



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 03:01 AM UTC

PDB ID : 7TUT / pdb_00007tut
EMDB ID : EMD-26133
Title : Structure of the rabbit 80S ribosome stalled on a 4-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 : 2022-02-03
Resolution : 3.88 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

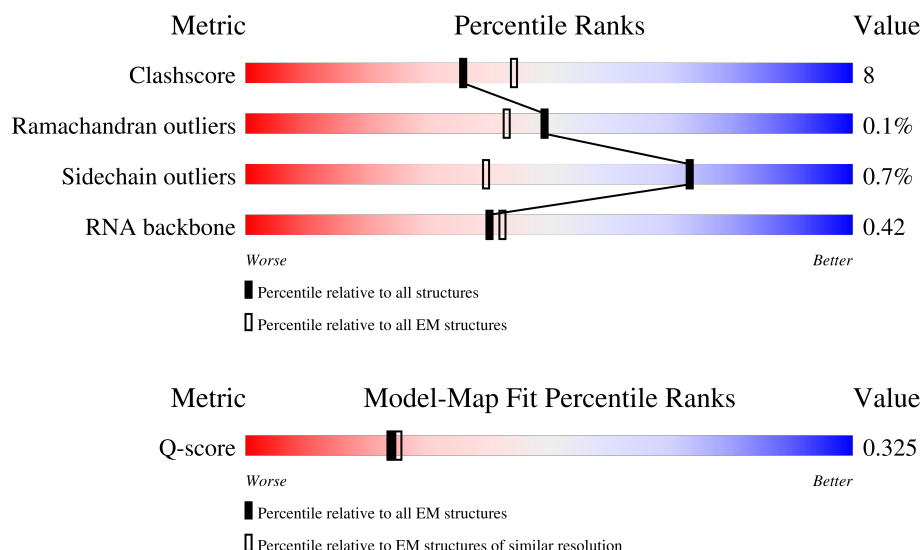
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.88 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	8773 (3.38 - 4.38)

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	C	413	
3	D	297	

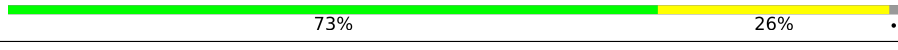
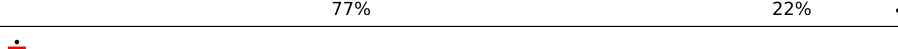
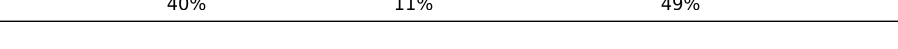
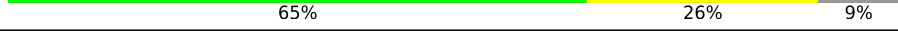
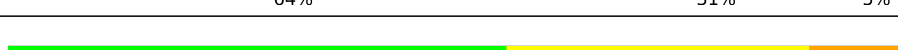
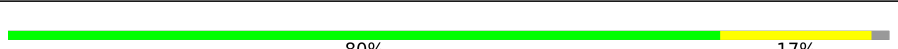
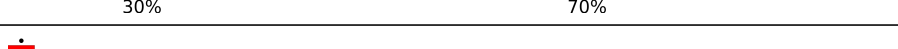
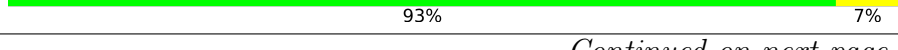
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Mol	Chain	Length	Quality of chain
4	E	291	
5	F	247	
6	G	319	
7	H	192	
8	I	214	
9	J	178	
10	L	211	
11	M	218	
12	N	204	
13	O	203	
14	P	184	
15	Q	188	
16	R	196	
17	S	176	
18	T	160	
19	U	128	
20	V	140	
21	W	157	
22	X	156	
23	Y	145	
24	Z	136	
25	a	148	
26	b	226	
27	c	115	
28	d	125	

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Mol	Chain	Length	Quality of chain
29	e	135	
30	f	110	
31	g	116	
32	h	123	
33	i	105	
34	j	97	
35	k	70	
36	l	51	
37	m	102	
38	n	25	
39	o	106	
40	p	92	
41	q	77	
42	r	137	
43	u	120	
44	v	156	
45	w	403	
46	B	273	
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	8	188	29% 77% 17% 6%
55	K	3543	51% 38% 11%
56	9	129	26% 74% 11% 16%

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 267107 atoms, of which 114508 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 uL4.

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

- Molecule 3 is a protein called uL18.

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

- Molecule 4 is a protein called eL6.

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

- Molecule 5 is a protein called uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	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

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Chain	Residue	Modelled	Actual	Comment	Reference
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 6 is a protein called eL8.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	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 7 is a protein called uL6.

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

- Molecule 8 is a protein called uL16.

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

- Molecule 9 is a protein called uL5.

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

- Molecule 10 is a protein called eL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 11 is a protein called eL14.

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

- Molecule 12 is a protein called eL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	N	202	Total	C	H	N	O	S	0	0
			3441	1069	1745	358	265	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	2	GLY	ALA	conflict	UNP G1T0C1

- Molecule 13 is a protein called uL13.

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

- Molecule 14 is a protein called uL22.

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

- Molecule 15 is a protein called eL18.

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

- Molecule 16 is a protein called eL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	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 17 is a protein called eL20.

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

- Molecule 18 is a protein called eL21.

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

- Molecule 19 is a protein called eL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	U	102	Total	C	H	N	O	S	0	0
			1690	534	856	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 20 is a protein called uL14.

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

- Molecule 21 is a protein called eL24.

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

- Molecule 22 is a protein called eL23.

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

- Molecule 23 is a protein called uL24.

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

- Molecule 24 is a protein called eL27.

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

- Molecule 25 is a protein called uL15.

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

- Molecule 26 is a protein called eL29.

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

- Molecule 27 is a protein called eL30.

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

- Molecule 28 is a protein called eL31.

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

- Molecule 29 is a protein called eL32.

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

- Molecule 30 is a protein called eL33.

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

- Molecule 31 is a protein called eL34.

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

- Molecule 32 is a protein called eL35.

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

- Molecule 33 is a protein called eL36.

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

- Molecule 34 is a protein called eL37.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	j	86	Total	C	H	N	O	S	0	0
			1443	434	738	155	111	5		

- Molecule 35 is a protein called eL38.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	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 36 is a protein called eL39.

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

- Molecule 37 is a protein called eL40.

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

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	1	MET	-	initiating methionine	UNP A0A2K5PSA0

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Chain	Residue	Modelled	Actual	Comment	Reference
m	2	GLY	-	expression tag	UNP A0A2K5PSA0
m	3	ASP	-	expression tag	UNP A0A2K5PSA0
m	4	PRO	-	expression tag	UNP A0A2K5PSA0
m	5	GLU	-	expression tag	UNP A0A2K5PSA0
m	6	SER	-	expression tag	UNP A0A2K5PSA0
m	7	GLY	-	expression tag	UNP A0A2K5PSA0
m	8	GLY	-	expression tag	UNP A0A2K5PSA0
m	9	CYS	-	expression tag	UNP A0A2K5PSA0

- Molecule 38 is a protein called eL41.

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

- Molecule 39 is a protein called eL42.

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

- Molecule 40 is a protein called eL43.

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

- Molecule 41 is a RNA chain called P-site tRNA.

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

- Molecule 42 is a protein called eL28.

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

- Molecule 43 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	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 44 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 45 is a protein called uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	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 46 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	B	70	Total	C	H	N	O	S	0	0
			1054	349	528	84	87	6		

- 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
			5595	1738	2817	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 protein called Calcium load-activated calcium channel.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	8	177	Total	C	H	N	O	S	0	0
			2884	900	1478	242	252	12		

- Molecule 55 is a RNA chain called 28S ribosomal RNA.

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

- Molecule 56 is a protein called Obligate partner of TMCO1 insertase.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	9	109	Total	C	H	N	O	S	0	0
			1784	610	881	134	156	3		

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	C	1	Total	Mg	0
			1	1	
57	D	1	Total	Mg	0
			1	1	
57	I	2	Total	Mg	0
			2	2	
57	J	1	Total	Mg	0
			1	1	
57	P	1	Total	Mg	0
			1	1	
57	V	1	Total	Mg	0
			1	1	
57	a	1	Total	Mg	0
			1	1	
57	u	4	Total	Mg	0
			4	4	
57	v	6	Total	Mg	0
			6	6	
57	K	202	Total	Mg	0
			202	202	

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	g	1	Total	Zn	0
			1	1	
58	j	1	Total	Zn	0
			1	1	
58	m	1	Total	Zn	0
			1	1	

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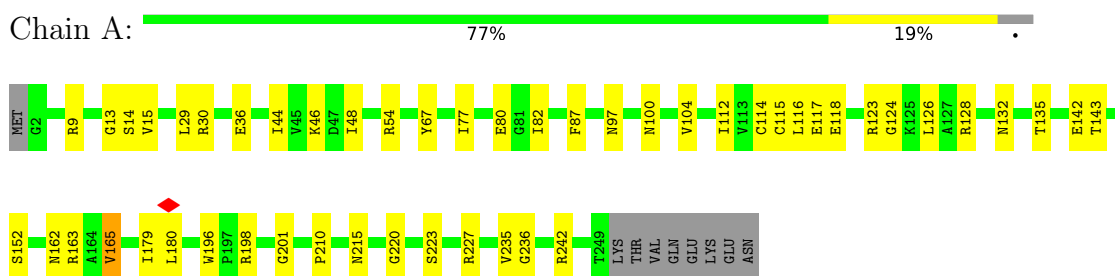
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
58	o	1	Total 1	Zn 1	0
58	p	1	Total 1	Zn 1	0

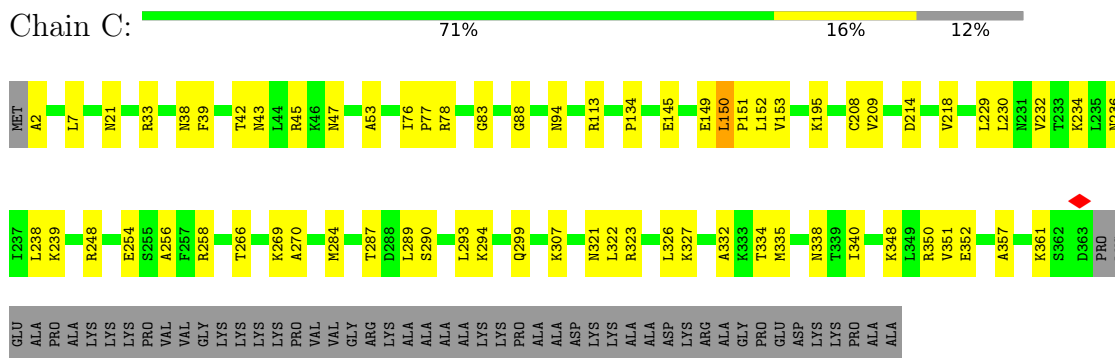
3 Residue-property plots

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.

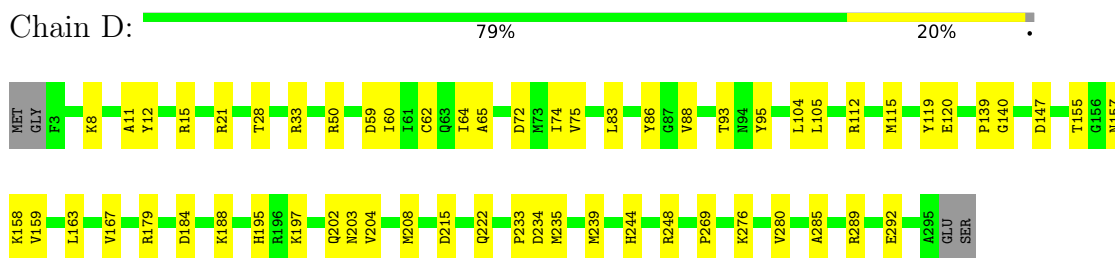
• Molecule 1: uL2



• Molecule 2: uL4



• Molecule 3: uL18



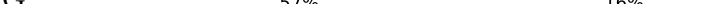
• Molecule 4: eL6



- Molecule 5: uL30

Chain F:  70% 21% 9%

- Molecule 6: eL8

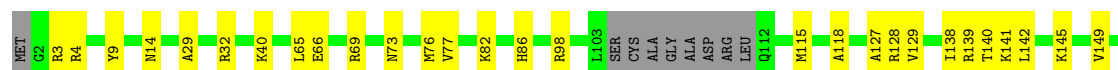
Chain G:  57% 16% 27%

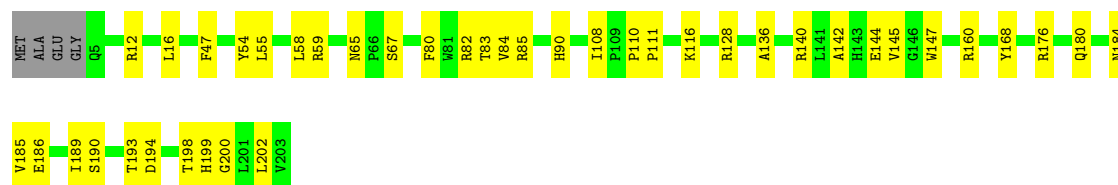
- Molecule 7: uL6

Chain H: 75% 23%

- Molecule 8: uL16

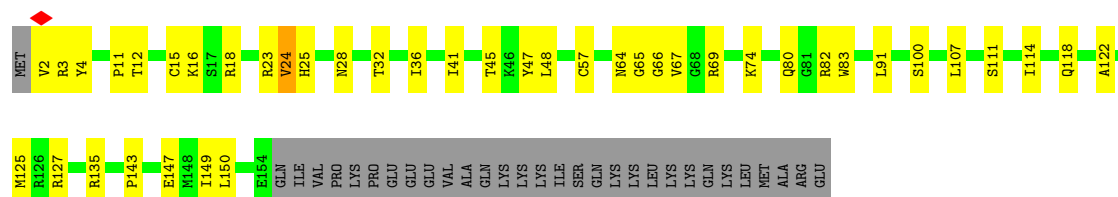
Chain I:  79% 16% 5%





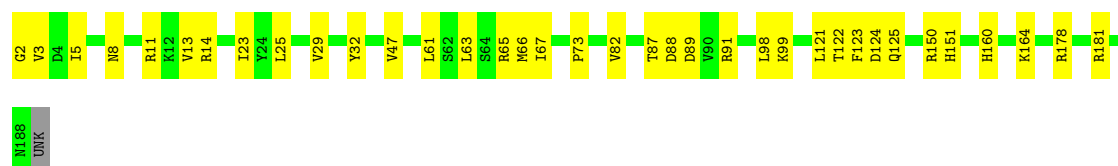
• Molecule 14: uL22

Chain P: 60% 22% 17%



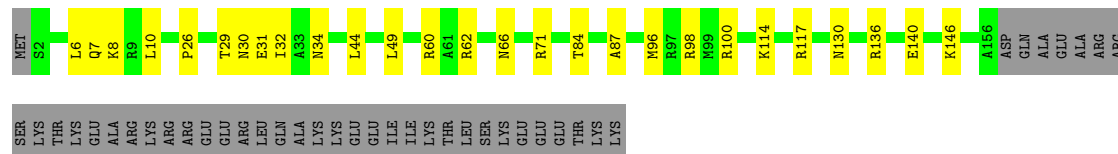
• Molecule 15: eL18

Chain Q: 80% 19%



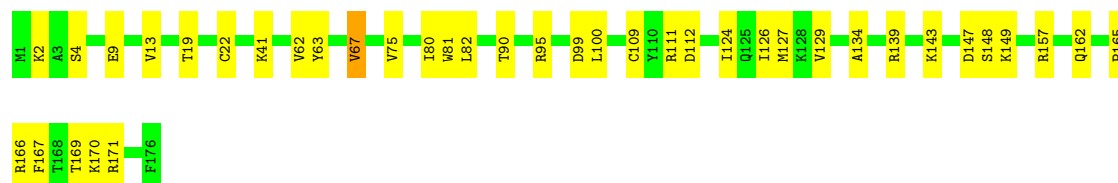
• Molecule 16: eL19

Chain R: 65% 14% 21%



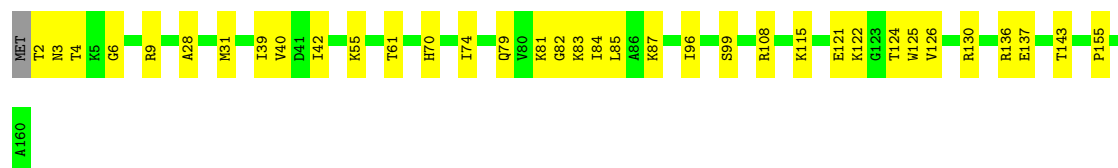
• Molecule 17: eL20

Chain S: 78% 22%

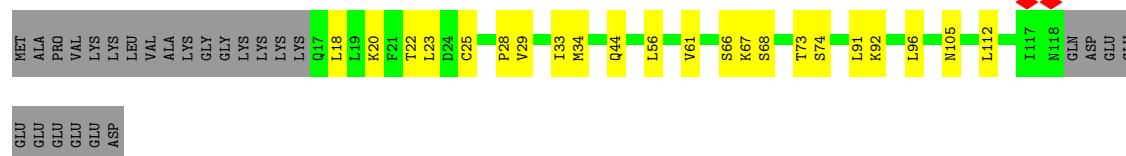


• Molecule 18: eL21

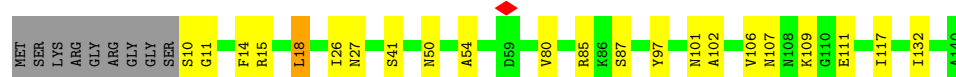
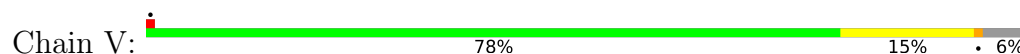
Chain T: 78% 22%



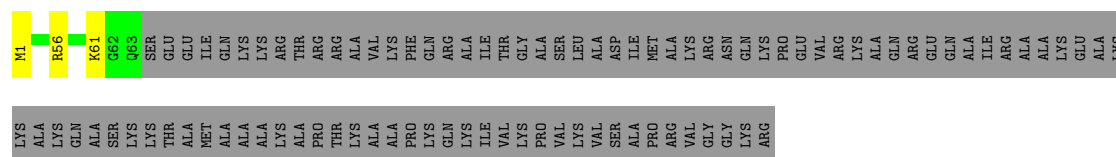
- Molecule 19: eL22



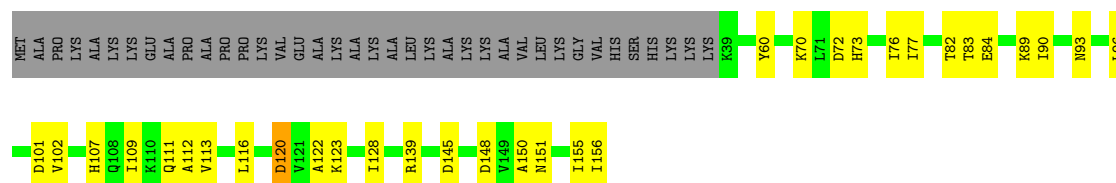
- Molecule 20: uL14



- Molecule 21: eL24

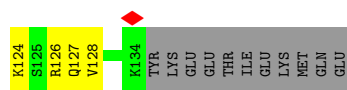


- Molecule 22: eL23



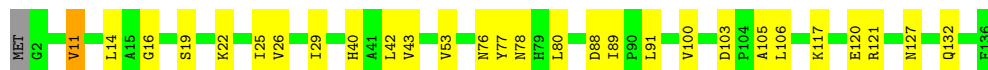
- Molecule 23: uL24





• Molecule 24: eL27

Chain Z: 79% 20% ..



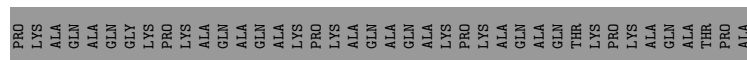
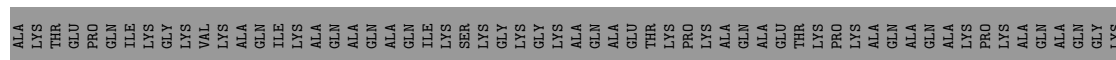
• Molecule 25: uL15

Chain a: 78% 22% .



• Molecule 26: eL29

Chain b: 38% 8% 54%



• Molecule 27: eL30

Chain c: 67% 18% 15%



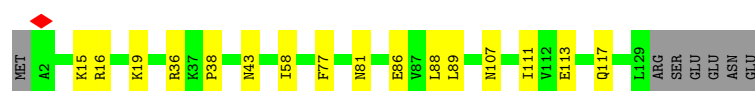
• Molecule 28: eL31

Chain d: 70% 15% 14%



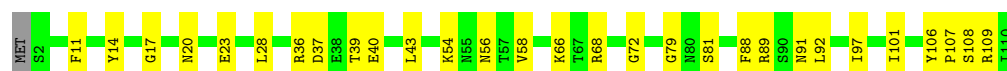
• Molecule 29: eL32

Chain e:  83% 12% 5%



- Molecule 30: eL33

Chain f:  73% 26%



- Molecule 31: eL34

Chain g:  77% 22%



- Molecule 32: eL35

Chain h:  78% 21%



- Molecule 33: eL36

Chain i:  81% 16%



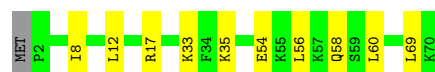
- Molecule 34: eL37

Chain j:  68% 20% 11%



- Molecule 35: eL38

Chain k:  84% 14%

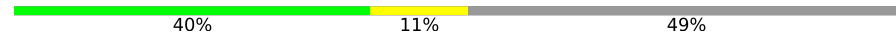


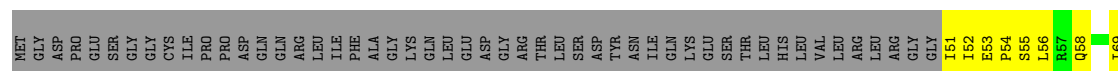
- Molecule 36: eL39

Chain l:  67% 31%



• Molecule 37: eL40

Chain m:  40% 11% 49%



• Molecule 38: eL41

Chain n:  88% 12%



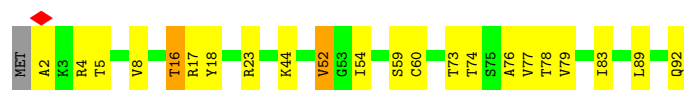
• Molecule 39: eL42

Chain o:  84% 14%



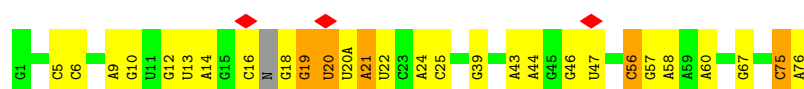
• Molecule 40: eL43

Chain p:  75% 22%



• Molecule 41: P-site tRNA

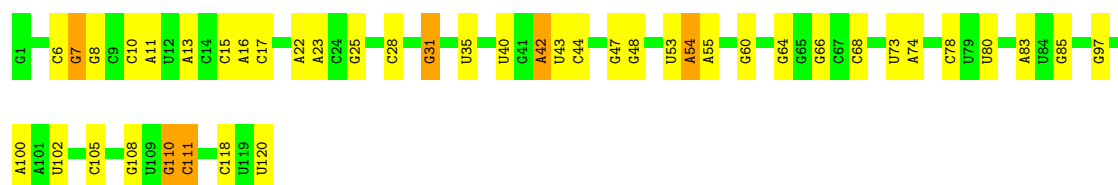
Chain q:  62% 30% 6%



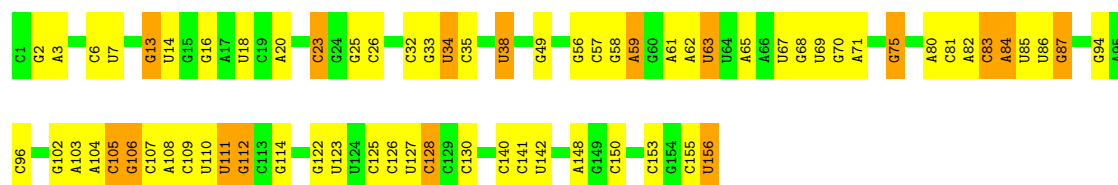
• Molecule 42: eL28

Chain r:  65% 26% 9%

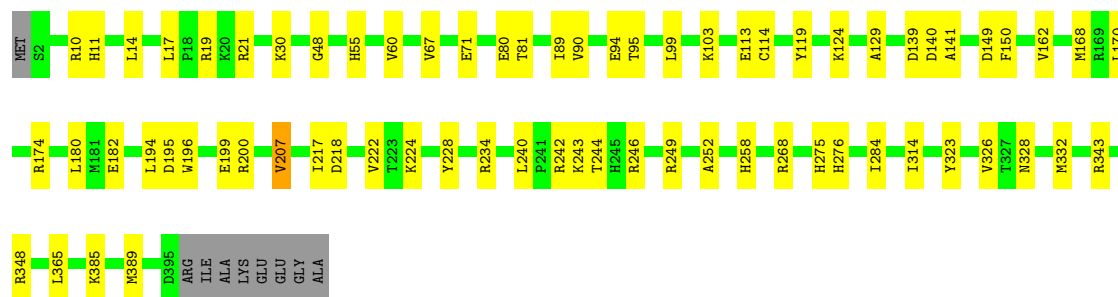
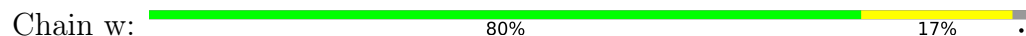
- Molecule 43: 5S ribosomal RNA



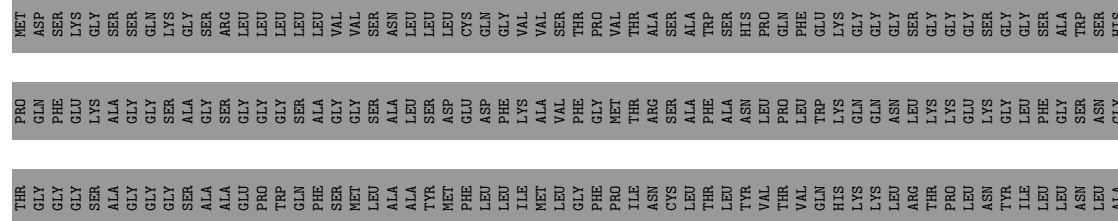
- Molecule 44: 5.8S ribosomal RNA



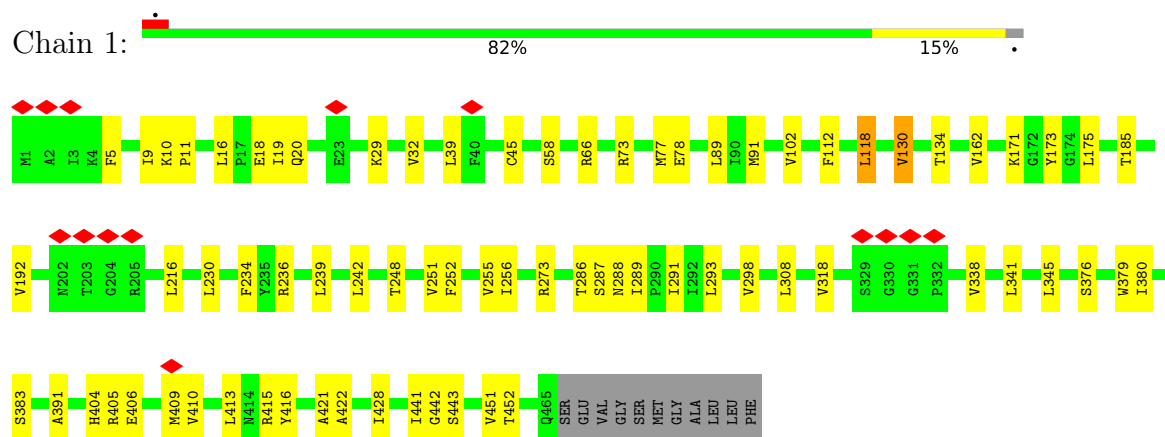
- Molecule 45: uL3



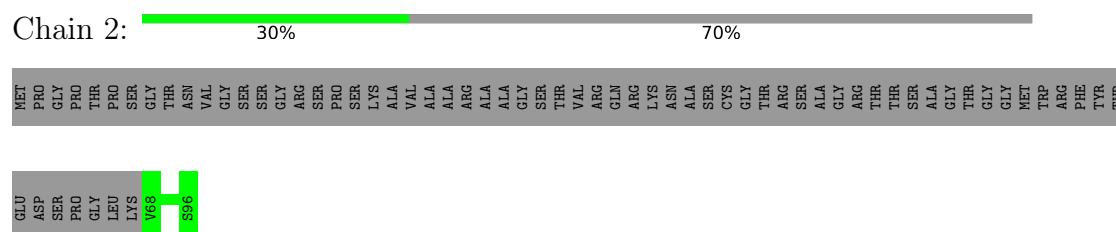
- Molecule 46: Nascent chain



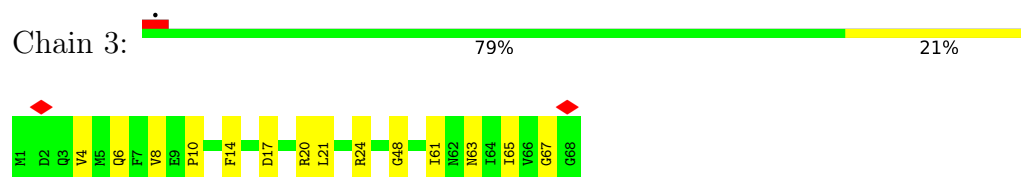
- Molecule 47: Protein transport protein Sec61 subunit alpha isoform 1



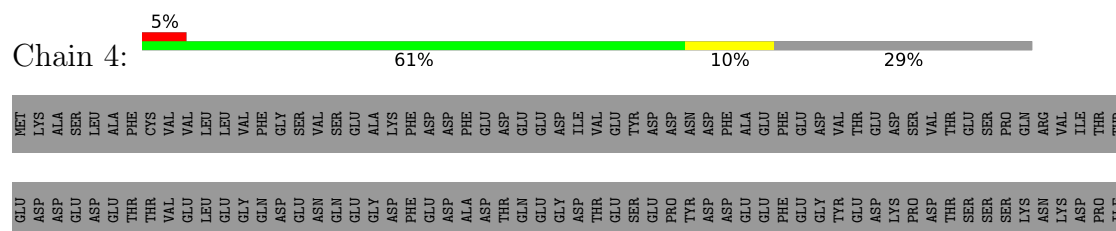
- Molecule 48: Protein transport protein Sec61 subunit beta



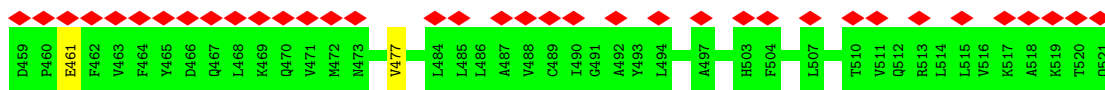
- Molecule 49: Protein transport protein Sec61 gamma



- Molecule 50: Coiled-coil domain containing 47



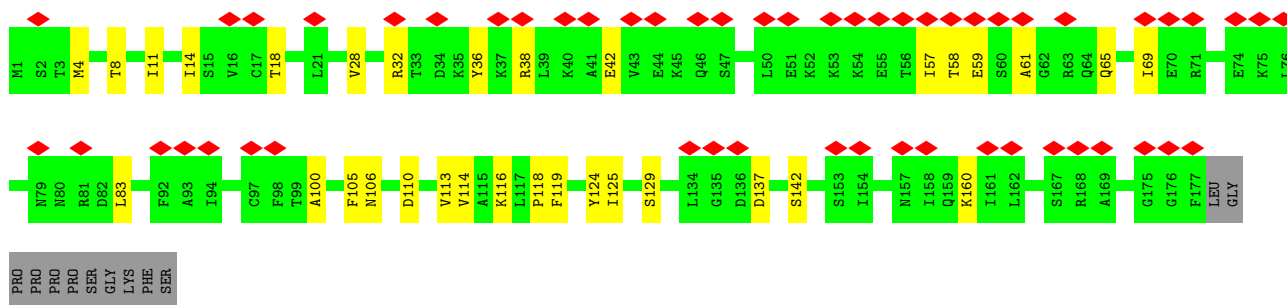
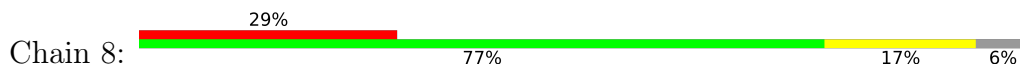




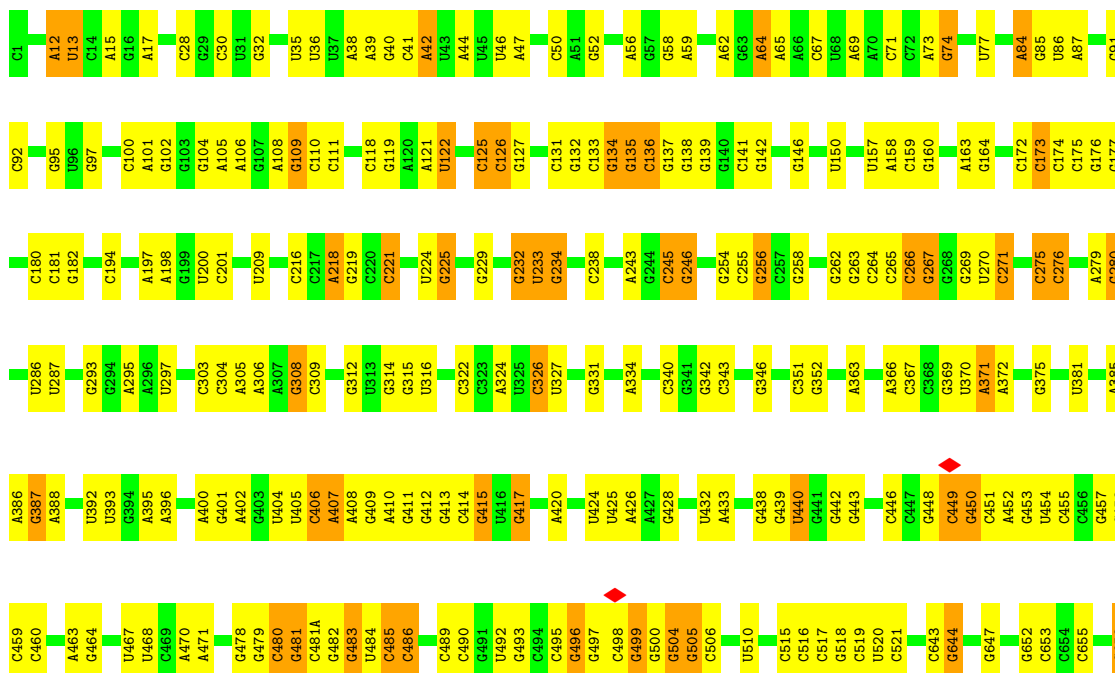
• Molecule 53: Transmembrane protein 147



• Molecule 54: Calcium load-activated calcium channel

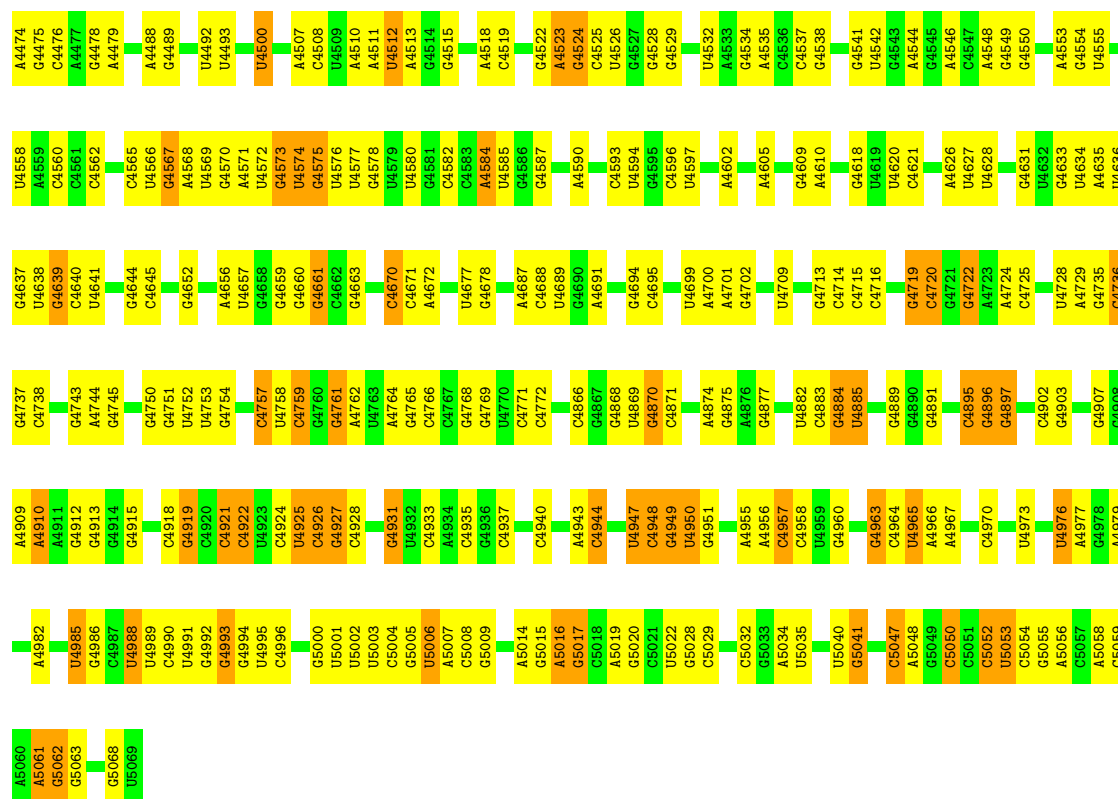


• Molecule 55: 28S ribosomal RNA

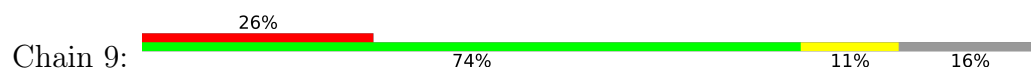


U2080	C2081	G2082	C2083	U2084	G2089	C2090	G2091	C2092	G2093	C2094	A2095	G2096	A2097	C2098	C2099	G2100	A2101	G2102	A2103	A2104	A2105	G2106	A2107	G2108	A2109	G2110	U2111	G2112	G2113	C2258	G2259	C2260	G2261	G2262	A2263	C2264	G2265	C2266	U2267	U2268	C2269	G2275	A2276	G2277	G2278	A2279	G2280	U2281	A2282	G2283	C2289	G2292	U2293	G2294	C2295						
U1997	A1998	A1999	G2000	G2001	A2002	G2003	U2004	G2005	U2006	G2007	U2008	A2009	A2097	U2010	C2011	A2017	C2018	C2019	U2020	G2021	G2022	C2023	G2024	A2025	A2026	U2029	A2030	A2040	A2041	G2045	G2046	A2047	U2048	U2052	C2053	U2054	G2055	G2056	A2057	C2062	G2063	G2064	G2065	A2069	U2070	C2071	C2072	C2073	C2074	C2077	C2078	G2079									
U1927	C1928	G1929	U1930	U1931	A1932	G1933	A1934	C1935	U1936	C1937	U1938	A1939	G1940	A1941	A1942	A1943	A1944	G1945	U1946	U1947	G1948	U1949	U1957	A1958	U1959	A1960	G1961	A1962	C1963	A1964	G1965	G1968	G1969	A1970	A1981	A1982	G1972	G1973	U1974	G1975	G1976	C1977	C1978	A1979	U1980	G1981	G1982	A1983	A1984	C1987	G1988	G1989	A1990	A1991	U1992						
G1840	C1841	U1842	A1843	U1844	U1845	G1846	C1847	A1850	G1851	U1852	G1853	G1854	G1855	G1864	G1865	U1866	A1867	A1868	G1869	G1872	A1801	A1802	G1803	A1874	C1875	U1876	G1877	C1881	U1882	G1886	U1889	G1890	A1891	A1892	C1893	G1894	G1895	A1896	A1897	C1898	G1909	G1910	C1911	G1912	G1913	C1914	C1915	G1916	A1917	U1918	G1919	C1920	C1921	G1922							
C1763	G1764	A1767	C1768	G1769	C1772	U1773	A1774	A1775	A1780	A1786	A1787	A1788	U1789	G1798	G1799	U1800	A1801	A1802	G1803	A1804	A1805	G1806	C1807	C1808	C1809	G1810	G1811	G1812	U1813	G1814	G1815	G1818	G1819	U1820	G1821	U1822	G1823	G1824	A1825	G1826	C1827	C1828	G1831	C1832	G1833	U1834	G1835	G1836	A1837	U1839											
C1637	A1638	U1639	C1640	C1645	A1646	G1651	G1654	C1655	G1658	U1659	U1660	C1661	C1666	U1676	U1677	A1682	U1683	A1684	G1688	C1689	C1690	C1696	U1727	U1730	C1731	G1732	G1733	U1602	G1612	A1613	A1621	U1622	A1623	G1624	G1625	G1626	A1627	C1628	G1629	A1630	A1631	A1632	G1660	C1761	C1762																
U1531	A1534	C1541	A1547	G1548	G1552	A1553	A1554	G1555	A1563	A1564	A1565	C1566	G1574	G1577	U1578	U1586	C1590	U1591	C1594	G1595	G1597	C1598	A1600	A1601	U1602	A1497	G1498	C1499	G1502	A1503	G1504	C1505	U1514	A1515	C1516	G1517	A1518	C1519	A1523	A1524																					
U1443	G1444	U1445	C1446	G1447	G1448	C1449	G1451	G1455	G1456	G1457	C1458	A1459	C1460	C1461	C1464	G1465	C1474	G1475	C1476	C1477	C1478	G1479	C1480	C1481	C1482	C1483	G1484	C1485	G1488	G1489	G1490	G1493	A1497	G1498	C1499	G1502	A1503	G1504	C1505	U1514	A1515	C1516	G1517	A1518	C1519	A1523	A1524														
G1377	C1378	C1379	G1380	U1381	G1382	G1383	C1384	G1385	A1387	G1390	A1391	A1392	C1393	G1394	A1397	A1398	G1399	G1400	C1401	C1402	G1403	G1404	C1405	G1406	G1406A	C1411	G1411A	C1411B	G1411C	G1412	C1413	C1414	G1415	C1416	C1417	C1418	G1419	A1420	G1421	G1426	C1430	C1431	G1432	A1433	G1435	C1436	C1437	U1438	U1440	C1441	C1442										
G1296	U1297	G1298	G1299	G1300	U1301	A1302	A1303	C1305	G1308	C1309	C1314	C1315	G1316	U1317	C1318	U1319	U1320	G1321	A1322	A1326	C1327	G1328	G1329	A1330	C1331	C1332	A1333	A1334	G1335	A1337	U1339	U1340	U1341	A1342	A1345	C1346	G1351	A1354	G1358	G1360	G1361	G1362	G1363	U1364	A1366	C1369	A1371														
G1195	G1196	C1197	G1198	G1199	C1202	G1203	C1204	G1205	U1208	C1209	C1210	G1211	G1212	G1215	C1216	G1217	G1218	G1219	G1223	G1234	C1235	G1236	C1237	G1238	A1239	C1248	C1249	C1250	C1251	G1252	G1271	C1272	G1273	A1274	G1275	C1276	G1277	C1278	A1279	C1280	G1281	U1285	G1286	G1287	G1288	C1289	G1290	G1291	C1292	G1293	A1294	U1295									
C972	G973	C974	C975	G976	C977	G978	C979	U980	C981	U982	C983	C984	C985	C986	C987	C988	U989	C990	G1070	C1071	G1072	C1073	G1075	C1076	C1077	A929	A832	G933	C934	A935	G935A	C936	U937	C938	G939	C940	C941	G1090	C942	A943	A944	U945	G952	C953	A956	G957	G958	G959	A960	G961	C962	G963	A964	G965	A966	G967	C968	C969	C1192	C1193	G1194
G659	G660	C661	C666	A667	C668	C669	C670	C678	C679	G684	C685	A686	U687	C690	A692	G695	C696	G697	G698	C699	G701	C704	G705	C706	C707	C724	G730	G731	G734	C737	C738	C739A	G739	G740	A746	A747	G748	G749	U750	G751	C752	G756	G757	G758																	





- Molecule 56: Obligate partner of TMCO1 insertase



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	136812	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	3.210	Depositor
Minimum map value	-1.145	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.183	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	552.08, 552.08, 552.08	wwPDB
Map dimensions	412, 412, 412	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.10	0/1936	0.29	0/2596
2	C	0.12	0/2937	0.34	0/3946
3	D	0.12	0/2437	0.36	0/3264
4	E	0.11	0/1914	0.32	0/2566
5	F	0.12	0/1911	0.33	0/2549
6	G	0.12	0/1910	0.37	0/2569
7	H	0.11	0/1535	0.34	0/2063
8	I	0.11	0/1702	0.31	0/2272
9	J	0.12	0/1385	0.36	0/1852
10	L	0.12	0/1733	0.35	0/2316
11	M	0.13	0/1158	0.38	0/1547
12	N	0.12	0/1741	0.36	0/2331
13	O	0.13	0/1662	0.36	0/2222
14	P	0.17	0/1268	0.40	0/1700
15	Q	0.12	0/1538	0.34	0/2054
16	R	0.13	0/1310	0.37	0/1734
17	S	0.12	0/1501	0.33	0/2012
18	T	0.10	0/1326	0.29	0/1770
19	U	0.11	0/848	0.32	0/1138
20	V	0.10	0/993	0.28	0/1332
21	W	0.11	0/541	0.33	0/720
22	X	0.12	0/984	0.35	0/1323
23	Y	0.11	0/1132	0.34	0/1504
24	Z	0.11	0/1130	0.30	0/1507
25	a	0.11	0/1191	0.31	0/1590
26	b	0.11	0/861	0.35	0/1138
27	c	0.11	0/771	0.31	0/1034
28	d	0.13	0/903	0.33	0/1216
29	e	0.11	0/1071	0.32	0/1429
30	f	0.12	0/895	0.31	0/1198
31	g	0.12	0/916	0.31	0/1220
32	h	0.12	0/1017	0.37	0/1344

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.13	0/841	0.36	0/1112
34	j	0.10	0/720	0.32	0/952
35	k	0.12	0/575	0.32	0/761
36	l	0.15	0/459	0.46	0/608
37	m	0.12	0/435	0.32	0/575
38	n	0.13	0/240	0.40	0/305
39	o	0.10	0/864	0.30	0/1140
40	p	0.13	0/718	0.36	0/953
41	q	0.13	0/1805	0.37	0/2809
42	r	0.12	0/1010	0.36	0/1354
43	u	0.14	0/2858	0.33	0/4455
44	v	0.14	0/3701	0.37	0/5766
45	w	0.10	0/3240	0.28	0/4339
46	B	0.21	0/541	0.63	0/738
47	1	0.13	0/3677	0.36	0/4986
48	2	0.12	0/237	0.28	0/321
49	3	0.13	0/553	0.33	0/738
50	4	0.13	0/2819	0.36	0/3772
51	5	0.12	0/730	0.30	0/988
52	7	0.10	0/4224	0.29	0/5728
53	6	0.10	0/1835	0.30	0/2495
54	8	0.12	0/1426	0.33	0/1908
55	K	0.16	0/84979	0.41	0/132532
56	9	0.12	0/932	0.37	0/1268
All	All	0.14	0/163576	0.38	0/239659

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
55	K	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
55	K	234	G	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1898	1993	1993	39	0
2	C	2883	3053	3053	54	0
3	D	2391	2424	2424	38	0
4	E	1877	2031	2031	49	0
5	F	1875	1995	1995	40	0
6	G	1879	2027	2027	36	0
7	H	1516	1597	1597	33	0
8	I	1664	1712	1712	24	0
9	J	1362	1399	1399	27	0
10	L	1702	1820	1820	27	0
11	M	1137	1211	1211	19	0
12	N	1696	1745	1744	35	0
13	O	1630	1778	1778	30	0
14	P	1242	1274	1274	35	0
15	Q	1514	1634	1634	27	0
16	R	1294	1434	1434	19	0
17	S	1462	1508	1508	29	0
18	T	1298	1367	1366	30	0
19	U	834	856	858	12	0
20	V	979	1039	1039	18	0
21	W	528	541	541	2	0
22	X	967	1040	1040	28	0
23	Y	1115	1205	1205	32	0
24	Z	1107	1182	1182	17	0
25	a	1162	1209	1209	23	0
26	b	848	920	920	18	0
27	c	761	794	794	13	0
28	d	888	930	930	10	0
29	e	1053	1147	1147	12	0
30	f	876	912	912	23	0
31	g	906	998	998	19	0
32	h	1009	1136	1136	20	0
33	i	830	916	916	12	0
34	j	705	738	738	17	0
35	k	569	637	637	8	0
36	l	447	480	480	19	0
37	m	429	466	466	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	n	239	289	289	2	0
39	o	851	922	922	12	0
40	p	708	757	757	19	0
41	q	1616	823	824	13	0
42	r	994	1051	1051	29	0
43	u	2558	1296	1296	28	0
44	v	3314	1683	1683	41	0
45	w	3172	3310	3310	59	0
46	B	526	528	528	48	0
47	1	3598	3722	3722	57	0
48	2	230	245	245	0	0
49	3	543	577	577	12	0
50	4	2778	2817	2819	47	0
51	5	711	710	710	4	0
52	7	4139	4121	4123	33	0
53	6	1783	1792	1792	11	0
54	8	1406	1478	1478	26	0
55	K	75972	38358	38378	1081	0
56	9	903	881	881	9	0
57	C	1	0	0	0	0
57	D	1	0	0	0	0
57	I	2	0	0	0	0
57	J	1	0	0	0	0
57	K	202	0	0	0	0
57	P	1	0	0	0	0
57	V	1	0	0	0	0
57	a	1	0	0	0	0
57	u	4	0	0	0	0
57	v	6	0	0	0	0
58	g	1	0	0	0	0
58	j	1	0	0	0	0
58	m	1	0	0	0	0
58	o	1	0	0	0	0
58	p	1	0	0	0	0
All	All	152599	114508	114533	2031	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 8.

All (2031) 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)
55:K:2638:G:N2	55:K:2697:A:N1	2.14	0.95
55:K:1442:C:O2	55:K:2112:G:N2	2.02	0.93
12:N:157:LYS:O	12:N:162:ARG:NH1	2.01	0.93
55:K:746:A:O2'	55:K:913:U:O4	1.87	0.93
55:K:1369:C:OP2	55:K:1370:G:O2'	1.87	0.92
55:K:759:G:N2	55:K:904:C:O2	2.02	0.91
55:K:180:C:O2	55:K:256:G:N2	2.04	0.91
55:K:1818:G:O2'	55:K:1819:G:OP1	1.88	0.90
55:K:245:C:O2'	55:K:246:G:OP2	1.90	0.90
23:Y:65:GLN:O	54:8:38:ARG:NH2	2.05	0.89
41:q:10:G:N2	41:q:25:C:O2	2.05	0.89
55:K:2869:U:O2'	55:K:2881:A:N7	2.07	0.88
55:K:2848:G:O2'	55:K:3838:U:O4	1.90	0.88
55:K:1326:A:OP2	55:K:4445:U:O2'	1.92	0.88
53:6:110:GLU:OE1	53:6:146:TYR:OH	1.90	0.88
55:K:2469:C:N4	55:K:2471:G:O6	2.06	0.88
8:I:191:ILE:HD11	8:I:212:LEU:HD11	1.57	0.87
55:K:1406:G:N2	55:K:1411(C):C:O2	2.07	0.87
43:u:23:A:N3	43:u:118:C:O2'	2.08	0.87
23:Y:121:ARG:NH2	55:K:194:C:O2	2.08	0.86
42:r:98:ARG:NH2	55:K:2262:G:OP2	2.07	0.86
26:b:44:ARG:NH1	55:K:1493:G:OP2	2.08	0.85
23:Y:8:THR:OG1	55:K:346:G:OP1	1.93	0.85
8:I:203:ARG:NH1	43:u:105:C:OP2	2.10	0.85
55:K:2601:A:N6	55:K:2744:A:OP2	2.10	0.84
55:K:4467:A:O2'	55:K:4510:A:N3	2.10	0.84
55:K:966:A:O4'	55:K:968:C:N4	2.10	0.84
55:K:738(A):C:O2'	55:K:740:G:OP2	1.96	0.84
44:v:102:G:OP2	44:v:104:A:O2'	1.95	0.84
5:F:231:ASP:OD1	5:F:235:ARG:NH2	2.10	0.83
13:O:186:GLU:O	13:O:190:SER:OG	1.95	0.83
55:K:4743:G:O6	55:K:4957:C:N4	2.11	0.83
55:K:2416:G:N2	55:K:2427:G:O6	2.12	0.83
55:K:1756:U:OP2	55:K:1768:C:N4	2.11	0.82
55:K:314:G:O2'	55:K:4355:G:OP1	1.97	0.81
20:V:50:ASN:ND2	55:K:4457:U:OP1	2.14	0.81
55:K:1320:U:O2'	55:K:1891:A:N1	2.13	0.81
7:H:120:GLU:OE1	7:H:124:ARG:NH2	2.14	0.81
55:K:62:A:N3	55:K:77:U:O2'	2.14	0.81
55:K:759:G:N1	55:K:904:C:N3	2.29	0.81
43:u:73:U:O2'	43:u:102:U:O4	1.99	0.81
55:K:1442:C:N3	55:K:2112:G:N1	2.28	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:107:HIS:O	22:X:111:GLN:NE2	2.14	0.81
13:O:168:TYR:OH	55:K:4768:G:OP1	1.98	0.80
23:Y:67:ILE:O	23:Y:84:ARG:NH2	2.12	0.80
9:J:56:THR:HG22	9:J:64:ARG:H	1.44	0.80
39:o:61:LYS:NZ	55:K:4372:U:OP2	2.15	0.80
17:S:95:ARG:NH2	17:S:112:ASP:OD2	2.15	0.80
55:K:1397:A:O2'	55:K:1467:C:O2'	1.97	0.80
32:h:48:ARG:NH2	44:v:63:U:OP1	2.15	0.80
45:w:246:ARG:NH2	55:K:4558:U:OP2	2.13	0.80
25:a:4:ARG:NH2	55:K:2341:A:OP2	2.15	0.80
55:K:1435:G:O2'	55:K:2105:A:N1	2.14	0.80
55:K:46:U:OP2	55:K:47:A:O2'	2.00	0.80
55:K:180:C:N3	55:K:256:G:N1	2.29	0.79
55:K:3766:A:OP2	55:K:3767:C:N4	2.14	0.79
1:A:117:GLU:OE2	1:A:123:ARG:N	2.14	0.79
15:Q:181:ARG:NH2	55:K:1391:A:OP1	2.14	0.79
11:M:71:LYS:NZ	55:K:737:C:OP2	2.16	0.79
55:K:67:C:OP2	55:K:312:G:N2	2.14	0.79
46:B:233:ILE:O	46:B:237:VAL:HG12	1.83	0.79
2:C:321:ASN:OD1	55:K:1280:C:O2'	2.01	0.79
55:K:704:C:O2'	55:K:705:G:OP1	2.00	0.79
23:Y:74:TYR:OH	44:v:75:G:OP2	1.99	0.79
17:S:170:LYS:NZ	55:K:4874:A:O2'	2.17	0.78
55:K:3811:G:O2'	55:K:3814:U:OP2	2.00	0.78
10:L:2:ALA:N	55:K:1514:U:OP1	2.17	0.78
4:E:97:LYS:NZ	55:K:687:U:O2	2.16	0.78
1:A:142:GLU:O	1:A:143:THR:OG1	2.00	0.78
55:K:3641:U:OP2	55:K:3646:A:N6	2.16	0.78
1:A:67:TYR:OH	55:K:4087:G:N7	2.17	0.78
55:K:2490:U:O2'	55:K:2491:C:O4'	2.02	0.78
55:K:4492:U:O2'	55:K:4512:U:O2	2.01	0.78
40:p:17:ARG:NH1	55:K:1577:G:OP1	2.16	0.78
22:X:128:ILE:O	36:l:10:LYS:NZ	2.13	0.77
8:I:40:LYS:NZ	55:K:1751:A:OP1	2.15	0.77
25:a:47:LYS:NZ	55:K:1684:A:OP1	2.18	0.77
15:Q:2:GLY:N	55:K:2072:C:OP1	2.17	0.77
34:j:49:TRP:O	55:K:1646:A:O2'	2.03	0.77
55:K:2418:A:N1	55:K:2429:A:O2'	2.16	0.76
15:Q:150:ARG:NH2	55:K:1499:C:OP1	2.18	0.76
55:K:1734:G:N2	55:K:1735:U:O4	2.17	0.76
10:L:110:LEU:O	10:L:114:VAL:HG23	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:e:15:LYS:NZ	55:K:2077:C:O2	2.16	0.76
55:K:1397:A:HO2'	55:K:1467:C:HO2'	1.19	0.76
40:p:44:LYS:NZ	55:K:2672:C:OP1	2.19	0.76
1:A:223:SER:OG	55:K:3748:A:O2'	2.03	0.76
32:h:95:LEU:O	55:K:135:G:N2	2.19	0.76
16:R:62:ARG:O	16:R:66:ASN:ND2	2.19	0.75
55:K:1523:A:N3	55:K:4389:C:O2'	2.19	0.75
23:Y:19:PHE:O	23:Y:26:ARG:NH2	2.19	0.75
36:l:28:TRP:NE1	46:B:250:GLU:OE2	2.18	0.75
12:N:193:ARG:O	12:N:197:THR:OG1	2.03	0.75
55:K:5047:C:O2'	55:K:5050:C:OP2	2.04	0.75
55:K:1787:A:N3	55:K:4210:U:O2'	2.20	0.75
55:K:1099:C:N4	55:K:1196:G:O6	2.19	0.75
55:K:2465:C:O2	55:K:3672:G:N2	2.19	0.75
55:K:2486:G:H1	55:K:2492:C:H42	1.33	0.75
6:G:302:ARG:NH2	55:K:4075:U:OP1	2.19	0.75
24:Z:22:LYS:NZ	24:Z:132:GLN:O	2.20	0.75
45:w:385:LYS:NZ	55:K:5002:U:OP2	2.20	0.75
55:K:2502:A:O2'	55:K:2503:G:O5'	2.04	0.75
29:e:86:GLU:HA	29:e:89:LEU:HD23	1.66	0.74
35:k:33:LYS:NZ	55:K:2695:A:OP2	2.20	0.74
36:l:41:ARG:NH1	55:K:2431:A:OP1	2.20	0.74
55:K:1440:U:O2'	55:K:1441:C:OP1	2.02	0.74
6:G:90:LYS:NZ	55:K:4126:C:OP1	2.20	0.74
18:T:87:LYS:NZ	55:K:4300:U:OP1	2.20	0.74
31:g:54:ARG:NH2	55:K:2651:C:O2'	2.19	0.74
34:j:52:LYS:NZ	55:K:375:G:OP2	2.20	0.74
55:K:369:G:N2	55:K:372:A:OP2	2.19	0.74
55:K:1802:A:O2'	55:K:1837:A:OP1	2.05	0.74
28:d:32:ARG:NH2	55:K:4995:U:O3'	2.21	0.74
44:v:107:C:O2	44:v:112:G:N2	2.17	0.74
55:K:308:G:OP2	55:K:308:G:N2	2.20	0.74
45:w:174:ARG:NH1	55:K:4985:U:O2	2.20	0.74
44:v:16:G:O2'	55:K:417:G:N2	2.20	0.74
55:K:406:C:O2'	55:K:407:A:OP1	2.03	0.74
55:K:4996:C:O2	55:K:5055:G:N2	2.17	0.74
55:K:1594:C:HO2'	55:K:1597:G:HO2'	1.35	0.74
55:K:1426:G:N2	55:K:1458:C:OP2	2.21	0.73
55:K:1481:C:O2'	55:K:1482:G:O4'	2.04	0.73
55:K:4925:U:O2'	55:K:4926:C:OP1	2.06	0.73
4:E:182:LEU:HD12	4:E:186:ARG:HA	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:107:ARG:NH2	55:K:2263:A:OP1	2.21	0.73
2:C:327:LYS:NZ	55:K:975:C:O2	2.17	0.72
50:4:273:GLN:NE2	50:4:283:CYS:O	2.22	0.72
43:u:11:A:N1	43:u:66:G:O2'	2.22	0.72
55:K:4474:A:OP2	55:K:4476:C:N4	2.23	0.72
18:T:2:THR:N	55:K:4220:A:OP2	2.22	0.72
30:f:28:LEU:HG	30:f:101:ILE:HD11	1.71	0.72
14:P:12:THR:HG23	50:4:414:GLU:OE2	1.89	0.72
30:f:23:GLU:OE2	55:K:438:G:N2	2.20	0.72
46:B:214:GLY:O	46:B:218:THR:HG23	1.89	0.72
3:D:86:TYR:CE2	3:D:104:LEU:HD21	2.24	0.72
5:F:133:ARG:NH1	43:u:97:G:O5'	2.23	0.72
36:l:2:SER:N	55:K:2407:G:O6	2.22	0.72
50:4:462:ARG:NH1	55:K:2378:G:OP1	2.23	0.72
55:K:1481:C:O2'	55:K:1482:G:N3	2.18	0.72
55:K:3809:G:N2	55:K:3809:G:OP2	2.23	0.72
55:K:1406(A):G:N2	55:K:1411(B):C:O2	2.15	0.71
41:q:18:G:N2	41:q:58:A:O4'	2.23	0.71
41:q:19:G:H4'	41:q:20:U:OP2	1.88	0.71
23:Y:91:ASN:OD1	23:Y:93:THR:HG22	1.89	0.71
46:B:225:LEU:O	46:B:229:VAL:HG13	1.91	0.71
55:K:3663:A:N6	55:K:4168:G:O2'	2.23	0.71
11:M:108:ASP:OD2	13:O:199:HIS:NE2	2.24	0.71
55:K:4448:G:O2'	55:K:4449:A:OP2	2.08	0.71
25:a:8:THR:HG21	55:K:1339:U:OP1	1.91	0.71
46:B:229:VAL:O	46:B:233:ILE:HG23	1.91	0.70
55:K:1591:U:N3	55:K:4555:U:OP1	2.23	0.70
10:L:47:ALA:HB3	10:L:48:PRO:HD3	1.73	0.70
32:h:109:ARG:NH2	55:K:267:G:OP1	2.24	0.70
43:u:11:A:O2'	43:u:13:A:OP2	2.09	0.70
55:K:2517:A:N3	55:K:2539:C:O2'	2.22	0.70
55:K:2529:A:O2'	55:K:2531:C:OP2	2.08	0.70
2:C:239:LYS:O	2:C:248:ARG:NH1	2.25	0.70
45:w:246:ARG:NH1	55:K:4525:C:OP1	2.25	0.70
45:w:249:ARG:NH1	55:K:2837:U:OP1	2.25	0.70
50:4:314:ASP:OD2	50:4:388:TYR:OH	2.08	0.70
17:S:80:ILE:HG21	17:S:126:ILE:HD12	1.73	0.70
32:h:81:LEU:HD23	32:h:84:ARG:HD2	1.72	0.70
55:K:3603:G:O2'	55:K:3604:A:O4'	2.10	0.70
55:K:1818:G:HO2'	55:K:1819:G:P	2.14	0.70
2:C:307:LYS:NZ	55:K:2090:U:OP2	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:12:ARG:O	17:S:171:ARG:NH2	2.25	0.69
20:V:41:SER:OG	55:K:4507:A:O2'	2.10	0.69
26:b:32:LEU:HD12	55:K:1464:C:H5''	1.72	0.69
50:4:433:ARG:HH11	55:K:392:U:P	2.14	0.69
17:S:9:GLU:HG3	17:S:67:VAL:HG13	1.74	0.69
24:Z:16:GLY:O	24:Z:19:SER:OG	2.06	0.69
10:L:39:ARG:NE	55:K:106:A:OP1	2.24	0.69
55:K:1477:C:O2'	55:K:1478:C:OP1	2.08	0.69
32:h:52:LYS:NZ	44:v:63:U:O2'	2.21	0.69
55:K:3625:G:O2'	55:K:3626:G:OP1	2.10	0.69
12:N:184:ILE:O	12:N:194:ARG:NH2	2.26	0.69
14:P:28:ASN:O	14:P:32:THR:HG22	1.92	0.69
47:1:19:ILE:O	47:1:171:LYS:NZ	2.26	0.69
55:K:1455:G:O2'	55:K:1456:C:OP1	2.07	0.69
15:Q:65:ARG:NH1	55:K:1502:G:OP1	2.26	0.69
54:8:57:ILE:HD13	54:8:69:ILE:HD11	1.75	0.69
55:K:1594:C:O2'	55:K:1597:G:O2'	2.07	0.69
18:T:55:LYS:NZ	55:K:4217:G:OP1	2.25	0.69
39:o:3:ASN:ND2	39:o:95:GLY:O	2.25	0.69
55:K:4098:A:N6	55:K:4111:U:O4	2.26	0.69
2:C:45:ARG:NH2	55:K:2295:C:O2'	2.25	0.69
5:F:93:ARG:NH1	5:F:95:ARG:O	2.25	0.69
22:X:89:LYS:NZ	55:K:2532:C:O2'	2.25	0.69
39:o:81:ARG:NH2	55:K:4293:U:O2'	2.26	0.68
23:Y:15:ARG:NH2	44:v:23:C:OP1	2.26	0.68
24:Z:88:ASP:O	24:Z:121:ARG:NH1	2.26	0.68
29:e:16:ARG:NH2	29:e:19:LYS:O	2.26	0.68
34:j:21:ARG:NH2	34:j:39:TYR:O	2.25	0.68
26:b:72:ILE:HG23	26:b:73:LYS:HD2	1.74	0.68
55:K:2490:U:O2'	55:K:2491:C:O5'	2.12	0.68
55:K:69:A:N1	55:K:324:A:O2'	2.25	0.68
18:T:83:LYS:HE2	18:T:85:LEU:HD21	1.76	0.68
55:K:4119:C:O2'	55:K:4120:U:O5'	2.12	0.68
20:V:18:LEU:HD13	20:V:54:ALA:HB3	1.76	0.68
14:P:18:ARG:NH1	14:P:147:GLU:OE1	2.25	0.68
36:l:29:MET:HE3	46:B:247:ARG:NH1	2.09	0.68
55:K:158:A:N1	55:K:276:C:O2'	2.19	0.68
56:9:49:ARG:NH1	56:9:78:ASN:OD1	2.26	0.68
5:F:69:ARG:NH1	55:K:1210:C:OP1	2.26	0.68
16:R:114:LYS:O	16:R:146:LYS:NZ	2.27	0.68
1:A:124:GLY:O	1:A:128:ARG:NH1	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:3893:C:O2'	55:K:4979:A:N1	2.27	0.67
6:G:156:ARG:NH2	6:G:245:ARG:O	2.28	0.67
22:X:123:LYS:NZ	55:K:2533:C:OP2	2.27	0.67
25:a:72:THR:HG22	25:a:110:LYS:HB3	1.76	0.67
2:C:234:LYS:NZ	55:K:1364:U:O2	2.19	0.67
12:N:123:GLU:OE1	12:N:128:LYS:NZ	2.26	0.67
40:p:5:THR:OG1	40:p:8:VAL:O	2.10	0.67
55:K:2586:G:N3	55:K:2770:C:O2'	2.27	0.67
55:K:5017:G:N2	55:K:5032:C:O2	2.17	0.67
33:i:50:PHE:O	33:i:55:ARG:NH2	2.28	0.67
55:K:2658:G:O2'	55:K:2675:G:N2	2.28	0.67
5:F:244:ARG:NH2	55:K:942:G:OP1	2.28	0.67
50:4:305:MET:HE1	50:4:402:GLY:HA2	1.76	0.67
3:D:88:VAL:HG12	3:D:239:MET:SD	2.35	0.67
15:Q:14:ARG:NH2	55:K:2083:C:OP2	2.28	0.67
55:K:5005:G:N2	55:K:5041:G:O2'	2.27	0.67
16:R:8:LYS:NZ	55:K:2387:G:OP1	2.26	0.67
34:j:72:ARG:NH1	44:v:94:G:OP2	2.28	0.67
55:K:1414:C:N4	55:K:1415:G:O6	2.28	0.66
9:J:75:ARG:NH1	43:u:40:U:O2	2.29	0.66
32:h:29:SER:O	32:h:33:VAL:HG23	1.96	0.66
52:7:40:ARG:NH1	54:8:110:ASP:OD1	2.28	0.66
14:P:82:ARG:NH2	55:K:2362:U:OP1	2.29	0.66
36:l:2:SER:OG	36:l:3:SER:N	2.24	0.66
15:Q:11:ARG:NH1	55:K:1689:G:OP1	2.28	0.66
55:K:233:U:O2'	55:K:2304:U:O4	2.11	0.66
55:K:1893:C:O2'	55:K:1936:C:N3	2.27	0.66
46:B:265:LEU:HD12	46:B:267:CYS:H	1.61	0.66
8:I:145:LYS:O	8:I:149:VAL:HG23	1.96	0.66
55:K:388:A:O2'	55:K:402:A:N1	2.27	0.66
55:K:1432:G:O2'	55:K:1451:G:N2	2.25	0.66
55:K:2870:A:OP2	55:K:2879:A:N6	2.28	0.66
34:j:2:THR:N	55:K:1601:A:HO2'	1.94	0.66
45:w:252:ALA:HB3	55:K:4457:U:O2	1.96	0.66
55:K:2407:G:OP2	55:K:2407:G:N2	2.30	0.66
54:8:124:TYR:CE1	54:8:125:ILE:HG23	2.30	0.65
55:K:2844:A:N6	55:K:3839:G:O2'	2.30	0.65
6:G:297:PRO:HA	6:G:300:VAL:HG12	1.77	0.65
2:C:83:GLY:O	55:K:367:C:O2'	2.11	0.65
45:w:17:LEU:O	45:w:19:ARG:N	2.29	0.65
55:K:1174:G:O2'	55:K:1175:A:OP1	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:1238:A:O2'	55:K:1239:C:OP1	2.14	0.65
45:w:21:ARG:NH2	55:K:4568:A:O3'	2.29	0.65
46:B:226:TRP:O	46:B:229:VAL:HG22	1.97	0.65
55:K:1918:U:O2	55:K:2064:G:O6	2.14	0.65
5:F:216:ARG:O	5:F:245:ARG:NH1	2.29	0.65
3:D:33:ARG:NH1	43:u:7:G:O3'	2.29	0.65
45:w:103:LYS:NZ	45:w:149:ASP:OD1	2.24	0.65
55:K:2368:A:N6	55:K:2827:G:O2'	2.29	0.65
4:E:269:GLN:N	55:K:4931:G:OP1	2.27	0.65
12:N:65:ARG:NH2	55:K:2457:G:OP1	2.30	0.65
18:T:42:ILE:HD11	18:T:74:ILE:HD11	1.79	0.65
55:K:2666:U:O2'	55:K:2668:G:N7	2.19	0.65
19:U:92:LYS:NZ	55:K:2627:C:OP2	2.30	0.65
45:w:228:TYR:O	55:K:2835:A:O2'	2.15	0.65
54:8:57:ILE:HG23	54:8:61:ALA:HB2	1.78	0.64
55:K:3717:A:OP2	55:K:3735:G:N2	2.29	0.64
55:K:4348:A:O2'	55:K:4350:C:OP2	2.15	0.64
32:h:87:LYS:O	32:h:92:ARG:NH1	2.29	0.64
24:Z:26:VAL:HG22	24:Z:42:LEU:O	1.96	0.64
26:b:44:ARG:NH2	55:K:1466:G:OP2	2.30	0.64
46:B:218:THR:CB	49:3:61:ILE:HD11	2.27	0.64
55:K:4232:U:H4'	55:K:4233:A:O5'	1.95	0.64
4:E:156:LEU:HD11	4:E:198:ILE:HG13	1.79	0.64
24:Z:121:ARG:NH2	24:Z:127:ASN:OD1	2.31	0.64
55:K:4949:G:H4'	55:K:4950:U:H5'	1.79	0.64
1:A:30:ARG:O	1:A:163:ARG:NH2	2.30	0.64
2:C:293:LEU:O	2:C:299:GLN:NE2	2.27	0.64
55:K:4454:G:HO2'	55:K:4500:U:HO2'	1.40	0.64
1:A:97:ASN:OD1	1:A:100:ASN:ND2	2.28	0.64
1:A:128:ARG:NE	55:K:3681:G:OP2	2.30	0.64
3:D:120:GLU:O	3:D:248:ARG:NH2	2.31	0.64
55:K:2520:C:O2	55:K:2640:G:N2	2.31	0.64
55:K:4761:G:N2	55:K:4766:C:O3'	2.31	0.64
1:A:104:VAL:HG22	1:A:162:ASN:O	1.98	0.64
13:O:116:LYS:N	55:K:4757:C:OP2	2.31	0.64
42:r:107:ARG:O	42:r:111:ILE:HD12	1.98	0.64
55:K:4947:U:O2'	55:K:4948:C:OP1	2.16	0.64
22:X:145:ASP:OD1	22:X:148:ASP:N	2.29	0.64
28:d:64:ILE:HG23	28:d:68:LEU:HD23	1.80	0.64
33:i:36:HIS:O	33:i:40:VAL:HG23	1.98	0.64
3:D:119:TYR:OH	3:D:139:PRO:O	2.16	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:111:LEU:HD12	7:H:127:ARG:HD2	1.80	0.63
23:Y:55:VAL:HG22	23:Y:104:VAL:HG22	1.79	0.63
45:w:242:ARG:NH2	55:K:2856:C:O2	2.29	0.63
55:K:2440:U:O2'	55:K:2441:C:OP1	2.16	0.63
3:D:208:MET:HE2	3:D:233:PRO:HG3	1.80	0.63
14:P:47:TYR:OH	14:P:57:CYS:O	2.09	0.63
52:7:250:ASN:CB	52:7:259:LEU:HD12	2.27	0.63
55:K:1833:G:N2	55:K:1835:G:O4'	2.31	0.63
3:D:50:ARG:NH1	3:D:147:ASP:OD2	2.31	0.63
5:F:236:GLU:OE2	17:S:41:LYS:NZ	2.29	0.63
7:H:134:CYS:SG	7:H:144:LEU:HD23	2.38	0.63
42:r:99:LYS:NZ	55:K:2260:C:O2	2.31	0.63
17:S:13:VAL:HG22	17:S:63:TYR:HB3	1.81	0.63
55:K:3692:A:H62	55:K:3823:G:H21	1.46	0.63
52:7:26:LEU:HD13	52:7:65:ALA:HB2	1.79	0.63
13:O:194:ASP:O	13:O:198:THR:HG23	1.98	0.63
39:o:39:ARG:NH1	55:K:295:A:OP2	2.32	0.63
30:f:91:ASN:ND2	55:K:439:G:O3'	2.32	0.63
55:K:371:A:N3	55:K:1531:U:O2'	2.29	0.63
55:K:2599:G:N2	55:K:2747:U:O4	2.31	0.63
2:C:323:ARG:CD	55:K:976:G:H21	2.12	0.62
2:C:323:ARG:HD3	55:K:976:G:H21	1.64	0.62
23:Y:4:ASN:N	55:K:243:A:OP1	2.29	0.62
32:h:33:VAL:O	32:h:37:THR:HG23	1.98	0.62
55:K:1390:G:N2	55:K:1393:G:OP2	2.30	0.62
55:K:3661:G:N1	55:K:3682:A:OP2	2.29	0.62
55:K:3878:C:N4	55:K:4518:A:O4'	2.32	0.62
12:N:155:VAL:O	12:N:162:ARG:NH2	2.31	0.62
54:8:116:LYS:NZ	54:8:137:ASP:OD2	2.32	0.62
55:K:1358:G:N2	55:K:1381:U:O4	2.32	0.62
5:F:59:GLU:OE1	5:F:191:HIS:NE2	2.32	0.62
23:Y:83:GLU:OE1	23:Y:84:ARG:NH1	2.32	0.62
39:o:20:PRO:O	39:o:73:VAL:HG22	1.99	0.62
40:p:73:THR:HG23	40:p:76:ALA:HB3	1.81	0.62
55:K:1622:U:O2'	55:K:1627:G:O3'	2.16	0.62
42:r:32:LEU:HD21	42:r:106:LEU:HD12	1.82	0.62
10:L:74:ARG:NH2	55:K:109:G:OP2	2.33	0.62
14:P:2:VAL:HG12	14:P:3:ARG:H	1.64	0.62
45:w:224:LYS:NZ	55:K:4626:A:OP2	2.20	0.62
55:K:1339:U:H2'	55:K:1340:C:C6	2.35	0.62
2:C:39:PHE:O	2:C:43:ASN:ND2	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:226:TRP:O	46:B:230:VAL:HG13	1.99	0.62
55:K:4902:C:N4	55:K:4919:G:O6	2.33	0.62
55:K:4948:C:H5''	55:K:4949:G:H5''	1.82	0.62
14:P:135:ARG:NH2	55:K:1596:U:O2'	2.33	0.62
3:D:155:THR:O	43:u:35:U:O2'	2.17	0.61
4:E:206:ILE:O	4:E:206:ILE:HG22	2.00	0.61
33:i:89:GLU:O	33:i:93:VAL:HG12	2.00	0.61
35:k:35:LYS:NZ	55:K:2695:A:OP1	2.21	0.61
50:4:233:VAL:HG22	50:4:236:ARG:HH22	1.64	0.61
2:C:209:VAL:HB	2:C:229:LEU:HD13	1.80	0.61
42:r:32:LEU:HD23	42:r:32:LEU:H	1.66	0.61
45:w:252:ALA:HB1	55:K:4524:G:N3	2.16	0.61
7:H:73:ILE:O	7:H:77:VAL:HG23	1.99	0.61
55:K:1073:G:H22	55:K:1238:A:H2	1.49	0.61
55:K:1556:C:O2'	55:K:2669:C:OP1	2.18	0.61
29:e:36:ARG:NH2	55:K:2322:G:OP1	2.34	0.61
40:p:23:ARG:NH1	55:K:2875:C:OP1	2.31	0.61
52:7:246:TRP:CH2	52:7:259:LEU:HD11	2.35	0.61
55:K:2361:G:O2'	55:K:3859:G:O6	2.16	0.61
55:K:4633:G:O2'	55:K:4635:A:OP2	2.11	0.61
12:N:15:GLN:NE2	55:K:305:A:OP2	2.33	0.61
46:B:204:VAL:O	46:B:208:THR:HG23	2.01	0.61
1:A:29:LEU:O	1:A:123:ARG:NH1	2.33	0.61
4:E:49:ASN:ND2	55:K:979:C:OP1	2.34	0.61
9:J:33:LEU:HD21	9:J:68:ILE:O	2.00	0.61
18:T:130:ARG:NH2	55:K:1802:A:N3	2.49	0.61
55:K:4661:G:N2	55:K:5004:C:O3'	2.34	0.61
55:K:4541:G:N2	55:K:4544:A:OP2	2.32	0.60
1:A:152:SER:OG	55:K:3661:G:N7	2.34	0.60
3:D:184:ASP:O	3:D:188:LYS:N	2.33	0.60
8:I:4:ARG:NH1	8:I:9:TYR:OH	2.34	0.60
23:Y:2:LYS:NZ	23:Y:7:VAL:O	2.29	0.60
32:h:56:ARG:O	32:h:60:VAL:HG23	2.01	0.60
55:K:1503:A:H4'	55:K:1504:G:H5'	1.82	0.60
27:c:28:VAL:HG21	27:c:37:MET:HG3	1.83	0.60
33:i:76:ARG:O	55:K:304:C:O2'	2.16	0.60
55:K:46:U:P	55:K:47:A:HO2'	2.21	0.60
30:f:14:TYR:OH	30:f:92:LEU:O	2.19	0.60
15:Q:88:ASP:OD1	15:Q:89:ASP:N	2.34	0.60
26:b:22:LYS:NZ	55:K:1845:U:OP2	2.35	0.60
42:r:107:ARG:NH1	42:r:108:MET:SD	2.75	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:312:LYS:HA	6:G:315:ALA:HB3	1.83	0.60
10:L:20:ARG:NH1	55:K:50:C:OP1	2.33	0.60
46:B:272:LEU:HD12	46:B:272:LEU:O	2.02	0.60
55:K:643:C:H2'	55:K:644:G:C8	2.36	0.60
55:K:1872:G:O2'	55:K:4219:A:N3	2.19	0.60
55:K:3911:C:H2'	55:K:3912:U:H6	1.67	0.60
36:l:25:GLN:O	46:B:247:ARG:NH1	2.35	0.60
13:O:142:ALA:HA	13:O:145:VAL:HG12	1.84	0.60
47:l:273:ARG:NH1	55:K:2432:U:OP1	2.34	0.60
49:3:61:ILE:HG22	49:3:65:ILE:HD12	1.83	0.60
10:L:36:ARG:NH1	55:K:1364:U:OP2	2.35	0.60
40:p:89:LEU:O	40:p:92:GLN:NE2	2.35	0.60
55:K:2094:C:H3'	55:K:2095:A:H5'	1.82	0.60
55:K:3788:C:N4	55:K:3812:C:O4'	2.35	0.60
20:V:41:SER:HG	55:K:4507:A:HO2'	1.43	0.59
22:X:90:ILE:HG12	22:X:96:LEU:HD23	1.84	0.59
9:J:156:ARG:NH2	43:u:17:C:OP1	2.35	0.59
15:Q:11:ARG:NH2	55:K:1690:C:OP2	2.35	0.59
55:K:2395:A:O2'	55:K:2806:A:H1'	2.02	0.59
5:F:145:ASN:O	5:F:149:VAL:HG23	2.02	0.59
13:O:16:LEU:HD21	13:O:83:THR:HG21	1.83	0.59
13:O:80:PHE:O	13:O:84:VAL:HG23	2.02	0.59
30:f:58:VAL:O	55:K:4944:C:N4	2.35	0.59
55:K:684:G:O2'	55:K:685:C:OP1	2.19	0.59
55:K:5017:G:N1	55:K:5032:C:N3	2.41	0.59
13:O:82:ARG:NH1	55:K:3887:C:OP1	2.36	0.59
15:Q:13:VAL:O	15:Q:13:VAL:HG12	2.03	0.59
39:o:105:GLN:OE1	39:o:105:GLN:N	2.36	0.59
54:8:57:ILE:CD1	54:8:69:ILE:HD11	2.32	0.59
55:K:1541:C:O2'	55:K:2448:G:N3	2.35	0.59
55:K:1742:A:N1	55:K:1790:U:O2'	2.33	0.59
55:K:2740:U:O2'	55:K:2742:G:N2	2.36	0.59
4:E:168:LEU:HD11	4:E:179:THR:HG22	1.84	0.59
6:G:253:THR:OG1	55:K:150:U:OP1	2.15	0.59
55:K:1666:C:O2'	55:K:1688:G:OP1	2.15	0.59
55:K:2491:C:H2'	55:K:2492:C:C6	2.38	0.59
10:L:116:ARG:NH2	10:L:155:MET:O	2.35	0.59
16:R:44:LEU:HD22	16:R:49:LEU:HD12	1.85	0.59
30:f:36:ARG:O	30:f:39:THR:HG22	2.01	0.59
55:K:4492:U:H5''	55:K:4493:U:H5'	1.84	0.59
8:I:3:ARG:NH2	55:K:4431:U:OP2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:56:ARG:O	10:L:116:ARG:NH1	2.36	0.59
12:N:116:LEU:HD22	12:N:135:ILE:HD11	1.83	0.59
5:F:130:ASN:ND2	55:K:1727:U:OP1	2.34	0.59
45:w:114:CYS:SG	45:w:180:LEU:HD11	2.43	0.59
5:F:75:ARG:NE	55:K:730:G:OP2	2.35	0.59
8:I:29:ALA:O	8:I:32:ARG:NH1	2.36	0.59
12:N:187:SER:OG	55:K:28:C:OP1	2.21	0.59
45:w:124:LYS:NZ	55:K:5063:G:O6	2.31	0.59
46:B:230:VAL:O	46:B:233:ILE:HG13	2.02	0.59
55:K:1168:G:H1	55:K:1193:C:H42	1.51	0.59
55:K:1850:A:N3	55:K:2283:G:O2'	2.35	0.59
3:D:72:ASP:OD2	43:u:6:C:O2'	2.07	0.58
12:N:103:GLU:OE2	12:N:118:SER:OG	2.17	0.58
45:w:170:LEU:O	45:w:328:ASN:ND2	2.31	0.58
28:d:94:GLU:HG3	28:d:95:ASP:H	1.68	0.58
45:w:55:HIS:CE1	55:K:4627:U:HO2'	2.21	0.58
46:B:237:VAL:O	46:B:237:VAL:HG13	2.03	0.58
55:K:1315:C:N4	55:K:1316:G:O6	2.36	0.58
7:H:91:LYS:HG2	7:H:145:VAL:HG22	1.86	0.58
12:N:181:HIS:O	12:N:195:ARG:NH2	2.35	0.58
16:R:117:ARG:NH2	55:K:2660:A:OP1	2.34	0.58
55:K:2045:G:O6	55:K:3870:C:O2'	2.22	0.58
22:X:120:ASP:OD1	22:X:120:ASP:N	2.36	0.58
23:Y:115:ARG:O	23:Y:119:LEU:HD13	2.04	0.58
37:m:53:GLU:OE1	37:m:55:SER:N	2.33	0.58
55:K:2811:G:N1	55:K:2814:C:OP2	2.34	0.58
55:K:4419:U:OP1	55:K:4421:C:N4	2.33	0.58
16:R:31:GLU:OE1	16:R:31:GLU:N	2.36	0.58
1:A:142:GLU:C	1:A:143:THR:HG1	2.08	0.58
29:e:107:ASN:ND2	55:K:2303:C:OP1	2.33	0.58
34:j:30:GLN:NE2	55:K:1621:A:OP2	2.36	0.58
55:K:1524:A:N7	55:K:3915:U:O2'	2.30	0.58
46:B:233:ILE:HD12	46:B:237:VAL:HG11	1.86	0.58
50:4:261:PHE:CZ	50:4:313:MET:HE3	2.38	0.58
54:8:4:MET:HE1	54:8:116:LYS:HG2	1.84	0.58
55:K:1633:G:H5'	55:K:1634:A:OP1	2.03	0.58
20:V:18:LEU:HD13	20:V:54:ALA:CB	2.32	0.58
22:X:93:ASN:OD1	55:K:2532:C:O2'	2.22	0.58
37:m:98:LYS:NZ	55:K:4473:A:OP1	2.37	0.58
55:K:1637:A:OP1	55:K:1640:C:N4	2.36	0.58
55:K:2093:G:H4'	55:K:2094:C:H5'	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:21:ARG:NH2	43:u:8:G:O6	2.37	0.57
5:F:89:ALA:HB2	5:F:124:LEU:HD21	1.86	0.57
7:H:152:GLU:OE2	55:K:4702:G:N2	2.37	0.57
14:P:69:ARG:NH1	55:K:4568:A:N3	2.51	0.57
22:X:72:ASP:OD1	22:X:73:HIS:N	2.37	0.57
54:8:57:ILE:HG23	54:8:61:ALA:CB	2.34	0.57
55:K:1482:G:O2'	55:K:1483:C:OP2	2.21	0.57
55:K:1927:U:OP1	55:K:1949:U:O2'	2.14	0.57
1:A:36:GLU:OE2	1:A:163:ARG:NE	2.37	0.57
14:P:12:THR:HG23	50:4:414:GLU:CG	2.34	0.57
22:X:156:ILE:O	49:3:24:ARG:NH1	2.38	0.57
42:r:39:ARG:NH1	42:r:105:ASP:OD2	2.36	0.57
55:K:102:G:HO2'	55:K:1381:U:HO2'	1.53	0.57
55:K:1755:C:O2'	55:K:1757:U:OP2	2.23	0.57
55:K:4602:A:N6	55:K:4609:G:O2'	2.37	0.57
3:D:28:THR:OG1	43:u:7:G:OP2	2.06	0.57
10:L:63:THR:O	10:L:65:ARG:N	2.38	0.57
27:c:49:ALA:HB2	27:c:81:LEU:HD12	1.87	0.57
17:S:80:ILE:HG23	17:S:129:VAL:HG22	1.86	0.57
19:U:66:SER:OG	19:U:67:LYS:N	2.38	0.57
47:1:234:PHE:CZ	47:1:242:LEU:HD23	2.39	0.57
55:K:85:G:O2'	55:K:97:G:O6	2.21	0.57
47:1:287:SER:OG	47:1:288:ASN:N	2.37	0.57
47:1:442:GLY:O	47:1:443:SER:OG	2.19	0.57
52:7:250:ASN:HB2	52:7:259:LEU:HD12	1.86	0.57
55:K:1198:G:H2'	55:K:1199:G:H8	1.69	0.57
55:K:2488:C:HO2'	55:K:2489:C:P	2.27	0.57
5:F:85:GLU:OE2	18:T:136:ARG:NH1	2.38	0.57
55:K:1354:A:N6	55:K:1503:A:O4'	2.38	0.57
4:E:179:THR:HG23	4:E:179:THR:O	2.03	0.56
55:K:1218:G:H2'	55:K:1219:G:C8	2.40	0.56
55:K:1563:A:H2'	55:K:1564:A:C8	2.40	0.56
55:K:4635:A:H2	55:K:4663:G:H21	1.52	0.56
3:D:65:ALA:HB2	3:D:74:ILE:HD13	1.87	0.56
5:F:33:ARG:NH1	55:K:1272:C:OP2	2.39	0.56
6:G:217:ILE:O	6:G:221:VAL:HG23	2.05	0.56
10:L:59:VAL:HG13	55:K:74:G:H5'	1.86	0.56
47:1:391:ALA:CB	47:1:410:VAL:HG22	2.35	0.56
55:K:959:G:O2'	55:K:2263:A:N6	2.34	0.56
55:K:1978:C:O2	55:K:1989:G:N1	2.38	0.56
55:K:2519:U:O2'	55:K:2530:U:O2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:2637:U:O2'	55:K:2718:U:O2'	2.15	0.56
17:S:147:ASP:OD1	17:S:149:LYS:N	2.38	0.56
18:T:108:ARG:NH2	55:K:1802:A:O2'	2.38	0.56
54:8:61:ALA:HB1	54:8:65:GLN:OE1	2.06	0.56
55:K:2658:G:H1	55:K:2675:G:HO2'	1.53	0.56
55:K:2758:G:O2'	55:K:2765:A:N3	2.24	0.56
45:w:10:ARG:NH2	45:w:14:LEU:HD21	2.21	0.56
46:B:230:VAL:O	46:B:234:GLU:HG2	2.05	0.56
47:1:291:ILE:HD11	47:1:428:ILE:CG2	2.36	0.56
2:C:145:GLU:N	2:C:145:GLU:OE1	2.37	0.56
13:O:85:ARG:NH2	55:K:3887:C:OP2	2.38	0.56
40:p:16:THR:HG22	55:K:2876:G:C8	2.40	0.56
55:K:132:G:N2	55:K:136:C:O2	2.38	0.56
23:Y:82:ILE:HG22	23:Y:83:GLU:H	1.71	0.56
45:w:182:GLU:OE2	55:K:4580:U:O2'	2.24	0.56
55:K:197:A:N1	55:K:225:G:O2'	2.33	0.56
55:K:2502:A:H4'	55:K:2503:G:OP1	2.04	0.56
18:T:40:VAL:HG13	18:T:96:ILE:HG23	1.87	0.56
54:8:4:MET:HE3	54:8:113:VAL:HG12	1.86	0.56
55:K:1438:U:O2'	55:K:1440:U:OP2	2.22	0.56
55:K:2520:C:OP2	55:K:2530:U:N3	2.35	0.56
55:K:2691:U:C2	55:K:2692:U:C5	2.94	0.56
55:K:2695:A:O2'	55:K:2696:A:OP2	2.18	0.56
11:M:57:LEU:HD23	11:M:57:LEU:H	1.69	0.56
22:X:156:ILE:OXT	47:1:416:TYR:OH	2.24	0.56
38:n:23:ARG:NH2	55:K:3782:C:OP2	2.38	0.56
55:K:2459:G:N2	55:K:2462:C:OP2	2.36	0.56
23:Y:56:GLN:NE2	23:Y:65:GLN:OE1	2.38	0.56
34:j:82:THR:OG1	44:v:94:G:N2	2.39	0.56
55:K:3700:C:O2'	55:K:3774:A:N3	2.30	0.56
12:N:17:ASP:OD1	12:N:18:VAL:N	2.38	0.56
32:h:96:ASN:ND2	55:K:136:C:OP2	2.38	0.56
50:4:422:HIS:CD2	55:K:401:G:HO2'	2.24	0.56
1:A:9:ARG:NH2	55:K:1629:G:N7	2.54	0.55
19:U:20:LYS:NZ	19:U:73:THR:OG1	2.37	0.55
20:V:107:ASN:OD1	20:V:111:GLU:N	2.40	0.55
40:p:74:THR:O	40:p:78:THR:HG23	2.06	0.55
47:1:20:GLN:O	47:1:173:TYR:OH	2.13	0.55
6:G:139:VAL:HG23	6:G:236:ILE:HG22	1.88	0.55
6:G:190:ARG:HD2	6:G:195:THR:HG21	1.88	0.55
7:H:105:ILE:HD13	7:H:136:VAL:HG23	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:j:35:GLY:O	34:j:45:ARG:NH2	2.36	0.55
54:8:28:VAL:O	54:8:32:ARG:NE	2.39	0.55
55:K:4510:A:O2'	55:K:4511:A:O4'	2.24	0.55
55:K:4729:A:OP2	55:K:5068:G:N2	2.37	0.55
4:E:168:LEU:HD11	4:E:179:THR:CG2	2.36	0.55
45:w:252:ALA:HB1	55:K:4524:G:C2	2.40	0.55
55:K:134:G:H4'	55:K:135:G:O5'	2.06	0.55
55:K:5006:U:H4'	55:K:5007:A:H5'	1.87	0.55
4:E:123:ASP:OD2	42:r:112:ARG:NH2	2.39	0.55
15:Q:73:PRO:O	55:K:1456:C:O2'	2.25	0.55
2:C:232:VAL:CG1	2:C:256:ALA:HB1	2.36	0.55
4:E:289:LEU:HD12	11:M:109:ARG:CZ	2.37	0.55
7:H:40:HIS:ND1	55:K:4701:A:O2'	2.35	0.55
11:M:10:GLY:O	11:M:62:LEU:HD23	2.07	0.55
19:U:29:VAL:HG11	19:U:68:SER:HB3	1.88	0.55
24:Z:14:LEU:HD21	31:g:92:LYS:HE3	1.89	0.55
45:w:89:ILE:HG22	45:w:162:VAL:HG23	1.88	0.55
45:w:119:TYR:OH	45:w:129:ALA:N	2.37	0.55
54:8:129:SER:O	54:8:142:SER:N	2.39	0.55
2:C:290:SER:O	2:C:294:LYS:HG2	2.07	0.55
34:j:48:ASN:OD1	34:j:54:LYS:NZ	2.39	0.55
41:q:14:A:N1	41:q:21:A:O2'	2.38	0.55
47:1:380:ILE:HD11	47:1:421:ALA:HB2	1.87	0.55
50:4:470:LYS:NZ	55:K:395:A:O3'	2.38	0.55
55:K:2000:G:O2'	55:K:2001:G:N7	2.37	0.55
4:E:126:ARG:O	55:K:958:G:O2'	2.23	0.55
12:N:73:ARG:NH1	55:K:32:G:OP1	2.39	0.55
23:Y:85:VAL:HG23	23:Y:85:VAL:O	2.07	0.55
55:K:1398:A:H62	55:K:1419:G:H21	1.55	0.55
55:K:1400:G:H2'	55:K:1401:C:C6	2.42	0.55
55:K:4729:A:OP2	55:K:5068:G:N1	2.37	0.55
54:8:8:THR:OG1	54:8:114:VAL:O	2.24	0.55
55:K:1406:G:N1	55:K:1411(C):C:N3	2.37	0.55
55:K:1481:C:O2'	55:K:1482:G:O5'	2.25	0.55
2:C:232:VAL:HG11	2:C:256:ALA:HB1	1.90	0.54
55:K:125:C:O2'	55:K:126:C:O5'	2.20	0.54
6:G:215:ASP:HB2	6:G:216:PRO:HD3	1.89	0.54
16:R:71:ARG:NE	55:K:3605:C:OP2	2.28	0.54
17:S:82:LEU:HD13	17:S:126:ILE:HD13	1.90	0.54
55:K:3689:G:O2'	55:K:3818:U:OP2	2.26	0.54
5:F:112:ARG:NH2	5:F:204:ASN:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:M:85:LYS:O	11:M:89:THR:HG23	2.07	0.54
15:Q:124:ASP:OD1	15:Q:125:GLN:N	2.40	0.54
27:c:35:LEU:HD11	27:c:63:TYR:CD2	2.43	0.54
46:B:269:ALA:O	46:B:271:PRO:HD3	2.07	0.54
55:K:1406(A):G:N1	55:K:1411(B):C:N3	2.44	0.54
4:E:109:VAL:HG13	4:E:109:VAL:O	2.08	0.54
19:U:28:PRO:HB3	19:U:33:ILE:HD11	1.89	0.54
40:p:2:ALA:N	55:K:1570:G:O6	2.40	0.54
4:E:289:LEU:HD12	11:M:109:ARG:NH1	2.22	0.54
7:H:41:ILE:HG22	7:H:43:VAL:HG13	1.88	0.54
12:N:36:LEU:HD12	12:N:64:ILE:HD12	1.90	0.54
19:U:22:THR:C	19:U:23:LEU:HD12	2.32	0.54
44:v:122:G:H21	44:v:128:C:H5	1.54	0.54
55:K:4378:A:O2'	55:K:4379:A:H2'	2.06	0.54
17:S:99:ASP:OD1	17:S:100:LEU:N	2.39	0.54
29:e:81:ASN:HA	29:e:111:ILE:HD11	1.90	0.54
55:K:1233:G:O2'	55:K:1234:G:OP2	2.22	0.54
14:P:48:LEU:HD21	14:P:91:LEU:HD11	1.89	0.54
18:T:4:THR:O	18:T:9:ARG:NE	2.40	0.54
23:Y:124:LYS:O	23:Y:128:VAL:HG23	2.08	0.54
36:l:25:GLN:O	46:B:247:ARG:CZ	2.55	0.54
55:K:36:U:OP1	55:K:1651:G:N2	2.36	0.54
55:K:1854:G:N2	55:K:4394:A:O4'	2.41	0.54
55:K:2440:U:HO2'	55:K:2441:C:P	2.30	0.54
55:K:2588:C:OP1	55:K:2768:C:O2'	2.19	0.54
50:4:305:MET:HE3	50:4:405:LYS:HD3	1.89	0.54
55:K:1757:U:OP1	55:K:1768:C:N4	2.39	0.54
6:G:215:ASP:HB2	6:G:216:PRO:CD	2.37	0.54
36:l:48:LYS:NZ	55:K:2791:C:OP1	2.28	0.54
38:n:21:ARG:O	38:n:24:SER:OG	2.21	0.54
45:w:48:GLY:HA3	45:w:81:THR:HG22	1.90	0.54
45:w:139:ASP:OD1	45:w:139:ASP:N	2.39	0.54
3:D:276:LYS:O	3:D:280:VAL:HG22	2.08	0.54
42:r:113:ARG:O	42:r:117:ILE:HG12	2.08	0.54
46:B:246:PHE:HD1	50:4:476:LYS:HG3	1.73	0.54
55:K:517:C:H2'	55:K:518:G:H8	1.73	0.54
47:1:291:ILE:HD11	47:1:428:ILE:HG21	1.90	0.53
55:K:1984:A:N6	55:K:2010:A:O2'	2.41	0.53
3:D:93:THR:O	3:D:93:THR:HG22	2.09	0.53
25:a:77:LYS:O	25:a:80:THR:OG1	2.25	0.53
55:K:2701:U:H2'	55:K:2702:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:54:LYS:O	30:f:66:LYS:NZ	2.38	0.53
33:i:42:ASP:OD1	33:i:43:MET:N	2.42	0.53
20:V:80:VAL:HG23	20:V:106:VAL:HG21	1.90	0.53
25:a:26:ARG:NH1	55:K:1655:C:OP2	2.42	0.53
32:h:81:LEU:HD22	44:v:38:U:C2	2.43	0.53
54:8:124:TYR:CD1	54:8:125:ILE:HG23	2.43	0.53
55:K:218:A:O2'	55:K:221:C:OP1	2.27	0.53
55:K:1931:C:O2'	55:K:1932:A:O5'	2.24	0.53
55:K:2378:G:O2'	55:K:2380:G:N7	2.41	0.53
17:S:19:THR:OG1	17:S:22:CYS:SG	2.66	0.53
42:r:85:ASN:O	42:r:89:THR:HG22	2.08	0.53
45:w:80:GLU:OE1	45:w:323:TYR:OH	2.26	0.53
45:w:268:ARG:NE	55:K:4565:C:O2	2.37	0.53
50:4:229:ASP:O	50:4:233:VAL:HG23	2.08	0.53
53:6:81:LEU:HD11	53:6:177:VAL:CG2	2.39	0.53
55:K:964:A:H2'	55:K:965:G:O4'	2.08	0.53
55:K:1300:G:O2'	55:K:1301:C:N4	2.41	0.53
55:K:4925:U:O2'	55:K:4926:C:P	2.66	0.53
1:A:114:CYS:SG	1:A:165:VAL:HG13	2.49	0.53
7:H:128:MET:HE1	7:H:161:ILE:HG21	1.91	0.53
41:q:58:A:O2'	41:q:60:A:OP2	2.14	0.53
42:r:85:ASN:HD22	55:K:690:C:H4'	1.74	0.53
43:u:28:C:H1'	43:u:54:A:H61	1.73	0.53
55:K:485:C:H2'	55:K:486:C:C6	2.44	0.53
55:K:4476:C:O2'	55:K:4478:G:OP2	2.21	0.53
12:N:93:LYS:NZ	55:K:4177:C:OP1	2.39	0.53
18:T:61:THR:OG1	55:K:1799:G:N2	2.40	0.53
29:e:86:GLU:CA	29:e:89:LEU:HD23	2.38	0.53
3:D:62:CYS:HB3	3:D:105:LEU:HD22	1.90	0.53
3:D:179:ARG:NH2	55:K:4323:A:OP1	2.40	0.53
55:K:914:U:H1'	55:K:915:A:C5	2.44	0.53
7:H:92:MET:HE2	7:H:179:ILE:HG22	1.91	0.53
27:c:14:ILE:HD13	27:c:17:ARG:HH21	1.72	0.53
50:4:213:VAL:HG12	50:4:214:CYS:SG	2.49	0.53
55:K:92:C:OP2	55:K:4341:C:O2'	2.19	0.53
55:K:2647:A:H62	55:K:2686:G:H8	1.56	0.53
3:D:285:ALA:O	3:D:289:ARG:HG2	2.09	0.53
20:V:10:SER:OG	20:V:11:GLY:N	2.41	0.53
52:7:10:GLN:NE2	52:7:187:GLY:O	2.41	0.53
55:K:1238:A:HO2'	55:K:1239:C:P	2.31	0.53
25:a:84:GLU:OE2	25:a:87:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:1477:C:HO2'	55:K:1478:C:P	2.30	0.52
55:K:2844:A:O2'	55:K:4631:G:H4'	2.09	0.52
3:D:115:MET:SD	55:K:1819:G:O2'	2.68	0.52
8:I:142:LEU:HD23	8:I:142:LEU:O	2.10	0.52
34:j:33:THR:HG22	34:j:40:PRO:HG2	1.91	0.52
34:j:56:ARG:NE	55:K:375:G:O6	2.42	0.52
55:K:695:G:O2'	55:K:697:G:OP2	2.24	0.52
9:J:98:ASN:O	55:K:4249:G:O2'	2.27	0.52
13:O:108:ILE:HD12	13:O:160:ARG:CZ	2.39	0.52
30:f:91:ASN:O	55:K:440:U:O2'	2.25	0.52
55:K:2638:G:H1	55:K:2697:A:H61	1.56	0.52
55:K:3692:A:H62	55:K:3823:G:N2	2.08	0.52
9:J:40:LEU:HD23	9:J:72:CYS:HB2	1.91	0.52
17:S:157:ARG:NE	55:K:4870:G:O6	2.37	0.52
23:Y:106:ILE:HG21	23:Y:109:LEU:HD23	1.91	0.52
31:g:99:GLU:O	31:g:103:VAL:HG23	2.10	0.52
55:K:963:G:HO2'	55:K:964:A:H8	1.57	0.52
55:K:4182:G:O2'	55:K:4184:G:N7	2.40	0.52
5:F:170:ASP:OD1	5:F:171:ASN:N	2.42	0.52
46:B:248:PHE:N	50:4:476:LYS:O	2.30	0.52
52:7:245:ARG:HB2	52:7:453:ILE:HD12	1.91	0.52
55:K:4371:G:O2'	55:K:4372:U:OP2	2.28	0.52
16:R:30:ASN:O	16:R:34:ASN:ND2	2.43	0.52
45:w:113:GLU:OE1	45:w:168:MET:N	2.33	0.52
50:4:333:PHE:CD1	50:4:359:LEU:HD22	2.45	0.52
53:6:72:MET:O	53:6:76:VAL:HG23	2.10	0.52
1:A:13:GLY:O	1:A:14:SER:OG	2.26	0.52
1:A:77:ILE:HD11	1:A:115:CYS:HB2	1.92	0.52
31:g:46:CYS:SG	31:g:47:GLY:N	2.83	0.52
44:v:105:C:H4'	44:v:106:G:H5''	1.91	0.52
55:K:685:C:O2'	55:K:686:A:OP2	2.18	0.52
55:K:759:G:O6	55:K:904:C:N4	2.43	0.52
4:E:134:LYS:O	4:E:139:HIS:NE2	2.43	0.52
55:K:12:A:H5'	55:K:13:U:OP2	2.10	0.52
55:K:1437:C:O2'	55:K:1438:U:O4'	2.28	0.52
55:K:3603:G:H2'	55:K:3604:A:C8	2.45	0.52
55:K:4237:C:O3'	55:K:4326:G:N2	2.43	0.52
1:A:48:ILE:HD11	1:A:82:ILE:HG22	1.92	0.52
23:Y:82:ILE:HB	23:Y:85:VAL:HG22	1.92	0.52
26:b:117:ARG:NH2	55:K:1272:C:OP1	2.43	0.52
45:w:81:THR:OG1	45:w:207:VAL:HG21	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:237:VAL:HG21	47:1:29:LYS:HG2	1.91	0.52
55:K:922(B):C:H3'	55:K:923:C:H5''	1.90	0.52
55:K:1235:G:O2'	55:K:1236:C:OP2	2.20	0.52
55:K:1276:C:H2'	55:K:1277:G:O4'	2.10	0.52
55:K:3759:A:N6	55:K:3765:G:O2'	2.43	0.52
55:K:3888:G:O2'	55:K:3889:G:OP1	2.23	0.52
55:K:4478:G:O2'	55:K:4602:A:N1	2.42	0.52
1:A:80:GLU:OE2	40:p:73:THR:HG22	2.10	0.52
30:f:89:ARG:NH1	55:K:708:G:O5'	2.43	0.52
45:w:240:LEU:HB3	45:w:244:THR:HG21	1.92	0.52
55:K:2491:C:H2'	55:K:2492:C:H6	1.75	0.52
5:F:106:LYS:HZ3	5:F:110:LEU:HD21	1.75	0.51
7:H:113:GLU:OE1	7:H:115:ARG:NH2	2.43	0.51
17:S:75:VAL:HA	17:S:100:LEU:HD23	1.91	0.51
17:S:82:LEU:HD12	17:S:124:ILE:HG23	1.92	0.51
53:6:53:LEU:HD21	53:6:76:VAL:HG21	1.92	0.51
55:K:2046:G:O2'	55:K:2047:A:OP2	2.18	0.51
47:1:45:CYS:HB3	47:1:77:MET:HE3	1.91	0.51
55:K:1332:C:H2'	55:K:1333:A:H8	1.76	0.51
6:G:142:ARG:NH1	44:v:155:C:OP2	2.41	0.51
6:G:164:LYS:O	6:G:168:LEU:HG	2.09	0.51
7:H:68:ALA:O	55:K:4691:A:O2'	2.29	0.51
13:O:65:ASN:OD1	13:O:67:SER:OG	2.24	0.51
52:7:428:ASP:O	52:7:434:LEU:HD12	2.10	0.51
14:P:36:ILE:O	14:P:36:ILE:HG22	2.10	0.51
18:T:3:ASN:ND2	55:K:4212:A:N1	2.58	0.51
23:Y:11:ARG:NH1	55:K:229:G:OP1	2.41	0.51
26:b:68:ARG:O	26:b:72:ILE:HG22	2.09	0.51
41:q:5:C:H2'	41:q:6:C:C6	2.45	0.51
5:F:106:LYS:O	5:F:110:LEU:HG	2.10	0.51
5:F:205:ASN:ND2	55:K:1841:C:OP2	2.42	0.51
9:J:157:ILE:HG22	9:J:158:SER:N	2.26	0.51
55:K:643:C:H2'	55:K:644:G:H8	1.76	0.51
55:K:1768:C:H4'	55:K:1769:G:H5''	1.91	0.51
7:H:95:VAL:HG22	37:m:56:LEU:HB3	1.93	0.51
16:R:84:THR:O	16:R:87:ALA:N	2.43	0.51
30:f:28:LEU:CG	30:f:101:ILE:HD11	2.39	0.51
36:l:29:MET:HE3	46:B:247:ARG:HH11	1.75	0.51
36:l:29:MET:SD	44:v:75:G:O2'	2.68	0.51
37:m:71:ARG:NH1	55:K:4424:A:OP1	2.44	0.51
53:6:117:ILE:HB	53:6:118:PRO:HD3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:1296:G:HO2'	55:K:1297:U:H6	1.58	0.51
2:C:338:ASN:C	2:C:340:ILE:H	2.19	0.51
14:P:66:GLY:N	55:K:3893:C:OP1	2.41	0.51
55:K:978:G:N2	55:K:1277:G:H22	2.08	0.51
55:K:4396:A:OP1	55:K:4443:C:O2'	2.20	0.51
3:D:83:LEU:HB3	3:D:88:VAL:CG2	2.40	0.51
23:Y:10:ASP:OD1	23:Y:11:ARG:N	2.44	0.51
31:g:11:LEU:HD23	31:g:13:TYR:H	1.76	0.51
36:l:20:ASN:O	36:l:41:ARG:NH2	2.44	0.51
47:1:32:VAL:HG22	47:1:175:LEU:HD11	1.93	0.51
47:1:380:ILE:CD1	47:1:421:ALA:HB2	2.41	0.51
55:K:2553:A:H2	55:K:2765:A:H62	1.58	0.51
2:C:150:LEU:O	2:C:152:LEU:N	2.44	0.51
2:C:208:CYS:SG	2:C:230:LEU:HD12	2.51	0.51
3:D:163:LEU:O	3:D:167:VAL:HG23	2.11	0.51
4:E:233:GLY:O	4:E:237:ASP:HA	2.11	0.51
8:I:65:LEU:HD23	8:I:159:PHE:HE1	1.76	0.51
9:J:31:ASP:OD2	9:J:35:ARG:NE	2.33	0.51
29:e:77:PHE:HB3	29:e:88:LEU:HD11	1.93	0.51
46:B:227:SER:O	46:B:230:VAL:HG22	2.11	0.51
55:K:3888:G:HO2'	55:K:3889:G:P	2.33	0.51
55:K:4493:U:H5	55:K:4512:U:HO2'	1.58	0.51
12:N:68:ARG:NH2	55:K:303:C:OP2	2.39	0.51
18:T:108:ARG:NH2	55:K:1837:A:OP1	2.44	0.51
42:r:26:SER:HG	42:r:28:GLU:CD	2.19	0.51
55:K:1317:U:H2'	55:K:1318:C:C6	2.46	0.51
55:K:1978:C:O2'	55:K:1989:G:N2	2.43	0.51
2:C:134:PRO:HA	2:C:150:LEU:HD11	1.91	0.50
15:Q:122:THR:HG22	15:Q:123:PHE:H	1.75	0.50
47:1:130:VAL:O	47:1:134:THR:HG23	2.11	0.50
55:K:1377:G:H21	55:K:1380:G:H5'	1.76	0.50
55:K:1445:U:O2'	55:K:1446:C:OP1	2.29	0.50
55:K:1991:A:OP1	55:K:1991:A:H4'	2.10	0.50
55:K:4412:C:H2'	55:K:4413:C:O2	2.11	0.50
2:C:348:LYS:HA	2:C:351:VAL:HG22	1.92	0.50
12:N:148:THR:O	12:N:151:ILE:HG22	2.11	0.50
32:h:66:LYS:O	32:h:70:ARG:HG2	2.11	0.50
39:o:104:ILE:HD13	41:q:56:C:C4	2.46	0.50
52:7:438:GLU:OE1	52:7:450:GLN:NE2	2.44	0.50
55:K:2041:A:N7	55:K:4434:C:O2'	2.42	0.50
5:F:91:VAL:HG13	5:F:139:ILE:HD12	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:115:ARG:HG2	7:H:123:ILE:HG22	1.94	0.50
14:P:114:ILE:HA	14:P:150:LEU:HD22	1.93	0.50
30:f:40:GLU:O	30:f:109:ARG:NH2	2.39	0.50
45:w:218:ASP:OD2	45:w:348:ARG:NH2	2.42	0.50
47:1:289:ILE:HG21	47:1:379:TRP:CE2	2.46	0.50
55:K:100:C:H2'	55:K:101:A:O4'	2.11	0.50
55:K:1326:A:H2'	55:K:1327:C:C6	2.47	0.50
55:K:1478:C:H2'	55:K:1479:G:H8	1.77	0.50
55:K:3598:C:H2'	55:K:3599:A:H8	1.76	0.50
55:K:3656:A:O2'	55:K:3747:A:O2'	2.17	0.50
13:O:116:LYS:HD2	17:S:169:THR:HG23	1.93	0.50
55:K:1440:U:O2'	55:K:1441:C:P	2.69	0.50
14:P:74:LYS:NZ	55:K:4970:C:OP1	2.27	0.50
19:U:61:VAL:HG12	19:U:74:SER:HB2	1.93	0.50
32:h:56:ARG:NH1	44:v:65:A:OP1	2.43	0.50
50:4:201:ASN:OD1	50:4:202:GLU:N	2.43	0.50
55:K:1442:C:C2	55:K:2112:G:N2	2.78	0.50
55:K:4208:U:H2'	55:K:4209:G:H8	1.76	0.50
55:K:4964:C:N4	55:K:4965:U:O4	2.45	0.50
10:L:197:LYS:NZ	55:K:4359:U:OP1	2.44	0.50
14:P:24:VAL:HG12	14:P:25:HIS:H	1.75	0.50
14:P:127:ARG:NH2	55:K:2422:C:OP1	2.45	0.50
18:T:81:LYS:O	26:b:16:TRP:NE1	2.45	0.50
47:1:248:THR:OG1	47:1:441:ILE:N	2.44	0.50
54:8:36:TYR:CE1	54:8:83:LEU:HD11	2.46	0.50
55:K:1475:G:H2'	55:K:1476:C:C6	2.46	0.50
55:K:1910:G:O2'	55:K:1917:A:N1	2.37	0.50
55:K:1920:C:H3'	55:K:1921:C:H5''	1.94	0.50
55:K:4067:U:H2'	55:K:4068:U:C6	2.47	0.50
55:K:4925:U:HO2'	55:K:4926:C:P	2.34	0.50
2:C:323:ARG:NH2	55:K:1280:C:OP1	2.44	0.50
3:D:75:VAL:O	3:D:112:ARG:NH1	2.44	0.50
31:g:54:ARG:NH2	55:K:2653:C:OP1	2.44	0.50
55:K:275:C:O2'	55:K:276:C:O5'	2.22	0.50
55:K:1076:C:H2'	55:K:1077:C:C6	2.46	0.50
55:K:1440:U:HO2'	55:K:1441:C:P	2.34	0.50
55:K:3644:U:O2	55:K:4554:G:O2'	2.24	0.50
55:K:4574:U:H3'	55:K:4575:G:H5''	1.93	0.50
5:F:49:ILE:HD12	5:F:185:CYS:SG	2.52	0.50
15:Q:89:ASP:OD1	15:Q:91:ARG:NH1	2.45	0.50
28:d:52:PHE:O	28:d:56:GLU:HG2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:g:66:ARG:NH1	55:K:2517:A:O2'	2.45	0.50
36:l:48:LYS:NZ	55:K:2406:G:O2'	2.45	0.50
47:1:89:LEU:HD12	47:1:293:LEU:HD22	1.94	0.50
47:1:234:PHE:CE2	47:1:242:LEU:HD23	2.47	0.50
2:C:195:LYS:NZ	55:K:2334:C:OP2	2.43	0.50
10:L:64:VAL:HG12	55:K:71:C:H4'	1.93	0.50
16:R:6:LEU:HD21	16:R:10:LEU:HD11	1.93	0.50
34:j:56:ARG:NH2	55:K:375:G:N7	2.60	0.50
55:K:485:C:O2'	55:K:486:C:O5'	2.24	0.50
55:K:1548:G:O2'	55:K:2812:A:N3	2.39	0.50
8:I:86:HIS:HB3	8:I:139:ARG:HG2	1.93	0.49
12:N:45:PRO:O	12:N:49:ARG:HG3	2.12	0.49
18:T:84:ILE:HG13	26:b:21:ILE:HG22	1.92	0.49
52:7:241:GLN:NE2	52:7:461:GLU:OE1	2.44	0.49
3:D:59:ASP:OD1	3:D:60:ILE:N	2.45	0.49
4:E:245:ILE:HD12	4:E:245:ILE:N	2.26	0.49
11:M:123:ILE:O	11:M:127:VAL:HG23	2.13	0.49
13:O:54:TYR:CD1	13:O:145:VAL:HG21	2.46	0.49
14:P:83:TRP:O	55:K:3856:A:H5''	2.12	0.49
29:e:86:GLU:OE1	29:e:86:GLU:N	2.44	0.49
55:K:245:C:HO2'	55:K:246:G:P	2.29	0.49
55:K:2718:U:H5''	55:K:2719:C:H5'	1.93	0.49
55:K:3625:G:O2'	55:K:3626:G:P	2.70	0.49
4:E:48:ARG:NH2	55:K:981:C:OP1	2.44	0.49
10:L:56:ARG:NH1	10:L:74:ARG:O	2.45	0.49
10:L:106:SER:OG	10:L:107:THR:N	2.43	0.49
14:P:12:THR:HG23	50:4:414:GLU:CD	2.37	0.49
23:Y:126:ARG:NH2	55:K:198:A:OP1	2.44	0.49
46:B:246:PHE:C	50:4:476:LYS:HA	2.37	0.49
55:K:958:G:N2	55:K:1285:U:OP1	2.29	0.49
6:G:195:THR:HG22	6:G:199:LEU:HD23	1.93	0.49
16:R:98:ARG:NH2	16:R:130:ASN:OD1	2.45	0.49
55:K:1743:A:N1	55:K:1789:C:O2'	2.41	0.49
55:K:1881:C:H5'	55:K:2281:U:H1'	1.94	0.49
55:K:1957:U:C2	55:K:1958:A:C8	2.99	0.49
55:K:1982:G:N2	55:K:2009:A:H4'	2.28	0.49
55:K:3934:G:H2'	55:K:3935:C:C6	2.47	0.49
15:Q:32:TYR:CE2	15:Q:47:VAL:HG11	2.47	0.49
22:X:150:ALA:HB1	22:X:155:ILE:HG13	1.93	0.49
27:c:10:SER:O	27:c:13:SER:OG	2.30	0.49
55:K:1197:C:H2'	55:K:1198:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:284:MET:HA	15:Q:122:THR:HG21	1.94	0.49
8:I:14:ASN:O	8:I:128:ARG:NH2	2.41	0.49
26:b:18:ARG:NH1	55:K:1669:A:OP1	2.40	0.49
55:K:658:C:N4	55:K:659:G:O6	2.43	0.49
55:K:1942:A:H2'	55:K:1943:A:H8	1.77	0.49
4:E:234:GLU:HG3	50:4:319:HIS:NE2	2.27	0.49
13:O:54:TYR:CE1	13:O:58:LEU:HD21	2.48	0.49
28:d:124:GLU:N	28:d:124:GLU:OE1	2.45	0.49
55:K:2627:C:H2'	55:K:2628:U:C6	2.48	0.49
9:J:26:VAL:HG23	9:J:28:GLU:H	1.77	0.49
37:m:54:PRO:O	37:m:58:GLN:HG2	2.12	0.49
55:K:1336:G:N1	55:K:2348:G:OP2	2.36	0.49
55:K:1384:C:O2'	55:K:1505:C:OP1	2.28	0.49
55:K:1914:C:OP2	55:K:1915:C:O2'	2.21	0.49
28:d:26:THR:HG23	55:K:4996:C:H4'	1.93	0.49
42:r:32:LEU:O	42:r:33:LYS:HB2	2.13	0.49
43:u:78:C:O2'	55:K:1736:A:N3	2.46	0.49
55:K:1411:C:H2'	55:K:1411(A):G:C8	2.48	0.49
55:K:1475:G:N2	55:K:1490:G:C4	2.81	0.49
55:K:3707:U:H2'	55:K:3708:C:C6	2.48	0.49
3:D:140:GLY:O	55:K:1819:G:O2'	2.23	0.49
10:L:66:TYR:OH	55:K:1382:G:OP1	2.17	0.49
13:O:110:PRO:N	13:O:111:PRO:CD	2.76	0.49
23:Y:45:ARG:NH2	55:K:238:C:OP2	2.46	0.49
23:Y:82:ILE:HG22	23:Y:83:GLU:N	2.28	0.49
25:a:76:ASP:OD1	25:a:76:ASP:N	2.46	0.49
43:u:83:A:O2'	43:u:85:G:OP1	2.29	0.49
45:w:243:LYS:NZ	55:K:2854:G:O6	2.46	0.49
47:1:5:PHE:CZ	47:1:9:ILE:HD11	2.48	0.49
4:E:144:ARG:HH21	4:E:147:ILE:HD11	1.78	0.48
27:c:29:LEU:HD13	27:c:89:TYR:HE2	1.77	0.48
44:v:155:C:H2'	44:v:156:U:O4'	2.13	0.48
46:B:248:PHE:CD2	50:4:476:LYS:HB3	2.48	0.48
47:1:192:VAL:HG21	49:3:48:GLY:HA3	1.94	0.48
55:K:1762:C:N3	55:K:1763:C:N4	2.60	0.48
55:K:4537:C:H2'	55:K:4538:G:H8	1.77	0.48
55:K:4719:G:H4'	55:K:4720:C:OP1	2.13	0.48
2:C:266:THR:HG23	2:C:269:LYS:H	1.78	0.48
8:I:171:TRP:O	8:I:174:THR:OG1	2.26	0.48
22:X:109:ILE:O	22:X:113:VAL:HG23	2.12	0.48
55:K:705:G:H2'	55:K:706:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:983:C:H2'	55:K:984:C:C6	2.48	0.48
4:E:167:PHE:HA	4:E:178:VAL:HG23	1.95	0.48
10:L:42:ARG:O	10:L:46:ILE:HG12	2.13	0.48
16:R:62:ARG:NH1	55:K:4645:C:OP2	2.45	0.48
25:a:59:ARG:NH2	25:a:61:TYR:OH	2.46	0.48
36:l:48:LYS:O	36:l:50:GLY:N	2.47	0.48
47:1:9:ILE:O	47:1:9:ILE:HG22	2.14	0.48
52:7:477:VAL:HG11	53:6:1:MET:HE3	1.95	0.48
55:K:2804:C:C2	55:K:2805:C:C5	3.01	0.48
55:K:3625:G:HO2'	55:K:3626:G:P	2.34	0.48
55:K:4258:C:H2'	55:K:4259:C:H6	1.78	0.48
56:9:90:LEU:HD23	56:9:92:ILE:CD1	2.44	0.48
2:C:149:GLU:OE2	42:r:71:ARG:NE	2.46	0.48
10:L:140:SER:N	10:L:143:GLU:OE1	2.46	0.48
45:w:80:GLU:HG3	45:w:326:VAL:HG13	1.95	0.48
55:K:2485:U:H2'	55:K:2486:G:C8	2.47	0.48
55:K:2553:A:O2'	55:K:2554:U:OP2	2.29	0.48
55:K:3695:U:H2'	55:K:3696:C:O4'	2.13	0.48
55:K:4260:U:H2'	55:K:4261:C:C6	2.48	0.48
55:K:5061:A:H3'	55:K:5062:G:H5'	1.95	0.48
1:A:112:ILE:HD13	1:A:135:THR:HG22	1.94	0.48
5:F:175:ALA:HB1	55:K:2102:G:C8	2.49	0.48
6:G:218:GLU:OE2	12:N:22:LEU:HD13	2.14	0.48
7:H:5:LEU:HD13	7:H:60:TRP:CH2	2.48	0.48
13:O:176:ARG:HD3	55:K:4769:G:H5'	1.95	0.48
16:R:60:ARG:HG3	16:R:60:ARG:O	2.14	0.48
55:K:138:G:H2'	55:K:139:G:C8	2.47	0.48
55:K:2502:A:HO2'	55:K:2503:G:P	2.33	0.48
55:K:4921:C:H4'	55:K:4922:C:OP1	2.13	0.48
2:C:348:LYS:O	2:C:352:GLU:HG2	2.13	0.48
6:G:126:ARG:NE	55:K:4076:G:OP1	2.42	0.48
9:J:53:ALA:HB2	9:J:68:ILE:HD11	1.94	0.48
33:i:93:VAL:O	33:i:97:MET:HG3	2.13	0.48
37:m:69:ILE:HD12	55:K:4473:A:H5''	1.96	0.48
55:K:1786:A:H2'	55:K:1789:C:C5	2.49	0.48
4:E:165:VAL:CG2	4:E:178:VAL:HG21	2.43	0.48
6:G:139:VAL:HG22	6:G:140:LEU:H	1.79	0.48
9:J:157:ILE:HG22	9:J:158:SER:H	1.78	0.48
42:r:85:ASN:OD1	42:r:88:ALA:HB3	2.13	0.48
52:7:442:SER:HA	52:7:448:VAL:HG21	1.94	0.48
54:8:14:ILE:O	54:8:18:THR:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:3848:U:H2'	55:K:3849:A:C8	2.49	0.48
2:C:76:ILE:HD12	2:C:77:PRO:HD2	1.95	0.48
15:Q:178:ARG:H	25:a:51:GLY:HA2	1.79	0.48
36:l:6:THR:OG1	36:l:9:ILE:HD12	2.13	0.48
46:B:260:THR:HG22	55:K:2794:C:C2	2.49	0.48
55:K:420:A:HO2'	55:K:1331:C:HO2'	1.62	0.48
2:C:287:THR:OG1	42:r:2:SER:OG	2.23	0.48
6:G:141:ASP:OD1	6:G:143:GLN:N	2.47	0.48
37:m:74:TYR:O	55:K:4472:G:O2'	2.29	0.48
55:K:480:C:O2'	55:K:481:G:P	2.72	0.48
55:K:1477:C:O2'	55:K:1478:C:P	2.71	0.48
55:K:1477:C:H2'	55:K:1478:C:C6	2.49	0.48
55:K:3910:C:H2'	55:K:3911:C:C6	2.49	0.48
55:K:4077:A:N1	55:K:4171:C:N4	2.60	0.48
3:D:215:ASP:OD1	3:D:215:ASP:N	2.47	0.48
26:b:11:ASN:ND2	55:K:1669:A:OP1	2.37	0.48
32:h:80:PRO:HD2	32:h:83:LEU:HD12	1.96	0.48
55:K:986:C:H2'	55:K:987:C:H6	1.79	0.48
55:K:4724:A:H2'	55:K:4725:C:O4'	2.14	0.48
1:A:220:GLY:O	55:K:4542:U:O2'	2.31	0.47
5:F:148:SER:OG	5:F:244:ARG:NH1	2.35	0.47
8:I:118:ALA:O	55:K:1864:G:O2'	2.28	0.47
45:w:389:MET:O	55:K:5041:G:N1	2.39	0.47
55:K:495:C:H2'	55:K:496:G:O4'	2.14	0.47
55:K:1437:C:O2'	55:K:1438:U:O5'	2.28	0.47
55:K:1772:C:H2'	55:K:1773:U:O4'	2.14	0.47
55:K:1846:G:H2'	55:K:1847:C:C6	2.49	0.47
55:K:4944:C:H4'	55:K:4944:C:OP1	2.13	0.47
5:F:215:PRO:HD3	5:F:246:MET:HE2	1.96	0.47
13:O:180:GLN:OE1	13:O:184:ASN:ND2	2.42	0.47
45:w:89:ILE:HD11	45:w:150:PHE:HE1	1.78	0.47
46:B:218:THR:HB	49:3:61:ILE:HD11	1.96	0.47
52:7:299:LEU:HD22	52:7:312:PHE:CE1	2.49	0.47
55:K:326:C:N4	55:K:327:U:O4	2.47	0.47
55:K:3890:A:N6	55:K:4571:A:O4'	2.47	0.47
55:K:4119:C:HO2'	55:K:4120:U:C5'	2.25	0.47
55:K:4582:C:N4	55:K:4722:G:O6	2.47	0.47
55:K:4988:U:HO2'	55:K:5061:A:H2	1.62	0.47
6:G:216:PRO:HG2	6:G:219:LEU:HD13	1.95	0.47
18:T:39:ILE:O	18:T:99:SER:OG	2.28	0.47
22:X:139:ARG:NH2	55:K:2534:C:OP1	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:b:40:LEU:O	26:b:44:ARG:HG3	2.13	0.47
27:c:64:ALA:HB1	27:c:69:THR:HB	1.96	0.47
50:4:470:LYS:NZ	55:K:395:A:O2'	2.42	0.47
55:K:1942:A:OP2	55:K:2040:A:N6	2.46	0.47
55:K:4572:U:H2'	55:K:4573:G:C8	2.49	0.47
56:9:103:LEU:H	56:9:103:LEU:HD12	1.79	0.47
12:N:99:GLN:O	12:N:103:GLU:HG3	2.13	0.47
25:a:88:VAL:O	25:a:92:LYS:HG2	2.14	0.47
31:g:37:LYS:NZ	55:K:2516:G:OP2	2.37	0.47
43:u:73:U:OP2	43:u:74:A:O2'	2.23	0.47
55:K:35:U:H5'	55:K:36:U:OP2	2.15	0.47
55:K:180:C:N4	55:K:256:G:O6	2.43	0.47
55:K:519:C:H2'	55:K:520:U:H6	1.80	0.47
55:K:1882:U:C4	55:K:2279:A:C2	3.02	0.47
55:K:2539:C:H2'	55:K:2540:C:C6	2.49	0.47
55:K:3873:G:H2'	55:K:3874:G:C8	2.50	0.47
55:K:4735:G:HO2'	55:K:4736:C:H6	1.59	0.47
9:J:44:THR:O	9:J:78:LYS:NZ	2.47	0.47
15:Q:11:ARG:HG3	55:K:2081:C:H5''	1.97	0.47
15:Q:25:LEU:O	15:Q:29:VAL:HG23	2.14	0.47
47:1:298:VAL:HG22	47:1:345:LEU:HD23	1.96	0.47
55:K:451:C:O2'	55:K:1293:G:H2'	2.14	0.47
55:K:691:C:H2'	55:K:692:A:C8	2.50	0.47
55:K:1308:C:H2'	55:K:1309:C:C6	2.49	0.47
55:K:4537:C:N4	55:K:4550:G:O6	2.48	0.47
6:G:267:ALA:O	6:G:271:LEU:HG	2.15	0.47
12:N:6:TYR:CE1	33:i:40:VAL:HG13	2.49	0.47
16:R:7:GLN:HG2	16:R:32:ILE:HG22	1.95	0.47
30:f:68:ARG:NH1	55:K:442:G:OP1	2.43	0.47
44:v:111:U:H4'	44:v:112:G:H5'	1.97	0.47
45:w:234:ARG:NH1	55:K:4566:U:O2'	2.47	0.47
53:6:2:THR:HG22	53:6:125:GLY:O	2.15	0.47
55:K:175:C:H2'	55:K:176:G:H8	1.80	0.47
55:K:914:U:O2'	55:K:915:A:O4'	2.32	0.47
55:K:1798:G:H2'	55:K:1799:G:H5''	1.96	0.47
55:K:2089:G:H1'	55:K:2090:U:OP2	2.14	0.47
3:D:222:GLN:O	43:u:48:G:O2'	2.27	0.47
4:E:179:THR:CB	4:E:189:LEU:HD23	2.45	0.47
12:N:12:ARG:NH2	55:K:279:A:OP2	2.45	0.47
13:O:47:PHE:HA	13:O:136:ALA:HB2	1.96	0.47
20:V:85:ARG:N	20:V:101:ASN:OD1	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:57:VAL:HA	23:Y:104:VAL:HG23	1.95	0.47
27:c:17:ARG:NH1	27:c:103:ASP:OD1	2.38	0.47
30:f:56:ASN:OD1	30:f:66:LYS:NZ	2.43	0.47
45:w:71:GLU:OE1	45:w:71:GLU:N	2.44	0.47
45:w:343:ARG:NH2	55:K:4976:U:O3'	2.47	0.47
47:1:39:LEU:HD11	47:1:185:THR:HG21	1.97	0.47
55:K:219:G:H2'	55:K:219:G:N3	2.30	0.47
55:K:392:U:H2'	55:K:393:U:C6	2.50	0.47
55:K:404:U:N3	55:K:411:G:O6	2.48	0.47
55:K:678:C:H2'	55:K:679:C:C6	2.49	0.47
55:K:738:C:OP1	55:K:739:G:H4'	2.14	0.47
55:K:2495:U:H2'	55:K:2496:G:H8	1.80	0.47
55:K:2503:G:N2	55:K:4084:G:C8	2.83	0.47
55:K:3652:A:H2'	55:K:3653:A:C8	2.50	0.47
55:K:3725:G:N1	55:K:3728:A:OP2	2.44	0.47
8:I:66:GLU:OE2	8:I:69:ARG:NH2	2.48	0.47
10:L:140:SER:OG	10:L:143:GLU:OE1	2.22	0.47
32:h:53:SER:O	32:h:57:VAL:HG23	2.14	0.47
42:r:114:ALA:O	42:r:118:LEU:HD23	2.15	0.47
55:K:1552:G:O2'	55:K:1574:G:N2	2.44	0.47
55:K:4524:G:OP2	55:K:4524:G:H4'	2.15	0.47
1:A:180:LEU:HD22	40:p:18:TYR:HB3	1.96	0.47
11:M:119:ARG:HG2	11:M:123:ILE:HD12	1.96	0.47
18:T:108:ARG:NH1	55:K:1836:G:O2'	2.43	0.47
36:l:2:SER:O	36:l:5:LYS:NZ	2.47	0.47
40:p:59:SER:OG	40:p:60:CYS:N	2.48	0.47
45:w:10:ARG:NH1	45:w:11:HIS:O	2.48	0.47
47:1:288:ASN:OD1	47:1:452:THR:HB	2.14	0.47
47:1:406:GLU:O	47:1:410:VAL:HG23	2.15	0.47
50:4:181:LEU:HD21	50:4:184:ASP:HB2	1.97	0.47
55:K:1449:C:O2	55:K:2105:A:O2'	2.25	0.47
55:K:3910:C:H2'	55:K:3911:C:H6	1.80	0.47
55:K:4761:G:H2'	55:K:4762:A:H8	1.79	0.47
55:K:5034:A:H2'	55:K:5035:U:O4'	2.15	0.47
1:A:44:ILE:HD11	1:A:46:LYS:NZ	2.29	0.47
1:A:117:GLU:HB2	1:A:162:ASN:HB2	1.96	0.47
42:r:14:SER:OG	42:r:15:SER:N	2.46	0.47
54:8:119:PHE:CZ	56:9:116:MET:HE1	2.49	0.47
55:K:2467:U:H4'	55:K:2468:U:H5'	1.96	0.47
55:K:2689:C:H2'	55:K:2690:C:H6	1.80	0.47
55:K:3725:G:N2	55:K:3728:A:OP2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:265:LYS:NZ	55:K:4933:C:OP2	2.48	0.46
5:F:79:ASN:HA	18:T:143:THR:HG22	1.97	0.46
13:O:185:VAL:HG12	13:O:185:VAL:O	2.15	0.46
15:Q:151:HIS:ND1	15:Q:164:LYS:O	2.47	0.46
18:T:70:HIS:NE2	55:K:4327:C:OP1	2.48	0.46
33:i:39:PHE:O	33:i:42:ASP:OD1	2.34	0.46
55:K:4119:C:H4'	55:K:4120:U:OP1	2.15	0.46
7:H:87:GLY:O	7:H:186:THR:HG22	2.14	0.46
42:r:96:MET:HE3	55:K:678:C:O2'	2.15	0.46
45:w:252:ALA:HB1	55:K:4524:G:C4	2.50	0.46
50:4:225:LEU:N	50:4:243:ASP:OD1	2.43	0.46
55:K:478:G:H2'	55:K:479:G:H8	1.80	0.46
55:K:751:G:H5'	55:K:752:G:OP2	2.15	0.46
55:K:1174:G:HO2'	55:K:1175:A:P	2.35	0.46
55:K:1236:C:O2'	55:K:1238:A:OP1	2.32	0.46
55:K:2640:G:O6	55:K:2693:G:O2'	2.23	0.46
55:K:4371:G:HO2'	55:K:4372:U:P	2.39	0.46
3:D:289:ARG:HA	3:D:292:GLU:HG2	1.96	0.46
11:M:95:ILE:O	11:M:99:GLU:HG3	2.16	0.46
25:a:36:GLY:HA3	25:a:40:HIS:CE1	2.51	0.46
39:o:2:VAL:HG22	39:o:3:ASN:H	1.81	0.46
55:K:351:C:N4	55:K:352:G:O6	2.49	0.46
55:K:1932:A:H2'	55:K:1933:G:C8	2.50	0.46
55:K:3598:C:H2'	55:K:3599:A:C8	2.51	0.46
55:K:4129:G:O6	55:K:4156:G:N2	2.48	0.46
7:H:92:MET:SD	7:H:161:ILE:HD11	2.55	0.46
15:Q:63:LEU:O	15:Q:67:ILE:HG12	2.14	0.46
17:S:111:ARG:NH2	55:K:2062:C:O2'	2.48	0.46
47:1:58:SER:OG	47:1:73:ARG:NH2	2.49	0.46
52:7:26:LEU:HD11	52:7:28:THR:OG1	2.14	0.46
52:7:250:ASN:HB3	52:7:259:LEU:HD12	1.97	0.46
55:K:684:G:H4'	55:K:685:C:OP2	2.15	0.46
55:K:739:G:C6	55:K:926:G:C5	3.04	0.46
55:K:2411:C:O2'	55:K:2526:C:O2	2.31	0.46
55:K:4413:C:H2'	55:K:4414:A:O4'	2.15	0.46
55:K:4414:A:OP2	55:K:4422:A:N6	2.49	0.46
55:K:4884:G:O2'	55:K:4885:U:P	2.74	0.46
6:G:103:ASP:OD1	6:G:105:THR:HG23	2.15	0.46
8:I:98:ARG:NH2	55:K:1865:G:OP2	2.49	0.46
14:P:41:ILE:O	14:P:45:THR:HG23	2.16	0.46
40:p:4:ARG:NH2	55:K:1555:G:N7	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:1300:G:HO2'	55:K:1301:C:N4	2.13	0.46
55:K:1402:C:H2'	55:K:1403:G:C8	2.51	0.46
6:G:163:LYS:O	6:G:167:LEU:HG	2.16	0.46
6:G:273:GLU:O	6:G:277:THR:HG22	2.16	0.46
9:J:13:ARG:NH1	9:J:154:LYS:O	2.48	0.46
11:M:132:ARG:NE	55:K:4895:C:O2	2.48	0.46
17:S:127:MET:HE1	18:T:155:PRO:HA	1.98	0.46
52:7:9:MET:HE3	52:7:93:LEU:HD23	1.98	0.46
52:7:205:VAL:HG22	52:7:373:THR:OG1	2.15	0.46
55:K:910:G:H2'	55:K:911:U:H6	1.81	0.46
55:K:1327:C:H2'	55:K:1328:G:H8	1.79	0.46
55:K:3599:A:H2'	55:K:3600:G:C8	2.51	0.46
55:K:4349:C:H3'	55:K:4350:C:H5'	1.98	0.46
55:K:4660:G:H2'	55:K:4661:G:H5''	1.97	0.46
5:F:213:SER:OG	5:F:214:SER:N	2.47	0.46
9:J:94:LEU:O	9:J:175:LEU:HD23	2.16	0.46
13:O:193:THR:HG23	13:O:202:LEU:HD23	1.98	0.46
52:7:24:ALA:O	52:7:102:TYR:OH	2.33	0.46
54:8:14:ILE:HG21	54:8:105:PHE:CE1	2.51	0.46
55:K:3770:U:H2'	55:K:3771:C:C6	2.50	0.46
55:K:3911:C:C2	55:K:3912:U:C5	3.04	0.46
55:K:4926:C:H3'	55:K:4927:G:H5''	1.97	0.46
7:H:12:ILE:HD13	7:H:18:ILE:HG21	1.98	0.46
22:X:112:ALA:O	22:X:116:LEU:HG	2.16	0.46
45:w:89:ILE:HD11	45:w:150:PHE:CE1	2.51	0.46
50:4:170:THR:HG21	50:4:377:GLU:HA	1.98	0.46
50:4:337:PHE:CE1	50:4:360:LEU:HD11	2.51	0.46
55:K:2552:G:N2	55:K:2767:U:C4	2.84	0.46
2:C:53:ALA:O	44:v:26:C:O2'	2.30	0.46
3:D:8:LYS:HA	3:D:12:TYR:CD2	2.50	0.46
3:D:203:ASN:OD1	3:D:204:VAL:N	2.49	0.46
12:N:104:GLU:HA	12:N:160:GLU:HG3	1.97	0.46
22:X:101:ASP:OD1	22:X:102:VAL:N	2.49	0.46
26:b:9:THR:O	26:b:9:THR:HG22	2.16	0.46
54:8:11:ILE:HD11	54:8:114:VAL:HG11	1.97	0.46
55:K:757:G:O2'	55:K:758:G:O5'	2.32	0.46
55:K:1090:G:H2'	55:K:1091:C:C6	2.50	0.46
55:K:2292:C:H2'	55:K:2293:U:C6	2.51	0.46
55:K:2632:U:H2'	55:K:2633:U:C6	2.51	0.46
55:K:4354:U:O2	55:K:4354:U:H2'	2.15	0.46
4:E:165:VAL:HG23	4:E:178:VAL:HG21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:15:CYS:SG	14:P:150:LEU:HB2	2.56	0.46
22:X:122:ALA:HB3	22:X:139:ARG:O	2.16	0.46
24:Z:117:LYS:HA	24:Z:120:GLU:HG2	1.98	0.46
26:b:117:ARG:NH2	55:K:1273:G:OP2	2.47	0.46
30:f:37:ASP:OD1	30:f:37:ASP:N	2.49	0.46
35:k:54:GLU:O	35:k:58:GLN:HG3	2.15	0.46
52:7:174:LEU:HD13	52:7:225:ALA:C	2.40	0.46
55:K:1198:G:H2'	55:K:1199:G:C8	2.50	0.46
55:K:1370:G:H4'	55:K:1371:A:O5'	2.15	0.46
55:K:3904:G:H1'	55:K:3905:A:OP1	2.15	0.46
55:K:4413:C:H5	55:K:4429:C:H42	1.64	0.46
7:H:93:ARG:HE	7:H:143:GLU:HB3	1.81	0.45
8:I:115:MET:HE3	55:K:1868:A:H61	1.80	0.45
8:I:115:MET:HG3	8:I:115:MET:O	2.16	0.45
12:N:169:ARG:HE	12:N:174:LEU:HD11	1.81	0.45
13:O:185:VAL:HG12	13:O:189:ILE:HG23	1.97	0.45
19:U:44:GLN:HA	19:U:56:LEU:HD21	1.98	0.45
47:1:252:PHE:CE2	47:1:256:ILE:HD11	2.51	0.45
50:4:333:PHE:CG	50:4:359:LEU:HD22	2.50	0.45
55:K:1942:A:H2'	55:K:1943:A:C8	2.51	0.45
55:K:4384:U:O2'	55:K:4386:C:OP1	2.25	0.45
11:M:62:LEU:HD23	11:M:62:LEU:H	1.81	0.45
15:Q:23:ILE:HD12	42:r:5:LEU:HD12	1.99	0.45
22:X:82:THR:O	47:1:404:HIS:NE2	2.49	0.45
46:B:241:LYS:C	46:B:243:MET:H	2.25	0.45
52:7:375:LEU:C	52:7:375:LEU:HD23	2.41	0.45
55:K:269:G:H2'	55:K:270:U:H6	1.80	0.45
55:K:519:C:H2'	55:K:520:U:C6	2.51	0.45
55:K:3700:C:H2'	55:K:3746:A:H61	1.81	0.45
55:K:5001:U:H2'	55:K:5002:U:O4'	2.17	0.45
22:X:83:THR:HG21	55:K:2434:G:H5'	1.97	0.45
27:c:45:LEU:HD12	27:c:70:GLY:O	2.16	0.45
34:j:48:ASN:N	55:K:52:G:OP1	2.42	0.45
50:4:233:VAL:HG22	50:4:236:ARG:NH2	2.29	0.45
55:K:121:A:H5'	55:K:122:U:OP2	2.16	0.45
55:K:987:C:H2'	55:K:988:C:C6	2.51	0.45
55:K:1174:G:O2'	55:K:1175:A:P	2.74	0.45
55:K:1443:A:H2'	55:K:1444:G:O4'	2.16	0.45
55:K:1590:C:H5''	55:K:1591:U:O5'	2.16	0.45
55:K:4451:G:N2	55:K:4452:U:O4	2.42	0.45
4:E:141:ARG:NE	4:E:172:SER:O	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:127:GLY:O	55:K:4251:A:N6	2.50	0.45
13:O:55:LEU:O	13:O:59:ARG:HG3	2.16	0.45
20:V:87:SER:HA	20:V:97:TYR:HB3	1.97	0.45
22:X:151:ASN:C	22:X:151:ASN:HD22	2.24	0.45
30:f:106:TYR:N	30:f:107:PRO:CD	2.79	0.45
32:h:28:LEU:HD12	32:h:54:ILE:HD12	1.98	0.45
44:v:57:C:O2	44:v:61:A:O2'	2.32	0.45
47:1:5:PHE:CE2	47:1:9:ILE:HD11	2.51	0.45
55:K:386:A:H3'	55:K:387:G:H5''	1.98	0.45
55:K:1612:G:H2'	55:K:1612:G:N3	2.31	0.45
55:K:1730:U:O2	55:K:1799:G:O6	2.35	0.45
55:K:2809:G:O2'	55:K:4644:G:H5''	2.16	0.45
55:K:2895:A:H2'	55:K:2896:G:O4'	2.17	0.45
55:K:4507:A:H2'	55:K:4508:C:C6	2.51	0.45
55:K:5000:G:H2'	55:K:5001:U:O4'	2.16	0.45
7:H:5:LEU:HD13	7:H:60:TRP:CZ2	2.52	0.45
19:U:28:PRO:HB2	19:U:34:MET:HG2	1.99	0.45
24:Z:89:ILE:HG23	24:Z:91:LEU:HD23	1.99	0.45
26:b:36:ASP:N	26:b:36:ASP:OD1	2.48	0.45
28:d:90:ARG:HD3	28:d:102:LEU:HD13	1.99	0.45
30:f:11:PHE:CE2	30:f:97:ILE:HD13	2.52	0.45
45:w:140:ASP:OD1	45:w:141:ALA:N	2.49	0.45
47:1:66:ARG:NH2	47:1:78:GLU:OE2	2.43	0.45
47:1:405:ARG:NH2	55:K:2526:C:C6	2.84	0.45
55:K:1411(C):C:H2'	55:K:1412:G:O4'	2.17	0.45
55:K:1973:G:P	55:K:1974:U:H3'	2.57	0.45
55:K:2258:C:H2'	55:K:2259:G:OP1	2.17	0.45
55:K:4753:U:C2	55:K:4947:U:C4	3.04	0.45
55:K:4759:C:O2	55:K:4759:C:O4'	2.35	0.45
4:E:164:ARG:NH1	4:E:276:SER:OG	2.50	0.45
4:E:227:LYS:N	4:E:228:PRO:HD3	2.32	0.45
5:F:106:LYS:NZ	5:F:110:LEU:HD21	2.31	0.45
11:M:118:MET:SD	55:K:4891:G:N2	2.90	0.45
14:P:111:SER:O	14:P:111:SER:OG	2.34	0.45
31:g:8:ARG:N	31:g:34:TYR:OH	2.41	0.45
42:r:17:LEU:HD21	42:r:19:LYS:HD2	1.98	0.45
42:r:19:LYS:HG2	42:r:24:THR:HG23	1.98	0.45
43:u:42:A:C5	43:u:43:U:C5	3.04	0.45
49:3:17:ASP:OD1	49:3:20:ARG:NH1	2.49	0.45
55:K:1337:A:O2'	55:K:1519:C:O2	2.32	0.45
55:K:2024:G:O2'	55:K:2025:A:OP2	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:2664:G:N1	55:K:2671:C:N3	2.65	0.45
55:K:3930:U:H2'	55:K:3931:C:C6	2.52	0.45
55:K:4569:U:OP1	55:K:4982:A:O2'	2.32	0.45
2:C:254:GLU:OE1	2:C:258:ARG:NH1	2.48	0.45
3:D:64:ILE:HG13	3:D:105:LEU:HD21	1.97	0.45
17:S:134:ALA:HB3	55:K:748:G:OP1	2.16	0.45
45:w:95:THR:HG22	55:K:4910:A:H4'	1.98	0.45
46:B:248:PHE:CD2	50:4:476:LYS:CB	3.00	0.45
55:K:1639:U:O2	55:K:1639:U:H2'	2.17	0.45
55:K:1875:C:H2'	55:K:1876:U:C6	2.51	0.45
55:K:2264:C:H2'	55:K:2265:G:O4'	2.17	0.45
55:K:2567:G:H2'	55:K:2568:C:C6	2.51	0.45
55:K:3664:G:H2'	55:K:3665:G:H8	1.82	0.45
55:K:4907:G:N2	55:K:4915:G:C2	2.85	0.45
1:A:44:ILE:HG22	1:A:87:PHE:CE1	2.51	0.45
3:D:157:ASN:CG	3:D:159:VAL:HG12	2.41	0.45
4:E:133:LYS:N	4:E:133:LYS:HD2	2.31	0.45
17:S:82:LEU:HD21	17:S:109:CYS:SG	2.56	0.45
22:X:60:TYR:OH	55:K:17:A:OP2	2.25	0.45
46:B:236:TYR:O	46:B:237:VAL:C	2.59	0.45
51:5:40:LEU:HD23	51:5:63:CYS:SG	2.57	0.45
55:K:1250:C:H2'	55:K:1251:C:O4'	2.16	0.45
55:K:1278:C:H2'	55:K:1279:A:O4'	2.17	0.45
55:K:1354:A:N7	55:K:1502:G:O2'	2.44	0.45
55:K:2579:G:N2	55:K:2582:A:OP2	2.32	0.45
55:K:4761:G:H2'	55:K:4762:A:C8	2.52	0.45
2:C:7:LEU:HG	2:C:21:ASN:HB3	1.99	0.45
6:G:101:LYS:HD3	6:G:101:LYS:HA	1.88	0.45
13:O:142:ALA:O	13:O:147:TRP:N	2.47	0.45
52:7:8:ARG:NH2	52:7:21:THR:O	2.49	0.45
55:K:485:C:H2'	55:K:486:C:H6	1.82	0.45
55:K:2412:A:H2'	55:K:2413:U:C6	2.51	0.45
55:K:2845:A:H61	55:K:3843:C:N4	2.14	0.45
55:K:3597:G:H5''	55:K:3598:C:C5	2.52	0.45
55:K:3667:C:H2'	55:K:3668:C:H6	1.82	0.45
1:A:44:ILE:HD11	1:A:46:LYS:HZ3	1.82	0.45
1:A:227:ARG:NH1	55:K:3666:C:OP1	2.50	0.45
6:G:113:TYR:OH	44:v:148:A:N3	2.28	0.45
15:Q:66:MET:HE3	15:Q:98:LEU:HD13	1.98	0.45
28:d:50:ARG:CG	28:d:54:MET:HE3	2.47	0.45
33:i:79:THR:HG22	33:i:81:ILE:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:669:C:O2'	55:K:670:G:H8	2.00	0.45
55:K:4918:C:H2'	55:K:4919:G:O4'	2.16	0.45
55:K:5002:U:H2'	55:K:5003:U:C6	2.52	0.45
2:C:322:LEU:O	2:C:326:LEU:HG	2.16	0.44
12:N:143:ARG:NH1	32:h:94:ARG:O	2.50	0.44
18:T:87:LYS:CE	55:K:4305:G:H22	2.29	0.44
35:k:17:ARG:NH2	55:K:2772:C:O2'	2.50	0.44
39:o:4:VAL:O	39:o:94:GLY:N	2.37	0.44
45:w:60:VAL:HG11	45:w:67:VAL:HG23	1.98	0.44
46:B:248:PHE:O	46:B:250:GLU:HG2	2.18	0.44
50:4:433:ARG:HD3	55:K:392:U:OP1	2.17	0.44
53:6:115:ARG:NH2	53:6:138:ASP:OD2	2.44	0.44
55:K:489:C:H2'	55:K:490:C:C6	2.52	0.44
55:K:495:C:C2	55:K:496:G:C8	3.05	0.44
55:K:704:C:C2'	55:K:705:G:OP1	2.64	0.44
55:K:952:G:H2'	55:K:953:C:C6	2.52	0.44
55:K:4537:C:H2'	55:K:4538:G:C8	2.51	0.44
2:C:332:ALA:HA	2:C:335:MET:HB2	1.98	0.44
3:D:11:ALA:O	3:D:15:ARG:HG2	2.17	0.44
30:f:17:GLY:N	30:f:20:ASN:O	2.49	0.44
55:K:38:A:H61	55:K:41:C:H3'	1.82	0.44
55:K:125:C:H2'	55:K:126:C:C6	2.52	0.44
55:K:406:C:O2'	55:K:407:A:P	2.74	0.44
55:K:2617:G:H2'	55:K:2618:G:O4'	2.16	0.44
55:K:2635:U:H2'	55:K:2636:U:C6	2.52	0.44
16:R:44:LEU:CD2	16:R:49:LEU:HD12	2.47	0.44
17:S:147:ASP:OD1	17:S:148:SER:N	2.50	0.44
18:T:115:LYS:HG2	18:T:126:VAL:HG21	1.99	0.44
19:U:25:CYS:HA	19:U:112:LEU:HB2	1.99	0.44
33:i:54:GLU:HG2	33:i:90:LEU:HD11	1.99	0.44
45:w:55:HIS:CD2	55:K:4627:U:HO2'	2.35	0.44
55:K:520:U:H2'	55:K:521:C:C6	2.53	0.44
55:K:917:A:N7	55:K:918:G:C8	2.86	0.44
55:K:2465:C:H1'	55:K:3672:G:H22	1.82	0.44
55:K:4195:G:O2'	55:K:4442:U:OP1	2.23	0.44
55:K:4670:C:O3'	55:K:4671:C:H3'	2.17	0.44
1:A:210:PRO:HG2	1:A:235:VAL:HG21	1.99	0.44
4:E:160:HIS:HB3	4:E:163:LYS:HD2	2.00	0.44
6:G:197:THR:O	6:G:201:GLU:HG3	2.17	0.44
12:N:14:LYS:HE2	55:K:280:G:H5''	1.99	0.44
15:Q:160:HIS:NE2	55:K:4298:A:OP1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:R:96:MET:HG2	55:K:2667:C:O4'	2.18	0.44
23:Y:23:SER:OG	23:Y:75:ARG:NH2	2.49	0.44
24:Z:100:VAL:HG23	24:Z:106:LEU:HB3	2.00	0.44
26:b:10:HIS:NE2	55:K:1877:G:O6	2.49	0.44
27:c:30:GLY:HA2	55:K:2673:G:O3'	2.18	0.44
45:w:258:HIS:HB2	55:K:4518:A:OP2	2.17	0.44
46:B:218:THR:HG21	49:3:61:ILE:CG1	2.47	0.44
55:K:181:C:H42	55:K:255:C:H42	1.65	0.44
55:K:1482:G:HO2'	55:K:1483:C:P	2.41	0.44
55:K:3876:A:O2'	55:K:3877:A:OP1	2.35	0.44
55:K:4119:C:O2'	55:K:4120:U:P	2.76	0.44
55:K:4135:G:H2'	55:K:4136:G:C8	2.53	0.44
55:K:4758:U:O2	55:K:4758:U:O4'	2.34	0.44
55:K:5008:C:H2'	55:K:5009:G:O4'	2.17	0.44
2:C:45:ARG:NH2	55:K:2296:G:O4'	2.51	0.44
9:J:175:LEU:HD23	9:J:175:LEU:H	1.83	0.44
11:M:132:ARG:NH2	55:K:4895:C:N3	2.66	0.44
18:T:79:GLN:OE1	26:b:21:ILE:HG21	2.16	0.44
21:W:1:MET:SD	21:W:1:MET:N	2.81	0.44
31:g:54:ARG:HB2	55:K:2583:C:OP1	2.18	0.44
43:u:31:G:C6	43:u:47:G:C6	3.06	0.44
44:v:108:A:C6	44:v:112:G:O6	2.71	0.44
47:1:77:MET:HE1	47:1:162:VAL:HG23	1.99	0.44
55:K:1474:C:H2'	55:K:1475:G:O4'	2.18	0.44
55:K:3912:U:O2'	55:K:3913:G:H5'	2.17	0.44
55:K:4577:U:H2'	55:K:4578:G:C8	2.53	0.44
1:A:54:ARG:NH2	55:K:3680:U:OP1	2.42	0.44
9:J:33:LEU:HD22	9:J:70:VAL:HG23	1.99	0.44
14:P:12:THR:O	14:P:107:LEU:HD21	2.17	0.44
25:a:44:ASN:ND2	55:K:1683:U:OP1	2.51	0.44
47:1:255:VAL:HG12	47:1:451:VAL:HG11	1.99	0.44
47:1:409:MET:O	47:1:413:LEU:HD13	2.17	0.44
54:8:118:PRO:O	56:9:67:GLY:N	2.39	0.44
55:K:914:U:HO2'	55:K:915:A:C1'	2.31	0.44
55:K:1405:C:H2'	55:K:1406:G:H8	1.82	0.44
55:K:2409:U:H4'	55:K:2428:A:H4'	2.00	0.44
55:K:2538:U:H2'	55:K:2539:C:C6	2.52	0.44
55:K:4459:U:H2'	55:K:4460:U:C6	2.53	0.44
55:K:4925:U:H1'	55:K:4926:C:OP2	2.17	0.44
4:E:66:SER:OG	55:K:1239:C:N4	2.50	0.44
4:E:261:LEU:N	4:E:262:PRO:HD2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:4:ARG:NH1	55:K:1866:U:OP1	2.42	0.44
20:V:27:ASN:OD1	20:V:102:ALA:HB2	2.18	0.44
24:Z:89:ILE:CG1	24:Z:91:LEU:HD23	2.48	0.44
25:a:121:PRO:HA	25:a:141:GLY:O	2.18	0.44
31:g:94:ALA:O	31:g:98:GLU:HG3	2.17	0.44
46:B:233:ILE:O	46:B:236:TYR:C	2.61	0.44
47:1:45:CYS:CB	47:1:77:MET:HE3	2.47	0.44
55:K:111:C:C2	55:K:331:G:C2	3.06	0.44
55:K:1210:C:H3'	55:K:1210:C:O2	2.17	0.44
55:K:1804:A:O4'	55:K:1806:G:C8	2.70	0.44
55:K:1962:A:C4	55:K:1963:C:C5	3.06	0.44
55:K:2464:C:H2'	55:K:2465:C:H6	1.81	0.44
55:K:2533:C:H2'	55:K:2534:C:C6	2.52	0.44
55:K:4199:C:H2'	55:K:4200:G:H5'	2.00	0.44
55:K:4453:C:C2	55:K:4529:G:C2	3.05	0.44
55:K:4461:C:O2'	55:K:4462:C:H5'	2.18	0.44
2:C:33:ARG:NH1	55:K:1351:G:OP1	2.42	0.44
3:D:234:ASP:OD1	3:D:235:MET:N	2.51	0.44
18:T:124:THR:OG1	18:T:125:TRP:N	2.51	0.44
20:V:18:LEU:HD12	20:V:18:LEU:O	2.18	0.44
30:f:79:GLY:HA2	55:K:1917:A:H4'	2.00	0.44
41:q:5:C:H2'	41:q:6:C:H6	1.83	0.44
42:r:26:SER:OG	42:r:28:GLU:OE1	2.35	0.44
50:4:229:ASP:OD2	50:4:232:ASN:ND2	2.46	0.44
55:K:408:A:H4'	55:K:409:G:H3'	2.00	0.44
55:K:658:C:C4	55:K:659:G:N7	2.86	0.44
55:K:1477:C:H2'	55:K:1478:C:H6	1.82	0.44
55:K:1504:G:H2'	55:K:1505:C:C6	2.53	0.44
55:K:3911:C:H2'	55:K:3912:U:C6	2.51	0.44
55:K:4096:C:H2'	55:K:4097:G:C8	2.53	0.44
55:K:4344:U:H2'	55:K:4345:C:C6	2.52	0.44
55:K:5052:C:H2'	55:K:5053:U:O4'	2.18	0.44
5:F:29:ILE:O	5:F:33:ARG:HG3	2.18	0.44
8:I:77:VAL:HG23	8:I:82:LYS:HA	2.00	0.44
36:l:15:LYS:O	36:l:19:GLN:HG3	2.18	0.44
53:6:1:MET:HA	53:6:4:PHE:HD2	1.83	0.44
55:K:975:C:H2'	55:K:976:G:C8	2.53	0.44
55:K:1248:C:H2'	55:K:1249:C:H5'	1.99	0.44
55:K:1478:C:H2'	55:K:1479:G:C8	2.53	0.44
55:K:3810:C:O2'	55:K:3811:G:OP1	2.32	0.44
55:K:4237:C:O2	55:K:4321:U:O2'	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:4273:A:H2'	55:K:4274:A:C8	2.53	0.44
1:A:242:ARG:O	55:K:3658:C:H5''	2.18	0.43
4:E:182:LEU:HD12	4:E:186:ARG:CA	2.43	0.43
6:G:189:LEU:HD21	6:G:257:PHE:CE1	2.53	0.43
22:X:70:LYS:NZ	44:v:59:A:OP2	2.51	0.43
25:a:43:ILE:HD12	55:K:1682:A:C2	2.52	0.43
34:j:66:HIS:O	34:j:70:VAL:HG23	2.18	0.43
55:K:174:C:H2'	55:K:175:C:H6	1.83	0.43
55:K:420:A:O2'	55:K:1331:C:O2'	2.32	0.43
55:K:1354:A:N1	55:K:1385:G:O2'	2.41	0.43
55:K:1645:C:H2'	55:K:1646:A:C8	2.53	0.43
55:K:1654:G:OP2	55:K:1655:C:N4	2.47	0.43
55:K:1669:A:C2	55:K:1852:U:H4'	2.53	0.43
9:J:24:ILE:HG12	9:J:128:LEU:HB3	2.01	0.43
12:N:97:SER:O	12:N:101:VAL:HG23	2.18	0.43
20:V:106:VAL:HG12	20:V:107:ASN:O	2.18	0.43
23:Y:61:HIS:N	55:K:232:G:O6	2.47	0.43
34:j:52:LYS:O	34:j:56:ARG:HG3	2.18	0.43
41:q:18:G:O2'	41:q:19:G:N7	2.51	0.43
41:q:57:G:H2'	41:q:58:A:H5''	2.00	0.43
44:v:56:G:H2'	44:v:57:C:O4'	2.18	0.43
45:w:89:ILE:HD12	45:w:194:LEU:HD11	1.99	0.43
46:B:218:THR:HG21	49:3:61:ILE:HD11	1.99	0.43
46:B:263:MET:SD	55:K:1600:A:C2	3.11	0.43
52:7:270:ASP:OD1	52:7:271:THR:HG23	2.18	0.43
55:K:342:G:H2'	55:K:343:C:C6	2.53	0.43
55:K:734:G:H1	55:K:929:A:H62	1.67	0.43
55:K:1188:C:H2'	55:K:1189:G:H8	1.83	0.43
55:K:1238:A:O2'	55:K:1239:C:P	2.75	0.43
55:K:2468:U:N3	55:K:2506:G:C5	2.86	0.43
55:K:2550:G:O2'	55:K:2587:A:N1	2.47	0.43
55:K:2573:A:H2'	55:K:2574:G:O4'	2.18	0.43
55:K:2607:C:H2'	55:K:2608:G:H8	1.84	0.43
55:K:2868:G:C2	55:K:2883:G:O6	2.72	0.43
55:K:4111:U:H2'	55:K:4112:C:O4'	2.17	0.43
55:K:4266:G:H2'	55:K:4266:G:N3	2.32	0.43
55:K:4354:U:C2'	55:K:4355:G:OP2	2.67	0.43
55:K:4534:G:O6	55:K:4553:A:C6	2.71	0.43
4:E:225:LEU:O	4:E:227:LYS:HG2	2.18	0.43
7:H:6:SER:HB3	7:H:67:LEU:HD22	2.00	0.43
47:1:102:VAL:HG21	47:1:112:PHE:CD1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1:289:ILE:HD13	47:1:379:TRP:CZ2	2.53	0.43
50:4:320:PHE:HB3	50:4:385:MET:SD	2.58	0.43
55:K:504:G:H4'	55:K:505:G:OP1	2.18	0.43
55:K:1763:C:H42	55:K:1769:G:H1	1.66	0.43
55:K:3648:A:H1'	55:K:3785:A:N6	2.34	0.43
45:w:276:HIS:O	55:K:4716:C:H5''	2.19	0.43
52:7:299:LEU:O	52:7:299:LEU:HD23	2.19	0.43
55:K:105:A:H5''	55:K:1362:G:H5'	2.01	0.43
55:K:504:G:O2'	55:K:505:G:P	2.77	0.43
55:K:519:C:C2	55:K:520:U:C5	3.06	0.43
55:K:1445:U:H2'	55:K:1446:C:C6	2.54	0.43
55:K:1839:U:H2'	55:K:1840:G:O4'	2.19	0.43
2:C:350:ARG:HD2	55:K:724:C:OP1	2.19	0.43
4:E:105:GLY:N	55:K:685:C:OP1	2.52	0.43
4:E:245:ILE:HD12	4:E:245:ILE:H	1.83	0.43
17:S:139:ARG:O	17:S:143:LYS:HG3	2.18	0.43
29:e:58:ILE:HD12	55:K:2319:C:C4	2.53	0.43
52:7:295:PHE:HA	52:7:383:VAL:HG21	2.00	0.43
55:K:64:A:C4	55:K:109:G:N7	2.87	0.43
55:K:923:C:H4'	55:K:923:C:OP1	2.17	0.43
55:K:1170:G:H2'	55:K:1171:G:H8	1.84	0.43
55:K:2079:G:H2'	55:K:2080:U:C6	2.54	0.43
55:K:2299:G:C2	55:K:2336:G:C5	3.07	0.43
55:K:2586:G:N2	55:K:2771:G:O4'	2.52	0.43
55:K:3637:U:O4	55:K:3651:A:H2	2.01	0.43
9:J:109:ILE:HG23	9:J:128:LEU:HD23	1.99	0.43
17:S:13:VAL:HG23	17:S:62:VAL:HB	2.01	0.43
17:S:165:PRO:O	17:S:167:PHE:N	2.51	0.43
18:T:61:THR:HG21	55:K:1800:U:O2'	2.19	0.43
23:Y:73:VAL:HG13	23:Y:80:ILE:HG22	2.00	0.43
36:l:28:TRP:CG	46:B:247:ARG:HH21	2.37	0.43
43:u:68:C:N3	43:u:108:G:N1	2.67	0.43
44:v:6:C:H2'	44:v:7:U:H6	1.84	0.43
45:w:258:HIS:NE2	55:K:3878:C:O2	2.52	0.43
50:4:421:THR:O	50:4:421:THR:HG22	2.18	0.43
55:K:385:A:N3	55:K:387:G:H5''	2.34	0.43
55:K:1345:A:H2'	55:K:1346:C:C6	2.53	0.43
55:K:1669:A:N3	55:K:1852:U:O2'	2.48	0.43
55:K:1803:G:H2'	55:K:1836:G:N2	2.34	0.43
55:K:2073:C:H2'	55:K:2074:C:C6	2.54	0.43
55:K:4301:U:OP2	55:K:4303:C:N4	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:4869:U:O2	55:K:4869:U:O4'	2.37	0.43
56:9:41:PHE:CE2	56:9:45:ILE:HD11	2.54	0.43
56:9:103:LEU:HD12	56:9:103:LEU:N	2.34	0.43
1:A:236:GLY:N	55:K:3687:A:O2'	2.52	0.43
2:C:151:PRO:O	2:C:153:VAL:HG23	2.19	0.43
5:F:161:ILE:HB	5:F:166:ILE:HD12	2.01	0.43
9:J:15:LEU:HD23	9:J:165:TRP:CG	2.54	0.43
9:J:155:HIS:HB2	43:u:55:A:H4'	2.01	0.43
10:L:81:LEU:HD11	10:L:98:VAL:HG22	2.00	0.43
12:N:177:GLY:HA2	55:K:67:C:O3'	2.19	0.43
14:P:4:TYR:OH	55:K:400:A:OP1	2.30	0.43
23:Y:1:MET:HG3	23:Y:2:LYS:H	1.83	0.43
37:m:51:ILE:HG23	37:m:52:ILE:N	2.34	0.43
42:r:97:ILE:HG21	42:r:107:ARG:HB3	2.00	0.43
55:K:2559:G:C6	55:K:2569:G:C6	3.07	0.43
55:K:3936:A:C6	55:K:4175:G:C6	3.07	0.43
55:K:5015:G:H2'	55:K:5016:A:C2	2.53	0.43
5:F:147:LYS:O	5:F:151:GLU:HG2	2.18	0.43
7:H:105:ILE:CD1	7:H:136:VAL:HG23	2.48	0.43
9:J:141:ILE:HD11	43:u:28:C:H5'	2.01	0.43
24:Z:25:ILE:HG12	24:Z:43:VAL:HG12	2.01	0.43
25:a:28:HIS:ND1	25:a:32:ARG:HG2	2.34	0.43
40:p:52:VAL:HG13	55:K:2739:C:H5'	1.99	0.43
50:4:167:TRP:HH2	50:4:220:ILE:HD13	1.83	0.43
55:K:448:G:H3'	55:K:449:C:H4'	2.00	0.43
55:K:459:C:H2'	55:K:460:C:H6	1.82	0.43
55:K:2627:C:O2	55:K:2627:C:O4'	2.37	0.43
55:K:3603:G:O2'	55:K:3604:A:P	2.77	0.43
55:K:4228:G:H4'	55:K:4229:U:OP2	2.18	0.43
55:K:4566:U:H2'	55:K:4567:G:O4'	2.19	0.43
55:K:4678:G:N2	55:K:4713:G:H1'	2.34	0.43
22:X:76:ILE:HG23	22:X:77:ILE:HG13	2.00	0.43
31:g:5:LEU:HD11	31:g:32:TYR:CD1	2.54	0.43
46:B:233:ILE:HG13	46:B:234:GLU:H	1.84	0.43
47:1:338:VAL:O	47:1:338:VAL:HG12	2.19	0.43
55:K:173:C:C6	55:K:174:C:C5	3.06	0.43
55:K:504:G:O2'	55:K:505:G:O5'	2.30	0.43
55:K:685:C:H1'	55:K:686:A:OP2	2.18	0.43
55:K:978:G:O2'	55:K:979:C:OP2	2.32	0.43
55:K:1189:G:C6	55:K:1190:C:C4	3.07	0.43
55:K:1402:C:C2	55:K:1416:G:C2	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:1655:C:O2	55:K:4390:A:O2'	2.37	0.43
55:K:1824:G:H2'	55:K:1825:A:C8	2.54	0.43
55:K:2429:A:H2'	55:K:2430:C:C6	2.54	0.43
55:K:3941:G:C6	55:K:4073:A:C6	3.07	0.43
6:G:105:THR:O	44:v:150:C:N4	2.43	0.43
6:G:258:THR:OG1	6:G:259:GLN:N	2.51	0.43
11:M:71:LYS:HE3	55:K:739:G:OP2	2.18	0.43
15:Q:99:LYS:HE2	15:Q:121:LEU:HD11	2.00	0.43
16:R:96:MET:O	16:R:100:ARG:HG3	2.19	0.43
43:u:16:A:H2'	43:u:17:C:C6	2.54	0.43
46:B:208:THR:O	46:B:212:LEU:HG	2.19	0.43
50:4:433:ARG:NH1	55:K:392:U:P	2.86	0.43
55:K:424:U:H2'	55:K:425:U:H6	1.84	0.43
55:K:1074:G:C2	55:K:1238:A:C2	3.07	0.43
55:K:1190:C:O2'	55:K:1191:C:H5'	2.18	0.43
55:K:1341:U:H2'	55:K:1342:A:H8	1.84	0.43
55:K:1483:C:O2	55:K:1483:C:O4'	2.36	0.43
55:K:1918:U:O4'	55:K:2065:G:N2	2.52	0.43
55:K:1929:A:H5'	55:K:1930:U:OP1	2.19	0.43
55:K:2533:C:H2'	55:K:2534:C:H6	1.84	0.43
55:K:2616:C:C2	55:K:2722:G:C2	3.07	0.43
55:K:3684:G:H2'	55:K:3685:C:C6	2.54	0.43
55:K:3783:A:C8	55:K:3792:G:C8	3.07	0.43
2:C:214:ASP:OD1	2:C:218:VAL:HG13	2.18	0.42
2:C:269:LYS:NZ	2:C:270:ALA:O	2.43	0.42
4:E:118:TYR:HB3	55:K:457:G:H5'	2.01	0.42
7:H:6:SER:CB	7:H:67:LEU:HD22	2.49	0.42
16:R:136:ARG:O	16:R:140:GLU:HG2	2.19	0.42
24:Z:29:ILE:HD13	24:Z:40:HIS:CD2	2.54	0.42
25:a:65:ARG:NH1	55:K:84:A:OP2	2.51	0.42
31:g:100:GLN:O	31:g:104:VAL:HG23	2.19	0.42
36:l:26:TRP:HA	46:B:247:ARG:HH12	1.84	0.42
39:o:13:LYS:NZ	55:K:4294:C:O3'	2.42	0.42
40:p:52:VAL:CG1	55:K:2739:C:H5'	2.49	0.42
44:v:107:C:N3	44:v:112:G:N1	2.44	0.42
47:1:252:PHE:CE1	47:1:451:VAL:HG22	2.54	0.42
55:K:686:A:H2'	55:K:686:A:N3	2.34	0.42
55:K:1430:C:C2	55:K:1455:G:C2	3.07	0.42
55:K:3888:G:O2'	55:K:3889:G:P	2.76	0.42
55:K:4737:G:C4	55:K:4963:G:N2	2.87	0.42
2:C:94:ASN:OD1	2:C:94:ASN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:106:ARG:NH2	55:K:4163:U:OP2	2.52	0.42
12:N:73:ARG:HB3	12:N:89:VAL:HG12	2.01	0.42
18:T:137:GLU:H	18:T:137:GLU:CD	2.27	0.42
40:p:74:THR:HA	40:p:77:VAL:HG22	2.01	0.42
55:K:163:A:H2'	55:K:164:G:H8	1.84	0.42
55:K:1327:C:H2'	55:K:1328:G:C8	2.54	0.42
55:K:1970:A:H5''	55:K:1971:U:O4'	2.19	0.42
55:K:2259:G:H5'	55:K:2260:C:OP2	2.19	0.42
55:K:4192:A:H2'	55:K:4193:C:H6	1.84	0.42
55:K:4699:U:C4	55:K:4702:G:O6	2.72	0.42
1:A:118:GLU:HB3	1:A:126:LEU:HD11	2.00	0.42
1:A:179:ILE:O	55:K:3653:A:H4'	2.18	0.42
10:L:126:LEU:HD12	32:h:119:TYR:HB3	2.00	0.42
11:M:29:ASP:OD1	11:M:30:VAL:N	2.53	0.42
24:Z:11:VAL:HG21	24:Z:80:LEU:HB3	2.01	0.42
26:b:54:LEU:O	26:b:57:MET:N	2.51	0.42
44:v:83:C:H1'	44:v:84:A:OP1	2.19	0.42
45:w:276:HIS:ND1	55:K:4716:C:OP1	2.52	0.42
47:1:422:ALA:HB3	49:3:14:PHE:HE1	1.85	0.42
50:4:252:ASN:HB2	50:4:255:ASP:OD2	2.20	0.42
52:7:278:LEU:HD11	52:7:343:LEU:HG	2.01	0.42
55:K:1378:C:H4'	55:K:1379:C:H5'	2.01	0.42
55:K:1959:U:O4'	55:K:1961:G:H1'	2.18	0.42
55:K:2418:A:C5	55:K:2419:C:C5	3.07	0.42
55:K:4390:A:H2'	55:K:4391:G:O4'	2.19	0.42
55:K:4479:A:OP1	55:K:4610:A:O2'	2.37	0.42
55:K:4523:A:H5''	55:K:4524:G:H5'	2.01	0.42
55:K:4633:G:O3'	55:K:4634:U:H3'	2.18	0.42
12:N:110:CYS:SG	12:N:134:LEU:HD13	2.60	0.42
22:X:122:ALA:N	22:X:139:ARG:O	2.41	0.42
44:v:6:C:H2'	44:v:7:U:C6	2.54	0.42
44:v:68:G:C5	44:v:69:U:C5	3.07	0.42
47:1:286:THR:HG21	47:1:376:SER:OG	2.19	0.42
52:7:278:LEU:HG	52:7:343:LEU:HD11	2.00	0.42
55:K:286:U:H2'	55:K:287:U:C6	2.55	0.42
55:K:433:A:N1	55:K:3866:C:O2'	2.32	0.42
55:K:971(A):G:O2'	55:K:972:C:O5'	2.23	0.42
55:K:1984:A:N6	55:K:2010:A:HO2'	2.18	0.42
55:K:2363:A:N6	55:K:3859:G:O2'	2.50	0.42
55:K:2793:G:C5'	55:K:2794:C:H5''	2.49	0.42
55:K:3770:U:H2'	55:K:3771:C:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:4188:U:H2'	55:K:4189:U:C6	2.54	0.42
1:A:201:GLY:N	55:K:3689:G:OP1	2.52	0.42
2:C:357:ALA:O	2:C:361:LYS:NZ	2.50	0.42
11:M:39:ASP:OD2	11:M:47:ARG:NE	2.45	0.42
12:N:178:HIS:O	55:K:293:G:N2	2.48	0.42
14:P:64:ASN:ND2	14:P:80:GLN:OE1	2.53	0.42
15:Q:61:LEU:O	15:Q:87:THR:OG1	2.33	0.42
20:V:117:ILE:HD11	20:V:132:ILE:HG23	2.02	0.42
24:Z:103:ASP:OD1	24:Z:105:ALA:N	2.52	0.42
45:w:222:VAL:HA	45:w:275:HIS:O	2.19	0.42
45:w:332:MET:HE1	45:w:365:LEU:CD1	2.48	0.42
52:7:89:GLU:OE2	52:7:188:VAL:N	2.46	0.42
55:K:504:G:N1	55:K:655:C:N3	2.68	0.42
55:K:1304:C:H2'	55:K:1305:C:C6	2.55	0.42
55:K:1813:U:C2	55:K:1826:G:N2	2.87	0.42
55:K:1969:G:H21	55:K:2017:A:H62	1.66	0.42
55:K:2597:G:H2'	55:K:2598:A:C8	2.55	0.42
55:K:4638:U:H2'	55:K:4639:G:N3	2.34	0.42
55:K:4735:G:O2'	55:K:4736:C:H6	2.02	0.42
2:C:334:THR:HG21	5:F:50:TYR:OH	2.19	0.42
3:D:93:THR:O	3:D:158:LYS:NZ	2.35	0.42
4:E:153:LEU:HD11	4:E:167:PHE:HB2	2.01	0.42
5:F:186:MET:O	5:F:190:ILE:HG13	2.20	0.42
6:G:195:THR:HA	6:G:198:THR:HG22	2.01	0.42
9:J:9:GLU:OE1	9:J:9:GLU:HA	2.20	0.42
22:X:73:HIS:O	22:X:116:LEU:HD11	2.19	0.42
27:c:10:SER:O	27:c:14:ILE:HG12	2.20	0.42
46:B:246:PHE:HB3	50:4:475:MET:O	2.19	0.42
55:K:1192:C:H2'	55:K:1193:C:O4'	2.20	0.42
55:K:1450:C:O2'	55:K:2104:A:H1'	2.19	0.42
55:K:4423:U:O2	55:K:4423:U:O4'	2.37	0.42
55:K:4510:A:O2'	55:K:4511:A:C8	2.71	0.42
7:H:63:ASN:O	7:H:67:LEU:HG	2.20	0.42
8:I:127:ALA:O	8:I:129:VAL:HG23	2.20	0.42
18:T:6:GLY:HA3	55:K:4208:U:P	2.60	0.42
31:g:6:THR:HG22	55:K:2400:G:H21	1.84	0.42
31:g:66:ARG:CD	55:K:2539:C:H5''	2.50	0.42
31:g:83:CYS:O	31:g:87:VAL:HG23	2.20	0.42
34:j:54:LYS:O	34:j:58:THR:HG23	2.19	0.42
35:k:69:LEU:HD21	55:K:2696:A:C4	2.54	0.42
42:r:54:ALA:HA	42:r:61:VAL:HG13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:71:A:OP2	44:v:83:C:N4	2.48	0.42
45:w:217:ILE:HD13	45:w:284:ILE:HD11	2.02	0.42
46:B:246:PHE:CA	50:4:476:LYS:HA	2.49	0.42
55:K:40:G:N2	55:K:4380:A:H62	2.17	0.42
55:K:425:U:N3	55:K:426:A:N7	2.67	0.42
55:K:1092:G:C6	55:K:1205:G:C6	3.08	0.42
55:K:1178:G:H5'	55:K:1179:U:OP2	2.20	0.42
55:K:1322:A:C6	55:K:1326:A:C8	3.07	0.42
55:K:1442:C:H2'	55:K:1443:A:C8	2.54	0.42
55:K:1504:G:H2'	55:K:1505:C:H6	1.82	0.42
55:K:1974:U:O3'	55:K:1975:G:H3'	2.19	0.42
55:K:2411:C:H2'	55:K:2412:A:H8	1.85	0.42
55:K:2430:C:O2'	55:K:2431:A:H5'	2.20	0.42
55:K:2732:G:H2'	55:K:2733:C:C6	2.55	0.42
55:K:4948:C:O2	55:K:4948:C:O4'	2.35	0.42
56:9:24:VAL:HG22	56:9:40:GLU:OE2	2.20	0.42
5:F:145:ASN:OD1	5:F:146:LEU:N	2.50	0.42
9:J:78:LYS:O	9:J:82:ILE:HG12	2.19	0.42
10:L:63:THR:O	10:L:63:THR:HG22	2.20	0.42
13:O:128:ARG:NH1	17:S:162:GLN:OE1	2.53	0.42
16:R:26:PRO:O	16:R:29:THR:OG1	2.36	0.42
17:S:81:TRP:O	17:S:127:MET:HG2	2.20	0.42
22:X:107:HIS:ND1	44:v:130:C:H4'	2.35	0.42
40:p:73:THR:CG2	40:p:76:ALA:HB3	2.49	0.42
47:1:286:THR:O	47:1:287:SER:HB3	2.20	0.42
55:K:42:A:N6	55:K:4379:A:O2'	2.53	0.42
55:K:1804:A:O2'	55:K:1833:G:O6	2.23	0.42
55:K:2409:U:C5	55:K:2783:A:N1	2.88	0.42
55:K:3736:A:H2'	55:K:3737:A:C8	2.55	0.42
55:K:3834:C:H2'	55:K:3835:C:H6	1.85	0.42
55:K:4067:U:H2'	55:K:4068:U:H6	1.84	0.42
1:A:132:ASN:ND2	55:K:3683:C:OP1	2.46	0.42
4:E:245:ILE:H	4:E:245:ILE:CD1	2.33	0.42
14:P:2:VAL:HG12	14:P:3:ARG:N	2.32	0.42
25:a:15:VAL:HG13	55:K:1659:U:OP2	2.20	0.42
50:4:252:ASN:ND2	50:4:255:ASP:OD2	2.43	0.42
55:K:405:U:N3	55:K:408:A:OP2	2.46	0.42
55:K:414:C:H5'	55:K:415:G:OP2	2.19	0.42
55:K:1808:C:H1'	55:K:1831:G:N2	2.35	0.42
55:K:2845:A:H61	55:K:3843:C:H42	1.68	0.42
55:K:3789:C:OP2	55:K:3790:U:O2'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:4073:A:C2	55:K:4074:C:C6	3.08	0.42
55:K:4532:U:OP2	55:K:4554:G:N1	2.48	0.42
55:K:4688:C:H2'	55:K:4689:U:C6	2.54	0.42
2:C:47:ASN:OD1	2:C:113:ARG:N	2.47	0.42
5:F:46:ARG:NH2	55:K:976:G:O3'	2.53	0.42
7:H:16:VAL:HG12	7:H:17:ASP:N	2.35	0.42
8:I:76:MET:HE2	8:I:138:ILE:HG21	2.02	0.42
18:T:28:ALA:HA	18:T:31:MET:HG2	2.01	0.42
28:d:29:ILE:O	28:d:33:ILE:HG22	2.20	0.42
42:r:118:LEU:O	42:r:122:LYS:HG3	2.20	0.42
47:1:406:GLU:HA	47:1:409:MET:HE3	2.01	0.42
50:4:422:HIS:CD2	55:K:401:G:O2'	2.73	0.42
55:K:1179:U:H3'	55:K:1179:U:O2	2.20	0.42
55:K:2099:C:H4'	55:K:2100:G:H5'	2.01	0.42
55:K:4575:G:C2	55:K:4576:U:C6	3.07	0.42
1:A:13:GLY:C	1:A:15:VAL:H	2.28	0.41
3:D:95:TYR:OH	3:D:195:HIS:NE2	2.47	0.41
5:F:58:LYS:O	5:F:62:GLN:HG3	2.20	0.41
5:F:91:VAL:CG1	5:F:139:ILE:HD12	2.50	0.41
9:J:27:GLY:HA2	9:J:68:ILE:HG23	2.01	0.41
10:L:71:ARG:HG2	10:L:72:ALA:H	1.84	0.41
20:V:26:ILE:HG22	20:V:101:ASN:HB3	2.02	0.41
24:Z:76:ASN:OD1	24:Z:77:TYR:N	2.53	0.41
27:c:17:ARG:O	27:c:21:VAL:HG23	2.20	0.41
30:f:36:ARG:HD2	30:f:79:GLY:O	2.19	0.41
40:p:54:ILE:O	40:p:54:ILE:HG13	2.19	0.41
47:1:91:MET:HG3	47:1:112:PHE:CE1	2.55	0.41
47:1:236:ARG:HD3	47:1:239:LEU:HB2	2.01	0.41
54:8:58:THR:HG22	54:8:59:GLU:N	2.35	0.41
55:K:926:G:C6	55:K:927:G:C5	3.08	0.41
55:K:963:G:C2	55:K:964:A:C5	3.08	0.41
55:K:1460:C:H2'	55:K:1461:C:C6	2.55	0.41
55:K:1554:A:H2'	55:K:1555:G:O4'	2.20	0.41
55:K:1786:A:O2'	55:K:1788:A:OP2	2.34	0.41
55:K:2309:G:O6	55:K:2330:G:C2	2.73	0.41
55:K:2490:U:H2'	55:K:2491:C:C6	2.54	0.41
55:K:2780:C:H2'	55:K:2781:G:H8	1.85	0.41
55:K:4874:A:C5	55:K:4877:G:H4'	2.55	0.41
3:D:244:HIS:O	3:D:248:ARG:HG3	2.20	0.41
4:E:178:VAL:HG22	4:E:179:THR:N	2.36	0.41
7:H:26:ILE:HG22	7:H:35:ARG:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:87:HIS:HB3	10:L:90:VAL:HG12	2.02	0.41
12:N:143:ARG:HB3	32:h:99:GLU:OE2	2.20	0.41
14:P:66:GLY:HA3	55:K:2362:U:H5''	2.01	0.41
25:a:84:GLU:O	25:a:88:VAL:HG12	2.20	0.41
25:a:85:GLN:HA	25:a:88:VAL:HG12	2.02	0.41
55:K:125:C:H2'	55:K:126:C:H6	1.84	0.41
55:K:2658:G:N1	55:K:2675:G:O2'	2.45	0.41
55:K:3893:C:H2'	55:K:3894:A:C8	2.55	0.41
55:K:4458:C:H2'	55:K:4459:U:C6	2.56	0.41
55:K:4714:C:C5	55:K:4715:C:C5	3.09	0.41
55:K:4994:G:C2	55:K:5058:A:C2	3.08	0.41
55:K:5028:G:H2'	55:K:5029:C:C6	2.55	0.41
5:F:52:LYS:NZ	5:F:188:ASP:OD2	2.40	0.41
7:H:88:PHE:CE2	7:H:151:ILE:HB	2.56	0.41
8:I:65:LEU:HD23	8:I:159:PHE:CE1	2.54	0.41
10:L:18:TRP:NE1	55:K:1516:G:O2'	2.44	0.41
14:P:4:TYR:CE1	14:P:18:ARG:HD2	2.55	0.41
17:S:165:PRO:O	17:S:166:ARG:C	2.63	0.41
21:W:56:ARG:HH21	21:W:61:LYS:HB3	1.85	0.41
23:Y:65:GLN:CB	54:8:42:GLU:OE2	2.68	0.41
23:Y:73:VAL:HG12	23:Y:75:ARG:HG2	2.03	0.41
25:a:131:ARG:O	25:a:135:GLU:HG3	2.20	0.41
50:4:146:LEU:HD11	51:5:65:PHE:CD2	2.55	0.41
50:4:422:HIS:NE2	55:K:401:G:O2'	2.49	0.41
50:4:470:LYS:HD3	55:K:396:A:OP1	2.20	0.41
54:8:106:ASN:O	54:8:110:ASP:HB2	2.20	0.41
55:K:916:C:H4'	55:K:917:A:OP2	2.20	0.41
55:K:963:G:O2'	55:K:964:A:H8	2.02	0.41
55:K:2804:C:H2'	55:K:2805:C:C6	2.56	0.41
55:K:2805:C:N4	55:K:2806:A:N6	2.69	0.41
55:K:4635:A:H8	55:K:5048:A:H61	1.68	0.41
55:K:4736:C:H2'	55:K:4737:G:H8	1.84	0.41
2:C:289:LEU:C	2:C:289:LEU:HD12	2.45	0.41
2:C:323:ARG:HD2	55:K:976:G:H21	1.85	0.41
4:E:116:PRO:HA	55:K:458:C:OP1	2.19	0.41
7:H:126:VAL:HG11	7:H:161:ILE:HG22	2.02	0.41
30:f:81:SER:HB2	55:K:1919:G:O2'	2.20	0.41
32:h:66:LYS:HG2	44:v:96:C:H5''	2.02	0.41
44:v:13:G:C4	44:v:14:U:C5	3.09	0.41
44:v:25:G:C6	55:K:351:C:N4	2.88	0.41
45:w:30:LYS:HG3	55:K:4716:C:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:265:LEU:HD12	46:B:266:ALA:N	2.36	0.41
47:1:16:LEU:HD11	47:1:118:LEU:HB2	2.02	0.41
47:1:308:LEU:HG	47:1:318:VAL:HG22	2.02	0.41
49:3:63:ASN:O	49:3:67:GLY:N	2.52	0.41
52:7:86:MET:HG2	52:7:356:SER:OG	2.20	0.41
55:K:1168:G:C2	55:K:1194:G:N1	2.88	0.41
55:K:2349:A:H5''	55:K:2350:U:H5''	2.03	0.41
55:K:2871:A:H2'	55:K:2872:C:O4'	2.21	0.41
55:K:3939:G:N7	55:K:4170:A:H2'	2.35	0.41
55:K:4323:A:H2'	55:K:4324:A:O4'	2.20	0.41
55:K:4896:G:H2'	55:K:4897:G:H8	1.86	0.41
3:D:197:LYS:O	3:D:202:GLN:N	2.53	0.41
4:E:144:ARG:NH1	30:f:108:SER:O	2.54	0.41
7:H:92:MET:O	7:H:143:GLU:HB2	2.21	0.41
7:H:123:ILE:O	7:H:123:ILE:HG13	2.21	0.41
12:N:47:LYS:O	12:N:51:LEU:HG	2.20	0.41
14:P:122:ALA:HB3	14:P:143:PRO:HG2	2.02	0.41
17:S:2:LYS:O	17:S:4:SER:N	2.51	0.41
30:f:72:GLY:HA2	30:f:88:PHE:HA	2.02	0.41
44:v:18:U:O2	55:K:2309:G:O2'	2.38	0.41
45:w:80:GLU:OE2	45:w:328:ASN:ND2	2.53	0.41
46:B:225:LEU:HA	46:B:228:LEU:HG	2.02	0.41
46:B:233:ILE:HG13	46:B:234:GLU:N	2.36	0.41
46:B:260:THR:HG22	55:K:2794:C:N3	2.35	0.41
47:1:10:LYS:N	47:1:11:PRO:HD2	2.35	0.41
47:1:273:ARG:HG3	55:K:2432:U:H5'	2.02	0.41
55:K:385:A:H4'	55:K:386:A:OP1	2.21	0.41
55:K:458:C:H2'	55:K:459:C:C6	2.56	0.41
55:K:1271:G:O2'	55:K:1272:C:O5'	2.35	0.41
55:K:1292:C:H5'	55:K:1293:G:OP2	2.20	0.41
55:K:1874:A:O4'	55:K:4213:A:N6	2.54	0.41
55:K:1990:A:H3'	55:K:1991:A:H5''	2.03	0.41
55:K:2504:C:H2'	55:K:2505:C:C2	2.56	0.41
55:K:2581:A:N3	55:K:2654:C:O2'	2.40	0.41
55:K:2599:G:N2	55:K:2747:U:C4	2.88	0.41
55:K:3653:A:C2	55:K:3692:A:H5'	2.55	0.41
55:K:4889:G:C6	55:K:4931:G:C6	3.08	0.41
1:A:116:LEU:HD12	1:A:117:GLU:H	1.86	0.41
2:C:134:PRO:CA	2:C:150:LEU:HD11	2.51	0.41
2:C:236:ASN:OD1	2:C:238:LEU:N	2.53	0.41
6:G:314:LEU:O	6:G:318:LEU:HD12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:75:VAL:O	12:N:76:PRO:O	2.39	0.41
14:P:11:PRO:HD2	50:4:414:GLU:CD	2.45	0.41
14:P:32:THR:O	14:P:36:ILE:HG12	2.21	0.41
15:Q:3:VAL:HG23	15:Q:5:ILE:HG12	2.01	0.41
19:U:91:LEU:O	19:U:96:LEU:N	2.50	0.41
35:k:8:ILE:O	35:k:12:LEU:HG	2.21	0.41
39:o:61:LYS:NZ	55:K:4371:G:O2'	2.52	0.41
47:1:341:LEU:O	47:1:345:LEU:HD13	2.20	0.41
50:4:332:HIS:NE2	50:4:334:SER:HB2	2.36	0.41
53:6:4:PHE:HZ	54:8:100:ALA:O	2.04	0.41
55:K:254:G:H2'	55:K:255:C:O4'	2.20	0.41
55:K:381:U:H4'	55:K:415:G:H5'	2.02	0.41
55:K:425:U:C2	55:K:426:A:C8	3.08	0.41
55:K:750:U:H2'	55:K:751:G:O4'	2.21	0.41
55:K:956:A:N6	55:K:1283:G:H1'	2.35	0.41
55:K:1328:G:O2'	55:K:2349:A:OP1	2.35	0.41
55:K:1445:U:O2'	55:K:1446:C:P	2.78	0.41
55:K:1563:A:O2'	55:K:1564:A:O4'	2.35	0.41
55:K:1886:G:O2'	55:K:1909:G:O2'	2.06	0.41
55:K:1937:C:OP2	55:K:1938:C:O2'	2.34	0.41
55:K:2279:A:H2'	55:K:2280:G:O4'	2.20	0.41
55:K:2793:G:H5'	55:K:2794:C:H5''	2.02	0.41
55:K:3662:A:H5'	55:K:3664:G:O4'	2.21	0.41
55:K:3795:A:C6	55:K:3806:G:C6	3.07	0.41
55:K:4699:U:H4'	55:K:4700:A:OP1	2.20	0.41
2:C:323:ARG:NH1	55:K:1279:A:O2'	2.54	0.41
6:G:199:LEU:CD1	6:G:205:ALA:HB2	2.51	0.41
41:q:43:A:H2'	41:q:44:A:C8	2.55	0.41
44:v:140:C:H2'	44:v:141:C:C6	2.56	0.41
55:K:86:U:H2'	55:K:87:A:C8	2.55	0.41
55:K:450:G:C6	55:K:1298:C:C4	3.09	0.41
55:K:470:A:H2'	55:K:471:A:O4'	2.21	0.41
55:K:759:G:N2	55:K:904:C:C2	2.79	0.41
55:K:1358:G:O2'	55:K:1360:G:O6	2.34	0.41
55:K:1381:U:O2	55:K:1381:U:O4'	2.37	0.41
55:K:2029:A:H2'	55:K:2030:A:C8	2.55	0.41
55:K:2325:C:O2	55:K:2325:C:H2'	2.21	0.41
55:K:3599:A:H2'	55:K:3600:G:H8	1.85	0.41
55:K:3784:A:O2'	55:K:3785:A:H3'	2.21	0.41
55:K:4525:C:C2	55:K:4526:U:C5	3.09	0.41
55:K:4620:U:OP2	55:K:4670:C:N4	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:4973:U:O2	55:K:4986:G:C6	2.74	0.41
1:A:196:TRP:O	1:A:198:ARG:N	2.54	0.41
4:E:179:THR:O	4:E:179:THR:CG2	2.69	0.41
4:E:206:ILE:O	4:E:206:ILE:CG2	2.66	0.41
6:G:313:GLU:OE1	6:G:314:LEU:N	2.54	0.41
14:P:16:LYS:HG2	14:P:149:ILE:HG12	2.03	0.41
23:Y:123:ALA:O	23:Y:127:GLN:HG3	2.20	0.41
24:Z:89:ILE:CG2	24:Z:91:LEU:HD23	2.50	0.41
29:e:113:GLU:O	29:e:117:GLN:HG3	2.21	0.41
34:j:63:ARG:NH2	44:v:58:G:O6	2.53	0.41
44:v:33:G:H5''	44:v:34:U:OP1	2.20	0.41
45:w:195:ASP:O	45:w:199:GLU:HG2	2.21	0.41
45:w:314:ILE:HD11	45:w:326:VAL:HG11	2.02	0.41
52:7:319:ILE:HD11	52:7:334:ALA:HB3	2.03	0.41
55:K:1483:C:H4'	55:K:1484:G:H5'	2.01	0.41
55:K:1767:A:H5''	55:K:1768:C:OP2	2.20	0.41
55:K:2089:G:H4'	55:K:2090:U:O5'	2.21	0.41
55:K:3936:A:N6	55:K:4175:G:O6	2.54	0.41
55:K:4168:G:H2'	55:K:4169:G:H5'	2.02	0.41
55:K:5019:A:H2'	55:K:5020:G:C8	2.55	0.41
55:K:5061:A:H3'	55:K:5062:G:C5'	2.51	0.41
4:E:165:VAL:HG11	4:E:187:VAL:HG11	2.02	0.41
5:F:49:ILE:HD12	5:F:185:CYS:HB3	2.03	0.41
6:G:195:THR:O	6:G:199:LEU:HG	2.21	0.41
8:I:140:THR:OG1	8:I:141:LYS:N	2.53	0.41
8:I:193:ASP:OD1	55:K:1750:G:N2	2.54	0.41
9:J:109:ILE:HD13	9:J:115:LEU:CD1	2.50	0.41
12:N:44:ARG:NH2	55:K:280:G:OP1	2.35	0.41
14:P:74:LYS:NZ	55:K:4982:A:OP1	2.45	0.41
15:Q:61:LEU:HD12	15:Q:82:VAL:HG21	2.03	0.41
18:T:121:GLU:HG2	18:T:122:LYS:HD2	2.03	0.41
20:V:109:LYS:NZ	20:V:111:GLU:OE1	2.53	0.41
22:X:156:ILE:HD11	47:1:415:ARG:HH12	1.86	0.41
28:d:57:MET:O	28:d:59:THR:N	2.47	0.41
35:k:8:ILE:HD12	35:k:8:ILE:H	1.86	0.41
35:k:56:LEU:O	35:k:60:LEU:HD12	2.20	0.41
40:p:79:VAL:O	40:p:83:ILE:HG12	2.21	0.41
43:u:15:C:H2'	43:u:16:A:C8	2.56	0.41
44:v:67:U:H2'	44:v:68:G:H8	1.86	0.41
44:v:70:G:N2	44:v:87:G:H1'	2.36	0.41
44:v:141:C:H2'	44:v:142:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:3:4:VAL:O	49:3:8:VAL:HG23	2.21	0.41
50:4:314:ASP:OD1	50:4:314:ASP:C	2.64	0.41
51:5:49:LEU:HD21	51:5:90:ALA:HA	2.02	0.41
52:7:423:ALA:O	52:7:427:VAL:HG23	2.21	0.41
55:K:132:G:H2'	55:K:133:C:O4'	2.20	0.41
55:K:967:C:H5''	55:K:968:C:H5	1.86	0.41
55:K:1078:A:C5	55:K:1233:G:C6	3.09	0.41
55:K:1188:C:H2'	55:K:1189:G:C8	2.56	0.41
55:K:1202:C:C2	55:K:1203:G:C8	3.09	0.41
55:K:1294:A:H5'	55:K:1296:G:N2	2.36	0.41
55:K:1328:G:C6	55:K:1329:G:C6	3.09	0.41
55:K:1333:A:H2'	55:K:1334:A:C8	2.56	0.41
55:K:1565:A:C5	55:K:1566:C:H1'	2.56	0.41
55:K:2294:G:C6	55:K:2341:A:C6	3.09	0.41
55:K:3652:A:H2'	55:K:3653:A:C5	2.56	0.41
55:K:3722:G:C6	55:K:3732:A:C6	3.09	0.41
55:K:3904:G:O2'	55:K:3905:A:P	2.79	0.41
55:K:4208:U:H2'	55:K:4209:G:C8	2.55	0.41
55:K:4238:G:H2'	55:K:4239:A:H8	1.85	0.41
55:K:4584:A:C2	55:K:4719:G:C4	3.09	0.41
55:K:4596:C:C4	55:K:4597:U:C4	3.08	0.41
55:K:4620:U:H2'	55:K:4621:C:O4'	2.21	0.41
55:K:4659:G:H2'	55:K:4660:G:O4'	2.21	0.41
56:9:90:LEU:HD23	56:9:92:ILE:HD12	2.03	0.41
3:D:269:PRO:O	43:u:60:G:H4'	2.21	0.41
6:G:247:VAL:HG21	6:G:249:ARG:NH1	2.36	0.41
11:M:97:ALA:HB1	13:O:200:GLY:CA	2.51	0.41
13:O:90:HIS:NE2	55:K:3886:G:OP2	2.51	0.41
13:O:140:ARG:O	13:O:144:GLU:OE1	2.39	0.41
13:O:142:ALA:HB1	13:O:147:TRP:HB2	2.03	0.41
30:f:43:LEU:O	30:f:109:ARG:NH1	2.54	0.41
41:q:10:G:N1	41:q:25:C:N3	2.45	0.41
41:q:75:C:H2'	41:q:76:A:O4'	2.21	0.41
47:1:379:TRP:CE2	47:1:383:SER:OG	2.74	0.41
55:K:442:G:H2'	55:K:443:G:O4'	2.21	0.41
55:K:1802:A:H5''	55:K:1803:G:H5'	2.03	0.41
55:K:1912:G:C6	55:K:2057:A:C2	3.09	0.41
55:K:3866:C:H2'	55:K:3867:A:O4'	2.20	0.41
55:K:3876:A:O2'	55:K:3877:A:P	2.78	0.41
55:K:3882:C:H2'	55:K:3883:U:C6	2.57	0.41
55:K:4205:A:C8	55:K:4375:C:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:4284:C:H2'	55:K:4285:U:C6	2.56	0.41
55:K:4640:C:H2'	55:K:4641:U:O4'	2.21	0.41
55:K:4769:G:C2	55:K:4866:C:C2	3.08	0.41
2:C:42:THR:HB	55:K:2340:C:H4'	2.02	0.40
2:C:214:ASP:OD1	2:C:218:VAL:HG22	2.20	0.40
4:E:160:HIS:CG	4:E:187:VAL:HG22	2.56	0.40
5:F:95:ARG:NH2	55:K:1895:G:OP1	2.54	0.40
20:V:14:PHE:HE2	45:w:67:VAL:HG13	1.86	0.40
20:V:15:ARG:HB3	55:K:4618:G:H5''	2.02	0.40
31:g:108:LYS:O	31:g:112:GLN:HG2	2.21	0.40
39:o:11:PHE:HA	39:o:17:LYS:O	2.21	0.40
46:B:240:CYS:HB2	46:B:242:PRO:HD3	2.02	0.40
51:5:10:ARG:O	51:5:11:ARG:NH1	2.54	0.40
55:K:485:C:H4'	55:K:486:C:OP1	2.21	0.40
55:K:4627:U:H2'	55:K:4628:U:H6	1.87	0.40
55:K:4992:G:H2'	55:K:4993:G:C8	2.56	0.40
55:K:5058:A:H2'	55:K:5059:C:O4'	2.21	0.40
1:A:215:ASN:ND2	55:K:4546:A:N7	2.68	0.40
2:C:38:ASN:O	2:C:42:THR:HG23	2.21	0.40
2:C:78:ARG:HB3	2:C:88:GLY:HA2	2.03	0.40
9:J:87:LEU:HD13	9:J:170:TYR:CD2	2.56	0.40
14:P:65:GLY:C	14:P:67:VAL:H	2.30	0.40
17:S:147:ASP:OD1	17:S:147:ASP:C	2.65	0.40
19:U:18:LEU:HD23	19:U:18:LEU:C	2.46	0.40
25:a:80:THR:H	25:a:80:THR:HG1	1.67	0.40
47:1:251:VAL:O	47:1:255:VAL:HG23	2.21	0.40
49:3:6:GLN:O	49:3:10:PRO:CD	2.69	0.40
53:6:4:PHE:CZ	54:8:100:ALA:O	2.74	0.40
55:K:270:U:C4	55:K:271:C:C5	3.09	0.40
55:K:504:G:C2	55:K:655:C:C2	3.08	0.40
55:K:922:C:H2'	55:K:922(A):G:C8	2.56	0.40
55:K:1191:C:H2'	55:K:1192:C:C6	2.57	0.40
55:K:1370:G:H1'	55:K:1371:A:OP2	2.21	0.40
55:K:2318:G:N1	55:K:2322:G:C6	2.90	0.40
55:K:2804:C:H2'	55:K:2805:C:H6	1.86	0.40
55:K:4235:G:N2	55:K:4292:A:OP1	2.43	0.40
55:K:4260:U:H2'	55:K:4261:C:H6	1.84	0.40
55:K:4322:G:N2	55:K:4325:A:OP2	2.43	0.40
2:C:2:ALA:N	55:K:667:A:N7	2.68	0.40
7:H:45:LEU:HD22	7:H:57:VAL:HG12	2.03	0.40
14:P:100:SER:HB2	55:K:393:U:H4'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:76:ASN:ND2	24:Z:78:ASN:OD1	2.55	0.40
33:i:31:GLY:O	55:K:308:G:O2'	2.23	0.40
42:r:10:VAL:O	42:r:10:VAL:CG1	2.70	0.40
45:w:94:GLU:HG2	45:w:99:LEU:HD13	2.03	0.40
45:w:196:TRP:O	45:w:200:ARG:HG2	2.21	0.40
47:1:216:LEU:HD22	47:1:242:LEU:HD22	2.04	0.40
52:7:422:ARG:HD2	52:7:433:LEU:HD21	2.03	0.40
55:K:138:G:H2'	55:K:139:G:H8	1.87	0.40
55:K:483:G:H5''	55:K:484:U:H2'	2.03	0.40
55:K:515:C:H2'	55:K:516:C:C6	2.57	0.40
55:K:652:G:H2'	55:K:653:C:C6	2.57	0.40
55:K:966:A:H4'	55:K:967:C:O5'	2.22	0.40
55:K:1381:U:H5'	55:K:1382:G:OP2	2.21	0.40
55:K:1391:A:H2'	55:K:1392:A:O4'	2.22	0.40
55:K:1417:C:H2'	55:K:1418:C:C6	2.56	0.40
55:K:1488:G:H2'	55:K:1489:G:O4'	2.21	0.40
55:K:1594:C:O2	55:K:1599:G:O6	2.40	0.40
55:K:2093:G:C4	55:K:2095:A:C6	3.09	0.40
55:K:2477:A:H2'	55:K:2478:C:C6	2.56	0.40
55:K:2553:A:H1'	55:K:2554:U:O4'	2.21	0.40
55:K:2617:G:C6	55:K:2721:G:C6	3.10	0.40
55:K:3653:A:N1	55:K:3692:A:H5'	2.37	0.40
55:K:4354:U:H2'	55:K:4355:G:OP2	2.22	0.40
55:K:4593:C:H2'	55:K:4594:U:H6	1.86	0.40
10:L:107:THR:HB	33:i:18:THR:HG23	2.03	0.40
22:X:84:GLU:HG2	47:1:404:HIS:CE1	2.56	0.40
27:c:32:LYS:NZ	55:K:2658:G:O6	2.48	0.40
29:e:38:PRO:HB2	29:e:43:ASN:ND2	2.36	0.40
31:g:63:VAL:O	31:g:63:VAL:HG12	2.20	0.40
42:r:28:GLU:HB2	42:r:31:ASN:HB2	2.04	0.40
43:u:110:G:H2'	43:u:111:C:C6	2.56	0.40
46:B:247:ARG:O	46:B:247:ARG:HG2	2.21	0.40
52:7:9:MET:HE2	52:7:20:GLY:HA2	2.02	0.40
55:K:499:G:H2'	55:K:500:G:C8	2.56	0.40
55:K:1089:G:N1	55:K:1208:G:C6	2.89	0.40
55:K:1171:G:H2'	55:K:1172:C:C6	2.56	0.40
55:K:1460:C:H2'	55:K:1461:C:H6	1.86	0.40
55:K:2784:C:C2	55:K:2785:C:C5	3.09	0.40
55:K:3753:G:N1	55:K:3772:U:O2	2.54	0.40
55:K:4254:G:H2'	55:K:4254:G:N3	2.36	0.40
4:E:117:ARG:NH2	55:K:691:C:OP2	2.49	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:269:GLN:OE1	11:M:111:LYS:HG2	2.21	0.40
4:E:286:PRO:HA	4:E:289:LEU:CD2	2.51	0.40
5:F:135:VAL:HG23	5:F:139:ILE:HD13	2.03	0.40
7:H:71:ARG:NH2	55:K:4695:C:OP1	2.54	0.40
10:L:80:GLU:HG2	10:L:110:LEU:HD12	2.03	0.40
14:P:23:ARG:HG3	14:P:125:MET:HE1	2.02	0.40
18:T:40:VAL:CG1	18:T:96:ILE:HG23	2.50	0.40
25:a:134:GLU:O	25:a:138:LYS:HG2	2.21	0.40
31:g:18:ASN:O	31:g:18:ASN:ND2	2.55	0.40
43:u:43:U:C4	43:u:44:C:C4	3.09	0.40
52:7:176:THR:O	52:7:264:ALA:N	2.50	0.40
55:K:126:C:H2'	55:K:127:G:H8	1.86	0.40
55:K:163:A:H2'	55:K:164:G:C8	2.56	0.40
55:K:264:C:O2'	55:K:266:C:N3	2.33	0.40
55:K:366:A:H2'	55:K:367:C:O4'	2.21	0.40
55:K:432:U:H4'	55:K:433:A:H5''	2.03	0.40
55:K:976:G:H22	55:K:1279:A:H2	1.68	0.40
55:K:1484:G:H2'	55:K:1484:G:N3	2.37	0.40
55:K:1485:C:C5	55:K:4349:C:C2	3.10	0.40
55:K:4299:U:H2'	55:K:4300:U:C6	2.57	0.40
55:K:4381:A:C6	55:K:4382:G:N7	2.90	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%)	220 (89%)	26 (11%)	0	100	100
2	C	360/413 (87%)	336 (93%)	24 (7%)	0	100	100
3	D	291/297 (98%)	270 (93%)	21 (7%)	0	100	100
4	E	227/291 (78%)	218 (96%)	8 (4%)	1 (0%)	30	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	F	223/247 (90%)	208 (93%)	15 (7%)	0	100	100
6	G	229/319 (72%)	214 (93%)	15 (7%)	0	100	100
7	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
8	I	201/214 (94%)	182 (90%)	19 (10%)	0	100	100
9	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100
10	L	208/211 (99%)	194 (93%)	13 (6%)	1 (0%)	24	59
11	M	136/218 (62%)	126 (93%)	10 (7%)	0	100	100
12	N	200/204 (98%)	185 (92%)	14 (7%)	1 (0%)	24	59
13	O	197/203 (97%)	187 (95%)	10 (5%)	0	100	100
14	P	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
15	Q	185/188 (98%)	171 (92%)	14 (8%)	0	100	100
16	R	153/196 (78%)	144 (94%)	9 (6%)	0	100	100
17	S	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
18	T	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	21	55
19	U	100/128 (78%)	90 (90%)	10 (10%)	0	100	100
20	V	129/140 (92%)	121 (94%)	8 (6%)	0	100	100
21	W	61/157 (39%)	55 (90%)	6 (10%)	0	100	100
22	X	116/156 (74%)	106 (91%)	10 (9%)	0	100	100
23	Y	132/145 (91%)	125 (95%)	7 (5%)	0	100	100
24	Z	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
25	a	145/148 (98%)	132 (91%)	13 (9%)	0	100	100
26	b	100/226 (44%)	95 (95%)	5 (5%)	0	100	100
27	c	96/115 (84%)	92 (96%)	4 (4%)	0	100	100
28	d	105/125 (84%)	94 (90%)	11 (10%)	0	100	100
29	e	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
30	f	107/110 (97%)	101 (94%)	6 (6%)	0	100	100
31	g	112/116 (97%)	106 (95%)	6 (5%)	0	100	100
32	h	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
33	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
34	j	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
35	k	67/70 (96%)	63 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	l	48/51 (94%)	39 (81%)	9 (19%)	0	100	100
37	m	50/102 (49%)	47 (94%)	3 (6%)	0	100	100
38	n	23/25 (92%)	23 (100%)	0	0	100	100
39	o	102/106 (96%)	93 (91%)	9 (9%)	0	100	100
40	p	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
42	r	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
45	w	392/403 (97%)	361 (92%)	31 (8%)	0	100	100
46	B	68/273 (25%)	56 (82%)	11 (16%)	1 (2%)	8	37
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%)	336 (99%)	3 (1%)	1 (0%)	36	69
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
54	8	175/188 (93%)	174 (99%)	1 (1%)	0	100	100
56	9	107/129 (83%)	101 (94%)	6 (6%)	0	100	100
All	All	8428/9902 (85%)	7941 (94%)	481 (6%)	6 (0%)	49	80

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	N	76	PRO
10	L	64	VAL
50	4	347	GLY
18	T	82	GLY
46	B	242	PRO
4	E	228	PRO

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	81
2	C	302/337 (90%)	301 (100%)	1 (0%)	86	85
3	D	247/250 (99%)	247 (100%)	0	100	100
4	E	206/251 (82%)	204 (99%)	2 (1%)	68	75
5	F	196/215 (91%)	195 (100%)	1 (0%)	81	81
6	G	200/272 (74%)	199 (100%)	1 (0%)	81	81
7	H	169/171 (99%)	168 (99%)	1 (1%)	78	80
8	I	175/181 (97%)	174 (99%)	1 (1%)	78	80
9	J	143/149 (96%)	142 (99%)	1 (1%)	76	78
10	L	175/176 (99%)	172 (98%)	3 (2%)	53	67
11	M	117/161 (73%)	116 (99%)	1 (1%)	70	75
12	N	171/172 (99%)	170 (99%)	1 (1%)	78	80
13	O	171/173 (99%)	171 (100%)	0	100	100
14	P	134/163 (82%)	132 (98%)	2 (2%)	57	69
15	Q	164/164 (100%)	163 (99%)	1 (1%)	78	80
16	R	138/175 (79%)	138 (100%)	0	100	100
17	S	157/157 (100%)	155 (99%)	2 (1%)	61	71
18	T	139/140 (99%)	139 (100%)	0	100	100
19	U	92/114 (81%)	91 (99%)	1 (1%)	65	73
20	V	101/107 (94%)	100 (99%)	1 (1%)	68	75
21	W	55/126 (44%)	55 (100%)	0	100	100
22	X	106/134 (79%)	105 (99%)	1 (1%)	70	75
23	Y	124/135 (92%)	123 (99%)	1 (1%)	73	77
24	Z	117/118 (99%)	115 (98%)	2 (2%)	53	67
25	a	119/120 (99%)	118 (99%)	1 (1%)	73	77
26	b	84/172 (49%)	83 (99%)	1 (1%)	63	72
27	c	84/98 (86%)	83 (99%)	1 (1%)	63	72
28	d	98/110 (89%)	96 (98%)	2 (2%)	48	65
29	e	114/121 (94%)	114 (100%)	0	100	100
30	f	88/89 (99%)	88 (100%)	0	100	100
31	g	98/99 (99%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	h	108/110 (98%)	107 (99%)	1 (1%)	70	75
33	i	86/89 (97%)	86 (100%)	0	100	100
34	j	73/80 (91%)	71 (97%)	2 (3%)	39	59
35	k	64/65 (98%)	64 (100%)	0	100	100
36	l	47/48 (98%)	47 (100%)	0	100	100
37	m	48/90 (53%)	48 (100%)	0	100	100
38	n	24/24 (100%)	24 (100%)	0	100	100
39	o	92/94 (98%)	92 (100%)	0	100	100
40	p	74/75 (99%)	72 (97%)	2 (3%)	39	59
42	r	108/121 (89%)	108 (100%)	0	100	100
45	w	342/348 (98%)	340 (99%)	2 (1%)	78	80
46	B	54/207 (26%)	52 (96%)	2 (4%)	30	53
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%)	58 (98%)	1 (2%)	53	67
50	4	306/435 (70%)	303 (99%)	3 (1%)	68	75
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	81
54	8	155/164 (94%)	154 (99%)	1 (1%)	78	80
56	9	93/108 (86%)	90 (97%)	3 (3%)	34	56
All	All	7336/8400 (87%)	7283 (99%)	53 (1%)	73	78

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	165	VAL
2	C	150	LEU
4	E	221	LYS
4	E	245	ILE
5	F	236	GLU
6	G	96	GLN
7	H	105	ILE
8	I	73	ASN
9	J	115	LEU

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Mol	Chain	Res	Type
10	L	10	LEU
10	L	70	VAL
10	L	154	VAL
11	M	43	THR
12	N	80	THR
14	P	24	VAL
14	P	118	GLN
15	Q	8	ASN
17	S	67	VAL
17	S	90	THR
19	U	105	ASN
20	V	18	LEU
22	X	120	ASP
23	Y	79	VAL
24	Z	11	VAL
24	Z	53	VAL
25	a	122	VAL
26	b	116	LEU
27	c	91	VAL
28	d	22	THR
28	d	86	VAL
32	h	82	ASP
34	j	67	LEU
34	j	82	THR
40	p	16	THR
40	p	52	VAL
45	w	90	VAL
45	w	207	VAL
46	B	230	VAL
46	B	233	ILE
47	1	18	GLU
47	1	118	LEU
47	1	130	VAL
47	1	230	LEU
49	3	21	LEU
50	4	323	HIS
50	4	434	GLU
50	4	468	LEU
52	7	314	MET
53	6	51	LEU
54	8	160	LYS
56	9	29	LEU

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Mol	Chain	Res	Type
56	9	100	THR
56	9	129	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	194	ASN
1	A	205	ASN
5	F	55	HIS
5	F	79	ASN
5	F	118	ASN
5	F	125	ASN
6	G	96	GLN
7	H	76	HIS
7	H	189	GLN
8	I	163	GLN
9	J	104	ASN
10	L	15	HIS
12	N	182	HIS
13	O	96	GLN
13	O	143	HIS
14	P	21	ASN
16	R	58	HIS
18	T	66	ASN
19	U	17	GLN
22	X	57	GLN
22	X	108	GLN
23	Y	61	HIS
25	a	19	HIS
25	a	120	GLN
26	b	60	ASN
27	c	15	ASN
28	d	18	ASN
28	d	30	HIS
31	g	28	ASN
32	h	98	HIS
38	n	22	GLN
42	r	21	ASN
45	w	68	ASN
47	1	186	ASN
47	1	218	HIS
47	1	275	GLN

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Mol	Chain	Res	Type
47	1	294	GLN
50	4	446	ASN
52	7	56	GLN
52	7	61	GLN
52	7	116	GLN
52	7	135	HIS
52	7	281	HIS
52	7	349	HIS
52	7	353	GLN
52	7	467	GLN
52	7	470	GLN
52	7	512	GLN
53	6	152	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
41	q	74/77 (96%)	16 (21%)	0
43	u	119/120 (99%)	14 (11%)	0
44	v	155/156 (99%)	37 (23%)	0
55	K	3520/3543 (99%)	819 (23%)	58 (1%)
All	All	3868/3896 (99%)	886 (22%)	58 (1%)

All (886) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
41	q	9	A
41	q	12	G
41	q	13	U
41	q	16	C
41	q	19	G
41	q	20	U
41	q	20(A)	U
41	q	21	A
41	q	22	U
41	q	24	A
41	q	39	G
41	q	46	G
41	q	47	U
41	q	56	C
41	q	67	G

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Mol	Chain	Res	Type
41	q	75	C
43	u	7	G
43	u	10	C
43	u	22	A
43	u	25	G
43	u	31	G
43	u	42	A
43	u	53	U
43	u	54	A
43	u	64	G
43	u	80	U
43	u	100	A
43	u	110	G
43	u	111	C
43	u	120	U
44	v	2	G
44	v	3	A
44	v	13	G
44	v	20	A
44	v	23	C
44	v	32	C
44	v	34	U
44	v	35	C
44	v	38	U
44	v	49	G
44	v	59	A
44	v	62	A
44	v	63	U
44	v	75	G
44	v	80	A
44	v	81	C
44	v	82	A
44	v	83	C
44	v	84	A
44	v	85	U
44	v	86	U
44	v	87	G
44	v	103	A
44	v	105	C
44	v	106	G
44	v	109	C
44	v	110	U

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Mol	Chain	Res	Type
44	v	111	U
44	v	112	G
44	v	114	G
44	v	123	U
44	v	125	C
44	v	126	C
44	v	127	U
44	v	128	C
44	v	153	C
44	v	156	U
55	K	12	A
55	K	13	U
55	K	15	A
55	K	30	C
55	K	39	A
55	K	42	A
55	K	44	A
55	K	56	A
55	K	58	G
55	K	59	A
55	K	64	A
55	K	65	A
55	K	73	A
55	K	74	G
55	K	84	A
55	K	91	G
55	K	95	G
55	K	104	G
55	K	108	A
55	K	109	G
55	K	110	C
55	K	118	C
55	K	119	G
55	K	122	U
55	K	126	C
55	K	131	C
55	K	134	G
55	K	135	G
55	K	136	C
55	K	137	G
55	K	141	C
55	K	142	G

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Mol	Chain	Res	Type
55	K	146	G
55	K	157	U
55	K	159	C
55	K	160	G
55	K	172	C
55	K	173	C
55	K	177	G
55	K	182	G
55	K	200	U
55	K	201	C
55	K	209	U
55	K	216	C
55	K	218	A
55	K	221	C
55	K	224	U
55	K	225	G
55	K	232	G
55	K	233	U
55	K	234	G
55	K	246	G
55	K	256	G
55	K	258	G
55	K	262	G
55	K	263	G
55	K	265	C
55	K	266	C
55	K	267	G
55	K	271	C
55	K	276	C
55	K	280	G
55	K	297	U
55	K	306	A
55	K	308	G
55	K	309	C
55	K	315	G
55	K	316	U
55	K	322	C
55	K	326	C
55	K	334	A
55	K	340	C
55	K	363	A
55	K	370	U

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Mol	Chain	Res	Type
55	K	371	A
55	K	387	G
55	K	407	A
55	K	410	A
55	K	412	G
55	K	413	G
55	K	415	G
55	K	417	G
55	K	428	G
55	K	440	U
55	K	446	C
55	K	449	C
55	K	450	G
55	K	452	A
55	K	453	G
55	K	454	U
55	K	455	C
55	K	463	A
55	K	464	G
55	K	467	U
55	K	468	U
55	K	481	G
55	K	481(A)	C
55	K	482	G
55	K	483	G
55	K	485	C
55	K	486	C
55	K	492	U
55	K	493	G
55	K	496	G
55	K	497	G
55	K	498	C
55	K	499	G
55	K	505	G
55	K	506	C
55	K	510	U
55	K	644	G
55	K	647	G
55	K	658	C
55	K	659	G
55	K	661	C
55	K	666	G

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Mol	Chain	Res	Type
55	K	667	A
55	K	668	C
55	K	669	C
55	K	670	G
55	K	685	C
55	K	686	A
55	K	687	U
55	K	696	C
55	K	697	G
55	K	699	C
55	K	701	G
55	K	704	C
55	K	705	G
55	K	708	G
55	K	731	G
55	K	738	C
55	K	749	G
55	K	756	G
55	K	758	G
55	K	914	U
55	K	917	A
55	K	918	G
55	K	923	C
55	K	925	C
55	K	926	G
55	K	929	A
55	K	932	A
55	K	933	G
55	K	934	C
55	K	935	A
55	K	935(A)	G
55	K	936	C
55	K	938	C
55	K	939	G
55	K	941	C
55	K	944	A
55	K	945	U
55	K	959	G
55	K	960	A
55	K	961	G
55	K	964	A
55	K	965	G

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Mol	Chain	Res	Type
55	K	966	A
55	K	967	C
55	K	968	C
55	K	969	C
55	K	971(A)	G
55	K	972	C
55	K	973	G
55	K	979	C
55	K	983	C
55	K	990	C
55	K	1070	G
55	K	1072	C
55	K	1073	G
55	K	1076	C
55	K	1078	A
55	K	1079	C
55	K	1081	C
55	K	1082	C
55	K	1099	C
55	K	1175	A
55	K	1179	U
55	K	1199	G
55	K	1210	C
55	K	1211	G
55	K	1212	G
55	K	1215	C
55	K	1216	C
55	K	1234	G
55	K	1235	G
55	K	1236	C
55	K	1237	C
55	K	1238	A
55	K	1239	C
55	K	1272	C
55	K	1273	G
55	K	1274	A
55	K	1275	G
55	K	1281	G
55	K	1284	G
55	K	1287	G
55	K	1289	C
55	K	1291	G

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Mol	Chain	Res	Type
55	K	1292	C
55	K	1293	G
55	K	1296	G
55	K	1301	C
55	K	1303	A
55	K	1304	C
55	K	1314	C
55	K	1326	A
55	K	1330	A
55	K	1354	A
55	K	1358	G
55	K	1359	G
55	K	1364	U
55	K	1370	G
55	K	1371	A
55	K	1377	G
55	K	1378	C
55	K	1379	C
55	K	1387	A
55	K	1392	A
55	K	1394	G
55	K	1397	A
55	K	1398	A
55	K	1403	G
55	K	1411(A)	G
55	K	1415	G
55	K	1419	G
55	K	1420	A
55	K	1421	G
55	K	1433	A
55	K	1436	C
55	K	1437	C
55	K	1438	U
55	K	1440	U
55	K	1441	C
55	K	1445	U
55	K	1446	C
55	K	1448	G
55	K	1456	C
55	K	1457	G
55	K	1458	C
55	K	1475	G

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Mol	Chain	Res	Type
55	K	1478	C
55	K	1481	C
55	K	1482	G
55	K	1483	C
55	K	1484	G
55	K	1489	G
55	K	1497	A
55	K	1498	G
55	K	1502	G
55	K	1514	U
55	K	1516	G
55	K	1518	A
55	K	1519	C
55	K	1523	A
55	K	1534	A
55	K	1547	A
55	K	1563	A
55	K	1564	A
55	K	1566	C
55	K	1578	U
55	K	1586	G
55	K	1591	U
55	K	1596	U
55	K	1597	G
55	K	1600	A
55	K	1602	U
55	K	1612	G
55	K	1613	A
55	K	1624	G
55	K	1625	G
55	K	1631	A
55	K	1633	G
55	K	1634	A
55	K	1640	C
55	K	1654	G
55	K	1658	G
55	K	1661	C
55	K	1676	C
55	K	1677	U
55	K	1696	C
55	K	1731	C
55	K	1733	G

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Mol	Chain	Res	Type
55	K	1741	G
55	K	1742	A
55	K	1750	G
55	K	1756	U
55	K	1760	G
55	K	1761	G
55	K	1764	G
55	K	1767	A
55	K	1768	C
55	K	1769	G
55	K	1772	C
55	K	1774	C
55	K	1775	A
55	K	1780	A
55	K	1787	A
55	K	1798	G
55	K	1799	G
55	K	1804	A
55	K	1807	C
55	K	1809	C
55	K	1811	G
55	K	1815	G
55	K	1818	G
55	K	1819	G
55	K	1821	G
55	K	1822	U
55	K	1828	C
55	K	1834	U
55	K	1835	G
55	K	1836	G
55	K	1837	A
55	K	1842	G
55	K	1843	A
55	K	1847	C
55	K	1855	G
55	K	1869	G
55	K	1882	U
55	K	1889	U
55	K	1892	A
55	K	1897	A
55	K	1898	C
55	K	1916	G

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Mol	Chain	Res	Type
55	K	1918	U
55	K	1920	C
55	K	1921	C
55	K	1922	G
55	K	1931	C
55	K	1932	A
55	K	1935	C
55	K	1940	G
55	K	1945	G
55	K	1947	U
55	K	1948	G
55	K	1957	U
55	K	1958	A
55	K	1960	A
55	K	1961	G
55	K	1962	A
55	K	1963	C
55	K	1964	A
55	K	1965	G
55	K	1968	G
55	K	1969	G
55	K	1971	U
55	K	1974	U
55	K	1975	G
55	K	1976	G
55	K	1978	C
55	K	1979	A
55	K	1980	U
55	K	1984	A
55	K	1987	C
55	K	1988	G
55	K	1990	A
55	K	1991	A
55	K	1997	U
55	K	1999	A
55	K	2001	G
55	K	2002	A
55	K	2003	G
55	K	2004	U
55	K	2008	U
55	K	2011	C
55	K	2018	C

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Mol	Chain	Res	Type
55	K	2020	U
55	K	2021	G
55	K	2022	C
55	K	2024	G
55	K	2026	A
55	K	2046	G
55	K	2047	A
55	K	2048	U
55	K	2052	G
55	K	2053	C
55	K	2055	G
55	K	2056	G
55	K	2063	G
55	K	2064	G
55	K	2069	A
55	K	2071	A
55	K	2084	U
55	K	2090	U
55	K	2092	G
55	K	2093	G
55	K	2094	C
55	K	2095	A
55	K	2097	A
55	K	2098	G
55	K	2099	C
55	K	2100	G
55	K	2101	A
55	K	2102	G
55	K	2104	A
55	K	2105	A
55	K	2107	A
55	K	2108	G
55	K	2110	G
55	K	2259	G
55	K	2260	C
55	K	2267	U
55	K	2268	A
55	K	2269	C
55	K	2275	G
55	K	2277	C
55	K	2279	A
55	K	2289	C

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Mol	Chain	Res	Type
55	K	2294	G
55	K	2299	G
55	K	2300	A
55	K	2301	G
55	K	2306	G
55	K	2313	A
55	K	2314	G
55	K	2316	G
55	K	2331	G
55	K	2333	G
55	K	2335	C
55	K	2348	G
55	K	2351	C
55	K	2364	G
55	K	2382	A
55	K	2395	A
55	K	2396	A
55	K	2398	U
55	K	2417	A
55	K	2422	C
55	K	2424	G
55	K	2425	U
55	K	2431	A
55	K	2433	G
55	K	2441	C
55	K	2447	U
55	K	2450	G
55	K	2453	A
55	K	2469	C
55	K	2475	G
55	K	2476	G
55	K	2487	G
55	K	2488	C
55	K	2489	C
55	K	2490	U
55	K	2491	C
55	K	2492	C
55	K	2498	C
55	K	2503	G
55	K	2504	C
55	K	2505	C
55	K	2506	G

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Mol	Chain	Res	Type
55	K	2511	A
55	K	2512	A
55	K	2513	A
55	K	2527	A
55	K	2529	A
55	K	2530	U
55	K	2536	A
55	K	2537	A
55	K	2546	G
55	K	2547	G
55	K	2553	A
55	K	2554	U
55	K	2566	G
55	K	2568	C
55	K	2570	U
55	K	2575	U
55	K	2583	C
55	K	2586	G
55	K	2587	A
55	K	2588	C
55	K	2599	G
55	K	2600	A
55	K	2602	G
55	K	2618	G
55	K	2620	G
55	K	2621	A
55	K	2627	C
55	K	2638	G
55	K	2653	C
55	K	2662	G
55	K	2669	C
55	K	2673	G
55	K	2674	A
55	K	2676	A
55	K	2677	G
55	K	2686	G
55	K	2687	U
55	K	2695	A
55	K	2696	A
55	K	2705	G
55	K	2707	U
55	K	2708	U

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Mol	Chain	Res	Type
55	K	2709	C
55	K	2711	G
55	K	2714	G
55	K	2721	G
55	K	2725	A
55	K	2726	G
55	K	2740	U
55	K	2743	A
55	K	2760	G
55	K	2761	U
55	K	2763	U
55	K	2764	A
55	K	2769	U
55	K	2772	C
55	K	2787	A
55	K	2788	U
55	K	2790	U
55	K	2794	C
55	K	2798	A
55	K	2803	U
55	K	2807	A
55	K	2808	G
55	K	2822	G
55	K	2826	U
55	K	2827	G
55	K	2828	U
55	K	2834	C
55	K	2842	G
55	K	2850	A
55	K	2855	G
55	K	2867	C
55	K	2875	C
55	K	2879	A
55	K	2895	A
55	K	3598	C
55	K	3603	G
55	K	3604	A
55	K	3605	C
55	K	3616	U
55	K	3617	G
55	K	3618	C
55	K	3622	C

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Mol	Chain	Res	Type
55	K	3625	G
55	K	3626	G
55	K	3630	A
55	K	3635	A
55	K	3644	U
55	K	3646	A
55	K	3648	A
55	K	3649	A
55	K	3657	U
55	K	3662	A
55	K	3664	G
55	K	3672	G
55	K	3673	C
55	K	3674	G
55	K	3682	A
55	K	3692	A
55	K	3696	C
55	K	3702	A
55	K	3711	A
55	K	3714	G
55	K	3728	A
55	K	3729	U
55	K	3743	G
55	K	3748	A
55	K	3750	G
55	K	3753	G
55	K	3756	A
55	K	3760	A
55	K	3763	A
55	K	3767	C
55	K	3772	U
55	K	3773	U
55	K	3776	G
55	K	3777	G
55	K	3780	G
55	K	3783	A
55	K	3784	A
55	K	3786	U
55	K	3787	G
55	K	3809	G
55	K	3810	C
55	K	3811	G

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Mol	Chain	Res	Type
55	K	3814	U
55	K	3817	A
55	K	3819	G
55	K	3822	U
55	K	3824	A
55	K	3838	U
55	K	3840	U
55	K	3876	A
55	K	3877	A
55	K	3878	C
55	K	3879	G
55	K	3880	G
55	K	3889	G
55	K	3897	G
55	K	3901	A
55	K	3904	G
55	K	3905	A
55	K	3906	A
55	K	3907	G
55	K	3908	A
55	K	3915	U
55	K	3916	G
55	K	3917	A
55	K	3923	A
55	K	3926	C
55	K	3938	G
55	K	3939	G
55	K	3943	A
55	K	3946	G
55	K	4066	U
55	K	4069	U
55	K	4070	U
55	K	4076	G
55	K	4084	G
55	K	4086	G
55	K	4088	C
55	K	4097	G
55	K	4111	U
55	K	4116	C
55	K	4118	U
55	K	4119	C
55	K	4120	U

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Mol	Chain	Res	Type
55	K	4121	G
55	K	4127	A
55	K	4128	A
55	K	4133	C
55	K	4136	G
55	K	4158	C
55	K	4162	C
55	K	4163	U
55	K	4166	G
55	K	4170	A
55	K	4171	C
55	K	4183	G
55	K	4184	G
55	K	4191	G
55	K	4203	A
55	K	4212	A
55	K	4215	C
55	K	4225	G
55	K	4229	U
55	K	4233	A
55	K	4237	C
55	K	4251	A
55	K	4254	G
55	K	4265	U
55	K	4266	G
55	K	4267	G
55	K	4268	A
55	K	4271	A
55	K	4273	A
55	K	4281	A
55	K	4282	A
55	K	4291	G
55	K	4297	G
55	K	4304	A
55	K	4305	G
55	K	4306	U
55	K	4314	C
55	K	4317	A
55	K	4324	A
55	K	4329	G
55	K	4330	G
55	K	4332	C

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Mol	Chain	Res	Type
55	K	4339	A
55	K	4349	C
55	K	4354	U
55	K	4355	G
55	K	4364	G
55	K	4373	G
55	K	4376	A
55	K	4377	G
55	K	4378	A
55	K	4379	A
55	K	4380	A
55	K	4387	C
55	K	4391	G
55	K	4393	G
55	K	4394	A
55	K	4395	U
55	K	4398	C
55	K	4401	G
55	K	4419	U
55	K	4421	C
55	K	4422	A
55	K	4430	G
55	K	4437	U
55	K	4438	U
55	K	4444	C
55	K	4448	G
55	K	4449	A
55	K	4452	U
55	K	4464	A
55	K	4466	C
55	K	4471	U
55	K	4472	G
55	K	4473	A
55	K	4475	G
55	K	4488	A
55	K	4489	G
55	K	4500	U
55	K	4512	U
55	K	4513	A
55	K	4515	G
55	K	4519	C
55	K	4522	G

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Mol	Chain	Res	Type
55	K	4523	A
55	K	4524	G
55	K	4528	G
55	K	4535	A
55	K	4548	A
55	K	4549	G
55	K	4560	C
55	K	4562	C
55	K	4567	G
55	K	4570	G
55	K	4573	G
55	K	4574	U
55	K	4575	G
55	K	4584	A
55	K	4585	U
55	K	4587	G
55	K	4590	A
55	K	4605	A
55	K	4636	U
55	K	4637	G
55	K	4639	G
55	K	4652	G
55	K	4656	A
55	K	4657	U
55	K	4661	G
55	K	4670	C
55	K	4672	A
55	K	4677	U
55	K	4687	A
55	K	4694	G
55	K	4709	U
55	K	4719	G
55	K	4720	C
55	K	4722	G
55	K	4728	U
55	K	4736	C
55	K	4738	C
55	K	4744	A
55	K	4745	G
55	K	4750	G
55	K	4751	G
55	K	4752	U

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Mol	Chain	Res	Type
55	K	4754	G
55	K	4757	C
55	K	4759	C
55	K	4761	G
55	K	4764	A
55	K	4765	G
55	K	4771	C
55	K	4772	C
55	K	4868	G
55	K	4870	G
55	K	4871	C
55	K	4875	G
55	K	4882	U
55	K	4883	C
55	K	4885	U
55	K	4895	C
55	K	4896	G
55	K	4897	G
55	K	4903	G
55	K	4909	A
55	K	4910	A
55	K	4912	G
55	K	4913	G
55	K	4919	G
55	K	4921	C
55	K	4922	C
55	K	4924	C
55	K	4925	U
55	K	4926	C
55	K	4927	G
55	K	4928	C
55	K	4931	G
55	K	4935	C
55	K	4937	C
55	K	4940	C
55	K	4943	A
55	K	4944	C
55	K	4948	C
55	K	4949	G
55	K	4950	U
55	K	4951	G
55	K	4955	A

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Mol	Chain	Res	Type
55	K	4956	A
55	K	4957	C
55	K	4958	C
55	K	4960	G
55	K	4963	G
55	K	4965	U
55	K	4966	A
55	K	4967	A
55	K	4976	U
55	K	4977	A
55	K	4985	U
55	K	4988	U
55	K	4989	U
55	K	4990	C
55	K	4991	U
55	K	4993	G
55	K	5006	U
55	K	5014	A
55	K	5016	A
55	K	5017	G
55	K	5022	U
55	K	5040	U
55	K	5041	G
55	K	5047	C
55	K	5050	C
55	K	5052	C
55	K	5053	U
55	K	5054	C
55	K	5056	A
55	K	5061	A
55	K	5062	G

All (58) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	K	12	A
55	K	125	C
55	K	134	G
55	K	245	C
55	K	265	C
55	K	275	C
55	K	406	C

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Mol	Chain	Res	Type
55	K	449	C
55	K	480	C
55	K	485	C
55	K	498	C
55	K	504	G
55	K	684	G
55	K	685	C
55	K	696	C
55	K	704	C
55	K	935(A)	G
55	K	959	G
55	K	971(A)	G
55	K	1072	C
55	K	1174	G
55	K	1211	G
55	K	1236	C
55	K	1238	A
55	K	1329	G
55	K	1370	G
55	K	1440	U
55	K	1445	U
55	K	1455	G
55	K	1477	C
55	K	1482	G
55	K	1633	G
55	K	1818	G
55	K	2046	G
55	K	2089	G
55	K	2266	C
55	K	2468	U
55	K	2488	C
55	K	2502	A
55	K	2546	G
55	K	2695	A
55	K	3603	G
55	K	3625	G
55	K	3876	A
55	K	3888	G
55	K	3904	G
55	K	4119	C
55	K	4170	A
55	K	4232	U

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Mol	Chain	Res	Type
55	K	4354	U
55	K	4378	A
55	K	4448	G
55	K	4719	G
55	K	4884	G
55	K	4921	C
55	K	4925	U
55	K	4947	U
55	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
55	K	24

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	40.45
1	K	1252:C	O3'	1271:G	P	37.04
1	K	1219:G	O3'	1233:G	P	18.73
1	K	3948:C	O3'	4065:G	P	18.66
1	K	4138:C	O3'	4146:G	P	17.71
1	K	990:C	O3'	1064:G	P	17.16
1	K	1696:C	O3'	1720:C	P	16.09
1	K	5022:U	O3'	5028:G	P	15.96
1	K	1406(C):G	O3'	1411:C	P	15.95
1	K	4777:C	O3'	4859:C	P	15.76
1	K	523:C	O3'	638:G	P	15.48
1	K	4101:C	O3'	4107:G	P	14.86
1	K	760:G	O3'	904:C	P	13.85
1	K	182:G	O3'	189:G	P	13.34
1	K	1364:U	O3'	1368:A	P	13.08
1	K	2901:G	O3'	3597:G	P	12.38
1	K	4729:A	O3'	4735:G	P	8.92
1	K	1180:C	O3'	1183:C	P	7.98
1	K	1100:U	O3'	1168:G	P	7.89
1	K	512:U	O3'	515:C	P	6.58
1	K	500:G	O3'	504:G	P	5.58
1	K	4740:G	O3'	4743:G	P	4.82
1	K	1239:C	O3'	1244:G	P	4.45
1	K	4899:G	O3'	4902:C	P	3.43

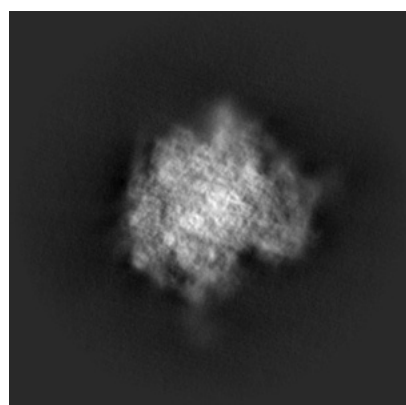
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26133. These allow visual inspection of the internal detail of the map and identification of artifacts.

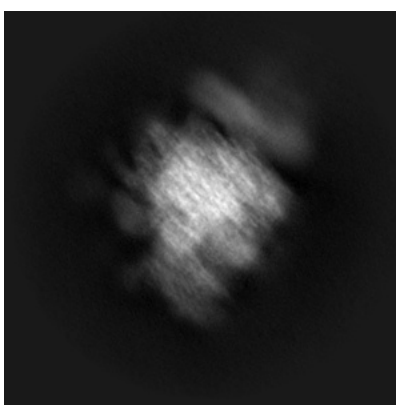
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

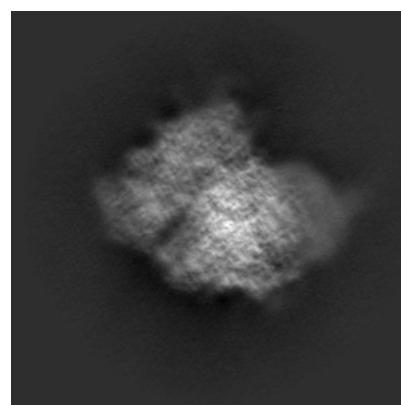
6.1.1 Primary map



X



Y

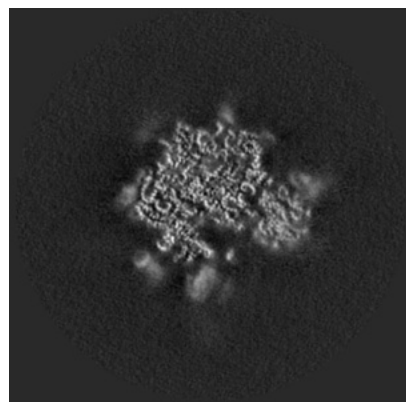


Z

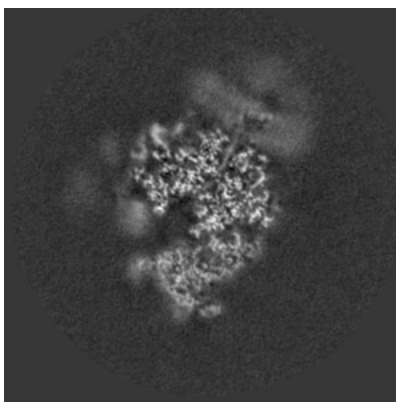
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

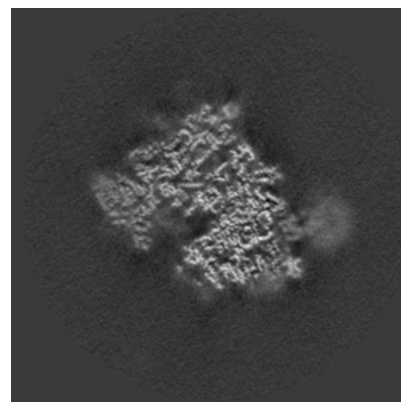
6.2.1 Primary map



X Index: 206



Y Index: 206

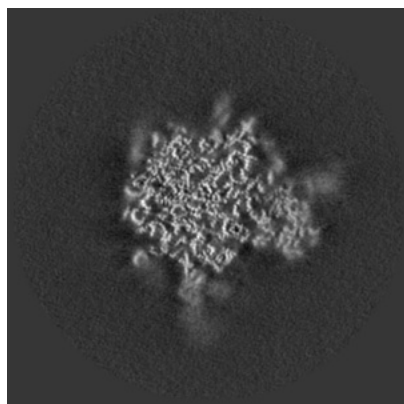


Z Index: 206

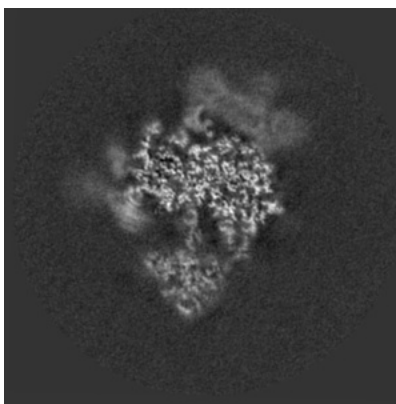
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

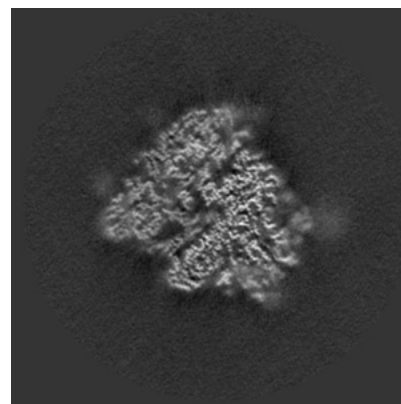
6.3.1 Primary map



X Index: 218



Y Index: 194

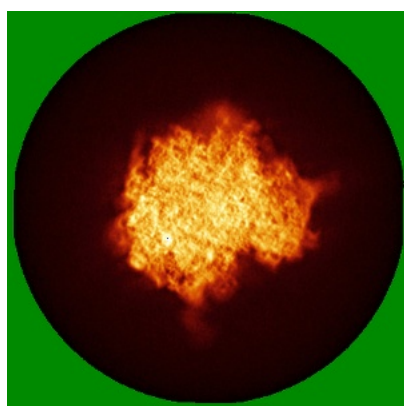


Z Index: 192

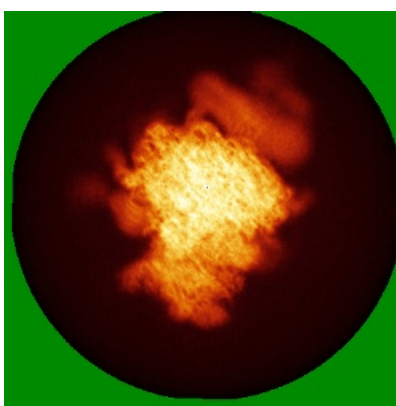
The images above show the largest variance slices of the map in three orthogonal directions.

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

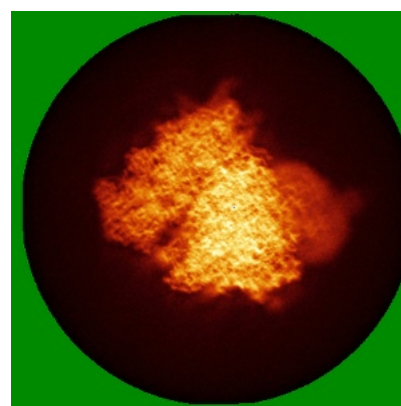
6.4.1 Primary map



X



Y

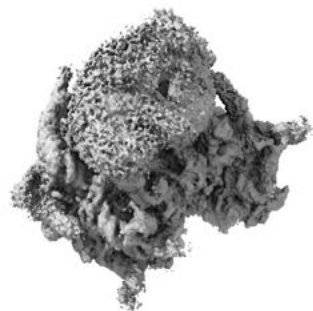


Z

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 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

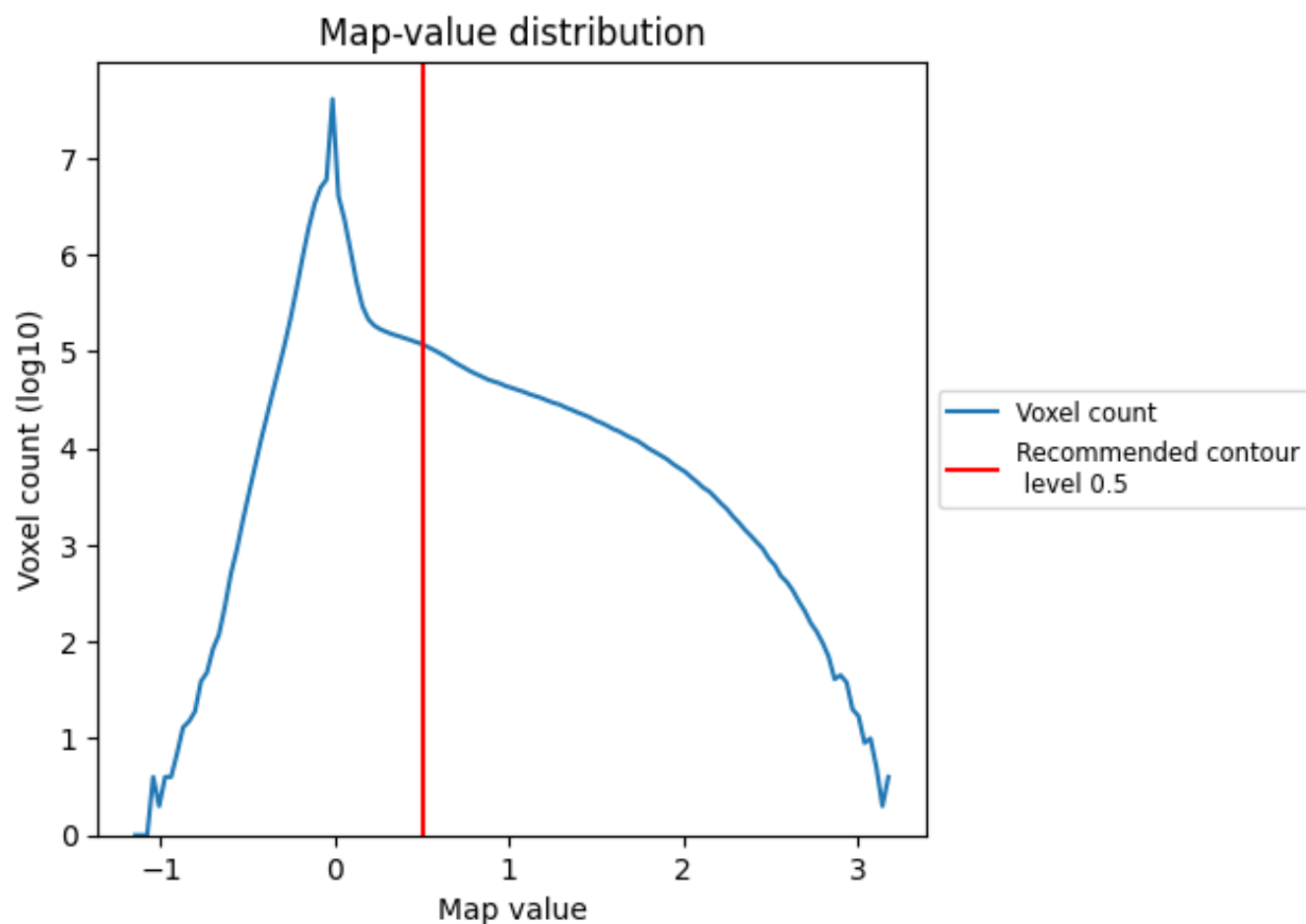
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

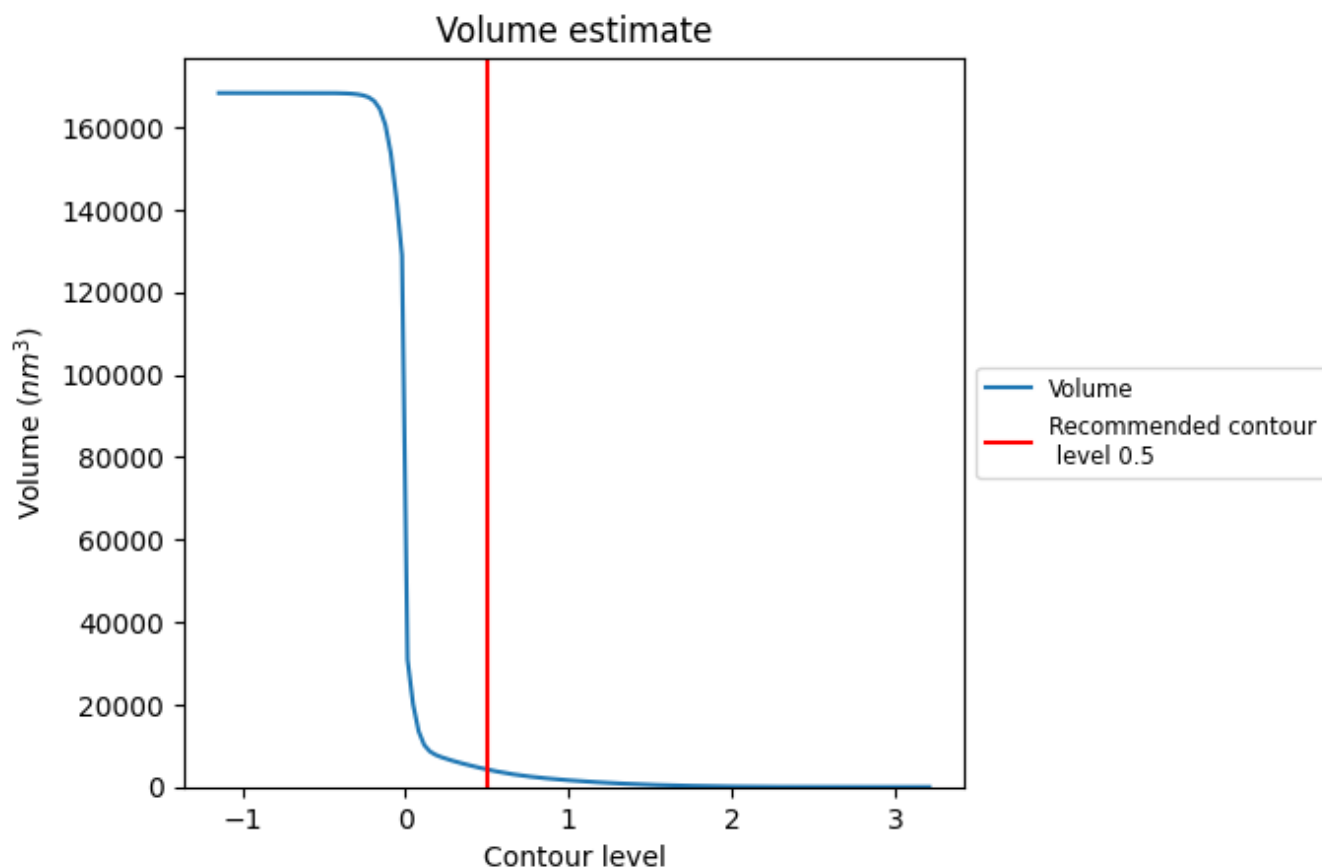
This section contains the results of statistical analysis of the map.

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.

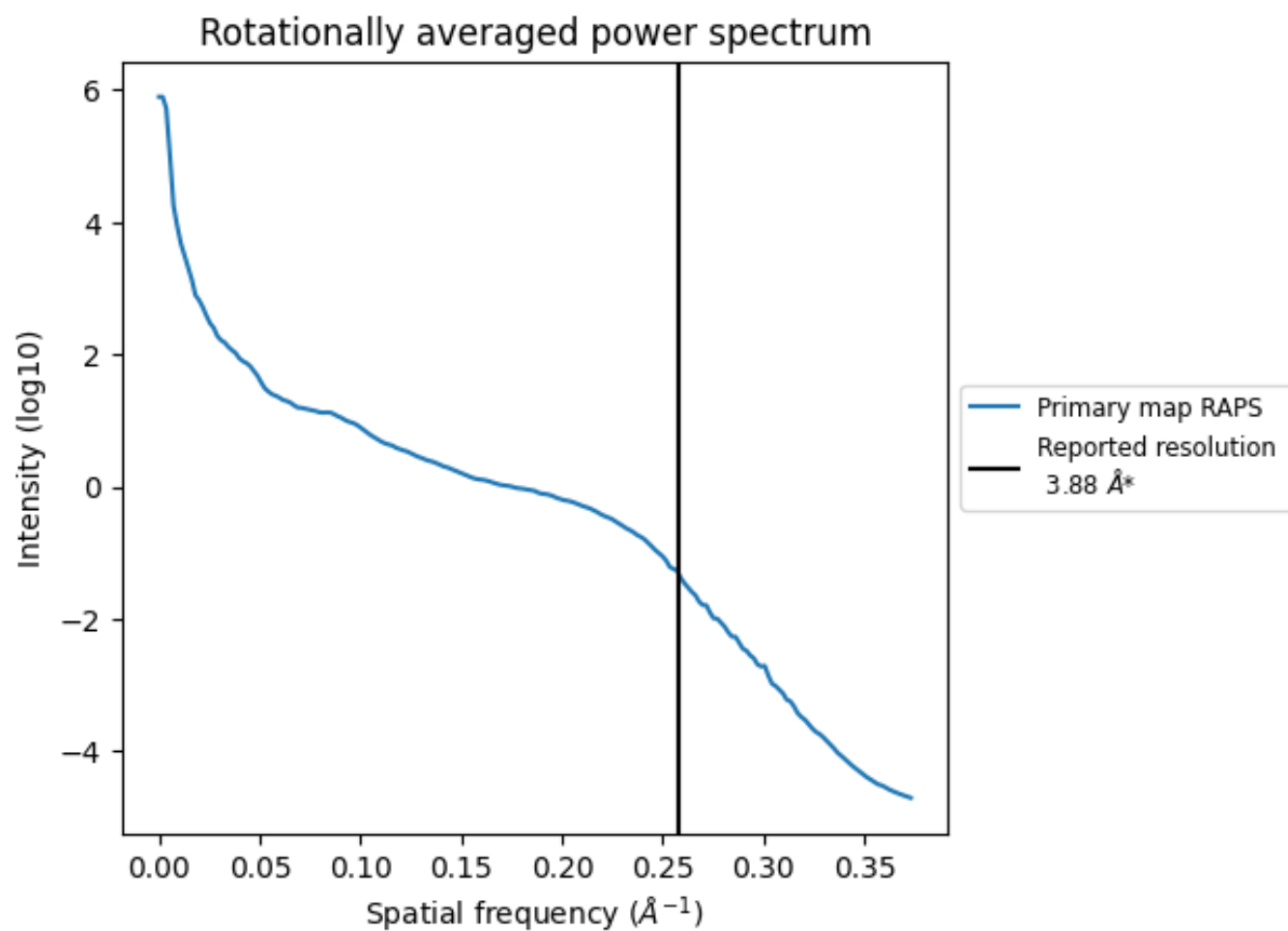
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4244 nm^3 ; this corresponds to an approximate mass of 3834 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 0.258 Å⁻¹

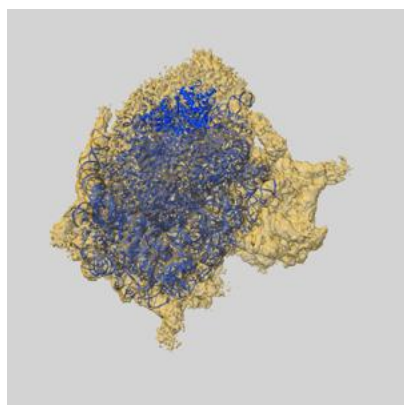
8 Fourier-Shell correlation

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

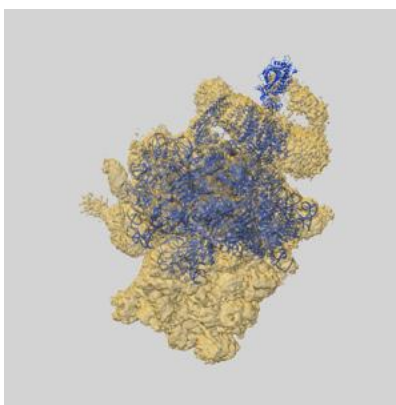
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26133 and PDB model 7TUT. Per-residue inclusion information can be found in section [3](#) on page [18](#).

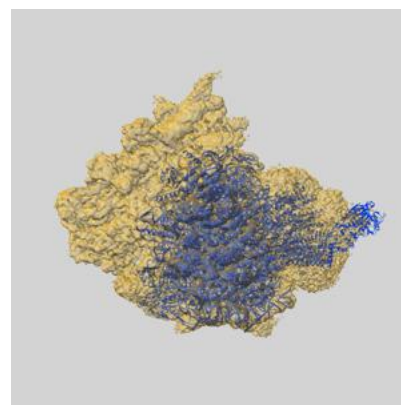
9.1 Map-model overlay [i](#)



X



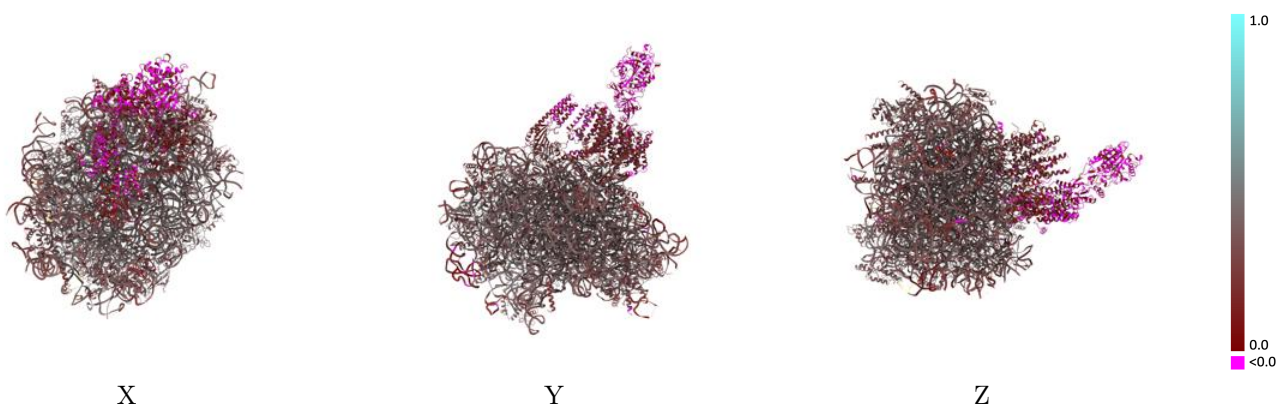
Y



Z

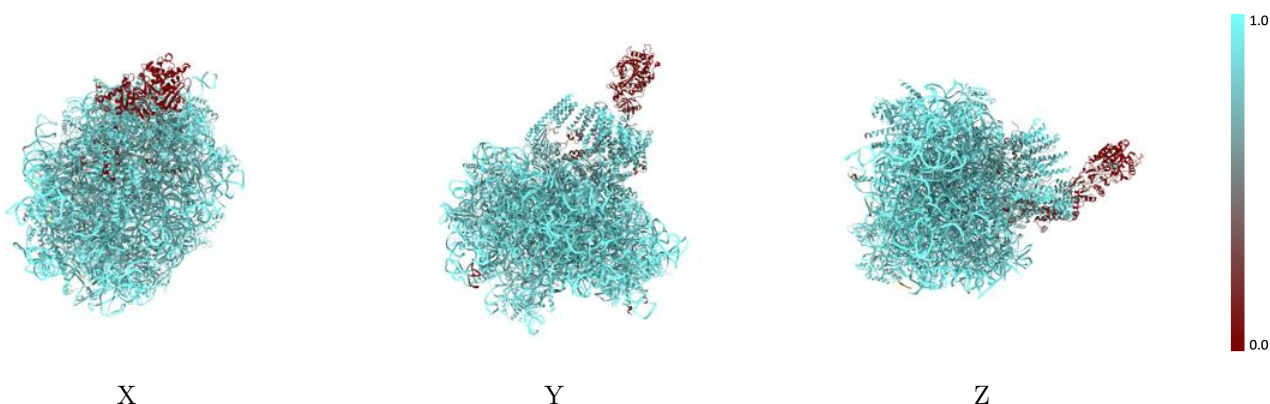
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



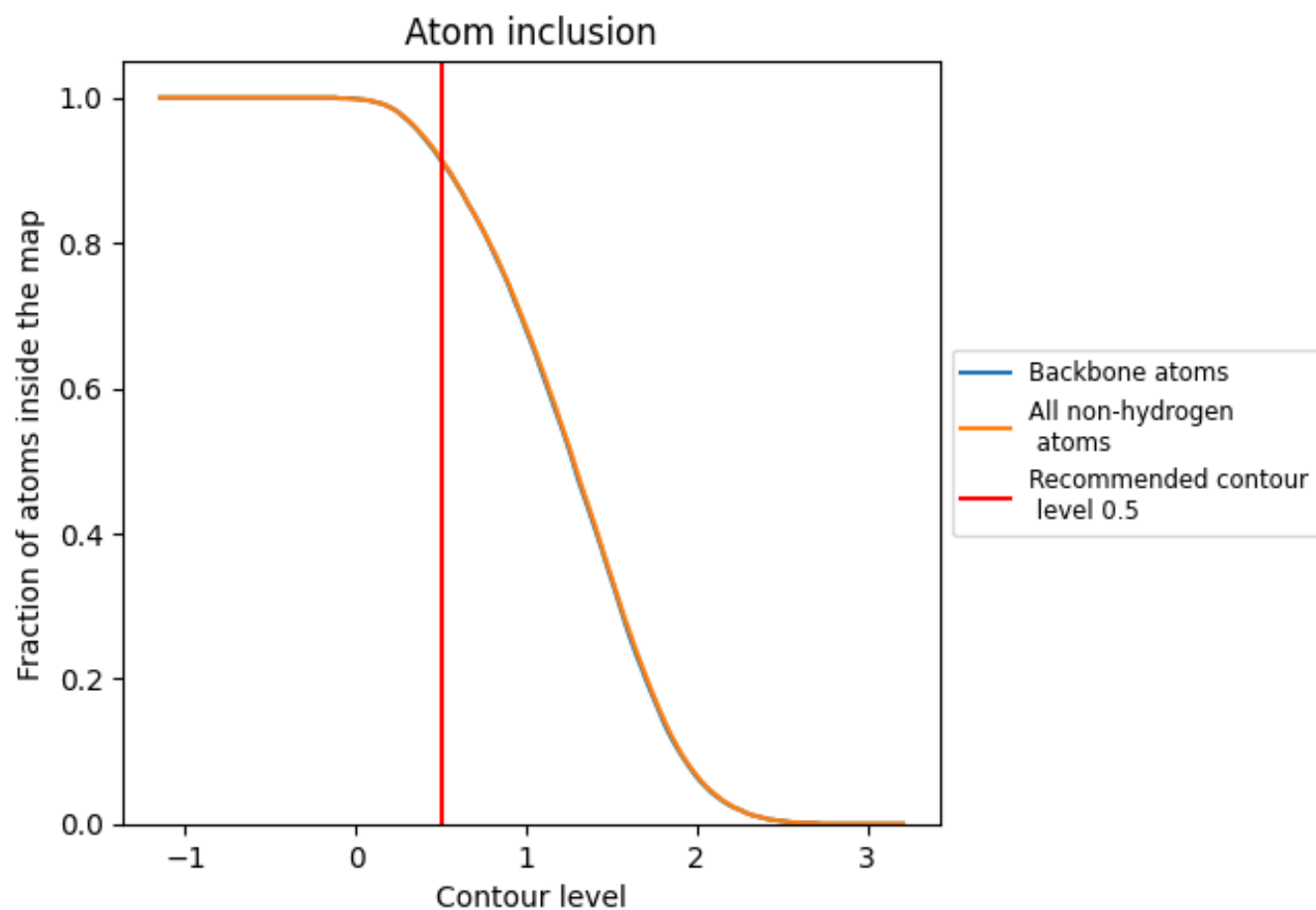
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9160	 0.3250
1	 0.8120	 0.2120
2	 0.8580	 0.1580
3	 0.7680	 0.1660
4	 0.7570	 0.1820
5	 0.8210	 0.0900
6	 0.8010	 0.1400
7	 0.1390	 0.0200
8	 0.6010	 0.1030
9	 0.6230	 0.0320
A	 0.9220	 0.3700
B	 0.7840	 0.2490
C	 0.9200	 0.3570
D	 0.9380	 0.3220
E	 0.9190	 0.3340
F	 0.9060	 0.3420
G	 0.8760	 0.3020
H	 0.8950	 0.3520
I	 0.9120	 0.3640
J	 0.9140	 0.3220
K	 0.9880	 0.3510
L	 0.8960	 0.3290
M	 0.9090	 0.3450
N	 0.9160	 0.3470
O	 0.8920	 0.3470
P	 0.8860	 0.3480
Q	 0.9390	 0.3670
R	 0.8840	 0.3280
S	 0.9230	 0.3740
T	 0.8960	 0.3620
U	 0.8580	 0.3010
V	 0.9110	 0.3820
W	 0.9080	 0.3630
X	 0.8900	 0.3420
Y	 0.8530	 0.3400



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Chain	Atom inclusion	Q-score
Z	 0.9150	 0.3380
a	 0.9340	 0.3580
b	 0.8740	 0.2900
c	 0.9340	 0.3320
d	 0.9280	 0.3540
e	 0.8980	 0.3730
f	 0.9130	 0.3800
g	 0.8880	 0.3390
h	 0.8730	 0.3120
i	 0.9080	 0.3200
j	 0.9350	 0.3480
k	 0.8560	 0.3050
l	 0.8950	 0.3240
m	 0.9280	 0.3500
n	 0.8490	 0.2300
o	 0.9250	 0.3640
p	 0.8910	 0.3330
q	 0.8890	 0.3160
r	 0.9310	 0.3650
u	 0.9950	 0.3740
v	 0.9860	 0.3500
w	 0.9170	 0.3710