OG	9:k:22:ALA:N	2.43	0.50
23:v:16:SER:HB2	23:v:101:PRO:HD2	1.93	0.50
7:i:132:VAL:HG11	7:i:146:ILE:HG12	1.94	0.50
21:w:148:LYS:C	21:w:150:TRP:H	2.18	0.50
22:d:174:LEU:N	22:d:174:LEU:CD1	2.73	0.50
3:e:179:VAL:HG22	3:e:189:VAL:HG12	1.93	0.50
23:v:184:ASN:HD21	23:v:194:ARG:NH2	2.09	0.50
6:h:19:ASN:ND2	20:a:775:U:O2'	2.45	0.50
6:h:67:ARG:CB	26:8:67:CYS:HA	2.41	0.50
8:j:143:CYS:SG	20:a:1316:G:O2'	2.67	0.50
21:w:119:PRO:HG3	21:w:150:TRP:CD1	2.46	0.50
24:n:41:TRP:N	24:n:41:TRP:CD1	2.77	0.50
1:b:31:MET:HE2	1:b:197:PRO:HD3	1.93	0.50
18:u:100:LEU:HD11	21:w:168:ASN:CG	2.35	0.50
20:a:185:G:C6	23:v:25:TYR:CD2	3.00	0.50
20:a:1176:C:H2'	20:a:1177:A:H8	1.76	0.50
20:a:227:U:H2'	20:a:228:G:H8	1.76	0.50
20:a:438:C:H2'	20:a:439:G:H8	1.77	0.50
1:b:90:ARG:NH2	26:8:359:ARG:HB2	2.26	0.50
20:a:258:U:H2'	20:a:259:A:H8	1.75	0.50
20:a:613:G:H1'	20:a:681:A:H5'	1.94	0.50
20:a:676:A:H2'	20:a:677:A:C8	2.47	0.50
6:h:67:ARG:CD	26:8:69:ASN:N	2.75	0.49
8:j:178:ASP:O	8:j:182:GLN:HB2	2.12	0.49
12:o:21:SER:N	20:a:699:U:O4'	2.45	0.49
20:a:1437:A:H2'	20:a:1438:G:H8	1.76	0.49
22:d:187:LYS:C	22:d:188:ILE:HG13	2.36	0.49
23:v:52:GLU:HB3	23:v:67:PHE:HB2	1.93	0.49
1:b:201:ASP:HB2	26:8:66:ARG:CB	2.42	0.49
3:e:142:LYS:HG2	3:e:146:GLU:HG3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:p:31:ARG:HH11	20:a:555:A:H1'	1.77	0.49
20:a:893:G:N1	20:a:1286:G:OP2	2.40	0.49
9:k:83:VAL:HG21	9:k:88:MET:HE2	1.93	0.49
18:u:106:GLU:N	21:w:138:TRP:HZ2	1.88	0.49
20:a:551:C:H2'	20:a:552:G:H8	1.77	0.49
23:v:42:VAL:HB	23:v:48:ILE:HD11	1.94	0.49
2:c:60:ILE:HG12	2:c:78:MET:HE2	1.94	0.49
3:e:147:LYS:O	3:e:149:ARG:N	2.45	0.49
6:h:67:ARG:CD	26:8:69:ASN:H	2.25	0.49
20:a:142:G:H1	20:a:147:C:N4	2.10	0.49
20:a:989:G:H2'	20:a:990:G:C8	2.48	0.49
20:a:139:G:H1	20:a:150:C:H42	1.60	0.49
20:a:1335:G:H2'	20:a:1336:G:H8	1.78	0.49
23:v:126:ILE:N	23:v:166:GLY:O	2.39	0.49
3:e:246:GLY:C	22:d:195:GLU:CG	2.86	0.49
20:a:1340:U:H2'	20:a:1341:G:C8	2.47	0.49
21:w:136:ASP:O	21:w:140:GLU:CG	2.61	0.49
21:w:139:GLU:O	21:w:143:VAL:HG23	2.12	0.49
26:8:63:ALA:HA	26:8:66:ARG:HB2	1.94	0.49
20:a:429:G:O2'	20:a:431:C:N4	2.45	0.49
23:v:33:LEU:HA	23:v:37:GLU:OE2	2.12	0.49
6:h:67:ARG:NH1	26:8:68:ARG:HG2	2.27	0.49
20:a:57:U:H2'	20:a:58:G:C8	2.47	0.49
21:w:114:LEU:HD11	21:w:159:LEU:HD13	1.94	0.49
6:h:117:ASP:O	6:h:121:ARG:HB2	2.12	0.49
9:k:66:ARG:NH2	20:a:639:G:O6	2.43	0.49
20:a:616:C:H2'	20:a:617:A:C8	2.47	0.49
20:a:616:C:H2'	20:a:617:A:H8	1.78	0.49
17:t:79:ALA:HB1	17:t:81:LYS:HD2	1.95	0.49
20:a:374:C:H5''	22:d:126:PRO:HD2	1.95	0.49
20:a:1439:U:H2'	20:a:1440:G:C8	2.48	0.49
26:8:315:LEU:O	26:8:317:HIS:N	2.45	0.49
18:u:99:LEU:HB2	21:w:171:GLN:NE2	2.28	0.48
20:a:978:U:H3	20:a:981:G:H22	1.61	0.48
20:a:1218:G:HO2'	20:a:1261:G:HO2'	1.55	0.48
24:n:34:VAL:HA	24:n:41:TRP:HH2	1.78	0.48
3:e:224:PRO:HD2	3:e:289:MET:HE2	1.93	0.48
14:q:81:LEU:HD22	14:q:90:ARG:HG2	1.95	0.48
17:t:152:THR:H	17:t:155:ARG:HD2	1.78	0.48
20:a:68:C:H2'	20:a:69:G:H8	1.77	0.48
20:a:206:C:H2'	20:a:207:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:a:228:G:H1	20:a:240:U:H3	1.61	0.48
22:d:58:TYR:OH	22:d:88:GLU:OE2	2.27	0.48
23:v:29:ILE:O	23:v:64:ARG:HG2	2.13	0.48
1:b:163:ASP:O	1:b:186:PRO:HG2	2.14	0.48
20:a:240:U:H2'	20:a:241:A:C8	2.48	0.48
7:i:78:ARG:HD3	7:i:141:GLY:HA2	1.96	0.48
20:a:68:C:H2'	20:a:69:G:C8	2.48	0.48
26:8:288:HIS:O	26:8:292:ILE:HG13	2.12	0.48
1:b:6:TRP:N	26:8:348:LYS:HG2	2.29	0.48
1:b:20:PHE:CD1	26:8:329:LYS:HG2	2.47	0.48
3:e:246:GLY:N	22:d:191:LEU:HD22	2.28	0.48
6:h:67:ARG:HG3	26:8:70:ALA:HB3	1.94	0.48
7:i:79:LYS:HB2	7:i:176:ARG:HD3	1.95	0.48
17:t:81:LYS:HE2	20:a:62:G:C8	2.44	0.48
18:u:106:GLU:HB2	21:w:138:TRP:CE2	2.43	0.48
20:a:467:C:N4	20:a:477:G:O2'	2.34	0.48
20:a:142:G:H1	20:a:147:C:H42	1.60	0.48
20:a:1181:G:O2'	20:a:1314:A:OP1	2.30	0.48
20:a:1256:U:H2'	20:a:1257:G:H8	1.78	0.48
20:a:1487:C:H2'	20:a:1488:C:C6	2.49	0.48
3:e:233:ALA:O	3:e:272:SER:OG	2.29	0.48
23:v:120:SER:O	23:v:122:TYR:N	2.46	0.48
1:b:60:LEU:CD1	26:8:65:GLU:HB3	2.39	0.48
3:e:254:ARG:HE	22:d:47:ARG:NH1	2.12	0.48
2:c:24:SER:OG	2:c:25:GLN:N	2.45	0.48
10:l:42:PRO:HB3	10:l:89:ASP:HB3	1.96	0.48
11:m:58:LYS:HE3	25:x:85:PRO:HD3	1.95	0.48
20:a:13:U:O2'	20:a:863:A:OP2	2.29	0.48
20:a:895:A:H2'	20:a:896:G:C8	2.48	0.48
25:x:70:SER:O	25:x:75:ARG:NH1	2.45	0.48
15:r:52:ASN:CA	21:w:149:PRO:HG3	2.44	0.47
20:a:941:U:O2	20:a:992:C:N4	2.47	0.47
22:d:13:ARG:NH1	22:d:31:ASP:OD2	2.47	0.47
20:a:306:C:H2'	20:a:307:A:C8	2.47	0.47
20:a:1035:U:H3	20:a:1048:G:H22	1.61	0.47
14:q:95:LYS:NZ	20:a:208:C:OP2	2.40	0.47
15:r:52:ASN:C	21:w:149:PRO:HG3	2.40	0.47
20:a:1009:U:OP1	24:n:84:ARG:NH1	2.47	0.47
23:v:45:HIS:CD2	23:v:79:VAL:HG23	2.50	0.47
20:a:127:A:H2	20:a:191:G:H1	1.60	0.47
22:d:19:PRO:HG3	22:d:186:LEU:HD12	1.91	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:v:125:TYR:CD2	23:v:167:PHE:CZ	3.02	0.47
9:k:39:THR:O	9:k:55:SER:OG	2.29	0.47
13:p:36:VAL:HG13	13:p:49:ASN:HB3	1.96	0.47
17:t:117:LYS:HD2	17:t:131:LEU:HD11	1.97	0.47
20:a:676:A:H2'	20:a:677:A:H8	1.79	0.47
23:v:24:LEU:HD11	23:v:68:VAL:HB	1.97	0.47
24:n:40:LYS:HA	24:n:40:LYS:HD3	1.59	0.47
26:8:63:ALA:O	26:8:66:ARG:O	2.33	0.47
5:g:99:LEU:HD23	5:g:102:ARG:HE	1.79	0.47
8:j:130:MET:HB2	8:j:168:ASP:HB2	1.96	0.47
22:d:188:ILE:HG22	22:d:189:ASN:H	1.79	0.47
26:8:61:GLU:O	26:8:65:GLU:HG3	2.15	0.47
2:c:183:ARG:HG2	20:a:1055:G:H5''	1.96	0.47
3:e:142:LYS:HG3	3:e:145:LYS:HB3	1.97	0.47
3:e:222:THR:OG1	3:e:223:PHE:N	2.47	0.47
8:j:104:ARG:NH1	20:a:1227:A:OP2	2.48	0.47
9:k:91:ALA:N	9:k:115:LEU:O	2.46	0.47
11:m:121:ARG:HH22	20:a:1257:G:H5'	1.79	0.47
20:a:685:U:H2'	20:a:686:G:C8	2.50	0.47
4:f:110:THR:HA	4:f:203:SER:HA	1.95	0.47
8:j:159:GLU:HB3	24:n:98:SER:HB3	1.97	0.47
15:r:54:LEU:HB3	15:r:58:GLN:HB2	1.97	0.47
20:a:280:A:O2'	20:a:555:A:N1	2.48	0.47
21:w:136:ASP:O	21:w:140:GLU:HG3	2.15	0.47
2:c:165:ALA:HB1	20:a:1006:G:H5''	1.97	0.47
12:o:24:PHE:O	12:o:28:CYS:CB	2.62	0.47
15:r:71:ILE:HD11	20:a:683:U:H1'	1.97	0.47
20:a:883:C:O2'	20:a:1292:C:OP2	2.26	0.47
1:b:5:TYR:CE1	26:8:344:LEU:HD21	2.49	0.47
4:f:114:LEU:HB2	4:f:172:ILE:HB	1.96	0.47
9:k:24:LYS:HA	9:k:86:GLN:HE22	1.80	0.47
10:l:44:LYS:HD2	20:a:1441:A:H5'	1.97	0.47
26:8:257:GLN:NE2	26:8:282:GLY:O	2.48	0.47
1:b:42:ILE:HD11	26:8:291:GLN:NE2	2.30	0.46
1:b:223:PHE:HE2	26:8:359:ARG:HD2	1.80	0.46
19:y:137:PHE:HA	19:y:143:VAL:HG12	1.97	0.46
11:m:136:THR:OG1	11:m:140:CYS:SG	2.73	0.46
1:b:201:ASP:OD2	26:8:66:ARG:HD2	2.15	0.46
20:a:716:A:O2'	20:a:1472:G:N2	2.49	0.46
20:a:1129:G:O2'	20:a:1130:G:N7	2.40	0.46
23:v:35:ASN:HD21	23:v:105:MET:HE3	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:e:246:GLY:CA	22:d:195:GLU:CG	2.94	0.46
10:l:4:ILE:HG12	14:q:89:ARG:HD2	1.98	0.46
20:a:162:C:H2'	20:a:163:G:C8	2.50	0.46
20:a:670:A:N6	20:a:681:A:H61	2.11	0.46
20:a:1304:G:H2'	20:a:1305:G:C8	2.50	0.46
22:d:155:SER:O	22:d:157:ARG:N	2.46	0.46
24:n:40:LYS:C	24:n:41:TRP:CD1	2.94	0.46
1:b:19:HIS:HE1	26:8:332:GLU:CD	2.24	0.46
18:u:100:LEU:CD1	21:w:168:ASN:ND2	2.55	0.46
20:a:527:C:H2'	20:a:528:U:C6	2.50	0.46
21:w:97:PRO:HB2	21:w:117:THR:HB	1.97	0.46
8:j:119:MET:SD	8:j:123:ARG:NE	2.89	0.46
8:j:150:VAL:HG21	20:a:912:G:H21	1.81	0.46
11:m:33:LYS:HA	11:m:39:HIS:HB3	1.96	0.46
20:a:133:A:H2'	20:a:134:C:C6	2.50	0.46
22:d:41:ARG:NH2	22:d:49:GLU:OE1	2.49	0.46
1:b:202:ILE:HD11	6:h:67:ARG:NH2	2.31	0.46
3:e:181:GLY:HA3	3:e:187:VAL:HG12	1.97	0.46
11:m:127:LEU:N	20:a:1256:U:OP1	2.44	0.46
20:a:449:C:O2	20:a:497:C:O2'	2.33	0.46
20:a:876:G:N2	20:a:1481:U:OP1	2.35	0.46
20:a:1374:C:H2'	20:a:1375:A:C8	2.51	0.46
1:b:20:PHE:CG	26:8:329:LYS:HE3	2.51	0.46
6:h:15:ASN:ND2	20:a:774:C:O2	2.49	0.46
6:h:67:ARG:NH1	26:8:65:GLU:C	2.74	0.46
17:t:145:LYS:HD3	17:t:150:ARG:HD2	1.97	0.46
20:a:869:U:H2'	20:a:870:U:C6	2.51	0.46
23:v:42:VAL:HA	23:v:45:HIS:CD2	2.44	0.46
26:8:343:LYS:HA	26:8:346:PHE:CE2	2.50	0.46
11:m:115:LYS:H	11:m:118:ARG:HH21	1.63	0.46
20:a:1271:G:O2'	20:a:1310:C:O2'	2.30	0.46
21:w:111:GLY:HA3	21:w:129:TYR:CZ	2.51	0.46
1:b:196:ASN:HB3	1:b:199:LEU:HG	1.97	0.46
3:e:181:GLY:CA	3:e:186:GLN:O	2.63	0.46
5:g:150:ALA:HA	9:k:70:PHE:HB3	1.98	0.46
6:h:44:PHE:HB3	6:h:77:PHE:HE1	1.81	0.46
9:k:121:ASP:H	15:r:81:GLU:HB2	1.80	0.46
9:k:128:ASN:ND2	20:a:666:A:H5'	2.31	0.46
20:a:255:C:H2'	20:a:256:A:H8	1.81	0.46
20:a:670:A:H61	20:a:681:A:N6	2.11	0.46
20:a:772:U:H2'	20:a:773:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:e:199:SER:O	3:e:203:LYS:HB2	2.16	0.45
6:h:64:ARG:HH12	6:h:75:ASN:HB2	1.81	0.45
7:i:82:ILE:HD11	7:i:135:HIS:CE1	2.52	0.45
9:k:62:ARG:HA	9:k:66:ARG:HD3	1.98	0.45
9:k:121:ASP:HB3	15:r:81:GLU:HG3	1.98	0.45
20:a:423:A:H2	20:a:428:U:H3	1.60	0.45
20:a:1081:C:N3	20:a:1087:G:O6	2.48	0.45
20:a:1166:C:H2'	20:a:1167:U:C6	2.51	0.45
20:a:1361:U:H2'	20:a:1362:A:H8	1.81	0.45
21:w:98:ARG:HA	21:w:99:LEU:HG	1.98	0.45
26:8:318:ASP:OD2	26:8:323:ARG:NH2	2.45	0.45
1:b:60:LEU:HD22	26:8:65:GLU:HG2	1.97	0.45
7:i:162:ARG:HD2	7:i:166:LYS:HD3	1.98	0.45
10:l:5:LYS:H	10:l:8:ILE:HG12	1.82	0.45
12:o:59:LYS:NZ	20:a:604:G:O3'	2.49	0.45
13:p:59:LYS:HD2	13:p:59:LYS:HA	1.69	0.45
15:r:52:ASN:HA	21:w:149:PRO:HG3	1.97	0.45
15:r:57:LYS:NZ	20:a:611:A:H5''	2.32	0.45
20:a:376:U:OP1	20:a:377:G:O2'	2.23	0.45
20:a:786:C:H2'	20:a:787:G:C8	2.51	0.45
20:a:1340:U:H2'	20:a:1341:G:H8	1.81	0.45
20:a:1375:A:H2	20:a:1423:G:H22	1.63	0.45
23:v:17:ASP:HA	23:v:100:LYS:HB3	1.98	0.45
23:v:21:ALA:HB3	23:v:73:VAL:HG13	1.98	0.45
7:i:77:ARG:HG3	7:i:82:ILE:HG22	1.97	0.45
9:k:55:SER:OG	9:k:56:ALA:N	2.50	0.45
20:a:272:G:H2'	20:a:273:G:H8	1.81	0.45
20:a:507:A:H4'	20:a:508:A:H3'	1.97	0.45
20:a:1166:C:H2'	20:a:1167:U:H6	1.81	0.45
22:d:43:GLN:HB3	22:d:47:ARG:HH22	1.81	0.45
22:d:142:GLN:NE2	22:d:145:ILE:O	2.49	0.45
26:8:356:PHE:O	26:8:359:ARG:HG2	2.16	0.45
1:b:79:LYS:NZ	26:8:316:SER:C	2.75	0.45
1:b:141:VAL:O	1:b:145:LEU:CB	2.65	0.45
2:c:27:LYS:NZ	2:c:31:GLU:OE2	2.49	0.45
5:g:120:LEU:O	5:g:124:LEU:HB2	2.15	0.45
9:k:116:LEU:HD21	9:k:119:VAL:HG13	1.98	0.45
20:a:112:G:H2'	20:a:113:A:C8	2.52	0.45
20:a:705:U:OP1	20:a:770:G:O2'	2.33	0.45
1:b:79:LYS:HZ3	26:8:318:ASP:N	2.14	0.45
1:b:177:LEU:HD21	1:b:199:LEU:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:k:128:ASN:HD22	20:a:665:C:H4'	1.81	0.45
20:a:23:G:H2'	20:a:24:C:C6	2.51	0.45
20:a:97:G:H2'	20:a:98:U:C6	2.51	0.45
20:a:232:U:N3	20:a:235:U:OP2	2.41	0.45
20:a:265:U:OP1	20:a:558:U:O2'	2.29	0.45
20:a:585:U:H2'	20:a:586:G:C8	2.51	0.45
22:d:12:ILE:HG23	22:d:17:ALA:HA	1.97	0.45
22:d:184:VAL:O	22:d:184:VAL:HG23	2.15	0.45
23:v:25:TYR:O	23:v:95:VAL:HA	2.15	0.45
23:v:123:LYS:CE	23:v:167:PHE:CG	2.96	0.45
23:v:127:GLY:O	23:v:193:ILE:CA	2.63	0.45
14:q:118:ARG:HD2	20:a:235:U:H4'	1.99	0.45
20:a:925:G:N2	20:a:1311:C:OP2	2.46	0.45
26:8:264:VAL:HG22	26:8:281:GLY:H	1.81	0.45
7:i:81:ALA:HB2	7:i:137:GLY:HA3	1.98	0.45
19:y:126:GLY:O	20:a:478:G:O2'	2.34	0.45
1:b:215:ARG:O	1:b:219:THR:CB	2.64	0.45
20:a:22:G:H2'	20:a:23:G:C8	2.52	0.45
20:a:198:G:H2'	20:a:199:A:C8	2.51	0.45
20:a:621:G:H2'	20:a:622:G:C8	2.52	0.45
20:a:785:G:O6	20:a:798:U:O4	2.35	0.45
20:a:899:U:H3	20:a:1179:G:H1	1.65	0.45
20:a:1253:G:H22	20:a:1279:G:HO2'	1.61	0.45
23:v:126:ILE:HB	23:v:166:GLY:O	2.17	0.45
24:n:9:ARG:HH11	24:n:13:ARG:HH11	1.64	0.45
7:i:90:GLY:H	7:i:128:TYR:HA	1.81	0.45
20:a:182:G:H2'	20:a:183:A:H8	1.82	0.45
20:a:566:C:H5'	20:a:567:U:H5''	1.98	0.45
20:a:607:C:H2'	20:a:608:G:C8	2.52	0.45
21:w:114:LEU:HD13	21:w:141:LEU:HD11	1.98	0.45
24:n:31:ILE:HG12	24:n:44:HIS:HD2	1.82	0.45
24:n:40:LYS:O	24:n:41:TRP:CG	2.70	0.45
26:8:329:LYS:HE2	26:8:332:GLU:OE2	2.16	0.45
10:l:47:SER:N	20:a:477:G:O6	2.42	0.45
20:a:541:U:H2'	20:a:542:U:C6	2.51	0.45
23:v:76:ALA:HA	23:v:79:VAL:HG12	1.97	0.45
23:v:130:ALA:HB2	23:v:191:GLN:HB2	1.99	0.45
8:j:133:VAL:HG13	8:j:166:LEU:HB3	1.98	0.44
9:k:114:ILE:O	9:k:116:LEU:N	2.50	0.44
20:a:662:G:H2'	20:a:663:A:C8	2.52	0.44
20:a:872:A:O2'	20:a:1348:C:OP2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:a:1300:C:P	25:x:56:ARG:HH22	2.40	0.44
23:v:127:GLY:O	23:v:128:ASN:HB3	2.17	0.44
26:8:317:HIS:CA	26:8:324:VAL:HA	2.33	0.44
26:8:329:LYS:HB3	26:8:332:GLU:OE2	2.17	0.44
2:c:141:PHE:O	2:c:145:MET:HB3	2.17	0.44
18:u:106:GLU:HB3	21:w:139:GLU:CD	2.37	0.44
20:a:1123:G:H2'	20:a:1124:A:H8	1.83	0.44
1:b:30:ARG:H	1:b:30:ARG:HD3	1.82	0.44
1:b:40:LYS:HD2	26:8:330:LYS:HE2	1.99	0.44
1:b:141:VAL:O	1:b:145:LEU:HB3	2.17	0.44
20:a:649:U:O2	20:a:651:G:N1	2.51	0.44
1:b:60:LEU:HD22	26:8:65:GLU:CG	2.47	0.44
1:b:135:LYS:O	1:b:139:ALA:HB2	2.17	0.44
18:u:96:GLU:HB3	21:w:172:GLN:NE2	2.31	0.44
24:n:3:ARG:HH21	24:n:6:LEU:HD11	1.81	0.44
26:8:69:ASN:HB3	26:8:73:GLU:HG2	1.99	0.44
1:b:136:ARG:NH1	20:a:1106:C:O3'	2.51	0.44
3:e:197:VAL:HG23	3:e:198:VAL:HG23	1.99	0.44
8:j:143:CYS:HG	20:a:1316:G:HO2'	1.63	0.44
19:y:134:VAL:O	19:y:145:ARG:HA	2.17	0.44
20:a:137:C:H2'	20:a:138:A:H8	1.83	0.44
20:a:1456:A:H2'	20:a:1457:G:C8	2.53	0.44
23:v:34:ASN:OD1	23:v:35:ASN:N	2.50	0.44
23:v:183:LEU:HD21	23:v:193:ILE:CG2	2.48	0.44
24:n:20:TYR:HE2	24:n:51:PRO:HB3	1.81	0.44
3:e:165:VAL:HG23	20:a:871:G:H1'	2.00	0.44
6:h:67:ARG:NH2	26:8:66:ARG:HA	2.32	0.44
17:t:85:GLN:O	17:t:89:ARG:HG2	2.18	0.44
20:a:585:U:H2'	20:a:586:G:H8	1.83	0.44
22:d:88:GLU:HA	22:d:93:ASN:HD22	1.82	0.44
5:g:98:ALA:O	5:g:102:ARG:HB2	2.18	0.44
20:a:1361:U:H2'	20:a:1362:A:C8	2.51	0.44
20:a:1363:U:H2'	20:a:1364:G:C8	2.51	0.44
22:d:191:LEU:O	22:d:195:GLU:HG3	2.18	0.44
24:n:37:LEU:O	24:n:41:TRP:CH2	2.70	0.44
26:8:354:GLN:HA	26:8:357:ARG:NH1	2.33	0.44
1:b:92:ARG:HE	1:b:229:ARG:HD2	1.82	0.44
1:b:201:ASP:HB2	26:8:66:ARG:HB3	1.99	0.44
1:b:211:ILE:CG1	26:8:317:HIS:CE1	2.98	0.44
9:k:83:VAL:HG22	9:k:86:GLN:HB2	1.98	0.44
20:a:14:U:H1'	20:a:863:A:H5''	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:a:283:C:H2'	20:a:284:A:C8	2.53	0.44
20:a:684:C:H2'	20:a:685:U:H6	1.82	0.44
20:a:1071:U:H2'	20:a:1072:A:H8	1.83	0.44
22:d:21:LEU:HB2	22:d:104:ILE:HD12	2.00	0.44
23:v:52:GLU:OE1	23:v:103:GLU:HA	2.18	0.44
2:c:15:THR:HG22	2:c:192:LYS:HD3	1.99	0.44
6:h:67:ARG:NH1	26:8:65:GLU:O	2.46	0.44
20:a:239:U:H2'	20:a:240:U:C6	2.53	0.44
26:8:364:GLU:HA	26:8:364:GLU:OE1	2.18	0.44
1:b:19:HIS:CE1	26:8:332:GLU:HB3	2.53	0.43
2:c:92:VAL:HA	2:c:95:LEU:HD13	2.00	0.43
4:f:158:ARG:HB2	4:f:168:TYR:HE2	1.82	0.43
20:a:155:A:H2'	20:a:156:A:C8	2.53	0.43
20:a:292:A:H2'	20:a:293:C:H6	1.84	0.43
20:a:387:G:H2'	20:a:388:G:H8	1.83	0.43
20:a:1274:U:H2'	20:a:1275:G:H8	1.82	0.43
20:a:1400:C:H3'	20:a:1401:A:C8	2.53	0.43
22:d:196:TYR:CD1	22:d:196:TYR:C	2.96	0.43
1:b:7:ASN:ND2	26:8:348:LYS:HB3	2.32	0.43
1:b:40:LYS:HB2	26:8:330:LYS:HZ3	1.82	0.43
6:h:66:ARG:HD3	6:h:74:LEU:HD13	2.00	0.43
7:i:180:ARG:HH21	20:a:1135:G:H4'	1.83	0.43
13:p:6:LEU:HD22	13:p:17:TYR:HB3	2.00	0.43
18:u:100:LEU:HG	21:w:164:THR:HG23	2.00	0.43
20:a:466:C:H2'	20:a:478:G:C8	2.52	0.43
20:a:1366:G:O2'	20:a:1432:A:N6	2.51	0.43
21:w:112:LEU:HD12	21:w:137:ALA:HB1	1.98	0.43
26:8:367:ALA:HB3	26:8:368:ARG:HG2	2.00	0.43
2:c:42:CYS:O	2:c:46:TYR:CB	2.66	0.43
19:y:151:GLU:H	19:y:151:GLU:HG3	1.60	0.43
20:a:185:G:H22	23:v:98:THR:HA	1.82	0.43
20:a:398:C:O2'	20:a:489:G:OP1	2.35	0.43
20:a:716:A:N3	20:a:1461:U:O2'	2.47	0.43
21:w:144:LEU:O	21:w:148:LYS:HG2	2.18	0.43
1:b:202:ILE:HG12	26:8:66:ARG:CG	2.48	0.43
1:b:223:PHE:CE1	26:8:355:THR:HB	2.54	0.43
6:h:67:ARG:HD3	26:8:69:ASN:N	2.33	0.43
11:m:47:ILE:HD11	20:a:1250:U:C4	2.53	0.43
12:o:43:HIS:CE1	12:o:46:ASP:HB2	2.53	0.43
20:a:610:U:H2'	20:a:611:A:C8	2.53	0.43
20:a:663:A:H2'	20:a:664:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:d:187:LYS:C	22:d:188:ILE:CG1	2.92	0.43
5:g:15:ASP:N	5:g:20:ASN:O	2.52	0.43
6:h:67:ARG:NH2	26:8:65:GLU:O	2.43	0.43
11:m:53:GLU:HB2	11:m:96:GLU:HG2	2.00	0.43
19:y:107:HIS:HA	19:y:140:ARG:CZ	2.49	0.43
24:n:43:ILE:O	24:n:46:LYS:CA	2.66	0.43
5:g:14:SER:O	5:g:24:ASN:ND2	2.52	0.43
6:h:96:ILE:HA	6:h:97:PRO:HD3	1.72	0.43
18:u:106:GLU:OE2	21:w:136:ASP:OD2	2.36	0.43
20:a:165:A:H2'	20:a:177:A:H61	1.84	0.43
20:a:732:G:H2'	20:a:733:G:H8	1.83	0.43
26:8:369:ALA:O	26:8:371:MET:HG2	2.18	0.43
1:b:52:ARG:CD	26:8:73:GLU:HG3	2.45	0.43
6:h:67:ARG:CD	26:8:67:CYS:C	2.91	0.43
6:h:109:SER:HA	6:h:114:ILE:HG22	2.00	0.43
16:s:23:ASN:ND2	16:s:43:THR:O	2.52	0.43
17:t:136:TYR:CE2	20:a:175:G:H4'	2.53	0.43
20:a:684:C:H2'	20:a:685:U:C6	2.53	0.43
22:d:51:LYS:HE3	22:d:51:LYS:HB3	1.92	0.43
1:b:21:GLY:HA2	1:b:207:ASN:HB2	2.01	0.43
2:c:147:LYS:O	2:c:151:LEU:CB	2.66	0.43
20:a:1212:C:N4	20:a:1220:G:O6	2.52	0.43
22:d:70:ARG:O	22:d:74:LYS:HB2	2.19	0.43
4:f:110:THR:O	4:f:175:LEU:HA	2.19	0.43
20:a:20:C:H2'	20:a:21:U:C6	2.54	0.43
20:a:574:U:H2'	20:a:575:G:C8	2.54	0.43
24:n:22:LEU:O	24:n:26:SER:OG	2.35	0.43
20:a:35:C:H2'	20:a:36:G:C8	2.52	0.43
20:a:227:U:H2'	20:a:228:G:C8	2.53	0.43
23:v:80:ILE:HD13	23:v:97:ILE:HG22	2.01	0.43
23:v:172:SER:HB3	23:v:175:GLU:OE1	2.19	0.43
26:8:72:MET:HB3	26:8:72:MET:HE3	1.71	0.43
8:j:119:MET:HE2	8:j:167:ILE:HD11	2.00	0.42
8:j:129:ILE:HA	8:j:170:LEU:HD13	2.01	0.42
8:j:150:VAL:HG13	20:a:921:C:O2'	2.19	0.42
16:s:13:ASN:HB3	24:n:46:LYS:HZ3	1.84	0.42
19:y:130:ARG:HG2	19:y:153:LEU:HG	2.00	0.42
20:a:372:C:O3'	22:d:67:LYS:NZ	2.48	0.42
23:v:156:THR:O	23:v:160:SER:HA	2.18	0.42
23:v:172:SER:HB3	23:v:175:GLU:CD	2.44	0.42
20:a:131:G:H2'	20:a:132:A:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:a:1384:G:H2'	20:a:1385:U:H6	1.83	0.42
21:w:111:GLY:HA2	21:w:130:TYR:O	2.19	0.42
22:d:80:GLY:HA3	22:d:190:GLU:HB3	2.01	0.42
1:b:209:ASP:HA	26:8:316:SER:HA	2.01	0.42
7:i:124:TYR:HA	7:i:127:ASN:HD22	1.84	0.42
21:w:119:PRO:HG3	21:w:150:TRP:CG	2.53	0.42
3:e:218:THR:OG1	3:e:219:LYS:N	2.52	0.42
6:h:67:ARG:NH1	26:8:67:CYS:H	2.17	0.42
6:h:81:ARG:HD2	6:h:131:CYS:HB3	2.02	0.42
11:m:44:ILE:HB	11:m:47:ILE:HD12	2.02	0.42
15:r:70:ARG:HB3	15:r:77:PHE:HE1	1.84	0.42
17:t:117:LYS:NZ	17:t:127:PRO:O	2.52	0.42
20:a:18:U:H2'	20:a:19:C:C6	2.55	0.42
20:a:1244:C:H1'	20:a:1250:U:H5	1.84	0.42
20:a:1275:G:H5''	25:x:73:ASN:ND2	2.33	0.42
23:v:127:GLY:O	23:v:193:ILE:HG23	2.18	0.42
7:i:78:ARG:H	7:i:145:ALA:HB2	1.84	0.42
20:a:1464:U:H2'	20:a:1465:G:H8	1.85	0.42
2:c:11:ARG:NH1	2:c:186:LEU:O	2.44	0.42
2:c:187:GLN:NE2	20:a:1137:U:O2'	2.47	0.42
3:e:241:ALA:HB2	3:e:266:LEU:HD12	2.01	0.42
20:a:486:G:H2'	20:a:487:A:C8	2.55	0.42
20:a:1214:G:N2	20:a:1217:A:OP2	2.30	0.42
23:v:24:LEU:HD13	23:v:79:VAL:CG1	2.49	0.42
10:l:52:VAL:HG12	10:l:66:TYR:HA	2.00	0.42
10:l:121:LYS:NZ	20:a:448:G:H5''	2.35	0.42
11:m:135:ARG:HD3	20:a:897:C:C5	2.54	0.42
17:t:89:ARG:HH12	20:a:300:A:H61	1.66	0.42
18:u:103:PHE:CE2	21:w:138:TRP:CB	2.98	0.42
20:a:139:G:H1	20:a:150:C:N4	2.16	0.42
20:a:182:G:H2'	20:a:183:A:C8	2.55	0.42
20:a:732:G:H2'	20:a:733:G:C8	2.55	0.42
20:a:1216:G:H2'	20:a:1217:A:C8	2.55	0.42
21:w:118:ILE:HG22	21:w:119:PRO:O	2.19	0.42
1:b:14:MET:O	1:b:19:HIS:NE2	2.36	0.42
3:e:199:SER:O	3:e:203:LYS:CB	2.68	0.42
20:a:1044:U:P	20:a:1057:G:H1	2.42	0.42
23:v:83:LEU:HD23	23:v:95:VAL:CG2	2.48	0.42
2:c:196:CYS:SG	2:c:197:ALA:N	2.93	0.42
16:s:30:ILE:HG23	16:s:59:PRO:HB3	2.01	0.42
17:t:137:SER:O	17:t:140:ASP:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:a:490:A:O3'	22:d:14:ARG:NH1	2.53	0.42
20:a:780:G:N2	20:a:803:U:O2	2.45	0.42
1:b:112:GLU:OE2	1:b:116:HIS:NE2	2.53	0.41
2:c:12:LEU:HD23	2:c:12:LEU:HA	1.88	0.41
14:q:66:ILE:HD11	14:q:77:GLU:HG3	2.02	0.41
19:y:124:SER:OG	19:y:125:LYS:N	2.52	0.41
6:h:67:ARG:NH1	26:8:67:CYS:N	2.67	0.41
20:a:449:C:H2'	20:a:450:A:H8	1.84	0.41
20:a:795:C:H2'	20:a:796:C:C6	2.55	0.41
26:8:271:LEU:CD1	26:8:304:LEU:HA	2.50	0.41
1:b:40:LYS:NZ	26:8:294:HIS:CE1	2.88	0.41
2:c:61:ALA:HA	2:c:125:ASN:HD22	1.84	0.41
17:t:99:GLU:HB2	17:t:150:ARG:NH2	2.36	0.41
21:w:114:LEU:O	21:w:127:SER:HA	2.20	0.41
23:v:16:SER:HA	23:v:22:ARG:HD2	2.02	0.41
1:b:40:LYS:HB2	26:8:330:LYS:NZ	2.35	0.41
1:b:196:ASN:HD22	1:b:199:LEU:HG	1.85	0.41
18:u:106:GLU:OE1	21:w:136:ASP:CG	2.64	0.41
24:n:8:GLN:HA	24:n:11:LYS:HB2	2.02	0.41
26:8:280:ILE:HD13	26:8:280:ILE:HG21	1.69	0.41
1:b:40:LYS:HD3	26:8:290:SER:CA	2.50	0.41
1:b:79:LYS:CE	26:8:317:HIS:C	2.93	0.41
3:e:247:VAL:O	22:d:195:GLU:CD	2.63	0.41
5:g:50:ILE:HD12	5:g:50:ILE:HA	1.85	0.41
8:j:129:ILE:HG23	8:j:169:ILE:HA	2.02	0.41
10:l:11:THR:OG1	10:l:12:ARG:N	2.42	0.41
20:a:205:U:H2'	20:a:206:C:C6	2.55	0.41
20:a:1373:C:H2'	20:a:1374:C:C6	2.55	0.41
22:d:57:HIS:CG	22:d:186:LEU:HD22	2.53	0.41
20:a:1440:G:O5'	20:a:1440:G:H8	2.03	0.41
24:n:25:ARG:HH11	24:n:55:ALA:HA	1.85	0.41
24:n:31:ILE:HG12	24:n:44:HIS:CD2	2.56	0.41
3:e:223:PHE:HB2	3:e:240:PRO:HB3	2.02	0.41
7:i:94:PHE:HB2	7:i:130:VAL:O	2.20	0.41
11:m:70:ILE:HG23	25:x:89:PRO:O	2.19	0.41
20:a:786:C:H42	20:a:797:G:H1	1.68	0.41
11:m:59:ARG:HA	11:m:62:TYR:HB2	2.03	0.41
11:m:137:LYS:HG2	11:m:140:CYS:HB2	2.03	0.41
20:a:785:G:N1	20:a:798:U:N3	2.66	0.41
20:a:1110:C:H2'	20:a:1111:G:H8	1.85	0.41
20:a:1176:C:H2'	20:a:1177:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:8:268:VAL:HG11	26:8:305:GLN:HB3	2.03	0.41
1:b:31:MET:HB3	1:b:35:ILE:HG13	2.02	0.41
1:b:79:LYS:NZ	26:8:317:HIS:C	2.72	0.41
2:c:77:HIS:HB3	2:c:117:ILE:HD11	2.02	0.41
6:h:9:ILE:HD12	6:h:32:THR:HG23	2.03	0.41
11:m:40:GLY:H	11:m:48:ARG:CZ	2.33	0.41
12:o:24:PHE:O	12:o:28:CYS:HB2	2.21	0.41
18:u:98:ARG:HE	21:w:168:ASN:CB	2.19	0.41
20:a:355:G:H2'	20:a:356:C:C6	2.56	0.41
20:a:660:A:H2'	20:a:661:A:C8	2.56	0.41
20:a:912:G:H2'	20:a:913:A:H8	1.86	0.41
20:a:1100:A:H2'	20:a:1101:A:C8	2.56	0.41
21:w:145:LEU:CD1	21:w:156:MET:HG3	2.51	0.41
23:v:100:LYS:HA	23:v:101:PRO:HD3	1.77	0.41
23:v:128:ASN:OD1	23:v:191:GLN:HB3	2.21	0.41
26:8:315:LEU:HD23	26:8:327:SER:H	1.85	0.41
3:e:297:ARG:HH12	6:h:66:ARG:NH1	2.19	0.41
6:h:77:PHE:HE2	6:h:79:LEU:HD12	1.85	0.41
6:h:80:LYS:O	6:h:131:CYS:HB2	2.21	0.41
15:r:44:GLY:O	15:r:70:ARG:NH1	2.54	0.41
20:a:198:G:H2'	20:a:199:A:H8	1.85	0.41
20:a:970:G:H2'	20:a:971:G:C8	2.57	0.40
20:a:1265:C:N3	24:n:52:ARG:NH1	2.69	0.40
20:a:1384:G:H2'	20:a:1385:U:C6	2.56	0.40
1:b:145:LEU:O	1:b:149:GLN:CB	2.68	0.40
2:c:100:GLN:O	2:c:104:ASN:ND2	2.54	0.40
3:e:254:ARG:HH22	22:d:195:GLU:HB3	1.85	0.40
4:f:147:ARG:HD2	4:f:147:ARG:HA	1.92	0.40
8:j:129:ILE:HG12	8:j:169:ILE:HG23	2.03	0.40
9:k:110:ARG:NH1	18:u:98:ARG:O	2.39	0.40
10:l:23:ALA:HB2	10:l:61:PHE:HD2	1.87	0.40
20:a:137:C:H2'	20:a:138:A:C8	2.55	0.40
20:a:175:G:H2'	20:a:176:C:C6	2.56	0.40
20:a:717:G:H4'	20:a:1462:A:H4'	2.02	0.40
10:l:51:LYS:HB2	10:l:51:LYS:HE2	1.90	0.40
11:m:120:TYR:HB2	11:m:127:LEU:HD21	2.04	0.40
11:m:126:LYS:HZ1	11:m:136:THR:HG22	1.84	0.40
17:t:85:GLN:O	17:t:88:THR:N	2.54	0.40
19:y:104:LYS:HE3	20:a:738:A:H1'	2.03	0.40
20:a:425:C:H2'	20:a:426:A:C8	2.56	0.40
20:a:1301:G:P	25:x:56:ARG:HH21	2.44	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:a:1422:A:H2'	20:a:1423:G:C8	2.56	0.40
20:a:3:U:H5'	20:a:4:C:OP2	2.22	0.40
20:a:461:C:H2'	20:a:462:U:C6	2.56	0.40
20:a:785:G:H2'	20:a:786:C:H6	1.86	0.40
8:j:110:LEU:O	8:j:114:SER:HB2	2.20	0.40
16:s:16:LEU:HD23	24:n:46:LYS:HZ1	1.85	0.40
18:u:134:ARG:NH1	20:a:671:C:O5'	2.54	0.40
19:y:107:HIS:HB3	19:y:109:VAL:HG23	2.04	0.40
20:a:292:A:H2'	20:a:293:C:C6	2.57	0.40
20:a:530:U:OP2	20:a:706:G:N1	2.48	0.40
20:a:1256:U:N3	20:a:1277:A:C2	2.90	0.40
21:w:99:LEU:HD22	21:w:116:GLN:HA	2.02	0.40
21:w:145:LEU:HA	21:w:145:LEU:HD23	1.79	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	
1	b	225/236 (95%)	195 (87%)	29 (13%)	1 (0%)	30	60
2	c	211/218 (97%)	181 (86%)	28 (13%)	2 (1%)	14	45
3	e	169/253 (67%)	150 (89%)	17 (10%)	2 (1%)	10	40
4	f	109/146 (75%)	85 (78%)	24 (22%)	0	100	100
5	g	147/155 (95%)	130 (88%)	16 (11%)	1 (1%)	18	50
6	h	132/134 (98%)	116 (88%)	16 (12%)	0	100	100
7	i	131/157 (83%)	107 (82%)	23 (18%)	1 (1%)	16	48
8	j	96/122 (79%)	83 (86%)	13 (14%)	0	100	100
9	k	116/138 (84%)	104 (90%)	12 (10%)	0	100	100
10	l	121/123 (98%)	100 (83%)	21 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	m	108/126 (86%)	90 (83%)	18 (17%)	0	100	100
12	o	60/90 (67%)	59 (98%)	1 (2%)	0	100	100
13	p	78/88 (89%)	61 (78%)	17 (22%)	0	100	100
14	q	76/108 (70%)	64 (84%)	12 (16%)	0	100	100
15	r	62/101 (61%)	58 (94%)	4 (6%)	0	100	100
16	s	76/92 (83%)	61 (80%)	15 (20%)	0	100	100
17	t	103/108 (95%)	93 (90%)	10 (10%)	0	100	100
18	u	42/137 (31%)	39 (93%)	3 (7%)	0	100	100
19	y	106/236 (45%)	96 (91%)	10 (9%)	0	100	100
21	w	82/121 (68%)	79 (96%)	0	3 (4%)	2	22
22	d	197/201 (98%)	173 (88%)	22 (11%)	2 (1%)	12	43
23	v	188/198 (95%)	171 (91%)	14 (7%)	3 (2%)	7	35
24	n	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
25	x	35/47 (74%)	30 (86%)	4 (11%)	1 (3%)	3	26
26	8	150/370 (40%)	116 (77%)	18 (12%)	16 (11%)	0	5
All	All	2917/3805 (77%)	2531 (87%)	354 (12%)	32 (1%)	14	42

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	e	148	ILE
21	w	149	PRO
23	v	105	MET
26	8	72	MET
26	8	73	GLU
26	8	299	ASP
26	8	300	ILE
26	8	303	VAL
26	8	316	SER
26	8	330	LYS
26	8	366	MET
26	8	367	ALA
26	8	370	ASP
26	8	371	MET
2	c	89	PRO
22	d	5	ARG
23	v	121	PRO

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Mol	Chain	Res	Type
26	8	360	ILE
26	8	368	ARG
1	b	169	ASP
7	i	159	ALA
21	w	150	TRP
2	c	88	ARG
3	e	302	PRO
25	x	90	ILE
26	8	306	PRO
26	8	364	GLU
5	g	9	GLU
22	d	168	PRO
23	v	120	SER
21	w	119	PRO
26	8	307	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	192/201 (96%)	191 (100%)	1 (0%)	81	80
2	c	185/188 (98%)	185 (100%)	0	100	100
3	e	132/203 (65%)	128 (97%)	4 (3%)	36	57
4	f	98/125 (78%)	97 (99%)	1 (1%)	68	74
5	g	120/126 (95%)	120 (100%)	0	100	100
6	h	117/117 (100%)	115 (98%)	2 (2%)	53	67
7	i	103/123 (84%)	103 (100%)	0	100	100
8	j	90/110 (82%)	89 (99%)	1 (1%)	65	73
9	k	92/109 (84%)	91 (99%)	1 (1%)	65	73
10	l	106/106 (100%)	106 (100%)	0	100	100
11	m	97/109 (89%)	97 (100%)	0	100	100
12	o	58/85 (68%)	58 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	p	71/79 (90%)	70 (99%)	1 (1%)	59	70
14	q	70/95 (74%)	70 (100%)	0	100	100
15	r	56/96 (58%)	56 (100%)	0	100	100
16	s	67/81 (83%)	67 (100%)	0	100	100
17	t	86/89 (97%)	86 (100%)	0	100	100
18	u	40/118 (34%)	40 (100%)	0	100	100
19	y	97/213 (46%)	95 (98%)	2 (2%)	47	64
21	w	75/109 (69%)	74 (99%)	1 (1%)	61	71
22	d	178/180 (99%)	175 (98%)	3 (2%)	53	67
23	v	160/168 (95%)	157 (98%)	3 (2%)	50	65
24	n	89/90 (99%)	89 (100%)	0	100	100
25	x	28/37 (76%)	28 (100%)	0	100	100
26	8	129/310 (42%)	123 (95%)	6 (5%)	23	48
All	All	2536/3267 (78%)	2510 (99%)	26 (1%)	65	74

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	201	ASP
3	e	212	ILE
3	e	266	LEU
3	e	303	MET
3	e	305	GLU
4	f	113	VAL
6	h	67	ARG
6	h	79	LEU
8	j	133	VAL
9	k	25	ILE
13	p	46	THR
19	y	114	VAL
19	y	159	LEU
21	w	167	ILE
22	d	21	LEU
22	d	160	LEU
22	d	174	LEU
23	v	24	LEU
23	v	37	GLU

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Mol	Chain	Res	Type
23	v	175	GLU
26	8	283	ILE
26	8	303	VAL
26	8	304	LEU
26	8	305	GLN
26	8	314	ILE
26	8	368	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
2	c	18	HIS
2	c	34	GLN
2	c	100	GLN
2	c	104	ASN
2	c	125	ASN
2	c	187	GLN
3	e	158	GLN
3	e	171	HIS
3	e	264	ASN
3	e	278	ASN
4	f	160	ASN
5	g	64	GLN
5	g	85	HIS
5	g	148	ASN
6	h	19	ASN
6	h	51	HIS
6	h	68	ASN
6	h	94	GLN
7	i	127	ASN
8	j	149	HIS
8	j	151	HIS
9	k	127	HIS
9	k	128	ASN
10	l	77	HIS
11	m	56	ASN
11	m	65	GLN
11	m	83	ASN
11	m	125	HIS
15	r	59	GLN
15	r	83	GLN
16	s	69	HIS

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Mol	Chain	Res	Type
17	t	85	GLN
18	u	124	ASN
19	y	165	GLN
21	w	109	ASN
21	w	116	GLN
21	w	155	GLN
21	w	162	GLN
22	d	57	HIS
22	d	112	ASN
22	d	115	HIS
22	d	142	GLN
23	v	45	HIS
23	v	96	ASN
23	v	154	GLN
23	v	163	ASN
23	v	196	ASN
24	n	15	ASN
24	n	44	HIS
26	8	58	GLN
26	8	257	GLN
26	8	269	GLN
26	8	294	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	a	1477/1491 (99%)	310 (20%)	0

All (310) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	a	5	A
20	a	6	U
20	a	7	G
20	a	10	G
20	a	31	U
20	a	32	G
20	a	33	A
20	a	40	G
20	a	45	A
20	a	48	C

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Mol	Chain	Res	Type
20	a	49	U
20	a	50	U
20	a	52	A
20	a	55	C
20	a	62	G
20	a	72	A
20	a	75	U
20	a	82	U
20	a	83	C
20	a	85	A
20	a	90	C
20	a	92	G
20	a	100	A
20	a	104	A
20	a	105	C
20	a	106	G
20	a	114	A
20	a	115	C
20	a	121	C
20	a	127	A
20	a	130	G
20	a	143	G
20	a	147	C
20	a	148	G
20	a	150	C
20	a	152	G
20	a	166	G
20	a	167	G
20	a	174	A
20	a	180	A
20	a	191	G
20	a	202	G
20	a	216	U
20	a	218	G
20	a	221	A
20	a	222	G
20	a	230	G
20	a	237	G
20	a	238	C
20	a	252	G
20	a	260	G
20	a	269	A

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Mol	Chain	Res	Type
20	a	277	A
20	a	287	C
20	a	296	A
20	a	299	C
20	a	300	A
20	a	303	G
20	a	315	A
20	a	317	G
20	a	322	G
20	a	323	C
20	a	324	A
20	a	325	G
20	a	338	U
20	a	343	C
20	a	344	A
20	a	349	G
20	a	353	A
20	a	355	G
20	a	358	U
20	a	360	A
20	a	369	U
20	a	377	G
20	a	382	C
20	a	383	A
20	a	384	G
20	a	392	A
20	a	393	C
20	a	395	G
20	a	399	G
20	a	400	U
20	a	410	U
20	a	411	U
20	a	416	G
20	a	423	A
20	a	424	G
20	a	426	A
20	a	429	G
20	a	432	G
20	a	433	G
20	a	434	U
20	a	443	A
20	a	444	A

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Mol	Chain	Res	Type
20	a	447	A
20	a	453	G
20	a	456	U
20	a	459	C
20	a	466	C
20	a	469	G
20	a	472	G
20	a	475	G
20	a	478	G
20	a	479	U
20	a	481	A
20	a	495	A
20	a	507	A
20	a	510	G
20	a	511	A
20	a	512	U
20	a	514	G
20	a	520	A
20	a	521	A
20	a	524	C
20	a	525	G
20	a	536	G
20	a	543	A
20	a	544	A
20	a	566	C
20	a	577	A
20	a	578	C
20	a	579	A
20	a	580	G
20	a	600	U
20	a	601	G
20	a	602	G
20	a	613	G
20	a	630	G
20	a	650	A
20	a	651	G
20	a	659	A
20	a	660	A
20	a	669	A
20	a	670	A
20	a	671	C
20	a	672	G

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Mol	Chain	Res	Type
20	a	695	A
20	a	696	C
20	a	697	A
20	a	703	A
20	a	725	A
20	a	741	U
20	a	742	A
20	a	757	G
20	a	762	A
20	a	763	A
20	a	765	C
20	a	766	G
20	a	768	U
20	a	769	G
20	a	775	U
20	a	776	A
20	a	780	G
20	a	784	U
20	a	790	U
20	a	791	C
20	a	794	C
20	a	795	C
20	a	796	C
20	a	797	G
20	a	798	U
20	a	799	G
20	a	821	A
20	a	822	A
20	a	825	A
20	a	834	G
20	a	838	A
20	a	849	A
20	a	851	G
20	a	863	A
20	a	875	G
20	a	876	G
20	a	883	C
20	a	884	A
20	a	909	U
20	a	915	G
20	a	918	A
20	a	920	G

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Mol	Chain	Res	Type
20	a	924	A
20	a	925	G
20	a	926	A
20	a	938	G
20	a	941	U
20	a	942	G
20	a	945	A
20	a	946	U
20	a	948	C
20	a	953	A
20	a	954	A
20	a	958	U
20	a	961	U
20	a	963	A
20	a	964	A
20	a	969	A
20	a	973	G
20	a	974	U
20	a	975	G
20	a	978	U
20	a	980	C
20	a	981	G
20	a	982	G
20	a	985	A
20	a	986	C
20	a	992	C
20	a	994	C
20	a	995	A
20	a	1003	C
20	a	1005	U
20	a	1014	U
20	a	1027	U
20	a	1034	U
20	a	1038	G
20	a	1041	A
20	a	1043	G
20	a	1044	U
20	a	1047	C
20	a	1050	A
20	a	1057	G
20	a	1066	G
20	a	1073	G

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Mol	Chain	Res	Type
20	a	1074	U
20	a	1075	U
20	a	1079	A
20	a	1080	A
20	a	1082	G
20	a	1088	U
20	a	1089	U
20	a	1091	G
20	a	1095	C
20	a	1099	G
20	a	1100	A
20	a	1105	A
20	a	1107	U
20	a	1114	G
20	a	1115	A
20	a	1116	U
20	a	1119	G
20	a	1130	G
20	a	1131	U
20	a	1132	G
20	a	1144	A
20	a	1149	A
20	a	1150	U
20	a	1160	U
20	a	1161	A
20	a	1162	U
20	a	1163	G
20	a	1174	C
20	a	1175	A
20	a	1184	A
20	a	1186	A
20	a	1187	A
20	a	1188	U
20	a	1189	G
20	a	1195	G
20	a	1198	A
20	a	1204	U
20	a	1205	C
20	a	1206	G
20	a	1208	G
20	a	1222	G
20	a	1223	A

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Mol	Chain	Res	Type
20	a	1227	A
20	a	1229	C
20	a	1233	A
20	a	1234	A
20	a	1235	A
20	a	1243	C
20	a	1246	C
20	a	1247	A
20	a	1248	G
20	a	1250	U
20	a	1253	G
20	a	1265	C
20	a	1266	A
20	a	1267	A
20	a	1271	G
20	a	1280	A
20	a	1288	A
20	a	1294	A
20	a	1295	G
20	a	1311	C
20	a	1312	A
20	a	1317	G
20	a	1319	G
20	a	1327	C
20	a	1328	G
20	a	1346	C
20	a	1347	A
20	a	1351	C
20	a	1368	G
20	a	1371	G
20	a	1390	A
20	a	1395	A
20	a	1397	C
20	a	1400	C
20	a	1401	A
20	a	1402	A
20	a	1403	G
20	a	1405	A
20	a	1418	A
20	a	1441	A
20	a	1443	G
20	a	1452	A

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Mol	Chain	Res	Type
20	a	1454	G
20	a	1455	U
20	a	1466	G
20	a	1478	G
20	a	1479	G
20	a	1480	A

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.

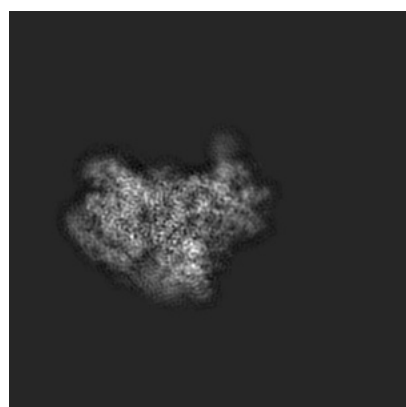
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6710. These allow visual inspection of the internal detail of the map and identification of artifacts.

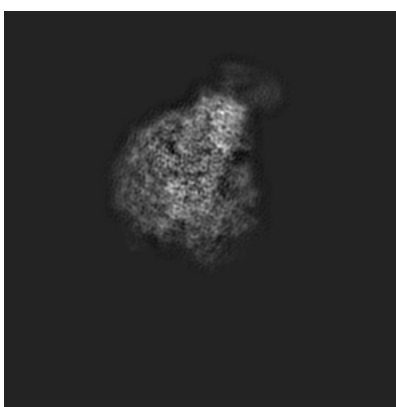
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

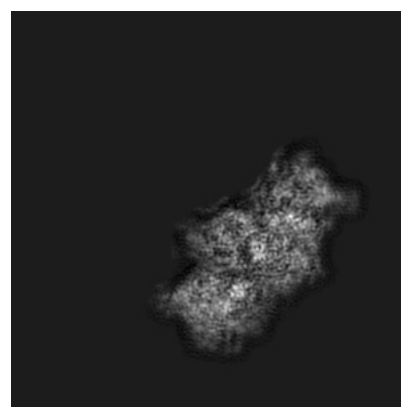
6.1.1 Primary map



X



Y

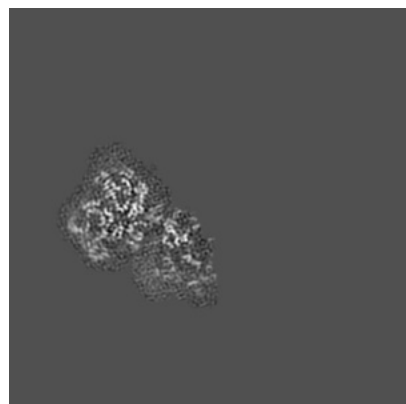


Z

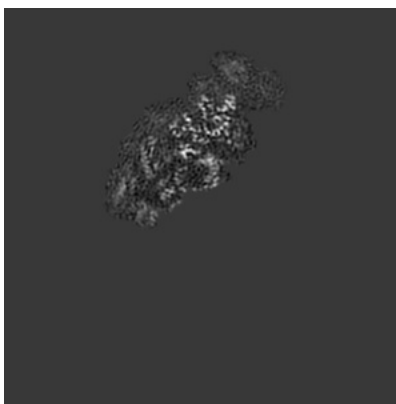
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

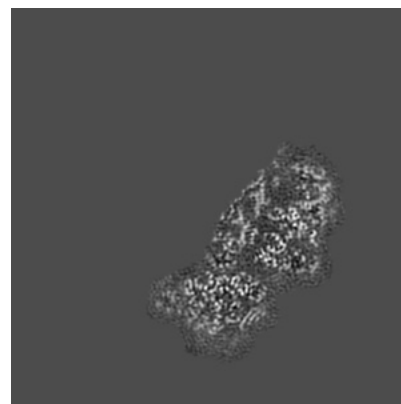
6.2.1 Primary map



X Index: 192



Y Index: 192

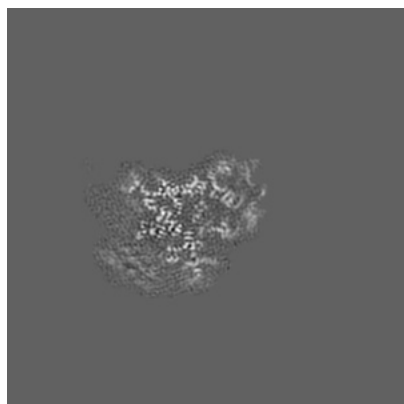


Z Index: 192

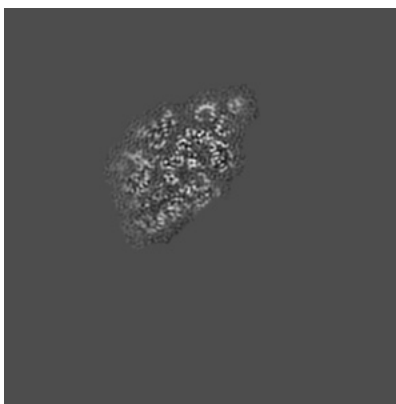
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

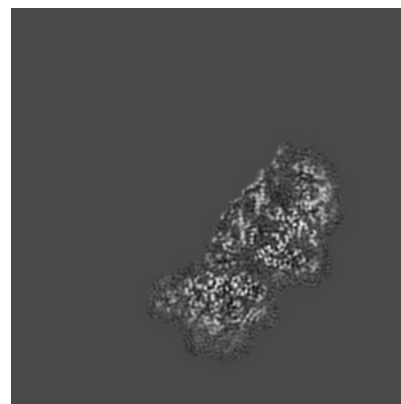
6.3.1 Primary map



X Index: 253



Y Index: 160

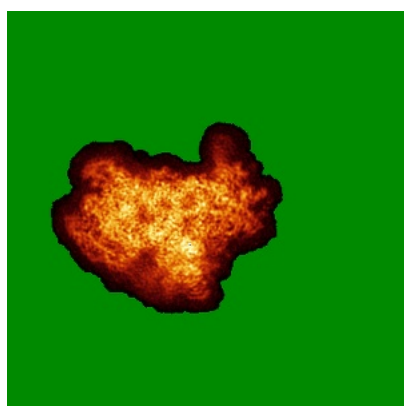


Z Index: 191

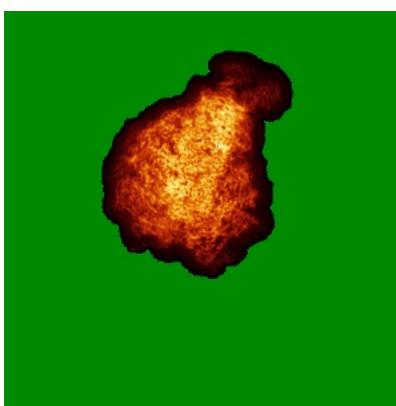
The images above show the largest variance slices of the map in three orthogonal directions.

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

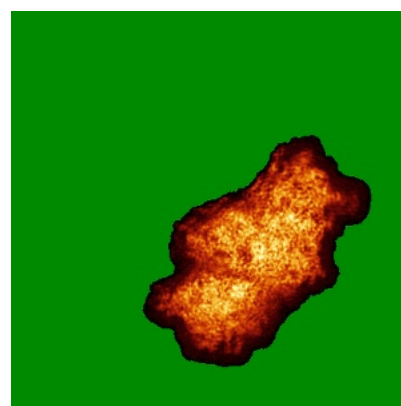
6.4.1 Primary map



X



Y

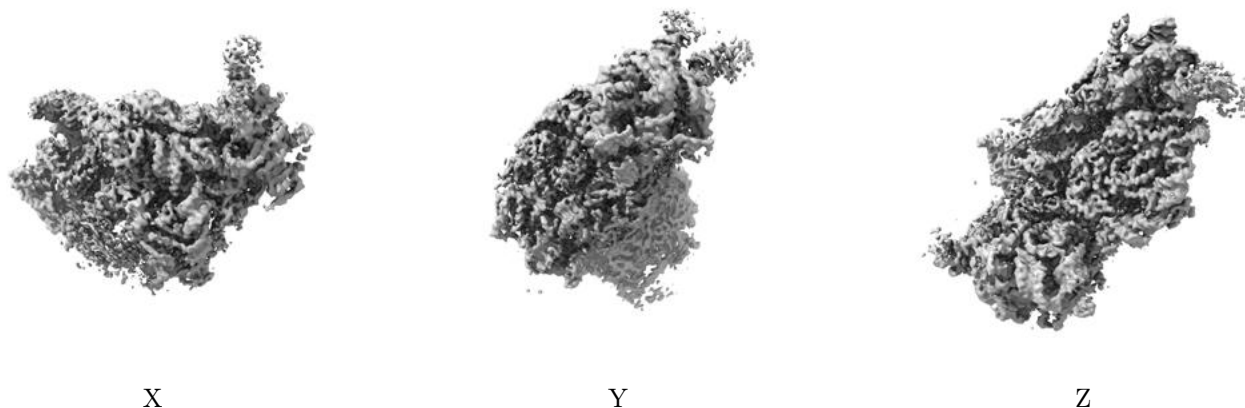


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

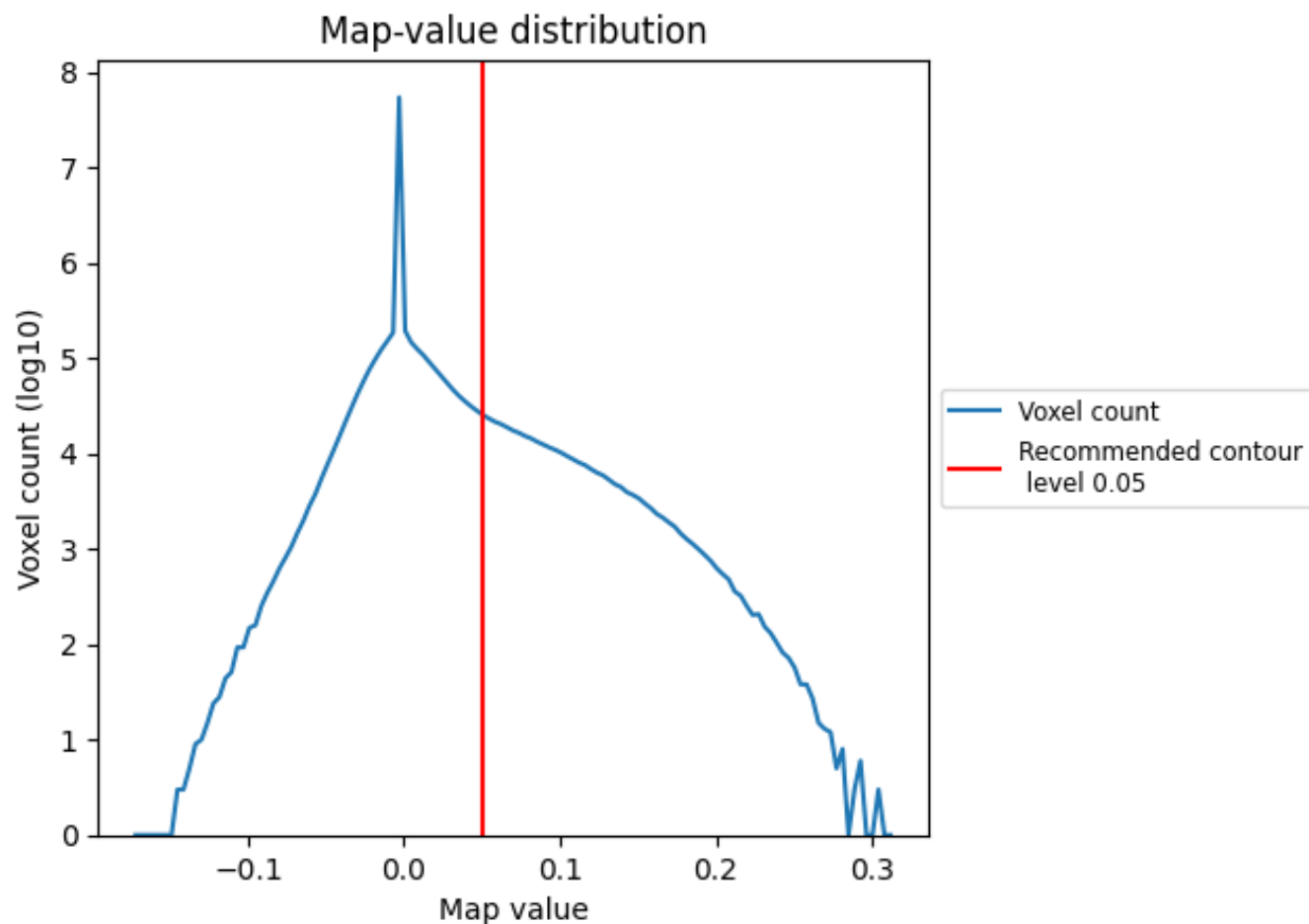
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

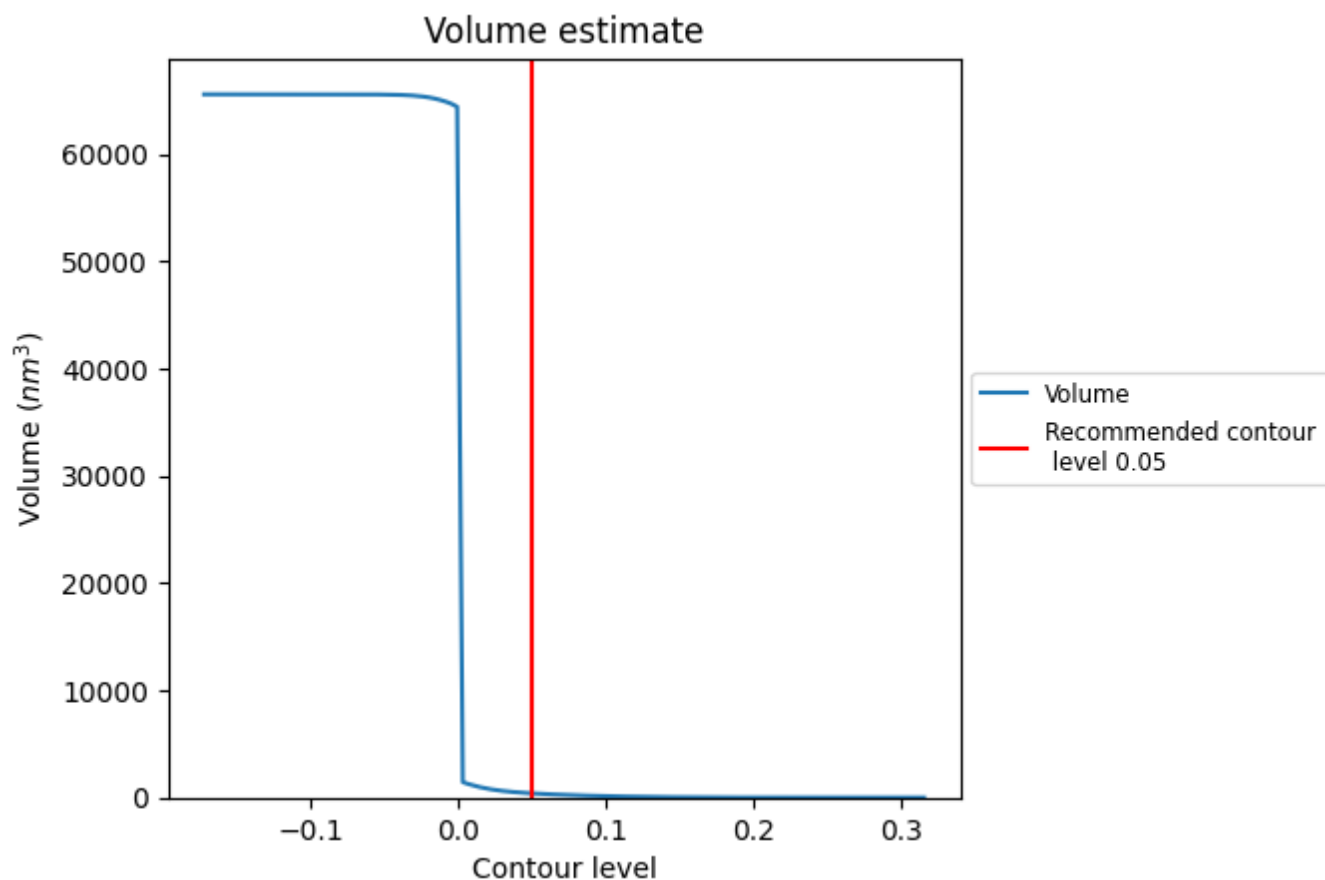
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

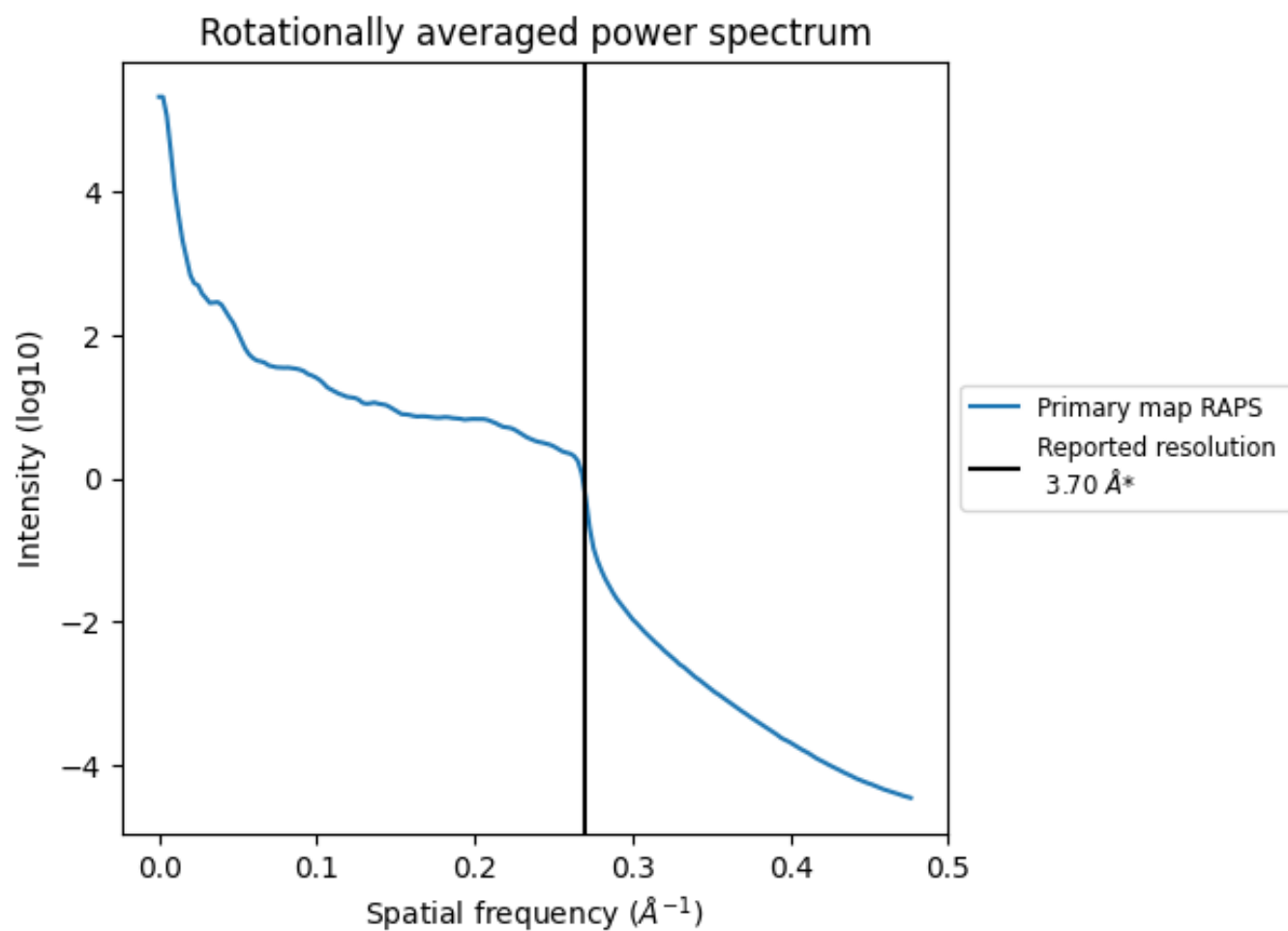
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 393 nm³; this corresponds to an approximate mass of 355 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 0.270 Å⁻¹

8 Fourier-Shell correlation

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

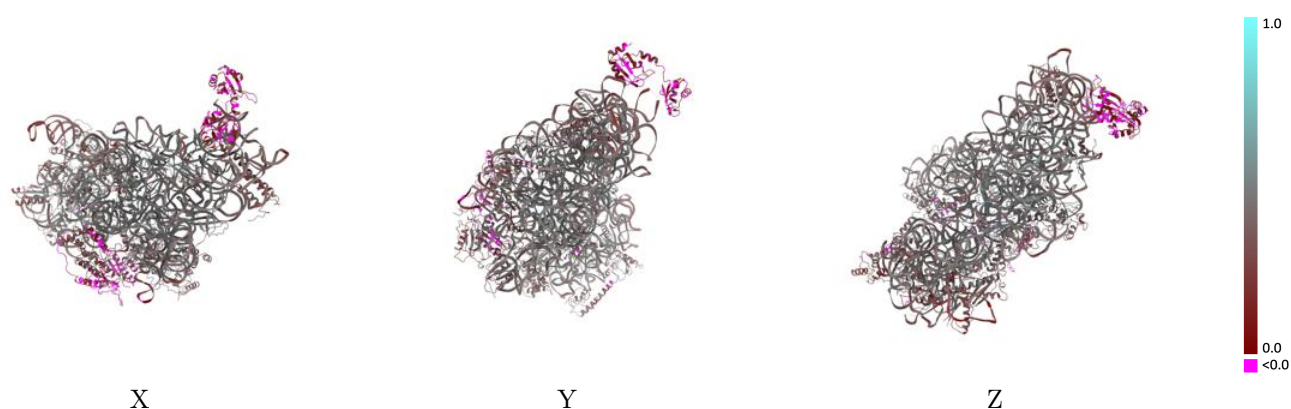
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6710 and PDB model 5X8R. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

This section was not generated.

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

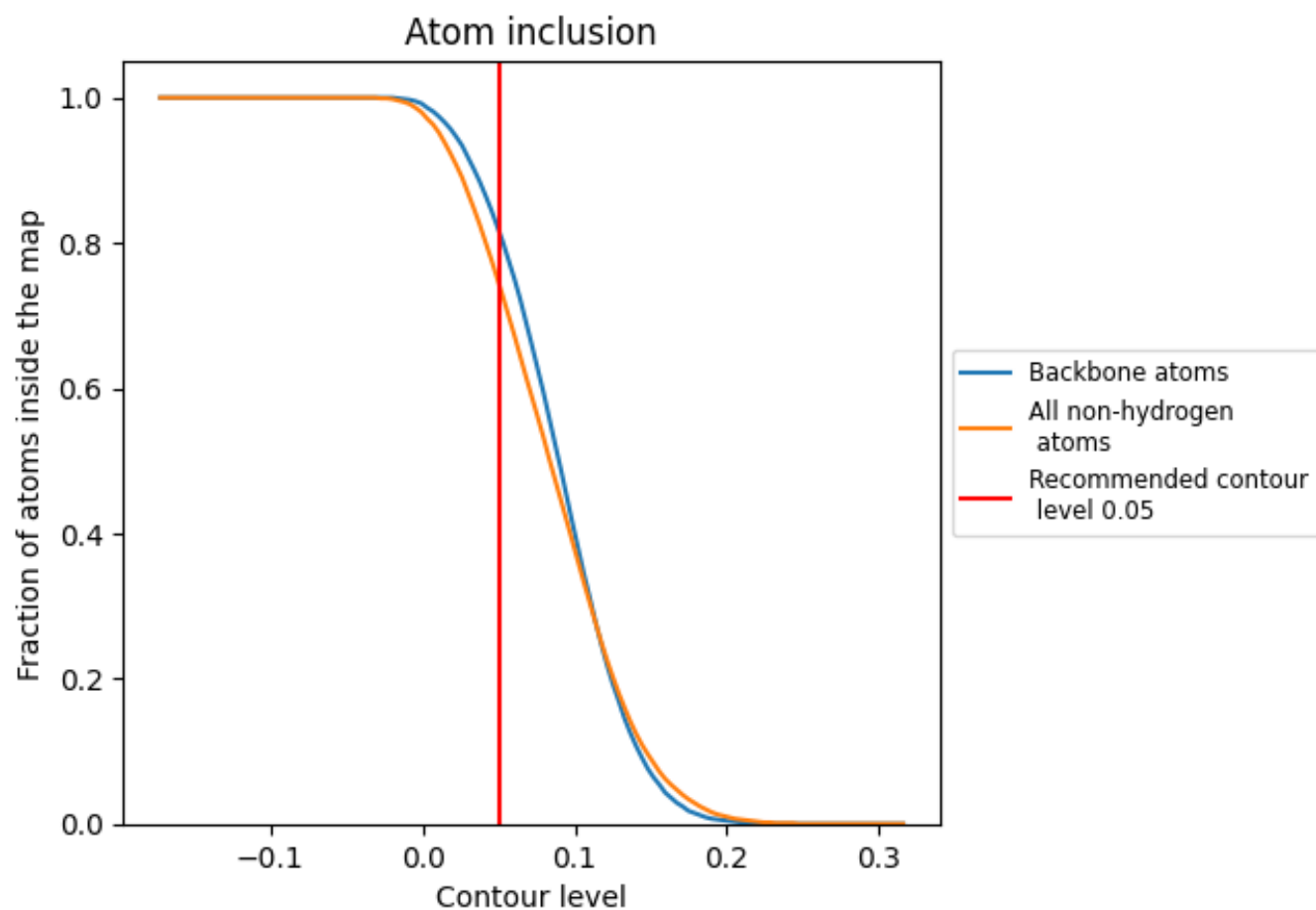


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 82% of all backbone atoms, 75% 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	 0.7460	 0.3930
8	 0.0280	 0.0120
a	 0.9010	 0.4330
b	 0.3430	 0.3270
c	 0.6460	 0.4160
d	 0.6610	 0.4040
e	 0.6890	 0.4310
f	 0.5410	 0.3560
g	 0.5160	 0.3730
h	 0.6780	 0.4220
i	 0.6850	 0.4000
j	 0.6210	 0.4020
k	 0.6330	 0.3940
l	 0.7070	 0.4640
m	 0.6100	 0.3210
n	 0.6470	 0.3870
o	 0.5350	 0.3860
p	 0.7280	 0.4350
q	 0.6890	 0.4520
r	 0.6290	 0.3840
s	 0.6500	 0.3850
t	 0.6510	 0.3400
u	 0.4920	 0.3180
v	 0.0850	 0.0540
w	 0.0620	 -0.0250
x	 0.6880	 0.4150
y	 0.5960	 0.4000

