



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:30 PM UTC

PDB ID : 7Q0F / pdb_00007q0f
EMDB ID : EMD-13744
Title : Structure of Candida albicans 80S ribosome in complex with phyllanthoside
Authors : Zgadzay, Y.; Kolosova, O.; Stetsenko, A.; Jenner, L.; Guskov, A.; Yusupova, G.; Yusupov, M.
Deposited on : 2021-10-14
Resolution : 2.64 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

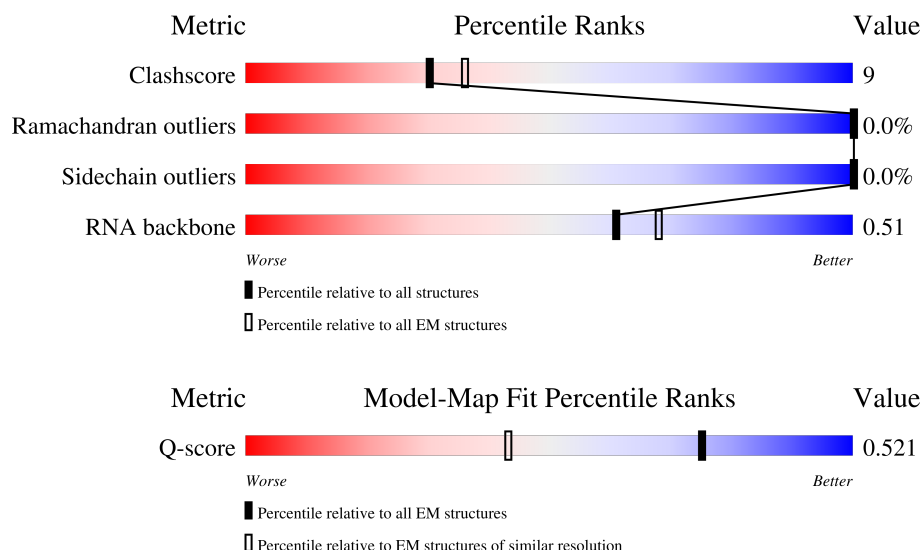
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.64 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.



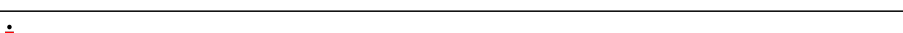
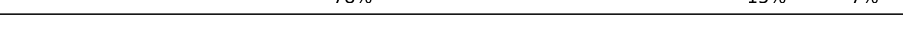
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8968 (2.14 - 3.14)

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

Mol	Chain	Length	Quality of chain
1	1	3359	
2	3	121	
3	4	158	

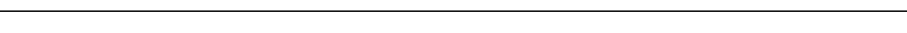
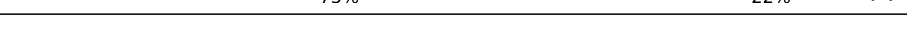
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Mol	Chain	Length	Quality of chain
4	j	254	 82% 16% .
5	k	389	 81% 19% .
6	l	363	 87% 13% .
7	m	298	 85% 13% .
8	n	176	 74% 14% 12%
9	o	241	 82% 15% .
10	p	262	 76% 15% 9%
11	q	191	 79% 21% .
12	r	220	 79% 16% 5%
13	s	174	 76% 22% ..
14	t	202	 89% 10% .
15	u	131	 82% 17% .
16	v	204	 85% 14%
17	w	200	 87% 12%
18	x	185	 78% 15% 7%
19	y	186	 83% 16% .
20	z	190	 82% 13% 6%
21	0	172	 83% 16% .
22	2	160	 87% 12% .
23	5	124	 63% 20% 17%
24	6	137	 80% 15% .
25	7	155	 34% 7% 59%
26	8	142	 75% 11% 15%
27	9	127	 84% 15% .
28	AA	136	 84% 15% .

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Mol	Chain	Length	Quality of chain
29	AB	149	
30	AC	63	
31	AD	106	
32	AE	112	
33	AF	131	
34	AG	107	
35	AH	122	
36	AI	120	
37	AJ	99	
38	AK	90	
39	AL	78	
40	AM	51	
41	AN	52	
42	AO	25	
43	AP	106	
44	AQ	92	
45	i	267	
46	A	1787	
47	B	261	
48	C	256	
49	D	249	
50	E	251	
51	F	262	
52	G	225	
53	H	236	

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Mol	Chain	Length	Quality of chain
54	I	186	
55	J	206	
56	K	189	
57	L	118	
58	M	155	
59	N	143	
60	O	151	
61	P	132	
62	Q	142	
63	R	142	
64	S	137	
65	T	145	
66	U	145	
67	V	119	
68	W	87	
69	X	130	
70	Y	145	
71	Z	135	
72	a	105	
73	b	119	
74	c	82	
75	d	67	
76	e	56	
77	f	63	
78	g	193	

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Mol	Chain	Length	Quality of chain
79	h	317	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
81	3K5	1	3402	X	-	-	-

2 Entry composition [i](#)

There are 82 unique types of molecules in this entry. The entry contains 199317 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3209	Total	C	N	O	P	0	0
			68595	30642	12317	22427	3209		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1153	463	842	121		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	585	1110	158		

- Molecule 4 is a protein called Ribosomal 60S subunit protein L2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	j	249	Total	C	N	O	S	1	0
			1894	1185	377	330	2		

- Molecule 5 is a protein called Ribosomal 60S subunit protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	k	386	Total	C	N	O	S	1	0
			3084	1955	584	538	7		

- Molecule 6 is a protein called Ribosomal 60S subunit protein L4B.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	l	361	Total	C	N	O	S	0	0
			2751	1729	529	490	3		

- Molecule 7 is a protein called Ribosomal 60S subunit protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	m	292	Total	C	N	O	S	0	0
			2394	1526	416	450	2		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	n	155	Total	C	N	O	S	1	0
			1237	794	226	217			

- Molecule 9 is a protein called Ribosomal 60S subunit protein L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	o	234	Total	C	N	O	S	1	0
			1893	1213	348	331	1		

- Molecule 10 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	p	238	Total	C	N	O	S	0	0
			1839	1175	327	334	3		

- Molecule 11 is a protein called Ribosomal 60S subunit protein L9B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	q	190	Total	C	N	O	S	0	0
			1519	958	276	281	4		

- Molecule 12 is a protein called Ribosomal 60S subunit protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	r	208	Total	C	N	O	S	0	0
			1689	1069	322	291	7		

- Molecule 13 is a protein called Ribosomal 60S subunit protein L11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	s	172	Total	C	N	O	S	1	0
			1385	864	262	255	4		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	t	200	Total	C	N	O	0	0
			1610	1009	318	283		

- Molecule 15 is a protein called Ribosomal 60S subunit protein L14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	u	130	Total	C	N	O	S	0	0
			1029	660	193	175	1		

- Molecule 16 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	v	203	Total	C	N	O	S	0	0
			1713	1075	356	280	2		

- Molecule 17 is a protein called Ribosomal 60S subunit protein L16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	w	199	Total	C	N	O	S	0	0
			1590	1025	294	269	2		

- Molecule 18 is a protein called Ribosomal 60S subunit protein L17B.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	x	172	Total	C	N	O	0	0
			1375	850	279	246		

- Molecule 19 is a protein called Ribosomal 60S subunit protein L18A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	y	185	Total	C	N	O	3	0
			1478	930	302	246		

- Molecule 20 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	z	179	Total	C	N	O	S	1	0
			1462	904	311	244	3		

- Molecule 21 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	171	Total	C	N	O	S	2	0
			1442	933	262	244	3		

- Molecule 22 is a protein called Ribosomal 60S subunit protein L21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	159	Total	C	N	O	S	2	0
			1276	807	244	223	2		

- Molecule 23 is a protein called Ribosomal 60S subunit protein L22B.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	5	103	Total	C	N	O	S	2	0
			848	553	139	156			

- Molecule 24 is a protein called Ribosomal 60S subunit protein L23B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	6	131	Total	C	N	O	S	1	0
			986	621	186	171	8		

- Molecule 25 is a protein called Ribosomal 60S subunit protein L24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	7	63	Total	C	N	O	S	0	0
			524	334	103	86	1		

- Molecule 26 is a protein called Ribosomal 60S subunit protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	8	121	Total	C	N	O	S	0	0
			974	622	175	176	1		

- Molecule 27 is a protein called Ribosomal 60S subunit protein L26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	9	126	Total	C	N	O	S	0	0
			989	618	190	181			

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AA	135	Total	C	N	O	S	0	0
			1087	705	197	183	2		

- Molecule 29 is a protein called Ribosomal 60S subunit protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AB	148	Total	C	N	O	S	0	0
			1170	741	231	197	1		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AC	63	Total	C	N	O	S	1	0
			509	317	109	82	1		

- Molecule 31 is a protein called Ribosomal 60S subunit protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AD	96	Total	C	N	O	S	0	0
			729	469	121	137	2		

- Molecule 32 is a protein called Ribosomal 60S subunit protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AE	109	Total	C	N	O	S	0	0
			889	562	167	158	2		

- Molecule 33 is a protein called Ribosomal 60S subunit protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AF	125	Total	C	N	O	S	1	0
			1015	649	197	168	1		

- Molecule 34 is a protein called Ribosomal 60S subunit protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AG	106	Total	C	N	O	S	3	0
			867	558	166	142	1		

- Molecule 35 is a protein called Ribosomal 60S subunit protein L34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AH	112	Total	C	N	O	S	4	0
			913	567	188	154	4		

- Molecule 36 is a protein called Ribosomal 60S subunit protein L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AI	119	Total	C	N	O		1	0
			990	629	195	166			

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AJ	98	Total	C	N	O	S	1	0
			772	481	158	131	2		

- Molecule 38 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AK	86	Total	C	N	O	S	0	0
			677	413	148	110	6		

- Molecule 39 is a protein called Ribosomal 60S subunit protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AL	77	Total	C	N	O		1	0
			623	398	116	109			

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AM	50	Total	C	N	O		1	0
			446	280	100	66			

- Molecule 41 is a protein called Rpl40bp.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AN	52	Total	C	N	O	S	1	0
			427	265	89	67	6		

- Molecule 42 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AO	24	Total	C	N	O	S	0	0
			227	138	61	27	1		

- Molecule 43 is a protein called Ribosomal 60S subunit protein L42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AP	103	Total	C	N	O	S	2	0
			843	533	168	137	5		

- Molecule 44 is a protein called Ribosomal 60S subunit protein L43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AQ	91	Total	C	N	O	S	0	0
			698	430	140	124	4		

- Molecule 45 is a protein called HABP4_PA1-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	113	Total	C	N	O		0	0
			853	512	155	186			

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A	1692	Total	C	N	O	P	0	0
			36083	16130	6412	11849	1692		

- Molecule 47 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B	208	Total	C	N	O	S	0	0
			1627	1041	284	297	5		

- Molecule 48 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	C	214	Total	C	N	O	S	0	0
			1724	1094	313	313	4		

- Molecule 49 is a protein called Ribosomal 40S subunit protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	D	216	Total	C	N	O	S	0	0
			1620	1033	287	295	5		

- Molecule 50 is a protein called Ribosomal 40S subunit protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	E	223	Total	C	N	O	S	0	0
			1707	1087	311	305	4		

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	F	260	Total	C	N	O	S	0	0
			2055	1306	386	358	5		

- Molecule 52 is a protein called Ribosomal 40S subunit protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	G	206	Total	C	N	O	S	0	0
			1614	1008	301	301	4		

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	H	226	Total	C	N	O	S	0	0
			1820	1133	351	330	6		

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	I	182	Total	C	N	O	S	0	0
			1466	939	264	263			

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	J	203	Total	C	N	O	S	0	0
			1579	973	322	283	1		

- Molecule 56 is a protein called Ribosomal 40S subunit protein S9B.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	K	178	Total	C	N	O	S	0	0
			1453	918	286	248	1		

- Molecule 57 is a protein called Ribosomal 40S subunit protein S10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	L	93	Total	C	N	O	S	0	0
			783	511	129	142	1		

- Molecule 58 is a protein called Ribosomal 40S subunit protein S11A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	M	141	Total	C	N	O	S	0	0
			1129	722	212	192	3		

- Molecule 59 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	N	116	Total	C	N	O	S	0	0
			885	550	158	172	5		

- Molecule 60 is a protein called Ribosomal 40S subunit protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	O	150	Total	C	N	O	S	0	0
			1187	757	219	210	1		

- Molecule 61 is a protein called Ribosomal 40S subunit protein S14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	P	127	Total	C	N	O	S	0	0
			942	579	186	174	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	119	IAS	ASP	modified residue	UNP A0A1D8PDT3

- Molecule 62 is a protein called Ribosomal 40S subunit protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Q	118	Total	C	N	O	S	0	0
			935	598	169	162	6		

- Molecule 63 is a protein called Ribosomal 40S subunit protein S16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	R	140	Total	C	N	O	S	0	0
			1091	700	198	192	1		

- Molecule 64 is a protein called Ribosomal 40S subunit protein S17B.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	S	125	Total	C	N	O	S	0	0
			1002	631	184	186	1		

- Molecule 65 is a protein called Ribosomal 40S subunit protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	T	142	Total	C	N	O	S	0	0
			1169	733	228	205	3		

- Molecule 66 is a protein called Ribosomal 40S subunit protein S19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	U	141	Total	C	N	O	S	0	0
			1100	689	210	200	1		

- Molecule 67 is a protein called Ribosomal 40S subunit protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	V	100	Total	C	N	O	S	0	0
			790	499	146	143	2		

- Molecule 68 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	W	87	Total	C	N	O	S	0	0
			676	415	126	133	2		

- Molecule 69 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	X	129	Total	C	N	O	S	0	0
			1032	655	191	183	3		

- Molecule 70 is a protein called Ribosomal 40S subunit protein S23B.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Y	143	Total	C	N	O	S	0	0
			1110	701	219	188	2		

- Molecule 71 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Z	132	Total	C	N	O		0	0
			1072	670	216	186			

- Molecule 72 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	a	72	Total	C	N	O		0	0
			578	369	103	106			

- Molecule 73 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	b	100	Total	C	N	O	S	0	0
			799	494	169	130	6		

- Molecule 74 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	c	81	Total	C	N	O	S	0	0
			614	383	110	114	7		

- Molecule 75 is a protein called Ribosomal 40S subunit protein S28B.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	d	62	Total	C	N	O	S	0	0
			487	299	98	88	2		

- Molecule 76 is a protein called Ribosomal 40S subunit protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	e	55	Total	C	N	O	S	0	0
			454	281	94	75	4		

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	f	56	Total	C	N	O	S	0	0
			444	278	89	75	2		

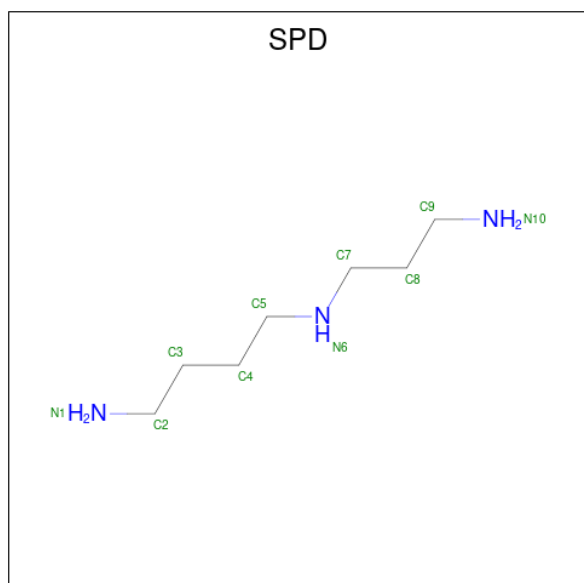
- Molecule 78 is a protein called Ubiquitin-ribosomal 40S subunit protein S31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	g	70	Total	C	N	O	S	0	0
			574	362	113	93	6		

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

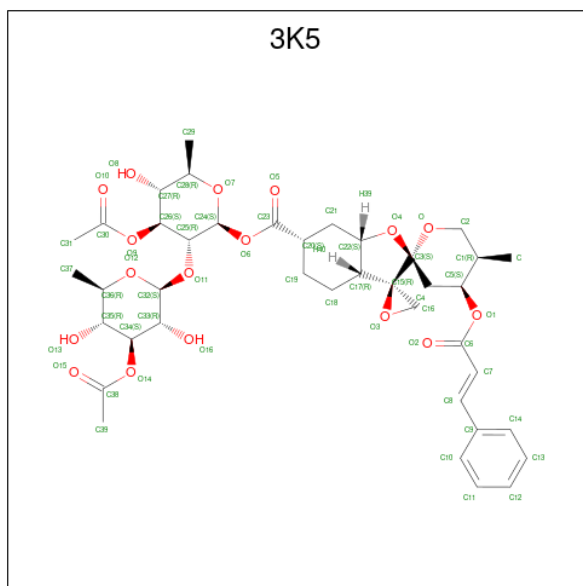
Mol	Chain	Residues	Atoms					AltConf	Trace
79	h	311	Total	C	N	O	S	0	0
			2398	1519	412	462	5		

- Molecule 80 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
80	1	1	Total	C	N	0
			10	7	3	

- Molecule 81 is 3-O-acetyl-2-O-(3-O-acetyl-6-deoxy-beta-D-glucopyranosyl)-6-deoxy-1-O-{[(2R,2'S,3a'R,4''S,5''R,6'S,7a'S)-5''-methyl-4''-{[(2E)-3-phenylprop-2-enoyl]oxy}decahydrodispiro[oxirane-2,3'-[1]benzofuran-2',2''-pyran]-6'-yl]carbonyl}-beta-D-glucopyranose (CCD ID: 3K5) (formula: C₄₀H₅₂O₁₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
81	1	1	Total	C	O	0
			57	40	17	

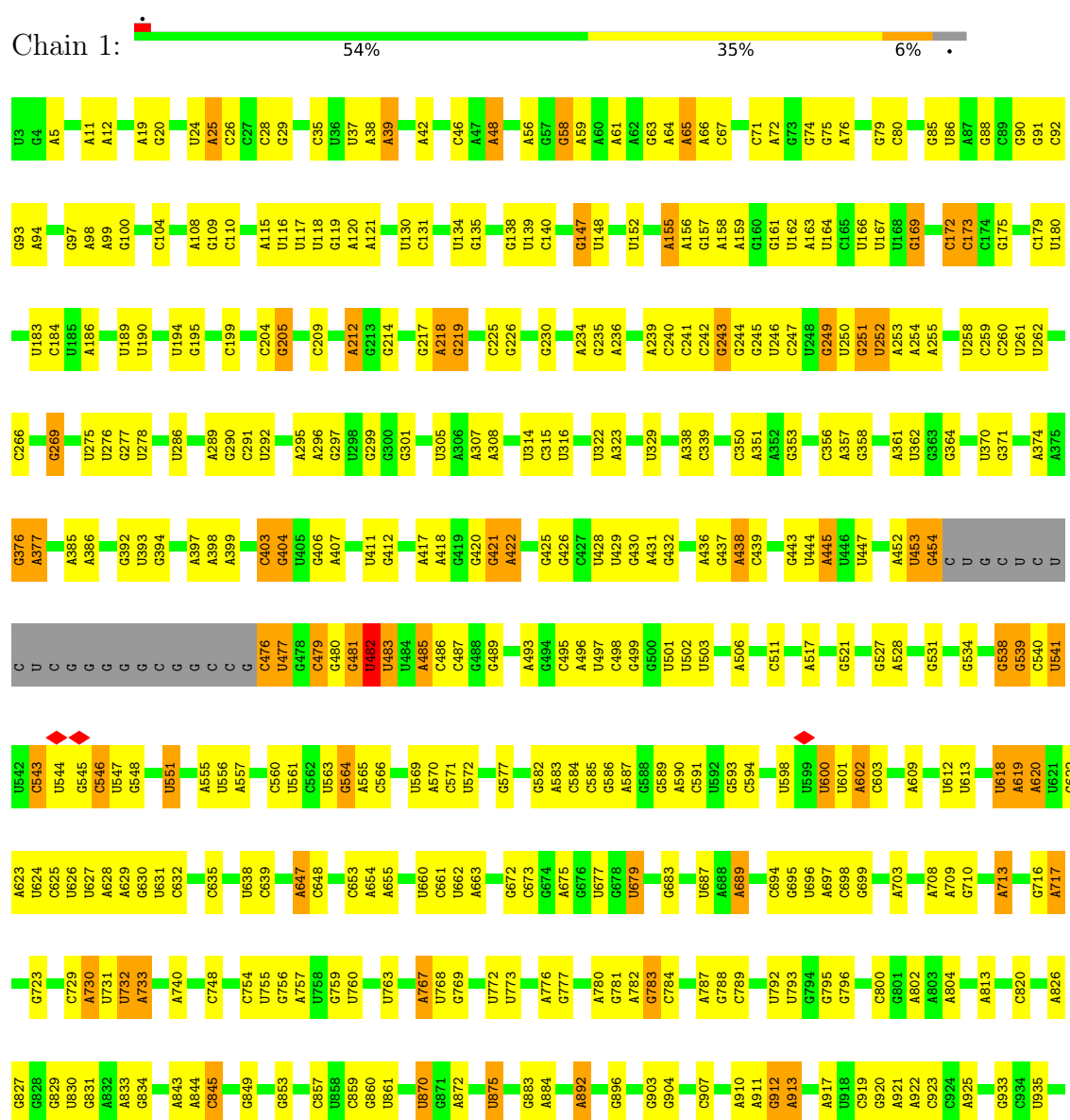
- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
82	AK	1	Total	Zn	0
			1	1	
82	AN	1	Total	Zn	0
			1	1	
82	AP	1	Total	Zn	0
			1	1	
82	AQ	1	Total	Zn	0
			1	1	
82	b	1	Total	Zn	0
			1	1	
82	c	1	Total	Zn	0
			1	1	
82	e	1	Total	Zn	0
			1	1	
82	g	1	Total	Zn	0
			1	1	

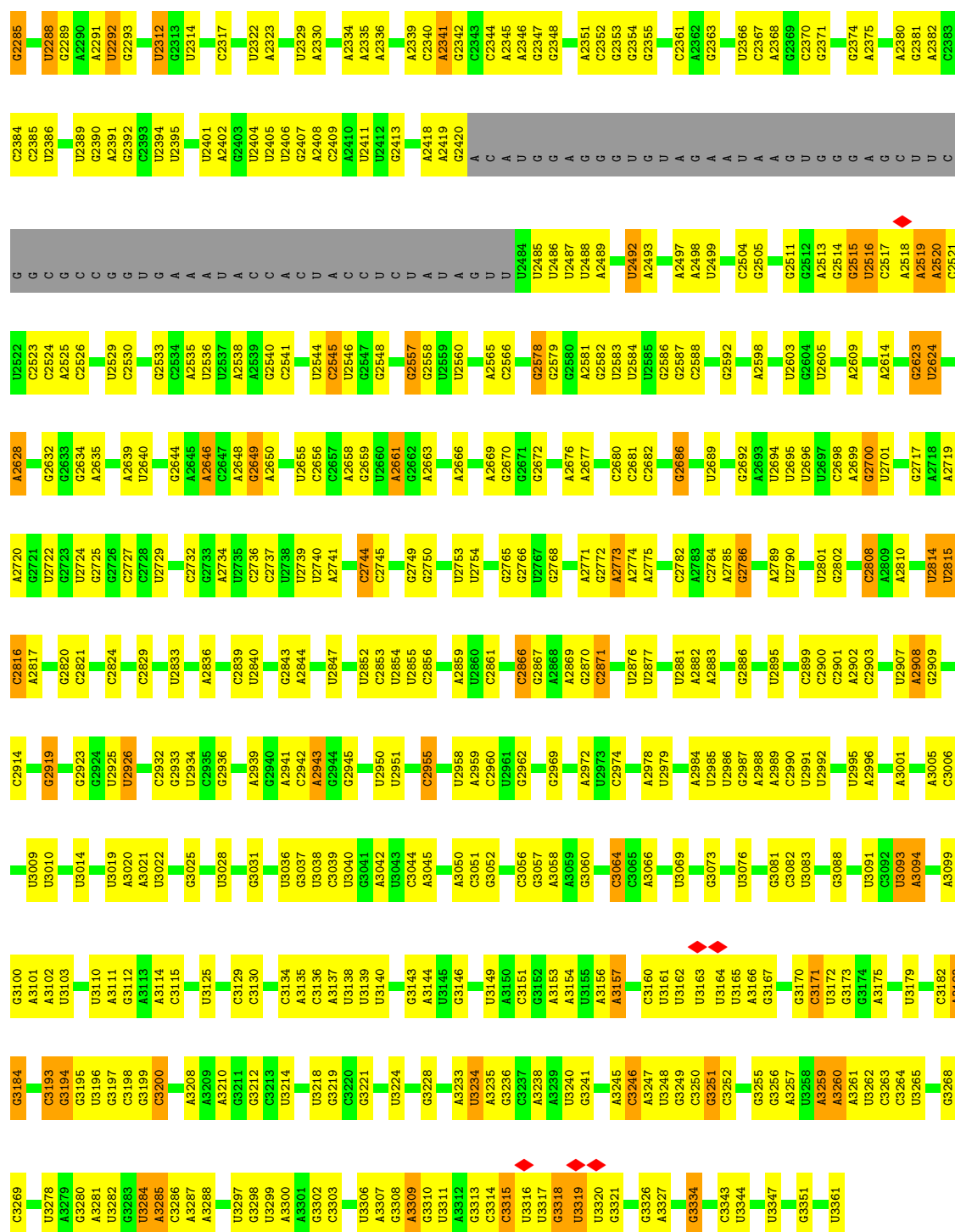
3 Residue-property plots [i](#)

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: 25S ribosomal RNA



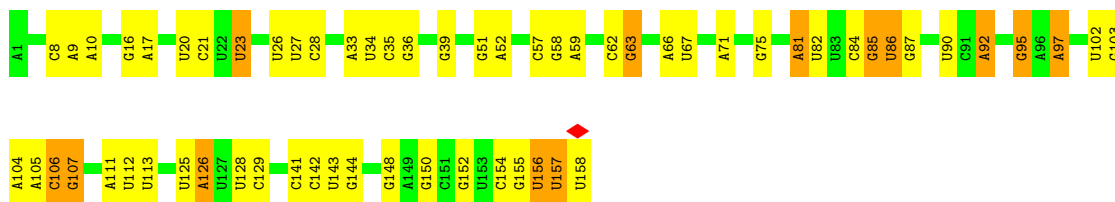






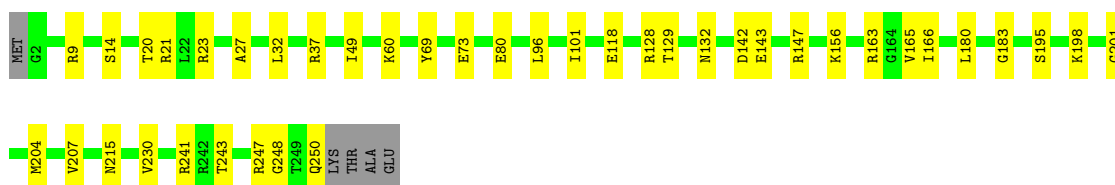
- Molecule 3: 5.8S ribosomal RNA

Chain 4: 61% 31% 8%



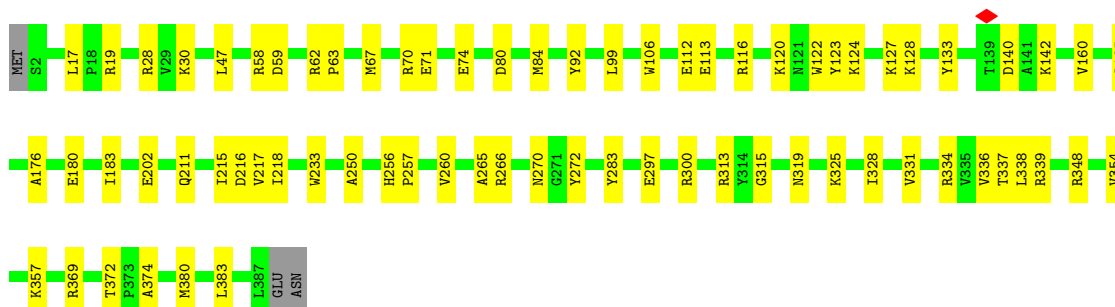
- Molecule 4: Ribosomal 60S subunit protein L2A

Chain j: 82% 16%



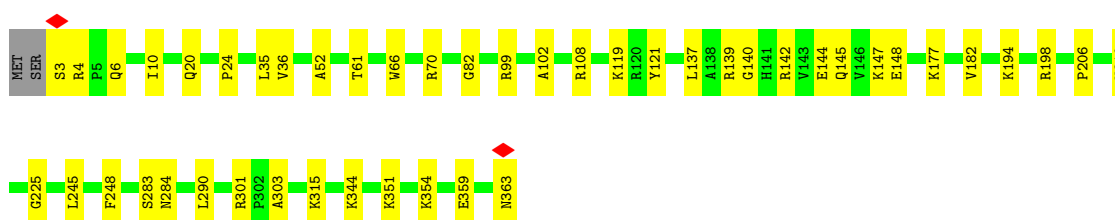
- Molecule 5: Ribosomal 60S subunit protein L3

Chain k: 81% 19%



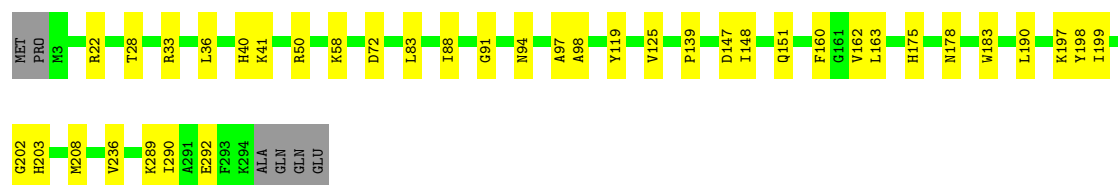
- Molecule 6: Ribosomal 60S subunit protein L4B

Chain l: 87% 13%



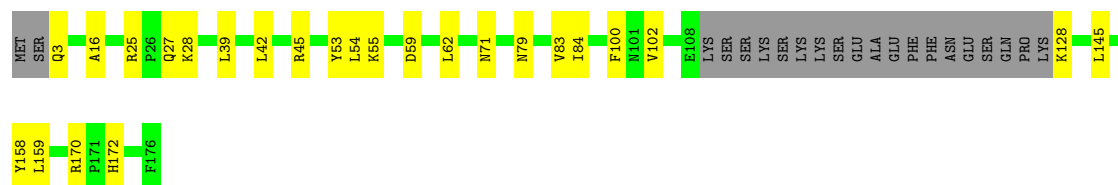
- Molecule 7: Ribosomal 60S subunit protein L5

Chain m:  85% 13%



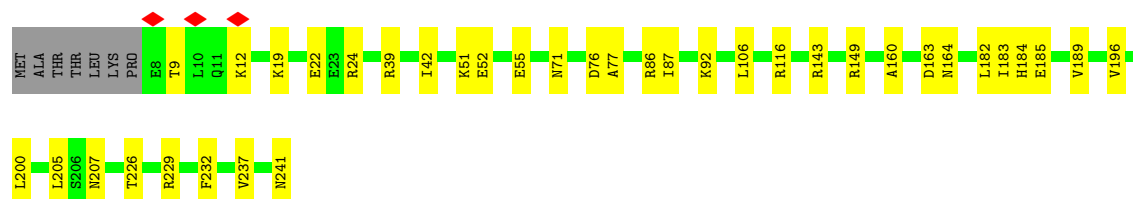
• Molecule 8: 60S ribosomal protein L6

Chain n:  74% 14% 12%



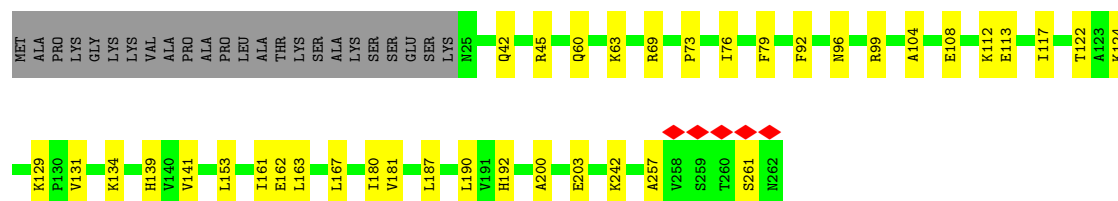
• Molecule 9: Ribosomal 60S subunit protein L7A

Chain o:  82% 15%



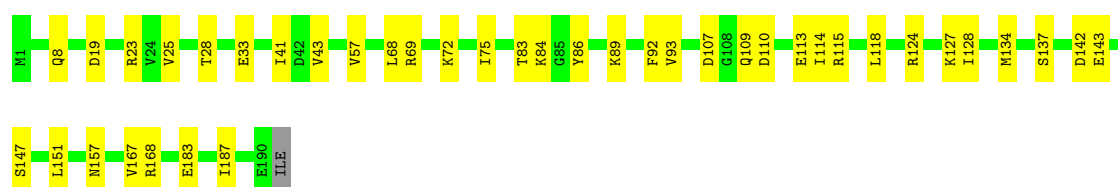
• Molecule 10: 60S ribosomal protein L8

Chain p:  76% 15% 9%



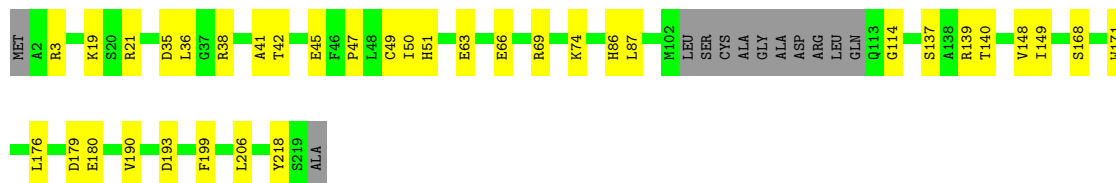
• Molecule 11: Ribosomal 60S subunit protein L9B

Chain q:  79% 21%



- Molecule 12: Ribosomal 60S subunit protein L10

Chain r:  79% 16% 5%



- Molecule 13: Ribosomal 60S subunit protein L11B

Chain s:  76% 22% ..



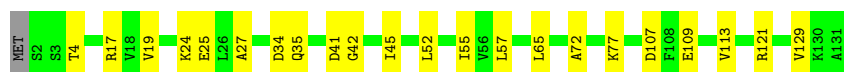
- Molecule 14: 60S ribosomal protein L13

Chain t:  89% 10% .



- Molecule 15: Ribosomal 60S subunit protein L14B

Chain u:  82% 17% .



- Molecule 16: Ribosomal protein L15

Chain v:  85% 14%

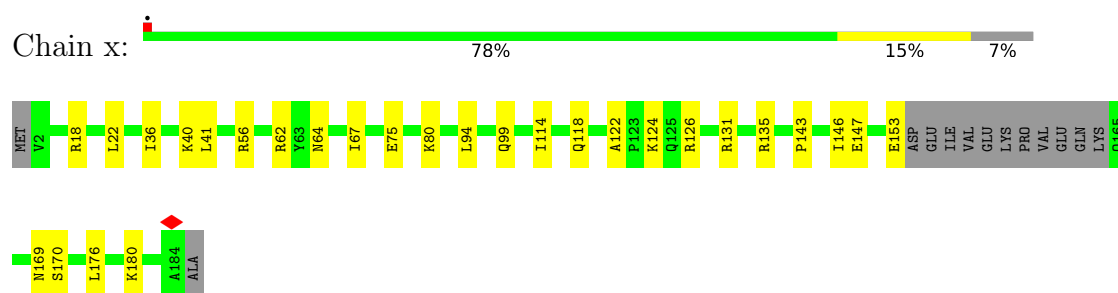


- Molecule 17: Ribosomal 60S subunit protein L16A

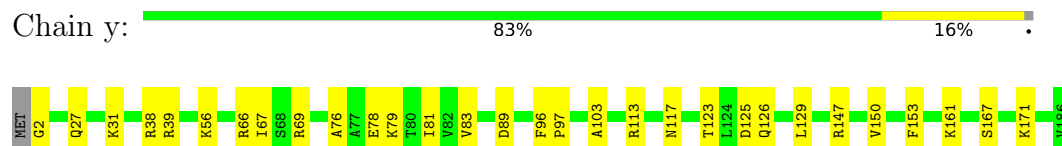
Chain w:  87% 12%



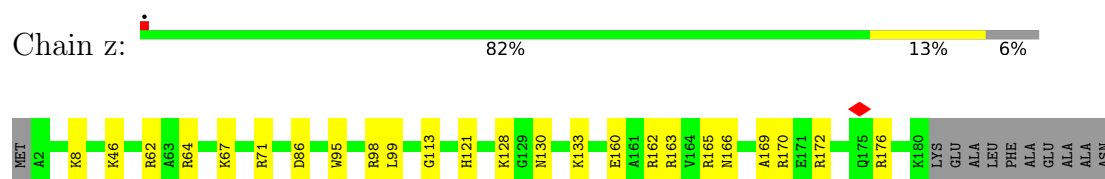
- Molecule 18: Ribosomal 60S subunit protein L17B



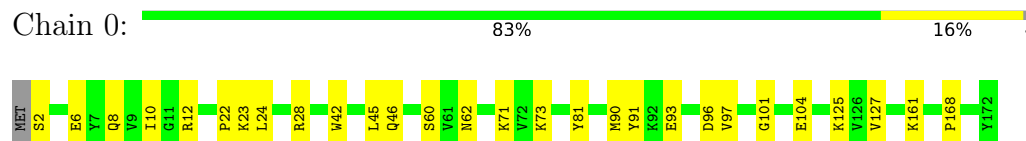
- Molecule 19: Ribosomal 60S subunit protein L18A



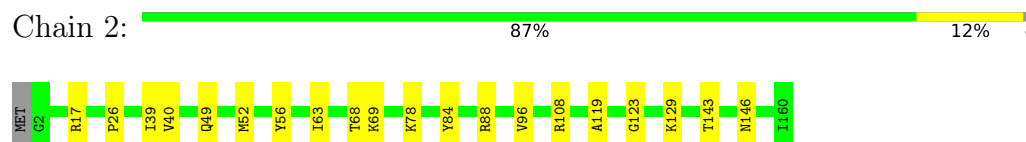
- Molecule 20: Ribosomal protein L19



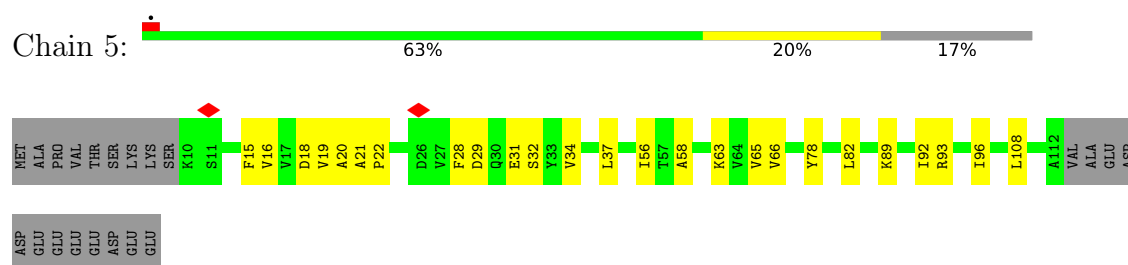
- Molecule 21: 60S ribosomal protein L20



- Molecule 22: Ribosomal 60S subunit protein L21A

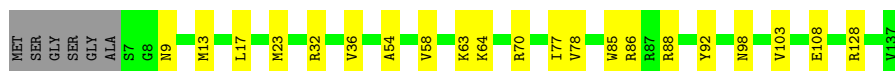


- Molecule 23: Ribosomal 60S subunit protein L22B



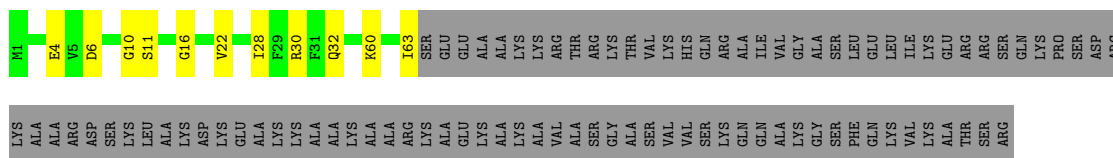
- Molecule 24: Ribosomal 60S subunit protein L23B

Chain 6:  80% 15% .



- Molecule 25: Ribosomal 60S subunit protein L24A

Chain 7:  34% 7% 59%



- Molecule 26: Ribosomal 60S subunit protein L25

Chain 8:  75% 11% 15%



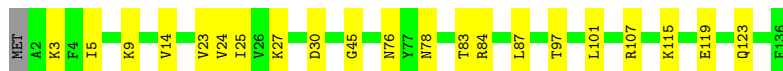
- Molecule 27: Ribosomal 60S subunit protein L26B

Chain 9:  84% 15% .



- Molecule 28: 60S ribosomal protein L27

Chain AA:  84% 15% .



- Molecule 29: Ribosomal 60S subunit protein L28

Chain AB:  83% 17% .



- Molecule 30: 60S ribosomal protein L29

Chain AC:  83% 17%



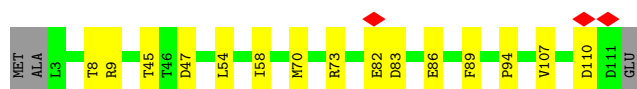
- Molecule 31: Ribosomal 60S subunit protein L30

Chain AD:  80% 10% 9%



- Molecule 32: Ribosomal 60S subunit protein L31B

Chain AE:  84% 13% 3%



- Molecule 33: Ribosomal 60S subunit protein L32

Chain AF:  85% 11% 5%



- Molecule 34: Ribosomal 60S subunit protein L33A

Chain AG:  90% 9% 1%



- Molecule 35: Ribosomal 60S subunit protein L34B

Chain AH:  80% 11% 8%

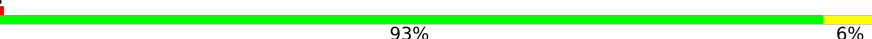


- Molecule 36: Ribosomal 60S subunit protein L35A

Chain AI:  82% 18% 0%



- Molecule 37: 60S ribosomal protein L36

Chain AJ:  93% 6% 1%



• Molecule 38: Ribosomal protein L37

Chain AK:  82% 13%

• Molecule 39: Ribosomal 60S subunit protein L38

Chain AL:  76% 23%

• Molecule 40: 60S ribosomal protein L39

Chain AM:  73% 25%

• Molecule 41: Rpl40bp

Chain AN:  85% 15%

• Molecule 42: 60S ribosomal protein eL41

Chain AO:  68% 28%

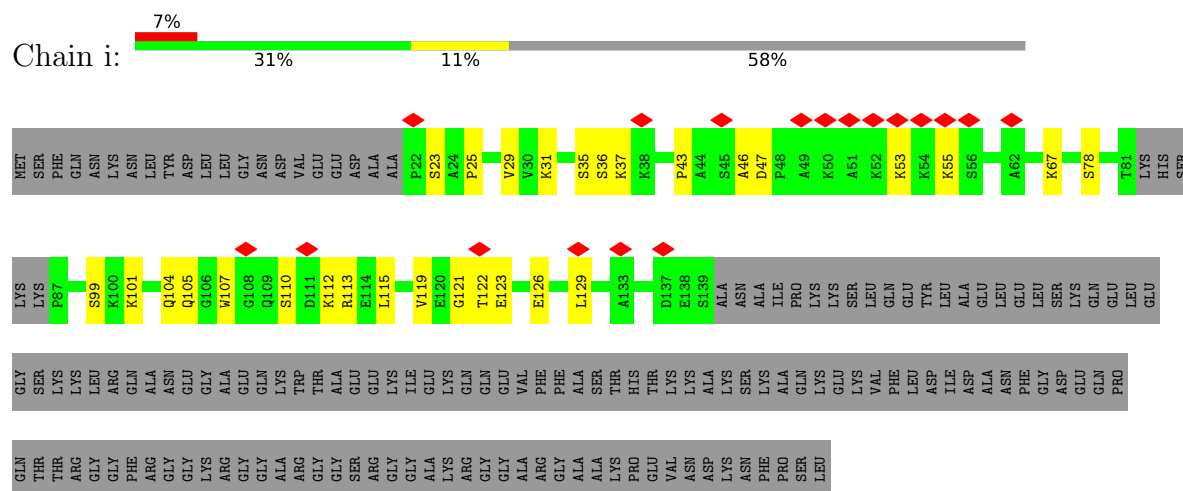
• Molecule 43: Ribosomal 60S subunit protein L42A

Chain AP:  75% 22%

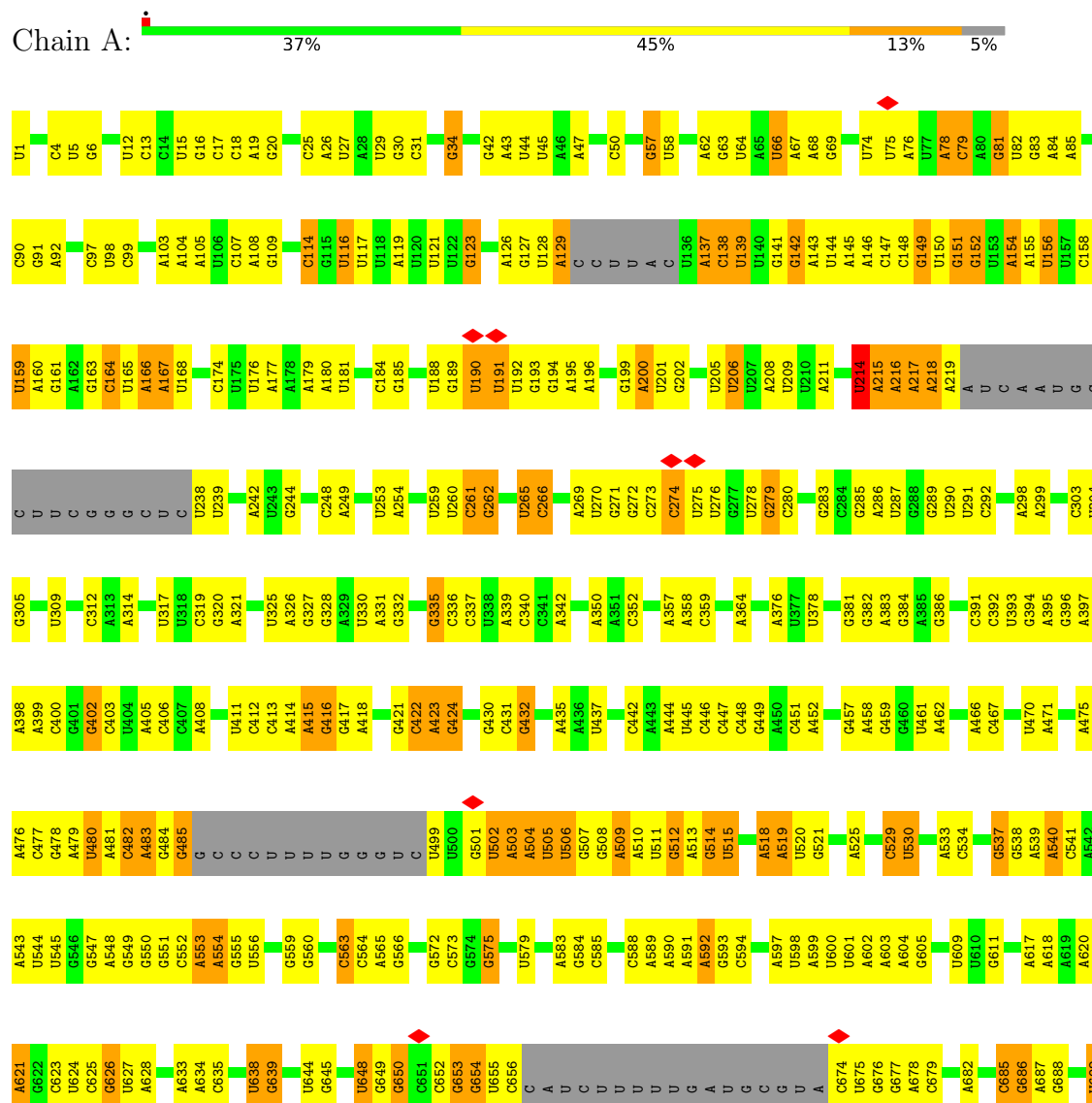
• Molecule 44: Ribosomal 60S subunit protein L43A

Chain AQ:  84% 15%

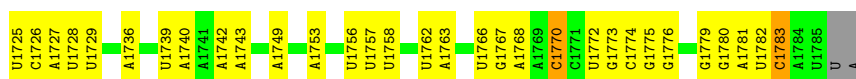
Chain i:



Chain A:

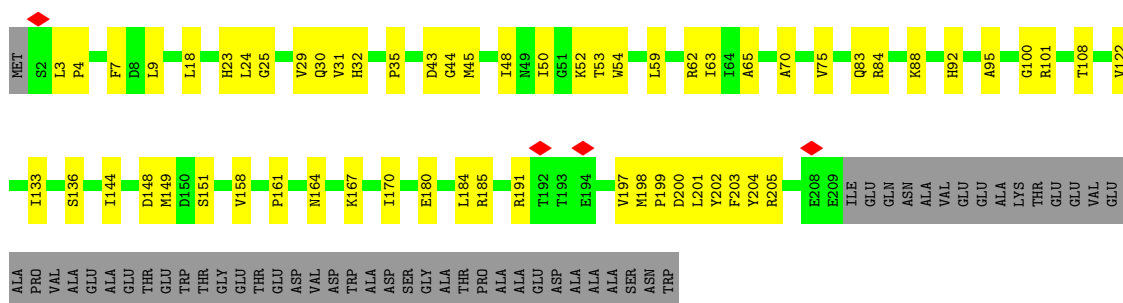


C1661	A1580	U1509	C1449	C1375	A1307	U1234	G1164	A1077	A909	C833	G761	U693
C1662	G1561	G1510	G1450	U1376	C1308	U1235	C1165	A1078	G910	C834	C762	C694
U1663	U1582	A1511	G1451	C1379	G1309	U1236	U1166	C1081	A911	A835	C763	C695
C1664	C1583	A1512	C1452	C1380	G1313	C1237	U1167	C1082	C912	U836	U764	U696
C1665	A1513	G1381	U1453	A1381	G1314	U1238	A1168	G1085	U914	C837	U765	U697
G1666	G1518	U1382	U1454	U1382	A1314	U1239	A1169	G1086	A913	G838	U766	C698
C1667	U1519	U1383	C1455	U1384	G1315	U1240	U1170	U1087	A915	U839	U767	U699
A1668	C1590	U1384	C1456	U1385	A1316	A1241	A1174	G1088	G916	A840	C768	G700
U1669	U1591	U1385	A1457	U1386	U1320	U1242	U1179	U1089	U917	A841	U769	G701
G1670	G1523	U1386	A1458	A1386	A1321	U1243	C1180	G1092	A918	G842	C770	G
C1671	U1524	U1387	U1459	A1387	C1322	U1247	A1181	G1093	C919	U843	C771	A
C1672	U1525	G1391	C1460	U1387	A1323	G1248	G1184	G1094	U920	A844	A772	G
U1673	G1526	G1395	C1462	U1395	C1324	G1249	G1185	U1099	A924	U845	A773	C
U1674	U1529	A1396	G1463	A1396	A1326	G1250	G1186	G1099	A925	U846	U776	C
U1675	A1530	A1397	U1464	A1397	U1327	U1251	G1187	G1099	A929	A847	U777	A
A1676	G1533	U1398	A1465	U1398	A1330	G1252	A1188	U1102	U930	U848	U778	U
G1677	A1534	U1399	C1466	U1399	A1331	G1253	A1189	G1103	U931	U849	U779	U
G	G1535	U1400	C1467	U1400	U1332	G1254	A1190	G1104	U932	A850	U780	U
A	C1536	U1401	C1468	U1401	A1333	G1255	C1190	U1105	U933	G853	U784	A
A	G1603	U1402	G1470	U1402	U1334	U1256	U1191	C1106	U934	A854	G785	U
C	U1537	G1403	C1471	G1403	G1335	G1257	C1192	G1115	U945	C855	G786	G
G	U1538	A1410	U1472	A1410	G1336	G1258	A1193	U1129	U946	G856	A787	G
C	U1539	U1411	C1473	U1411	U1337	G1259	A1194	U1130	G938	G857	C	C
G	G1540	U1412	U1474	U1412	U1338	A1260	C1195	A1122	G939	A796	A796	G
U	U1541	A1413	G1475	A1413	G1339	U1261	C1196	A1123	A940	U797	U797	A
C	A1542	G1414	U1476	G1414	C1340	G1262	A1196	G1127	C941	U798	U798	A
C	U1543	G1415	U1477	G1415	U1341	G1263	G1197	U1039	U942	U799	U799	C
A	U1544	U1416	U1478	U1416	U1342	G1264	G1198	U1040	U943	C868	G800	C720
A	U1545	U1417	A1479	U1417	G1343	G1265	C1201	A1128	U944	C869	G801	C721
C	U1546	U1479	C1480	U1479	U1344	G1266	A1202	U1129	U945	G870	A722	A722
U	U1547	U1480	G1481	U1480	C1345	U1270	G1203	U1130	A949	G871	G802	G723
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C	G1549	U1423	U1483	U1423	U1347	A1272	C1207	A1046	A952	U873	U805	U729
U	C1550	G1424	C1425	G1424	U1348	U1275	A1212	U1047	U953	U874	A806	U730
U	U1551	U1425	C1426	U1425	U1349	G1276	C1208	U1048	C954	A875	U807	U730
C	C1552	C1427	U1428	C1427	G1350	U1279	A1211	A1050	A955	G877	G808	G736
U	U1553	U1428	U1429	U1428	U1351	G1282	A1212	G1052	A956	U878	U810	U737
A	C1555	A1430	U1430	A1430	G1352	U1283	G1213	A1055	G965	G880	U811	A738
U	A1556	G1431	U1431	G1431	U1353	G1284	G1214	U1056	U973	U881	A741	A741
G	G1559	A1432	U1432	A1432	U1354	U1285	A1215	C1057	A974	U815	A742	A742
C	U1560	C1433	U1433	C1433	U1355	U1286	U1216	G1058	C975	U816	U743	U743
U	G1561	G1434	U1434	G1434	A1357	U1286	U1217	G1059	A977	U817	U744	U744
C	G1562	U1435	U1435	U1435	G1358	U1292	G1218	C1060	U978	U818	A745	A745
U	U1565	U1436	U1436	U1436	U1359	U1293	A1219	A1061	A890	U820	G746	G746
U	U1566	C1437	U1437	C1437	C1360	G1294	A1220	U1062	A891	U821	A747	A747
C	C1567	U1438	U1438	U1438	U1361	U1295	A1221	C1063	A892	G822	G750	G750
U	U1568	G1439	G1439	G1439	C1362	C1296	A1222	U1064	A893	G823	U751	U751
U	U1569	U1440	U1440	U1440	C1363	U1297	A1223	U1065	U989	U824	U752	U752
C	A1570	G1441	U1441	G1441	U1364	A1298	G1226	U1066	G988	U825	A754	A754
U	G1571	C1442	U1442	C1442	U1365	U1299	U1227	A1067	U903	U826	A755	A755
U	U1572	C1443	U1443	C1443	U1366	U1300	G1228	C1067	A904	G827	A756	A756
A	A1573	G1444	U1444	G1444	U1367	G1301	G1229	G1068	C905	U828	G757	G757
C	U1574	C1445	U1445	C1445	A1370	C1302	U1230	U1069	U906	A829	C758	C758
U	G1575	A1446	U1446	A1446	G1371	G1303	U1231	A1072	A908	G830	A759	A759
U	C1578	U1447	U1447	U1447	G1372	U1304	U1232	A1073	U1003	G831	G831	G831
C	A1579	G1448	U1448	G1448	A1374	A1305	U1233	A1074	A1004	G832	G832	G832
U	U1580	U1449	U1449	U1449	U1375	U1306	U1234	G1163	A1005	A908	A832	A832



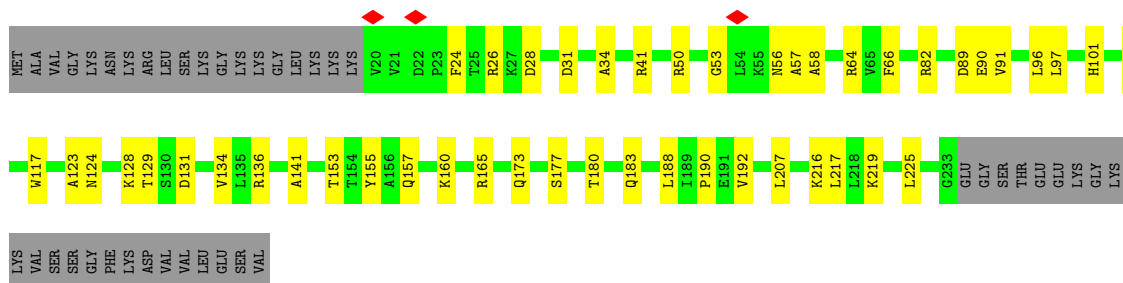
- Molecule 47: 40S ribosomal protein S0

Chain B: 57% 23% 20%



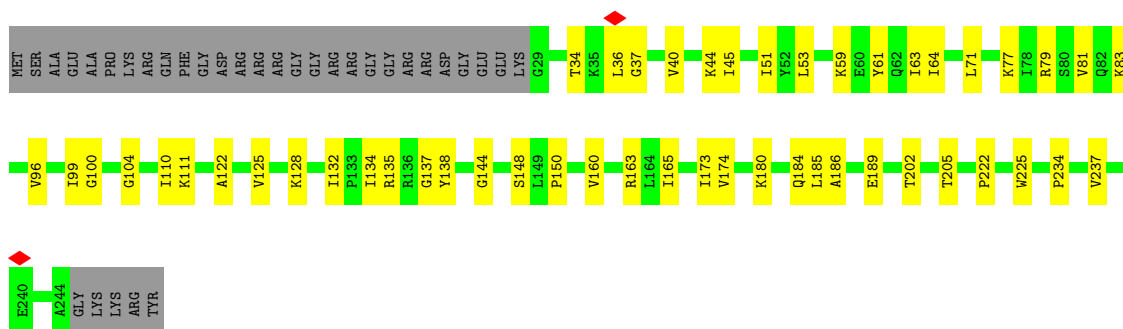
- Molecule 48: 40S ribosomal protein S1

Chain C: 65% 18% 16%



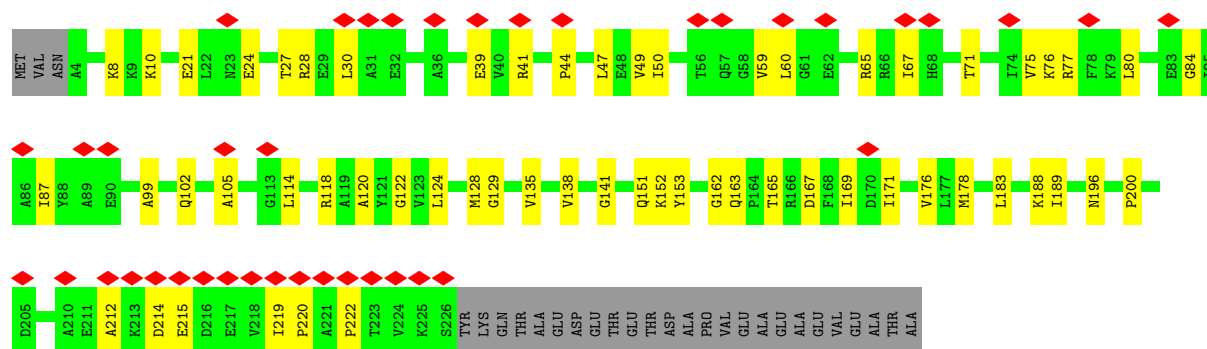
- Molecule 49: Ribosomal 40S subunit protein S2

Chain D: 67% 20% 13%



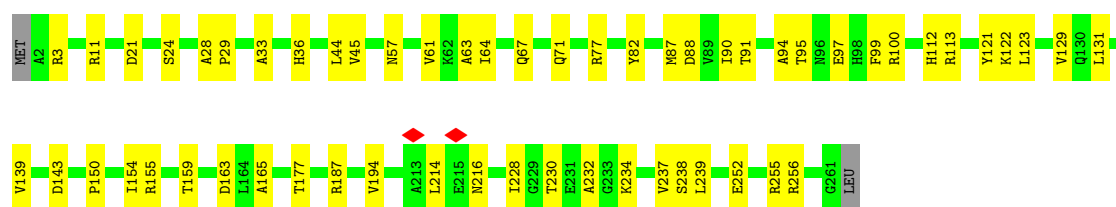
- Molecule 50: Ribosomal 40S subunit protein S3

Chain E: 16% 65% 24% 11%



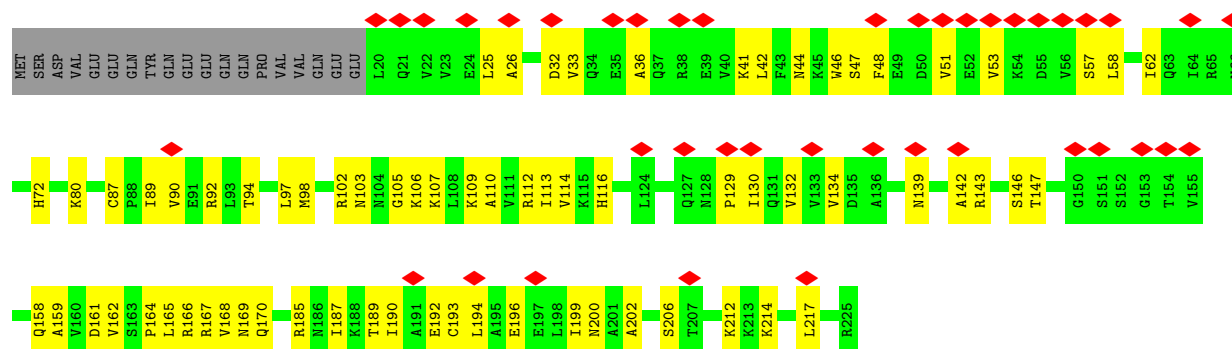
- Molecule 51: 40S ribosomal protein S4

Chain F: 77% 22% .



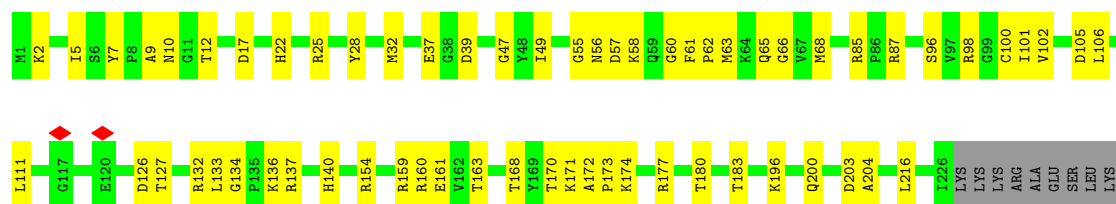
- Molecule 52: Ribosomal 40S subunit protein S5

Chain G: 18% 60% 32% 8% .



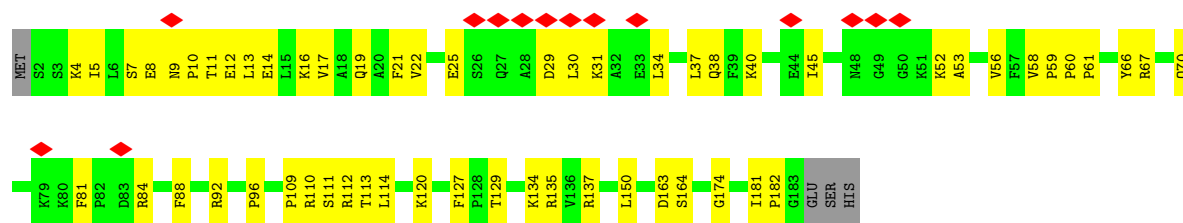
- Molecule 53: 40S ribosomal protein S6

Chain H: 69% 27% .



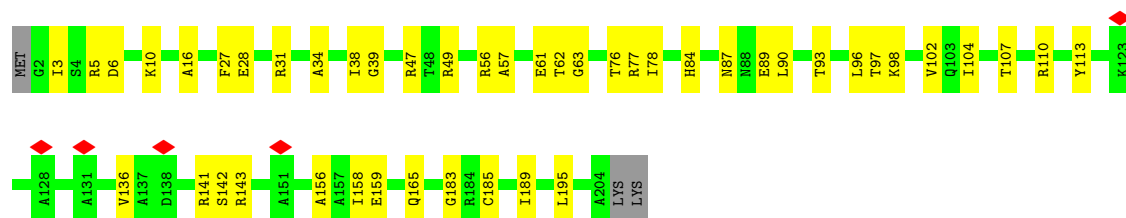
- Molecule 54: 40S ribosomal protein S7

Chain I: 8% 67% 31% .



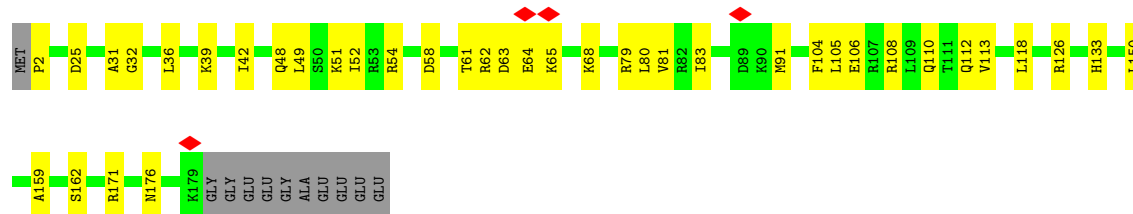
- Molecule 55: 40S ribosomal protein S8

Chain J: 76% 22%



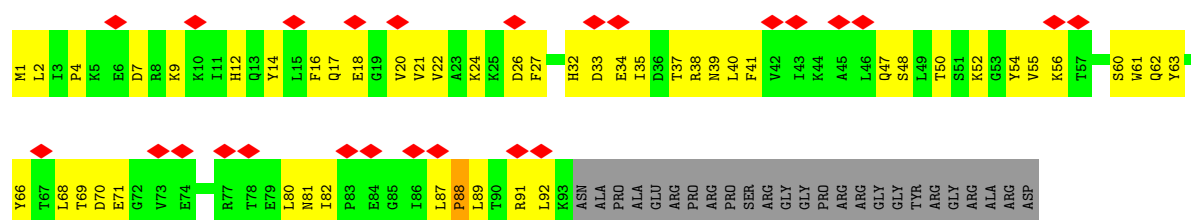
- Molecule 56: Ribosomal 40S subunit protein S9B

Chain K: 74% 21% 6%



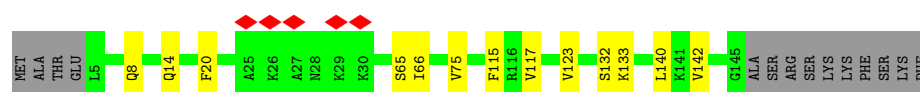
- Molecule 57: Ribosomal 40S subunit protein S10A

Chain L: 21% 37% 41% 21%

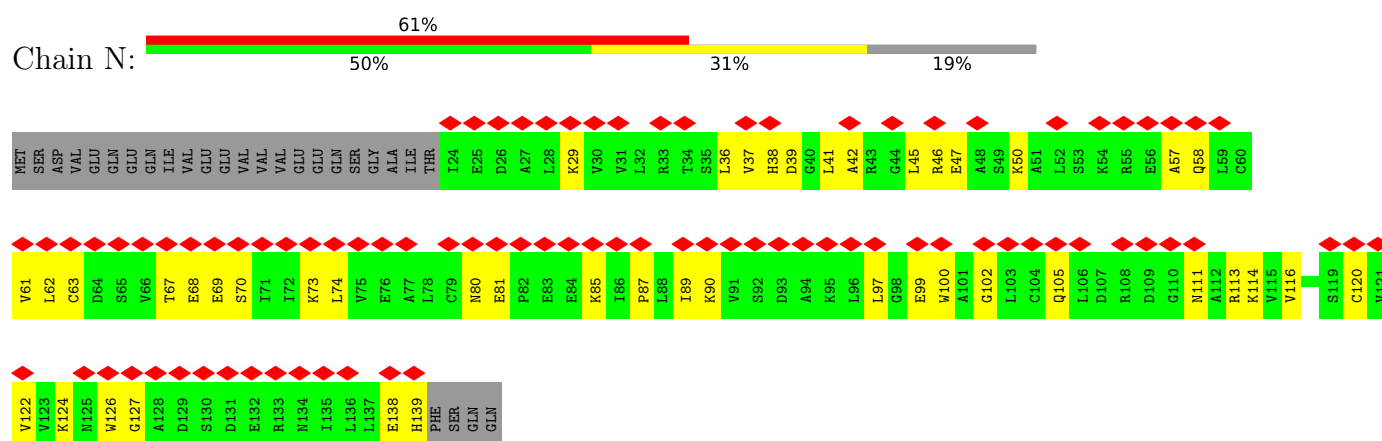


- Molecule 58: Ribosomal 40S subunit protein S11A

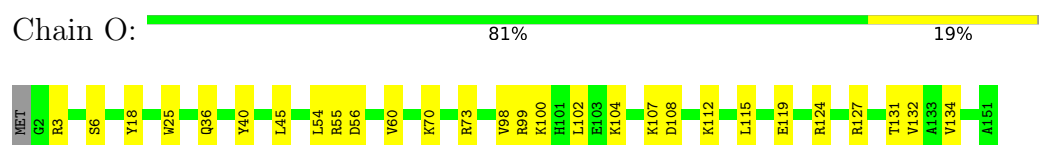
Chain M: 83% 8% 9%



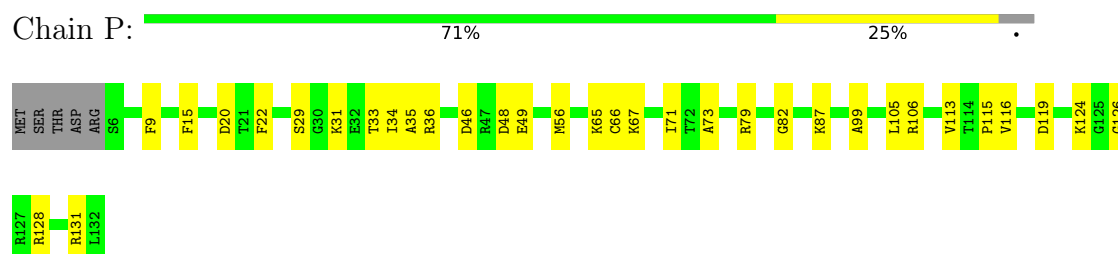
- Molecule 59: 40S ribosomal protein S12



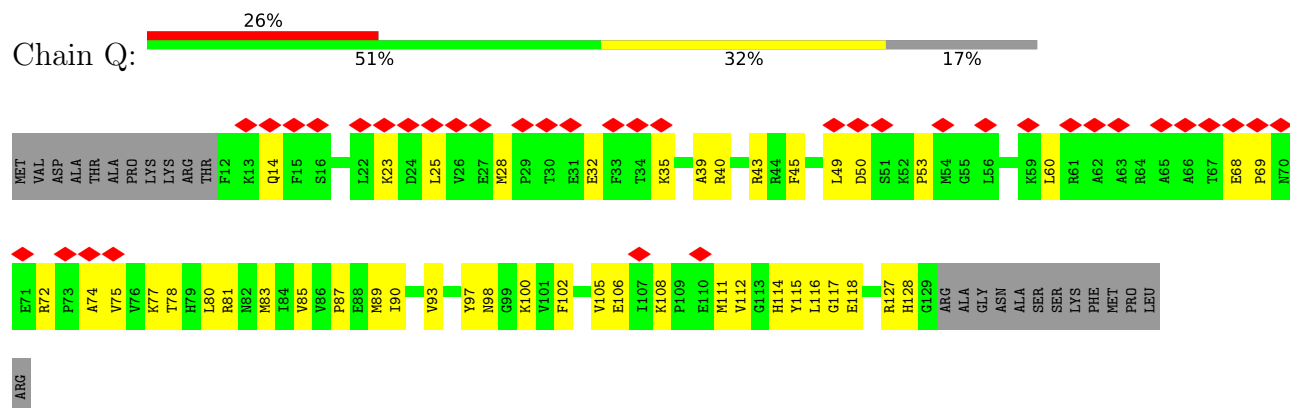
- Molecule 60: Ribosomal 40S subunit protein S13



- Molecule 61: Ribosomal 40S subunit protein S14B

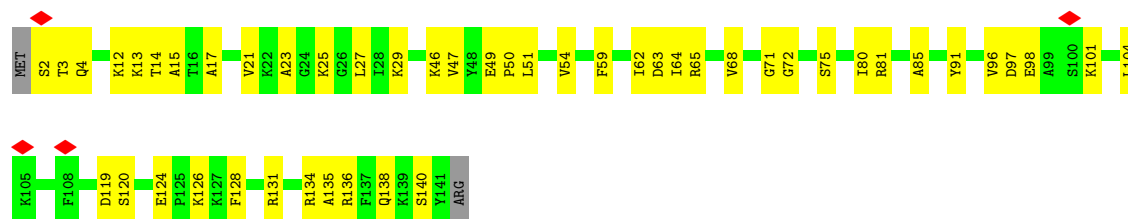


- Molecule 62: Ribosomal 40S subunit protein S15

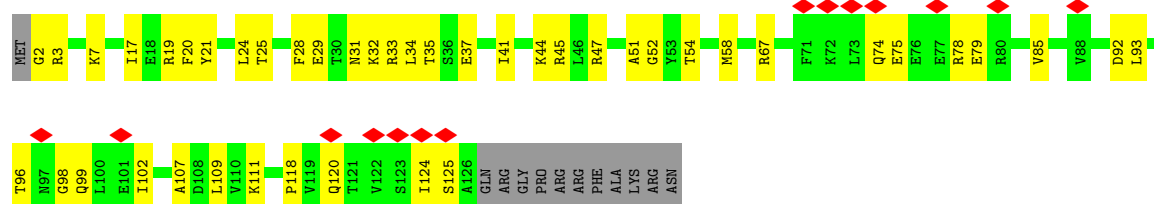


- Molecule 63: Ribosomal 40S subunit protein S16A

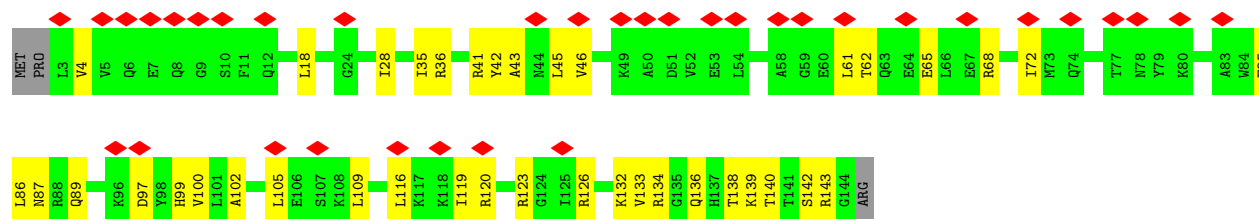




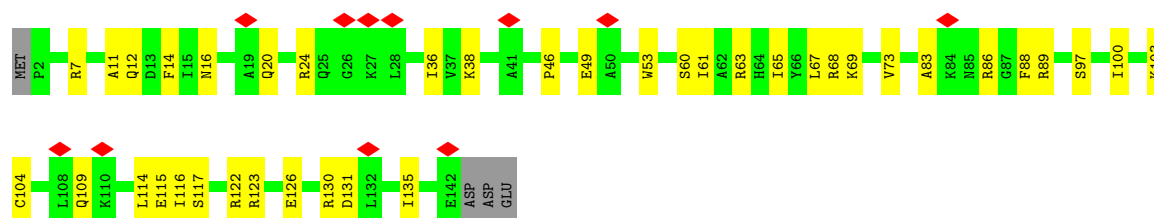
• Molecule 64: Ribosomal 40S subunit protein S17B



• Molecule 65: Ribosomal 40S subunit protein S18B



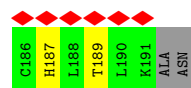
• Molecule 66: Ribosomal 40S subunit protein S19A



• Molecule 67: Ribosomal 40S subunit protein S20

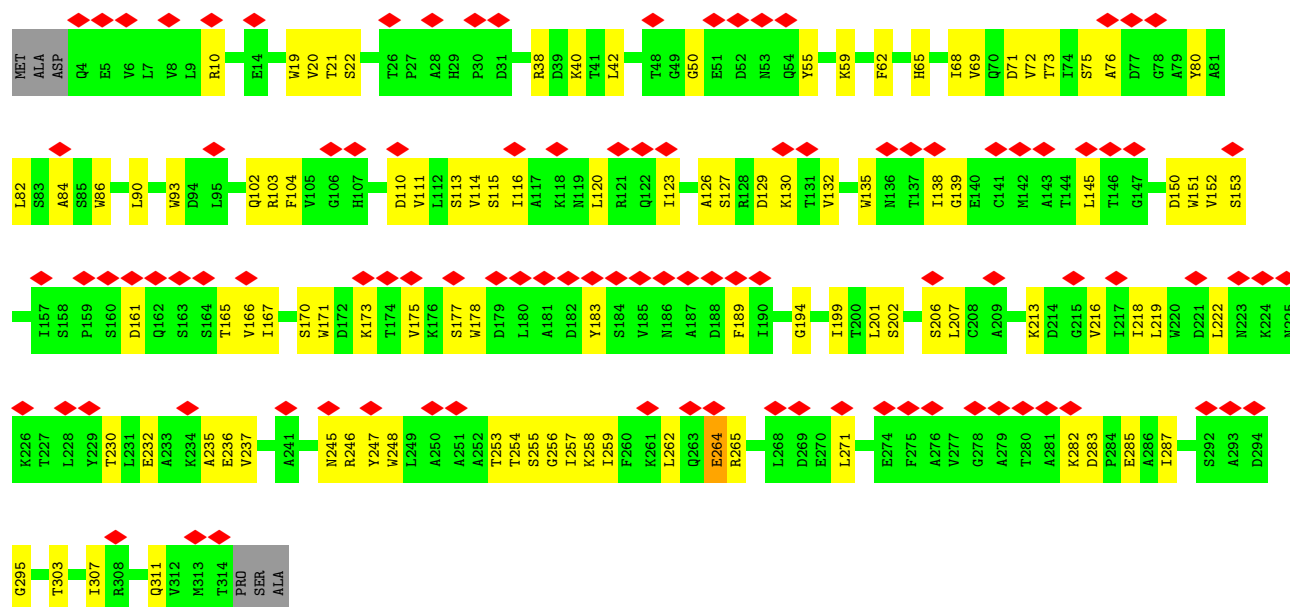


- [illegible]



- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein

Chain h: 32% 66% 32%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	132328	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.771	Depositor
Minimum map value	-1.536	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.134	Depositor
Recommended contour level	0.3	Depositor
Map size ($\text{\AA}$)	426.36002, 426.36002, 426.36002	wwPDB
Map dimensions	510, 510, 510	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.836, 0.836, 0.836	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, IAS, MLZ, SPD, OMC, OMG, 3K5

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.22	9/76718 (0.0%)	0.30	4/119600 (0.0%)
2	3	0.17	0/2884	0.22	0/4492
3	4	0.19	0/3746	0.26	0/5832
4	j	0.19	0/1931	0.32	0/2592
5	k	0.20	0/3156	0.35	0/4246
6	l	0.17	0/2799	0.33	0/3777
7	m	0.15	0/2447	0.30	0/3294
8	n	0.15	0/1258	0.29	0/1696
9	o	0.18	0/1929	0.32	0/2589
10	p	0.15	0/1869	0.30	0/2519
11	q	0.15	0/1537	0.30	0/2067
12	r	0.17	0/1724	0.32	0/2314
13	s	0.35	1/1404 (0.1%)	0.56	4/1880 (0.2%)
14	t	0.16	0/1637	0.32	0/2195
15	u	0.16	0/1044	0.29	0/1407
16	v	0.21	0/1753	0.31	0/2347
17	w	0.18	0/1620	0.30	0/2167
18	x	0.17	0/1398	0.31	0/1879
19	y	0.17	0/1511	0.28	0/2022
20	z	0.14	0/1483	0.25	0/1972
21	0	0.18	0/1483	0.30	0/1997
22	2	0.17	0/1305	0.28	0/1749
23	5	0.15	0/871	0.38	0/1175
24	6	0.17	0/994	0.33	0/1339
25	7	0.16	0/536	0.31	0/712
26	8	0.17	0/990	0.31	0/1337
27	9	0.15	0/999	0.30	0/1334
28	AA	0.15	0/1112	0.31	0/1488
29	AB	0.19	0/1199	0.30	0/1607
30	AC	0.16	0/522	0.31	0/692
31	AD	0.14	0/738	0.27	0/994
32	AE	0.17	0/902	0.29	0/1212

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AF	0.17	0/1039	0.31	0/1390
34	AG	0.19	0/895	0.31	0/1201
35	AH	0.16	0/934	0.36	0/1242
36	AI	0.15	0/1004	0.33	0/1337
37	AJ	0.13	0/780	0.27	0/1033
38	AK	0.19	0/690	0.32	0/916
39	AL	0.16	0/632	0.35	0/842
40	AM	0.18	0/458	0.27	0/609
41	AN	0.15	0/436	0.35	0/577
42	AO	0.12	0/228	0.29	0/293
43	AP	0.19	0/840	0.40	0/1108
44	AQ	0.17	0/705	0.31	0/940
45	i	0.13	0/864	0.36	0/1156
46	A	0.14	0/40362	0.32	7/62888 (0.0%)
47	B	0.13	0/1666	0.32	0/2273
48	C	0.12	0/1750	0.30	0/2354
49	D	0.14	0/1648	0.32	0/2237
50	E	0.13	0/1731	0.36	0/2324
51	F	0.12	0/2096	0.32	0/2822
52	G	0.11	0/1631	0.34	0/2199
53	H	0.12	0/1845	0.31	0/2464
54	I	0.14	0/1490	0.34	0/2004
55	J	0.16	0/1606	0.36	0/2150
56	K	0.11	0/1478	0.29	0/1978
57	L	0.18	0/801	0.49	0/1081
58	M	0.14	0/1154	0.32	0/1553
59	N	0.15	0/892	0.47	0/1203
60	O	0.12	0/1210	0.30	0/1631
61	P	0.13	0/944	0.32	0/1265
62	Q	0.16	0/954	0.44	0/1282
63	R	0.12	0/1109	0.37	0/1486
64	S	0.12	0/1014	0.38	0/1361
65	T	0.13	0/1186	0.33	0/1590
66	U	0.13	0/1120	0.34	0/1508
67	V	0.17	0/800	0.40	0/1082
68	W	0.13	0/683	0.35	0/918
69	X	0.17	0/1049	0.39	0/1412
70	Y	0.13	0/1128	0.33	0/1505
71	Z	0.10	0/1086	0.30	0/1447
72	a	0.12	0/585	0.30	0/789
73	b	0.14	0/811	0.35	0/1085
74	c	0.13	0/624	0.32	0/843
75	d	0.13	0/489	0.41	0/654

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	e	0.15	0/466	0.40	0/620
77	f	0.18	0/451	0.49	0/601
78	g	0.16	0/585	0.48	0/778
79	h	0.18	0/2451	0.42	0/3337
All	All	0.18	10/213899 (0.0%)	0.32	15/313891 (0.0%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1737	A	O3'-P	-12.69	1.42	1.61
13	s	118	PRO	CG-CD	-9.73	1.17	1.50
1	1	482	U	C1'-N1	6.32	1.57	1.48
1	1	477	U	C1'-N1	6.31	1.57	1.48
1	1	483	U	C1'-N1	6.12	1.57	1.48
1	1	479	C	C1'-N1	5.66	1.56	1.48
1	1	476	C	C1'-N1	5.64	1.56	1.48
1	1	1738	U	P-OP1	-5.43	1.38	1.49
1	1	1017	G	O3'-P	-5.38	1.53	1.61
1	1	1738	U	O3'-P	-5.25	1.53	1.61

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1017	G	P-O3'-C3'	21.59	152.59	120.20
46	A	822	G	O3'-P-O5'	18.80	132.21	104.00
13	s	118	PRO	CA-N-CD	-12.09	95.08	112.00
46	A	822	G	P-O3'-C3'	12.05	138.28	120.20
46	A	214	U	OP2-P-O3'	-12.00	71.99	108.00
13	s	118	PRO	N-CD-CG	-10.91	86.83	103.20
46	A	214	U	P-O3'-C3'	-9.69	105.67	120.20
1	1	1017	G	OP2-P-O3'	-9.37	79.90	108.00
46	A	214	U	OP1-P-O3'	8.10	132.31	108.00
1	1	1017	G	OP1-P-O3'	7.86	131.57	108.00
1	1	1738	U	C1'-C2'-O2'	-6.81	98.19	108.40
13	s	118	PRO	CA-CB-CG	-6.54	92.08	104.50
13	s	118	PRO	N-CA-CB	-6.45	97.46	103.46
46	A	214	U	O3'-P-O5'	5.22	111.84	104.00
46	A	822	G	OP2-P-O3'	-5.06	92.81	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68595	0	34479	879	0
2	3	2579	0	1304	27	0
3	4	3353	0	1694	45	0
4	j	1894	0	1975	31	0
5	k	3084	0	3173	55	0
6	l	2751	0	2879	37	0
7	m	2394	0	2362	25	0
8	n	1237	0	1316	20	0
9	o	1893	0	1990	21	0
10	p	1839	0	1957	27	0
11	q	1519	0	1588	23	0
12	r	1689	0	1731	24	0
13	s	1385	0	1418	36	0
14	t	1610	0	1686	20	0
15	u	1029	0	1116	15	0
16	v	1713	0	1764	22	0
17	w	1590	0	1705	17	0
18	x	1375	0	1403	20	0
19	y	1478	0	1590	24	0
20	z	1462	0	1570	24	0
21	0	1442	0	1500	22	0
22	2	1276	0	1333	18	0
23	5	848	0	864	17	0
24	6	986	0	1040	14	0
25	7	524	0	545	8	0
26	8	974	0	1032	10	0
27	9	989	0	1064	13	0
28	AA	1087	0	1154	14	0
29	AB	1170	0	1203	21	0
30	AC	509	0	545	8	0
31	AD	729	0	775	6	0
32	AE	889	0	936	9	0
33	AF	1015	0	1095	11	0
34	AG	867	0	932	7	0
35	AH	913	0	1002	14	0
36	AI	990	0	1094	16	0
37	AJ	772	0	863	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	AK	677	0	697	9	0
39	AL	623	0	688	11	0
40	AM	446	0	488	9	0
41	AN	427	0	473	8	0
42	AO	227	0	272	6	0
43	AP	843	0	914	19	0
44	AQ	698	0	734	11	0
45	i	853	0	830	26	0
46	A	36083	0	18151	841	0
47	B	1627	0	1644	46	0
48	C	1724	0	1805	33	0
49	D	1620	0	1715	35	0
50	E	1707	0	1807	45	0
51	F	2055	0	2137	40	0
52	G	1614	0	1688	55	0
53	H	1820	0	1896	52	0
54	I	1466	0	1561	45	0
55	J	1579	0	1602	31	0
56	K	1453	0	1532	26	0
57	L	783	0	799	40	0
58	M	1129	0	1183	10	0
59	N	885	0	915	31	0
60	O	1187	0	1249	23	0
61	P	942	0	980	27	0
62	Q	935	0	970	42	0
63	R	1091	0	1155	39	0
64	S	1002	0	1058	35	0
65	T	1169	0	1216	35	0
66	U	1100	0	1114	37	0
67	V	790	0	855	36	0
68	W	676	0	677	17	0
69	X	1032	0	1066	22	0
70	Y	1110	0	1182	32	0
71	Z	1072	0	1123	32	0
72	a	578	0	613	16	0
73	b	799	0	860	15	0
74	c	614	0	627	8	0
75	d	487	0	523	25	0
76	e	454	0	431	21	0
77	f	444	0	483	24	0
78	g	574	0	606	24	0
79	h	2398	0	2374	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	1	10	0	19	0	0
81	1	57	0	52	6	0
82	AK	1	0	0	0	0
82	AN	1	0	0	0	0
82	AP	1	0	0	0	0
82	AQ	1	0	0	0	0
82	b	1	0	0	0	0
82	c	1	0	0	0	0
82	e	1	0	0	0	0
82	g	1	0	0	0	0
All	All	199317	0	148441	3064	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 9.

All (3064) 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)
46:A:215:A:H62	46:A:830:G:C1'	1.14	1.55
46:A:215:A:N6	46:A:830:G:H1'	1.09	1.38
1:1:445:A:N6	1:1:485:A:N1	2.00	1.08
77:f:50:THR:OG1	77:f:53:LYS:HB2	1.56	1.04
70:Y:89:ASN:ND2	70:Y:92:CYS:SG	2.36	0.99
46:A:215:A:C6	46:A:830:G:H1'	1.97	0.99
46:A:214:U:O2'	46:A:215:A:OP1	1.81	0.97
46:A:216:A:N6	46:A:829:A:H1'	1.79	0.97
81:1:3402:3K5:O15	43:AP:57:ILE:HG23	1.63	0.96
46:A:216:A:H61	46:A:829:A:H1'	1.32	0.94
1:1:961:A:H5''	14:t:4:SER:HB2	1.47	0.93
46:A:218:A:N6	46:A:827:C:N4	2.17	0.93
46:A:701:G:N2	46:A:720:C:H42	1.67	0.92
46:A:1486:G:H1	46:A:1495:U:H3	1.11	0.92
46:A:811:U:H3	46:A:831:G:H1	1.04	0.91
46:A:218:A:N6	46:A:827:C:H42	1.68	0.91
1:1:2736:C:N3	81:1:3402:3K5:O3	2.05	0.88
62:Q:60:LEU:HB3	62:Q:89:MET:HE2	1.53	0.88
1:1:1014:G:H1	1:1:1030:U:H3	0.88	0.87
46:A:218:A:C6	46:A:827:C:N4	2.41	0.87
35:AH:58:ARG:HD3	35:AH:59:PRO:HD2	1.56	0.87
79:h:90:LEU:HB2	79:h:104:PHE:HB2	1.56	0.87
1:1:445:A:N6	1:1:485:A:C6	2.39	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:h:19:TRP:HB2	79:h:38:ARG:HG3	1.59	0.85
46:A:853:G:H1	46:A:945:U:H3	1.24	0.84
46:A:1666:G:H21	46:A:1709:A:H62	1.24	0.83
55:J:87:ASN:HB3	55:J:90:LEU:HD23	1.62	0.81
1:1:2116:A:HO2'	38:AK:2:GLY:N	1.80	0.80
46:A:757:G:H21	46:A:759:A:H1'	1.46	0.79
46:A:759:A:H61	46:A:770:C:H42	1.30	0.79
61:P:15:PHE:HB3	61:P:22:PHE:HB2	1.64	0.79
47:B:108:THR:O	49:D:59:LYS:NZ	2.15	0.79
46:A:739:A:H5''	46:A:740:A:H5'	1.63	0.79
49:D:34:THR:HG23	49:D:37:GLY:H	1.48	0.78
79:h:42:LEU:HB2	79:h:62:PHE:HB2	1.64	0.78
1:1:2334:A:N3	18:x:131:ARG:NH2	2.30	0.78
46:A:44:U:OP2	46:A:435:A:N6	2.17	0.78
1:1:2086:C:H1'	1:1:3309:A:H8	1.47	0.78
46:A:1668:A:H1'	53:H:66:GLY:HA2	1.65	0.78
1:1:454:G:C6	1:1:476:C:C4	2.72	0.78
23:5:19:VAL:HG23	23:5:20:ALA:H	1.48	0.78
46:A:701:G:H22	46:A:720:C:N4	1.83	0.77
73:b:51:ARG:NH1	75:d:60:GLU:O	2.18	0.77
46:A:869:A:O2'	48:C:124:ASN:ND2	2.16	0.77
46:A:214:U:O2'	46:A:215:A:P	2.42	0.77
48:C:82:ARG:NH2	48:C:188:LEU:O	2.17	0.76
9:o:9:THR:HA	9:o:12:LYS:HD3	1.65	0.76
46:A:1226:G:H4'	62:Q:78:THR:HA	1.69	0.75
1:1:2171:U:H5'	1:1:2172:G:H5'	1.66	0.75
13:s:157:GLU:O	13:s:161:GLN:NE2	2.19	0.75
46:A:126:A:H62	46:A:289:G:H21	1.33	0.75
46:A:1324:C:O2'	46:A:1326:A:N7	2.19	0.75
1:1:3010:U:O2	24:6:9:ASN:ND2	2.18	0.75
1:1:1019:U:H4'	1:1:1019:U:OP1	1.87	0.75
1:1:1242:G:C5	1:1:1260:G:O2'	2.38	0.75
1:1:935:U:OP2	29:AB:26:ARG:NH2	2.21	0.74
3:4:75:G:OP2	27:9:74:TYR:OH	2.05	0.74
51:F:64:ILE:HD11	71:Z:18:LEU:HB2	1.68	0.74
1:1:1021:A:H2'	1:1:1021:A:N3	2.02	0.74
46:A:1276:G:H1	46:A:1309:G:H22	1.35	0.74
13:s:109:HIS:HD2	13:s:114:ILE:HD11	1.52	0.73
39:AL:63:LYS:O	39:AL:67:GLN:NE2	2.21	0.73
79:h:257:ILE:HB	79:h:271:LEU:HB2	1.70	0.73
1:1:2628:A:H4'	43:AP:98:LYS:HE3	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:U:86:ARG:HH21	66:U:89:ARG:HE	1.34	0.73
1:1:1225:G:H2'	1:1:1226:G:C8	2.23	0.73
46:A:1156:A:H2'	46:A:1157:G:C8	2.24	0.73
46:A:1535:G:O2'	65:T:89:GLN:NE2	2.21	0.73
46:A:1320:U:H3	46:A:1402:G:H1	1.36	0.72
50:E:128:MET:HE2	50:E:135:VAL:HG12	1.71	0.72
46:A:847:A:O2'	46:A:948:A:N1	2.21	0.72
46:A:478:G:H1	46:A:506:U:H3	1.35	0.72
46:A:588:C:OP1	77:f:42:ARG:NH2	2.21	0.72
52:G:57:SER:OG	52:G:167:ARG:NH2	2.22	0.72
51:F:45:VAL:HG23	51:F:61:VAL:HG11	1.71	0.72
1:1:2808:OMC:H5	1:1:2824:C:H42	1.36	0.72
1:1:2814:U:OP1	1:1:2816:C:N4	2.23	0.72
45:i:78:SER:HG	46:A:1164:G:HO2'	1.30	0.72
46:A:1460:G:H2'	46:A:1461:A:H8	1.54	0.72
63:R:21:VAL:HG22	63:R:64:ILE:HG12	1.72	0.72
1:1:1678:U:O4	23:5:93:ARG:NH1	2.22	0.72
46:A:217:A:H8	46:A:217:A:H5''	1.55	0.72
54:I:150:LEU:HB2	54:I:181:ILE:HG13	1.70	0.72
1:1:1091:U:H4'	1:1:1092:U:H5'	1.70	0.72
46:A:759:A:H61	46:A:770:C:N4	1.86	0.72
46:A:1600:U:OP1	52:G:92:ARG:NH2	2.22	0.72
20:z:160:GLU:OE1	20:z:163:ARG:NH1	2.23	0.71
75:d:12:VAL:HG22	75:d:52:ASP:H	1.55	0.71
78:g:175:ALA:HB1	78:g:177:MET:HE2	1.71	0.71
6:l:4:ARG:NH1	6:l:24:PRO:O	2.23	0.71
1:1:1936:G:H21	1:1:3327:A:H8	1.38	0.71
1:1:2086:C:H1'	1:1:3309:A:C8	2.25	0.71
35:AH:87:GLU:OE1	35:AH:91[B]:ARG:NH2	2.22	0.71
79:h:10:ARG:NH1	79:h:311:GLN:OE1	2.24	0.71
13:s:90:GLN:HE22	13:s:170:GLU:HB2	1.56	0.71
46:A:79:C:H1'	53:H:174:LYS:HB2	1.72	0.71
47:B:92:HIS:HD1	47:B:202:TYR:HH	1.38	0.71
1:1:2696:U:OP1	22:2:78:LYS:NZ	2.24	0.71
46:A:938:G:H2'	46:A:939:G:H8	1.56	0.71
54:I:40:LYS:HG3	54:I:59:PRO:HD3	1.71	0.71
52:G:164:PRO:HD3	75:d:54:LEU:HB3	1.73	0.70
79:h:255:SER:OG	79:h:258:LYS:NZ	2.21	0.70
45:i:104:GLN:HG3	45:i:110:SER:HB2	1.72	0.70
46:A:1546:G:N2	46:A:1548:U:OP2	2.24	0.70
1:1:3179:U:OP2	15:u:121:ARG:NH2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1156:A:H2'	46:A:1157:G:H8	1.56	0.70
51:F:44:LEU:HD23	51:F:82:TYR:HB3	1.72	0.70
46:A:1592:G:OP2	63:R:126:LYS:NZ	2.23	0.70
11:q:8:GLN:HB3	11:q:72:LYS:HD2	1.71	0.70
17:w:35:VAL:HG22	17:w:104:LYS:HB2	1.74	0.70
49:D:36:LEU:HD11	49:D:51:ILE:HD12	1.73	0.70
53:H:137:ARG:HB3	53:H:140:HIS:HD2	1.56	0.70
57:L:27:PHE:HB3	57:L:40:LEU:HD13	1.74	0.70
79:h:153:SER:H	79:h:170:SER:HA	1.57	0.70
1:1:1006:G:N2	12:r:193:ASP:OD2	2.25	0.69
1:1:1240:A:N6	1:1:1267:A:OP1	2.25	0.69
13:s:118:PRO:HD2	13:s:119:SER:N	2.07	0.69
46:A:1448:G:OP2	65:T:143:ARG:NH1	2.24	0.69
46:A:1475:U:O2'	46:A:1501:A:N6	2.24	0.69
54:I:52:LYS:HB2	54:I:84:ARG:HD3	1.74	0.69
1:1:800:C:OP1	6:l:99:ARG:NH2	2.25	0.69
46:A:766:U:H4'	46:A:767:G:H5''	1.74	0.69
50:E:44:PRO:HD3	67:V:107:ILE:HG12	1.72	0.69
31:AD:16:LEU:HD22	31:AD:82:VAL:HG12	1.74	0.69
46:A:155:A:OP2	71:Z:132:ARG:NH2	2.26	0.69
60:O:3:ARG:HB3	60:O:6:SER:HB3	1.74	0.69
49:D:138:TYR:OH	49:D:144:GLY:O	2.10	0.69
50:E:77:ARG:HB2	57:L:22:VAL:HG11	1.74	0.69
5:k:218:ILE:HB	5:k:337:THR:HB	1.74	0.69
46:A:1335:U:H2'	46:A:1336:G:C8	2.28	0.69
1:1:443:G:C2	1:1:487:C:O2	2.45	0.69
27:9:55:GLU:OE1	27:9:107:THR:OG1	2.11	0.69
46:A:485:G:H1	46:A:499:U:H3	0.75	0.69
71:Z:36:SER:OG	71:Z:38:ASP:OD1	2.10	0.69
46:A:1154:G:N1	46:A:1562:G:OP2	2.22	0.69
1:1:1014:G:O6	1:1:1030:U:O4	2.11	0.68
8:n:71:ASN:ND2	8:n:159:LEU:O	2.19	0.68
46:A:784:U:H2'	46:A:785:G:H8	1.58	0.68
56:K:106:GLU:O	56:K:112:GLN:NE2	2.25	0.68
1:1:71:C:O2'	14:t:66:ASN:OD1	2.12	0.68
1:1:3022:U:O2'	25:7:16:GLY:O	2.09	0.68
13:s:118:PRO:HD2	13:s:119:SER:H	1.58	0.68
1:1:1218:G:N2	1:1:1281:G:O2'	2.26	0.68
1:1:2504:C:OP1	4:j:37:ARG:NH2	2.25	0.68
46:A:948:A:N7	60:O:70:LYS:NZ	2.41	0.68
51:F:230:THR:OG1	51:F:234:LYS:NZ	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3010:U:OP1	5:k:348:ARG:NH1	2.27	0.68
1:1:3014:U:OP2	1:1:3064:C:N4	2.26	0.68
52:G:146:SER:HA	52:G:159:ALA:HA	1.74	0.68
79:h:175:VAL:HB	79:h:189:PHE:HB2	1.75	0.68
21:0:60:SER:OG	21:0:62:ASN:ND2	2.25	0.68
46:A:1343:G:H4'	66:U:130:ARG:HD2	1.76	0.68
65:T:134:ARG:HB2	65:T:136:GLN:HE22	1.58	0.68
1:1:438:A:N1	1:1:489:G:O2'	2.26	0.68
1:1:834:G:O6	44:AQ:4:ARG:NH2	2.26	0.68
1:1:1344:U:OP1	19:y:39:ARG:NH1	2.25	0.68
20:z:98:ARG:NH2	20:z:130:ASN:OD1	2.27	0.68
46:A:850:A:OP1	69:X:3:ARG:NH2	2.26	0.68
52:G:187:ILE:HD13	72:a:66:VAL:HG11	1.75	0.68
1:1:2155:G:OP2	4:j:128:ARG:NH1	2.26	0.68
1:1:3157:A:OP1	11:q:23:ARG:NH1	2.25	0.68
1:1:2370:C:O2'	5:k:266:ARG:NH2	2.27	0.68
70:Y:69:ARG:HG3	70:Y:117:ILE:HG13	1.76	0.68
1:1:1892:A:H61	1:1:2317:C:H42	1.41	0.68
46:A:915:A:N3	48:C:111:ARG:NH2	2.42	0.68
47:B:24:LEU:HD23	47:B:45:MET:HE3	1.75	0.68
1:1:3199:G:H1	1:1:3218:U:H3	1.41	0.67
46:A:1511:A:H2'	46:A:1512:A:C8	2.29	0.67
64:S:25:THR:O	64:S:31:ASN:ND2	2.27	0.67
46:A:144:U:H2'	46:A:145:A:H8	1.59	0.67
46:A:1240:G:N7	59:N:46:ARG:NH2	2.42	0.67
46:A:1255:G:O2'	78:g:122:ARG:NH1	2.27	0.67
52:G:94:THR:HG22	52:G:114:VAL:HG21	1.76	0.67
75:d:12:VAL:HG12	75:d:30:VAL:HG12	1.76	0.67
1:1:925:A:O2'	38:AK:49:TRP:O	2.13	0.67
1:1:1657:G:H2'	1:1:1658:G:C8	2.29	0.67
1:1:3233:A:OP1	8:n:45:ARG:NH2	2.28	0.67
1:1:3262:U:O4	5:k:124:LYS:NZ	2.28	0.67
28:AA:27:LYS:HE3	28:AA:97:THR:HG22	1.77	0.67
46:A:1316:A:H61	50:E:162:GLY:HA3	1.58	0.67
18:x:40:LYS:NZ	18:x:153:GLU:OE2	2.28	0.67
7:m:289:LYS:HD2	12:r:206:LEU:HD23	1.75	0.67
46:A:747:A:OP1	56:K:79:ARG:NH2	2.28	0.67
1:1:1577:C:O5'	1:1:1577:C:H6	1.77	0.67
1:1:2815:U:OP2	1:1:2816:C:N4	2.25	0.67
48:C:190:PRO:HG2	48:C:192:VAL:HG23	1.77	0.67
1:1:498:C:OP1	8:n:25:ARG:NH2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Y:70:LYS:HD3	70:Y:93:LEU:HD22	1.75	0.67
1:1:454:G:C6	1:1:476:C:N3	2.63	0.67
1:1:429:U:H2'	1:1:430:G:H8	1.60	0.66
46:A:644:U:H2'	46:A:645:G:H8	1.61	0.66
32:AE:45:THR:HG22	32:AE:47:ASP:H	1.59	0.66
47:B:63:ILE:HG12	68:W:36:ILE:HG12	1.77	0.66
46:A:1019:C:HO2'	69:X:2:THR:N	1.94	0.66
1:1:454:G:C2	1:1:476:C:C2	2.82	0.66
46:A:485:G:O6	46:A:499:U:O4	2.14	0.66
46:A:1578:C:H2'	46:A:1579:A:H8	1.60	0.66
62:Q:32:GLU:HA	62:Q:35:LYS:HE2	1.78	0.66
63:R:4:GLN:HB2	63:R:23:ALA:HB2	1.75	0.66
71:Z:87:PRO:HD2	71:Z:90:ARG:HD2	1.76	0.66
50:E:21:GLU:HG3	57:L:61:TRP:CD1	2.31	0.66
63:R:29:LYS:HB2	63:R:65:ARG:HG2	1.76	0.66
21:O:73:LYS:NZ	21:O:97:VAL:O	2.24	0.66
1:1:1021:A:H62	62:Q:74:ALA:HA	1.60	0.66
46:A:148:C:O5'	46:A:148:C:H6	1.78	0.66
46:A:1699:G:N1	46:A:1700:G:N3	2.44	0.66
1:1:716:G:H3'	1:1:717:A:H5''	1.78	0.66
1:1:1560:U:H3	1:1:1571:G:H1	1.43	0.66
51:F:154:ILE:O	51:F:155:ARG:NH1	2.29	0.66
46:A:261:C:O2'	46:A:262:G:N2	2.29	0.66
79:h:116:ILE:HG22	79:h:123:ILE:HG12	1.78	0.66
77:f:24:GLN:HE22	77:f:26:LYS:HB2	1.60	0.65
7:m:197:LYS:HG2	7:m:202:GLY:HA3	1.79	0.65
3:4:63:G:O2'	36:AI:49:LYS:NZ	2.29	0.65
46:A:856:G:H2'	46:A:857:G:C8	2.31	0.65
1:1:147:G:OP2	16:v:4:TYR:OH	2.13	0.65
81:1:3402:3K5:O16	81:1:3402:3K5:H24	1.96	0.65
57:L:17:GLN:H	57:L:88:PRO:HB3	1.62	0.65
1:1:1352:C:N4	19:y:27[A]:GLN:OE1	2.22	0.65
37:AJ:2:ALA:O	37:AJ:11:ASN:ND2	2.29	0.65
46:A:881:U:O2	61:P:36:ARG:NH1	2.24	0.65
46:A:1265:C:H2'	46:A:1266:G:H8	1.61	0.65
67:V:100:LYS:O	67:V:104:GLN:NE2	2.30	0.65
1:1:653:C:H2'	1:1:654:A:H8	1.61	0.65
35:AH:87:GLU:OE1	35:AH:91[A]:ARG:NH2	2.30	0.65
46:A:512:G:HO2'	46:A:513:A:H8	1.45	0.65
46:A:653:G:H4'	46:A:654:G:H5'	1.79	0.65
46:A:1579:A:H2'	46:A:1580:A:H8	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:k:19:ARG:NH2	5:k:270:ASN:OD1	2.29	0.65
46:A:509:A:OP2	56:K:176:ASN:ND2	2.29	0.65
62:Q:108:LYS:HB2	62:Q:111:MET:HG3	1.79	0.65
1:l:88:G:N7	19:y:171:LYS:NZ	2.44	0.65
46:A:1579:A:H2'	46:A:1580:A:C8	2.31	0.65
46:A:1666:G:N2	46:A:1709:A:H62	1.94	0.65
46:A:1460:G:H2'	46:A:1461:A:C8	2.31	0.65
47:B:84:ARG:NH1	47:B:203:PHE:O	2.28	0.65
1:l:316:U:O2'	37:AJ:29:LYS:NZ	2.30	0.64
2:3:7:G:OP1	7:m:33:ARG:NH1	2.30	0.64
46:A:1303:G:OP2	64:S:67:ARG:NH2	2.30	0.64
52:G:162:VAL:HG13	52:G:166:ARG:HD3	1.79	0.64
46:A:1445:C:OP2	65:T:138:THR:OG1	2.15	0.64
1:l:1148:G:OP2	1:l:1148:G:N2	2.29	0.64
46:A:655:U:O2'	46:A:674:C:N4	2.29	0.64
46:A:1593:C:H2'	46:A:1594:G:C8	2.32	0.64
63:R:12:LYS:HG3	63:R:13:LYS:H	1.62	0.64
1:l:716:G:OP2	1:l:716:G:N2	2.21	0.64
46:A:811:U:O2	46:A:831:G:O6	2.15	0.64
65:T:36:ARG:HB3	65:T:102:ALA:HA	1.78	0.64
1:l:3287:A:H2'	1:l:3288:A:C8	2.32	0.64
46:A:99:C:OP2	46:A:376:A:O2'	2.13	0.64
46:A:364:A:OP1	46:A:743:U:O2'	2.15	0.64
46:A:869:A:H62	46:A:913:U:H3	1.46	0.64
52:G:57:SER:HA	75:d:53:ILE:HB	1.79	0.64
1:l:2941:A:N7	4:j:215:ASN:ND2	2.45	0.64
10:p:42:GLN:OE1	10:p:45:ARG:NH2	2.30	0.64
46:A:126:A:H62	46:A:289:G:N2	1.96	0.64
46:A:1474:G:O2'	46:A:1481:C:O2	2.14	0.64
1:l:3199:G:N2	1:l:3218:U:O2	2.28	0.64
46:A:17:C:O2'	46:A:1122:A:N1	2.29	0.64
74:c:64:CYS:HB3	74:c:73:LEU:HD23	1.80	0.64
79:h:264:GLU:O	79:h:264:GLU:HG2	1.98	0.64
46:A:1160:U:H2'	46:A:1161:G:H8	1.62	0.64
46:A:1266:G:H4'	67:V:75:SER:H	1.62	0.64
51:F:129:VAL:HG22	51:F:139:VAL:HG12	1.80	0.64
67:V:62:LEU:HB3	67:V:83:MET:HB2	1.78	0.64
79:h:127:SER:OG	79:h:129:ASP:OD1	2.15	0.64
1:l:1243:U:H2'	1:l:1264:G:H1	1.62	0.64
8:n:39:LEU:HD13	8:n:83:VAL:HG11	1.79	0.64
46:A:829:A:H2'	46:A:830:G:H8	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1379:C:H2'	46:A:1380:G:H8	1.62	0.64
1:1:2163:G:O2'	1:1:2292:U:OP2	2.13	0.63
56:K:31:ALA:HB2	56:K:42:ILE:HD11	1.78	0.63
4:j:27:ALA:O	4:j:128:ARG:NH2	2.30	0.63
23:5:34:VAL:HG21	23:5:58:ALA:HB2	1.80	0.63
46:A:1367:U:H2'	46:A:1368:A:C8	2.34	0.63
69:X:77:PRO:HD2	69:X:79:PHE:CZ	2.34	0.63
18:x:122:ALA:HB3	18:x:143:PRO:HB2	1.79	0.63
46:A:701:G:N2	46:A:720:C:N4	2.39	0.63
46:A:1131:G:H2'	46:A:1132:A:C8	2.34	0.63
1:1:1152:C:OP2	9:o:92:LYS:NZ	2.32	0.63
1:1:1837:A:H1'	40:AM:45:ARG:HH22	1.62	0.63
46:A:215:A:N7	46:A:830:G:O4'	2.32	0.63
46:A:1302:C:O2'	46:A:1386:A:N3	2.28	0.63
49:D:53:LEU:O	68:W:15:ARG:NH1	2.31	0.63
57:L:12:HIS:HB3	57:L:80:LEU:HD21	1.80	0.63
66:U:114:LEU:HD11	66:U:122:ARG:HB3	1.81	0.63
6:l:10:ILE:HD11	6:l:147:LYS:HZ1	1.64	0.63
46:A:57:G:OP2	71:Z:116:LYS:NZ	2.29	0.63
46:A:1401:U:OP1	64:S:45:ARG:NH2	2.31	0.63
28:AA:115:LYS:NZ	28:AA:119:GLU:OE1	2.31	0.63
46:A:626:G:OP1	60:O:124:ARG:NH1	2.31	0.63
54:I:58:VAL:HG21	54:I:66:TYR:HE2	1.63	0.63
23:5:22:PRO:HB2	23:5:28:PHE:HB2	1.81	0.63
36:AI:5:LYS:HB2	36:AI:8:GLU:HG3	1.80	0.63
46:A:78:A:H8	53:H:154:ARG:HG3	1.63	0.63
49:D:71:LEU:HB3	49:D:99:ILE:HD11	1.79	0.63
52:G:53:VAL:HG21	52:G:62:ILE:HG21	1.80	0.63
1:1:476:C:H2'	1:1:477:U:C6	2.33	0.63
1:1:2560:U:OP1	10:p:242:LYS:NZ	2.30	0.63
45:i:101:LYS:NZ	46:A:579:U:O2	2.31	0.63
46:A:821:U:H2'	46:A:822:G:C8	2.33	0.63
52:G:41:LYS:HD3	52:G:47:SER:HB3	1.80	0.63
46:A:164:C:O2'	53:H:133:LEU:O	2.17	0.62
46:A:871:U:O2'	61:P:116:VAL:O	2.17	0.62
67:V:29:LYS:HG3	67:V:32:GLN:HB3	1.81	0.62
1:1:1190:G:H2'	1:1:1191:A:C8	2.34	0.62
1:1:1713:U:H2'	1:1:1714:G:C8	2.33	0.62
46:A:1160:U:H2'	46:A:1161:G:C8	2.34	0.62
48:C:58:ALA:HB1	48:C:91:VAL:HG11	1.80	0.62
7:m:91:GLY:O	7:m:94:ASN:ND2	2.27	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:S:35:THR:HG21	64:S:51:ALA:HB2	1.82	0.62
79:h:73:THR:OG1	79:h:114:VAL:O	2.16	0.62
46:A:485:G:N2	46:A:499:U:O2	2.27	0.62
46:A:768:C:H2'	46:A:769:U:O4'	1.99	0.62
46:A:1399:U:OP2	64:S:3:ARG:NH2	2.28	0.62
1:l:591:C:O2	9:o:24:ARG:NH1	2.33	0.62
46:A:952:A:OP2	60:O:124:ARG:NH2	2.32	0.62
49:D:222:PRO:HA	49:D:225:TRP:CD2	2.35	0.62
52:G:51:VAL:HG21	52:G:130:ILE:HG13	1.81	0.62
75:d:11:LYS:O	75:d:31:GLU:N	2.33	0.62
76:e:21:CYS:SG	76:e:39:CYS:HB2	2.39	0.62
1:l:2115:U:OP2	1:l:2120:A:N6	2.29	0.62
1:l:2516:U:O2'	1:l:2520:A:N1	2.33	0.62
1:l:2535:A:OP1	4:j:69:TYR:OH	2.13	0.62
46:A:1451:C:OP1	63:R:138:GLN:NE2	2.32	0.62
65:T:45:LEU:HD11	66:U:36:ILE:HG12	1.82	0.62
75:d:42:ARG:NH1	75:d:58:GLU:O	2.33	0.62
1:l:2925:U:H2'	1:l:2926:U:H2'	1.82	0.62
46:A:1704:C:H2'	46:A:1705:G:H8	1.65	0.62
32:AE:45:THR:HG21	32:AE:89:PHE:HA	1.82	0.62
46:A:908:A:H2'	46:A:909:A:C8	2.35	0.62
1:l:716:G:OP1	29:AB:117:ARG:NH2	2.33	0.61
1:l:1022:A:N3	62:Q:72:ARG:NH1	2.47	0.61
2:3:21:G:OP2	13:s:2:SER:N	2.32	0.61
5:k:47:LEU:HB2	5:k:84:MET:HE3	1.81	0.61
12:r:3:ARG:NH2	12:r:63:GLU:OE2	2.32	0.61
25:7:6:ASP:OD2	25:7:32:GLN:N	2.32	0.61
46:A:151:G:H2'	46:A:152:G:H8	1.65	0.61
46:A:1238:U:OP2	78:g:147:TYR:OH	2.13	0.61
55:J:84:HIS:NE2	55:J:97:THR:OG1	2.23	0.61
65:T:116:LEU:HD12	65:T:119:ILE:HD11	1.81	0.61
72:a:65:LEU:HG	72:a:69:LEU:HD12	1.80	0.61
1:l:3256:G:H2'	1:l:3257:A:H8	1.64	0.61
24:6:108:GLU:OE1	24:6:128[B]:ARG:NH1	2.32	0.61
46:A:1444:G:OP1	65:T:138:THR:N	2.31	0.61
54:I:129:THR:HG21	54:I:150:LEU:HB3	1.81	0.61
1:l:1242:G:C8	1:l:1260:G:H2'	2.35	0.61
13:s:134:ALA:O	13:s:152:HIS:NE2	2.30	0.61
67:V:26:THR:HG22	67:V:87:LYS:HG2	1.81	0.61
70:Y:107:PHE:HE1	70:Y:123:LYS:HB3	1.66	0.61
1:l:3139:U:OP2	34:AG:63:LYS:NZ	2.27	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:156:U:O2'	46:A:158:C:OP2	2.19	0.61
47:B:18:LEU:HD21	64:S:102:ILE:HD13	1.81	0.61
47:B:197:VAL:HG13	47:B:201:LEU:HD23	1.83	0.61
50:E:99:ALA:HB2	50:E:189:ILE:HB	1.81	0.61
78:g:162:GLU:HA	78:g:173:PHE:HA	1.80	0.61
1:l:795:G:O2'	14:t:18:TRP:NE1	2.32	0.61
1:l:2988:A:H2'	1:l:2989:A:H8	1.65	0.61
13:s:148:ILE:O	13:s:153:LYS:NZ	2.32	0.61
46:A:872:A:H5''	61:P:115:PRO:HB2	1.83	0.61
46:A:938:G:H2'	46:A:939:G:C8	2.35	0.61
46:A:1529:G:N2	46:A:1556:A:OP2	2.33	0.61
46:A:1602:C:N4	52:G:80:LYS:O	2.33	0.61
1:l:1680:U:OP1	23:5:89:LYS:NZ	2.31	0.61
1:l:2867:G:O2'	41:AN:24:TYR:O	2.18	0.61
46:A:216:A:N3	46:A:216:A:H2'	2.15	0.61
52:G:109:LYS:HG3	52:G:112:ARG:HH21	1.66	0.61
71:Z:52:LYS:NZ	71:Z:53:ASP:OD1	2.34	0.61
79:h:202:SER:HB3	79:h:207:LEU:HB2	1.82	0.61
1:l:653:C:H2'	1:l:654:A:C8	2.35	0.61
29:AB:112:VAL:HB	29:AB:130:VAL:HG12	1.83	0.61
46:A:1043:U:O2'	46:A:1045:U:OP2	2.17	0.61
46:A:1168:A:C2	62:Q:100:LYS:HB2	2.35	0.61
65:T:138:THR:O	65:T:142:SER:OG	2.19	0.61
6:l:283:SER:N	19:y:125:ASP:OD1	2.26	0.61
7:m:50:ARG:NH1	7:m:147:ASP:OD2	2.34	0.61
11:q:92:PHE:HB2	11:q:142:ASP:HB3	1.82	0.61
26:8:73:MET:HE2	26:8:142:ILE:HD12	1.83	0.61
46:A:58:U:O2'	46:A:449:G:N3	2.34	0.61
46:A:215:A:N6	46:A:830:G:C1'	1.98	0.61
46:A:839:U:O4	46:A:840:A:N6	2.33	0.61
46:A:1529:G:H22	46:A:1555:C:H1'	1.66	0.61
49:D:64:ILE:HD11	49:D:128:LYS:HB3	1.80	0.61
67:V:23:ILE:HG12	67:V:115:VAL:HG13	1.81	0.61
72:a:50:ILE:HG12	72:a:69:LEU:HD13	1.82	0.61
79:h:38:ARG:HD3	79:h:68:ILE:HG21	1.81	0.61
1:l:892:A:H5'	4:j:183:GLY:HA2	1.83	0.61
46:A:218:A:N3	46:A:218:A:H2'	2.14	0.61
46:A:396:G:OP2	55:J:47:ARG:NH2	2.32	0.61
46:A:1305:U:H3'	47:B:101:ARG:HH12	1.65	0.61
47:B:35:PRO:O	47:B:52:LYS:NZ	2.34	0.61
67:V:32:GLN:HE22	67:V:108:GLU:HB3	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:654:A:H2'	1:1:655:A:C8	2.36	0.60
6:l:301:ARG:NH2	19:y:38:ARG:O	2.34	0.60
11:q:57:VAL:HG23	11:q:68:LEU:HD13	1.81	0.60
46:A:1067:C:O4'	68:W:62:ARG:NH1	2.34	0.60
1:1:827:G:O2'	1:1:1860:A:N3	2.34	0.60
1:1:2866:C:OP2	11:q:168:ARG:NH1	2.34	0.60
4:j:129:THR:OG1	4:j:132:ASN:OD1	2.19	0.60
28:AA:101:LEU:O	28:AA:107:ARG:NH2	2.34	0.60
46:A:635:C:O2	54:I:110:ARG:NH2	2.34	0.60
46:A:821:U:H2'	46:A:822:G:H8	1.66	0.60
63:R:124:GLU:OE2	63:R:134:ARG:NH1	2.34	0.60
1:1:394:G:N1	1:1:397:A:OP2	2.34	0.60
5:k:216:ASP:OD2	5:k:339:ARG:NH2	2.29	0.60
11:q:107:ASP:O	11:q:109:GLN:NE2	2.34	0.60
54:I:17:VAL:O	54:I:21:PHE:N	2.33	0.60
1:1:358:G:N2	1:1:361:A:OP2	2.29	0.60
1:1:875:U:O2'	18:x:135:ARG:NH2	2.29	0.60
1:1:1720:U:H1'	1:1:1721:C:C6	2.36	0.60
1:1:2699:A:OP2	1:1:2700:G:N2	2.28	0.60
46:A:1026:G:H2'	46:A:1027:G:C8	2.37	0.60
1:1:1774:G:O2'	1:1:1776:G:OP2	2.19	0.60
46:A:1024:A:O2'	46:A:1025:G:O5'	2.15	0.60
46:A:1214:G:N2	46:A:1240:G:O2'	2.34	0.60
48:C:180:THR:HG23	48:C:183:GLN:H	1.66	0.60
57:L:35:ILE:HG22	57:L:37:THR:HG22	1.83	0.60
46:A:648:U:OP1	56:K:65:LYS:NZ	2.32	0.60
46:A:1272:A:N1	46:A:1313:G:O2'	2.32	0.60
46:A:1473:A:OP1	76:e:34:TYR:OH	2.19	0.60
1:1:454:G:O6	1:1:476:C:C4	2.55	0.60
25:7:60:LYS:HA	25:7:63:ILE:HD12	1.83	0.60
50:E:75:VAL:HG12	50:E:80:LEU:HD23	1.83	0.60
1:1:403:C:O2'	1:1:404:G:OP1	2.18	0.60
3:4:23:U:OP1	27:9:16:ARG:NH1	2.34	0.60
5:k:71:GLU:OE2	5:k:357:LYS:NZ	2.34	0.60
46:A:1152:G:N2	63:R:138:GLN:OE1	2.28	0.60
46:A:1240:G:OP2	59:N:50:LYS:NZ	2.34	0.60
46:A:1582:U:H3	46:A:1587:A:H62	1.50	0.60
79:h:132:VAL:HB	79:h:145:LEU:HB2	1.82	0.60
46:A:699:U:H2'	46:A:700:G:C8	2.36	0.60
79:h:235:ALA:HB3	79:h:253:THR:HB	1.83	0.60
1:1:831:G:O2'	1:1:853:G:N2	2.28	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:j:80:GLU:HG3	44:AQ:66:GLY:HA2	1.83	0.60
24:6:17:LEU:HD13	24:6:23:MET:HE2	1.84	0.60
46:A:759:A:N6	46:A:770:C:H42	1.98	0.60
48:C:129:THR:OG1	48:C:131:ASP:OD1	2.18	0.60
75:d:9:LEU:HA	75:d:55:CYS:HA	1.83	0.60
77:f:42:ARG:NH1	77:f:56:MET:HE1	2.16	0.60
1:1:2869:A:H2'	1:1:2871:C:H5''	1.84	0.59
1:1:2932:C:H2'	1:1:2933:G:C8	2.36	0.59
6:l:351:LYS:O	6:l:354:LYS:NZ	2.31	0.59
21:0:60:SER:HG	21:0:62:ASN:ND2	1.98	0.59
46:A:600:U:OP2	70:Y:110:ARG:NH2	2.35	0.59
46:A:1339:G:O6	46:A:1354:U:O2	2.20	0.59
60:O:99:ARG:NH2	60:O:119:GLU:OE2	2.30	0.59
1:1:437:G:N2	1:1:620:A:H61	1.99	0.59
46:A:965:G:H4'	46:A:1763:A:H4'	1.83	0.59
55:J:76:THR:HG21	55:J:104:ILE:HD12	1.83	0.59
70:Y:54:LEU:HD11	70:Y:75:GLN:HB2	1.84	0.59
1:1:1611:U:H2'	1:1:1612:U:C6	2.38	0.59
40:AM:25:GLN:OE1	40:AM:28:ARG:NH2	2.34	0.59
46:A:29:U:H2'	46:A:30:G:H8	1.67	0.59
61:P:82:GLY:HA3	61:P:115:PRO:HG2	1.84	0.59
1:1:2810:A:H4'	12:r:74:LYS:HD3	1.83	0.59
1:1:3256:G:H2'	1:1:3257:A:C8	2.37	0.59
12:r:42:THR:OG1	12:r:45:GLU:OE1	2.17	0.59
18:x:118:GLN:NE2	18:x:147:GLU:OE2	2.35	0.59
46:A:146:A:N6	46:A:165:U:O2	2.35	0.59
46:A:1463:G:H2'	46:A:1464:G:H8	1.66	0.59
54:I:5:ILE:HG12	54:I:10:PRO:HB3	1.82	0.59
46:A:1353:G:H5''	66:U:69:LYS:HE3	1.84	0.59
46:A:1664:C:H42	46:A:1711:C:H42	1.47	0.59
49:D:77:LYS:NZ	49:D:202:THR:OG1	2.33	0.59
49:D:134:ILE:HD13	49:D:186:ALA:HB1	1.83	0.59
52:G:169:ASN:OD1	52:G:170:GLN:N	2.36	0.59
1:1:1199:A:H2'	1:1:1200:A:C8	2.38	0.59
1:1:1795:A:H2'	1:1:1796:A:C8	2.36	0.59
76:e:21:CYS:HB2	76:e:25:SER:N	2.18	0.59
1:1:2932:C:H2'	1:1:2933:G:H8	1.68	0.59
46:A:924:A:H2'	46:A:925:A:C8	2.37	0.59
46:A:470:U:O2'	46:A:754:A:N3	2.35	0.59
46:A:676:G:N3	46:A:677:G:N2	2.51	0.59
47:B:83:GLN:HE22	47:B:100:GLY:HA2	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:V:52:LYS:HB2	67:V:91:ASP:HB2	1.85	0.59
71:Z:38:ASP:OD1	71:Z:39:GLU:N	2.35	0.59
5:k:58:ARG:HD2	5:k:354:VAL:HG13	1.84	0.59
19:y:123:THR:OG1	19:y:125:ASP:OD2	2.18	0.59
46:A:151:G:H2'	46:A:152:G:C8	2.36	0.59
46:A:1442:C:H5''	46:A:1443:C:H5''	1.84	0.59
1:1:1110:U:OP1	29:AB:23:GLY:N	2.36	0.59
1:1:1264:G:O5'	1:1:1264:G:H8	1.86	0.59
45:i:35:SER:OG	45:i:37:LYS:NZ	2.30	0.59
58:M:66:ILE:HG21	58:M:140:LEU:HD11	1.84	0.59
77:f:42:ARG:NH1	77:f:43:ARG:HB3	2.18	0.59
1:1:628:A:H2'	1:1:629:A:C8	2.37	0.58
1:1:1021:A:OP1	1:1:1021:A:H3'	2.03	0.58
10:p:134:LYS:HD2	10:p:139:HIS:HE1	1.66	0.58
24:6:13:MET:HE1	24:6:54:ALA:HB3	1.85	0.58
46:A:869:A:OP1	48:C:136:ARG:NH2	2.35	0.58
46:A:1320:U:O2	46:A:1402:G:N2	2.28	0.58
59:N:57:ALA:HB3	59:N:124:LYS:HA	1.84	0.58
1:1:2335:A:H2'	1:1:2336:A:C8	2.38	0.58
26:8:67:ILE:HD12	26:8:121:LYS:HG3	1.85	0.58
1:1:157:G:H2'	1:1:158:A:H8	1.66	0.58
1:1:730:A:H2'	1:1:731:U:H2'	1.86	0.58
46:A:191:U:H4'	46:A:192:U:H5'	1.86	0.58
46:A:519:A:H2'	46:A:520:U:C6	2.39	0.58
75:d:19:THR:HG23	75:d:25:VAL:HG13	1.85	0.58
76:e:21:CYS:HB2	76:e:25:SER:H	1.67	0.58
1:1:242:C:HO2'	1:1:243:G:H8	1.51	0.58
1:1:370:U:H4'	1:1:404:G:H5'	1.85	0.58
1:1:1177:U:O4	17:w:22:SER:OG	2.20	0.58
1:1:3064:C:O2'	1:1:3066:A:OP2	2.18	0.58
2:3:112:G:H2'	2:3:113:C:C6	2.38	0.58
46:A:722:A:OP1	51:F:177:THR:OG1	2.21	0.58
46:A:1036:U:H3	46:A:1052:G:H1	1.51	0.58
46:A:1067:C:O2	68:W:62:ARG:NH1	2.37	0.58
46:A:1198:G:H1	46:A:1436:U:H3	1.51	0.58
1:1:3040:U:OP2	20:z:62:ARG:NH2	2.35	0.58
1:1:1017:G:H2'	1:1:1018:U:C6	2.38	0.58
1:1:3039:C:H3'	20:z:62:ARG:HH22	1.69	0.58
46:A:148:C:O2	46:A:163:G:N2	2.37	0.58
46:A:432:G:N1	46:A:435:A:OP2	2.34	0.58
46:A:1582:U:H5''	46:A:1583:C:H5	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:870:G:H2'	46:A:871:U:C6	2.39	0.58
46:A:891:A:H2'	46:A:892:A:C8	2.38	0.58
46:A:929:A:OP2	73:b:19:LYS:NZ	2.37	0.58
46:A:1335:U:H2'	46:A:1336:G:H8	1.68	0.58
48:C:64:ARG:HG2	61:P:31:LYS:HD2	1.86	0.58
56:K:81:VAL:HG21	56:K:91:MET:HE2	1.86	0.58
57:L:21:VAL:HB	57:L:66:TYR:HB2	1.85	0.58
67:V:92:LEU:HD13	67:V:99:VAL:HG12	1.85	0.58
1:1:437:G:O2'	1:1:438:A:OP1	2.20	0.58
5:k:63:PRO:HD2	5:k:348:ARG:NH2	2.18	0.58
17:w:11:ASP:HB2	17:w:118:ARG:HB3	1.85	0.58
50:E:49:VAL:HB	50:E:87:ILE:HG12	1.83	0.58
53:H:63:MET:HG2	53:H:98:ARG:HG3	1.86	0.58
72:a:71:ILE:HB	72:a:75:LEU:HD23	1.85	0.58
1:1:782:A:H4'	1:1:783:G:H5'	1.86	0.58
3:4:66:A:OP1	36:AI:10:ARG:NH2	2.36	0.58
9:o:51:LYS:NZ	9:o:55:GLU:OE2	2.36	0.58
46:A:1376:U:H5'	64:S:3:ARG:HG2	1.86	0.58
53:H:57:ASP:OD1	53:H:61:PHE:N	2.36	0.58
63:R:128:PHE:O	63:R:136:ARG:NH2	2.36	0.58
75:d:12:VAL:HA	75:d:30:VAL:HA	1.85	0.58
79:h:90:LEU:HD21	79:h:111:VAL:HG11	1.84	0.58
1:1:2988:A:H2'	1:1:2989:A:C8	2.38	0.58
1:1:3166:A:H2'	1:1:3167:G:H8	1.69	0.58
35:AH:38:ALA:O	35:AH:58:ARG:NH2	2.37	0.58
1:1:564:G:H2'	1:1:565:A:C8	2.39	0.57
1:1:1029:U:H2'	1:1:1030:U:C6	2.38	0.57
1:1:1691:U:O2'	1:1:1745:A:N1	2.35	0.57
46:A:1064:U:H2'	46:A:1065:U:C6	2.39	0.57
46:A:1637:U:H2'	46:A:1638:A:C8	2.39	0.57
23:5:16:VAL:HG12	23:5:65:VAL:HG22	1.86	0.57
46:A:64:U:O2'	46:A:166:A:N3	2.31	0.57
46:A:1198:G:N2	46:A:1436:U:O2	2.37	0.57
46:A:1659:G:H2'	46:A:1660:G:C8	2.39	0.57
50:E:41:ARG:HA	67:V:109:PRO:HB3	1.85	0.57
6:l:6:GLN:HB3	6:l:20:GLN:HB3	1.87	0.57
46:A:317:U:H4'	46:A:321:A:C8	2.40	0.57
1:1:353:G:O6	38:AK:55:ARG:NH2	2.38	0.57
1:1:437:G:H22	1:1:620:A:H61	1.51	0.57
1:1:2051:G:H2'	1:1:2052:G:C8	2.38	0.57
46:A:1239:U:OP2	59:N:46:ARG:NH1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1486:G:O6	46:A:1495:U:O4	2.23	0.57
50:E:114:LEU:HD23	50:E:118:ARG:HD3	1.85	0.57
1:1:1172:C:H4'	17:w:90:PRO:HD3	1.86	0.57
1:1:2322:U:H2'	1:1:2323:A:C8	2.38	0.57
17:w:122:PRO:HA	17:w:125:LEU:HD12	1.87	0.57
46:A:415:A:H5'	46:A:416:G:C4	2.40	0.57
46:A:1475:U:HO2'	46:A:1501:A:H62	1.51	0.57
46:A:1597:G:N7	63:R:13:LYS:NZ	2.52	0.57
59:N:67:THR:O	59:N:68:GLU:HG3	2.04	0.57
78:g:182:TYR:CZ	78:g:184:GLY:HA2	2.39	0.57
1:1:252:U:H5'	1:1:253:A:H8	1.68	0.57
1:1:362:U:O4	38:AK:24:ARG:NH2	2.37	0.57
1:1:1692:A:H2'	1:1:1693:A:C8	2.39	0.57
62:Q:81:ARG:HH12	62:Q:98:ASN:HA	1.69	0.57
1:1:1276:C:H2'	1:1:1277:G:O4'	2.03	0.57
48:C:134:VAL:HG21	48:C:219:LYS:HE3	1.86	0.57
53:H:180:THR:HG23	53:H:183:THR:H	1.70	0.57
13:s:109:HIS:CE1	13:s:122:ILE:HA	2.40	0.57
46:A:1395:G:N2	46:A:1398:G:OP2	2.34	0.57
46:A:1459:U:OP2	52:G:189:THR:OG1	2.14	0.57
46:A:1491:G:N3	46:A:1550:C:O2'	2.37	0.57
46:A:1541:U:H3'	46:A:1542:A:H8	1.69	0.57
1:1:820:C:H5''	4:j:21:ARG:HD3	1.86	0.57
1:1:3308:G:O2'	1:1:3327:A:N6	2.38	0.57
39:AL:17:ARG:NH2	39:AL:19:ASP:OD2	2.36	0.57
46:A:5:U:H2'	46:A:6:G:H8	1.68	0.57
1:1:730:A:H8	1:1:733:A:H62	1.53	0.57
1:1:1115:C:H2'	1:1:1116:A:H8	1.70	0.57
29:AB:36:GLY:HA3	29:AB:40:HIS:CE1	2.39	0.57
46:A:530:U:OP1	71:Z:64:PHE:HA	2.05	0.57
46:A:829:A:H2'	46:A:830:G:C8	2.39	0.57
63:R:68:VAL:HG11	63:R:80:ILE:HD11	1.86	0.57
1:1:1104:U:H2'	1:1:1105:U:C6	2.40	0.56
1:1:2068:U:N3	20:z:113:GLY:O	2.37	0.56
3:4:95:G:OP2	38:AK:72:ARG:NE	2.38	0.56
46:A:518:A:H2'	46:A:519:A:C8	2.39	0.56
46:A:1351:U:O3'	66:U:7:ARG:NH1	2.38	0.56
1:1:1260:G:H8	1:1:1260:G:O5'	1.87	0.56
1:1:2079:C:HO2'	1:1:2080:U:H6	1.53	0.56
1:1:2347:G:H2'	1:1:2348:G:C8	2.40	0.56
1:1:3060:G:OP1	5:k:313:ARG:NH1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:y:76:ALA:HA	19:y:79:LYS:HG3	1.87	0.56
46:A:327:G:H5''	55:J:98:LYS:HB3	1.86	0.56
62:Q:93:VAL:HA	62:Q:106:GLU:HA	1.86	0.56
1:1:454:G:O6	1:1:476:C:N4	2.39	0.56
1:1:672:G:O6	19:y:56:LYS:NZ	2.38	0.56
1:1:1592:C:H2'	1:1:1593:C:C6	2.40	0.56
1:1:1950:G:H21	1:1:2065:C:H42	1.54	0.56
1:1:2744:C:H4'	1:1:2745:C:H5'	1.87	0.56
6:l:290:LEU:HD22	19:y:129:LEU:HD21	1.85	0.56
9:o:71:ASN:O	22:2:143:THR:OG1	2.23	0.56
10:p:63:LYS:NZ	16:v:29:GLU:OE1	2.31	0.56
23:5:19:VAL:HG12	23:5:108:LEU:HD13	1.88	0.56
27:9:55:GLU:HA	27:9:69:LYS:HA	1.87	0.56
46:A:119:A:H1'	46:A:395:A:C5	2.40	0.56
48:C:34:ALA:HB3	48:C:41:ARG:HA	1.86	0.56
77:f:49:LEU:HD12	77:f:52:GLY:H	1.68	0.56
1:1:212:A:OP1	27:9:2:ALA:N	2.39	0.56
1:1:1238:G:N2	1:1:1266:A:O2'	2.39	0.56
1:1:1787:U:H2'	1:1:1788:C:C6	2.40	0.56
1:1:2045:C:H2'	1:1:2046:U:C6	2.41	0.56
13:s:51:ARG:HD2	45:i:31:LYS:HZ2	1.70	0.56
46:A:841:A:N6	54:I:111:SER:O	2.35	0.56
65:T:86:LEU:HD22	65:T:99:HIS:HB2	1.85	0.56
1:1:2680:C:H5'	45:i:29:VAL:HB	1.86	0.56
5:k:297:GLU:O	5:k:300:ARG:NE	2.39	0.56
18:x:18:ARG:NH1	18:x:147:GLU:OE1	2.39	0.56
21:0:81:TYR:CE1	21:0:90:MET:HE3	2.41	0.56
46:A:1437:C:H2'	46:A:1438:U:C6	2.41	0.56
46:A:1566:U:H2'	46:A:1567:C:C6	2.41	0.56
48:C:90:GLU:HB3	48:C:97:LEU:HB2	1.87	0.56
60:O:100:LYS:O	60:O:104:LYS:NZ	2.37	0.56
1:1:976:A:N6	1:1:1100:G:O2'	2.34	0.56
20:z:67:LYS:HE2	20:z:71:ARG:HH12	1.71	0.56
43:AP:8:ARG:HD3	43:AP:72:LEU:HD21	1.86	0.56
46:A:1042:U:H3'	46:A:1043:U:H2'	1.88	0.56
46:A:1087:G:OP2	70:Y:7:ARG:NH1	2.32	0.56
46:A:1715:U:H2'	46:A:1716:C:C6	2.41	0.56
51:F:122:LYS:NZ	51:F:143:ASP:OD2	2.38	0.56
65:T:28:ILE:HG12	65:T:61:LEU:HD11	1.88	0.56
73:b:32:LYS:O	73:b:37:LYS:NZ	2.36	0.56
78:g:182:TYR:HB2	78:g:189:THR:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:833:A:OP2	44:AQ:4:ARG:NH1	2.38	0.56
1:1:1782:G:H2'	1:1:1783:A:C8	2.41	0.56
1:1:3309:A:N6	1:1:3326:G:O2'	2.31	0.56
4:j:142:ASP:OD1	4:j:143:GLU:N	2.39	0.56
24:6:17:LEU:HD11	24:6:98:ASN:HB3	1.86	0.56
47:B:200:ASP:HB2	64:S:85:VAL:HG23	1.88	0.56
79:h:42:LEU:HD21	79:h:69:VAL:HG11	1.87	0.56
79:h:207:LEU:HB3	79:h:219:LEU:HD11	1.88	0.56
1:1:1386:A:N6	1:1:1414:A:O2'	2.38	0.56
21:0:125:LYS:HG2	21:0:127:VAL:HG23	1.87	0.56
76:e:19:ARG:NE	76:e:32:ARG:HD3	2.21	0.56
78:g:182:TYR:HE1	78:g:187:HIS:HA	1.71	0.56
1:1:411:U:H2'	1:1:412:G:H8	1.71	0.56
1:1:2285:G:O2'	1:1:2288:U:OP2	2.21	0.56
81:1:3402:3K5:H39	81:1:3402:3K5:H16	1.88	0.56
46:A:1040:U:O2	46:A:1049:G:N2	2.32	0.56
46:A:1550:C:H2'	46:A:1551:U:H6	1.70	0.56
54:I:29:ASP:OD1	54:I:30:LEU:N	2.38	0.56
1:1:623:A:H2'	1:1:624:U:C6	2.41	0.56
1:1:1943:G:O2'	1:1:1944:G:OP1	2.18	0.56
1:1:2669:A:H2'	1:1:2670:G:C8	2.41	0.56
15:u:52:LEU:HD23	15:u:55:ILE:HD11	1.87	0.56
46:A:291:U:H2'	46:A:292:C:C6	2.41	0.56
46:A:760:G:O6	46:A:769:U:O2	2.24	0.56
55:J:6:ASP:HB3	55:J:28:GLU:HG3	1.88	0.56
1:1:679:U:O4	6:l:119:LYS:NZ	2.38	0.55
1:1:1018:U:O5'	1:1:1018:U:H6	1.89	0.55
1:1:1964:G:N1	1:1:2051:G:O6	2.39	0.55
46:A:824:U:H5''	46:A:824:U:O2	2.06	0.55
52:G:106:LYS:HD3	52:G:109:LYS:HE3	1.88	0.55
55:J:136:VAL:O	55:J:141:ARG:NH2	2.38	0.55
67:V:81:TYR:HB3	76:e:52:PHE:HB3	1.88	0.55
1:1:662:U:H2'	1:1:663:A:C8	2.42	0.55
1:1:820:C:OP1	4:j:21:ARG:NE	2.38	0.55
1:1:246:U:H2'	1:1:247:C:C6	2.42	0.55
1:1:2191:A:H2'	1:1:2192:A:C8	2.41	0.55
2:3:12:U:OP2	2:3:68:C:O2'	2.24	0.55
17:w:125:LEU:HD13	21:0:168:PRO:HG3	1.88	0.55
46:A:253:U:H2'	46:A:254:A:C8	2.41	0.55
46:A:422:C:O2'	46:A:424:G:OP1	2.17	0.55
46:A:1247:U:H2'	46:A:1248:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:D:163:ARG:HD3	49:D:165:ILE:HD11	1.89	0.55
51:F:71:GLN:HB3	51:F:91:THR:HB	1.87	0.55
61:P:67:LYS:HE2	61:P:105:LEU:HD23	1.88	0.55
1:1:1286:A:H2'	1:1:1287:A:C8	2.41	0.55
46:A:248:C:H2'	46:A:249:A:H8	1.71	0.55
46:A:908:A:H2'	46:A:909:A:H8	1.71	0.55
46:A:1203:G:N2	46:A:1430:A:OP2	2.40	0.55
46:A:1580:A:H2'	46:A:1581:G:C8	2.41	0.55
47:B:30:GLN:NE2	47:B:151:SER:O	2.39	0.55
70:Y:93:LEU:HD21	77:f:8:LEU:HD22	1.89	0.55
79:h:285:GLU:O	79:h:303:THR:HG23	2.07	0.55
1:1:3260:A:H2'	1:1:3261:A:C8	2.42	0.55
5:k:211:GLN:NE2	5:k:283:TYR:O	2.37	0.55
53:H:102:VAL:HG13	53:H:106:LEU:HD12	1.89	0.55
1:1:92:C:OP2	1:1:2736:C:O2'	2.20	0.55
1:1:1720:U:OP2	20:z:128:LYS:NZ	2.29	0.55
3:4:21:C:OP1	6:l:194:LYS:NZ	2.30	0.55
46:A:815:U:O2'	46:A:816:U:O5'	2.23	0.55
1:1:417:A:H2'	1:1:418:A:C8	2.41	0.55
1:1:872:A:H5''	1:1:1886:U:H5''	1.88	0.55
15:u:41:ASP:OD2	15:u:42:GLY:N	2.40	0.55
16:v:11:GLN:HA	16:v:19:MET:HE3	1.88	0.55
46:A:445:U:H2'	46:A:446:C:O4'	2.07	0.55
46:A:907:G:H2'	46:A:908:A:C8	2.41	0.55
46:A:1336:G:H2'	46:A:1337:C:C6	2.42	0.55
51:F:63:ALA:O	51:F:67:GLN:NE2	2.39	0.55
67:V:57:MET:SD	67:V:58:PRO:HD2	2.47	0.55
70:Y:90:ASP:O	70:Y:136:TRP:NE1	2.39	0.55
1:1:2260:U:OP1	1:1:2945:G:O2'	2.24	0.55
1:1:2655:U:H2'	1:1:2656:C:C6	2.41	0.55
1:1:3088:G:OP1	1:1:3088:G:N2	2.38	0.55
2:3:84:A:H2'	2:3:85:G:C8	2.41	0.55
11:q:83:THR:HG23	11:q:84:LYS:HG3	1.88	0.55
54:I:11:THR:HG22	54:I:14:GLU:OE1	2.07	0.55
75:d:20:GLY:HA2	75:d:66:LEU:HB2	1.87	0.55
1:1:907:C:OP1	4:j:14:SER:OG	2.23	0.55
1:1:3170:G:OP2	1:1:3171:C:N4	2.37	0.55
9:o:19:LYS:O	9:o:22:GLU:HG3	2.07	0.55
14:t:61:PRO:O	14:t:62:THR:HG23	2.06	0.55
47:B:50:ILE:HA	47:B:53:THR:HB	1.89	0.55
57:L:80:LEU:HB3	57:L:82:ILE:HG23	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:527:G:H2'	1:1:528:A:C8	2.42	0.55
1:1:1043:A:N3	1:1:2605:U:O2'	2.40	0.55
16:v:27:CYS:SG	16:v:31:ARG:NH1	2.80	0.55
46:A:330:U:OP1	55:J:31:ARG:NH1	2.33	0.55
46:A:397:A:H4'	51:F:3:ARG:HG2	1.87	0.55
46:A:634:A:H5''	69:X:31:SER:HB3	1.89	0.55
46:A:1089:U:OP1	70:Y:14:LYS:NZ	2.39	0.55
46:A:1580:A:H2'	46:A:1581:G:H8	1.70	0.55
1:1:1795:A:H2'	1:1:1796:A:H8	1.73	0.54
1:1:1909:A:N3	1:1:2098:A:H2'	2.22	0.54
1:1:2206:A:H2'	1:1:2207:A:C8	2.42	0.54
1:1:2766:G:N2	81:1:3402:3K5:H42	2.21	0.54
6:l:140:GLY:O	6:l:142:ARG:NH1	2.41	0.54
32:AE:73:ARG:NH2	32:AE:110:ASP:OD1	2.39	0.54
46:A:149:G:H8	46:A:149:G:OP2	1.90	0.54
46:A:188:U:O4	55:J:142:SER:OG	2.25	0.54
46:A:253:U:H2'	46:A:254:A:H8	1.72	0.54
46:A:1546:G:N7	65:T:134:ARG:HD3	2.22	0.54
47:B:31:VAL:HG13	47:B:32:HIS:HD2	1.72	0.54
48:C:26:ARG:HA	48:C:50:ARG:NH1	2.23	0.54
10:p:163:LEU:HA	16:v:7:LEU:HD21	1.87	0.54
46:A:85:A:N3	46:A:146:A:O2'	2.39	0.54
46:A:291:U:H2'	46:A:292:C:H6	1.71	0.54
56:K:105:LEU:HD23	56:K:108:ARG:HD2	1.88	0.54
63:R:98:GLU:N	79:h:59:LYS:O	2.40	0.54
1:1:1045:C:OP2	12:r:21:ARG:NH2	2.40	0.54
46:A:692:U:N3	54:I:92:ARG:O	2.39	0.54
46:A:1399:U:N3	46:A:1570:A:OP2	2.34	0.54
1:1:158:A:H2'	1:1:159:A:C8	2.42	0.54
1:1:1612:U:H2'	1:1:1613:G:C8	2.42	0.54
46:A:1457:A:O2'	46:A:1458:C:OP1	2.25	0.54
46:A:1606:C:O2	75:d:22:ARG:NE	2.39	0.54
47:B:23:HIS:HA	47:B:48:ILE:HB	1.89	0.54
79:h:207:LEU:HD22	79:h:219:LEU:HD21	1.90	0.54
1:1:1268:C:H3'	1:1:1269:A:H4'	1.90	0.54
1:1:2107:U:H2'	1:1:2108:G:C8	2.42	0.54
14:t:76:THR:HG22	14:t:101:ARG:HB3	1.88	0.54
46:A:484:G:H2'	46:A:485:G:C8	2.42	0.54
46:A:644:U:H2'	46:A:645:G:C8	2.41	0.54
46:A:907:G:H2'	46:A:908:A:H8	1.72	0.54
46:A:1127:A:H5''	73:b:2:PRO:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:T:41:ARG:HH12	66:U:46:PRO:HB3	1.72	0.54
66:U:109:GLN:HE22	66:U:116:ILE:HG12	1.72	0.54
1:1:454:G:N2	1:1:476:C:C1'	2.71	0.54
18:x:124:LYS:HB2	18:x:126:ARG:NH1	2.22	0.54
38:AK:36:SER:OG	38:AK:57:ARG:NH2	2.38	0.54
46:A:771:G:OP1	51:F:255:ARG:NH2	2.41	0.54
46:A:1145:A:H2'	46:A:1146:C:C6	2.43	0.54
46:A:1189:A:H61	76:e:15:GLY:HA2	1.73	0.54
46:A:1437:C:H2'	46:A:1438:U:H6	1.73	0.54
46:A:1559:G:O2'	52:G:185:ARG:NE	2.41	0.54
62:Q:105:VAL:HA	65:T:120:ARG:HH22	1.72	0.54
65:T:62:THR:HG23	65:T:65:GLU:H	1.71	0.54
1:1:1093:G:H4'	22:2:129:LYS:HG2	1.89	0.54
1:1:1663:A:H2'	1:1:1664:G:C8	2.43	0.54
3:4:9:A:H2'	3:4:10:A:C8	2.43	0.54
7:m:208:MET:HE1	7:m:236:VAL:HG21	1.90	0.54
13:s:90:GLN:NE2	13:s:170:GLU:HB2	2.22	0.54
46:A:605:G:H5'	46:A:611:G:N2	2.21	0.54
46:A:1276:G:H22	46:A:1309:G:H22	1.56	0.54
46:A:1478:A:O2'	46:A:1479:A:O4'	2.20	0.54
47:B:84:ARG:NH1	47:B:205:ARG:HG3	2.22	0.54
52:G:143:ARG:HH21	52:G:214:LYS:HD3	1.72	0.54
52:G:192:GLU:OE2	72:a:63:SER:OG	2.25	0.54
65:T:126:ARG:NH1	65:T:133:VAL:O	2.41	0.54
1:1:25:A:H2'	1:1:26:C:H6	1.73	0.54
1:1:1895:G:O2'	1:1:2312:U:O4	2.17	0.54
4:j:248:GLY:O	4:j:250:GLN:NE2	2.39	0.54
5:k:17:LEU:HD21	5:k:233:TRP:HH2	1.73	0.54
46:A:189:G:N7	55:J:143:ARG:NH2	2.50	0.54
57:L:48:SER:O	57:L:52:LYS:HG2	2.08	0.54
69:X:53:ILE:HD13	74:c:24:LEU:HD11	1.90	0.54
71:Z:39:GLU:OE2	71:Z:43:LYS:NZ	2.41	0.54
1:1:1635:C:OP2	35:AH:74:ARG:NH1	2.38	0.54
1:1:2514:G:C4	1:1:2515:G:N2	2.76	0.54
26:8:106:ASP:HB2	26:8:130:TYR:HE2	1.73	0.54
46:A:249:A:H2	51:F:131:LEU:HD22	1.71	0.54
46:A:415:A:H4'	46:A:416:G:O5'	2.07	0.54
47:B:167:LYS:NZ	47:B:204:TYR:O	2.34	0.54
1:1:627:U:H2'	1:1:628:A:C8	2.43	0.54
1:1:1106:U:H2'	1:1:1107:U:C6	2.43	0.54
1:1:1250:C:C5	1:1:1259:A:OP1	2.61	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2354:G:H2'	1:1:2355:G:C8	2.43	0.54
1:1:3019:U:O2'	1:1:3020:A:H5'	2.08	0.54
5:k:217:VAL:HG11	5:k:328:ILE:HB	1.90	0.54
8:n:42:LEU:HD21	8:n:84:ILE:HG13	1.90	0.54
8:n:55:LYS:NZ	8:n:100:PHE:O	2.41	0.54
12:r:179:ASP:OD1	12:r:180:GLU:N	2.41	0.54
46:A:331:A:H2'	46:A:332:G:C8	2.43	0.54
46:A:1469:A:H2	46:A:1594:G:H1'	1.72	0.54
46:A:1588:G:C2	66:U:88:PHE:HB3	2.43	0.54
48:C:101:HIS:HA	48:C:217:LEU:HD12	1.89	0.54
57:L:56:LYS:NZ	57:L:69:THR:HG22	2.23	0.54
1:1:72:A:N7	14:t:66:ASN:HB3	2.23	0.53
1:1:618:U:H5''	1:1:619:A:C8	2.43	0.53
1:1:1668:U:OP1	20:z:64:ARG:NH1	2.33	0.53
1:1:2632:G:OP1	1:1:2722:U:O2'	2.26	0.53
1:1:2696:U:OP2	1:1:2698:C:N4	2.41	0.53
3:4:103:G:OP2	3:4:105:A:O2'	2.22	0.53
4:j:49:ILE:HD11	4:j:60:LYS:HE2	1.88	0.53
21:0:71:LYS:O	21:0:73:LYS:NZ	2.38	0.53
46:A:543:A:H4'	46:A:544:U:H5'	1.90	0.53
46:A:553:A:H2'	46:A:554:A:C8	2.43	0.53
46:A:803:G:H2'	46:A:806:A:C8	2.42	0.53
46:A:1666:G:H21	46:A:1709:A:N6	2.02	0.53
51:F:11:ARG:HH12	51:F:24:SER:HB2	1.73	0.53
52:G:97:LEU:HD11	52:G:194:LEU:HD12	1.90	0.53
53:H:25:ARG:HA	53:H:28:TYR:HD2	1.73	0.53
57:L:4:PRO:HG2	57:L:7:ASP:HB2	1.90	0.53
60:O:18:TYR:H	74:c:27:GLN:HE22	1.55	0.53
66:U:7:ARG:HH21	66:U:67:LEU:HA	1.73	0.53
79:h:50:GLY:H	79:h:55:TYR:HA	1.73	0.53
1:1:1631:G:N2	1:1:1634:A:OP2	2.36	0.53
1:1:2587:G:H2'	1:1:2588:C:H6	1.74	0.53
46:A:1049:G:H2'	46:A:1050:A:C8	2.43	0.53
46:A:1185:G:OP1	46:A:1582:U:O2'	2.26	0.53
46:A:1383:U:H3'	46:A:1385:C:H42	1.73	0.53
54:I:81:PHE:HB3	54:I:84:ARG:HG3	1.90	0.53
64:S:124:ILE:HG13	64:S:125:SER:H	1.73	0.53
66:U:86:ARG:HH21	66:U:89:ARG:NE	2.05	0.53
1:1:243:G:H2'	1:1:244:G:H8	1.73	0.53
1:1:496:A:H4'	8:n:27:GLN:HG3	1.89	0.53
1:1:1180:A:H2'	1:1:1181:C:C6	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2492:U:OP2	1:1:2558:G:N2	2.41	0.53
6:l:35:LEU:HD22	6:l:121:TYR:HD2	1.73	0.53
46:A:1040:U:H3	46:A:1049:G:H1	1.55	0.53
46:A:1094:G:OP2	70:Y:27:GLN:NE2	2.41	0.53
1:1:2384:C:H2'	1:1:2385:C:C6	2.44	0.53
1:1:2732:C:N3	43:AP:63:LYS:NZ	2.57	0.53
1:1:3197:G:H2'	1:1:3198:C:C6	2.43	0.53
6:l:147:LYS:HG3	6:l:148:GLU:HG2	1.91	0.53
8:n:54:LEU:HD21	8:n:145:LEU:HD21	1.90	0.53
10:p:104:ALA:O	10:p:108:GLU:HG3	2.08	0.53
46:A:504:A:O2'	46:A:505:U:OP1	2.26	0.53
46:A:1232:U:H5''	78:g:135:HIS:N	2.24	0.53
46:A:1572:U:OP1	63:R:124:GLU:N	2.29	0.53
50:E:67:ILE:HD11	50:E:87:ILE:HG22	1.89	0.53
53:H:136:LYS:NZ	53:H:174:LYS:O	2.36	0.53
60:O:25:TRP:CE3	74:c:82:LYS:HE2	2.44	0.53
1:1:158:A:H2'	1:1:159:A:H8	1.72	0.53
1:1:406:G:H1'	3:4:16:G:N2	2.23	0.53
1:1:486:C:H2'	1:1:487:C:C6	2.43	0.53
1:1:965:C:O2'	30:AC:18:ARG:NH1	2.41	0.53
1:1:1042:A:H2'	1:1:1045:C:C5	2.43	0.53
1:1:1258:G:H1'	1:1:1274:A:H61	1.73	0.53
1:1:2836:A:H5''	12:r:114:GLY:HA2	1.91	0.53
12:r:38:ARG:HG2	12:r:41:ALA:HB2	1.91	0.53
28:AA:3:LYS:NZ	28:AA:30:ASP:OD2	2.25	0.53
28:AA:14:VAL:HB	35:AH:86:LYS:HG3	1.91	0.53
45:i:129:LEU:HD11	50:E:129:GLY:HA3	1.91	0.53
46:A:242:A:OP1	51:F:155:ARG:NE	2.42	0.53
46:A:827:C:O2	46:A:827:C:H2'	2.08	0.53
46:A:1275:U:H2'	46:A:1276:G:C8	2.44	0.53
46:A:1396:A:O2'	46:A:1397:A:OP1	2.26	0.53
47:B:92:HIS:ND1	47:B:202:TYR:OH	2.31	0.53
54:I:5:ILE:HG13	54:I:7:SER:H	1.74	0.53
59:N:97:LEU:HA	59:N:100:TRP:CZ2	2.44	0.53
71:Z:91:LEU:HB3	71:Z:97:ALA:HB3	1.91	0.53
1:1:2138:G:H2'	1:1:2139:G:H8	1.73	0.53
13:s:32:ARG:NH1	13:s:123:TYR:OH	2.42	0.53
46:A:1431:G:N2	78:g:129:THR:O	2.39	0.53
1:1:297:G:OP2	1:1:297:G:N2	2.26	0.53
1:1:3166:A:H2'	1:1:3167:G:C8	2.44	0.53
10:p:92:PHE:O	10:p:96:ASN:ND2	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:p:257:ALA:O	10:p:261:SER:HB2	2.08	0.53
39:AL:7:ASP:HB3	39:AL:10:GLU:HB3	1.91	0.53
46:A:67:A:O2'	46:A:69:G:OP1	2.26	0.53
46:A:107:C:OP1	46:A:381:G:O2'	2.26	0.53
46:A:160:A:H3'	46:A:161:G:H21	1.72	0.53
46:A:1063:C:H2'	46:A:1064:U:C6	2.44	0.53
46:A:1578:C:H2'	46:A:1579:A:C8	2.41	0.53
47:B:144:ILE:HG23	47:B:158:VAL:HB	1.90	0.53
55:J:107:THR:HA	55:J:110:ARG:HG2	1.90	0.53
14:t:57:VAL:HG22	14:t:69:VAL:HG22	1.90	0.53
46:A:16:G:H2'	46:A:17:C:C6	2.44	0.53
46:A:1131:G:H2'	46:A:1132:A:H8	1.73	0.53
46:A:1282:G:N2	46:A:1285:A:OP2	2.27	0.53
46:A:1379:C:H2'	46:A:1380:G:C8	2.43	0.53
1:1:1662:G:H2'	1:1:1663:A:H8	1.74	0.53
1:1:2592:G:OP1	30:AC:1:MET:N	2.41	0.53
46:A:12:U:H2'	46:A:13:C:C6	2.44	0.53
46:A:57:G:OP1	71:Z:112:LYS:NZ	2.28	0.53
46:A:217:A:H5''	46:A:217:A:C8	2.41	0.53
46:A:572:G:O6	70:Y:65:ASN:ND2	2.38	0.53
46:A:1469:A:C2	46:A:1594:G:H1'	2.43	0.53
46:A:1512:A:H4'	66:U:83:ALA:HB2	1.90	0.53
54:I:163:ASP:OD1	54:I:164:SER:N	2.42	0.53
63:R:14:THR:HB	63:R:71:GLY:HA2	1.90	0.53
1:1:1230:G:N2	1:1:1251:C:N3	2.57	0.53
1:1:1482:G:H21	35:AH:6:THR:HG22	1.74	0.53
1:1:3344:U:H4'	5:k:315:GLY:HA2	1.91	0.53
40:AM:36:ARG:HG3	40:AM:37:TYR:CD1	2.43	0.53
43:AP:28:TYR:HB3	43:AP:69:VAL:HB	1.90	0.53
46:A:405:A:H2'	46:A:406:C:C6	2.44	0.53
46:A:638:U:H2'	46:A:639:G:O4'	2.08	0.53
46:A:1129:U:H2'	46:A:1130:U:C6	2.44	0.53
46:A:1196:A:N6	46:A:1439:G:O6	2.41	0.53
48:C:128:LYS:HB3	48:C:134:VAL:HG22	1.91	0.53
52:G:25:LEU:HA	63:R:25:LYS:HZ1	1.73	0.53
59:N:99:GLU:O	59:N:111:ASN:ND2	2.41	0.53
75:d:8:THR:HG23	75:d:56:LEU:HB2	1.91	0.53
1:1:1617:A:H2'	1:1:1618:U:C6	2.44	0.52
46:A:148:C:O2	46:A:163:G:C2	2.62	0.52
46:A:518:A:O2'	46:A:519:A:OP1	2.27	0.52
46:A:1145:A:H2'	46:A:1146:C:H6	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1483:U:O2	46:A:1498:G:O6	2.27	0.52
47:B:29:VAL:HG23	47:B:149:MET:HB3	1.90	0.52
63:R:49:GLU:OE1	63:R:81:ARG:NH2	2.41	0.52
1:1:437:G:H22	1:1:620:A:N6	2.06	0.52
1:1:1559:C:O2'	1:1:1560:U:OP1	2.23	0.52
25:7:6:ASP:HB3	25:7:10:GLY:H	1.74	0.52
29:AB:88:ASP:OD1	29:AB:89:GLU:N	2.42	0.52
46:A:188:U:O2	46:A:193:G:O6	2.27	0.52
46:A:1099:G:O2'	46:A:1115:G:O6	2.26	0.52
47:B:75:VAL:HG12	47:B:122:VAL:HB	1.91	0.52
69:X:23:ARG:HD3	69:X:65:LEU:O	2.09	0.52
70:Y:86:PHE:HD1	70:Y:88:PRO:HG3	1.74	0.52
1:1:67:C:OP2	1:1:301:G:N2	2.41	0.52
1:1:2740:U:H2'	1:1:2741:A:H8	1.75	0.52
1:1:2974:C:O2'	5:k:180:GLU:OE2	2.23	0.52
3:4:150:G:OP1	26:8:27:ARG:NH2	2.42	0.52
7:m:178:ASN:HA	7:m:183:TRP:CD2	2.44	0.52
10:p:76:ILE:HG23	10:p:161:ILE:HD13	1.91	0.52
23:5:37:LEU:HB3	23:5:56:ILE:HD13	1.91	0.52
41:AN:3:GLU:OE1	41:AN:5:SER:OG	2.21	0.52
46:A:66:U:C5	53:H:173:PRO:HD3	2.44	0.52
46:A:185:G:H21	46:A:196:A:H62	1.58	0.52
46:A:1265:C:H2'	46:A:1266:G:C8	2.42	0.52
46:A:1398:G:H4'	46:A:1399:U:O5'	2.10	0.52
46:A:1550:C:H2'	46:A:1551:U:C6	2.45	0.52
53:H:22:HIS:CE1	53:H:25:ARG:HH22	2.27	0.52
64:S:74:GLN:O	64:S:78:ARG:HG2	2.09	0.52
5:k:67:MET:HE2	24:6:88:ARG:HB2	1.92	0.52
7:m:83:LEU:HD13	7:m:88:ILE:HD12	1.90	0.52
12:r:66:GLU:OE1	12:r:69:ARG:NH1	2.43	0.52
46:A:68:A:N6	53:H:132:ARG:HG2	2.25	0.52
46:A:446:C:H2'	46:A:447:C:H6	1.74	0.52
46:A:945:U:H5'	60:O:55:ARG:HE	1.75	0.52
46:A:1472:G:N2	46:A:1580:A:OP1	2.42	0.52
46:A:1539:U:O4	62:Q:40:ARG:NH1	2.37	0.52
1:1:422:A:C2	1:1:2341:A:H4'	2.45	0.52
1:1:612:U:H2'	1:1:613:U:C6	2.44	0.52
1:1:660:U:H2'	1:1:661:C:C6	2.44	0.52
8:n:3:GLN:HG2	33:AF:76:LEU:H	1.74	0.52
9:o:143[B]:ARG:HG3	9:o:183:ILE:HD13	1.91	0.52
11:q:28:THR:OG1	11:q:33:GLU:OE2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:97:C:H1'	46:A:424:G:H5'	1.92	0.52
50:E:196:ASN:ND2	50:E:200:PRO:O	2.41	0.52
57:L:81:ASN:ND2	59:N:37:VAL:O	2.42	0.52
61:P:87:LYS:HD2	61:P:116:VAL:HG22	1.91	0.52
64:S:29:GLU:HB2	79:h:38:ARG:HH12	1.74	0.52
1:1:511:C:H5''	6:l:344:LYS:HE2	1.92	0.52
1:1:547:U:H2'	1:1:548:G:H8	1.74	0.52
1:1:1662:G:H2'	1:1:1663:A:C8	2.44	0.52
46:A:1170:U:O2'	46:A:1444:G:N7	2.42	0.52
46:A:1427:C:H2'	46:A:1428:U:C6	2.45	0.52
62:Q:81:ARG:NH1	62:Q:98:ASN:HA	2.25	0.52
1:1:269:G:H5''	16:v:14:LYS:HE2	1.91	0.52
1:1:1494:A:H2'	1:1:1495:U:C6	2.45	0.52
1:1:1966:G:H1	1:1:2049:A:H2	1.55	0.52
1:1:2985:U:H2'	1:1:2986:U:C6	2.45	0.52
3:4:36:G:C5	36:AI:86:ARG:HD3	2.44	0.52
20:z:172:ARG:NH2	46:A:836:U:H5''	2.25	0.52
46:A:418:A:OP1	53:H:96:SER:OG	2.24	0.52
52:G:206:SER:O	52:G:212:LYS:NZ	2.24	0.52
54:I:66:TYR:O	54:I:70:GLN:N	2.43	0.52
69:X:77:PRO:HD3	70:Y:7:ARG:O	2.10	0.52
76:e:20:GLN:HB2	76:e:25:SER:HA	1.90	0.52
79:h:102:GLN:HE22	79:h:139:GLY:HA3	1.73	0.52
1:1:74:G:H1'	14:t:61:PRO:HG3	1.90	0.52
1:1:412:G:OP1	18:x:62:ARG:NH1	2.41	0.52
1:1:454:G:N1	1:1:476:C:C2	2.78	0.52
1:1:870:U:N3	1:1:2950:U:OP1	2.40	0.52
1:1:2418:A:H4'	48:C:53:GLY:HA3	1.92	0.52
46:A:154:A:H2'	46:A:155:A:O4'	2.10	0.52
46:A:159:U:H2'	46:A:160:A:H8	1.74	0.52
46:A:1236:U:O2'	46:A:1237:C:H5''	2.10	0.52
46:A:1276:G:H22	46:A:1309:G:N2	2.08	0.52
52:G:142:ALA:HB1	52:G:217:LEU:HD22	1.91	0.52
72:a:65:LEU:HD23	72:a:71:ILE:HD11	1.90	0.52
1:1:1302:G:O6	1:1:2344:C:O2'	2.23	0.52
1:1:2869:A:H5''	41:AN:49:LYS:HD2	1.92	0.52
3:4:57:C:H4'	3:4:63:G:N7	2.25	0.52
9:o:163:ASP:OD1	9:o:164:ASN:N	2.42	0.52
13:s:43:GLN:NE2	13:s:70:THR:O	2.43	0.52
24:6:63:LYS:O	24:6:70:ARG:NH1	2.43	0.52
30:AC:33:LYS:HE2	30:AC:33:LYS:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:216:A:N3	46:A:216:A:C2'	2.73	0.52
46:A:510:A:H2'	46:A:511:U:C6	2.45	0.52
50:E:76:LYS:HD2	57:L:20:VAL:HG23	1.91	0.52
1:1:480:G:H2'	1:1:480:G:N3	2.25	0.52
3:4:90:U:O2'	3:4:92:A:OP1	2.23	0.52
11:q:113:GLU:OE2	11:q:115:ARG:NE	2.37	0.52
46:A:335:G:O2'	55:J:10:LYS:NZ	2.42	0.52
1:1:406:G:H1'	3:4:16:G:H22	1.75	0.51
3:4:154:C:H2'	3:4:155:G:H8	1.74	0.51
10:p:153:LEU:HD13	10:p:181:VAL:HG11	1.92	0.51
12:r:140:THR:HG21	12:r:148:VAL:HG21	1.92	0.51
20:z:176:ARG:NH2	46:A:838:G:OP2	2.40	0.51
46:A:166:A:H2'	46:A:167:A:C8	2.46	0.51
46:A:1369:G:O5'	67:V:88:ARG:NH2	2.44	0.51
49:D:150:PRO:HB3	68:W:1:MET:HE1	1.93	0.51
75:d:9:LEU:HD23	75:d:53:ILE:HG22	1.92	0.51
1:1:172:C:O2'	1:1:173:C:OP1	2.24	0.51
1:1:1021:A:N6	62:Q:74:ALA:HA	2.24	0.51
1:1:1199:A:H2'	1:1:1200:A:H8	1.75	0.51
1:1:3259:A:H2'	1:1:3260:A:O4'	2.10	0.51
1:1:3287:A:H2'	1:1:3288:A:H8	1.75	0.51
7:m:125:VAL:HG11	7:m:199:ILE:HG21	1.91	0.51
46:A:413:C:O2'	46:A:416:G:O6	2.27	0.51
46:A:564:C:H2'	46:A:565:A:O4'	2.10	0.51
46:A:600:U:H2'	46:A:601:U:C6	2.46	0.51
46:A:1286:U:H5'	49:D:83:LYS:HD2	1.92	0.51
62:Q:105:VAL:HG12	65:T:120:ARG:HH12	1.75	0.51
66:U:100:ILE:O	66:U:104:CYS:N	2.37	0.51
1:1:1115:C:H2'	1:1:1116:A:C8	2.45	0.51
1:1:2183:U:H2'	1:1:2184:G:C8	2.45	0.51
1:1:2992:U:H2'	1:1:3005:A:H61	1.74	0.51
6:l:10:ILE:HD11	6:l:147:LYS:NZ	2.25	0.51
16:v:100:SER:O	16:v:104:GLU:HG3	2.11	0.51
30:AC:11:ASN:OD1	30:AC:14[B]:ARG:NH1	2.42	0.51
36:AI:31:LEU:HD22	36:AI:41:LEU:HD21	1.92	0.51
46:A:189:G:C5	46:A:190:U:H1'	2.46	0.51
46:A:512:G:H1	46:A:541:C:H5	1.57	0.51
46:A:1025:G:H5'	47:B:31:VAL:HG11	1.93	0.51
46:A:1248:G:H2'	46:A:1249:G:O4'	2.10	0.51
46:A:1359:U:O2'	46:A:1360:C:OP2	2.24	0.51
50:E:163:GLN:NE2	50:E:167:ASP:OD2	2.37	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:h:248:TRP:HB3	79:h:259:ILE:HD11	1.92	0.51
3:4:8:C:H2'	3:4:9:A:C8	2.45	0.51
9:o:237:VAL:O	9:o:241:ASN:N	2.38	0.51
46:A:1659:G:H2'	46:A:1660:G:H8	1.74	0.51
46:A:1757:U:H2'	46:A:1758:U:C6	2.45	0.51
53:H:7:TYR:HD2	53:H:10:ASN:HB2	1.75	0.51
54:I:110:ARG:HA	54:I:113:THR:HG23	1.92	0.51
61:P:66:CYS:HB3	61:P:71:ILE:HB	1.92	0.51
66:U:20:GLN:HG2	66:U:24:ARG:HE	1.76	0.51
77:f:50:THR:HG1	77:f:53:LYS:HB2	1.72	0.51
1:1:39:A:H5''	29:AB:35:ALA:HB1	1.91	0.51
1:1:385:A:H2'	1:1:386:A:C8	2.46	0.51
1:1:541:U:O4	1:1:546:C:N4	2.44	0.51
1:1:628:A:H2'	1:1:629:A:H8	1.75	0.51
1:1:647:A:OP2	1:1:2840:U:O2'	2.28	0.51
1:1:830:U:H2'	1:1:831:G:O4'	2.10	0.51
1:1:1966:G:O6	1:1:2049:A:N1	2.44	0.51
1:1:2933:G:H2'	1:1:2934:U:C6	2.45	0.51
5:k:70:ARG:HG2	5:k:70:ARG:HH11	1.76	0.51
11:q:137:SER:HB2	11:q:143:GLU:OE1	2.11	0.51
46:A:1384:U:OP2	46:A:1385:C:N4	2.44	0.51
46:A:1677:G:N2	46:A:1699:G:O4'	2.44	0.51
54:I:109:PRO:HG2	54:I:112:ARG:HD3	1.93	0.51
1:1:732:U:H3'	1:1:733:A:H8	1.76	0.51
1:1:1261:U:H2'	1:1:1262:G:C8	2.46	0.51
1:1:1892:A:H61	1:1:2317:C:N4	2.05	0.51
15:u:34:ASP:OD1	15:u:35:GLN:N	2.40	0.51
31:AD:18:LEU:HB3	31:AD:100:SER:HB2	1.93	0.51
46:A:30:G:H4'	70:Y:131:SER:HB2	1.93	0.51
46:A:530:U:O2'	71:Z:33:ALA:O	2.27	0.51
46:A:538:G:N2	77:f:25:GLU:OE2	2.43	0.51
46:A:1227:A:O2'	46:A:1229:A:OP1	2.19	0.51
46:A:1670:U:H3	46:A:1705:G:H1	1.58	0.51
57:L:88:PRO:O	57:L:89:LEU:HD22	2.11	0.51
62:Q:77:LYS:CE	62:Q:102:PHE:HB3	2.41	0.51
1:1:1242:G:C8	1:1:1260:G:C2'	2.93	0.51
1:1:2244:U:H2'	1:1:2245:C:C6	2.46	0.51
7:m:198:TYR:CE1	7:m:203:HIS:HB3	2.46	0.51
13:s:118:PRO:CD	13:s:119:SER:H	2.23	0.51
14:t:115:ARG:NH2	14:t:147:PHE:O	2.38	0.51
18:x:22:LEU:HD12	18:x:146:ILE:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AP:46:LYS:HE3	43:AP:54:THR:HB	1.93	0.51
46:A:1072:A:H2'	46:A:1073:A:C8	2.46	0.51
55:J:34:ALA:HB2	55:J:56:ARG:HD2	1.93	0.51
66:U:65:ILE:HG21	66:U:114:LEU:HD13	1.92	0.51
1:1:315:C:OP2	37:AJ:27:TYR:OH	2.25	0.51
1:1:1157:G:O2'	33:AF:55:ASN:OD1	2.28	0.51
1:1:1456:A:H2'	1:1:1457:A:C8	2.45	0.51
11:q:93:VAL:HG22	41:AN:6:LEU:HD12	1.93	0.51
19:y:125:ASP:OD2	19:y:126:GLN:N	2.43	0.51
28:AA:84:ARG:HH11	28:AA:84:ARG:HG3	1.74	0.51
46:A:330:U:O2'	55:J:5:ARG:NH2	2.44	0.51
46:A:1481:C:H2'	46:A:1482:C:C6	2.45	0.51
46:A:1489:G:N2	46:A:1492:A:OP2	2.32	0.51
1:1:582:G:H2'	1:1:583:A:H8	1.76	0.51
1:1:2251:G:O2'	1:1:2289:G:O6	2.24	0.51
5:k:215:ILE:HD12	5:k:338:LEU:HB3	1.93	0.51
22:2:49:GLN:HA	22:2:52:MET:HE3	1.93	0.51
22:2:84:TYR:HB2	30:AC:24:PRO:HD3	1.93	0.51
26:8:73:MET:HE3	26:8:73:MET:HA	1.92	0.51
34:AG:42:LYS:HA	34:AG:45:LEU:HG	1.93	0.51
46:A:549:G:H2'	46:A:550:G:H8	1.74	0.51
74:c:33:MET:HB3	74:c:79:PHE:HB2	1.93	0.51
1:1:624:U:H2'	1:1:625:C:C6	2.46	0.51
1:1:1246:G:H2'	1:1:1247:A:C8	2.46	0.51
19:y:147:ARG:HB3	19:y:150:VAL:HG23	1.92	0.51
46:A:215:A:N6	46:A:830:G:C4	2.79	0.51
46:A:589:A:H2'	46:A:590:A:C8	2.46	0.51
46:A:903:U:H2'	46:A:904:A:C8	2.47	0.51
46:A:1216:U:P	78:g:136:LYS:HZ1	2.34	0.51
46:A:1551:U:H2'	46:A:1552:C:H6	1.76	0.51
51:F:112:HIS:NE2	51:F:238:SER:O	2.44	0.51
59:N:50:LYS:HG3	78:g:172:ILE:HD11	1.94	0.51
63:R:98:GLU:HG3	63:R:101:LYS:HE3	1.93	0.51
65:T:18:LEU:HD12	65:T:35:ILE:HG21	1.93	0.51
1:1:79:G:H2'	1:1:80:C:H6	1.76	0.50
1:1:638:U:OP1	29:AB:21:ARG:NH1	2.39	0.50
1:1:2090:U:H4'	1:1:2091:A:O5'	2.10	0.50
8:n:39:LEU:HD11	8:n:53:TYR:HB2	1.92	0.50
46:A:854:A:H61	46:A:943:U:H5	1.58	0.50
46:A:1336:G:H2'	46:A:1337:C:H6	1.76	0.50
46:A:1469:A:OP2	46:A:1508:G:N2	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1549:G:OP1	66:U:89:ARG:NH2	2.44	0.50
1:1:19:A:OP2	36:AI:90:ARG:NH2	2.28	0.50
1:1:1030:U:H2'	1:1:1031:A:C8	2.46	0.50
1:1:2222:A:H5''	4:j:243:THR:HB	1.92	0.50
1:1:2485:U:H2'	1:1:2486:U:C6	2.46	0.50
12:r:176:LEU:HB3	12:r:180:GLU:HG3	1.93	0.50
46:A:97:C:O2	46:A:423:A:O2'	2.29	0.50
46:A:1142:A:H2'	46:A:1145:A:N7	2.27	0.50
78:g:174:MET:HB3	78:g:181:GLN:HB3	1.92	0.50
1:1:93:G:H2'	1:1:94:A:C8	2.46	0.50
1:1:792:U:H2'	1:1:793:U:C6	2.45	0.50
1:1:941:C:H2'	1:1:942:U:C6	2.46	0.50
4:j:20:THR:HA	4:j:23:ARG:HG3	1.92	0.50
4:j:195:SER:O	4:j:198:LYS:NZ	2.39	0.50
17:w:86:ARG:HG3	17:w:100:LEU:HD11	1.93	0.50
34:AG:16:TYR:OH	34:AG:89:LEU:O	2.14	0.50
46:A:1477:U:H4'	46:A:1478:A:H5'	1.93	0.50
51:F:123:LEU:HD12	51:F:159:THR:HG22	1.93	0.50
57:L:55:VAL:HA	57:L:69:THR:HG23	1.92	0.50
67:V:32:GLN:HG2	67:V:110:GLY:HA3	1.92	0.50
70:Y:107:PHE:CD2	70:Y:114:LYS:HB3	2.47	0.50
79:h:86:TRP:CD1	79:h:110:ASP:HB3	2.46	0.50
1:1:3196:U:H2'	1:1:3197:G:H8	1.75	0.50
39:AL:31:VAL:HG12	39:AL:33:ALA:H	1.76	0.50
54:I:67:ARG:HD2	54:I:127:PHE:CE1	2.46	0.50
69:X:81:VAL:HG21	69:X:125:ILE:HB	1.94	0.50
70:Y:56:LYS:HG2	70:Y:72:VAL:HG12	1.92	0.50
71:Z:83:LYS:NZ	71:Z:96:LEU:O	2.35	0.50
1:1:429:U:H2'	1:1:430:G:C8	2.43	0.50
1:1:432:G:OP1	34:AG:57:LYS:HB2	2.11	0.50
1:1:538:G:H2'	1:1:539:G:C8	2.47	0.50
1:1:1241:A:N6	1:1:1268:C:O2'	2.38	0.50
1:1:2646:A:H5''	13:s:105:GLY:HA3	1.93	0.50
2:3:19:C:H2'	2:3:20:A:H8	1.76	0.50
19:y:78:GLU:H	19:y:78:GLU:CD	2.20	0.50
24:6:23:MET:HE1	24:6:78:VAL:HG22	1.93	0.50
46:A:217:A:N1	46:A:828:U:O2'	2.41	0.50
46:A:298:A:H2'	46:A:299:A:C8	2.47	0.50
46:A:331:A:N6	55:J:27:PHE:HB2	2.27	0.50
57:L:1:MET:HE1	57:L:40:LEU:HG	1.93	0.50
62:Q:114:HIS:ND1	62:Q:118:GLU:OE2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:307:A:H2'	1:1:308:A:C8	2.46	0.50
1:1:2184:G:O2'	1:1:2187:U:O4	2.23	0.50
1:1:2717:G:N2	1:1:2720:A:OP2	2.40	0.50
1:1:2719:A:H2'	1:1:2720:A:C8	2.47	0.50
1:1:2876:U:H2'	1:1:2877:U:C6	2.47	0.50
15:u:19:VAL:HG11	15:u:55:ILE:HD12	1.93	0.50
16:v:68:ARG:NH1	16:v:124:ASP:O	2.32	0.50
46:A:1400:U:H5''	64:S:3:ARG:HE	1.77	0.50
57:L:52:LYS:HG3	57:L:54:TYR:HD2	1.77	0.50
64:S:96:THR:HG23	64:S:98:GLY:H	1.76	0.50
1:1:1493:C:H2'	1:1:1494:A:C8	2.47	0.50
1:1:1689:C:O2'	1:1:1768:U:O2'	2.25	0.50
3:4:8:C:H2'	3:4:9:A:H8	1.77	0.50
4:j:60:LYS:HB3	4:j:73:GLU:OE2	2.12	0.50
46:A:5:U:H2'	46:A:6:G:C8	2.47	0.50
46:A:985:C:H5	46:A:988:A:H5''	1.76	0.50
46:A:1308:C:H2'	46:A:1309:G:O4'	2.12	0.50
46:A:1484:U:HO2'	46:A:1485:G:P	2.35	0.50
47:B:88:LYS:HB3	47:B:92:HIS:CE1	2.46	0.50
48:C:123:ALA:HB2	48:C:165:ARG:HG3	1.93	0.50
56:K:48:GLN:O	56:K:52:ILE:HG12	2.12	0.50
66:U:117:SER:HB2	66:U:123:ARG:HB2	1.92	0.50
67:V:83:MET:HE3	76:e:52:PHE:CD1	2.47	0.50
70:Y:88:PRO:O	70:Y:89:ASN:HB3	2.12	0.50
79:h:104:PHE:CD2	79:h:139:GLY:HA2	2.47	0.50
1:1:729:C:H3'	1:1:730:A:H5''	1.93	0.50
1:1:730:A:H4'	1:1:730:A:OP1	2.11	0.50
1:1:3236:G:O6	8:n:128:LYS:NZ	2.43	0.50
1:1:3309:A:N3	1:1:3309:A:H2'	2.26	0.50
5:k:122:TRP:CE2	5:k:127:LYS:HE3	2.47	0.50
13:s:32:ARG:NH1	13:s:120:ILE:O	2.45	0.50
46:A:511:U:O4	56:K:171:ARG:NH2	2.45	0.50
65:T:89:GLN:HA	65:T:97:ASP:HA	1.92	0.50
70:Y:46:SER:OG	70:Y:47:SER:N	2.45	0.50
71:Z:56:SER:HB3	71:Z:74:LEU:HB2	1.93	0.50
76:e:47:ALA:HB1	76:e:52:PHE:HB2	1.93	0.50
79:h:102:GLN:NE2	79:h:103:ARG:O	2.45	0.50
1:1:1400:G:N2	1:1:1403:A:OP2	2.34	0.50
1:1:1530:A:H2'	1:1:1531:A:C8	2.46	0.50
20:z:162:ARG:NH2	46:A:834:C:OP1	2.36	0.50
46:A:261:C:O2'	46:A:262:G:H5'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:378:U:H4'	56:K:2:PRO:HD2	1.94	0.50
46:A:382:G:H2'	46:A:383:A:C8	2.47	0.50
46:A:1063:C:H2'	46:A:1064:U:H6	1.77	0.50
58:M:66:ILE:HG13	58:M:140:LEU:HD21	1.94	0.50
1:1:65:A:N6	1:1:75:G:H1'	2.27	0.49
1:1:85:G:O2'	1:1:97:G:O6	2.24	0.49
1:1:1060:A:H4'	1:1:1061:A:O5'	2.11	0.49
1:1:2158:A:H2'	1:1:2159:C:C6	2.47	0.49
1:1:2587:G:H2'	1:1:2588:C:C6	2.47	0.49
2:3:91:G:H2'	2:3:92:A:C8	2.47	0.49
4:j:247:ARG:HB3	46:A:997:U:H4'	1.94	0.49
21:0:8:GLN:HE21	21:0:10:ILE:HD11	1.77	0.49
46:A:66:U:O2	53:H:160:ARG:NE	2.42	0.49
46:A:551:G:H3'	46:A:552:C:H2'	1.94	0.49
46:A:1022:C:O2	69:X:16:ASN:ND2	2.45	0.49
50:E:219:ILE:HD11	50:E:222:PRO:HG3	1.94	0.49
76:e:33:LYS:HG2	76:e:34:TYR:CD2	2.47	0.49
79:h:22:SER:OG	79:h:72:VAL:N	2.44	0.49
1:1:163:A:N1	1:1:258:U:N3	2.60	0.49
1:1:259:C:H2'	1:1:260:C:H6	1.76	0.49
1:1:539:G:H2'	1:1:540:C:C6	2.47	0.49
1:1:565:A:H2'	1:1:566:C:O4'	2.12	0.49
1:1:2384:C:H2'	1:1:2385:C:H6	1.77	0.49
1:1:3193:C:H4'	1:1:3194:G:O5'	2.12	0.49
1:1:3261:A:H2'	1:1:3262:U:H6	1.77	0.49
46:A:78:A:H2	53:H:174:LYS:HG3	1.78	0.49
46:A:123:G:OP1	51:F:77:ARG:NH2	2.42	0.49
46:A:1719:A:H2'	46:A:1720:C:C6	2.47	0.49
50:E:47:LEU:N	50:E:84:GLY:O	2.45	0.49
66:U:11:ALA:HA	66:U:63:ARG:HH12	1.77	0.49
1:1:117:U:O2	1:1:120:A:H5''	2.11	0.49
1:1:252:U:H5'	1:1:253:A:C8	2.46	0.49
1:1:1059:G:N7	1:1:1093:G:O2'	2.36	0.49
1:1:1197:C:N4	1:1:2829:C:OP1	2.42	0.49
1:1:1762:G:O2'	1:1:1763:C:OP1	2.27	0.49
1:1:1794:A:H2'	1:1:1795:A:C8	2.47	0.49
1:1:2081:U:H2'	1:1:2082:A:C8	2.47	0.49
14:t:2:ALA:HB3	29:AB:41:HIS:CE1	2.47	0.49
15:u:65:LEU:HD12	15:u:77:LYS:HD2	1.94	0.49
24:6:77:ILE:HD12	24:6:103:VAL:HG11	1.94	0.49
43:AP:8:ARG:HG2	43:AP:10:THR:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:167:A:OP2	46:A:167:A:H8	1.95	0.49
46:A:184:C:H2'	46:A:185:G:O4'	2.12	0.49
46:A:820:U:O2'	46:A:821:U:OP1	2.25	0.49
56:K:126:ARG:HD2	77:f:33:ARG:NH1	2.26	0.49
79:h:253:THR:OG1	79:h:256:GLY:O	2.19	0.49
1:l:683:G:OP1	14:t:39:ARG:NH2	2.46	0.49
1:l:844:A:C5	1:l:845:C:H1'	2.47	0.49
6:l:36:VAL:HG21	6:l:245:LEU:HD21	1.94	0.49
46:A:265:U:H2'	46:A:266:C:C6	2.46	0.49
46:A:1719:A:H2'	46:A:1720:C:H6	1.77	0.49
47:B:50:ILE:HG12	64:S:109:LEU:HD21	1.94	0.49
49:D:45:ILE:HG21	49:D:51:ILE:HD11	1.93	0.49
1:l:431:A:H2'	1:l:432:G:C8	2.47	0.49
1:l:695:G:H2'	1:l:696:U:C6	2.47	0.49
1:l:1576:A:H3'	1:l:1577:C:C6	2.47	0.49
4:j:180:LEU:HD21	44:AQ:22:LEU:HB3	1.93	0.49
42:AO:11:ARG:NH2	46:A:1762:U:OP1	2.45	0.49
45:i:123:GLU:HA	45:i:126:GLU:HB2	1.95	0.49
46:A:1048:U:H2'	46:A:1049:G:C8	2.46	0.49
46:A:1157:G:H2'	46:A:1158:C:C6	2.47	0.49
46:A:1782:U:H3'	73:b:5:ARG:HH21	1.77	0.49
57:L:56:LYS:HZ2	57:L:69:THR:HG22	1.77	0.49
64:S:19:ARG:HD2	64:S:20:PHE:CE1	2.47	0.49
1:l:1779:U:H2'	1:l:1780:A:C8	2.48	0.49
1:l:2498:A:H2'	1:l:2499:U:C6	2.47	0.49
1:l:2852:U:H1'	5:k:250:ALA:HB3	1.95	0.49
46:A:50:C:H2'	46:A:422:C:H41	1.77	0.49
46:A:209:U:OP1	58:M:20:PHE:HB2	2.12	0.49
46:A:309:U:OP2	70:Y:20:ARG:HD3	2.13	0.49
46:A:741:A:H3'	46:A:742:A:H8	1.77	0.49
48:C:34:ALA:O	48:C:41:ARG:NH1	2.46	0.49
51:F:11:ARG:HA	51:F:28:ALA:HB2	1.93	0.49
52:G:143:ARG:HG3	52:G:167:ARG:HD2	1.95	0.49
59:N:58:GLN:HB3	59:N:87:PRO:HD2	1.95	0.49
64:S:99:GLN:N	64:S:99:GLN:OE1	2.46	0.49
1:l:437:G:H1	1:l:620:A:N6	2.11	0.49
1:l:896:G:H1'	1:l:1585:A:N6	2.26	0.49
1:l:1050:A:H5''	1:l:2609:A:H61	1.78	0.49
1:l:1077:U:H5'	1:l:1078:U:C5	2.47	0.49
1:l:2634:G:H2'	1:l:2635:A:C8	2.48	0.49
1:l:2650:A:H8	45:i:47:ASP:HB3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:126:A:O2'	3:4:129:C:N4	2.45	0.49
13:s:109:HIS:HE1	13:s:122:ILE:HA	1.75	0.49
46:A:875:C:H2'	46:A:876:A:H8	1.77	0.49
46:A:1265:C:O2'	67:V:69:THR:HG22	2.12	0.49
65:T:87:ASN:N	65:T:99:HIS:HD2	2.11	0.49
69:X:15:ASN:ND2	69:X:72:CYS:O	2.45	0.49
79:h:216:VAL:HA	79:h:232:GLU:HA	1.94	0.49
79:h:265:ARG:HD3	79:h:265:ARG:H	1.78	0.49
1:1:1079:G:H2'	1:1:1080:A:C8	2.48	0.49
1:1:2201:A:H2'	1:1:2202:A:C8	2.46	0.49
1:1:2987:G:H2'	1:1:2988:A:H8	1.77	0.49
13:s:82:ARG:HH22	13:s:114:ILE:HG23	1.78	0.49
46:A:415:A:H5'	46:A:416:G:C5	2.47	0.49
46:A:1474:G:H3'	46:A:1502:A:H61	1.76	0.49
46:A:1483:U:HO2'	46:A:1506:U:HO2'	1.56	0.49
46:A:1635:A:H2'	46:A:1636:C:C6	2.47	0.49
53:H:58:LYS:HG2	53:H:105:ASP:O	2.13	0.49
65:T:87:ASN:H	65:T:99:HIS:HD2	1.61	0.49
74:c:18:GLN:NE2	74:c:22:LYS:O	2.46	0.49
1:1:541:U:N3	1:1:543:C:O2'	2.44	0.49
1:1:2183:U:O2'	1:1:2184:G:OP1	2.28	0.49
1:1:2239:G:H21	1:1:2240:A:N6	2.10	0.49
1:1:3135:A:H2'	1:1:3136:C:C6	2.48	0.49
17:w:62:ALA:HA	17:w:71:PRO:HD2	1.94	0.49
46:A:290:U:H2'	46:A:291:U:C6	2.48	0.49
46:A:529:C:O2'	46:A:530:U:OP1	2.30	0.49
49:D:137:GLY:N	49:D:148:SER:O	2.26	0.49
63:R:15:ALA:HB2	63:R:71:GLY:HA3	1.95	0.49
75:d:43:ASN:ND2	75:d:63:ALA:HB1	2.28	0.49
1:1:1021:A:N3	1:1:1021:A:C2'	2.75	0.49
1:1:1022:A:C2	62:Q:72:ARG:CD	2.96	0.49
1:1:1080:A:H2'	1:1:1081:A:C8	2.47	0.49
1:1:1612:U:H2'	1:1:1613:G:H8	1.78	0.49
1:1:1944:G:H2'	1:1:1945:A:H8	1.77	0.49
1:1:2583:U:H2'	1:1:2584:U:C6	2.48	0.49
13:s:118:PRO:CD	13:s:119:SER:N	2.75	0.49
46:A:479:A:H2'	46:A:480:U:C6	2.47	0.49
46:A:554:A:H4'	77:f:56:MET:HG2	1.92	0.49
46:A:1149:G:H2'	46:A:1150:G:C8	2.48	0.49
46:A:1541:U:H3'	46:A:1542:A:C8	2.48	0.49
46:A:1551:U:H2'	46:A:1552:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1727:A:H2'	46:A:1728:U:C6	2.48	0.49
47:B:62:ARG:HD2	68:W:36:ILE:HG22	1.93	0.49
1:1:1329:C:OP1	19:y:2:GLY:N	2.46	0.48
1:1:1965:U:H2'	1:1:1966:G:C4	2.48	0.48
7:m:148:ILE:O	7:m:151:GLN:HG2	2.13	0.48
29:AB:24:LYS:O	29:AB:26:ARG:HG2	2.13	0.48
46:A:502:U:O2'	46:A:503:A:OP1	2.27	0.48
46:A:876:A:H2'	46:A:877:G:H8	1.77	0.48
46:A:1021:A:H2'	46:A:1022:C:H6	1.77	0.48
46:A:1187:A:H1'	46:A:1192:C:H42	1.76	0.48
46:A:1257:U:O2'	46:A:1260:A:OP2	2.24	0.48
46:A:1315:G:C2	46:A:1316:A:H1'	2.47	0.48
49:D:96:VAL:HG22	49:D:110:ILE:HG12	1.93	0.48
54:I:8:GLU:OE1	54:I:9:ASN:ND2	2.38	0.48
57:L:70:ASP:OD1	57:L:71:GLU:N	2.45	0.48
75:d:8:THR:O	75:d:56:LEU:N	2.31	0.48
79:h:218:ILE:HG23	79:h:230:THR:HG22	1.94	0.48
1:1:204:C:H2'	1:1:205:G:O4'	2.13	0.48
1:1:444:U:H2'	1:1:445:A:C8	2.48	0.48
1:1:2485:U:H2'	1:1:2486:U:H6	1.78	0.48
1:1:2492:U:H5'	10:p:69:ARG:HG3	1.94	0.48
1:1:2649:G:H2'	1:1:2649:G:N3	2.28	0.48
3:4:154:C:H2'	3:4:155:G:C8	2.47	0.48
7:m:40:HIS:CE1	22:2:69:LYS:HA	2.48	0.48
11:q:86:TYR:CE2	11:q:151:LEU:HB2	2.48	0.48
25:7:6:ASP:HB3	25:7:10:GLY:N	2.28	0.48
33:AF:112:LYS:HG2	33:AF:116:LEU:HD13	1.95	0.48
39:AL:24:ILE:HB	39:AL:44:LYS:HB2	1.94	0.48
46:A:1396:A:H2'	46:A:1397:A:C8	2.48	0.48
46:A:1523:G:O2'	46:A:1524:C:OP1	2.31	0.48
46:A:1783:C:O2'	73:b:95:ARG:NH2	2.46	0.48
57:L:18:GLU:N	57:L:89:LEU:HD23	2.27	0.48
62:Q:68:GLU:N	62:Q:69:PRO:HD3	2.28	0.48
63:R:72:GLY:H	63:R:75:SER:HB3	1.78	0.48
70:Y:59:ILE:O	70:Y:69:ARG:N	2.45	0.48
1:1:445:A:N6	1:1:485:A:N6	2.60	0.48
1:1:740:A:OP1	19:y:66:ARG:NH1	2.44	0.48
1:1:2773:A:O2'	1:1:2774:A:H2'	2.13	0.48
1:1:3218:U:H2'	1:1:3219:G:C8	2.48	0.48
5:k:92:TYR:HB3	5:k:99:LEU:HD22	1.95	0.48
39:AL:29:ALA:HB1	39:AL:37:LYS:HE3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1425:C:C2	46:A:1426:C:C5	3.02	0.48
54:I:37:LEU:HB2	54:I:66:TYR:HE1	1.78	0.48
66:U:114:LEU:HD21	66:U:122:ARG:HD3	1.96	0.48
72:a:61:SER:H	72:a:64:VAL:HB	1.78	0.48
1:1:538:G:O2'	1:1:539:G:OP1	2.25	0.48
45:i:107:TRP:HB3	50:E:151:GLN:NE2	2.29	0.48
46:A:918:A:OP1	73:b:70:LYS:NZ	2.35	0.48
46:A:1463:G:H2'	46:A:1464:G:C8	2.47	0.48
47:B:148:ASP:OD2	47:B:149:MET:N	2.35	0.48
59:N:63:CYS:HB3	59:N:97:LEU:HD11	1.96	0.48
64:S:92:ASP:OD1	64:S:93:LEU:N	2.47	0.48
79:h:126:ALA:HB1	79:h:152:VAL:HG23	1.96	0.48
1:1:90:G:OP2	1:1:92:C:N4	2.42	0.48
1:1:92:C:C2	29:AB:55:LYS:HE2	2.48	0.48
1:1:629:A:H2'	1:1:630:G:C8	2.48	0.48
1:1:990:G:N2	1:1:991:U:O4	2.35	0.48
1:1:2936:G:N2	1:1:2939:A:OP2	2.36	0.48
5:k:260:VAL:HG11	5:k:266:ARG:NH1	2.29	0.48
46:A:148:C:C2	46:A:163:G:N2	2.82	0.48
46:A:1218:G:H1	46:A:1237:C:H5	1.61	0.48
49:D:104:GLY:HA2	49:D:134:ILE:HG12	1.95	0.48
50:E:24:GLU:O	50:E:27:THR:OG1	2.31	0.48
52:G:161:ASP:HB2	75:d:43:ASN:O	2.13	0.48
54:I:30:LEU:HD12	54:I:30:LEU:O	2.13	0.48
59:N:38:HIS:CD2	59:N:127:GLY:HA3	2.48	0.48
59:N:70:SER:O	59:N:74:LEU:HD23	2.13	0.48
62:Q:87:PRO:HA	62:Q:90:ILE:HG13	1.96	0.48
64:S:99:GLN:NE2	64:S:120:GLN:OE1	2.47	0.48
79:h:237:VAL:HG22	79:h:253:THR:HG22	1.94	0.48
1:1:638:U:H2'	1:1:639:C:C6	2.49	0.48
1:1:1911:A:H2'	1:1:1912:U:C6	2.49	0.48
1:1:2134:U:OP2	4:j:241:ARG:NH2	2.46	0.48
1:1:2385:C:H2'	1:1:2386:U:H6	1.78	0.48
1:1:2942:C:H4'	1:1:2943:A:C6	2.49	0.48
7:m:94:ASN:HB2	7:m:97:ALA:H	1.78	0.48
10:p:261:SER:HB3	48:C:225:LEU:HD11	1.96	0.48
12:r:86:HIS:HB3	12:r:139:ARG:HG3	1.95	0.48
16:v:183:THR:HG22	16:v:187:ARG:HB2	1.95	0.48
46:A:501:G:H2'	46:A:502:U:C6	2.48	0.48
46:A:563:C:O2'	46:A:575:G:N2	2.38	0.48
46:A:1610:C:H2'	46:A:1611:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:B:198:MET:SD	47:B:199:PRO:HD2	2.54	0.48
49:D:53:LEU:HA	68:W:12:TYR:HE1	1.78	0.48
50:E:151:GLN:HB3	50:E:153:TYR:HE1	1.78	0.48
51:F:94:ALA:HB3	71:Z:17:LEU:HD23	1.96	0.48
56:K:36:LEU:O	77:f:36:MET:HG2	2.13	0.48
56:K:63:ASP:OD1	56:K:64:GLU:N	2.47	0.48
62:Q:25:LEU:HA	62:Q:28:MET:HE2	1.96	0.48
1:1:130:U:H2'	1:1:131:C:C6	2.48	0.48
1:1:583:A:H2'	1:1:584:C:C6	2.48	0.48
1:1:1476:G:O2'	1:1:1867:U:O4	2.30	0.48
1:1:2411:U:H1'	16:v:125:SER:HB3	1.94	0.48
1:1:2740:U:H2'	1:1:2741:A:C8	2.48	0.48
3:4:63:G:H22	3:4:97:A:H2	1.59	0.48
11:q:110:ASP:HB3	11:q:128:ILE:HD12	1.95	0.48
22:2:119:ALA:O	22:2:123:GLY:N	2.46	0.48
23:5:19:VAL:HG23	23:5:20:ALA:N	2.24	0.48
46:A:639:G:H21	54:I:174:GLY:HA3	1.77	0.48
46:A:810:U:H2'	46:A:811:U:O4'	2.13	0.48
46:A:1036:U:O2	46:A:1052:G:N2	2.41	0.48
46:A:1489:G:C2	46:A:1493:G:C6	3.02	0.48
52:G:62:ILE:HG12	52:G:89:ILE:HG21	1.96	0.48
52:G:102:ARG:HG3	52:G:103:ASN:OD1	2.14	0.48
57:L:47:GLN:HA	57:L:50:THR:HG22	1.96	0.48
60:O:54:LEU:HB3	60:O:60:VAL:HB	1.96	0.48
1:1:214:G:OP1	27:9:12:ARG:NH1	2.41	0.48
1:1:783:G:H2'	1:1:784:C:C6	2.48	0.48
1:1:2978:A:H2'	1:1:2979:U:O4'	2.14	0.48
35:AH:54:ILE:HD11	35:AH:78:GLY:HA2	1.96	0.48
46:A:82:U:H2'	46:A:83:G:O4'	2.13	0.48
46:A:382:G:H2'	46:A:383:A:H8	1.78	0.48
46:A:953:U:H2'	46:A:954:C:O4'	2.14	0.48
46:A:1495:U:H2'	46:A:1496:C:C6	2.49	0.48
46:A:1537:A:H2'	46:A:1538:U:C6	2.49	0.48
46:A:1543:A:OP1	62:Q:115:TYR:OH	2.24	0.48
52:G:53:VAL:HA	52:G:134:VAL:HG11	1.96	0.48
59:N:80:ASN:HB3	59:N:85:LYS:HZ2	1.79	0.48
64:S:75:GLU:O	64:S:79:GLU:HG3	2.14	0.48
1:1:169:G:N1	1:1:249:G:H1'	2.29	0.48
1:1:694:C:H2'	1:1:695:G:C8	2.48	0.48
1:1:2634:G:H2'	1:1:2635:A:H8	1.78	0.48
1:1:2853:C:H2'	1:1:2854:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:r:49:CYS:HB3	12:r:168:SER:HB3	1.96	0.48
14:t:158:LEU:HB3	29:AB:98:ALA:HB1	1.94	0.48
23:5:56:ILE:HG23	23:5:66:VAL:HG22	1.95	0.48
46:A:871:U:C2	46:A:872:A:C8	3.02	0.48
46:A:1158:C:H2'	46:A:1159:C:C6	2.49	0.48
46:A:1423:U:H2'	46:A:1424:G:H8	1.79	0.48
48:C:173:GLN:O	48:C:177:SER:OG	2.28	0.48
51:F:100:ARG:NH2	51:F:121:TYR:O	2.46	0.48
54:I:135:ARG:HB3	69:X:51:GLU:OE2	2.14	0.48
76:e:30:LEU:HA	76:e:39:CYS:HA	1.95	0.48
79:h:245:ASN:OD1	79:h:246:ARG:N	2.47	0.48
79:h:282:LYS:HD3	79:h:283:ASP:O	2.14	0.48
1:1:619:A:H2'	1:1:620:A:C8	2.49	0.48
1:1:1010:U:H2'	1:1:1011:C:O4'	2.14	0.48
1:1:1022:A:C2	62:Q:72:ARG:HD3	2.48	0.48
1:1:1273:C:O2'	1:1:1274:A:H2'	2.14	0.48
1:1:2186:A:O2'	1:1:2187:U:H5'	2.14	0.48
11:q:147:SER:HB2	11:q:187:ILE:HD11	1.96	0.48
18:x:41:LEU:HD21	18:x:99:GLN:HG3	1.96	0.48
43:AP:7:THR:OG1	43:AP:22:GLN:OE1	2.32	0.48
46:A:391:C:H2'	46:A:392:C:C6	2.49	0.48
46:A:1067:C:HO2'	68:W:58:TYR:HE1	1.62	0.48
46:A:1475:U:OP1	50:E:10:LYS:NZ	2.34	0.48
46:A:1486:G:OP2	66:U:73:VAL:HG12	2.14	0.48
46:A:1656:U:H2'	46:A:1657:G:O4'	2.14	0.48
49:D:160:VAL:HG11	49:D:205:THR:HA	1.96	0.48
49:D:234:PRO:HA	49:D:237:VAL:HG22	1.95	0.48
61:P:119:IAS:N	61:P:119:IAS:OD1	2.47	0.48
69:X:6:VAL:HG22	69:X:34:ILE:HD11	1.96	0.48
1:1:218:A:O2'	1:1:219:G:N2	2.35	0.47
1:1:429:U:H5''	34:AG:87:LYS:HE3	1.95	0.47
1:1:619:A:O2'	34:AG:60:ARG:NH2	2.39	0.47
1:1:1258:G:H1'	1:1:1274:A:N6	2.28	0.47
1:1:2603:U:OP1	1:1:2729:U:O2'	2.29	0.47
2:3:45:A:H2'	2:3:46:A:C8	2.49	0.47
3:4:71:A:N1	3:4:82:U:O2'	2.40	0.47
6:l:284:ASN:HB3	6:l:290:LEU:HD11	1.95	0.47
8:n:170:ARG:HB3	8:n:172:HIS:CE1	2.49	0.47
12:r:36:LEU:HD11	12:r:69:ARG:HD2	1.97	0.47
13:s:38:GLU:HB3	13:s:45:PRO:HD3	1.95	0.47
44:AQ:38:ASP:HA	44:AQ:45:ARG:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:844:A:C5	60:O:73:ARG:HD3	2.48	0.47
46:A:845:U:O4'	54:I:110:ARG:HG3	2.13	0.47
46:A:1021:A:H2'	46:A:1022:C:C6	2.49	0.47
46:A:1331:A:OP2	46:A:1333:A:N6	2.45	0.47
46:A:1674:U:H2'	46:A:1675:U:C5	2.48	0.47
59:N:36:LEU:C	59:N:39:ASP:H	2.22	0.47
75:d:19:THR:HG21	75:d:27:GLN:HE21	1.79	0.47
1:1:1058:A:O2'	22:2:108:ARG:NH2	2.43	0.47
1:1:2855:U:H2'	1:1:2856:C:C6	2.48	0.47
1:1:3005:A:H2'	1:1:3006:C:H6	1.79	0.47
7:m:50:ARG:NH2	7:m:72:ASP:OD2	2.47	0.47
29:AB:76:ASP:OD2	29:AB:76:ASP:N	2.44	0.47
46:A:1519:U:H3'	72:a:77:ARG:NH2	2.29	0.47
46:A:1546:G:C5	65:T:134:ARG:HB3	2.49	0.47
46:A:1671:G:H2'	46:A:1672:G:O4'	2.15	0.47
55:J:57:ALA:HB2	55:J:183:GLY:HA2	1.96	0.47
56:K:113:VAL:HG13	56:K:118:LEU:HB2	1.96	0.47
62:Q:45:PHE:HA	62:Q:49:LEU:HD21	1.97	0.47
63:R:135:ALA:O	63:R:136:ARG:HD2	2.14	0.47
64:S:21:TYR:CD1	64:S:58:MET:HE1	2.49	0.47
67:V:22:ARG:NE	67:V:91:ASP:OD2	2.47	0.47
79:h:59:LYS:HD3	79:h:59:LYS:HA	1.68	0.47
1:1:1549:U:H4'	1:1:1550:U:H5'	1.96	0.47
1:1:2814:U:O2	1:1:2814:U:H2'	2.13	0.47
1:1:3297:U:H2'	1:1:3298:G:O4'	2.14	0.47
1:1:3318:G:H5''	1:1:3319:U:H4'	1.95	0.47
2:3:4:U:H2'	2:3:5:G:H8	1.79	0.47
2:3:19:C:H2'	2:3:20:A:C8	2.48	0.47
46:A:446:C:H2'	46:A:447:C:C6	2.49	0.47
46:A:590:A:OP1	56:K:39:LYS:HG3	2.14	0.47
46:A:761:G:H2'	46:A:762:C:C6	2.50	0.47
46:A:1029:U:H2'	46:A:1030:C:C6	2.49	0.47
46:A:1140:G:H2'	46:A:1141:C:C6	2.48	0.47
46:A:1383:U:O2'	46:A:1386:A:N6	2.46	0.47
52:G:58:LEU:HD22	52:G:168:VAL:HG23	1.96	0.47
52:G:196:GLU:HA	52:G:199:ILE:HG22	1.96	0.47
53:H:58:LYS:N	53:H:105:ASP:O	2.48	0.47
55:J:165:GLN:HE22	55:J:195:LEU:HD11	1.78	0.47
63:R:63:ASP:OD1	63:R:63:ASP:N	2.46	0.47
65:T:100:VAL:HG21	65:T:105:LEU:HA	1.96	0.47
1:1:1965:U:H2'	1:1:1966:G:C5	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2126:U:H2'	1:1:2127:A:C8	2.50	0.47
1:1:2322:U:H2'	1:1:2323:A:H8	1.77	0.47
1:1:2784:C:H2'	1:1:2785:A:C8	2.50	0.47
3:4:58:G:O6	38:AK:63:ARG:NH1	2.47	0.47
9:o:185:GLU:HG2	9:o:196:VAL:HG21	1.95	0.47
10:p:76:ILE:HD11	16:v:18:VAL:HG13	1.96	0.47
22:2:39:ILE:HG12	22:2:63:ILE:HD13	1.97	0.47
23:5:15:PHE:HB2	23:5:66:VAL:HB	1.96	0.47
46:A:5:U:O2'	46:A:551:G:H4'	2.14	0.47
46:A:559:G:H2'	46:A:560:G:H8	1.78	0.47
46:A:1648:U:H2'	46:A:1649:G:C8	2.49	0.47
50:E:178:MET:HE3	50:E:183:LEU:HD12	1.96	0.47
53:H:5:ILE:HA	53:H:111:LEU:HB2	1.96	0.47
59:N:29:LYS:HE2	59:N:100:TRP:CE3	2.49	0.47
64:S:28:PHE:CE2	64:S:32:LYS:HD3	2.49	0.47
1:1:169:G:C6	1:1:249:G:H1'	2.50	0.47
1:1:1653:C:O2'	1:1:1793:A:OP2	2.31	0.47
1:1:3069:U:OP1	5:k:325:LYS:NZ	2.34	0.47
1:1:3110:U:OP2	5:k:30:LYS:HG3	2.14	0.47
21:0:12:ARG:HB3	21:0:24:LEU:HD23	1.95	0.47
27:9:51:ARG:HG2	27:9:52:GLN:H	1.79	0.47
46:A:215:A:N6	46:A:830:G:N9	2.52	0.47
46:A:215:A:C5	46:A:830:G:H1'	2.47	0.47
46:A:841:A:C6	54:I:92:ARG:HG3	2.49	0.47
70:Y:42:PRO:O	70:Y:79:ASN:ND2	2.37	0.47
1:1:569:U:H2'	1:1:570:A:H8	1.80	0.47
1:1:912:G:H5'	1:1:913:A:OP1	2.14	0.47
1:1:1593:C:H2'	1:1:1594:G:C8	2.50	0.47
1:1:2084:A:H2'	1:1:2085:A:H8	1.79	0.47
1:1:2404:U:H2'	1:1:2405:U:C6	2.49	0.47
1:1:2405:U:H2'	1:1:2406:U:C6	2.49	0.47
1:1:2669:A:H2'	1:1:2670:G:H8	1.80	0.47
1:1:3194:G:H5'	15:u:129:VAL:HG21	1.96	0.47
1:1:3247:A:H2'	1:1:3248:U:C6	2.50	0.47
12:r:19:LYS:HE2	12:r:19:LYS:HB3	1.61	0.47
32:AE:54:LEU:HA	32:AE:94:PRO:HG3	1.96	0.47
57:L:62:GLN:NE2	76:e:23:HIS:O	2.45	0.47
64:S:24:LEU:HD23	64:S:34:LEU:HD23	1.95	0.47
73:b:99:GLN:HG2	73:b:99:GLN:O	2.14	0.47
1:1:259:C:H2'	1:1:260:C:C6	2.49	0.47
1:1:261:U:H2'	1:1:262:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:296:A:N3	1:1:299:G:O2'	2.48	0.47
1:1:849:G:N7	44:AQ:2:THR:HG23	2.30	0.47
1:1:1534:G:H21	1:1:1579:A:H62	1.62	0.47
1:1:1617:A:H2'	1:1:1618:U:H6	1.79	0.47
1:1:2050:U:H2'	1:1:2051:G:N7	2.30	0.47
1:1:2145:A:H2'	1:1:2146:A:C8	2.50	0.47
1:1:2488:U:O2'	1:1:2489:A:H8	1.97	0.47
1:1:2739:U:H2'	1:1:2740:U:C6	2.49	0.47
1:1:3137:A:H2'	1:1:3138:U:C6	2.50	0.47
2:3:27:A:H2'	2:3:28:C:C6	2.49	0.47
5:k:331:VAL:HG22	5:k:334:ARG:NE	2.30	0.47
13:s:92:ARG:HG2	13:s:92:ARG:HH11	1.79	0.47
33:AF:24:ASP:OD1	33:AF:25:ARG:N	2.47	0.47
46:A:286:A:H2'	46:A:287:U:O4'	2.14	0.47
46:A:383:A:H2'	46:A:384:G:C8	2.49	0.47
46:A:1196:A:H4'	62:Q:100:LYS:HG3	1.96	0.47
46:A:1293:G:H2'	46:A:1294:C:C6	2.49	0.47
46:A:1413:A:O2'	46:A:1414:G:OP1	2.33	0.47
46:A:1555:C:H4'	46:A:1556:A:O5'	2.14	0.47
46:A:1636:C:H2'	46:A:1637:U:C6	2.49	0.47
47:B:52:LYS:HD3	68:W:82:VAL:HG23	1.97	0.47
48:C:28:ASP:CG	48:C:50:ARG:HG2	2.39	0.47
50:E:60:LEU:HD12	50:E:67:ILE:HD13	1.95	0.47
51:F:88:ASP:OD1	51:F:122:LYS:NZ	2.47	0.47
57:L:24:LYS:HG3	57:L:63:TYR:HE1	1.79	0.47
57:L:52:LYS:HG3	57:L:54:TYR:CD2	2.50	0.47
63:R:27:LEU:HD11	63:R:29:LYS:HE3	1.97	0.47
79:h:75:SER:HA	79:h:116:ILE:HD11	1.97	0.47
1:1:37:U:H2'	1:1:38:A:O4'	2.14	0.47
1:1:1357:U:H2'	1:1:1358:C:C6	2.50	0.47
1:1:2050:U:H2'	1:1:2051:G:C8	2.50	0.47
1:1:2648:A:H5'	1:1:2649:G:C8	2.50	0.47
1:1:2658:A:H2'	1:1:2659:G:O4'	2.15	0.47
1:1:2919:G:N3	5:k:250:ALA:HB1	2.29	0.47
3:4:97:A:OP1	36:AI:67:ARG:NH2	2.45	0.47
3:4:156:U:H2'	3:4:157:U:C5	2.49	0.47
41:AN:3:GLU:HG2	41:AN:4:PRO:HD2	1.95	0.47
46:A:265:U:H2'	46:A:266:C:H6	1.79	0.47
46:A:597:A:H4'	70:Y:105:ALA:HB1	1.96	0.47
46:A:948:A:OP2	46:A:948:A:H8	1.98	0.47
46:A:1105:U:H2'	46:A:1106:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1498:G:H2'	46:A:1499:G:C8	2.49	0.47
47:B:59:LEU:HD11	68:W:36:ILE:HD13	1.96	0.47
54:I:45:ILE:O	54:I:53:ALA:N	2.47	0.47
59:N:36:LEU:HD13	59:N:102:GLY:HA3	1.95	0.47
60:O:115:LEU:O	60:O:119:GLU:HG3	2.15	0.47
78:g:160:ARG:HB3	78:g:173:PHE:HB3	1.96	0.47
79:h:173:LYS:HG2	79:h:194:GLY:C	2.40	0.47
1:1:99:A:H3'	1:1:100:G:H21	1.79	0.47
1:1:314:U:H2'	1:1:315:C:C6	2.50	0.47
1:1:2239:G:O2'	1:1:2241:C:N4	2.48	0.47
1:1:3259:A:H5'	5:k:128:LYS:HG3	1.96	0.47
1:1:3319:U:O3'	55:J:77:ARG:NH1	2.48	0.47
3:4:52:A:OP1	40:AM:21[B]:ARG:NH1	2.38	0.47
3:4:141:C:H2'	3:4:142:C:H6	1.79	0.47
3:4:142:C:H2'	3:4:143:U:C6	2.50	0.47
3:4:156:U:O2'	3:4:157:U:OP1	2.33	0.47
9:o:87:ILE:HD11	9:o:226:THR:HG22	1.97	0.47
21:0:8:GLN:NE2	21:0:10:ILE:HD11	2.29	0.47
46:A:15:U:H2'	46:A:16:G:O4'	2.15	0.47
46:A:457:G:P	71:Z:105:ARG:HH22	2.38	0.47
46:A:1444:G:H2'	46:A:1444:G:N3	2.30	0.47
46:A:1502:A:OP2	50:E:8:LYS:HG2	2.15	0.47
46:A:1524:C:O4'	46:A:1559:G:N2	2.48	0.47
46:A:1589:C:H2'	46:A:1590:U:C6	2.50	0.47
50:E:165:THR:O	50:E:169:ILE:HB	2.14	0.47
54:I:56:VAL:HB	54:I:88:PHE:HD2	1.80	0.47
60:O:55:ARG:NH1	60:O:56:ASP:OD1	2.48	0.47
75:d:35:ASP:O	75:d:37:SER:N	2.47	0.47
79:h:73:THR:HG21	79:h:115:SER:HA	1.96	0.47
1:1:19:A:H2'	1:1:20:G:C8	2.50	0.47
1:1:843:A:H2'	1:1:844:A:C8	2.50	0.47
1:1:1172:C:H2'	1:1:1173:G:N2	2.30	0.47
1:1:1218:G:H1'	1:1:1282:A:N6	2.30	0.47
1:1:1456:A:H2'	1:1:1457:A:H8	1.79	0.47
1:1:1466:U:H2'	1:1:1467:U:C6	2.50	0.47
1:1:3139:U:H2'	1:1:3140:U:C6	2.50	0.47
12:r:51:HIS:ND1	12:r:137:SER:OG	2.45	0.47
19:y:89:ASP:OD1	19:y:113[B]:ARG:NH1	2.45	0.47
45:i:119:VAL:HA	45:i:122:THR:HG22	1.96	0.47
46:A:141:G:O6	53:H:177:ARG:NH2	2.47	0.47
46:A:327:G:H2'	46:A:328:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:444:A:H62	46:A:459:G:H21	1.63	0.47
46:A:1538:U:OP2	62:Q:43:ARG:NH1	2.47	0.47
46:A:1670:U:O2'	46:A:1671:G:O5'	2.33	0.47
46:A:1772:U:H2'	46:A:1773:G:H8	1.80	0.47
48:C:157:GLN:HB2	48:C:160:LYS:HD3	1.97	0.47
51:F:90:ILE:HB	51:F:99:PHE:HB2	1.97	0.47
52:G:132:VAL:HG13	52:G:202:ALA:HB2	1.97	0.47
52:G:166:ARG:HB2	75:d:46:GLY:HA3	1.97	0.47
55:J:38:ILE:HG12	55:J:96:LEU:HD11	1.97	0.47
62:Q:50:ASP:O	62:Q:53:PRO:HD2	2.15	0.47
79:h:150:ASP:OD2	79:h:171:TRP:HD1	1.98	0.47
1:1:955:C:H41	1:1:2773:A:H5''	1.80	0.46
1:1:1917:A:H2'	1:1:1918:A:C8	2.50	0.46
1:1:2181:U:H2'	1:1:2182:C:C6	2.50	0.46
6:l:66:TRP:HB3	6:l:70:ARG:HD3	1.96	0.46
10:p:162:GLU:CD	16:v:26:ARG:HH22	2.22	0.46
20:z:162:ARG:HA	20:z:165:ARG:HD3	1.96	0.46
21:0:22:PRO:O	22:2:146:ASN:ND2	2.46	0.46
32:AE:9:ARG:HG2	32:AE:107:VAL:HA	1.98	0.46
33:AF:83:LEU:HD12	33:AF:112:LYS:HD3	1.95	0.46
39:AL:13:GLU:HA	39:AL:16:ARG:HG2	1.96	0.46
46:A:648:U:H2'	46:A:649:G:C8	2.50	0.46
46:A:1190:C:O2	76:e:17:GLY:N	2.40	0.46
46:A:1510:G:N7	66:U:68:ARG:NE	2.63	0.46
53:H:12:THR:HG21	53:H:127:THR:HG23	1.96	0.46
53:H:163:THR:HA	53:H:168:THR:HG22	1.96	0.46
66:U:131:ASP:O	66:U:135:ILE:HG12	2.16	0.46
77:f:42:ARG:HH22	77:f:43:ARG:NH2	2.13	0.46
1:1:496:A:H2'	1:1:497:U:C6	2.49	0.46
1:1:624:U:H2'	1:1:625:C:H6	1.79	0.46
1:1:3261:A:H2'	1:1:3262:U:C6	2.50	0.46
81:1:3402:3K5:O15	81:1:3402:3K5:H13	2.14	0.46
2:3:55:A:H5''	13:s:3:ASP:HA	1.97	0.46
8:n:158:TYR:OH	15:u:107:ASP:OD2	2.25	0.46
9:o:86:ARG:NH1	9:o:106:LEU:O	2.43	0.46
51:F:139:VAL:HG13	51:F:150:PRO:HG3	1.96	0.46
54:I:12:GLU:HG2	54:I:13:LEU:N	2.30	0.46
62:Q:75:VAL:HG22	62:Q:93:VAL:HB	1.97	0.46
65:T:43:ALA:HA	65:T:46:VAL:HG22	1.98	0.46
1:1:403:C:HO2'	1:1:404:G:P	2.36	0.46
1:1:829:G:OP1	20:z:86:ASP:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1343:C:H5''	6:l:303:ALA:HB1	1.96	0.46
1:1:3138:U:H2'	1:1:3139:U:C6	2.50	0.46
2:3:23:A:H2'	2:3:24:A:C8	2.50	0.46
3:4:85:G:H4'	3:4:86:U:OP1	2.15	0.46
10:p:122:THR:HG23	10:p:124:LYS:H	1.80	0.46
46:A:209:U:H5''	58:M:20:PHE:CG	2.50	0.46
46:A:874:U:O2'	46:A:875:C:OP1	2.33	0.46
46:A:1449:C:N4	65:T:140:THR:OG1	2.48	0.46
46:A:1487:C:OP1	66:U:122:ARG:NH2	2.39	0.46
49:D:44:LYS:HA	49:D:44:LYS:HD3	1.76	0.46
52:G:98:MET:HB2	52:G:103:ASN:O	2.15	0.46
53:H:7:TYR:CE2	53:H:9:ALA:HB3	2.50	0.46
53:H:196:LYS:O	53:H:200:GLN:HG2	2.14	0.46
55:J:62:THR:HG22	55:J:77:ARG:HA	1.97	0.46
57:L:14:TYR:OH	57:L:34:GLU:OE1	2.34	0.46
57:L:18:GLU:H	57:L:89:LEU:HD23	1.80	0.46
73:b:41:ILE:HG12	73:b:68:TYR:CD2	2.50	0.46
1:1:48:A:N7	16:v:187:ARG:HD2	2.30	0.46
1:1:754:C:OP1	43:AP:15:LYS:NZ	2.48	0.46
1:1:989:G:N3	1:1:2609:A:H2'	2.31	0.46
1:1:1637:U:O2'	1:1:1638:A:H3'	2.15	0.46
1:1:1655:U:H2'	1:1:1656:C:C6	2.50	0.46
1:1:2992:U:H2'	1:1:3005:A:N6	2.30	0.46
15:u:24:LYS:HB2	15:u:25:GLU:OE2	2.15	0.46
23:5:19:VAL:C	23:5:21:ALA:H	2.24	0.46
46:A:29:U:H2'	46:A:30:G:C8	2.50	0.46
46:A:147:C:H2'	46:A:148:C:C6	2.51	0.46
46:A:511:U:H2'	46:A:512:G:C8	2.50	0.46
46:A:565:A:N3	77:f:14:VAL:HG21	2.31	0.46
46:A:694:C:H1'	54:I:96:PRO:HB2	1.96	0.46
46:A:1258:G:N2	46:A:1263:G:O6	2.49	0.46
46:A:1335:U:O2'	46:A:1336:G:OP1	2.27	0.46
46:A:1498:G:H2'	46:A:1499:G:H8	1.80	0.46
46:A:1626:C:H2'	46:A:1627:C:O4'	2.15	0.46
62:Q:83:MET:O	62:Q:116:LEU:N	2.46	0.46
1:1:1358:C:H2'	1:1:1359:A:C8	2.50	0.46
1:1:1562:G:C2	1:1:1563:A:H1'	2.51	0.46
1:1:2081:U:H2'	1:1:2082:A:H8	1.79	0.46
1:1:3245:A:O2'	1:1:3246:C:H6	1.97	0.46
6:l:182:VAL:HG11	6:l:225:GLY:HA3	1.98	0.46
13:s:82:ARG:HA	13:s:85:LYS:HE2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:107:C:H2'	46:A:108:A:H8	1.81	0.46
46:A:411:U:H2'	46:A:412:C:C6	2.50	0.46
46:A:1597:G:H5''	52:G:107:LYS:HD2	1.98	0.46
50:E:30:LEU:HD22	50:E:59:VAL:HG22	1.97	0.46
52:G:165:LEU:HD23	75:d:47:PRO:HG2	1.97	0.46
55:J:39:GLY:O	55:J:61:GLU:HG3	2.15	0.46
57:L:38:ARG:HB2	57:L:41:PHE:CD2	2.50	0.46
1:1:393:U:H2'	1:1:394:G:O4'	2.15	0.46
1:1:411:U:H2'	1:1:412:G:C8	2.50	0.46
1:1:436:A:H2'	1:1:437:G:C8	2.50	0.46
1:1:623:A:H2'	1:1:624:U:H6	1.81	0.46
1:1:1762:G:HO2'	1:1:1763:C:P	2.38	0.46
1:1:1825:A:H5''	1:1:1826:G:H5'	1.97	0.46
1:1:2084:A:H2'	1:1:2085:A:C8	2.51	0.46
1:1:2950:U:O2'	1:1:2951:U:H5'	2.15	0.46
10:p:131:VAL:HG13	10:p:203:GLU:HG3	1.97	0.46
24:6:36:VAL:HG22	24:6:58:VAL:HG11	1.98	0.46
43:AP:24[A]:LYS:HE3	43:AP:24[A]:LYS:HB2	1.41	0.46
46:A:601:U:H2'	46:A:602:A:C8	2.51	0.46
46:A:876:A:H2'	46:A:877:G:C8	2.50	0.46
46:A:1180:C:N4	63:R:140:SER:OG	2.49	0.46
46:A:1704:C:H2'	46:A:1705:G:C8	2.47	0.46
69:X:115:GLU:O	69:X:119:LYS:HG2	2.14	0.46
1:1:493:A:O2'	1:1:3238:A:N1	2.44	0.46
1:1:788:G:H2'	1:1:789:C:C6	2.51	0.46
1:1:981:U:H2'	1:1:982:U:H6	1.80	0.46
1:1:1007:A:H2'	1:1:1008:A:C8	2.51	0.46
4:j:32:LEU:HD13	4:j:163:ARG:HD3	1.96	0.46
4:j:180:LEU:HD22	44:AQ:18:TYR:HB3	1.98	0.46
22:2:56:TYR:CE2	22:2:78:LYS:HD3	2.51	0.46
58:M:8:GLN:HE22	58:M:14:GLN:H	1.64	0.46
67:V:32:GLN:HG3	67:V:111:VAL:HG23	1.98	0.46
1:1:63:G:OP2	16:v:169:LYS:NZ	2.36	0.46
1:1:412:G:O2'	18:x:118:GLN:HB2	2.16	0.46
1:1:859:C:H2'	1:1:860:G:O4'	2.16	0.46
1:1:1493:C:H2'	1:1:1494:A:H8	1.80	0.46
1:1:2335:A:H2'	1:1:2336:A:H8	1.79	0.46
1:1:2689:U:O3'	43:AP:13:LYS:NZ	2.32	0.46
1:1:2719:A:H5'	7:m:175:HIS:HA	1.97	0.46
1:1:2801:U:C2	1:1:2802:G:C8	3.04	0.46
1:1:3248:U:H2'	1:1:3249:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:u:17:ARG:HG2	15:u:57:LEU:HD22	1.97	0.46
28:AA:5:ILE:HG23	28:AA:25:ILE:HD13	1.97	0.46
46:A:103:A:H4'	46:A:105:A:C8	2.51	0.46
46:A:141:G:H2'	46:A:142:G:C8	2.51	0.46
46:A:477:C:O2	46:A:508:G:N2	2.49	0.46
46:A:787:A:H8	46:A:787:A:OP2	1.98	0.46
46:A:871:U:OP2	48:C:216:LYS:NZ	2.48	0.46
46:A:1194:C:N3	46:A:1441:G:N2	2.63	0.46
46:A:1465:A:H5''	66:U:60:SER:HB2	1.98	0.46
46:A:1518:G:H2'	46:A:1519:U:C6	2.50	0.46
46:A:1575:G:H1	46:A:1595:U:H3	1.64	0.46
50:E:24:GLU:OE1	57:L:61:TRP:NE1	2.49	0.46
57:L:55:VAL:HG12	57:L:68:LEU:HA	1.97	0.46
59:N:105:GLN:HE21	59:N:113:ARG:HD3	1.80	0.46
62:Q:80:LEU:O	62:Q:80:LEU:HD12	2.16	0.46
70:Y:50:LYS:HB3	70:Y:101:GLU:OE2	2.16	0.46
1:1:547:U:H2'	1:1:548:G:C8	2.50	0.46
1:1:1130:G:O2'	1:1:2614:A:N3	2.34	0.46
1:1:1242:G:C4	1:1:1260:G:O2'	2.65	0.46
1:1:1807:G:H2'	1:1:1808:G:O4'	2.16	0.46
1:1:2230:A:H61	1:1:2242:U:H3	1.64	0.46
1:1:3042:A:OP1	20:z:62:ARG:NH1	2.49	0.46
1:1:3088:G:H4'	11:q:69:ARG:NH1	2.31	0.46
24:6:13:MET:HE3	24:6:85:TRP:CE2	2.51	0.46
27:9:85:LEU:HD23	27:9:85:LEU:HA	1.79	0.46
41:AN:4:PRO:HA	41:AN:7:LYS:HB3	1.97	0.46
46:A:325:U:H2'	46:A:326:A:C8	2.51	0.46
46:A:626:G:H21	46:A:956:A:H62	1.64	0.46
46:A:940:A:H4'	46:A:1058:G:O2'	2.15	0.46
46:A:1323:C:H2'	46:A:1324:C:C6	2.51	0.46
46:A:1573:A:O2'	46:A:1574:A:OP1	2.29	0.46
53:H:203:ASP:OD1	53:H:204:ALA:N	2.49	0.46
69:X:81:VAL:O	69:X:122:SER:OG	2.34	0.46
70:Y:107:PHE:CE1	70:Y:123:LYS:HB3	2.50	0.46
1:1:560:C:H2'	1:1:561:U:C6	2.51	0.46
12:r:35:ASP:C	12:r:36:LEU:HD12	2.40	0.46
17:w:114:ASP:OD1	17:w:114:ASP:N	2.47	0.46
18:x:56:ARG:NH2	18:x:75:GLU:OE2	2.38	0.46
33:AF:67:LEU:HD23	33:AF:73:LYS:HG3	1.98	0.46
46:A:1437:C:OP2	76:e:12:ARG:NH2	2.49	0.46
46:A:1631:C:H2'	46:A:1632:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1716:C:H2'	46:A:1717:A:O4'	2.16	0.46
78:g:172:ILE:CG2	78:g:185:LYS:HZ3	2.29	0.46
79:h:236:GLU:O	79:h:253:THR:HA	2.16	0.46
1:1:11:A:H2'	1:1:12:A:C8	2.51	0.45
1:1:166:U:H2'	1:1:167:U:H6	1.81	0.45
1:1:983:U:H2'	1:1:984:U:C6	2.51	0.45
1:1:1303:G:H5'	17:w:61:LYS:HE3	1.98	0.45
1:1:2557:G:H2'	1:1:2557:G:N3	2.31	0.45
1:1:3299:U:H4'	1:1:3300:A:H5'	1.98	0.45
14:t:63:VAL:HA	14:t:66:ASN:ND2	2.31	0.45
15:u:27:ALA:HB2	15:u:45:ILE:HG21	1.98	0.45
15:u:109:GLU:O	15:u:113:VAL:HG23	2.16	0.45
18:x:67:ILE:HD11	18:x:80:LYS:HB3	1.98	0.45
46:A:66:U:H5	53:H:173:PRO:HD3	1.81	0.45
46:A:90:C:O2'	46:A:449:G:H5''	2.15	0.45
46:A:824:U:O2	46:A:824:U:H3'	2.16	0.45
46:A:844:A:C6	60:O:73:ARG:HD3	2.51	0.45
46:A:1003:U:OP1	60:O:107:LYS:NZ	2.49	0.45
46:A:1774:C:H2'	46:A:1775:G:C8	2.51	0.45
48:C:28:ASP:OD2	48:C:50:ARG:HG2	2.17	0.45
50:E:39:GLU:HB3	50:E:50:ILE:HB	1.97	0.45
59:N:36:LEU:HB2	59:N:41:LEU:HD21	1.97	0.45
70:Y:75:GLN:NE2	70:Y:80:GLY:HA2	2.30	0.45
71:Z:12:VAL:HG22	71:Z:23:PHE:HB3	1.98	0.45
79:h:123:ILE:HB	79:h:135:TRP:HB2	1.98	0.45
1:1:732:U:H3'	1:1:733:A:C8	2.50	0.45
1:1:1153:G:O2'	1:1:1165:A:N3	2.46	0.45
1:1:1824:A:H2'	1:1:1825:A:C8	2.52	0.45
1:1:2196:G:H2'	1:1:2197:A:H8	1.80	0.45
1:1:2385:C:H2'	1:1:2386:U:C6	2.52	0.45
1:1:2519:A:H4'	1:1:2520:A:O5'	2.15	0.45
1:1:3173:G:HO2'	21:O:161:LYS:HD2	1.82	0.45
1:1:3284:U:O2'	1:1:3285:A:OP1	2.32	0.45
46:A:248:C:H2'	46:A:249:A:C8	2.51	0.45
46:A:1222:G:H2'	46:A:1223:A:H8	1.81	0.45
46:A:1340:C:H2'	46:A:1341:U:O4'	2.16	0.45
46:A:1545:U:H5'	65:T:126:ARG:HH22	1.80	0.45
49:D:132:ILE:HG22	68:W:27:LYS:HE2	1.97	0.45
52:G:147:THR:N	52:G:158:GLN:O	2.49	0.45
63:R:51:LEU:HA	63:R:59:PHE:CE2	2.51	0.45
79:h:152:VAL:HA	79:h:170:SER:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:h:167:ILE:HD13	79:h:201:LEU:HD21	1.97	0.45
79:h:167:ILE:HA	79:h:177:SER:HA	1.98	0.45
1:1:708:A:H2'	1:1:709:A:C8	2.52	0.45
1:1:1020:G:H3'	1:1:1021:A:H5''	1.97	0.45
1:1:2391:A:H2'	1:1:2392:G:H8	1.82	0.45
1:1:2406:U:H2'	1:1:2407:G:H8	1.82	0.45
1:1:3262:U:H2'	1:1:3263:C:H6	1.81	0.45
14:t:106:GLN:NE2	14:t:110:ASP:OD1	2.49	0.45
45:i:101:LYS:HD3	46:A:573:C:H4'	1.98	0.45
45:i:112:LYS:HG2	45:i:113:ARG:H	1.81	0.45
46:A:66:U:H4'	53:H:171:LYS:HE2	1.98	0.45
46:A:1168:A:H2'	46:A:1169:A:C5	2.52	0.45
46:A:1168:A:H4'	46:A:1169:A:OP1	2.14	0.45
46:A:1334:G:H2'	46:A:1335:U:C6	2.51	0.45
46:A:1455:A:H2'	46:A:1456:C:C6	2.51	0.45
46:A:1776:G:OP1	73:b:17:HIS:NE2	2.34	0.45
52:G:42:LEU:HB2	52:G:48:PHE:CZ	2.52	0.45
55:J:104:ILE:HD11	55:J:189:ILE:HD11	1.99	0.45
59:N:62:LEU:HG	59:N:90:LYS:HE3	1.98	0.45
65:T:123:ARG:HA	65:T:126:ARG:HH21	1.81	0.45
79:h:22:SER:HB2	79:h:71:ASP:HA	1.98	0.45
1:1:289:A:H2'	1:1:290:G:H8	1.81	0.45
1:1:1019:U:H3	1:1:1025:G:H1	1.64	0.45
1:1:1658:G:H22	1:1:1783:A:H2	1.63	0.45
1:1:2855:U:H2'	1:1:2856:C:H6	1.82	0.45
1:1:3093:U:H1'	1:1:3094:A:H5''	1.99	0.45
1:1:3197:G:H2'	1:1:3198:C:H6	1.81	0.45
1:1:3199:G:H2'	1:1:3200:C:C6	2.51	0.45
5:k:331:VAL:HG22	5:k:334:ARG:HE	1.82	0.45
5:k:372:THR:HG22	5:k:374:ALA:H	1.82	0.45
46:A:78:A:H4'	46:A:79:C:OP1	2.16	0.45
46:A:933:A:H2'	46:A:934:C:C6	2.51	0.45
46:A:1165:C:O2'	62:Q:128:HIS:ND1	2.39	0.45
46:A:1195:C:OP1	78:g:123:LYS:HD3	2.16	0.45
46:A:1202:A:N6	76:e:7:TRP:HE1	2.14	0.45
46:A:1261:U:H2'	46:A:1262:G:H8	1.81	0.45
46:A:1323:C:H1'	46:A:1396:A:C5	2.51	0.45
46:A:1423:U:H2'	46:A:1424:G:C8	2.51	0.45
46:A:1452:G:H2'	46:A:1453:C:C6	2.51	0.45
46:A:1499:G:H2'	46:A:1500:G:C8	2.51	0.45
49:D:40:VAL:HG11	49:D:63:ILE:HG12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:D:111:LYS:HG2	49:D:122:ALA:HB3	1.98	0.45
61:P:35:ALA:HB2	61:P:65:LYS:HG2	1.98	0.45
61:P:126:GLY:O	73:b:22:ARG:NH2	2.50	0.45
1:1:502:U:H2'	1:1:503:U:C6	2.52	0.45
1:1:1767:G:H2'	1:1:1768:U:O4'	2.15	0.45
1:1:3112:G:N7	5:k:28:ARG:NH2	2.64	0.45
7:m:290:ILE:HG21	12:r:218:TYR:CD2	2.51	0.45
8:n:59:ASP:HB2	8:n:102:VAL:HG22	1.99	0.45
42:AO:1:MET:HB2	46:A:1770:C:OP2	2.16	0.45
46:A:17:C:H2'	46:A:18:C:C6	2.51	0.45
46:A:766:U:O2	71:Z:21:ARG:NH1	2.49	0.45
46:A:886:G:H2'	46:A:887:G:C8	2.52	0.45
46:A:1026:G:H2'	46:A:1027:G:H8	1.78	0.45
46:A:1491:G:H21	46:A:1550:C:H1'	1.81	0.45
46:A:1571:G:H22	46:A:1598:A:P	2.40	0.45
46:A:1661:C:H2'	46:A:1662:C:C6	2.52	0.45
47:B:53:THR:OG1	47:B:161:PRO:HG2	2.16	0.45
47:B:84:ARG:HD3	47:B:203:PHE:O	2.17	0.45
50:E:120:ALA:O	50:E:124:LEU:HG	2.17	0.45
52:G:26:ALA:HB2	63:R:25:LYS:HG3	1.99	0.45
64:S:37:GLU:OE1	79:h:151:TRP:NE1	2.41	0.45
1:1:437:G:H1	1:1:620:A:H61	1.63	0.45
1:1:443:G:N1	1:1:487:C:C2	2.85	0.45
1:1:498:C:H2'	1:1:499:G:H8	1.82	0.45
1:1:1857:G:O2'	1:1:3038:U:OP1	2.30	0.45
1:1:1891:A:O2'	1:1:3025:G:H4'	2.16	0.45
1:1:2138:G:H2'	1:1:2139:G:C8	2.50	0.45
1:1:2261:G:H1'	1:1:2263:C:N4	2.31	0.45
1:1:2406:U:H2'	1:1:2407:G:C8	2.51	0.45
1:1:2486:U:H2'	1:1:2487:U:C6	2.50	0.45
1:1:3153:A:H2'	1:1:3154:A:C8	2.52	0.45
2:3:4:U:H2'	2:3:5:G:C8	2.52	0.45
7:m:119:TYR:OH	7:m:139:PRO:O	2.27	0.45
46:A:599:A:H2'	46:A:600:U:C6	2.51	0.45
46:A:800:G:H2'	46:A:801:A:H8	1.82	0.45
46:A:873:U:H2'	46:A:874:U:C6	2.51	0.45
46:A:1596:U:O2'	52:G:105:GLY:O	2.24	0.45
51:F:21:ASP:OD2	51:F:24:SER:OG	2.31	0.45
53:H:37:GLU:HA	53:H:49:ILE:HD13	1.98	0.45
59:N:73:LYS:HB2	78:g:150:VAL:HG11	1.97	0.45
78:g:182:TYR:OH	78:g:184:GLY:HA2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:h:167:ILE:HD12	79:h:199:ILE:HD13	1.99	0.45
1:1:119:G:C6	10:p:129:LYS:HB2	2.52	0.45
1:1:453:U:H2'	1:1:454:G:H5'	1.99	0.45
1:1:622:G:H2'	1:1:623:A:H8	1.82	0.45
1:1:1587:G:H5''	35:AH:37:LYS:HZ2	1.82	0.45
1:1:2345:A:H2'	1:1:2346:A:C8	2.52	0.45
1:1:3082:C:H2'	1:1:3083:U:C6	2.52	0.45
2:3:44:C:OP2	13:s:137:ARG:NH1	2.39	0.45
2:3:49:G:C4	7:m:58:LYS:HE2	2.52	0.45
6:l:359:GLU:OE1	6:l:363:ASN:ND2	2.50	0.45
21:0:71:LYS:HE3	21:0:73:LYS:HG2	1.98	0.45
46:A:478:G:C2	46:A:479:A:C5	3.05	0.45
46:A:857:G:N2	46:A:1032:G:H4'	2.32	0.45
46:A:975:C:H5'	61:P:124:LYS:HB3	1.99	0.45
46:A:1247:U:H2'	46:A:1248:G:H8	1.82	0.45
46:A:1772:U:OP1	61:P:131:ARG:NH2	2.47	0.45
51:F:87:MET:HE1	51:F:237:VAL:HG21	1.98	0.45
52:G:46:TRP:CE2	52:G:129:PRO:HG2	2.52	0.45
59:N:42:ALA:N	59:N:122:VAL:O	2.28	0.45
63:R:96:VAL:HG12	63:R:97:ASP:N	2.32	0.45
1:1:481:G:C8	1:1:482:U:C4	3.05	0.45
1:1:647:A:H2'	1:1:648:C:C6	2.52	0.45
1:1:883:G:H2'	1:1:884:A:C8	2.52	0.45
1:1:962:U:H2'	1:1:963:A:C8	2.52	0.45
1:1:1035:U:H2'	1:1:1036:A:C8	2.52	0.45
1:1:1229:G:H2'	1:1:1229:G:N3	2.32	0.45
1:1:1580:U:H2'	1:1:1581:C:H6	1.82	0.45
13:s:46:VAL:HG12	45:i:25:PRO:HB2	1.99	0.45
26:8:87:ASP:OD1	26:8:88:ILE:N	2.50	0.45
46:A:549:G:H2'	46:A:550:G:C8	2.51	0.45
46:A:1725:U:H2'	46:A:1726:C:C6	2.52	0.45
46:A:1766:U:H2'	46:A:1768:A:OP2	2.17	0.45
48:C:24:PHE:HZ	61:P:34:ILE:HA	1.81	0.45
52:G:139:ASN:O	52:G:214:LYS:HE2	2.17	0.45
79:h:166:VAL:HG13	79:h:178:TRP:HB2	1.99	0.45
79:h:194:GLY:HA3	79:h:213:LYS:HG2	1.99	0.45
1:1:172:C:HO2'	1:1:173:C:P	2.37	0.45
1:1:907:C:OP2	4:j:9:ARG:HD2	2.16	0.45
1:1:1093:G:H5''	22:2:129:LYS:HE2	1.98	0.45
1:1:1210:U:H2'	1:1:1211:U:C6	2.51	0.45
1:1:1944:G:H2'	1:1:1945:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2273:A:N3	1:1:2901:C:O2'	2.43	0.45
1:1:2367:C:H2'	1:1:2368:A:C8	2.52	0.45
1:1:2544:U:O2'	1:1:2545:C:O5'	2.34	0.45
1:1:2902:A:H2'	1:1:2903:C:C6	2.52	0.45
30:AC:20:GLY:HA3	30:AC:21:ILE:HA	1.84	0.45
46:A:17:C:H2'	46:A:18:C:H6	1.82	0.45
46:A:108:A:H2'	46:A:109:G:C8	2.52	0.45
46:A:507:G:H2'	46:A:508:G:C8	2.52	0.45
46:A:623:C:H2'	46:A:624:U:C6	2.51	0.45
46:A:817:U:O2'	46:A:818:U:O2	2.35	0.45
46:A:1166:U:H4'	62:Q:127:ARG:O	2.17	0.45
46:A:1187:A:H62	46:A:1443:C:P	2.40	0.45
46:A:1424:G:H2'	46:A:1425:C:H6	1.82	0.45
46:A:1512:A:H2'	46:A:1513:A:C8	2.52	0.45
53:H:85:ARG:O	53:H:87:ARG:NH1	2.49	0.45
60:O:36:GLN:O	60:O:40:TYR:HD1	2.00	0.45
1:1:139:U:H2'	1:1:140:C:C6	2.51	0.45
1:1:161:G:H2'	1:1:162:U:O4'	2.16	0.45
1:1:243:G:H2'	1:1:244:G:C8	2.51	0.45
1:1:1011:C:N4	1:1:1031:A:H61	2.15	0.45
1:1:1021:A:OP2	1:1:1021:A:C8	2.70	0.45
1:1:1029:U:H2'	1:1:1030:U:H6	1.81	0.45
1:1:2672:G:H5''	22:2:17:ARG:HG2	1.98	0.45
1:1:3009:U:H5''	5:k:348:ARG:HD2	1.98	0.45
1:1:3137:A:H2'	1:1:3138:U:H6	1.81	0.45
2:3:56:A:H4'	13:s:152:HIS:HB2	1.99	0.45
3:4:157:U:H2'	3:4:158:U:C6	2.52	0.45
8:n:53:TYR:CE1	8:n:62:LEU:HB3	2.51	0.45
11:q:118:LEU:HD11	11:q:167:VAL:HG22	1.99	0.45
22:2:40:VAL:HB	22:2:96:VAL:HG13	1.99	0.45
46:A:461:U:H2'	46:A:462:A:C8	2.52	0.45
46:A:621:A:N6	46:A:1089:U:O2'	2.46	0.45
46:A:738:A:OP1	51:F:187:ARG:N	2.45	0.45
46:A:815:U:O2'	46:A:816:U:H6	2.00	0.45
46:A:1226:G:H2'	46:A:1227:A:C8	2.52	0.45
46:A:1300:U:O2'	46:A:1301:G:H8	2.00	0.45
46:A:1307:A:H2'	46:A:1308:C:C6	2.52	0.45
50:E:102:GLN:HA	50:E:105:ALA:HB3	1.98	0.45
56:K:133:HIS:O	56:K:159:ALA:N	2.40	0.45
64:S:33:ARG:NE	79:h:110:ASP:OD2	2.50	0.45
72:a:54:VAL:HG11	72:a:83:LEU:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:h:75:SER:HB3	79:h:80:TYR:HB2	1.99	0.45
1:1:241:C:H2'	1:1:242:C:C6	2.52	0.44
1:1:364:G:OP1	6:l:61:THR:HG23	2.17	0.44
1:1:975:U:H4'	1:1:976:A:O4'	2.17	0.44
1:1:2523:C:H2'	1:1:2524:C:C6	2.52	0.44
1:1:2919:G:C2	5:k:250:ALA:HB1	2.52	0.44
1:1:2958:U:H2'	1:1:2959:A:C8	2.52	0.44
1:1:2995:U:H2'	1:1:2996:A:H8	1.82	0.44
2:3:45:A:H2'	2:3:46:A:H8	1.83	0.44
13:s:44:THR:HG21	45:i:23:SER:HB2	2.00	0.44
32:AE:58:ILE:HA	32:AE:70:MET:HE1	1.99	0.44
36:AI:118:ILE:HG22	36:AI:119:LYS:N	2.31	0.44
40:AM:20:ASN:ND2	40:AM:42:ARG:O	2.42	0.44
46:A:1:U:H1'	49:D:174:VAL:HG13	1.99	0.44
46:A:303:C:H2'	46:A:304:U:C6	2.52	0.44
46:A:887:G:H2'	46:A:888:U:C6	2.53	0.44
46:A:1368:A:H5'	67:V:58:PRO:HA	2.00	0.44
46:A:1444:G:OP2	65:T:139:LYS:HB2	2.16	0.44
51:F:194:VAL:HG11	51:F:232:ALA:HB2	1.99	0.44
58:M:123:VAL:HG12	58:M:142:VAL:HA	1.98	0.44
71:Z:40:LEU:HD12	71:Z:60:PHE:HE2	1.82	0.44
79:h:62:PHE:HB3	79:h:93:TRP:CZ2	2.52	0.44
79:h:111:VAL:HA	79:h:127:SER:HA	1.99	0.44
79:h:254:THR:HA	79:h:285:GLU:CG	2.47	0.44
1:1:1275:C:H2'	1:1:1276:C:C6	2.52	0.44
1:1:1346:U:H1'	1:1:1347:U:OP2	2.18	0.44
1:1:1427:G:N7	29:AB:9:ARG:NH2	2.66	0.44
1:1:1474:C:H2'	1:1:1475:U:C6	2.52	0.44
1:1:1951:U:H2'	1:1:1952:G:H8	1.82	0.44
1:1:2281:A:OP1	42:AO:23:ARG:NE	2.50	0.44
1:1:3280:G:OP2	5:k:116:ARG:NH2	2.51	0.44
1:1:3313:G:H2'	1:1:3314:C:C6	2.52	0.44
2:3:3:U:H2'	2:3:4:U:C6	2.53	0.44
21:0:6:GLU:OE1	21:0:28:ARG:NE	2.42	0.44
23:5:29:ASP:HB3	23:5:32:SER:HB3	1.99	0.44
31:AD:20:ILE:HG23	31:AD:25:TYR:CZ	2.52	0.44
46:A:272:G:H2'	46:A:273:C:C6	2.52	0.44
46:A:1088:U:H2'	46:A:1089:U:H6	1.82	0.44
46:A:1483:U:O2'	46:A:1506:U:O2'	2.31	0.44
46:A:1669:U:O2'	46:A:1670:U:O5'	2.35	0.44
48:C:66:PHE:CE2	61:P:29:SER:HB3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:I:25:GLU:HB2	54:I:31:LYS:HG3	1.99	0.44
57:L:32:HIS:HD2	57:L:33:ASP:N	2.14	0.44
65:T:68:ARG:HH21	65:T:72:ILE:HG13	1.82	0.44
79:h:19:TRP:HB3	79:h:287:ILE:HD11	1.99	0.44
1:1:662:U:H5'	6:l:108:ARG:HA	1.98	0.44
1:1:951:U:H2'	1:1:952:U:C6	2.52	0.44
1:1:1139:A:H5'	1:1:1364:U:H1'	2.00	0.44
1:1:1923:G:C8	44:AQ:16:VAL:HG12	2.52	0.44
1:1:2987:G:H2'	1:1:2988:A:C8	2.52	0.44
1:1:3039:C:H3'	20:z:62:ARG:NH2	2.32	0.44
4:j:96:LEU:HD12	4:j:166:ILE:HD13	1.98	0.44
5:k:256:HIS:HA	5:k:257:PRO:C	2.43	0.44
6:l:3:SER:OG	6:l:4:ARG:N	2.51	0.44
8:n:39:LEU:HB3	8:n:83:VAL:HG13	1.98	0.44
27:9:57:LEU:HD13	27:9:67:GLU:OE2	2.17	0.44
44:AQ:29:LEU:HD12	44:AQ:69:TYR:CD2	2.52	0.44
46:A:820:U:H2'	46:A:821:U:C2	2.51	0.44
46:A:1279:G:O2'	46:A:1306:A:N1	2.38	0.44
46:A:1609:G:H2'	46:A:1610:C:C6	2.51	0.44
61:P:106:ARG:HA	61:P:106:ARG:HD2	1.81	0.44
1:1:28:C:H4'	1:1:61:A:H4'	1.99	0.44
1:1:687:U:O4	6:l:210:TYR:OH	2.26	0.44
1:1:757:A:C2	1:1:767:A:H1'	2.53	0.44
1:1:1561:U:O2'	1:1:1562:G:OP1	2.29	0.44
1:1:2401:U:H2'	1:1:2402:A:C8	2.53	0.44
1:1:2408:A:H2'	1:1:2409:C:C6	2.52	0.44
1:1:2785:A:H2'	1:1:2786:G:O4'	2.17	0.44
1:1:3044:C:H2'	1:1:3045:A:O4'	2.17	0.44
7:m:41:LYS:HB2	22:2:68:THR:O	2.18	0.44
10:p:134:LYS:HB2	10:p:200:ALA:HB3	1.99	0.44
13:s:51:ARG:HB3	45:i:31:LYS:HZ2	1.82	0.44
29:AB:94:SER:HB3	29:AB:121:VAL:HG13	2.00	0.44
46:A:444:A:H5''	51:F:57:ASN:HD22	1.81	0.44
46:A:444:A:N6	46:A:459:G:H21	2.15	0.44
46:A:836:U:H2'	46:A:837:C:C6	2.53	0.44
46:A:1427:C:H2'	46:A:1428:U:H6	1.82	0.44
46:A:1612:C:H2'	46:A:1613:U:C6	2.52	0.44
46:A:1699:G:C6	46:A:1700:G:H1'	2.53	0.44
50:E:212:ALA:HB2	64:S:19:ARG:HG2	1.99	0.44
51:F:21:ASP:OD1	51:F:21:ASP:N	2.51	0.44
61:P:79:ARG:HB3	61:P:113:VAL:HG23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:Q:14:GLN:OE1	62:Q:23:LYS:N	2.39	0.44
66:U:61:ILE:O	66:U:65:ILE:HG12	2.18	0.44
1:1:357:A:O4'	6:l:82:GLY:HA3	2.18	0.44
1:1:582:G:H2'	1:1:583:A:C8	2.53	0.44
1:1:755:U:H2'	1:1:756:G:O4'	2.17	0.44
1:1:1521:G:H5'	1:1:1826:G:OP2	2.17	0.44
1:1:2519:A:H1'	1:1:2520:A:OP2	2.17	0.44
1:1:2753:U:H2'	1:1:2754:U:C6	2.52	0.44
3:4:26:U:H2'	3:4:27:U:C6	2.53	0.44
5:k:106:TRP:HB2	5:k:133:TYR:CE1	2.53	0.44
5:k:331:VAL:H	5:k:334:ARG:HG3	1.82	0.44
9:o:52:GLU:OE2	9:o:184:HIS:NE2	2.50	0.44
21:0:2:SER:O	21:0:104:GLU:HG2	2.17	0.44
42:AO:9:ARG:HH12	46:A:1630:U:P	2.40	0.44
46:A:537:G:OP2	46:A:537:G:N2	2.40	0.44
46:A:540:A:N6	77:f:25:GLU:OE2	2.50	0.44
46:A:931:U:H2'	46:A:932:U:C6	2.52	0.44
46:A:1425:C:H2'	46:A:1426:C:H6	1.82	0.44
47:B:59:LEU:HD22	68:W:79:LEU:HD11	2.00	0.44
53:H:133:LEU:HD12	53:H:134:GLY:H	1.83	0.44
57:L:16:PHE:O	57:L:17:GLN:HG3	2.17	0.44
59:N:67:THR:C	59:N:69:GLU:H	2.25	0.44
61:P:48:ASP:OD1	61:P:48:ASP:N	2.50	0.44
62:Q:72:ARG:HE	62:Q:93:VAL:HG21	1.83	0.44
63:R:2:SER:OG	63:R:3:THR:N	2.50	0.44
64:S:17:ILE:HD11	64:S:54:THR:HG23	2.00	0.44
1:1:768:U:H2'	1:1:769:G:O4'	2.18	0.44
1:1:911:A:H8	1:1:2114:C:O2'	2.01	0.44
1:1:2515:G:H1'	1:1:2516:U:O5'	2.18	0.44
3:4:26:U:O2'	6:l:52:ALA:O	2.34	0.44
3:4:51:G:O6	40:AM:30:ARG:NH2	2.51	0.44
7:m:160:PHE:HA	7:m:163:LEU:HB3	1.99	0.44
11:q:19:ASP:OD2	15:u:4:THR:OG1	2.35	0.44
13:s:61:ARG:HD3	45:i:36:SER:OG	2.17	0.44
19:y:67:ILE:HG23	19:y:81:ILE:HG13	2.00	0.44
46:A:470:U:H2'	46:A:471:A:C8	2.53	0.44
46:A:832:A:H2'	46:A:833:C:O4'	2.18	0.44
46:A:1345:A:N1	46:A:1349:G:C6	2.85	0.44
46:A:1579:A:O2'	46:A:1580:A:OP1	2.32	0.44
47:B:184:LEU:HB3	68:W:45:ALA:HB2	1.99	0.44
54:I:4:LYS:HA	54:I:38:GLN:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:K:159:ALA:HB3	56:K:162:SER:HB3	1.99	0.44
57:L:1:MET:HG2	57:L:2:LEU:N	2.33	0.44
57:L:9:LYS:O	57:L:12:HIS:N	2.50	0.44
66:U:7:ARG:HE	66:U:67:LEU:HD23	1.82	0.44
79:h:194:GLY:HA3	79:h:213:LYS:HE3	2.00	0.44
1:1:631:U:H2'	1:1:632:C:C6	2.53	0.44
1:1:1377:A:OP1	6:l:198:ARG:NE	2.42	0.44
1:1:1755:U:H3	1:1:1762:G:H1	1.64	0.44
2:3:70:A:H2'	2:3:71:U:C6	2.53	0.44
5:k:369:ARG:HH11	25:7:11:SER:HB3	1.83	0.44
46:A:62:A:H2'	46:A:286:A:H1'	2.00	0.44
46:A:352:C:H5''	55:J:16:ALA:HB2	2.00	0.44
46:A:867:U:H2'	46:A:868:C:C6	2.53	0.44
46:A:874:U:H2'	46:A:875:C:C6	2.52	0.44
46:A:891:A:P	61:P:46:ASP:HB2	2.58	0.44
46:A:1165:C:H2'	46:A:1166:U:C6	2.53	0.44
46:A:1772:U:P	61:P:128:ARG:HH22	2.40	0.44
62:Q:39:ALA:O	62:Q:43:ARG:N	2.45	0.44
66:U:109:GLN:HG3	66:U:115:GLU:HA	1.99	0.44
67:V:18:ILE:HD11	67:V:93:GLN:HB3	1.99	0.44
67:V:68:LYS:HE3	67:V:79:ASP:OD1	2.17	0.44
71:Z:7:ILE:HD11	71:Z:47:ILE:HD12	1.98	0.44
75:d:11:LYS:HA	75:d:52:ASP:O	2.18	0.44
79:h:71:ASP:HB2	79:h:113:SER:HA	2.00	0.44
1:1:1336:G:H2'	1:1:1337:U:C6	2.53	0.44
1:1:3005:A:H2'	1:1:3006:C:C6	2.53	0.44
4:j:101:ILE:HG13	4:j:165:VAL:HG22	2.00	0.44
9:o:182:LEU:HD21	9:o:200:LEU:HD11	1.99	0.44
23:5:19:VAL:O	23:5:21:ALA:N	2.49	0.44
29:AB:104:THR:OG1	29:AB:126:LYS:O	2.33	0.44
36:AI:83:LYS:HG3	36:AI:83:LYS:O	2.18	0.44
46:A:142:G:OP2	46:A:142:G:H8	2.01	0.44
46:A:484:G:H2'	46:A:485:G:H8	1.83	0.44
46:A:875:C:H2'	46:A:876:A:C8	2.53	0.44
46:A:1158:C:H2'	46:A:1159:C:H6	1.82	0.44
46:A:1276:G:H1	46:A:1309:G:N2	2.11	0.44
46:A:1669:U:H4'	53:H:65:GLN:NE2	2.33	0.44
47:B:180:GLU:OE1	47:B:191:ARG:NH2	2.51	0.44
53:H:22:HIS:HA	53:H:25:ARG:NH1	2.33	0.44
71:Z:8:ARG:HB2	71:Z:26:ASP:HB2	1.98	0.44
78:g:160:ARG:HB3	78:g:173:PHE:CG	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1153:G:H2'	1:1:1154:A:O4'	2.18	0.44
1:1:2854:U:H2'	1:1:2855:U:C6	2.53	0.44
1:1:2972:A:H5''	5:k:120:LYS:HZ2	1.83	0.44
10:p:108:GLU:O	10:p:112:LYS:HG2	2.17	0.44
12:r:42:THR:O	12:r:139:ARG:NH2	2.50	0.44
28:AA:76:ASN:OD1	28:AA:78:ASN:ND2	2.50	0.44
46:A:559:G:C6	46:A:583:A:C6	3.06	0.44
46:A:598:U:OP2	70:Y:108:GLY:HA2	2.17	0.44
46:A:1207:C:H2'	46:A:1208:A:C8	2.53	0.44
55:J:113:TYR:OH	55:J:156:ALA:O	2.29	0.44
65:T:42:TYR:HA	65:T:85:PHE:HE2	1.83	0.44
69:X:88:ARG:HD2	69:X:88:ARG:C	2.43	0.44
74:c:67:THR:HG22	74:c:68:GLY:N	2.33	0.44
1:1:35:C:H4'	1:1:804:A:H2	1.83	0.43
1:1:454:G:C2	1:1:476:C:N1	2.85	0.43
1:1:1124:U:H2'	1:1:1125:A:O4'	2.18	0.43
1:1:1639:A:H2'	1:1:1640:C:C2	2.53	0.43
1:1:3285:A:H2'	1:1:3286:C:C6	2.53	0.43
8:n:28[B]:LYS:HE3	8:n:28[B]:LYS:HB3	1.84	0.43
13:s:94[B]:LYS:HB3	13:s:94[B]:LYS:HE3	1.71	0.43
20:z:166:ASN:HA	20:z:169:ALA:HB3	2.00	0.43
24:6:88:ARG:HA	24:6:88:ARG:HD2	1.83	0.43
46:A:91:G:H2'	46:A:92:A:O4'	2.18	0.43
46:A:152:G:N2	53:H:60:GLY:O	2.50	0.43
46:A:598:U:H2'	46:A:599:A:H8	1.82	0.43
46:A:1092:G:O2'	46:A:1093:G:H5'	2.18	0.43
46:A:1211:A:N6	59:N:114:LYS:HB2	2.33	0.43
46:A:1574:A:OP2	63:R:131:ARG:NH2	2.51	0.43
54:I:4:LYS:NZ	54:I:34:LEU:O	2.51	0.43
63:R:17:ALA:HA	63:R:68:VAL:HA	1.99	0.43
64:S:28:PHE:O	64:S:32:LYS:N	2.42	0.43
77:f:43:ARG:HG3	77:f:44:PHE:CD2	2.53	0.43
79:h:201:LEU:HD22	79:h:222:LEU:HD21	1.99	0.43
1:1:46:C:OP1	14:t:16:LYS:HE2	2.18	0.43
1:1:79:G:H2'	1:1:80:C:C6	2.53	0.43
1:1:962:U:OP1	29:AB:44:ASN:ND2	2.50	0.43
1:1:1482:G:N2	35:AH:6:THR:HG22	2.32	0.43
1:1:1967:U:H3'	1:1:1968:A:C8	2.53	0.43
1:1:2525:A:H2'	1:1:2526:C:O4'	2.17	0.43
3:4:150:G:O2'	10:p:60:GLN:NE2	2.51	0.43
7:m:183:TRP:HE3	7:m:190:LEU:HB2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:13:C:P	49:D:79:ARG:HH12	2.40	0.43
46:A:79:C:OP1	53:H:159:ARG:NH2	2.44	0.43
46:A:809:G:H2'	46:A:810:U:H6	1.83	0.43
48:C:141:ALA:HB1	48:C:207:LEU:HD13	1.99	0.43
50:E:65:ARG:HD3	57:L:91:ARG:NE	2.32	0.43
57:L:16:PHE:CZ	57:L:88:PRO:HG3	2.53	0.43
57:L:50:THR:HB	57:L:55:VAL:HG23	1.99	0.43
1:1:444:U:H3	1:1:445:A:H62	1.65	0.43
1:1:820:C:O2'	1:1:1530:A:N3	2.49	0.43
12:r:87:LEU:HD12	12:r:137:SER:O	2.19	0.43
17:w:47:GLU:H	17:w:47:GLU:CD	2.26	0.43
17:w:57:ASP:OD2	17:w:60:ARG:NH1	2.39	0.43
30:AC:36:ASP:OD1	30:AC:37:ALA:N	2.51	0.43
35:AH:111:LYS:HE3	35:AH:111:LYS:HB3	1.65	0.43
46:A:116:U:H2'	46:A:117:U:C6	2.54	0.43
46:A:604:A:H4'	46:A:605:G:H3'	1.99	0.43
46:A:627:U:H2'	46:A:628:A:H8	1.83	0.43
46:A:1434:G:H2'	46:A:1435:U:O4'	2.17	0.43
52:G:189:THR:HG22	52:G:192:GLU:HG2	2.00	0.43
68:W:16:LYS:HE3	68:W:23:ILE:HG12	1.99	0.43
73:b:42:ARG:O	73:b:67:LEU:N	2.37	0.43
1:1:277:G:H2'	1:1:278:U:C6	2.53	0.43
1:1:421:G:O6	1:1:2361:C:O2'	2.26	0.43
1:1:454:G:N1	1:1:476:C:C4	2.86	0.43
5:k:70:ARG:HG2	5:k:70:ARG:NH1	2.33	0.43
5:k:140:ASP:OD1	5:k:142:LYS:HB2	2.18	0.43
16:v:73:ARG:HG2	16:v:75:VAL:HG13	2.00	0.43
24:6:86:ARG:HB2	24:6:92:TYR:CE2	2.53	0.43
32:AE:8:THR:HG21	32:AE:73:ARG:HE	1.84	0.43
39:AL:27:VAL:HG13	39:AL:39:LYS:HD2	1.99	0.43
46:A:218:A:H61	46:A:827:C:N4	2.10	0.43
46:A:1066:A:O2'	46:A:1068:G:N7	2.50	0.43
46:A:1168:A:H1'	46:A:1195:C:O2'	2.18	0.43
46:A:1194:C:C4	46:A:1441:G:N2	2.86	0.43
46:A:1339:G:O6	46:A:1354:U:C2	2.71	0.43
60:O:127:ARG:O	60:O:131:THR:HG23	2.19	0.43
63:R:54:VAL:HG11	63:R:104:LEU:HD22	2.00	0.43
67:V:70:PRO:O	76:e:41:GLN:NE2	2.48	0.43
70:Y:42:PRO:HA	70:Y:81:LYS:HD2	2.00	0.43
1:1:38:A:H5''	29:AB:35:ALA:HB2	2.00	0.43
1:1:242:C:H5''	36:AI:115:LYS:NZ	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:249:G:H2'	1:1:251:G:OP2	2.19	0.43
1:1:1561:U:H2'	1:1:1562:G:C8	2.53	0.43
1:1:1660:G:H2'	1:1:1661:U:C6	2.53	0.43
9:o:39:ARG:HA	9:o:42:ILE:HG12	2.01	0.43
10:p:141:VAL:HG22	10:p:167:LEU:HD21	2.00	0.43
17:w:152:SER:HA	17:w:155:GLU:HG2	2.00	0.43
18:x:64:ASN:O	18:x:80:LYS:NZ	2.47	0.43
21:0:91:TYR:OH	21:0:93:GLU:OE2	2.30	0.43
46:A:1088:U:P	70:Y:7:ARG:H	2.39	0.43
46:A:1149:G:H2'	46:A:1150:G:H8	1.83	0.43
46:A:1371:G:H2'	46:A:1372:G:C8	2.53	0.43
48:C:117:TRP:HB3	48:C:153:THR:HA	1.99	0.43
51:F:36:HIS:CE1	51:F:143:ASP:HB3	2.53	0.43
53:H:161:GLU:HB3	53:H:170:THR:HG22	2.00	0.43
54:I:60:PRO:N	54:I:61:PRO:HD2	2.33	0.43
64:S:107:ALA:O	64:S:111:LYS:HG2	2.19	0.43
78:g:149:LYS:H	78:g:157:GLU:HB3	1.82	0.43
1:1:620:A:O5'	1:1:620:A:H8	2.01	0.43
1:1:696:U:H2'	1:1:697:A:O4'	2.18	0.43
1:1:1058:A:H5''	1:1:1059:G:H5'	2.00	0.43
1:1:1363:G:OP1	33:AF:46:ARG:NH2	2.50	0.43
1:1:1623:U:H2'	1:1:1810:A:H62	1.83	0.43
1:1:2196:G:H2'	1:1:2197:A:C8	2.53	0.43
1:1:2486:U:H2'	1:1:2487:U:H6	1.83	0.43
6:l:145:GLN:HG2	6:l:177:LYS:HZ2	1.83	0.43
46:A:30:G:H2'	46:A:31:C:C6	2.53	0.43
46:A:137:A:H1'	46:A:138:C:OP2	2.19	0.43
46:A:649:G:H2'	46:A:650:G:O4'	2.19	0.43
46:A:863:G:O2'	60:O:108:ASP:OD1	2.29	0.43
46:A:1012:A:OP1	46:A:1776:G:O2'	2.30	0.43
46:A:1024:A:O2'	46:A:1025:G:H8	2.02	0.43
46:A:1321:A:C6	46:A:1402:G:C6	3.07	0.43
70:Y:19:ARG:O	70:Y:23:ARG:HG3	2.19	0.43
71:Z:10:ARG:NH1	71:Z:26:ASP:OD2	2.52	0.43
1:1:66:A:O2'	1:1:315:C:O2	2.36	0.43
1:1:116:U:O2'	1:1:118:U:OP2	2.32	0.43
1:1:275:U:H2'	1:1:276:U:C6	2.54	0.43
1:1:377:A:H1'	1:1:392:G:N2	2.33	0.43
1:1:625:C:H2'	1:1:626:U:C6	2.53	0.43
1:1:1030:U:H2'	1:1:1031:A:H8	1.83	0.43
1:1:1062:G:H2'	1:1:1063:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:3:U:H2'	2:3:4:U:H6	1.83	0.43
2:3:113:C:H2'	2:3:114:U:O4'	2.19	0.43
5:k:62:ARG:HG3	5:k:348:ARG:HH12	1.84	0.43
9:o:116:ARG:HD3	9:o:189:VAL:HG11	2.00	0.43
18:x:153:GLU:N	18:x:153:GLU:OE1	2.51	0.43
28:AA:9:LYS:HE2	28:AA:83:THR:O	2.19	0.43
29:AB:132:LYS:O	29:AB:136:GLU:HG3	2.19	0.43
46:A:274:C:O2'	46:A:275:U:O5'	2.36	0.43
46:A:466:A:N1	46:A:592:A:O2'	2.50	0.43
46:A:544:U:H2'	46:A:545:U:C6	2.54	0.43
46:A:1503:A:O2'	46:A:1504:U:H5'	2.19	0.43
47:B:48:ILE:HD12	47:B:149:MET:HE3	2.01	0.43
47:B:164:ASN:O	47:B:170:ILE:HD11	2.19	0.43
52:G:87:CYS:HB3	52:G:92:ARG:HD2	2.01	0.43
52:G:112:ARG:HH11	72:a:95:HIS:CE1	2.37	0.43
52:G:116:HIS:HB3	72:a:100:ILE:HD11	2.00	0.43
53:H:126:ASP:OD1	53:H:127:THR:N	2.52	0.43
54:I:19:GLN:HA	54:I:22:VAL:HG22	2.01	0.43
55:J:63:GLY:HA3	55:J:185:CYS:O	2.18	0.43
57:L:87:LEU:HD23	57:L:87:LEU:H	1.83	0.43
63:R:4:GLN:OE1	63:R:91:TYR:OH	2.34	0.43
67:V:26:THR:OG1	67:V:112:ASP:OD1	2.33	0.43
69:X:30:SER:HB2	69:X:61:ILE:HG13	2.01	0.43
79:h:236:GLU:HB3	79:h:254:THR:HG23	2.00	0.43
1:1:152:U:H4'	1:1:157:G:H4'	2.01	0.43
1:1:179:C:H2'	1:1:180:U:H6	1.83	0.43
1:1:425:G:H5'	33:AF:24:ASP:OD2	2.19	0.43
1:1:521:G:H5''	15:u:72:ALA:HB2	1.99	0.43
1:1:730:A:H8	1:1:733:A:N6	2.17	0.43
1:1:974:G:N2	1:1:975:U:O4	2.39	0.43
1:1:1469:G:OP2	20:z:8:LYS:NZ	2.48	0.43
5:k:123:TYR:CZ	5:k:124:LYS:HG3	2.54	0.43
46:A:114:C:O2'	58:M:65:SER:OG	2.30	0.43
46:A:165:U:H1'	53:H:133:LEU:HD23	2.01	0.43
46:A:304:U:H2'	46:A:305:G:C8	2.54	0.43
46:A:327:G:H2'	46:A:328:G:C8	2.54	0.43
46:A:482:C:H3'	46:A:483:A:H5''	2.00	0.43
46:A:904:A:H2'	46:A:905:C:C6	2.53	0.43
46:A:1062:C:C2	46:A:1063:C:C5	3.07	0.43
46:A:1335:U:HO2'	46:A:1336:G:P	2.39	0.43
46:A:1348:U:H5'	46:A:1349:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1530:A:H1'	46:A:1556:A:C2	2.53	0.43
46:A:1579:A:HO2'	46:A:1580:A:P	2.41	0.43
48:C:89:ASP:OD1	48:C:89:ASP:N	2.50	0.43
59:N:81:GLU:HG3	78:g:156:VAL:HG12	2.00	0.43
60:O:40:TYR:HB3	60:O:45:LEU:HD12	2.01	0.43
65:T:134:ARG:HB2	65:T:136:GLN:NE2	2.28	0.43
79:h:206:SER:HA	79:h:222:LEU:HB2	2.01	0.43
1:1:35:C:H4'	1:1:804:A:C2	2.53	0.43
1:1:371:G:N1	1:1:374:A:OP2	2.38	0.43
1:1:698:C:H2'	1:1:699:G:H8	1.84	0.43
1:1:1022:A:H2	62:Q:72:ARG:HD2	1.84	0.43
1:1:1494:A:H2'	1:1:1495:U:H6	1.84	0.43
1:1:1655:U:H2'	1:1:1656:C:H6	1.84	0.43
1:1:1656:C:H2'	1:1:1657:G:H8	1.84	0.43
1:1:1805:A:H2'	1:1:1806:A:O4'	2.17	0.43
1:1:2958:U:H2'	1:1:2959:A:H8	1.83	0.43
5:k:112:GLU:O	5:k:116:ARG:HG3	2.18	0.43
5:k:113:GLU:HG3	5:k:176:ALA:HB2	2.01	0.43
9:o:76:ASP:OD1	9:o:77:ALA:N	2.52	0.43
13:s:51:ARG:HB3	45:i:31:LYS:NZ	2.34	0.43
20:z:95:TRP:CZ2	20:z:99:LEU:HD22	2.53	0.43
46:A:393:U:H2'	46:A:394:G:O4'	2.17	0.43
46:A:888:U:O2'	46:A:890:A:N7	2.34	0.43
46:A:1701:A:H2'	46:A:1702:A:O4'	2.18	0.43
51:F:97:GLU:OE2	51:F:113:ARG:NH1	2.50	0.43
53:H:98:ARG:HE	53:H:105:ASP:CG	2.26	0.43
63:R:25:LYS:HA	63:R:25:LYS:HD2	1.83	0.43
66:U:103:LYS:HD3	66:U:103:LYS:HA	1.81	0.43
71:Z:20:ARG:HD2	71:Z:74:LEU:HD22	2.00	0.43
79:h:84:ALA:HB2	79:h:114:VAL:HB	2.00	0.43
1:1:46:C:H5''	14:t:16:LYS:HG2	2.00	0.43
1:1:266:C:N4	37:AJ:29:LYS:HA	2.33	0.43
1:1:299:G:C8	37:AJ:30:GLY:HA3	2.54	0.43
1:1:1099:A:N6	1:1:1359:A:H1'	2.34	0.43
1:1:1226:G:N2	1:1:1256:A:N3	2.67	0.43
1:1:1313:A:O2'	1:1:1314:A:H3'	2.19	0.43
1:1:1713:U:H2'	1:1:1714:G:H8	1.84	0.43
1:1:3161:U:H2'	1:1:3162:U:C6	2.53	0.43
1:1:3195:G:H2'	1:1:3196:U:C6	2.53	0.43
5:k:272:TYR:HE1	5:k:334:ARG:HH12	1.67	0.43
11:q:114:ILE:HB	11:q:124:ARG:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:w:9:VAL:HG12	17:w:118:ARG:HG3	2.01	0.43
17:w:131:LYS:HB3	17:w:134:ARG:HG2	2.00	0.43
21:0:42:TRP:O	21:0:46:GLN:HG3	2.19	0.43
46:A:386:G:C6	46:A:408:A:C6	3.07	0.43
46:A:1255:G:H4'	78:g:122:ARG:HH12	1.84	0.43
46:A:1353:G:H2'	46:A:1354:U:C6	2.54	0.43
46:A:1456:C:H5''	46:A:1457:A:O4'	2.19	0.43
46:A:1615:U:H2'	46:A:1616:G:C8	2.54	0.43
50:E:176:VAL:HG12	50:E:178:MET:HE2	2.00	0.43
53:H:56:ASN:HD22	53:H:62:PRO:HA	1.84	0.43
62:Q:81:ARG:HA	62:Q:116:LEU:HD23	2.01	0.43
66:U:49:GLU:O	66:U:53:TRP:HB3	2.19	0.43
69:X:10:ALA:HB1	69:X:27:ILE:HD13	2.01	0.43
72:a:54:VAL:HA	72:a:57:TYR:CD2	2.53	0.43
79:h:247:TYR:CD1	79:h:262:LEU:HD12	2.54	0.43
1:1:79:G:OP1	16:v:189:HIS:NE2	2.46	0.42
1:1:583:A:H2'	1:1:584:C:H6	1.84	0.42
1:1:654:A:H2'	1:1:655:A:H8	1.80	0.42
1:1:673:C:O2'	1:1:677:U:OP1	2.33	0.42
1:1:912:G:N1	4:j:207:VAL:HG11	2.34	0.42
1:1:995:G:H2'	1:1:996:C:C6	2.54	0.42
1:1:1218:G:H1'	1:1:1282:A:H62	1.84	0.42
1:1:1705:C:H2'	1:1:1706:C:H6	1.83	0.42
1:1:2130:A:H2'	1:1:2131:U:H6	1.84	0.42
1:1:2334:A:H61	1:1:2955:C:H5	1.65	0.42
1:1:2744:C:H4'	1:1:2745:C:C5'	2.47	0.42
10:p:113:GLU:O	10:p:117:ILE:HG12	2.19	0.42
11:q:89:LYS:HB2	11:q:183:GLU:HB3	2.00	0.42
35:AH:29[B]:LYS:HB2	35:AH:29[B]:LYS:HE2	1.91	0.42
40:AM:18:LYS:HG2	40:AM:21[A]:ARG:HH21	1.83	0.42
46:A:78:A:H2'	46:A:79:C:H6	1.84	0.42
46:A:239:U:H5''	53:H:216:LEU:HD11	2.00	0.42
46:A:744:U:C2	46:A:745:A:C8	3.07	0.42
46:A:1593:C:H2'	46:A:1594:G:H8	1.81	0.42
47:B:88:LYS:HE3	47:B:201:LEU:HD11	2.00	0.42
51:F:95:THR:HG22	71:Z:16:PRO:HG2	2.01	0.42
63:R:119:ASP:OD1	63:R:120:SER:N	2.52	0.42
65:T:4:VAL:HG22	72:a:82:GLN:OE1	2.19	0.42
70:Y:75:GLN:HE21	70:Y:80:GLY:HA2	1.83	0.42
1:1:627:U:H2'	1:1:628:A:H8	1.83	0.42
1:1:1258:G:C2'	1:1:1259:A:H5'	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1949:G:N1	1:1:2070:A:H2'	2.34	0.42
1:1:2191:A:H2'	1:1:2192:A:H8	1.82	0.42
1:1:2497:A:H2'	1:1:2498:A:C8	2.54	0.42
1:1:2899:C:H2'	1:1:2900:C:C6	2.54	0.42
1:1:3234:U:H1'	8:n:128:LYS:HD2	2.00	0.42
2:3:9:C:OP1	22:2:26:PRO:HB2	2.18	0.42
21:0:23:LYS:HD3	21:0:23:LYS:HA	1.82	0.42
27:9:31:LEU:HB3	27:9:101:PRO:HG2	2.00	0.42
33:AF:17[B]:LYS:HE3	33:AF:19:LYS:HG2	2.00	0.42
39:AL:31:VAL:HG22	39:AL:37:LYS:HA	2.01	0.42
46:A:200:A:H2'	46:A:201:U:C6	2.54	0.42
46:A:1063:C:C2	46:A:1064:U:C5	3.06	0.42
46:A:1332:U:P	67:V:22:ARG:HH12	2.42	0.42
52:G:42:LEU:HD22	52:G:90:VAL:HG11	2.01	0.42
57:L:26:ASP:O	57:L:39:ASN:ND2	2.53	0.42
62:Q:85:VAL:HG23	62:Q:112:VAL:HA	2.01	0.42
1:1:1113:G:OP1	30:AC:4:SER:HB2	2.19	0.42
1:1:1353:G:H2'	1:1:1354:C:C6	2.54	0.42
1:1:1714:G:H2'	1:1:1715:G:C8	2.54	0.42
1:1:1959:G:H2'	1:1:1960:C:C6	2.53	0.42
1:1:2210:A:H2'	1:1:2211:A:C8	2.54	0.42
1:1:2394:U:H2'	1:1:2395:U:C6	2.54	0.42
2:3:107:A:H2'	2:3:108:U:C6	2.54	0.42
3:4:66:A:H2'	3:4:67:U:C6	2.54	0.42
10:p:79:PHE:HA	10:p:180:ILE:HD13	2.00	0.42
13:s:93:SER:N	13:s:172:LEU:O	2.40	0.42
16:v:64:ILE:HG21	16:v:102:ALA:HB1	2.01	0.42
20:z:165:ARG:CZ	46:A:835:A:H5''	2.49	0.42
46:A:325:U:H2'	46:A:326:A:H8	1.85	0.42
46:A:402:G:H2'	46:A:403:C:C6	2.54	0.42
46:A:601:U:H2'	46:A:602:A:H8	1.84	0.42
46:A:1523:G:H2'	46:A:1525:U:C6	2.54	0.42
71:Z:45:ALA:HB1	71:Z:50:ALA:O	2.20	0.42
72:a:48:ASP:OD1	72:a:48:ASP:N	2.51	0.42
79:h:123:ILE:N	79:h:135:TRP:O	2.46	0.42
79:h:165:THR:OG1	79:h:178:TRP:O	2.36	0.42
1:1:58:G:H2'	3:4:33:A:O2'	2.20	0.42
1:1:534:G:H1	1:1:551:U:H3	1.68	0.42
1:1:589:G:O2'	8:n:16:ALA:O	2.33	0.42
1:1:602:A:H2'	1:1:603:C:C6	2.54	0.42
1:1:972:U:H2'	1:1:973:C:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:j:147:ARG:HG3	4:j:147:ARG:HH11	1.84	0.42
4:j:201:GLY:HA2	4:j:204:MET:SD	2.59	0.42
19:y:96:PHE:CD1	19:y:97:PRO:HD2	2.54	0.42
26:8:105:VAL:HG21	26:8:126:LEU:HD13	2.01	0.42
46:A:137:A:H4'	46:A:138:C:O5'	2.19	0.42
46:A:547:G:H2'	46:A:548:A:C8	2.55	0.42
46:A:828:U:O4	46:A:829:A:N6	2.53	0.42
46:A:880:G:N2	61:P:33:THR:OG1	2.52	0.42
46:A:1438:U:H2'	46:A:1439:G:C8	2.53	0.42
47:B:65:ALA:HA	47:B:185:ARG:HE	1.84	0.42
50:E:171:ILE:HG12	50:E:188:LYS:HG3	2.01	0.42
64:S:41:ILE:HG21	64:S:47:ARG:HB2	1.99	0.42
67:V:92:LEU:HD23	67:V:92:LEU:HA	1.83	0.42
79:h:40:LYS:HD2	79:h:65:HIS:O	2.19	0.42
1:1:787:A:H2'	1:1:788:G:C8	2.54	0.42
1:1:976:A:H2	1:1:1100:G:H21	1.68	0.42
1:1:1892:A:N6	1:1:2317:C:H42	2.11	0.42
1:1:2342:G:H22	1:1:2374:G:H1'	1.84	0.42
1:1:2504:C:H2'	1:1:2505:G:C8	2.55	0.42
1:1:2661:A:H2'	1:1:2661:A:N3	2.34	0.42
1:1:3302:G:H2'	1:1:3303:C:C6	2.54	0.42
3:4:143:U:H2'	3:4:144:G:O4'	2.20	0.42
9:o:149:ARG:HD2	9:o:205:LEU:HD23	2.01	0.42
43:AP:65:THR:HG22	43:AP:89:LYS:HD3	2.00	0.42
46:A:78:A:H5'	53:H:154:ARG:CG	2.50	0.42
46:A:147:C:N3	46:A:164:C:N4	2.68	0.42
46:A:279:G:P	46:A:279:G:H8	2.41	0.42
46:A:1162:C:H4'	46:A:1174:A:N1	2.34	0.42
46:A:1231:C:H2'	46:A:1232:U:O4'	2.20	0.42
46:A:1351:U:O2'	66:U:7:ARG:NH1	2.52	0.42
46:A:1457:A:HO2'	46:A:1458:C:P	2.41	0.42
50:E:141:GLY:HA3	50:E:183:LEU:HD23	2.00	0.42
52:G:32:ASP:OD1	52:G:33:VAL:N	2.52	0.42
54:I:137:ARG:HG2	69:X:51:GLU:OE1	2.19	0.42
66:U:14:PHE:HB3	66:U:63:ARG:NH1	2.34	0.42
69:X:66:ASN:OD1	69:X:68:ARG:HG2	2.19	0.42
75:d:27:GLN:NE2	75:d:43:ASN:OD1	2.52	0.42
77:f:42:ARG:HH12	77:f:56:MET:HE1	1.84	0.42
78:g:158:ARG:NH1	78:g:162:GLU:OE2	2.52	0.42
1:1:291:C:H2'	1:1:292:U:C6	2.55	0.42
1:1:683:G:OP2	14:t:35:ARG:NH1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1663:A:H2'	1:1:1664:G:H8	1.84	0.42
1:1:1852:C:C2	1:1:1853:C:C5	3.08	0.42
1:1:1970:A:H2'	1:1:1971:C:H6	1.84	0.42
1:1:2130:A:H2'	1:1:2131:U:C6	2.54	0.42
1:1:2686:G:OP2	43:AP:10:THR:HG22	2.19	0.42
1:1:2774:A:H5'	43:AP:56:GLN:HB3	2.01	0.42
1:1:3314:C:H2'	1:1:3315:C:C6	2.54	0.42
11:q:109:GLN:HB3	11:q:127:LYS:HE2	1.99	0.42
26:8:50:SER:HB2	36:AI:66:VAL:HG11	2.02	0.42
35:AH:106[A]:LYS:HB3	35:AH:106[A]:LYS:HE2	1.82	0.42
45:i:99:SER:HB3	46:A:573:C:OP1	2.18	0.42
46:A:119:A:H1'	46:A:395:A:C4	2.55	0.42
46:A:121:U:O2'	51:F:33:ALA:O	2.36	0.42
46:A:520:U:H2'	46:A:521:G:O4'	2.20	0.42
46:A:1195:C:C2	46:A:1440:G:C2	3.07	0.42
46:A:1212:A:C8	59:N:116:VAL:HG11	2.55	0.42
46:A:1218:G:H22	78:g:184:GLY:HA3	1.84	0.42
46:A:1252:G:H1	46:A:1428:U:H3	1.66	0.42
46:A:1258:G:N7	46:A:1416:U:H3'	2.35	0.42
46:A:1369:G:O2'	46:A:1370:A:H8	2.02	0.42
46:A:1424:G:H2'	46:A:1425:C:C6	2.55	0.42
46:A:1565:U:H2'	46:A:1566:U:H6	1.83	0.42
46:A:1612:C:H2'	46:A:1613:U:H6	1.85	0.42
49:D:138:TYR:O	69:X:98:GLN:NE2	2.53	0.42
53:H:57:ASP:HA	53:H:106:LEU:HA	2.01	0.42
54:I:12:GLU:O	54:I:16:LYS:HG2	2.20	0.42
58:M:115:PHE:HB3	58:M:142:VAL:HG21	2.01	0.42
71:Z:83:LYS:HE2	71:Z:96:LEU:HD12	2.00	0.42
1:1:138:G:H2'	1:1:139:U:C6	2.54	0.42
1:1:194:U:H2'	1:1:195:G:O4'	2.19	0.42
1:1:593:G:H2'	1:1:594:C:C6	2.55	0.42
1:1:1287:A:H2'	1:1:1288:C:O4'	2.19	0.42
1:1:1547:C:O2'	1:1:2148:U:O2'	2.32	0.42
1:1:2276:U:O2'	1:1:2277:A:H5'	2.19	0.42
5:k:74:GLU:OE1	5:k:325:LYS:HE3	2.20	0.42
23:5:92:ILE:HB	23:5:96:ILE:HD13	2.02	0.42
27:9:54:ASP:CG	27:9:115:ARG:HH12	2.26	0.42
46:A:331:A:C5	55:J:49:ARG:HD3	2.55	0.42
46:A:446:C:OP1	51:F:29:PRO:HG3	2.19	0.42
46:A:461:U:H2'	46:A:462:A:H8	1.85	0.42
46:A:475:A:H2'	46:A:476:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:721:C:O2'	46:A:722:A:H8	2.03	0.42
46:A:1143:C:O2'	46:A:1568:C:OP2	2.32	0.42
46:A:1369:G:P	67:V:88:ARG:HH22	2.42	0.42
46:A:1439:G:H1'	62:Q:97:TYR:HD1	1.85	0.42
54:I:92:ARG:NH1	54:I:120:LYS:HB3	2.34	0.42
65:T:105:LEU:O	65:T:109:LEU:HD23	2.19	0.42
70:Y:27:GLN:OE1	70:Y:27:GLN:N	2.49	0.42
71:Z:29:HIS:CE1	71:Z:34:ASN:HA	2.55	0.42
73:b:88:SER:O	73:b:92:ARG:HG3	2.20	0.42
1:1:2060:G:N1	1:1:2061:G:O6	2.53	0.42
1:1:2402:A:N1	4:j:230:VAL:HG11	2.35	0.42
1:1:2418:A:H2'	1:1:2419:A:C8	2.55	0.42
1:1:2808:OMC:HM23	1:1:2808:OMC:H1'	1.75	0.42
3:4:106:C:H4'	3:4:107:G:H5''	2.01	0.42
5:k:160:VAL:HB	5:k:183:ILE:HD11	2.01	0.42
23:5:18:ASP:HB2	23:5:63:LYS:HG2	2.02	0.42
26:8:108:LEU:N	26:8:125:ARG:O	2.49	0.42
44:AQ:84:ARG:O	44:AQ:88:GLU:HG2	2.20	0.42
46:A:271:G:H2'	46:A:272:G:H8	1.85	0.42
46:A:551:G:OP2	46:A:552:C:O2'	2.25	0.42
46:A:590:A:H2'	46:A:591:A:O4'	2.20	0.42
46:A:1375:C:O2'	64:S:52:GLY:HA3	2.20	0.42
46:A:1437:C:H5''	76:e:10:HIS:HB2	2.01	0.42
46:A:1491:G:H5'	66:U:97:SER:HA	2.02	0.42
47:B:43:ASP:OD1	47:B:44:GLY:N	2.53	0.42
48:C:31:ASP:O	48:C:96:LEU:N	2.53	0.42
50:E:28:ARG:HD2	57:L:60:SER:HB2	2.02	0.42
74:c:33:MET:HE3	74:c:33:MET:HB2	1.90	0.42
79:h:21:THR:HG22	79:h:287:ILE:HD12	2.02	0.42
1:1:1656:C:H2'	1:1:1657:G:C8	2.55	0.42
1:1:2720:A:H1'	7:m:36:LEU:HD23	2.01	0.42
1:1:3260:A:H2'	1:1:3261:A:H8	1.84	0.42
1:1:3264:C:C2	1:1:3265:U:C5	3.08	0.42
21:0:90:MET:HE2	21:0:90:MET:HB3	1.94	0.42
32:AE:82:GLU:HA	32:AE:83:ASP:HA	1.76	0.42
40:AM:41:ARG:HA	40:AM:41:ARG:HD2	1.81	0.42
45:i:107:TRP:HB3	50:E:151:GLN:HE22	1.85	0.42
46:A:97:C:H2'	46:A:98:U:C6	2.54	0.42
46:A:1399:U:O2'	46:A:1400:U:OP1	2.34	0.42
56:K:49:LEU:HD13	56:K:104:PHE:CE2	2.55	0.42
1:1:428:U:H2'	1:1:429:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:498:C:H2'	1:1:499:G:C8	2.54	0.42
1:1:1311:U:OP2	17:w:45:SER:OG	2.34	0.42
1:1:1408:G:OP1	33:AF:106:ARG:NH2	2.53	0.42
1:1:1444:U:OP1	18:x:67:ILE:HG22	2.20	0.42
1:1:1592:C:H2'	1:1:1593:C:H6	1.85	0.42
1:1:1661:U:H2'	1:1:1662:G:H8	1.84	0.42
1:1:3264:C:H2'	1:1:3265:U:C6	2.55	0.42
3:4:81:A:H2'	3:4:82:U:C6	2.55	0.42
5:k:165:GLN:NE2	5:k:202:GLU:OE2	2.39	0.42
11:q:134:MET:HE1	11:q:157:ASN:HB3	2.02	0.42
35:AH:58:ARG:CD	35:AH:59:PRO:HD2	2.38	0.42
36:AI:50:ASN:OD1	36:AI:53:ARG:NH1	2.53	0.42
38:AK:69:HIS:O	38:AK:73:ARG:HG3	2.20	0.42
46:A:34:G:O2'	46:A:513:A:O2'	2.37	0.42
46:A:205:U:H2'	46:A:206:U:C6	2.54	0.42
46:A:480:U:H2'	46:A:481:A:O4'	2.18	0.42
46:A:1195:C:N4	46:A:1196:A:H62	2.18	0.42
46:A:1396:A:O2'	46:A:1397:A:P	2.78	0.42
46:A:1739:U:H2'	46:A:1740:A:H8	1.85	0.42
52:G:98:MET:HG2	52:G:98:MET:O	2.20	0.42
55:J:78:ILE:HD11	55:J:102:VAL:HG21	2.01	0.42
60:O:132:VAL:HG23	60:O:134:VAL:HG23	2.02	0.42
67:V:21:ILE:HG12	67:V:117:ILE:HG13	2.02	0.42
79:h:102:GLN:NE2	79:h:138:ILE:O	2.53	0.42
1:1:86:U:OP1	19:y:167:SER:OG	2.27	0.41
1:1:1029:U:H4'	1:1:1030:U:OP1	2.20	0.41
1:1:1569:C:H2'	1:1:1570:A:C8	2.55	0.41
1:1:1936:G:N2	1:1:3327:A:H8	2.13	0.41
1:1:2540:G:H2'	1:1:2541:C:C6	2.55	0.41
1:1:3129:C:H2'	1:1:3130:C:H6	1.84	0.41
6:l:35:LEU:HD13	6:l:121:TYR:CE2	2.55	0.41
6:l:206:PRO:HB3	6:l:248:PHE:CD2	2.55	0.41
10:p:73:PRO:HG3	16:v:18:VAL:HA	2.02	0.41
11:q:41:ILE:HG22	11:q:43:VAL:HG13	2.02	0.41
14:t:69:VAL:HG11	14:t:152:PRO:HD3	2.02	0.41
19:y:83:VAL:O	19:y:103:ALA:HA	2.19	0.41
19:y:153:PHE:O	19:y:161:LYS:NZ	2.41	0.41
20:z:98:ARG:HD2	20:z:133:LYS:O	2.20	0.41
25:7:22:VAL:HG22	25:7:28:ILE:HG22	2.02	0.41
28:AA:119:GLU:O	28:AA:123:GLN:HG2	2.20	0.41
46:A:137:A:O4'	46:A:139:U:H5'	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:330:U:P	55:J:56:ARG:HH22	2.43	0.41
46:A:339:A:H2'	46:A:340:C:C6	2.55	0.41
46:A:1141:C:H2'	46:A:1142:A:C8	2.54	0.41
46:A:1348:U:H3'	46:A:1349:G:H8	1.85	0.41
46:A:1552:C:H5''	65:T:41:ARG:HG2	2.02	0.41
46:A:1739:U:C2	46:A:1740:A:C8	3.08	0.41
65:T:132:LYS:HD2	65:T:138:THR:HG22	2.02	0.41
67:V:31:LYS:HA	67:V:31:LYS:HE2	2.02	0.41
79:h:76:ALA:HB3	79:h:120:LEU:HD11	2.02	0.41
79:h:130:LYS:HG2	79:h:150:ASP:C	2.45	0.41
1:1:783:G:H2'	1:1:784:C:H6	1.84	0.41
1:1:1355:U:H2'	1:1:1356:U:C6	2.55	0.41
1:1:1616:U:H2'	1:1:1617:A:C8	2.55	0.41
1:1:1939:C:H4'	1:1:3311:U:H4'	2.01	0.41
1:1:2204:U:H2'	1:1:2205:C:C6	2.55	0.41
1:1:2694:U:O2'	22:2:88:ARG:O	2.32	0.41
1:1:2881:U:H2'	1:1:2882:A:O4'	2.21	0.41
13:s:110:ILE:HG21	13:s:116:TYR:HD1	1.85	0.41
14:t:173:ARG:HD2	14:t:173:ARG:HA	1.88	0.41
34:AG:49:ILE:HD11	34:AG:71:VAL:HG22	2.02	0.41
45:i:105:GLN:HA	45:i:113:ARG:HH12	1.85	0.41
45:i:121:GLY:O	50:E:122:GLY:HA2	2.21	0.41
46:A:481:A:H2	46:A:504:A:N6	2.19	0.41
46:A:625:C:H2'	46:A:626:G:O4'	2.19	0.41
46:A:655:U:H5'	46:A:676:G:C6	2.55	0.41
46:A:1196:A:C6	46:A:1439:G:C6	3.08	0.41
46:A:1470:G:H2'	46:A:1471:C:H6	1.85	0.41
46:A:1495:U:H2'	46:A:1496:C:H6	1.84	0.41
46:A:1581:G:O2'	46:A:1582:U:OP1	2.31	0.41
61:P:56:MET:HE2	61:P:56:MET:HB3	1.97	0.41
66:U:126:GLU:O	66:U:130:ARG:HG2	2.20	0.41
71:Z:22:GLN:HB2	71:Z:72:PHE:CZ	2.55	0.41
79:h:145:LEU:HD21	79:h:183:TYR:HB3	2.03	0.41
1:1:108:A:N1	1:1:322:U:O2'	2.52	0.41
1:1:622:G:H2'	1:1:623:A:C8	2.55	0.41
1:1:1328:A:H2	9:o:207:ASN:ND2	2.19	0.41
1:1:1474:C:H2'	1:1:1475:U:H6	1.85	0.41
1:1:2540:G:H2'	1:1:2541:C:H6	1.85	0.41
2:3:77:G:H3'	21:0:46:GLN:O	2.21	0.41
20:z:165:ARG:NH2	46:A:835:A:H5''	2.35	0.41
21:0:96:ASP:OD1	21:0:101:GLY:HA3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:7:4:GLU:CD	25:7:30:ARG:HD2	2.46	0.41
29:AB:35:ALA:O	29:AB:41:HIS:ND1	2.49	0.41
38:AK:18:LEU:HA	38:AK:25:ARG:HA	2.01	0.41
46:A:81:G:H2'	46:A:82:U:C6	2.55	0.41
46:A:279:G:H2'	46:A:280:C:C6	2.55	0.41
46:A:483:A:H2'	46:A:484:G:O4'	2.20	0.41
46:A:547:G:H2'	46:A:548:A:H8	1.85	0.41
46:A:685:C:O2'	46:A:686:G:OP1	2.34	0.41
46:A:809:G:H2'	46:A:810:U:C6	2.55	0.41
46:A:1233:C:N4	46:A:1234:U:O4	2.53	0.41
46:A:1285:A:H5''	49:D:81:VAL:HG21	2.03	0.41
46:A:1366:U:O2'	46:A:1503:A:N1	2.47	0.41
49:D:225:TRP:CE3	69:X:68:ARG:NH2	2.88	0.41
50:E:10:LYS:HE2	76:e:34:TYR:HA	2.02	0.41
50:E:71:THR:HB	50:E:87:ILE:HD12	2.03	0.41
52:G:36:ALA:HB2	52:G:44:ASN:ND2	2.36	0.41
53:H:39:ASP:OD1	53:H:47:GLY:N	2.29	0.41
54:I:13:LEU:O	54:I:17:VAL:HG22	2.20	0.41
58:M:75:VAL:HG21	58:M:117:VAL:HG21	2.02	0.41
59:N:47:GLU:HA	59:N:50:LYS:HB3	2.02	0.41
59:N:57:ALA:HB1	59:N:126:TRP:HZ3	1.84	0.41
69:X:21:GLY:HA2	69:X:23:ARG:HH21	1.84	0.41
71:Z:18:LEU:HD23	71:Z:20:ARG:HD3	2.01	0.41
71:Z:21:ARG:CZ	71:Z:75:ILE:HD11	2.50	0.41
1:1:183:U:H2'	1:1:184:C:C6	2.55	0.41
1:1:406:G:N3	3:4:16:G:C2	2.89	0.41
1:1:796:G:H22	6:l:102:ALA:HA	1.85	0.41
1:1:1242:G:C8	1:1:1260:G:C8	3.08	0.41
1:1:1308:C:H2'	1:1:1309:G:O4'	2.20	0.41
1:1:1777:C:H2'	1:1:1778:U:C6	2.55	0.41
1:1:3196:U:H2'	1:1:3197:G:C8	2.54	0.41
2:3:81:U:H2'	2:3:82:G:C8	2.55	0.41
3:4:27:U:H2'	3:4:28:C:C6	2.55	0.41
12:r:47:PRO:HB3	12:r:171:TRP:CZ2	2.55	0.41
20:z:166:ASN:O	20:z:170:ARG:HG3	2.19	0.41
23:5:78:TYR:CE2	23:5:82:LEU:HD11	2.55	0.41
24:6:32:ARG:HD2	24:6:64:LYS:NZ	2.35	0.41
31:AD:27:LEU:HD11	31:AD:85:LYS:HE3	2.03	0.41
46:A:238:U:H2'	46:A:239:U:C6	2.56	0.41
46:A:1102:U:H2'	46:A:1103:G:C8	2.56	0.41
62:Q:87:PRO:HG3	62:Q:112:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:R:59:PHE:HA	63:R:62:ILE:HG12	2.02	0.41
68:W:15:ARG:HG3	68:W:24:ILE:HD12	2.01	0.41
1:1:241:C:O2'	1:1:242:C:H5'	2.21	0.41
1:1:600:U:C2	1:1:602:A:H1'	2.56	0.41
1:1:689:A:N1	3:4:28:C:O2'	2.49	0.41
1:1:2524:C:H2'	1:1:2525:A:C8	2.55	0.41
1:1:2581:A:H2'	1:1:2582:G:C8	2.55	0.41
1:1:2623:G:H5''	1:1:2624:U:O4'	2.20	0.41
1:1:3056:C:H2'	1:1:3057:G:O4'	2.21	0.41
1:1:3313:G:H2'	1:1:3314:C:H6	1.85	0.41
10:p:187:LEU:HD23	10:p:187:LEU:HA	1.92	0.41
16:v:94:TYR:CE2	16:v:96:LYS:HB2	2.56	0.41
46:A:194:G:C2	46:A:195:A:H1'	2.56	0.41
46:A:208:A:H2'	46:A:209:U:C6	2.55	0.41
46:A:217:A:P	46:A:217:A:O4'	2.79	0.41
46:A:478:G:C4	46:A:507:G:N2	2.89	0.41
46:A:1276:G:N2	46:A:1309:G:H22	2.17	0.41
46:A:1297:A:OP1	64:S:2:GLY:N	2.53	0.41
46:A:1533:G:H2'	46:A:1534:A:H8	1.85	0.41
46:A:1573:A:HO2'	46:A:1574:A:P	2.41	0.41
46:A:1604:U:H2'	46:A:1605:C:C6	2.55	0.41
56:K:25:ASP:HB3	77:f:44:PHE:HZ	1.85	0.41
79:h:20:VAL:HG21	79:h:307:ILE:HG12	2.02	0.41
79:h:75:SER:HB2	79:h:120:LEU:HD21	2.01	0.41
1:1:482:U:H2'	1:1:483:U:C4	2.54	0.41
1:1:571:C:H2'	1:1:572:U:C6	2.56	0.41
1:1:1170:G:H2'	1:1:1171:C:C6	2.56	0.41
1:1:1220:C:C2	1:1:1221:A:C8	3.08	0.41
1:1:1385:G:H5''	33:AF:102:SER:HB3	2.01	0.41
1:1:1755:U:H2'	1:1:1756:A:H5''	2.03	0.41
1:1:2339:A:H2'	1:1:2340:C:C6	2.56	0.41
1:1:2700:G:O6	22:2:78:LYS:HE3	2.20	0.41
1:1:2737:C:O3'	43:AP:39:GLY:HA3	2.21	0.41
12:r:50:ILE:HD13	12:r:149:ILE:HG13	2.03	0.41
31:AD:94:ILE:HD13	31:AD:102:ILE:HG21	2.02	0.41
43:AP:65:THR:OG1	43:AP:87:ARG:HB3	2.21	0.41
46:A:518:A:HO2'	46:A:519:A:P	2.44	0.41
46:A:678:A:H2'	46:A:679:C:O4'	2.21	0.41
46:A:698:C:H2'	46:A:699:U:C6	2.56	0.41
46:A:1088:U:H2'	46:A:1089:U:C6	2.55	0.41
46:A:1535:G:H2'	46:A:1536:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:B:9:LEU:HD13	47:B:54:TRP:CG	2.55	0.41
51:F:214:LEU:HB2	51:F:216:ASN:OD1	2.21	0.41
56:K:62:ARG:CZ	56:K:68:LYS:HD3	2.51	0.41
56:K:110:GLN:OE1	56:K:126:ARG:HB2	2.20	0.41
58:M:132:SER:OG	58:M:133:LYS:N	2.54	0.41
60:O:102:LEU:HD23	60:O:102:LEU:HA	1.82	0.41
60:O:102:LEU:HD11	60:O:112:LYS:HA	2.02	0.41
67:V:24:THR:OG1	67:V:89:VAL:HG12	2.20	0.41
75:d:43:ASN:ND2	75:d:66:LEU:HD11	2.35	0.41
76:e:15:GLY:H	76:e:18:SER:HB3	1.86	0.41
1:1:713:A:O2'	1:1:748:C:O2'	2.35	0.41
1:1:716:G:O2'	1:1:717:A:OP1	2.32	0.41
1:1:756:G:H1'	1:1:767:A:N6	2.36	0.41
1:1:1194:C:OP2	1:1:1195:C:O2'	2.29	0.41
1:1:1231:U:N3	1:1:1259:A:C8	2.89	0.41
1:1:1322:A:H2'	1:1:1323:C:O4'	2.19	0.41
1:1:1714:G:H2'	1:1:1715:G:H8	1.86	0.41
1:1:2694:U:H2'	1:1:2695:U:H6	1.84	0.41
1:1:3001:A:H8	1:1:3001:A:O5'	2.04	0.41
1:1:3091:U:H4'	41:AN:28:PRO:HG2	2.03	0.41
1:1:3250:C:H2'	1:1:3251:G:H8	1.86	0.41
1:1:3264:C:H2'	1:1:3265:U:H6	1.86	0.41
1:1:3298:G:N2	1:1:3334:G:O2'	2.53	0.41
15:u:25:GLU:OE2	15:u:25:GLU:N	2.54	0.41
16:v:91:GLN:O	16:v:93:LYS:NZ	2.52	0.41
40:AM:23:LEU:HD12	40:AM:24:PRO:HD2	2.02	0.41
45:i:43:PRO:HG2	45:i:46:ALA:HB2	2.03	0.41
46:A:736:G:H2'	46:A:737:A:H8	1.85	0.41
46:A:881:U:H2'	46:A:882:C:C6	2.56	0.41
46:A:1160:U:H3	46:A:1450:G:H1	1.68	0.41
46:A:1459:U:O3'	52:G:109:LYS:HD3	2.21	0.41
46:A:1533:G:H2'	46:A:1534:A:C8	2.56	0.41
46:A:1613:U:H2'	46:A:1614:U:C6	2.56	0.41
46:A:1712:U:H2'	46:A:1713:G:C8	2.55	0.41
47:B:4:PRO:HG3	68:W:41:GLU:HA	2.02	0.41
47:B:25:GLY:HA3	47:B:48:ILE:HD11	2.02	0.41
47:B:133:ILE:O	47:B:136:SER:OG	2.32	0.41
52:G:72:HIS:CD2	52:G:107:LYS:HD3	2.56	0.41
53:H:32:MET:HG3	53:H:100:CYS:SG	2.61	0.41
55:J:89:GLU:O	55:J:93:THR:HG22	2.20	0.41
61:P:9:PHE:HD1	61:P:73:ALA:HB3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:f:41:THR:O	77:f:45:VAL:HB	2.21	0.41
1:1:445:A:H61	1:1:485:A:N6	2.10	0.41
1:1:495:C:H4'	8:n:79:ASN:HD21	1.85	0.41
1:1:948:A:H4'	1:1:964:G:N2	2.35	0.41
1:1:1068:G:H2'	1:1:1069:U:C6	2.56	0.41
1:1:1230:G:H8	1:1:1230:G:OP2	2.04	0.41
1:1:1260:G:O5'	1:1:1260:G:C8	2.70	0.41
1:1:1415:A:OP1	3:4:20:U:O2'	2.35	0.41
1:1:1502:A:H1'	1:1:1844:G:O6	2.21	0.41
1:1:2185:A:H2'	46:A:898:G:H4'	2.02	0.41
1:1:2391:A:H2'	1:1:2392:G:C8	2.55	0.41
1:1:2395:U:OP2	1:1:2578:G:O2'	2.31	0.41
6:l:315:LYS:HE2	9:o:160:ALA:HB1	2.02	0.41
12:r:190:VAL:HG22	12:r:199:PHE:HD1	1.86	0.41
16:v:193:LYS:HB3	16:v:193:LYS:HE2	1.84	0.41
18:x:169:ASN:OD1	18:x:170:SER:N	2.53	0.41
19:y:67:ILE:HG12	19:y:81:ILE:HG21	2.02	0.41
39:AL:46:ARG:HD3	39:AL:47:GLY:O	2.20	0.41
42:AO:2:ARG:HD3	42:AO:5:TRP:NE1	2.35	0.41
46:A:62:A:H4'	46:A:266:C:O2'	2.21	0.41
46:A:392:C:H2'	46:A:393:U:C6	2.55	0.41
46:A:1535:G:H2'	46:A:1536:C:H6	1.86	0.41
49:D:173:ILE:HD11	49:D:189:GLU:HA	2.02	0.41
51:F:64:ILE:CD1	71:Z:18:LEU:HB2	2.45	0.41
63:R:12:LYS:HB3	63:R:75:SER:OG	2.21	0.41
66:U:12:GLN:HE22	66:U:16:ASN:HD21	1.68	0.41
67:V:102:ILE:O	67:V:106:THR:HG23	2.20	0.41
77:f:42:ARG:HD2	77:f:42:ARG:C	2.45	0.41
77:f:49:LEU:HD12	77:f:52:GLY:N	2.34	0.41
1:1:148:U:P	16:v:49:ARG:HH12	2.44	0.41
1:1:155:A:OP2	37:AJ:24:LYS:HB3	2.21	0.41
1:1:225:C:H2'	1:1:226:G:O4'	2.21	0.41
1:1:356:C:O2'	6:l:82:GLY:O	2.31	0.41
1:1:425:G:H2'	1:1:426:G:H8	1.86	0.41
1:1:698:C:H2'	1:1:699:G:C8	2.56	0.41
1:1:754:C:H5''	43:AP:18:ARG:HH22	1.86	0.41
1:1:780:A:H2'	19:y:69:ARG:HH21	1.86	0.41
1:1:1218:G:O2'	1:1:1219:A:OP2	2.35	0.41
1:1:1277:G:H3'	1:1:1278:G:H8	1.85	0.41
1:1:1291:G:H2'	1:1:1292:C:C6	2.56	0.41
1:1:2339:A:H2'	1:1:2340:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2418:A:H2'	1:1:2419:A:H8	1.85	0.41
1:1:2639:A:H2'	1:1:2640:U:O4'	2.20	0.41
1:1:2695:U:H2'	1:1:2696:U:C6	2.56	0.41
1:1:2876:U:H2'	1:1:2877:U:H6	1.85	0.41
1:1:2908:A:H2'	1:1:2909:G:C8	2.56	0.41
1:1:3036:U:H2'	1:1:3037:G:H8	1.86	0.41
1:1:3111:A:H2'	1:1:3112:G:O4'	2.21	0.41
1:1:3183:A:H5''	1:1:3184:G:C5	2.56	0.41
1:1:3248:U:H2'	1:1:3249:G:H8	1.84	0.41
5:k:80:ASP:OD1	5:k:319:ASN:HB2	2.21	0.41
6:l:137:LEU:HD21	6:l:144:GLU:HG3	2.03	0.41
10:p:99:ARG:NH1	10:p:190:LEU:HA	2.34	0.41
13:s:82:ARG:HH21	13:s:112:LEU:HB3	1.86	0.41
18:x:176:LEU:HG	18:x:180:LYS:NZ	2.36	0.41
27:9:74:TYR:HD2	27:9:77:LYS:HB2	1.86	0.41
28:AA:23:VAL:HG12	28:AA:45:GLY:HA3	2.02	0.41
28:AA:84:ARG:HG3	28:AA:84:ARG:NH1	2.36	0.41
31:AD:63:MET:HE3	31:AD:63:MET:HB3	1.89	0.41
42:AO:13:LEU:HD11	46:A:1736:A:O2'	2.21	0.41
45:i:115:LEU:O	45:i:119:VAL:HG22	2.20	0.41
46:A:19:A:H2'	46:A:20:G:O4'	2.20	0.41
46:A:180:A:H2'	46:A:181:U:C6	2.56	0.41
46:A:430:G:H2'	46:A:431:C:C6	2.56	0.41
46:A:514:G:O2'	46:A:515:U:OP1	2.36	0.41
46:A:553:A:H4'	46:A:554:A:OP1	2.21	0.41
46:A:872:A:H5''	61:P:115:PRO:CB	2.50	0.41
46:A:909:A:H2'	46:A:910:G:C8	2.56	0.41
46:A:917:U:OP2	48:C:155:TYR:OH	2.25	0.41
46:A:975:C:H2'	46:A:976:G:O4'	2.21	0.41
46:A:1229:A:H2'	46:A:1231:C:O2	2.21	0.41
46:A:1386:A:H2'	46:A:1387:A:C8	2.56	0.41
46:A:1551:U:OP1	66:U:38:LYS:NZ	2.38	0.41
47:B:70:ALA:O	47:B:95:ALA:HA	2.20	0.41
48:C:56:ASN:OD1	48:C:57:ALA:N	2.54	0.41
49:D:61:TYR:CD1	49:D:125:VAL:HG13	2.56	0.41
50:E:151:GLN:HB3	50:E:153:TYR:CE1	2.54	0.41
51:F:228:ILE:HD12	51:F:239:LEU:HD21	2.03	0.41
52:G:110:ALA:HA	52:G:113:ILE:HD12	2.02	0.41
53:H:2:LYS:HA	53:H:17:ASP:HA	2.03	0.41
53:H:68:MET:HA	53:H:101:ILE:HD11	2.03	0.41
54:I:150:LEU:O	54:I:182:PRO:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:K:32:GLY:HA3	77:f:40:TYR:CG	2.56	0.41
57:L:89:LEU:HA	57:L:92:LEU:HD23	2.03	0.41
60:O:98:VAL:HG13	60:O:115:LEU:HD13	2.03	0.41
63:R:47:VAL:HA	63:R:81:ARG:HB3	2.03	0.41
77:f:42:ARG:CZ	77:f:56:MET:HE1	2.51	0.41
79:h:82:LEU:HD11	79:h:123:ILE:HD13	2.03	0.41
79:h:102:GLN:NE2	79:h:139:GLY:HA3	2.35	0.41
79:h:161:ASP:OD1	79:h:161:ASP:N	2.42	0.41
79:h:166:VAL:O	79:h:178:TRP:N	2.38	0.41
1:1:1116:A:H2'	1:1:1117:U:H6	1.86	0.41
1:1:1740:G:H2'	1:1:1741:C:C6	2.55	0.41
1:1:1917:A:H2'	1:1:1918:A:H8	1.83	0.41
1:1:3197:G:C6	1:1:3221:G:C6	3.09	0.41
11:q:25:VAL:HG11	11:q:75:ILE:HG23	2.03	0.41
36:AI:92:LEU:HD22	36:AI:96:GLU:HB3	2.03	0.41
45:i:53:LYS:C	45:i:55:LYS:H	2.29	0.41
46:A:405:A:H2'	46:A:406:C:H6	1.86	0.41
46:A:603:A:OP2	46:A:604:A:O2'	2.26	0.41
46:A:638:U:C4	54:I:114:LEU:HD11	2.55	0.41
46:A:919:C:C4	46:A:1062:C:H4'	2.56	0.41
46:A:1301:G:OP1	64:S:7:LYS:N	2.40	0.41
46:A:1519:U:H3'	72:a:77:ARG:HH22	1.86	0.41
46:A:1588:G:OP1	66:U:86:ARG:NH2	2.54	0.41
46:A:1665:C:H2'	46:A:1666:G:O4'	2.21	0.41
50:E:138:VAL:HG22	50:E:152:LYS:HG3	2.03	0.41
52:G:196:GLU:O	52:G:200:ASN:ND2	2.53	0.41
64:S:37:GLU:CD	79:h:151:TRP:HE1	2.26	0.41
64:S:99:GLN:HB2	64:S:118:PRO:O	2.21	0.41
67:V:27:SER:HB3	67:V:111:VAL:HG22	2.03	0.41
67:V:40:ILE:HG23	67:V:102:ILE:HG21	2.03	0.41
71:Z:5:VAL:HB	71:Z:43:LYS:HE2	2.03	0.41
75:d:10:ALA:HB1	75:d:30:VAL:HB	2.03	0.41
76:e:39:CYS:O	76:e:43:PHE:N	2.54	0.41
1:1:585:C:O2'	1:1:586:G:H5'	2.21	0.40
1:1:1163:U:H2'	1:1:1164:U:O4'	2.21	0.40
1:1:1827:U:H2'	1:1:1828:C:C6	2.56	0.40
13:s:13:ARG:HH22	13:s:134:ALA:HA	1.86	0.40
18:x:94:LEU:HD23	18:x:94:LEU:HA	1.87	0.40
43:AP:90[B]:HIS:NE2	43:AP:92:GLU:OE1	2.54	0.40
46:A:78:A:H2'	46:A:79:C:C6	2.56	0.40
46:A:1187:A:H3'	46:A:1187:A:N3	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1373:G:N7	64:S:44:LYS:NZ	2.51	0.40
49:D:37:GLY:HA2	49:D:40:VAL:HG12	2.03	0.40
49:D:100:GLY:HA3	49:D:185:LEU:HB3	2.04	0.40
54:I:134:LYS:C	54:I:135:ARG:HD2	2.46	0.40
56:K:150:LEU:HD23	56:K:150:LEU:HA	1.89	0.40
67:V:41:ILE:HD13	67:V:51:LYS:NZ	2.36	0.40
78:g:162:GLU:OE1	78:g:171:GLY:N	2.40	0.40
1:1:922:A:H2'	1:1:923:C:C6	2.56	0.40
1:1:1265:U:H2'	1:1:1267:A:O5'	2.20	0.40
1:1:2329:U:H2'	1:1:2330:A:H8	1.86	0.40
1:1:3099:A:H2'	1:1:3100:G:O4'	2.21	0.40
14:t:2:ALA:HB1	29:AB:33:GLY:O	2.21	0.40
18:x:36:ILE:HD12	18:x:114:ILE:HD13	2.04	0.40
19:y:31[A]:LYS:HE3	19:y:31[A]:LYS:HB2	1.95	0.40
27:9:11:SER:HB3	27:9:14:LYS:HB2	2.02	0.40
28:AA:24:VAL:HG11	28:AA:87:LEU:HD23	2.03	0.40
46:A:107:C:H2'	46:A:108:A:C8	2.56	0.40
46:A:518:A:H2'	46:A:519:A:H8	1.81	0.40
46:A:1030:C:H2'	46:A:1031:G:H8	1.86	0.40
46:A:1168:A:N3	46:A:1195:C:O2'	2.52	0.40
46:A:1293:G:H2'	46:A:1294:C:H6	1.85	0.40
46:A:1565:U:H2'	46:A:1566:U:C6	2.56	0.40
46:A:1566:U:O2'	63:R:138:GLN:HG3	2.22	0.40
46:A:1594:G:C2	46:A:1595:U:C5	3.10	0.40
47:B:3:LEU:HG	47:B:7:PHE:HD2	1.85	0.40
49:D:180:LYS:HG2	49:D:184:GLN:OE1	2.21	0.40
50:E:214:ASP:CG	50:E:215:GLU:H	2.29	0.40
50:E:219:ILE:HB	50:E:220:PRO:HD2	2.03	0.40
51:F:252:GLU:HG3	51:F:256:ARG:HH12	1.86	0.40
52:G:193:CYS:HA	52:G:196:GLU:HG2	2.04	0.40
53:H:55:GLY:O	53:H:56:ASN:ND2	2.55	0.40
54:I:67:ARG:HD3	54:I:67:ARG:HA	1.85	0.40
59:N:45:LEU:HD23	59:N:120:CYS:HB3	2.02	0.40
59:N:138:GLU:HG2	59:N:139:HIS:ND1	2.37	0.40
61:P:20:ASP:OD1	61:P:49:GLU:HB3	2.22	0.40
61:P:56:MET:HB2	61:P:99:ALA:HB2	2.03	0.40
62:Q:81:ARG:HE	62:Q:117:GLY:HA3	1.85	0.40
63:R:50:PRO:HB3	63:R:85:ALA:HB2	2.03	0.40
73:b:82:ARG:HD2	73:b:85:ARG:NH1	2.36	0.40
77:f:24:GLN:NE2	77:f:26:LYS:HB2	2.30	0.40
79:h:246:ARG:NH2	79:h:295:GLY:O	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:179:C:H2'	1:1:180:U:C6	2.56	0.40
1:1:374:A:N3	1:1:376:G:H5''	2.37	0.40
1:1:501:U:H2'	1:1:502:U:O4'	2.22	0.40
1:1:1007:A:H2'	1:1:1008:A:H8	1.86	0.40
1:1:1580:U:H2'	1:1:1581:C:C6	2.57	0.40
1:1:2820:G:OP1	41:AN:24:TYR:OH	2.32	0.40
1:1:2990:C:C4	1:1:2991:U:C4	3.08	0.40
6:l:139:ARG:HG3	6:l:139:ARG:HH11	1.87	0.40
10:p:99:ARG:HH21	10:p:192:HIS:CD2	2.39	0.40
46:A:79:C:OP1	53:H:172:ALA:HB3	2.22	0.40
46:A:194:G:H2'	46:A:195:A:O4'	2.20	0.40
46:A:512:G:O2'	46:A:513:A:H8	2.04	0.40
46:A:1166:U:H2'	46:A:1167:U:O4'	2.22	0.40
46:A:1207:C:H2'	46:A:1208:A:H8	1.86	0.40
46:A:1354:U:H2'	46:A:1355:A:C8	2.56	0.40
46:A:1579:A:C2	46:A:1580:A:C5	3.10	0.40
46:A:1661:C:H2'	46:A:1662:C:H6	1.86	0.40
46:A:1724:G:H2'	46:A:1725:U:C6	2.56	0.40
49:D:135:ARG:HE	68:W:10:GLU:CD	2.28	0.40
51:F:163:ASP:C	51:F:165:ALA:H	2.28	0.40
55:J:3:ILE:H	55:J:3:ILE:HD12	1.86	0.40
56:K:58:ASP:O	56:K:61:THR:OG1	2.38	0.40
56:K:80:LEU:HD23	56:K:83:ILE:HD11	2.04	0.40
59:N:61:VAL:HG12	59:N:89:ILE:HD11	2.03	0.40
62:Q:77:LYS:HE3	62:Q:102:PHE:HB3	2.02	0.40
1:1:162:U:H2'	1:1:163:A:N7	2.36	0.40
1:1:234:A:H2'	1:1:235:G:O4'	2.22	0.40
1:1:242:C:O2'	1:1:243:G:H8	2.04	0.40
1:1:672:G:H5'	6:l:35:LEU:HD11	2.04	0.40
1:1:767:A:H2'	1:1:768:U:O4'	2.22	0.40
1:1:999:A:N1	1:1:1045:C:O2'	2.49	0.40
1:1:1715:G:N7	20:z:121:HIS:HE1	2.19	0.40
1:1:2680:C:OP2	43:AP:100:LYS:NZ	2.52	0.40
3:4:126:A:O2'	3:4:128:U:OP2	2.30	0.40
4:j:118:GLU:OE2	4:j:156:LYS:NZ	2.54	0.40
5:k:217:VAL:HG13	5:k:336:VAL:HG13	2.04	0.40
5:k:380:MET:HE2	5:k:383:LEU:HD21	2.03	0.40
9:o:229:ARG:HD3	9:o:232:PHE:HB2	2.02	0.40
32:AE:47:ASP:HB2	32:AE:86:GLU:HG2	2.03	0.40
36:AI:28:LEU:HG	36:AI:32:LYS:HE2	2.03	0.40
36:AI:49:LYS:HA	36:AI:49:LYS:HD3	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:78:A:H5'	53:H:154:ARG:HG3	2.04	0.40
46:A:545:U:H1'	46:A:594:C:H1'	2.04	0.40
46:A:584:G:C6	46:A:585:C:C4	3.10	0.40
46:A:874:U:H2'	46:A:875:C:H6	1.85	0.40
46:A:940:A:H2'	46:A:941:C:H6	1.86	0.40
46:A:1161:G:C6	46:A:1450:G:C6	3.09	0.40
46:A:1305:U:H3'	47:B:101:ARG:NH1	2.33	0.40
54:I:37:LEU:HB2	54:I:66:TYR:CE1	2.56	0.40
54:I:129:THR:CG2	54:I:150:LEU:HB3	2.50	0.40
56:K:51:LYS:HA	56:K:54:ARG:HB3	2.03	0.40
67:V:33:LEU:HD23	67:V:86:HIS:HB2	2.04	0.40
72:a:54:VAL:N	72:a:55:PRO:HD2	2.36	0.40
73:b:40:THR:HG23	73:b:42:ARG:HH11	1.86	0.40
1:1:254:A:H2'	1:1:255:A:C8	2.56	0.40
1:1:407:A:C2	3:4:17:A:H1'	2.57	0.40
1:1:1022:A:C2	62:Q:72:ARG:HD2	2.56	0.40
1:1:1568:U:C4	1:1:1569:C:H1'	2.56	0.40
1:1:1576:A:OP1	26:8:33:ARG:NH2	2.47	0.40
1:1:1762:G:N7	20:z:46:LYS:HE2	2.37	0.40
1:1:2681:C:H2'	1:1:2682:C:C6	2.56	0.40
2:3:26:C:H2'	2:3:27:A:O4'	2.21	0.40
5:k:59:ASP:OD2	5:k:357:LYS:HD3	2.21	0.40
5:k:233:TRP:CD1	5:k:265:ALA:HB1	2.56	0.40
7:m:22:ARG:NE	7:m:28:THR:OG1	2.51	0.40
7:m:98:ALA:HB1	7:m:162:VAL:HG23	2.04	0.40
7:m:289:LYS:HA	7:m:292:GLU:HG2	2.04	0.40
13:s:87:LYS:O	13:s:88:GLU:HG3	2.22	0.40
17:w:156:LYS:O	17:w:159:GLU:HG2	2.21	0.40
28:AA:3:LYS:HE3	28:AA:5:ILE:O	2.22	0.40
39:AL:27:VAL:CG1	39:AL:39:LYS:HD2	2.52	0.40
44:AQ:7:LYS:O	44:AQ:27:LYS:NZ	2.39	0.40
45:i:67:LYS:HD3	45:i:67:LYS:HA	1.97	0.40
46:A:129:A:N6	46:A:180:A:N1	2.70	0.40
46:A:447:C:H2'	46:A:448:C:C6	2.57	0.40
46:A:699:U:H2'	46:A:700:G:H8	1.85	0.40
46:A:1306:A:H4'	46:A:1307:A:O5'	2.21	0.40
46:A:1459:U:OP2	52:G:190:ILE:HG22	2.22	0.40
46:A:1486:G:H5''	66:U:122:ARG:NH1	2.36	0.40
48:C:128:LYS:HA	48:C:134:VAL:HA	2.02	0.40
50:E:99:ALA:HA	50:E:189:ILE:HD12	2.03	0.40
53:H:2:LYS:HE2	53:H:17:ASP:OD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:J:158:ILE:HG22	55:J:159:GLU:N	2.37	0.40
63:R:46:LYS:HA	63:R:46:LYS:HD2	1.84	0.40
67:V:79:ASP:HB3	67:V:81:TYR:CE1	2.57	0.40
79:h:19:TRP:H	79:h:38:ARG:HB2	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	j	248/254 (98%)	240 (97%)	8 (3%)	0	100	100
5	k	385/389 (99%)	376 (98%)	9 (2%)	0	100	100
6	l	359/363 (99%)	354 (99%)	5 (1%)	0	100	100
7	m	290/298 (97%)	283 (98%)	7 (2%)	0	100	100
8	n	152/176 (86%)	148 (97%)	4 (3%)	0	100	100
9	o	233/241 (97%)	225 (97%)	8 (3%)	0	100	100
10	p	236/262 (90%)	232 (98%)	4 (2%)	0	100	100
11	q	188/191 (98%)	185 (98%)	3 (2%)	0	100	100
12	r	204/220 (93%)	204 (100%)	0	0	100	100
13	s	171/174 (98%)	166 (97%)	5 (3%)	0	100	100
14	t	198/202 (98%)	193 (98%)	5 (2%)	0	100	100
15	u	128/131 (98%)	124 (97%)	4 (3%)	0	100	100
16	v	201/204 (98%)	200 (100%)	1 (0%)	0	100	100
17	w	197/200 (98%)	195 (99%)	2 (1%)	0	100	100
18	x	168/185 (91%)	165 (98%)	3 (2%)	0	100	100
19	y	186/186 (100%)	182 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	z	178/190 (94%)	176 (99%)	2 (1%)	0	100	100
21	0	171/172 (99%)	170 (99%)	1 (1%)	0	100	100
22	2	159/160 (99%)	158 (99%)	1 (1%)	0	100	100
23	5	103/124 (83%)	97 (94%)	6 (6%)	0	100	100
24	6	129/137 (94%)	128 (99%)	1 (1%)	0	100	100
25	7	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
26	8	119/142 (84%)	117 (98%)	2 (2%)	0	100	100
27	9	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
28	AA	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
29	AB	146/149 (98%)	141 (97%)	5 (3%)	0	100	100
30	AC	62/63 (98%)	62 (100%)	0	0	100	100
31	AD	94/106 (89%)	94 (100%)	0	0	100	100
32	AE	107/112 (96%)	106 (99%)	1 (1%)	0	100	100
33	AF	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
34	AG	107/107 (100%)	104 (97%)	3 (3%)	0	100	100
35	AH	114/122 (93%)	113 (99%)	1 (1%)	0	100	100
36	AI	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
37	AJ	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
38	AK	84/90 (93%)	83 (99%)	1 (1%)	0	100	100
39	AL	76/78 (97%)	72 (95%)	4 (5%)	0	100	100
40	AM	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
41	AN	51/52 (98%)	50 (98%)	1 (2%)	0	100	100
42	AO	22/25 (88%)	22 (100%)	0	0	100	100
43	AP	101/106 (95%)	100 (99%)	1 (1%)	0	100	100
44	AQ	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	i	109/267 (41%)	104 (95%)	5 (5%)	0	100	100
47	B	206/261 (79%)	200 (97%)	6 (3%)	0	100	100
48	C	212/256 (83%)	209 (99%)	3 (1%)	0	100	100
49	D	214/249 (86%)	212 (99%)	2 (1%)	0	100	100
50	E	221/251 (88%)	214 (97%)	7 (3%)	0	100	100
51	F	258/262 (98%)	256 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	G	204/225 (91%)	195 (96%)	9 (4%)	0	100	100
53	H	224/236 (95%)	221 (99%)	3 (1%)	0	100	100
54	I	180/186 (97%)	177 (98%)	3 (2%)	0	100	100
55	J	201/206 (98%)	199 (99%)	2 (1%)	0	100	100
56	K	176/189 (93%)	174 (99%)	2 (1%)	0	100	100
57	L	91/118 (77%)	83 (91%)	7 (8%)	1 (1%)	11	16
58	M	139/155 (90%)	136 (98%)	3 (2%)	0	100	100
59	N	114/143 (80%)	100 (88%)	14 (12%)	0	100	100
60	O	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
61	P	123/132 (93%)	120 (98%)	3 (2%)	0	100	100
62	Q	116/142 (82%)	106 (91%)	10 (9%)	0	100	100
63	R	138/142 (97%)	131 (95%)	7 (5%)	0	100	100
64	S	123/137 (90%)	117 (95%)	6 (5%)	0	100	100
65	T	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
66	U	139/145 (96%)	135 (97%)	4 (3%)	0	100	100
67	V	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
68	W	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
69	X	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
70	Y	141/145 (97%)	139 (99%)	2 (1%)	0	100	100
71	Z	130/135 (96%)	130 (100%)	0	0	100	100
72	a	70/105 (67%)	68 (97%)	2 (3%)	0	100	100
73	b	98/119 (82%)	95 (97%)	3 (3%)	0	100	100
74	c	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
75	d	60/67 (90%)	56 (93%)	4 (7%)	0	100	100
76	e	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
77	f	54/63 (86%)	53 (98%)	1 (2%)	0	100	100
78	g	68/193 (35%)	60 (88%)	8 (12%)	0	100	100
79	h	309/317 (98%)	294 (95%)	15 (5%)	0	100	100
All	All	11010/12138 (91%)	10737 (98%)	272 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
57	L	88	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	
4	j	191/194 (98%)	191 (100%)	0	100	100
5	k	326/328 (99%)	326 (100%)	0	100	100
6	l	290/292 (99%)	290 (100%)	0	100	100
7	m	247/252 (98%)	247 (100%)	0	100	100
8	n	135/154 (88%)	135 (100%)	0	100	100
9	o	199/204 (98%)	199 (100%)	0	100	100
10	p	198/216 (92%)	198 (100%)	0	100	100
11	q	169/170 (99%)	169 (100%)	0	100	100
12	r	178/186 (96%)	178 (100%)	0	100	100
13	s	148/149 (99%)	148 (100%)	0	100	100
14	t	166/168 (99%)	166 (100%)	0	100	100
15	u	108/109 (99%)	108 (100%)	0	100	100
16	v	177/178 (99%)	177 (100%)	0	100	100
17	w	166/167 (99%)	166 (100%)	0	100	100
18	x	142/154 (92%)	142 (100%)	0	100	100
19	y	156/154 (101%)	156 (100%)	0	100	100
20	z	147/153 (96%)	147 (100%)	0	100	100
21	0	158/157 (101%)	158 (100%)	0	100	100
22	2	135/134 (101%)	135 (100%)	0	100	100
23	5	95/112 (85%)	93 (98%)	2 (2%)	47	67
24	6	101/103 (98%)	101 (100%)	0	100	100
25	7	57/127 (45%)	57 (100%)	0	100	100
26	8	108/121 (89%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	9	111/112 (99%)	111 (100%)	0	100	100
28	AA	117/118 (99%)	117 (100%)	0	100	100
29	AB	120/121 (99%)	120 (100%)	0	100	100
30	AC	50/49 (102%)	50 (100%)	0	100	100
31	AD	81/90 (90%)	81 (100%)	0	100	100
32	AE	98/100 (98%)	98 (100%)	0	100	100
33	AF	111/115 (96%)	111 (100%)	0	100	100
34	AG	94/92 (102%)	94 (100%)	0	100	100
35	AH	99/102 (97%)	99 (100%)	0	100	100
36	AI	106/106 (100%)	106 (100%)	0	100	100
37	AJ	79/79 (100%)	79 (100%)	0	100	100
38	AK	70/73 (96%)	70 (100%)	0	100	100
39	AL	69/69 (100%)	69 (100%)	0	100	100
40	AM	47/47 (100%)	47 (100%)	0	100	100
41	AN	48/47 (102%)	48 (100%)	0	100	100
42	AO	23/24 (96%)	23 (100%)	0	100	100
43	AP	88/89 (99%)	86 (98%)	2 (2%)	44	65
44	AQ	72/73 (99%)	72 (100%)	0	100	100
45	i	92/212 (43%)	92 (100%)	0	100	100
47	B	176/215 (82%)	176 (100%)	0	100	100
48	C	194/229 (85%)	194 (100%)	0	100	100
49	D	174/198 (88%)	174 (100%)	0	100	100
50	E	174/196 (89%)	174 (100%)	0	100	100
51	F	218/220 (99%)	218 (100%)	0	100	100
52	G	178/197 (90%)	178 (100%)	0	100	100
53	H	195/204 (96%)	195 (100%)	0	100	100
54	I	163/167 (98%)	163 (100%)	0	100	100
55	J	157/160 (98%)	157 (100%)	0	100	100
56	K	153/160 (96%)	153 (100%)	0	100	100
57	L	87/104 (84%)	87 (100%)	0	100	100
58	M	122/134 (91%)	122 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	N	98/123 (80%)	98 (100%)	0	100	100
60	O	129/130 (99%)	129 (100%)	0	100	100
61	P	96/101 (95%)	96 (100%)	0	100	100
62	Q	102/121 (84%)	102 (100%)	0	100	100
63	R	114/116 (98%)	114 (100%)	0	100	100
64	S	112/122 (92%)	112 (100%)	0	100	100
65	T	126/129 (98%)	126 (100%)	0	100	100
66	U	113/117 (97%)	113 (100%)	0	100	100
67	V	90/105 (86%)	90 (100%)	0	100	100
68	W	71/71 (100%)	71 (100%)	0	100	100
69	X	112/113 (99%)	112 (100%)	0	100	100
70	Y	116/118 (98%)	116 (100%)	0	100	100
71	Z	109/112 (97%)	109 (100%)	0	100	100
72	a	64/85 (75%)	64 (100%)	0	100	100
73	b	86/102 (84%)	86 (100%)	0	100	100
74	c	72/73 (99%)	72 (100%)	0	100	100
75	d	54/58 (93%)	54 (100%)	0	100	100
76	e	47/48 (98%)	46 (98%)	1 (2%)	47	67
77	f	48/54 (89%)	48 (100%)	0	100	100
78	g	62/175 (35%)	62 (100%)	0	100	100
79	h	259/263 (98%)	258 (100%)	1 (0%)	84	91
All	All	9443/10220 (92%)	9437 (100%)	6 (0%)	100	95

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	5	31[A]	GLU
23	5	31[B]	GLU
43	AP	24[A]	LYS
43	AP	24[B]	LYS
76	e	27	HIS
79	h	264	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
4	j	211	HIS
5	k	109	HIS
5	k	182	GLN
5	k	316	ASN
6	l	6	GLN
6	l	297	GLN
7	m	17	GLN
7	m	32	GLN
7	m	111	GLN
7	m	225	ASN
8	n	91	ASN
9	o	91	ASN
9	o	198	ASN
9	o	228	ASN
9	o	231	GLN
9	o	241	ASN
10	p	192	HIS
11	q	58	HIS
13	s	90	GLN
13	s	109	HIS
13	s	161	GLN
15	u	35	GLN
15	u	104	GLN
15	u	112	GLN
17	w	51	ASN
17	w	193	GLN
18	x	34	GLN
18	x	97	ASN
18	x	118	GLN
18	x	137	ASN
19	y	126	GLN
20	z	166	ASN
21	0	8	GLN
21	0	13	ASN
21	0	62	ASN
22	2	107	ASN
27	9	86	GLN
28	AA	78	ASN
28	AA	122	HIS
31	AD	11	ASN
34	AG	77	ASN
35	AH	14	ASN
36	AI	59	ASN

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Mol	Chain	Res	Type
43	AP	23	HIS
44	AQ	48	GLN
44	AQ	56	ASN
47	B	21	ASN
47	B	30	GLN
48	C	124	ASN
48	C	146	GLN
48	C	149	GLN
48	C	178	ASN
48	C	202	GLN
49	D	50	GLN
49	D	145	GLN
50	E	23	ASN
51	F	17	HIS
51	F	98	HIS
51	F	130	GLN
51	F	157	ASN
52	G	37	GLN
52	G	170	GLN
53	H	140	HIS
53	H	217	HIS
54	I	19	GLN
55	J	132	HIS
55	J	181	GLN
56	K	48	GLN
56	K	110	GLN
57	L	29	GLN
57	L	32	HIS
57	L	81	ASN
60	O	62	GLN
61	P	7	GLN
65	T	19	ASN
65	T	21	ASN
65	T	89	GLN
65	T	99	HIS
66	U	16	ASN
67	V	32	GLN
68	W	29	HIS
70	Y	75	GLN
70	Y	89	ASN
71	Z	106	GLN
73	b	43	ASN

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Mol	Chain	Res	Type
74	c	27	GLN
75	d	27	GLN
75	d	43	ASN
76	e	53	ASN
77	f	24	GLN
78	g	140	HIS
79	h	29	HIS
79	h	70	GLN
79	h	102	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3205/3359 (95%)	549 (17%)	32 (0%)
2	3	120/121 (99%)	9 (7%)	0
3	4	157/158 (99%)	26 (16%)	2 (1%)
46	A	1685/1787 (94%)	402 (23%)	42 (2%)
All	All	5167/5425 (95%)	986 (19%)	76 (1%)

All (986) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	A
1	1	24	U
1	1	25	A
1	1	29	G
1	1	39	A
1	1	42	A
1	1	48	A
1	1	56	A
1	1	58	G
1	1	59	A
1	1	64	A
1	1	65	A
1	1	76	A
1	1	91	G
1	1	98	A
1	1	104	C
1	1	109	G
1	1	110	C
1	1	115	A

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Mol	Chain	Res	Type
1	1	121	A
1	1	134	U
1	1	135	G
1	1	147	G
1	1	155	A
1	1	156	A
1	1	164	U
1	1	169	G
1	1	173	C
1	1	175	G
1	1	186	A
1	1	189	U
1	1	190	U
1	1	199	C
1	1	205	G
1	1	209	C
1	1	212	A
1	1	217	G
1	1	218	A
1	1	219	G
1	1	230	G
1	1	236	A
1	1	239	A
1	1	240	C
1	1	243	G
1	1	245	G
1	1	249	G
1	1	250	U
1	1	251	G
1	1	252	U
1	1	269	G
1	1	286	U
1	1	295	A
1	1	305	U
1	1	323	A
1	1	329	U
1	1	338	A
1	1	339	C
1	1	350	C
1	1	351	A
1	1	376	G
1	1	377	A

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Mol	Chain	Res	Type
1	1	398	A
1	1	399	A
1	1	403	C
1	1	404	G
1	1	420	G
1	1	421	G
1	1	422	A
1	1	438	A
1	1	439	C
1	1	445	A
1	1	447	U
1	1	452	A
1	1	453	U
1	1	454	G
1	1	479	C
1	1	481	G
1	1	482	U
1	1	485	A
1	1	506	A
1	1	517	A
1	1	531	G
1	1	538	G
1	1	539	G
1	1	541	U
1	1	543	C
1	1	544	U
1	1	545	G
1	1	546	C
1	1	551	U
1	1	555	A
1	1	556	U
1	1	557	A
1	1	564	G
1	1	577	G
1	1	587	A
1	1	590	A
1	1	598	U
1	1	600	U
1	1	601	U
1	1	602	A
1	1	609	A
1	1	618	U

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Mol	Chain	Res	Type
1	1	619	A
1	1	620	A
1	1	635	C
1	1	647	A
1	1	675	A
1	1	679	U
1	1	689	A
1	1	703	A
1	1	710	G
1	1	713	A
1	1	717	A
1	1	723	G
1	1	730	A
1	1	732	U
1	1	733	A
1	1	760	U
1	1	763	U
1	1	767	A
1	1	772	U
1	1	773	U
1	1	776	A
1	1	777	G
1	1	781	G
1	1	783	G
1	1	802	A
1	1	813	A
1	1	826	A
1	1	845	C
1	1	857	C
1	1	861	U
1	1	870	U
1	1	875	U
1	1	892	A
1	1	903	G
1	1	904	G
1	1	910	A
1	1	912	G
1	1	913	A
1	1	917	A
1	1	919	C
1	1	920	G
1	1	921	A

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Mol	Chain	Res	Type
1	1	933	G
1	1	940	C
1	1	955	C
1	1	956	U
1	1	976	A
1	1	978	C
1	1	990	G
1	1	997	G
1	1	998	A
1	1	1006	G
1	1	1011	C
1	1	1012	U
1	1	1014	G
1	1	1019	U
1	1	1020	G
1	1	1021	A
1	1	1022	A
1	1	1023	A
1	1	1024	U
1	1	1030	U
1	1	1033	C
1	1	1043	A
1	1	1045	C
1	1	1060	A
1	1	1061	A
1	1	1068	G
1	1	1077	U
1	1	1078	U
1	1	1089	A
1	1	1090	A
1	1	1091	U
1	1	1092	U
1	1	1094	A
1	1	1099	A
1	1	1100	G
1	1	1113	G
1	1	1127	G
1	1	1140	U
1	1	1149	A
1	1	1155	A
1	1	1174	G
1	1	1176	A

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Mol	Chain	Res	Type
1	1	1177	U
1	1	1178	G
1	1	1182	G
1	1	1188	C
1	1	1189	A
1	1	1192	C
1	1	1196	A
1	1	1197	C
1	1	1202	G
1	1	1204	U
1	1	1215	C
1	1	1218	G
1	1	1223	C
1	1	1224	C
1	1	1225	G
1	1	1228	C
1	1	1229	G
1	1	1230	G
1	1	1232	G
1	1	1234	C
1	1	1237	U
1	1	1238	G
1	1	1239	G
1	1	1241	A
1	1	1242	G
1	1	1243	U
1	1	1244	C
1	1	1245	G
1	1	1253	C
1	1	1255	A
1	1	1258	G
1	1	1259	A
1	1	1262	G
1	1	1264	G
1	1	1265	U
1	1	1266	A
1	1	1267	A
1	1	1268	C
1	1	1269	A
1	1	1270	A
1	1	1273	C
1	1	1274	A

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Mol	Chain	Res	Type
1	1	1278	G
1	1	1280	C
1	1	1282	A
1	1	1283	A
1	1	1301	U
1	1	1303	G
1	1	1304	A
1	1	1305	U
1	1	1326	A
1	1	1327	U
1	1	1346	U
1	1	1347	U
1	1	1348	U
1	1	1349	U
1	1	1376	G
1	1	1382	A
1	1	1388	G
1	1	1395	U
1	1	1415	A
1	1	1421	U
1	1	1430	G
1	1	1433	C
1	1	1442	A
1	1	1446	G
1	1	1471	A
1	1	1477	A
1	1	1484	G
1	1	1504	C
1	1	1520	A
1	1	1532	G
1	1	1552	C
1	1	1556	G
1	1	1558	G
1	1	1559	C
1	1	1560	U
1	1	1561	U
1	1	1562	G
1	1	1563	A
1	1	1565	U
1	1	1566	U
1	1	1567	U
1	1	1568	U

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Mol	Chain	Res	Type
1	1	1569	C
1	1	1571	G
1	1	1572	G
1	1	1574	C
1	1	1576	A
1	1	1577	C
1	1	1585	A
1	1	1586	G
1	1	1589	A
1	1	1601	A
1	1	1625	U
1	1	1635	C
1	1	1638	A
1	1	1639	A
1	1	1641	U
1	1	1648	G
1	1	1653	C
1	1	1720	U
1	1	1721	C
1	1	1732	G
1	1	1746	A
1	1	1747	G
1	1	1755	U
1	1	1756	A
1	1	1758	U
1	1	1760	U
1	1	1761	U
1	1	1762	G
1	1	1763	C
1	1	1771	G
1	1	1776	G
1	1	1793	A
1	1	1804	G
1	1	1810	A
1	1	1812	A
1	1	1814	U
1	1	1815	U
1	1	1816	U
1	1	1817	U
1	1	1835	A
1	1	1838	A
1	1	1842	C

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Mol	Chain	Res	Type
1	1	1845	C
1	1	1846	A
1	1	1862	C
1	1	1874	G
1	1	1876	U
1	1	1882	A
1	1	1889	A
1	1	1902	G
1	1	1944	G
1	1	1950	G
1	1	1951	U
1	1	1968	A
1	1	2043	G
1	1	2045	C
1	1	2051	G
1	1	2054	C
1	1	2055	G
1	1	2066	G
1	1	2068	U
1	1	2069	U
1	1	2070	A
1	1	2071	A
1	1	2078	A
1	1	2088	G
1	1	2089	G
1	1	2090	U
1	1	2091	A
1	1	2092	C
1	1	2099	G
1	1	2100	G
1	1	2109	A
1	1	2118	U
1	1	2122	A
1	1	2136	A
1	1	2147	G
1	1	2149	G
1	1	2166	A
1	1	2183	U
1	1	2184	G
1	1	2185	A
1	1	2186	A
1	1	2187	U

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Mol	Chain	Res	Type
1	1	2188	G
1	1	2201	A
1	1	2222	A
1	1	2227	G
1	1	2234	A
1	1	2235	C
1	1	2250	G
1	1	2251	G
1	1	2259	A
1	1	2260	U
1	1	2276	U
1	1	2285	G
1	1	2288	U
1	1	2291	A
1	1	2292	U
1	1	2293	G
1	1	2312	U
1	1	2314	U
1	1	2341	A
1	1	2351	A
1	1	2352	C
1	1	2353	G
1	1	2363	G
1	1	2366	U
1	1	2371	G
1	1	2375	A
1	1	2380	A
1	1	2381	G
1	1	2382	A
1	1	2389	U
1	1	2390	G
1	1	2413	G
1	1	2420	G
1	1	2492	U
1	1	2493	A
1	1	2511	G
1	1	2513	A
1	1	2515	G
1	1	2516	U
1	1	2517	C
1	1	2518	A
1	1	2519	A

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Mol	Chain	Res	Type
1	1	2520	A
1	1	2521	C
1	1	2529	U
1	1	2530	C
1	1	2533	G
1	1	2536	U
1	1	2538	A
1	1	2545	C
1	1	2546	U
1	1	2548	G
1	1	2557	G
1	1	2565	A
1	1	2566	C
1	1	2578	G
1	1	2579	G
1	1	2586	G
1	1	2598	A
1	1	2623	G
1	1	2624	U
1	1	2628	A
1	1	2644	G
1	1	2646	A
1	1	2649	G
1	1	2661	A
1	1	2663	A
1	1	2666	A
1	1	2676	A
1	1	2677	A
1	1	2686	G
1	1	2692	G
1	1	2700	G
1	1	2701	U
1	1	2724	U
1	1	2725	G
1	1	2727	C
1	1	2734	A
1	1	2744	C
1	1	2749	G
1	1	2750	G
1	1	2768	G
1	1	2771	A
1	1	2772	G

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Mol	Chain	Res	Type
1	1	2773	A
1	1	2775	A
1	1	2782	C
1	1	2786	G
1	1	2789	A
1	1	2790	U
1	1	2814	U
1	1	2815	U
1	1	2816	C
1	1	2817	A
1	1	2821	C
1	1	2833	U
1	1	2839	C
1	1	2843	G
1	1	2844	A
1	1	2847	U
1	1	2859	A
1	1	2861	C
1	1	2866	C
1	1	2870	G
1	1	2871	C
1	1	2883	A
1	1	2886	G
1	1	2895	U
1	1	2907	U
1	1	2908	A
1	1	2914	C
1	1	2919	G
1	1	2923	G
1	1	2926	U
1	1	2943	A
1	1	2955	C
1	1	2960	C
1	1	2962	G
1	1	2969	G
1	1	2984	A
1	1	3021	A
1	1	3028	U
1	1	3031	G
1	1	3050	A
1	1	3051	C
1	1	3052	G

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Mol	Chain	Res	Type
1	1	3058	A
1	1	3064	C
1	1	3073	G
1	1	3076	U
1	1	3081	G
1	1	3094	A
1	1	3101	A
1	1	3102	A
1	1	3103	U
1	1	3114	A
1	1	3115	C
1	1	3125	U
1	1	3134	C
1	1	3143	G
1	1	3144	A
1	1	3146	G
1	1	3149	U
1	1	3151	C
1	1	3156	A
1	1	3157	A
1	1	3160	C
1	1	3163	U
1	1	3164	U
1	1	3165	U
1	1	3171	C
1	1	3172	U
1	1	3175	A
1	1	3182	C
1	1	3183	A
1	1	3184	G
1	1	3194	G
1	1	3200	C
1	1	3208	A
1	1	3210	A
1	1	3212	G
1	1	3214	U
1	1	3224	U
1	1	3228	G
1	1	3235	A
1	1	3241	G
1	1	3246	C
1	1	3251	G

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Mol	Chain	Res	Type
1	1	3252	C
1	1	3255	G
1	1	3259	A
1	1	3260	A
1	1	3268	G
1	1	3269	C
1	1	3278	U
1	1	3281	A
1	1	3282	U
1	1	3284	U
1	1	3285	A
1	1	3306	U
1	1	3307	A
1	1	3309	A
1	1	3310	G
1	1	3316	U
1	1	3317	U
1	1	3318	G
1	1	3319	U
1	1	3320	U
1	1	3321	G
1	1	3334	G
1	1	3343	C
1	1	3347	U
1	1	3351	G
1	1	3361	U
2	3	7	G
2	3	22	A
2	3	54	U
2	3	55	A
2	3	65	G
2	3	73	C
2	3	76	A
2	3	102	A
2	3	112	G
3	4	23	U
3	4	34	U
3	4	35	C
3	4	39	G
3	4	59	A
3	4	62	C
3	4	63	G

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Mol	Chain	Res	Type
3	4	81	A
3	4	84	C
3	4	86	U
3	4	87	G
3	4	92	A
3	4	95	G
3	4	97	A
3	4	102	U
3	4	104	A
3	4	106	C
3	4	107	G
3	4	111	A
3	4	112	U
3	4	113	U
3	4	125	U
3	4	126	A
3	4	148	G
3	4	152	G
3	4	157	U
46	A	4	C
46	A	25	C
46	A	26	A
46	A	27	U
46	A	34	G
46	A	42	G
46	A	43	A
46	A	45	U
46	A	47	A
46	A	57	G
46	A	63	G
46	A	66	U
46	A	74	U
46	A	75	U
46	A	76	A
46	A	78	A
46	A	79	C
46	A	81	G
46	A	84	A
46	A	104	A
46	A	114	C
46	A	116	U
46	A	123	G

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Mol	Chain	Res	Type
46	A	127	G
46	A	128	U
46	A	129	A
46	A	138	C
46	A	139	U
46	A	142	G
46	A	143	A
46	A	149	G
46	A	150	U
46	A	151	G
46	A	152	G
46	A	154	A
46	A	156	U
46	A	159	U
46	A	164	C
46	A	166	A
46	A	167	A
46	A	168	U
46	A	174	C
46	A	176	U
46	A	177	A
46	A	179	A
46	A	190	U
46	A	191	U
46	A	199	G
46	A	200	A
46	A	202	G
46	A	206	U
46	A	211	A
46	A	215	A
46	A	216	A
46	A	217	A
46	A	218	A
46	A	219	A
46	A	244	G
46	A	259	U
46	A	260	U
46	A	261	C
46	A	262	G
46	A	266	C
46	A	269	A
46	A	270	U

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Mol	Chain	Res	Type
46	A	274	C
46	A	276	U
46	A	278	U
46	A	279	G
46	A	283	G
46	A	285	G
46	A	312	C
46	A	314	A
46	A	319	C
46	A	320	G
46	A	335	G
46	A	336	C
46	A	337	C
46	A	342	A
46	A	350	A
46	A	357	A
46	A	358	A
46	A	359	C
46	A	398	A
46	A	399	A
46	A	400	C
46	A	402	G
46	A	414	A
46	A	416	G
46	A	417	G
46	A	421	G
46	A	422	C
46	A	423	A
46	A	424	G
46	A	432	G
46	A	437	U
46	A	442	C
46	A	452	A
46	A	458	A
46	A	467	C
46	A	480	U
46	A	482	C
46	A	483	A
46	A	485	G
46	A	502	U
46	A	503	A
46	A	504	A

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Mol	Chain	Res	Type
46	A	505	U
46	A	506	U
46	A	509	A
46	A	512	G
46	A	515	U
46	A	518	A
46	A	519	A
46	A	525	A
46	A	530	U
46	A	534	C
46	A	537	G
46	A	539	A
46	A	540	A
46	A	553	A
46	A	554	A
46	A	555	G
46	A	556	U
46	A	563	C
46	A	566	G
46	A	575	G
46	A	592	A
46	A	593	G
46	A	609	U
46	A	617	A
46	A	618	A
46	A	620	A
46	A	621	A
46	A	626	G
46	A	633	A
46	A	639	G
46	A	648	U
46	A	650	G
46	A	652	C
46	A	653	G
46	A	654	G
46	A	656	C
46	A	675	U
46	A	682	A
46	A	686	G
46	A	687	A
46	A	688	G
46	A	692	U

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Mol	Chain	Res	Type
46	A	694	C
46	A	695	C
46	A	696	U
46	A	698	C
46	A	701	G
46	A	721	C
46	A	722	A
46	A	723	G
46	A	726	C
46	A	729	U
46	A	730	U
46	A	739	A
46	A	740	A
46	A	741	A
46	A	750	G
46	A	751	U
46	A	756	A
46	A	759	A
46	A	760	G
46	A	762	C
46	A	764	U
46	A	765	U
46	A	766	U
46	A	767	G
46	A	768	C
46	A	770	C
46	A	771	G
46	A	773	A
46	A	776	U
46	A	778	U
46	A	779	U
46	A	787	A
46	A	796	A
46	A	797	U
46	A	798	A
46	A	799	G
46	A	802	C
46	A	803	G
46	A	804	U
46	A	805	U
46	A	807	U
46	A	808	G

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Mol	Chain	Res	Type
46	A	814	A
46	A	815	U
46	A	816	U
46	A	818	U
46	A	819	G
46	A	821	U
46	A	823	G
46	A	824	U
46	A	825	U
46	A	827	C
46	A	828	U
46	A	831	G
46	A	832	A
46	A	841	A
46	A	842	U
46	A	848	A
46	A	856	G
46	A	857	G
46	A	869	A
46	A	871	U
46	A	875	C
46	A	877	G
46	A	879	U
46	A	880	G
46	A	881	U
46	A	909	A
46	A	910	G
46	A	911	A
46	A	918	A
46	A	920	U
46	A	945	U
46	A	951	A
46	A	973	A
46	A	975	C
46	A	977	A
46	A	988	A
46	A	989	U
46	A	998	A
46	A	1004	A
46	A	1005	A
46	A	1011	A
46	A	1013	C

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Mol	Chain	Res	Type
46	A	1015	A
46	A	1017	G
46	A	1025	G
46	A	1036	U
46	A	1038	G
46	A	1039	U
46	A	1042	U
46	A	1043	U
46	A	1044	U
46	A	1047	U
46	A	1055	A
46	A	1056	U
46	A	1057	C
46	A	1058	G
46	A	1059	G
46	A	1061	A
46	A	1067	C
46	A	1077	A
46	A	1078	A
46	A	1081	C
46	A	1085	G
46	A	1094	G
46	A	1123	A
46	A	1135	G
46	A	1143	C
46	A	1145	A
46	A	1152	G
46	A	1168	A
46	A	1169	A
46	A	1170	U
46	A	1179	A
46	A	1181	A
46	A	1184	G
46	A	1185	G
46	A	1186	G
46	A	1187	A
46	A	1201	C
46	A	1202	A
46	A	1203	G
46	A	1206	A
46	A	1212	A
46	A	1213	G

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Mol	Chain	Res	Type
46	A	1214	G
46	A	1215	A
46	A	1219	A
46	A	1220	C
46	A	1221	A
46	A	1229	A
46	A	1230	G
46	A	1231	C
46	A	1236	U
46	A	1237	C
46	A	1243	U
46	A	1250	G
46	A	1270	U
46	A	1284	G
46	A	1292	U
46	A	1299	U
46	A	1300	U
46	A	1306	A
46	A	1325	U
46	A	1326	A
46	A	1330	A
46	A	1336	G
46	A	1339	G
46	A	1342	A
46	A	1343	G
46	A	1344	C
46	A	1345	A
46	A	1346	U
46	A	1348	U
46	A	1349	G
46	A	1351	U
46	A	1352	G
46	A	1355	A
46	A	1356	U
46	A	1357	A
46	A	1359	U
46	A	1360	C
46	A	1364	U
46	A	1365	C
46	A	1369	G
46	A	1370	A
46	A	1376	U

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Mol	Chain	Res	Type
46	A	1380	G
46	A	1381	A
46	A	1382	U
46	A	1384	U
46	A	1385	C
46	A	1391	G
46	A	1396	A
46	A	1397	A
46	A	1398	G
46	A	1399	U
46	A	1400	U
46	A	1401	U
46	A	1410	A
46	A	1413	A
46	A	1414	G
46	A	1415	G
46	A	1416	U
46	A	1420	U
46	A	1422	A
46	A	1431	G
46	A	1433	C
46	A	1445	C
46	A	1446	A
46	A	1455	A
46	A	1458	C
46	A	1460	G
46	A	1461	A
46	A	1462	C
46	A	1463	G
46	A	1467	C
46	A	1468	C
46	A	1473	A
46	A	1476	A
46	A	1477	U
46	A	1480	G
46	A	1483	U
46	A	1485	G
46	A	1491	G
46	A	1503	A
46	A	1510	G
46	A	1511	A
46	A	1523	G

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Mol	Chain	Res	Type
46	A	1524	C
46	A	1526	G
46	A	1529	G
46	A	1530	A
46	A	1541	U
46	A	1544	U
46	A	1546	G
46	A	1556	A
46	A	1560	A
46	A	1561	G
46	A	1571	G
46	A	1574	A
46	A	1575	G
46	A	1580	A
46	A	1582	U
46	A	1583	C
46	A	1588	G
46	A	1589	C
46	A	1606	C
46	A	1622	A
46	A	1644	U
46	A	1645	G
46	A	1667	G
46	A	1670	U
46	A	1671	G
46	A	1672	G
46	A	1673	U
46	A	1674	U
46	A	1677	G
46	A	1700	G
46	A	1704	C
46	A	1729	U
46	A	1742	A
46	A	1743	A
46	A	1749	A
46	A	1753	A
46	A	1756	U
46	A	1767	G
46	A	1770	C
46	A	1779	G
46	A	1780	G
46	A	1781	A

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Mol	Chain	Res	Type
46	A	1783	C

All (76) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	172	C
1	1	403	C
1	1	538	G
1	1	563	U
1	1	601	U
1	1	759	G
1	1	912	G
1	1	1029	U
1	1	1060	A
1	1	1099	A
1	1	1224	C
1	1	1346	U
1	1	1347	U
1	1	1559	C
1	1	1561	U
1	1	1762	G
1	1	1815	U
1	1	1943	G
1	1	2090	U
1	1	2182	C
1	1	2183	U
1	1	2515	G
1	1	2519	A
1	1	2520	A
1	1	2545	C
1	1	3093	U
1	1	3193	C
1	1	3234	U
1	1	3240	U
1	1	3284	U
1	1	3315	C
1	1	3317	U
3	4	85	G
3	4	156	U
46	A	78	A
46	A	137	A
46	A	151	G

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Mol	Chain	Res	Type
46	A	176	U
46	A	214	U
46	A	259	U
46	A	265	U
46	A	278	U
46	A	415	A
46	A	451	C
46	A	502	U
46	A	504	A
46	A	505	U
46	A	514	G
46	A	518	A
46	A	529	C
46	A	533	A
46	A	553	A
46	A	638	U
46	A	685	C
46	A	763	C
46	A	820	U
46	A	824	U
46	A	855	C
46	A	874	U
46	A	876	A
46	A	1168	A
46	A	1335	U
46	A	1355	A
46	A	1359	U
46	A	1369	G
46	A	1396	A
46	A	1398	G
46	A	1457	A
46	A	1467	C
46	A	1479	A
46	A	1484	U
46	A	1523	G
46	A	1555	C
46	A	1573	A
46	A	1579	A
46	A	1581	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OMC	1	2808	1	19,22,23	2.97	8 (42%)	25,31,34	1.15	2 (8%)
61	IAS	P	119	61	6,7,8	1.06	0	3,8,10	1.79	0
43	MLZ	AP	55	43	8,9,10	0.71	0	4,9,11	0.93	0
24	MLZ	6	110	24	8,9,10	0.72	0	4,9,11	0.87	0
1	OMG	1	2765	1	23,26,27	2.35	9 (39%)	32,38,41	1.89	8 (25%)
43	MLZ	AP	40	43	8,9,10	0.71	0	4,9,11	0.95	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	1	2808	1	-	3/9/27/28	0/2/2/2
61	IAS	P	119	61	-	0/7/7/8	-
43	MLZ	AP	55	43	-	2/7/8/10	-
24	MLZ	6	110	24	-	3/7/8/10	-
1	OMG	1	2765	1	-	0/9/27/28	0/3/3/3
43	MLZ	AP	40	43	-	0/7/8/10	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2765	OMG	C4-N3	6.36	1.48	1.34
1	1	2808	OMC	C2-N3	6.25	1.48	1.36
1	1	2808	OMC	C6-C5	5.88	1.48	1.35
1	1	2765	OMG	C2-N3	5.48	1.46	1.33
1	1	2808	OMC	C2-N1	4.88	1.50	1.40
1	1	2808	OMC	C4-N4	4.72	1.45	1.33
1	1	2808	OMC	C4-N3	4.71	1.43	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2765	OMG	C2-N2	4.01	1.43	1.34
1	1	2808	OMC	O2-C2	-3.10	1.17	1.23
1	1	2808	OMC	C6-N1	3.07	1.45	1.38
1	1	2765	OMG	O6-C6	-2.89	1.18	1.23
1	1	2765	OMG	C5-N7	-2.76	1.33	1.39
1	1	2765	OMG	C2-N1	2.44	1.43	1.37
1	1	2765	OMG	C5-C6	2.38	1.53	1.44
1	1	2765	OMG	C6-N1	2.35	1.43	1.38
1	1	2808	OMC	C5-C4	2.30	1.48	1.42
1	1	2765	OMG	C4-N9	-2.07	1.32	1.38

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2765	OMG	C5-C4-N3	-4.96	120.49	128.39
1	1	2765	OMG	C2-N3-C4	4.48	120.02	112.30
1	1	2765	OMG	N9-C8-N7	-3.22	107.42	113.40
1	1	2808	OMC	O2-C2-N3	-3.13	117.40	122.33
1	1	2765	OMG	C2-N1-C6	-3.05	119.58	125.11
1	1	2765	OMG	N9-C4-N3	2.92	131.79	125.95
1	1	2765	OMG	C5-C6-N1	2.72	120.19	113.25
1	1	2765	OMG	O6-C6-C5	-2.48	120.00	126.53
1	1	2808	OMC	C1'-N1-C2	2.45	123.86	118.44
1	1	2765	OMG	C8-N7-C5	2.21	108.19	104.26

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	2808	OMC	O4'-C1'-N1-C2
1	1	2808	OMC	O4'-C1'-N1-C6
1	1	2808	OMC	C1'-C2'-O2'-CM2
24	6	110	MLZ	C-CA-CB-CG
43	AP	55	MLZ	N-CA-CB-CG
43	AP	55	MLZ	C-CA-CB-CG
24	6	110	MLZ	CG-CD-CE-NZ
24	6	110	MLZ	CE-CD-CG-CB

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	2808	OMC	2	0
61	P	119	IAS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	3K5	1	3402	-	63,63,63	0.33	0	84,95,95	0.68	3 (3%)
80	SPD	1	3401	-	9,9,9	0.32	0	8,8,8	0.78	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	3K5	1	3402	-	1/1/21/23	8/29/121/121	0/7/7/7
80	SPD	1	3401	-	-	3/7/7/7	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	1	3402	3K5	O-C3-C15	2.53	112.25	107.32
81	1	3402	3K5	C20-C21-C22	-2.22	107.20	111.93
81	1	3402	3K5	C4-C3-C15	-2.07	110.82	114.34

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
81	1	3402	3K5	C15

All (11) torsion outliers are listed below:

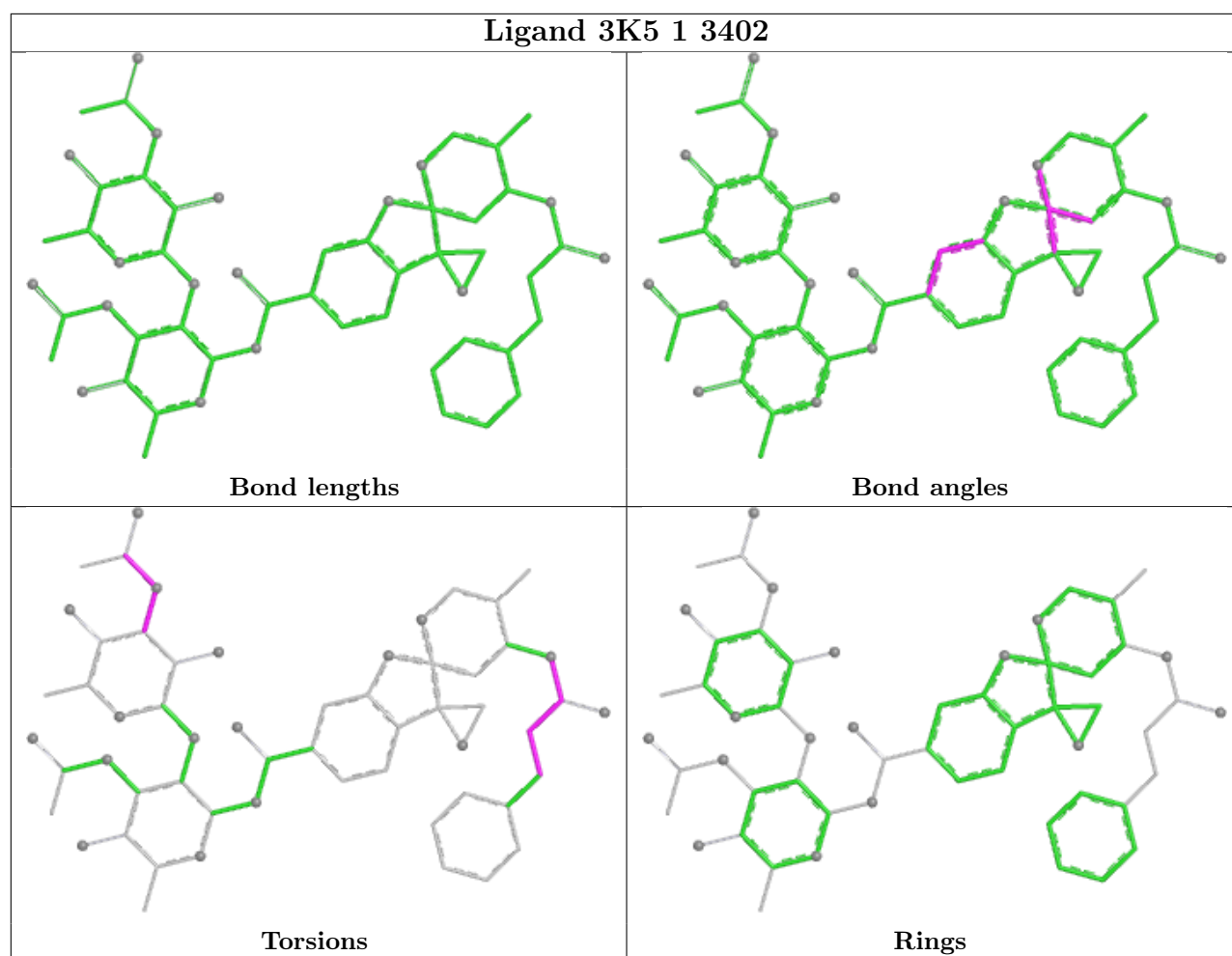
Mol	Chain	Res	Type	Atoms
81	1	3402	3K5	C39-C38-O14-C34
81	1	3402	3K5	C35-C34-O14-C38
81	1	3402	3K5	O15-C38-O14-C34
81	1	3402	3K5	C6-C7-C8-C9
81	1	3402	3K5	O1-C6-C7-C8
81	1	3402	3K5	O2-C6-C7-C8
81	1	3402	3K5	O2-C6-O1-C5
80	1	3401	SPD	C8-C7-N6-C5
81	1	3402	3K5	C7-C6-O1-C5
80	1	3401	SPD	C2-C3-C4-C5
80	1	3401	SPD	C4-C5-N6-C7

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	1	3402	3K5	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

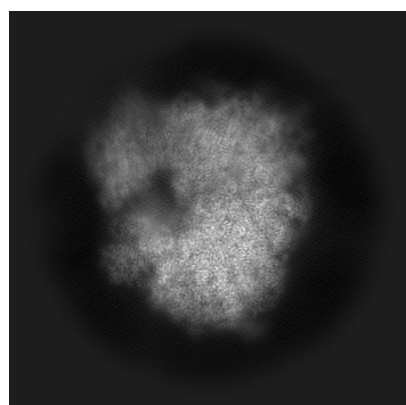
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13744. These allow visual inspection of the internal detail of the map and identification of artifacts.

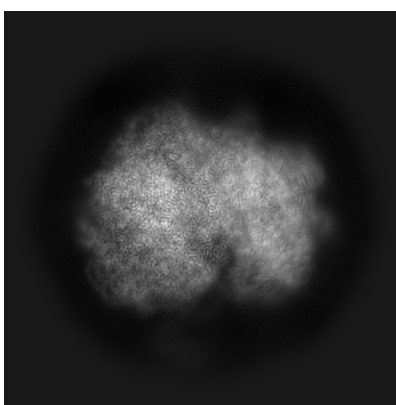
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

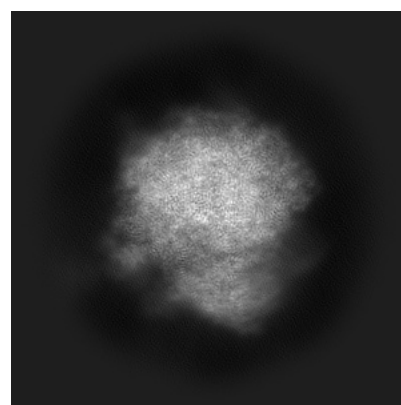
6.1.1 Primary map



X



Y

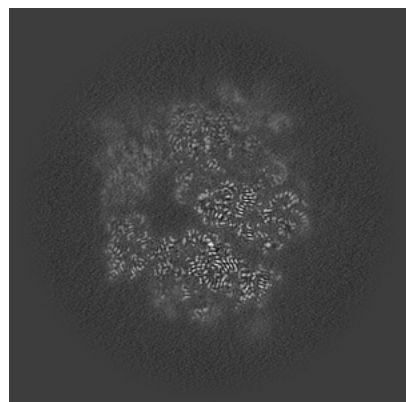


Z

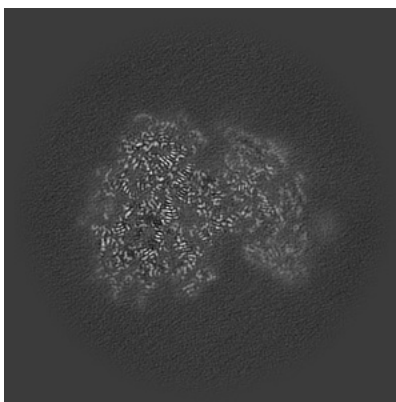
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

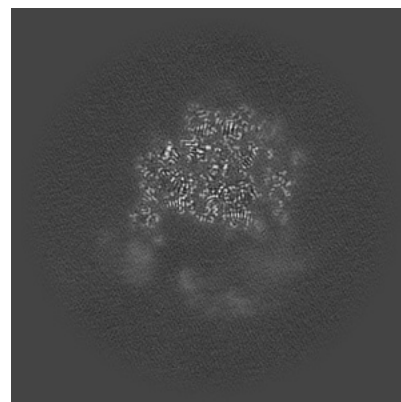
6.2.1 Primary map



X Index: 255



Y Index: 255

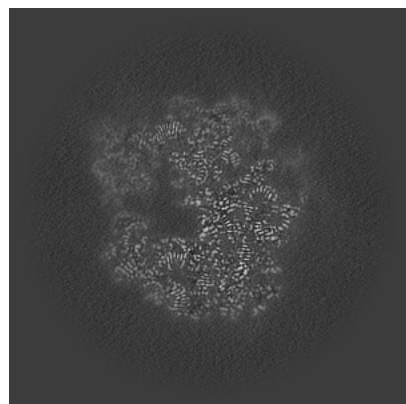


Z Index: 255

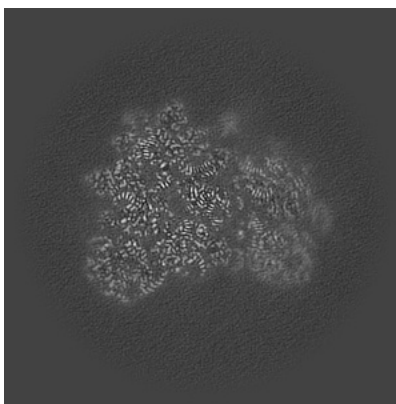
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

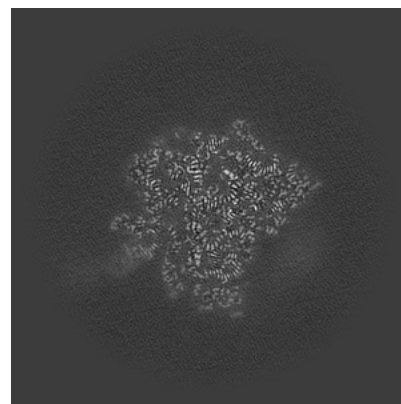
6.3.1 Primary map



X Index: 274



Y Index: 274

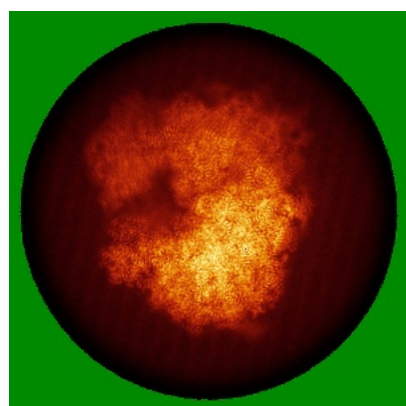


Z Index: 206

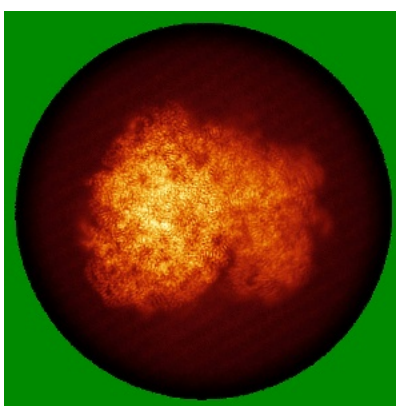
The images above show the largest variance slices of the map in three orthogonal directions.

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

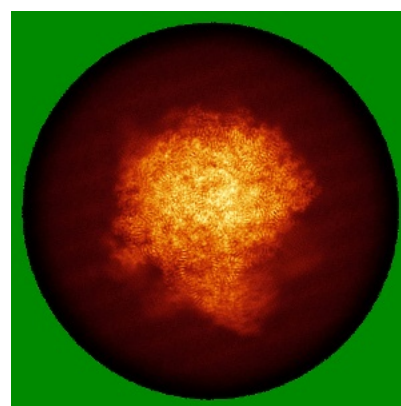
6.4.1 Primary map



X



Y

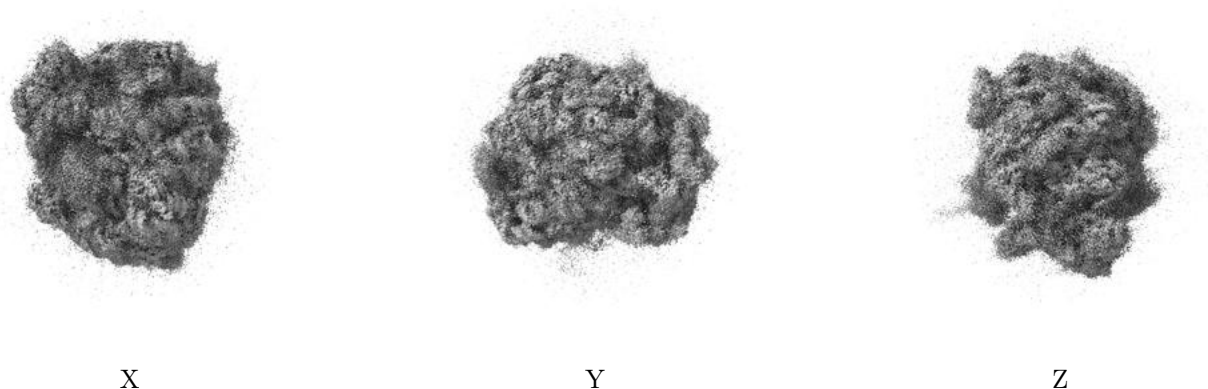


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

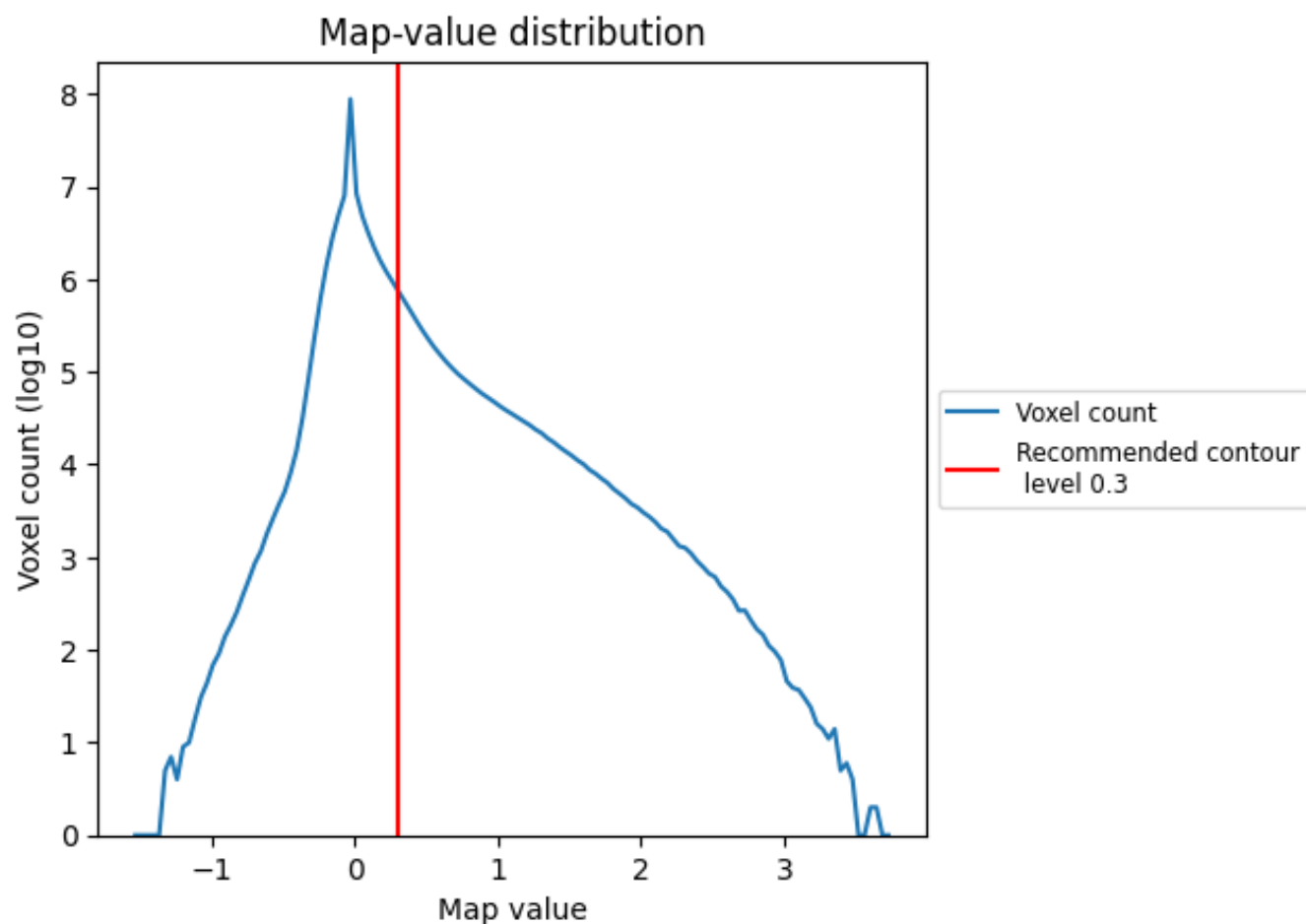
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

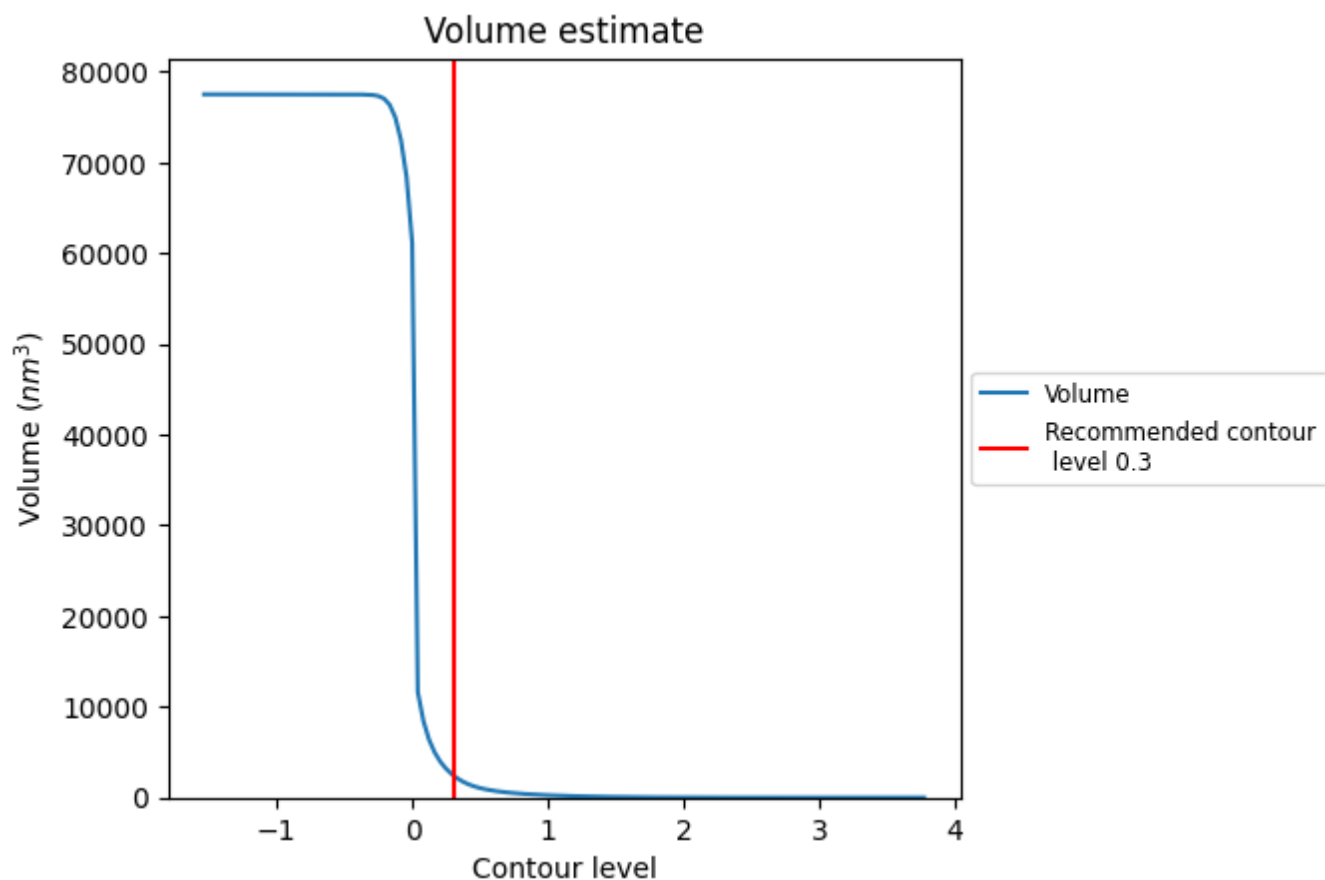
This section contains the results of statistical analysis of the map.

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.

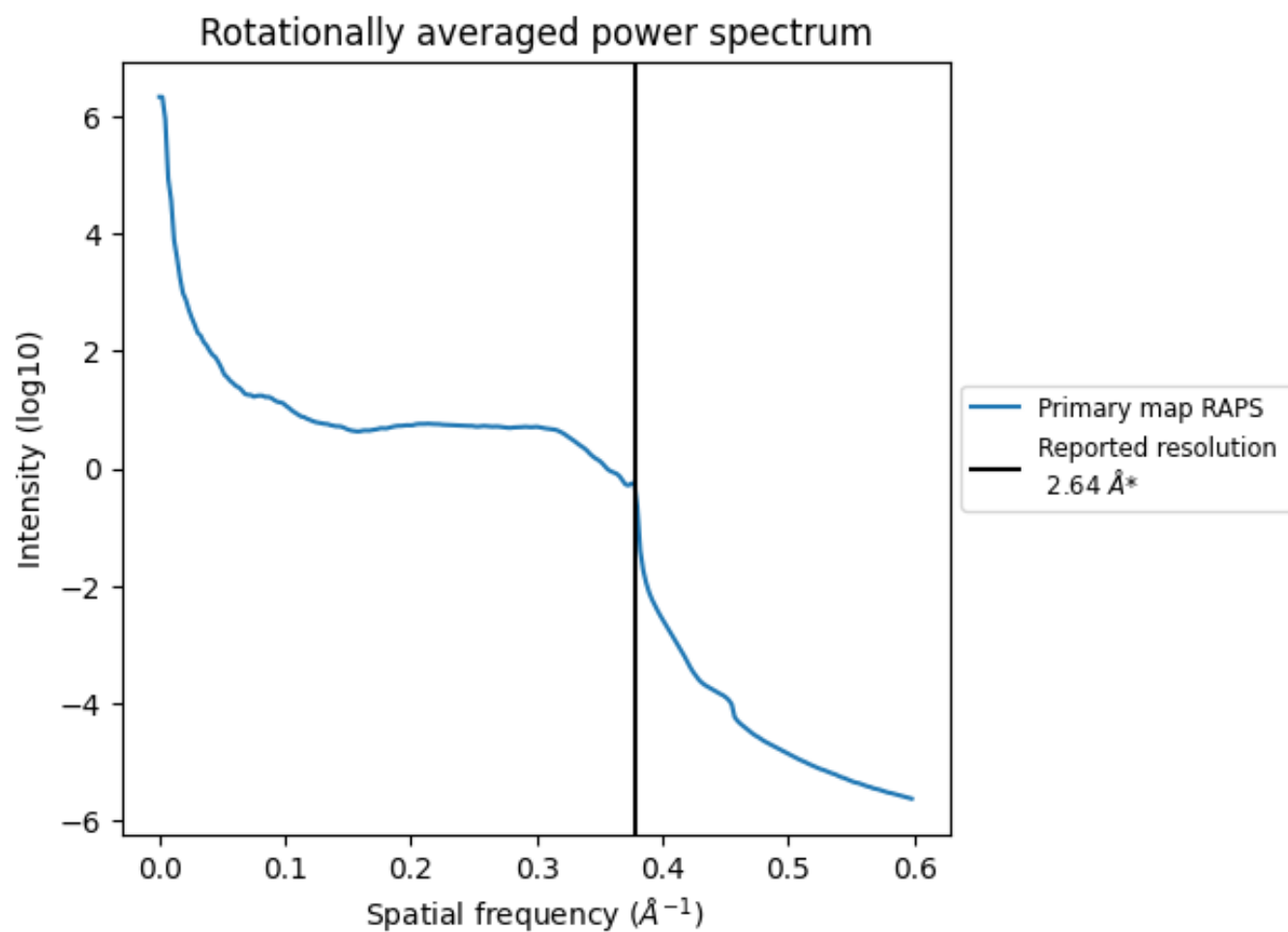
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2466 nm^3 ; this corresponds to an approximate mass of 2228 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 ⓘ

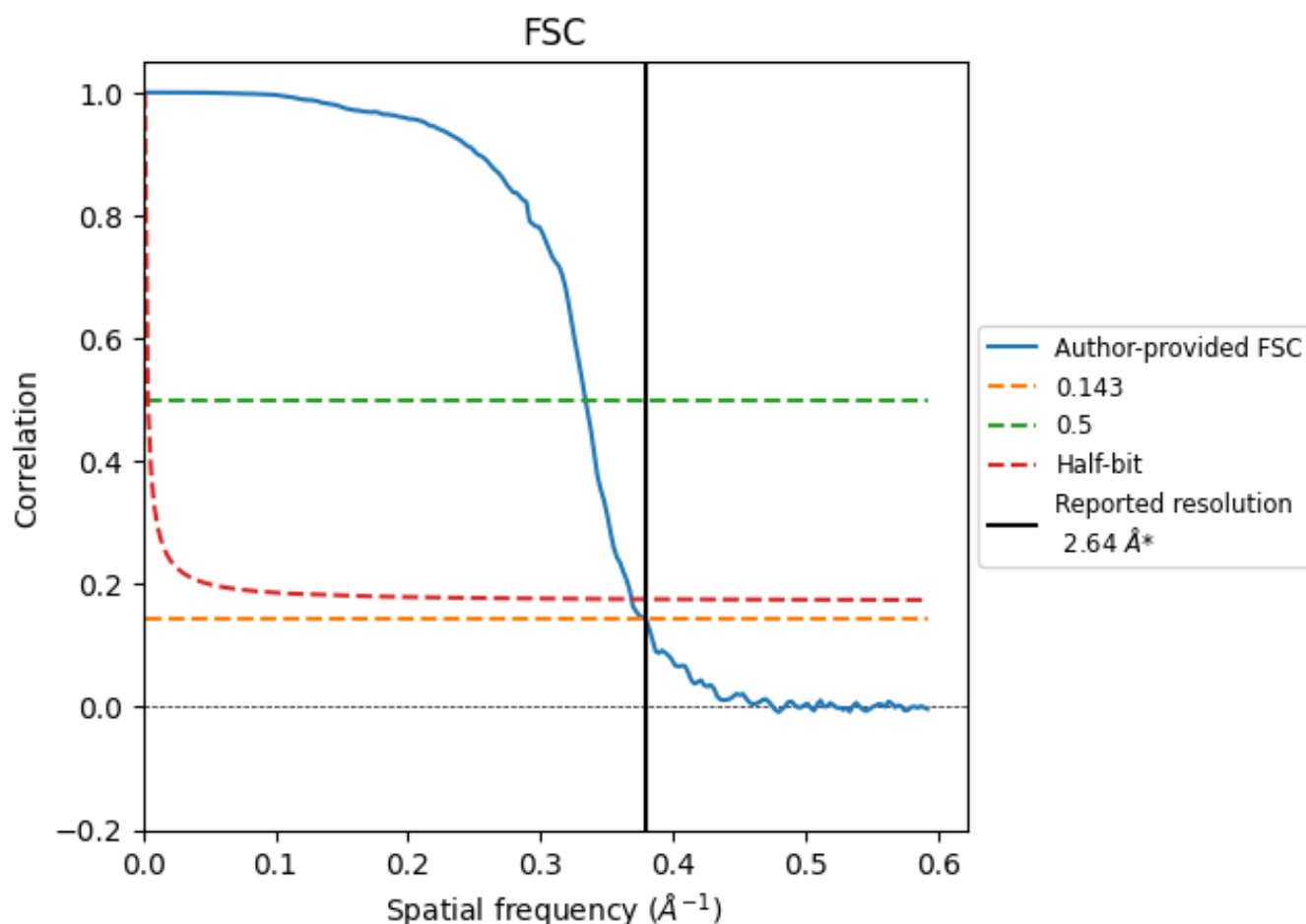


*Reported resolution corresponds to spatial frequency of 0.379 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.379 Å⁻¹

8.2 Resolution estimates [i](#)

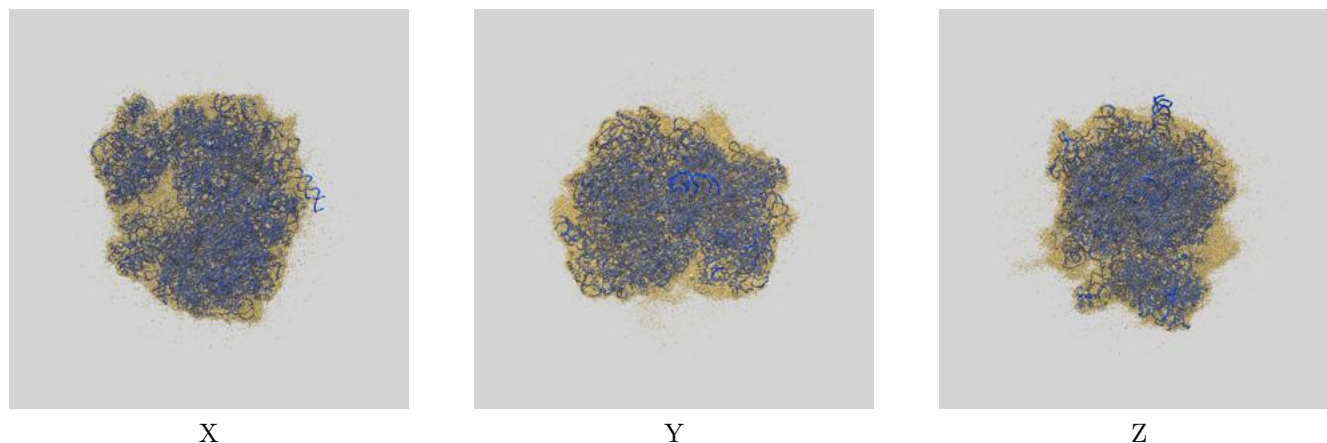
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.64	-	-
Author-provided FSC curve	2.64	2.99	2.71
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

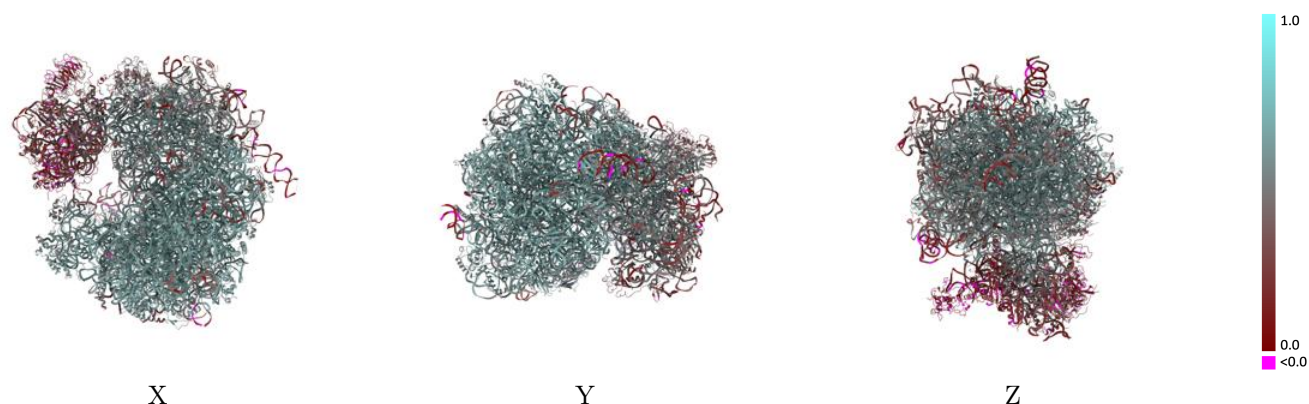
This section contains information regarding the fit between EMDB map EMD-13744 and PDB model 7Q0F. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

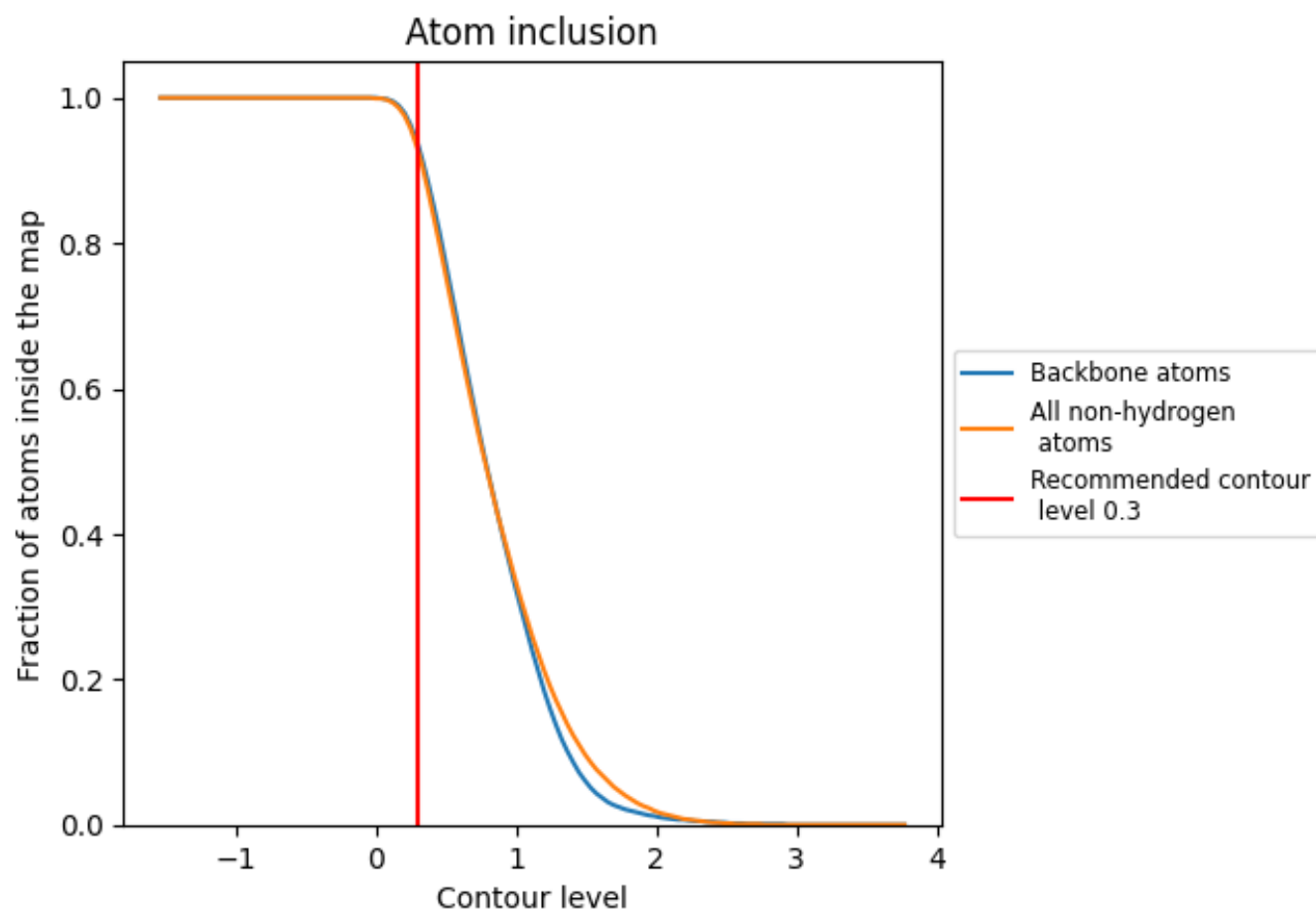


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9280	 0.5210
0	 0.9830	 0.6200
1	 0.9680	 0.5830
2	 0.9750	 0.6010
3	 0.9940	 0.6120
4	 0.9870	 0.6080
5	 0.9050	 0.5050
6	 0.9770	 0.6110
7	 0.9800	 0.5980
8	 0.9750	 0.6000
9	 0.9660	 0.5910
A	 0.9370	 0.4450
AA	 0.9570	 0.5860
AB	 0.9840	 0.6260
AC	 0.9550	 0.5650
AD	 0.9830	 0.5830
AE	 0.9450	 0.5910
AF	 0.9830	 0.6110
AG	 0.9850	 0.6400
AH	 0.9650	 0.6000
AI	 0.9750	 0.5870
AJ	 0.9530	 0.5710
AK	 0.9850	 0.6310
AL	 0.9340	 0.5450
AM	 0.9860	 0.6100
AN	 0.9510	 0.5910
AO	 0.9130	 0.5560
AP	 0.9680	 0.6130
AQ	 0.9790	 0.6050
B	 0.8830	 0.4450
C	 0.9220	 0.4850
D	 0.9240	 0.5010
E	 0.6850	 0.2600
F	 0.9330	 0.4690
G	 0.6520	 0.2120



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Chain	Atom inclusion	Q-score
H	 0.8620	 0.3860
I	 0.8140	 0.4280
J	 0.9110	 0.5140
K	 0.9010	 0.4540
L	 0.6040	 0.1490
M	 0.9220	 0.5440
N	 0.2430	 0.1120
O	 0.9620	 0.5350
P	 0.9400	 0.5080
Q	 0.5490	 0.1730
R	 0.8180	 0.3210
S	 0.7360	 0.3370
T	 0.6170	 0.1970
U	 0.7690	 0.2830
V	 0.7300	 0.2890
W	 0.8960	 0.4770
X	 0.9520	 0.5410
Y	 0.9450	 0.4910
Z	 0.8830	 0.3990
a	 0.4310	 0.1500
b	 0.9570	 0.5350
c	 0.9180	 0.4730
d	 0.5590	 0.2020
e	 0.8380	 0.2810
f	 0.8400	 0.3820
g	 0.3040	 0.1310
h	 0.5440	 0.2200
i	 0.6460	 0.2820
j	 0.9950	 0.6360
k	 0.9800	 0.6180
l	 0.9680	 0.5950
m	 0.9550	 0.5620
n	 0.9470	 0.5650
o	 0.9490	 0.5920
p	 0.9320	 0.5640
q	 0.9530	 0.5800
r	 0.9700	 0.6030
s	 0.9270	 0.5300
t	 0.9490	 0.5850
u	 0.9710	 0.5900
v	 0.9950	 0.6400
w	 0.9850	 0.6210

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Chain	Atom inclusion	Q-score
x	 0.9890	 0.6220
y	 0.9920	 0.6180
z	 0.9630	 0.5840