



Full wwPDB EM Validation Report ⓘ

Mar 4, 2026 – 10:52 PM UTC

PDB ID : 8Q5I / pdb_00008q5i
EMDB ID : EMD-18156
Title : Structure of Candida albicans 80S ribosome in complex with cephaeline
Authors : Kolosova, O.; Zgadzay, Y.; Stetsenko, A.; Atamas, A.; Guskov, A.; Yusupov, M.
Deposited on : 2023-08-09
Resolution : 2.45 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:

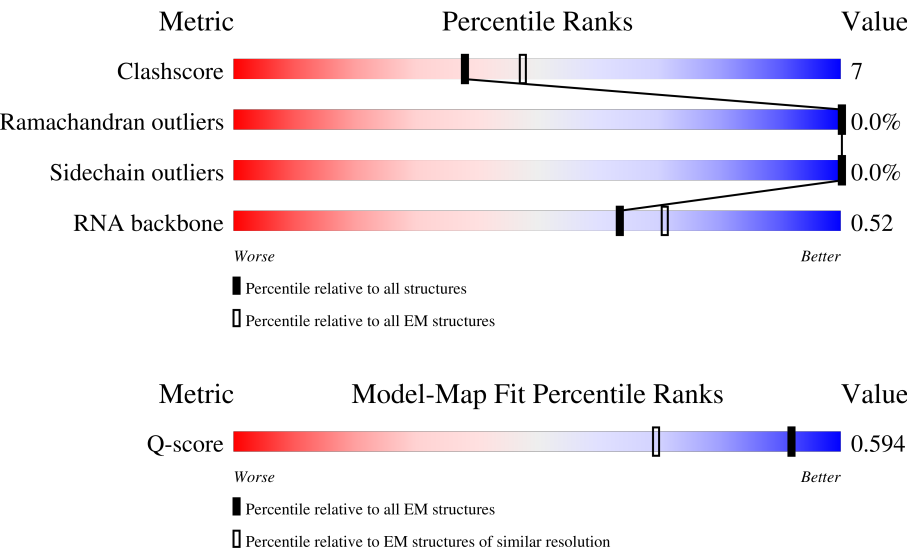
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 2.45 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	5931 (1.96 - 2.95)

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	10	14	
5	j	254	
6	k	389	
7	l	363	
8	m	298	
9	n	176	
10	o	241	
11	p	262	
12	q	191	
13	r	220	
14	s	174	
15	t	202	
16	u	131	
17	v	204	
18	w	200	
19	x	185	
20	y	186	
21	z	190	
22	0	172	
23	2	160	
24	5	124	
25	6	137	
26	7	155	
27	8	142	
28	9	127	

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Mol	Chain	Length	Quality of chain
29	AA	136	
30	AB	149	
31	AC	63	
32	AD	106	
33	AE	112	
34	AF	131	
35	AG	107	
36	AH	122	
37	AI	120	
38	AJ	99	
39	AK	90	
40	AL	78	
41	AM	51	
42	AN	52	
43	AO	25	
44	AP	106	
45	AQ	92	
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	O	151	
60	P	132	
61	Q	142	
62	R	142	
63	S	137	
64	T	145	
65	U	145	
66	V	119	
67	W	87	
68	X	130	
69	Y	145	
70	Z	135	
71	b	119	
72	c	82	
73	d	67	
74	e	56	
75	f	63	
76	g	5	

2 Entry composition [i](#)

There are 82 unique types of molecules in this entry. The entry contains 189590 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3073	Total	C	N	O	P	0	0
			65690	29348	11807	21462	3073		

- Molecule 2 is a RNA chain called 5S.

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 rRNA.

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 RNA chain called Mixture of endogenous E-tRNAs.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	10	9	Total	C	N	O	P	0	0
			187	84	31	63	9		

- Molecule 5 is a protein called 60S ribosomal protein L2-B.

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

- Molecule 6 is a protein called 60S ribosomal protein L3.

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

- Molecule 7 is a protein called 60S ribosomal protein L4-B.

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

- Molecule 8 is a protein called 60S ribosomal protein L5.

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

- Molecule 9 is a protein called 60S ribosomal protein L6.

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

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	o	226	Total	C	N	O	S	1	0
			1824	1170	336	317	1		

- Molecule 11 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	p	232	Total	C	N	O	S	0	0
			1800	1153	320	324	3		

- Molecule 12 is a protein called 60S ribosomal protein L9-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	q	188	Total	C	N	O	S	0	0
			1501	948	274	275	4		

- Molecule 13 is a protein called 60S ribosomal protein L10.

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

- Molecule 14 is a protein called 60S ribosomal protein L11-B.

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

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	t	191	Total	C	N	O		0	0
			1545	970	307	268			

- Molecule 16 is a protein called 60S ribosomal protein L14-B.

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

- Molecule 17 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 18 is a protein called Ribosomal protein L13.

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

- Molecule 19 is a protein called Ribosomal protein L22.

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

- Molecule 20 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0	171	Total	C	N	O	S	2	0
			1442	933	262	244	3		

- Molecule 23 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	159	Total	C	N	O	S	2	0
			1276	807	244	223	2		

- Molecule 24 is a protein called 60S ribosomal protein L22-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	5	101	Total	C	N	O		2	0
			833	544	136	153			

- Molecule 25 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	6	131	Total	C	N	O	S	1	0
			986	621	186	171	8		

- Molecule 26 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	7	63	Total	C	N	O	S	0	0
			524	334	103	86	1		

- Molecule 27 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	8	121	Total	C	N	O	S	0	0
			974	622	175	176	1		

- Molecule 28 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	9	125	Total	C	N	O		
			980	613	189	178	0	0

- Molecule 29 is a protein called 60S ribosomal protein L27.

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

- Molecule 30 is a protein called 60S ribosomal protein L28.

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

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AC	57	Total	C	N	O	S		
			464	291	99	73	1	1	0

- Molecule 32 is a protein called 60S ribosomal protein L30.

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

- Molecule 33 is a protein called 60S ribosomal protein L31-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AE	103	Total	C	N	O	S		
			839	536	161	140	2	0	0

- Molecule 34 is a protein called 60S ribosomal protein L32.

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

- Molecule 35 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L34-B.

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

- Molecule 37 is a protein called Ribosomal protein L29.

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

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AJ	97	Total	C	N	O	S	1	0
			764	476	157	130	1		

- Molecule 39 is a protein called 60S ribosomal protein L37-B.

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

- Molecule 40 is a protein called 60S ribosomal protein L38.

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

- Molecule 41 is a protein called 60S ribosomal protein L39.

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

- Molecule 42 is a protein called 60S ribosomal protein L40-B.

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

- Molecule 43 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AO	25	Total	C	N	O	S	0	0
			236	144	63	28	1		

- Molecule 44 is a protein called 60S ribosomal protein L42-B.

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

- Molecule 45 is a protein called 60S ribosomal protein L43-A.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A	1558	Total	C	N	O	P	0	0
			33257	14866	5947	10886	1558		

- 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 protein S5.

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 protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	E	206	Total	C	N	O	S	0	0
			1582	1010	292	276	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 protein S7.

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	185	Total	C	N	O	S	0	0
			1461	902	297	261	1		

- Molecule 56 is a protein called Ribosomal protein S4.

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 40S ribosomal protein S10-A.

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 40S ribosomal protein S11A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	M	135	Total	C	N	O	S	0	0
			1084	694	202	185	3		

- Molecule 59 is a protein called 40S ribosomal protein S13.

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

- Molecule 60 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	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	conflict	UNP A0A8H6F0V4

- Molecule 61 is a protein called 40S ribosomal protein S15.

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

- Molecule 62 is a protein called 40S ribosomal protein S16.

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

- Molecule 63 is a protein called 40S ribosomal protein S17-B.

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

- Molecule 64 is a protein called 40S ribosomal protein S18-B.

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

- Molecule 65 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 66 is a protein called Ribosomal protein S10.

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

- Molecule 67 is a protein called 40S ribosomal protein S21.

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

- Molecule 68 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 69 is a protein called Ribosomal protein S23 (S12).

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

- Molecule 70 is a protein called 40S ribosomal protein S24.

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

- Molecule 71 is a protein called 40S ribosomal protein S26.

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

- Molecule 72 is a protein called 40S ribosomal protein S27.

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

- Molecule 73 is a protein called 40S ribosomal protein S28-B.

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

- Molecule 74 is a protein called 40S ribosomal protein S29A.

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

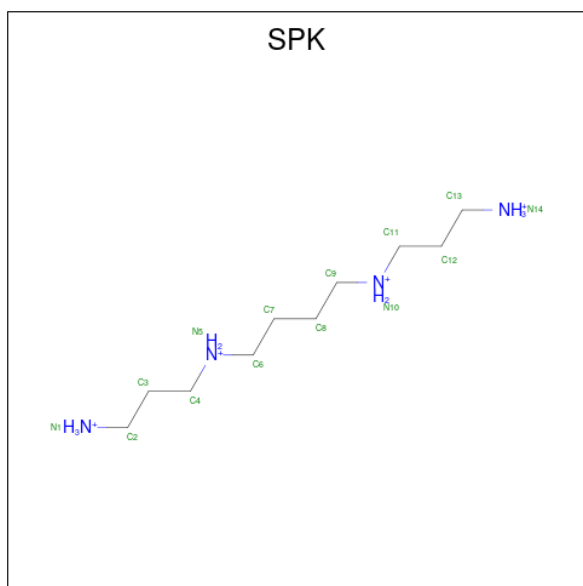
- Molecule 75 is a protein called 40S ribosomal protein S30.

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

- Molecule 76 is a RNA chain called DNA (5'-R(P*GP*GP*CP*AP*G)-3').

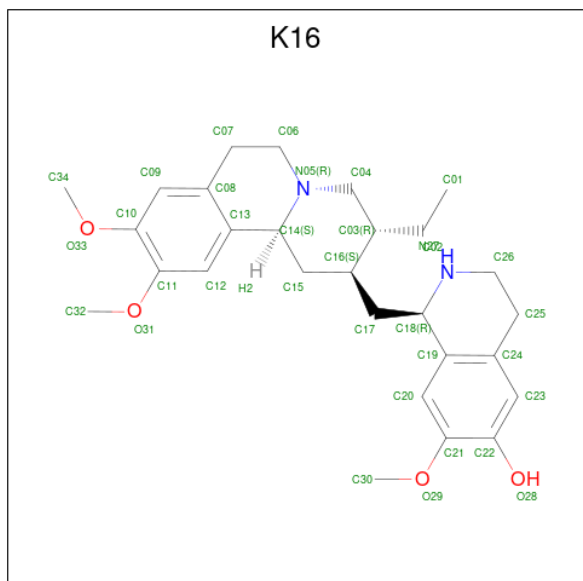
Mol	Chain	Residues	Atoms					AltConf	Trace
76	g	5	Total	C	N	O	P	0	0
			111	49	23	34	5		

- Molecule 77 is SPERMINE (FULLY PROTONATED FORM) (CCD ID: SPK) (formula: $C_{10}H_{30}N_4$).



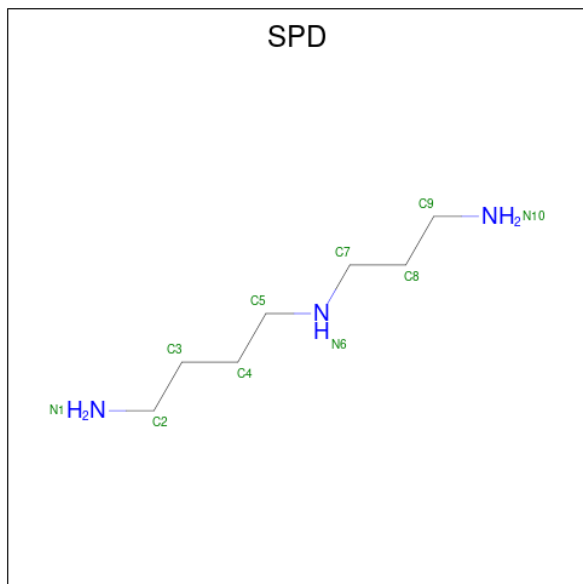
Mol	Chain	Residues	Atoms			AltConf
77	1	1	Total	C	N	0
			14	10	4	

- Molecule 78 is Cephaeline (CCD ID: K16) (formula: $C_{28}H_{38}N_2O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
78	1	1	Total	C	N	O	0
			34	28	2	4	
78	1	1	Total	C	N	O	0
			34	28	2	4	
78	A	1	Total	C	N	O	0
			34	28	2	4	

- Molecule 79 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
79	1	1	Total	C	N	0
			10	7	3	

- Molecule 80 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
80	1	255	Total	Mg	0
			255	255	
80	3	1	Total	Mg	0
			1	1	
80	4	2	Total	Mg	0
			2	2	
80	j	1	Total	Mg	0
			1	1	
80	k	1	Total	Mg	0
			1	1	
80	o	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
80	r	1	Total 1	Mg 1	0
80	v	1	Total 1	Mg 1	0
80	x	1	Total 1	Mg 1	0
80	6	1	Total 1	Mg 1	0
80	AH	1	Total 1	Mg 1	0
80	AP	1	Total 1	Mg 1	0
80	A	97	Total 97	Mg 97	0
80	C	1	Total 1	Mg 1	0
80	X	1	Total 1	Mg 1	0
80	Y	1	Total 1	Mg 1	0

- Molecule 81 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 82 is water.

Mol	Chain	Residues	Atoms	AltConf
82	1	632	Total O 632 632	0
82	3	2	Total O 2 2	0
82	4	14	Total O 14 14	0
82	10	1	Total O 1 1	0
82	j	17	Total O 17 17	0
82	k	16	Total O 16 16	0
82	l	11	Total O 11 11	0
82	m	2	Total O 2 2	0
82	o	5	Total O 5 5	0
82	q	2	Total O 2 2	0
82	r	5	Total O 5 5	0
82	t	1	Total O 1 1	0
82	v	7	Total O 7 7	0
82	w	3	Total O 3 3	0
82	x	8	Total O 8 8	0
82	y	1	Total O 1 1	0
82	z	1	Total O 1 1	0
82	2	1	Total O 1 1	0
82	6	6	Total O 6 6	0
82	8	2	Total O 2 2	0
82	AA	1	Total O 1 1	0
82	AB	1	Total O 1 1	0

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Mol	Chain	Residues	Atoms		AltConf
82	AC	3	Total 3	O 3	0
82	AF	5	Total 5	O 5	0
82	AG	3	Total 3	O 3	0
82	AH	4	Total 4	O 4	0
82	AI	2	Total 2	O 2	0
82	AK	7	Total 7	O 7	0
82	AP	3	Total 3	O 3	0
82	AQ	2	Total 2	O 2	0
82	A	321	Total 321	O 321	0
82	C	1	Total 1	O 1	0
82	D	5	Total 5	O 5	0
82	F	3	Total 3	O 3	0
82	H	3	Total 3	O 3	0
82	I	6	Total 6	O 6	0
82	J	5	Total 5	O 5	0
82	K	1	Total 1	O 1	0
82	M	5	Total 5	O 5	0
82	O	7	Total 7	O 7	0
82	P	1	Total 1	O 1	0
82	W	1	Total 1	O 1	0
82	X	15	Total 15	O 15	0

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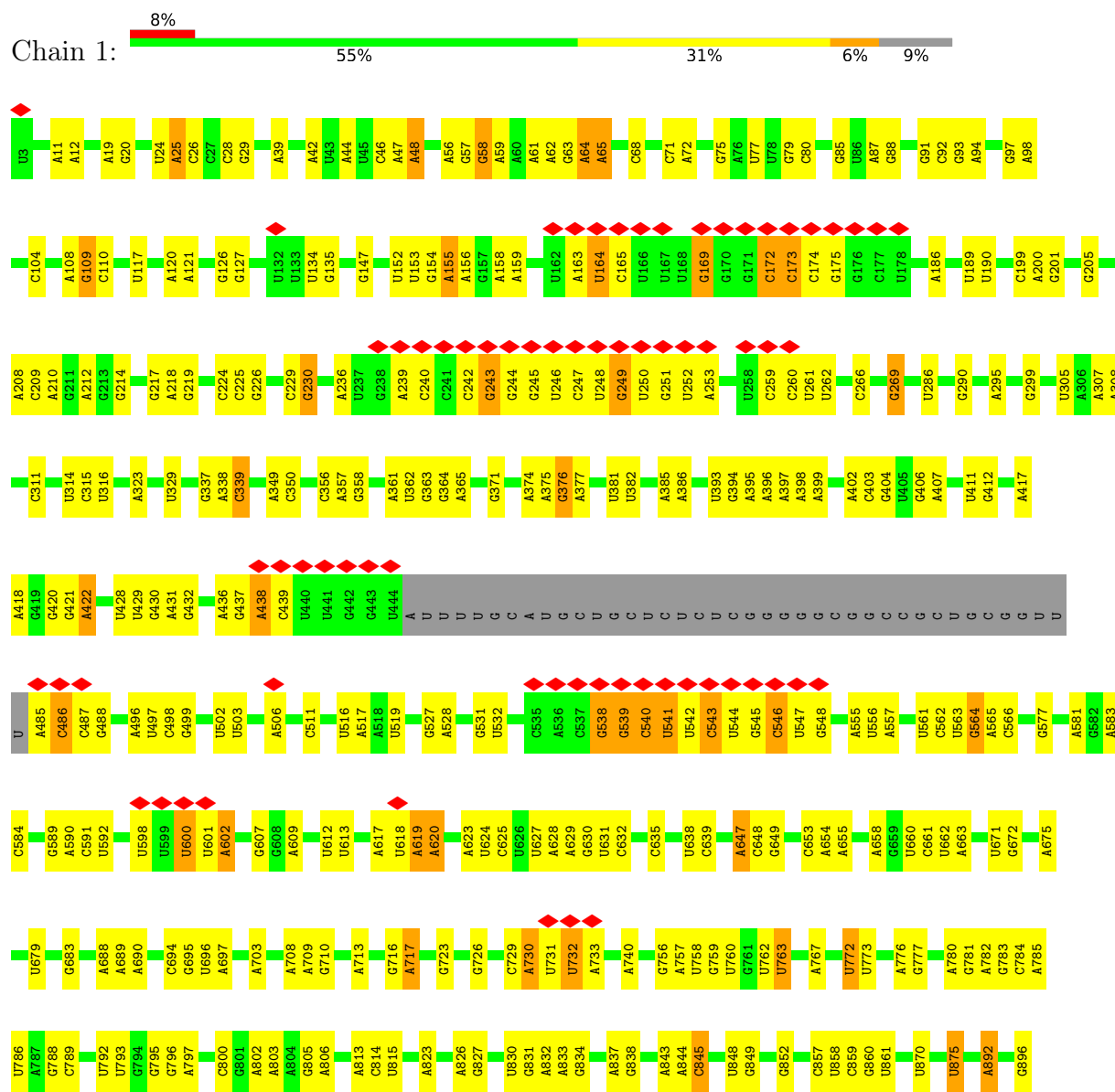
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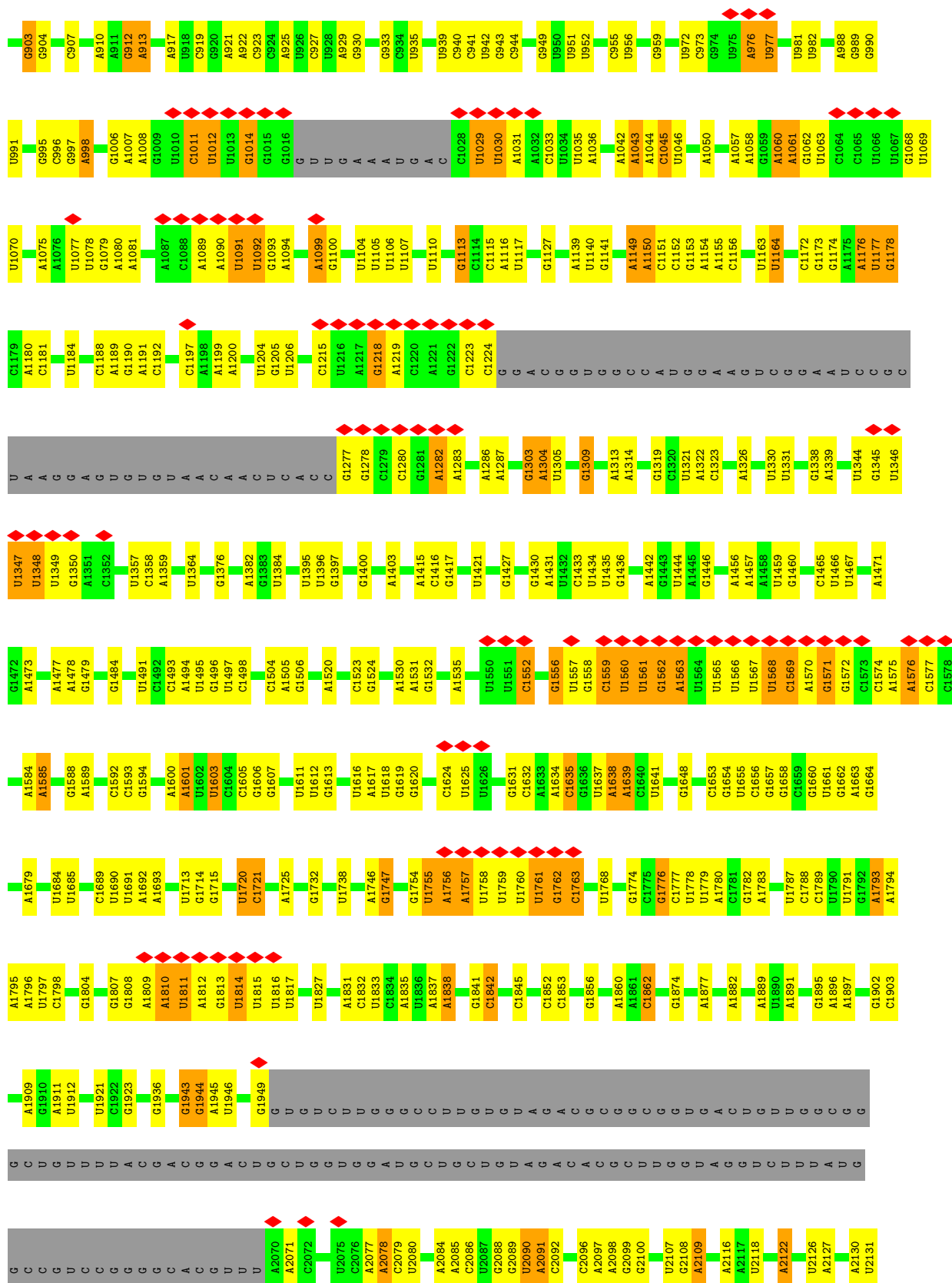
Mol	Chain	Residues	Atoms		AltConf
82	Y	11	Total 11	O 11	0
82	b	9	Total 9	O 9	0
82	c	3	Total 3	O 3	0
82	e	1	Total 1	O 1	0

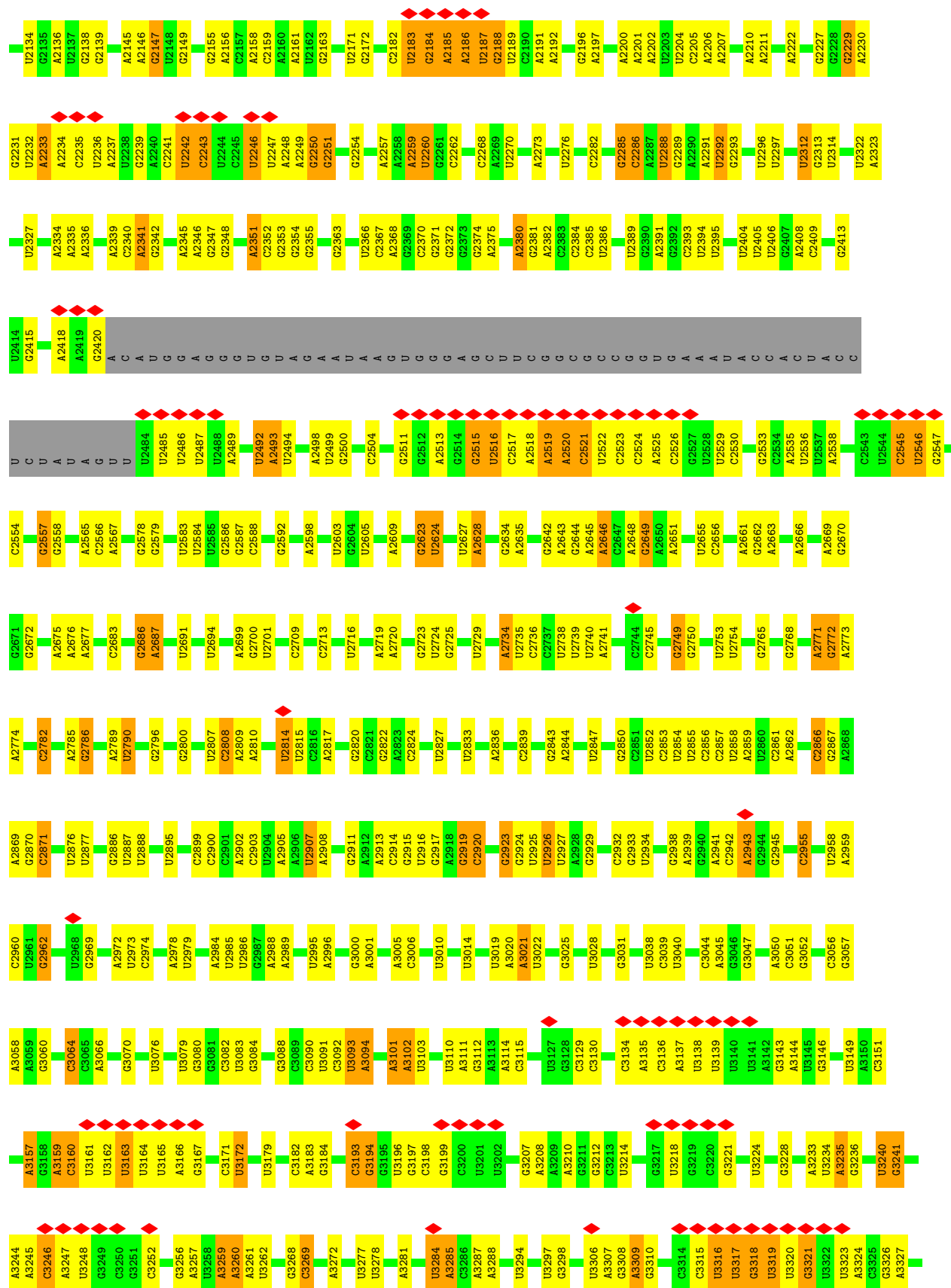
3 Residue-property plots

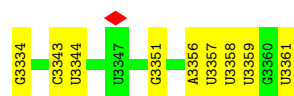
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 25S rRNA





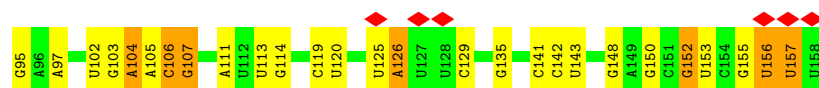




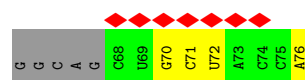
- Molecule 2: 5S



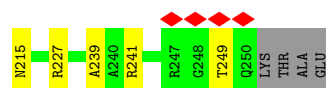
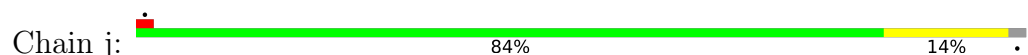
- Molecule 3: 5.8S rRNA



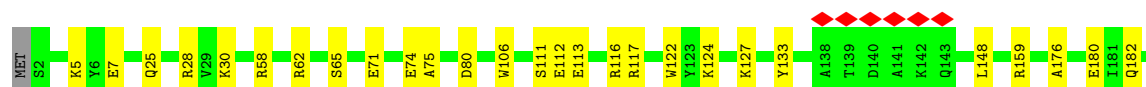
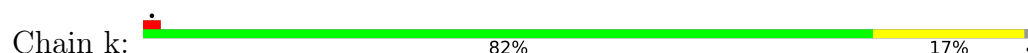
- Molecule 4: Mixture of endogenous E-tRNAs



- Molecule 5: 60S ribosomal protein L2-B

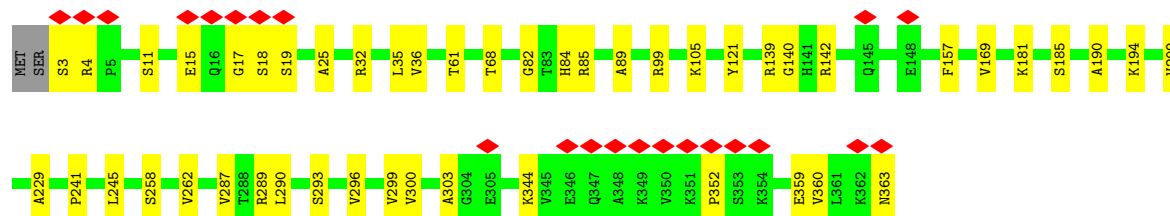
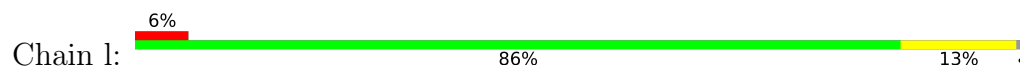


- Molecule 6: 60S ribosomal protein L3

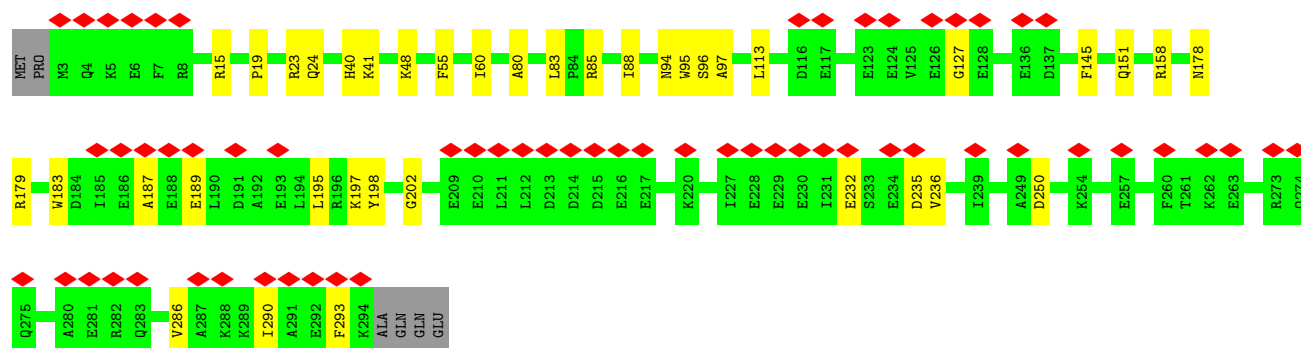
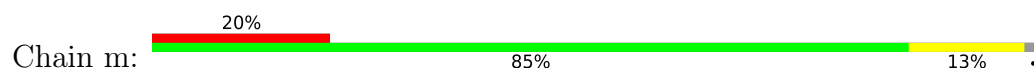




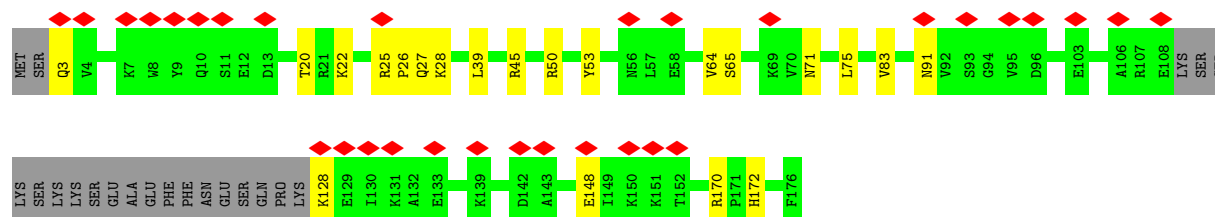
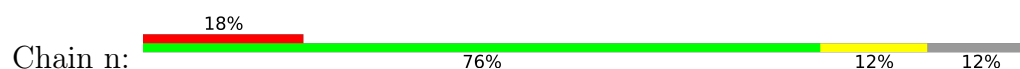
• Molecule 7: 60S ribosomal protein L4-B



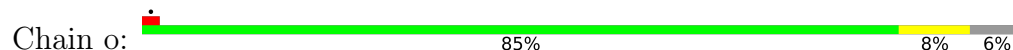
• Molecule 8: 60S ribosomal protein L5

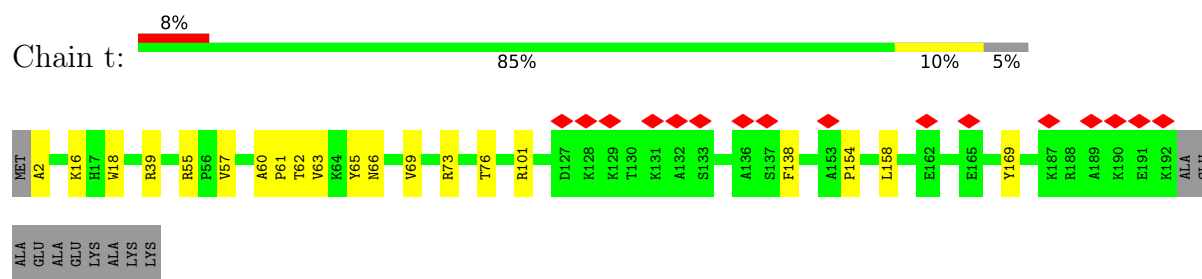


• Molecule 9: 60S ribosomal protein L6

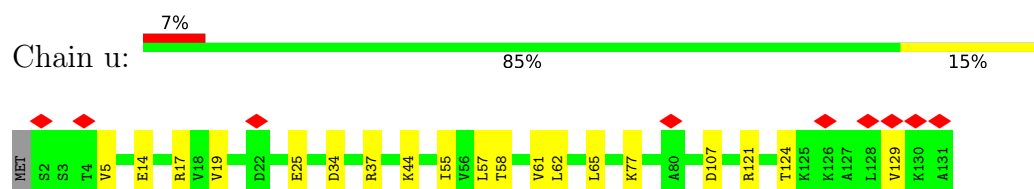


• Molecule 10: 60S ribosomal protein L7-A

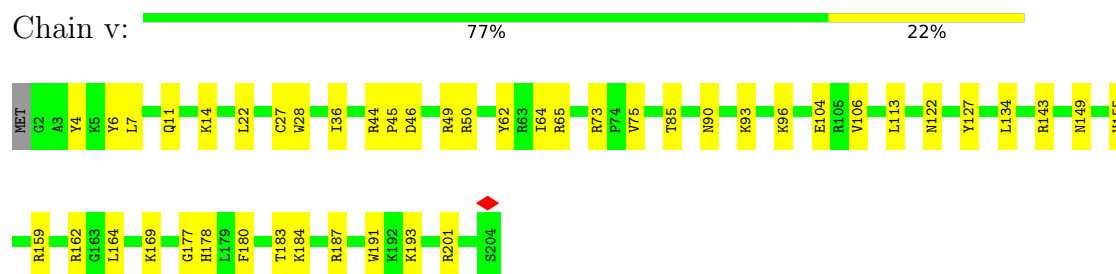




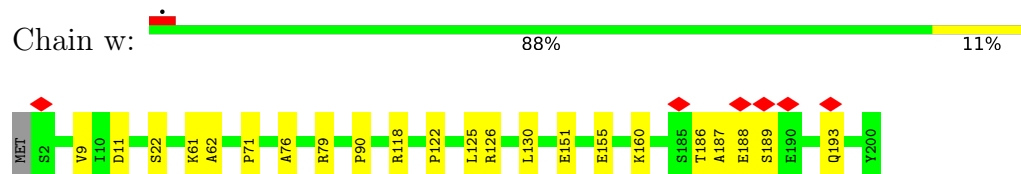
- Molecule 16: 60S ribosomal protein L14-B



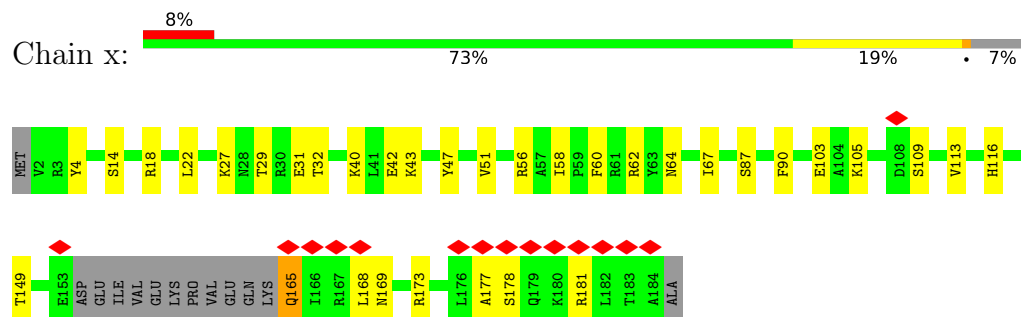
- Molecule 17: 60S ribosomal protein L15-A



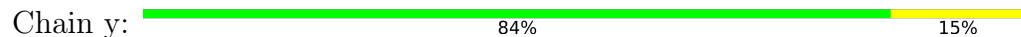
- Molecule 18: Ribosomal protein L13

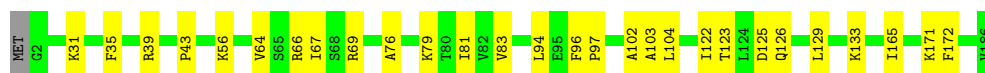


- Molecule 19: Ribosomal protein L22

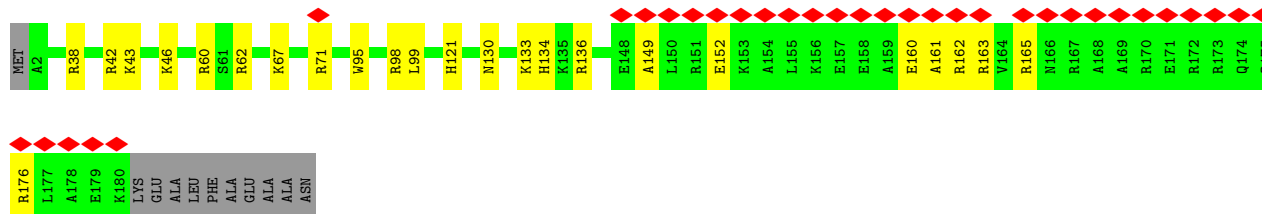
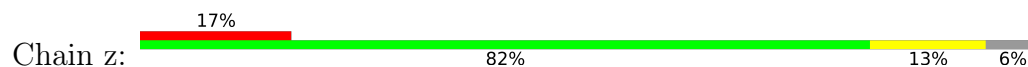


- Molecule 20: 60S ribosomal protein L18-A

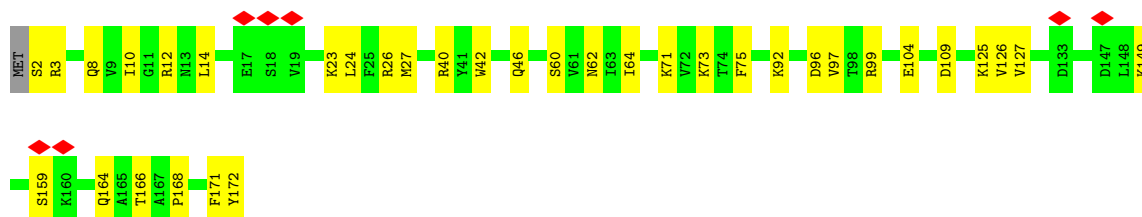




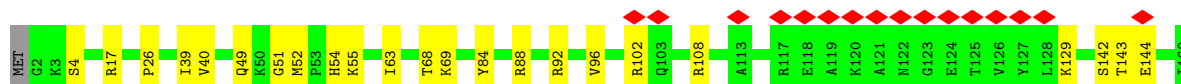
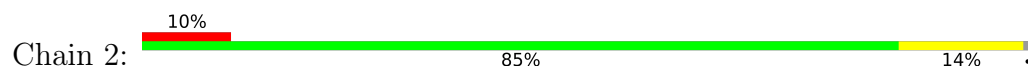
- Molecule 21: 60S ribosomal protein L19-A



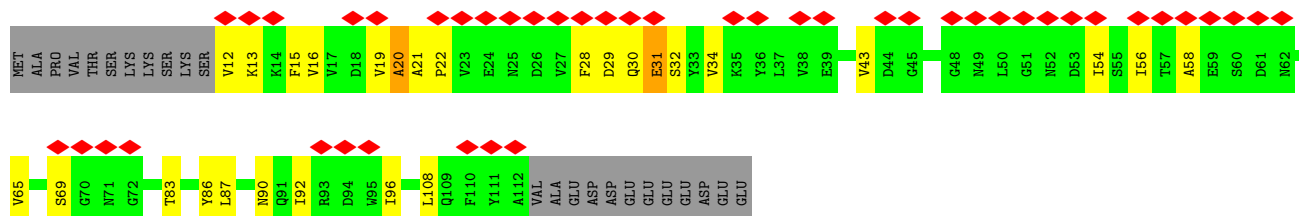
- Molecule 22: 60S ribosomal protein L20



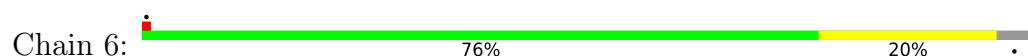
- Molecule 23: 60S ribosomal protein L21-A

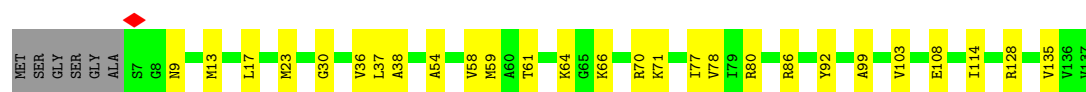


- Molecule 24: 60S ribosomal protein L22-B

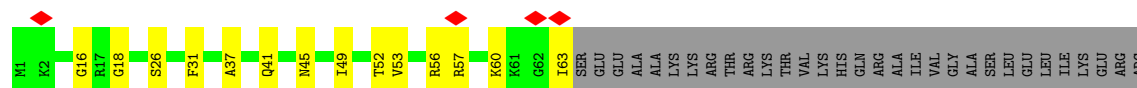


- Molecule 25: 60S ribosomal protein L23-A

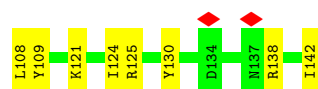




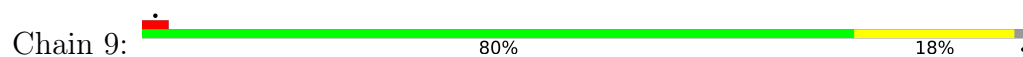
- Molecule 26: 60S ribosomal protein L24-A



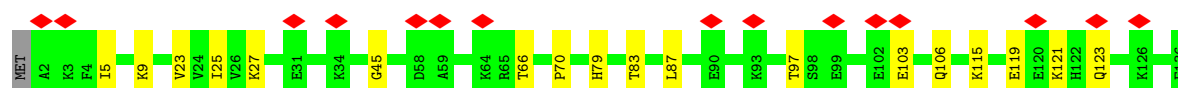
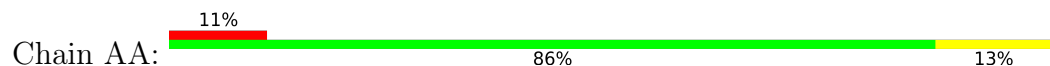
- Molecule 27: 60S ribosomal protein L25



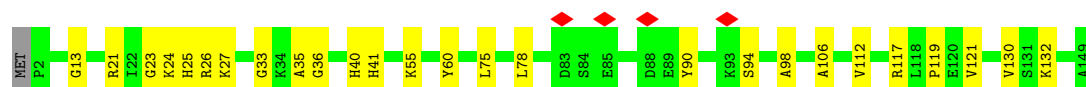
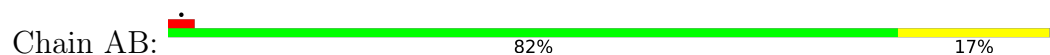
- Molecule 28: Ribosomal protein L24



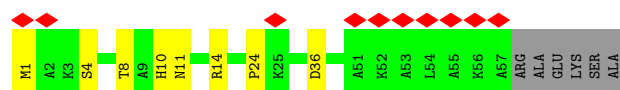
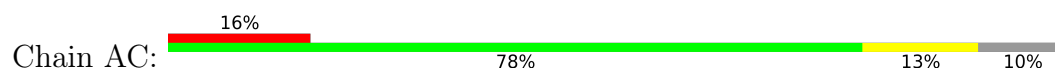
- Molecule 29: 60S ribosomal protein L27



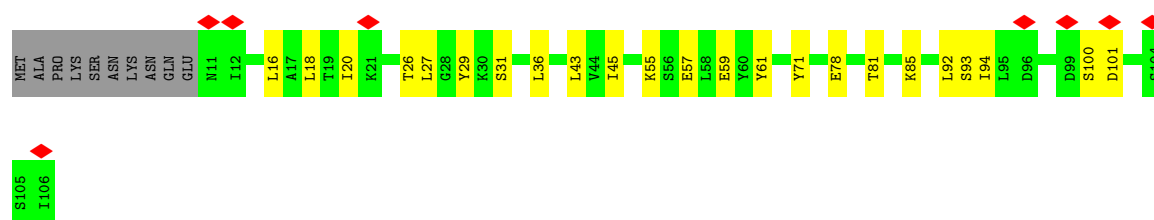
- Molecule 30: 60S ribosomal protein L28



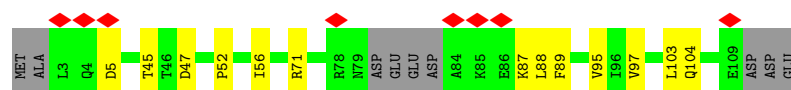
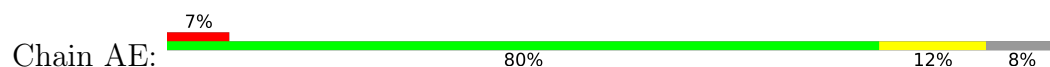
- Molecule 31: 60S ribosomal protein L29



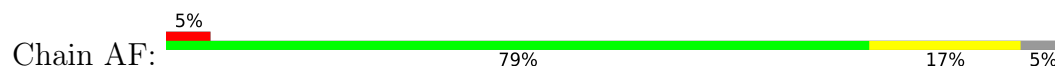
- Molecule 32: 60S ribosomal protein L30



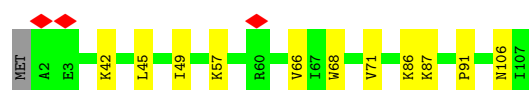
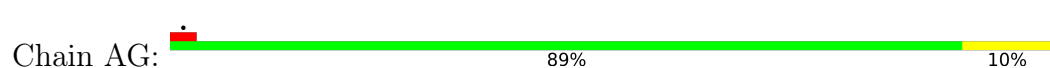
- Molecule 33: 60S ribosomal protein L31-B



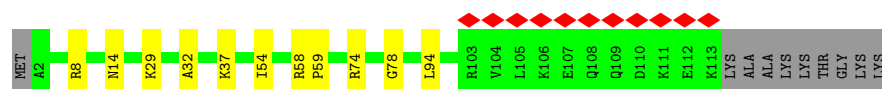
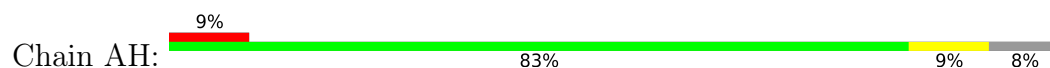
- Molecule 34: 60S ribosomal protein L32



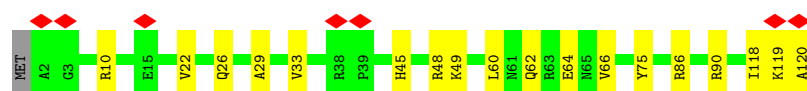
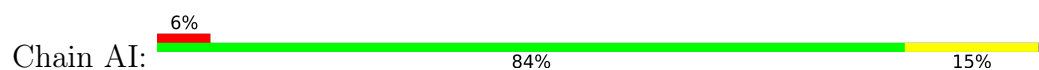
- Molecule 35: 60S ribosomal protein L33-A



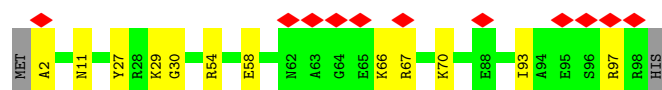
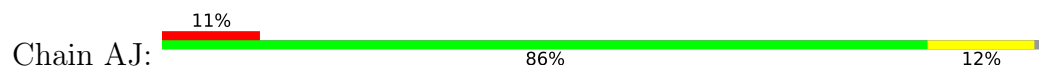
- Molecule 36: 60S ribosomal protein L34-B



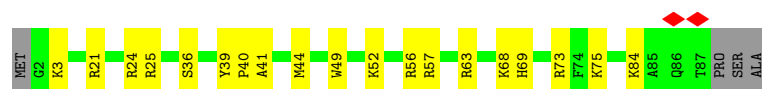
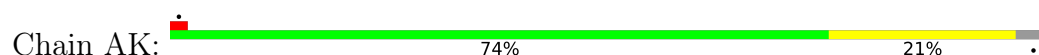
- Molecule 37: Ribosomal protein L29



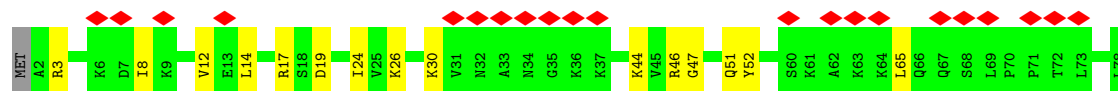
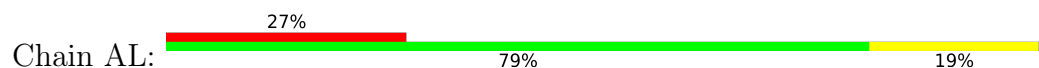
- Molecule 38: 60S ribosomal protein L36



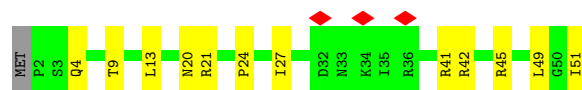
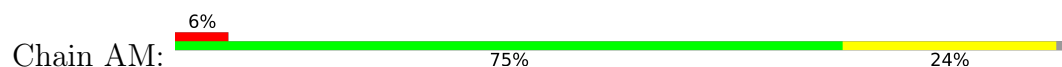
- Molecule 39: 60S ribosomal protein L37-B



- Molecule 40: 60S ribosomal protein L38



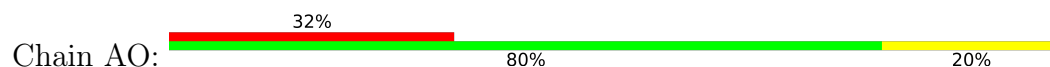
- Molecule 41: 60S ribosomal protein L39



- Molecule 42: 60S ribosomal protein L40-B

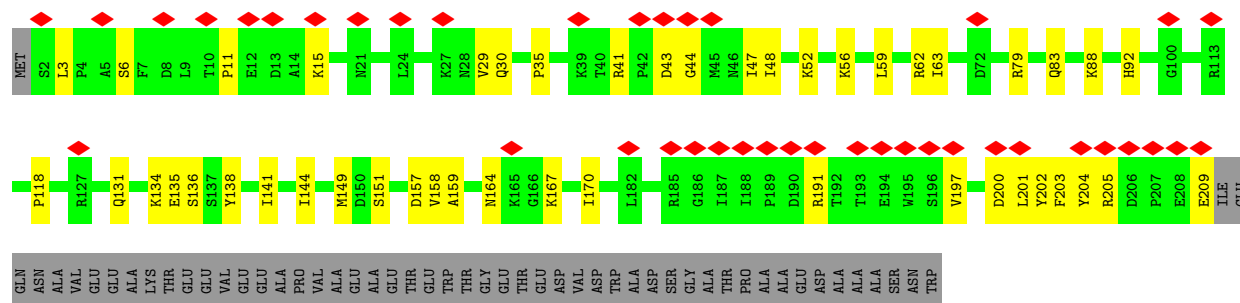


- Molecule 43: 60S ribosomal protein L41

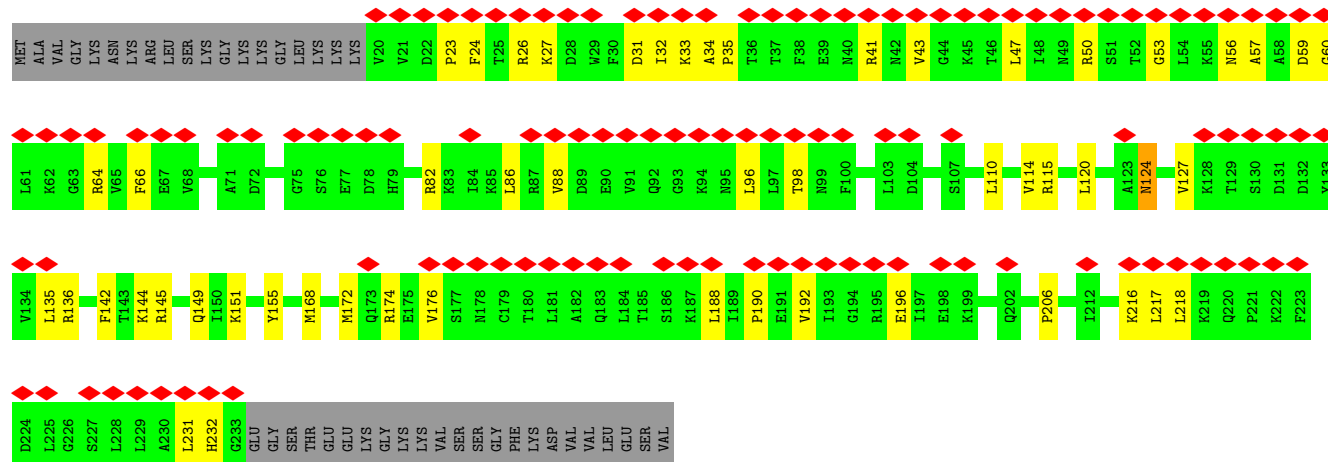




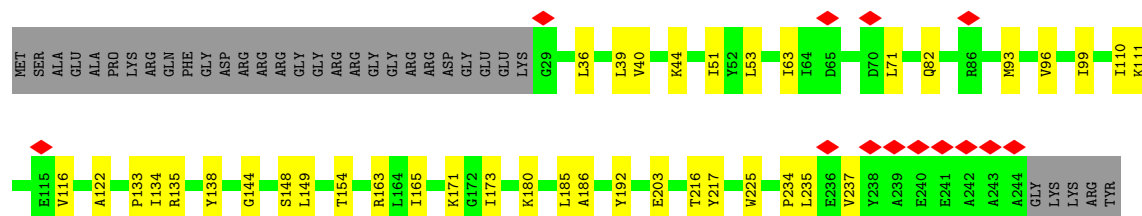
- Molecule 47: 40S ribosomal protein S0



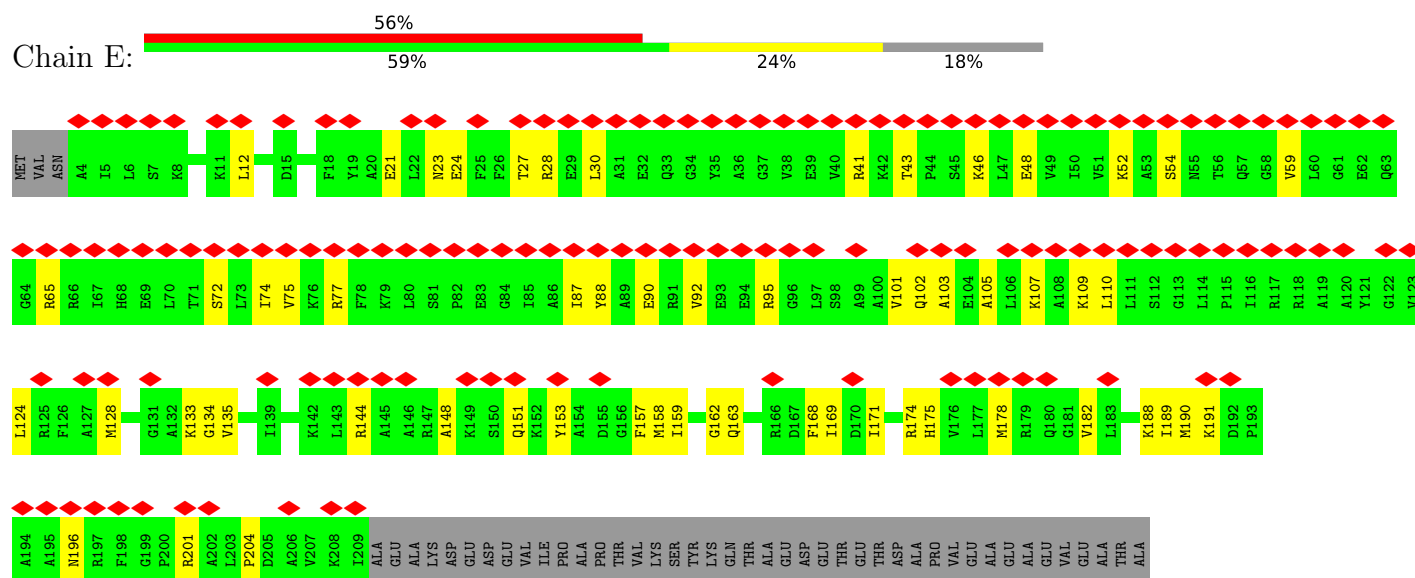
- Molecule 48: 40S ribosomal protein S1



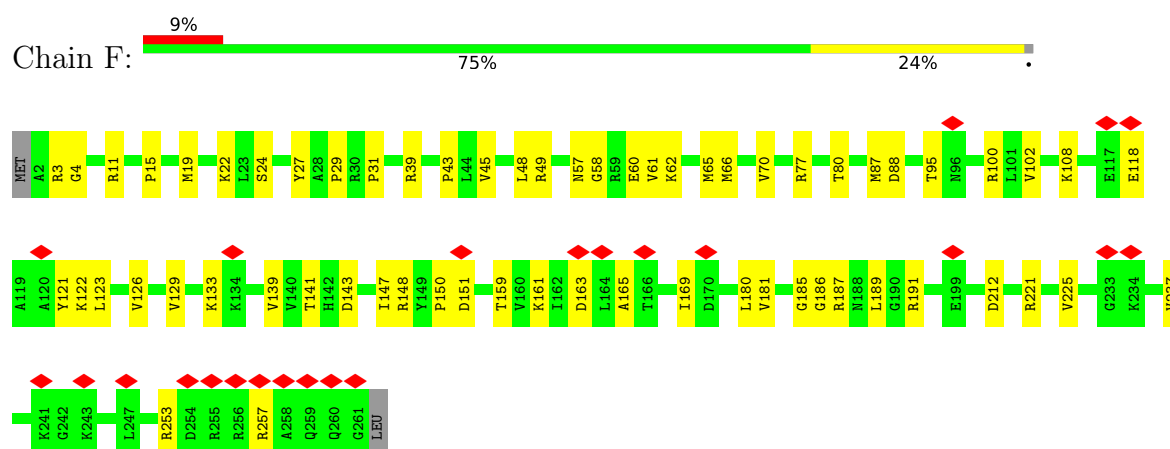
- Molecule 49: Ribosomal protein S5



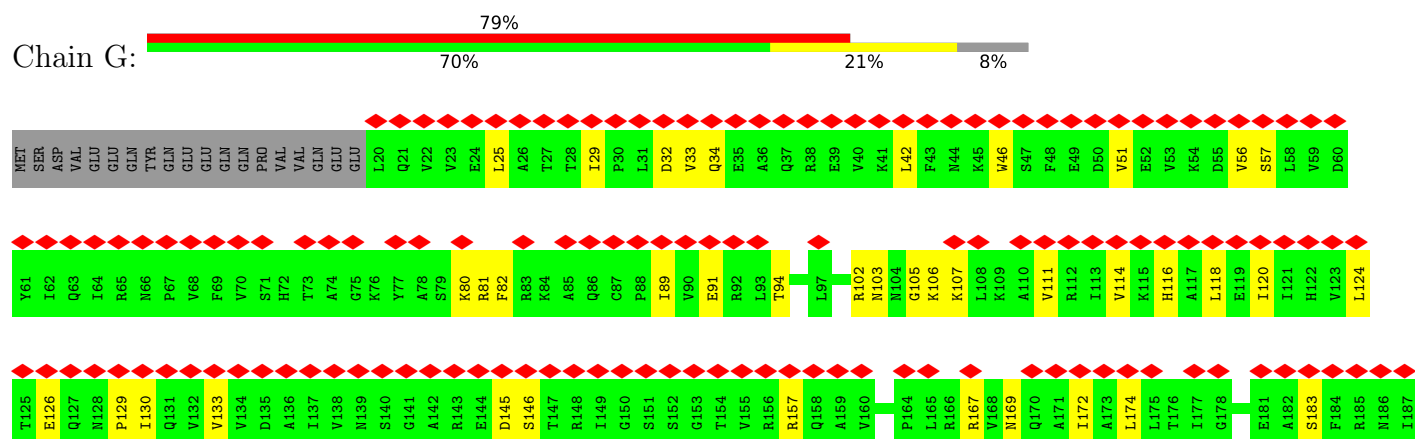
- Molecule 50: Ribosomal protein S3

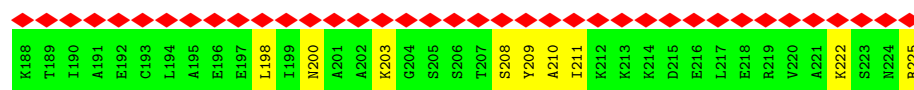


- Molecule 51: 40S ribosomal protein S4

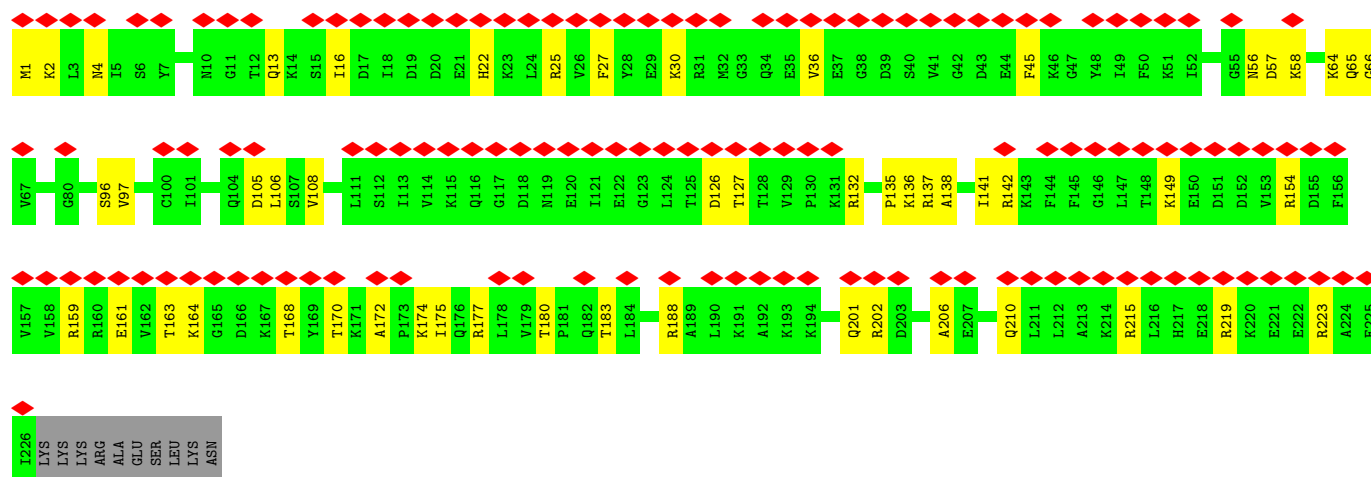
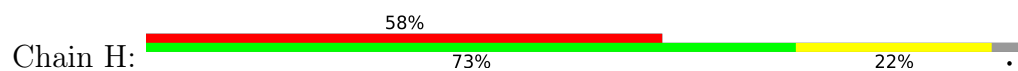


- Molecule 52: Ribosomal protein S7

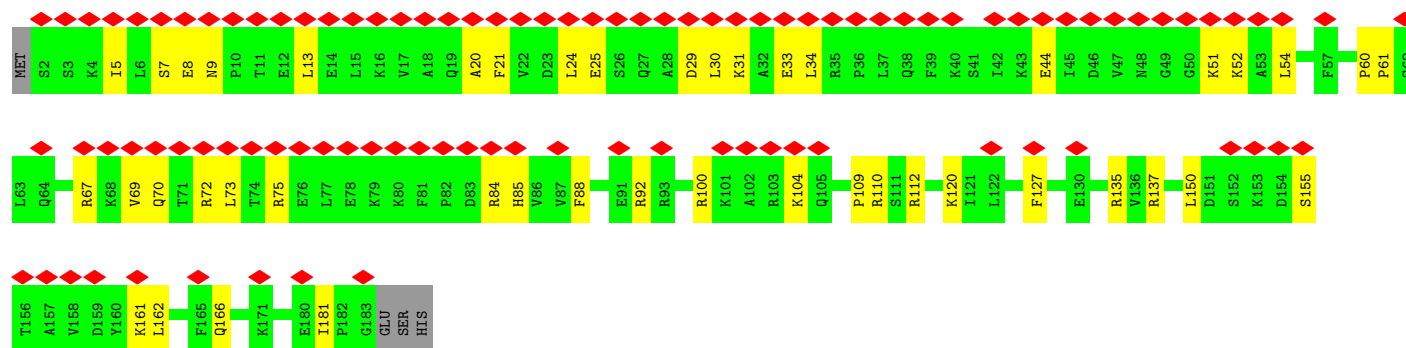
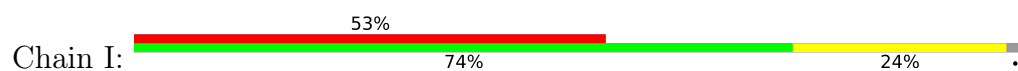




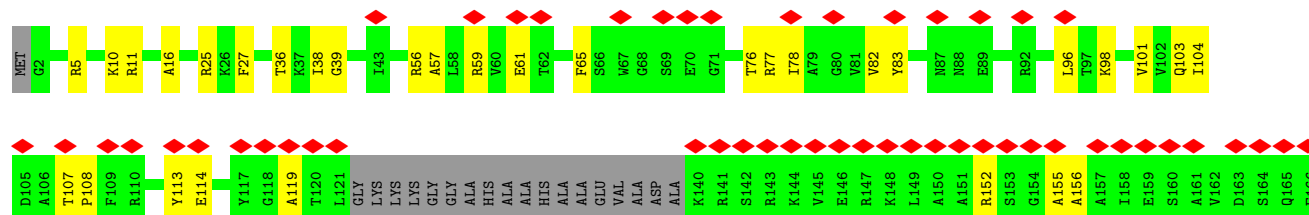
• Molecule 53: 40S ribosomal protein S6



• Molecule 54: 40S ribosomal protein S7

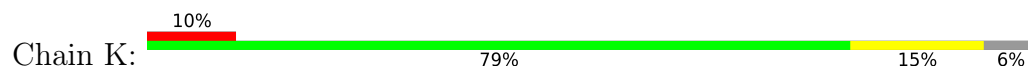


• Molecule 55: 40S ribosomal protein S8

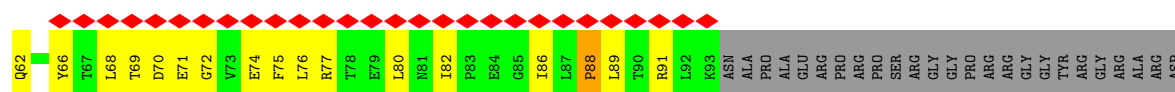
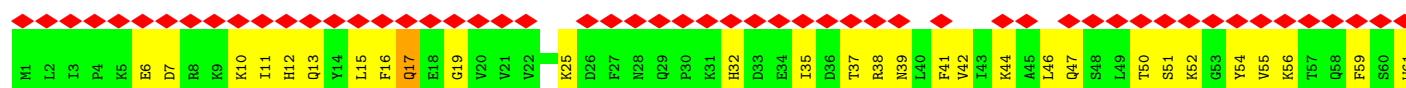




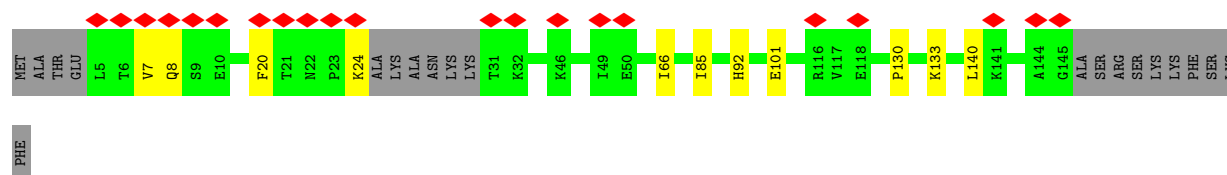
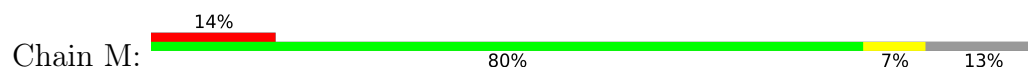
• Molecule 56: Ribosomal protein S4



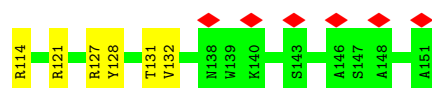
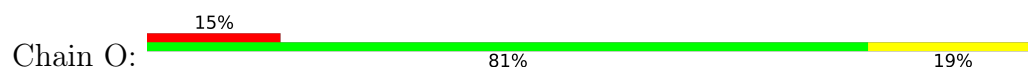
• Molecule 57: 40S ribosomal protein S10-A



• Molecule 58: 40S ribosomal protein S11A

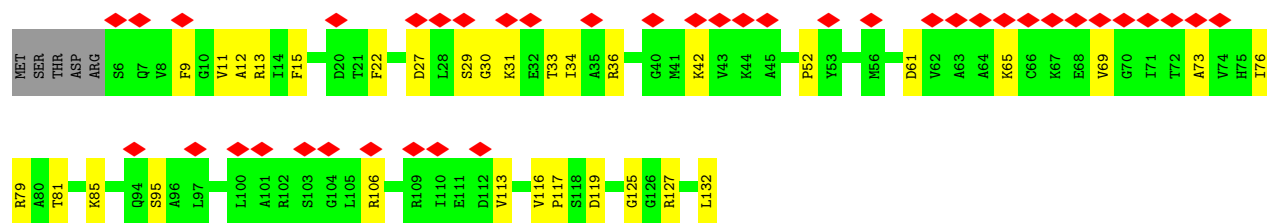


• Molecule 59: 40S ribosomal protein S13

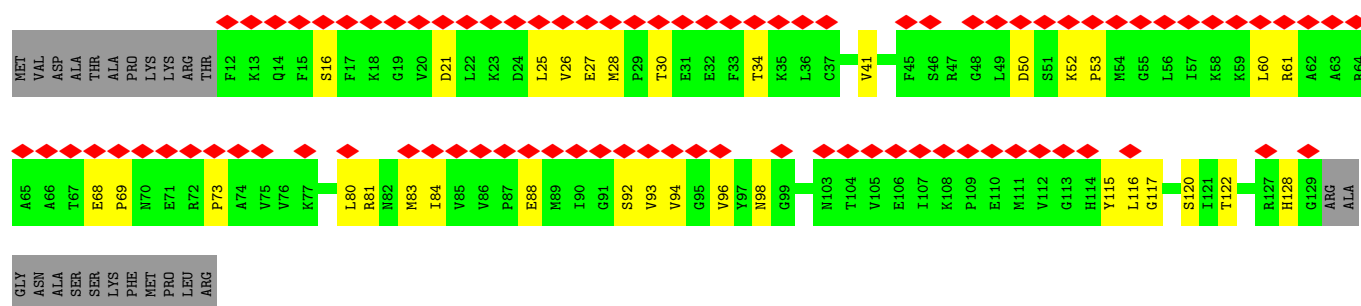


• Molecule 60: 40S ribosomal protein S14-A

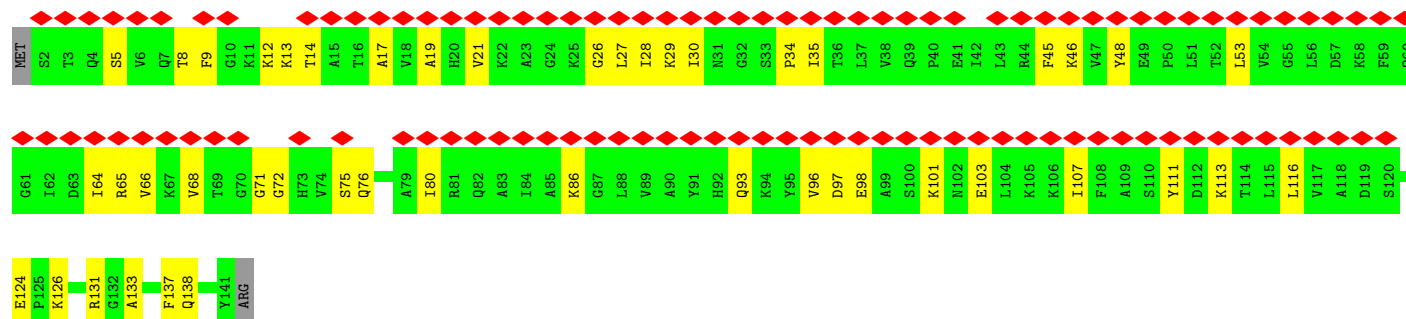
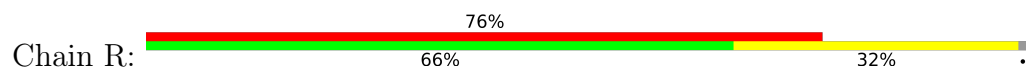




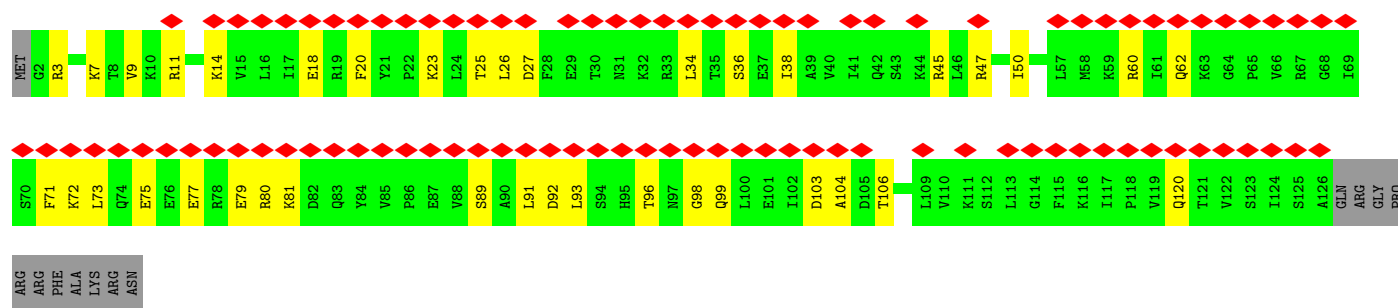
• Molecule 61: 40S ribosomal protein S15



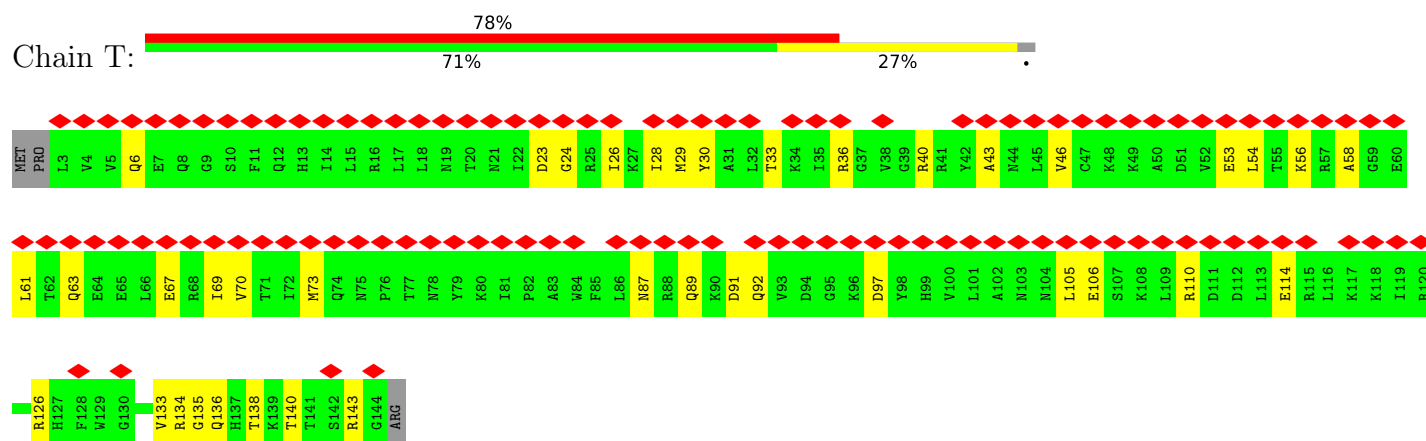
• Molecule 62: 40S ribosomal protein S16



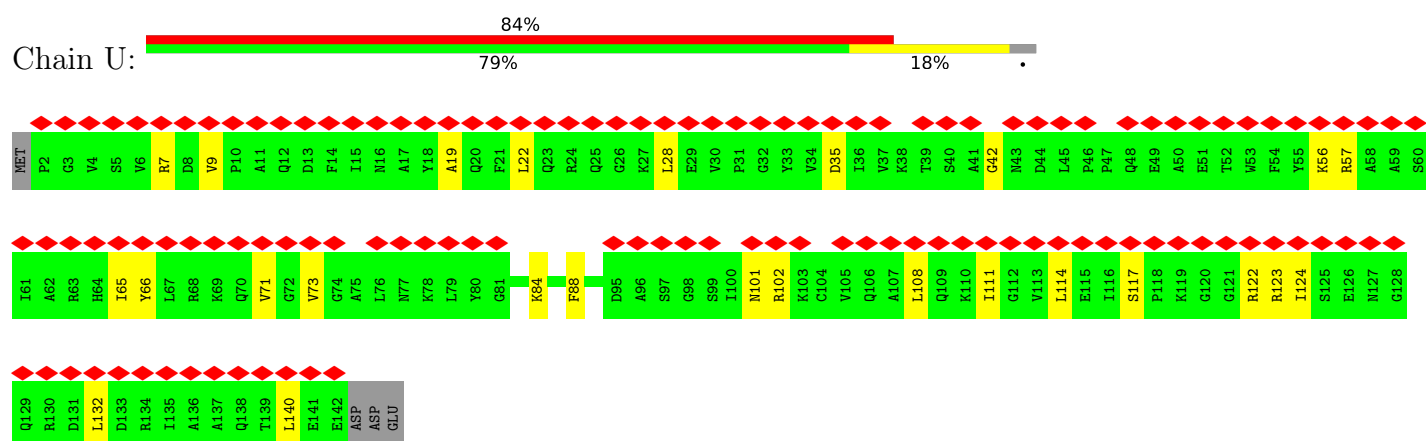
• Molecule 63: 40S ribosomal protein S17-B



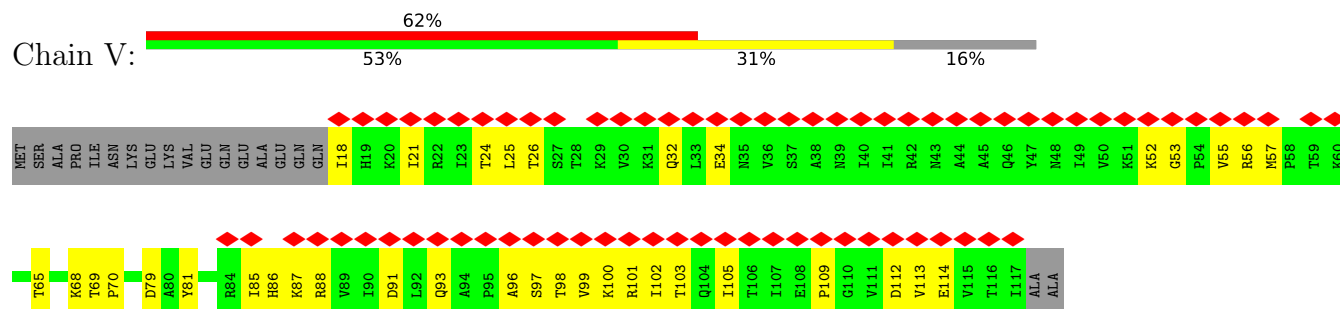
• Molecule 64: 40S ribosomal protein S18-B



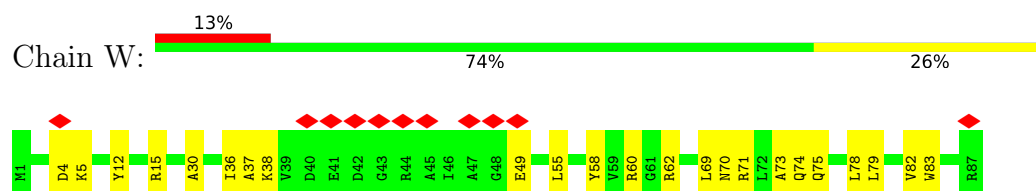
• Molecule 65: 40S ribosomal protein S19-A



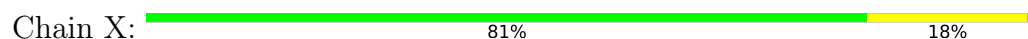
• Molecule 66: Ribosomal protein S10



• Molecule 67: 40S ribosomal protein S21

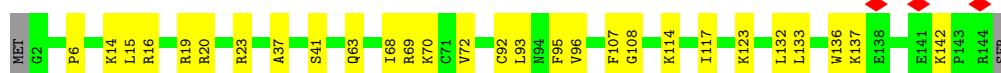
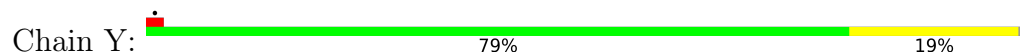


• Molecule 68: 40S ribosomal protein S22-A

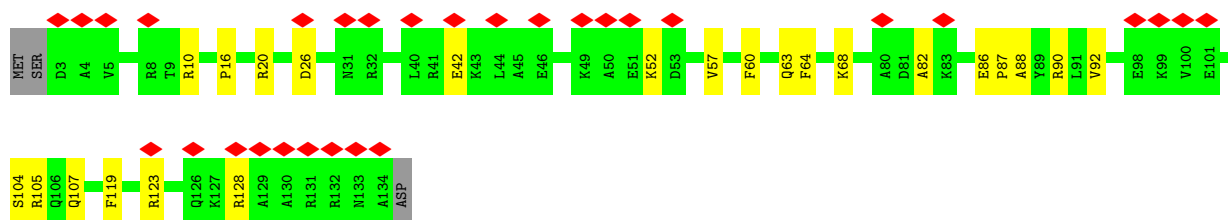
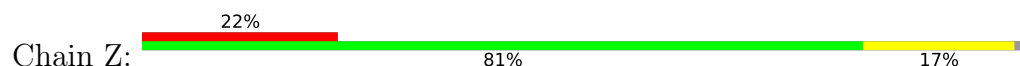




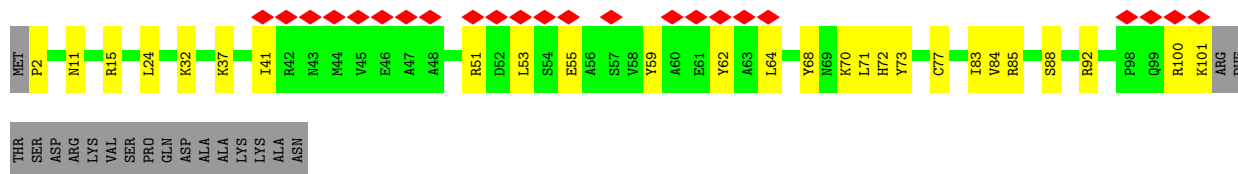
- Molecule 69: Ribosomal protein S23 (S12)



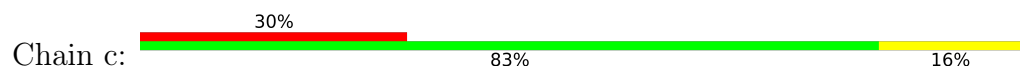
- Molecule 70: 40S ribosomal protein S24



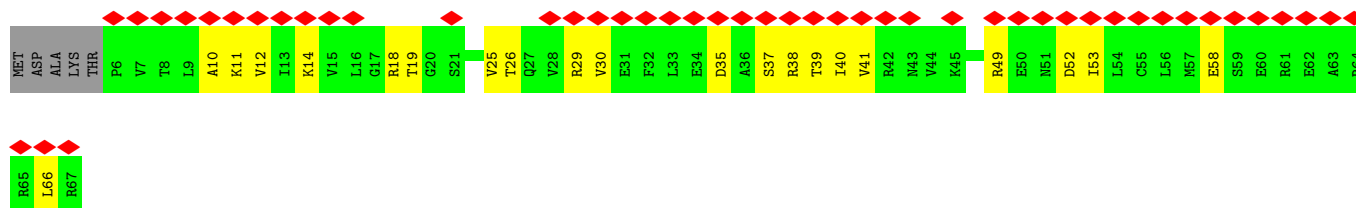
- Molecule 71: 40S ribosomal protein S26



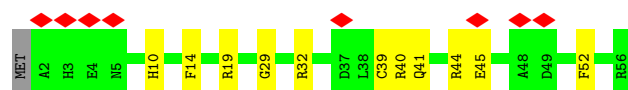
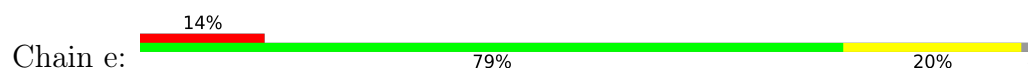
- Molecule 72: 40S ribosomal protein S27



- Molecule 73: 40S ribosomal protein S28-B



- Molecule 74: 40S ribosomal protein S29A



- Molecule 75: 40S ribosomal protein S30



- Molecule 76: DNA (5'-R(P*GP*GP*CP*AP*G)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	254047	Depositor
Resolution determination method	FSC 3 SIGMA CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.815	Depositor
Minimum map value	-0.331	Depositor
Average map value	0.023	Depositor
Map value standard deviation	0.062	Depositor
Recommended contour level	0.274	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: K16, MLZ, OMC, SPD, IAS, OMG, ZN, SPK, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.37	0/73469	0.38	0/114528
2	3	0.31	0/2884	0.29	0/4492
3	4	0.36	0/3746	0.35	0/5832
4	10	0.17	0/207	0.30	0/319
5	j	0.34	0/1931	0.44	0/2592
6	k	0.31	0/3156	0.42	0/4246
7	l	0.29	0/2799	0.41	0/3777
8	m	0.24	0/2447	0.40	0/3294
9	n	0.24	0/1258	0.35	0/1696
10	o	0.31	0/1860	0.42	0/2499
11	p	0.26	0/1830	0.39	0/2465
12	q	0.26	0/1519	0.42	0/2043
13	r	0.28	0/1724	0.39	0/2314
14	s	0.22	0/1404	0.42	0/1880
15	t	0.28	0/1572	0.44	0/2109
16	u	0.26	0/1044	0.39	0/1407
17	v	0.35	0/1753	0.45	0/2347
18	w	0.31	0/1620	0.42	0/2167
19	x	0.33	0/1398	0.45	0/1879
20	y	0.30	0/1511	0.43	0/2022
21	z	0.29	0/1483	0.46	0/1972
22	0	0.31	0/1483	0.45	0/1997
23	2	0.30	0/1305	0.43	0/1749
24	5	0.21	0/856	0.46	0/1156
25	6	0.30	0/994	0.45	0/1339
26	7	0.30	0/536	0.41	0/712
27	8	0.31	0/990	0.45	0/1337
28	9	0.27	0/990	0.43	0/1322
29	AA	0.26	0/1112	0.39	0/1488
30	AB	0.32	0/1199	0.39	0/1607
31	AC	0.28	0/477	0.43	0/633
32	AD	0.27	0/738	0.41	0/994

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AE	0.30	0/851	0.46	0/1141
34	AF	0.30	0/1039	0.41	0/1390
35	AG	0.32	0/895	0.37	0/1201
36	AH	0.29	0/934	0.44	0/1242
37	AI	0.29	0/1004	0.50	0/1337
38	AJ	0.28	0/772	0.44	0/1023
39	AK	0.37	0/690	0.49	0/916
40	AL	0.27	0/632	0.48	0/842
41	AM	0.28	0/458	0.38	0/609
42	AN	0.25	0/436	0.40	0/577
43	AO	0.24	0/237	0.52	0/304
44	AP	0.29	0/840	0.43	0/1108
45	AQ	0.31	0/705	0.44	0/940
46	A	0.33	0/37205	0.40	0/57962
47	B	0.26	0/1666	0.43	0/2273
48	C	0.20	0/1750	0.44	0/2354
49	D	0.31	0/1648	0.42	0/2237
50	E	0.22	0/1604	0.46	0/2150
51	F	0.26	0/2096	0.41	0/2822
52	G	0.17	0/1631	0.45	0/2199
53	H	0.19	0/1845	0.45	0/2464
54	I	0.21	0/1490	0.42	0/2004
55	J	0.23	0/1485	0.45	0/1987
56	K	0.27	0/1478	0.42	0/1978
57	L	0.22	0/801	0.60	0/1081
58	M	0.28	0/1108	0.38	0/1492
59	O	0.25	0/1210	0.43	0/1631
60	P	0.24	0/944	0.44	0/1265
61	Q	0.20	0/954	0.48	0/1282
62	R	0.19	0/1109	0.45	0/1486
63	S	0.20	0/1014	0.47	0/1361
64	T	0.17	0/1186	0.44	0/1590
65	U	0.18	0/1120	0.46	0/1508
66	V	0.23	0/800	0.53	0/1082
67	W	0.28	0/683	0.45	0/918
68	X	0.37	0/1049	0.45	0/1412
69	Y	0.34	0/1128	0.47	0/1505
70	Z	0.23	0/1086	0.38	0/1447
71	b	0.30	0/811	0.45	0/1085
72	c	0.25	0/624	0.41	0/843
73	d	0.20	0/489	0.51	0/654
74	e	0.28	0/466	0.41	0/620
75	f	0.22	0/451	0.40	0/601

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	g	0.12	0/124	0.30	0/192
All	All	0.32	0/201843	0.40	0/296329

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	65690	0	33022	730	0
2	3	2579	0	1304	20	0
3	4	3353	0	1694	48	0
4	10	187	0	98	3	0
5	j	1894	0	1975	32	0
6	k	3084	0	3173	52	0
7	l	2751	0	2879	41	0
8	m	2394	0	2362	27	0
9	n	1237	0	1316	19	0
10	o	1824	0	1913	13	0
11	p	1800	0	1920	13	0
12	q	1501	0	1576	25	0
13	r	1689	0	1731	23	0
14	s	1385	0	1418	24	0
15	t	1545	0	1622	20	0
16	u	1029	0	1116	18	0
17	v	1713	0	1764	34	0
18	w	1590	0	1705	15	0
19	x	1375	0	1403	29	0
20	y	1478	0	1590	25	0
21	z	1462	0	1570	22	0
22	0	1442	0	1500	29	0
23	2	1276	0	1333	18	0
24	5	833	0	846	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	6	986	0	1040	18	0
26	7	524	0	545	9	0
27	8	974	0	1032	18	0
28	9	980	0	1058	16	0
29	AA	1087	0	1154	12	0
30	AB	1170	0	1203	23	0
31	AC	464	0	498	8	0
32	AD	729	0	775	14	0
33	AE	839	0	907	11	0
34	AF	1015	0	1095	14	0
35	AG	867	0	932	9	0
36	AH	913	0	1002	8	0
37	AI	990	0	1094	16	0
38	AJ	764	0	851	9	0
39	AK	677	0	697	16	0
40	AL	623	0	688	10	0
41	AM	446	0	488	11	0
42	AN	427	0	473	3	0
43	AO	236	0	285	5	0
44	AP	843	0	914	13	0
45	AQ	698	0	734	20	0
46	A	33257	0	16733	550	0
47	B	1627	0	1644	33	0
48	C	1724	0	1805	40	0
49	D	1620	0	1715	28	0
50	E	1582	0	1685	43	0
51	F	2055	0	2137	49	0
52	G	1614	0	1688	37	0
53	H	1820	0	1896	45	0
54	I	1466	0	1561	32	0
55	J	1461	0	1485	31	0
56	K	1453	0	1532	20	0
57	L	783	0	799	40	0
58	M	1084	0	1127	9	0
59	O	1187	0	1249	22	0
60	P	942	0	980	23	0
61	Q	935	0	970	24	0
62	R	1091	0	1155	35	0
63	S	1002	0	1058	31	0
64	T	1169	0	1216	30	0
65	U	1100	0	1114	18	0
66	V	790	0	855	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
67	W	676	0	677	19	0
68	X	1032	0	1066	23	0
69	Y	1110	0	1182	24	0
70	Z	1072	0	1123	16	0
71	b	799	0	860	18	0
72	c	614	0	627	8	0
73	d	487	0	523	17	0
74	e	454	0	431	10	0
75	f	444	0	483	13	0
76	g	111	0	56	3	0
77	1	14	0	30	1	0
78	1	68	0	0	0	0
78	A	34	0	0	0	0
79	1	10	0	19	1	0
80	1	255	0	0	0	0
80	3	1	0	0	0	0
80	4	2	0	0	0	0
80	6	1	0	0	0	0
80	A	97	0	0	0	0
80	AH	1	0	0	0	0
80	AP	1	0	0	0	0
80	C	1	0	0	0	0
80	X	1	0	0	0	0
80	Y	1	0	0	0	0
80	j	1	0	0	0	0
80	k	1	0	0	0	0
80	o	1	0	0	0	0
80	r	1	0	0	0	0
80	v	1	0	0	0	0
80	x	1	0	0	0	0
81	AK	1	0	0	0	0
81	AN	1	0	0	0	0
81	AP	1	0	0	0	0
81	AQ	1	0	0	0	0
81	b	1	0	0	0	0
81	c	1	0	0	0	0
81	e	1	0	0	0	0
82	1	632	0	0	29	0
82	10	1	0	0	0	0
82	2	1	0	0	0	0
82	3	2	0	0	0	0
82	4	14	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
82	6	6	0	0	1	0
82	8	2	0	0	0	0
82	A	321	0	0	37	0
82	AA	1	0	0	0	0
82	AB	1	0	0	0	0
82	AC	3	0	0	0	0
82	AF	5	0	0	0	0
82	AG	3	0	0	0	0
82	AH	4	0	0	0	0
82	AI	2	0	0	0	0
82	AK	7	0	0	1	0
82	AP	3	0	0	0	0
82	AQ	2	0	0	4	0
82	C	1	0	0	0	0
82	D	5	0	0	1	0
82	F	3	0	0	1	0
82	H	3	0	0	0	0
82	I	6	0	0	0	0
82	J	5	0	0	4	0
82	K	1	0	0	0	0
82	M	5	0	0	1	0
82	O	7	0	0	1	0
82	P	1	0	0	1	0
82	W	1	0	0	1	0
82	X	15	0	0	6	0
82	Y	11	0	0	7	0
82	b	9	0	0	1	0
82	c	3	0	0	1	0
82	e	1	0	0	1	0
82	j	17	0	0	0	0
82	k	16	0	0	1	0
82	l	11	0	0	0	0
82	m	2	0	0	1	0
82	o	5	0	0	1	0
82	q	2	0	0	0	0
82	r	5	0	0	0	0
82	t	1	0	0	0	0
82	v	7	0	0	0	0
82	w	3	0	0	0	0
82	x	8	0	0	0	0
82	y	1	0	0	0	0
82	z	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	189590	0	139776	2413	0

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

All (2413) 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)
1:1:2246:U:H3	1:1:2250:G:H1	0.98	0.95
46:A:485:G:H1	46:A:499:U:H3	1.02	0.94
36:AH:58:ARG:HD3	36:AH:59:PRO:HD2	1.53	0.91
1:1:1014:G:H1	1:1:1030:U:H3	0.99	0.91
8:m:197:LYS:HG2	8:m:202:GLY:HA3	1.53	0.89
1:1:1936:G:H21	1:1:3327:A:H8	1.21	0.88
21:z:98:ARG:NH2	21:z:130:ASN:OD1	2.08	0.86
1:1:3199:G:H1	1:1:3218:U:H3	1.21	0.86
46:A:853:G:H1	46:A:945:U:H3	1.23	0.85
57:L:17:GLN:H	57:L:88:PRO:HB3	1.41	0.83
68:X:72:CYS:SG	82:X:301:HOH:O	2.35	0.83
68:X:80:ASN:OD1	68:X:124:LYS:NZ	2.11	0.82
33:AE:45:THR:HG21	33:AE:89:PHE:HA	1.62	0.82
1:1:2686:G:H4'	1:1:2687:A:H5''	1.62	0.82
34:AF:106:ARG:NH2	34:AF:122:ASN:O	2.13	0.82
67:W:38:LYS:HD2	67:W:49:GLU:HG3	1.59	0.81
4:10:72:U:H3	76:g:1:G:H1	1.27	0.81
21:z:134:HIS:HE1	21:z:136:ARG:HE	1.29	0.81
46:A:635:C:O2	54:I:110:ARG:NH2	2.12	0.81
23:2:142:SER:OG	23:2:144:GLU:OE1	1.98	0.80
7:l:290:LEU:HD22	20:y:129:LEU:HD11	1.63	0.80
46:A:500:U:O2'	46:A:501:G:N7	2.15	0.80
46:A:484:G:N2	46:A:501:G:O6	2.15	0.80
69:Y:92:CYS:O	82:Y:301:HOH:O	2.00	0.80
52:G:200:ASN:OD1	52:G:203:LYS:NZ	2.15	0.80
1:1:832:A:N6	82:1:3702:HOH:O	2.14	0.79
19:x:165:GLN:HE21	19:x:165:GLN:N	1.80	0.79
71:b:77:CYS:SG	82:b:309:HOH:O	2.40	0.79
66:V:24:THR:HB	66:V:114:GLU:HG2	1.63	0.79
45:AQ:11:THR:O	82:AQ:201:HOH:O	2.01	0.78
46:A:1276:G:H22	46:A:1309:G:H22	1.31	0.78
1:1:935:U:OP2	30:AB:26:ARG:NH2	2.17	0.78
1:1:2334:A:H61	1:1:2955:C:H5	1.31	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:I:33:GLU:HG3	54:I:69:VAL:HG11	1.64	0.78
1:l:2929:G:N2	82:l:3708:HOH:O	2.17	0.78
46:A:766:U:H4'	46:A:767:G:H5''	1.66	0.78
51:F:45:VAL:HG23	51:F:61:VAL:HG11	1.64	0.78
24:5:19:VAL:HG23	24:5:20:ALA:H	1.49	0.77
1:l:437:G:N2	1:l:620:A:H61	1.83	0.77
54:I:72:ARG:HG2	54:I:75:ARG:HH21	1.51	0.77
46:A:1040:U:H3	46:A:1049:G:H1	1.32	0.76
46:A:1422:A:OP2	50:E:28:ARG:NH2	2.17	0.76
14:s:109:HIS:HD2	14:s:114:ILE:HD11	1.48	0.76
16:u:34:ASP:OD2	16:u:37:ARG:NH2	2.18	0.76
46:A:381:G:N2	82:A:1911:HOH:O	2.17	0.76
1:l:3194:G:H4'	16:u:129:VAL:HG11	1.68	0.76
1:l:1091:U:H4'	1:l:1092:U:H5'	1.68	0.76
46:A:1472:G:N2	46:A:1580:A:OP1	2.15	0.76
31:AC:8:THR:HG22	31:AC:10:HIS:H	1.50	0.76
46:A:1276:G:H22	46:A:1309:G:N2	1.84	0.76
49:D:111:LYS:HG2	49:D:122:ALA:HB3	1.68	0.76
46:A:747:A:OP1	56:K:79:ARG:NH2	2.18	0.76
5:j:27:ALA:O	5:j:128:ARG:NH2	2.18	0.75
7:l:300:VAL:HB	20:y:39:ARG:HG2	1.67	0.75
1:l:1560:U:H3	1:l:1571:G:H1	1.34	0.75
17:v:143:ARG:O	17:v:149:ASN:ND2	2.17	0.75
62:R:21:VAL:HG22	62:R:64:ILE:HG12	1.69	0.75
29:AA:27:LYS:HE3	29:AA:97:THR:HG22	1.68	0.74
1:l:2109:A:N6	82:l:3716:HOH:O	2.20	0.74
46:A:1324:C:O2'	46:A:1326:A:N7	2.19	0.74
1:l:2254:G:OP1	43:AO:16:LYS:NZ	2.21	0.74
73:d:25:VAL:HG11	73:d:66:LEU:HD22	1.68	0.74
1:l:805:G:N2	82:l:3701:HOH:O	2.20	0.73
46:A:945:U:H5'	59:O:55:ARG:HD3	1.68	0.73
51:F:100:ARG:NH2	51:F:121:TYR:O	2.22	0.73
46:A:352:C:H5''	55:J:16:ALA:HB2	1.69	0.73
46:A:1474:G:H3'	46:A:1502:A:H61	1.53	0.73
46:A:1668:A:H1'	53:H:66:GLY:HA2	1.70	0.73
52:G:29:ILE:HB	52:G:34:GLN:HE21	1.53	0.73
46:A:403:C:OP2	82:A:1901:HOH:O	2.07	0.73
33:AE:45:THR:HG22	33:AE:47:ASP:H	1.54	0.72
46:A:880:G:H1	46:A:902:U:H3	1.37	0.72
25:6:30:GLY:HA3	25:6:66:LYS:HE2	1.70	0.72
61:Q:25:LEU:HA	61:Q:28:MET:HE2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:u:17:ARG:NH2	16:u:58:THR:O	2.21	0.72
50:E:52:LYS:NZ	50:E:90:GLU:OE1	2.23	0.72
53:H:57:ASP:HA	53:H:106:LEU:HA	1.72	0.72
73:d:12:VAL:HG22	73:d:52:ASP:H	1.53	0.72
1:1:2334:A:N3	19:x:131:ARG:NH2	2.38	0.72
1:1:834:G:O6	45:AQ:4:ARG:NH2	2.23	0.72
1:1:1897:A:N7	82:1:3720:HOH:O	2.23	0.72
63:S:103:ASP:OD1	63:S:104:ALA:N	2.23	0.72
46:A:125:U:OP1	53:H:201:GLN:NE2	2.22	0.72
46:A:1181:A:OP2	46:A:1450:G:N2	2.19	0.72
46:A:921:G:OP1	46:A:1059:G:N2	2.22	0.71
54:I:5:ILE:HG22	54:I:7:SER:H	1.55	0.71
66:V:26:THR:OG1	66:V:112:ASP:OD1	2.07	0.71
70:Z:87:PRO:HD2	70:Z:90:ARG:HD2	1.71	0.71
45:AQ:26:THR:O	82:AQ:202:HOH:O	2.07	0.71
1:1:3039:C:H3'	21:z:62:ARG:HH22	1.54	0.71
46:A:1445:C:OP2	64:T:138:THR:OG1	2.08	0.71
55:J:113:TYR:OH	55:J:156:ALA:O	2.08	0.71
46:A:512:G:H1	46:A:541:C:H5	1.39	0.71
12:q:92:PHE:HB2	12:q:142:ASP:HB3	1.72	0.71
46:A:1156:A:H2'	46:A:1157:G:C8	2.26	0.71
1:1:1657:G:H2'	1:1:1658:G:C8	2.25	0.70
1:1:2603:U:OP2	23:2:4:SER:OG	2.09	0.70
69:Y:142:LYS:HD2	82:Y:303:HOH:O	1.92	0.70
1:1:3010:U:O2	25:6:9:ASN:ND2	2.24	0.70
64:T:69:ILE:HG22	64:T:73:MET:HE2	1.73	0.70
46:A:538:G:N2	75:f:25:GLU:OE2	2.24	0.70
72:c:18:GLN:NE2	82:c:201:HOH:O	2.22	0.70
1:1:1774:G:O2'	1:1:1776:G:OP2	2.09	0.70
1:1:3318:G:OP1	55:J:170:ARG:NH2	2.24	0.70
46:A:4:C:H5	46:A:20:G:H1	1.40	0.70
46:A:148:C:H42	46:A:162:A:H61	1.39	0.70
46:A:357:A:OP2	82:A:1902:HOH:O	2.09	0.70
46:A:556:U:O2	50:E:144:ARG:NH1	2.25	0.70
1:1:800:C:OP1	7:l:99:ARG:NH2	2.24	0.70
1:1:2808:OMC:H5	1:1:2824:C:H42	1.36	0.70
46:A:1460:G:H2'	46:A:1461:A:H8	1.57	0.70
82:A:2170:HOH:O	68:X:124:LYS:HD2	1.90	0.70
1:1:2932:C:H2'	1:1:2933:G:C8	2.27	0.69
51:F:129:VAL:HG22	51:F:139:VAL:HG22	1.74	0.69
1:1:581:A:H5''	35:AG:106:ASN:HD21	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1057:A:O2'	23:2:102:ARG:NH2	2.26	0.69
46:A:1658:A:N7	82:A:1922:HOH:O	2.25	0.69
50:E:30:LEU:HD22	50:E:59:VAL:HG22	1.74	0.69
69:Y:6:PRO:O	82:Y:302:HOH:O	2.11	0.69
46:A:1535:G:H1'	64:T:89:GLN:HE21	1.58	0.69
57:L:76:LEU:O	57:L:80:LEU:HB2	1.93	0.68
1:1:2645:A:O2'	14:s:126:ASP:OD1	2.09	0.68
46:A:1600:U:OP1	52:G:169:ASN:HB2	1.93	0.68
48:C:82:ARG:NH2	48:C:188:LEU:O	2.24	0.68
64:T:134:ARG:HB2	64:T:136:GLN:HE22	1.58	0.68
1:1:365:A:OP1	7:l:85:ARG:NH1	2.26	0.68
46:A:1417:C:O2'	46:A:1423:U:O4	2.11	0.68
74:e:39:CYS:SG	82:e:201:HOH:O	2.51	0.68
1:1:437:G:H22	1:1:620:A:H61	1.39	0.68
1:1:538:G:H1	1:1:547:U:H3	1.39	0.68
1:1:2535:A:OP1	5:j:69:TYR:OH	2.12	0.68
46:A:100:A:OP1	82:A:1903:HOH:O	2.11	0.68
46:A:856:G:H2'	46:A:857:G:C8	2.28	0.68
55:J:155:ALA:O	58:M:24:LYS:NZ	2.25	0.68
1:1:2134:U:OP2	5:j:241:ARG:NH2	2.27	0.68
1:1:3309:A:H2	1:1:3326:G:H21	1.41	0.68
1:1:2171:U:H5'	1:1:2172:G:H5'	1.76	0.68
1:1:2869:A:H2'	1:1:2871:C:H5''	1.75	0.68
46:A:122:U:H2'	46:A:123:G:H5''	1.76	0.68
1:1:837:A:N6	82:1:3717:HOH:O	2.27	0.68
46:A:1478:A:OP2	46:A:1479:A:N6	2.25	0.68
1:1:2229:G:H2'	1:1:2230:A:C8	2.29	0.68
18:w:125:LEU:HD13	22:0:168:PRO:HG3	1.75	0.68
46:A:1579:A:H2'	46:A:1580:A:H8	1.59	0.68
46:A:2:A:OP1	49:D:171:LYS:NZ	2.23	0.67
1:1:2233:A:O2'	46:A:1744:G:O2'	2.13	0.67
67:W:79:LEU:HD13	67:W:82:VAL:HG11	1.76	0.67
55:J:27:PHE:O	82:J:301:HOH:O	2.12	0.67
1:1:730:A:H8	1:1:733:A:H62	1.42	0.67
1:1:564:G:H2'	1:1:565:A:C8	2.30	0.67
1:1:3235:A:N6	19:x:178:SER:OG	2.28	0.67
17:v:62:TYR:HD2	17:v:106:VAL:HG13	1.59	0.67
46:A:768:C:H2'	46:A:769:U:O4'	1.95	0.67
1:1:2735:U:O2	79:1:3404:SPD:N1	2.28	0.67
20:y:123:THR:OG1	20:y:125:ASP:OD1	2.12	0.67
46:A:150:U:O2	53:H:4:ASN:ND2	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2189:U:OP1	76:g:3:C:O2'	2.11	0.67
7:l:4:ARG:HH12	7:l:25:ALA:HA	1.58	0.67
10:o:185:GLU:HG2	10:o:196:VAL:HG21	1.76	0.67
44:AP:24[B]:LYS:HE2	44:AP:75:VAL:HG12	1.76	0.67
54:I:25:GLU:HB2	54:I:31:LYS:HG3	1.77	0.67
1:1:2086:C:H1'	1:1:3309:A:C8	2.29	0.67
1:1:3157:A:OP1	12:q:23:ARG:NH1	2.27	0.67
46:A:282:G:O6	53:H:188:ARG:NH2	2.28	0.67
61:Q:61:ARG:NH1	61:Q:88:GLU:OE2	2.27	0.67
22:0:96:ASP:OD1	22:0:97:VAL:N	2.29	0.66
1:1:740:A:OP1	20:y:66:ARG:NH2	2.29	0.66
7:l:11:SER:OG	7:l:15:GLU:OE1	2.12	0.66
46:A:577:A:H61	50:E:144:ARG:H	1.44	0.66
69:Y:69:ARG:HG3	69:Y:117:ILE:HG12	1.77	0.66
1:1:927:C:O2	82:1:3701:HOH:O	2.11	0.66
1:1:1713:U:H2'	1:1:1714:G:C8	2.31	0.66
1:1:1895:G:O2'	1:1:2312:U:O4	2.14	0.66
46:A:65:A:H2	46:A:84:A:H62	1.43	0.66
46:A:446:C:OP2	51:F:49:ARG:NH1	2.23	0.66
46:A:789:U:H1'	82:A:2170:HOH:O	1.96	0.66
46:A:1063:C:OP2	82:A:1906:HOH:O	2.13	0.66
46:A:1529:G:N2	46:A:1556:A:OP2	2.28	0.66
46:A:452:A:H4'	51:F:62:LYS:HE3	1.78	0.66
46:A:317:U:H4'	46:A:321:A:C8	2.30	0.66
46:A:1007:C:N3	82:A:1928:HOH:O	2.28	0.66
46:A:1399:U:OP2	63:S:3:ARG:NH2	2.29	0.66
46:A:1776:G:OP2	60:P:127:ARG:NH2	2.26	0.66
46:A:327:G:H5''	55:J:98:LYS:HB3	1.77	0.66
23:2:49:GLN:HA	23:2:52:MET:HE3	1.78	0.66
64:T:36:ARG:HE	64:T:105:LEU:HD22	1.61	0.66
46:A:1597:G:N7	62:R:13:LYS:NZ	2.44	0.65
62:R:12:LYS:HG3	62:R:13:LYS:H	1.61	0.65
65:U:108:LEU:HA	65:U:111:ILE:HG22	1.78	0.65
12:q:110:ASP:HB3	12:q:128:ILE:HD12	1.76	0.65
57:L:7:ASP:OD1	57:L:10:LYS:NZ	2.22	0.65
12:q:109:GLN:HB3	12:q:127:LYS:HE2	1.77	0.65
46:A:881:U:H5'	48:C:23:PRO:HG2	1.78	0.65
55:J:5:ARG:NH2	82:J:301:HOH:O	2.30	0.65
16:u:14:GLU:HG2	16:u:17:ARG:HG2	1.77	0.65
23:2:84:TYR:HB2	31:AC:24:PRO:HD3	1.76	0.65
46:A:1383:U:O2'	46:A:1386:A:N6	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:L:70:ASP:OD1	57:L:71:GLU:N	2.30	0.65
66:V:81:TYR:HB3	74:e:52:PHE:HB3	1.78	0.65
1:l:2941:A:N7	5:j:215:ASN:ND2	2.45	0.65
46:A:1463:G:H2'	46:A:1464:G:H8	1.60	0.65
58:M:92:HIS:ND1	82:M:201:HOH:O	2.28	0.65
13:r:30:LYS:HG3	13:r:63:GLU:HG3	1.79	0.65
25:6:17:LEU:HD13	25:6:23:MET:HE2	1.78	0.65
46:A:530:U:OP1	70:Z:64:PHE:HA	1.96	0.65
46:A:1154:G:N1	46:A:1562:G:OP2	2.25	0.65
46:A:1335:U:H2'	46:A:1336:G:C8	2.32	0.65
46:A:589:A:H2'	46:A:590:A:C8	2.32	0.64
46:A:49:C:OP1	82:A:1905:HOH:O	2.13	0.64
46:A:948:A:N7	59:O:70:LYS:NZ	2.44	0.64
46:A:1002:U:OP1	82:A:1909:HOH:O	2.15	0.64
66:V:70:PRO:O	74:e:41:GLN:NE2	2.29	0.64
46:A:1066:A:N1	82:A:1934:HOH:O	2.30	0.64
65:U:42:GLY:HA2	65:U:84:LYS:HG3	1.79	0.64
66:V:68:LYS:O	74:e:44:ARG:NH1	2.29	0.64
54:I:92:ARG:NH1	54:I:120:LYS:HB3	2.12	0.64
69:Y:70:LYS:HB3	69:Y:93:LEU:HD22	1.79	0.64
30:AB:90:TYR:O	30:AB:94:SER:HB2	1.97	0.64
7:l:359:GLU:OE2	7:l:363:ASN:ND2	2.31	0.64
46:A:345:G:H5''	58:M:85:ILE:HD11	1.79	0.64
1:l:2155:G:OP2	5:j:128:ARG:NH1	2.30	0.64
1:l:2923:G:OP2	82:l:3703:HOH:O	2.15	0.64
57:L:15:LEU:HD21	57:L:55:VAL:HG11	1.80	0.64
67:W:74:GLN:NE2	67:W:83:TRP:O	2.31	0.64
15:t:158:LEU:HB3	30:AB:98:ALA:HB1	1.81	0.63
46:A:142:G:O2'	46:A:143:A:O5'	2.16	0.63
51:F:139:VAL:HG23	51:F:150:PRO:HG3	1.81	0.63
3:4:52:A:OP1	41:AM:21[A]:ARG:NH1	2.31	0.63
3:4:57:C:OP2	39:AK:68:LYS:NZ	2.31	0.63
52:G:25:LEU:HD12	62:R:26:GLY:HA3	1.80	0.63
1:l:362:U:O4	39:AK:24:ARG:NH2	2.31	0.63
1:l:2233:A:OP2	1:l:2239:G:N1	2.30	0.63
46:A:1026:G:H2'	46:A:1027:G:C8	2.33	0.63
12:q:8:GLN:HB3	12:q:72:LYS:HD2	1.81	0.63
47:B:197:VAL:HG13	47:B:201:LEU:HD23	1.80	0.63
48:C:190:PRO:HG2	48:C:192:VAL:HG23	1.81	0.63
50:E:107:LYS:NZ	50:E:175:HIS:O	2.24	0.63
1:l:3356:A:O2'	19:x:56:ARG:NH2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:O:73:LYS:NZ	22:O:97:VAL:O	2.32	0.63
53:H:1:MET:HE2	53:H:106:LEU:HB2	1.80	0.63
17:v:183:THR:HG22	17:v:187:ARG:HB2	1.81	0.63
1:1:844:A:C5	1:1:845:C:H1'	2.34	0.63
1:1:2246:U:O4	1:1:2250:G:N2	2.29	0.63
24:5:16:VAL:HG12	24:5:65:VAL:HG22	1.80	0.63
49:D:234:PRO:HA	49:D:237:VAL:HG22	1.81	0.63
61:Q:41:VAL:HG13	61:Q:84:ILE:HD13	1.79	0.63
46:A:141:G:O6	53:H:177:ARG:NH2	2.31	0.63
46:A:1489:G:O6	65:U:102:ARG:NH1	2.24	0.63
46:A:1602:C:N4	52:G:80:LYS:O	2.32	0.63
47:B:35:PRO:O	47:B:52:LYS:NZ	2.32	0.63
68:X:11:LEU:O	82:X:301:HOH:O	2.15	0.62
1:1:2942:C:H4'	1:1:2943:A:C6	2.34	0.62
46:A:501:G:H2'	46:A:502:U:C6	2.35	0.62
48:C:124:ASN:HD22	48:C:124:ASN:C	2.07	0.62
1:1:498:C:H5''	9:n:25:ARG:NH2	2.14	0.62
1:1:1344:U:OP1	20:y:39:ARG:NH2	2.33	0.62
33:AE:71:ARG:HH11	33:AE:103:LEU:HD13	1.63	0.62
45:AQ:14:PHE:HB2	82:AQ:201:HOH:O	1.98	0.62
46:A:903:U:H2'	46:A:904:A:C8	2.34	0.62
1:1:71:C:O2'	15:t:66:ASN:OD1	2.12	0.62
12:q:80:THR:HA	12:q:83:THR:HG22	1.81	0.62
62:R:45:PHE:HA	62:R:48:TYR:HB2	1.81	0.62
64:T:29:MET:HB2	64:T:54:LEU:HD22	1.81	0.62
66:V:57:MET:HB2	66:V:87:LYS:HB3	1.81	0.62
1:1:307:A:H2'	1:1:308:A:C8	2.35	0.62
1:1:2191:A:H2'	1:1:2192:A:C8	2.35	0.62
50:E:65:ARG:HD3	57:L:91:ARG:HE	1.64	0.62
54:I:8:GLU:OE1	54:I:9:ASN:ND2	2.32	0.62
57:L:77:ARG:HH22	57:L:86:ILE:N	1.96	0.62
46:A:860:G:N3	82:A:1916:HOH:O	2.31	0.62
64:T:36:ARG:HG2	64:T:105:LEU:HD13	1.82	0.62
6:k:284:ARG:NH2	6:k:295:ALA:O	2.33	0.62
11:p:42:GLN:OE1	11:p:45:ARG:NH2	2.30	0.62
46:A:1511:A:H2'	46:A:1512:A:C8	2.34	0.62
54:I:137:ARG:HG2	68:X:51:GLU:OE1	1.99	0.62
46:A:1579:A:H2'	46:A:1580:A:C8	2.34	0.62
58:M:7:VAL:HG23	58:M:8:GLN:HG2	1.81	0.62
19:x:47:TYR:HD1	19:x:56:ARG:HD2	1.64	0.61
19:x:103:GLU:OE2	19:x:109:SER:OG	2.17	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:0:71:LYS:O	22:0:73:LYS:NZ	2.29	0.61
46:A:1469:A:H2'	46:A:1470:G:C8	2.35	0.61
1:1:1635:C:OP2	36:AH:74:ARG:NH1	2.33	0.61
39:AK:57:ARG:NH1	82:AK:202:HOH:O	2.31	0.61
46:A:4:C:O2'	56:K:17:ARG:NH2	2.31	0.61
53:H:161:GLU:HB3	53:H:170:THR:HG22	1.81	0.61
46:A:1276:G:N2	46:A:1309:G:H22	1.97	0.61
82:A:1913:HOH:O	68:X:76:GLN:HB2	1.99	0.61
50:E:92:VAL:HG11	50:E:101:VAL:HG21	1.82	0.61
63:S:96:THR:HG23	63:S:98:GLY:H	1.65	0.61
46:A:1183:G:OP1	46:A:1184:G:O2'	2.14	0.61
1:1:2494:U:O2'	1:1:2567:A:N1	2.25	0.61
1:1:2988:A:H2'	1:1:2989:A:C8	2.36	0.61
46:A:1419:G:N2	74:e:45:GLU:OE2	2.32	0.61
1:1:1030:U:H2'	1:1:1031:A:C8	2.36	0.61
46:A:485:G:N2	46:A:499:U:O2	2.27	0.61
46:A:880:G:O2'	60:P:33:THR:N	2.25	0.61
48:C:145:ARG:NH2	48:C:151:LYS:O	2.34	0.61
1:1:1436:G:OP1	7:l:84:HIS:NE2	2.29	0.61
1:1:1720:U:H1'	1:1:1721:C:C6	2.35	0.61
57:L:80:LEU:HB3	57:L:82:ILE:HG23	1.83	0.61
28:9:51:ARG:HG2	28:9:52:GLN:H	1.65	0.61
29:AA:115:LYS:NZ	29:AA:119:GLU:OE2	2.34	0.61
52:G:57:SER:HA	73:d:53:ILE:HB	1.83	0.61
1:1:3308:G:H21	1:1:3327:A:H2	1.47	0.61
6:k:331:VAL:H	6:k:334:ARG:HG3	1.66	0.61
7:l:3:SER:OG	7:l:4:ARG:N	2.30	0.61
24:5:30:GLN:HE22	24:5:58:ALA:HB1	1.66	0.61
46:A:1596:U:O2'	52:G:105:GLY:O	2.18	0.61
1:1:1663:A:H2'	1:1:1664:G:C8	2.36	0.61
11:p:115:ALA:O	11:p:119:GLU:HG2	2.01	0.61
14:s:32:ARG:NH1	14:s:120:ILE:O	2.33	0.61
27:8:108:LEU:N	27:8:125:ARG:O	2.34	0.61
46:A:1397:A:OP2	62:R:113:LYS:NZ	2.27	0.61
1:1:2651:A:O2'	14:s:52:TYR:OH	2.16	0.60
46:A:1275:U:H2'	46:A:1276:G:C8	2.35	0.60
1:1:437:G:H22	1:1:620:A:N6	1.99	0.60
1:1:628:A:H2'	1:1:629:A:C8	2.35	0.60
1:1:1782:G:H2'	1:1:1783:A:C8	2.35	0.60
46:A:1204:A:N3	57:L:51:SER:OG	2.33	0.60
49:D:53:LEU:HA	67:W:12:TYR:HE1	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:D:134:ILE:HD13	49:D:186:ALA:HB1	1.82	0.60
50:E:128:MET:HE2	50:E:135:VAL:HG12	1.83	0.60
54:I:44:GLU:OE2	54:I:52:LYS:HE3	2.00	0.60
1:1:660:U:H2'	1:1:661:C:C6	2.35	0.60
1:1:730:A:H4'	1:1:730:A:OP1	2.01	0.60
1:1:2655:U:H2'	1:1:2656:C:C6	2.37	0.60
17:v:159:ARG:HB2	17:v:164:LEU:HB2	1.83	0.60
1:1:2248:A:H2'	1:1:2249:A:C8	2.36	0.60
3:4:150:G:OP1	27:8:27:ARG:NH2	2.34	0.60
19:x:47:TYR:CD1	19:x:56:ARG:HD2	2.36	0.60
30:AB:24:LYS:O	30:AB:26:ARG:HG2	2.01	0.60
46:A:418:A:OP1	53:H:96:SER:OG	2.14	0.60
46:A:1145:A:H2'	46:A:1146:C:C6	2.36	0.60
57:L:16:PHE:O	57:L:17:GLN:HG3	2.02	0.60
3:4:66:A:OP1	37:AI:10:ARG:NH2	2.34	0.60
46:A:78:A:H8	53:H:154:ARG:HG3	1.66	0.60
46:A:1718:A:N6	82:A:1922:HOH:O	2.35	0.60
67:W:55:LEU:HD11	67:W:69:LEU:HD21	1.83	0.60
46:A:577:A:N6	50:E:144:ARG:H	1.98	0.60
45:AQ:84:ARG:O	45:AQ:88:GLU:HG2	2.02	0.60
68:X:15:ASN:ND2	68:X:72:CYS:O	2.34	0.60
1:1:976:A:H2'	1:1:977:U:H5'	1.84	0.60
1:1:1556:G:N7	27:8:36:LYS:HE2	2.17	0.60
1:1:1592:C:H2'	1:1:1593:C:C6	2.37	0.60
26:7:53:VAL:HG13	26:7:57:ARG:HH11	1.65	0.60
17:v:46:ASP:OD2	17:v:50:ARG:NH2	2.32	0.60
46:A:518:A:H2'	46:A:519:A:C8	2.36	0.60
46:A:1669:U:O4	46:A:1707:G:N2	2.35	0.60
1:1:1319:G:H4'	22:0:2:SER:HA	1.84	0.60
6:k:372:THR:HG22	6:k:374:ALA:H	1.66	0.60
7:l:32:ARG:HG3	7:l:121:TYR:HE2	1.66	0.60
46:A:457:G:OP2	70:Z:105:ARG:NH2	2.31	0.60
1:1:92:C:OP2	1:1:2736:C:O2'	2.17	0.59
1:1:795:G:O2'	15:t:18:TRP:NE1	2.30	0.59
1:1:2391:A:OP2	82:1:3705:HOH:O	2.16	0.59
5:j:129:THR:OG1	5:j:132:ASN:ND2	2.31	0.59
50:E:95:ARG:O	50:E:102:GLN:NE2	2.31	0.59
51:F:126:VAL:HG13	51:F:139:VAL:HG13	1.84	0.59
1:1:3262:U:O4	6:k:124:LYS:NZ	2.35	0.59
46:A:334:G:O6	55:J:5:ARG:NH1	2.34	0.59
46:A:1529:G:H22	46:A:1555:C:H1'	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1578:C:H2'	46:A:1579:A:H8	1.67	0.59
46:A:1578:C:H2'	46:A:1579:A:C8	2.38	0.59
57:L:38:ARG:HB2	57:L:41:PHE:CD2	2.37	0.59
1:1:2288:U:O4	82:1:3707:HOH:O	2.17	0.59
19:x:40:LYS:HD2	19:x:113:VAL:HG22	1.83	0.59
22:0:8:GLN:HG3	22:0:26:ARG:HD2	1.84	0.59
46:A:784:U:H2'	46:A:785:G:C8	2.37	0.59
1:1:2384:C:H2'	1:1:2385:C:C6	2.37	0.59
19:x:165:GLN:N	19:x:165:GLN:NE2	2.50	0.59
45:AQ:11:THR:HB	82:AQ:201:HOH:O	2.02	0.59
1:1:617:A:H5'	1:1:619:A:H1'	1.85	0.59
1:1:827:G:O2'	1:1:1860:A:N3	2.33	0.59
57:L:52:LYS:HG3	57:L:54:TYR:CD2	2.38	0.59
70:Z:82:ALA:O	70:Z:86:GLU:HB2	2.02	0.59
1:1:93:G:H2'	1:1:94:A:C8	2.37	0.59
1:1:3179:U:OP2	16:u:121:ARG:NH2	2.36	0.59
11:p:134:LYS:HD2	11:p:139:HIS:HE1	1.68	0.59
46:A:68:A:N6	53:H:132:ARG:HG2	2.18	0.59
46:A:952:A:N3	82:A:1938:HOH:O	2.32	0.59
48:C:24:PHE:HZ	60:P:34:ILE:HA	1.67	0.59
56:K:38:ASN:HA	75:f:36:MET:HE3	1.83	0.59
63:S:89:SER:HB3	63:S:92:ASP:HB2	1.85	0.59
1:1:1199:A:H2'	1:1:1200:A:C8	2.37	0.59
1:1:2867:G:O2'	42:AN:24:TYR:O	2.21	0.59
46:A:332:G:O6	82:J:301:HOH:O	2.17	0.59
75:f:50:THR:OG1	75:f:53:LYS:HB2	2.03	0.59
1:1:2962:G:N3	82:1:3745:HOH:O	2.32	0.59
1:1:2974:C:O2'	6:k:180:GLU:OE2	2.16	0.59
25:6:23:MET:HE1	25:6:78:VAL:HG22	1.85	0.59
46:A:477:C:H4'	56:K:120:ARG:HG3	1.85	0.59
46:A:1463:G:H2'	46:A:1464:G:C8	2.37	0.59
1:1:2740:U:H2'	1:1:2741:A:H8	1.68	0.58
46:A:557:C:OP1	75:f:59:SER:OG	2.19	0.58
54:I:92:ARG:HH12	54:I:120:LYS:HB3	1.68	0.58
1:1:627:U:H2'	1:1:628:A:C8	2.37	0.58
1:1:844:A:C6	1:1:845:C:H1'	2.39	0.58
46:A:509:A:OP2	56:K:176:ASN:ND2	2.33	0.58
46:A:1149:G:O2'	46:A:1599:U:O2	2.19	0.58
51:F:45:VAL:HA	51:F:61:VAL:HG21	1.85	0.58
62:R:124:GLU:HG2	62:R:133:ALA:HB1	1.85	0.58
66:V:26:THR:HG22	66:V:87:LYS:HG3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:0:60:SER:OG	22:0:62:ASN:ND2	2.34	0.58
1:1:164:U:H2'	1:1:165:C:H6	1.67	0.58
1:1:316:U:O2'	38:AJ:29:LYS:NZ	2.36	0.58
1:1:662:U:H2'	1:1:663:A:C8	2.39	0.58
1:1:716:G:OP1	30:AB:117:ARG:NH2	2.35	0.58
1:1:2709:C:O2'	31:AC:36:ASP:OD1	2.19	0.58
1:1:2850:G:H5''	6:k:5:LYS:HE2	1.84	0.58
49:D:36:LEU:HD21	49:D:51:ILE:HD12	1.84	0.58
1:1:925:A:O2'	39:AK:49:TRP:O	2.22	0.58
3:4:52:A:H62	41:AM:27:ILE:HD13	1.69	0.58
46:A:778:U:O2'	46:A:779:U:O2	2.16	0.58
46:A:1472:G:N2	46:A:1509:U:O4	2.36	0.58
63:S:25:THR:HG23	63:S:27:ASP:H	1.68	0.58
1:1:1177:U:O4	18:w:22:SER:OG	2.20	0.58
1:1:2239:G:O2'	1:1:2241:C:N4	2.37	0.58
1:1:2249:A:H2'	1:1:2250:G:O4'	2.04	0.58
46:A:511:U:H2'	46:A:512:G:C8	2.38	0.58
1:1:1653:C:O2'	1:1:1793:A:OP2	2.15	0.58
1:1:3260:A:H2'	1:1:3261:A:C8	2.39	0.58
46:A:151:G:H2'	46:A:152:G:C8	2.39	0.58
46:A:184:C:OP1	55:J:152:ARG:NH2	2.37	0.58
46:A:870:G:H2'	46:A:871:U:C6	2.38	0.58
64:T:63:GLN:O	64:T:67:GLU:HG3	2.04	0.58
32:AD:29:TYR:OH	32:AD:57:GLU:OE2	2.22	0.58
73:d:12:VAL:HG12	73:d:30:VAL:HG12	1.85	0.58
73:d:29:ARG:HE	73:d:41:VAL:HG22	1.68	0.58
1:1:1079:G:H2'	1:1:1080:A:C8	2.39	0.58
1:1:2163:G:O2'	1:1:2292:U:OP2	2.17	0.58
1:1:2925:U:H2'	1:1:2926:U:H2'	1.86	0.58
6:k:58:ARG:HD2	6:k:354:VAL:HG13	1.86	0.58
19:x:122:ALA:HB3	19:x:143:PRO:HB2	1.86	0.58
46:A:485:G:O6	46:A:499:U:O4	2.22	0.58
47:B:56:LYS:NZ	67:W:70:ASN:OD1	2.33	0.58
1:1:2184:G:O2'	1:1:2187:U:O4	2.16	0.57
1:1:2988:A:H2'	1:1:2989:A:H8	1.69	0.57
46:A:940:A:H4'	46:A:1058:G:O2'	2.04	0.57
46:A:1024:A:H4'	67:W:62:ARG:HH22	1.70	0.57
60:P:81:THR:HG21	60:P:85:LYS:HD2	1.85	0.57
64:T:36:ARG:NE	64:T:105:LEU:HD22	2.19	0.57
1:1:654:A:H2'	1:1:655:A:C8	2.39	0.57
1:1:896:G:H1'	1:1:1585:A:N6	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:17:C:H2'	46:A:18:C:C6	2.38	0.57
46:A:1007:C:O2'	46:A:1110:A:N1	2.35	0.57
46:A:1523:G:O2'	46:A:1524:C:OP1	2.22	0.57
1:1:315:C:OP2	38:AJ:27:TYR:OH	2.19	0.57
1:1:1478:A:N1	1:1:1862:C:O2'	2.37	0.57
11:p:163:LEU:HA	17:v:7:LEU:HD21	1.86	0.57
18:w:11:ASP:HB2	18:w:118:ARG:HB3	1.85	0.57
46:A:10:G:O2'	49:D:82:GLN:OE1	2.21	0.57
49:D:133:PRO:HB2	49:D:217:TYR:HE2	1.69	0.57
55:J:57:ALA:HB2	55:J:183:GLY:HA2	1.86	0.57
62:R:93:GLN:HB2	62:R:101:LYS:HG3	1.87	0.57
64:T:30:TYR:O	64:T:33:THR:OG1	2.21	0.57
68:X:28:ARG:HD3	68:X:60:LYS:HE2	1.86	0.57
1:1:248:U:H2'	1:1:249:G:H4'	1.87	0.57
9:n:39:LEU:HD13	9:n:83:VAL:HG11	1.86	0.57
46:A:116:U:H2'	46:A:117:U:C6	2.40	0.57
46:A:391:C:H2'	46:A:392:C:C6	2.40	0.57
49:D:225:TRP:NE1	82:D:301:HOH:O	2.29	0.57
26:7:37:ALA:O	26:7:41:GLN:HG2	2.05	0.57
46:A:1048:U:H2'	46:A:1049:G:C8	2.40	0.57
1:1:496:A:H4'	9:n:27:GLN:HG3	1.87	0.57
1:1:1617:A:H2'	1:1:1618:U:C6	2.39	0.57
1:1:1692:A:H2'	1:1:1693:A:C8	2.39	0.57
46:A:965:G:H4'	46:A:1763:A:H4'	1.86	0.57
53:H:159:ARG:NH1	53:H:170:THR:OG1	2.38	0.57
62:R:27:LEU:HD11	62:R:29:LYS:HE3	1.85	0.57
63:S:99:GLN:N	63:S:99:GLN:OE1	2.37	0.57
1:1:1093:G:H4'	23:2:129:LYS:HG2	1.87	0.57
1:1:1561:U:H2'	1:1:1562:G:C8	2.40	0.57
1:1:1896:A:H8	82:1:3709:HOH:O	1.88	0.57
1:1:2347:G:H2'	1:1:2348:G:C8	2.40	0.57
14:s:60:ARG:NH1	44:AP:104:LEU:O	2.38	0.57
46:A:1131:G:H2'	46:A:1132:A:C8	2.40	0.57
1:1:1190:G:H2'	1:1:1191:A:C8	2.39	0.57
1:1:1895:G:O3'	82:1:3709:HOH:O	2.17	0.57
1:1:2327:U:OP1	82:1:3706:HOH:O	2.17	0.57
30:AB:112:VAL:HB	30:AB:130:VAL:HG12	1.87	0.57
46:A:152:G:OP1	53:H:2:LYS:HD2	2.04	0.57
1:1:1662:G:H2'	1:1:1663:A:C8	2.39	0.57
46:A:1160:U:H2'	46:A:1161:G:H8	1.69	0.57
63:S:20:PHE:HD2	63:S:23:LYS:HD3	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:619:A:H2'	1:1:620:A:C8	2.40	0.56
1:1:858:U:OP2	82:1:3710:HOH:O	2.17	0.56
1:1:2418:A:H4'	48:C:53:GLY:HA3	1.85	0.56
1:1:3287:A:H2'	1:1:3288:A:C8	2.40	0.56
46:A:1024:A:O2'	46:A:1025:G:O5'	2.21	0.56
1:1:358:G:N2	1:1:361:A:OP2	2.36	0.56
18:w:122:PRO:HA	18:w:125:LEU:HD12	1.87	0.56
43:AO:11:ARG:NH2	46:A:1762:U:OP1	2.36	0.56
1:1:690:A:OP1	17:v:201:ARG:NH2	2.26	0.56
1:1:939:U:H3'	30:AB:13:GLY:HA2	1.87	0.56
1:1:1611:U:H2'	1:1:1612:U:C6	2.40	0.56
1:1:2183:U:O2'	1:1:2184:G:OP1	2.22	0.56
1:1:3277:U:H4'	6:k:25:GLN:OE1	2.05	0.56
9:n:65:SER:HB2	9:n:75:LEU:HD23	1.87	0.56
46:A:881:U:O2	60:P:36:ARG:NH1	2.38	0.56
46:A:1460:G:H2'	46:A:1461:A:C8	2.39	0.56
47:B:144:ILE:HG12	47:B:158:VAL:HB	1.87	0.56
60:P:79:ARG:HB3	60:P:113:VAL:HG23	1.86	0.56
69:Y:95:PHE:O	82:Y:303:HOH:O	2.18	0.56
46:A:209:U:H5''	58:M:20:PHE:CG	2.40	0.56
46:A:738:A:OP1	51:F:186:GLY:HA3	2.05	0.56
50:E:48:GLU:HG2	50:E:88:TYR:HE2	1.70	0.56
66:V:101:ARG:O	66:V:105:ILE:HG12	2.05	0.56
1:1:1631:G:N2	1:1:1634:A:OP2	2.28	0.56
13:r:77:THR:HG22	13:r:82:ARG:HA	1.87	0.56
16:u:57:LEU:HG	22:0:172:TYR:OH	2.06	0.56
24:5:86:TYR:O	24:5:90:ASN:ND2	2.35	0.56
46:A:149:G:N2	53:H:13:GLN:OE1	2.25	0.56
48:C:168:MET:O	48:C:172:MET:HG3	2.04	0.56
51:F:88:ASP:OD1	51:F:122:LYS:NZ	2.39	0.56
51:F:253:ARG:HD2	51:F:257:ARG:NH2	2.21	0.56
1:1:3060:G:OP1	6:k:313:ARG:NH1	2.38	0.56
27:8:99:VAL:HG11	27:8:124:ILE:HD13	1.88	0.56
46:A:405:A:H2'	46:A:406:C:C6	2.41	0.56
46:A:1715:U:H2'	46:A:1716:C:C6	2.41	0.56
47:B:48:ILE:HD12	47:B:149:MET:HE3	1.87	0.56
57:L:88:PRO:O	57:L:89:LEU:HD22	2.05	0.56
3:4:21:C:OP1	7:l:194:LYS:NZ	2.31	0.56
40:AL:44:LYS:HB3	40:AL:51:GLN:HE21	1.70	0.56
46:A:123:G:OP1	51:F:77:ARG:NH2	2.29	0.56
46:A:530:U:OP2	56:K:132:ARG:NH2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2932:C:H2'	1:1:2933:G:H8	1.68	0.56
46:A:1535:G:O2'	64:T:89:GLN:NE2	2.37	0.56
61:Q:81:ARG:NH1	61:Q:98:ASN:HA	2.21	0.56
51:F:191:ARG:NH2	51:F:212:ASP:OD2	2.36	0.56
41:AM:49:LEU:HB3	41:AM:51:ILE:HG12	1.87	0.55
46:A:1282:G:N2	46:A:1285:A:OP2	2.31	0.55
47:B:131:GLN:NE2	47:B:135:GLU:OE2	2.33	0.55
54:I:85:HIS:CD2	54:I:161:LYS:HG2	2.41	0.55
3:4:75:G:OP2	28:9:74:TYR:OH	2.24	0.55
13:r:53:VAL:HG21	13:r:166:ILE:HD12	1.88	0.55
46:A:16:G:H2'	46:A:17:C:C6	2.41	0.55
46:A:1019:C:HO2'	68:X:2:THR:N	2.04	0.55
51:F:11:ARG:HH12	51:F:24:SER:HB3	1.70	0.55
57:L:54:TYR:HD1	57:L:72:GLY:HA2	1.71	0.55
65:U:124:ILE:HD11	65:U:132:LEU:HD12	1.88	0.55
46:A:1413:A:O2'	46:A:1414:G:OP1	2.25	0.55
46:A:1575:G:H1	46:A:1595:U:H3	1.53	0.55
66:V:99:VAL:O	66:V:103:THR:HG23	2.06	0.55
1:1:2740:U:H2'	1:1:2741:A:C8	2.41	0.55
3:4:126:A:O2'	3:4:129:C:N4	2.40	0.55
47:B:52:LYS:HD3	67:W:82:VAL:HG23	1.88	0.55
1:1:1738:U:OP2	82:1:3711:HOH:O	2.18	0.55
1:1:1837:A:H1'	41:AM:45:ARG:HH22	1.71	0.55
46:A:79:C:OP1	53:H:159:ARG:NH2	2.39	0.55
46:A:1399:U:O2'	46:A:1400:U:OP1	2.25	0.55
1:1:429:U:H5''	35:AG:87:LYS:HE3	1.87	0.55
1:1:1833:U:OP1	82:1:3712:HOH:O	2.18	0.55
1:1:2185:A:H2'	46:A:898:G:H4'	1.88	0.55
1:1:3040:U:OP2	21:z:62:ARG:NH2	2.39	0.55
24:5:19:VAL:HG12	24:5:108:LEU:HG	1.89	0.55
46:A:511:U:O4	56:K:171:ARG:NH2	2.39	0.55
46:A:784:U:H2'	46:A:785:G:H8	1.71	0.55
46:A:892:A:H1'	46:A:982:G:O2'	2.06	0.55
46:A:924:A:H2'	46:A:925:A:C8	2.41	0.55
47:B:63:ILE:HG12	67:W:36:ILE:HG12	1.89	0.55
52:G:103:ASN:HA	52:G:106:LYS:HD2	1.87	0.55
1:1:428:U:H2'	1:1:429:U:C6	2.41	0.55
1:1:487:C:H2'	1:1:488:G:O4'	2.06	0.55
13:r:48:LEU:HD22	13:r:142:ASP:HA	1.89	0.55
46:A:1615:U:H2'	46:A:1616:G:C8	2.42	0.55
65:U:117:SER:HB2	65:U:123:ARG:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1218:G:HO2'	1:1:1219:A:P	2.30	0.55
46:A:78:A:H1'	53:H:175:ILE:HG13	1.89	0.55
19:x:32:THR:HG21	19:x:87:SER:HB3	1.88	0.55
24:5:19:VAL:O	24:5:21:ALA:N	2.39	0.55
46:A:1257:U:O2'	46:A:1260:A:OP2	2.16	0.55
46:A:1669:U:HO2'	46:A:1670:U:H6	1.54	0.55
28:9:48:LEU:HD13	28:9:115:ARG:HH21	1.72	0.55
46:A:1189:A:N3	74:e:10:HIS:HE1	2.05	0.55
46:A:1400:U:H5''	63:S:3:ARG:HE	1.71	0.55
46:A:1739:U:H2'	46:A:1740:A:H8	1.72	0.55
48:C:174:ARG:NH2	48:C:196:GLU:OE2	2.40	0.55
73:d:19:THR:HG23	73:d:25:VAL:HG13	1.89	0.55
1:1:716:G:OP2	1:1:716:G:N2	2.34	0.54
46:A:334:G:N7	82:A:1945:HOH:O	2.34	0.54
46:A:479:A:H2'	46:A:480:U:C6	2.43	0.54
46:A:1396:A:O2'	46:A:1397:A:OP1	2.23	0.54
64:T:28:ILE:HG12	64:T:61:LEU:HD11	1.89	0.54
1:1:72:A:N7	15:t:66:ASN:HB3	2.22	0.54
1:1:2634:G:H2'	1:1:2635:A:C8	2.42	0.54
9:n:50:ARG:O	9:n:71:ASN:ND2	2.41	0.54
16:u:25:GLU:OE2	16:u:44:LYS:HB2	2.07	0.54
54:I:109:PRO:HG2	54:I:112:ARG:HD3	1.88	0.54
1:1:172:C:O2'	1:1:173:C:OP1	2.22	0.54
1:1:2646:A:H5''	14:s:105:GLY:HA3	1.90	0.54
1:1:2808:OMC:H5	1:1:2824:C:N4	2.04	0.54
22:0:92:LYS:HE2	22:0:109:ASP:OD2	2.07	0.54
51:F:87:MET:HE1	51:F:237:VAL:HG21	1.89	0.54
62:R:98:GLU:HG3	62:R:101:LYS:HE3	1.88	0.54
69:Y:132:LEU:HD11	82:Y:301:HOH:O	2.06	0.54
1:1:653:C:H2'	1:1:654:A:C8	2.43	0.54
1:1:683:G:OP1	15:t:39:ARG:NH2	2.41	0.54
1:1:941:C:H2'	1:1:942:U:C6	2.43	0.54
1:1:2090:U:H4'	1:1:2091:A:O5'	2.06	0.54
1:1:2790:U:H5''	31:AC:1:MET:HA	1.88	0.54
15:t:57:VAL:HG22	15:t:69:VAL:HG22	1.88	0.54
24:5:29:ASP:HB3	24:5:32:SER:OG	2.07	0.54
32:AD:59:GLU:OE1	32:AD:71:TYR:OH	2.20	0.54
39:AK:21:ARG:HD3	39:AK:44:MET:SD	2.48	0.54
46:A:405:A:H2'	46:A:406:C:H6	1.72	0.54
46:A:1265:C:H5'	74:e:44:ARG:HH12	1.71	0.54
46:A:1659:G:H2'	46:A:1660:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:W:30:ALA:O	67:W:60:ARG:NE	2.38	0.54
1:1:1795:A:H2'	1:1:1796:A:C8	2.42	0.54
2:3:112:G:H2'	2:3:113:C:C6	2.42	0.54
46:A:350:A:N6	82:A:1961:HOH:O	2.40	0.54
54:I:29:ASP:OD1	54:I:30:LEU:N	2.40	0.54
1:1:1559:C:O2'	1:1:1560:U:OP1	2.26	0.54
1:1:2782:C:OP1	1:1:2927:U:O2'	2.22	0.54
1:1:2924:G:OP2	82:1:3703:HOH:O	2.19	0.54
46:A:1635:A:H2'	46:A:1636:C:C6	2.42	0.54
59:O:113:PHE:O	82:O:201:HOH:O	2.18	0.54
1:1:1286:A:H2'	1:1:1287:A:C8	2.43	0.54
1:1:3159:A:O2'	1:1:3160:C:OP1	2.25	0.54
1:1:2079:C:HO2'	1:1:2080:U:H6	1.55	0.54
21:z:134:HIS:HE1	21:z:136:ARG:NE	2.03	0.54
46:A:12:U:H2'	46:A:13:C:C6	2.43	0.54
46:A:915:A:N6	82:A:1962:HOH:O	2.40	0.54
46:A:1160:U:H2'	46:A:1161:G:C8	2.42	0.54
47:B:59:LEU:HD22	67:W:79:LEU:HD11	1.89	0.54
48:C:144:LYS:HE2	48:C:206:PRO:HB3	1.89	0.54
63:S:89:SER:C	63:S:91:LEU:H	2.15	0.54
1:1:2242:U:O3'	46:A:987:G:H4'	2.08	0.54
1:1:2292:U:OP1	82:1:3713:HOH:O	2.18	0.54
4:10:70:G:H2'	4:10:71:C:C6	2.43	0.54
29:AA:87:LEU:HD11	29:AA:121:LYS:HD3	1.90	0.54
52:G:133:VAL:HG22	52:G:198:LEU:HD13	1.90	0.54
57:L:77:ARG:HD3	57:L:82:ILE:HD11	1.90	0.54
67:W:73:ALA:HB1	67:W:78:LEU:HB2	1.89	0.54
1:1:3256:G:H2'	1:1:3257:A:C8	2.42	0.54
29:AA:103:GLU:HB2	29:AA:106:GLN:HB2	1.88	0.54
1:1:88:G:N7	20:y:171:LYS:NZ	2.57	0.53
1:1:164:U:H2'	1:1:165:C:C6	2.41	0.53
1:1:1060:A:H4'	1:1:1061:A:O5'	2.08	0.53
1:1:3236:G:O6	9:n:128:LYS:NZ	2.40	0.53
46:A:518:A:O2'	46:A:519:A:OP1	2.26	0.53
70:Z:10:ARG:NH1	70:Z:26:ASP:OD2	2.41	0.53
1:1:407:A:C2	3:4:17:A:H1'	2.44	0.53
1:1:1747:G:H5'	40:AL:26:LYS:HE2	1.90	0.53
17:v:65:ARG:HG2	17:v:127:TYR:CD1	2.43	0.53
39:AK:21:ARG:NH2	39:AK:41:ALA:O	2.28	0.53
1:1:653:C:H2'	1:1:654:A:H8	1.74	0.53
1:1:788:G:H2'	1:1:789:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1042:A:H2'	1:1:1045:C:C5	2.43	0.53
1:1:1632:C:O2'	29:AA:79:HIS:ND1	2.39	0.53
1:1:2852:U:H1'	6:k:250:ALA:HB3	1.90	0.53
37:AI:22:VAL:O	37:AI:26:GLN:HG3	2.08	0.53
1:1:68:C:OP1	17:v:178:HIS:ND1	2.27	0.53
1:1:797:A:OP1	30:AB:27:LYS:HE3	2.09	0.53
1:1:3344:U:H4'	6:k:315:GLY:HA2	1.89	0.53
6:k:218:ILE:HB	6:k:337:THR:HB	1.89	0.53
13:r:38:ARG:NH1	13:r:45:GLU:OE1	2.40	0.53
21:z:162:ARG:HA	21:z:165:ARG:HD3	1.90	0.53
46:A:446:C:OP1	51:F:29:PRO:HD3	2.08	0.53
57:L:17:GLN:N	57:L:88:PRO:HB3	2.18	0.53
71:b:51:ARG:O	71:b:55:GLU:HG3	2.08	0.53
1:1:75:G:H3'	15:t:73:ARG:HD2	1.90	0.53
1:1:600:U:C2	1:1:602:A:H1'	2.44	0.53
1:1:2158:A:H2'	1:1:2159:C:C6	2.43	0.53
1:1:2335:A:H2'	1:1:2336:A:C8	2.43	0.53
51:F:15:PRO:HG3	51:F:39:ARG:HD3	1.90	0.53
51:F:253:ARG:HD2	51:F:257:ARG:HH21	1.73	0.53
61:Q:81:ARG:NH2	61:Q:117:GLY:O	2.41	0.53
1:1:1218:G:H1'	1:1:1282:A:N6	2.24	0.53
1:1:1787:U:H2'	1:1:1788:C:C6	2.44	0.53
8:m:85:ARG:NH2	8:m:250:ASP:OD2	2.42	0.53
17:v:62:TYR:CD2	17:v:106:VAL:HG13	2.43	0.53
46:A:265:U:H2'	46:A:266:C:H6	1.73	0.53
54:I:155:SER:HB2	54:I:181:ILE:HD13	1.90	0.53
57:L:6:GLU:OE1	57:L:10:LYS:NZ	2.41	0.53
66:V:25:LEU:HD23	66:V:113:VAL:HG22	1.90	0.53
1:1:2669:A:H2'	1:1:2670:G:C8	2.44	0.53
1:1:2938:G:H2'	1:1:2939:A:C8	2.44	0.53
32:AD:55:LYS:O	32:AD:59:GLU:HG2	2.08	0.53
43:AO:1:MET:HB3	46:A:1629:G:H5'	1.91	0.53
46:A:1451:C:OP1	62:R:138:GLN:NE2	2.41	0.53
1:1:2516:U:O2'	1:1:2520:A:N1	2.40	0.53
1:1:3019:U:O2'	1:1:3020:A:H5'	2.08	0.53
1:1:3256:G:H2'	1:1:3257:A:H8	1.74	0.53
10:o:130:PRO:HG2	10:o:131:TYR:CE2	2.44	0.53
44:AP:15:LYS:HG2	44:AP:18:ARG:HH21	1.74	0.53
46:A:1664:C:H42	46:A:1711:C:H42	1.57	0.53
55:J:76:THR:HG21	55:J:104:ILE:HD12	1.91	0.53
24:5:34:VAL:HG13	24:5:56:ILE:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:AE:71:ARG:NH2	33:AE:104:GLN:O	2.41	0.53
46:A:757:G:OP1	51:F:22:LYS:NZ	2.25	0.53
46:A:1487:C:OP1	65:U:122:ARG:NH2	2.33	0.53
64:T:43:ALA:HA	64:T:46:VAL:HG22	1.89	0.53
1:1:581:A:H5''	35:AG:106:ASN:ND2	2.24	0.53
9:n:50:ARG:NH2	16:u:107:ASP:OD2	2.40	0.53
12:q:86:TYR:CE2	12:q:151:LEU:HB2	2.44	0.53
18:w:151:GLU:O	18:w:155:GLU:HG2	2.08	0.53
46:A:78:A:C8	53:H:154:ARG:HG3	2.43	0.53
46:A:685:C:OP1	68:X:118:ARG:NH1	2.42	0.53
46:A:988:A:H2'	46:A:990:A:N7	2.24	0.53
46:A:1415:G:H2'	46:A:1416:U:O2	2.08	0.53
54:I:67:ARG:HD2	54:I:127:PHE:CE1	2.44	0.53
1:1:243:G:H2'	1:1:244:G:H8	1.75	0.52
1:1:1303:G:HO2'	1:1:2345:A:HO2'	1.57	0.52
46:A:1665:C:OP1	55:J:59:ARG:NH2	2.31	0.52
50:E:171:ILE:HG12	50:E:188:LYS:HG3	1.90	0.52
52:G:91:GLU:HA	52:G:94:THR:HG22	1.91	0.52
1:1:208:A:H4'	1:1:210:A:N7	2.24	0.52
1:1:649:G:O2'	1:1:1431:A:OP1	2.26	0.52
1:1:1491:U:H5	1:1:1831:A:N1	2.06	0.52
1:1:2810:A:N6	1:1:2822:G:O2'	2.39	0.52
46:A:1470:G:H5'	62:R:14:THR:HG21	1.92	0.52
46:A:1479:A:H4'	46:A:1480:G:O5'	2.08	0.52
46:A:1551:U:H2'	46:A:1552:C:C6	2.44	0.52
69:Y:107:PHE:CD2	69:Y:114:LYS:HB3	2.43	0.52
1:1:46:C:OP2	1:1:47:A:O2'	2.22	0.52
1:1:290:G:H1'	17:v:93:LYS:HD2	1.91	0.52
1:1:848:U:C6	45:AQ:2:THR:HG22	2.44	0.52
1:1:1115:C:H2'	1:1:1116:A:H8	1.74	0.52
64:T:67:GLU:HA	64:T:70:VAL:HG22	1.91	0.52
1:1:729:C:H3'	1:1:730:A:H5''	1.92	0.52
1:1:3194:G:H5'	16:u:129:VAL:HG21	1.91	0.52
19:x:29:THR:HA	19:x:32:THR:HG22	1.90	0.52
1:1:1493:C:H2'	1:1:1494:A:C8	2.45	0.52
1:1:2862:A:O2'	1:1:2905:A:N3	2.42	0.52
1:1:2933:G:H2'	1:1:2934:U:C6	2.44	0.52
1:1:3093:U:H1'	1:1:3094:A:H5''	1.90	0.52
20:y:94:LEU:HD22	30:AB:119:PRO:HG3	1.90	0.52
33:AE:71:ARG:NH1	33:AE:103:LEU:HB3	2.25	0.52
44:AP:25:VAL:HG22	44:AP:72:LEU:HD22	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1325:U:O4	62:R:8:THR:HA	2.10	0.52
47:B:167:LYS:NZ	47:B:204:TYR:O	2.40	0.52
1:1:1936:G:N2	1:1:3327:A:H8	1.99	0.52
1:1:3000:G:H2'	1:1:3001:A:C8	2.45	0.52
8:m:55:PHE:H	8:m:151:GLN:HE22	1.58	0.52
18:w:9:VAL:HG12	18:w:118:ARG:HG3	1.91	0.52
21:z:98:ARG:HD2	21:z:133:LYS:O	2.10	0.52
24:5:92:ILE:HD12	24:5:96:ILE:HD13	1.92	0.52
32:AD:78:GLU:HA	32:AD:81:THR:HG22	1.90	0.52
46:A:309:U:OP2	69:Y:20:ARG:HD3	2.09	0.52
46:A:1602:C:P	52:G:81:ARG:HE	2.32	0.52
66:V:34:GLU:OE1	66:V:56:ARG:NH2	2.43	0.52
1:1:1400:G:N2	1:1:1403:A:OP2	2.39	0.52
1:1:1562:G:C2	1:1:1563:A:H1'	2.44	0.52
1:1:2184:G:H1'	1:1:2186:A:N6	2.24	0.52
14:s:20:ASN:HB3	14:s:126:ASP:HB3	1.91	0.52
18:w:76:ALA:HB3	18:w:79:ARG:HG2	1.92	0.52
40:AL:8:ILE:O	40:AL:12:VAL:HG23	2.09	0.52
45:AQ:85:ARG:O	45:AQ:89:LEU:HG	2.10	0.52
46:A:108:A:H2'	46:A:109:G:C8	2.44	0.52
46:A:1302:C:H2'	46:A:1303:G:O4'	2.09	0.52
48:C:59:ASP:OD1	48:C:60:GLY:N	2.42	0.52
71:b:37:LYS:HG2	71:b:72:HIS:ND1	2.25	0.52
6:k:260:VAL:HG11	6:k:266:ARG:NH1	2.23	0.52
14:s:109:HIS:CD2	14:s:114:ILE:HD11	2.37	0.52
25:6:77:ILE:HD12	25:6:103:VAL:HG11	1.92	0.52
46:A:904:A:H2'	46:A:905:C:C6	2.45	0.52
46:A:1369:G:O2'	46:A:1370:A:H8	1.93	0.52
1:1:1184:U:OP1	1:1:1206:U:O2'	2.21	0.52
1:1:2260:U:OP1	1:1:2945:G:O2'	2.26	0.52
3:4:57:C:H4'	3:4:63:G:N7	2.24	0.52
6:k:211:GLN:NE2	6:k:283:TYR:O	2.43	0.52
7:l:140:GLY:O	7:l:142:ARG:NH1	2.43	0.52
12:q:27:VAL:HG12	12:q:82:VAL:HG21	1.91	0.52
40:AL:14:LEU:HD21	40:AL:52:TYR:CG	2.45	0.52
46:A:17:C:O2'	46:A:1122:A:N1	2.38	0.52
46:A:1582:U:H5'	46:A:1583:C:OP2	2.10	0.52
46:A:1637:U:H2'	46:A:1638:A:C8	2.45	0.52
59:O:127:ARG:O	59:O:131:THR:HG23	2.10	0.52
64:T:23:ASP:HB3	64:T:26:ILE:HG13	1.92	0.52
64:T:24:GLY:HA2	64:T:58:ALA:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:V:32:GLN:N	66:V:32:GLN:OE1	2.43	0.52
66:V:96:ALA:HA	66:V:99:VAL:HG22	1.92	0.52
68:X:40:VAL:HG11	68:X:103:ILE:HD12	1.92	0.52
71:b:32:LYS:O	71:b:37:LYS:NZ	2.42	0.52
1:1:1277:G:H2'	1:1:1278:G:C8	2.46	0.51
1:1:1277:G:H2'	1:1:1278:G:H8	1.75	0.51
1:1:2583:U:H2'	1:1:2584:U:C6	2.45	0.51
1:1:3166:A:H2'	1:1:3167:G:C8	2.44	0.51
7:l:289:ARG:O	7:l:293:SER:HB3	2.10	0.51
53:H:163:THR:HA	53:H:168:THR:HG22	1.92	0.51
68:X:15:ASN:N	82:X:301:HOH:O	2.44	0.51
1:1:117:U:O2	1:1:120:A:H5''	2.11	0.51
1:1:1689:C:O2'	1:1:1768:U:O2'	2.21	0.51
1:1:2282:C:O2'	82:1:3704:HOH:O	2.16	0.51
1:1:2866:C:OP2	12:q:168:ARG:NH1	2.42	0.51
7:l:139:ARG:HH21	7:l:241:PRO:HG2	1.75	0.51
36:AH:54:ILE:HD11	36:AH:78:GLY:HA2	1.92	0.51
46:A:770:C:OP1	46:A:770:C:H6	1.93	0.51
46:A:1072:A:H2'	46:A:1073:A:C8	2.45	0.51
46:A:1145:A:H2'	46:A:1146:C:H6	1.75	0.51
1:1:1807:G:H2'	1:1:1808:G:O4'	2.09	0.51
1:1:1810:A:H4'	1:1:1811:U:O4'	2.10	0.51
1:1:2814:U:O2	1:1:2814:U:H2'	2.10	0.51
6:k:284:ARG:HH11	6:k:356:LEU:HD12	1.75	0.51
20:y:76:ALA:HA	20:y:79:LYS:HG3	1.92	0.51
20:y:125:ASP:OD1	20:y:126:GLN:N	2.44	0.51
28:9:51:ARG:HG2	28:9:52:GLN:N	2.25	0.51
41:AM:24:PRO:HG2	41:AM:27:ILE:HD12	1.92	0.51
46:A:69:G:P	70:Z:123:ARG:HH12	2.34	0.51
46:A:881:U:H3	60:P:36:ARG:HH12	1.58	0.51
46:A:1581:G:H2'	46:A:1582:U:O4'	2.11	0.51
49:D:138:TYR:OH	49:D:144:GLY:O	2.28	0.51
50:E:41:ARG:HG3	66:V:109:PRO:HB3	1.93	0.51
60:P:52:PRO:HB3	60:P:95:SER:OG	2.11	0.51
69:Y:133:LEU:HG	69:Y:137:LYS:HD2	1.93	0.51
1:1:2404:U:H2'	1:1:2405:U:C6	2.46	0.51
46:A:685:C:O2'	46:A:686:G:OP1	2.27	0.51
46:A:1543:A:OP1	61:Q:115:TYR:OH	2.21	0.51
50:E:135:VAL:HG23	50:E:189:ILE:HG12	1.91	0.51
51:F:141:THR:OG1	51:F:143:ASP:OD1	2.22	0.51
57:L:7:ASP:O	57:L:11:ILE:HG13	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:L:56:LYS:NZ	57:L:69:THR:HG22	2.26	0.51
62:R:131:ARG:HG3	62:R:137:PHE:HE1	1.75	0.51
1:1:25:A:H2'	1:1:26:C:H6	1.76	0.51
1:1:2649:G:O2'	1:1:2651:A:N1	2.38	0.51
1:1:3233:A:OP1	9:n:45:ARG:NH2	2.41	0.51
5:j:80:GLU:HG3	45:AQ:66:GLY:HA2	1.92	0.51
8:m:94:ASN:HB2	8:m:97:ALA:H	1.75	0.51
8:m:178:ASN:HA	8:m:183:TRP:CD2	2.46	0.51
20:y:96:PHE:CD1	20:y:97:PRO:HD2	2.45	0.51
46:A:634:A:OP1	82:A:1912:HOH:O	2.19	0.51
46:A:1546:G:H5''	64:T:135:GLY:HA3	1.93	0.51
1:1:58:G:H2'	3:4:33:A:O2'	2.11	0.51
1:1:1106:U:H2'	1:1:1107:U:C6	2.46	0.51
1:1:2145:A:H2'	1:1:2146:A:C8	2.46	0.51
12:q:90:MET:HE3	12:q:181:VAL:HG23	1.93	0.51
17:v:90:ASN:O	44:AP:50:TYR:OH	2.28	0.51
46:A:1138:G:OP1	71:b:85:ARG:NH1	2.42	0.51
48:C:64:ARG:HG2	60:P:31:LYS:HD2	1.92	0.51
1:1:437:G:O2'	1:1:438:A:OP1	2.27	0.51
1:1:1655:U:H2'	1:1:1656:C:C6	2.46	0.51
1:1:2888:U:H5	1:1:2907:U:HO2'	1.58	0.51
14:s:32:ARG:HD2	14:s:120:ILE:HA	1.92	0.51
25:6:36:VAL:HG22	25:6:58:VAL:HG11	1.93	0.51
29:AA:66:THR:HB	29:AA:123:GLN:HE22	1.76	0.51
32:AD:16:LEU:O	32:AD:20:ILE:HG12	2.10	0.51
39:AK:25:ARG:O	39:AK:25:ARG:HG2	2.10	0.51
46:A:64:U:O2'	46:A:166:A:N3	2.36	0.51
50:E:74:ILE:HD12	50:E:87:ILE:HD11	1.91	0.51
62:R:103:GLU:O	62:R:107:ILE:HD12	2.10	0.51
1:1:547:U:H2'	1:1:548:G:H8	1.76	0.51
1:1:1347:U:O2'	1:1:1348:U:OP2	2.26	0.51
6:k:25:GLN:HE21	6:k:334:ARG:HD3	1.76	0.51
7:l:4:ARG:NH1	7:l:25:ALA:HA	2.24	0.51
9:n:39:LEU:HB3	9:n:83:VAL:HG13	1.93	0.51
26:7:18:GLY:HA3	26:7:31:PHE:O	2.11	0.51
46:A:871:U:C2	46:A:872:A:C8	2.98	0.51
54:I:52:LYS:HB2	54:I:84:ARG:HD3	1.93	0.51
62:R:76:GLN:O	62:R:80:ILE:HG13	2.11	0.51
64:T:91:ASP:OD1	64:T:92:GLN:N	2.44	0.51
1:1:3207:G:OP1	18:w:160:LYS:NZ	2.41	0.51
14:s:47:GLN:OE1	14:s:64:LYS:HD3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:52:U:H2'	46:A:53:G:C8	2.46	0.51
51:F:185:GLY:HA2	51:F:189:LEU:HD12	1.91	0.51
1:1:2260:U:O2	1:1:2288:U:H4'	2.12	0.50
1:1:3309:A:N3	1:1:3309:A:H2'	2.24	0.50
1:1:3357:U:H5'	19:x:56:ARG:HH22	1.75	0.50
2:3:19:C:H2'	2:3:20:A:C8	2.46	0.50
28:9:39:LEU:HD22	28:9:43:TYR:HE2	1.74	0.50
46:A:563:C:O2'	46:A:575:G:N2	2.44	0.50
46:A:1265:C:O2'	66:V:69:THR:HG22	2.11	0.50
46:A:1783:C:O2	71:b:92:ARG:HB3	2.10	0.50
53:H:2:LYS:O	53:H:108:VAL:HA	2.12	0.50
69:Y:95:PHE:HB3	82:Y:303:HOH:O	2.12	0.50
1:1:422:A:C2	1:1:2341:A:H4'	2.46	0.50
1:1:1617:A:H2'	1:1:1618:U:H6	1.74	0.50
1:1:3241:G:O6	19:x:169:ASN:ND2	2.44	0.50
3:4:135:G:OP1	27:8:49:LYS:NZ	2.40	0.50
24:5:22:PRO:HB2	24:5:28:PHE:HB2	1.92	0.50
33:AE:71:ARG:NH1	33:AE:103:LEU:HD13	2.26	0.50
45:AQ:28:LYS:O	45:AQ:32:GLN:HG3	2.11	0.50
46:A:1276:G:H1	46:A:1309:G:H22	1.59	0.50
59:O:39:LYS:NZ	59:O:43:LYS:HE2	2.26	0.50
1:1:716:G:O2'	1:1:717:A:OP1	2.26	0.50
1:1:796:G:O6	7:l:105:LYS:NZ	2.34	0.50
1:1:2525:A:H2'	1:1:2526:C:O4'	2.12	0.50
15:t:61:PRO:O	15:t:62:THR:OG1	2.26	0.50
46:A:335:G:O2'	55:J:10:LYS:NZ	2.45	0.50
46:A:1719:A:H2'	46:A:1720:C:C6	2.46	0.50
52:G:32:ASP:OD1	52:G:33:VAL:N	2.44	0.50
52:G:42:LEU:HB3	52:G:46:TRP:HB2	1.93	0.50
65:U:65:ILE:HG12	65:U:71:VAL:CG2	2.42	0.50
1:1:1030:U:H2'	1:1:1031:A:H8	1.77	0.50
1:1:1199:A:N3	1:1:2827:U:O2'	2.44	0.50
1:1:2134:U:P	5:j:241:ARG:HH22	2.33	0.50
1:1:2229:G:H2'	1:1:2230:A:H8	1.75	0.50
6:k:74:GLU:OE1	6:k:325:LYS:HE3	2.12	0.50
21:z:160:GLU:OE1	21:z:163:ARG:NH1	2.45	0.50
32:AD:26:THR:OG1	32:AD:93:SER:OG	2.28	0.50
46:A:745:A:N7	82:A:1948:HOH:O	2.34	0.50
46:A:1470:G:H2'	46:A:1471:C:C6	2.46	0.50
48:C:56:ASN:OD1	48:C:57:ALA:N	2.44	0.50
48:C:127:VAL:HG13	48:C:176:VAL:HG11	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:V:21:ILE:HG21	66:V:99:VAL:HG21	1.93	0.50
1:1:1662:G:H2'	1:1:1663:A:H8	1.76	0.50
1:1:1794:A:H2'	1:1:1795:A:C8	2.46	0.50
1:1:2694:U:O2'	23:2:88:ARG:O	2.26	0.50
1:1:2734:A:H2'	1:1:2735:U:H6	1.77	0.50
1:1:2739:U:H2'	1:1:2740:U:C6	2.46	0.50
1:1:3163:U:H1'	1:1:3165:U:O4	2.10	0.50
14:s:148:ILE:O	14:s:153:LYS:NZ	2.43	0.50
22:0:171:PHE:O	22:0:172:TYR:HB2	2.10	0.50
29:AA:70:PRO:HG3	29:AA:115:LYS:HB2	1.93	0.50
46:A:15:U:H2'	46:A:16:G:O4'	2.11	0.50
46:A:70:C:OP1	53:H:164:LYS:NZ	2.45	0.50
46:A:638:U:H2'	46:A:639:G:O4'	2.12	0.50
46:A:932:U:H2'	46:A:933:A:C8	2.46	0.50
46:A:1453:C:O2'	65:U:88:PHE:O	2.19	0.50
52:G:200:ASN:HB3	52:G:208:SER:HB3	1.93	0.50
53:H:206:ALA:O	53:H:210:GLN:HG2	2.12	0.50
54:I:30:LEU:HD12	54:I:30:LEU:O	2.11	0.50
57:L:55:VAL:HG12	57:L:68:LEU:HA	1.93	0.50
73:d:29:ARG:NE	73:d:41:VAL:HG22	2.26	0.50
1:1:1576:A:H5''	1:1:1576:A:C8	2.47	0.50
1:1:2210:A:H2'	1:1:2211:A:C8	2.47	0.50
1:1:2262:C:N4	1:1:2286:C:OP2	2.42	0.50
34:AF:67:LEU:HD23	34:AF:73:LYS:HG3	1.93	0.50
66:V:18:ILE:HD11	66:V:93:GLN:HB3	1.92	0.50
1:1:716:G:H3'	1:1:717:A:H5''	1.94	0.50
1:1:907:C:N4	5:j:3:ARG:HD3	2.27	0.50
1:1:972:U:H2'	1:1:973:C:O4'	2.12	0.50
1:1:2498:A:H2'	1:1:2499:U:C6	2.46	0.50
7:l:360:VAL:HG22	22:0:64:ILE:HG12	1.94	0.50
19:x:60:PHE:HB3	19:x:64:ASN:HB3	1.93	0.50
21:z:149:ALA:HA	21:z:152:GLU:HG3	1.93	0.50
46:A:93:A:O2'	51:F:4:GLY:HA3	2.12	0.50
46:A:1298:A:N3	46:A:1300:U:H5'	2.27	0.50
46:A:1398:G:H4'	46:A:1399:U:O5'	2.12	0.50
46:A:1508:G:O2'	46:A:1510:G:OP2	2.26	0.50
69:Y:37:ALA:HA	69:Y:41:SER:HB2	1.93	0.50
70:Z:57:VAL:HB	70:Z:60:PHE:HE2	1.76	0.50
73:d:18:ARG:HD2	73:d:26:THR:HG22	1.94	0.50
1:1:92:C:C2	30:AB:55:LYS:HE2	2.47	0.50
1:1:3244:A:O2'	1:1:3245:A:H5'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:8:105:VAL:HG23	27:8:130:TYR:CG	2.47	0.50
44:AP:10:THR:O	44:AP:20:HIS:HA	2.12	0.50
46:A:330:U:P	55:J:56:ARG:HH22	2.34	0.50
46:A:1571:G:O2'	46:A:1597:G:O6	2.24	0.50
47:B:92:HIS:ND1	47:B:202:TYR:OH	2.34	0.50
63:S:77:GLU:OE2	63:S:81:LYS:HD2	2.12	0.50
1:1:783:G:H2'	1:1:784:C:C6	2.47	0.50
1:1:1218:G:O2'	1:1:1219:A:OP2	2.26	0.50
1:1:2116:A:C4	39:AK:3:LYS:HB3	2.47	0.50
1:1:2713:C:O2	44:AP:20:HIS:HE1	1.94	0.50
1:1:3064:C:O2'	1:1:3066:A:OP2	2.25	0.50
46:A:29:U:H2'	46:A:30:G:H8	1.76	0.50
1:1:912:G:N1	5:j:207:VAL:HG11	2.27	0.49
1:1:1115:C:H2'	1:1:1116:A:C8	2.47	0.49
2:3:23:A:H2'	2:3:24:A:C8	2.46	0.49
46:A:31:C:O2'	46:A:545:U:OP1	2.30	0.49
46:A:129:A:H61	46:A:179:A:H61	1.60	0.49
47:B:118:PRO:HG2	47:B:141:ILE:HD13	1.94	0.49
48:C:135:LEU:HA	48:C:216:LYS:O	2.12	0.49
66:V:52:LYS:HB2	66:V:91:ASP:HB2	1.94	0.49
67:W:4:ASP:OD1	67:W:5:LYS:N	2.45	0.49
1:1:1637:U:O2'	1:1:1638:A:H3'	2.12	0.49
1:1:2634:G:H2'	1:1:2635:A:H8	1.75	0.49
29:AA:23:VAL:HG12	29:AA:45:GLY:HA3	1.95	0.49
46:A:357:A:H5'	82:A:2050:HOH:O	2.12	0.49
46:A:797:U:OP2	59:O:76:LYS:NZ	2.27	0.49
46:A:903:U:H4'	60:P:13:ARG:HD3	1.94	0.49
46:A:1092:G:O2'	46:A:1093:G:H5'	2.12	0.49
46:A:1165:C:O2'	61:Q:128:HIS:ND1	2.45	0.49
63:S:77:GLU:HG2	63:S:80:ARG:CZ	2.43	0.49
1:1:357:A:O4'	7:l:82:GLY:HA3	2.12	0.49
1:1:432:G:OP1	35:AG:57:LYS:HB2	2.12	0.49
1:1:1152:C:OP2	10:o:92:LYS:NZ	2.45	0.49
1:1:1923:G:C8	45:AQ:16:VAL:HG12	2.48	0.49
1:1:2985:U:H2'	1:1:2986:U:C6	2.47	0.49
19:x:168:LEU:HB2	19:x:173:ARG:HG3	1.93	0.49
46:A:1369:G:OP1	66:V:86:HIS:ND1	2.46	0.49
61:Q:80:LEU:O	61:Q:80:LEU:HD12	2.12	0.49
1:1:1035:U:H2'	1:1:1036:A:C8	2.48	0.49
1:1:1199:A:H2'	1:1:1200:A:H8	1.78	0.49
1:1:3297:U:O5'	82:1:3715:HOH:O	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:3:U:H2'	2:3:4:U:C6	2.47	0.49
10:o:82:VAL:HG21	10:o:134:TYR:HD2	1.77	0.49
46:A:1475:U:O2'	46:A:1501:A:N6	2.44	0.49
60:P:65:LYS:O	60:P:69:VAL:HG23	2.12	0.49
1:1:169:G:C6	1:1:249:G:H1'	2.47	0.49
1:1:782:A:H4'	1:1:783:G:H5'	1.93	0.49
7:l:36:VAL:HG21	7:l:245:LEU:HD21	1.94	0.49
18:w:126:ARG:HG2	18:w:130:LEU:HD12	1.93	0.49
26:7:53:VAL:O	26:7:57:ARG:HG2	2.13	0.49
46:A:290:U:H2'	46:A:291:U:C6	2.46	0.49
46:A:1369:G:O2'	46:A:1370:A:O5'	2.27	0.49
46:A:1470:G:H2'	46:A:1471:C:H6	1.77	0.49
52:G:145:ASP:OD1	52:G:146:SER:N	2.45	0.49
1:1:2130:A:H2'	1:1:2131:U:H6	1.78	0.49
1:1:2504:C:OP1	5:j:37:ARG:NH2	2.44	0.49
1:1:3269:C:O2	6:k:25:GLN:NE2	2.46	0.49
3:4:141:C:O3'	17:v:62:TYR:OH	2.31	0.49
26:7:60:LYS:HA	26:7:63:ILE:HD12	1.94	0.49
44:AP:90[B]:HIS:NE2	44:AP:92:GLU:OE1	2.45	0.49
46:A:932:U:H2'	46:A:933:A:H8	1.77	0.49
46:A:1584:A:C8	74:e:14:PHE:HD1	2.29	0.49
52:G:82:PHE:CE1	73:d:49:ARG:HG3	2.47	0.49
52:G:225:ARG:NH1	73:d:58:GLU:HG2	2.28	0.49
53:H:58:LYS:HG2	53:H:105:ASP:O	2.12	0.49
54:I:44:GLU:OE2	54:I:52:LYS:HB3	2.12	0.49
64:T:36:ARG:NH1	64:T:106:GLU:HB3	2.28	0.49
68:X:115:GLU:O	68:X:119:LYS:HG2	2.12	0.49
69:Y:107:PHE:HE1	69:Y:123:LYS:HB3	1.76	0.49
19:x:22:LEU:HD13	19:x:90:PHE:CD1	2.48	0.49
22:0:99:ARG:NH1	22:0:126:VAL:O	2.44	0.49
46:A:903:U:H2'	46:A:904:A:H8	1.76	0.49
46:A:1635:A:H2'	46:A:1636:C:H6	1.78	0.49
46:A:1668:A:H2'	46:A:1669:U:H5'	1.94	0.49
67:W:58:TYR:N	82:W:101:HOH:O	2.45	0.49
1:1:229:C:H2'	1:1:230:G:O4'	2.13	0.49
1:1:951:U:H2'	1:1:952:U:C6	2.47	0.49
1:1:2790:U:H5'	1:1:2790:U:H6	1.77	0.49
1:1:2899:C:H2'	1:1:2900:C:C6	2.48	0.49
21:z:176:ARG:NH2	46:A:838:G:OP2	2.45	0.49
46:A:291:U:H2'	46:A:292:C:C6	2.47	0.49
46:A:598:U:OP2	69:Y:108:GLY:HA2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1716:C:H2'	46:A:1717:A:O4'	2.12	0.49
58:M:66:ILE:HG13	58:M:140:LEU:HD21	1.95	0.49
1:1:62:A:N3	1:1:77:U:O2'	2.39	0.49
1:1:485:A:H2'	1:1:486:C:C6	2.48	0.49
1:1:1043:A:N3	1:1:2605:U:O2'	2.45	0.49
3:4:8:C:H2'	3:4:9:A:C8	2.48	0.49
39:AK:39:TYR:CD1	39:AK:40:PRO:HA	2.48	0.49
46:A:139:U:OP1	53:H:149:LYS:NZ	2.45	0.49
46:A:165:U:H2'	46:A:166:A:H5''	1.95	0.49
46:A:364:A:OP1	46:A:743:U:O2'	2.29	0.49
46:A:1268:U:H5	46:A:1410:A:H62	1.59	0.49
50:E:151:GLN:OE1	50:E:153:TYR:OH	2.28	0.49
57:L:12:HIS:HB3	57:L:80:LEU:HD21	1.95	0.49
1:1:438:A:N7	34:AF:2:ALA:N	2.60	0.49
1:1:803:A:H61	1:1:930:G:H22	1.61	0.49
1:1:2186:A:H5'	46:A:898:G:OP2	2.13	0.49
8:m:41:LYS:HB2	23:2:68:THR:O	2.12	0.49
28:9:5:SER:HB3	28:9:8:VAL:HG23	1.95	0.49
34:AF:97:ILE:HG21	34:AF:106:ARG:HG3	1.94	0.49
38:AJ:93:ILE:O	38:AJ:97:ARG:HG3	2.13	0.49
46:A:944:U:H4'	82:A:1933:HOH:O	2.13	0.49
46:A:985:C:H5	46:A:988:A:H5''	1.77	0.49
46:A:1146:C:H2'	46:A:1147:C:H6	1.76	0.49
46:A:1279:G:N2	82:A:1946:HOH:O	2.34	0.49
46:A:1323:C:H1'	46:A:1396:A:C5	2.48	0.49
47:B:6:SER:O	47:B:191:ARG:NH1	2.46	0.49
47:B:136:SER:HB2	47:B:141:ILE:HB	1.93	0.49
47:B:205:ARG:NH1	47:B:209:GLU:HG2	2.28	0.49
48:C:124:ASN:C	48:C:124:ASN:ND2	2.71	0.49
53:H:159:ARG:HB3	53:H:172:ALA:HB2	1.95	0.49
68:X:40:VAL:HG13	82:X:303:HOH:O	2.12	0.49
1:1:2672:G:H5''	23:2:17:ARG:HG2	1.95	0.48
23:2:51:GLY:HA3	23:2:92:ARG:HG3	1.95	0.48
46:A:298:A:H2'	46:A:299:A:C8	2.48	0.48
46:A:1330:A:OP1	66:V:53:GLY:N	2.46	0.48
46:A:1659:G:H2'	46:A:1660:G:H8	1.78	0.48
63:S:7:LYS:O	63:S:11:ARG:HG2	2.13	0.48
1:1:1080:A:H2'	1:1:1081:A:C8	2.48	0.48
1:1:2370:C:H1'	6:k:266:ARG:HH21	1.78	0.48
1:1:2810:A:H4'	13:r:74:LYS:HD3	1.95	0.48
5:j:49:ILE:HD11	5:j:60:LYS:HE2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:l:157:PHE:CD1	7:l:169:VAL:HG11	2.47	0.48
13:r:202:ARG:C	13:r:203:LYS:HD3	2.38	0.48
46:A:944:U:H5'	59:O:15:ALA:O	2.14	0.48
58:M:101:GLU:OE1	69:Y:16:ARG:NH2	2.46	0.48
59:O:54:LEU:HB3	59:O:60:VAL:HB	1.95	0.48
1:1:417:A:H2'	1:1:418:A:C8	2.47	0.48
1:1:1110:U:OP1	30:AB:23:GLY:N	2.39	0.48
1:1:1303:G:C4	18:w:61:LYS:HD3	2.49	0.48
1:1:2184:G:H4'	1:1:2185:A:C5	2.48	0.48
1:1:2342:G:H22	1:1:2374:G:H1'	1.78	0.48
38:AJ:54:ARG:O	38:AJ:58:GLU:HG2	2.14	0.48
46:A:1302:C:O2'	46:A:1386:A:N3	2.39	0.48
64:T:110:ARG:HG2	64:T:114:GLU:OE1	2.13	0.48
1:1:242:C:O2'	1:1:243:G:H8	1.97	0.48
1:1:1530:A:H2'	1:1:1531:A:C8	2.48	0.48
28:9:58:VAL:HA	28:9:104:VAL:HG12	1.95	0.48
46:A:137:A:O4'	46:A:139:U:H5'	2.13	0.48
46:A:1425:C:H2'	46:A:1426:C:H6	1.78	0.48
46:A:1628:C:H2'	46:A:1629:G:C8	2.49	0.48
48:C:26:ARG:HA	48:C:50:ARG:NH1	2.29	0.48
51:F:60:GLU:CD	70:Z:20:ARG:HH22	2.22	0.48
51:F:123:LEU:HD23	51:F:159:THR:HG21	1.95	0.48
57:L:35:ILE:HG22	57:L:37:THR:HG22	1.96	0.48
1:1:299:G:C8	38:AJ:30:GLY:HA3	2.48	0.48
1:1:2161:A:H5''	5:j:7:ASN:OD1	2.14	0.48
27:8:46:TYR:CD1	37:AI:75:TYR:HB3	2.48	0.48
46:A:865:U:OP1	59:O:107:LYS:HD3	2.12	0.48
46:A:904:A:H2'	46:A:905:C:H6	1.78	0.48
50:E:23:ASN:O	50:E:27:THR:HG23	2.14	0.48
51:F:148:ARG:NH2	53:H:201:GLN:OE1	2.46	0.48
55:J:11:ARG:O	82:J:302:HOH:O	2.20	0.48
61:Q:83:MET:O	61:Q:116:LEU:N	2.45	0.48
62:R:68:VAL:HG11	62:R:80:ILE:HD11	1.96	0.48
1:1:308:A:H1'	1:1:2200:A:N3	2.29	0.48
1:1:541:U:N3	1:1:543:C:O2'	2.46	0.48
1:1:2285:G:O2'	1:1:2288:U:OP2	2.27	0.48
15:t:169:TYR:CD2	30:AB:132:LYS:HG3	2.49	0.48
21:z:67:LYS:HE2	21:z:71:ARG:HH22	1.78	0.48
35:AG:68:TRP:O	35:AG:86[B]:LYS:HG2	2.13	0.48
46:A:469:A:H5''	56:K:10:LYS:HG3	1.95	0.48
51:F:181:VAL:HG11	51:F:225:VAL:HG13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:J:196:ALA:O	55:J:200:ARG:HG3	2.14	0.48
60:P:11:VAL:HG12	60:P:13:ARG:HG3	1.96	0.48
1:1:892:A:H5'	5:j:183:GLY:HA2	1.95	0.48
1:1:907:C:OP1	5:j:14:SER:OG	2.31	0.48
1:1:1029:U:H2'	1:1:1030:U:C6	2.49	0.48
1:1:1116:A:H2'	1:1:1117:U:H6	1.79	0.48
1:1:2370:C:O2'	6:k:266:ARG:NH2	2.47	0.48
8:m:15:ARG:NH1	82:m:301:HOH:O	2.41	0.48
37:AI:62:GLN:O	37:AI:66:VAL:HG23	2.13	0.48
46:A:361:G:N3	82:A:1953:HOH:O	2.35	0.48
46:A:415:A:H4'	46:A:416:G:O5'	2.13	0.48
46:A:1458:C:OP1	52:G:102:ARG:NH1	2.43	0.48
46:A:1489:G:N2	46:A:1492:A:OP2	2.46	0.48
46:A:1636:C:H2'	46:A:1637:U:C6	2.48	0.48
57:L:38:ARG:O	57:L:42:VAL:HG23	2.14	0.48
57:L:52:LYS:HG3	57:L:54:TYR:HD2	1.79	0.48
65:U:57:ARG:NH2	65:U:101:ASN:OD1	2.46	0.48
66:V:100:LYS:O	66:V:103:THR:OG1	2.25	0.48
1:1:2785:A:H2'	1:1:2786:G:O4'	2.14	0.48
2:3:113:C:H2'	2:3:114:U:O4'	2.14	0.48
3:4:37:A:H5''	3:4:39:G:O4'	2.13	0.48
9:n:3:GLN:HG2	34:AF:76:LEU:H	1.79	0.48
46:A:260:U:O2'	46:A:261:C:H5'	2.13	0.48
46:A:1149:G:H2'	46:A:1150:G:C8	2.49	0.48
46:A:1156:A:H2'	46:A:1157:G:H8	1.76	0.48
46:A:1742:A:OP1	69:Y:63:GLN:HG2	2.14	0.48
53:H:56:ASN:HB2	53:H:108:VAL:HG12	1.95	0.48
55:J:83:TYR:HB3	55:J:101:VAL:HB	1.96	0.48
69:Y:107:PHE:CE1	69:Y:123:LYS:HB3	2.49	0.48
1:1:3022:U:O2'	26:7:16:GLY:O	2.32	0.48
1:1:3319:U:O2'	55:J:77:ARG:NH1	2.47	0.48
12:q:134:MET:SD	12:q:146:VAL:HG22	2.54	0.48
30:AB:36:GLY:HA3	30:AB:40:HIS:CE1	2.48	0.48
46:A:82:U:H2'	46:A:83:G:O4'	2.13	0.48
46:A:502:U:O2'	46:A:503:A:OP1	2.30	0.48
46:A:1123:A:H2'	46:A:1124:A:C8	2.49	0.48
46:A:1205:C:H2'	46:A:1206:A:C8	2.49	0.48
46:A:1739:U:H2'	46:A:1740:A:C8	2.48	0.48
54:I:150:LEU:HB2	54:I:181:ILE:HG12	1.95	0.48
61:Q:73:PRO:HD2	61:Q:93:VAL:HG23	1.95	0.48
1:1:158:A:H2'	1:1:159:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:173:C:H2'	1:1:174:C:C6	2.49	0.48
1:1:1058:A:O2'	23:2:108:ARG:NH2	2.44	0.48
1:1:1104:U:H2'	1:1:1105:U:C6	2.49	0.48
1:1:1322:A:H2'	1:1:1323:C:O4'	2.14	0.48
1:1:2719:A:H2'	1:1:2720:A:C8	2.49	0.48
1:1:3112:G:N7	6:k:28:ARG:NH2	2.62	0.48
17:v:180:PHE:O	17:v:184:LYS:HG3	2.13	0.48
21:z:134:HIS:CE1	21:z:136:ARG:HB3	2.49	0.48
46:A:1129:U:H2'	46:A:1130:U:C6	2.49	0.48
50:E:21:GLU:OE2	50:E:77:ARG:NE	2.44	0.48
50:E:124:LEU:HD11	50:E:153:TYR:HB3	1.95	0.48
61:Q:94:VAL:HG21	61:Q:116:LEU:HD11	1.95	0.48
1:1:726:G:H5''	20:y:43:PRO:HB2	1.96	0.47
3:4:142:C:H2'	3:4:143:U:C6	2.49	0.47
14:s:82:ARG:HA	14:s:85:LYS:HE2	1.95	0.47
17:v:36:ILE:HG12	17:v:64:ILE:HG13	1.95	0.47
22:0:42:TRP:O	22:0:46:GLN:HG3	2.14	0.47
46:A:160:A:H3'	46:A:161:G:H21	1.79	0.47
46:A:335:G:H3'	58:M:133:LYS:HB2	1.95	0.47
46:A:854:A:H61	46:A:943:U:H5	1.62	0.47
46:A:1551:U:H2'	46:A:1552:C:H6	1.78	0.47
49:D:163:ARG:HD3	49:D:165:ILE:HD11	1.96	0.47
59:O:31:ASP:O	59:O:34:VAL:N	2.46	0.47
61:Q:60:LEU:HD22	61:Q:92:SER:HB3	1.96	0.47
71:b:24:LEU:HD22	71:b:71:LEU:HD22	1.96	0.47
1:1:147:G:OP2	17:v:4:TYR:OH	2.21	0.47
1:1:339:C:OP1	1:1:1376:G:O2'	2.26	0.47
1:1:583:A:H2'	1:1:584:C:C6	2.49	0.47
1:1:772:U:H5	1:1:2691:U:O2	1.97	0.47
1:1:1478:A:H4'	1:1:1479:G:OP2	2.14	0.47
1:1:1762:G:N7	21:z:46:LYS:HE2	2.29	0.47
1:1:2107:U:H2'	1:1:2108:G:C8	2.49	0.47
1:1:2492:U:H5'	11:p:69:ARG:HG3	1.96	0.47
1:1:2603:U:OP1	1:1:2729:U:O2'	2.30	0.47
1:1:2853:C:H2'	1:1:2854:U:C6	2.49	0.47
1:1:2876:U:H2'	1:1:2877:U:C6	2.49	0.47
1:1:3039:C:H3'	21:z:62:ARG:NH2	2.24	0.47
2:3:55:A:H5''	14:s:3:ASP:HA	1.96	0.47
12:q:12:ILE:HD11	12:q:53:ILE:HG13	1.96	0.47
12:q:47:LYS:HB2	16:u:5:VAL:HB	1.97	0.47
25:6:38:ALA:HB3	25:6:59:MET:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:AP:8:ARG:HG2	44:AP:10:THR:HG23	1.95	0.47
46:A:1155:G:C2	46:A:1156:A:C8	3.02	0.47
57:L:10:LYS:HA	57:L:13:GLN:CD	2.39	0.47
66:V:65:THR:HA	66:V:79:ASP:O	2.13	0.47
74:e:19:ARG:HD2	74:e:32:ARG:HD3	1.94	0.47
1:1:1172:C:H4'	18:w:90:PRO:HD3	1.95	0.47
1:1:3166:A:H2'	1:1:3167:G:H8	1.80	0.47
46:A:953:U:OP1	46:A:1018:C:O2'	2.31	0.47
66:V:21:ILE:HD13	66:V:99:VAL:HG21	1.95	0.47
1:1:46:C:H5''	15:t:16:LYS:HG2	1.96	0.47
1:1:2675:A:OP2	8:m:23:ARG:NH2	2.43	0.47
1:1:2919:G:N3	6:k:250:ALA:HB1	2.30	0.47
1:1:2978:A:H2'	1:1:2979:U:O4'	2.14	0.47
1:1:3014:U:OP2	1:1:3064:C:N4	2.43	0.47
1:1:3193:C:H4'	1:1:3194:G:O5'	2.14	0.47
5:j:112:ILE:HG13	45:AQ:79:VAL:HG22	1.95	0.47
7:l:209:VAL:HA	7:l:229:ALA:O	2.14	0.47
37:AI:118:ILE:HG22	37:AI:119:LYS:N	2.29	0.47
46:A:151:G:H2'	46:A:152:G:H8	1.77	0.47
46:A:1566:U:H2'	46:A:1567:C:C6	2.49	0.47
48:C:135:LEU:HD23	48:C:217:LEU:HD23	1.95	0.47
49:D:165:ILE:HB	49:D:192:TYR:HB2	1.97	0.47
49:D:173:ILE:HG21	49:D:180:LYS:HA	1.96	0.47
52:G:57:SER:OG	52:G:167:ARG:NH2	2.47	0.47
53:H:180:THR:HG23	53:H:183:THR:H	1.78	0.47
55:J:172:TYR:HB3	55:J:190:LEU:HD12	1.96	0.47
62:R:53:LEU:HD11	62:R:111:TYR:CD2	2.49	0.47
1:1:85:G:O2'	1:1:97:G:O6	2.28	0.47
1:1:527:G:H2'	1:1:528:A:C8	2.49	0.47
1:1:3110:U:OP1	6:k:274:HIS:ND1	2.47	0.47
1:1:3298:G:N7	82:1:3715:HOH:O	2.35	0.47
10:o:71:ASN:O	23:2:143:THR:OG1	2.29	0.47
18:w:187:ALA:O	18:w:188:GLU:HG3	2.14	0.47
46:A:788:A:C8	68:X:107:SER:HA	2.50	0.47
46:A:1495:U:H2'	46:A:1496:C:C6	2.49	0.47
52:G:222:LYS:HG3	52:G:225:ARG:NH2	2.29	0.47
53:H:22:HIS:HA	53:H:25:ARG:NH1	2.29	0.47
55:J:65:PHE:HA	55:J:187:GLY:O	2.14	0.47
66:V:68:LYS:HE2	66:V:79:ASP:OD1	2.15	0.47
70:Z:88:ALA:O	70:Z:92:VAL:HG23	2.14	0.47
1:1:3070:G:OP1	6:k:349:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:k:112:GLU:O	6:k:116:ARG:HG3	2.13	0.47
16:u:17:ARG:HD2	16:u:61:VAL:HG22	1.95	0.47
17:v:155:VAL:O	17:v:162:ARG:NH2	2.38	0.47
20:y:35:PHE:CZ	20:y:39:ARG:HD2	2.50	0.47
41:AM:20:ASN:ND2	41:AM:42:ARG:O	2.46	0.47
46:A:119:A:H1'	46:A:395:A:C5	2.50	0.47
46:A:122:U:C2'	46:A:123:G:H5''	2.45	0.47
46:A:184:C:H2'	46:A:185:G:O4'	2.14	0.47
46:A:484:G:H2'	46:A:485:G:C8	2.49	0.47
46:A:504:A:O2'	46:A:505:U:OP1	2.32	0.47
46:A:871:U:O2'	60:P:116:VAL:O	2.33	0.47
47:B:88:LYS:HG3	47:B:201:LEU:HD11	1.96	0.47
62:R:12:LYS:HB3	62:R:75:SER:OG	2.15	0.47
1:1:269:G:OP2	17:v:44:ARG:NH2	2.42	0.47
1:1:396:A:O2'	1:1:399:A:OP1	2.28	0.47
1:1:792:U:H2'	1:1:793:U:C6	2.50	0.47
1:1:843:A:H2'	1:1:844:A:C8	2.50	0.47
1:1:1309:G:O2'	1:1:1314:A:N1	2.46	0.47
1:1:1684:U:H2'	1:1:1685:U:C6	2.50	0.47
3:4:58:G:O6	39:AK:63:ARG:NH1	2.47	0.47
5:j:101:ILE:HG13	5:j:165:VAL:HG22	1.97	0.47
6:k:106:TRP:HB2	6:k:133:TYR:CE1	2.50	0.47
7:l:303:ALA:HB2	20:y:39:ARG:HH12	1.80	0.47
10:o:52:GLU:OE2	10:o:184:HIS:NE2	2.47	0.47
13:r:50:ILE:HD13	13:r:149:ILE:HG13	1.97	0.47
14:s:136:ALA:HA	14:s:148:ILE:HD11	1.97	0.47
40:AL:24:ILE:HB	40:AL:44:LYS:HB2	1.96	0.47
46:A:605:G:H5'	46:A:611:G:N2	2.30	0.47
46:A:736:G:H2'	46:A:737:A:C8	2.50	0.47
46:A:869:A:H62	46:A:913:U:H3	1.63	0.47
46:A:953:U:H2'	46:A:954:C:O4'	2.15	0.47
50:E:105:ALA:O	50:E:109:LYS:HG2	2.14	0.47
50:E:196:ASN:O	50:E:201:ARG:NH1	2.48	0.47
53:H:27:PHE:CE1	53:H:36:VAL:HG21	2.50	0.47
53:H:64:LYS:HB2	53:H:97:VAL:HG21	1.96	0.47
57:L:59:PHE:CZ	57:L:62:GLN:HA	2.50	0.47
61:Q:81:ARG:HB2	61:Q:117:GLY:HA3	1.96	0.47
68:X:111:MET:SD	68:X:115:GLU:HG2	2.54	0.47
71:b:53:LEU:HD22	71:b:64:LEU:HD11	1.97	0.47
1:1:314:U:H2'	1:1:315:C:C6	2.50	0.47
1:1:412:G:OP1	19:x:62:ARG:NH1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1762:G:O2'	1:1:1763:C:OP1	2.29	0.47
16:u:19:VAL:HG11	16:u:55:ILE:HD12	1.97	0.47
46:A:250:U:OP1	51:F:133:LYS:NZ	2.41	0.47
46:A:561:U:H4'	75:f:17:GLN:OE1	2.15	0.47
46:A:1516:C:H2'	46:A:1517:C:C6	2.49	0.47
46:A:1770:C:O2'	82:A:1910:HOH:O	2.16	0.47
63:S:71:PHE:CE2	63:S:73:LEU:HB3	2.49	0.47
6:k:122:TRP:CE2	6:k:127:LYS:HE3	2.50	0.47
15:t:138:PHE:HE1	37:AI:120:ALA:HB2	1.79	0.47
21:z:67:LYS:HE2	21:z:71:ARG:HH12	1.79	0.47
24:5:29:ASP:OD1	24:5:31[A]:GLU:HG3	2.15	0.47
46:A:1573:A:H2'	46:A:1574:A:O4'	2.14	0.47
46:A:1784:A:N6	71:b:84:VAL:HB	2.29	0.47
57:L:15:LEU:O	57:L:19:GLY:HA2	2.15	0.47
59:O:102:LEU:HD11	59:O:112:LYS:HA	1.96	0.47
1:1:619:A:H2'	1:1:620:A:N7	2.30	0.47
1:1:859:C:H2'	1:1:860:G:O4'	2.15	0.47
1:1:1552:C:H2'	1:1:2147:G:N2	2.30	0.47
1:1:2385:C:H2'	1:1:2386:U:C6	2.50	0.47
11:p:160:PRO:HB2	11:p:162:GLU:OE1	2.15	0.47
16:u:124:THR:HA	18:w:186:THR:HG21	1.97	0.47
46:A:988:A:H2'	46:A:990:A:C8	2.50	0.47
46:A:1168:A:O2'	46:A:1169:A:OP1	2.30	0.47
46:A:1375:C:OP2	63:S:45:ARG:HG3	2.15	0.47
46:A:1469:A:N3	46:A:1594:G:O2'	2.36	0.47
46:A:1757:U:H2'	46:A:1758:U:C6	2.50	0.47
54:I:69:VAL:HG12	54:I:72:ARG:NH2	2.30	0.47
59:O:5:HIS:HB2	59:O:121:ARG:HH21	1.80	0.47
62:R:28:ILE:HA	62:R:64:ILE:O	2.14	0.47
64:T:6:GLN:OE1	64:T:6:GLN:N	2.48	0.47
1:1:730:A:H8	1:1:733:A:N6	2.10	0.46
1:1:757:A:H2'	1:1:758:U:C6	2.51	0.46
1:1:2126:U:H2'	1:1:2127:A:C5	2.50	0.46
3:4:155:G:H5'	11:p:186:ARG:HD2	1.97	0.46
23:2:40:VAL:HB	23:2:96:VAL:HG13	1.96	0.46
46:A:327:G:H2'	46:A:328:G:H8	1.80	0.46
46:A:366:U:H2'	46:A:367:A:O4'	2.15	0.46
46:A:1396:A:H2'	46:A:1397:A:C8	2.50	0.46
47:B:131:GLN:O	47:B:135:GLU:HG3	2.16	0.46
50:E:41:ARG:HA	66:V:109:PRO:HB3	1.97	0.46
52:G:51:VAL:HG21	52:G:130:ILE:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:R:28:ILE:HG22	62:R:35:ILE:HG21	1.97	0.46
1:1:437:G:H1	1:1:620:A:N6	2.13	0.46
1:1:623:A:H2'	1:1:624:U:C6	2.49	0.46
1:1:1007:A:H2'	1:1:1008:A:C8	2.50	0.46
1:1:1045:C:H2'	1:1:1046:U:C6	2.51	0.46
1:1:1943:G:O2'	1:1:1944:G:OP1	2.21	0.46
6:k:217:VAL:HG11	6:k:328:ILE:HB	1.97	0.46
32:AD:101:ASP:OD1	32:AD:101:ASP:N	2.47	0.46
46:A:180:A:H2'	46:A:181:U:C6	2.50	0.46
46:A:769:U:O2'	46:A:770:C:OP2	2.30	0.46
46:A:871:U:H2'	46:A:872:A:H8	1.78	0.46
46:A:1003:U:OP1	59:O:107:LYS:NZ	2.48	0.46
46:A:1503:A:H8	66:V:57:MET:HE1	1.78	0.46
46:A:1670:U:O2'	46:A:1671:G:O5'	2.28	0.46
49:D:44:LYS:HD3	49:D:44:LYS:HA	1.68	0.46
51:F:147:ILE:HG21	51:F:169:ILE:HG13	1.96	0.46
54:I:33:GLU:HG2	54:I:34:LEU:HD12	1.97	0.46
54:I:135:ARG:HB3	68:X:51:GLU:OE2	2.14	0.46
1:1:2546:U:H5'	1:1:2547:G:O4'	2.16	0.46
1:1:3088:G:H4'	12:q:69:ARG:NH1	2.31	0.46
17:v:27:CYS:HB2	17:v:122:ASN:ND2	2.30	0.46
39:AK:52:LYS:O	39:AK:56:ARG:HG3	2.15	0.46
40:AL:8:ILE:HG23	40:AL:65:LEU:HD12	1.98	0.46
46:A:160:A:H2'	46:A:161:G:N3	2.30	0.46
46:A:736:G:H2'	46:A:737:A:H8	1.80	0.46
46:A:1316:A:H61	50:E:162:GLY:HA3	1.80	0.46
52:G:33:VAL:HG21	62:R:48:TYR:CD2	2.50	0.46
53:H:136:LYS:NZ	53:H:174:LYS:O	2.39	0.46
53:H:161:GLU:HA	53:H:170:THR:HA	1.96	0.46
61:Q:96:VAL:HB	61:Q:120:SER:OG	2.15	0.46
1:1:624:U:H2'	1:1:625:C:C6	2.50	0.46
1:1:833:A:OP2	45:AQ:4:ARG:NH1	2.48	0.46
3:4:63:G:H22	3:4:97:A:H2	1.62	0.46
8:m:286:VAL:HG13	13:r:206:LEU:HD22	1.98	0.46
22:0:2:SER:O	22:0:104:GLU:HG2	2.15	0.46
22:0:8:GLN:HB2	22:0:64:ILE:HD11	1.98	0.46
25:6:70:ARG:HG2	25:6:71:LYS:HG3	1.97	0.46
35:AG:42:LYS:HA	35:AG:45:LEU:HG	1.97	0.46
46:A:1555:C:H4'	46:A:1556:A:O5'	2.15	0.46
46:A:1561:G:H5''	46:A:1562:G:OP1	2.15	0.46
1:1:730:A:H2'	1:1:731:U:H2'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:757:A:C2	1:1:767:A:H1'	2.51	0.46
8:m:232:GLU:O	8:m:236:VAL:HG23	2.16	0.46
12:q:45:PHE:CE1	12:q:55:ILE:HG12	2.51	0.46
46:A:1335:U:O2'	46:A:1336:G:OP1	2.30	0.46
70:Z:104:SER:OG	70:Z:107:GLN:HG2	2.16	0.46
1:1:943:G:H2'	1:1:944:C:C6	2.51	0.46
10:o:39:ARG:HA	10:o:42:ILE:HG12	1.97	0.46
13:r:73:ASN:O	13:r:77:THR:HG23	2.15	0.46
22:0:164:GLN:HG2	22:0:166:THR:H	1.81	0.46
33:AE:5:ASP:OD2	33:AE:87:LYS:NZ	2.49	0.46
46:A:261:C:O2'	46:A:262:G:H5'	2.15	0.46
73:d:38:ARG:O	73:d:40:ILE:HG13	2.16	0.46
1:1:79:G:H2'	1:1:80:C:H6	1.81	0.46
1:1:806:A:N3	82:1:3701:HOH:O	2.36	0.46
1:1:989:G:N3	1:1:2609:A:H2'	2.31	0.46
1:1:2126:U:H2'	1:1:2127:A:C8	2.51	0.46
1:1:3196:U:H2'	1:1:3197:G:H8	1.80	0.46
6:k:217:VAL:HG13	6:k:336:VAL:HG13	1.98	0.46
6:k:256:HIS:HA	6:k:257:PRO:C	2.41	0.46
51:F:121:TYR:CD1	51:F:161:LYS:HE3	2.50	0.46
73:d:11:LYS:HA	73:d:52:ASP:O	2.16	0.46
1:1:169:G:N1	1:1:249:G:H1'	2.31	0.46
1:1:1496:G:H2'	1:1:1497:U:O4'	2.15	0.46
1:1:2251:G:N2	1:1:2289:G:H2'	2.31	0.46
1:1:2345:A:H2'	1:1:2346:A:C8	2.51	0.46
1:1:2919:G:N2	82:1:3761:HOH:O	2.38	0.46
21:z:161:ALA:O	21:z:165:ARG:HG3	2.15	0.46
25:6:135:VAL:HG11	26:7:26:SER:HB3	1.98	0.46
46:A:583:A:OP1	75:f:15:LYS:NZ	2.48	0.46
46:A:883:A:N3	46:A:884:G:H1'	2.30	0.46
49:D:135:ARG:HB3	49:D:216:THR:HB	1.97	0.46
51:F:57:ASN:HB3	82:F:302:HOH:O	2.15	0.46
51:F:58:GLY:HA2	51:F:61:VAL:HG12	1.98	0.46
1:1:849:G:OP2	45:AQ:2:THR:HG21	2.16	0.46
1:1:1347:U:H5	1:1:1350:G:OP1	1.99	0.46
1:1:2130:A:H2'	1:1:2131:U:C6	2.50	0.46
1:1:2385:C:H2'	1:1:2386:U:H6	1.80	0.46
1:1:3161:U:H2'	1:1:3162:U:C6	2.51	0.46
6:k:216:ASP:OD2	6:k:339:ARG:NH2	2.28	0.46
11:p:150:LYS:N	11:p:201:LEU:O	2.46	0.46
17:v:113:LEU:HB2	17:v:134:LEU:HD23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:w:62:ALA:HA	18:w:71:PRO:HD2	1.97	0.46
46:A:1085:G:O3'	82:A:1913:HOH:O	2.21	0.46
56:K:36:LEU:HA	56:K:126:ARG:NH2	2.31	0.46
62:R:66:VAL:HG21	62:R:80:ILE:HG23	1.97	0.46
1:1:2545:C:O2'	1:1:2546:U:OP1	2.32	0.46
1:1:2916:U:H4'	82:k:514:HOH:O	2.16	0.46
1:1:3199:G:N2	1:1:3218:U:O2	2.38	0.46
9:n:91:ASN:O	9:n:148:GLU:HG2	2.16	0.46
22:0:3:ARG:NH1	22:0:104:GLU:OE2	2.49	0.46
46:A:642:C:H2'	46:A:643:U:C6	2.52	0.46
46:A:767:G:O2'	46:A:768:C:H6	1.98	0.46
46:A:1029:U:H2'	46:A:1030:C:C6	2.50	0.46
46:A:1127:A:H5''	71:b:2:PRO:HB3	1.99	0.46
46:A:1335:U:H2'	46:A:1336:G:H8	1.75	0.46
46:A:1393:U:H2'	46:A:1394:G:C8	2.51	0.46
54:I:70:GLN:NE2	54:I:88:PHE:HB2	2.30	0.46
55:J:199:LEU:O	55:J:203:THR:HG23	2.15	0.46
71:b:41:ILE:HG12	71:b:68:TYR:CD2	2.51	0.46
73:d:14:LYS:HB3	73:d:29:ARG:HB3	1.98	0.46
75:f:43:ARG:HD3	75:f:56:MET:HE1	1.98	0.46
1:1:48:A:OP1	17:v:191:TRP:NE1	2.46	0.45
1:1:498:C:H2'	1:1:499:G:C8	2.51	0.45
3:4:156:U:O2'	3:4:157:U:OP1	2.34	0.45
9:n:26:PRO:HG2	9:n:28[A]:LYS:NZ	2.31	0.45
21:z:134:HIS:CE1	21:z:136:ARG:HE	2.19	0.45
46:A:151:G:O6	70:Z:128:ARG:NH2	2.48	0.45
46:A:883:A:N1	46:A:896:U:O2'	2.40	0.45
46:A:974:U:H2'	46:A:975:C:C6	2.50	0.45
48:C:33:LYS:O	48:C:232:HIS:HE1	1.99	0.45
55:J:39:GLY:O	55:J:61:GLU:HG3	2.16	0.45
60:P:42:LYS:NZ	60:P:61:ASP:OD2	2.38	0.45
1:1:1584:A:C6	41:AM:4:GLN:HB3	2.50	0.45
1:1:2486:U:H2'	1:1:2487:U:C6	2.52	0.45
9:n:28[B]:LYS:HB3	9:n:28[B]:LYS:HE3	1.79	0.45
12:q:41:ILE:HG22	12:q:43:VAL:HG13	1.98	0.45
17:v:45:PRO:O	17:v:49:ARG:HG3	2.16	0.45
46:A:71:A:OP2	53:H:164:LYS:HE2	2.16	0.45
47:B:30:GLN:NE2	47:B:151:SER:O	2.49	0.45
50:E:43:THR:CG2	50:E:46:LYS:HB3	2.46	0.45
50:E:54:SER:HA	50:E:92:VAL:HG12	1.97	0.45
59:O:46:THR:OG1	59:O:49:GLN:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:R:30:ILE:HG12	62:R:35:ILE:HG22	1.97	0.45
1:1:11:A:H2'	1:1:12:A:C8	2.51	0.45
1:1:1909:A:N3	1:1:2098:A:H2'	2.31	0.45
1:1:2492:U:OP2	1:1:2558:G:N2	2.49	0.45
1:1:2627:U:H4'	1:1:2628:A:O4'	2.16	0.45
1:1:3245:A:O2'	1:1:3246:C:H6	1.98	0.45
13:r:42:THR:O	13:r:139:ARG:NH2	2.48	0.45
13:r:150:GLU:O	13:r:154:ARG:HG3	2.15	0.45
30:AB:94:SER:HB3	30:AB:121:VAL:HG13	1.98	0.45
46:A:78:A:H2	53:H:174:LYS:HG3	1.82	0.45
46:A:78:A:H2'	46:A:79:C:H6	1.81	0.45
46:A:1423:U:O2'	50:E:182:VAL:HG23	2.17	0.45
47:B:43:ASP:OD1	47:B:44:GLY:N	2.50	0.45
49:D:133:PRO:HB2	49:D:217:TYR:CE2	2.50	0.45
53:H:16:ILE:HD13	53:H:45:PHE:HZ	1.81	0.45
62:R:19:ALA:HB2	62:R:66:VAL:HG12	1.98	0.45
1:1:126:G:H2'	1:1:127:G:H8	1.81	0.45
1:1:172:C:HO2'	1:1:173:C:P	2.37	0.45
1:1:411:U:H2'	1:1:412:G:H8	1.81	0.45
1:1:1616:U:H2'	1:1:1617:A:C8	2.51	0.45
1:1:2919:G:H8	82:1:3972:HOH:O	1.97	0.45
3:4:156:U:H2'	3:4:157:U:C6	2.52	0.45
20:y:31[A]:LYS:HE3	20:y:31[A]:LYS:HB2	1.75	0.45
23:2:102:ARG:NE	23:2:102:ARG:HA	2.31	0.45
46:A:1396:A:HO2'	46:A:1397:A:P	2.38	0.45
48:C:34:ALA:O	48:C:41:ARG:NH1	2.49	0.45
61:Q:16:SER:HA	61:Q:21:ASP:HA	1.97	0.45
61:Q:68:GLU:N	61:Q:69:PRO:HD3	2.32	0.45
1:1:2084:A:H2'	1:1:2085:A:C8	2.52	0.45
1:1:2322:U:H2'	1:1:2323:A:C8	2.51	0.45
1:1:2408:A:H2'	1:1:2409:C:C6	2.52	0.45
6:k:148:LEU:HD13	6:k:196:LYS:HD2	1.98	0.45
19:x:4:TYR:CZ	19:x:18:ARG:HG3	2.52	0.45
46:A:1316:A:N6	50:E:162:GLY:HA3	2.31	0.45
46:A:1593:C:H2'	46:A:1594:G:C8	2.52	0.45
63:S:72:LYS:HD2	63:S:72:LYS:HA	1.85	0.45
63:S:75:GLU:O	63:S:79:GLU:HG3	2.17	0.45
1:1:214:G:OP1	28:9:12:ARG:NH1	2.44	0.45
1:1:696:U:H2'	1:1:697:A:O4'	2.17	0.45
1:1:1075:A:C2	8:m:113:LEU:HD22	2.51	0.45
1:1:1921:U:O2'	1:1:1923:G:N7	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2351:A:N3	1:1:2796:G:O2'	2.40	0.45
1:1:2915:G:H2'	1:1:2916:U:O4'	2.17	0.45
1:1:3261:A:H2'	1:1:3262:U:H6	1.80	0.45
2:3:4:U:H2'	2:3:5:G:C8	2.52	0.45
2:3:9:C:OP1	23:2:26:PRO:HB2	2.16	0.45
3:4:9:A:H2'	3:4:10:A:C8	2.50	0.45
7:l:299:VAL:HG21	20:y:133:LYS:HG3	1.98	0.45
8:m:95:TRP:CD1	8:m:158:ARG:HA	2.52	0.45
11:p:65:ILE:O	11:p:69:ARG:HG2	2.17	0.45
20:y:67:ILE:HG12	20:y:81:ILE:HG21	1.98	0.45
46:A:393:U:H2'	46:A:394:G:O4'	2.16	0.45
46:A:878:U:H5'	46:A:879:U:OP2	2.17	0.45
46:A:975:C:H2'	46:A:976:G:O4'	2.17	0.45
46:A:1478:A:O2'	46:A:1479:A:O4'	2.27	0.45
54:I:51:LYS:HG3	54:I:85:HIS:CE1	2.51	0.45
61:Q:26:VAL:HG23	61:Q:27:GLU:OE1	2.16	0.45
66:V:98:THR:O	66:V:102:ILE:HG13	2.17	0.45
1:1:393:U:H2'	1:1:394:G:O4'	2.16	0.45
1:1:1358:C:H2'	1:1:1359:A:C8	2.51	0.45
1:1:2370:C:H1'	6:k:266:ARG:NH2	2.31	0.45
1:1:2523:C:H2'	1:1:2524:C:C6	2.52	0.45
1:1:2587:G:H2'	1:1:2588:C:C6	2.52	0.45
1:1:2686:G:H8	1:1:2723:G:H2'	1.81	0.45
2:3:3:U:H2'	2:3:4:U:H6	1.82	0.45
5:j:32:LEU:HD13	5:j:163:ARG:HD3	1.99	0.45
8:m:187:ALA:O	8:m:189:GLU:N	2.48	0.45
8:m:235:ASP:OD1	8:m:235:ASP:N	2.44	0.45
26:7:45:ASN:O	26:7:49:ILE:HG12	2.17	0.45
34:AF:98:ALA:HB3	34:AF:101:VAL:HG23	1.97	0.45
46:A:728:U:P	54:I:104:LYS:H	2.40	0.45
46:A:1527:G:OP2	64:T:40:ARG:NH2	2.49	0.45
48:C:32:ILE:HA	48:C:96:LEU:HB2	1.98	0.45
62:R:86:LYS:HG2	62:R:116:LEU:HD13	1.97	0.45
5:j:118:GLU:HG3	5:j:126:LEU:HD21	1.99	0.45
8:m:40:HIS:CE1	23:2:69:LYS:HA	2.51	0.45
28:9:106:ILE:HG21	28:9:109:LEU:HD23	1.98	0.45
29:AA:103:GLU:HG3	29:AA:106:GLN:OE1	2.17	0.45
46:A:917:U:OP2	48:C:155:TYR:OH	2.31	0.45
46:A:1317:C:H4'	50:E:204:PRO:HB3	1.98	0.45
56:K:112:GLN:OE1	56:K:153:GLN:NE2	2.33	0.45
1:1:788:G:H2'	1:1:789:C:H6	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1473:A:OP1	1:1:3047:G:O2'	2.29	0.45
1:1:1715:G:N7	21:z:121:HIS:HE1	2.15	0.45
1:1:1903:C:O2	6:k:240:ARG:NH2	2.48	0.45
1:1:2188:G:H4'	76:g:4:A:O2'	2.17	0.45
1:1:2515:G:H1'	1:1:2516:U:O5'	2.17	0.45
1:1:2623:G:H5''	1:1:2624:U:O4'	2.17	0.45
2:3:19:C:H2'	2:3:20:A:H8	1.80	0.45
2:3:45:A:H2'	2:3:46:A:C8	2.52	0.45
7:l:287:VAL:HG11	20:y:31[B]:LYS:HD3	1.98	0.45
21:z:38:ARG:O	21:z:42:ARG:HG3	2.16	0.45
35:AG:49:ILE:HD11	35:AG:71:VAL:HG22	1.99	0.45
46:A:247:U:O2'	82:A:1915:HOH:O	2.21	0.45
46:A:553:A:H2'	46:A:554:A:C8	2.52	0.45
46:A:1083:U:OP1	49:D:154:THR:OG1	2.23	0.45
46:A:1575:G:H5'	46:A:1576:C:OP2	2.17	0.45
46:A:1602:C:H5''	46:A:1603:G:O5'	2.17	0.45
48:C:66:PHE:CE1	60:P:29:SER:HB3	2.52	0.45
48:C:88:VAL:HA	48:C:98:THR:HA	1.97	0.45
54:I:162:LEU:O	54:I:166:GLN:HG3	2.16	0.45
56:K:100:LYS:HB3	56:K:102:GLU:OE1	2.16	0.45
57:L:74:GLU:HA	57:L:77:ARG:HB2	1.98	0.45
1:1:1384:U:OP1	34:AF:105:LYS:NZ	2.43	0.45
1:1:1588:G:OP2	36:AH:37:LYS:NZ	2.37	0.45
1:1:1789:C:OP1	5:j:177:LYS:NZ	2.44	0.45
1:1:2122:A:H1'	1:1:2259:A:N6	2.32	0.45
1:1:2521:C:H2'	1:1:2522:U:H6	1.82	0.45
1:1:3044:C:H2'	1:1:3045:A:O4'	2.17	0.45
27:8:67:ILE:HD12	27:8:121:LYS:HG3	1.99	0.45
45:AQ:13:LYS:NZ	45:AQ:30:GLU:OE2	2.36	0.45
46:A:176:U:O2'	46:A:177:A:OP2	2.34	0.45
46:A:919:C:H1'	71:b:11:ASN:OD1	2.16	0.45
46:A:1306:A:H4'	46:A:1307:A:O5'	2.16	0.45
56:K:63:ASP:OD1	56:K:64:GLU:N	2.50	0.45
63:S:26:LEU:HD11	63:S:62:GLN:HG3	1.99	0.45
1:1:385:A:H2'	1:1:386:A:C8	2.52	0.44
1:1:1050:A:H5''	1:1:2609:A:H61	1.80	0.44
1:1:2520:A:H1'	1:1:2521:C:C5	2.52	0.44
1:1:2919:G:C2	6:k:250:ALA:HB1	2.52	0.44
12:q:114:ILE:HB	12:q:124:ARG:HB2	1.99	0.44
22:0:27:MET:HE2	22:0:27:MET:HB3	1.85	0.44
45:AQ:8:VAL:O	45:AQ:11:THR:OG1	2.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:398:A:H5''	55:J:25:ARG:HA	1.97	0.44
46:A:445:U:H2'	46:A:446:C:O4'	2.17	0.44
46:A:918:A:OP1	71:b:70:LYS:NZ	2.46	0.44
46:A:1259:C:O2	46:A:1413:A:O2'	2.24	0.44
46:A:1414:G:C2'	46:A:1415:G:H5'	2.47	0.44
46:A:1452:G:H2'	46:A:1453:C:C6	2.52	0.44
53:H:137:ARG:O	53:H:141:ILE:HG13	2.16	0.44
57:L:44:LYS:HA	57:L:44:LYS:HD3	1.87	0.44
57:L:52:LYS:HG3	57:L:54:TYR:CE2	2.52	0.44
1:1:511:C:H5''	7:l:344:LYS:HD2	1.99	0.44
1:1:1330:U:H2'	1:1:1331:U:C6	2.53	0.44
1:1:1434:U:H2'	1:1:1435:U:C6	2.53	0.44
1:1:1600:A:H4'	1:1:1831:A:H4'	1.99	0.44
1:1:2270:U:OP1	82:1:3718:HOH:O	2.21	0.44
1:1:2587:G:H2'	1:1:2588:C:H6	1.82	0.44
3:4:106:C:H4'	3:4:107:G:H5''	1.98	0.44
11:p:162:GLU:OE2	17:v:22:LEU:HD13	2.17	0.44
13:r:43:VAL:HG21	13:r:197:VAL:HG13	1.98	0.44
19:x:42:GLU:HG2	19:x:43:LYS:N	2.31	0.44
24:5:12:VAL:HG22	24:5:69:SER:HA	1.99	0.44
28:9:32:SER:HA	28:9:49:PRO:HA	1.99	0.44
39:AK:69:HIS:O	39:AK:73:ARG:HG3	2.17	0.44
42:AN:23:CYS:HB2	42:AN:38:LYS:HD2	1.98	0.44
46:A:350:A:H5''	82:A:2034:HOH:O	2.16	0.44
46:A:590:A:O2'	46:A:594:C:OP1	2.29	0.44
46:A:613:A:O2'	46:A:619:A:N1	2.45	0.44
46:A:891:A:H2'	46:A:892:A:C8	2.52	0.44
46:A:1597:G:H5''	52:G:107:LYS:HD2	2.00	0.44
47:B:157:ASP:OD1	67:W:60:ARG:NH1	2.42	0.44
48:C:35:PRO:HA	48:C:231:LEU:O	2.16	0.44
50:E:159:ILE:HG22	50:E:169:ILE:HD11	1.99	0.44
51:F:100:ARG:HG2	51:F:102:VAL:HG13	1.98	0.44
59:O:87:ASP:OD1	59:O:87:ASP:N	2.50	0.44
61:Q:50:ASP:O	61:Q:53:PRO:HD2	2.17	0.44
67:W:55:LEU:HD11	67:W:69:LEU:CD2	2.48	0.44
69:Y:132:LEU:HA	69:Y:132:LEU:HD12	1.70	0.44
1:1:163:A:H2'	1:1:164:U:O4'	2.17	0.44
1:1:516:U:OP1	7:l:352:PRO:HD2	2.16	0.44
1:1:538:G:H2'	1:1:539:G:C8	2.53	0.44
1:1:844:A:N6	1:1:845:C:O2	2.50	0.44
1:1:1172:C:H2'	1:1:1173:G:N2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3101:A:H2'	1:1:3102:A:H5''	1.99	0.44
3:4:52:A:OP1	41:AM:21[B]:ARG:NH1	2.46	0.44
8:m:83:LEU:HD13	8:m:88:ILE:HD12	1.99	0.44
9:n:170:ARG:HB3	9:n:172:HIS:CE1	2.53	0.44
12:q:129:HIS:H	12:q:157:ASN:HD21	1.64	0.44
14:s:94[B]:LYS:HE3	14:s:94[B]:LYS:HB3	1.68	0.44
46:A:399:A:H4'	51:F:3:ARG:HD2	1.98	0.44
46:A:607:U:H2'	82:A:2082:HOH:O	2.17	0.44
46:A:1064:U:H2'	46:A:1065:U:C6	2.52	0.44
46:A:1303:G:H2'	46:A:1304:A:C8	2.52	0.44
46:A:1604:U:H2'	46:A:1605:C:C6	2.53	0.44
49:D:40:VAL:HG21	49:D:63:ILE:HG23	1.99	0.44
50:E:133:LYS:HB3	50:E:190:MET:HG2	2.00	0.44
55:J:77:ARG:HG2	55:J:78:ILE:N	2.31	0.44
65:U:35:ASP:OD1	65:U:35:ASP:N	2.41	0.44
71:b:59:TYR:HB2	71:b:62:TYR:HB2	1.99	0.44
1:1:252:U:H5'	1:1:253:A:C8	2.52	0.44
1:1:631:U:H2'	1:1:632:C:C6	2.53	0.44
1:1:1069:U:H2'	1:1:1070:U:C6	2.52	0.44
1:1:2790:U:C5'	31:AC:1:MET:HA	2.47	0.44
25:6:38:ALA:O	25:6:58:VAL:HG13	2.17	0.44
29:AA:9:LYS:HE2	29:AA:83:THR:O	2.18	0.44
52:G:146:SER:HG	52:G:157:ARG:NH2	2.15	0.44
56:K:32:GLY:HA3	75:f:40:TYR:CG	2.51	0.44
69:Y:92:CYS:HG	69:Y:136:TRP:CD1	2.36	0.44
71:b:100:ARG:HG2	71:b:101:LYS:HD3	2.00	0.44
1:1:612:U:H2'	1:1:613:U:C6	2.52	0.44
1:1:912:G:H5'	1:1:913:A:OP1	2.18	0.44
1:1:1663:A:H2'	1:1:1664:G:H8	1.81	0.44
1:1:1755:U:H2'	1:1:1756:A:H5''	1.99	0.44
1:1:2557:G:C6	27:8:24:LEU:HD21	2.53	0.44
1:1:3261:A:H2'	1:1:3262:U:C6	2.52	0.44
3:4:81:A:H2'	3:4:82:U:C6	2.52	0.44
5:j:227:ARG:HB2	5:j:239:ALA:HB2	2.00	0.44
9:n:39:LEU:HB3	9:n:83:VAL:CG1	2.47	0.44
11:p:114:ALA:HA	11:p:117:ILE:HG22	2.00	0.44
46:A:644:U:H2'	46:A:645:G:H8	1.82	0.44
46:A:728:U:OP2	54:I:104:LYS:N	2.48	0.44
46:A:1062:C:H2'	46:A:1063:C:H6	1.82	0.44
46:A:1105:U:H2'	46:A:1106:C:C6	2.53	0.44
56:K:92:LYS:C	56:K:94:ASP:H	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:T:134:ARG:HB2	64:T:136:GLN:NE2	2.27	0.44
65:U:114:LEU:HD23	65:U:122:ARG:HD3	1.98	0.44
1:1:1163:U:H2'	1:1:1164:U:O4'	2.17	0.44
1:1:1303:G:H4'	1:1:1304:A:O5'	2.16	0.44
1:1:1757:A:O2'	1:1:1759:U:OP2	2.31	0.44
1:1:1827:U:O2'	3:4:114:G:OP1	2.22	0.44
3:4:39:G:H1'	3:4:104:A:N6	2.33	0.44
5:j:118:GLU:OE2	5:j:156:LYS:NZ	2.50	0.44
7:l:32:ARG:HG3	7:l:121:TYR:CE2	2.49	0.44
19:x:177:ALA:O	19:x:181:ARG:HG3	2.18	0.44
22:0:10:ILE:HG12	22:0:26:ARG:HG3	1.99	0.44
46:A:327:G:H2'	46:A:328:G:C8	2.53	0.44
46:A:585:C:H5'	75:f:24:GLN:OE1	2.17	0.44
48:C:115:ARG:HA	48:C:115:ARG:HD3	1.78	0.44
48:C:120:LEU:HD12	48:C:142:PHE:CE2	2.52	0.44
75:f:13:LYS:O	75:f:17:GLN:HG2	2.16	0.44
1:1:838:G:O6	82:1:3717:HOH:O	2.21	0.44
1:1:1093:G:H2'	1:1:1093:G:N3	2.33	0.44
1:1:1113:G:OP1	31:AC:4:SER:HB2	2.17	0.44
1:1:1556:G:O2'	1:1:1557:U:H5'	2.18	0.44
1:1:3005:A:H2'	1:1:3006:C:H6	1.83	0.44
1:1:3110:U:OP2	6:k:30:LYS:HG3	2.18	0.44
2:3:27:A:H2'	2:3:28:C:C6	2.53	0.44
14:s:87:LYS:HB2	14:s:87:LYS:HE2	1.76	0.44
20:y:64:VAL:HG22	20:y:96:PHE:CE1	2.53	0.44
27:8:50:SER:HB2	37:AI:66:VAL:HG11	1.99	0.44
29:AA:119:GLU:O	29:AA:123:GLN:HG2	2.17	0.44
46:A:1248:G:H2'	46:A:1249:G:O4'	2.17	0.44
46:A:1300:U:O2'	46:A:1301:G:H8	2.01	0.44
63:S:89:SER:C	63:S:91:LEU:N	2.76	0.44
65:U:22:LEU:HD21	65:U:28:LEU:HD22	2.00	0.44
1:1:28:C:H4'	1:1:61:A:H4'	2.00	0.44
1:1:1911:A:H2'	1:1:1912:U:C6	2.53	0.44
1:1:1945:A:H2'	1:1:1946:U:C6	2.52	0.44
7:l:17:GLY:C	7:l:19:SER:H	2.26	0.44
12:q:94:TYR:HA	12:q:177:ASP:OD1	2.17	0.44
32:AD:43:LEU:HD23	32:AD:94:ILE:HD12	1.99	0.44
33:AE:52:PRO:O	33:AE:56:ILE:HG12	2.18	0.44
46:A:29:U:H2'	46:A:30:G:C8	2.53	0.44
46:A:261:C:O2'	46:A:262:G:N2	2.35	0.44
46:A:302:U:H2'	46:A:303:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:844:A:N3	59:O:73:ARG:NH1	2.65	0.44
46:A:1276:G:H1	46:A:1309:G:H1	1.66	0.44
51:F:19:MET:HE2	51:F:108:LYS:HG2	1.99	0.44
53:H:135:PRO:HB2	53:H:141:ILE:HG12	2.00	0.44
60:P:73:ALA:HB2	60:P:106:ARG:HB2	1.99	0.44
62:R:9:PHE:HA	62:R:17:ALA:O	2.18	0.44
62:R:46:LYS:HA	62:R:46:LYS:HD2	1.84	0.44
1:1:830:U:H2'	1:1:831:G:O4'	2.18	0.44
1:1:1313:A:O2'	1:1:1314:A:H3'	2.18	0.44
1:1:2394:U:H2'	1:1:2395:U:C6	2.52	0.44
1:1:3136:C:H2'	1:1:3137:A:C8	2.53	0.44
2:3:48:C:P	8:m:94:ASN:HD21	2.41	0.44
6:k:62:ARG:HG2	6:k:65:SER:HB2	1.99	0.44
8:m:41:LYS:HA	8:m:41:LYS:HD3	1.84	0.44
15:t:76:THR:HG22	15:t:101:ARG:HB3	2.00	0.44
18:w:189:SER:O	18:w:193:GLN:HG2	2.17	0.44
46:A:260:U:C2'	46:A:261:C:H5'	2.48	0.44
46:A:445:U:O2'	51:F:27:TYR:O	2.36	0.44
46:A:1089:U:OP1	69:Y:14:LYS:NZ	2.51	0.44
46:A:1334:G:H2'	46:A:1335:U:C6	2.53	0.44
1:1:591:C:O2	10:o:24:ARG:NH1	2.50	0.43
1:1:638:U:OP1	30:AB:21:ARG:NH1	2.46	0.43
1:1:1153:G:H2'	1:1:1154:A:O4'	2.17	0.43
1:1:1493:C:H2'	1:1:1494:A:H8	1.82	0.43
1:1:2354:G:H2'	1:1:2355:G:C8	2.53	0.43
1:1:2913:A:H8	1:1:2913:A:OP2	2.01	0.43
1:1:3323:U:H2'	1:1:3324:A:H8	1.83	0.43
5:j:20:THR:HA	5:j:23:ARG:HG3	1.99	0.43
46:A:907:G:O2'	46:A:908:A:H5'	2.18	0.43
47:B:200:ASP:O	47:B:203:PHE:HB2	2.18	0.43
48:C:149:GLN:HE21	48:C:151:LYS:HG3	1.83	0.43
50:E:158:MET:HE2	50:E:158:MET:HB2	1.83	0.43
51:F:123:LEU:HD13	51:F:237:VAL:HG13	2.00	0.43
53:H:2:LYS:HE3	53:H:2:LYS:HB2	1.77	0.43
1:1:364:G:OP1	7:l:61:THR:HG23	2.17	0.43
1:1:638:U:H2'	1:1:639:C:C6	2.53	0.43
1:1:1605:C:OP1	27:8:109:TYR:OH	2.32	0.43
1:1:2405:U:H2'	1:1:2406:U:C6	2.53	0.43
9:n:39:LEU:HD11	9:n:53:TYR:HB2	2.00	0.43
38:AJ:66:LYS:HE2	38:AJ:70:LYS:HD2	2.00	0.43
46:A:103:A:H4'	46:A:105:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:394:G:N7	82:A:1957:HOH:O	2.36	0.43
46:A:1719:A:H2'	46:A:1720:C:H6	1.82	0.43
1:1:431:A:H2'	1:1:432:G:C8	2.53	0.43
1:1:539:G:H2'	1:1:540:C:C6	2.53	0.43
1:1:561:U:H2'	1:1:562:C:C6	2.54	0.43
1:1:981:U:H2'	1:1:982:U:H6	1.82	0.43
1:1:2077:A:O2'	1:1:2078:A:H5'	2.18	0.43
1:1:2339:A:H2'	1:1:2340:C:C6	2.54	0.43
1:1:2854:U:H2'	1:1:2855:U:C6	2.53	0.43
1:1:3259:A:H2'	1:1:3260:A:O4'	2.18	0.43
5:j:68:LYS:HE3	5:j:68:LYS:HB2	1.92	0.43
6:k:260:VAL:HG11	6:k:266:ARG:HH11	1.83	0.43
8:m:127:GLY:O	8:m:195:LEU:HD23	2.18	0.43
8:m:179:ARG:HA	8:m:179:ARG:HD3	1.79	0.43
20:y:102:ALA:HA	20:y:122:ILE:O	2.18	0.43
27:8:103:TYR:O	27:8:138:ARG:NH2	2.46	0.43
46:A:4:C:H5	46:A:20:G:N1	2.10	0.43
46:A:922:C:O2'	82:A:1916:HOH:O	2.21	0.43
48:C:136:ARG:HG3	48:C:218:LEU:HD11	1.99	0.43
54:I:20:ALA:O	54:I:24:LEU:HD23	2.19	0.43
55:J:107:THR:OG1	55:J:108:PRO:HD3	2.19	0.43
62:R:5:SER:HA	62:R:21:VAL:O	2.19	0.43
69:Y:68:ILE:HD12	75:f:6:GLY:HA3	1.99	0.43
1:1:109:G:OP2	15:t:73:ARG:NH2	2.47	0.43
1:1:200:A:H2'	1:1:201:G:H8	1.84	0.43
1:1:565:A:H2'	1:1:566:C:O4'	2.18	0.43
1:1:907:C:H42	5:j:3:ARG:HD3	1.84	0.43
1:1:1416:C:C5	7:l:190:ALA:HB2	2.53	0.43
1:1:1755:U:H3	1:1:1762:G:H1	1.65	0.43
1:1:1779:U:H2'	1:1:1780:A:C8	2.53	0.43
1:1:2384:C:H2'	1:1:2385:C:H6	1.82	0.43
1:1:3358:U:H2'	1:1:3359:U:C6	2.54	0.43
6:k:117:ARG:HD2	6:k:176:ALA:O	2.19	0.43
7:l:35:LEU:HD13	7:l:121:TYR:CD2	2.53	0.43
8:m:290:ILE:HG13	13:r:206:LEU:HD21	2.01	0.43
13:r:202:ARG:NH1	13:r:216:TYR:OH	2.51	0.43
14:s:63:GLU:O	14:s:65:ILE:HG12	2.18	0.43
14:s:132:GLY:HA2	14:s:154:THR:HG21	1.99	0.43
17:v:73:ARG:HG2	17:v:75:VAL:HG13	1.99	0.43
17:v:96:LYS:NZ	17:v:104:GLU:OE2	2.45	0.43
46:A:872:A:H1'	60:P:117:PRO:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:1317:C:O2'	50:E:163:GLN:HB3	2.17	0.43
46:A:1455:A:H2'	46:A:1456:C:C6	2.54	0.43
68:X:14:ILE:HG12	68:X:25:VAL:HG11	2.00	0.43
1:1:394:G:N1	1:1:397:A:OP2	2.51	0.43
1:1:429:U:H2'	1:1:430:G:H8	1.83	0.43
1:1:498:C:H2'	1:1:499:G:H8	1.84	0.43
1:1:547:U:H2'	1:1:548:G:C8	2.53	0.43
1:1:708:A:H2'	1:1:709:A:C8	2.54	0.43
1:1:2086:C:H1'	1:1:3309:A:H8	1.77	0.43
1:1:2734:A:H2'	1:1:2735:U:C6	2.54	0.43
2:3:4:U:H2'	2:3:5:G:H8	1.82	0.43
13:r:19:LYS:HE2	13:r:19:LYS:HB3	1.65	0.43
16:u:62:LEU:HD22	16:u:65:LEU:HB2	2.00	0.43
37:AI:29:ALA:O	37:AI:33:VAL:HG23	2.19	0.43
46:A:685:C:H2'	46:A:686:G:O4'	2.19	0.43
46:A:1141:C:H2'	46:A:1142:A:C8	2.53	0.43
46:A:1494:G:H2'	46:A:1495:U:C6	2.54	0.43
47:B:201:LEU:O	47:B:202:TYR:HB2	2.18	0.43
1:1:762:U:H4'	1:1:763:U:O4'	2.19	0.43
1:1:1552:C:H2'	1:1:2147:G:H22	1.84	0.43
1:1:2393:C:H5''	5:j:207:VAL:HG12	2.01	0.43
1:1:2485:U:H2'	1:1:2486:U:C6	2.52	0.43
1:1:2493:A:H5''	17:v:28:TRP:CD1	2.54	0.43
1:1:2738:U:H2'	1:1:2739:U:C6	2.53	0.43
1:1:3247:A:H2'	1:1:3248:U:C6	2.54	0.43
15:t:60:ALA:HB3	15:t:65:TYR:O	2.19	0.43
24:5:19:VAL:C	24:5:21:ALA:H	2.26	0.43
30:AB:35:ALA:O	30:AB:41:HIS:ND1	2.46	0.43
34:AF:22:HIS:CE1	34:AF:25:ARG:HE	2.37	0.43
46:A:1311:A:O3'	50:E:157:PHE:HE1	2.02	0.43
46:A:1452:G:O2'	46:A:1589:C:OP1	2.36	0.43
47:B:164:ASN:O	47:B:170:ILE:HD11	2.19	0.43
50:E:24:GLU:OE1	57:L:61:TRP:NE1	2.45	0.43
51:F:151:ASP:OD1	53:H:215:ARG:NH2	2.47	0.43
53:H:126:ASP:OD1	53:H:127:THR:N	2.51	0.43
54:I:60:PRO:N	54:I:61:PRO:HD2	2.33	0.43
63:S:34:LEU:O	63:S:38:ILE:HG12	2.18	0.43
1:1:624:U:H2'	1:1:625:C:H6	1.83	0.43
1:1:1396:U:H2'	1:1:1397:G:O4'	2.19	0.43
1:1:1456:A:H2'	1:1:1457:A:C8	2.53	0.43
1:1:1459:U:H2'	1:1:1460:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1494:A:H2'	1:1:1495:U:C6	2.53	0.43
1:1:1568:U:C4	1:1:1569:C:H1'	2.54	0.43
1:1:1754:G:H2'	1:1:1755:U:O4'	2.18	0.43
1:1:2186:A:O2'	1:1:2187:U:H5'	2.18	0.43
1:1:2196:G:OP1	38:AJ:67:ARG:NH1	2.52	0.43
1:1:3138:U:H2'	1:1:3139:U:C6	2.53	0.43
7:l:359:GLU:OE2	22:0:26:ARG:HD3	2.18	0.43
12:q:57:VAL:HG13	12:q:64:HIS:CE1	2.53	0.43
12:q:135:GLU:O	12:q:144:LEU:HD12	2.19	0.43
25:6:108:GLU:HG2	25:6:128[B]:ARG:HG3	2.00	0.43
32:AD:18:LEU:HB3	32:AD:100:SER:HB2	2.01	0.43
34:AF:33:TRP:CH2	34:AF:53:GLN:HG2	2.53	0.43
40:AL:17:ARG:NE	40:AL:19:ASP:OD2	2.46	0.43
46:A:923:G:N2	46:A:926:A:OP2	2.40	0.43
46:A:1626:C:H2'	46:A:1627:C:O4'	2.18	0.43
47:B:56:LYS:HE2	47:B:159:ALA:O	2.19	0.43
51:F:48:LEU:HD11	51:F:70:VAL:HG21	2.00	0.43
64:T:126:ARG:HB2	64:T:133:VAL:HG12	2.00	0.43
72:c:12:PRO:HA	72:c:15:GLU:HB3	2.01	0.43
1:1:154:G:H5''	1:1:155:A:H2'	2.01	0.43
1:1:261:U:H2'	1:1:262:U:C6	2.54	0.43
1:1:814:C:H2'	1:1:815:U:O4'	2.19	0.43
1:1:875:U:O2'	19:x:131:ARG:HD2	2.18	0.43
1:1:2156:A:H5''	5:j:129:THR:OG1	2.18	0.43
3:4:36:G:C5	37:AI:86:ARG:HD3	2.54	0.43
6:k:159:ARG:HG2	6:k:182:GLN:HA	1.99	0.43
8:m:60:ILE:HB	8:m:80:ALA:HB2	1.99	0.43
12:q:34:LEU:HB3	12:q:78:LEU:HD22	2.00	0.43
28:9:85:LEU:HD23	28:9:85:LEU:HA	1.75	0.43
45:AQ:38:ASP:HA	45:AQ:45:ARG:HA	2.01	0.43
46:A:71:A:H2'	46:A:72:A:C8	2.54	0.43
46:A:291:U:H2'	46:A:292:C:H6	1.84	0.43
46:A:518:A:H2'	46:A:519:A:H8	1.81	0.43
46:A:583:A:H2'	46:A:584:G:C8	2.54	0.43
46:A:1636:C:H2'	46:A:1637:U:H6	1.83	0.43
49:D:53:LEU:O	67:W:15:ARG:NE	2.51	0.43
51:F:100:ARG:HH12	51:F:118:GLU:HG2	1.83	0.43
55:J:82:VAL:HG11	55:J:103:GLN:HG3	2.01	0.43
60:P:125:GLY:O	82:P:201:HOH:O	2.20	0.43
62:R:34:PRO:HD2	65:U:7:ARG:O	2.19	0.43
63:S:9:VAL:HG23	63:S:50:ILE:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:X:23:ARG:HG3	72:c:4:VAL:HG22	2.01	0.43
73:d:10:ALA:HB1	73:d:30:VAL:HB	2.01	0.43
1:1:2771:A:H5''	1:1:2772:G:O5'	2.18	0.43
31:AC:11:ASN:OD1	31:AC:14[B]:ARG:NH1	2.51	0.43
33:AE:95:VAL:HG12	33:AE:97:VAL:HG13	1.99	0.43
34:AF:17[B]:LYS:HE3	34:AF:19:LYS:HG2	1.99	0.43
46:A:514:G:H2'	46:A:515:U:O4'	2.19	0.43
46:A:578:A:O2'	46:A:580:U:OP1	2.37	0.43
46:A:1011:A:N3	46:A:1777:A:O2'	2.50	0.43
46:A:1168:A:H1'	46:A:1195:C:O2'	2.18	0.43
57:L:54:TYR:CE1	57:L:75:PHE:HB2	2.54	0.43
69:Y:15:LEU:HD11	82:Y:302:HOH:O	2.19	0.43
1:1:1444:U:OP1	19:x:67:ILE:HG22	2.19	0.43
1:1:1601:A:O2'	1:1:1603:U:OP2	2.30	0.43
1:1:2206:A:H2'	1:1:2207:A:C8	2.54	0.43
1:1:2557:G:H2'	1:1:2557:G:N3	2.34	0.43
1:1:3172:U:O4	22:0:159:SER:HB2	2.18	0.43
3:4:63:G:HO2'	37:AI:49:LYS:HZ2	1.62	0.43
6:k:283:TYR:CZ	6:k:325:LYS:HB2	2.54	0.43
8:m:48:LYS:HG2	8:m:145:PHE:HE2	1.84	0.43
16:u:65:LEU:HD12	16:u:77:LYS:HD2	2.01	0.43
22:0:40:ARG:HA	22:0:40:ARG:HD2	1.87	0.43
43:AO:9:ARG:HH12	46:A:1630:U:P	2.42	0.43
46:A:158:C:H2'	46:A:159:U:O4'	2.19	0.43
46:A:470:U:H5''	56:K:11:THR:HG23	2.00	0.43
46:A:938:G:H2'	46:A:939:G:C8	2.54	0.43
46:A:1191:U:OP2	46:A:1192:C:O2'	2.30	0.43
51:F:221:ARG:O	51:F:225:VAL:HG23	2.19	0.43
56:K:123:HIS:CE1	75:f:37:ARG:HB2	2.54	0.43
60:P:12:ALA:HB3	60:P:76:ILE:HD13	2.00	0.43
1:1:269:G:H5''	17:v:14:LYS:HE2	2.00	0.42
1:1:436:A:H2'	1:1:437:G:C8	2.54	0.42
1:1:1139:A:H5'	1:1:1364:U:H1'	2.01	0.42
1:1:1321:U:H2'	1:1:1322:A:O4'	2.19	0.42
1:1:2592:G:OP1	31:AC:1:MET:HG2	2.18	0.42
1:1:2649:G:H2'	1:1:2649:G:N3	2.34	0.42
2:3:77:G:H3'	22:0:46:GLN:O	2.19	0.42
4:10:70:G:H2'	4:10:71:C:H6	1.81	0.42
8:m:293:PHE:CE2	13:r:210:LEU:HB3	2.54	0.42
9:n:20:THR:HG22	9:n:22:LYS:H	1.84	0.42
13:r:31:ILE:HA	13:r:66:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:x:27:LYS:O	19:x:31:GLU:HG2	2.18	0.42
46:A:544:U:H2'	46:A:545:U:C6	2.54	0.42
46:A:1206:A:H2'	46:A:1207:C:O4'	2.19	0.42
48:C:120:LEU:HD12	48:C:142:PHE:HE2	1.84	0.42
50:E:110:LEU:O	50:E:178:MET:HE1	2.19	0.42
73:d:29:ARG:HD2	73:d:39:THR:HG22	2.01	0.42
1:1:496:A:H2'	1:1:497:U:C6	2.53	0.42
1:1:903:G:H2'	1:1:922:A:H62	1.83	0.42
1:1:1116:A:H2'	1:1:1117:U:C6	2.53	0.42
1:1:1655:U:H2'	1:1:1656:C:H6	1.84	0.42
1:1:1761:U:C5	21:z:43:LYS:HE3	2.53	0.42
1:1:1762:G:HO2'	1:1:1763:C:P	2.42	0.42
1:1:2243:C:OP1	46:A:987:G:H5''	2.19	0.42
1:1:3129:C:H2'	1:1:3130:C:H6	1.83	0.42
3:4:63:G:O2'	37:AI:49:LYS:NZ	2.42	0.42
6:k:215:ILE:HD12	6:k:338:LEU:HB3	2.02	0.42
8:m:19:PRO:HG2	8:m:24:GLN:HB2	2.00	0.42
9:n:3:GLN:HG2	34:AF:75:TYR:HA	2.00	0.42
16:u:14:GLU:HG2	16:u:17:ARG:CG	2.46	0.42
29:AA:5:ILE:HG23	29:AA:25:ILE:HD13	2.00	0.42
41:AM:41:ARG:HD2	41:AM:41:ARG:HA	1.76	0.42
44:AP:71:ARG:NH1	44:AP:80:LYS:HG2	2.33	0.42
46:A:442:C:H5	70:Z:105:ARG:NH2	2.17	0.42
46:A:452:A:O4'	51:F:66:MET:HG3	2.19	0.42
47:B:47:ILE:HD12	63:S:106:THR:HG22	2.01	0.42
48:C:23:PRO:HB3	48:C:26:ARG:NH2	2.34	0.42
50:E:103:ALA:HB1	50:E:174:ARG:HD3	2.01	0.42
52:G:89:ILE:HD11	52:G:172:ILE:HD11	2.00	0.42
52:G:129:PRO:O	52:G:133:VAL:HG23	2.19	0.42
57:L:25:LYS:HD2	57:L:59:PHE:CZ	2.54	0.42
1:1:374:A:N3	1:1:376:G:H5''	2.34	0.42
1:1:2183:U:HO2'	1:1:2184:G:P	2.40	0.42
1:1:2196:G:H2'	1:1:2197:A:C8	2.54	0.42
1:1:2296:U:H2'	1:1:2297:U:O4'	2.19	0.42
1:1:3111:A:H2'	1:1:3112:G:O4'	2.19	0.42
3:4:49:G:OP1	37:AI:45:HIS:HB2	2.19	0.42
6:k:292:ALA:HB1	6:k:295:ALA:HB3	2.01	0.42
10:o:82:VAL:HG21	10:o:134:TYR:CD2	2.54	0.42
38:AJ:2:ALA:O	38:AJ:11:ASN:ND2	2.31	0.42
51:F:95:THR:HG22	70:Z:16:PRO:HG2	2.01	0.42
52:G:124:LEU:C	52:G:126:GLU:H	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:H:138:ALA:O	53:H:142:ARG:HG3	2.19	0.42
55:J:36:THR:OG1	55:J:57:ALA:O	2.34	0.42
62:R:29:LYS:HB2	62:R:65:ARG:HG2	2.01	0.42
73:d:35:ASP:O	73:d:37:SER:N	2.52	0.42
1:1:371:G:N1	1:1:374:A:OP2	2.38	0.42
1:1:502:U:H2'	1:1:503:U:C6	2.54	0.42
1:1:1099:A:N3	1:1:1099:A:H2'	2.34	0.42
1:1:3297:U:H2'	1:1:3298:G:O4'	2.20	0.42
3:4:37:A:OP2	37:AI:86:ARG:HD2	2.18	0.42
5:j:79:ASN:ND2	5:j:165:VAL:HG12	2.34	0.42
20:y:165:ILE:HD11	20:y:172:PHE:HB3	2.01	0.42
24:5:43:VAL:HG22	24:5:54:ILE:HD12	2.01	0.42
46:A:167:A:OP2	46:A:167:A:H8	2.01	0.42
46:A:600:U:H3'	82:A:2008:HOH:O	2.19	0.42
46:A:1533:G:N2	64:T:87:ASN:OD1	2.52	0.42
46:A:1548:U:H4'	46:A:1586:C:H4'	2.01	0.42
48:C:27:LYS:HD2	48:C:47:LEU:HD13	2.02	0.42
49:D:96:VAL:HG22	49:D:110:ILE:HG12	2.02	0.42
55:J:38:ILE:HG12	55:J:96:LEU:HD11	2.00	0.42
60:P:9:PHE:HA	60:P:73:ALA:O	2.18	0.42
63:S:77:GLU:O	63:S:81:LYS:HB2	2.19	0.42
75:f:37:ARG:O	75:f:41:THR:HG23	2.20	0.42
1:1:785:A:H2'	1:1:786:U:C6	2.54	0.42
1:1:1569:C:H2'	1:1:1570:A:C8	2.54	0.42
1:1:1841:G:H5''	1:1:1842:C:H5'	2.02	0.42
1:1:1852:C:H2'	1:1:1853:C:C6	2.54	0.42
3:4:23:U:OP1	28:9:16:ARG:NH1	2.53	0.42
3:4:78:G:H2'	3:4:79:A:N3	2.34	0.42
3:4:103:G:OP2	3:4:105:A:O2'	2.31	0.42
5:j:27:ALA:HB1	5:j:77:ILE:HG13	2.01	0.42
15:t:154:PRO:HB3	30:AB:106:ALA:CB	2.49	0.42
21:z:95:TRP:CZ2	21:z:99:LEU:HD22	2.54	0.42
25:6:13:MET:HE1	25:6:54:ALA:HB3	2.01	0.42
27:8:70:GLU:HG2	27:8:74:LYS:NZ	2.35	0.42
32:AD:27:LEU:HD11	32:AD:85:LYS:HE3	2.01	0.42
46:A:119:A:H1'	46:A:395:A:C4	2.54	0.42
46:A:151:G:O2'	46:A:152:G:OP1	2.34	0.42
46:A:273:C:H2'	46:A:274:C:O4'	2.19	0.42
46:A:649:G:O6	46:A:682:A:N6	2.52	0.42
48:C:23:PRO:HB3	48:C:26:ARG:HH21	1.84	0.42
57:L:10:LYS:HA	57:L:13:GLN:NE2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:S:36:SER:OG	63:S:47:ARG:NH1	2.45	0.42
63:S:103:ASP:O	63:S:106:THR:OG1	2.33	0.42
68:X:119:LYS:HG3	68:X:121:VAL:HG22	2.01	0.42
72:c:57:ASP:OD1	72:c:58:SER:N	2.52	0.42
1:1:538:G:O2'	1:1:539:G:OP1	2.32	0.42
1:1:671:U:H2'	1:1:672:G:C8	2.55	0.42
1:1:694:C:H2'	1:1:695:G:C8	2.55	0.42
1:1:1891:A:O2'	1:1:3025:G:H4'	2.20	0.42
1:1:2876:U:H2'	1:1:2877:U:H6	1.84	0.42
1:1:3318:G:C6	1:1:3321:G:C5	3.08	0.42
25:6:80:ARG:HG2	25:6:99:ALA:HB3	2.02	0.42
46:A:286:A:H2'	46:A:287:U:O4'	2.19	0.42
46:A:1482:C:O2'	46:A:1506:U:O2	2.34	0.42
46:A:1668:A:H8	53:H:65:GLN:HG3	1.84	0.42
46:A:1741:A:H2'	46:A:1742:A:C8	2.54	0.42
47:B:62:ARG:HD3	67:W:37:ALA:O	2.19	0.42
49:D:148:SER:OG	49:D:149:LEU:N	2.53	0.42
60:P:15:PHE:HB3	60:P:22:PHE:HB2	2.02	0.42
60:P:27:ASP:OD1	60:P:30:GLY:N	2.51	0.42
1:1:252:U:H5'	1:1:253:A:H8	1.85	0.42
1:1:629:A:H2'	1:1:630:G:C8	2.55	0.42
1:1:1813:G:C5	1:1:1814:U:H5	2.38	0.42
1:1:2836:A:H5''	13:r:114:GLY:HA2	2.00	0.42
1:1:2995:U:H2'	1:1:2996:A:H8	1.84	0.42
3:4:152:G:H2'	3:4:153:U:O4'	2.19	0.42
7:l:258:SER:O	7:l:262:VAL:HG23	2.19	0.42
15:t:2:ALA:HB1	30:AB:33:GLY:O	2.20	0.42
27:8:63:ILE:HG13	27:8:102:LEU:HD12	2.01	0.42
28:9:63:LYS:HA	28:9:63:LYS:HD3	1.86	0.42
46:A:738:A:OP2	51:F:187:ARG:HG2	2.20	0.42
46:A:1071:A:H2'	46:A:1072:A:C8	2.53	0.42
46:A:1160:U:O4	64:T:140:THR:HG21	2.20	0.42
47:B:134:LYS:O	47:B:138:TYR:HD1	2.03	0.42
57:L:32:HIS:HB2	57:L:39:ASN:HD22	1.84	0.42
61:Q:30:THR:O	61:Q:34:THR:HG23	2.20	0.42
65:U:66:TYR:HD2	65:U:124:ILE:HD13	1.84	0.42
72:c:36:LYS:HZ1	72:c:43:ILE:HD13	1.84	0.42
1:1:375:A:H1'	28:9:87:LYS:HE2	2.01	0.42
1:1:1044:A:H2'	13:r:22:TYR:CZ	2.55	0.42
1:1:1180:A:H2'	1:1:1181:C:C6	2.54	0.42
1:1:2236:U:C2	1:1:2237:A:C8	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2753:U:H2'	1:1:2754:U:C6	2.55	0.42
1:1:3079:U:H2'	1:1:3080:G:C8	2.55	0.42
3:4:155:G:C5	3:4:156:U:C4	3.07	0.42
6:k:293:ASN:HB2	6:k:304:THR:HA	2.02	0.42
12:q:89:LYS:HB2	12:q:183:GLU:HB3	2.00	0.42
33:AE:5:ASP:CG	33:AE:88:LEU:HD11	2.45	0.42
46:A:852:G:O3'	59:O:121:ARG:HD3	2.20	0.42
46:A:1425:C:H2'	46:A:1426:C:C6	2.54	0.42
48:C:110:LEU:O	48:C:114:VAL:HG23	2.20	0.42
49:D:39:LEU:HD12	49:D:235:LEU:HD23	2.00	0.42
50:E:12:LEU:HD12	66:V:85:ILE:HG12	2.00	0.42
51:F:133:LYS:HD3	51:F:133:LYS:HA	1.82	0.42
57:L:35:ILE:O	57:L:37:THR:N	2.52	0.42
61:Q:81:ARG:HH12	61:Q:122:THR:HG22	1.85	0.42
71:b:15:ARG:CZ	71:b:15:ARG:HB2	2.50	0.42
1:1:363:G:OP2	39:AK:56:ARG:NH2	2.47	0.42
1:1:1338:G:H2'	1:1:1339:A:O4'	2.20	0.42
1:1:1466:U:H2'	1:1:1467:U:C6	2.55	0.42
1:1:1714:G:H2'	1:1:1715:G:C8	2.55	0.42
1:1:1797:U:H2'	1:1:1798:C:C6	2.54	0.42
1:1:3197:G:H2'	1:1:3198:C:C6	2.54	0.42
2:3:21:G:OP2	14:s:2:SER:N	2.52	0.42
3:4:104:A:C8	3:4:105:A:C8	3.08	0.42
10:o:201:TRP:CD1	10:o:202:PRO:HD2	2.55	0.42
11:p:125:ASP:OD1	11:p:126:VAL:N	2.52	0.42
13:r:86:HIS:HB3	13:r:139:ARG:CG	2.50	0.42
14:s:37:LEU:HD23	14:s:37:LEU:HA	1.90	0.42
15:t:63:VAL:HA	15:t:66:ASN:ND2	2.35	0.42
30:AB:24:LYS:O	30:AB:25:HIS:C	2.62	0.42
43:AO:14:LYS:HB3	43:AO:14:LYS:HE2	1.83	0.42
46:A:933:A:H2'	46:A:934:C:C6	2.55	0.42
46:A:972:G:N2	46:A:998:A:OP1	2.53	0.42
49:D:71:LEU:HB3	49:D:99:ILE:HD11	2.02	0.42
55:J:114:GLU:HG2	55:J:119:ALA:O	2.19	0.42
71:b:88:SER:O	71:b:92:ARG:HG3	2.20	0.42
1:1:246:U:H2'	1:1:247:C:C6	2.54	0.42
1:1:995:G:N3	1:1:998:A:N6	2.67	0.42
1:1:1620:G:O2'	1:1:1639:A:N1	2.45	0.42
1:1:2686:G:C8	1:1:2723:G:H2'	2.54	0.42
1:1:2800:G:H5'	13:r:8:CYS:SG	2.59	0.42
17:v:177:GLY:H	17:v:184:LYS:HE3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AH:8:ARG:HD2	36:AH:32:ALA:O	2.20	0.42
46:A:254:A:H2'	46:A:255:A:O4'	2.19	0.42
46:A:873:U:H2'	46:A:874:U:C6	2.55	0.42
46:A:1378:U:H2'	46:A:1379:C:C6	2.55	0.42
46:A:1448:G:OP2	64:T:143:ARG:NH1	2.52	0.42
46:A:1487:C:P	65:U:122:ARG:HH22	2.41	0.42
49:D:96:VAL:HG21	49:D:203:GLU:HG3	2.01	0.42
52:G:146:SER:OG	52:G:157:ARG:NH2	2.53	0.42
56:K:105:LEU:HD23	56:K:108:ARG:HD2	2.01	0.42
59:O:38:ILE:HG23	59:O:80:LEU:HD11	2.02	0.42
1:1:224:C:H5'	28:9:34:PRO:HD3	2.02	0.41
1:1:1575:A:OP1	1:1:2500:G:N2	2.33	0.41
1:1:1612:U:H2'	1:1:1613:G:C8	2.55	0.41
1:1:1618:U:H2'	1:1:1619:G:H8	1.85	0.41
1:1:2251:G:O2'	1:1:2289:G:O6	2.33	0.41
1:1:2268:C:H3'	82:1:3734:HOH:O	2.20	0.41
1:1:3284:U:O2'	1:1:3285:A:OP1	2.34	0.41
2:3:16:U:H2'	2:3:17:A:C8	2.55	0.41
7:l:296:VAL:O	7:l:300:VAL:HG13	2.19	0.41
12:q:44:THR:HG23	12:q:56:THR:HB	2.01	0.41
22:0:14:LEU:HD23	22:0:14:LEU:HA	1.90	0.41
37:AI:60:LEU:O	37:AI:64:GLU:OE1	2.37	0.41
39:AK:84:LYS:HB2	39:AK:84:LYS:HE3	1.75	0.41
46:A:78:A:H2'	46:A:79:C:C6	2.55	0.41
46:A:504:A:O2'	46:A:505:U:P	2.78	0.41
46:A:944:U:OP2	72:c:20:LYS:NZ	2.52	0.41
51:F:65:MET:SD	51:F:80:THR:HA	2.60	0.41
57:L:47:GLN:HA	57:L:50:THR:HG22	2.02	0.41
61:Q:81:ARG:HB2	61:Q:117:GLY:CA	2.49	0.41
66:V:97:SER:O	66:V:100:LYS:HG3	2.19	0.41
1:1:57:G:H4'	17:v:155:VAL:HG12	2.01	0.41
1:1:648:C:H2'	1:1:649:G:C8	2.55	0.41
1:1:732:U:C4	1:1:733:A:H1'	2.55	0.41
1:1:976:A:C2'	1:1:977:U:H5'	2.49	0.41
1:1:1079:G:H2'	1:1:1080:A:H8	1.82	0.41
1:1:1505:A:H2'	1:1:1506:G:C8	2.55	0.41
1:1:2079:C:O2'	1:1:2080:U:H6	2.02	0.41
7:l:17:GLY:O	7:l:18:SER:OG	2.32	0.41
17:v:193:LYS:HE2	17:v:193:LYS:HB3	1.75	0.41
46:A:64:U:H2'	46:A:65:A:H5''	2.02	0.41
46:A:127:G:N7	53:H:202:ARG:NH2	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:283:G:H2'	46:A:284:C:C6	2.55	0.41
46:A:481:A:H2	46:A:504:A:C6	2.39	0.41
46:A:642:C:H2'	46:A:643:U:H6	1.85	0.41
46:A:1529:G:N2	46:A:1555:C:H1'	2.33	0.41
47:B:29:VAL:HG23	47:B:149:MET:HB3	2.02	0.41
49:D:93:MET:HG3	49:D:116:VAL:HG23	2.02	0.41
52:G:116:HIS:O	52:G:120:ILE:HG13	2.19	0.41
53:H:30:LYS:NZ	53:H:36:VAL:HG12	2.36	0.41
61:Q:80:LEU:HD12	61:Q:83:MET:HB2	2.03	0.41
65:U:19:ALA:HB2	65:U:56:LYS:HA	2.03	0.41
70:Z:63:GLN:CD	70:Z:68:LYS:HD3	2.45	0.41
71:b:73:TYR:CE2	71:b:83:ILE:HD13	2.55	0.41
1:1:225:C:H2'	1:1:226:G:O4'	2.19	0.41
1:1:647:A:H2'	1:1:648:C:C6	2.56	0.41
1:1:823:A:H5''	36:AH:14:ASN:O	2.20	0.41
1:1:1007:A:H2'	1:1:1008:A:H8	1.85	0.41
1:1:1852:C:H2'	1:1:1853:C:H6	1.85	0.41
1:1:3082:C:H2'	1:1:3083:U:C6	2.55	0.41
6:k:71:GLU:OE2	6:k:357:LYS:NZ	2.52	0.41
10:o:17:GLN:O	10:o:20:THR:HG22	2.21	0.41
14:s:19:LEU:HD11	14:s:79:ILE:HG21	2.02	0.41
25:6:86:ARG:HB2	25:6:92:TYR:CE2	2.55	0.41
30:AB:75:LEU:HD23	30:AB:78:LEU:HD22	2.01	0.41
32:AD:57:GLU:HB2	36:AH:94:LEU:HD11	2.02	0.41
36:AH:29[B]:LYS:HB2	36:AH:29[B]:LYS:HE2	1.87	0.41
46:A:1515:U:H2'	46:A:1516:C:C6	2.55	0.41
51:F:100:ARG:NH1	51:F:118:GLU:OE2	2.53	0.41
63:S:14:LYS:O	63:S:18:GLU:HG3	2.20	0.41
63:S:99:GLN:HG2	63:S:120:GLN:HG2	2.02	0.41
69:Y:19:ARG:O	69:Y:23:ARG:HG3	2.20	0.41
1:1:922:A:H2'	1:1:923:C:C6	2.55	0.41
1:1:1832:C:O2'	1:1:1838:A:N1	2.50	0.41
1:1:2273:A:C4	25:6:37:LEU:HD22	2.56	0.41
1:1:2642:G:H2'	1:1:2643:A:C8	2.56	0.41
1:1:3090:C:H2'	1:1:3091:U:O4'	2.21	0.41
3:4:51:G:C8	41:AM:27:ILE:HD11	2.55	0.41
3:4:62:C:OP1	37:AI:48:ARG:NH2	2.48	0.41
22:0:23:LYS:HD3	22:0:23:LYS:HA	1.80	0.41
25:6:114:ILE:HG12	82:6:302:HOH:O	2.20	0.41
33:AE:45:THR:HG22	33:AE:47:ASP:N	2.28	0.41
41:AM:9:THR:O	41:AM:13:LEU:HG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:94:U:H2'	46:A:95:G:O4'	2.20	0.41
46:A:148:C:H42	46:A:162:A:N6	2.12	0.41
46:A:451:C:O2	46:A:451:C:H2'	2.20	0.41
46:A:558:U:H2'	46:A:559:G:H8	1.86	0.41
46:A:844:A:C5	59:O:73:ARG:HD3	2.55	0.41
46:A:1277:G:H2'	46:A:1278:U:C6	2.55	0.41
46:A:1376:U:C5	63:S:3:ARG:HG3	2.55	0.41
46:A:1469:A:C6	46:A:1470:G:C6	3.09	0.41
46:A:1481:C:H2'	46:A:1482:C:C6	2.55	0.41
54:I:21:PHE:CZ	54:I:73:LEU:HD21	2.55	0.41
63:S:93:LEU:HD23	63:S:93:LEU:H	1.85	0.41
69:Y:72:VAL:HG11	69:Y:96:VAL:HG11	2.02	0.41
1:1:1660:G:H2'	1:1:1661:U:C6	2.55	0.41
1:1:1777:C:H2'	1:1:1778:U:C6	2.55	0.41
1:1:2522:U:H2'	1:1:2523:C:C6	2.56	0.41
1:1:2669:A:H2'	1:1:2670:G:H8	1.86	0.41
1:1:2749:G:C2	30:AB:60:TYR:CE2	3.08	0.41
1:1:3088:G:H4'	12:q:69:ARG:HH12	1.86	0.41
10:o:98:ARG:HD3	82:o:405:HOH:O	2.19	0.41
11:p:145:GLU:OE2	17:v:6:TYR:OH	2.17	0.41
19:x:51:VAL:HA	19:x:56:ARG:O	2.20	0.41
22:0:12:ARG:HB3	22:0:24:LEU:HD23	2.03	0.41
23:2:39:ILE:HG12	23:2:63:ILE:HD13	2.03	0.41
24:5:83:THR:O	24:5:87:LEU:HG	2.20	0.41
37:AI:86:ARG:O	37:AI:90:ARG:HD3	2.21	0.41
44:AP:61:LYS:NZ	44:AP:63:LYS:O	2.53	0.41
46:A:331:A:N6	55:J:27:PHE:HB2	2.35	0.41
46:A:1261:U:OP1	50:E:148:ALA:N	2.52	0.41
46:A:1546:G:N7	64:T:134:ARG:HD3	2.36	0.41
46:A:1595:U:O3'	62:R:72:GLY:HA3	2.21	0.41
47:B:11:PRO:O	47:B:15:LYS:HG3	2.21	0.41
48:C:86:LEU:HB3	48:C:98:THR:HB	2.02	0.41
51:F:180:LEU:HD12	51:F:180:LEU:HA	1.89	0.41
68:X:84:ASN:HB2	82:X:304:HOH:O	2.20	0.41
70:Z:42:GLU:HG3	70:Z:52:LYS:HE3	2.02	0.41
74:e:29:GLY:O	74:e:40:ARG:N	2.49	0.41
1:1:1357:U:H2'	1:1:1358:C:C6	2.56	0.41
1:1:1491:U:C5	1:1:1831:A:N1	2.87	0.41
1:1:1791:U:H2'	5:j:50:HIS:CD2	2.54	0.41
1:1:1856:G:O3'	21:z:60:ARG:NH1	2.53	0.41
1:1:2367:C:H2'	1:1:2368:A:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2645:A:H4'	14:s:103:GLY:C	2.46	0.41
1:1:2655:U:H2'	1:1:2656:C:H6	1.83	0.41
1:1:2972:A:H2'	1:1:2973:U:C6	2.56	0.41
1:1:3038:U:H2'	1:1:3039:C:C6	2.55	0.41
3:4:27:U:H2'	3:4:28:C:C6	2.56	0.41
5:j:249:THR:HG21	46:A:973:A:OP2	2.20	0.41
15:t:2:ALA:HB3	30:AB:41:HIS:CE1	2.56	0.41
19:x:4:TYR:OH	19:x:18:ARG:HG3	2.20	0.41
27:8:142:ILE:HD12	27:8:142:ILE:HA	1.89	0.41
46:A:86:A:H5'	70:Z:119:PHE:CE1	2.54	0.41
46:A:147:C:C2	46:A:148:C:C5	3.09	0.41
46:A:404:U:H2'	46:A:405:A:C8	2.56	0.41
46:A:600:U:H4'	82:A:1918:HOH:O	2.20	0.41
46:A:770:C:P	46:A:770:C:O4'	2.79	0.41
47:B:79:ARG:O	47:B:83:GLN:HG3	2.20	0.41
1:1:63:G:OP2	17:v:169:LYS:NZ	2.44	0.41
1:1:152:U:O2'	1:1:153:U:H5'	2.21	0.41
1:1:259:C:H2'	1:1:260:C:H6	1.86	0.41
1:1:356:C:O2'	7:l:82:GLY:O	2.28	0.41
1:1:654:A:H2'	1:1:655:A:H8	1.83	0.41
1:1:929:A:C2	7:l:99:ARG:NH2	2.89	0.41
1:1:1011:C:H4'	1:1:1012:U:H6	1.85	0.41
1:1:1099:A:N6	1:1:1359:A:H1'	2.36	0.41
1:1:2887:U:C5	6:k:7:GLU:HG3	2.56	0.41
1:1:3135:A:H2'	1:1:3136:C:C6	2.55	0.41
3:4:40:A:H2'	3:4:41:A:C8	2.56	0.41
3:4:85:G:H4'	3:4:86:U:OP1	2.21	0.41
3:4:156:U:O2'	3:4:157:U:P	2.78	0.41
6:k:80:ASP:OD1	6:k:319:ASN:HB2	2.20	0.41
9:n:64:VAL:O	9:n:75:LEU:HA	2.21	0.41
34:AF:80:VAL:HB	34:AF:112:LYS:HD2	2.03	0.41
40:AL:3:ARG:O	40:AL:52:TYR:HA	2.20	0.41
46:A:30:G:H2'	46:A:31:C:C6	2.55	0.41
46:A:787:A:H8	46:A:787:A:OP2	2.04	0.41
46:A:931:U:H2'	46:A:932:U:C6	2.55	0.41
46:A:1459:U:OP1	52:G:183:SER:OG	2.38	0.41
46:A:1580:A:O2'	46:A:1581:G:H5'	2.21	0.41
47:B:88:LYS:HD3	47:B:88:LYS:HA	1.81	0.41
50:E:72:SER:HA	50:E:75:VAL:HG22	2.03	0.41
53:H:219:ARG:HD3	53:H:223:ARG:HH12	1.86	0.41
61:Q:81:ARG:NH1	61:Q:122:THR:HG22	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:c:31:PHE:CD2	72:c:81:ARG:HG3	2.55	0.41
1:1:1618:U:H2'	1:1:1619:G:C8	2.56	0.41
1:1:2486:U:H2'	1:1:2487:U:H6	1.86	0.41
1:1:2648:A:H5'	1:1:2649:G:C8	2.56	0.41
1:1:3084:G:O6	1:1:3092:C:H5''	2.21	0.41
15:t:154:PRO:HB3	30:AB:106:ALA:HB1	2.02	0.41
20:y:69:ARG:HG3	20:y:69:ARG:HH11	1.85	0.41
20:y:104:LEU:HD23	20:y:104:LEU:HA	1.95	0.41
22:0:125:LYS:HG2	22:0:127:VAL:HG23	2.01	0.41
28:9:55:GLU:HB2	28:9:108:LYS:HB3	2.02	0.41
40:AL:46:ARG:HD3	40:AL:47:GLY:O	2.20	0.41
46:A:505:U:O2'	46:A:506:U:O5'	2.30	0.41
46:A:1012:A:OP1	46:A:1776:G:O2'	2.36	0.41
46:A:1148:A:H2'	46:A:1149:G:O4'	2.20	0.41
47:B:3:LEU:CD2	47:B:62:ARG:HH22	2.34	0.41
49:D:111:LYS:HE3	49:D:122:ALA:HB1	2.02	0.41
51:F:31:PRO:HG3	51:F:43:PRO:HG3	2.01	0.41
51:F:163:ASP:C	51:F:165:ALA:H	2.29	0.41
52:G:102:ARG:O	52:G:106:LYS:NZ	2.41	0.41
52:G:174:LEU:HB3	52:G:210:ALA:CB	2.51	0.41
54:I:13:LEU:HD21	54:I:54:LEU:HD11	2.03	0.41
68:X:86:ILE:HG23	82:X:315:HOH:O	2.20	0.41
1:1:406:G:N3	3:4:16:G:C2	2.89	0.41
1:1:546:C:H2'	1:1:547:U:O4'	2.21	0.41
1:1:1014:G:O6	1:1:1030:U:O4	2.38	0.41
1:1:1176:A:C4	1:1:1178:G:C8	3.09	0.41
1:1:1524:G:O2'	1:1:1584:A:N3	2.51	0.41
1:1:1725:A:C6	45:AQ:42:CYS:HA	2.56	0.41
1:1:2096:C:H2'	1:1:2097:A:O4'	2.20	0.41
1:1:2138:G:H2'	1:1:2139:G:H8	1.85	0.41
1:1:2857:C:O2'	1:1:2858:U:H5'	2.20	0.41
1:1:2917:G:O2'	1:1:2920:C:OP2	2.30	0.41
1:1:3056:C:H2'	1:1:3057:G:O4'	2.21	0.41
1:1:3240:U:H5'	35:AG:66:VAL:HG21	2.03	0.41
1:1:3260:A:H2'	1:1:3261:A:H8	1.85	0.41
1:1:3287:A:H2'	1:1:3288:A:H8	1.85	0.41
1:1:3316:U:O2'	1:1:3317:U:OP1	2.36	0.41
3:4:5:U:H2'	3:4:6:U:C6	2.55	0.41
3:4:94:C:OP1	39:AK:75:LYS:NZ	2.51	0.41
6:k:236:LYS:HE2	6:k:236:LYS:HB2	1.91	0.41
14:s:50:ALA:HB2	14:s:65:ILE:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:u:14:GLU:HB3	22:0:149:LYS:HG2	2.02	0.41
22:0:73:LYS:HD2	22:0:75:PHE:CZ	2.55	0.41
23:2:54:HIS:CE1	23:2:55:LYS:HG2	2.56	0.41
45:AQ:30:GLU:HA	45:AQ:33:GLN:HG2	2.02	0.41
46:A:154:A:H2'	46:A:155:A:O4'	2.21	0.41
46:A:165:U:C2'	46:A:166:A:H5''	2.50	0.41
46:A:333:U:O2'	58:M:130:PRO:O	2.37	0.41
46:A:470:U:O2'	46:A:754:A:N3	2.43	0.41
46:A:883:A:C8	46:A:897:U:C4	3.09	0.41
46:A:1084:U:O2'	82:A:1914:HOH:O	2.21	0.41
46:A:1099:G:O2'	46:A:1115:G:O6	2.34	0.41
46:A:1634:U:H2'	46:A:1635:A:C8	2.55	0.41
46:A:1749:A:H1'	46:A:1770:C:H5'	2.02	0.41
48:C:23:PRO:O	48:C:26:ARG:HG2	2.21	0.41
52:G:94:THR:HB	52:G:114:VAL:HG21	2.03	0.41
52:G:114:VAL:O	52:G:118:LEU:HG	2.21	0.41
55:J:175:ILE:HD12	55:J:185:CYS:SG	2.61	0.41
56:K:110:GLN:NE2	56:K:122:ILE:HG13	2.35	0.41
57:L:46:LEU:HD23	57:L:66:TYR:CG	2.55	0.41
62:R:14:THR:HB	62:R:71:GLY:HA2	2.01	0.41
62:R:96:VAL:HG12	62:R:97:ASP:N	2.36	0.41
63:S:89:SER:O	63:S:91:LEU:N	2.54	0.41
66:V:55:VAL:O	66:V:88:ARG:HA	2.19	0.41
1:1:19:A:H2'	1:1:20:G:C8	2.55	0.41
1:1:592:U:H2'	1:1:607:G:O6	2.21	0.41
1:1:1062:G:H2'	1:1:1063:U:C6	2.56	0.41
1:1:1434:U:H4'	7:l:89:ALA:HB3	2.03	0.41
1:1:1606:G:H2'	1:1:1607:G:O4'	2.21	0.41
1:1:2085:A:H2	1:1:3309:A:C8	2.39	0.41
1:1:2380:A:H5''	7:l:68:THR:OG1	2.21	0.41
1:1:2516:U:O2'	1:1:2519:A:N6	2.54	0.41
1:1:2807:U:H2'	1:1:2808:OMC:O2	2.21	0.41
1:1:2808:OMC:H2'	1:1:2809:A:O4'	2.21	0.41
1:1:2855:U:H2'	1:1:2856:C:C6	2.55	0.41
1:1:3021:A:C5	6:k:75:ALA:HB2	2.56	0.41
2:3:84:A:H2'	2:3:85:G:C8	2.56	0.41
7:l:181:LYS:O	7:l:185:SER:HB3	2.21	0.41
16:u:14:GLU:OE2	16:u:17:ARG:HD3	2.21	0.41
27:8:96:LYS:HG3	27:8:107:ALA:HB3	2.02	0.41
46:A:149:G:HO2'	46:A:150:U:H6	1.68	0.41
46:A:405:A:H2	82:A:1919:HOH:O	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:472:A:H5''	56:K:144:PRO:HD2	2.02	0.41
46:A:623:C:H2'	46:A:624:U:C6	2.56	0.41
46:A:857:G:H2'	46:A:858:U:O4'	2.21	0.41
46:A:1669:U:O2'	46:A:1670:U:H6	2.02	0.41
50:E:168:PHE:HA	50:E:191:LYS:HE2	2.02	0.41
59:O:128:TYR:O	59:O:132:VAL:HG22	2.21	0.41
61:Q:52:LYS:HB2	61:Q:53:PRO:HD3	2.02	0.41
64:T:53:GLU:OE2	64:T:56:LYS:HD2	2.21	0.41
1:1:64:A:C4	1:1:109:G:N7	2.89	0.40
1:1:65:A:N6	1:1:75:G:H1'	2.36	0.40
1:1:158:A:H2'	1:1:159:A:H8	1.86	0.40
1:1:628:A:H2'	1:1:629:A:H8	1.81	0.40
1:1:988:A:O2'	1:1:989:G:H5'	2.21	0.40
1:1:1141:G:OP1	34:AF:45:ARG:HD2	2.22	0.40
1:1:1690:U:O2'	1:1:1691:U:H5'	2.22	0.40
1:1:2201:A:H2'	1:1:2202:A:C8	2.57	0.40
1:1:2958:U:H2'	1:1:2959:A:C8	2.56	0.40
5:j:168:VAL:CG2	45:AQ:79:VAL:HG21	2.51	0.40
6:k:218:ILE:CD1	6:k:276:THR:HG23	2.51	0.40
13:r:140:THR:HG21	13:r:148:VAL:HG21	2.02	0.40
17:v:7:LEU:O	17:v:11:GLN:HG2	2.22	0.40
24:5:13:LYS:HD2	24:5:15:PHE:CZ	2.55	0.40
27:8:87:ASP:OD1	27:8:88:ILE:N	2.54	0.40
32:AD:26:THR:HB	32:AD:31:SER:HB3	2.03	0.40
32:AD:36:LEU:HD13	32:AD:61:TYR:HB3	2.03	0.40
40:AL:30[B]:LYS:HE3	40:AL:30[B]:LYS:HB3	1.61	0.40
46:A:25:C:H4'	46:A:26:A:O5'	2.21	0.40
46:A:560:G:H2'	46:A:561:U:O2	2.21	0.40
46:A:986:A:H2'	46:A:987:G:C8	2.56	0.40
46:A:1024:A:O2'	46:A:1025:G:H8	2.04	0.40
46:A:1467:C:O2'	46:A:1468:C:O5'	2.33	0.40
48:C:26:ARG:HA	48:C:50:ARG:HH12	1.85	0.40
50:E:110:LEU:HA	50:E:110:LEU:HD23	1.81	0.40
52:G:209:TYR:C	52:G:211:ILE:H	2.29	0.40
60:P:132:LEU:HD23	60:P:132:LEU:HA	1.90	0.40
64:T:89:GLN:HA	64:T:97:ASP:HA	2.03	0.40
67:W:71:ARG:O	67:W:75:GLN:HG3	2.20	0.40
1:1:381:U:H2'	1:1:382:U:C6	2.56	0.40
1:1:411:U:H2'	1:1:412:G:C8	2.55	0.40
1:1:629:A:C2	35:AG:91:PRO:HG2	2.56	0.40
1:1:672:G:O6	20:y:56:LYS:NZ	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:k:111:SER:OG	6:k:113:GLU:HG2	2.21	0.40
7:l:300:VAL:HB	20:y:39:ARG:CG	2.45	0.40
10:o:189:VAL:HG13	10:o:193:PHE:CD2	2.56	0.40
14:s:103:GLY:HA3	14:s:128:TYR:CD1	2.56	0.40
17:v:85:THR:HA	44:AP:51:GLY:HA2	2.02	0.40
19:x:14:SER:O	19:x:105:LYS:NZ	2.44	0.40
19:x:47:TYR:OH	19:x:58:ILE:HD13	2.21	0.40
19:x:116:HIS:HB3	19:x:149:THR:HB	2.04	0.40
27:8:73:MET:HE2	27:8:142:ILE:HD13	2.03	0.40
46:A:107:C:H2'	46:A:108:A:C8	2.56	0.40
46:A:180:A:H2'	46:A:181:U:H6	1.86	0.40
46:A:1300:U:OP1	46:A:1313:G:N2	2.40	0.40
46:A:1663:U:H2'	46:A:1664:C:C6	2.56	0.40
47:B:41:ARG:NH2	47:B:43:ASP:OD2	2.49	0.40
52:G:56:VAL:HG12	73:d:53:ILE:HG21	2.02	0.40
56:K:148:VAL:HG11	56:K:156:ILE:HD11	2.04	0.40
1:1:44:A:H5''	77:1:3401:SPK:H8A	2.04	0.40
1:1:87:A:H2'	1:1:88:G:O4'	2.21	0.40
1:1:2204:U:H2'	1:1:2205:C:C6	2.57	0.40
1:1:2683:C:O2'	1:1:2716:U:OP1	2.31	0.40
8:m:83:LEU:HD23	8:m:83:LEU:HA	1.90	0.40
34:AF:39:ILE:O	34:AF:44:ARG:NH2	2.55	0.40
46:A:179:A:H2'	46:A:180:A:O4'	2.22	0.40
46:A:274:C:O2'	46:A:275:U:O5'	2.39	0.40
46:A:787:A:O2'	54:I:100:ARG:NE	2.44	0.40
46:A:1168:A:H2'	46:A:1169:A:C8	2.57	0.40
46:A:1265:C:H2'	46:A:1266:G:H8	1.86	0.40
46:A:1325:U:O4'	46:A:1364:U:H5''	2.21	0.40
46:A:1414:G:O2'	46:A:1415:G:H5'	2.21	0.40
46:A:1486:G:OP2	65:U:73:VAL:HG12	2.22	0.40
82:A:2170:HOH:O	68:X:105:THR:HG23	2.20	0.40
48:C:31:ASP:O	48:C:96:LEU:N	2.47	0.40
48:C:34:ALA:HB3	48:C:41:ARG:HA	2.03	0.40
49:D:135:ARG:HD2	49:D:217:TYR:CD1	2.57	0.40
50:E:134:GLY:HA3	50:E:157:PHE:O	2.21	0.40
57:L:13:GLN:O	57:L:17:GLN:NE2	2.35	0.40
65:U:9:VAL:HB	65:U:140:LEU:HD23	2.04	0.40
1:1:266:C:N4	38:AJ:29:LYS:HA	2.36	0.40
1:1:852:G:N3	82:1:3702:HOH:O	2.37	0.40
1:1:1029:U:HO2'	1:1:1030:U:P	2.41	0.40
1:1:1149:A:O2'	1:1:1150:A:H5'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1593:C:H2'	1:1:1594:G:C8	2.57	0.40
1:1:2339:A:H2'	1:1:2340:C:H6	1.86	0.40
1:1:2522:U:H2'	1:1:2523:C:H6	1.84	0.40
1:1:3294:U:H5''	6:k:308:MET:HE2	2.04	0.40
2:3:107:A:H2'	2:3:108:U:C6	2.57	0.40
15:t:55:ARG:NH1	15:t:73:ARG:O	2.49	0.40
24:5:30:GLN:HE22	24:5:58:ALA:CB	2.33	0.40
25:6:37:LEU:HD23	25:6:61:THR:HG23	2.02	0.40
25:6:64:LYS:HE3	25:6:64:LYS:HB2	1.81	0.40
26:7:52:THR:O	26:7:56:ARG:HG3	2.20	0.40
32:AD:45:ILE:HD12	32:AD:92:LEU:HD11	2.04	0.40
39:AK:36:SER:OG	39:AK:57:ARG:NH2	2.46	0.40
46:A:266:C:O2'	46:A:267:G:H5'	2.22	0.40
46:A:779:U:C2	46:A:780:A:C8	3.10	0.40
46:A:861:G:H2'	46:A:921:G:N2	2.36	0.40
46:A:1378:U:H2'	46:A:1379:C:H6	1.87	0.40
46:A:1396:A:O2'	46:A:1397:A:P	2.79	0.40
46:A:1441:G:H2'	46:A:1442:C:O4'	2.22	0.40
46:A:1575:G:O6	46:A:1595:U:O4	2.38	0.40
48:C:32:ILE:HB	48:C:43:VAL:HB	2.03	0.40
52:G:107:LYS:O	52:G:111:VAL:HG23	2.22	0.40
57:L:76:LEU:HB3	57:L:80:LEU:HD23	2.02	0.40
63:S:36:SER:HG	63:S:47:ARG:HH11	1.66	0.40
66:V:25:LEU:CD2	66:V:113:VAL:HG22	2.51	0.40
1:1:756:G:H1'	1:1:767:A:N6	2.37	0.40
1:1:2820:G:OP1	42:AN:24:TYR:OH	2.35	0.40
1:1:2902:A:H2'	1:1:2903:C:C6	2.57	0.40
2:3:26:C:H2'	2:3:27:A:O4'	2.21	0.40
3:4:119:C:H2'	3:4:120:U:C6	2.57	0.40
8:m:96:SER:OG	8:m:198:TYR:O	2.40	0.40
20:y:83:VAL:O	20:y:103:ALA:HA	2.21	0.40
44:AP:35:LEU:HA	44:AP:40:MLZ:HG3	2.04	0.40
46:A:107:C:H2'	46:A:108:A:H8	1.86	0.40
46:A:620:A:H4'	46:A:621:A:O5'	2.21	0.40
46:A:1386:A:H4'	63:S:60:ARG:NH2	2.36	0.40
46:A:1469:A:C5	46:A:1511:A:C5	3.10	0.40
46:A:1512:A:N3	46:A:1576:C:O2'	2.42	0.40
46:A:1556:A:OP2	46:A:1556:A:C8	2.74	0.40
46:A:1592:G:OP2	62:R:126:LYS:NZ	2.43	0.40
49:D:185:LEU:HD23	49:D:185:LEU:HA	1.95	0.40
59:O:39:LYS:HZ3	59:O:43:LYS:HE2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:O:110:ASP:O	59:O:114:ARG:HG2	2.20	0.40
72:c:56:CYS:HB3	72:c:63:LEU:HD11	2.02	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	
5	j	248/254 (98%)	241 (97%)	7 (3%)	0	100	100
6	k	385/389 (99%)	374 (97%)	11 (3%)	0	100	100
7	l	359/363 (99%)	350 (98%)	9 (2%)	0	100	100
8	m	290/298 (97%)	280 (97%)	10 (3%)	0	100	100
9	n	152/176 (86%)	150 (99%)	2 (1%)	0	100	100
10	o	225/241 (93%)	217 (96%)	8 (4%)	0	100	100
11	p	230/262 (88%)	225 (98%)	5 (2%)	0	100	100
12	q	186/191 (97%)	182 (98%)	4 (2%)	0	100	100
13	r	204/220 (93%)	201 (98%)	3 (2%)	0	100	100
14	s	171/174 (98%)	166 (97%)	5 (3%)	0	100	100
15	t	189/202 (94%)	187 (99%)	2 (1%)	0	100	100
16	u	128/131 (98%)	125 (98%)	3 (2%)	0	100	100
17	v	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
18	w	197/200 (98%)	195 (99%)	2 (1%)	0	100	100
19	x	168/185 (91%)	165 (98%)	3 (2%)	0	100	100
20	y	186/186 (100%)	182 (98%)	4 (2%)	0	100	100
21	z	178/190 (94%)	175 (98%)	3 (2%)	0	100	100
22	0	171/172 (99%)	170 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	2	159/160 (99%)	157 (99%)	2 (1%)	0	100	100
24	5	101/124 (82%)	96 (95%)	4 (4%)	1 (1%)	12	14
25	6	129/137 (94%)	126 (98%)	3 (2%)	0	100	100
26	7	61/155 (39%)	61 (100%)	0	0	100	100
27	8	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
28	9	123/127 (97%)	122 (99%)	1 (1%)	0	100	100
29	AA	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
30	AB	146/149 (98%)	138 (94%)	8 (6%)	0	100	100
31	AC	56/63 (89%)	55 (98%)	1 (2%)	0	100	100
32	AD	94/106 (89%)	93 (99%)	1 (1%)	0	100	100
33	AE	99/112 (88%)	98 (99%)	1 (1%)	0	100	100
34	AF	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
35	AG	107/107 (100%)	104 (97%)	3 (3%)	0	100	100
36	AH	114/122 (93%)	112 (98%)	2 (2%)	0	100	100
37	AI	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
38	AJ	96/99 (97%)	95 (99%)	1 (1%)	0	100	100
39	AK	84/90 (93%)	81 (96%)	3 (4%)	0	100	100
40	AL	76/78 (97%)	73 (96%)	3 (4%)	0	100	100
41	AM	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
42	AN	51/52 (98%)	51 (100%)	0	0	100	100
43	AO	23/25 (92%)	23 (100%)	0	0	100	100
44	AP	101/106 (95%)	100 (99%)	1 (1%)	0	100	100
45	AQ	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
47	B	206/261 (79%)	200 (97%)	6 (3%)	0	100	100
48	C	212/256 (83%)	207 (98%)	5 (2%)	0	100	100
49	D	214/249 (86%)	210 (98%)	4 (2%)	0	100	100
50	E	204/251 (81%)	202 (99%)	2 (1%)	0	100	100
51	F	258/262 (98%)	255 (99%)	3 (1%)	0	100	100
52	G	204/225 (91%)	197 (97%)	7 (3%)	0	100	100
53	H	224/236 (95%)	222 (99%)	2 (1%)	0	100	100
54	I	180/186 (97%)	174 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	J	181/206 (88%)	180 (99%)	1 (1%)	0	100	100
56	K	176/189 (93%)	175 (99%)	1 (1%)	0	100	100
57	L	91/118 (77%)	84 (92%)	5 (6%)	2 (2%)	5	3
58	M	131/155 (84%)	130 (99%)	1 (1%)	0	100	100
59	O	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
60	P	123/132 (93%)	119 (97%)	4 (3%)	0	100	100
61	Q	116/142 (82%)	107 (92%)	9 (8%)	0	100	100
62	R	138/142 (97%)	134 (97%)	4 (3%)	0	100	100
63	S	123/137 (90%)	121 (98%)	2 (2%)	0	100	100
64	T	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
65	U	139/145 (96%)	137 (99%)	2 (1%)	0	100	100
66	V	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
67	W	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
68	X	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
69	Y	141/145 (97%)	139 (99%)	2 (1%)	0	100	100
70	Z	130/135 (96%)	130 (100%)	0	0	100	100
71	b	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
72	c	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
73	d	60/67 (90%)	55 (92%)	5 (8%)	0	100	100
74	e	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
75	f	54/63 (86%)	52 (96%)	2 (4%)	0	100	100
All	All	10253/11113 (92%)	10025 (98%)	225 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
57	L	88	PRO
24	5	20	ALA
57	L	17	GLN

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	
5	j	191/194 (98%)	191 (100%)	0	100	100
6	k	326/328 (99%)	326 (100%)	0	100	100
7	l	290/292 (99%)	290 (100%)	0	100	100
8	m	247/252 (98%)	247 (100%)	0	100	100
9	n	135/154 (88%)	135 (100%)	0	100	100
10	o	191/204 (94%)	191 (100%)	0	100	100
11	p	193/216 (89%)	193 (100%)	0	100	100
12	q	167/170 (98%)	167 (100%)	0	100	100
13	r	178/186 (96%)	178 (100%)	0	100	100
14	s	148/149 (99%)	148 (100%)	0	100	100
15	t	161/168 (96%)	161 (100%)	0	100	100
16	u	108/109 (99%)	108 (100%)	0	100	100
17	v	177/178 (99%)	177 (100%)	0	100	100
18	w	166/167 (99%)	166 (100%)	0	100	100
19	x	142/154 (92%)	141 (99%)	1 (1%)	76	84
20	y	156/154 (101%)	156 (100%)	0	100	100
21	z	147/153 (96%)	147 (100%)	0	100	100
22	0	158/157 (101%)	158 (100%)	0	100	100
23	2	135/134 (101%)	135 (100%)	0	100	100
24	5	93/112 (83%)	91 (98%)	2 (2%)	45	60
25	6	101/103 (98%)	101 (100%)	0	100	100
26	7	57/127 (45%)	57 (100%)	0	100	100
27	8	108/121 (89%)	108 (100%)	0	100	100
28	9	110/112 (98%)	110 (100%)	0	100	100
29	AA	117/118 (99%)	117 (100%)	0	100	100
30	AB	120/121 (99%)	120 (100%)	0	100	100
31	AC	46/49 (94%)	46 (100%)	0	100	100
32	AD	81/90 (90%)	81 (100%)	0	100	100
33	AE	92/100 (92%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	AF	111/115 (96%)	111 (100%)	0	100	100
35	AG	94/92 (102%)	94 (100%)	0	100	100
36	AH	99/102 (97%)	99 (100%)	0	100	100
37	AI	106/106 (100%)	106 (100%)	0	100	100
38	AJ	78/79 (99%)	78 (100%)	0	100	100
39	AK	70/73 (96%)	70 (100%)	0	100	100
40	AL	69/69 (100%)	69 (100%)	0	100	100
41	AM	47/47 (100%)	47 (100%)	0	100	100
42	AN	48/47 (102%)	48 (100%)	0	100	100
43	AO	24/24 (100%)	24 (100%)	0	100	100
44	AP	88/89 (99%)	88 (100%)	0	100	100
45	AQ	72/73 (99%)	72 (100%)	0	100	100
47	B	176/215 (82%)	176 (100%)	0	100	100
48	C	194/229 (85%)	193 (100%)	1 (0%)	81	87
49	D	174/198 (88%)	174 (100%)	0	100	100
50	E	160/196 (82%)	160 (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	149/160 (93%)	149 (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	118/134 (88%)	118 (100%)	0	100	100
59	O	129/130 (99%)	129 (100%)	0	100	100
60	P	96/101 (95%)	96 (100%)	0	100	100
61	Q	102/121 (84%)	102 (100%)	0	100	100
62	R	114/116 (98%)	114 (100%)	0	100	100
63	S	112/122 (92%)	112 (100%)	0	100	100
64	T	126/129 (98%)	126 (100%)	0	100	100
65	U	113/117 (97%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	V	90/105 (86%)	90 (100%)	0	100	100
67	W	71/71 (100%)	71 (100%)	0	100	100
68	X	112/113 (99%)	112 (100%)	0	100	100
69	Y	116/118 (98%)	116 (100%)	0	100	100
70	Z	109/112 (97%)	109 (100%)	0	100	100
71	b	86/102 (84%)	86 (100%)	0	100	100
72	c	72/73 (99%)	72 (100%)	0	100	100
73	d	54/58 (93%)	54 (100%)	0	100	100
74	e	47/48 (98%)	47 (100%)	0	100	100
75	f	48/54 (89%)	48 (100%)	0	100	100
All	All	8809/9362 (94%)	8805 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	x	165	GLN
24	5	31[A]	GLU
24	5	31[B]	GLU
48	C	124	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
5	j	132	ASN
6	k	25	GLN
6	k	259	ASN
6	k	316	ASN
7	l	117	ASN
7	l	141	HIS
7	l	321	ASN
8	m	17	GLN
8	m	151	GLN
8	m	242	ASN
9	n	56	ASN
10	o	50	GLN
10	o	91	ASN
10	o	110	ASN

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Mol	Chain	Res	Type
11	p	146	ASN
11	p	222	ASN
12	q	129	HIS
13	r	92	HIS
14	s	109	HIS
15	t	37	GLN
16	u	112	GLN
17	v	95	GLN
18	w	193	GLN
19	x	50	GLN
20	y	158	HIS
21	z	134	HIS
24	5	25	ASN
24	5	30	GLN
25	6	9	ASN
27	8	93	HIS
28	9	81	GLN
28	9	98	ASN
29	AA	122	HIS
33	AE	68	ASN
34	AF	36	GLN
35	AG	5	HIS
37	AI	59	ASN
39	AK	69	HIS
44	AP	22	GLN
44	AP	99	GLN
45	AQ	56	ASN
47	B	30	GLN
48	C	74	GLN
48	C	149	GLN
48	C	183	GLN
48	C	209	ASN
50	E	23	ASN
51	F	130	GLN
51	F	197	HIS
54	I	19	GLN
57	L	29	GLN
57	L	39	ASN
57	L	62	GLN
58	M	81	HIS
61	Q	79	HIS
61	Q	103	ASN

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Mol	Chain	Res	Type
62	R	31	ASN
64	T	89	GLN
64	T	92	GLN
73	d	27	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3067/3359 (91%)	512 (16%)	35 (1%)
2	3	120/121 (99%)	9 (7%)	0
3	4	157/158 (99%)	24 (15%)	3 (1%)
4	10	8/14 (57%)	1 (12%)	0
46	A	1546/1787 (86%)	327 (21%)	41 (2%)
76	g	4/5 (80%)	1 (25%)	0
All	All	4902/5444 (90%)	874 (17%)	79 (1%)

All (874) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
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	91	G
1	1	98	A
1	1	104	C
1	1	108	A
1	1	109	G
1	1	110	C
1	1	121	A
1	1	134	U
1	1	135	G
1	1	155	A
1	1	156	A

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Mol	Chain	Res	Type
1	1	164	U
1	1	169	G
1	1	172	C
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	269	G
1	1	286	U
1	1	295	A
1	1	305	U
1	1	311	C
1	1	323	A
1	1	329	U
1	1	337	G
1	1	338	A
1	1	339	C
1	1	349	A
1	1	350	C
1	1	376	G
1	1	377	A
1	1	395	A
1	1	398	A
1	1	402	A
1	1	403	C

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Mol	Chain	Res	Type
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	486	C
1	1	506	A
1	1	517	A
1	1	519	U
1	1	531	G
1	1	532	U
1	1	538	G
1	1	539	G
1	1	540	C
1	1	541	U
1	1	542	U
1	1	543	C
1	1	544	U
1	1	545	G
1	1	546	C
1	1	555	A
1	1	556	U
1	1	557	A
1	1	564	G
1	1	577	G
1	1	589	G
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
1	1	619	A
1	1	620	A
1	1	635	C
1	1	647	A
1	1	658	A
1	1	675	A
1	1	679	U
1	1	688	A

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Mol	Chain	Res	Type
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	760	U
1	1	763	U
1	1	772	U
1	1	773	U
1	1	776	A
1	1	777	G
1	1	780	A
1	1	781	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	921	A
1	1	933	G
1	1	940	C
1	1	949	G
1	1	955	C
1	1	956	U
1	1	959	G
1	1	976	A
1	1	977	U
1	1	990	G

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Mol	Chain	Res	Type
1	1	991	U
1	1	996	C
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	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	1150	A
1	1	1151	C
1	1	1155	A
1	1	1156	C
1	1	1164	U
1	1	1174	G
1	1	1176	A
1	1	1177	U
1	1	1178	G
1	1	1188	C
1	1	1189	A
1	1	1192	C
1	1	1197	C
1	1	1204	U

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Mol	Chain	Res	Type
1	1	1205	G
1	1	1215	C
1	1	1218	G
1	1	1223	C
1	1	1224	C
1	1	1280	C
1	1	1282	A
1	1	1283	A
1	1	1303	G
1	1	1304	A
1	1	1305	U
1	1	1309	G
1	1	1326	A
1	1	1345	G
1	1	1346	U
1	1	1347	U
1	1	1348	U
1	1	1349	U
1	1	1382	A
1	1	1395	U
1	1	1415	A
1	1	1417	G
1	1	1421	U
1	1	1427	G
1	1	1430	G
1	1	1433	C
1	1	1442	A
1	1	1446	G
1	1	1465	C
1	1	1471	A
1	1	1477	A
1	1	1484	G
1	1	1498	C
1	1	1504	C
1	1	1520	A
1	1	1523	C
1	1	1532	G
1	1	1535	A
1	1	1552	C
1	1	1556	G
1	1	1558	G
1	1	1559	C

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Mol	Chain	Res	Type
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
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	1589	A
1	1	1601	A
1	1	1603	U
1	1	1624	C
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	1654	G
1	1	1679	A
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	1757	A
1	1	1758	U
1	1	1760	U
1	1	1761	U
1	1	1762	G
1	1	1763	C
1	1	1776	G
1	1	1793	A

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Mol	Chain	Res	Type
1	1	1804	G
1	1	1809	A
1	1	1810	A
1	1	1811	U
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
1	1	1845	C
1	1	1862	C
1	1	1874	G
1	1	1877	A
1	1	1882	A
1	1	1889	A
1	1	1902	G
1	1	1944	G
1	1	1949	G
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	2183	U
1	1	2184	G
1	1	2185	A
1	1	2186	A
1	1	2187	U
1	1	2188	G

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Mol	Chain	Res	Type
1	1	2222	A
1	1	2227	G
1	1	2229	G
1	1	2231	G
1	1	2232	U
1	1	2233	A
1	1	2234	A
1	1	2235	C
1	1	2242	U
1	1	2243	C
1	1	2246	U
1	1	2247	U
1	1	2250	G
1	1	2251	G
1	1	2257	A
1	1	2259	A
1	1	2260	U
1	1	2276	U
1	1	2285	G
1	1	2286	C
1	1	2288	U
1	1	2291	A
1	1	2292	U
1	1	2293	G
1	1	2312	U
1	1	2313	G
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	2372	G
1	1	2375	A
1	1	2380	A
1	1	2381	G
1	1	2382	A
1	1	2389	U
1	1	2413	G
1	1	2415	G

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Mol	Chain	Res	Type
1	1	2420	G
1	1	2489	A
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
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	2554	C
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	2662	G
1	1	2663	A
1	1	2666	A
1	1	2676	A
1	1	2677	A
1	1	2686	G
1	1	2687	A

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Mol	Chain	Res	Type
1	1	2699	A
1	1	2700	G
1	1	2701	U
1	1	2724	U
1	1	2725	G
1	1	2734	A
1	1	2745	C
1	1	2749	G
1	1	2750	G
1	1	2768	G
1	1	2771	A
1	1	2772	G
1	1	2773	A
1	1	2774	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	2817	A
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	2886	G
1	1	2895	U
1	1	2907	U
1	1	2908	A
1	1	2911	G
1	1	2914	C
1	1	2919	G
1	1	2920	C
1	1	2923	G
1	1	2926	U
1	1	2943	A

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Mol	Chain	Res	Type
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
1	1	3058	A
1	1	3064	C
1	1	3076	U
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	3134	C
1	1	3143	G
1	1	3144	A
1	1	3146	G
1	1	3149	U
1	1	3151	C
1	1	3157	A
1	1	3160	C
1	1	3163	U
1	1	3164	U
1	1	3171	C
1	1	3172	U
1	1	3182	C
1	1	3183	A
1	1	3184	G
1	1	3194	G
1	1	3208	A
1	1	3210	A
1	1	3212	G
1	1	3214	U
1	1	3221	G
1	1	3224	U

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Mol	Chain	Res	Type
1	1	3228	G
1	1	3235	A
1	1	3241	G
1	1	3246	C
1	1	3252	C
1	1	3259	A
1	1	3260	A
1	1	3268	G
1	1	3269	C
1	1	3272	A
1	1	3278	U
1	1	3281	A
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	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	59	A
3	4	62	C

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Mol	Chain	Res	Type
3	4	63	G
3	4	81	A
3	4	84	C
3	4	85	G
3	4	86	U
3	4	87	G
3	4	92	A
3	4	95	G
3	4	102	U
3	4	104	A
3	4	106	C
3	4	107	G
3	4	111	A
3	4	113	U
3	4	125	U
3	4	126	A
3	4	148	G
3	4	152	G
3	4	157	U
4	10	76	A
46	A	17	C
46	A	25	C
46	A	26	A
46	A	27	U
46	A	34	G
46	A	47	A
46	A	57	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	115	G
46	A	123	G
46	A	126	A
46	A	127	G
46	A	128	U

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Mol	Chain	Res	Type
46	A	129	A
46	A	138	C
46	A	139	U
46	A	142	G
46	A	143	A
46	A	150	U
46	A	151	G
46	A	152	G
46	A	154	A
46	A	159	U
46	A	166	A
46	A	168	U
46	A	173	G
46	A	176	U
46	A	177	A
46	A	179	A
46	A	190	U
46	A	191	U
46	A	193	G
46	A	199	G
46	A	200	A
46	A	202	G
46	A	206	U
46	A	211	A
46	A	247	U
46	A	255	A
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
46	A	274	C
46	A	276	U
46	A	277	G
46	A	278	U
46	A	279	G
46	A	283	G
46	A	285	G
46	A	297	A
46	A	312	C

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Mol	Chain	Res	Type
46	A	314	A
46	A	318	U
46	A	320	G
46	A	335	G
46	A	336	C
46	A	350	A
46	A	357	A
46	A	358	A
46	A	359	C
46	A	388	G
46	A	398	A
46	A	400	C
46	A	402	G
46	A	414	A
46	A	416	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	446	C
46	A	452	A
46	A	458	A
46	A	466	A
46	A	475	A
46	A	480	U
46	A	482	C
46	A	483	A
46	A	485	G
46	A	501	G
46	A	502	U
46	A	503	A
46	A	504	A
46	A	505	U
46	A	506	U
46	A	509	A
46	A	512	G
46	A	513	A
46	A	515	U
46	A	518	A

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Mol	Chain	Res	Type
46	A	519	A
46	A	525	A
46	A	530	U
46	A	534	C
46	A	536	A
46	A	537	G
46	A	539	A
46	A	540	A
46	A	547	G
46	A	553	A
46	A	554	A
46	A	555	G
46	A	556	U
46	A	557	C
46	A	563	C
46	A	566	G
46	A	575	G
46	A	576	U
46	A	580	U
46	A	592	A
46	A	593	G
46	A	604	A
46	A	609	U
46	A	617	A
46	A	618	A
46	A	620	A
46	A	621	A
46	A	639	G
46	A	648	U
46	A	682	A
46	A	686	G
46	A	687	A
46	A	688	G
46	A	729	U
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

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Mol	Chain	Res	Type
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	775	A
46	A	778	U
46	A	779	U
46	A	796	A
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	840	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	878	U
46	A	879	U
46	A	881	U
46	A	891	A
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

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Mol	Chain	Res	Type
46	A	988	A
46	A	989	U
46	A	997	U
46	A	998	A
46	A	1004	A
46	A	1005	A
46	A	1011	A
46	A	1013	C
46	A	1017	G
46	A	1024	A
46	A	1025	G
46	A	1039	U
46	A	1055	A
46	A	1056	U
46	A	1057	C
46	A	1058	G
46	A	1059	G
46	A	1060	C
46	A	1061	A
46	A	1067	C
46	A	1077	A
46	A	1081	C
46	A	1085	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	1193	A
46	A	1202	A
46	A	1203	G
46	A	1206	A
46	A	1207	C

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Mol	Chain	Res	Type
46	A	1229	A
46	A	1230	G
46	A	1231	C
46	A	1250	G
46	A	1270	U
46	A	1284	G
46	A	1299	U
46	A	1300	U
46	A	1301	G
46	A	1306	A
46	A	1325	U
46	A	1330	A
46	A	1336	G
46	A	1364	U
46	A	1365	C
46	A	1369	G
46	A	1370	A
46	A	1376	U
46	A	1380	G
46	A	1381	A
46	A	1382	U
46	A	1384	U
46	A	1385	C
46	A	1392	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	1422	A
46	A	1431	G
46	A	1433	C
46	A	1445	C
46	A	1446	A
46	A	1455	A
46	A	1457	A
46	A	1458	C
46	A	1461	A

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Mol	Chain	Res	Type
46	A	1462	C
46	A	1463	G
46	A	1468	C
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	1508	G
46	A	1510	G
46	A	1511	A
46	A	1523	G
46	A	1524	C
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	1577	G
46	A	1580	A
46	A	1582	U
46	A	1584	A
46	A	1588	G
46	A	1621	C
46	A	1644	U
46	A	1645	G
46	A	1665	C
46	A	1667	G
46	A	1670	U
46	A	1671	G
46	A	1672	G
46	A	1737	A
46	A	1743	A
46	A	1747	G

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Mol	Chain	Res	Type
46	A	1749	A
46	A	1753	A
46	A	1756	U
46	A	1767	G
46	A	1769	A
46	A	1770	C
46	A	1779	G
46	A	1780	G
46	A	1781	A
46	A	1782	U
46	A	1783	C
76	g	2	G

All (79) 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	1346	U
1	1	1347	U
1	1	1559	C
1	1	1561	U
1	1	1576	A
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	2545	C
1	1	2789	A
1	1	2790	U

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Mol	Chain	Res	Type
1	1	3093	U
1	1	3159	A
1	1	3193	C
1	1	3234	U
1	1	3240	U
1	1	3284	U
1	1	3309	A
1	1	3315	C
1	1	3317	U
3	4	85	G
3	4	125	U
3	4	156	U
46	A	25	C
46	A	78	A
46	A	137	A
46	A	151	G
46	A	176	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	556	U
46	A	638	U
46	A	685	C
46	A	740	A
46	A	763	C
46	A	769	U
46	A	855	C
46	A	874	U
46	A	876	A
46	A	1168	A
46	A	1335	U
46	A	1369	G

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Mol	Chain	Res	Type
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	2.90	8 (42%)	25,31,34	1.19	3 (12%)
1	OMG	1	2765	1	23,26,27	2.31	9 (39%)	32,38,41	1.87	9 (28%)
25	MLZ	6	110	25	8,9,10	0.74	0	4,9,11	0.97	0
44	MLZ	AP	55	44	8,9,10	0.67	0	4,9,11	0.73	0
60	IAS	P	119	60	6,7,8	1.03	0	3,8,10	1.64	1 (33%)
44	MLZ	AP	40	44	8,9,10	0.68	0	4,9,11	1.05	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
1	OMG	1	2765	1	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	MLZ	6	110	25	-	3/7/8/10	-
44	MLZ	AP	55	44	-	3/7/8/10	-
60	IAS	P	119	60	-	1/7/7/8	-
44	MLZ	AP	40	44	-	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	6.19	1.48	1.34
1	1	2808	OMC	C2-N3	5.91	1.48	1.36
1	1	2808	OMC	C6-C5	5.87	1.48	1.35
1	1	2765	OMG	C2-N3	5.18	1.45	1.33
1	1	2808	OMC	C2-N1	4.86	1.50	1.40
1	1	2808	OMC	C4-N4	4.43	1.44	1.33
1	1	2808	OMC	C4-N3	4.42	1.43	1.34
1	1	2765	OMG	C2-N2	3.94	1.43	1.34
1	1	2808	OMC	O2-C2	-3.26	1.17	1.23
1	1	2765	OMG	O6-C6	-3.09	1.17	1.23
1	1	2808	OMC	C6-N1	3.08	1.45	1.38
1	1	2765	OMG	C5-N7	-2.98	1.33	1.39
1	1	2765	OMG	C4-N9	-2.29	1.32	1.38
1	1	2765	OMG	C2-N1	2.24	1.43	1.37
1	1	2808	OMC	C5-C4	2.19	1.48	1.42
1	1	2765	OMG	C5-C6	2.12	1.52	1.44
1	1	2765	OMG	C6-N1	2.09	1.42	1.38

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2765	OMG	C5-C4-N3	-4.72	120.88	128.39
1	1	2765	OMG	C2-N3-C4	4.58	120.19	112.30
1	1	2808	OMC	O2-C2-N3	-3.60	116.66	122.33
1	1	2765	OMG	N9-C8-N7	-3.29	107.31	113.40
1	1	2765	OMG	C2-N1-C6	-2.88	119.88	125.11
1	1	2765	OMG	C5-C6-N1	2.83	120.47	113.25
1	1	2765	OMG	N9-C4-N3	2.70	131.35	125.95
1	1	2765	OMG	O6-C6-C5	-2.57	119.76	126.53
1	1	2765	OMG	N1-C2-N3	-2.12	119.44	123.32
1	1	2765	OMG	C8-N7-C5	2.11	108.02	104.26
1	1	2808	OMC	C6-C5-C4	2.05	120.89	117.53
1	1	2808	OMC	C1'-N1-C2	2.02	122.91	118.44
60	P	119	IAS	OXT-C-O	-2.00	119.54	124.08

There are no chirality outliers.

All (10) 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
25	6	110	MLZ	N-CA-CB-CG
25	6	110	MLZ	C-CA-CB-CG
25	6	110	MLZ	CD-CE-NZ-CM
44	AP	55	MLZ	CG-CD-CE-NZ
44	AP	55	MLZ	CE-CD-CG-CB
44	AP	55	MLZ	CA-CB-CG-CD
60	P	119	IAS	CA-CB-CG-OD1

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	2808	OMC	4	0
44	AP	40	MLZ	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 379 ligands modelled in this entry, 374 are monoatomic - leaving 5 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	$\# Z > 2$
78	K16	1	3402	-	38,38,38	3.13	21 (55%)	50,55,55	1.92	17 (34%)
78	K16	1	3403	-	38,38,38	3.05	21 (55%)	50,55,55	1.92	17 (34%)
79	SPD	1	3404	-	9,9,9	0.33	0	8,8,8	1.04	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
78	K16	A	1801	-	38,38,38	3.01	19 (50%)	50,55,55	2.04	19 (38%)
77	SPK	1	3401	-	13,13,13	0.36	0	12,12,12	0.69	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
78	K16	1	3402	-	-	6/12/47/47	0/5/5/5
78	K16	1	3403	-	-	2/12/47/47	1/5/5/5
79	SPD	1	3404	-	-	1/7/7/7	-
78	K16	A	1801	-	-	8/12/47/47	0/5/5/5
77	SPK	1	3401	-	-	7/11/11/11	-

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
78	1	3402	K16	C15-C14	8.97	1.63	1.53
78	1	3403	K16	C15-C14	7.56	1.61	1.53
78	A	1801	K16	C15-C14	6.20	1.60	1.53
78	A	1801	K16	C17-C18	5.70	1.59	1.53
78	1	3403	K16	C06-C07	5.55	1.62	1.51
78	1	3402	K16	C06-C07	5.51	1.62	1.51
78	1	3402	K16	C17-C16	5.50	1.64	1.53
78	A	1801	K16	C06-C07	5.43	1.62	1.51
78	A	1801	K16	C17-C16	5.36	1.64	1.53
78	1	3403	K16	C17-C16	5.23	1.64	1.53
78	1	3402	K16	C06-N05	-5.14	1.37	1.47
78	A	1801	K16	C06-N05	-5.10	1.37	1.47
78	1	3403	K16	C06-N05	-4.91	1.38	1.47
78	1	3403	K16	C07-C08	4.88	1.59	1.51
78	1	3402	K16	C07-C08	4.88	1.59	1.51
78	A	1801	K16	C07-C08	4.78	1.59	1.51
78	1	3403	K16	C17-C18	4.69	1.58	1.53
78	1	3403	K16	C08-C13	-4.65	1.32	1.40
78	1	3402	K16	C17-C18	4.63	1.58	1.53
78	A	1801	K16	C08-C13	-4.37	1.32	1.40
78	1	3402	K16	O33-C10	4.31	1.44	1.37
78	A	1801	K16	C19-C18	4.24	1.56	1.52
78	1	3403	K16	O33-C10	4.04	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
78	A	1801	K16	O33-C10	4.04	1.43	1.37
78	1	3403	K16	C04-C03	4.01	1.59	1.53
78	A	1801	K16	C04-C03	3.97	1.59	1.53
78	1	3402	K16	C08-C13	-3.87	1.33	1.40
78	1	3403	K16	C09-C08	3.80	1.45	1.39
78	A	1801	K16	C09-C08	3.77	1.45	1.39
78	1	3402	K16	C09-C08	3.61	1.45	1.39
78	1	3403	K16	C19-C18	3.59	1.55	1.52
78	1	3403	K16	C23-C24	3.52	1.45	1.39
78	A	1801	K16	C20-C19	3.36	1.45	1.39
78	1	3402	K16	C04-C03	3.30	1.58	1.53
78	A	1801	K16	C24-C19	-3.29	1.34	1.40
78	1	3402	K16	C23-C24	3.29	1.44	1.39
78	1	3402	K16	C24-C19	-3.28	1.34	1.40
78	1	3402	K16	C20-C19	3.28	1.44	1.39
78	A	1801	K16	C23-C24	3.22	1.44	1.39
78	1	3402	K16	C19-C18	3.19	1.55	1.52
78	1	3403	K16	C20-C19	3.18	1.44	1.39
78	A	1801	K16	O29-C21	2.98	1.42	1.37
78	1	3403	K16	C24-C19	-2.91	1.35	1.40
78	1	3402	K16	C12-C13	2.90	1.44	1.39
78	1	3402	K16	C18-N27	-2.87	1.44	1.47
78	1	3402	K16	O29-C21	2.87	1.41	1.37
78	A	1801	K16	C12-C13	2.84	1.44	1.39
78	1	3403	K16	O29-C21	2.82	1.41	1.37
78	1	3403	K16	C12-C13	2.80	1.44	1.39
78	1	3403	K16	C15-C16	-2.78	1.46	1.53
78	1	3402	K16	O31-C11	2.72	1.41	1.37
78	1	3403	K16	C18-N27	-2.64	1.44	1.47
78	1	3403	K16	O31-C11	2.51	1.41	1.37
78	1	3402	K16	C03-C16	-2.42	1.46	1.53
78	A	1801	K16	O31-C11	2.37	1.41	1.37
78	A	1801	K16	C15-C16	-2.32	1.47	1.53
78	1	3402	K16	C15-C16	-2.27	1.48	1.53
78	1	3403	K16	O28-C22	2.21	1.40	1.36
78	A	1801	K16	O28-C22	2.20	1.40	1.36
78	1	3403	K16	C03-C16	-2.20	1.47	1.53
78	1	3402	K16	O28-C22	2.12	1.40	1.36

All (53) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	1	3402	K16	C25-C26-N27	4.81	115.55	109.02
78	A	1801	K16	C25-C26-N27	4.66	115.34	109.02
78	A	1801	K16	C15-C16-C03	4.36	117.72	110.57
78	1	3403	K16	C04-N05-C14	4.34	116.45	110.12
78	1	3403	K16	C06-N05-C14	4.14	119.44	111.21
78	1	3402	K16	O33-C10-C11	4.01	120.84	115.40
78	A	1801	K16	C15-C14-C13	-3.81	107.65	113.07
78	1	3403	K16	C06-N05-C04	3.76	117.56	110.32
78	A	1801	K16	C06-N05-C04	3.55	117.14	110.32
78	A	1801	K16	C04-C03-C16	3.42	114.79	108.12
78	1	3403	K16	O29-C21-C22	3.41	119.67	114.55
78	1	3403	K16	C25-C26-N27	3.41	113.65	109.02
78	A	1801	K16	C26-N27-C18	3.27	117.92	111.51
78	1	3402	K16	O29-C21-C22	3.25	119.42	114.55
78	1	3403	K16	C04-C03-C16	3.21	114.38	108.12
78	1	3402	K16	C17-C16-C03	-3.17	106.27	114.34
78	A	1801	K16	C34-O33-C10	-3.17	112.86	117.51
78	1	3403	K16	O31-C11-C10	3.14	119.66	115.40
78	1	3402	K16	O33-C10-C09	-3.13	118.68	124.08
78	A	1801	K16	C16-C15-C14	3.12	117.57	111.76
78	1	3402	K16	O31-C11-C10	3.12	119.63	115.40
78	A	1801	K16	O29-C21-C22	3.08	119.16	114.55
78	1	3402	K16	C04-N05-C14	3.05	114.57	110.12
78	1	3402	K16	C24-C19-C18	-2.98	117.80	121.38
78	1	3402	K16	C03-C04-N05	-2.95	108.28	112.17
78	A	1801	K16	O33-C10-C11	2.82	119.22	115.40
78	1	3402	K16	C06-N05-C14	2.75	116.69	111.21
78	A	1801	K16	O31-C11-C10	2.71	119.09	115.40
78	1	3403	K16	C17-C16-C03	-2.69	107.50	114.34
78	1	3403	K16	O33-C10-C11	2.66	119.01	115.40
78	A	1801	K16	C06-N05-C14	2.60	116.38	111.21
78	A	1801	K16	O33-C10-C09	-2.51	119.75	124.08
78	1	3402	K16	O31-C11-C12	-2.48	119.80	124.08
78	1	3403	K16	C12-C13-C14	-2.46	115.46	119.36
78	1	3402	K16	C07-C08-C09	-2.44	115.10	119.91
78	1	3402	K16	C06-N05-C04	2.41	114.96	110.32
78	1	3403	K16	O33-C10-C09	-2.40	119.94	124.08
78	A	1801	K16	C17-C16-C03	-2.31	108.47	114.34
78	1	3403	K16	O31-C11-C12	-2.30	120.11	124.08
78	A	1801	K16	C10-C09-C08	-2.29	117.66	121.10
78	1	3403	K16	C15-C14-C13	-2.29	109.82	113.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	1	3402	K16	C26-C25-C24	2.28	114.70	110.66
78	A	1801	K16	O31-C11-C12	-2.26	120.19	124.08
78	1	3402	K16	C34-O33-C10	-2.23	114.24	117.51
78	A	1801	K16	C32-O31-C11	-2.21	114.27	117.51
78	1	3403	K16	C10-C09-C08	-2.20	117.80	121.10
78	A	1801	K16	C12-C13-C14	-2.13	115.99	119.36
78	1	3402	K16	O29-C21-C20	-2.11	120.44	124.08
78	1	3403	K16	O29-C21-C20	-2.09	120.48	124.08
78	A	1801	K16	C06-C07-C08	-2.08	107.75	111.34
78	1	3402	K16	C09-C08-C13	2.05	122.07	119.49
78	1	3403	K16	C34-O33-C10	-2.01	114.56	117.51
78	1	3403	K16	C02-C03-C16	-2.01	109.43	114.56

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
78	1	3402	K16	C01-C02-C03-C04
78	A	1801	K16	C01-C02-C03-C16
78	A	1801	K16	C01-C02-C03-C04
78	A	1801	K16	C10-C11-O31-C32
77	1	3401	SPK	C7-C8-C9-N10
78	1	3402	K16	C22-C21-O29-C30
78	A	1801	K16	C12-C11-O31-C32
77	1	3401	SPK	N5-C6-C7-C8
78	A	1801	K16	C11-C10-O33-C34
78	1	3402	K16	C20-C21-O29-C30
77	1	3401	SPK	C7-C6-N5-C4
77	1	3401	SPK	C12-C11-N10-C9
78	1	3402	K16	C01-C02-C03-C16
78	A	1801	K16	C09-C10-O33-C34
77	1	3401	SPK	C3-C4-N5-C6
79	1	3404	SPD	C2-C3-C4-C5
77	1	3401	SPK	C11-C12-C13-N14
78	A	1801	K16	C03-C16-C17-C18
77	1	3401	SPK	C2-C3-C4-N5
78	1	3403	K16	C01-C02-C03-C04
78	1	3402	K16	C10-C11-O31-C32
78	A	1801	K16	C22-C21-O29-C30
78	1	3403	K16	C01-C02-C03-C16
78	1	3402	K16	C12-C11-O31-C32

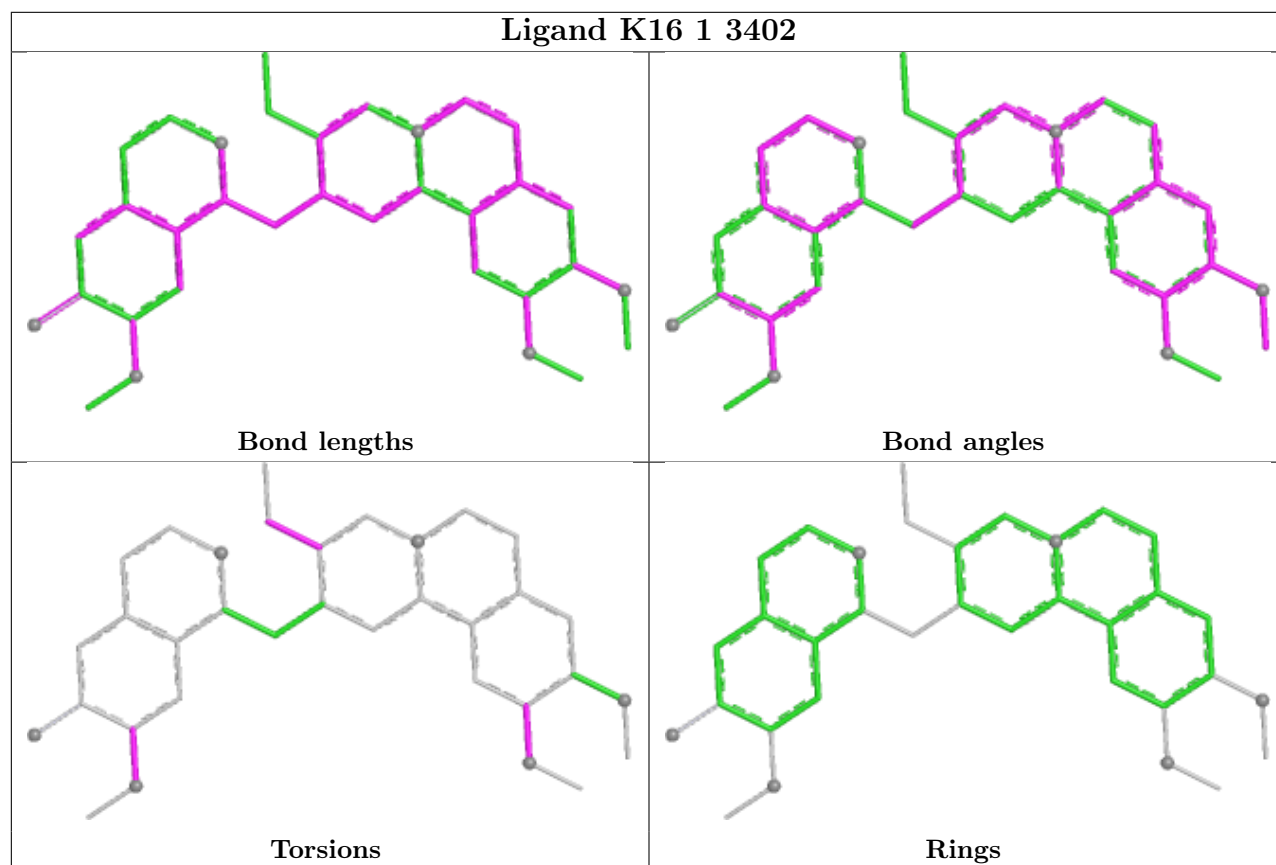
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
78	1	3403	K16	C03-C04-C14-C15-C16-N05

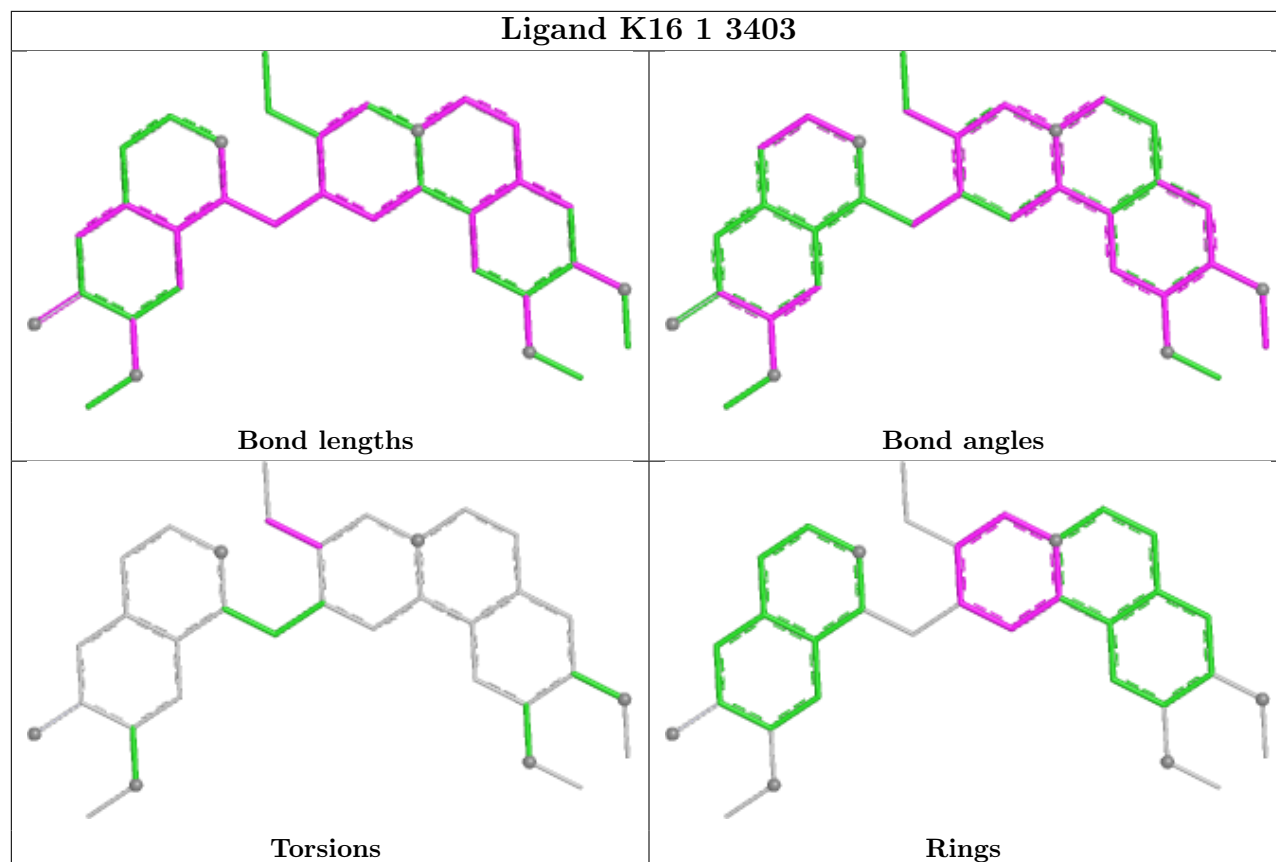
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
79	1	3404	SPD	1	0
77	1	3401	SPK	1	0

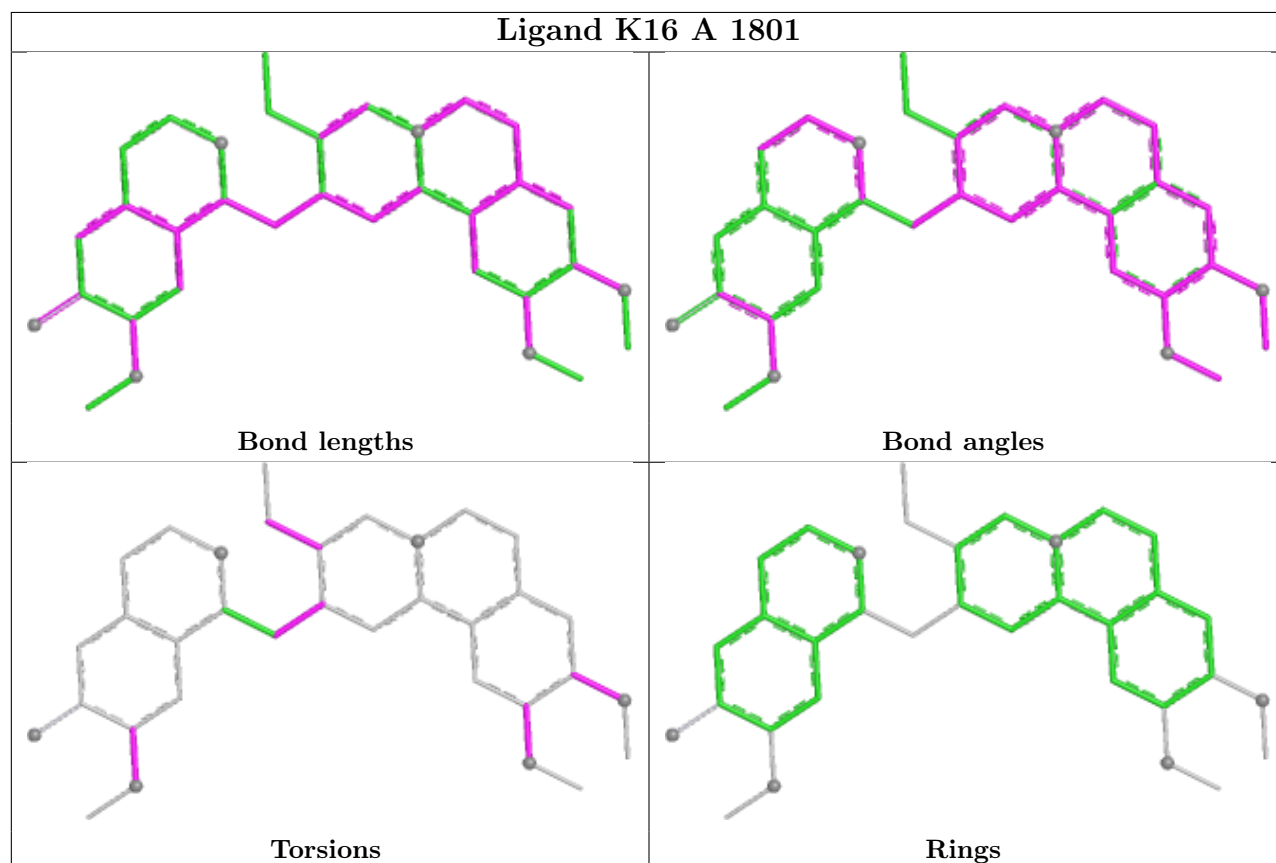
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



Ligand K16 1 3403



Ligand K16 A 1801



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.

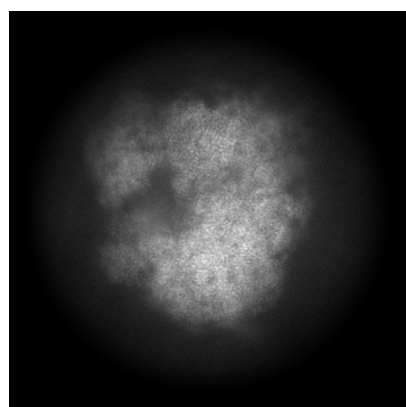
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18156. These allow visual inspection of the internal detail of the map and identification of artifacts.

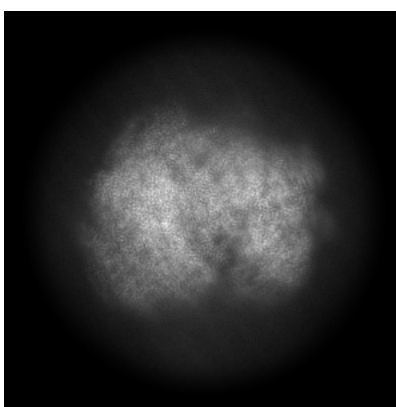
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

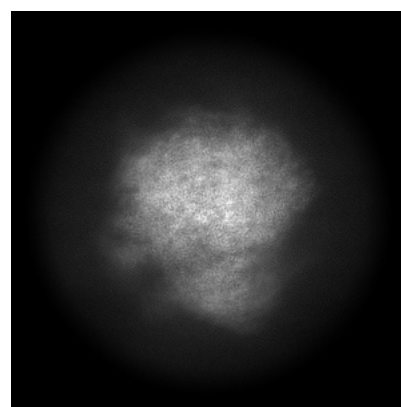
6.1.1 Primary map



X



Y

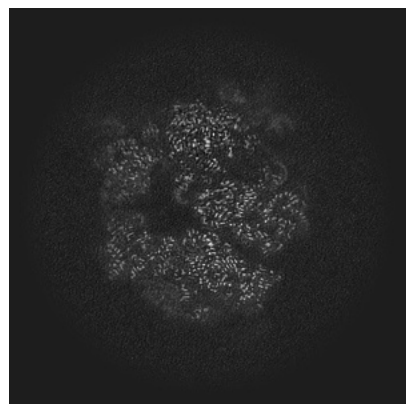


Z

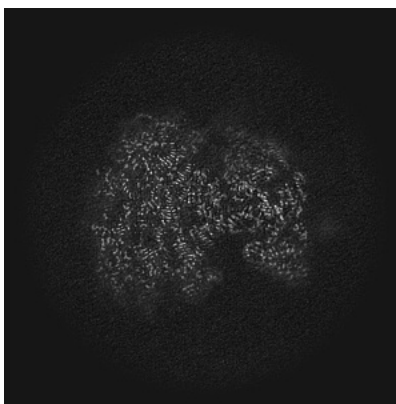
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

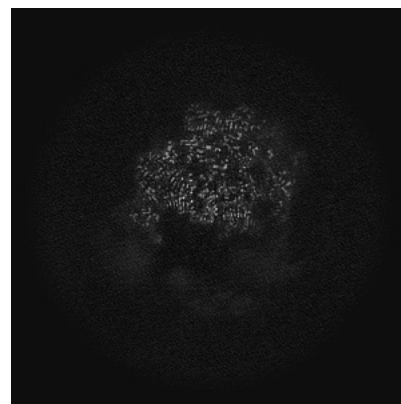
6.2.1 Primary map



X Index: 255



Y Index: 255

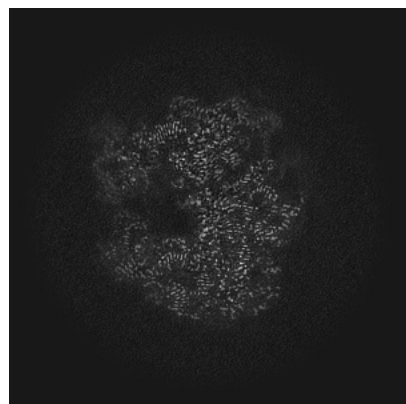


Z Index: 255

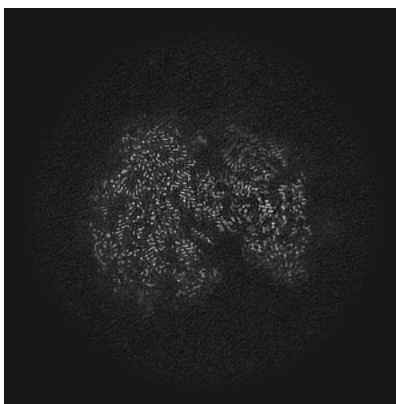
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

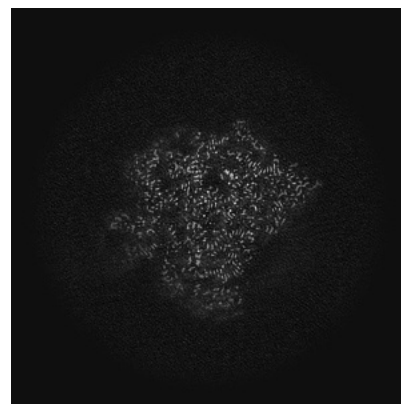
6.3.1 Primary map



X Index: 274



Y Index: 252

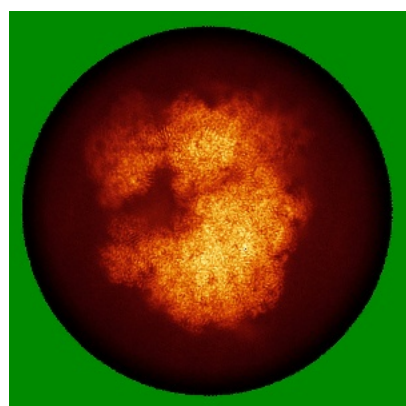


Z Index: 206

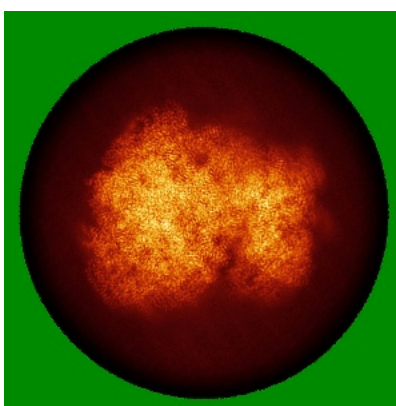
The images above show the largest variance slices of the map in three orthogonal directions.

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

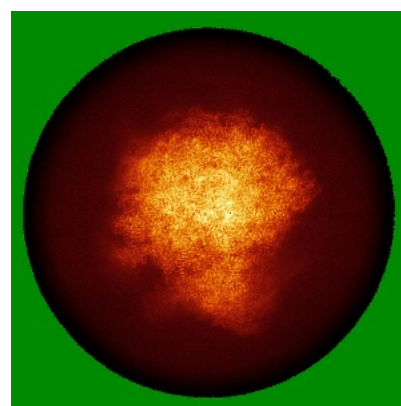
6.4.1 Primary map



X



Y

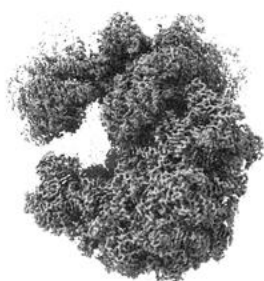


Z

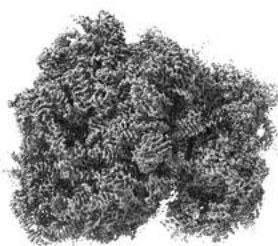
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.274. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

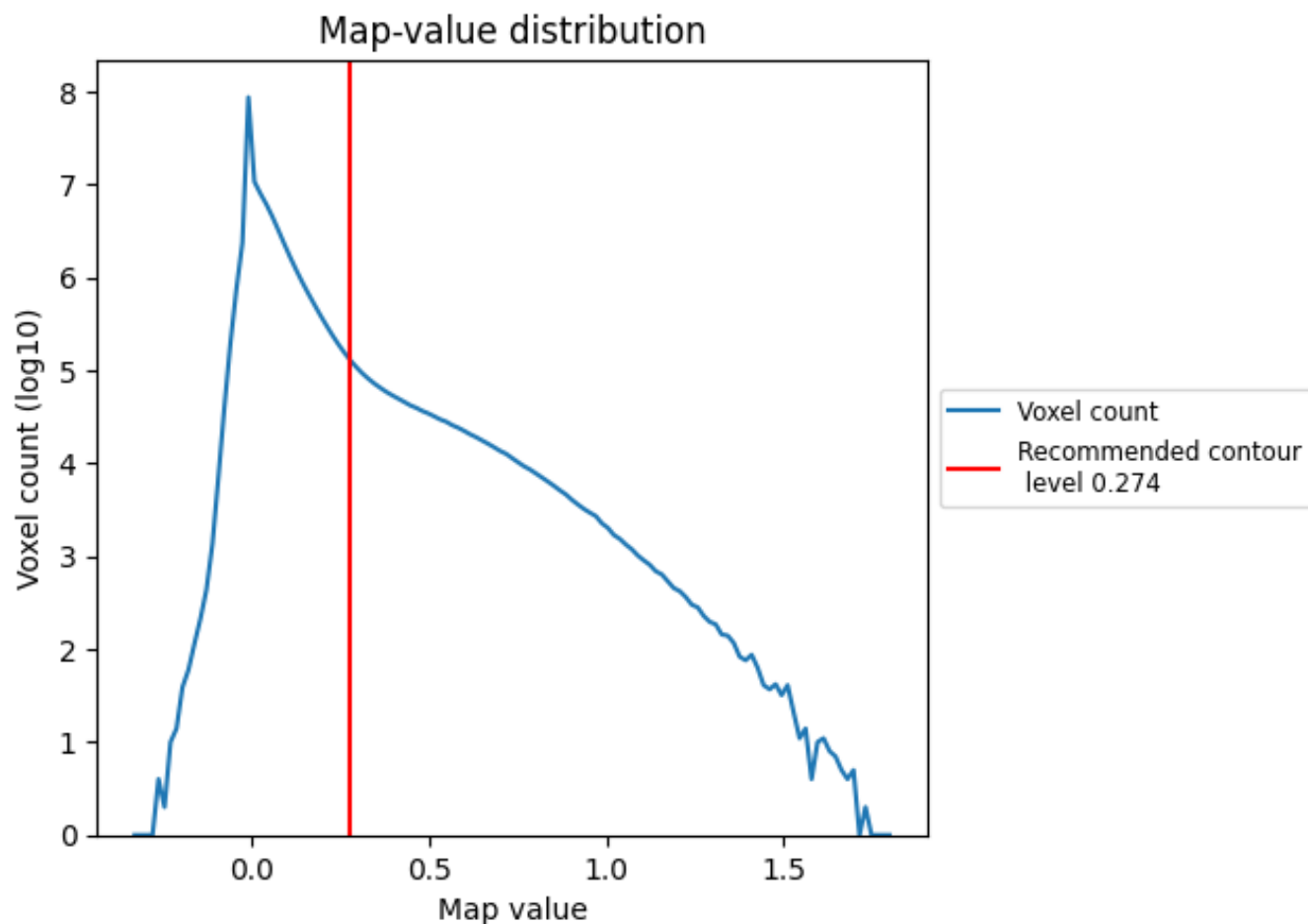
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

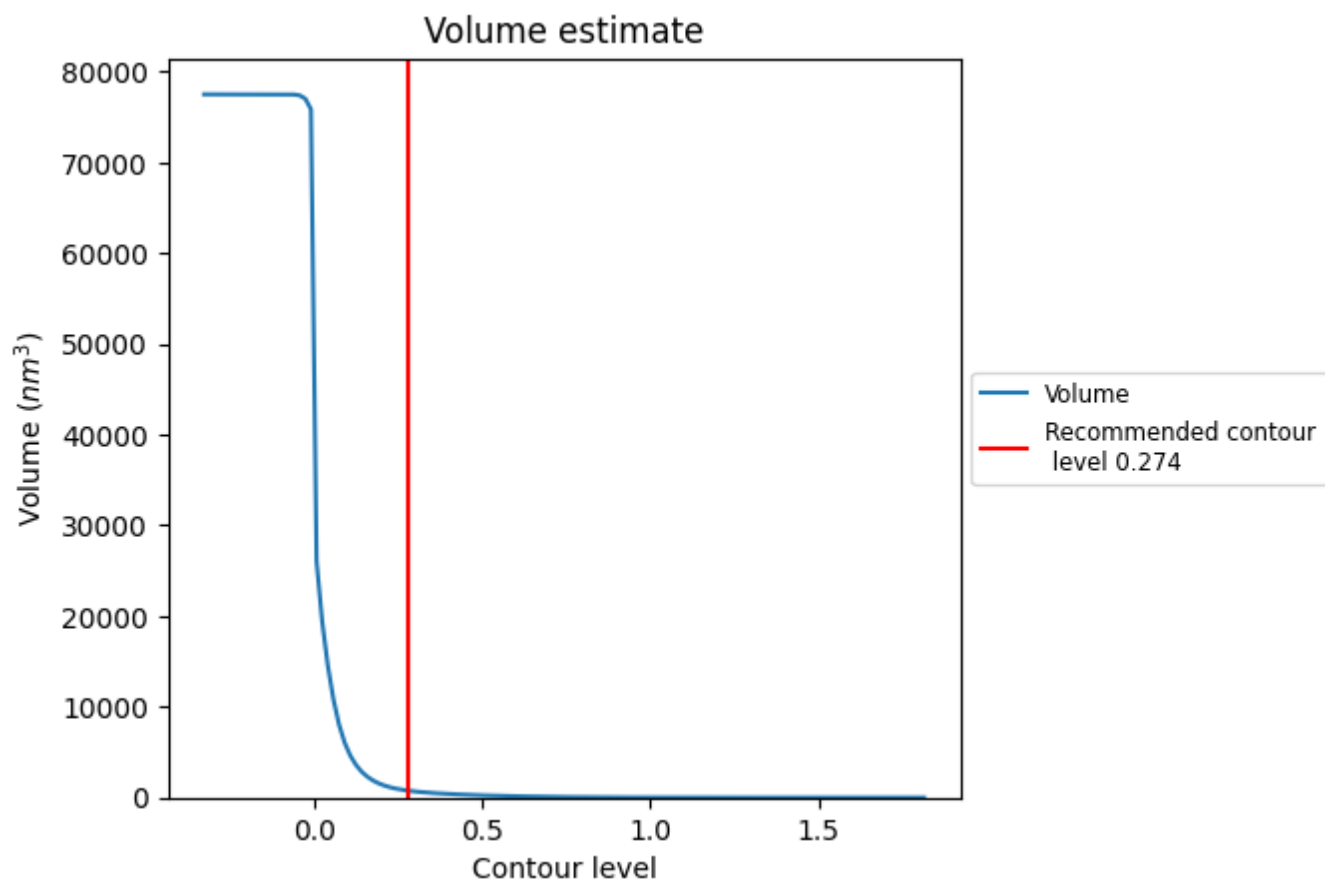
This section contains the results of statistical analysis of the map.

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.

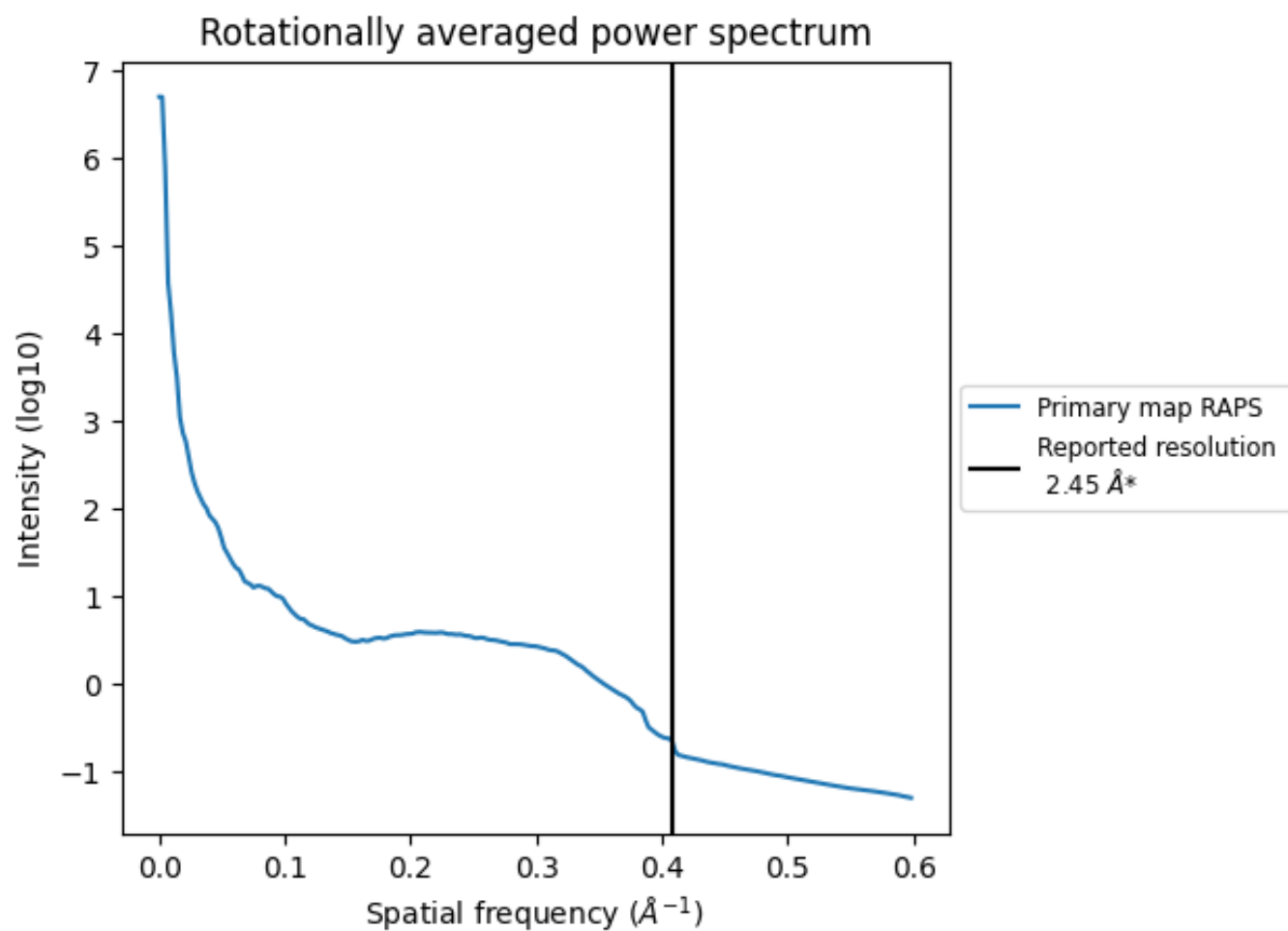
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 775 nm³; this corresponds to an approximate mass of 700 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 0.408 Å⁻¹

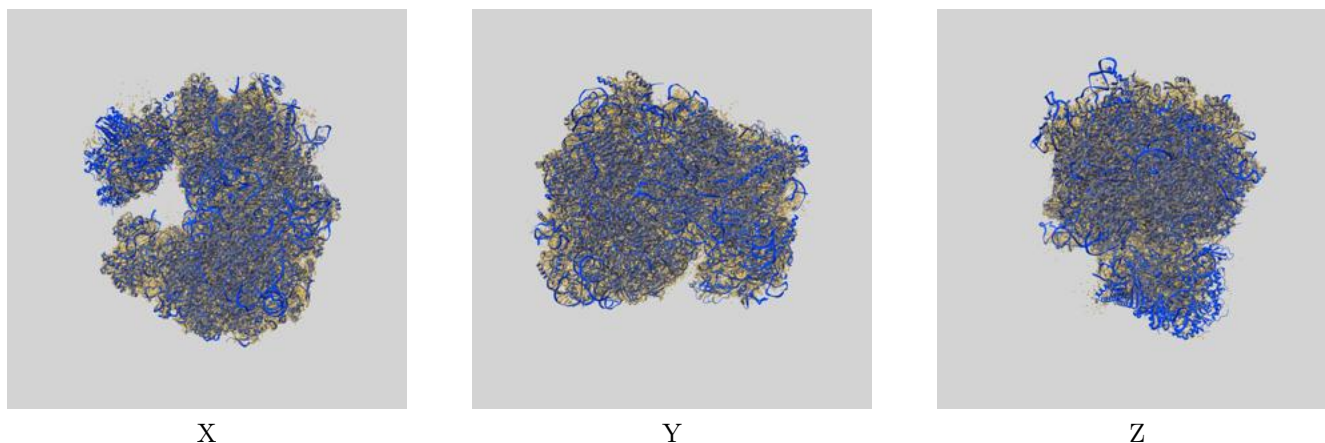
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

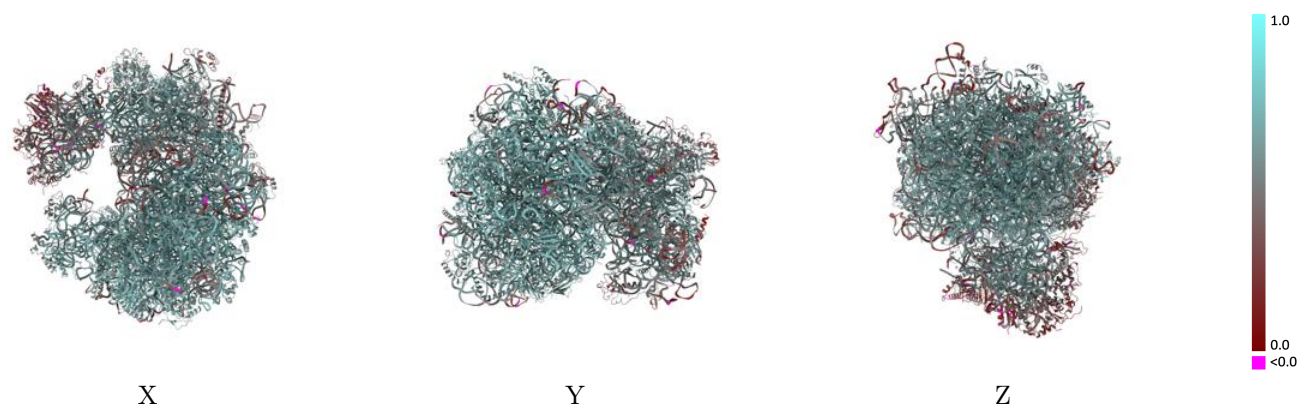
This section contains information regarding the fit between EMDB map EMD-18156 and PDB model 8Q5I. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.274 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](#)

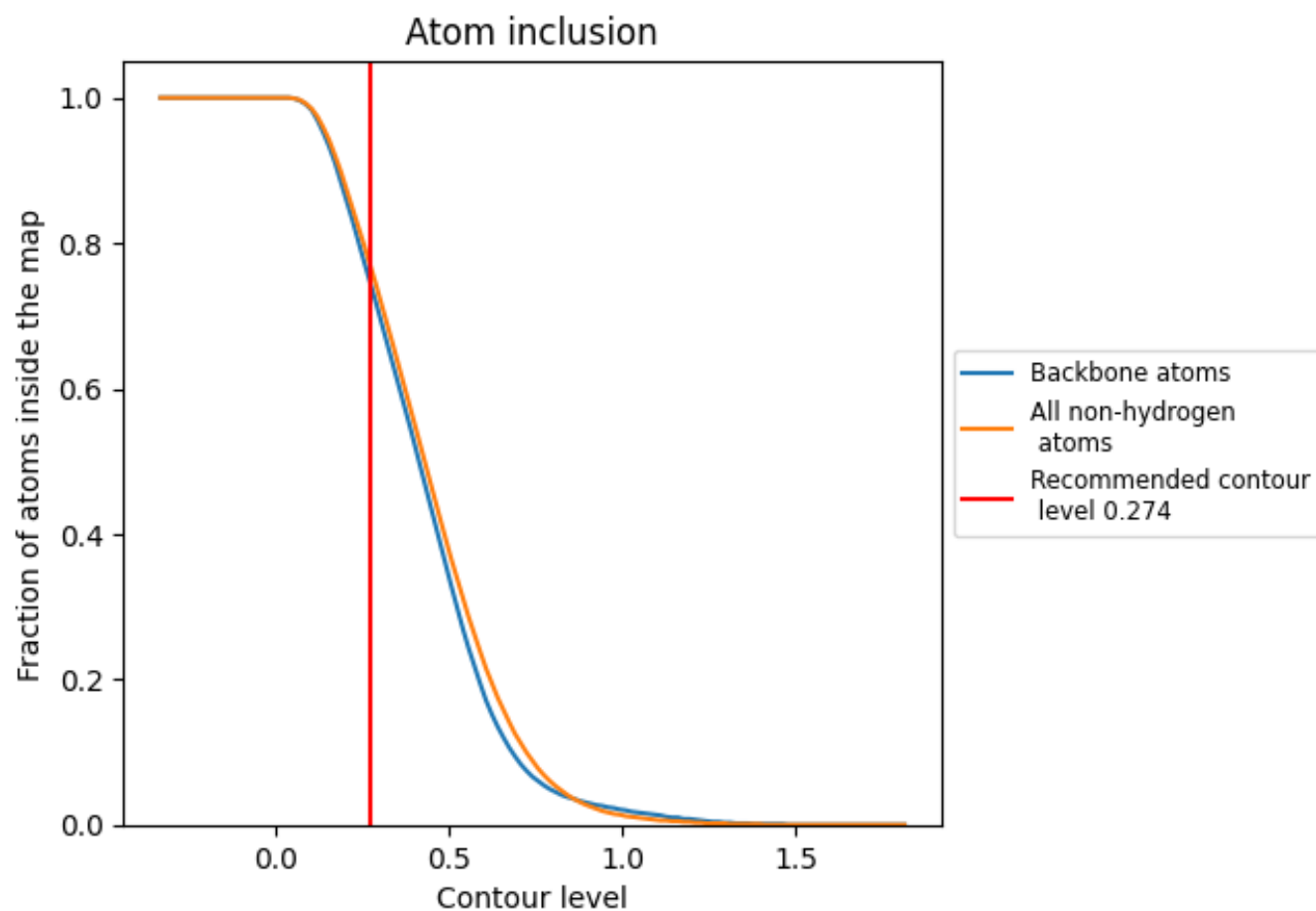


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 74% of all backbone atoms, 77% 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 (0.274) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7690	 0.5940
0	 0.8470	 0.6540
1	 0.8760	 0.6310
10	 0.1870	 0.3830
2	 0.7950	 0.6290
3	 0.9040	 0.6390
4	 0.9000	 0.6400
5	 0.4390	 0.5030
6	 0.8840	 0.6550
7	 0.8440	 0.6420
8	 0.8180	 0.6480
9	 0.7950	 0.6360
A	 0.7820	 0.5630
AA	 0.7160	 0.6080
AB	 0.8960	 0.6730
AC	 0.7280	 0.5900
AD	 0.7600	 0.6140
AE	 0.8420	 0.6530
AF	 0.8490	 0.6550
AG	 0.8800	 0.6760
AH	 0.8110	 0.6370
AI	 0.7750	 0.6240
AJ	 0.7110	 0.5910
AK	 0.9100	 0.6810
AL	 0.6170	 0.5640
AM	 0.8510	 0.6470
AN	 0.7760	 0.6320
AO	 0.5670	 0.5460
AP	 0.7810	 0.6460
AQ	 0.8340	 0.6450
B	 0.6420	 0.5530
C	 0.3840	 0.4380
D	 0.8190	 0.6180
E	 0.2930	 0.4040
F	 0.7160	 0.5760



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Chain	Atom inclusion	Q-score
G	 0.1550	 0.3440
H	 0.3420	 0.4270
I	 0.3980	 0.4720
J	 0.5330	 0.5140
K	 0.7310	 0.5890
L	 0.1510	 0.3320
M	 0.7130	 0.6030
O	 0.6850	 0.5600
P	 0.5190	 0.5020
Q	 0.2620	 0.4200
R	 0.2260	 0.3720
S	 0.2510	 0.3940
T	 0.2190	 0.3810
U	 0.1580	 0.3710
V	 0.2350	 0.3360
W	 0.7250	 0.5950
X	 0.9310	 0.6540
Y	 0.8660	 0.6220
Z	 0.5500	 0.5230
b	 0.6980	 0.5680
c	 0.5850	 0.5270
d	 0.1540	 0.3400
e	 0.6990	 0.5750
f	 0.5120	 0.4770
g	 0.0000	 0.3270
j	 0.9240	 0.6850
k	 0.8750	 0.6600
l	 0.8270	 0.6420
m	 0.6610	 0.5820
n	 0.6220	 0.5850
o	 0.8600	 0.6650
p	 0.7130	 0.6110
q	 0.7350	 0.6120
r	 0.7810	 0.6260
s	 0.5190	 0.5330
t	 0.7920	 0.6290
u	 0.7660	 0.6150
v	 0.9320	 0.6850
w	 0.8630	 0.6590
x	 0.8280	 0.6480
y	 0.8940	 0.6650
z	 0.7470	 0.5950