



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 09:07 AM UTC

PDB ID : 7TM3 / pdb_00007tm3
EMDB ID : EMD-25994
Title : Structure of the rabbit 80S ribosome stalled on a 2-TMD Rhodopsin intermediate in complex with the multipass translocon
Authors : Kim, M.K.; Lewis, A.J.O.; Keenan, R.J.; Hegde, R.S.
Deposited on : 2022-01-19
Resolution : 3.25 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

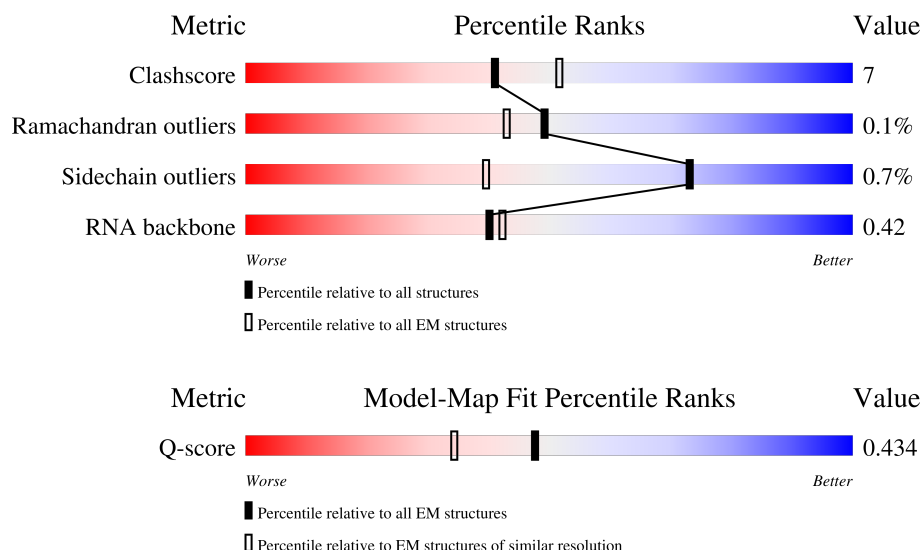
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.25 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.



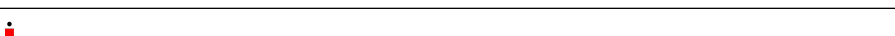
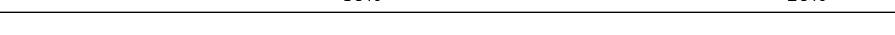
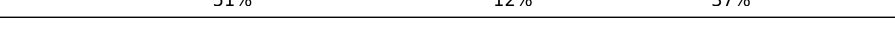
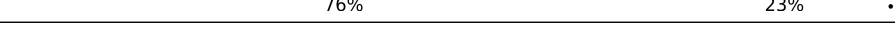
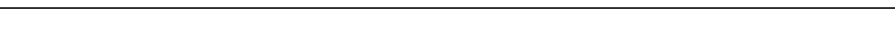
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14599 (2.75 - 3.75)

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

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	229	
3	C	425	

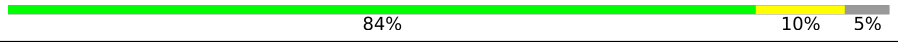
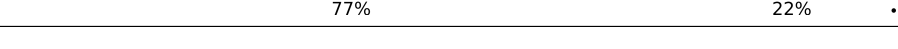
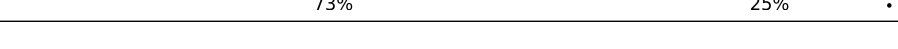
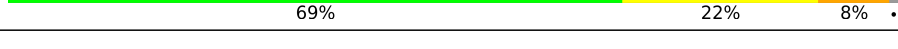
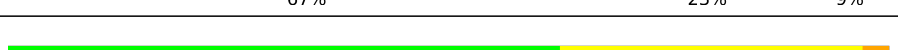
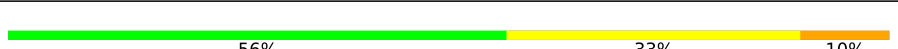
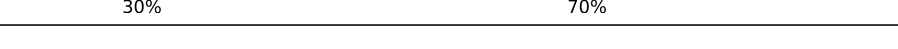
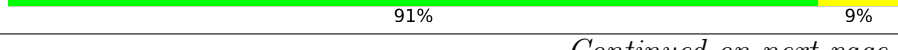
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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	247	
7	G	319	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	226	
28	c	115	

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Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	116	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	102	
39	n	25	
40	o	106	
41	p	92	
42	q	77	
43	r	137	
44	u	120	
45	v	156	
46	w	403	
47	1	476	
48	2	96	
49	3	68	
50	4	483	
51	5	106	
52	7	563	
53	6	224	

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Mol	Chain	Length	Quality of chain
54	K	3543	54% 36% 10%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 261738 atoms, of which 111794 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 uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	248	Total	C	H	N	O	S	0	0
			3891	1189	1993	389	314	6		

- Molecule 2 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	27	Total	C	H	N	O	S	0	0
			351	112	171	31	36	1		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	362	Total	C	H	N	O	S	0	0
			5936	1812	3053	577	480	14		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	378	LYS	-	insertion	UNP G1SVW5
C	379	VAL	-	insertion	UNP G1SVW5
C	380	LYS	-	insertion	UNP G1SVW5
C	381	LYS	-	insertion	UNP G1SVW5
C	382	PRO	-	insertion	UNP G1SVW5
C	383	ARG	-	insertion	UNP G1SVW5
C	384	ALA	-	insertion	UNP G1SVW5
C	385	VAL	-	insertion	UNP G1SVW5
C	386	GLY	-	insertion	UNP G1SVW5
C	387	ILE	-	insertion	UNP G1SVW5
C	388	LYS	-	insertion	UNP G1SVW5
C	389	GLN	-	insertion	UNP G1SVW5

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	293	Total	C	H	N	O	S	0	0
			4815	1512	2424	438	427	14		

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	233	Total	C	H	N	O	S	0	0
			3908	1206	2031	357	311	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	225	Total	C	H	N	O	S	0	0
			3870	1205	1995	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	233	Total	C	H	N	O	S	0	0
			3906	1199	2027	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	190	Total	C	H	N	O	S	0	0
			3113	954	1597	284	272	6		

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	205	Total	C	H	N	O	S	0	0
			3376	1056	1712	321	274	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	170	Total	C	H	N	O	S	0	0
			2761	861	1399	254	241	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	L	210	Total	C	H	N	O	S	0	0
			3522	1065	1820	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	M	138	Total	C	H	N	O	S	0	0
			2348	727	1211	221	182	7		

- Molecule 13 is a protein called eL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	N	202	Total	C	H	N	O	S	0	0
			3440	1069	1744	358	265	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	O	199	Total	C	H	N	O	S	0	0
			3408	1051	1778	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	P	153	Total	C	H	N	O	S	0	0
			2516	777	1274	241	215	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	Q	187	Total	C	H	N	O	S	0	0
			3148	946	1634	315	249	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	R	155	Total	C	H	N	O	S	0	0
			2728	808	1434	278	199	9		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	S	176	Total	C	H	N	O	S	0	0
			2970	930	1508	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	T	159	Total	C	H	N	O	S	0	0
			2665	823	1367	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	U	102	Total	C	H	N	O	S	0	0
			1692	534	858	146	152	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	V	131	Total	C	H	N	O	S	0	0
			2018	618	1039	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	W	63	Total	C	H	N	O	S	0	0
			1069	337	541	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	X	118	Total	C	H	N	O	S	0	0
			2007	618	1040	181	167	1		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Y	134	Total	C	H	N	O	S	0	0
			2320	700	1205	226	186	3		

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Z	135	Total	C	H	N	O	S	0	0
			2289	714	1182	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	a	147	Total	C	H	N	O	S	0	0
			2371	734	1209	239	185	4		

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	b	104	Total	C	H	N	O	S	0	0
			1768	527	920	189	129	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	c	98	Total	C	H	N	O	S	0	0
			1555	481	794	134	140	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	d	107	Total	C	H	N	O	S	0	0
			1818	560	930	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	e	128	Total	C	H	N	O	S	0	0
			2200	667	1147	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	f	109	Total	C	H	N	O	S	0	0
			1788	555	912	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	g	114	Total	C	H	N	O	S	0	0
			1904	566	998	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	h	122	Total	C	H	N	O	S	0	0
			2145	637	1136	203	168	1		

- Molecule 34 is a protein called eL36.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	i	102	Total	C	H	N	O	S	0	0
			1746	520	916	176	129	5		

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	j	86	Total	C	H	N	O	S	0	0
			1442	434	737	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	k	69	Total	C	H	N	O	S	0	0
			1206	366	637	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	l	50	Total	C	H	N	O	S	0	0
			927	286	480	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	m	52	Total	C	H	N	O	S	0	0
			895	266	466	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	n	25	Total	C	H	N	O	S	0	0
			528	145	289	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	o	104	Total	C	H	N	O	S	0	0
			1773	533	922	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	p	91	Total	C	H	N	O	S	0	0
			1465	445	757	136	120	7		

- Molecule 42 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	q	76	Total	C	H	N	O	P	0	0
			2439	723	823	291	527	75		

- Molecule 43 is a protein called eL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	r	124	Total	C	H	N	O	S	0	0
			2045	616	1051	205	167	6		

- Molecule 44 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	u	120	Total	C	H	N	O	P	0	0
			3854	1141	1296	456	842	119		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	2	U	N	conflict	GB X06789.1
u	36	C	N	conflict	GB X06789.1
u	102	U	N	conflict	GB X06789.1
u	112	U	N	conflict	GB X06789.1
u	114	U	N	conflict	GB X06789.1
u	119	U	C	conflict	GB X06789.1
u	120	U	N	conflict	GB X06789.1

- Molecule 45 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	v	156	Total	C	H	N	O	P	0	0
			4997	1480	1683	585	1094	155		

- Molecule 46 is a protein called uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	w	394	Total	C	H	N	O	S	0	0
			6482	2020	3310	597	542	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	1	MET	-	insertion	UNP G1TL06

- Molecule 47 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	1	465	Total	C	H	N	O	S	0	0
			7320	2360	3722	580	634	24		

- Molecule 48 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	2	29	Total	C	H	N	O	S	0	0
			475	157	245	36	35	2		

- Molecule 49 is a protein called Protein transport protein Sec61 gamma.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	3	68	Total	C	H	N	O	S	0	0
			1120	355	577	94	89	5		

- Molecule 50 is a protein called Coiled-coil domain containing 47.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	4	342	Total	C	H	N	O	S	0	0
			5597	1738	2819	495	522	23		

- Molecule 51 is a protein called PAT complex subunit Asterix.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	5	90	Total	C	H	N	O	S	0	0
			1421	456	710	115	128	12		

- Molecule 52 is a protein called Nicalin.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	7	521	Total	C	H	N	O	S	0	0
			8260	2625	4121	726	771	17		

- Molecule 53 is a protein called Transmembrane protein 147.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	6	224	Total	C	H	N	O	S	0	0
			3575	1190	1792	277	300	16		

- Molecule 54 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	K	3543	Total	C	H	N	O	P	0	0
			114330	33833	38358	13910	24686	3543		

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	P	2	Total	Mg	0
			2	2	
55	V	1	Total	Mg	0
			1	1	
55	a	1	Total	Mg	0
			1	1	
55	g	1	Total	Mg	0
			1	1	
55	j	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
55	u	7	Total 7	Mg 7	0
55	v	6	Total 6	Mg 6	0
55	K	201	Total 201	Mg 201	0

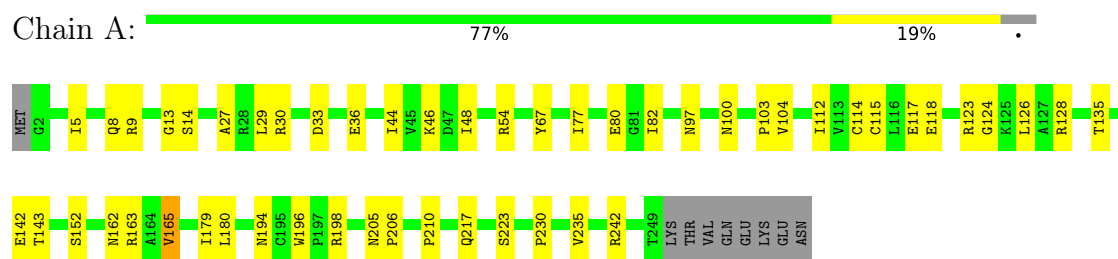
- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	g	1	Total 1	Zn 1	0
56	j	1	Total 1	Zn 1	0
56	m	1	Total 1	Zn 1	0
56	o	1	Total 1	Zn 1	0
56	p	1	Total 1	Zn 1	0

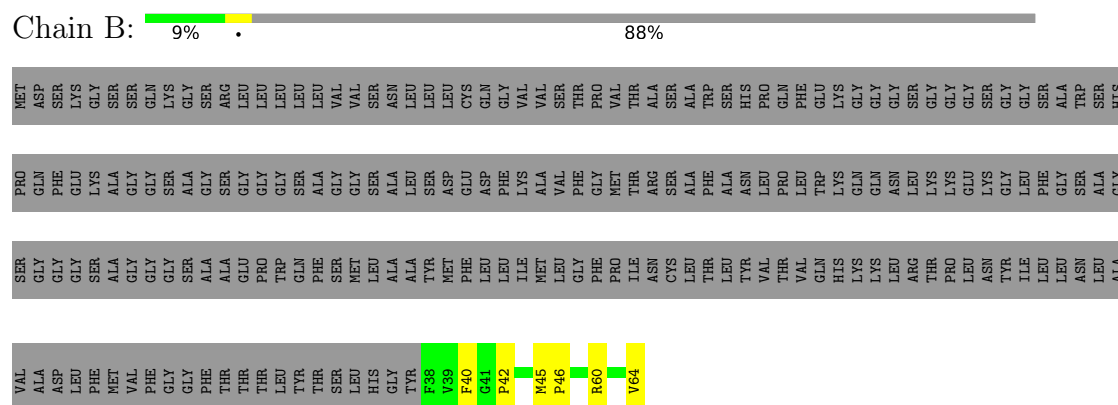
3 Residue-property plots

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

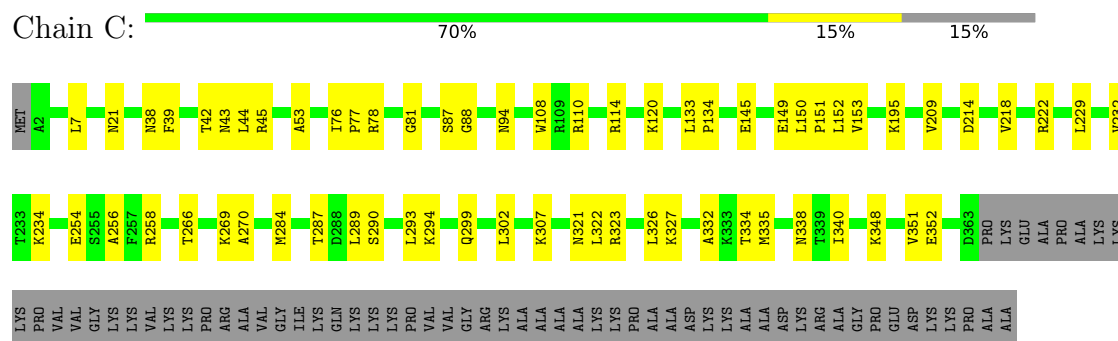
• Molecule 1: uL2



• Molecule 2: Nascent chain



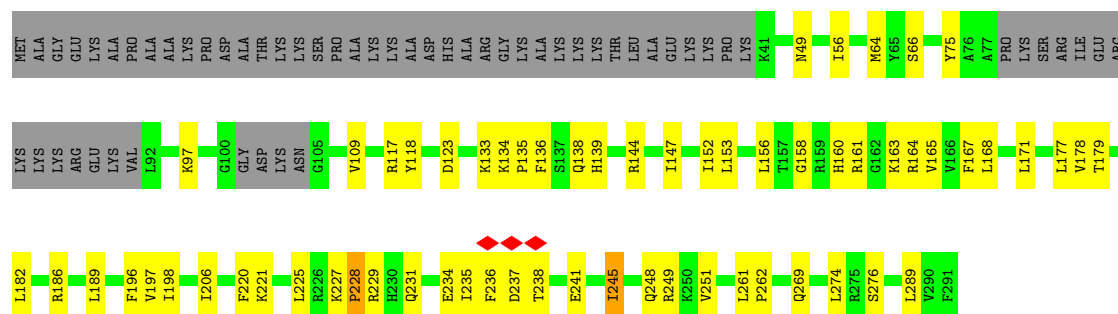
• Molecule 3: uL4



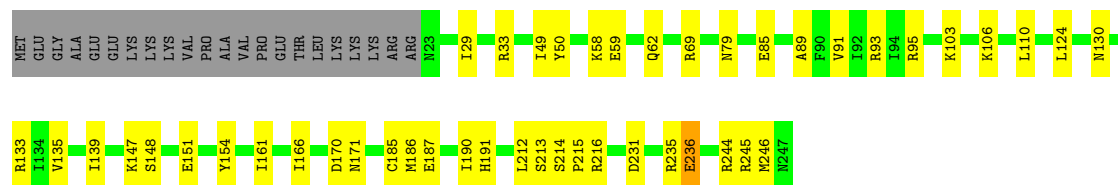
• Molecule 4: uL18

L163	L175	D184	K188	N203	V204	M208	D215	Q222	V231	T232	P233	D234	M235	M239	H244	R248	V261	K276	V280	A285	S296	R299	E292	A295	GLU	SER															
Met	GLY	F3	R23	T28	R33	V37	Y44	R50	D59	I60	I61	G62	G63	I64	A65	T66	A67	D72	W73	I74	W75	L83	Y86	S87	V88	R89	V90	T93	L104	L105	R112	Y119	E120	P139	L146	D147	T155	G156	N157	K158	Y159

Chain E: 58% 21% 20%



Chain F: 72% 18% 9%

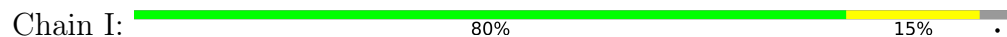


Chain G: 59% 14% 27%

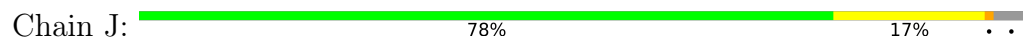


Chain H: 79% 20% .

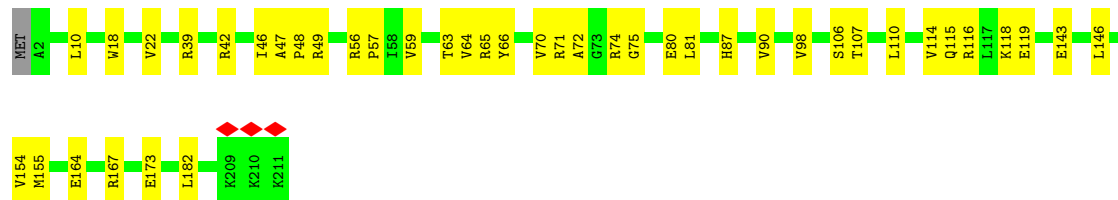
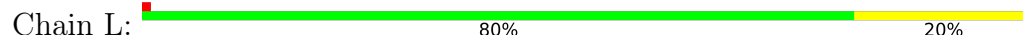
- Molecule 9: uL16



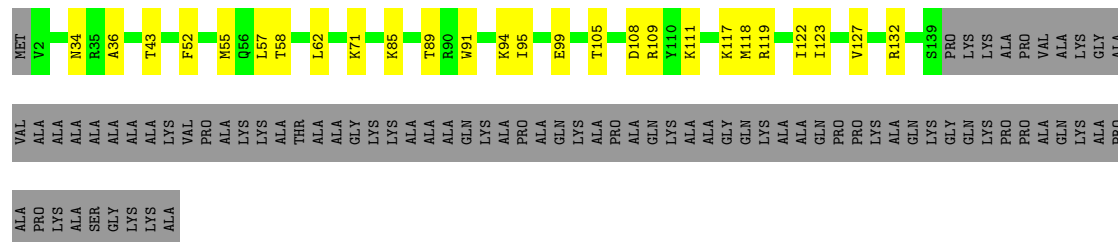
- Molecule 10: uL5



- Molecule 11: eL13

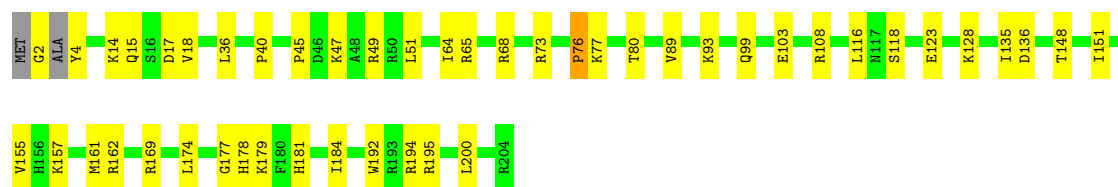


- Molecule 12: eL14



- Molecule 13: eL15

Chain N:  76% 23% .



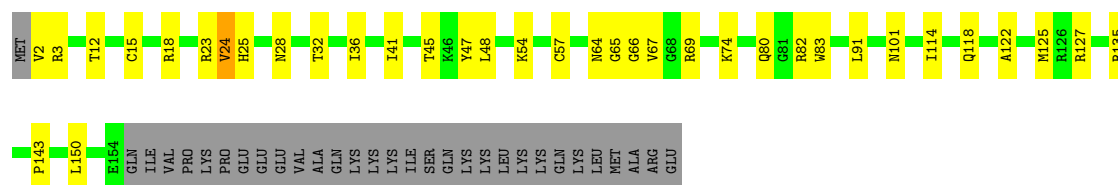
• Molecule 14: uL13

Chain O:  77% 21% .



• Molecule 15: uL22

Chain P:  64% 19% 17% .



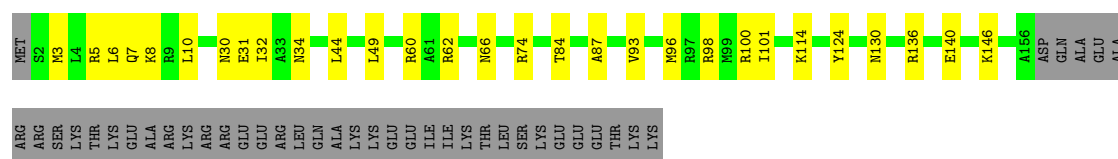
• Molecule 16: eL18

Chain Q:  83% 16% .



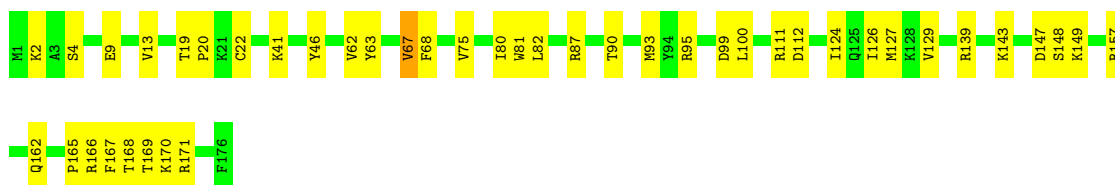
• Molecule 17: eL19

Chain R:  64% 15% 21% .

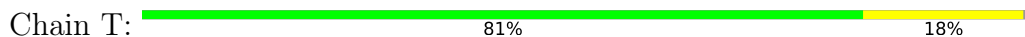


• Molecule 18: eL20

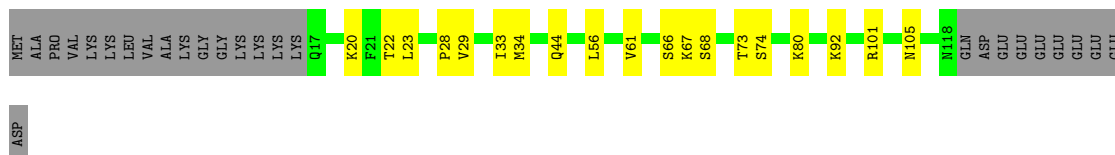
Chain S:  76% 24% .



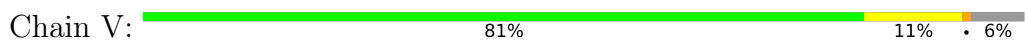
- Molecule 19: eL21



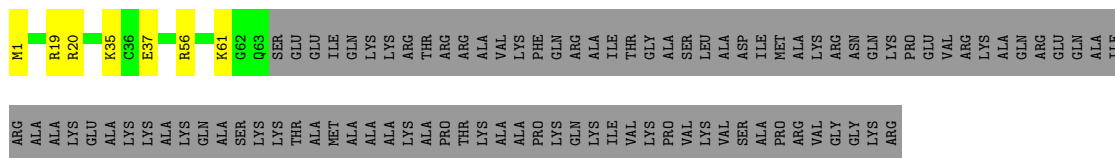
- Molecule 20: eL22



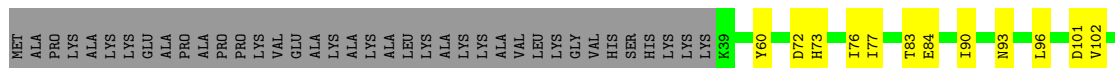
- Molecule 21: uL14



- Molecule 22: eL24



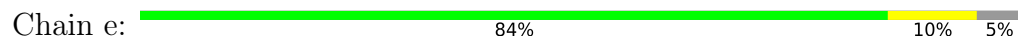
- Molecule 23: uL23



- Molecule 24: uL24



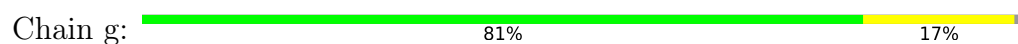
• Molecule 30: eL32



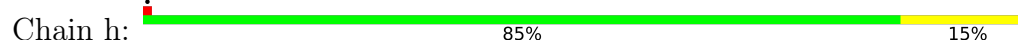
• Molecule 31: eL33



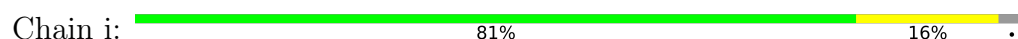
• Molecule 32: eL34



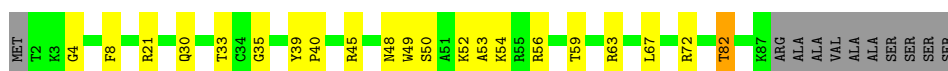
• Molecule 33: uL29



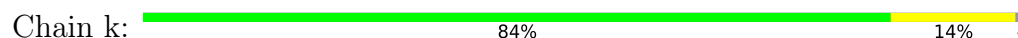
• Molecule 34: eL36

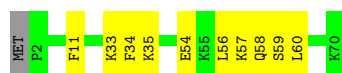


• Molecule 35: eL37



• Molecule 36: eL38





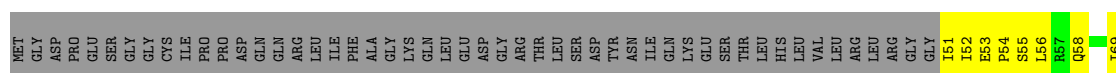
- Molecule 37: eL39

Chain l: 73% 25% .



- Molecule 38: eL40

Chain m: 38% 13% 49%



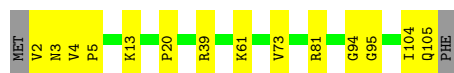
- Molecule 39: eL41

Chain n: 72% 28%



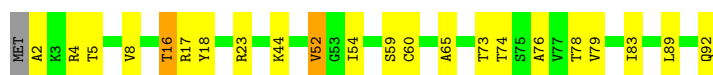
- Molecule 40: eL42

Chain o: 85% 13% .



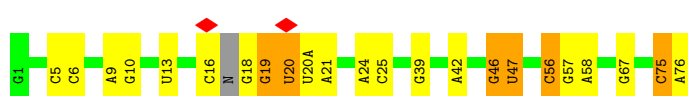
- Molecule 41: eL43

Chain p: 75% 22% ..



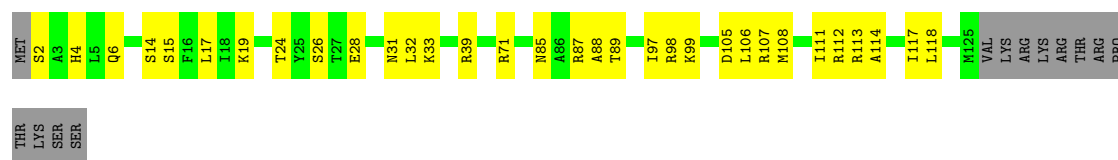
- Molecule 42: P-site tRNA

Chain q: 69% 22% 8% .



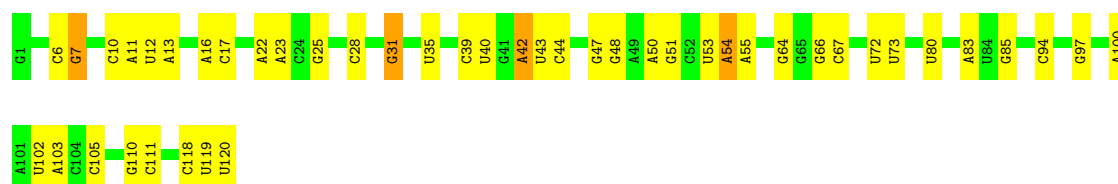
- Molecule 43: eL28

Chain r: 



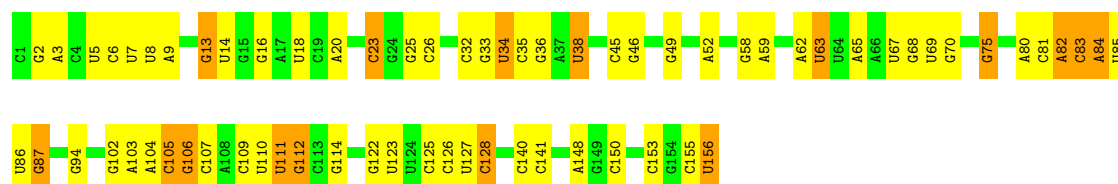
• Molecule 44: 5S ribosomal RNA

Chain u: 



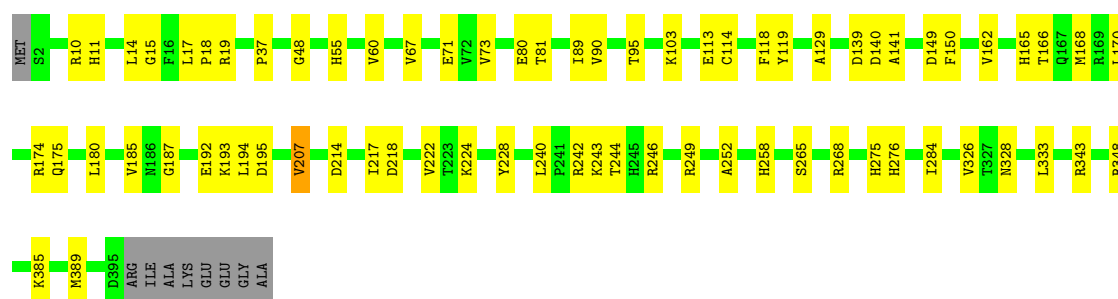
• Molecule 45: 5.8S ribosomal RNA

Chain v: 



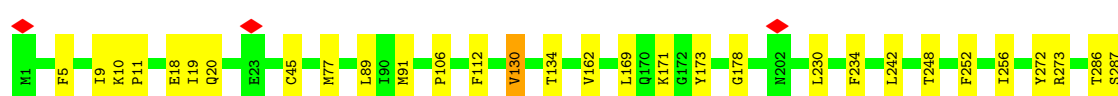
• Molecule 46: uL3

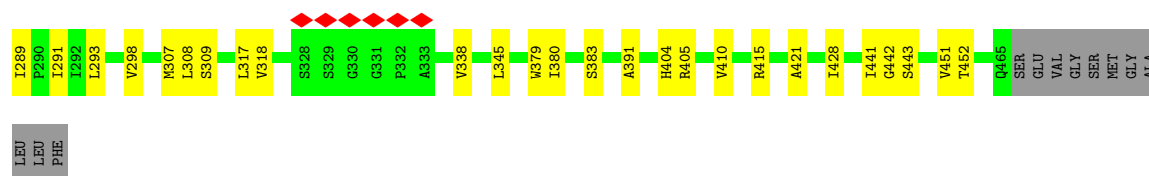
Chain w: 



• Molecule 47: Protein transport protein Sec61 subunit alpha isoform 1

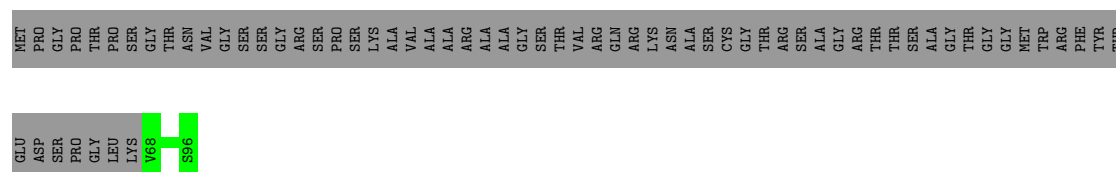
Chain 1: 





- Molecule 48: Protein transport protein Sec61 subunit beta

Chain 2: 30% 70%



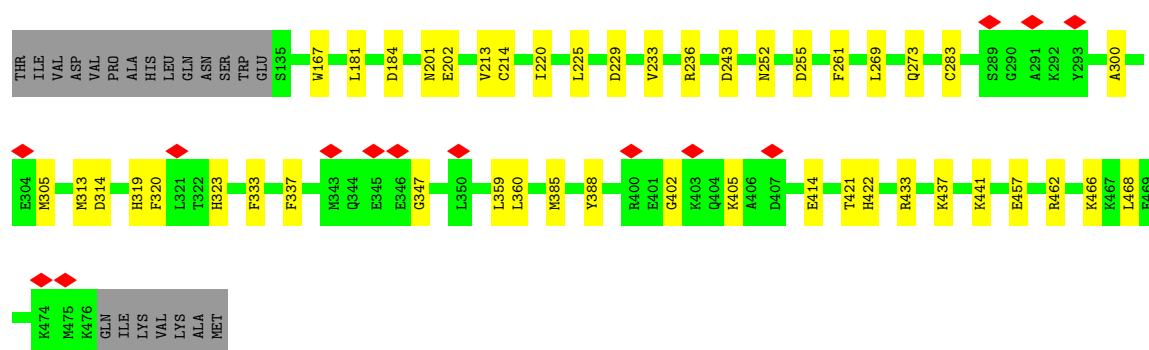
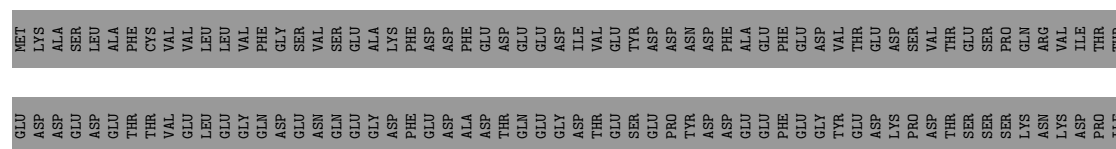
- Molecule 49: Protein transport protein Sec61 gamma

Chain 3: 87% 13%



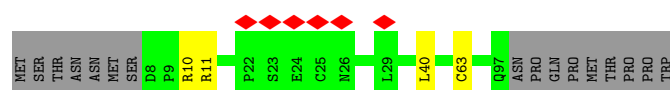
- Molecule 50: Coiled-coil domain containing 47

Chain 4: 61% 10% 29%



- Molecule 51: PAT complex subunit Asterix

Chain 5: 6% 81% 15%



Chain 7: 51% 86% 7% 7%





C41294	C4297	U4300	C4303	A4304	G4305	U4306	C4314	A4317	U4321	A4322	A4324	A4325	G4326	G4327	G4328	G4329	G4330	G4331	C4332	A4339	U4344	C4345	A4348	C4349	C4350	U4354	G4355	U4371	U4372	G4373	A4376	A4377	A4378	A4379	A4380	U4384	A4385	C4386	C4387	A4388	A4389	U4390	U4391	U4293																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
G4087	C4088	C4096	G4097	A4098	U4111	C4112	C4116	U4117	U4118	C4119	U4120	G4121	G4122	C4123	G4124	C4125	C4126	A4127	A4128	G4129	C4133	C4134	G4135	G4136	G4137	G4138	G4139	C4140	C4141	C4142	C4143	C4144	C4145	C4146	C4147	C4148	G4156	A4157	C4158	C4162	U4163	G4166	G4167	U4168	G4169	U4069	U4070	A4073	C4074	A4075	A4076	A4077	C4078	C4079	C4080	G4081	G3887	G3888	G3889																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
C3893	G3897	A3901	G3904	A3905	G3907	A3908	C3909	C3910	C3911	U3912	U3915	G3916	A3917	A3923	C3926	U3927	A3928	G3929	U3930	C3931	G3934	C3935	G3938	G3939	A3943	G3946	A3947	C3948	U4065	U4066	U4067	U4068	U4069	U4070	A4073	C4074	A4075	A4076	A4077	C4078	C4079	C4080	G4081	G3887	G3888	A4084	A4085	G4086																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
A3774	A3775	G3777	G3780	C3781	C3782	A3783	A3784	A3785	U3786	G3787	C3788	G3809	C3810	G3811	C3812	A3813	U3814	A3817	U3818	G3819	U3822	G3823	A3824	C3834	C3835	U3838	G3839	U3840	A3845	C3855	A3856	G3859	C3870	A3871	C3872	G3873	G3874	G3875	A3876	A3877	C3878	G3879	G3880	C3887	G3888	G3889																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
C3685	G3689	A3692	U3695	C3696	C3700	C3701	A3702	U3707	C3708	A3711	G3714	A3717	G3722	A3723	A3724	G3725	A3728	U3729	G3735	A3736	A3737	G3743	A3747	A3748	C3749	G3750	G3751	C3752	G3753	G3754	G3755	A3756	A3759	A3760	A3763	U3764	G3765	A3766	C3767	U3770	C3771	U3772	U3773	A3774	A3775	G3776	G3777	G3778	G3779	G3780	G3781	U3782	A3783	A3787	U3788	A3789	A3790	C3791	U3792	G3793	C3794	A3795	A3796	A3797	A3798	A3799	A3800	A3801	A3802	A3803	A3804	A3805	A3806	A3807	A3808	A3809	A3810	A3811	A3812	A3813	A3814	A3815	A3816	A3817	A3818	A3819	A3820	A3821	A3822	A3823	A3824	A3825	A3826	A3827	A3828	A3829	A3830	A3831	A3832	A3833	A3834	A3835	A3836	A3837	A3838	A3839	A3840	A3841	A3842	A3843	A3844	A3845	A3846	A3847	A3848	A3849	A3850	A3851	A3852	A3853	A3854	A3855	A3856	A3857	A3858	A3859	A3860	A3861	A3862	A3863	A3864	A3865	A3866	A3867	A3868	A3869	A3870	A3871	A3872	A3873	A3874	A3875	A3876	A3877	A3878	A3879	A3880	A3881	A3882	A3883	A3884	A3885	A3886	A3887	A3888	A3889	A3890	A3891	A3892	A3893	A3894	A3895	A3896	A3897	A3898	A3899	A3900	A3901	A3902	A3903	A3904	A3905	A3906	A3907	A3908	A3909	A3910	A3911	A3912	A3913	A3914	A3915	A3916	A3917	A3918	A3919	A3920	A3921	A3922	A3923	A3924	A3925	A3926	A3927	A3928	A3929	A3930	A3931	A3932	A3933	A3934	A3935	A3936	A3937	A3938	A3939	A3940	A3941	A3942	A3943	A3944	A3945	A3946	A3947	A3948	A3949	A3950	A3951	A3952	A3953	A3954	A3955	A3956	A3957	A3958	A3959	A3960	A3961	A3962	A3963	A3964	A3965	A3966	A3967	A3968	A3969	A3970	A3971	A3972	A3973	A3974	A3975	A3976	A3977	A3978	A3979	A3980	A3981	A3982	A3983	A3984	A3985	A3986	A3987	A3988	A3989	A3990	A3991	A3992	A3993	A3994	A3995	A3996	A3997	A3998	A3999	A4000	A4001	A4002	A4003	A4004	A4005	A4006	A4007	A4008	A4009	A4010	A4011	A4012	A4013	A4014	A4015	A4016	A4017	A4018	A4019	A4020	A4021	A4022	A4023	A4024	A4025	A4026	A4027	A4028	A4029	A4030	A4031	A4032	A4033	A4034	A4035	A4036	A4037	A4038	A4039	A4040	A4041	A4042	A4043	A4044	A4045	A4046	A4047	A4048	A4049	A4050	A4051	A4052	A4053	A4054	A4055	A4056	A4057	A4058	A4059	A4060	A4061	A4062	A4063	A4064	A4065	A4066	A4067	A4068	A4069	A4070	A4071	A4072	A4073	A4074	A4075	A4076	A4077	A4078	A4079	A4080	A4081	A4082	A4083	A4084	A4085	A4086	A4087	A4088	A4089	A4090	A4091	A4092	A4093	A4094	A4095	A4096	A4097	A4098	A4099	A4100	A4101	A4102	A4103	A4104	A4105	A4106	A4107	A4108	A4109	A4110	A4111	A4112	A4113	A4114	A4115	A4116	A4117	A4118	A4119	A4120	A4121	A4122	A4123	A4124	A4125	A4126	A4127	A4128	A4129	A4130	A4131	A4132	A4133	A4134	A4135	A4136	A4137	A4138	A4139	A4140	A4141	A4142	A4143	A4144	A4145	A4146	A4147	A4148	A4149	A4150	A4151	A4152	A4153	A4154	A4155	A4156	A4157	A4158	A4159	A4160	A4161	A4162	A4163	A4164	A4165	A4166	A4167	A4168	A4169	A4170	A4171	A4172	A4173	A4174	A4175	A4176	A4177	A4178	A4179	A4180	A4181	A4182	A4183	A4184	A4185	A4186	A4187	A4188	A4189	A4190	A4191	A4192	A4193	A4194	A4195	A4196	A4197	A4198	A4199	A4200	A4201	A4202	A4203	A4204	A4205	A4206	A4207	A4208	A4209	A4210	A4211	A4212	A4213	A4214	A4215	A4216	A4217	A4218	A4219	A4220	A4221	A4222	A4223	A4224	A4225	A4226	A4227	A4228	A4229	A4230	A4231	A4232	A4233	A4234	A4235	A4236	A4237	A4238	A4239	A4240	A4241	A4242	A4243	A4244	A4245	A4246	A4247	A4248	A4249	A4250	A4251	A4252	A4253	A4254	A4255	A4256	A4257	A4258	A4259	A4260	A4261	A4262	A4263	A4264	A4265	A4266	A4267	A4268	A4269	A4270	A4271	A4272	A4273	A4274	A4275	A4276	A4277	A4278	A4279	A4280	A4281	A4282	A4283	A4284	A4285	A4286	A4287	A4288	A4289	A4290	A4291	A4292	A4293	A4294	A4295	A4296	A4297	A4298	A4299	A4300	A4301	A4302	A4303	A4304	A4305	A4306	A4307	A4308	A4309	A4310	A4311	A4312	A4313	A4314	A4315	A4316	A4317	A4318	A4319	A4320	A4321	A4322	A4323	A4324	A4325	A4326	A4327	A4328	A4329	A4330	A4331	A4332	A4333	A4334	A4335	A4336	A4337	A4338	A4339	A4340	A4341	A4342	A4343	A4344	A4345	A4346	A4347	A4348	A4349	A4350	A4351	A4352	A4353	A4354	A4355	A4356	A4357	A4358	A4359	A4360	A4361	A4362	A4363	A4364	A4365	A4366	A4367	A4368	A4369	A4370	A4371	A4372	A4373	A4374	A4375	A4376	A4377	A4378	A4379	A4380	A4381	A4382	A4383	A4384	A4385	A4386	A4387	A4388	A4389	A4390	A4391	A4392	A4393	A4394	A4395	A4396	A4397	A4398	A4399	A4400	A4401	A4402	A4403	A4404	A4405	A4406	A4407	A4408	A4409	A4410	A4411	A4412	A4413	A4414	A4415	A4416	A4417	A4418	A4419	A4420	A4421	A4422	A4423	A4424	A4425	A4426	A4427	A4428	A4429	A4430	A4431	A4432	A4433	A4434	A4435	A4436	A4437	A4438	A4439	A4440	A4441	A4442	A4443	A4444	A4445	A4446	A4447	A4448	A4449	A4450	A4451	A4452	A4453	A4454	A4455	A4456	A4457	A4458	A4459	A4460	A4461	A4462	A4463	A4464	A4465	A4466	A4467	A4468	A4469	A4470	A4471	A4472	A4473	A4474	A4475	A4476	A4477	A4478	A4479	A4480	A4481	A4482	A4483	A4484	A4485	A4486	A4487	A4488	A4489	A4490	A4491	A4492	A4493	A4494	A4495	A4496	A4497	A4498	A4499	A4500	A4501	A4502	A4503	A4504	A4505	A4506	A4507	A4508	A4509	A4510	A4511	A4512	A4513	A4514	A4515	A4516	A4517	A4518	A4519	A4520	A4521	A4522	A4523	A4524	A4525	A4526	A4527	A4528	A4529	A4530	A4531	A4532	A4533	A4534	A4535	A4536	A4537	A4538	A4539	A4540	A4541	A4542	A4543	A4544	A4545	A4546	A4547	A4548	A4549	A4550	A4551	A4552	A4553	A4554	A4555	A4556	A4557	A4558	A4559	A4560	A4561	A4562	A4563	A4564	A4565	A4566	A4567	A4568	A4569	A4570	A4571	A4572	A4573	A4574	A4575	A4576	A4577	A4578	A4579	A4580	A4581	A4582	A4583	A4584	A4585	A4586	A4587	A4588	A4589	A4590	A4591	A4592	A4593	A4594	A4595	A4596	A4597	A4598	A4599	A4600	A4601	A4602	A4603	A4604	A4605	A4606	A4607	A4608	A4609	A4610	A4611	A4612	A4613	A4614	A4615	A4616	A4617	A4618	A4619	A4620	A4621	A4622	A4623	A4624	A4625	A4626	A4627	A4628	A4629	A4630	A4631	A4632	A4633	A4634	A4635	A4636	A4637	A4638	A4639	A4640	A4641	A4642	A4643	A4644	A4645	A4646	A4647	A4648	A4649	A4650	A4651	A4652	A4653	A4654	A4655	A4656	A4657	A4658	A4659	A4660	A4661	A4662	A4663	A4664	A4665	A4666	A4667	A4668	A4669	A4670	A4671	A4672	A4673	A4674	A4675	A4676	A4677	A4678	A4679	A4680	A4681	A4682	A4683	A4684	A4685	A4686	A4687	A4688	A4689	A4690	A4691	A4692	A4693	A4694	A4695	A4696	A4697	A4698	A4699	A4700	A4701	A4702	A4703	A4704	A4705	A4706	A4707	A4708	A4709	A4710	A4711	A4712	A4713	A4714	A4715	A4716	A4717	A4718	A4719	A4720	A4721	A4722	A4723	A4724	A4725	A4726	A4727	A4728	A4729	A4730	A4731	A4732	A4733	A4734	A4735	A4736	A4737	A4738	A4739	A4740	A4741	A4742	A4743	A4744	A4745	A4746	A4747	A4748	A4749	A4750	A4751	A4752	A4753	A4754	A4755	A4756	A4757	A4758	A4759	A4760	A4761	A4762	A4763	A4764	A4765	A4766	A4767	A4768	A4769	A4770	A4771	A4772	A4773	A4774	A4775	A4776	A4777	A4778	A4779	A4780	A4781	A4782	A4783	A4784	A4785	A4786	A4787	A4788	A4789	A4790	A4791	A4792	A4793	A4794	A4795	A4796	A4797	A4798	A4799	A4800	A4801	A4802	A4803	A4804	A4805	A4806	A4807	A4808	A4809	A4810	A4811	A4812	A4813	A4814	A4815	A4816	A4817	A4818	A4819	A4820	A4821	A4822	A4823	A4824	A4825	A4826	A4827	A4828	A4829	A4830	A4831	A4832	A4833	A4834	A4835	A4836	A4837	A4838	A4839	A4840	A4841	A4842	A4843	A4844	A4845	A4846	A4847	A4848	A4849	A4850	A4851	A4852	A4853	A4854	A4855	A4856	A4857	A4858	A4859	A4860	A4861	A4862	A4863	A4864	A4865	A4866	A4867	A4868	A4869	A4870	A4871	A4872	A4873	A4874	A4875	A4876	A4877	A4878	A4879	A4880	A4881	A4882	A4883	A4884	A4885	A4886	A4887	A4888	A4889	A4890	A4891	A4892	A4893	A4894	A4895	A4896	A4897	A4898	A4899	A4900

C5008	G4931	A4762	G4660	C4560	U4471	G4392
G5009		U4763	G4661	C4561	G4472	G4393
A5014	C4935	A4764	G4662	C4562	A4473	A4394
G5015	G4936	G4765	G4663	U4563	A4474	U4395
G5017	C4937			A4564	G4475	
A5016		G4768	C4670	C4565	C4476	C4398
G5018	C4940	G4769	G4671	U4566	A4477	U4399
A5019	G4941	U4770	A4672	G4567	G4478	G4400
G5020	C4942	C4771		A4568		C4401
C5021	A4943	C4772	U4677	U4569	A4488	G4402
U5022	C4944			G4570	G4489	U4403
G5028	A4945	G4860	A4687	A4571	U4492	U4406
C5029	U4946	G4861	C4688	U4572	U4493	G4407
	U4947		U4689	G4573		
A5034	C4948	G4868	G4694	U4574		C4412
U5035	G4949	G4869		G4575	U4500	C4413
	U4950	C4870	G4699	U4576		A4414
U5040	G4951	G4871	U4700	U4577	A4507	
G5041		G4872	A4701	G4578	U4508	
A5042	A4955	G4873	G4702		U4509	U4419
A5043	A4956	A4874		A4584	A4510	U4420
A5044	C4957	G4875	U4709	U4585	A4511	C4421
	C4958			G4586	U4512	A4422
C5047	U4959	U4882	G4713	G4587	A4513	U4423
A5048	G4960	C4883		A4590	G4514	A4424
G5049		G4884			G4515	
C5050	G4963	U4885	C4716	A4602	A4518	C4429
C5051	C4964	C4886	A4717		G4430	G4430
C5052	U4965	C4887	G4718	A4605	U4431	U4431
U5053	A4966		G4719		G4522	C4432
C5054	A4967	C4895	C4720	G4609	G4523	G4433
G5055	U4976	G4896	G4721		G4524	C4434
A5056	G4977	G4897	G4722	U4618	C4525	
C5057	A4978	C4902	A4723	G4619		U4437
A5058	A4979	G4903	U4724	U4620	G4528	U4438
C5059	C4980		C4725		G4529	
A5060	G4981	G4907		A4626		U4442
A5061	A4982	G4908	U4728	U4627		C4443
G5062		A4909	A4729	U4628	U4532	C4444
G5063	U4985	A4910	G4735	U4629	A4535	U4445
		A4911	C4736	G4630	C4536	
G5068		G4912	G4737	G4631	G4448	G4448
U5069	C4988	C4913	C4738	U4632	A4449	
	U4989	G4914	C4739	G4633		U4452
	C4990	G4915	G4740	U4634	C4453	C4453
	U4991	G4916	A4743	A4635	G4541	G4454
	G4992	C4917	G4744	U4636	A4544	
	G4993	C4918	G4745	G4637		U4457
	U4994	G4919		U4638	A4548	C4458
	C4995	C4920	G4750	G4639	G4549	U4459
		C4921	U4751		U4550	U4460
	G5000	C4922	U4752	C4645	C4461	C4461
	U5001	U4923	G4753		U4552	U4463
	U5002	C4924	G4754	A4651	A4553	A4464
	U5003	U4925		G4652	G4554	U4465
	C5004	C4926	C4757		U4555	
	G5005	G4927	U4758	A4656		C4466
	U5006	C4928	C4759	U4657	U4558	A4467
	A5007		G4760		A4559	
			G4761			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1665551	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.070	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.007	Depositor
Map size ($\text{\AA}$)	552.0, 552.0, 552.0	wwPDB
Map dimensions	412, 412, 412	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3398058, 1.3398058, 1.3398058	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.12	0/1936	0.30	0/2596
2	B	0.14	0/186	0.36	0/254
3	C	0.13	0/2937	0.36	0/3946
4	D	0.14	0/2437	0.37	0/3264
5	E	0.13	0/1914	0.34	0/2566
6	F	0.14	0/1911	0.36	0/2549
7	G	0.14	0/1910	0.37	0/2569
8	H	0.13	0/1535	0.35	0/2063
9	I	0.12	0/1702	0.34	0/2272
10	J	0.13	0/1385	0.38	0/1852
11	L	0.13	0/1733	0.36	0/2316
12	M	0.15	0/1158	0.40	0/1547
13	N	0.15	0/1740	0.39	0/2328
14	O	0.15	0/1662	0.38	0/2222
15	P	0.19	0/1268	0.43	0/1700
16	Q	0.14	0/1538	0.35	0/2054
17	R	0.16	0/1310	0.41	0/1734
18	S	0.14	0/1501	0.36	0/2012
19	T	0.11	0/1326	0.30	0/1770
20	U	0.11	0/848	0.35	0/1138
21	V	0.12	0/993	0.34	1/1332 (0.1%)
22	W	0.13	0/541	0.35	0/720
23	X	0.14	0/984	0.37	0/1323
24	Y	0.12	0/1132	0.35	0/1504
25	Z	0.13	0/1130	0.32	0/1507
26	a	0.13	0/1191	0.32	0/1590
27	b	0.12	0/861	0.36	0/1138
28	c	0.13	0/771	0.34	0/1034
29	d	0.14	0/903	0.36	0/1216
30	e	0.13	0/1071	0.33	0/1429
31	f	0.13	0/895	0.33	0/1198
32	g	0.15	0/916	0.35	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.14	0/1017	0.40	0/1344
34	i	0.14	0/841	0.38	0/1112
35	j	0.11	0/720	0.30	0/952
36	k	0.13	0/575	0.34	0/761
37	l	0.14	0/459	0.37	0/608
38	m	0.13	0/435	0.33	0/575
39	n	0.16	0/240	0.45	0/305
40	o	0.11	0/864	0.32	0/1140
41	p	0.15	0/718	0.37	0/953
42	q	0.14	0/1805	0.38	0/2809
43	r	0.13	0/1010	0.37	0/1354
44	u	0.15	0/2858	0.34	0/4455
45	v	0.15	0/3701	0.37	0/5766
46	w	0.12	0/3240	0.30	0/4339
47	1	0.13	0/3677	0.37	0/4986
48	2	0.13	0/237	0.28	0/321
49	3	0.14	0/553	0.35	0/738
50	4	0.13	0/2819	0.35	0/3772
51	5	0.14	0/730	0.31	0/988
52	7	0.11	0/4224	0.30	0/5728
53	6	0.11	0/1835	0.30	0/2495
54	K	0.17	0/84978	0.42	0/132528
All	All	0.15	0/160861	0.39	1/235992 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
13	N	0	1
50	4	0	1
54	K	0	1
All	All	0	3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	V	132	ILE	N-CA-C	-5.50	107.08	111.81

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	4	433	ARG	Sidechain
54	K	234	G	Sidechain
13	N	76	PRO	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1898	1993	1993	39	0
2	B	180	171	171	4	0
3	C	2883	3053	3053	52	0
4	D	2391	2424	2424	37	0
5	E	1877	2031	2031	58	0
6	F	1875	1995	1995	31	0
7	G	1879	2027	2027	29	0
8	H	1516	1597	1597	26	0
9	I	1664	1712	1712	20	0
10	J	1362	1399	1399	23	0
11	L	1702	1820	1820	28	0
12	M	1137	1211	1211	21	0
13	N	1696	1744	1743	37	0
14	O	1630	1778	1778	31	0
15	P	1242	1274	1274	34	0
16	Q	1514	1634	1634	25	0
17	R	1294	1434	1434	21	0
18	S	1462	1508	1508	34	0
19	T	1298	1367	1366	24	0
20	U	834	858	858	11	0
21	V	979	1039	1039	15	0
22	W	528	541	541	5	0
23	X	967	1040	1040	23	0
24	Y	1115	1205	1205	26	0
25	Z	1107	1182	1182	18	0
26	a	1162	1209	1209	26	0
27	b	848	920	920	18	0
28	c	761	794	794	12	0
29	d	888	930	930	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	e	1053	1147	1147	10	0
31	f	876	912	912	20	0
32	g	906	998	998	16	0
33	h	1009	1136	1136	14	0
34	i	830	916	916	11	0
35	j	705	737	737	14	0
36	k	569	637	637	7	0
37	l	447	480	480	12	0
38	m	429	466	466	9	0
39	n	239	289	289	5	0
40	o	851	922	922	11	0
41	p	708	757	757	18	0
42	q	1616	823	824	11	0
43	r	994	1051	1051	30	0
44	u	2558	1296	1296	29	0
45	v	3314	1683	1683	40	0
46	w	3172	3310	3310	58	0
47	1	3598	3722	3722	42	0
48	2	230	245	245	0	0
49	3	543	577	577	5	0
50	4	2778	2819	2819	35	0
51	5	711	710	710	2	0
52	7	4139	4121	4123	24	0
53	6	1783	1792	1792	11	0
54	K	75972	38358	38382	939	0
55	K	201	0	0	0	0
55	P	2	0	0	0	0
55	V	1	0	0	0	0
55	a	1	0	0	0	0
55	g	1	0	0	0	0
55	j	1	0	0	0	0
55	u	7	0	0	0	0
55	v	6	0	0	0	0
56	g	1	0	0	0	0
56	j	1	0	0	0	0
56	m	1	0	0	0	0
56	o	1	0	0	0	0
56	p	1	0	0	0	0
All	All	149944	111794	111819	1755	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (1755) 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)
54:K:1397:A:HO2'	54:K:1467:C:HO2'	1.00	0.92
54:K:2638:G:N2	54:K:2697:A:N1	2.16	0.92
21:V:50:ASN:ND2	54:K:4457:U:OP1	2.04	0.90
43:r:98:ARG:NH2	54:K:2262:G:OP2	2.05	0.89
42:q:10:G:N2	42:q:25:C:O2	2.04	0.89
54:K:746:A:O2'	54:K:913:U:O4	1.90	0.89
54:K:180:C:O2	54:K:256:G:N2	2.05	0.88
54:K:1369:C:OP2	54:K:1370:G:O2'	1.90	0.88
6:F:231:ASP:OD1	6:F:235:ARG:NH2	2.08	0.87
54:K:2469:C:N4	54:K:2471:G:O6	2.07	0.86
13:N:157:LYS:O	13:N:162:ARG:NH1	2.08	0.86
54:K:245:C:O2'	54:K:246:G:OP2	1.93	0.86
16:Q:150:ARG:NH2	54:K:1499:C:OP1	2.09	0.86
54:K:1818:G:O2'	54:K:1819:G:OP1	1.93	0.86
24:Y:8:THR:OG1	54:K:346:G:OP1	1.94	0.85
54:K:1406:G:N2	54:K:1411(C):C:O2	2.08	0.85
53:6:110:GLU:OE1	53:6:146:TYR:OH	1.93	0.85
54:K:759:G:N2	54:K:904:C:O2	2.09	0.85
54:K:164:G:O6	54:K:271:C:N4	2.10	0.85
54:K:62:A:N3	54:K:77:U:O2'	2.10	0.85
16:Q:181:ARG:NH2	54:K:1391:A:OP1	2.09	0.84
27:b:44:ARG:NH1	54:K:1493:G:OP2	2.10	0.84
44:u:23:A:N3	44:u:118:C:O2'	2.10	0.84
54:K:1326:A:OP2	54:K:4445:U:O2'	1.94	0.84
24:Y:121:ARG:NH2	54:K:194:C:O2	2.11	0.83
7:G:90:LYS:NZ	54:K:4126:C:OP1	2.11	0.83
9:I:191:ILE:HD11	9:I:212:LEU:HD11	1.59	0.83
54:K:4467:A:O2'	54:K:4510:A:N3	2.10	0.83
54:K:4743:G:O6	54:K:4957:C:N4	2.12	0.82
54:K:3766:A:OP2	54:K:3767:C:N4	2.12	0.82
54:K:1756:U:OP2	54:K:1768:C:N4	2.12	0.82
54:K:2416:G:N2	54:K:2427:G:O6	2.12	0.82
54:K:1320:U:O2'	54:K:1891:A:N1	2.12	0.81
9:I:203:ARG:NH1	44:u:105:C:OP2	2.14	0.81
7:G:302:ARG:NH2	54:K:4075:U:OP1	2.14	0.81
54:K:1406(A):G:N2	54:K:1411(B):C:O2	2.14	0.80
8:H:120:GLU:OE1	8:H:124:ARG:NH2	2.15	0.80
43:r:107:ARG:NH2	54:K:2263:A:OP1	2.14	0.80
25:Z:121:ARG:NH2	25:Z:127:ASN:OD1	2.16	0.79
26:a:4:ARG:NH2	54:K:2341:A:OP2	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:r:99:LYS:NZ	54:K:2260:C:O2	2.15	0.79
14:O:12:ARG:O	18:S:171:ARG:NH2	2.15	0.79
54:K:738(A):C:O2'	54:K:740:G:OP2	2.01	0.79
54:K:755:C:O2	54:K:908:G:N2	2.14	0.79
40:o:61:LYS:NZ	54:K:4372:U:OP2	2.16	0.79
9:I:40:LYS:NZ	54:K:1751:A:OP1	2.16	0.78
54:K:2465:C:O2	54:K:3672:G:N2	2.17	0.78
24:Y:74:TYR:OH	45:v:75:G:OP2	2.02	0.78
54:K:180:C:N3	54:K:256:G:N1	2.30	0.78
54:K:966:A:O4'	54:K:968:C:N4	2.16	0.78
1:A:117:GLU:OE2	1:A:123:ARG:N	2.16	0.78
54:K:67:C:OP2	54:K:312:G:N2	2.17	0.78
54:K:3641:U:OP2	54:K:3646:A:N6	2.16	0.78
1:A:142:GLU:O	1:A:143:THR:OG1	2.00	0.78
4:D:72:ASP:OD2	44:u:6:C:O2'	2.01	0.77
13:N:2:GLY:O	13:N:4:TYR:N	2.17	0.77
54:K:2490:U:O2'	54:K:2491:C:O4'	2.01	0.77
54:K:2869:U:O2'	54:K:2881:A:N7	2.17	0.77
1:A:36:GLU:OE2	1:A:163:ARG:NE	2.18	0.77
21:V:41:SER:OG	54:K:4507:A:O2'	2.02	0.77
36:k:33:LYS:NZ	54:K:2695:A:OP2	2.18	0.77
44:u:72:U:O2	44:u:103:A:N6	2.18	0.77
3:C:327:LYS:NZ	54:K:975:C:O2	2.16	0.77
26:a:8:THR:HG21	54:K:1339:U:OP1	1.86	0.76
35:j:52:LYS:NZ	54:K:375:G:OP2	2.17	0.76
3:C:287:THR:HG1	43:r:2:SER:HG	1.27	0.76
38:m:74:TYR:O	54:K:4472:G:O2'	2.03	0.76
3:C:234:LYS:NZ	54:K:1364:U:O2	2.13	0.76
21:V:41:SER:HG	54:K:4507:A:HO2'	1.33	0.75
54:K:5047:C:O2'	54:K:5050:C:OP2	2.04	0.75
10:J:56:THR:HG22	10:J:64:ARG:H	1.51	0.75
17:R:114:LYS:O	17:R:146:LYS:NZ	2.19	0.75
41:p:44:LYS:NZ	54:K:2672:C:OP1	2.19	0.75
17:R:62:ARG:O	17:R:66:ASN:ND2	2.19	0.75
23:X:107:HIS:O	23:X:111:GLN:NE2	2.20	0.75
54:K:369:G:N2	54:K:372:A:OP2	2.18	0.75
19:T:87:LYS:NZ	54:K:4300:U:OP1	2.19	0.74
54:K:406:C:O2'	54:K:407:A:OP1	2.04	0.74
29:d:32:ARG:NH2	54:K:4995:U:O3'	2.21	0.74
37:l:41:ARG:NH1	54:K:2431:A:OP1	2.21	0.74
54:K:1872:G:O2'	54:K:4219:A:N3	2.16	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:w:385:LYS:NZ	54:K:5002:U:OP2	2.21	0.74
54:K:1435:G:O2'	54:K:2105:A:N1	2.19	0.74
54:K:1481:C:O2'	54:K:1482:G:O4'	2.03	0.74
24:Y:91:ASN:OD1	24:Y:93:THR:HG22	1.86	0.74
18:S:95:ARG:NH2	18:S:112:ASP:OD2	2.20	0.74
19:T:55:LYS:NZ	54:K:4217:G:OP1	2.19	0.74
54:K:2601:A:N6	54:K:2744:A:OP2	2.21	0.74
54:K:2418:A:N1	54:K:2429:A:O2'	2.21	0.74
45:v:112:G:OP1	54:K:2779:C:O2'	2.02	0.74
16:Q:14:ARG:NH2	54:K:2083:C:OP2	2.21	0.73
25:Z:22:LYS:NZ	25:Z:132:GLN:O	2.21	0.73
54:K:2486:G:H1	54:K:2492:C:H42	1.36	0.73
54:K:1440:U:O2'	54:K:1441:C:OP1	2.05	0.73
54:K:759:G:N1	54:K:904:C:N3	2.34	0.73
12:M:71:LYS:NZ	54:K:737:C:OP2	2.22	0.73
54:K:1404:G:N2	54:K:1413:C:O2	2.20	0.73
42:q:18:G:N2	42:q:58:A:O4'	2.22	0.72
45:v:102:G:OP2	45:v:104:A:O2'	2.05	0.72
18:S:111:ARG:NH2	54:K:2062:C:O2'	2.22	0.72
46:w:174:ARG:NH1	54:K:4985:U:O2	2.22	0.72
50:4:273:GLN:NE2	50:4:283:CYS:O	2.21	0.72
15:P:12:THR:HG23	50:4:414:GLU:OE2	1.88	0.72
54:K:2529:A:O2'	54:K:2531:C:OP2	2.07	0.72
4:D:86:TYR:CE2	4:D:104:LEU:HD21	2.24	0.72
4:D:88:VAL:HG12	4:D:239:MET:SD	2.29	0.72
12:M:108:ASP:OD2	14:O:199:HIS:NE2	2.23	0.72
46:w:249:ARG:NH2	54:K:3845:A:OP2	2.22	0.72
33:h:81:LEU:HD23	33:h:84:ARG:HD2	1.71	0.72
54:K:704:C:O2'	54:K:705:G:OP1	2.05	0.72
54:K:233:U:O2'	54:K:2304:U:O4	2.06	0.72
54:K:2490:U:O2'	54:K:2491:C:O5'	2.07	0.72
3:C:287:THR:OG1	43:r:2:SER:OG	2.06	0.72
41:p:17:ARG:NH1	54:K:1577:G:OP1	2.21	0.72
19:T:42:ILE:HD11	19:T:74:ILE:HD11	1.72	0.71
24:Y:67:ILE:O	24:Y:84:ARG:NH2	2.22	0.71
54:K:2502:A:O2'	54:K:2503:G:O5'	2.07	0.71
4:D:222:GLN:O	44:u:48:G:O2'	2.09	0.71
27:b:32:LEU:HD12	54:K:1464:C:H5''	1.71	0.71
1:A:30:ARG:O	1:A:163:ARG:NH2	2.23	0.71
54:K:4492:U:O2'	54:K:4512:U:O2	2.07	0.71
54:K:1477:C:O2'	54:K:1478:C:OP1	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:3603:G:O2'	54:K:3604:A:O4'	2.09	0.71
35:j:30:GLN:NE2	54:K:1621:A:OP2	2.24	0.70
54:K:308:G:N2	54:K:308:G:OP2	2.21	0.70
54:K:3692:A:H62	54:K:3823:G:H21	1.36	0.70
3:C:321:ASN:OD1	54:K:1280:C:O2'	2.08	0.70
45:v:107:C:O2	45:v:112:G:N2	2.19	0.70
42:q:19:G:H4'	42:q:20:U:OP2	1.89	0.70
54:K:4925:U:O2'	54:K:4926:C:OP1	2.09	0.70
18:S:9:GLU:HG3	18:S:67:VAL:HG13	1.74	0.70
46:w:246:ARG:NH2	54:K:4558:U:OP2	2.24	0.70
11:L:47:ALA:HB3	11:L:48:PRO:HD3	1.74	0.70
54:K:1591:U:N3	54:K:4555:U:OP1	2.22	0.70
3:C:45:ARG:NH2	54:K:2295:C:O2'	2.24	0.70
54:K:2517:A:N3	54:K:2539:C:O2'	2.25	0.70
25:Z:88:ASP:O	25:Z:121:ARG:NH1	2.24	0.70
1:A:9:ARG:NH2	54:K:1629:G:N7	2.40	0.69
54:K:46:U:OP2	54:K:47:A:O2'	2.09	0.69
13:N:184:ILE:O	13:N:194:ARG:NH2	2.25	0.69
35:j:21:ARG:NH2	35:j:39:TYR:O	2.24	0.69
14:O:168:TYR:OH	54:K:4768:G:OP1	2.08	0.69
7:G:96:GLN:O	54:K:4124:G:N2	2.25	0.69
54:K:4448:G:O2'	54:K:4449:A:OP2	2.10	0.69
19:T:83:LYS:HE2	19:T:85:LEU:HD21	1.74	0.69
52:7:26:LEU:HD13	52:7:65:ALA:HB2	1.74	0.69
40:o:81:ARG:NH2	54:K:4293:U:O2'	2.25	0.69
50:4:462:ARG:NH1	54:K:2378:G:OP1	2.26	0.69
54:K:3811:G:O2'	54:K:3814:U:OP2	2.10	0.69
54:K:4620:U:OP2	54:K:4670:C:N4	2.26	0.69
1:A:223:SER:HG	54:K:3748:A:HO2'	1.26	0.68
13:N:2:GLY:N	54:K:115:C:OP1	2.27	0.68
30:e:107:ASN:ND2	54:K:2303:C:OP1	2.26	0.68
54:K:4949:G:H4'	54:K:4950:U:H5'	1.75	0.68
46:w:114:CYS:SG	46:w:180:LEU:HD11	2.34	0.68
13:N:116:LEU:HD22	13:N:135:ILE:HD11	1.75	0.68
46:w:17:LEU:O	46:w:19:ARG:N	2.27	0.68
46:w:224:LYS:NZ	54:K:4626:A:OP2	2.18	0.68
13:N:155:VAL:O	13:N:162:ARG:NH2	2.27	0.68
43:r:32:LEU:HD21	43:r:106:LEU:HD12	1.76	0.68
5:E:182:LEU:HD12	5:E:186:ARG:HA	1.74	0.67
46:w:80:GLU:HG3	46:w:326:VAL:HG13	1.75	0.67
9:I:3:ARG:NH2	54:K:4431:U:OP2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:3625:G:O2'	54:K:3626:G:OP1	2.12	0.67
6:F:95:ARG:NH2	54:K:1895:G:OP1	2.27	0.67
54:K:102:G:HO2'	54:K:1381:U:HO2'	1.32	0.67
54:K:5005:G:N2	54:K:5041:G:O2'	2.27	0.67
33:h:95:LEU:O	54:K:135:G:N2	2.26	0.66
37:l:2:SER:OG	37:l:3:SER:N	2.24	0.66
13:N:123:GLU:OE1	13:N:128:LYS:NZ	2.29	0.66
10:J:33:LEU:HD21	10:J:68:ILE:O	1.95	0.66
13:N:65:ARG:NH2	54:K:2457:G:OP1	2.28	0.66
11:L:59:VAL:HG13	54:K:74:G:H5'	1.76	0.66
25:Z:14:LEU:HD21	32:g:92:LYS:HE3	1.76	0.66
54:K:3809:G:N2	54:K:3809:G:OP2	2.26	0.66
6:F:89:ALA:HB2	6:F:124:LEU:HD21	1.77	0.66
26:a:47:LYS:NZ	54:K:1684:A:OP1	2.29	0.66
29:d:64:ILE:HG23	29:d:68:LEU:HD23	1.76	0.66
46:w:246:ARG:NH1	54:K:4525:C:OP1	2.29	0.66
54:K:1893:C:O2'	54:K:1936:C:N3	2.27	0.66
54:K:2519:U:O2'	54:K:2530:U:O2	2.14	0.66
11:L:110:LEU:O	11:L:114:VAL:HG23	1.95	0.65
16:Q:65:ARG:NH1	54:K:1502:G:OP1	2.30	0.65
24:Y:15:ARG:NH2	45:v:23:C:OP1	2.28	0.65
54:K:2395:A:O2'	54:K:2806:A:H1'	1.97	0.65
33:h:96:ASN:ND2	54:K:136:C:OP2	2.29	0.65
4:D:33:ARG:NH1	44:u:7:G:O3'	2.29	0.65
4:D:120:GLU:O	4:D:248:ARG:NH2	2.29	0.65
12:M:117:LYS:NZ	54:K:4882:U:OP1	2.29	0.65
54:K:1666:C:O2'	54:K:1688:G:OP1	2.09	0.65
54:K:2740:U:O2'	54:K:2742:G:N2	2.30	0.65
54:K:2758:G:O2'	54:K:2765:A:N3	2.23	0.65
26:a:72:THR:HG22	26:a:110:LYS:HB3	1.78	0.65
54:K:1818:G:HO2'	54:K:1819:G:P	2.16	0.65
27:b:72:ILE:HG23	27:b:73:LYS:HD2	1.76	0.65
47:1:273:ARG:NH1	54:K:2432:U:OP1	2.29	0.65
40:o:20:PRO:O	40:o:73:VAL:HG22	1.97	0.65
54:K:1455:G:O2'	54:K:1456:C:OP1	2.11	0.64
54:K:4232:U:H4'	54:K:4233:A:O5'	1.95	0.64
5:E:269:GLN:N	54:K:4931:G:OP1	2.28	0.64
34:i:76:ARG:O	54:K:304:C:O2'	2.11	0.64
16:Q:2:GLY:N	54:K:2072:C:OP1	2.30	0.64
30:e:15:LYS:NZ	54:K:2077:C:O2	2.23	0.64
31:f:28:LEU:HG	31:f:101:ILE:HD11	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:1174:G:O2'	54:K:1175:A:OP1	2.15	0.64
33:h:48:ARG:NH2	45:v:63:U:OP1	2.31	0.64
50:4:470:LYS:NZ	54:K:395:A:O2'	2.28	0.64
52:7:250:ASN:CB	52:7:259:LEU:HD12	2.27	0.64
54:K:1339:U:H2'	54:K:1340:C:C6	2.33	0.64
54:K:4098:A:N6	54:K:4111:U:O4	2.30	0.64
8:H:111:LEU:HD12	8:H:127:ARG:HD2	1.78	0.64
15:P:28:ASN:O	15:P:32:THR:HG22	1.97	0.64
54:K:2000:G:O2'	54:K:2001:G:N7	2.31	0.64
8:H:134:CYS:SG	8:H:144:LEU:HD23	2.38	0.64
54:K:1440:U:HO2'	54:K:1441:C:P	2.20	0.64
54:K:2368:A:N6	54:K:2827:G:O2'	2.29	0.64
35:j:72:ARG:NH1	45:v:94:G:OP2	2.31	0.64
54:K:734:G:H1	54:K:929:A:H62	1.44	0.64
54:K:1397:A:O2'	54:K:1467:C:O2'	1.92	0.64
54:K:1594:C:O2'	54:K:1597:G:O2'	2.13	0.64
54:K:3878:C:N4	54:K:4518:A:O4'	2.31	0.64
32:g:54:ARG:NH2	54:K:2651:C:O2'	2.31	0.63
54:K:158:A:N1	54:K:276:C:O2'	2.23	0.63
1:A:124:GLY:O	1:A:128:ARG:NH1	2.32	0.63
54:K:1238:A:O2'	54:K:1239:C:OP1	2.16	0.63
46:w:242:ARG:NH2	54:K:2856:C:O2	2.30	0.63
54:K:1548:G:O2'	54:K:2812:A:N3	2.31	0.63
16:Q:11:ARG:NH2	54:K:1690:C:OP2	2.31	0.63
54:K:314:G:O2'	54:K:4355:G:OP1	2.04	0.63
15:P:12:THR:HG23	50:4:414:GLU:CG	2.29	0.63
54:K:3717:A:OP2	54:K:3735:G:N2	2.31	0.63
5:E:66:SER:OG	54:K:1239:C:N4	2.32	0.63
15:P:2:VAL:HG12	15:P:3:ARG:H	1.63	0.63
43:r:107:ARG:NH1	43:r:108:MET:SD	2.72	0.62
54:K:2440:U:O2'	54:K:2441:C:OP1	2.17	0.62
54:K:3946:G:N2	54:K:4067:U:O2	2.29	0.62
18:S:13:VAL:HG22	18:S:63:TYR:HB3	1.81	0.62
54:K:4902:C:N4	54:K:4919:G:O6	2.32	0.62
43:r:39:ARG:NH1	43:r:105:ASP:OD2	2.32	0.62
36:k:35:LYS:NZ	54:K:2695:A:OP1	2.25	0.62
54:K:218:A:O2'	54:K:221:C:OP1	2.18	0.62
6:F:216:ARG:O	6:F:245:ARG:NH1	2.32	0.62
50:4:314:ASP:OD2	50:4:388:TYR:OH	2.17	0.62
54:K:1426:G:N2	54:K:1458:C:OP2	2.31	0.62
43:r:32:LEU:HD23	43:r:32:LEU:H	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:4:470:LYS:NZ	54:K:395:A:O3'	2.32	0.62
54:K:410:A:O2'	54:K:414:C:O2'	2.06	0.62
41:p:23:ARG:NH1	54:K:2875:C:OP1	2.31	0.62
50:4:233:VAL:HG22	50:4:236:ARG:HH22	1.64	0.62
54:K:2094:C:H3'	54:K:2095:A:H5'	1.81	0.62
6:F:93:ARG:NH1	6:F:95:ARG:O	2.31	0.62
54:K:4948:C:H5''	54:K:4949:G:H5''	1.82	0.62
5:E:206:ILE:O	5:E:206:ILE:HG22	1.99	0.61
1:A:104:VAL:HG22	1:A:162:ASN:O	2.00	0.61
28:c:28:VAL:HG21	28:c:37:MET:HG3	1.82	0.61
46:w:119:TYR:OH	46:w:129:ALA:N	2.32	0.61
54:K:2848:G:O2'	54:K:3838:U:O4	2.12	0.61
54:K:4077:A:N1	54:K:4171:C:N4	2.48	0.61
39:n:21:ARG:O	39:n:24:SER:OG	2.18	0.61
50:4:305:MET:HE1	50:4:402:GLY:HA2	1.81	0.61
24:Y:55:VAL:HG22	24:Y:104:VAL:HG22	1.82	0.61
34:i:50:PHE:O	34:i:55:ARG:NH2	2.34	0.61
6:F:59:GLU:OE1	6:F:191:HIS:NE2	2.33	0.61
9:I:115:MET:HE3	54:K:1868:A:H61	1.65	0.61
46:w:89:ILE:HD12	46:w:194:LEU:HD11	1.81	0.61
3:C:284:MET:HA	16:Q:122:THR:HG21	1.83	0.61
23:X:83:THR:HG21	54:K:2434:G:H5'	1.81	0.61
4:D:62:CYS:HB3	4:D:105:LEU:HD22	1.83	0.61
44:u:11:A:O2'	44:u:13:A:OP2	2.19	0.61
47:1:19:ILE:O	47:1:171:LYS:NZ	2.27	0.61
16:Q:88:ASP:OD1	16:Q:89:ASP:N	2.33	0.61
1:A:54:ARG:NH2	54:K:3680:U:OP1	2.30	0.61
4:D:75:VAL:O	4:D:112:ARG:NH1	2.33	0.61
6:F:85:GLU:OE2	19:T:136:ARG:NH1	2.34	0.61
31:f:58:VAL:O	54:K:4944:C:N4	2.34	0.60
46:w:249:ARG:NH1	54:K:2837:U:OP1	2.31	0.60
5:E:144:ARG:NH1	31:f:108:SER:O	2.34	0.60
7:G:297:PRO:HA	7:G:300:VAL:HG12	1.82	0.60
19:T:2:THR:N	54:K:4220:A:OP2	2.34	0.60
1:A:152:SER:OG	54:K:3661:G:N7	2.35	0.60
11:L:63:THR:O	11:L:65:ARG:N	2.35	0.60
54:K:85:G:O2'	54:K:97:G:O6	2.19	0.60
14:O:148:LYS:NZ	54:K:4713:G:OP1	2.23	0.60
24:Y:115:ARG:O	24:Y:119:LEU:HD13	2.02	0.60
54:K:2093:G:H4'	54:K:2094:C:H5'	1.84	0.60
3:C:195:LYS:NZ	54:K:2334:C:OP2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:75:ARG:NH1	44:u:40:U:O2	2.35	0.60
45:v:16:G:O2'	54:K:417:G:N2	2.35	0.60
54:K:2046:G:O2'	54:K:2047:A:OP2	2.19	0.60
16:Q:13:VAL:O	16:Q:13:VAL:HG12	2.02	0.60
23:X:93:ASN:OD1	54:K:2532:C:O2'	2.20	0.60
13:N:93:LYS:NZ	54:K:4177:C:OP1	2.32	0.59
46:w:252:ALA:HB1	54:K:4524:G:N3	2.17	0.59
54:K:1503:A:H4'	54:K:1504:G:H5'	1.83	0.59
54:K:2459:G:N2	54:K:2462:C:OP2	2.33	0.59
54:K:3893:C:O2'	54:K:4979:A:N1	2.34	0.59
54:K:1481:C:O2'	54:K:1482:G:N3	2.26	0.59
11:L:116:ARG:NH2	11:L:155:MET:O	2.34	0.59
12:M:94:LYS:NZ	54:K:4872:G:OP2	2.35	0.59
54:K:1398:A:H62	54:K:1419:G:H21	1.51	0.59
54:K:2491:C:H2'	54:K:2492:C:C6	2.37	0.59
54:K:2695:A:O2'	54:K:2696:A:OP2	2.16	0.59
24:Y:83:GLU:OE1	24:Y:84:ARG:NH1	2.36	0.59
25:Z:16:GLY:O	25:Z:19:SER:OG	2.14	0.59
40:o:105:GLN:OE1	40:o:105:GLN:N	2.36	0.59
1:A:142:GLU:C	1:A:143:THR:HG1	2.08	0.59
5:E:49:ASN:ND2	54:K:979:C:OP1	2.36	0.59
40:o:39:ARG:NH1	54:K:295:A:OP2	2.36	0.59
46:w:81:THR:OG1	46:w:207:VAL:HG21	2.03	0.59
54:K:2870:A:OP2	54:K:2879:A:N6	2.32	0.59
11:L:66:TYR:OH	54:K:1382:G:OP1	2.19	0.59
27:b:44:ARG:NH2	54:K:1466:G:OP2	2.36	0.59
34:i:89:GLU:O	34:i:93:VAL:HG12	2.02	0.59
54:K:3700:C:O2'	54:K:3774:A:N3	2.31	0.59
14:O:142:ALA:HA	14:O:145:VAL:HG12	1.85	0.59
37:l:20:ASN:O	37:l:41:ARG:NH2	2.36	0.59
46:w:55:HIS:CE1	54:K:4627:U:HO2'	2.20	0.59
3:C:39:PHE:O	3:C:43:ASN:ND2	2.33	0.58
20:U:66:SER:OG	20:U:67:LYS:N	2.36	0.58
21:V:18:LEU:HD13	21:V:54:ALA:HB3	1.85	0.58
29:d:94:GLU:HG3	29:d:95:ASP:H	1.68	0.58
54:K:4419:U:OP1	54:K:4421:C:N4	2.35	0.58
4:D:65:ALA:HB2	4:D:74:ILE:HD13	1.84	0.58
50:4:261:PHE:CZ	50:4:313:MET:HE3	2.39	0.58
54:K:2041:A:N7	54:K:4434:C:O2'	2.34	0.58
14:O:186:GLU:O	14:O:190:SER:OG	2.19	0.58
30:e:86:GLU:HA	30:e:89:LEU:HD23	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:i:36:HIS:O	34:i:40:VAL:HG23	2.03	0.58
52:7:246:TRP:CH2	52:7:259:LEU:HD11	2.37	0.58
5:E:289:LEU:HD12	12:M:109:ARG:CZ	2.33	0.58
54:K:1482:G:O2'	54:K:1483:C:OP2	2.20	0.58
3:C:254:GLU:OE1	3:C:258:ARG:NH1	2.37	0.58
13:N:181:HIS:O	13:N:195:ARG:NH2	2.36	0.58
15:P:127:ARG:NH2	54:K:2422:C:OP1	2.37	0.58
54:K:1411:C:H2'	54:K:1411(A):G:C8	2.39	0.58
46:w:89:ILE:HG22	46:w:162:VAL:HG23	1.85	0.58
54:K:1218:G:H2'	54:K:1219:G:C8	2.39	0.58
33:h:29:SER:O	33:h:33:VAL:HG23	2.03	0.58
41:p:89:LEU:O	41:p:92:GLN:NE2	2.36	0.58
54:K:684:G:O2'	54:K:685:C:OP1	2.21	0.58
54:K:1637:A:OP1	54:K:1640:C:N4	2.37	0.58
3:C:307:LYS:NZ	54:K:2090:U:OP2	2.36	0.58
54:K:4661:G:N2	54:K:5004:C:O3'	2.37	0.58
3:C:150:LEU:O	3:C:152:LEU:N	2.37	0.58
5:E:75:TYR:OH	54:K:983:C:OP1	2.13	0.58
44:u:73:U:O2'	44:u:102:U:O4	2.20	0.58
54:K:1073:G:H22	54:K:1238:A:H2	1.50	0.58
54:K:1477:C:HO2'	54:K:1478:C:P	2.27	0.58
16:Q:11:ARG:NH1	54:K:1689:G:OP1	2.31	0.57
20:U:20:LYS:NZ	20:U:73:THR:OG1	2.35	0.57
23:X:72:ASP:OD1	23:X:73:HIS:N	2.37	0.57
25:Z:26:VAL:HG22	25:Z:42:LEU:O	2.03	0.57
47:1:442:GLY:O	47:1:443:SER:OG	2.18	0.57
5:E:234:GLU:HG3	50:4:319:HIS:NE2	2.20	0.57
18:S:80:ILE:HG21	18:S:126:ILE:HD12	1.87	0.57
19:T:40:VAL:HG13	19:T:96:ILE:HG23	1.86	0.57
52:7:438:GLU:OE1	52:7:450:GLN:NE2	2.37	0.57
54:K:1633:G:H5'	54:K:1634:A:OP1	2.03	0.57
54:K:4492:U:H5''	54:K:4493:U:H5'	1.86	0.57
54:K:4633:G:O2'	54:K:4635:A:OP2	2.15	0.57
54:K:4635:A:H2	54:K:4663:G:H21	1.52	0.57
38:m:98:LYS:NZ	54:K:4473:A:OP1	2.37	0.57
12:M:57:LEU:HD23	12:M:57:LEU:H	1.67	0.57
4:D:155:THR:O	44:u:35:U:O2'	2.19	0.57
8:H:41:ILE:HG22	8:H:43:VAL:HG13	1.85	0.57
24:Y:126:ARG:NH2	54:K:198:A:OP1	2.37	0.57
5:E:123:ASP:OD2	43:r:112:ARG:NH2	2.37	0.57
5:E:156:LEU:HD11	5:E:198:ILE:HG13	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:8:LYS:NZ	54:K:2387:G:OP1	2.37	0.57
43:r:107:ARG:O	43:r:111:ILE:HD12	2.03	0.57
54:K:4378:A:O2'	54:K:4379:A:H2'	2.04	0.57
17:R:31:GLU:OE1	17:R:31:GLU:N	2.37	0.57
19:T:87:LYS:CE	54:K:4305:G:H22	2.18	0.57
33:h:33:VAL:O	33:h:37:THR:HG23	2.04	0.57
46:w:95:THR:HG22	54:K:4910:A:H4'	1.87	0.57
52:7:10:GLN:NE2	52:7:187:GLY:O	2.37	0.57
52:7:250:ASN:HB2	52:7:259:LEU:HD12	1.86	0.57
5:E:164:ARG:NH1	5:E:276:SER:OG	2.38	0.57
13:N:73:ARG:NH1	54:K:32:G:OP1	2.37	0.57
31:f:36:ARG:O	31:f:39:THR:HG22	2.04	0.57
54:K:1168:G:H1	54:K:1193:C:H42	1.50	0.57
5:E:109:VAL:HG13	5:E:109:VAL:O	2.05	0.57
14:O:116:LYS:N	54:K:4757:C:OP2	2.34	0.57
37:l:2:SER:N	54:K:2407:G:O6	2.38	0.57
54:K:1198:G:H2'	54:K:1199:G:H8	1.70	0.57
54:K:3876:A:HO2'	54:K:3877:A:P	2.28	0.57
5:E:97:LYS:NZ	54:K:687:U:O2	2.37	0.56
6:F:148:SER:OG	6:F:244:ARG:NH1	2.37	0.56
23:X:120:ASP:OD1	23:X:120:ASP:N	2.35	0.56
35:j:48:ASN:OD1	35:j:54:LYS:NZ	2.37	0.56
47:1:234:PHE:CZ	47:1:242:LEU:HD23	2.40	0.56
54:K:125:C:H2'	54:K:126:C:H6	1.71	0.56
5:E:179:THR:HG23	5:E:179:THR:O	2.03	0.56
14:O:16:LEU:HD21	14:O:83:THR:HG21	1.88	0.56
18:S:147:ASP:OD1	18:S:149:LYS:N	2.38	0.56
28:c:35:LEU:HD11	28:c:63:TYR:CD2	2.40	0.56
38:m:53:GLU:OE1	38:m:55:SER:N	2.31	0.56
45:v:105:C:H4'	45:v:106:G:H5''	1.87	0.56
54:K:3753:G:N1	54:K:3772:U:O2	2.37	0.56
23:X:90:ILE:HG12	23:X:96:LEU:HD23	1.88	0.56
33:h:56:ARG:O	33:h:60:VAL:HG23	2.05	0.56
46:w:228:TYR:O	54:K:2835:A:O2'	2.15	0.56
46:w:252:ALA:HB3	54:K:4457:U:O2	2.06	0.56
54:K:4119:C:O2'	54:K:4120:U:O5'	2.22	0.56
47:1:291:ILE:HD11	47:1:428:ILE:CG2	2.35	0.56
7:G:106:ARG:NH2	54:K:4163:U:OP2	2.38	0.56
18:S:170:LYS:NZ	54:K:4874:A:O2'	2.34	0.56
3:C:108:TRP:HB2	13:N:200:LEU:HD13	1.86	0.56
54:K:4478:G:O2'	54:K:4602:A:N1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:17:ASP:OD1	13:N:18:VAL:N	2.39	0.56
39:n:23:ARG:NH2	54:K:3782:C:OP2	2.39	0.56
47:1:380:ILE:HD11	47:1:421:ALA:HB2	1.87	0.56
54:K:2502:A:H4'	54:K:2503:G:OP1	2.05	0.56
4:D:50:ARG:NH1	4:D:147:ASP:OD2	2.37	0.56
5:E:289:LEU:HD12	12:M:109:ARG:NH1	2.21	0.56
8:H:105:ILE:HD13	8:H:136:VAL:HG23	1.87	0.56
14:O:54:TYR:CD1	14:O:145:VAL:HG21	2.41	0.56
41:p:2:ALA:N	54:K:1570:G:O6	2.39	0.56
54:K:1321:G:OP1	54:K:1880:G:O2'	2.23	0.56
4:D:119:TYR:OH	4:D:139:PRO:O	2.12	0.55
5:E:168:LEU:HD11	5:E:179:THR:HG22	1.88	0.55
6:F:49:ILE:HD12	6:F:185:CYS:HB3	1.88	0.55
13:N:68:ARG:NH2	54:K:303:C:OP2	2.36	0.55
53:6:81:LEU:HD11	53:6:177:VAL:CG2	2.35	0.55
15:P:135:ARG:NH2	54:K:1596:U:O2'	2.39	0.55
54:K:1235:G:O2'	54:K:1236:C:OP2	2.18	0.55
54:K:1563:A:H2'	54:K:1564:A:C8	2.40	0.55
17:R:7:GLN:HG2	17:R:32:ILE:HG22	1.89	0.55
54:K:181:C:H42	54:K:255:C:H42	1.52	0.55
24:Y:82:ILE:HB	24:Y:85:VAL:HG22	1.89	0.55
18:S:82:LEU:HD12	18:S:124:ILE:HG23	1.87	0.55
30:e:81:ASN:HA	30:e:111:ILE:HD11	1.89	0.55
47:1:298:VAL:HG22	47:1:345:LEU:HD23	1.87	0.55
54:K:5006:U:H4'	54:K:5007:A:H5'	1.88	0.55
3:C:145:GLU:N	3:C:145:GLU:OE1	2.38	0.55
17:R:84:THR:O	17:R:87:ALA:N	2.39	0.55
47:1:287:SER:OG	47:1:288:ASN:N	2.40	0.55
54:K:4510:A:O2'	54:K:4511:A:O4'	2.24	0.55
23:X:156:ILE:O	49:3:24:ARG:NH1	2.40	0.55
24:Y:19:PHE:O	24:Y:26:ARG:NH2	2.40	0.55
34:i:79:THR:HG22	34:i:81:ILE:H	1.72	0.55
54:K:1276:C:H2'	54:K:1277:G:O4'	2.07	0.55
54:K:1481:C:O2'	54:K:1482:G:O5'	2.25	0.55
54:K:1978:C:O2	54:K:1989:G:N1	2.40	0.55
54:K:2465:C:H1'	54:K:3672:G:H22	1.72	0.55
54:K:4237:C:O2	54:K:4321:U:O2'	2.25	0.55
54:K:4348:A:O2'	54:K:4350:C:OP2	2.25	0.55
5:E:228:PRO:O	5:E:229:ARG:HG3	2.07	0.55
8:H:40:HIS:ND1	54:K:4701:A:O2'	2.36	0.55
23:X:145:ASP:OD1	23:X:148:ASP:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Y:106:ILE:HG21	24:Y:109:LEU:HD23	1.89	0.55
3:C:290:SER:O	3:C:294:LYS:HG2	2.07	0.54
14:O:54:TYR:HD1	14:O:145:VAL:HG21	1.72	0.54
27:b:11:ASN:ND2	54:K:1669:A:OP1	2.34	0.54
54:K:1802:A:O2'	54:K:1837:A:OP1	2.22	0.54
46:w:139:ASP:OD1	46:w:139:ASP:N	2.39	0.54
54:K:69:A:N1	54:K:324:A:O2'	2.34	0.54
14:O:194:ASP:O	14:O:198:THR:HG23	2.07	0.54
54:K:1984:A:N6	54:K:2010:A:O2'	2.41	0.54
7:G:215:ASP:HB2	7:G:216:PRO:HD3	1.89	0.54
5:E:168:LEU:HD11	5:E:179:THR:CG2	2.37	0.54
26:a:26:ARG:NH1	54:K:1655:C:OP2	2.40	0.54
54:K:3938:G:N2	54:K:4171:C:OP2	2.41	0.54
15:P:47:TYR:OH	15:P:57:CYS:O	2.14	0.54
24:Y:82:ILE:HG22	24:Y:83:GLU:H	1.72	0.54
54:K:1400:G:H2'	54:K:1401:C:C6	2.42	0.54
54:K:2440:U:HO2'	54:K:2441:C:P	2.31	0.54
54:K:4195:G:O2'	54:K:4442:U:OP1	2.15	0.54
6:F:133:ARG:NH1	44:u:97:G:O5'	2.41	0.54
7:G:217:ILE:O	7:G:221:VAL:HG23	2.07	0.54
7:G:312:LYS:HA	7:G:315:ALA:HB3	1.90	0.54
44:u:11:A:N1	44:u:66:G:O2'	2.34	0.54
13:N:169:ARG:HE	13:N:174:LEU:HD11	1.72	0.54
45:v:122:G:H21	45:v:128:C:H5	1.55	0.54
46:w:48:GLY:HA3	46:w:81:THR:HG22	1.90	0.54
16:Q:124:ASP:OD1	16:Q:125:GLN:N	2.41	0.53
54:K:1438:U:O2'	54:K:1440:U:OP2	2.24	0.53
54:K:4977:A:O2'	54:K:4982:A:N1	2.41	0.53
1:A:97:ASN:OD1	1:A:100:ASN:ND2	2.35	0.53
28:c:17:ARG:NH1	28:c:103:ASP:OD1	2.38	0.53
42:q:5:C:H2'	42:q:6:C:C6	2.43	0.53
7:G:215:ASP:HB2	7:G:216:PRO:CD	2.38	0.53
43:r:87:ARG:NH2	54:K:458:C:OP1	2.41	0.53
46:w:103:LYS:NZ	46:w:149:ASP:OD1	2.26	0.53
54:K:2647:A:H62	54:K:2686:G:H8	1.56	0.53
3:C:134:PRO:HA	3:C:150:LEU:HD11	1.91	0.53
3:C:209:VAL:HB	3:C:229:LEU:HD13	1.91	0.53
4:D:93:THR:O	4:D:93:THR:HG22	2.08	0.53
18:S:99:ASP:OD1	18:S:100:LEU:N	2.39	0.53
54:K:759:G:O6	54:K:904:C:N4	2.42	0.53
54:K:2844:A:O2'	54:K:4631:G:H4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:l:48:LYS:NZ	54:K:2791:C:OP1	2.39	0.53
54:K:275:C:O2'	54:K:276:C:O5'	2.24	0.53
54:K:963:G:HO2'	54:K:964:A:H8	1.55	0.53
54:K:2579:G:N2	54:K:2582:A:OP2	2.32	0.53
10:J:40:LEU:HD23	10:J:72:CYS:HB2	1.91	0.53
35:j:35:GLY:O	35:j:45:ARG:NH2	2.38	0.53
54:K:388:A:O2'	54:K:402:A:N1	2.38	0.53
54:K:1432:G:O2'	54:K:1451:G:N2	2.35	0.53
46:w:10:ARG:NH2	46:w:14:LEU:HD21	2.23	0.53
54:K:1332:C:H2'	54:K:1333:A:H8	1.74	0.53
54:K:1552:G:O2'	54:K:1574:G:N2	2.36	0.53
54:K:3661:G:N1	54:K:3682:A:OP2	2.32	0.53
54:K:4541:G:N2	54:K:4544:A:OP2	2.39	0.53
45:v:18:U:O2	54:K:2309:G:O2'	2.27	0.53
16:Q:89:ASP:OD1	16:Q:91:ARG:NH1	2.42	0.53
23:X:119:ILE:HG21	23:X:149:VAL:HG21	1.90	0.53
1:A:77:ILE:HD11	1:A:115:CYS:HB2	1.91	0.53
46:w:113:GLU:OE1	46:w:168:MET:N	2.37	0.53
54:K:125:C:O2'	54:K:126:C:O5'	2.21	0.53
54:K:978:G:N2	54:K:1277:G:H22	2.06	0.53
54:K:1390:G:N2	54:K:1393:G:OP2	2.38	0.53
54:K:1406(C):G:N2	54:K:1411:C:N3	2.57	0.53
54:K:1798:G:H2'	54:K:1799:G:H5''	1.90	0.53
54:K:2407:G:OP2	54:K:2407:G:N2	2.42	0.53
54:K:4371:G:O2'	54:K:4372:U:OP2	2.27	0.53
21:V:10:SER:OG	21:V:11:GLY:N	2.42	0.52
23:X:128:ILE:O	37:l:10:LYS:NZ	2.32	0.52
54:K:485:C:O2'	54:K:486:C:O5'	2.23	0.52
54:K:2701:U:H2'	54:K:2702:C:C6	2.44	0.52
54:K:5061:A:H3'	54:K:5062:G:H5'	1.91	0.52
5:E:165:VAL:CG2	5:E:178:VAL:HG21	2.39	0.52
43:r:17:LEU:HD21	43:r:19:LYS:HD2	1.91	0.52
46:w:252:ALA:HB1	54:K:4524:G:C2	2.44	0.52
54:K:1768:C:H4'	54:K:1769:G:H5''	1.90	0.52
54:K:2553:A:H2	54:K:2765:A:H62	1.57	0.52
1:A:112:ILE:HD13	1:A:135:THR:HG22	1.91	0.52
4:D:83:LEU:HB3	4:D:88:VAL:CG2	2.39	0.52
5:E:144:ARG:HH21	5:E:147:ILE:HD11	1.74	0.52
10:J:53:ALA:HB2	10:J:68:ILE:HD11	1.91	0.52
16:Q:178:ARG:H	26:a:51:GLY:HA2	1.75	0.52
31:f:23:GLU:OE2	54:K:438:G:N2	2.29	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:h:66:LYS:O	33:h:70:ARG:HG2	2.10	0.52
54:K:914:U:H1'	54:K:915:A:C5	2.45	0.52
54:K:3663:A:N6	54:K:4168:G:O2'	2.42	0.52
3:C:338:ASN:C	3:C:340:ILE:H	2.18	0.52
4:D:59:ASP:OD1	4:D:60:ILE:N	2.43	0.52
8:H:115:ARG:HG2	8:H:123:ILE:HG22	1.91	0.52
14:O:85:ARG:HG3	14:O:99:LEU:HD11	1.91	0.52
34:i:54:GLU:HG2	34:i:90:LEU:HD11	1.92	0.52
46:w:170:LEU:O	46:w:328:ASN:ND2	2.39	0.52
54:K:1238:A:HO2'	54:K:1239:C:P	2.31	0.52
54:K:1562:G:N2	54:K:1565:A:OP2	2.42	0.52
19:T:130:ARG:NH2	54:K:1802:A:N3	2.55	0.52
47:1:380:ILE:CD1	47:1:421:ALA:HB2	2.40	0.52
50:4:213:VAL:HG12	50:4:214:CYS:SG	2.50	0.52
54:K:4476:C:O2'	54:K:4478:G:OP2	2.21	0.52
8:H:73:ILE:O	8:H:77:VAL:HG23	2.09	0.52
8:H:95:VAL:HG22	38:m:56:LEU:HB3	1.90	0.52
14:O:85:ARG:NH2	54:K:3887:C:OP2	2.38	0.52
23:X:60:TYR:OH	54:K:17:A:OP2	2.15	0.52
46:w:218:ASP:OD2	46:w:348:ARG:NH2	2.42	0.52
54:K:517:C:H2'	54:K:518:G:H8	1.75	0.52
54:K:1991:A:OP1	54:K:1991:A:H4'	2.08	0.52
27:b:68:ARG:O	27:b:72:ILE:HG22	2.10	0.52
35:j:49:TRP:O	54:K:1646:A:O2'	2.24	0.52
5:E:249:ARG:NH2	54:K:4940:C:O2'	2.40	0.52
8:H:128:MET:HE1	8:H:161:ILE:HG21	1.91	0.52
17:R:93:VAL:HG11	54:K:2725:A:H1'	1.90	0.52
46:w:55:HIS:CD2	54:K:4627:U:HO2'	2.27	0.52
50:4:466:LYS:NZ	54:K:2379:A:OP1	2.43	0.52
52:7:245:ARG:HB2	52:7:453:ILE:HD12	1.92	0.52
17:R:6:LEU:HD21	17:R:10:LEU:HD11	1.92	0.52
23:X:150:ALA:HB1	23:X:155:ILE:HG13	1.92	0.52
34:i:42:ASP:OD1	34:i:43:MET:N	2.43	0.52
54:K:4925:U:O2'	54:K:4926:C:P	2.67	0.52
24:Y:10:ASP:OD1	24:Y:11:ARG:N	2.43	0.51
27:b:22:LYS:NZ	54:K:1845:U:OP2	2.43	0.51
46:w:89:ILE:HD11	46:w:150:PHE:HE1	1.74	0.51
54:K:1854:G:N2	54:K:4394:A:O4'	2.43	0.51
54:K:3662:A:O4'	54:K:3664:G:C8	2.63	0.51
1:A:114:CYS:SG	1:A:165:VAL:HG13	2.50	0.51
9:I:86:HIS:HB3	9:I:139:ARG:HG2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:f:3:GLY:O	54:K:4945:G:N1	2.37	0.51
40:o:3:ASN:ND2	40:o:95:GLY:O	2.43	0.51
47:1:130:VAL:O	47:1:134:THR:HG23	2.10	0.51
54:K:2844:A:N6	54:K:3839:G:O2'	2.43	0.51
6:F:91:VAL:HG13	6:F:139:ILE:HD12	1.93	0.51
7:G:139:VAL:HG23	7:G:236:ILE:HG22	1.92	0.51
9:I:14:ASN:O	9:I:128:ARG:NH2	2.37	0.51
15:P:12:THR:HG23	50:4:414:GLU:CD	2.35	0.51
41:p:5:THR:OG1	41:p:8:VAL:O	2.15	0.51
54:K:12:A:H5'	54:K:13:U:OP2	2.10	0.51
54:K:134:G:H4'	54:K:135:G:O5'	2.09	0.51
54:K:1882:U:C4	54:K:2279:A:C2	2.98	0.51
4:D:90:VAL:HG11	4:D:231:VAL:HG21	1.93	0.51
9:I:142:LEU:HD23	9:I:142:LEU:O	2.11	0.51
19:T:4:THR:O	19:T:9:ARG:NE	2.43	0.51
20:U:22:THR:C	20:U:23:LEU:HD12	2.34	0.51
54:K:4537:C:H2'	54:K:4538:G:H8	1.75	0.51
6:F:79:ASN:HA	19:T:143:THR:HG22	1.92	0.51
54:K:1326:A:H2'	54:K:1327:C:C6	2.46	0.51
1:A:48:ILE:HD11	1:A:82:ILE:HG22	1.93	0.51
5:E:237:ASP:OD1	5:E:238:THR:N	2.44	0.51
15:P:36:ILE:O	15:P:36:ILE:HG22	2.11	0.51
29:d:26:THR:HG23	54:K:4996:C:H4'	1.93	0.51
29:d:59:THR:HG1	29:d:104:THR:HG1	1.41	0.51
54:K:964:A:H2'	54:K:965:G:O4'	2.11	0.51
54:K:1169:G:H1	54:K:1192:C:H42	1.58	0.51
54:K:2467:U:H4'	54:K:2468:U:H5'	1.91	0.51
54:K:3603:G:H2'	54:K:3604:A:C8	2.45	0.51
4:D:50:ARG:NH2	4:D:72:ASP:OD2	2.44	0.51
13:N:45:PRO:O	13:N:49:ARG:HG3	2.10	0.51
27:b:15:LYS:NZ	54:K:1670:G:OP1	2.35	0.51
53:6:53:LEU:HD21	53:6:76:VAL:HG21	1.93	0.51
54:K:4067:U:H2'	54:K:4068:U:C6	2.46	0.51
54:K:4413:C:H5	54:K:4429:C:H42	1.59	0.51
54:K:4454:G:HO2'	54:K:4500:U:HO2'	1.54	0.51
1:A:13:GLY:O	1:A:14:SER:OG	2.26	0.51
1:A:223:SER:OG	54:K:3748:A:O2'	2.04	0.51
3:C:293:LEU:O	3:C:299:GLN:NE2	2.40	0.51
5:E:165:VAL:HG23	5:E:178:VAL:HG21	1.93	0.51
24:Y:85:VAL:HG23	24:Y:85:VAL:O	2.10	0.51
47:1:391:ALA:CB	47:1:410:VAL:HG22	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:691:C:H2'	54:K:692:A:C8	2.46	0.51
1:A:117:GLU:HB2	1:A:162:ASN:HB2	1.93	0.51
13:N:136:ASP:OD2	45:v:141:C:O2'	2.25	0.51
37:l:48:LYS:O	37:l:50:GLY:N	2.44	0.51
43:r:26:SER:HG	43:r:28:GLU:CD	2.19	0.51
53:6:119:LEU:O	53:6:123:ALA:HB3	2.11	0.51
54:K:1317:U:H2'	54:K:1318:C:C6	2.46	0.51
6:F:170:ASP:OD1	6:F:171:ASN:N	2.44	0.50
7:G:139:VAL:HG22	7:G:140:LEU:H	1.76	0.50
50:4:229:ASP:O	50:4:233:VAL:HG23	2.11	0.50
53:6:117:ILE:HB	53:6:118:PRO:HD3	1.94	0.50
4:D:289:ARG:HA	4:D:292:GLU:HG2	1.92	0.50
7:G:190:ARG:HD2	7:G:195:THR:HG21	1.92	0.50
16:Q:11:ARG:HG3	54:K:2081:C:H5''	1.93	0.50
32:g:46:CYS:SG	32:g:47:GLY:N	2.85	0.50
54:K:2485:U:H2'	54:K:2486:G:C8	2.45	0.50
8:H:93:ARG:HE	8:H:143:GLU:HB3	1.76	0.50
11:L:106:SER:OG	11:L:107:THR:N	2.43	0.50
54:K:4947:U:O2'	54:K:4948:C:OP1	2.22	0.50
54:K:4964:C:N4	54:K:4965:U:O4	2.44	0.50
5:E:231:GLN:O	5:E:234:GLU:HG2	2.11	0.50
11:L:56:ARG:O	11:L:116:ARG:NH1	2.41	0.50
28:c:14:ILE:HD13	28:c:17:ARG:HH21	1.77	0.50
33:h:52:LYS:NZ	45:v:63:U:O2'	2.31	0.50
46:w:89:ILE:HD11	46:w:150:PHE:CE1	2.46	0.50
3:C:348:LYS:O	3:C:352:GLU:HG2	2.11	0.50
15:P:15:CYS:SG	15:P:150:LEU:HB2	2.52	0.50
33:h:56:ARG:NH1	45:v:65:A:OP1	2.43	0.50
50:4:201:ASN:OD1	50:4:202:GLU:N	2.44	0.50
54:K:1931:C:O2'	54:K:1932:A:O5'	2.27	0.50
9:I:4:ARG:NH1	9:I:9:TYR:OH	2.44	0.50
16:Q:63:LEU:O	16:Q:67:ILE:HG12	2.10	0.50
21:V:15:ARG:HB3	54:K:4618:G:H5''	1.94	0.50
21:V:94:VAL:HG11	22:W:20:ARG:HE	1.77	0.50
25:Z:10:VAL:O	25:Z:83:THR:OG1	2.25	0.50
31:f:28:LEU:CG	31:f:101:ILE:HD11	2.42	0.50
54:K:2718:U:H5''	54:K:2719:C:H5'	1.92	0.50
54:K:4135:G:H2'	54:K:4136:G:C8	2.47	0.50
54:K:4944:C:H4'	54:K:4944:C:OP1	2.11	0.50
1:A:210:PRO:HG2	1:A:235:VAL:HG21	1.93	0.50
4:D:208:MET:HE2	4:D:233:PRO:HG3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:245:ILE:HD12	5:E:245:ILE:N	2.26	0.50
7:G:111:PRO:HD2	7:G:114:ILE:HD12	1.92	0.50
26:a:84:GLU:OE2	26:a:87:ARG:NH2	2.45	0.50
38:m:71:ARG:NH1	54:K:4424:A:OP1	2.45	0.50
54:K:392:U:H2'	54:K:393:U:C6	2.47	0.50
54:K:1328:G:O2'	54:K:2349:A:OP1	2.26	0.50
8:H:105:ILE:CD1	8:H:136:VAL:HG23	2.42	0.50
10:J:157:ILE:HG22	10:J:158:SER:N	2.27	0.50
45:v:111:U:H4'	45:v:112:G:H5'	1.94	0.50
46:w:10:ARG:NH1	46:w:11:HIS:O	2.45	0.50
50:4:305:MET:HE3	50:4:405:LYS:HD3	1.93	0.50
52:7:24:ALA:O	52:7:102:TYR:OH	2.30	0.50
54:K:35:U:O2'	54:K:1525:A:N1	2.44	0.50
54:K:3620:G:OP1	54:K:3622:C:N4	2.45	0.50
54:K:3707:U:H2'	54:K:3708:C:C6	2.47	0.50
35:j:82:THR:OG1	45:v:94:G:N2	2.45	0.50
46:w:118:PHE:O	54:K:4578:G:O2'	2.29	0.50
54:K:420:A:O2'	54:K:1331:C:O2'	2.27	0.50
54:K:1920:C:H3'	54:K:1921:C:H5''	1.94	0.50
3:C:53:ALA:O	45:v:26:C:O2'	2.25	0.49
6:F:69:ARG:NH1	54:K:1210:C:OP1	2.45	0.49
38:m:69:ILE:HD12	54:K:4473:A:H5''	1.93	0.49
54:K:1477:C:O2'	54:K:1478:C:P	2.70	0.49
3:C:76:ILE:HD12	3:C:77:PRO:HD2	1.93	0.49
7:G:105:THR:O	45:v:150:C:N4	2.40	0.49
41:p:4:ARG:NH2	54:K:1555:G:N7	2.58	0.49
43:r:97:ILE:HG21	43:r:107:ARG:HB3	1.93	0.49
46:w:217:ILE:HD11	46:w:333:LEU:HD21	1.94	0.49
54:K:1377:G:H21	54:K:1380:G:H5'	1.77	0.49
54:K:2811:G:N1	54:K:2814:C:OP2	2.35	0.49
54:K:4079:C:H2'	54:K:4080:C:H6	1.78	0.49
54:K:4574:U:H3'	54:K:4575:G:H5''	1.94	0.49
15:P:101:ASN:OD1	54:K:399:G:N2	2.45	0.49
17:R:44:LEU:HD22	17:R:49:LEU:HD12	1.94	0.49
54:K:685:C:O2'	54:K:686:A:OP2	2.19	0.49
54:K:2488:C:HO2'	54:K:2489:C:P	2.34	0.49
3:C:323:ARG:NH2	54:K:1280:C:OP1	2.46	0.49
53:6:115:ARG:NH2	53:6:138:ASP:OD2	2.41	0.49
5:E:167:PHE:HA	5:E:178:VAL:HG23	1.93	0.49
6:F:212:LEU:O	54:K:2072:C:O2'	2.30	0.49
8:H:91:LYS:HG2	8:H:145:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:O:47:PHE:HA	14:O:136:ALA:HB2	1.95	0.49
16:Q:55:ARG:HH21	54:K:1352:C:H41	1.60	0.49
33:h:109:ARG:NH2	54:K:267:G:OP1	2.46	0.49
47:1:248:THR:OG1	47:1:441:ILE:N	2.45	0.49
54:K:983:C:H2'	54:K:984:C:C6	2.46	0.49
54:K:2491:C:H2'	54:K:2492:C:H6	1.78	0.49
54:K:4111:U:H2'	54:K:4112:C:O4'	2.12	0.49
6:F:33:ARG:NH1	54:K:1272:C:OP2	2.46	0.49
14:O:110:PRO:N	14:O:111:PRO:CD	2.76	0.49
14:O:116:LYS:HD2	18:S:169:THR:HG23	1.93	0.49
23:X:156:ILE:HD11	47:1:415:ARG:HH12	1.77	0.49
38:m:54:PRO:O	38:m:58:GLN:HG2	2.12	0.49
40:o:13:LYS:NZ	54:K:4294:C:O3'	2.37	0.49
54:K:971(A):G:O2'	54:K:972:C:O5'	2.26	0.49
54:K:1308:C:H2'	54:K:1309:C:C6	2.47	0.49
54:K:1932:A:H2'	54:K:1933:G:C8	2.47	0.49
54:K:2042:A:N3	54:K:4462:C:O2'	2.41	0.49
4:D:286:SER:OG	54:K:1179:U:O2	2.30	0.49
20:U:92:LYS:NZ	54:K:2627:C:OP2	2.46	0.49
28:c:10:SER:O	28:c:13:SER:OG	2.30	0.49
54:K:1437:C:O2'	54:K:1438:U:O4'	2.30	0.49
54:K:264:C:O2'	54:K:266:C:N3	2.38	0.49
54:K:695:G:O2'	54:K:697:G:OP2	2.29	0.49
54:K:1402:C:H2'	54:K:1403:G:C8	2.48	0.49
54:K:1655:C:O2	54:K:4390:A:O2'	2.31	0.49
54:K:2520:C:O2	54:K:2640:G:N2	2.46	0.49
54:K:3911:C:H2'	54:K:3912:U:H6	1.78	0.49
24:Y:57:VAL:HA	24:Y:104:VAL:HG23	1.94	0.49
25:Z:95:VAL:HG11	25:Z:113:GLU:HG2	1.94	0.49
43:r:114:ALA:O	43:r:118:LEU:HD23	2.13	0.49
46:w:343:ARG:NH2	54:K:4976:U:O3'	2.45	0.49
54:K:2638:G:H22	54:K:2697:A:N6	2.11	0.49
17:R:60:ARG:NH1	54:K:2808:G:O3'	2.45	0.49
24:Y:82:ILE:HG22	24:Y:83:GLU:N	2.28	0.49
32:g:44:SER:OG	32:g:46:CYS:SG	2.65	0.49
47:1:45:CYS:HB3	47:1:77:MET:HE3	1.95	0.49
50:4:337:PHE:CE1	50:4:360:LEU:HD11	2.48	0.49
54:K:407:A:O2'	54:K:410:A:OP1	2.28	0.49
14:O:65:ASN:OD1	14:O:67:SER:OG	2.28	0.48
54:K:1192:C:H2'	54:K:1193:C:O4'	2.12	0.48
54:K:2607:C:H2'	54:K:2608:G:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:3625:G:O2'	54:K:3626:G:P	2.71	0.48
54:K:4195:G:OP1	54:K:4221:C:O2'	2.28	0.48
1:A:180:LEU:HD22	41:p:18:TYR:HB3	1.95	0.48
5:E:118:TYR:HB3	54:K:457:G:H5'	1.95	0.48
10:J:26:VAL:HG23	10:J:28:GLU:H	1.78	0.48
16:Q:122:THR:HG22	16:Q:123:PHE:H	1.77	0.48
43:r:32:LEU:O	43:r:33:LYS:HB2	2.13	0.48
44:u:83:A:O2'	44:u:85:G:OP1	2.30	0.48
54:K:4237:C:O3'	54:K:4326:G:N2	2.46	0.48
54:K:4602:A:N6	54:K:4609:G:O2'	2.46	0.48
54:K:4925:U:HO2'	54:K:4926:C:P	2.36	0.48
9:I:171:TRP:O	9:I:174:THR:OG1	2.27	0.48
10:J:141:ILE:HD11	44:u:28:C:H5'	1.95	0.48
15:P:48:LEU:HD21	15:P:91:LEU:HD11	1.94	0.48
54:K:922(B):C:H3'	54:K:923:C:H5''	1.93	0.48
54:K:2363:A:N6	54:K:3859:G:O2'	2.46	0.48
10:J:157:ILE:HG22	10:J:158:SER:H	1.78	0.48
18:S:82:LEU:HD13	18:S:126:ILE:HD13	1.95	0.48
45:v:155:C:H2'	45:v:156:U:O4'	2.14	0.48
54:K:1198:G:H2'	54:K:1199:G:C8	2.47	0.48
54:K:3725:G:N1	54:K:3728:A:OP2	2.43	0.48
54:K:4572:U:H2'	54:K:4573:G:C8	2.48	0.48
20:U:29:VAL:HG11	20:U:68:SER:HB3	1.94	0.48
27:b:117:ARG:NH2	54:K:1273:G:OP2	2.43	0.48
43:r:14:SER:OG	43:r:15:SER:N	2.46	0.48
47:1:288:ASN:OD1	47:1:452:THR:HB	2.12	0.48
54:K:1314:C:C2	54:K:1315:C:C5	3.02	0.48
54:K:4258:C:H2'	54:K:4259:C:H6	1.78	0.48
54:K:4724:A:H2'	54:K:4725:C:O4'	2.14	0.48
54:K:4761:G:H2'	54:K:4762:A:C8	2.48	0.48
44:u:28:C:O2'	44:u:54:A:N1	2.44	0.48
54:K:519:C:H2'	54:K:520:U:C6	2.49	0.48
54:K:2488:C:O2'	54:K:2489:C:OP2	2.32	0.48
8:H:5:LEU:HD13	8:H:60:TRP:CH2	2.49	0.48
14:O:121:PRO:HD3	18:S:168:THR:HG22	1.95	0.48
17:R:96:MET:HG2	54:K:2667:C:O4'	2.14	0.48
30:e:86:GLU:OE1	30:e:86:GLU:N	2.45	0.48
52:7:26:LEU:HD11	52:7:28:THR:OG1	2.13	0.48
54:K:2582:A:HO2'	54:K:2653:C:HO2'	1.42	0.48
54:K:2632:U:H2'	54:K:2633:U:C6	2.49	0.48
54:K:3692:A:H62	54:K:3823:G:N2	2.09	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:4182:G:O2'	54:K:4184:G:N7	2.46	0.48
3:C:348:LYS:HA	3:C:351:VAL:HG22	1.95	0.48
4:D:215:ASP:OD1	4:D:215:ASP:N	2.46	0.48
21:V:18:LEU:HD13	21:V:54:ALA:CB	2.43	0.48
29:d:124:GLU:N	29:d:124:GLU:OE1	2.46	0.48
40:o:104:ILE:HD13	42:q:56:C:C4	2.49	0.48
45:v:107:C:N3	45:v:112:G:N1	2.44	0.48
54:K:115:C:O2'	54:K:276:C:OP1	2.31	0.48
54:K:643:C:H2'	54:K:644:G:C8	2.49	0.48
54:K:2264:C:H2'	54:K:2265:G:O4'	2.14	0.48
54:K:2378:G:O2'	54:K:2380:G:N7	2.46	0.48
54:K:3934:G:H2'	54:K:3935:C:C6	2.48	0.48
1:A:67:TYR:OH	54:K:4087:G:N7	2.44	0.48
6:F:215:PRO:HD3	6:F:246:MET:HE2	1.95	0.48
20:U:61:VAL:HG12	20:U:74:SER:HB2	1.95	0.48
40:o:2:VAL:HG22	40:o:3:ASN:H	1.79	0.48
46:w:165:HIS:ND1	46:w:166:THR:O	2.40	0.48
47:1:9:ILE:O	47:1:9:ILE:HG22	2.14	0.48
54:K:1990:A:C2	54:K:1991:A:H1'	2.49	0.48
9:I:145:LYS:O	9:I:149:VAL:HG23	2.14	0.48
15:P:24:VAL:HG12	15:P:25:HIS:H	1.78	0.48
19:T:88:ARG:NH1	27:b:33:LYS:O	2.47	0.48
54:K:1762:C:N3	54:K:1763:C:N4	2.62	0.48
54:K:4719:G:H4'	54:K:4720:C:OP1	2.14	0.48
2:B:64:VAL:O	42:q:76:A:O3'	2.30	0.47
6:F:106:LYS:O	6:F:110:LEU:HG	2.13	0.47
36:k:54:GLU:O	36:k:58:GLN:HG3	2.14	0.47
43:r:85:ASN:HD22	54:K:690:C:H4'	1.78	0.47
52:7:250:ASN:HB3	52:7:259:LEU:HD12	1.96	0.47
54:K:100:C:H2'	54:K:101:A:O4'	2.13	0.47
54:K:1440:U:O2'	54:K:1441:C:P	2.70	0.47
54:K:4921:C:H4'	54:K:4922:C:OP1	2.14	0.47
8:H:152:GLU:OE2	54:K:4702:G:N2	2.42	0.47
13:N:103:GLU:OE2	13:N:118:SER:OG	2.29	0.47
15:P:74:LYS:NZ	54:K:4982:A:OP1	2.44	0.47
54:K:986:C:H2'	54:K:987:C:H6	1.79	0.47
54:K:1076:C:H2'	54:K:1077:C:C6	2.49	0.47
54:K:1197:C:H2'	54:K:1198:G:C8	2.49	0.47
54:K:4735:G:HO2'	54:K:4736:C:H6	1.58	0.47
3:C:149:GLU:OE2	43:r:71:ARG:NE	2.47	0.47
4:D:184:ASP:O	4:D:188:LYS:N	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:141:ASP:OD1	7:G:143:GLN:N	2.48	0.47
18:S:80:ILE:HG23	18:S:129:VAL:HG22	1.96	0.47
26:a:76:ASP:OD1	26:a:76:ASP:N	2.46	0.47
50:4:422:HIS:CD2	54:K:401:G:HO2'	2.32	0.47
52:7:9:MET:HE3	52:7:93:LEU:HD23	1.96	0.47
54:K:910:G:H2'	54:K:911:U:H6	1.80	0.47
54:K:3911:C:H2'	54:K:3912:U:C6	2.49	0.47
54:K:4474:A:OP2	54:K:4476:C:N4	2.46	0.47
54:K:1846:G:H2'	54:K:1847:C:C6	2.49	0.47
54:K:4384:U:O2'	54:K:4386:C:OP1	2.24	0.47
54:K:4860:G:C2	54:K:4861:G:C8	3.02	0.47
3:C:266:THR:HG23	3:C:269:LYS:H	1.79	0.47
11:L:167:ARG:NH2	11:L:173:GLU:OE2	2.46	0.47
12:M:132:ARG:NE	54:K:4895:C:O2	2.48	0.47
13:N:179:LYS:O	54:K:297:U:O2'	2.32	0.47
15:P:32:THR:HG23	15:P:91:LEU:HD21	1.97	0.47
17:R:30:ASN:O	17:R:34:ASN:ND2	2.47	0.47
18:S:95:ARG:NH1	54:K:1951:G:O2'	2.46	0.47
19:T:108:ARG:NH2	54:K:1802:A:O2'	2.47	0.47
24:Y:11:ARG:NH1	54:K:229:G:OP1	2.45	0.47
28:c:64:ALA:HB1	28:c:69:THR:HB	1.96	0.47
54:K:40:G:N2	54:K:4380:A:H62	2.12	0.47
54:K:1170:G:H2'	54:K:1171:G:H8	1.79	0.47
54:K:3625:G:HO2'	54:K:3626:G:P	2.35	0.47
54:K:3759:A:N6	54:K:3765:G:O2'	2.47	0.47
54:K:4638:U:OP1	54:K:5044:A:O2'	2.27	0.47
54:K:4660:G:H2'	54:K:4661:G:H5''	1.96	0.47
54:K:5034:A:H2'	54:K:5035:U:O4'	2.15	0.47
46:w:71:GLU:OE1	46:w:71:GLU:N	2.45	0.47
47:1:289:ILE:HG21	47:1:379:TRP:CE2	2.50	0.47
50:4:470:LYS:HZ3	54:K:396:A:P	2.38	0.47
54:K:495:C:H2'	54:K:496:G:O4'	2.14	0.47
54:K:734:G:C2	54:K:735:G:C8	3.01	0.47
2:B:45:MET:HE3	2:B:46:PRO:HD2	1.95	0.47
4:D:23:ARG:NH2	54:K:4280:A:OP2	2.45	0.47
6:F:236:GLU:OE2	18:S:41:LYS:NZ	2.36	0.47
11:L:42:ARG:O	11:L:46:ILE:HG12	2.14	0.47
11:L:143:GLU:O	11:L:146:LEU:N	2.47	0.47
13:N:36:LEU:HD12	13:N:64:ILE:HD12	1.96	0.47
15:P:23:ARG:HG3	15:P:125:MET:HE1	1.97	0.47
18:S:82:LEU:HB2	18:S:93:MET:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:70:HIS:NE2	54:K:4327:C:OP1	2.48	0.47
23:X:101:ASP:OD1	23:X:102:VAL:N	2.48	0.47
32:g:54:ARG:NH2	54:K:2653:C:OP1	2.47	0.47
46:w:214:ASP:N	46:w:284:ILE:O	2.45	0.47
47:1:5:PHE:CZ	47:1:9:ILE:HD11	2.49	0.47
54:K:125:C:H2'	54:K:126:C:C6	2.49	0.47
54:K:705:G:H2'	54:K:706:C:C6	2.50	0.47
54:K:914:U:O2'	54:K:915:A:O4'	2.32	0.47
54:K:3656:A:O2'	54:K:3747:A:O2'	2.31	0.47
54:K:3689:G:O2'	54:K:3818:U:OP2	2.30	0.47
54:K:4199:C:H2'	54:K:4200:G:H5'	1.97	0.47
4:D:234:ASP:OD1	4:D:235:MET:N	2.48	0.47
28:c:29:LEU:HD13	28:c:89:TYR:HE2	1.79	0.47
41:p:59:SER:OG	41:p:60:CYS:N	2.48	0.47
54:K:326:C:N4	54:K:327:U:O4	2.47	0.47
54:K:1345:A:H2'	54:K:1346:C:C6	2.50	0.47
54:K:2045:G:O6	54:K:3870:C:O2'	2.28	0.47
46:w:185:VAL:O	46:w:193:LYS:HD3	2.14	0.47
47:1:291:ILE:HD11	47:1:428:ILE:HG21	1.95	0.47
49:3:61:ILE:HG22	49:3:65:ILE:HD12	1.96	0.47
54:K:1645:C:H2'	54:K:1646:A:C8	2.50	0.47
54:K:2533:C:H2'	54:K:2534:C:C6	2.50	0.47
54:K:4551:U:H2'	54:K:4552:U:C6	2.50	0.47
6:F:130:ASN:ND2	54:K:1727:U:OP1	2.46	0.47
6:F:213:SER:OG	6:F:214:SER:N	2.46	0.47
8:H:12:ILE:HD13	8:H:18:ILE:HG21	1.97	0.47
13:N:49:ARG:NH2	54:K:152:U:OP2	2.42	0.47
13:N:99:GLN:O	13:N:103:GLU:HG3	2.15	0.47
21:V:93:GLY:HA3	46:w:73:VAL:HB	1.97	0.47
27:b:117:ARG:NH2	54:K:1272:C:OP1	2.47	0.47
31:f:89:ARG:NH1	54:K:708:G:O5'	2.48	0.47
54:K:2588:C:OP1	54:K:2768:C:O2'	2.29	0.47
1:A:179:ILE:O	54:K:3653:A:H4'	2.15	0.46
1:A:217:GLN:NE2	54:K:3650:C:OP1	2.39	0.46
5:E:133:LYS:N	5:E:133:LYS:HD2	2.29	0.46
5:E:135:PRO:HG2	5:E:138:GLN:HG3	1.97	0.46
11:L:74:ARG:NH2	54:K:109:G:OP2	2.48	0.46
13:N:76:PRO:O	13:N:77:LYS:C	2.57	0.46
13:N:148:THR:O	13:N:151:ILE:HG22	2.15	0.46
24:Y:2:LYS:NZ	24:Y:7:VAL:O	2.35	0.46
25:Z:74:VAL:HG23	25:Z:101:PHE:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:r:19:LYS:HG2	43:r:24:THR:HG23	1.97	0.46
43:r:113:ARG:O	43:r:117:ILE:HG12	2.15	0.46
54:K:508:G:O2'	54:K:510:U:OP2	2.29	0.46
54:K:2539:C:H2'	54:K:2540:C:C6	2.50	0.46
19:T:115:LYS:HG2	19:T:126:VAL:HG21	1.97	0.46
21:V:107:ASN:OD1	21:V:111:GLU:N	2.49	0.46
33:h:81:LEU:HD22	45:v:38:U:C2	2.49	0.46
46:w:243:LYS:NZ	54:K:2854:G:O6	2.48	0.46
54:K:36:U:OP1	54:K:1651:G:N2	2.43	0.46
54:K:2089:G:H1'	54:K:2090:U:OP2	2.15	0.46
54:K:2520:C:OP2	54:K:2530:U:N3	2.38	0.46
7:G:267:ALA:O	7:G:271:LEU:HG	2.16	0.46
8:H:25:VAL:HG23	8:H:80:MET:HE1	1.97	0.46
54:K:1413:C:H2'	54:K:1414:C:C6	2.50	0.46
54:K:1942:A:H2'	54:K:1943:A:C8	2.51	0.46
54:K:2042:A:O4'	54:K:4462:C:O2'	2.32	0.46
54:K:4537:C:H2'	54:K:4538:G:C8	2.49	0.46
5:E:160:HIS:HB3	5:E:163:LYS:HD2	1.98	0.46
8:H:92:MET:HE2	8:H:179:ILE:HG22	1.98	0.46
13:N:177:GLY:HA2	54:K:67:C:O3'	2.15	0.46
50:4:167:TRP:HH2	50:4:220:ILE:HD13	1.79	0.46
54:K:2412:A:H2'	54:K:2413:U:C6	2.50	0.46
54:K:2590:G:O2'	54:K:2755:A:N6	2.46	0.46
13:N:178:HIS:O	54:K:293:G:N2	2.41	0.46
28:c:49:ALA:HB2	28:c:81:LEU:HD12	1.98	0.46
54:K:35:U:H5'	54:K:36:U:OP2	2.15	0.46
54:K:2024:G:O2'	54:K:2025:A:OP2	2.28	0.46
54:K:2502:A:HO2'	54:K:2503:G:P	2.35	0.46
1:A:242:ARG:O	54:K:3658:C:H5''	2.15	0.46
4:D:261:VAL:HG11	44:u:119:U:C2	2.51	0.46
16:Q:66:MET:HE3	16:Q:98:LEU:HD13	1.97	0.46
21:V:80:VAL:HG23	21:V:106:VAL:HG21	1.98	0.46
41:p:16:THR:HG22	54:K:2876:G:C8	2.51	0.46
46:w:240:LEU:HB3	46:w:244:THR:HG21	1.98	0.46
50:4:233:VAL:HG22	50:4:236:ARG:NH2	2.28	0.46
52:7:442:SER:HA	52:7:448:VAL:HG21	1.96	0.46
54:K:4761:G:H2'	54:K:4762:A:H8	1.79	0.46
6:F:154:TYR:OH	6:F:187:GLU:OE2	2.31	0.46
9:I:118:ALA:O	54:K:1864:G:O2'	2.31	0.46
10:J:78:LYS:O	10:J:82:ILE:HG12	2.16	0.46
11:L:39:ARG:NH2	54:K:1362:G:OP1	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:108:ARG:HB2	13:N:161:MET:CE	2.46	0.46
17:R:62:ARG:NH1	54:K:4645:C:OP2	2.49	0.46
20:U:44:GLN:HA	20:U:56:LEU:HD21	1.98	0.46
47:1:169:LEU:HD12	47:1:178:GLY:CA	2.46	0.46
54:K:448:G:H3'	54:K:449:C:H4'	1.97	0.46
54:K:1370:G:H4'	54:K:1371:A:O5'	2.15	0.46
54:K:2666:U:O2'	54:K:2668:G:N7	2.37	0.46
3:C:214:ASP:OD1	3:C:218:VAL:HG13	2.15	0.46
9:I:65:LEU:HD23	9:I:159:PHE:HE1	1.80	0.46
54:K:66:A:H61	54:K:282:C:HO2'	1.64	0.46
54:K:245:C:HO2'	54:K:246:G:P	2.32	0.46
54:K:4119:C:H4'	54:K:4120:U:OP1	2.16	0.46
54:K:4354:U:O2	54:K:4354:U:H2'	2.15	0.46
54:K:4629:U:C2	54:K:4630:G:C8	3.04	0.46
3:C:114:ARG:NH2	54:K:1357:C:O2'	2.45	0.46
4:D:28:THR:O	54:K:4280:A:N6	2.49	0.46
7:G:197:THR:O	7:G:201:GLU:HG3	2.15	0.46
52:7:428:ASP:O	52:7:434:LEU:HD12	2.16	0.46
54:K:1411(C):C:H2'	54:K:1412:G:O4'	2.16	0.46
54:K:2895:A:H2'	54:K:2896:G:O4'	2.16	0.46
54:K:4067:U:H2'	54:K:4068:U:H6	1.81	0.46
54:K:4524:G:OP2	54:K:4524:G:H4'	2.15	0.46
54:K:4884:G:O2'	54:K:4885:U:P	2.74	0.46
14:O:185:VAL:HG12	14:O:185:VAL:O	2.16	0.46
14:O:185:VAL:HG12	14:O:189:ILE:HG23	1.97	0.46
15:P:83:TRP:O	54:K:3856:A:H5''	2.16	0.46
20:U:80:LYS:N	54:K:2620:G:OP1	2.43	0.46
28:c:30:GLY:HA2	54:K:2673:G:O3'	2.16	0.46
31:f:43:LEU:O	31:f:109:ARG:NH1	2.49	0.46
44:u:12:U:OP2	44:u:67:C:O2'	2.33	0.46
54:K:1563:A:O2'	54:K:1564:A:O4'	2.31	0.46
54:K:2361:G:O2'	54:K:3859:G:O6	2.26	0.46
54:K:2552:G:N2	54:K:2767:U:C4	2.84	0.46
54:K:3888:G:O2'	54:K:3889:G:OP1	2.30	0.46
3:C:322:LEU:O	3:C:326:LEU:HG	2.15	0.45
8:H:93:ARG:HG2	8:H:182:SER:HB3	1.98	0.45
9:I:66:GLU:OE2	9:I:69:ARG:NH2	2.50	0.45
12:M:132:ARG:NH2	54:K:4895:C:N3	2.65	0.45
22:W:19:ARG:NH1	22:W:37:GLU:OE2	2.49	0.45
31:f:37:ASP:OD1	31:f:37:ASP:N	2.49	0.45
42:q:5:C:H2'	42:q:6:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:2258:C:H2'	54:K:2259:G:OP1	2.16	0.45
54:K:2866:C:H2'	54:K:2867:C:O4'	2.15	0.45
54:K:3695:U:H2'	54:K:3696:C:O4'	2.15	0.45
54:K:4371:G:HO2'	54:K:4372:U:P	2.39	0.45
5:E:179:THR:CB	5:E:189:LEU:HD23	2.47	0.45
10:J:27:GLY:HA2	10:J:68:ILE:HG23	1.98	0.45
17:R:98:ARG:NH2	17:R:130:ASN:OD1	2.49	0.45
28:c:55:LEU:HD13	32:g:93:ARG:HB2	1.98	0.45
54:K:138:G:H2'	54:K:139:G:C8	2.51	0.45
54:K:180:C:N4	54:K:256:G:O6	2.45	0.45
54:K:504:G:H2'	54:K:505:G:H8	1.81	0.45
54:K:1188:C:H2'	54:K:1189:G:H8	1.81	0.45
54:K:4925:U:H1'	54:K:4926:C:OP2	2.15	0.45
13:N:192:TRP:NE1	54:K:48:G:OP1	2.45	0.45
14:O:128:ARG:NH1	18:S:162:GLN:OE1	2.49	0.45
45:v:82:A:H1'	53:6:92:ALA:HB1	1.99	0.45
54:K:451:C:O2'	54:K:1293:G:H2'	2.16	0.45
54:K:2804:C:C2	54:K:2805:C:C5	3.04	0.45
54:K:4260:U:H2'	54:K:4261:C:C6	2.51	0.45
54:K:4759:C:O2	54:K:4759:C:O4'	2.34	0.45
1:A:80:GLU:OE2	41:p:73:THR:HG22	2.17	0.45
8:H:92:MET:SD	8:H:161:ILE:HD11	2.56	0.45
15:P:66:GLY:HA3	54:K:2362:U:H5''	1.99	0.45
17:R:136:ARG:O	17:R:140:GLU:HG2	2.16	0.45
23:X:151:ASN:C	23:X:151:ASN:HD22	2.24	0.45
41:p:52:VAL:HG13	54:K:2739:C:H5'	1.96	0.45
50:4:437:LYS:HG2	50:4:441:LYS:HE3	1.98	0.45
2:B:40:PHE:CE1	47:1:272:TYR:CE1	3.04	0.45
4:D:285:ALA:O	4:D:289:ARG:HG2	2.16	0.45
8:H:113:GLU:OE1	8:H:115:ARG:NH2	2.47	0.45
9:I:115:MET:HG3	9:I:115:MET:O	2.17	0.45
14:O:80:PHE:O	14:O:84:VAL:HG23	2.16	0.45
46:w:217:ILE:HD13	46:w:284:ILE:HD11	1.99	0.45
54:K:1174:G:HO2'	54:K:1175:A:P	2.36	0.45
54:K:2503:G:N2	54:K:4084:G:C8	2.84	0.45
54:K:4638:U:H2'	54:K:4639:G:N3	2.31	0.45
18:S:165:PRO:O	18:S:167:PHE:N	2.49	0.45
19:T:81:LYS:O	27:b:16:TRP:CE2	2.70	0.45
19:T:124:THR:OG1	19:T:125:TRP:N	2.50	0.45
20:U:28:PRO:HB2	20:U:34:MET:HG2	1.98	0.45
24:Y:123:ALA:O	24:Y:127:GLN:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z:100:VAL:HG23	25:Z:106:LEU:HB3	1.99	0.45
25:Z:117:LYS:HA	25:Z:120:GLU:HG2	1.98	0.45
26:a:17:HIS:O	26:a:17:HIS:ND1	2.50	0.45
31:f:20:ASN:ND2	54:K:1885:G:OP1	2.44	0.45
52:7:17:GLN:NE2	52:7:324:ASP:OD2	2.50	0.45
52:7:375:LEU:C	52:7:375:LEU:HD23	2.42	0.45
53:6:72:MET:O	53:6:76:VAL:HG23	2.17	0.45
54:K:219:G:H2'	54:K:219:G:N3	2.32	0.45
54:K:386:A:H3'	54:K:387:G:H5''	1.98	0.45
3:C:323:ARG:CD	54:K:976:G:H21	2.29	0.45
11:L:18:TRP:NE1	54:K:1516:G:O2'	2.42	0.45
17:R:74:ARG:NE	54:K:2891:U:OP2	2.50	0.45
54:K:2627:C:H2'	54:K:2628:U:C6	2.51	0.45
12:M:95:ILE:O	12:M:99:GLU:HG3	2.16	0.45
24:Y:73:VAL:HG12	24:Y:75:ARG:HG2	1.99	0.45
27:b:9:THR:O	27:b:9:THR:HG22	2.17	0.45
29:d:52:PHE:O	29:d:56:GLU:HG2	2.17	0.45
35:j:59:THR:HG23	54:K:23:C:H4'	1.98	0.45
38:m:84:CYS:SG	38:m:85:ARG:N	2.89	0.45
45:v:6:C:H2'	45:v:7:U:H6	1.82	0.45
54:K:480:C:O2'	54:K:481:G:P	2.75	0.45
54:K:520:U:H2'	54:K:521:C:C6	2.52	0.45
54:K:1233:G:O2'	54:K:1234:G:OP2	2.24	0.45
54:K:1442:C:H2'	54:K:1443:A:C8	2.52	0.45
54:K:1763:C:H42	54:K:1769:G:H1	1.65	0.45
54:K:2804:C:H2'	54:K:2805:C:H6	1.82	0.45
54:K:4586:G:O6	54:K:4717:A:N6	2.50	0.45
54:K:4729:A:OP2	54:K:5068:G:N1	2.41	0.45
3:C:332:ALA:HA	3:C:335:MET:HB2	1.98	0.45
15:P:32:THR:O	15:P:36:ILE:HG12	2.16	0.45
32:g:94:ALA:O	32:g:98:GLU:HG3	2.16	0.45
54:K:199:G:C4	54:K:201:C:C5	3.05	0.45
54:K:1612:G:H2'	54:K:1612:G:N3	2.32	0.45
54:K:4926:C:H3'	54:K:4927:G:H5''	1.99	0.45
54:K:5002:U:H2'	54:K:5003:U:C6	2.52	0.45
3:C:44:LEU:HD21	3:C:120:LYS:HE2	1.99	0.45
5:E:245:ILE:HD12	5:E:245:ILE:H	1.82	0.45
6:F:29:ILE:O	6:F:33:ARG:HG3	2.16	0.45
19:T:28:ALA:HA	19:T:31:MET:HG2	1.98	0.45
26:a:113:GLY:O	54:K:1397:A:H5'	2.17	0.45
30:e:17:THR:HG21	54:K:1301:C:H2'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:q:57:G:H2'	42:q:58:A:H5''	1.99	0.45
47:1:45:CYS:CB	47:1:77:MET:HE3	2.47	0.45
50:4:320:PHE:HB3	50:4:385:MET:SD	2.57	0.45
54:K:1327:C:H2'	54:K:1328:G:H8	1.82	0.45
54:K:1443:A:H2'	54:K:1444:G:O4'	2.17	0.45
54:K:3648:A:H1'	54:K:3785:A:N6	2.31	0.45
54:K:3652:A:H2'	54:K:3653:A:C8	2.52	0.45
54:K:3751:G:H21	54:K:3775:A:H8	1.65	0.45
54:K:4129:G:O6	54:K:4156:G:N2	2.49	0.45
54:K:4523:A:H5''	54:K:4524:G:H5'	1.99	0.45
54:K:5001:U:H2'	54:K:5002:U:O4'	2.17	0.45
7:G:164:LYS:O	7:G:168:LEU:HG	2.17	0.44
21:V:106:VAL:HG12	21:V:107:ASN:O	2.17	0.44
26:a:43:ILE:HD12	54:K:1682:A:C2	2.52	0.44
37:l:15:LYS:NZ	45:v:45:C:OP2	2.50	0.44
45:v:5:U:H2'	45:v:6:C:C6	2.52	0.44
54:K:684:G:H4'	54:K:685:C:OP2	2.17	0.44
54:K:1378:C:H4'	54:K:1379:C:H5'	1.99	0.44
54:K:2803:U:C2	54:K:2804:C:C5	3.05	0.44
54:K:3736:A:H2'	54:K:3737:A:C8	2.52	0.44
54:K:4146:G:C2	54:K:4147:G:C8	3.05	0.44
3:C:334:THR:HG21	6:F:50:TYR:OH	2.16	0.44
10:J:156:ARG:NH2	44:u:17:C:OP1	2.50	0.44
16:Q:144:LYS:HG2	54:K:1460:C:H5''	1.99	0.44
22:W:1:MET:SD	22:W:1:MET:N	2.82	0.44
47:1:77:MET:HE1	47:1:162:VAL:HG23	1.99	0.44
47:1:234:PHE:CE2	47:1:242:LEU:HD23	2.52	0.44
54:K:406:C:O2'	54:K:407:A:P	2.75	0.44
54:K:504:G:H4'	54:K:505:G:OP1	2.17	0.44
54:K:987:C:H2'	54:K:988:C:C6	2.53	0.44
54:K:1639:U:O2	54:K:1639:U:H2'	2.17	0.44
54:K:2465:C:O2'	54:K:3672:G:N1	2.47	0.44
54:K:2567:G:H2'	54:K:2568:C:C6	2.52	0.44
54:K:2804:C:H2'	54:K:2805:C:C6	2.52	0.44
54:K:4758:U:O4'	54:K:4758:U:O2	2.34	0.44
54:K:5061:A:H3'	54:K:5062:G:C5'	2.48	0.44
4:D:146:LEU:HD12	4:D:163:LEU:HB2	1.99	0.44
7:G:216:PRO:HG2	7:G:219:LEU:HD13	1.99	0.44
31:f:11:PHE:CE2	31:f:97:ILE:HD13	2.53	0.44
54:K:969:C:N4	54:K:2095:A:N1	2.64	0.44
54:K:1174:G:O2'	54:K:1175:A:P	2.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:1445:U:H2'	54:K:1446:C:C6	2.53	0.44
4:D:28:THR:OG1	44:u:7:G:OP2	2.22	0.44
18:S:75:VAL:HA	18:S:100:LEU:HD23	1.99	0.44
18:S:81:TRP:O	18:S:127:MET:HG2	2.18	0.44
19:T:23:GLY:N	54:K:4278:C:OP1	2.49	0.44
54:K:132:G:N2	54:K:136:C:O2	2.51	0.44
54:K:307:A:N3	54:K:310:G:O2'	2.48	0.44
54:K:1236:C:O2'	54:K:1238:A:OP1	2.34	0.44
54:K:2553:A:O2'	54:K:2554:U:OP2	2.30	0.44
54:K:2793:G:C5'	54:K:2794:C:H5''	2.47	0.44
54:K:3788:C:N4	54:K:3812:C:O4'	2.50	0.44
54:K:4635:A:H8	54:K:5048:A:H61	1.65	0.44
5:E:225:LEU:O	5:E:227:LYS:HG2	2.18	0.44
18:S:13:VAL:HG23	18:S:62:VAL:HB	2.00	0.44
18:S:157:ARG:NE	54:K:4870:G:O6	2.42	0.44
23:X:84:GLU:HG2	47:1:404:HIS:ND1	2.33	0.44
35:j:56:ARG:NE	54:K:375:G:O6	2.50	0.44
47:1:252:PHE:CE2	47:1:451:VAL:HG22	2.52	0.44
54:K:1590:C:H5''	54:K:1591:U:O5'	2.17	0.44
54:K:2292:C:H2'	54:K:2293:U:C6	2.53	0.44
54:K:2411:C:H2'	54:K:2412:A:H8	1.83	0.44
54:K:4096:C:H2'	54:K:4097:G:C8	2.53	0.44
54:K:4322:G:N2	54:K:4325:A:OP2	2.40	0.44
54:K:4886:C:C2	54:K:4887:C:C5	3.06	0.44
17:R:101:ILE:HD13	54:K:2897:G:H4'	2.00	0.44
32:g:22:LEU:HD12	32:g:30:ILE:CG2	2.48	0.44
50:4:333:PHE:CD1	50:4:359:LEU:HD22	2.53	0.44
50:4:421:THR:O	50:4:421:THR:HG22	2.17	0.44
54:K:406:C:HO2'	54:K:407:A:P	2.36	0.44
54:K:1398:A:H62	54:K:1419:G:N2	2.13	0.44
54:K:3930:U:H2'	54:K:3931:C:C6	2.53	0.44
54:K:4627:U:H2'	54:K:4628:U:H6	1.83	0.44
4:D:203:ASN:OD1	4:D:204:VAL:N	2.51	0.44
7:G:273:GLU:O	7:G:277:THR:HG22	2.18	0.44
10:J:49:VAL:HG21	44:u:39:C:C6	2.53	0.44
19:T:87:LYS:NZ	54:K:4305:G:H22	2.15	0.44
34:i:39:PHE:O	34:i:42:ASP:OD1	2.36	0.44
37:l:27:ILE:HD13	45:v:52:A:H62	1.82	0.44
54:K:269:G:H2'	54:K:270:U:H6	1.82	0.44
54:K:922:C:H2'	54:K:922(A):G:C8	2.52	0.44
54:K:4412:C:H2'	54:K:4413:C:O2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:4413:C:H2'	54:K:4414:A:O4'	2.17	0.44
3:C:94:ASN:OD1	3:C:94:ASN:N	2.51	0.44
3:C:110:ARG:NH1	54:K:1508:A:OP1	2.38	0.44
11:L:81:LEU:HD11	11:L:98:VAL:HG22	1.99	0.44
11:L:107:THR:HB	34:i:18:THR:HG23	1.99	0.44
13:N:40:PRO:HG3	54:K:8:U:H5'	1.99	0.44
30:e:14:LYS:NZ	54:K:2318:G:OP2	2.51	0.44
42:q:75:C:H2'	42:q:76:A:O4'	2.18	0.44
44:u:28:C:H1'	44:u:54:A:H61	1.82	0.44
47:1:338:VAL:O	47:1:338:VAL:HG12	2.18	0.44
54:K:2780:C:H2'	54:K:2781:G:H8	1.83	0.44
54:K:4288:C:O2'	54:K:4321:U:OP1	2.31	0.44
54:K:4896:G:H2'	54:K:4897:G:H8	1.83	0.44
11:L:164:GLU:HG2	26:a:100:ILE:HD12	2.00	0.44
14:O:193:THR:HG23	14:O:202:LEU:HD23	1.99	0.44
24:Y:71:VAL:N	24:Y:81:TYR:O	2.48	0.44
54:K:121:A:H5'	54:K:122:U:OP2	2.17	0.44
54:K:179:G:H2'	54:K:180:C:C6	2.53	0.44
54:K:424:U:H2'	54:K:425:U:H6	1.83	0.44
54:K:485:C:H4'	54:K:486:C:OP1	2.17	0.44
54:K:3722:G:H2'	54:K:3723:A:H8	1.83	0.44
54:K:4736:C:H2'	54:K:4737:G:H8	1.83	0.44
5:E:134:LYS:O	5:E:139:HIS:NE2	2.50	0.43
5:E:153:LEU:HB3	5:E:197:VAL:HG22	2.00	0.43
8:H:151:ILE:O	8:H:155:SER:OG	2.25	0.43
10:J:155:HIS:HB2	44:u:55:A:H4'	1.99	0.43
18:S:2:LYS:O	18:S:4:SER:N	2.49	0.43
35:j:4:GLY:O	35:j:8:PHE:HD1	2.01	0.43
41:p:52:VAL:CG1	54:K:2739:C:H5'	2.47	0.43
43:r:85:ASN:O	43:r:89:THR:HG22	2.17	0.43
54:K:1248:C:H2'	54:K:1249:C:H5'	1.98	0.43
54:K:1772:C:H2'	54:K:1773:U:O4'	2.18	0.43
54:K:2553:A:H1'	54:K:2554:U:O4'	2.18	0.43
54:K:3910:C:H2'	54:K:3911:C:C6	2.53	0.43
1:A:29:LEU:O	1:A:123:ARG:NH1	2.51	0.43
3:C:232:VAL:CG1	3:C:256:ALA:HB1	2.48	0.43
5:E:152:ILE:HD12	5:E:274:LEU:HD21	2.00	0.43
9:I:76:MET:HE2	9:I:138:ILE:HG21	2.00	0.43
12:M:85:LYS:O	12:M:89:THR:HG23	2.17	0.43
13:N:14:LYS:NZ	54:K:280:G:OP2	2.43	0.43
14:O:55:LEU:O	14:O:59:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:S:147:ASP:OD1	18:S:148:SER:N	2.51	0.43
26:a:36:GLY:HA3	26:a:40:HIS:CE1	2.52	0.43
30:e:38:PRO:HB2	30:e:43:ASN:ND2	2.32	0.43
44:u:42:A:C5	44:u:43:U:C5	3.05	0.43
46:w:276:HIS:ND1	54:K:4716:C:OP1	2.50	0.43
54:K:504:G:N1	54:K:655:C:N3	2.67	0.43
54:K:686:A:H2'	54:K:686:A:N3	2.33	0.43
54:K:1210:C:H3'	54:K:1210:C:O2	2.18	0.43
54:K:1482:G:HO2'	54:K:1483:C:P	2.41	0.43
54:K:1759:G:N1	54:K:1774:C:O2	2.50	0.43
54:K:2490:U:O2'	54:K:2491:C:C6	2.70	0.43
54:K:4266:G:H2'	54:K:4266:G:N3	2.32	0.43
13:N:49:ARG:HH12	54:K:152:U:P	2.42	0.43
13:N:108:ARG:HB2	13:N:161:MET:HE1	1.99	0.43
32:g:99:GLU:O	32:g:103:VAL:HG23	2.19	0.43
37:l:18:LYS:NZ	45:v:46:G:OP1	2.44	0.43
37:l:23:ILE:HG23	37:l:38:ASN:HB2	2.00	0.43
43:r:26:SER:OG	43:r:28:GLU:OE1	2.36	0.43
52:7:270:ASP:OD1	52:7:271:THR:HG23	2.18	0.43
54:K:1195:G:H2'	54:K:1196:G:C8	2.52	0.43
54:K:1307:A:H2'	54:K:1308:C:C6	2.53	0.43
54:K:1477:C:H2'	54:K:1478:C:C6	2.54	0.43
54:K:1622:U:O2'	54:K:1627:G:O3'	2.31	0.43
54:K:2468:U:O4	54:K:2506:G:O2'	2.20	0.43
54:K:2483:G:H2'	54:K:2484:A:C8	2.54	0.43
5:E:227:LYS:N	5:E:228:PRO:HD3	2.33	0.43
23:X:146:ALA:HA	23:X:149:VAL:HG12	2.01	0.43
27:b:36:ASP:N	27:b:36:ASP:OD1	2.50	0.43
38:m:51:ILE:HG23	38:m:52:ILE:N	2.34	0.43
47:1:89:LEU:HD12	47:1:293:LEU:HD22	2.00	0.43
52:7:299:LEU:HD22	52:7:312:PHE:CE1	2.53	0.43
54:K:350:C:OP1	54:K:2294:G:O2'	2.36	0.43
54:K:1090:G:H2'	54:K:1091:C:C6	2.53	0.43
54:K:1450:C:O2'	54:K:2104:A:H1'	2.19	0.43
54:K:4228:G:H4'	54:K:4229:U:OP2	2.18	0.43
54:K:4869:U:O2	54:K:4869:U:O4'	2.36	0.43
6:F:147:LYS:O	6:F:151:GLU:HG2	2.18	0.43
15:P:82:ARG:NH2	54:K:2362:U:OP1	2.50	0.43
25:Z:89:ILE:HG23	25:Z:91:LEU:HD23	2.01	0.43
31:f:17:GLY:N	31:f:20:ASN:O	2.51	0.43
31:f:72:GLY:HA2	31:f:88:PHE:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:h:60:VAL:O	33:h:64:THR:HG22	2.18	0.43
39:n:13:LEU:O	39:n:17:ARG:HG3	2.18	0.43
51:5:10:ARG:O	51:5:11:ARG:NH1	2.51	0.43
54:K:130:C:H2'	54:K:131:C:O4'	2.19	0.43
54:K:385:A:N3	54:K:387:G:H5''	2.34	0.43
54:K:432:U:H4'	54:K:433:A:H5''	2.00	0.43
54:K:976:G:H1	54:K:1279:A:H2	1.66	0.43
54:K:1914:C:OP2	54:K:1915:C:O2'	2.35	0.43
54:K:1978:C:O2	54:K:1989:G:C6	2.72	0.43
54:K:3598:C:H2'	54:K:3599:A:H8	1.82	0.43
54:K:3656:A:HO2'	54:K:3747:A:HO2'	1.63	0.43
54:K:4459:U:H2'	54:K:4460:U:C6	2.53	0.43
54:K:4735:G:O2'	54:K:4736:C:H6	2.01	0.43
10:J:9:GLU:OE1	10:J:9:GLU:HA	2.19	0.43
26:a:28:HIS:ND1	26:a:32:ARG:HG2	2.32	0.43
46:w:10:ARG:NH2	46:w:265:SER:O	2.52	0.43
46:w:37:PRO:HA	46:w:187:GLY:O	2.18	0.43
54:K:1211:G:HO2'	54:K:1212:G:P	2.41	0.43
54:K:1474:C:H2'	54:K:1475:G:O4'	2.19	0.43
54:K:2582:A:O2'	54:K:2653:C:O2'	2.22	0.43
54:K:2601:A:N6	54:K:2743:A:H3'	2.33	0.43
54:K:2616:C:C2	54:K:2722:G:N2	2.87	0.43
54:K:2633:U:H2'	54:K:2634:C:C6	2.53	0.43
54:K:4349:C:H3'	54:K:4350:C:H5'	2.01	0.43
6:F:106:LYS:HZ3	6:F:110:LEU:HD21	1.84	0.43
14:O:81:TRP:HB2	14:O:104:VAL:HG21	1.99	0.43
15:P:2:VAL:HG12	15:P:3:ARG:N	2.32	0.43
20:U:101:ARG:NH2	54:K:2702:C:OP1	2.52	0.43
21:V:87:SER:HA	21:V:97:TYR:HB3	1.99	0.43
29:d:29:ILE:O	29:d:33:ILE:HG22	2.19	0.43
32:g:11:LEU:HD23	32:g:13:TYR:H	1.84	0.43
41:p:74:THR:O	41:p:78:THR:HG23	2.18	0.43
46:w:15:GLY:O	54:K:4587:G:N2	2.49	0.43
46:w:140:ASP:OD1	46:w:141:ALA:N	2.51	0.43
53:6:119:LEU:HG	53:6:135:MET:HE3	2.01	0.43
54:K:2464:C:H2'	54:K:2465:C:H6	1.82	0.43
54:K:2830:G:C6	54:K:3856:A:N6	2.87	0.43
54:K:3684:G:H2'	54:K:3685:C:C6	2.54	0.43
54:K:3784:A:O2'	54:K:3785:A:H3'	2.19	0.43
54:K:4354:U:C2'	54:K:4355:G:OP2	2.67	0.43
54:K:4907:G:N2	54:K:4915:G:C2	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:5062:G:C2	54:K:5063:G:C8	3.06	0.43
1:A:103:PRO:HA	1:A:163:ARG:HA	2.01	0.43
3:C:81:GLY:O	3:C:87:SER:OG	2.26	0.43
7:G:103:ASP:OD1	7:G:105:THR:HG23	2.19	0.43
7:G:247:VAL:HG21	7:G:249:ARG:NH1	2.34	0.43
17:R:124:TYR:OH	54:K:2666:U:OP2	2.28	0.43
18:S:87:ARG:HG3	54:K:2034:G:OP1	2.19	0.43
19:T:81:LYS:O	27:b:16:TRP:NE1	2.51	0.43
26:a:35:ALA:HB2	54:K:38:A:H5''	2.00	0.43
29:d:90:ARG:HD3	29:d:102:LEU:HD13	2.00	0.43
47:1:20:GLN:O	47:1:173:TYR:OH	2.20	0.43
47:1:291:ILE:HD11	47:1:428:ILE:HG23	2.01	0.43
54:K:1250:C:H2'	54:K:1251:C:O4'	2.19	0.43
54:K:2021:G:H2'	54:K:2022:C:C2	2.54	0.43
54:K:2495:U:H2'	54:K:2496:G:H8	1.84	0.43
54:K:3603:G:O2'	54:K:3604:A:P	2.77	0.43
54:K:3637:U:O4	54:K:3651:A:H2	2.02	0.43
3:C:322:LEU:HD21	5:E:56:ILE:HG13	2.01	0.43
10:J:24:ILE:HG12	10:J:128:LEU:HB3	2.01	0.43
13:N:47:LYS:O	13:N:51:LEU:HG	2.18	0.43
54:K:342:G:H2'	54:K:343:C:C6	2.54	0.43
54:K:658:C:C4	54:K:659:G:N7	2.87	0.43
54:K:1354:A:N1	54:K:1385:G:O2'	2.44	0.43
54:K:2079:G:H2'	54:K:2080:U:C6	2.54	0.43
54:K:2599:G:N2	54:K:2747:U:O4	2.52	0.43
54:K:3810:C:O2'	54:K:3811:G:OP1	2.33	0.43
54:K:4918:C:H2'	54:K:4919:G:O4'	2.18	0.43
4:D:244:HIS:O	4:D:248:ARG:HG3	2.19	0.43
4:D:276:LYS:O	4:D:280:VAL:HG22	2.19	0.43
6:F:161:ILE:HB	6:F:166:ILE:HD12	2.00	0.43
9:I:29:ALA:O	9:I:32:ARG:NH1	2.52	0.43
11:L:115:GLN:OE1	11:L:119:GLU:HG2	2.17	0.43
15:P:41:ILE:HD12	15:P:150:LEU:CD1	2.49	0.43
17:R:3:MET:HE1	17:R:5:ARG:CZ	2.49	0.43
19:T:137:GLU:H	19:T:137:GLU:CD	2.27	0.43
24:Y:1:MET:HG3	24:Y:2:LYS:H	1.84	0.43
45:v:33:G:H5''	45:v:34:U:OP1	2.19	0.43
52:7:299:LEU:O	52:7:299:LEU:HD23	2.19	0.43
54:K:425:U:C2	54:K:426:A:C8	3.07	0.43
54:K:923:C:H4'	54:K:923:C:OP1	2.18	0.43
54:K:1173:G:H2'	54:K:1174:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:1952:G:C2	54:K:2032:U:O2	2.72	0.43
54:K:2259:G:H5'	54:K:2260:C:OP2	2.18	0.43
54:K:2793:G:H5'	54:K:2794:C:H5''	2.01	0.43
54:K:4344:U:H2'	54:K:4345:C:C6	2.54	0.43
2:B:60:ARG:HD2	2:B:60:ARG:HA	1.92	0.42
3:C:38:ASN:O	3:C:42:THR:HG23	2.19	0.42
12:M:62:LEU:H	12:M:62:LEU:HD23	1.83	0.42
15:P:54:LYS:NZ	54:K:3855:C:O2'	2.47	0.42
23:X:112:ALA:O	23:X:116:LEU:HG	2.19	0.42
26:a:85:GLN:HA	26:a:88:VAL:HG12	2.01	0.42
26:a:113:GLY:N	26:a:133:ALA:HB2	2.34	0.42
31:f:14:TYR:OH	31:f:92:LEU:O	2.28	0.42
31:f:106:TYR:N	31:f:107:PRO:CD	2.82	0.42
32:g:76:ARG:NH1	54:K:2583:C:OP2	2.46	0.42
46:w:17:LEU:HB3	46:w:18:PRO:HD3	2.00	0.42
49:3:49:PHE:CZ	49:3:53:PHE:CE1	3.07	0.42
54:K:64:A:N1	54:K:108:A:O2'	2.50	0.42
54:K:478:G:H2'	54:K:479:G:H8	1.83	0.42
54:K:1195:G:H2'	54:K:1196:G:H8	1.84	0.42
54:K:1974:U:O3'	54:K:1975:G:H3'	2.19	0.42
54:K:2638:G:H22	54:K:2697:A:H61	1.66	0.42
54:K:2740:U:HO2'	54:K:2742:G:N2	2.16	0.42
1:A:44:ILE:HD11	1:A:46:LYS:NZ	2.34	0.42
5:E:269:GLN:OE1	12:M:111:LYS:HG2	2.19	0.42
14:O:176:ARG:HD3	54:K:4769:G:H5'	2.00	0.42
18:S:127:MET:HE1	19:T:155:PRO:HA	2.00	0.42
20:U:28:PRO:HB3	20:U:33:ILE:HD11	1.99	0.42
36:k:57:LYS:HA	36:k:60:LEU:HD13	2.01	0.42
49:3:17:ASP:OD1	49:3:20:ARG:NH1	2.51	0.42
52:7:86:MET:HG2	52:7:356:SER:OG	2.19	0.42
52:7:141:GLY:N	52:7:477:VAL:O	2.48	0.42
52:7:295:PHE:HA	52:7:383:VAL:HG21	2.01	0.42
54:K:1833:G:N2	54:K:1835:G:O4'	2.52	0.42
54:K:2429:A:H2'	54:K:2430:C:C6	2.54	0.42
54:K:2430:C:O2'	54:K:2431:A:H5'	2.19	0.42
54:K:2706:G:N2	54:K:2710:C:OP2	2.52	0.42
4:D:64:ILE:HG13	4:D:105:LEU:HD21	2.00	0.42
5:E:158:GLY:HA2	54:K:4942:C:H5''	2.00	0.42
5:E:171:LEU:HD21	5:E:177:LEU:HB2	2.01	0.42
5:E:261:LEU:N	5:E:262:PRO:HD2	2.35	0.42
14:O:140:ARG:HG2	14:O:144:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:69:ARG:NH1	54:K:4568:A:N3	2.60	0.42
54:K:644:G:N2	54:K:645:G:O4'	2.52	0.42
54:K:916:C:H4'	54:K:917:A:OP2	2.19	0.42
54:K:1278:C:H2'	54:K:1279:A:O4'	2.19	0.42
54:K:1300:G:O2'	54:K:1301:C:N4	2.53	0.42
54:K:1767:A:H5''	54:K:1768:C:OP2	2.18	0.42
54:K:2689:C:H2'	54:K:2690:C:H6	1.84	0.42
54:K:4458:C:H2'	54:K:4459:U:C6	2.55	0.42
54:K:4916:G:H2'	54:K:4917:C:O4'	2.19	0.42
11:L:87:HIS:HB3	11:L:90:VAL:HG12	2.01	0.42
18:S:19:THR:HG1	18:S:22:CYS:HG	1.65	0.42
26:a:76:ASP:HB3	26:a:115:GLY:HA3	2.00	0.42
54:K:414:C:H5'	54:K:415:G:OP2	2.19	0.42
54:K:2409:U:H4'	54:K:2428:A:H4'	2.01	0.42
54:K:2477:A:H2'	54:K:2478:C:C6	2.54	0.42
54:K:2538:U:H2'	54:K:2539:C:C6	2.54	0.42
54:K:3904:G:H1'	54:K:3905:A:OP1	2.19	0.42
54:K:4079:C:H2'	54:K:4080:C:C6	2.54	0.42
54:K:4948:C:O2	54:K:4948:C:O4'	2.36	0.42
4:D:157:ASN:CG	4:D:159:VAL:HG12	2.44	0.42
5:E:49:ASN:HB3	5:E:64:MET:SD	2.60	0.42
9:I:38:ARG:HG2	9:I:41:ALA:HB2	2.02	0.42
12:M:58:THR:HG22	12:M:91:TRP:CZ3	2.55	0.42
16:Q:3:VAL:HG23	16:Q:5:ILE:HG12	2.01	0.42
18:S:165:PRO:O	18:S:166:ARG:C	2.62	0.42
21:V:18:LEU:HD12	21:V:18:LEU:O	2.19	0.42
23:X:119:ILE:HG22	23:X:144:TYR:CD2	2.54	0.42
35:j:50:SER:OG	35:j:53:ALA:HB3	2.19	0.42
45:v:83:C:H1'	45:v:84:A:OP1	2.19	0.42
47:1:106:PRO:CD	50:4:457:GLU:OE2	2.68	0.42
47:1:379:TRP:CE2	47:1:383:SER:OG	2.72	0.42
54:K:499:G:H2'	54:K:500:G:C8	2.54	0.42
54:K:669:C:O2'	54:K:670:G:H8	2.02	0.42
54:K:738:C:OP1	54:K:739:G:H4'	2.20	0.42
54:K:1074:G:C2	54:K:1238:A:C2	3.07	0.42
54:K:1412:G:H2'	54:K:1413:C:H5'	2.00	0.42
54:K:3599:A:H2'	54:K:3600:G:C8	2.53	0.42
54:K:3888:G:HO2'	54:K:3889:G:P	2.41	0.42
54:K:4303:C:O2'	54:K:4304:A:H2'	2.20	0.42
12:M:36:ALA:HB2	12:M:52:PHE:CZ	2.54	0.42
15:P:66:GLY:N	54:K:3893:C:OP1	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:S:19:THR:HB	18:S:20:PRO:HD2	2.02	0.42
35:j:63:ARG:NH2	45:v:58:G:O6	2.53	0.42
41:p:73:THR:HG23	41:p:76:ALA:HB3	2.00	0.42
46:w:276:HIS:O	54:K:4716:C:H5''	2.19	0.42
54:K:679:C:H2'	54:K:680:G:H8	1.85	0.42
54:K:956:A:H1'	54:K:2076:G:H5''	2.02	0.42
54:K:1202:C:C2	54:K:1203:G:C8	3.08	0.42
54:K:1824:G:H2'	54:K:1825:A:C8	2.54	0.42
54:K:2418:A:C5	54:K:2419:C:C5	3.08	0.42
54:K:2627:C:O2	54:K:2627:C:O4'	2.37	0.42
54:K:4080:C:H2'	54:K:4081:G:H8	1.84	0.42
54:K:5008:C:H2'	54:K:5009:G:O4'	2.20	0.42
3:C:78:ARG:HB3	3:C:88:GLY:HA2	2.00	0.42
11:L:22:VAL:HG13	13:N:200:LEU:HD12	2.00	0.42
16:Q:25:LEU:O	16:Q:29:VAL:HG23	2.20	0.42
22:W:35:LYS:HD3	54:K:5004:C:OP1	2.20	0.42
24:Y:45:ARG:NH1	54:K:199:G:OP2	2.51	0.42
26:a:132:ARG:NH2	54:K:1468:C:OP1	2.42	0.42
27:b:18:ARG:NH1	54:K:1669:A:OP1	2.45	0.42
28:c:10:SER:O	28:c:14:ILE:HG12	2.20	0.42
33:h:28:LEU:HD12	33:h:54:ILE:HD12	2.01	0.42
43:r:24:THR:OG1	54:K:2289:C:N4	2.52	0.42
43:r:107:ARG:HG3	43:r:108:MET:N	2.34	0.42
46:w:168:MET:HE2	46:w:175:GLN:HG3	2.02	0.42
54:K:425:U:N3	54:K:426:A:N7	2.66	0.42
54:K:1178:G:H5''	54:K:1179:U:OP2	2.20	0.42
54:K:1294:A:H5'	54:K:1296:G:N2	2.35	0.42
54:K:1468:C:H2'	54:K:1469:C:H6	1.84	0.42
54:K:4453:C:C2	54:K:4529:G:C2	3.07	0.42
54:K:4510:A:O2'	54:K:4511:A:C8	2.71	0.42
54:K:4568:A:O2'	54:K:4981:G:N7	2.53	0.42
54:K:4575:G:C2	54:K:4576:U:C6	3.07	0.42
54:K:5007:A:N7	54:K:5042:A:O2'	2.49	0.42
7:G:313:GLU:OE1	7:G:314:LEU:N	2.52	0.42
14:O:54:TYR:CE1	14:O:58:LEU:HD21	2.55	0.42
18:S:46:TYR:OH	44:u:94:C:OP1	2.38	0.42
23:X:109:ILE:O	23:X:113:VAL:HG23	2.20	0.42
31:f:81:SER:HB2	54:K:1919:G:O2'	2.20	0.42
34:i:93:VAL:O	34:i:97:MET:HG3	2.20	0.42
45:v:67:U:H2'	45:v:68:G:H8	1.85	0.42
51:5:40:LEU:HD23	51:5:63:CYS:SG	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:136:C:O2'	54:K:137:G:OP2	2.29	0.42
54:K:310:G:C4	54:K:311:G:C8	3.07	0.42
54:K:1292:C:H5'	54:K:1293:G:OP2	2.19	0.42
54:K:1927:U:OP1	54:K:1949:U:O2'	2.27	0.42
54:K:1957:U:OP2	54:K:1957:U:H6	2.03	0.42
54:K:3823:G:H8	54:K:3823:G:O5'	2.03	0.42
54:K:4423:U:O2	54:K:4423:U:O4'	2.38	0.42
5:E:117:ARG:NH2	54:K:691:C:OP2	2.51	0.42
7:G:82:ASN:OD1	7:G:83:PRO:HD2	2.20	0.42
7:G:258:THR:OG1	7:G:259:GLN:N	2.52	0.42
13:N:15:GLN:NE2	54:K:305:A:OP2	2.53	0.42
23:X:73:HIS:O	23:X:116:LEU:HD11	2.20	0.42
23:X:76:ILE:HG23	23:X:77:ILE:HG13	2.00	0.42
25:Z:76:ASN:OD1	25:Z:77:TYR:N	2.53	0.42
26:a:77:LYS:O	26:a:80:THR:OG1	2.38	0.42
26:a:134:GLU:O	26:a:138:LYS:HG2	2.19	0.42
42:q:18:G:O2'	42:q:19:G:N7	2.53	0.42
43:r:28:GLU:HB2	43:r:31:ASN:HB2	2.02	0.42
45:v:140:C:H2'	45:v:141:C:C6	2.55	0.42
46:w:60:VAL:HG11	46:w:67:VAL:HG23	2.01	0.42
54:K:102:G:O2'	54:K:1381:U:O2'	2.08	0.42
54:K:324:A:H2'	54:K:325:U:O4'	2.20	0.42
54:K:750:U:H2'	54:K:751:G:O4'	2.20	0.42
54:K:2533:C:H2'	54:K:2534:C:H6	1.85	0.42
54:K:4661:G:H21	54:K:5005:G:P	2.42	0.42
54:K:4670:C:O3'	54:K:4671:C:H3'	2.20	0.42
54:K:4737:G:C4	54:K:4963:G:N2	2.88	0.42
4:D:163:LEU:HD21	4:D:175:HIS:HB3	2.01	0.42
5:E:134:LYS:NZ	54:K:1279:A:OP1	2.51	0.42
5:E:158:GLY:O	5:E:161:ARG:HG3	2.20	0.42
10:J:56:THR:HG22	10:J:64:ARG:N	2.29	0.42
11:L:63:THR:O	11:L:63:THR:HG22	2.20	0.42
23:X:151:ASN:OD1	49:3:20:ARG:HG3	2.20	0.42
40:o:5:PRO:HD3	54:K:4232:U:C2	2.55	0.42
47:1:286:THR:O	47:1:287:SER:HB3	2.19	0.42
54:K:168:C:H2'	54:K:169:A:O4'	2.20	0.42
54:K:907:C:H2'	54:K:908:G:H8	1.84	0.42
54:K:1168:G:C2	54:K:1169:G:C8	3.08	0.42
54:K:1188:C:H2'	54:K:1189:G:C8	2.54	0.42
54:K:1445:U:HO2'	54:K:1446:C:P	2.42	0.42
54:K:2055:G:H5'	54:K:2056:G:H5''	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:4389:C:H2'	54:K:4390:A:C8	2.54	0.42
54:K:4633:G:O3'	54:K:4634:U:H3'	2.19	0.42
54:K:4688:C:H2'	54:K:4689:U:C6	2.54	0.42
54:K:4988:U:HO2'	54:K:5061:A:H2	1.66	0.42
1:A:48:ILE:HD13	41:p:65:ALA:HB2	2.02	0.41
3:C:269:LYS:NZ	3:C:270:ALA:O	2.45	0.41
5:E:133:LYS:NZ	54:K:1284:G:OP1	2.46	0.41
5:E:179:THR:O	5:E:179:THR:CG2	2.68	0.41
5:E:196:PHE:HD1	31:f:106:TYR:HB2	1.85	0.41
7:G:113:TYR:OH	45:v:148:A:N3	2.40	0.41
10:J:33:LEU:HD22	10:J:70:VAL:HG23	2.01	0.41
12:M:55:MET:O	18:S:157:ARG:NH2	2.53	0.41
13:N:73:ARG:HB3	13:N:89:VAL:HG12	2.02	0.41
18:S:139:ARG:O	18:S:143:LYS:HG3	2.20	0.41
44:u:50:A:H2'	44:u:51:G:O4'	2.20	0.41
54:K:321:U:H2'	54:K:322:C:O4'	2.19	0.41
54:K:907:C:H2'	54:K:908:G:C8	2.54	0.41
54:K:978:G:N2	54:K:1277:G:H1	2.18	0.41
54:K:1332:C:H2'	54:K:1333:A:C8	2.55	0.41
54:K:1867:A:N3	54:K:4403:U:O2'	2.45	0.41
54:K:4168:G:H2'	54:K:4169:G:H5'	2.02	0.41
54:K:4738:C:H2'	54:K:4739:C:C6	2.55	0.41
54:K:5058:A:H2'	54:K:5059:C:O4'	2.20	0.41
4:D:37:VAL:HG13	4:D:67:ALA:CB	2.50	0.41
5:E:245:ILE:H	5:E:245:ILE:CD1	2.32	0.41
10:J:73:THR:N	44:u:39:C:O2	2.39	0.41
15:P:114:ILE:HA	15:P:150:LEU:HD22	2.02	0.41
15:P:122:ALA:HB3	15:P:143:PRO:HG2	2.02	0.41
25:Z:36:ARG:NH1	25:Z:38:TYR:OH	2.53	0.41
26:a:121:PRO:HA	26:a:141:GLY:O	2.19	0.41
31:f:40:GLU:O	31:f:109:ARG:NH2	2.48	0.41
37:l:15:LYS:O	37:l:19:GLN:HG3	2.19	0.41
44:u:31:G:C6	44:u:47:G:C6	3.09	0.41
47:1:130:VAL:HG22	47:1:307:MET:HE1	2.03	0.41
47:1:252:PHE:CE1	47:1:256:ILE:HD11	2.55	0.41
50:4:181:LEU:HD21	50:4:184:ASP:HB2	2.02	0.41
54:K:385:A:H4'	54:K:386:A:OP1	2.20	0.41
54:K:1477:C:H2'	54:K:1478:C:H6	1.83	0.41
54:K:2686:G:H5'	54:K:2687:U:OP1	2.20	0.41
3:C:290:SER:OG	43:r:4:HIS:NE2	2.45	0.41
3:C:323:ARG:HD3	54:K:976:G:H21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:135:VAL:HG23	6:F:139:ILE:HD13	2.02	0.41
10:J:94:LEU:O	10:J:175:LEU:HD23	2.20	0.41
14:O:108:ILE:HD12	14:O:160:ARG:CZ	2.51	0.41
21:V:14:PHE:HE2	46:w:67:VAL:HG13	1.85	0.41
24:Y:124:LYS:O	24:Y:128:VAL:HG23	2.20	0.41
31:f:89:ARG:NH2	54:K:709:C:OP1	2.53	0.41
45:v:36:G:N1	54:K:20:U:OP2	2.50	0.41
46:w:389:MET:O	54:K:5041:G:N1	2.44	0.41
47:1:106:PRO:HG3	50:4:457:GLU:OE2	2.20	0.41
47:1:308:LEU:HG	47:1:318:VAL:HG22	2.01	0.41
54:K:1483:C:O2	54:K:1483:C:O4'	2.37	0.41
54:K:1504:G:H2'	54:K:1505:C:C6	2.54	0.41
54:K:1881:C:H5'	54:K:2281:U:H1'	2.02	0.41
54:K:1942:A:H2'	54:K:1943:A:H8	1.86	0.41
54:K:2635:U:H2'	54:K:2636:U:C6	2.56	0.41
54:K:2863:G:N1	54:K:3619:G:O4'	2.52	0.41
54:K:3598:C:H2'	54:K:3599:A:C8	2.55	0.41
54:K:3873:G:H2'	54:K:3874:G:C8	2.56	0.41
54:K:4886:C:H2'	54:K:4887:C:H6	1.84	0.41
1:A:205:ASN:HB3	1:A:206:PRO:HD2	2.01	0.41
3:C:232:VAL:HG11	3:C:256:ALA:HB1	2.02	0.41
3:C:302:LEU:HD23	16:Q:39:THR:HG22	2.02	0.41
6:F:186:MET:O	6:F:190:ILE:HG13	2.20	0.41
8:H:16:VAL:HG12	8:H:17:ASP:N	2.35	0.41
8:H:123:ILE:HG13	8:H:123:ILE:O	2.20	0.41
25:Z:89:ILE:CG1	25:Z:91:LEU:HD23	2.51	0.41
30:e:77:PHE:HB3	30:e:88:LEU:HD11	2.02	0.41
40:o:4:VAL:O	40:o:94:GLY:N	2.41	0.41
46:w:192:GLU:HA	46:w:195:ASP:OD1	2.20	0.41
54:K:2560:C:H2'	54:K:2561:C:H6	1.85	0.41
3:C:133:LEU:HD23	43:r:6:GLN:OE1	2.20	0.41
4:D:44:TYR:O	54:K:1823:G:O2'	2.39	0.41
5:E:177:LEU:HD13	5:E:220:PHE:CE2	2.54	0.41
5:E:248:GLN:HA	5:E:251:VAL:HG12	2.01	0.41
10:J:175:LEU:HD23	10:J:175:LEU:H	1.86	0.41
13:N:89:VAL:CG2	54:K:3928:A:H5'	2.51	0.41
14:O:140:ARG:O	14:O:144:GLU:OE1	2.38	0.41
15:P:12:THR:HG23	50:4:414:GLU:HG3	2.00	0.41
17:R:60:ARG:HG3	17:R:60:ARG:O	2.20	0.41
19:T:3:ASN:ND2	54:K:4212:A:N1	2.65	0.41
42:q:46:G:H3'	42:q:47:U:H5''	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:r:85:ASN:OD1	43:r:88:ALA:HB3	2.21	0.41
47:1:5:PHE:CE2	47:1:9:ILE:HD11	2.56	0.41
50:4:314:ASP:C	50:4:314:ASP:OD1	2.64	0.41
54:K:495:C:C2	54:K:496:G:C8	3.08	0.41
54:K:1186:U:H2'	54:K:1187:G:N3	2.35	0.41
54:K:1238:A:O2'	54:K:1239:C:P	2.76	0.41
54:K:2382:A:N1	54:K:2829:U:O2'	2.44	0.41
54:K:2409:U:C5	54:K:2783:A:N1	2.89	0.41
54:K:2546:G:O2'	54:K:2547:G:OP1	2.27	0.41
54:K:3664:G:H2'	54:K:3665:G:H8	1.85	0.41
1:A:5:ILE:HG13	1:A:8:GLN:H	1.84	0.41
6:F:58:LYS:O	6:F:62:GLN:HG3	2.20	0.41
7:G:126:ARG:NE	54:K:4076:G:OP1	2.40	0.41
7:G:266:GLY:O	7:G:270:LYS:HG2	2.19	0.41
12:M:119:ARG:HG2	12:M:123:ILE:HD12	2.02	0.41
15:P:65:GLY:C	15:P:67:VAL:H	2.29	0.41
36:k:56:LEU:O	36:k:60:LEU:HD12	2.20	0.41
54:K:381:U:H4'	54:K:415:G:H5'	2.02	0.41
54:K:1962:A:C4	54:K:1963:C:C5	3.08	0.41
54:K:2597:G:H2'	54:K:2598:A:C8	2.56	0.41
54:K:4097:G:H22	54:K:4111:U:H3	1.69	0.41
54:K:4883:C:H2'	54:K:4884:G:H8	1.85	0.41
1:A:118:GLU:HB3	1:A:126:LEU:HD11	2.01	0.41
1:A:128:ARG:NE	54:K:3681:G:OP2	2.47	0.41
3:C:7:LEU:HG	3:C:21:ASN:HB3	2.03	0.41
3:C:151:PRO:O	3:C:153:VAL:HG23	2.20	0.41
15:P:41:ILE:O	15:P:45:THR:HG23	2.21	0.41
54:K:1929:A:H5'	54:K:1930:U:OP1	2.20	0.41
54:K:2459:G:H2'	54:K:2461:G:OP2	2.21	0.41
54:K:4073:A:C2	54:K:4074:C:C6	3.09	0.41
54:K:4080:C:H2'	54:K:4081:G:C8	2.55	0.41
11:L:182:LEU:HD23	34:i:7:MET:HE2	2.02	0.41
12:M:123:ILE:O	12:M:127:VAL:HG23	2.21	0.41
15:P:18:ARG:HB3	54:K:399:G:H4'	2.02	0.41
28:c:35:LEU:HD13	28:c:60:ILE:HD13	2.02	0.41
44:u:16:A:H2'	44:u:17:C:C6	2.56	0.41
47:1:309:SER:HA	47:1:318:VAL:HG11	2.03	0.41
52:7:7:TYR:O	52:7:103:PHE:N	2.47	0.41
54:K:86:U:H2'	54:K:87:A:C8	2.55	0.41
54:K:163:A:H2'	54:K:164:G:H8	1.85	0.41
54:K:1179:U:O2	54:K:1179:U:H3'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:2266:C:H4'	54:K:2267:U:O5'	2.20	0.41
54:K:2418:A:C2	54:K:2429:A:O2'	2.73	0.41
3:C:289:LEU:HD12	3:C:289:LEU:C	2.46	0.41
5:E:206:ILE:O	5:E:206:ILE:CG2	2.65	0.41
6:F:103:LYS:NZ	54:K:1797:G:OP1	2.54	0.41
9:I:140:THR:OG1	9:I:141:LYS:N	2.53	0.41
11:L:63:THR:C	11:L:65:ARG:N	2.79	0.41
11:L:71:ARG:HG2	11:L:72:ALA:H	1.85	0.41
11:L:114:VAL:O	11:L:118:LYS:HG2	2.21	0.41
15:P:64:ASN:ND2	15:P:80:GLN:OE1	2.54	0.41
25:Z:29:ILE:HB	25:Z:40:HIS:CD2	2.55	0.41
27:b:56:LYS:HD2	54:K:1812:C:H5''	2.03	0.41
32:g:6:THR:HG22	54:K:2400:G:H21	1.86	0.41
32:g:63:VAL:O	32:g:63:VAL:HG12	2.20	0.41
32:g:108:LYS:O	32:g:112:GLN:HG2	2.21	0.41
36:k:11:PHE:CZ	36:k:34:PHE:HB3	2.56	0.41
45:v:6:C:H2'	45:v:7:U:C6	2.55	0.41
50:4:269:LEU:HD11	50:4:300:ALA:O	2.21	0.41
53:6:11:ALA:HB1	53:6:15:PHE:CE2	2.56	0.41
54:K:707:C:O2'	54:K:4943:A:N1	2.39	0.41
54:K:975:C:H2'	54:K:976:G:C8	2.55	0.41
54:K:1406(A):G:N1	54:K:1411(B):C:N3	2.49	0.41
54:K:1406(A):G:H2'	54:K:1406(B):C:C6	2.56	0.41
54:K:1430:C:H2'	54:K:1431:C:H6	1.86	0.41
54:K:1959:U:O4'	54:K:1961:G:H1'	2.21	0.41
54:K:2488:C:O2'	54:K:2489:C:P	2.78	0.41
54:K:4119:C:O2'	54:K:4120:U:P	2.79	0.41
54:K:4238:G:H2'	54:K:4239:A:H8	1.85	0.41
54:K:4273:A:H2'	54:K:4274:A:C8	2.56	0.41
54:K:4389:C:H2'	54:K:4390:A:H8	1.85	0.41
54:K:4406:U:C2	54:K:4407:G:C8	3.08	0.41
54:K:4433:G:H2'	54:K:4434:C:H6	1.86	0.41
54:K:4729:A:OP2	54:K:5068:G:N2	2.51	0.41
54:K:4886:C:H2'	54:K:4887:C:C6	2.55	0.41
54:K:5000:G:H2'	54:K:5001:U:O4'	2.21	0.41
1:A:33:ASP:OD1	1:A:33:ASP:N	2.53	0.41
16:Q:61:LEU:HD12	16:Q:82:VAL:HG21	2.03	0.41
26:a:103:VAL:CG1	26:a:108:TYR:HB2	2.51	0.41
30:e:41:ILE:HG13	30:e:42:ASP:H	1.85	0.41
36:k:59:SER:O	36:k:59:SER:OG	2.34	0.41
45:v:70:G:N2	45:v:87:G:H1'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:w:258:HIS:HB2	54:K:4518:A:OP2	2.20	0.41
46:w:268:ARG:NE	54:K:4565:C:O2	2.46	0.41
50:4:252:ASN:HB2	50:4:255:ASP:OD2	2.21	0.41
54:K:408:A:H4'	54:K:409:G:H3'	2.03	0.41
54:K:1808:C:H2'	54:K:1809:C:C6	2.55	0.41
54:K:2411:C:H2'	54:K:2412:A:C8	2.56	0.41
54:K:2478:C:H2'	54:K:2479:G:C8	2.56	0.41
54:K:3755:G:C2	54:K:3770:U:O2	2.74	0.41
54:K:4305:G:N3	54:K:4305:G:C2'	2.83	0.41
7:G:195:THR:HG22	7:G:199:LEU:HD23	2.02	0.40
11:L:46:ILE:HB	11:L:49:ARG:HB2	2.03	0.40
12:M:118:MET:O	12:M:122:ILE:HG13	2.21	0.40
16:Q:90:VAL:HG22	54:K:1502:G:O6	2.21	0.40
27:b:8:THR:HG22	54:K:1671:U:O5'	2.21	0.40
32:g:98:GLU:OE2	54:K:4122:G:N2	2.54	0.40
45:v:13:G:C4	45:v:14:U:C5	3.08	0.40
45:v:68:G:C5	45:v:69:U:C5	3.09	0.40
54:K:1327:C:H2'	54:K:1328:G:C8	2.56	0.40
54:K:2708:U:O2'	54:K:2709:C:H6	2.04	0.40
54:K:3770:U:H2'	54:K:3771:C:H6	1.86	0.40
54:K:3834:C:H2'	54:K:3835:C:H6	1.87	0.40
54:K:4233:A:C4	54:K:4235:G:N7	2.90	0.40
54:K:5019:A:H2'	54:K:5020:G:C8	2.56	0.40
54:K:5028:G:H2'	54:K:5029:C:C6	2.56	0.40
5:E:136:PHE:HA	5:E:139:HIS:ND1	2.36	0.40
5:E:234:GLU:HG3	50:4:319:HIS:CD2	2.57	0.40
5:E:235:ILE:HG22	5:E:236:PHE:CD1	2.57	0.40
8:H:5:LEU:HD13	8:H:60:TRP:CZ2	2.56	0.40
10:J:93:GLU:HG2	10:J:173:ILE:HG12	2.02	0.40
11:L:80:GLU:HG2	11:L:110:LEU:HD12	2.02	0.40
12:M:105:THR:HG22	12:M:108:ASP:OD1	2.21	0.40
26:a:131:ARG:O	26:a:135:GLU:HG3	2.21	0.40
39:n:1:MET:HE3	39:n:1:MET:HA	2.04	0.40
39:n:20:MET:HE1	39:n:23:ARG:HD3	2.02	0.40
45:v:25:G:C6	45:v:26:C:C4	3.09	0.40
47:1:91:MET:HG3	47:1:112:PHE:CE1	2.56	0.40
47:1:405:ARG:NH2	54:K:2526:C:C6	2.89	0.40
54:K:173:C:C6	54:K:174:C:C5	3.10	0.40
54:K:470:A:H2'	54:K:471:A:O4'	2.21	0.40
54:K:685:C:H1'	54:K:686:A:OP2	2.21	0.40
54:K:1168:G:C2	54:K:1194:G:N1	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:K:1475:G:N2	54:K:1490:G:C4	2.90	0.40
54:K:2279:A:H2'	54:K:2280:G:O4'	2.22	0.40
54:K:2412:A:H2'	54:K:2413:U:H6	1.87	0.40
54:K:2492:C:H2'	54:K:2493:G:H8	1.86	0.40
54:K:2519:U:H1'	54:K:2520:C:C6	2.56	0.40
54:K:2654:C:H2'	54:K:2655:C:H6	1.86	0.40
54:K:2894:A:H2'	54:K:2895:A:C8	2.56	0.40
54:K:4699:U:C4	54:K:4702:G:O6	2.74	0.40
5:E:97:LYS:HE3	54:K:687:U:O2'	2.21	0.40
8:H:6:SER:CB	8:H:67:LEU:HD22	2.52	0.40
10:J:57:VAL:HG23	10:J:60:PHE:HB2	2.02	0.40
15:P:41:ILE:HD12	15:P:150:LEU:HD13	2.04	0.40
17:R:96:MET:O	17:R:100:ARG:HG3	2.22	0.40
18:S:68:PHE:N	54:K:729:G:O6	2.47	0.40
22:W:56:ARG:HH21	22:W:61:LYS:HB3	1.85	0.40
25:Z:25:ILE:HG12	25:Z:43:VAL:HG12	2.04	0.40
41:p:54:ILE:O	41:p:54:ILE:HG13	2.21	0.40
44:u:43:U:C4	44:u:44:C:C4	3.09	0.40
46:w:222:VAL:HA	46:w:275:HIS:O	2.21	0.40
47:1:10:LYS:N	47:1:11:PRO:HD2	2.36	0.40
53:6:153:VAL:O	53:6:156:ILE:HG22	2.22	0.40
54:K:132:G:H2'	54:K:133:C:O4'	2.21	0.40
54:K:458:C:H2'	54:K:459:C:C6	2.56	0.40
54:K:504:G:O2'	54:K:505:G:P	2.80	0.40
54:K:971(A):G:H4'	54:K:972:C:H5'	2.03	0.40
54:K:1175:A:H2'	54:K:1176:C:C6	2.56	0.40
54:K:1187:G:H2'	54:K:1188:C:H6	1.86	0.40
54:K:1354:A:N6	54:K:1503:A:O4'	2.54	0.40
54:K:1400:G:H2'	54:K:1401:C:H6	1.86	0.40
54:K:1475:G:H2'	54:K:1476:C:C6	2.56	0.40
54:K:1554:A:H2'	54:K:1555:G:O4'	2.21	0.40
54:K:2573:A:H2'	54:K:2574:G:O4'	2.21	0.40
54:K:2586:G:N3	54:K:2770:C:O2'	2.52	0.40
54:K:2655:C:H2'	54:K:2656:U:H6	1.86	0.40
54:K:2864:A:H2'	54:K:2865:U:H6	1.87	0.40
54:K:3870:C:H2'	54:K:3871:A:H8	1.87	0.40
54:K:4188:U:H2'	54:K:4189:U:C6	2.57	0.40
54:K:4303:C:O2	54:K:4303:C:O5'	2.40	0.40
54:K:4563:U:H2'	54:K:4564:A:H8	1.86	0.40
54:K:4569:U:OP1	54:K:4982:A:O2'	2.32	0.40
1:A:27:ALA:O	1:A:128:ARG:NH2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:TRP:O	1:A:198:ARG:N	2.55	0.40
1:A:230:PRO:HB3	54:K:3928:A:N1	2.36	0.40
3:C:293:LEU:HD22	16:Q:34:PHE:CD2	2.56	0.40
9:I:206:LEU:O	9:I:210:ARG:HG3	2.21	0.40
14:O:69:GLY:O	14:O:70:PRO:C	2.64	0.40
15:P:67:VAL:O	15:P:80:GLN:NE2	2.46	0.40
26:a:15:VAL:HG13	54:K:1659:U:OP2	2.22	0.40
41:p:79:VAL:O	41:p:83:ILE:HG12	2.22	0.40
50:4:225:LEU:N	50:4:243:ASP:OD1	2.49	0.40
52:7:163:GLU:O	52:7:448:VAL:HA	2.21	0.40
54:K:459:C:H2'	54:K:460:C:H6	1.85	0.40
54:K:1984:A:H5'	54:K:1986:U:OP2	2.21	0.40
54:K:2732:G:H2'	54:K:2733:C:C6	2.56	0.40
54:K:4136:G:H1	54:K:4148:C:H42	1.70	0.40
54:K:4400:G:C6	54:K:4401:G:N7	2.90	0.40
54:K:4532:U:OP2	54:K:4554:G:N1	2.47	0.40
54:K:4651:A:H2'	54:K:4652:G:O4'	2.22	0.40
1:A:194:ASN:HB2	54:K:1539:G:H4'	2.03	0.40
3:C:218:VAL:O	3:C:222:ARG:HB3	2.22	0.40
3:C:289:LEU:O	3:C:293:LEU:HG	2.22	0.40
11:L:57:PRO:HG3	11:L:75:GLY:O	2.22	0.40
12:M:34:ASN:HA	12:M:52:PHE:HD2	1.86	0.40
25:Z:59:LYS:HD3	54:K:4148:C:H5'	2.03	0.40
26:a:32:ARG:HD2	54:K:37:U:H4'	2.03	0.40
32:g:18:ASN:O	32:g:18:ASN:ND2	2.54	0.40
35:j:33:THR:HG22	35:j:40:PRO:HG2	2.03	0.40
45:v:8:U:H2'	45:v:9:A:H8	1.87	0.40
52:7:278:LEU:HG	52:7:343:LEU:HD11	2.02	0.40
54:K:1238:A:O2'	54:K:1239:C:H5'	2.22	0.40
54:K:1279:A:H8	54:K:1279:A:OP2	2.04	0.40
54:K:1381:U:O2	54:K:1381:U:O4'	2.38	0.40
54:K:1804:A:O4'	54:K:1806:G:C8	2.74	0.40
54:K:4507:A:H2'	54:K:4508:C:C6	2.57	0.40
54:K:5050:C:H2'	54:K:5051:C:H6	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	246/257 (96%)	219 (89%)	27 (11%)	0	100	100
2	B	25/229 (11%)	22 (88%)	2 (8%)	1 (4%)	2	14
3	C	360/425 (85%)	335 (93%)	25 (7%)	0	100	100
4	D	291/297 (98%)	269 (92%)	22 (8%)	0	100	100
5	E	227/291 (78%)	217 (96%)	9 (4%)	1 (0%)	30	59
6	F	223/247 (90%)	205 (92%)	18 (8%)	0	100	100
7	G	229/319 (72%)	213 (93%)	16 (7%)	0	100	100
8	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
10	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100
11	L	208/211 (99%)	193 (93%)	14 (7%)	1 (0%)	24	55
12	M	136/218 (62%)	125 (92%)	11 (8%)	0	100	100
13	N	199/204 (98%)	183 (92%)	16 (8%)	0	100	100
14	O	197/203 (97%)	186 (94%)	11 (6%)	0	100	100
15	P	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
16	Q	185/188 (98%)	171 (92%)	14 (8%)	0	100	100
17	R	153/196 (78%)	144 (94%)	9 (6%)	0	100	100
18	S	174/176 (99%)	159 (91%)	15 (9%)	0	100	100
19	T	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	21	51
20	U	100/128 (78%)	90 (90%)	10 (10%)	0	100	100
21	V	129/140 (92%)	121 (94%)	8 (6%)	0	100	100
22	W	61/157 (39%)	55 (90%)	6 (10%)	0	100	100
23	X	116/156 (74%)	106 (91%)	10 (9%)	0	100	100
24	Y	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
25	Z	133/136 (98%)	122 (92%)	11 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	145/148 (98%)	132 (91%)	13 (9%)	0	100	100
27	b	100/226 (44%)	96 (96%)	4 (4%)	0	100	100
28	c	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
29	d	105/125 (84%)	94 (90%)	11 (10%)	0	100	100
30	e	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
31	f	107/110 (97%)	99 (92%)	8 (8%)	0	100	100
32	g	112/116 (97%)	104 (93%)	8 (7%)	0	100	100
33	h	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
34	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
35	j	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
36	k	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
37	l	48/51 (94%)	38 (79%)	10 (21%)	0	100	100
38	m	50/102 (49%)	46 (92%)	4 (8%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	90 (88%)	12 (12%)	0	100	100
41	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
43	r	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
46	w	392/403 (97%)	360 (92%)	32 (8%)	0	100	100
47	1	463/476 (97%)	460 (99%)	3 (1%)	0	100	100
48	2	27/96 (28%)	27 (100%)	0	0	100	100
49	3	66/68 (97%)	66 (100%)	0	0	100	100
50	4	340/483 (70%)	338 (99%)	1 (0%)	1 (0%)	36	66
51	5	88/106 (83%)	87 (99%)	1 (1%)	0	100	100
52	7	519/563 (92%)	512 (99%)	7 (1%)	0	100	100
53	6	222/224 (99%)	222 (100%)	0	0	100	100
All	All	8102/9553 (85%)	7610 (94%)	487 (6%)	5 (0%)	49	76

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	L	64	VAL
50	4	347	GLY
2	B	42	PRO

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Mol	Chain	Res	Type
5	E	228	PRO
19	T	82	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	A	190/199 (96%)	189 (100%)	1 (0%)	81	82
2	B	21/172 (12%)	21 (100%)	0	100	100
3	C	302/347 (87%)	302 (100%)	0	100	100
4	D	247/250 (99%)	247 (100%)	0	100	100
5	E	206/251 (82%)	203 (98%)	3 (2%)	57	71
6	F	196/215 (91%)	195 (100%)	1 (0%)	81	82
7	G	200/272 (74%)	199 (100%)	1 (0%)	81	82
8	H	169/171 (99%)	168 (99%)	1 (1%)	78	81
9	I	175/181 (97%)	174 (99%)	1 (1%)	78	81
10	J	143/149 (96%)	141 (99%)	2 (1%)	59	72
11	L	175/176 (99%)	172 (98%)	3 (2%)	53	69
12	M	117/161 (73%)	116 (99%)	1 (1%)	70	76
13	N	171/172 (99%)	170 (99%)	1 (1%)	78	81
14	O	171/173 (99%)	171 (100%)	0	100	100
15	P	134/163 (82%)	132 (98%)	2 (2%)	57	71
16	Q	164/164 (100%)	163 (99%)	1 (1%)	78	81
17	R	138/175 (79%)	138 (100%)	0	100	100
18	S	157/157 (100%)	155 (99%)	2 (1%)	61	73
19	T	139/140 (99%)	139 (100%)	0	100	100
20	U	92/114 (81%)	91 (99%)	1 (1%)	65	75
21	V	101/107 (94%)	100 (99%)	1 (1%)	68	75
22	W	55/126 (44%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	X	106/134 (79%)	105 (99%)	1 (1%)	70	76
24	Y	124/135 (92%)	123 (99%)	1 (1%)	73	78
25	Z	117/118 (99%)	115 (98%)	2 (2%)	53	69
26	a	119/120 (99%)	118 (99%)	1 (1%)	73	78
27	b	84/172 (49%)	83 (99%)	1 (1%)	63	74
28	c	84/98 (86%)	83 (99%)	1 (1%)	63	74
29	d	98/110 (89%)	96 (98%)	2 (2%)	48	66
30	e	114/121 (94%)	114 (100%)	0	100	100
31	f	88/89 (99%)	88 (100%)	0	100	100
32	g	98/99 (99%)	98 (100%)	0	100	100
33	h	108/110 (98%)	107 (99%)	1 (1%)	70	76
34	i	86/89 (97%)	86 (100%)	0	100	100
35	j	73/80 (91%)	71 (97%)	2 (3%)	39	61
36	k	64/65 (98%)	64 (100%)	0	100	100
37	l	47/48 (98%)	47 (100%)	0	100	100
38	m	48/90 (53%)	48 (100%)	0	100	100
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	92/94 (98%)	92 (100%)	0	100	100
41	p	74/75 (99%)	72 (97%)	2 (3%)	39	61
43	r	108/121 (89%)	108 (100%)	0	100	100
46	w	342/348 (98%)	340 (99%)	2 (1%)	78	81
47	1	390/398 (98%)	386 (99%)	4 (1%)	68	75
48	2	26/74 (35%)	26 (100%)	0	100	100
49	3	59/59 (100%)	57 (97%)	2 (3%)	32	57
50	4	306/435 (70%)	304 (99%)	2 (1%)	76	79
51	5	83/99 (84%)	83 (100%)	0	100	100
52	7	443/476 (93%)	442 (100%)	1 (0%)	87	87
53	6	187/187 (100%)	186 (100%)	1 (0%)	81	82
All	All	7055/8103 (87%)	7007 (99%)	48 (1%)	73	79

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	165	VAL
5	E	221	LYS
5	E	241	GLU
5	E	245	ILE
6	F	236	GLU
7	G	96	GLN
8	H	105	ILE
9	I	73	ASN
10	J	115	LEU
10	J	173	ILE
11	L	10	LEU
11	L	70	VAL
11	L	154	VAL
12	M	43	THR
13	N	80	THR
15	P	24	VAL
15	P	118	GLN
16	Q	8	ASN
18	S	67	VAL
18	S	90	THR
20	U	105	ASN
21	V	18	LEU
23	X	120	ASP
24	Y	79	VAL
25	Z	11	VAL
25	Z	53	VAL
26	a	122	VAL
27	b	116	LEU
28	c	91	VAL
29	d	22	THR
29	d	86	VAL
33	h	82	ASP
35	j	67	LEU
35	j	82	THR
41	p	16	THR
41	p	52	VAL
46	w	90	VAL
46	w	207	VAL
47	1	18	GLU
47	1	130	VAL
47	1	230	LEU
47	1	317	LEU
49	3	5	MET

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Mol	Chain	Res	Type
49	3	21	LEU
50	4	323	HIS
50	4	468	LEU
52	7	314	MET
53	6	51	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	HIS
1	A	205	ASN
4	D	63	GLN
4	D	198	HIS
4	D	275	GLN
6	F	125	ASN
7	G	147	GLN
9	I	163	GLN
10	J	104	ASN
12	M	48	GLN
13	N	91	GLN
14	O	167	HIS
15	P	25	HIS
16	Q	40	ASN
17	R	58	HIS
19	T	66	ASN
20	U	17	GLN
23	X	57	GLN
26	a	19	HIS
29	d	18	ASN
32	g	18	ASN
33	h	63	GLN
33	h	98	HIS
34	i	80	HIS
46	w	184	GLN
46	w	209	GLN
47	1	186	ASN
47	1	294	GLN
47	1	398	GLN
50	4	165	GLN
50	4	199	GLN
52	7	56	GLN
52	7	116	GLN

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Mol	Chain	Res	Type
52	7	349	HIS
52	7	409	GLN
53	6	152	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
42	q	74/77 (96%)	15 (20%)	0
44	u	119/120 (99%)	14 (11%)	0
45	v	155/156 (99%)	37 (23%)	0
54	K	3520/3543 (99%)	822 (23%)	58 (1%)
All	All	3868/3896 (99%)	888 (22%)	58 (1%)

All (888) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
42	q	9	A
42	q	13	U
42	q	16	C
42	q	19	G
42	q	20	U
42	q	20(A)	U
42	q	21	A
42	q	24	A
42	q	39	G
42	q	42	A
42	q	46	G
42	q	47	U
42	q	56	C
42	q	67	G
42	q	75	C
44	u	7	G
44	u	10	C
44	u	22	A
44	u	25	G
44	u	31	G
44	u	42	A
44	u	53	U
44	u	54	A
44	u	64	G
44	u	80	U

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Mol	Chain	Res	Type
44	u	100	A
44	u	110	G
44	u	111	C
44	u	120	U
45	v	2	G
45	v	3	A
45	v	13	G
45	v	20	A
45	v	23	C
45	v	32	C
45	v	34	U
45	v	35	C
45	v	38	U
45	v	49	G
45	v	59	A
45	v	62	A
45	v	63	U
45	v	75	G
45	v	80	A
45	v	81	C
45	v	82	A
45	v	83	C
45	v	84	A
45	v	85	U
45	v	86	U
45	v	87	G
45	v	103	A
45	v	105	C
45	v	106	G
45	v	109	C
45	v	110	U
45	v	111	U
45	v	112	G
45	v	114	G
45	v	123	U
45	v	125	C
45	v	126	C
45	v	127	U
45	v	128	C
45	v	153	C
45	v	156	U
54	K	12	A

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Mol	Chain	Res	Type
54	K	13	U
54	K	15	A
54	K	30	C
54	K	39	A
54	K	42	A
54	K	44	A
54	K	56	A
54	K	58	G
54	K	59	A
54	K	64	A
54	K	65	A
54	K	72	C
54	K	73	A
54	K	74	G
54	K	84	A
54	K	91	G
54	K	95	G
54	K	104	G
54	K	108	A
54	K	109	G
54	K	110	C
54	K	118	C
54	K	119	G
54	K	122	U
54	K	126	C
54	K	131	C
54	K	134	G
54	K	135	G
54	K	136	C
54	K	137	G
54	K	141	C
54	K	142	G
54	K	146	G
54	K	157	U
54	K	159	C
54	K	160	G
54	K	172	C
54	K	173	C
54	K	177	G
54	K	182	G
54	K	200	U
54	K	201	C

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Mol	Chain	Res	Type
54	K	209	U
54	K	216	C
54	K	218	A
54	K	221	C
54	K	224	U
54	K	225	G
54	K	232	G
54	K	233	U
54	K	234	G
54	K	246	G
54	K	256	G
54	K	258	G
54	K	262	G
54	K	263	G
54	K	265	C
54	K	266	C
54	K	267	G
54	K	276	C
54	K	280	G
54	K	297	U
54	K	306	A
54	K	308	G
54	K	309	C
54	K	315	G
54	K	316	U
54	K	322	C
54	K	326	C
54	K	334	A
54	K	340	C
54	K	363	A
54	K	370	U
54	K	371	A
54	K	387	G
54	K	407	A
54	K	410	A
54	K	412	G
54	K	413	G
54	K	415	G
54	K	417	G
54	K	428	G
54	K	440	U
54	K	446	C

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Mol	Chain	Res	Type
54	K	449	C
54	K	450	G
54	K	452	A
54	K	453	G
54	K	454	U
54	K	455	C
54	K	463	A
54	K	467	U
54	K	468	U
54	K	481	G
54	K	481(A)	C
54	K	482	G
54	K	483	G
54	K	485	C
54	K	486	C
54	K	492	U
54	K	493	G
54	K	496	G
54	K	497	G
54	K	498	C
54	K	499	G
54	K	505	G
54	K	506	C
54	K	510	U
54	K	644	G
54	K	647	G
54	K	658	C
54	K	659	G
54	K	661	C
54	K	666	G
54	K	667	A
54	K	668	C
54	K	669	C
54	K	670	G
54	K	685	C
54	K	686	A
54	K	687	U
54	K	696	C
54	K	697	G
54	K	699	C
54	K	701	G
54	K	704	C

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Mol	Chain	Res	Type
54	K	705	G
54	K	708	G
54	K	731	G
54	K	738	C
54	K	749	G
54	K	756	G
54	K	758	G
54	K	914	U
54	K	917	A
54	K	918	G
54	K	923	C
54	K	925	C
54	K	926	G
54	K	929	A
54	K	930	G
54	K	932	A
54	K	933	G
54	K	934	C
54	K	935	A
54	K	935(A)	G
54	K	936	C
54	K	938	C
54	K	939	G
54	K	941	C
54	K	944	A
54	K	945	U
54	K	959	G
54	K	960	A
54	K	961	G
54	K	964	A
54	K	965	G
54	K	966	A
54	K	967	C
54	K	968	C
54	K	969	C
54	K	971(A)	G
54	K	972	C
54	K	973	G
54	K	979	C
54	K	983	C
54	K	990	C
54	K	1070	G

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Mol	Chain	Res	Type
54	K	1072	C
54	K	1073	G
54	K	1076	C
54	K	1078	A
54	K	1079	C
54	K	1081	C
54	K	1082	C
54	K	1099	C
54	K	1175	A
54	K	1179	U
54	K	1199	G
54	K	1210	C
54	K	1211	G
54	K	1212	G
54	K	1215	C
54	K	1216	C
54	K	1234	G
54	K	1235	G
54	K	1236	C
54	K	1237	C
54	K	1238	A
54	K	1239	C
54	K	1272	C
54	K	1273	G
54	K	1274	A
54	K	1275	G
54	K	1281	G
54	K	1284	G
54	K	1287	G
54	K	1289	C
54	K	1291	G
54	K	1292	C
54	K	1293	G
54	K	1296	G
54	K	1301	C
54	K	1303	A
54	K	1304	C
54	K	1314	C
54	K	1326	A
54	K	1330	A
54	K	1354	A
54	K	1358	G

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Mol	Chain	Res	Type
54	K	1359	G
54	K	1364	U
54	K	1370	G
54	K	1371	A
54	K	1377	G
54	K	1378	C
54	K	1379	C
54	K	1387	A
54	K	1392	A
54	K	1394	G
54	K	1397	A
54	K	1398	A
54	K	1403	G
54	K	1411(A)	G
54	K	1415	G
54	K	1419	G
54	K	1420	A
54	K	1421	G
54	K	1433	A
54	K	1436	C
54	K	1437	C
54	K	1438	U
54	K	1440	U
54	K	1441	C
54	K	1445	U
54	K	1446	C
54	K	1448	G
54	K	1456	C
54	K	1457	G
54	K	1458	C
54	K	1475	G
54	K	1478	C
54	K	1481	C
54	K	1482	G
54	K	1483	C
54	K	1484	G
54	K	1489	G
54	K	1497	A
54	K	1498	G
54	K	1502	G
54	K	1514	U
54	K	1516	G

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Mol	Chain	Res	Type
54	K	1518	A
54	K	1519	C
54	K	1523	A
54	K	1534	A
54	K	1547	A
54	K	1563	A
54	K	1564	A
54	K	1566	C
54	K	1578	U
54	K	1586	G
54	K	1591	U
54	K	1596	U
54	K	1597	G
54	K	1600	A
54	K	1602	U
54	K	1612	G
54	K	1613	A
54	K	1624	G
54	K	1625	G
54	K	1631	A
54	K	1633	G
54	K	1634	A
54	K	1640	C
54	K	1654	G
54	K	1658	G
54	K	1661	C
54	K	1676	C
54	K	1677	U
54	K	1696	C
54	K	1731	C
54	K	1733	G
54	K	1741	G
54	K	1742	A
54	K	1750	G
54	K	1756	U
54	K	1760	G
54	K	1761	G
54	K	1764	G
54	K	1767	A
54	K	1768	C
54	K	1769	G
54	K	1772	C

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Mol	Chain	Res	Type
54	K	1774	C
54	K	1775	A
54	K	1780	A
54	K	1787	A
54	K	1798	G
54	K	1799	G
54	K	1804	A
54	K	1807	C
54	K	1809	C
54	K	1811	G
54	K	1815	G
54	K	1818	G
54	K	1819	G
54	K	1821	G
54	K	1822	U
54	K	1828	C
54	K	1834	U
54	K	1835	G
54	K	1836	G
54	K	1837	A
54	K	1842	G
54	K	1843	A
54	K	1847	C
54	K	1855	G
54	K	1869	G
54	K	1882	U
54	K	1889	U
54	K	1892	A
54	K	1897	A
54	K	1898	C
54	K	1916	G
54	K	1918	U
54	K	1920	C
54	K	1921	C
54	K	1922	G
54	K	1931	C
54	K	1932	A
54	K	1935	C
54	K	1940	G
54	K	1945	G
54	K	1947	U
54	K	1948	G

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Mol	Chain	Res	Type
54	K	1957	U
54	K	1958	A
54	K	1960	A
54	K	1961	G
54	K	1962	A
54	K	1963	C
54	K	1964	A
54	K	1965	G
54	K	1968	G
54	K	1969	G
54	K	1971	U
54	K	1974	U
54	K	1975	G
54	K	1976	G
54	K	1978	C
54	K	1979	A
54	K	1980	U
54	K	1984	A
54	K	1987	C
54	K	1988	G
54	K	1990	A
54	K	1991	A
54	K	1997	U
54	K	1999	A
54	K	2001	G
54	K	2002	A
54	K	2003	G
54	K	2004	U
54	K	2008	U
54	K	2011	C
54	K	2018	C
54	K	2020	U
54	K	2021	G
54	K	2022	C
54	K	2024	G
54	K	2026	A
54	K	2043	A
54	K	2046	G
54	K	2047	A
54	K	2048	U
54	K	2052	G
54	K	2053	C

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Mol	Chain	Res	Type
54	K	2055	G
54	K	2056	G
54	K	2063	G
54	K	2064	G
54	K	2069	A
54	K	2071	A
54	K	2084	U
54	K	2090	U
54	K	2092	G
54	K	2093	G
54	K	2094	C
54	K	2095	A
54	K	2097	A
54	K	2098	G
54	K	2099	C
54	K	2100	G
54	K	2101	A
54	K	2102	G
54	K	2104	A
54	K	2105	A
54	K	2107	A
54	K	2108	G
54	K	2110	G
54	K	2259	G
54	K	2260	C
54	K	2267	U
54	K	2268	A
54	K	2269	C
54	K	2275	G
54	K	2277	C
54	K	2279	A
54	K	2289	C
54	K	2294	G
54	K	2299	G
54	K	2300	A
54	K	2301	G
54	K	2306	G
54	K	2313	A
54	K	2314	G
54	K	2316	G
54	K	2331	G
54	K	2333	G

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Mol	Chain	Res	Type
54	K	2335	C
54	K	2348	G
54	K	2351	C
54	K	2364	G
54	K	2382	A
54	K	2395	A
54	K	2396	A
54	K	2398	U
54	K	2417	A
54	K	2422	C
54	K	2424	G
54	K	2425	U
54	K	2431	A
54	K	2433	G
54	K	2441	C
54	K	2447	U
54	K	2450	G
54	K	2453	A
54	K	2469	C
54	K	2475	G
54	K	2476	G
54	K	2487	G
54	K	2488	C
54	K	2489	C
54	K	2490	U
54	K	2491	C
54	K	2492	C
54	K	2498	C
54	K	2503	G
54	K	2504	C
54	K	2505	C
54	K	2506	G
54	K	2511	A
54	K	2512	A
54	K	2513	A
54	K	2527	A
54	K	2529	A
54	K	2530	U
54	K	2536	A
54	K	2537	A
54	K	2546	G
54	K	2547	G

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Mol	Chain	Res	Type
54	K	2553	A
54	K	2554	U
54	K	2566	G
54	K	2568	C
54	K	2570	U
54	K	2575	U
54	K	2583	C
54	K	2586	G
54	K	2587	A
54	K	2588	C
54	K	2599	G
54	K	2600	A
54	K	2602	G
54	K	2618	G
54	K	2620	G
54	K	2621	A
54	K	2627	C
54	K	2638	G
54	K	2653	C
54	K	2662	G
54	K	2669	C
54	K	2673	G
54	K	2674	A
54	K	2676	A
54	K	2677	G
54	K	2686	G
54	K	2687	U
54	K	2695	A
54	K	2696	A
54	K	2705	G
54	K	2707	U
54	K	2708	U
54	K	2709	C
54	K	2711	G
54	K	2714	G
54	K	2721	G
54	K	2725	A
54	K	2726	G
54	K	2740	U
54	K	2743	A
54	K	2760	G
54	K	2761	U

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Mol	Chain	Res	Type
54	K	2763	U
54	K	2764	A
54	K	2769	U
54	K	2772	C
54	K	2787	A
54	K	2788	U
54	K	2790	U
54	K	2794	C
54	K	2798	A
54	K	2803	U
54	K	2807	A
54	K	2808	G
54	K	2822	G
54	K	2826	U
54	K	2827	G
54	K	2828	U
54	K	2834	C
54	K	2842	G
54	K	2850	A
54	K	2855	G
54	K	2867	C
54	K	2875	C
54	K	2879	A
54	K	2895	A
54	K	3598	C
54	K	3603	G
54	K	3604	A
54	K	3605	C
54	K	3616	U
54	K	3617	G
54	K	3618	C
54	K	3622	C
54	K	3625	G
54	K	3626	G
54	K	3630	A
54	K	3635	A
54	K	3644	U
54	K	3646	A
54	K	3648	A
54	K	3649	A
54	K	3657	U
54	K	3662	A

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Mol	Chain	Res	Type
54	K	3664	G
54	K	3672	G
54	K	3673	C
54	K	3674	G
54	K	3682	A
54	K	3692	A
54	K	3696	C
54	K	3702	A
54	K	3711	A
54	K	3714	G
54	K	3728	A
54	K	3729	U
54	K	3743	G
54	K	3748	A
54	K	3750	G
54	K	3753	G
54	K	3756	A
54	K	3760	A
54	K	3763	A
54	K	3767	C
54	K	3772	U
54	K	3773	U
54	K	3776	G
54	K	3777	G
54	K	3780	G
54	K	3783	A
54	K	3784	A
54	K	3786	U
54	K	3787	G
54	K	3809	G
54	K	3810	C
54	K	3811	G
54	K	3814	U
54	K	3817	A
54	K	3819	G
54	K	3822	U
54	K	3824	A
54	K	3838	U
54	K	3840	U
54	K	3876	A
54	K	3877	A
54	K	3878	C

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Mol	Chain	Res	Type
54	K	3879	G
54	K	3880	G
54	K	3889	G
54	K	3897	G
54	K	3901	A
54	K	3904	G
54	K	3905	A
54	K	3906	A
54	K	3907	G
54	K	3908	A
54	K	3915	U
54	K	3916	G
54	K	3917	A
54	K	3923	A
54	K	3926	C
54	K	3938	G
54	K	3939	G
54	K	3943	A
54	K	3946	G
54	K	4066	U
54	K	4069	U
54	K	4070	U
54	K	4076	G
54	K	4084	G
54	K	4086	G
54	K	4088	C
54	K	4097	G
54	K	4111	U
54	K	4116	C
54	K	4118	U
54	K	4119	C
54	K	4120	U
54	K	4121	G
54	K	4127	A
54	K	4128	A
54	K	4133	C
54	K	4136	G
54	K	4158	C
54	K	4162	C
54	K	4163	U
54	K	4166	G
54	K	4170	A

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Mol	Chain	Res	Type
54	K	4171	C
54	K	4183	G
54	K	4184	G
54	K	4191	G
54	K	4203	A
54	K	4212	A
54	K	4215	C
54	K	4225	G
54	K	4229	U
54	K	4233	A
54	K	4237	C
54	K	4251	A
54	K	4254	G
54	K	4265	U
54	K	4266	G
54	K	4267	G
54	K	4268	A
54	K	4271	A
54	K	4273	A
54	K	4281	A
54	K	4282	A
54	K	4291	G
54	K	4297	G
54	K	4304	A
54	K	4305	G
54	K	4306	U
54	K	4314	C
54	K	4317	A
54	K	4324	A
54	K	4329	G
54	K	4330	G
54	K	4332	C
54	K	4339	A
54	K	4349	C
54	K	4354	U
54	K	4355	G
54	K	4364	G
54	K	4373	G
54	K	4376	A
54	K	4377	G
54	K	4378	A
54	K	4379	A

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Mol	Chain	Res	Type
54	K	4380	A
54	K	4387	C
54	K	4391	G
54	K	4393	G
54	K	4394	A
54	K	4395	U
54	K	4398	C
54	K	4401	G
54	K	4419	U
54	K	4421	C
54	K	4422	A
54	K	4430	G
54	K	4437	U
54	K	4438	U
54	K	4444	C
54	K	4448	G
54	K	4449	A
54	K	4452	U
54	K	4453	C
54	K	4464	A
54	K	4466	C
54	K	4471	U
54	K	4472	G
54	K	4473	A
54	K	4475	G
54	K	4488	A
54	K	4489	G
54	K	4500	U
54	K	4512	U
54	K	4513	A
54	K	4515	G
54	K	4519	C
54	K	4522	G
54	K	4523	A
54	K	4524	G
54	K	4528	G
54	K	4535	A
54	K	4548	A
54	K	4549	G
54	K	4560	C
54	K	4562	C
54	K	4567	G

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Mol	Chain	Res	Type
54	K	4570	G
54	K	4573	G
54	K	4574	U
54	K	4575	G
54	K	4584	A
54	K	4585	U
54	K	4587	G
54	K	4590	A
54	K	4605	A
54	K	4636	U
54	K	4637	G
54	K	4639	G
54	K	4652	G
54	K	4656	A
54	K	4657	U
54	K	4661	G
54	K	4670	C
54	K	4672	A
54	K	4677	U
54	K	4687	A
54	K	4694	G
54	K	4709	U
54	K	4719	G
54	K	4720	C
54	K	4722	G
54	K	4728	U
54	K	4736	C
54	K	4738	C
54	K	4744	A
54	K	4745	G
54	K	4750	G
54	K	4751	G
54	K	4752	U
54	K	4754	G
54	K	4757	C
54	K	4759	C
54	K	4761	G
54	K	4764	A
54	K	4765	G
54	K	4771	C
54	K	4772	C
54	K	4868	G

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Mol	Chain	Res	Type
54	K	4870	G
54	K	4871	C
54	K	4875	G
54	K	4882	U
54	K	4883	C
54	K	4885	U
54	K	4895	C
54	K	4896	G
54	K	4897	G
54	K	4903	G
54	K	4909	A
54	K	4910	A
54	K	4912	G
54	K	4913	G
54	K	4919	G
54	K	4921	C
54	K	4922	C
54	K	4924	C
54	K	4925	U
54	K	4926	C
54	K	4927	G
54	K	4928	C
54	K	4931	G
54	K	4935	C
54	K	4937	C
54	K	4940	C
54	K	4943	A
54	K	4944	C
54	K	4948	C
54	K	4949	G
54	K	4950	U
54	K	4951	G
54	K	4955	A
54	K	4956	A
54	K	4957	C
54	K	4958	C
54	K	4960	G
54	K	4963	G
54	K	4965	U
54	K	4966	A
54	K	4967	A
54	K	4976	U

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Mol	Chain	Res	Type
54	K	4977	A
54	K	4985	U
54	K	4988	U
54	K	4989	U
54	K	4990	C
54	K	4991	U
54	K	4993	G
54	K	5006	U
54	K	5014	A
54	K	5016	A
54	K	5017	G
54	K	5022	U
54	K	5040	U
54	K	5041	G
54	K	5047	C
54	K	5050	C
54	K	5052	C
54	K	5053	U
54	K	5054	C
54	K	5056	A
54	K	5058	A
54	K	5061	A
54	K	5062	G

All (58) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	K	12	A
54	K	125	C
54	K	134	G
54	K	245	C
54	K	265	C
54	K	275	C
54	K	406	C
54	K	449	C
54	K	480	C
54	K	485	C
54	K	498	C
54	K	504	G
54	K	684	G
54	K	685	C
54	K	696	C

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Mol	Chain	Res	Type
54	K	704	C
54	K	935(A)	G
54	K	959	G
54	K	971(A)	G
54	K	1072	C
54	K	1174	G
54	K	1211	G
54	K	1236	C
54	K	1238	A
54	K	1329	G
54	K	1370	G
54	K	1440	U
54	K	1445	U
54	K	1455	G
54	K	1477	C
54	K	1482	G
54	K	1633	G
54	K	1818	G
54	K	2046	G
54	K	2089	G
54	K	2266	C
54	K	2468	U
54	K	2488	C
54	K	2502	A
54	K	2546	G
54	K	2695	A
54	K	3603	G
54	K	3625	G
54	K	3876	A
54	K	3888	G
54	K	3904	G
54	K	4119	C
54	K	4170	A
54	K	4232	U
54	K	4354	U
54	K	4378	A
54	K	4448	G
54	K	4719	G
54	K	4884	G
54	K	4921	C
54	K	4925	U
54	K	4947	U

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Mol	Chain	Res	Type
54	K	4989	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 225 ligands modelled in this entry, 225 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
54	K	25

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	2113:G	O3'	2258:C	P	40.63
1	K	1252:C	O3'	1271:G	P	36.90

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	1219:G	O3'	1233:G	P	19.23
1	K	3948:C	O3'	4065:G	P	18.79
1	K	4138:C	O3'	4146:G	P	18.12
1	K	990:C	O3'	1064:G	P	17.54
1	K	1696:C	O3'	1720:C	P	16.44
1	K	523:C	O3'	638:G	P	16.21
1	K	4777:C	O3'	4859:C	P	16.19
1	K	5022:U	O3'	5028:G	P	16.09
1	K	1406(C):G	O3'	1411:C	P	15.82
1	K	4101:C	O3'	4107:G	P	15.03
1	K	760:G	O3'	904:C	P	13.89
1	K	1364:U	O3'	1368:A	P	13.51
1	K	182:G	O3'	189:G	P	12.54
1	K	2901:G	O3'	3597:G	P	12.45
1	K	4729:A	O3'	4735:G	P	9.07
1	K	1180:C	O3'	1183:C	P	8.56
1	K	1100:U	O3'	1168:G	P	8.11
1	K	512:U	O3'	515:C	P	6.98
1	K	500:G	O3'	504:G	P	5.70
1	K	4740:G	O3'	4743:G	P	4.85
1	K	1239:C	O3'	1244:G	P	4.61
1	K	4899:G	O3'	4902:C	P	3.31
1	K	751:G	O3'	752:G	P	2.87

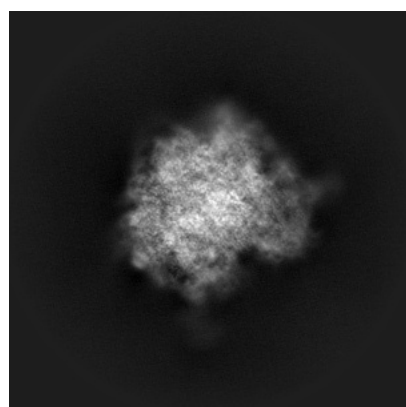
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25994. These allow visual inspection of the internal detail of the map and identification of artifacts.

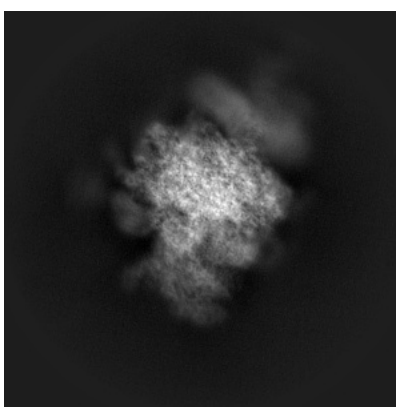
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

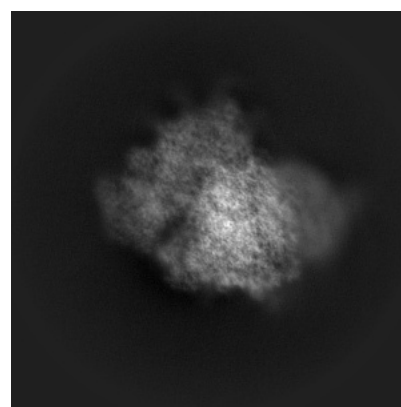
6.1.1 Primary map



X



Y

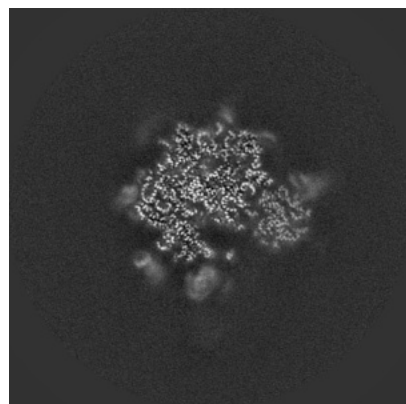


Z

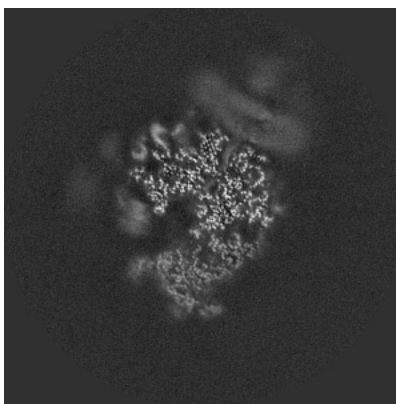
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

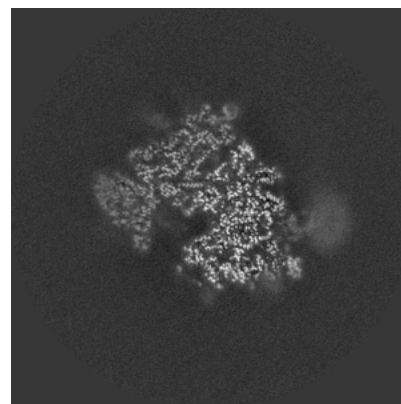
6.2.1 Primary map



X Index: 206



Y Index: 206

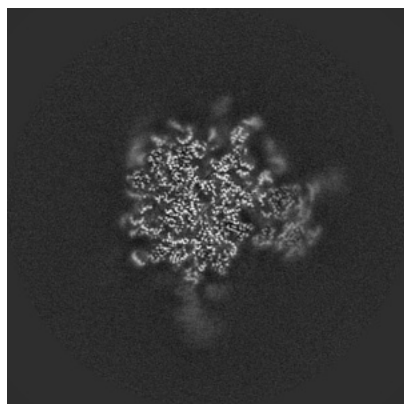


Z Index: 206

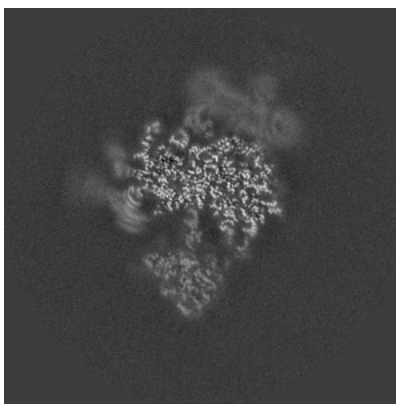
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

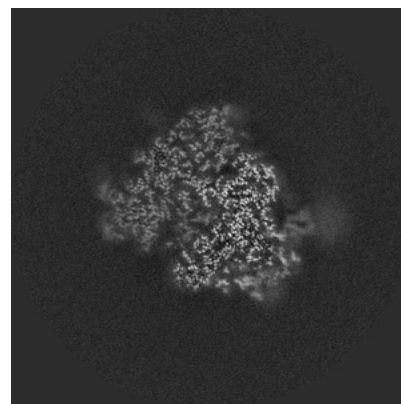
6.3.1 Primary map



X Index: 224



Y Index: 193

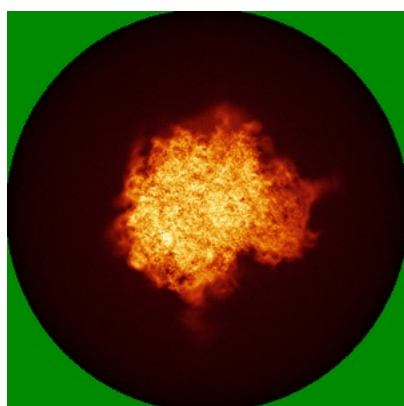


Z Index: 196

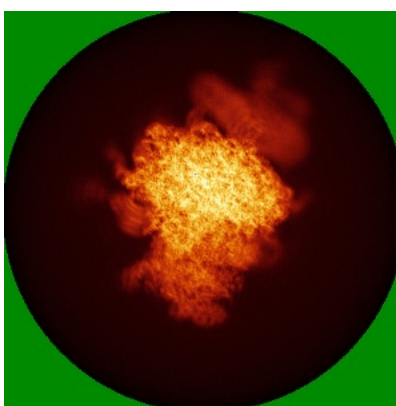
The images above show the largest variance slices of the map in three orthogonal directions.

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

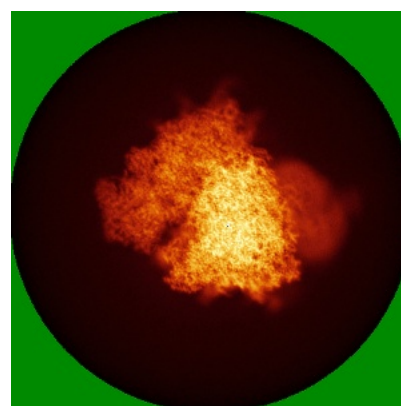
6.4.1 Primary map



X



Y

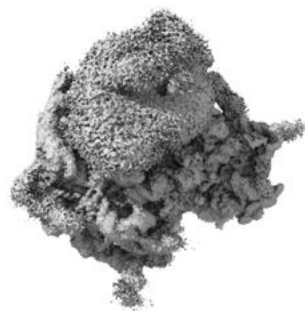


Z

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](#)

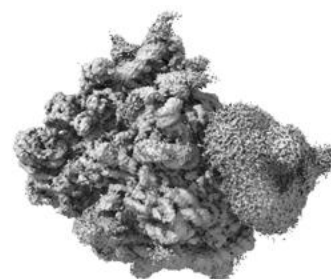
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

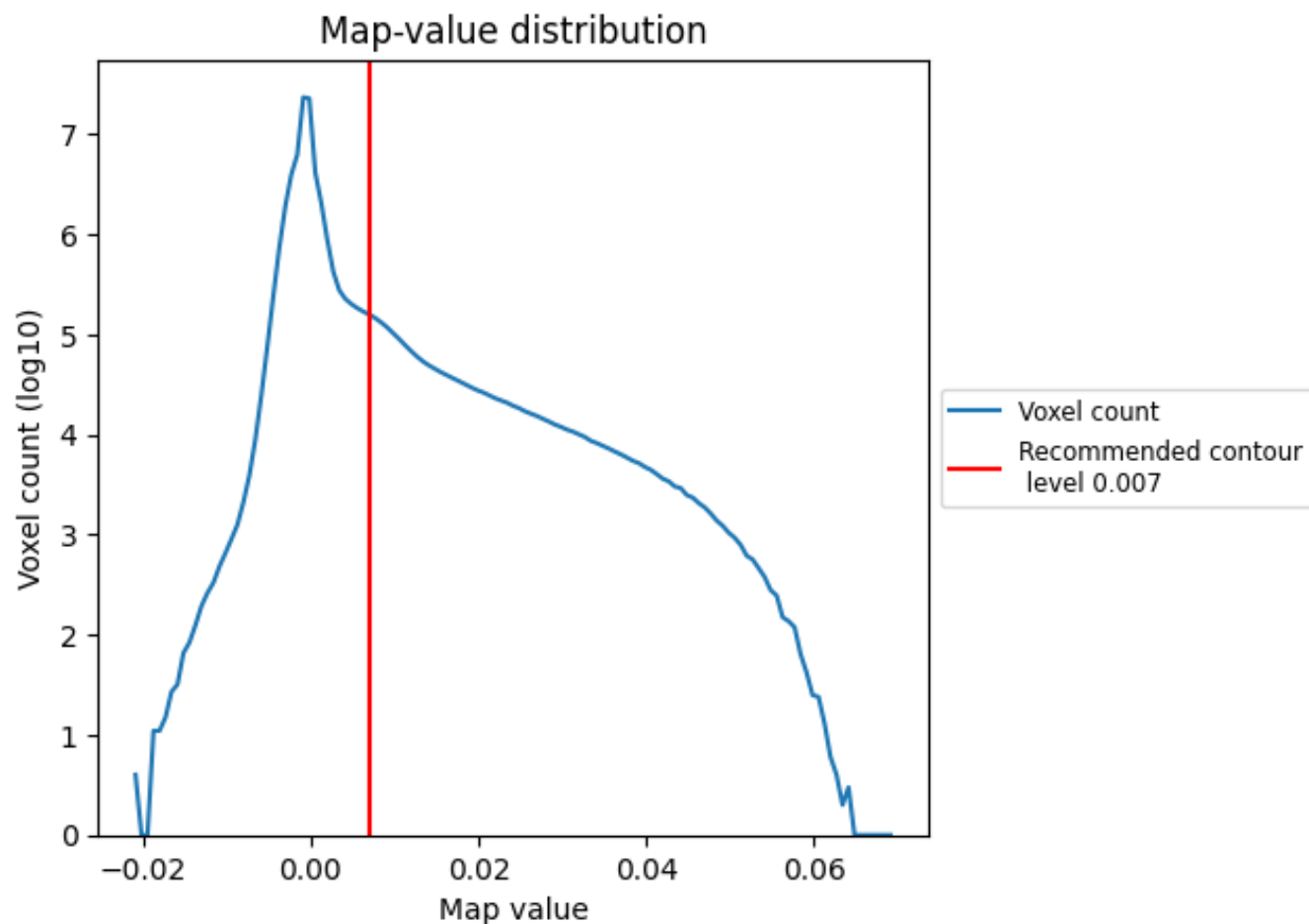
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

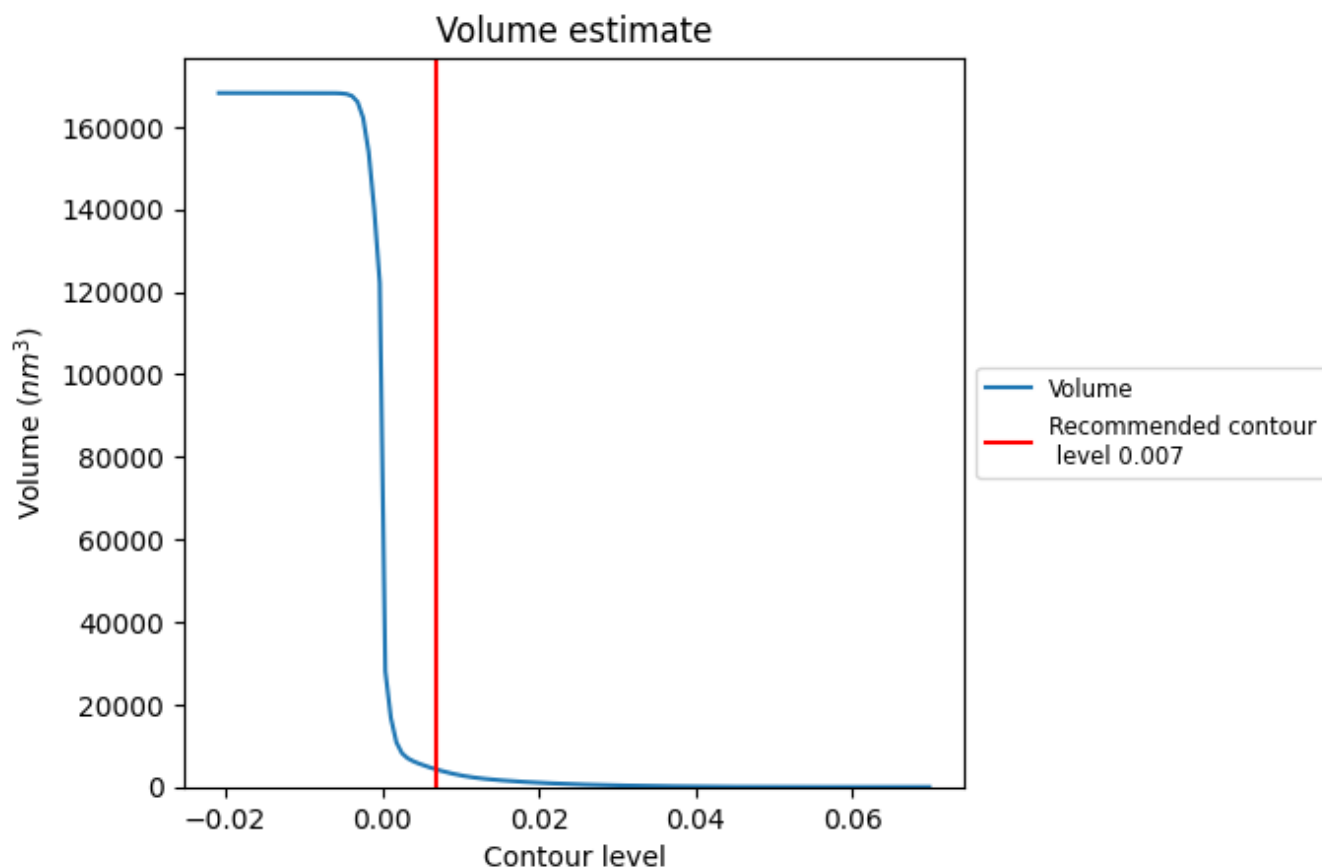
This section contains the results of statistical analysis of the map.

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.

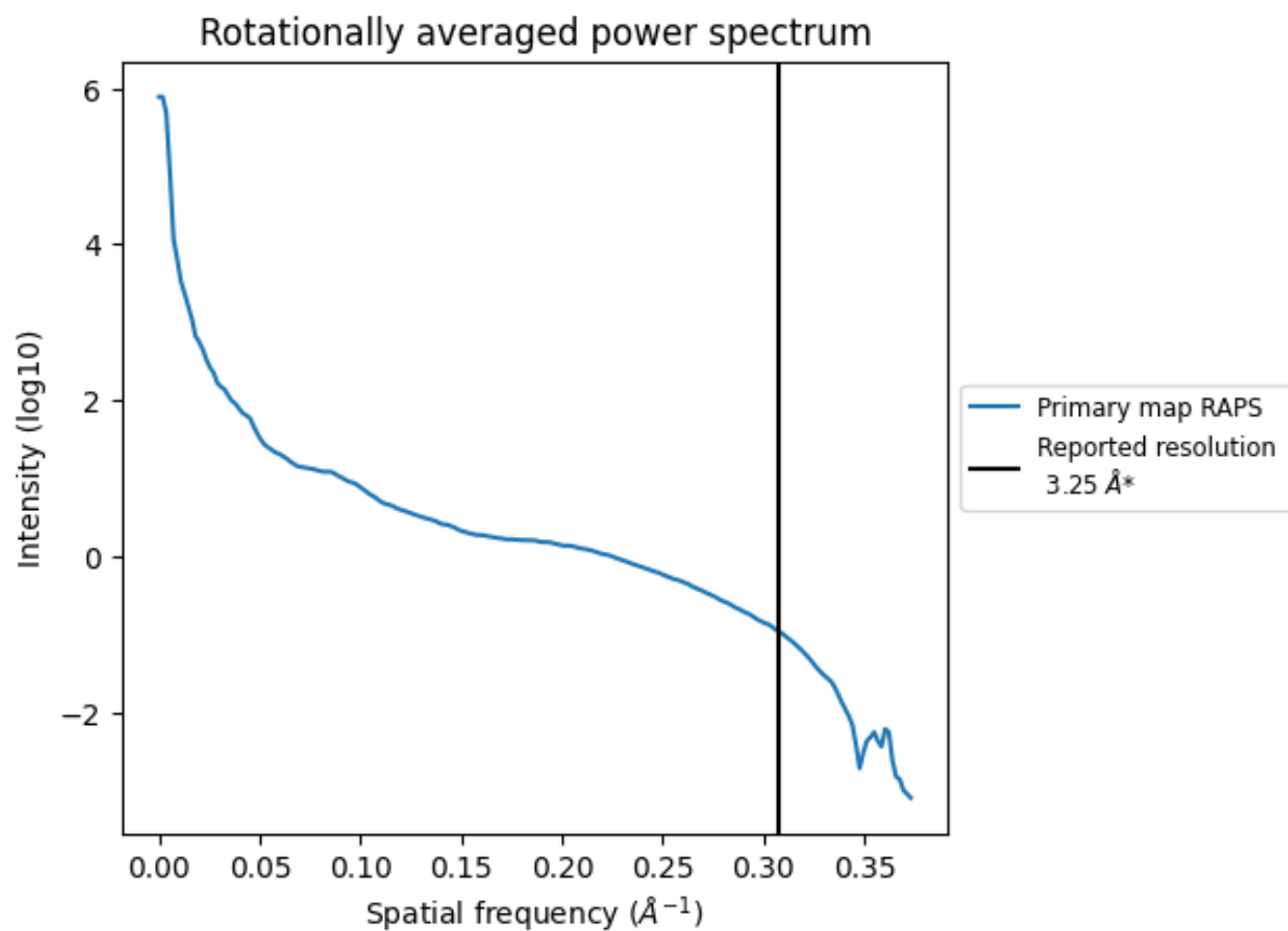
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4210 nm^3 ; this corresponds to an approximate mass of 3803 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 0.308 Å⁻¹

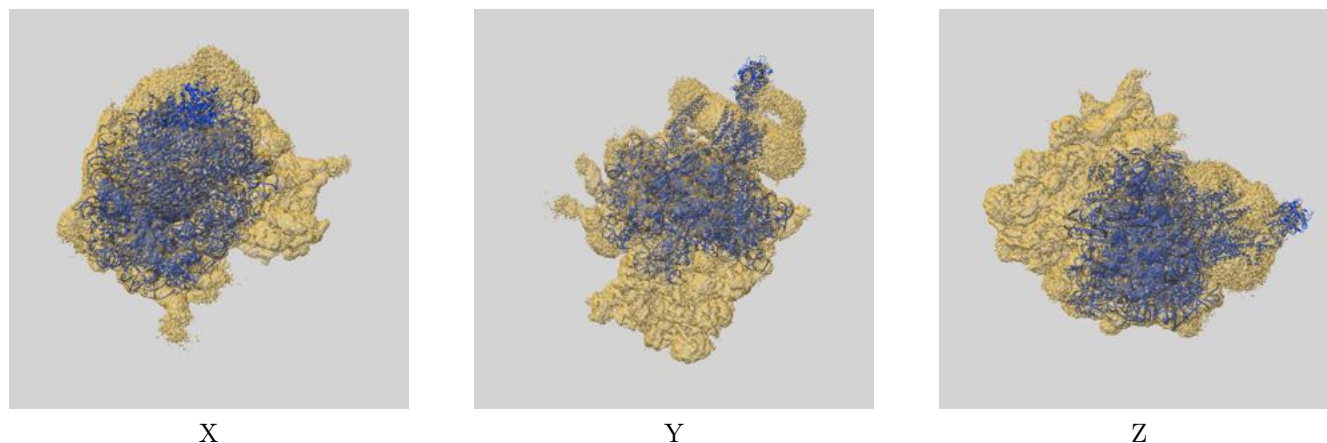
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

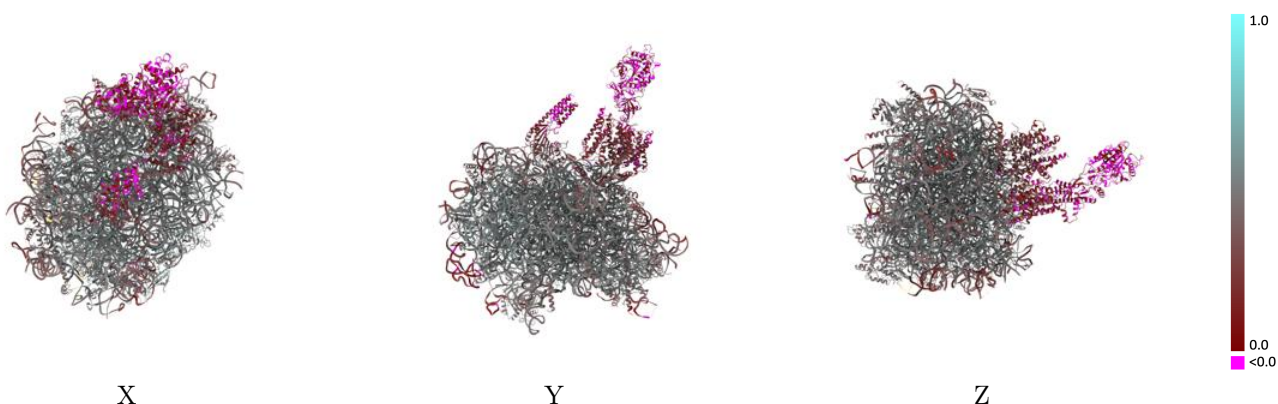
This section contains information regarding the fit between EMDB map EMD-25994 and PDB model 7TM3. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



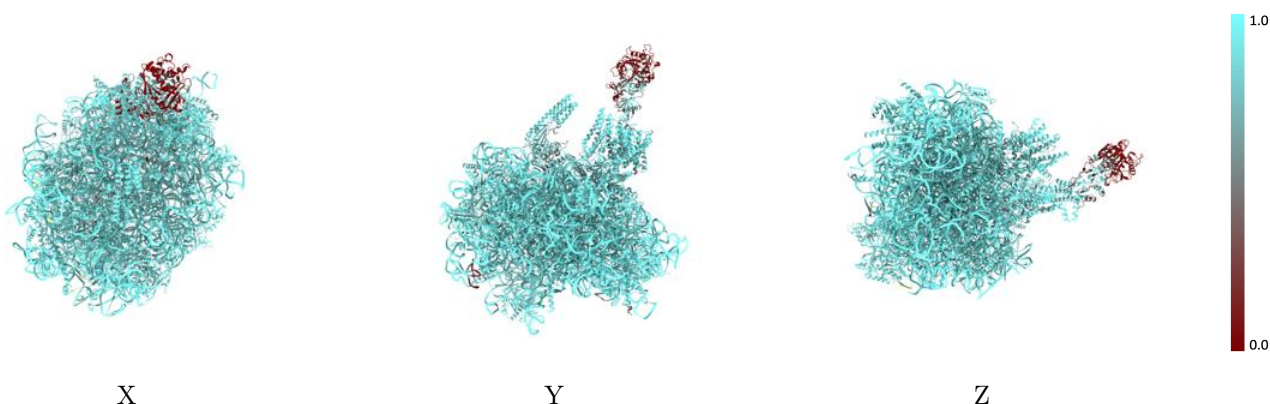
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



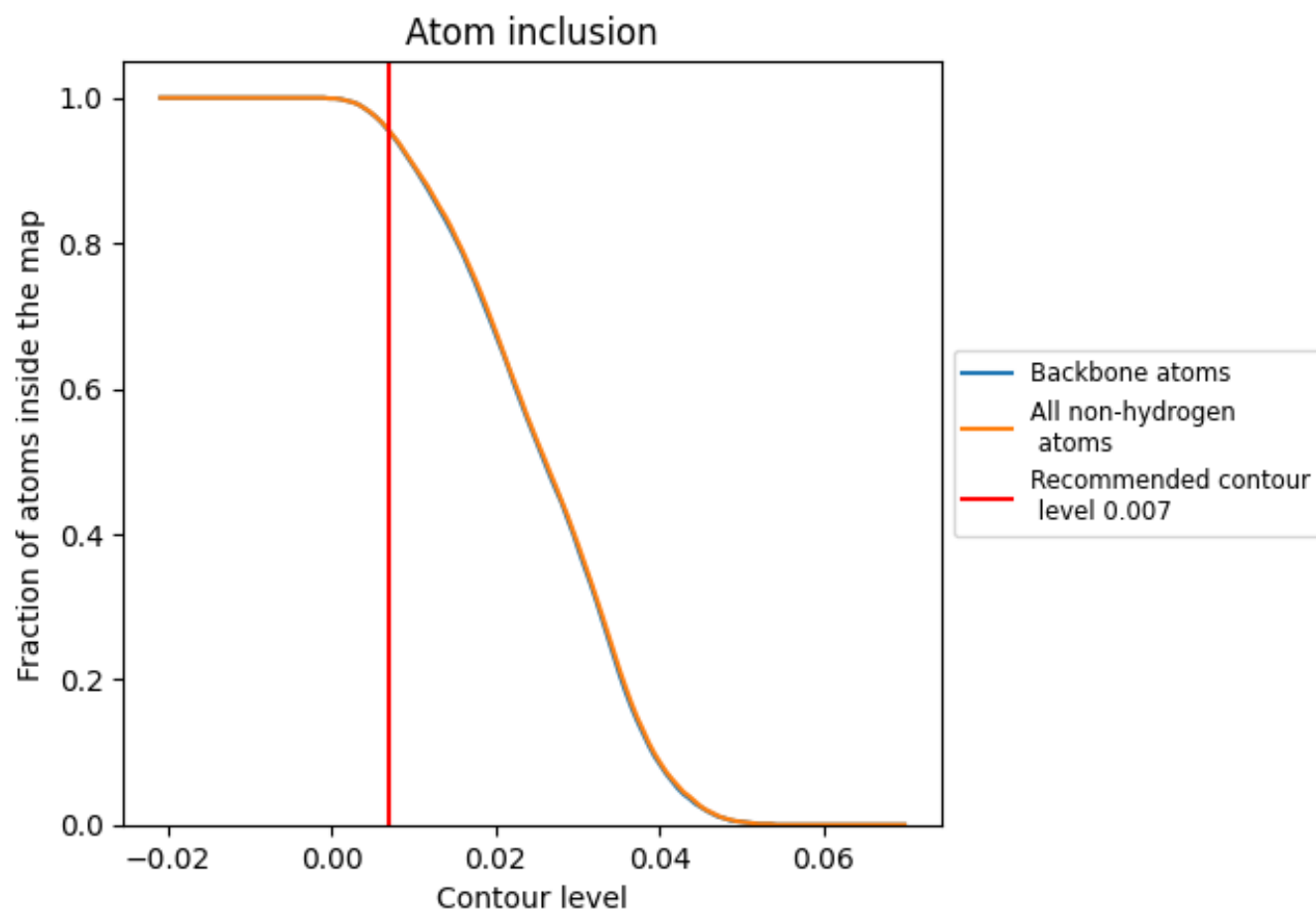
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 96% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9550	 0.4340
1	 0.8860	 0.2370
2	 0.9160	 0.1090
3	 0.8920	 0.2370
4	 0.7890	 0.2040
5	 0.8890	 0.0330
6	 0.8760	 0.1460
7	 0.3910	 0.0360
A	 0.9700	 0.5070
B	 0.9380	 0.3230
C	 0.9760	 0.4970
D	 0.9690	 0.4510
E	 0.9580	 0.4530
F	 0.9660	 0.4930
G	 0.9440	 0.4320
H	 0.9590	 0.4780
I	 0.9690	 0.4940
J	 0.9580	 0.4330
K	 0.9920	 0.4550
L	 0.9520	 0.4610
M	 0.9700	 0.4770
N	 0.9750	 0.5040
O	 0.9710	 0.4930
P	 0.9550	 0.4920
Q	 0.9770	 0.5040
R	 0.9560	 0.4660
S	 0.9760	 0.5050
T	 0.9620	 0.4830
U	 0.9350	 0.3940
V	 0.9680	 0.5100
W	 0.9610	 0.4900
X	 0.9490	 0.4690
Y	 0.9310	 0.4710
Z	 0.9680	 0.4620
a	 0.9810	 0.5030



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Chain	Atom inclusion	Q-score
b	 0.9460	 0.4210
c	 0.9490	 0.4500
d	 0.9460	 0.4690
e	 0.9710	 0.5100
f	 0.9790	 0.5240
g	 0.9530	 0.4730
h	 0.9340	 0.4560
i	 0.9520	 0.4510
j	 0.9810	 0.5080
k	 0.8890	 0.4190
l	 0.9650	 0.4830
m	 0.9710	 0.4900
n	 0.8990	 0.3970
o	 0.9650	 0.4910
p	 0.9550	 0.4660
q	 0.9480	 0.4000
r	 0.9750	 0.4960
u	 0.9970	 0.4790
v	 0.9970	 0.4530
w	 0.9720	 0.5050