



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 06:28 PM UTC

PDB ID : 7Q0P / pdb_00007q0p
EMDB ID : EMD-13749
Title : Structure of the *Candida albicans* 80S ribosome in complex with anisomycin
Authors : Kolosova, O.; Zgadzay, Y.; Stetsenko, A.; Jenner, L.; Guskov, A.; Yusupova, G.; Yusupov, M.
Deposited on : 2021-10-15
Resolution : 2.77 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:

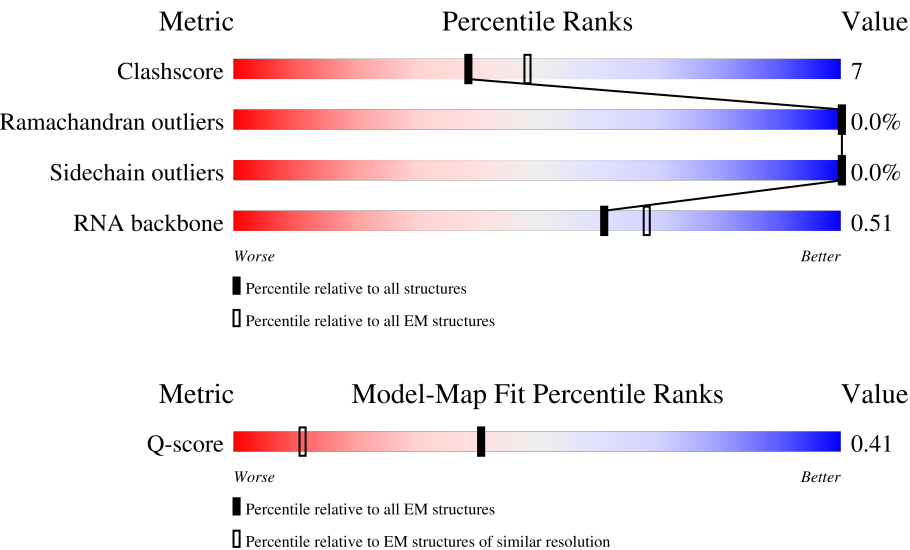
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.77 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	10695 (2.27 - 3.27)

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	77	
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	i	267	
47	A	1787	
48	B	261	
49	C	256	
50	D	249	
51	E	251	
52	F	262	
53	G	225	

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Mol	Chain	Length	Quality of chain
54	H	236	
55	I	186	
56	J	206	
57	K	189	
58	L	118	
59	M	155	
60	N	143	
61	O	151	
62	P	132	
63	Q	142	
64	R	142	
65	S	137	
66	T	145	
67	U	145	
68	V	119	
69	W	87	
70	X	130	
71	Y	145	
72	Z	135	
73	a	105	
74	b	119	
75	c	82	
76	d	67	
77	e	56	
78	f	63	

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Mol	Chain	Length	Quality of chain
79	g	193	
80	h	317	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
82	ANM	1	3403	-	-	X	-

2 Entry composition [i](#)

There are 83 unique types of molecules in this entry. The entry contains 199587 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

- Molecule 4 is a RNA chain called Mixture of endogenous E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	10	14	Total	C	N	O	P	0	0
			298	133	54	97	14		

- Molecule 5 is a protein called Ribosomal 60S subunit protein L2A.

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 Ribosomal 60S subunit 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 Ribosomal 60S subunit protein L4B.

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 Ribosomal 60S subunit 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 Ribosomal 60S subunit protein L7A.

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

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

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

- Molecule 12 is a protein called Ribosomal 60S subunit protein L9B.

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

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

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	200	Total	C	N	O		0	0
			1610	1009	318	283			

- Molecule 16 is a protein called Ribosomal 60S subunit protein L14B.

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 Ribosomal protein L15.

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 60S subunit protein L16A.

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 60S subunit protein L17B.

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 Ribosomal 60S subunit protein L18A.

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 Ribosomal protein L19.

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 Ribosomal 60S subunit protein L21A.

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 Ribosomal 60S subunit protein L22B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	5	103	Total	C	N	O		2	0
			848	553	139	156			

- Molecule 25 is a protein called Ribosomal 60S subunit protein L23B.

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 Ribosomal 60S subunit protein L24A.

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 Ribosomal 60S subunit 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 60S subunit protein L26B.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	9	126	Total	C	N	O		
			989	618	190	181	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 Ribosomal 60S subunit 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	63	Total	C	N	O	S		
			509	317	109	82	1	1	0

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

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

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

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 Ribosomal 60S subunit protein L34B.

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 60S subunit protein L35A.

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	98	Total	C	N	O	S	1	0
			772	481	158	131	2		

- Molecule 39 is a protein called Ribosomal protein L37.

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 Ribosomal 60S subunit 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 Rpl40bp.

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	24	Total	C	N	O	S	0	0
			227	138	61	27	1		

- Molecule 44 is a protein called Ribosomal 60S subunit protein L42A.

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 Ribosomal 60S subunit protein L43A.

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 protein called HABP4_PAI-RBP1 domain-containing protein.

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

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 48 is a protein called 40S ribosomal protein S0.

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

- Molecule 49 is a protein called 40S ribosomal protein S1.

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

- Molecule 50 is a protein called Ribosomal 40S subunit protein S2.

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

- Molecule 51 is a protein called Ribosomal 40S subunit protein S3.

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

- Molecule 52 is a protein called 40S ribosomal protein S4.

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

- Molecule 53 is a protein called Ribosomal 40S subunit protein S5.

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

- Molecule 54 is a protein called 40S ribosomal protein S6.

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

- Molecule 55 is a protein called 40S ribosomal protein S7.

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

- Molecule 56 is a protein called 40S ribosomal protein S8.

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

- Molecule 57 is a protein called Ribosomal 40S subunit protein S9B.

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

- Molecule 58 is a protein called Ribosomal 40S subunit protein S10A.

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

- Molecule 59 is a protein called Ribosomal 40S subunit protein S11A.

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

- Molecule 60 is a protein called 40S ribosomal protein S12.

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

- Molecule 61 is a protein called Ribosomal 40S subunit protein S13.

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

- Molecule 62 is a protein called Ribosomal 40S subunit protein S14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	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 A0A1D8PDT3

- Molecule 63 is a protein called Ribosomal 40S subunit protein S15.

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

- Molecule 64 is a protein called Ribosomal 40S subunit protein S16A.

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

- Molecule 65 is a protein called Ribosomal 40S subunit protein S17B.

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

- Molecule 66 is a protein called Ribosomal 40S subunit protein S18B.

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

- Molecule 67 is a protein called Ribosomal 40S subunit protein S19A.

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

- Molecule 68 is a protein called Ribosomal 40S subunit protein S20.

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

- Molecule 69 is a protein called 40S ribosomal protein S21.

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

- Molecule 70 is a protein called 40S ribosomal protein S22-B.

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

- Molecule 71 is a protein called Ribosomal 40S subunit protein S23B.

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

- Molecule 72 is a protein called 40S ribosomal protein S24.

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

- Molecule 73 is a protein called 40S ribosomal protein S25.

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

- Molecule 74 is a protein called 40S ribosomal protein S26.

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

- Molecule 75 is a protein called 40S ribosomal protein S27.

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

- Molecule 76 is a protein called Ribosomal 40S subunit protein S28B.

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

- Molecule 77 is a protein called Ribosomal 40S subunit protein S29A.

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

- Molecule 78 is a protein called 40S ribosomal protein S30.

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

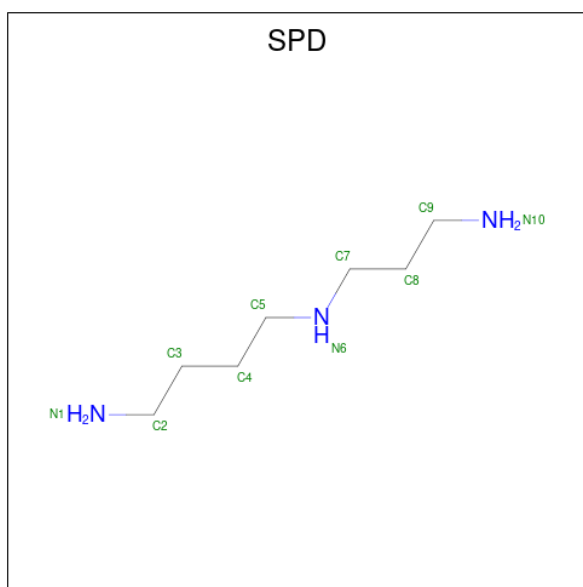
- Molecule 79 is a protein called Ubiquitin-ribosomal 40S subunit protein S31 fusion protein.

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

- Molecule 80 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

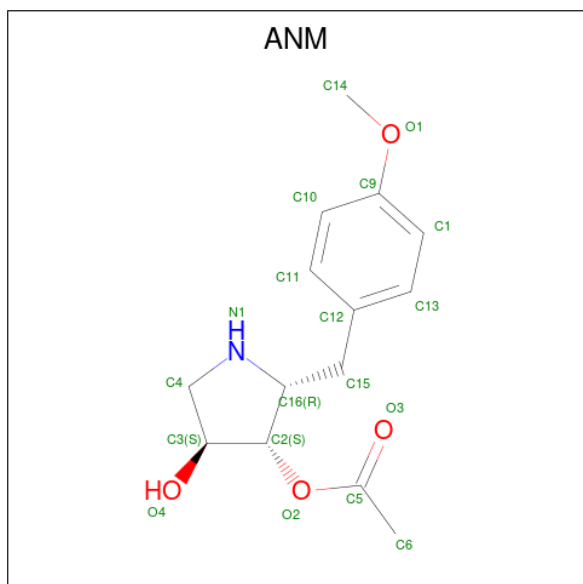
Mol	Chain	Residues	Atoms					AltConf	Trace
80	h	311	Total	C	N	O	S	0	0
			2398	1519	412	462	5		

- Molecule 81 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
81	1	1	Total	C	N	0
			10	7	3	
81	1	1	Total	C	N	0
			10	7	3	

- Molecule 82 is ANISOMYCIN (CCD ID: ANM) (formula: $C_{14}H_{19}NO_4$) (labeled as "Ligand of Interest" by depositor).

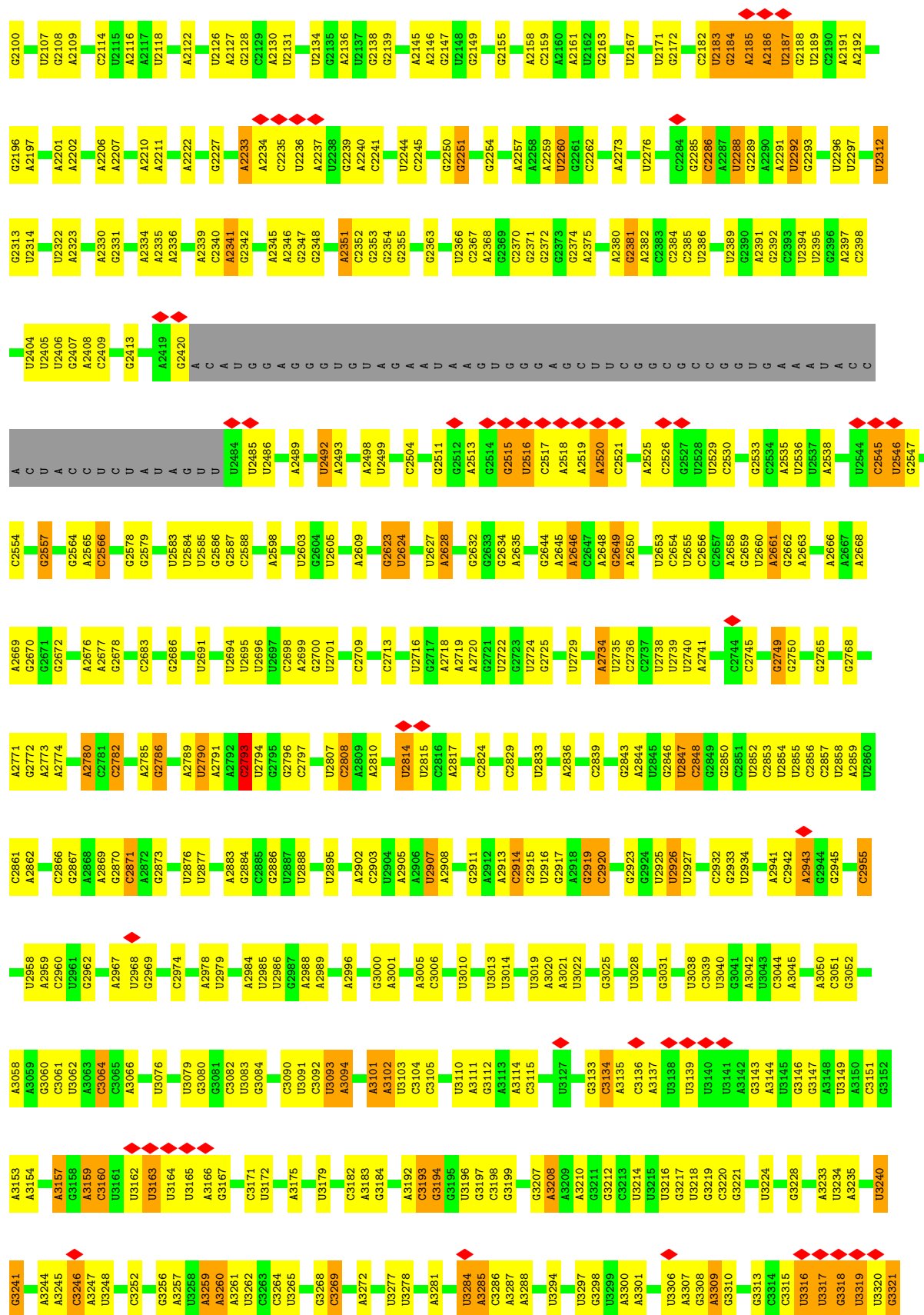


Mol	Chain	Residues	Atoms				AltConf
82	1	1	Total	C	N	O	0
			19	14	1	4	

- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

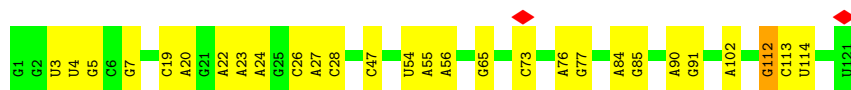
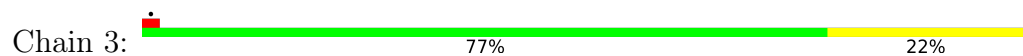
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83	AN	1	Total 1	Zn 1	0
83	AP	1	Total 1	Zn 1	0
83	AQ	1	Total 1	Zn 1	0
83	b	1	Total 1	Zn 1	0
83	c	1	Total 1	Zn 1	0
83	e	1	Total 1	Zn 1	0
83	g	1	Total 1	Zn 1	0

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C	G2042	U	A1870	U1779	G1642	G1562	G1460	C1329	C1253	C1188	A1081	G903
A	G2043	C	G1870	A1780	G1648	A1563	A1464	U1330	U1254	A1189	C996	G904
C	G2044	C	G1874	G1782	C1653	U1564	C1465	A1189	A1255	G1190	A1089	C907
U	G2045	U	A1875	A1783	G1654	U1565	U1466	A1191	A1256	U1091	A1090	A910
U	U2046	C	A1876	U1787	U1655	U1566	U1467	C1192	G1257	U1092	A1099	A911
G	U2047	G	A1877	C1788	C1656	U1567	U1468	C1197	G1258	G1093	A1007	A912
G	U2048	U	A1882	U1791	G1657	U1568	U1469	C1199	G1259	A1094	A1008	A913
U	U2049	U	G1883	G1792	G1658	C1569	A1470	C1199	A1259	A1099	C1011	A917
G	U2050	A	A1793	A1792	C1659	A1570	A1471	A1198	G1260	G1100	U1012	U918
C	G2051	C	A1794	A1794	U1661	G1571	G1472	A1199	U1261	U1105	U1013	C919
U	U2052	U	A1795	A1795	G1662	G1572	C1473	U1200	G1262	U1106	U1014	G920
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- Molecule 2: 5S ribosomal RNA



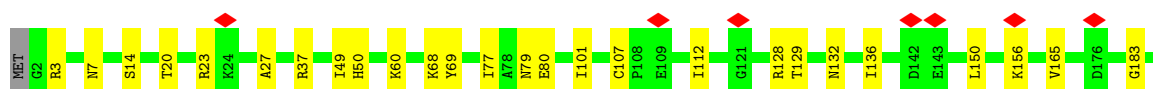
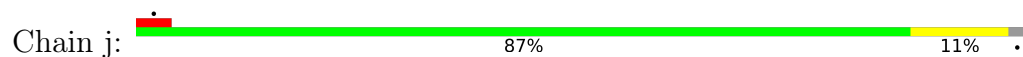
- Molecule 3: 5.8S ribosomal RNA



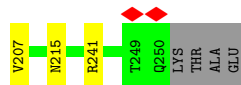
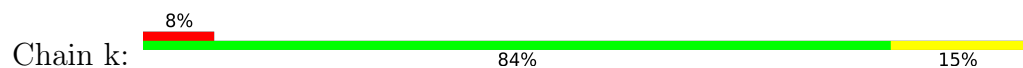
- Molecule 4: Mixture of endogenous E-tRNA

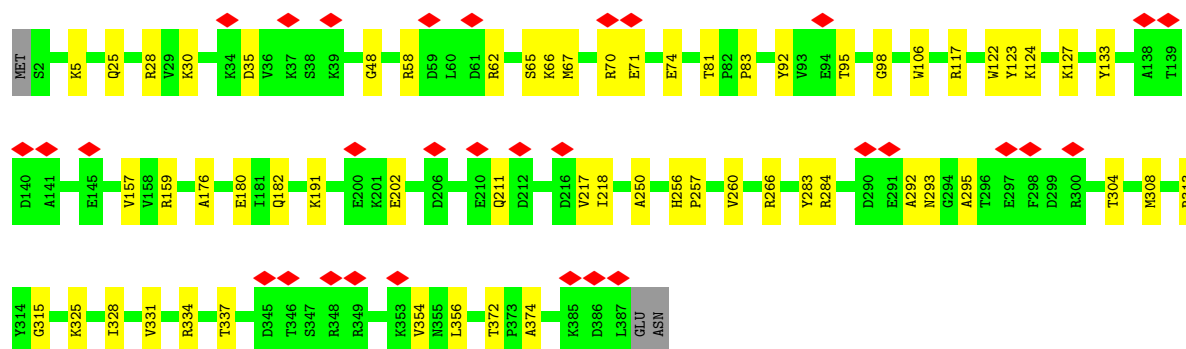


- Molecule 5: Ribosomal 60S subunit protein L2A

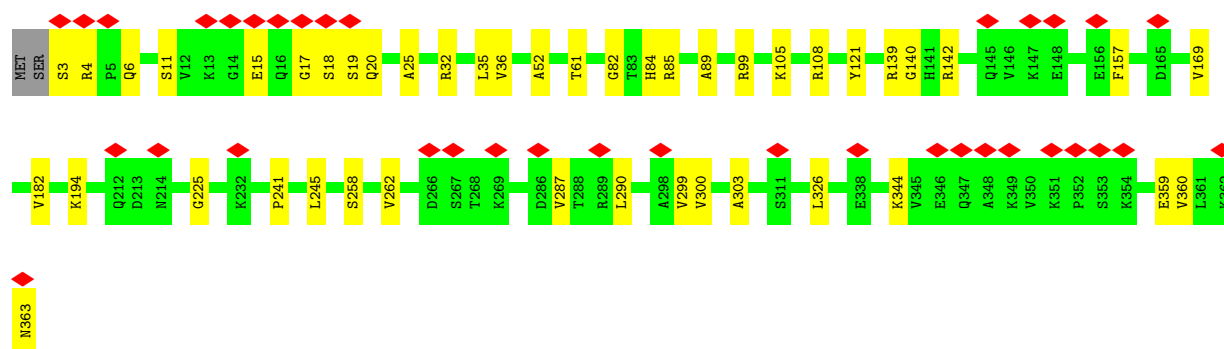
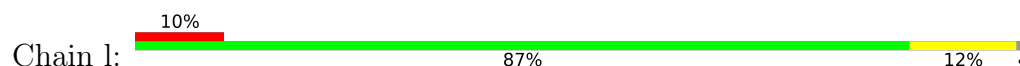


- Molecule 6: Ribosomal 60S subunit protein L3

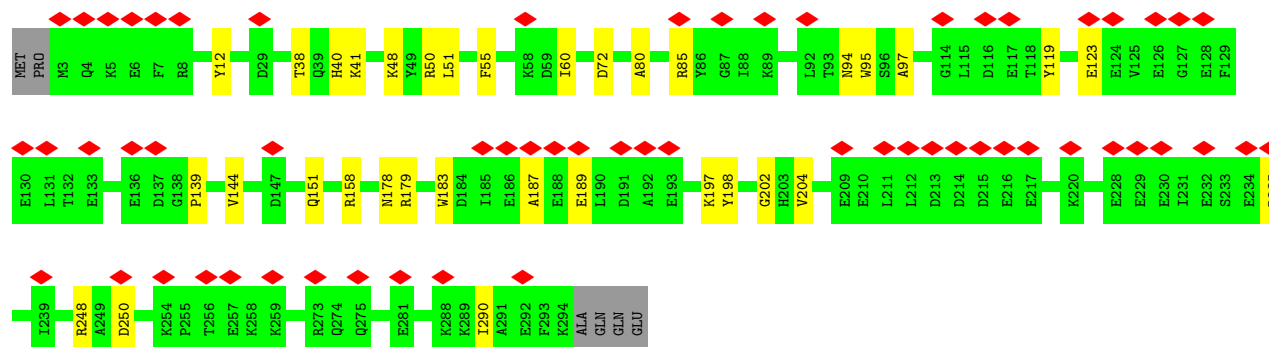
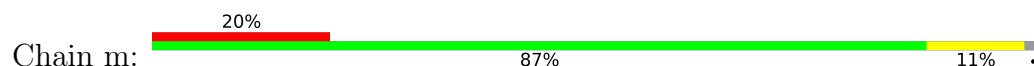




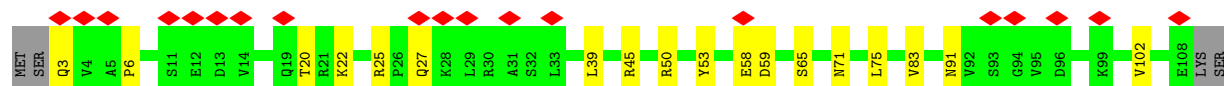
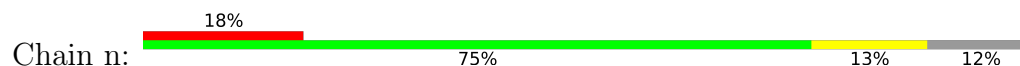
• Molecule 7: Ribosomal 60S subunit protein L4B



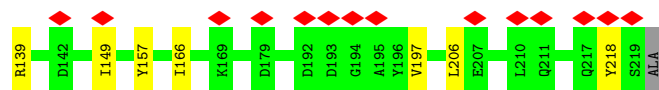
• Molecule 8: Ribosomal 60S subunit protein L5



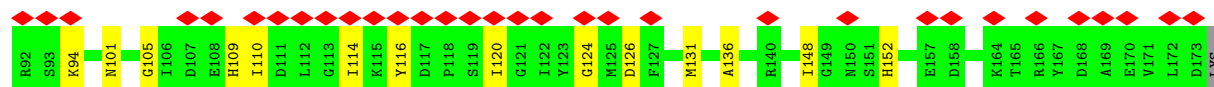
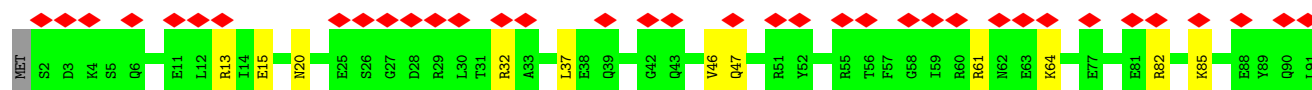
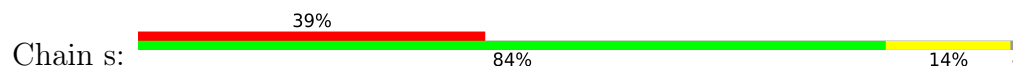
• Molecule 9: 60S ribosomal protein L6



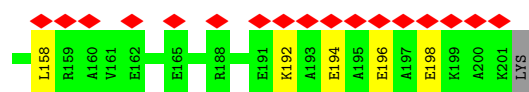
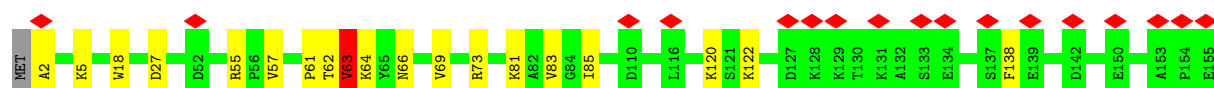
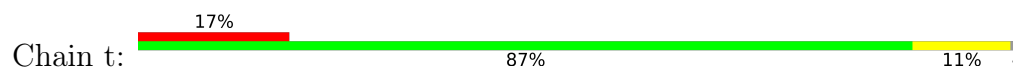




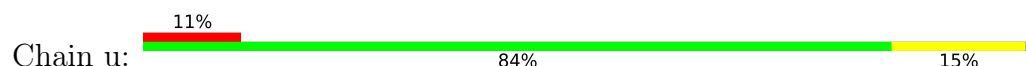
- Molecule 14: Ribosomal 60S subunit protein L11B



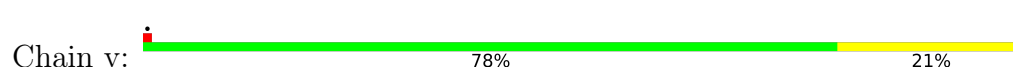
- Molecule 15: 60S ribosomal protein L13



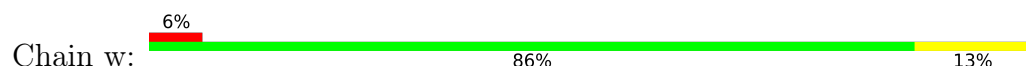
- Molecule 16: Ribosomal 60S subunit protein L14B

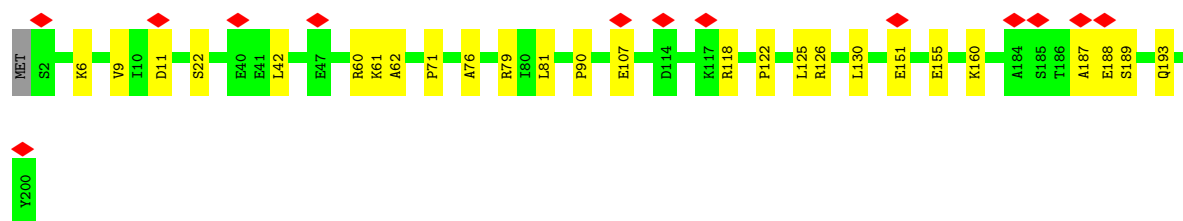


- Molecule 17: Ribosomal protein L15

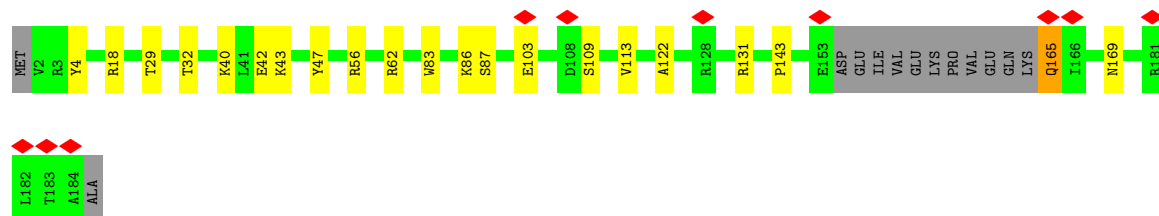
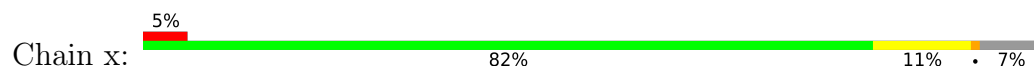


- Molecule 18: Ribosomal 60S subunit protein L16A

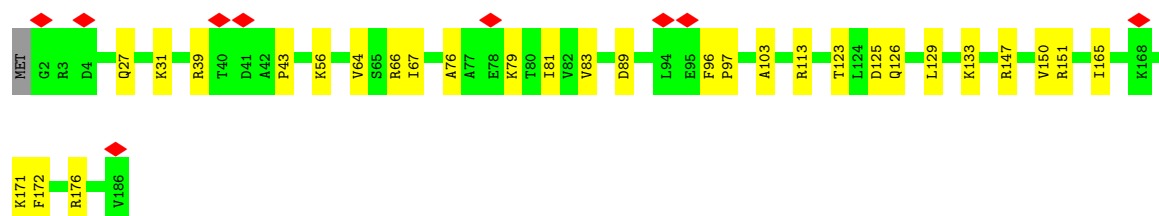
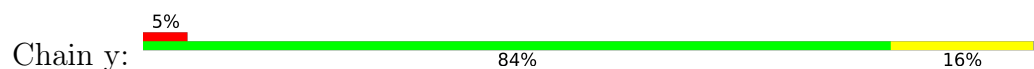




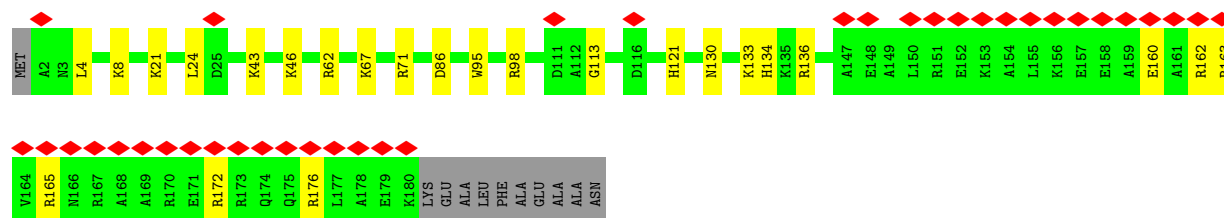
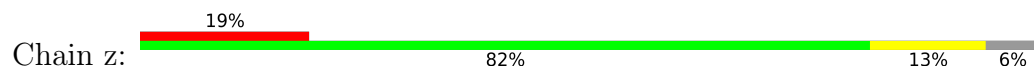
- Molecule 19: Ribosomal 60S subunit protein L17B



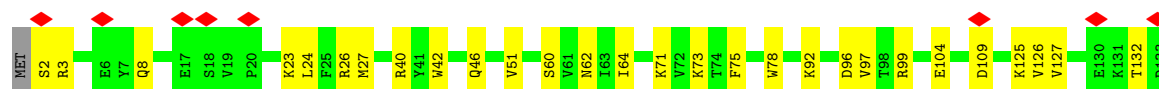
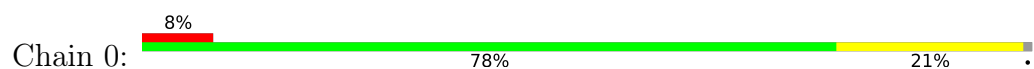
- Molecule 20: Ribosomal 60S subunit protein L18A

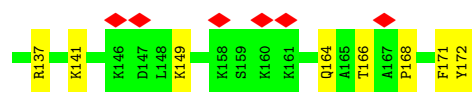


- Molecule 21: Ribosomal protein L19

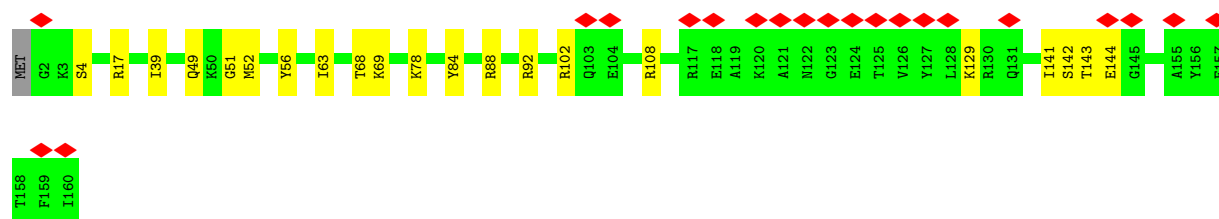
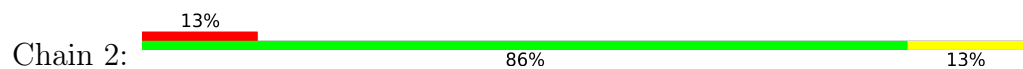


- Molecule 22: 60S ribosomal protein L20

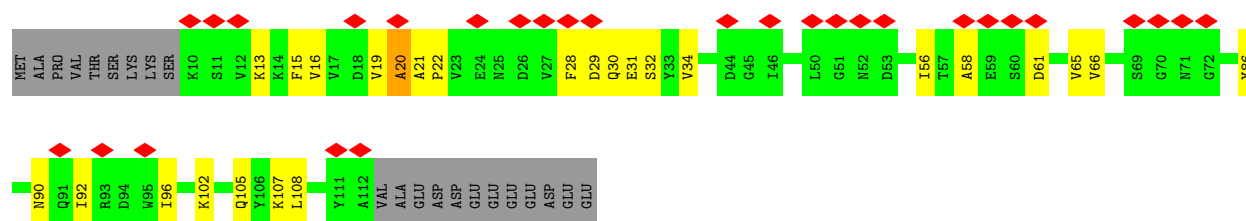




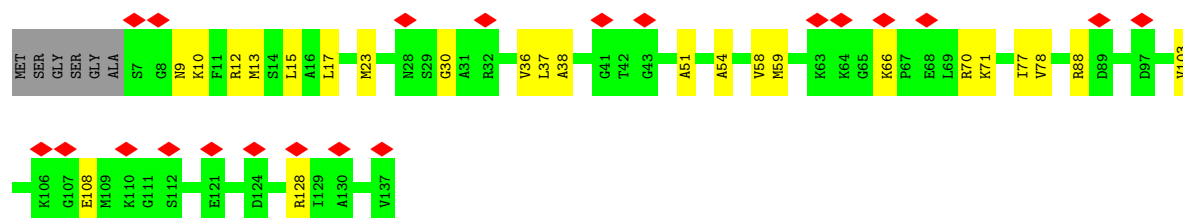
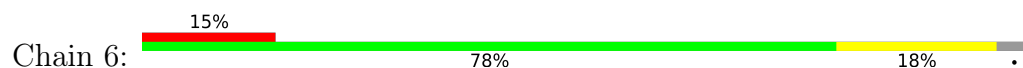
- Molecule 23: Ribosomal 60S subunit protein L21A



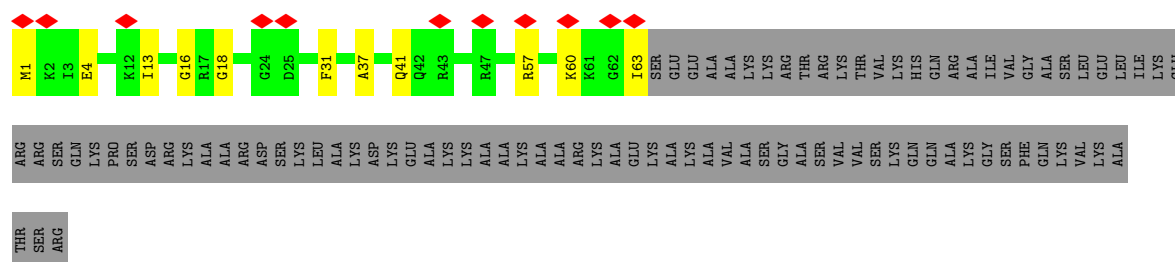
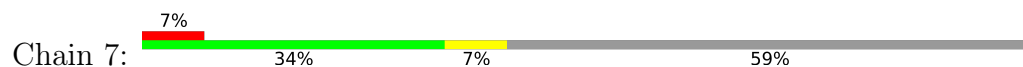
- Molecule 24: Ribosomal 60S subunit protein L22B



- Molecule 25: Ribosomal 60S subunit protein L23B

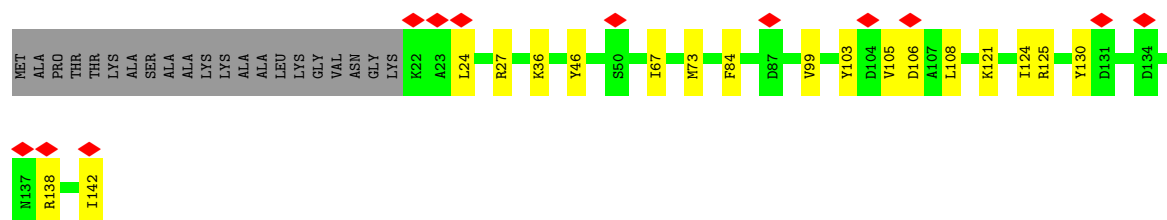


- Molecule 26: Ribosomal 60S subunit protein L24A



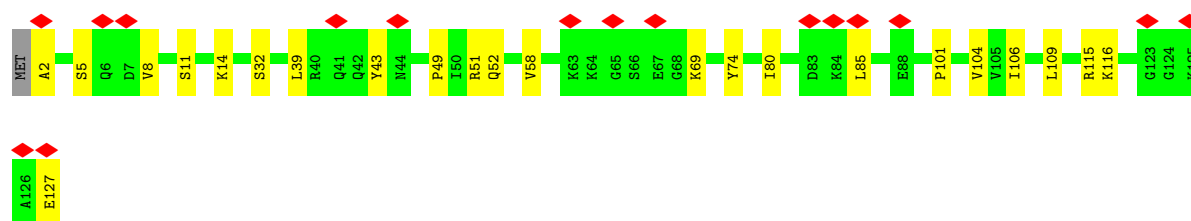
- Molecule 27: Ribosomal 60S subunit protein L25

Chain 8: 



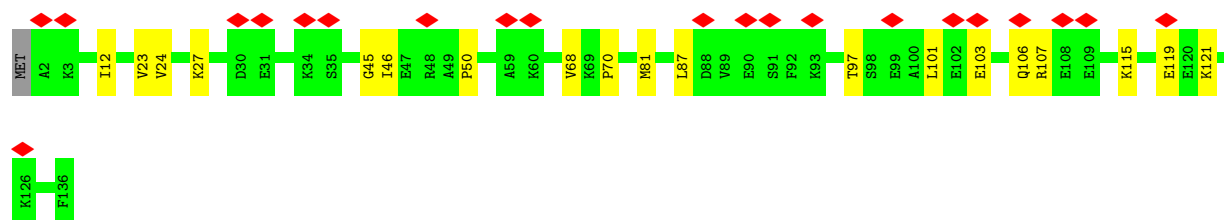
- Molecule 28: Ribosomal 60S subunit protein L26B

Chain 9: 



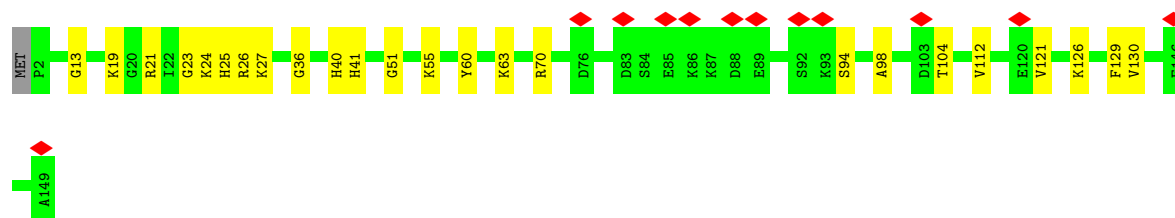
- Molecule 29: 60S ribosomal protein L27

Chain AA: 



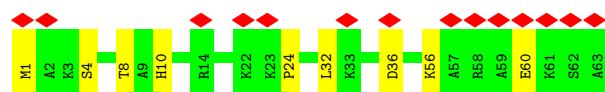
- Molecule 30: Ribosomal 60S subunit protein L28

Chain AB: 

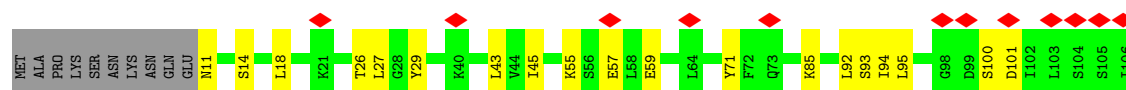
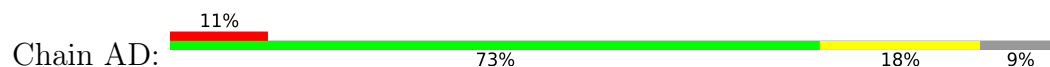


- Molecule 31: 60S ribosomal protein L29

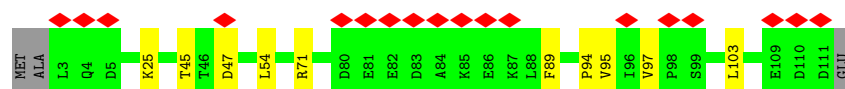
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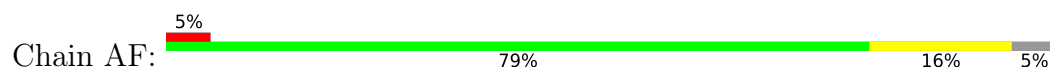
- Molecule 32: Ribosomal 60S subunit protein L30



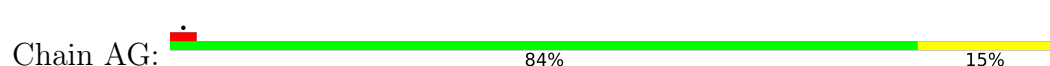
- Molecule 33: Ribosomal 60S subunit protein L31B



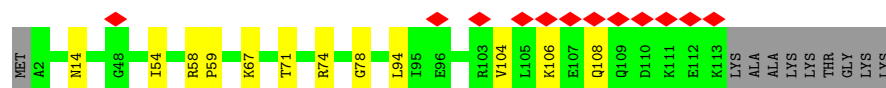
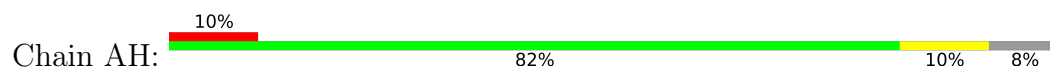
- Molecule 34: Ribosomal 60S subunit protein L32



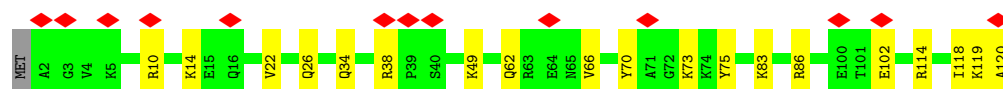
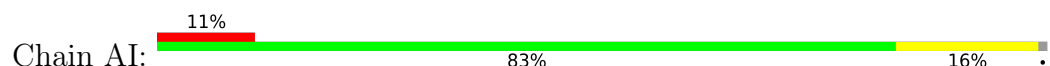
- Molecule 35: Ribosomal 60S subunit protein L33A



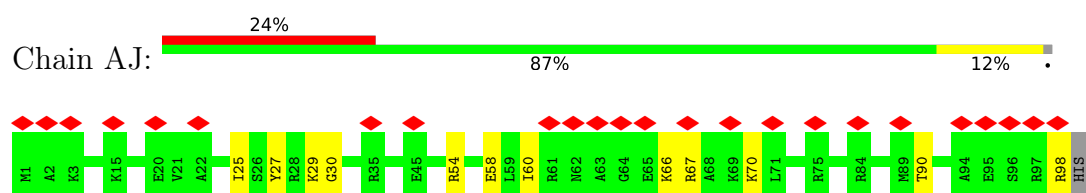
- Molecule 36: Ribosomal 60S subunit protein L34B



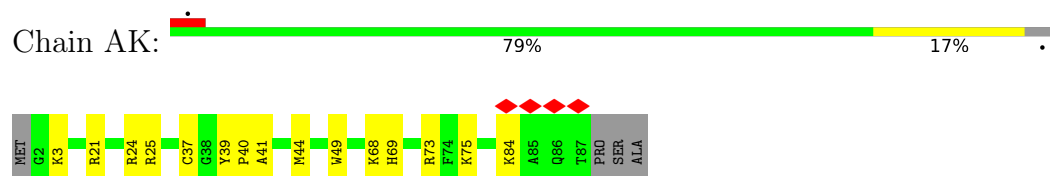
- Molecule 37: Ribosomal 60S subunit protein L35A



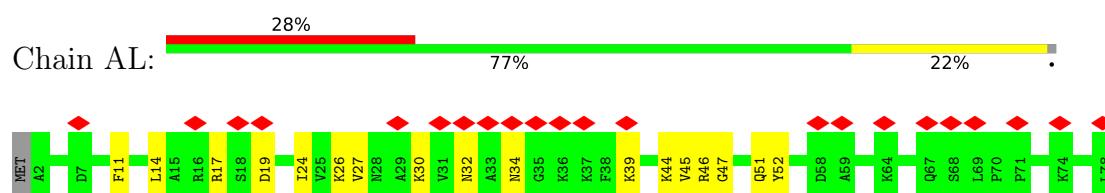
- Molecule 38: 60S ribosomal protein L36



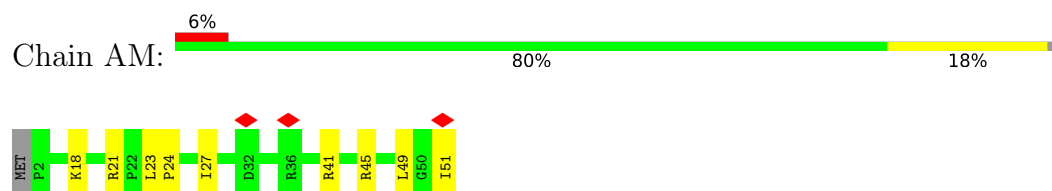
- Molecule 39: Ribosomal protein L37



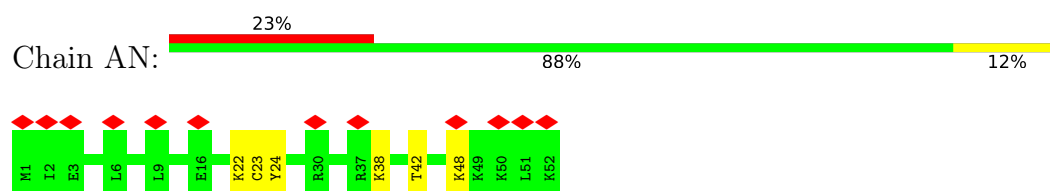
- Molecule 40: Ribosomal 60S subunit protein L38



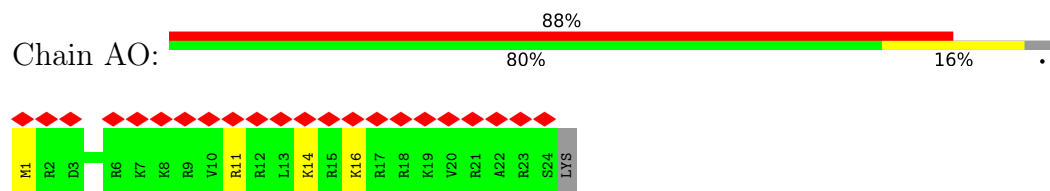
- Molecule 41: 60S ribosomal protein L39



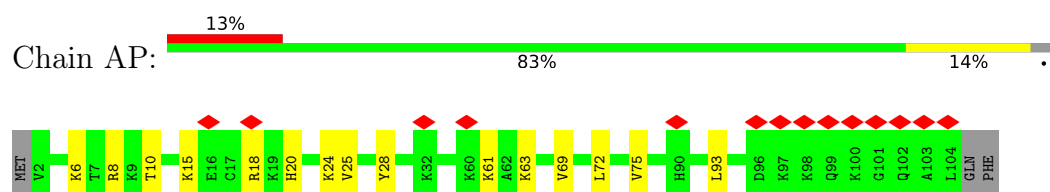
- Molecule 42: Rpl40bp



- Molecule 43: 60S ribosomal protein L41



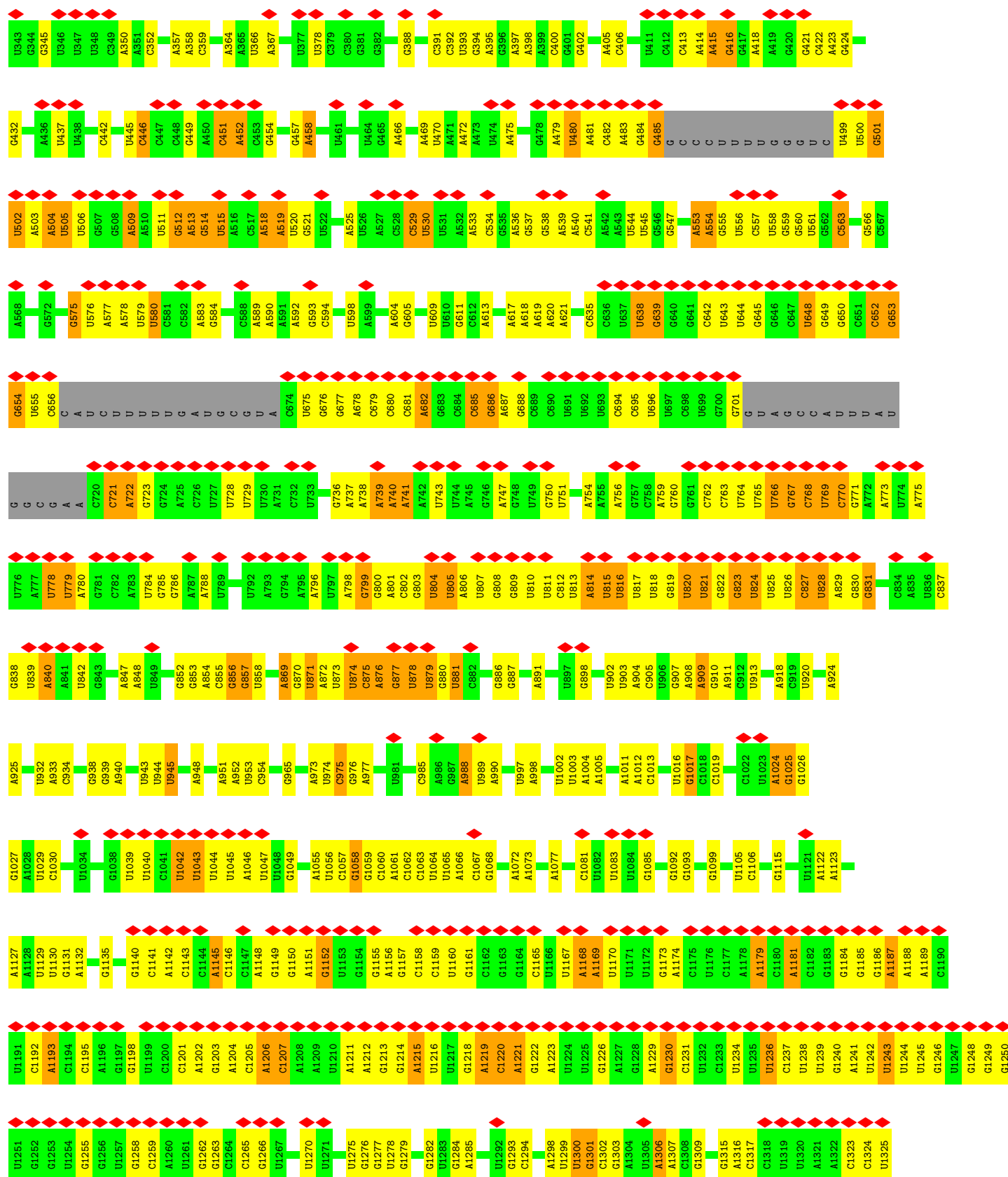
- Molecule 44: Ribosomal 60S subunit protein L42A

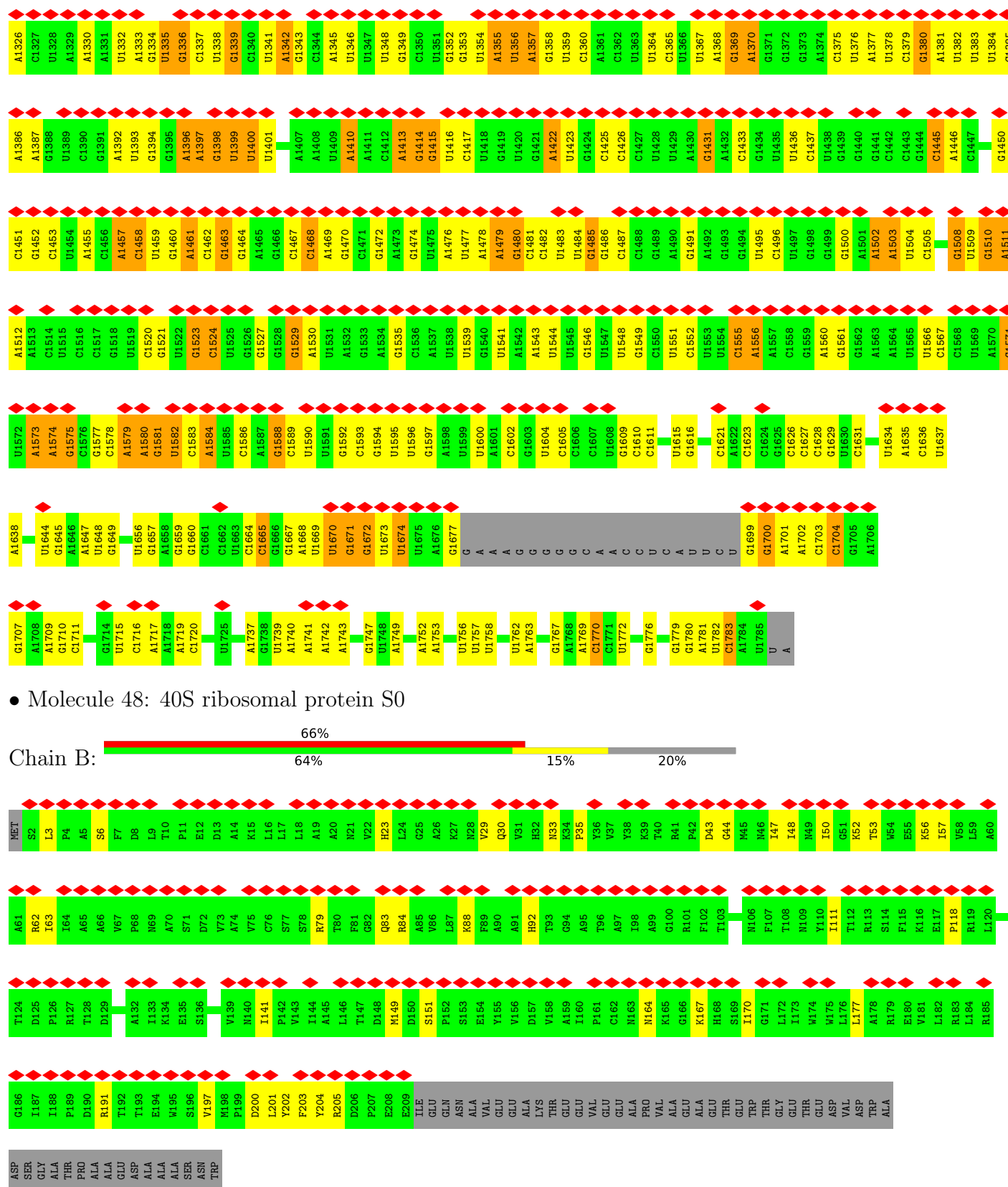


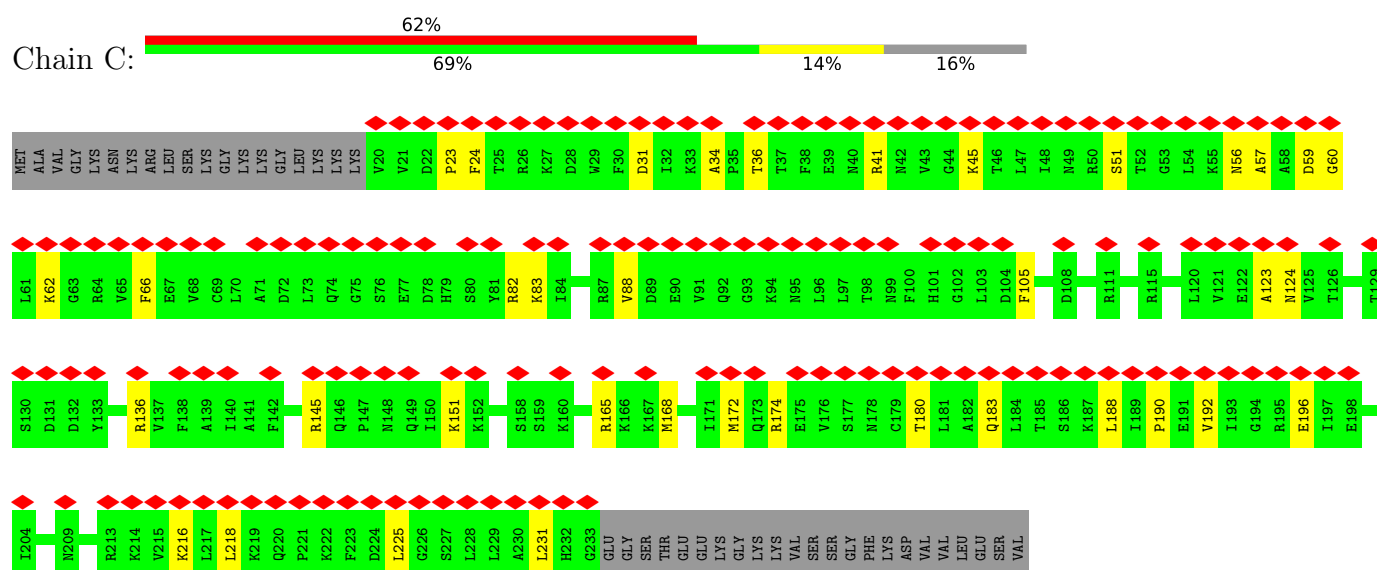
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- | | | | | |
|-----|-----|--------|------|-----|
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| ARG | GLU | TI122 | A62 | SER |
| ARG | GLU | TI123 | A63 | PHE |
| GLY | LYS | D124 | L64 | GLN |
| ALA | GLU | A125 | K65 | ASN |
| LYS | LYS | E126 | N66 | LYS |
| ARG | GLN | A127 | N67 | ASN |
| GLY | GLN | E128 | K68 | LEU |
| GLY | GLU | LI129 | F69 | ASP |
| ALA | VAL | E130 | N70 | LEU |
| ARG | PHE | A131 | K71 | GLY |
| GLY | ALA | E132 | P76 | LEU |
| ALA | SER | A133 | D72 | ASN |
| LYS | THR | E134 | V73 | ASP |
| PRO | HIS | E135 | A74 | VAL |
| GLU | THR | N136 | P75 | GLU |
| VAL | LYS | D137 | T77 | GLY |
| LYS | LYS | E138 | S78 | ASP |
| ASP | ALA | S139 | T79 | GLY |
| PHE | LYS | ALA | A80 | GLU |
| PRO | GLN | ASN | T81 | ASP |
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| LEU | GLU | ILE | HIS | ALA |
| | LYS | PRO | SER | ALA |
| | VAL | LYS | LYS | ALA |
| | PHE | LYS | LYS | ALA |
| | LEU | SER | LYS | ALA |
| | ASP | LEU | P87 | ALA |
| | ILE | GLN | F88 | ALA |
| | ASP | GLU | D89 | ALA |
| | ALA | TYR | R90 | ALA |
| | ASN | LEU | H91 | ALA |
| | PHE | ALA | S92 | ALA |
| | GLY | GLU | R93 | ALA |
| | ASP | LEU | T94 | ALA |
| | GLU | LEU | G95 | ALA |
| | PRO | SER | K96 | ALA |
| | GLN | LYS | T97 | ALA |
| | THR | GLN | D98 | ALA |
| | THR | GLU | S99 | ALA |
| | ARG | LEU | K100 | ALA |
| | GLY | GLU | K101 | ALA |
| | GLY | SER | K102 | ALA |
| | PHE | LYS | L103 | ALA |
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| | GLY | ARG | W107 | ALA |
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| | ALA | GLU | Q109 | ALA |
| | ARG | GLN | S110 | ALA |
| | GLY | LYS | D111 | ALA |
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| | THR | THR | R113 | ALA |
| | | | E114 | ALA |
| | | | L115 | ALA |
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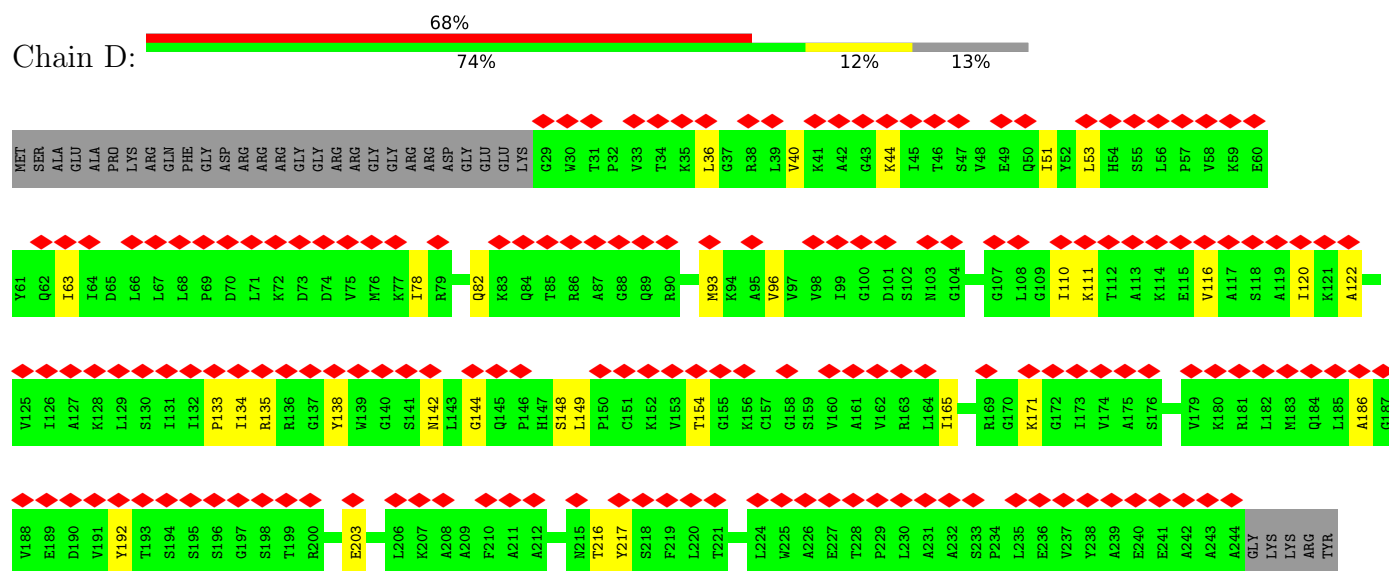
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| U201 | G202 | U203 | A204 | U205 | U206 | U210 | A211 | G212 | A213 | U214 | A215 | A216 | A217 | A218 | A219 | A | U | C | A | U | G | C | C | U | U | C | C | U238 | U239 | U240 | G241 | U242 | U243 | G244 | A245 | U246 | U247 | U250 | A251 | A252 | U253 | A254 | A255 | U258 | U259 | U260 | C261 | G262 | A263 | A264 | | | | | | | | | |
| U139 | | G142 | A143 | U144 | | C147 | G148 | G149 | U150 | G151 | G152 | U153 | A154 | A155 | U156 | U157 | C158 | U159 | A160 | G161 | A162 | G163 | C164 | U165 | A166 | U167 | U168 | A169 | C170 | A171 | U172 | G173 | C174 | U175 | U176 | A177 | A178 | A179 | A180 | U181 | C182 | C183 | C184 | G185 | A186 | G187 | U188 | G189 | U190 | U191 | U192 | G193 | G194 | A195 | A196 | G197 | G198 | G199 | A200 |
| U1 | A2 | U3 | C4 | | G10 | A11 | U12 | C13 | C14 | U15 | G16 | C17 | C18 | A19 | G20 | U21 | A22 | G23 | U24 | C25 | A26 | U27 | A28 | U29 | G30 | C31 | U32 | U33 | G34 | C38 | A39 | U45 | A46 | A47 | G48 | A51 | U52 | G53 | C54 | A55 | U56 | G57 | U58 | C59 | U60 | A61 | A62 | G63 | U64 | A65 | U66 | A67 | A68 | G69 | C70 | | | | |



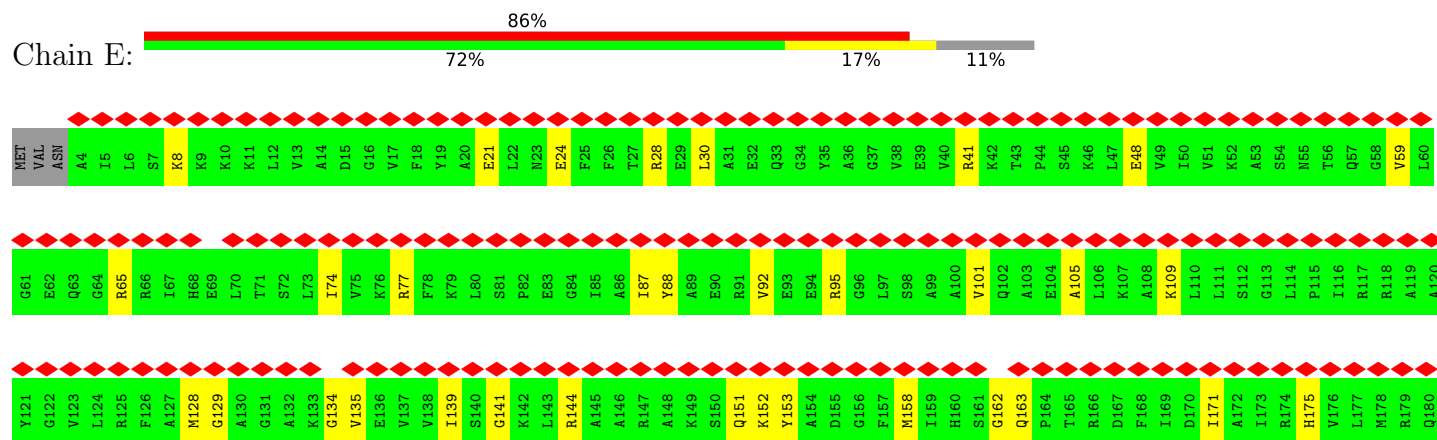




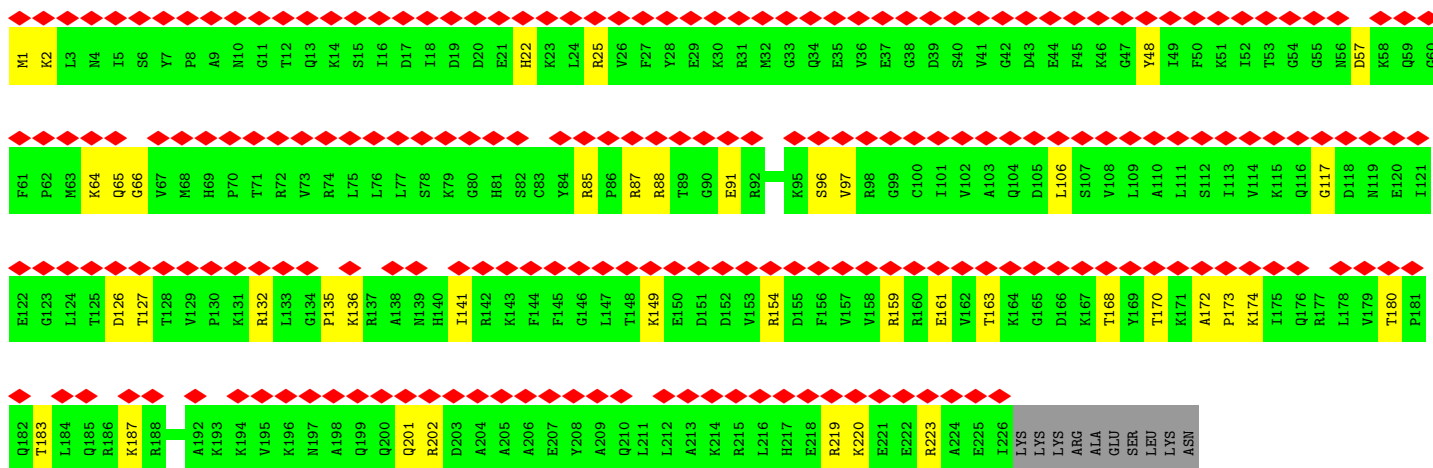
- Molecule 50: Ribosomal 40S subunit protein S2



- Molecule 51: Ribosomal 40S subunit protein S3

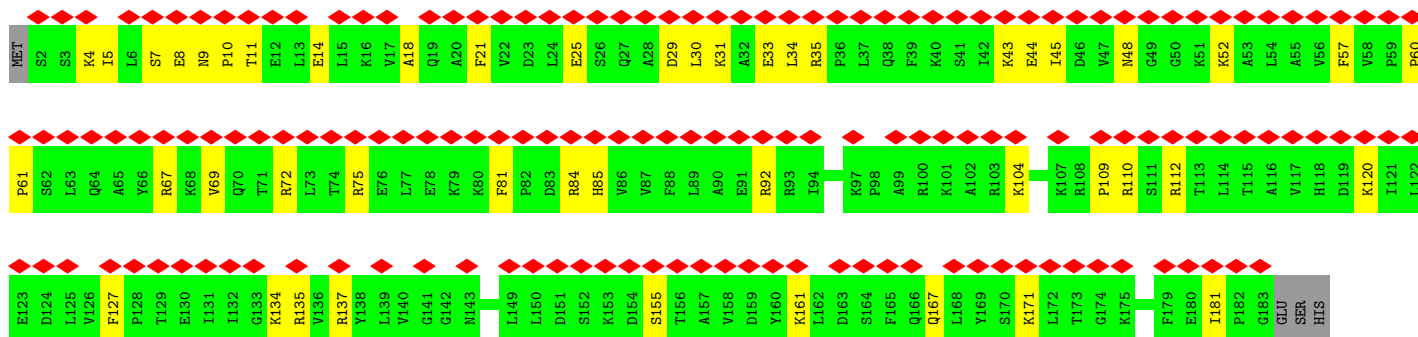






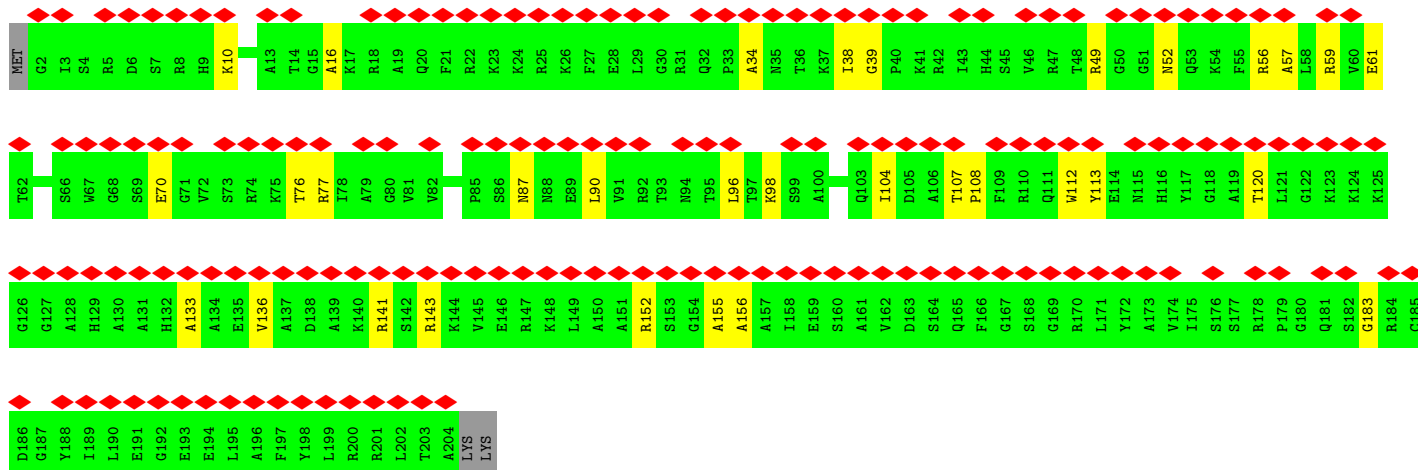
• Molecule 55: 40S ribosomal protein S7

Chain I:



• Molecule 56: 40S ribosomal protein S8

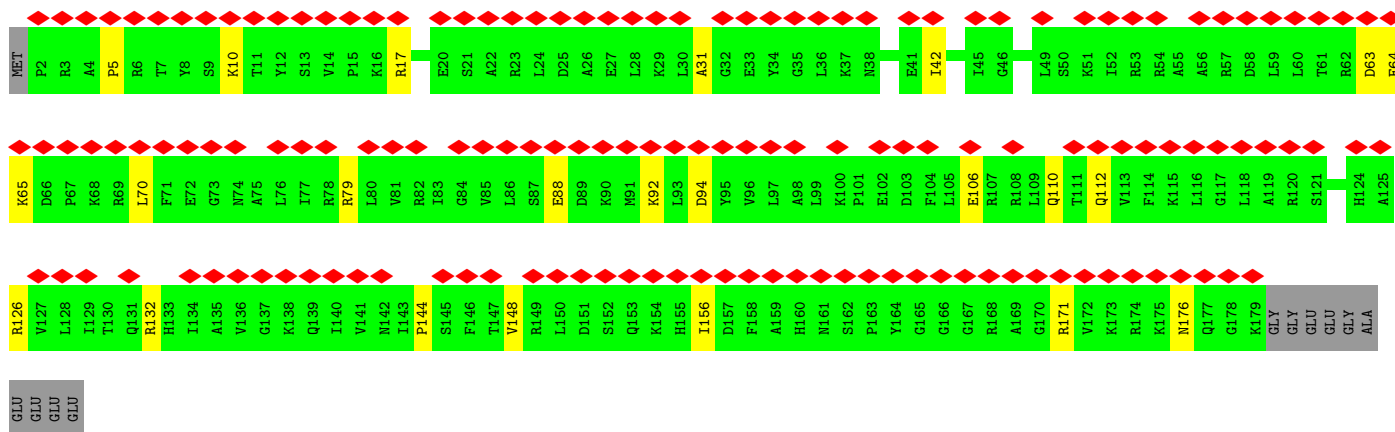
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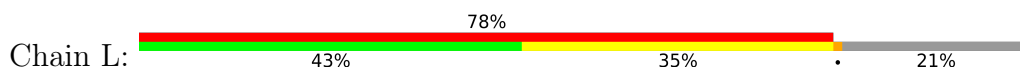
• Molecule 57: Ribosomal 40S subunit protein S9B

Chain K:

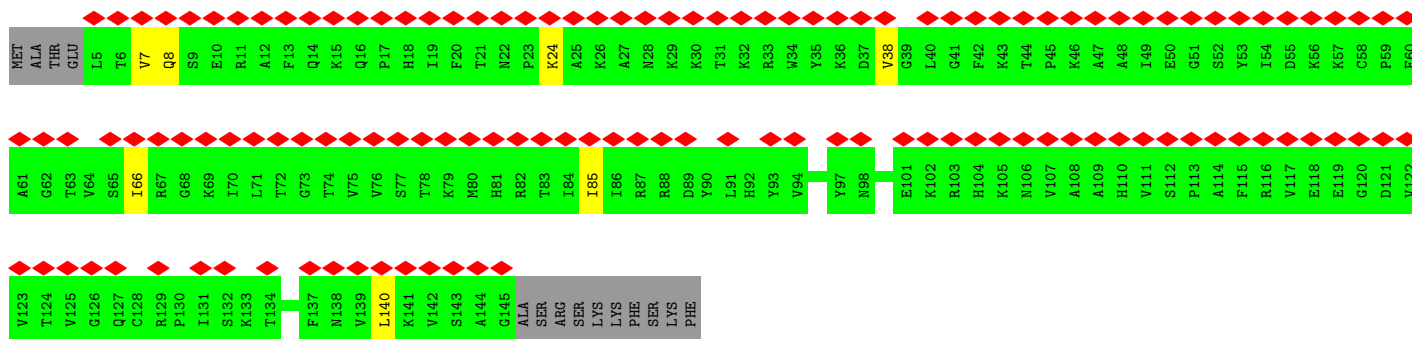
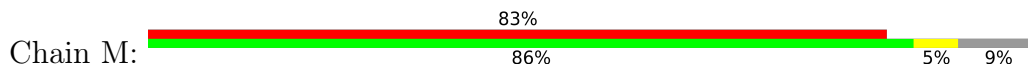




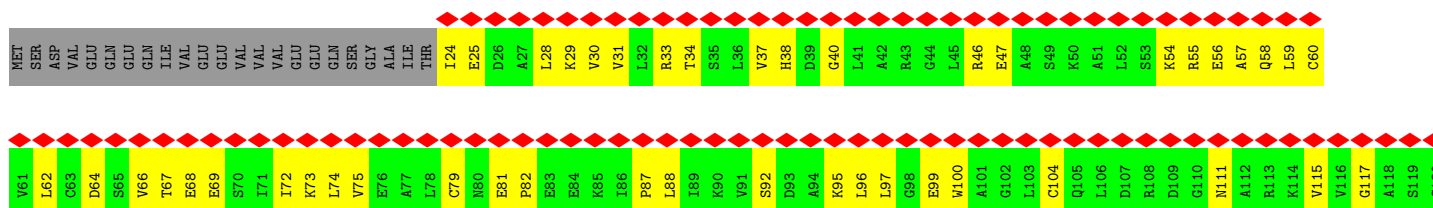
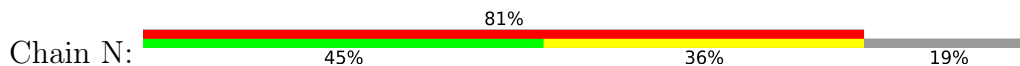
• Molecule 58: Ribosomal 40S subunit protein S10A



• Molecule 59: Ribosomal 40S subunit protein S11A

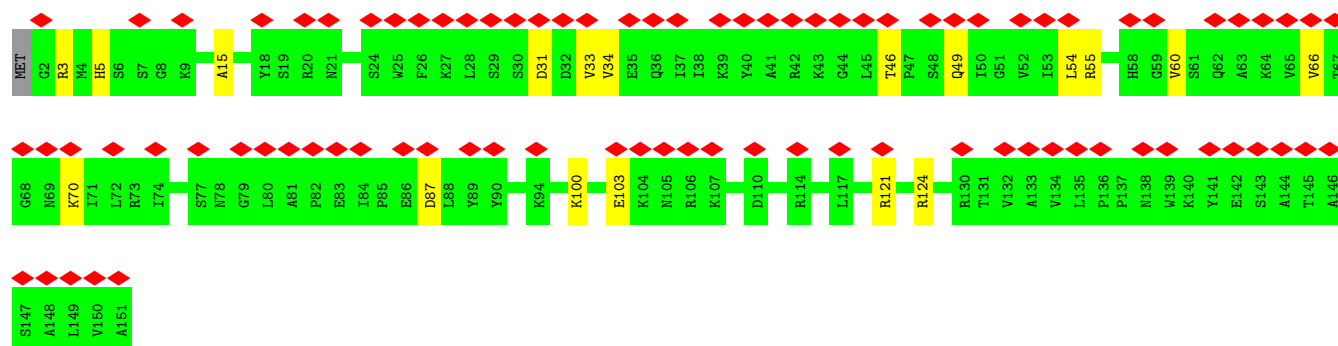
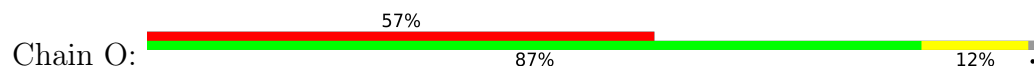


• Molecule 60: 40S ribosomal protein S12

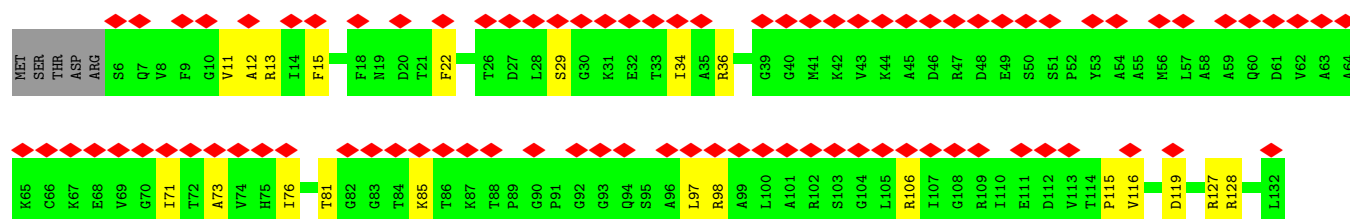




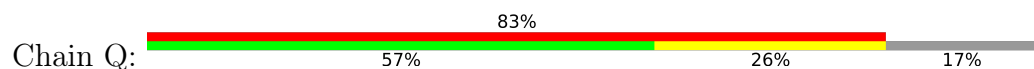
• Molecule 61: Ribosomal 40S subunit protein S13



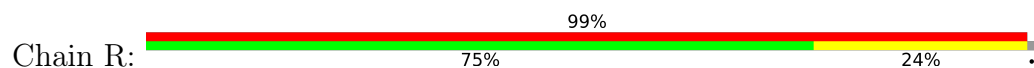
• Molecule 62: Ribosomal 40S subunit protein S14B

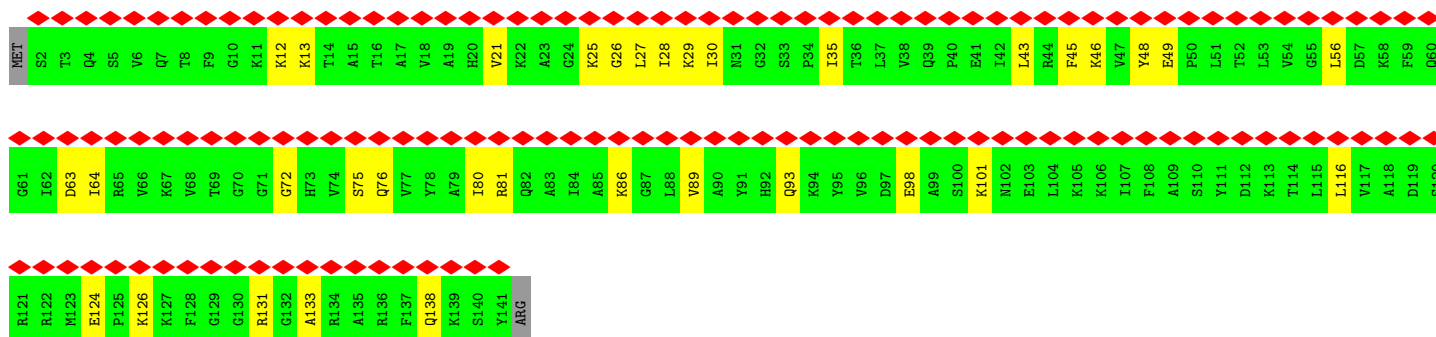


• Molecule 63: Ribosomal 40S subunit protein S15



• Molecule 64: Ribosomal 40S subunit protein S16A

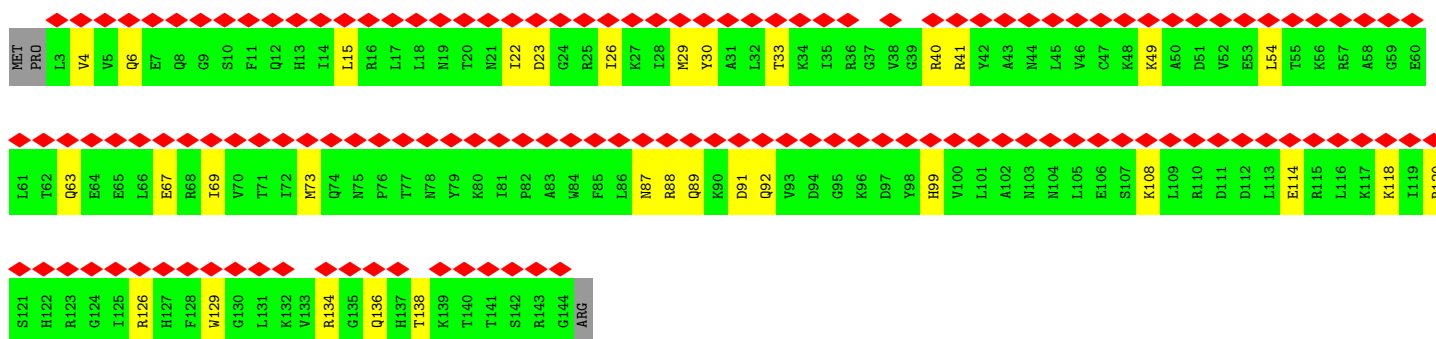
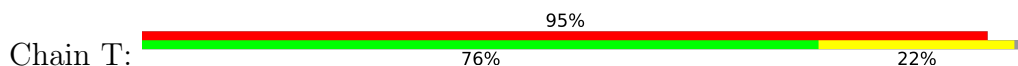




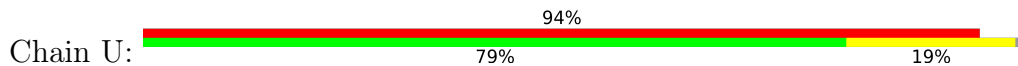
• Molecule 65: Ribosomal 40S subunit protein S17B

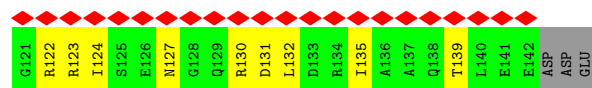


• Molecule 66: Ribosomal 40S subunit protein S18B

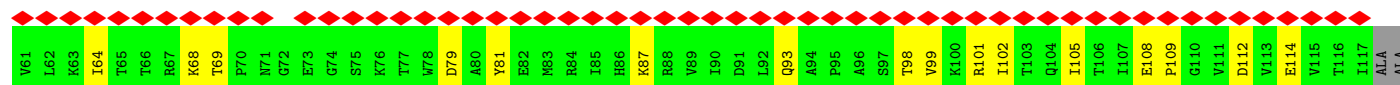
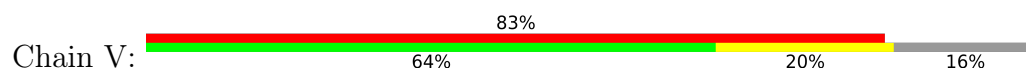


• Molecule 67: Ribosomal 40S subunit protein S19A

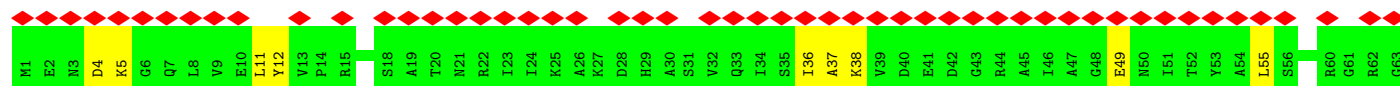
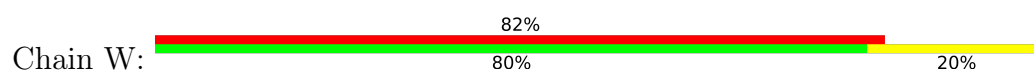




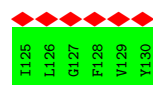
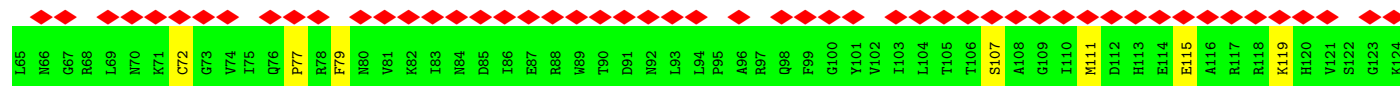
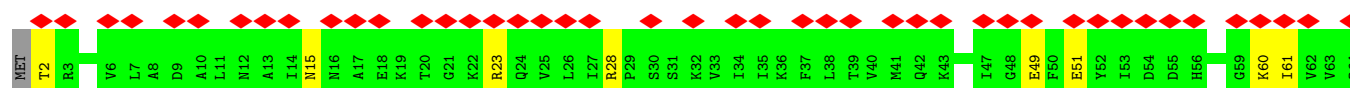
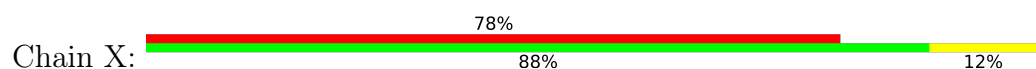
• Molecule 68: Ribosomal 40S subunit protein S20



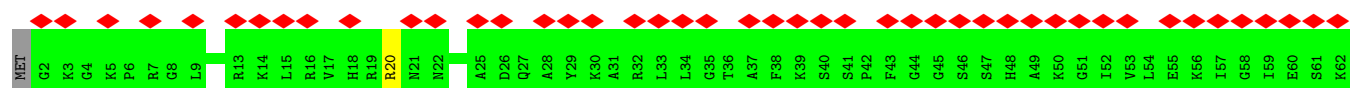
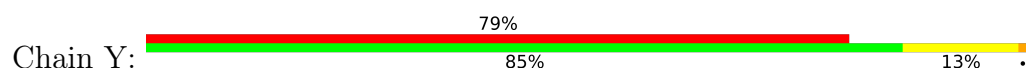
• Molecule 69: 40S ribosomal protein S21

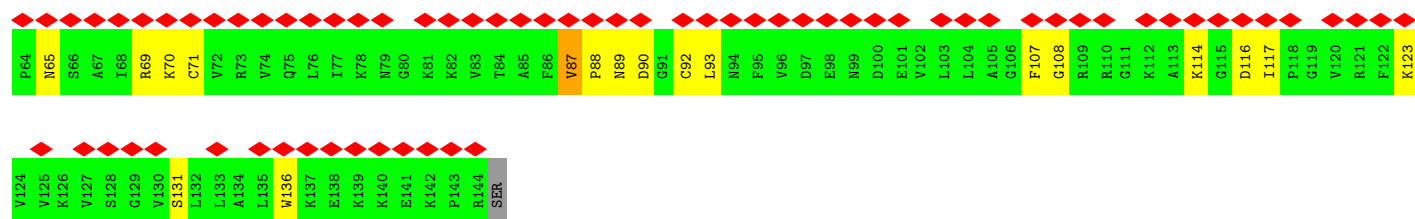


• Molecule 70: 40S ribosomal protein S22-B

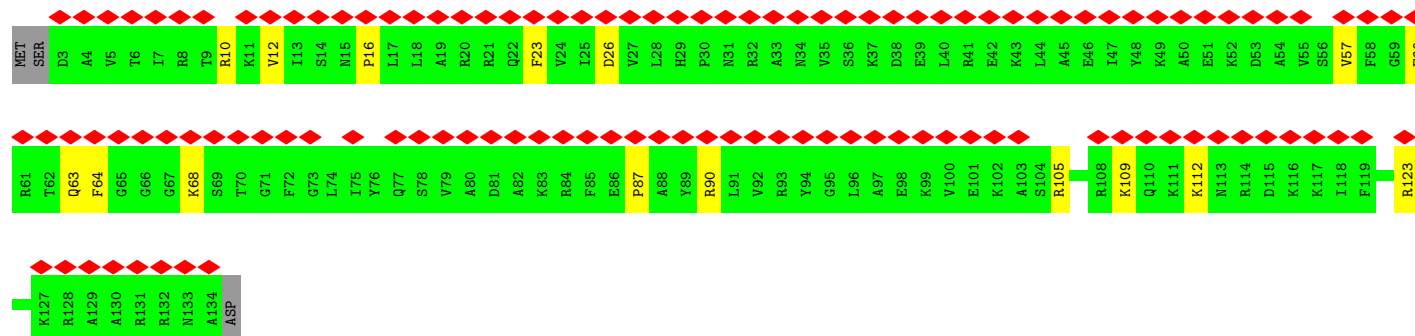


• Molecule 71: Ribosomal 40S subunit protein S23B

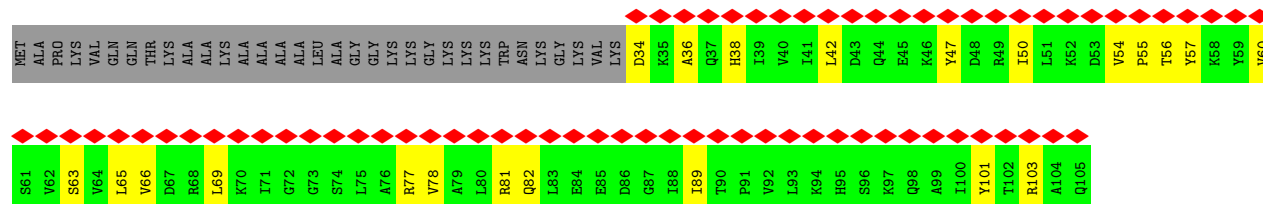




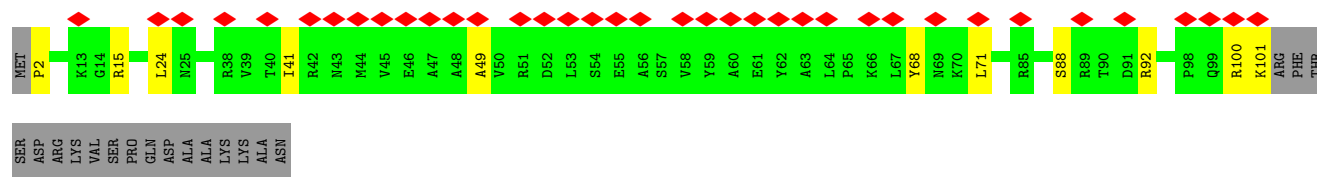
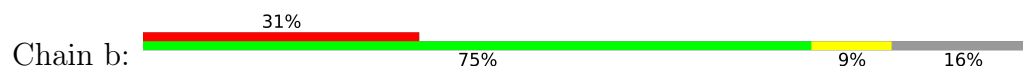
• Molecule 72: 40S ribosomal protein S24



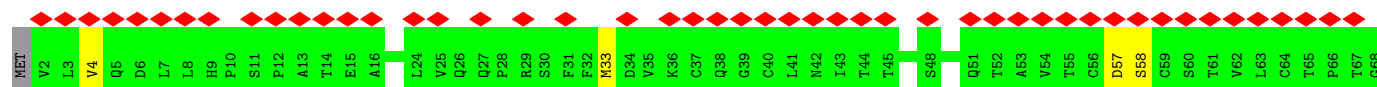
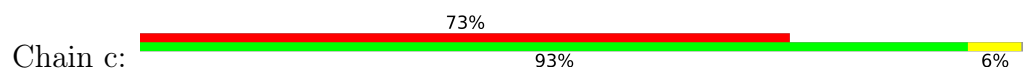
• Molecule 73: 40S ribosomal protein S25

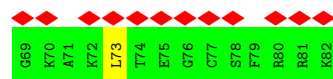


• Molecule 74: 40S ribosomal protein S26

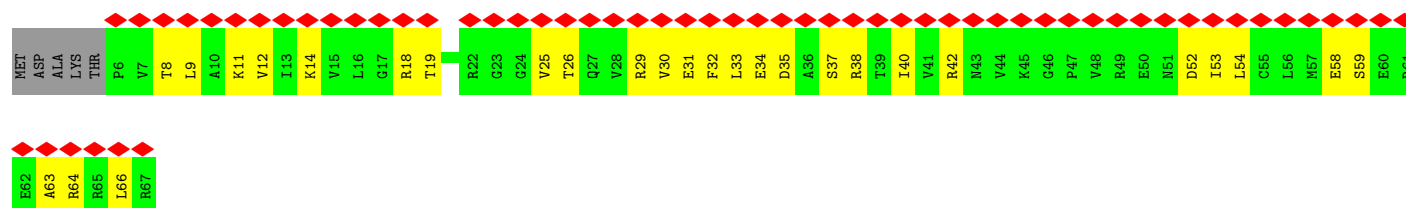
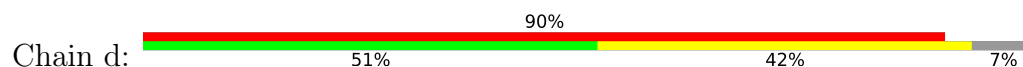


• Molecule 75: 40S ribosomal protein S27

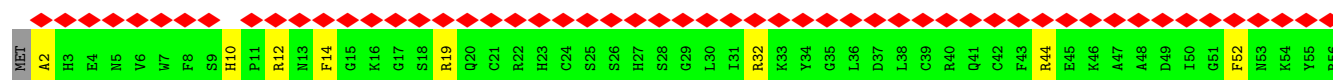
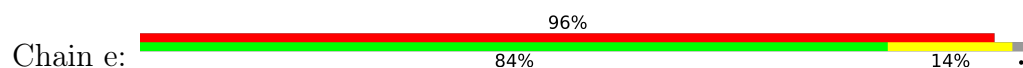




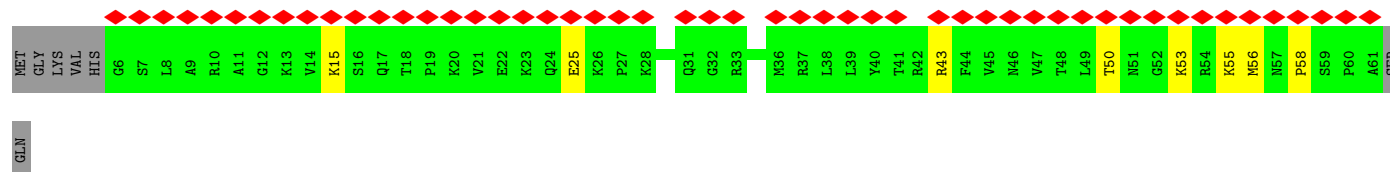
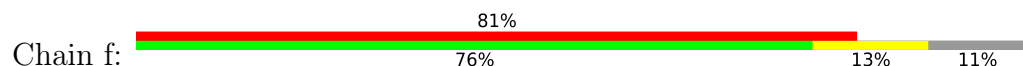
- Molecule 76: Ribosomal 40S subunit protein S28B



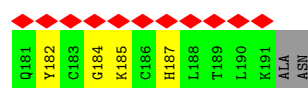
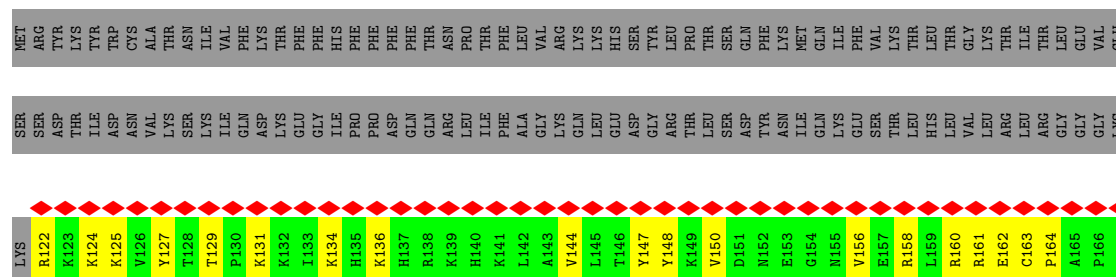
- Molecule 77: Ribosomal 40S subunit protein S29A



- Molecule 78: 40S ribosomal protein S30

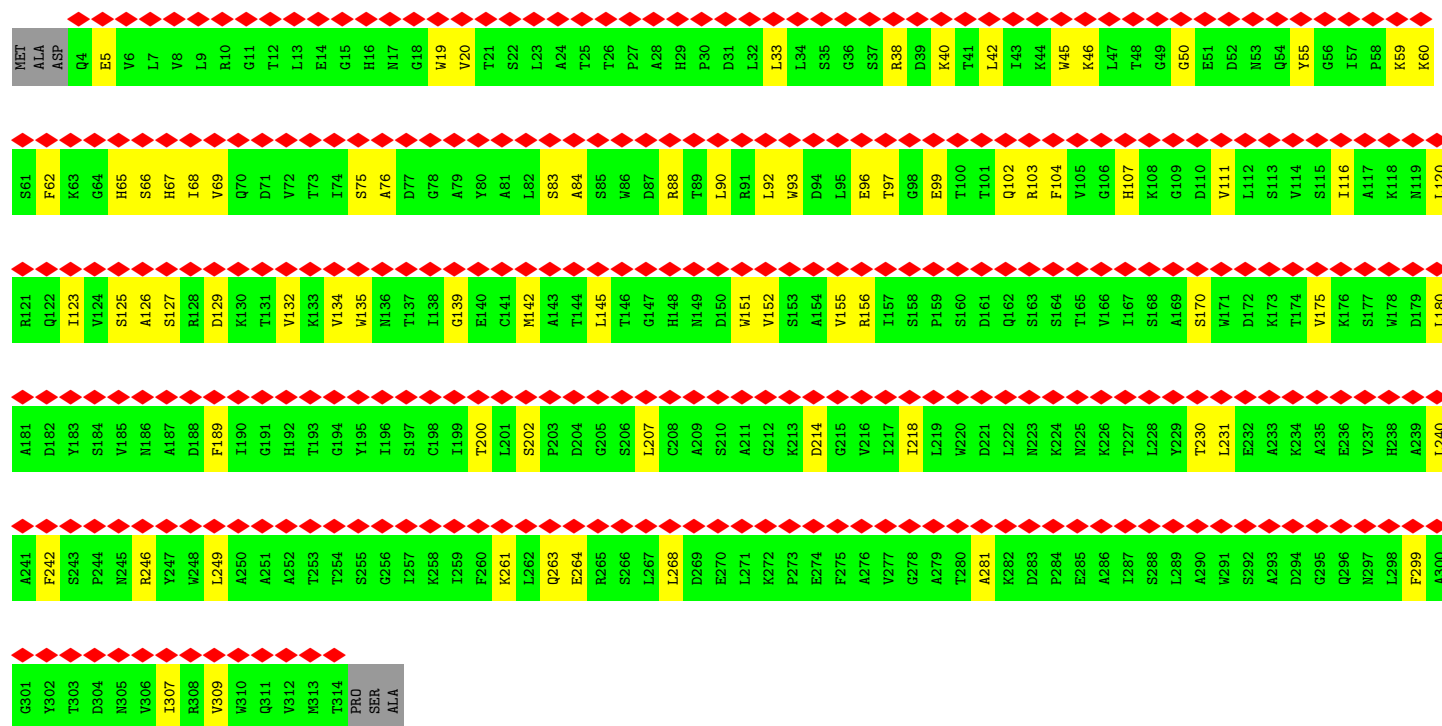


- Molecule 79: Ubiquitin-ribosomal 40S subunit protein S31 fusion protein



- Molecule 80: Guanine nucleotide-binding protein subunit beta-like protein

Category	Percentage
Very bad	98%
Bad	74%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	156607	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.912	Depositor
Minimum map value	-1.096	Depositor
Average map value	0.012	Depositor
Map value standard deviation	0.114	Depositor
Recommended contour level	0.55	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: OMG, ANM, SPD, OMC, IAS, MLZ, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.24	11/76718 (0.0%)	0.34	5/119600 (0.0%)
2	3	0.18	0/2884	0.25	0/4492
3	4	0.21	0/3746	0.29	0/5832
4	10	0.16	0/331	0.19	0/511
5	j	0.20	0/1931	0.33	0/2592
6	k	0.20	0/3156	0.35	0/4246
7	l	0.17	0/2799	0.35	0/3777
8	m	0.15	0/2447	0.31	0/3294
9	n	0.16	0/1258	0.30	0/1696
10	o	0.18	0/1929	0.36	0/2589
11	p	0.15	0/1869	0.30	0/2519
12	q	0.16	0/1537	0.29	0/2067
13	r	0.16	0/1724	0.29	0/2314
14	s	0.14	0/1404	0.29	0/1880
15	t	0.24	0/1637	0.40	0/2195
16	u	0.17	0/1044	0.33	0/1407
17	v	0.20	0/1753	0.35	0/2347
18	w	0.18	0/1620	0.32	0/2167
19	x	0.18	0/1398	0.33	0/1879
20	y	0.18	0/1511	0.34	0/2022
21	z	0.16	0/1483	0.27	0/1972
22	0	0.19	0/1483	0.32	0/1997
23	2	0.17	0/1305	0.29	0/1749
24	5	0.14	0/871	0.37	0/1175
25	6	0.17	0/994	0.36	0/1339
26	7	0.17	0/536	0.29	0/712
27	8	0.18	0/990	0.32	0/1337
28	9	0.17	0/999	0.35	0/1334
29	AA	0.16	0/1112	0.26	0/1488
30	AB	0.19	0/1199	0.32	0/1607
31	AC	0.15	0/522	0.27	0/692
32	AD	0.16	0/738	0.25	0/994

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AE	0.17	0/902	0.31	0/1212
34	AF	0.18	0/1039	0.35	0/1390
35	AG	0.20	0/895	0.31	0/1201
36	AH	0.17	0/934	0.34	0/1242
37	AI	0.16	0/1004	0.38	0/1337
38	AJ	0.14	0/780	0.27	0/1033
39	AK	0.22	0/690	0.41	0/916
40	AL	0.18	0/632	0.33	0/842
41	AM	0.17	0/458	0.27	0/609
42	AN	0.15	0/436	0.31	0/577
43	AO	0.10	0/228	0.32	0/293
44	AP	0.16	0/840	0.29	0/1108
45	AQ	0.18	0/705	0.33	0/940
46	i	0.12	0/864	0.35	0/1156
47	A	0.20	1/40362 (0.0%)	0.32	0/62888
48	B	0.16	0/1666	0.29	0/2273
49	C	0.15	0/1750	0.27	0/2354
50	D	0.17	0/1648	0.28	0/2237
51	E	0.14	0/1731	0.32	0/2324
52	F	0.17	0/2096	0.30	0/2822
53	G	0.14	0/1631	0.32	0/2199
54	H	0.14	0/1845	0.27	0/2464
55	I	0.16	0/1490	0.31	0/2004
56	J	0.16	0/1606	0.28	0/2150
57	K	0.16	0/1478	0.25	0/1978
58	L	0.17	0/801	0.52	0/1081
59	M	0.18	0/1154	0.28	0/1553
60	N	0.14	0/892	0.49	0/1203
61	O	0.15	0/1210	0.26	0/1631
62	P	0.15	0/944	0.28	0/1265
63	Q	0.15	0/954	0.41	0/1282
64	R	0.15	0/1109	0.35	0/1486
65	S	0.13	0/1014	0.32	0/1361
66	T	0.12	0/1186	0.28	0/1590
67	U	0.15	0/1120	0.33	0/1508
68	V	0.14	0/800	0.29	0/1082
69	W	0.17	0/683	0.37	0/918
70	X	0.19	0/1049	0.27	0/1412
71	Y	0.21	0/1128	0.37	0/1505
72	Z	0.16	0/1086	0.24	0/1447
73	a	0.14	0/585	0.30	0/789
74	b	0.16	0/811	0.30	0/1085
75	c	0.17	0/624	0.30	0/843

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	d	0.15	0/489	0.39	0/654
77	e	0.14	0/466	0.31	0/620
78	f	0.15	0/451	0.31	0/601
79	g	0.13	0/585	0.41	0/778
80	h	0.14	0/2451	0.33	0/3337
All	All	0.20	12/214230 (0.0%)	0.33	5/314402 (0.0%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	A	218	A	O3'-P	-11.02	1.44	1.61
1	1	1738	U	O3'-P	-8.78	1.48	1.61
1	1	1259	A	O3'-P	-8.18	1.48	1.61
1	1	2848	C	O3'-P	6.80	1.71	1.61
1	1	482	U	C1'-N1	6.32	1.57	1.48
1	1	477	U	C1'-N1	6.31	1.57	1.48
1	1	483	U	C1'-N1	6.12	1.57	1.48
1	1	2793	C	O3'-P	-5.76	1.52	1.61
1	1	479	C	C1'-N1	5.66	1.56	1.48
1	1	476	C	C1'-N1	5.64	1.56	1.48
1	1	1738	U	P-OP1	-5.43	1.38	1.49
1	1	2791	A	O3'-P	-5.40	1.53	1.61

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1259	A	P-O3'-C3'	18.97	148.66	120.20
1	1	1259	A	OP2-P-O3'	7.61	130.84	108.00
1	1	1738	U	C1'-C2'-O2'	-6.81	98.19	108.40
1	1	1259	A	OP1-P-O3'	-6.80	87.60	108.00
1	1	2848	C	C1'-C2'-O2'	-6.55	98.58	108.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68595	0	34479	826	0
2	3	2579	0	1304	16	0
3	4	3353	0	1694	47	0
4	10	298	0	154	5	0
5	j	1894	0	1975	25	0
6	k	3084	0	3173	48	0
7	l	2751	0	2879	38	0
8	m	2394	0	2362	25	0
9	n	1237	0	1316	17	0
10	o	1893	0	1990	16	0
11	p	1839	0	1957	18	0
12	q	1519	0	1588	18	0
13	r	1689	0	1731	20	0
14	s	1385	0	1418	19	0
15	t	1610	0	1686	26	0
16	u	1029	0	1116	16	0
17	v	1713	0	1764	32	0
18	w	1590	0	1705	18	0
19	x	1375	0	1403	18	0
20	y	1478	0	1590	26	0
21	z	1462	0	1570	29	0
22	0	1442	0	1500	31	0
23	2	1276	0	1333	16	0
24	5	848	0	864	19	0
25	6	986	0	1040	16	0
26	7	524	0	545	7	0
27	8	974	0	1032	13	0
28	9	989	0	1064	15	0
29	AA	1087	0	1154	12	0
30	AB	1170	0	1203	19	0
31	AC	509	0	545	10	0
32	AD	729	0	775	12	0
33	AE	889	0	936	8	0
34	AF	1015	0	1095	14	0
35	AG	867	0	932	13	0
36	AH	913	0	1002	9	0
37	AI	990	0	1094	16	0
38	AJ	772	0	863	9	0
39	AK	677	0	697	12	0
40	AL	623	0	688	11	0
41	AM	446	0	488	9	0
42	AN	427	0	473	4	0
43	AO	227	0	272	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	AP	843	0	914	9	0
45	AQ	698	0	734	10	0
46	i	853	0	830	23	0
47	A	36083	0	18151	598	0
48	B	1627	0	1644	32	0
49	C	1724	0	1805	24	0
50	D	1620	0	1715	20	0
51	E	1707	0	1807	35	0
52	F	2055	0	2137	32	0
53	G	1614	0	1688	37	0
54	H	1820	0	1896	34	0
55	I	1466	0	1561	35	0
56	J	1579	0	1602	23	0
57	K	1453	0	1532	16	0
58	L	783	0	799	33	0
59	M	1129	0	1183	6	0
60	N	885	0	915	33	0
61	O	1187	0	1249	12	0
62	P	942	0	980	16	0
63	Q	935	0	970	31	0
64	R	1091	0	1155	26	0
65	S	1002	0	1058	32	0
66	T	1169	0	1216	24	0
67	U	1100	0	1114	19	0
68	V	790	0	855	19	0
69	W	676	0	677	14	0
70	X	1032	0	1066	13	0
71	Y	1110	0	1182	19	0
72	Z	1072	0	1123	13	0
73	a	578	0	613	18	0
74	b	799	0	860	8	0
75	c	614	0	627	3	0
76	d	487	0	523	20	0
77	e	454	0	431	9	0
78	f	444	0	483	7	0
79	g	574	0	606	29	0
80	h	2398	0	2374	55	0
81	1	20	0	38	1	0
82	1	19	0	19	12	0
83	AK	1	0	0	0	0
83	AN	1	0	0	0	0
83	AP	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	AQ	1	0	0	0	0
83	b	1	0	0	0	0
83	c	1	0	0	0	0
83	e	1	0	0	0	0
83	g	1	0	0	0	0
All	All	199587	0	148581	2507	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 (2507) 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)
78:f:50:THR:OG1	78:f:53:LYS:HB2	1.28	1.33
1:1:2793:C:C1'	82:1:3403:ANM:H143	1.68	1.23
1:1:2793:C:O4'	82:1:3403:ANM:C14	1.86	1.22
71:Y:70:LYS:O	71:Y:87:VAL:HG23	1.33	1.21
1:1:1108:A:P	15:t:5:LYS:NZ	2.16	1.17
71:Y:70:LYS:O	71:Y:87:VAL:CG2	1.92	1.16
1:1:2793:C:H1'	82:1:3403:ANM:H143	1.35	1.08
1:1:2793:C:C1'	82:1:3403:ANM:C14	2.29	1.06
1:1:1108:A:OP1	15:t:5:LYS:NZ	1.94	0.98
1:1:1108:A:P	15:t:5:LYS:HZ1	1.81	0.96
1:1:2793:C:O4'	82:1:3403:ANM:H142	1.67	0.93
4:10:1:G:H1	4:10:72:U:H3	1.10	0.92
36:AH:58:ARG:HD3	36:AH:59:PRO:HD2	1.50	0.92
47:A:853:G:H1	47:A:945:U:H3	1.18	0.89
25:6:30:GLY:HA3	25:6:66:LYS:HE2	1.55	0.89
1:1:1014:G:H1	1:1:1030:U:H3	0.89	0.89
47:A:1040:U:H3	47:A:1049:G:H1	1.21	0.86
47:A:216:A:N6	47:A:829:A:H1'	1.91	0.86
1:1:443:G:N2	1:1:487:C:O2	2.09	0.85
1:1:2847:U:OP2	1:1:2917:G:N1	2.08	0.85
1:1:2793:C:H1'	82:1:3403:ANM:C14	2.00	0.85
80:h:42:LEU:HB2	80:h:62:PHE:HB2	1.58	0.85
1:1:2808:OMC:H5	1:1:2824:C:H42	1.23	0.84
47:A:218:A:N6	47:A:827:C:H42	1.74	0.84
1:1:1240:A:N6	1:1:1267:A:OP1	2.13	0.82
1:1:2793:C:O4'	82:1:3403:ANM:H143	1.57	0.82
78:f:50:THR:OG1	78:f:53:LYS:CB	2.22	0.81
19:x:165:GLN:HE21	19:x:165:GLN:N	1.79	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:s:109:HIS:HD2	14:s:114:ILE:HD11	1.47	0.80
1:1:1936:G:H21	1:1:3327:A:H8	1.27	0.79
31:AC:8:THR:HG22	31:AC:10:HIS:H	1.46	0.79
24:5:19:VAL:HG23	24:5:20:ALA:H	1.48	0.79
47:A:1042:U:H3'	47:A:1043:U:H2'	1.64	0.79
47:A:484:G:N2	47:A:501:G:O6	2.16	0.78
80:h:90:LEU:HB2	80:h:104:PHE:HB2	1.65	0.78
34:AF:106:ARG:NH2	34:AF:122:ASN:O	2.16	0.78
47:A:1324:C:O2'	47:A:1326:A:N7	2.14	0.78
1:1:2836:A:H5''	13:r:114:GLY:HA2	1.66	0.78
21:z:98:ARG:NH2	21:z:130:ASN:OD1	2.17	0.78
47:A:500:U:O2'	47:A:501:G:N7	2.18	0.77
16:u:17:ARG:NH2	16:u:58:THR:O	2.18	0.76
1:1:437:G:H22	1:1:620:A:H61	1.31	0.76
10:o:9:THR:HA	10:o:12:LYS:HD3	1.67	0.76
47:A:1597:G:N7	64:R:13:LYS:NZ	2.32	0.76
47:A:880:G:H1	47:A:902:U:H3	1.30	0.76
1:1:3194:G:H5'	16:u:129:VAL:HG21	1.67	0.76
47:A:869:A:O2'	49:C:124:ASN:ND2	2.18	0.76
17:v:143:ARG:O	17:v:149:ASN:ND2	2.18	0.76
47:A:512:G:H1	47:A:541:C:H5	1.33	0.76
47:A:215:A:N3	47:A:215:A:H2'	2.01	0.75
5:j:27:ALA:O	5:j:128:ARG:NH2	2.18	0.75
47:A:1579:A:H2'	47:A:1580:A:H8	1.51	0.75
52:F:45:VAL:HG23	52:F:61:VAL:HG11	1.66	0.75
47:A:216:A:H61	47:A:829:A:H1'	1.50	0.75
1:1:935:U:OP2	30:AB:26:ARG:NH2	2.20	0.75
1:1:1019:U:H4'	1:1:1019:U:OP1	1.87	0.75
47:A:766:U:H4'	47:A:767:G:H5''	1.69	0.74
17:v:183:THR:HG22	17:v:187:ARG:HB2	1.69	0.74
29:AA:27:LYS:HE3	29:AA:97:THR:HG22	1.70	0.74
69:W:38:LYS:HD2	69:W:49:GLU:HG3	1.67	0.74
47:A:1276:G:H1	47:A:1309:G:H22	1.34	0.74
47:A:1043:U:O2'	47:A:1045:U:OP2	2.04	0.74
1:1:1021:A:H2'	1:1:1021:A:N3	2.03	0.74
33:AE:45:THR:HG21	33:AE:89:PHE:HA	1.70	0.74
47:A:79:C:OP1	54:H:159:ARG:NH2	2.20	0.73
1:1:1091:U:H4'	1:1:1092:U:H5'	1.71	0.73
1:1:2793:C:C1'	82:1:3403:ANM:H142	2.15	0.73
1:1:1657:G:H2'	1:1:1658:G:C8	2.22	0.73
23:2:142:SER:OG	23:2:144:GLU:OE1	2.04	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:f:50:THR:HG1	78:f:53:LYS:HB2	1.49	0.73
58:L:17:GLN:H	58:L:88:PRO:HB3	1.52	0.73
21:z:67:LYS:HE2	21:z:71:ARG:HH12	1.54	0.73
49:C:82:ARG:NH2	49:C:188:LEU:O	2.21	0.73
1:1:1269:A:H3'	1:1:1270:A:H8	1.53	0.73
47:A:1699:G:N1	47:A:1700:G:N3	2.37	0.73
54:H:1:MET:HE2	54:H:106:LEU:HB2	1.69	0.73
71:Y:89:ASN:HB2	71:Y:92:CYS:SG	2.28	0.73
1:1:3309:A:H2	1:1:3326:G:H21	1.37	0.72
47:A:1529:G:N2	47:A:1556:A:OP2	2.22	0.72
1:1:834:G:O6	45:AQ:4:ARG:NH2	2.22	0.72
1:1:3157:A:OP1	12:q:23:ARG:NH1	2.21	0.72
1:1:3139:U:OP2	35:AG:63:LYS:NZ	2.23	0.72
47:A:217:A:H8	47:A:217:A:H5''	1.55	0.72
58:L:54:TYR:HD1	58:L:72:GLY:HA2	1.55	0.72
1:1:71:C:O2'	15:t:66:ASN:OD1	2.08	0.71
1:1:1352:C:N4	20:y:27[A]:GLN:OE1	2.23	0.71
47:A:635:C:O2	55:I:110:ARG:NH2	2.22	0.71
52:F:11:ARG:HH12	52:F:24:SER:HB3	1.53	0.71
55:I:5:ILE:HG22	55:I:7:SER:H	1.55	0.71
47:A:65:A:H2	47:A:84:A:H62	1.37	0.71
1:1:1560:U:H3	1:1:1571:G:H1	1.38	0.71
12:q:92:PHE:HB2	12:q:142:ASP:HB3	1.73	0.71
47:A:747:A:OP1	57:K:79:ARG:NH2	2.22	0.71
7:l:290:LEU:HD22	20:y:129:LEU:HD11	1.73	0.71
16:u:34:ASP:OD2	16:u:37:ARG:NH2	2.22	0.71
1:1:2988:A:H2'	1:1:2989:A:C8	2.26	0.71
47:A:854:A:H61	47:A:943:U:H5	1.39	0.70
3:4:66:A:OP1	37:AI:10:ARG:NH2	2.23	0.70
47:A:211:A:H62	47:A:250:U:H3	1.39	0.70
1:1:362:U:O4	39:AK:24:ARG:NH2	2.24	0.70
1:1:581:A:H5''	35:AG:106:ASN:HD21	1.56	0.70
47:A:1240:G:N7	60:N:46:ARG:NH2	2.38	0.70
1:1:437:G:H1	1:1:620:A:H61	1.38	0.70
47:A:653:G:H4'	47:A:654:G:H5'	1.72	0.70
32:AD:29:TYR:OH	32:AD:57:GLU:OE2	2.09	0.70
33:AE:45:THR:HG22	33:AE:47:ASP:H	1.56	0.70
47:A:1383:U:O2'	47:A:1386:A:N6	2.23	0.70
52:F:100:ARG:NH2	52:F:121:TYR:O	2.24	0.70
47:A:1474:G:H3'	47:A:1502:A:H61	1.56	0.70
1:1:1225:G:H2'	1:1:1226:G:C8	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2504:C:OP1	5:j:37:ARG:NH2	2.23	0.70
47:A:1156:A:H2'	47:A:1157:G:C8	2.26	0.70
1:1:2645:A:O2'	14:s:126:ASP:OD1	2.05	0.70
47:A:1575:G:H1	47:A:1595:U:H3	1.39	0.70
65:S:103:ASP:OD1	65:S:104:ALA:N	2.25	0.70
1:1:564:G:H2'	1:1:565:A:C8	2.27	0.69
66:T:134:ARG:HB2	66:T:136:GLN:HE22	1.56	0.69
1:1:2334:A:H61	1:1:2955:C:H5	1.38	0.69
1:1:2988:A:H2'	1:1:2989:A:H8	1.57	0.69
76:d:12:VAL:HG22	76:d:52:ASP:H	1.56	0.69
1:1:1774:G:O2'	1:1:1776:G:OP2	2.10	0.69
1:1:307:A:H2'	1:1:308:A:C8	2.28	0.69
7:l:359:GLU:OE2	7:l:363:ASN:ND2	2.25	0.69
47:A:1236:U:O2'	47:A:1237:C:O2	2.09	0.69
13:r:30:LYS:HG3	13:r:63:GLU:HG3	1.72	0.69
22:0:60:SER:OG	22:0:62:ASN:ND2	2.24	0.69
1:1:2847:U:C6	1:1:2847:U:H5''	2.28	0.69
47:A:345:G:H5''	59:M:85:ILE:HD11	1.74	0.69
79:g:144:VAL:HA	79:g:147:TYR:HD2	1.58	0.69
1:1:3039:C:H3'	21:z:62:ARG:HH22	1.58	0.69
39:AK:21:ARG:NH2	39:AK:41:ALA:O	2.19	0.69
47:A:1460:G:H2'	47:A:1461:A:H8	1.58	0.69
47:A:1535:G:H1'	66:T:89:GLN:HE21	1.57	0.69
1:1:2171:U:H5'	1:1:2172:G:H5'	1.75	0.68
47:A:869:A:H62	47:A:913:U:H3	1.41	0.68
47:A:1445:C:OP2	66:T:138:THR:OG1	2.11	0.68
51:E:30:LEU:HD22	51:E:59:VAL:HG22	1.74	0.68
1:1:437:G:N2	1:1:620:A:H61	1.90	0.68
1:1:3194:G:H4'	16:u:129:VAL:HG11	1.75	0.68
1:1:1243:U:H2'	1:1:1264:G:H1	1.59	0.68
3:4:150:G:OP1	27:8:27:ARG:NH2	2.27	0.68
53:G:57:SER:OG	53:G:167:ARG:NH2	2.26	0.68
64:R:12:LYS:HG3	64:R:13:LYS:H	1.58	0.68
69:W:55:LEU:HD11	69:W:69:LEU:HD21	1.76	0.68
1:1:2932:C:H2'	1:1:2933:G:C8	2.29	0.68
24:5:16:VAL:HG12	24:5:65:VAL:HG22	1.74	0.68
47:A:1335:U:H2'	47:A:1336:G:C8	2.28	0.68
8:m:50:ARG:NH2	8:m:72:ASP:OD2	2.27	0.67
47:A:1579:A:H2'	47:A:1580:A:C8	2.28	0.67
21:z:134:HIS:HE1	21:z:136:ARG:HE	1.40	0.67
41:AM:18:LYS:HG2	41:AM:21[A]:ARG:HH21	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1219:A:OP1	77:e:2:ALA:N	2.27	0.67
46:i:57:PRO:HG2	46:i:60:ASN:HB2	1.76	0.67
47:A:530:U:OP1	72:Z:64:PHE:HA	1.93	0.67
47:A:652:C:H5''	47:A:653:G:H8	1.58	0.67
1:1:1238:G:N2	1:1:1266:A:O2'	2.27	0.67
1:1:2254:G:OP1	43:AO:16:LYS:NZ	2.28	0.67
80:h:102:GLN:NE2	80:h:103:ARG:O	2.28	0.67
47:A:4:C:O2'	57:K:17:ARG:NH2	2.26	0.67
47:A:122:U:H2'	47:A:123:G:H5''	1.77	0.67
47:A:948:A:N7	61:O:70:LYS:NZ	2.43	0.67
80:h:175:VAL:HB	80:h:189:PHE:HB2	1.74	0.67
1:1:653:C:H2'	1:1:654:A:H8	1.60	0.67
1:1:3356:A:O2'	19:x:56:ARG:NH2	2.28	0.67
47:A:1669:U:O4	47:A:1707:G:N2	2.28	0.67
80:h:218:ILE:HG23	80:h:230:THR:HG22	1.77	0.67
10:o:185:GLU:HG2	10:o:196:VAL:HG21	1.77	0.67
1:1:662:U:H2'	1:1:663:A:C8	2.31	0.67
1:1:2086:C:H1'	1:1:3309:A:C8	2.30	0.66
63:Q:61:ARG:NH1	63:Q:88:GLU:OE2	2.27	0.66
17:v:62:TYR:HD2	17:v:106:VAL:HG13	1.60	0.66
47:A:856:G:H2'	47:A:857:G:C8	2.30	0.66
47:A:1422:A:OP2	51:E:28:ARG:NH2	2.24	0.66
50:D:53:LEU:HA	69:W:12:TYR:HE1	1.59	0.66
1:1:3262:U:O4	6:k:124:LYS:NZ	2.28	0.66
1:1:3308:G:H21	1:1:3327:A:H2	1.43	0.66
47:A:1026:G:H2'	47:A:1027:G:C8	2.31	0.66
55:I:92:ARG:HH12	55:I:120:LYS:HB3	1.60	0.66
47:A:485:G:O6	47:A:499:U:O4	2.14	0.66
47:A:218:A:N6	47:A:827:C:N4	2.43	0.66
47:A:1276:G:H22	47:A:1309:G:N2	1.93	0.66
47:A:1463:G:H2'	47:A:1464:G:H8	1.60	0.66
1:1:730:A:H8	1:1:733:A:H62	1.42	0.66
47:A:1019:C:HO2'	70:X:2:THR:N	1.93	0.66
68:V:81:TYR:HB3	77:e:52:PHE:HB3	1.78	0.66
1:1:1713:U:H2'	1:1:1714:G:C8	2.31	0.66
22:O:60:SER:HG	22:O:62:ASN:ND2	1.94	0.66
47:A:1451:C:OP1	64:R:138:GLN:NE2	2.27	0.66
49:C:174:ARG:NH2	49:C:196:GLU:OE2	2.29	0.66
53:G:200:ASN:HB3	53:G:208:SER:HB3	1.76	0.66
1:1:740:A:OP1	20:y:66:ARG:NH2	2.29	0.65
49:C:145:ARG:NH2	49:C:151:LYS:O	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:437:G:H22	1:1:620:A:N6	1.93	0.65
49:C:190:PRO:HG2	49:C:192:VAL:HG23	1.78	0.65
8:m:197:LYS:HG2	8:m:202:GLY:HA3	1.76	0.65
46:i:104:GLN:HG3	46:i:110:SER:HB2	1.79	0.65
1:1:437:G:H1	1:1:620:A:N6	1.93	0.65
1:1:2189:U:OP1	4:10:3:C:O2'	2.13	0.65
1:1:2869:A:H2'	1:1:2871:C:H5''	1.77	0.65
32:AD:59:GLU:OE1	32:AD:71:TYR:OH	2.14	0.65
47:A:1578:C:H2'	47:A:1579:A:H8	1.61	0.65
70:X:15:ASN:ND2	70:X:72:CYS:O	2.29	0.65
63:Q:25:LEU:HA	63:Q:28:MET:HE2	1.78	0.65
1:1:2191:A:H2'	1:1:2192:A:C8	2.32	0.65
46:i:93:ARG:H	47:A:1259:C:H5	1.45	0.65
47:A:1156:A:H2'	47:A:1157:G:H8	1.60	0.65
23:2:84:TYR:HB2	31:AC:24:PRO:HD3	1.78	0.65
47:A:881:U:H5'	49:C:23:PRO:HG2	1.79	0.65
55:I:25:GLU:HB2	55:I:31:LYS:HG3	1.78	0.65
1:1:315:C:OP2	38:AJ:27:TYR:OH	2.13	0.65
47:A:485:G:N2	47:A:499:U:O2	2.17	0.65
47:A:501:G:H2'	47:A:502:U:C6	2.31	0.65
1:1:3010:U:O2	25:6:9:ASN:ND2	2.30	0.65
47:A:1472:G:N2	47:A:1580:A:OP1	2.29	0.65
1:1:654:A:H2'	1:1:655:A:C8	2.33	0.64
1:1:1592:C:H2'	1:1:1593:C:C6	2.32	0.64
16:u:14:GLU:HG2	16:u:17:ARG:HG2	1.79	0.64
55:I:33:GLU:HG3	55:I:69:VAL:HG11	1.80	0.64
55:I:92:ARG:NH1	55:I:120:LYS:HB3	2.12	0.64
1:1:800:C:OP1	7:l:99:ARG:NH2	2.28	0.64
1:1:2780:A:H8	1:1:2780:A:H5'	1.62	0.64
1:1:1014:G:O6	1:1:1030:U:O4	2.15	0.64
1:1:2334:A:N3	19:x:131:ARG:NH2	2.45	0.64
47:A:826:U:H6	47:A:826:U:H3'	1.63	0.64
76:d:19:THR:HG23	76:d:25:VAL:HG13	1.79	0.64
1:1:2925:U:H2'	1:1:2926:U:H2'	1.79	0.64
1:1:1230:G:N2	1:1:1259:A:OP1	2.28	0.64
1:1:1692:A:H2'	1:1:1693:A:C8	2.32	0.64
1:1:2535:A:OP1	5:j:69:TYR:OH	2.14	0.64
1:1:2847:U:H5''	1:1:2847:U:H6	1.62	0.64
1:1:2867:G:O2'	42:AN:24:TYR:O	2.16	0.64
6:k:218:ILE:HB	6:k:337:THR:HB	1.78	0.64
1:1:316:U:O2'	38:AJ:29:LYS:NZ	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2051:G:H2'	1:1:2052:G:C8	2.33	0.64
3:4:57:C:OP2	39:AK:68:LYS:NZ	2.31	0.64
48:B:167:LYS:NZ	48:B:204:TYR:O	2.28	0.64
76:d:12:VAL:HG12	76:d:30:VAL:HG12	1.80	0.64
1:1:1663:A:H2'	1:1:1664:G:C8	2.33	0.64
47:A:1511:A:H2'	47:A:1512:A:C8	2.33	0.64
1:1:1030:U:H2'	1:1:1031:A:C8	2.33	0.64
14:s:32:ARG:HD2	14:s:120:ILE:HA	1.79	0.64
29:AA:87:LEU:HD11	29:AA:121:LYS:HD3	1.79	0.64
1:1:925:A:O2'	39:AK:49:TRP:O	2.17	0.63
12:q:8:GLN:HB3	12:q:72:LYS:HD2	1.79	0.63
23:2:49:GLN:HA	23:2:52:MET:HE3	1.80	0.63
55:I:45:ILE:HG21	55:I:171:LYS:HG2	1.81	0.63
80:h:75:SER:HA	80:h:116:ILE:HD11	1.80	0.63
46:i:55:LYS:HB3	46:i:61:GLU:HB3	1.79	0.63
1:1:1231:U:H4'	1:1:1232:G:H5'	1.81	0.63
53:G:187:ILE:HD13	73:a:66:VAL:HG11	1.79	0.63
64:R:124:GLU:HG2	64:R:133:ALA:HB1	1.78	0.63
1:1:498:C:H5''	9:n:25:ARG:NH2	2.13	0.63
1:1:3269:C:O2	6:k:25:GLN:NE2	2.32	0.63
7:l:300:VAL:HB	20:y:39:ARG:HG2	1.80	0.63
51:E:151:GLN:OE1	51:E:153:TYR:OH	2.16	0.63
69:W:79:LEU:HD13	69:W:82:VAL:HG11	1.80	0.63
80:h:127:SER:OG	80:h:129:ASP:OD1	2.16	0.63
1:1:1057:A:O2'	23:2:102:ARG:NH2	2.31	0.63
47:A:405:A:H2'	47:A:406:C:H6	1.63	0.63
47:A:457:G:OP2	72:Z:105:ARG:NH2	2.26	0.63
47:A:1024:A:O2'	47:A:1025:G:O5'	2.16	0.63
73:a:78:VAL:HG12	73:a:81:ARG:HH21	1.63	0.63
47:A:142:G:O2'	47:A:143:A:O5'	2.14	0.63
47:A:405:A:H2'	47:A:406:C:C6	2.33	0.63
47:A:509:A:OP2	57:K:176:ASN:ND2	2.28	0.63
80:h:116:ILE:HG22	80:h:123:ILE:HG12	1.81	0.63
1:1:1720:U:H1'	1:1:1721:C:C6	2.33	0.63
1:1:2052:G:H2'	1:1:2053:C:C6	2.34	0.63
22:0:73:LYS:NZ	22:0:97:VAL:O	2.32	0.63
47:A:1219:A:O2'	79:g:187:HIS:ND1	2.32	0.63
49:C:136:ARG:HG3	49:C:218:LEU:HD11	1.81	0.63
1:1:476:C:H2'	1:1:477:U:C6	2.33	0.63
1:1:1653:C:O2'	1:1:1793:A:OP2	2.14	0.63
1:1:2846:G:O6	1:1:2917:G:H2'	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:h:202:SER:HB3	80:h:207:LEU:HB2	1.80	0.63
1:1:2709:C:O2'	31:AC:36:ASP:OD1	2.16	0.62
47:A:511:U:H2'	47:A:512:G:C8	2.33	0.62
58:L:70:ASP:OD1	58:L:71:GLU:N	2.32	0.62
1:1:67:C:OP2	1:1:301:G:N2	2.32	0.62
1:1:976:A:N6	1:1:1100:G:O2'	2.30	0.62
1:1:2239:G:O2'	1:1:2241:C:N4	2.32	0.62
6:k:331:VAL:H	6:k:334:ARG:HG3	1.63	0.62
47:A:452:A:H4'	52:F:62:LYS:HE3	1.80	0.62
66:T:29:MET:HB2	66:T:54:LEU:HD22	1.80	0.62
29:AA:115:LYS:NZ	29:AA:119:GLU:OE2	2.32	0.62
47:A:317:U:H4'	47:A:321:A:C8	2.34	0.62
47:A:1339:G:O6	47:A:1354:U:O2	2.16	0.62
67:U:117:SER:HB2	67:U:123:ARG:HB2	1.80	0.62
1:1:653:C:H2'	1:1:654:A:C8	2.34	0.62
47:A:123:G:OP1	52:F:77:ARG:NH2	2.25	0.62
47:A:214:U:O5'	47:A:214:U:H6	1.82	0.62
47:A:768:C:H2'	47:A:769:U:O4'	1.99	0.62
47:A:1596:U:O2'	53:G:105:GLY:O	2.15	0.62
60:N:58:GLN:HB3	60:N:87:PRO:HD2	1.82	0.62
1:1:443:G:N2	1:1:487:C:C2	2.67	0.62
25:6:17:LEU:HD13	25:6:23:MET:HE2	1.80	0.62
9:n:3:GLN:HG2	34:AF:76:LEU:H	1.63	0.62
47:A:530:U:OP2	57:K:132:ARG:NH2	2.33	0.62
6:k:284:ARG:NH2	6:k:295:ALA:O	2.33	0.62
47:A:1245:U:H2'	47:A:1246:G:H8	1.65	0.62
1:1:1957:G:O2'	1:1:1958:G:O5'	2.17	0.62
7:l:11:SER:OG	7:l:15:GLU:OE1	2.18	0.62
33:AE:71:ARG:HH11	33:AE:103:LEU:HD13	1.65	0.62
46:i:60:ASN:OD1	66:T:120:ARG:NH1	2.33	0.62
47:A:648:U:H2'	47:A:649:G:C8	2.35	0.62
47:A:1668:A:H8	54:H:65:GLN:HG3	1.65	0.62
53:G:25:LEU:HD12	64:R:26:GLY:HA3	1.82	0.62
56:J:120:THR:HG21	56:J:133:ALA:HA	1.80	0.62
1:1:628:A:H2'	1:1:629:A:C8	2.34	0.61
1:1:1837:A:H1'	41:AM:45:ARG:HH22	1.64	0.61
80:h:107:HIS:NE2	80:h:125:SER:OG	2.29	0.61
1:1:2780:A:H5'	1:1:2780:A:C8	2.35	0.61
58:L:12:HIS:HB3	58:L:80:LEU:HD21	1.81	0.61
1:1:2163:G:O2'	1:1:2292:U:OP2	2.18	0.61
47:A:589:A:H2'	47:A:590:A:C8	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1561:U:H2'	1:1:1562:G:C8	2.35	0.61
1:1:2158:A:H2'	1:1:2159:C:C6	2.35	0.61
18:w:11:ASP:HB2	18:w:118:ARG:HB3	1.82	0.61
60:N:69:GLU:OE1	60:N:73:LYS:NZ	2.33	0.61
64:R:27:LEU:HB3	64:R:63:ASP:HB2	1.82	0.61
1:1:2130:A:H2'	1:1:2131:U:H6	1.66	0.61
19:x:40:LYS:HD2	19:x:113:VAL:HG22	1.82	0.61
24:5:30:GLN:HE22	24:5:58:ALA:HB1	1.64	0.61
47:A:1275:U:H2'	47:A:1276:G:C8	2.36	0.61
53:G:72:HIS:CD2	53:G:107:LYS:HD3	2.36	0.61
1:1:1021:A:H62	63:Q:74:ALA:HA	1.65	0.61
47:A:216:A:N3	47:A:216:A:H2'	2.15	0.61
47:A:1668:A:H1'	54:H:66:GLY:HA2	1.81	0.61
60:N:57:ALA:HB3	60:N:124:LYS:HA	1.82	0.61
64:R:86:LYS:HG2	64:R:116:LEU:HD13	1.82	0.61
47:A:1417:C:O2'	47:A:1423:U:O4	2.16	0.61
1:1:1617:A:H2'	1:1:1618:U:C6	2.35	0.61
22:0:71:LYS:O	22:0:73:LYS:NZ	2.33	0.61
50:D:134:ILE:HD13	50:D:186:ALA:HB1	1.81	0.61
64:R:30:ILE:HG12	64:R:35:ILE:HG22	1.82	0.61
47:A:218:A:N3	47:A:218:A:H2'	2.14	0.61
47:A:945:U:H5'	61:O:55:ARG:HD3	1.81	0.61
60:N:99:GLU:O	60:N:111:ASN:ND2	2.34	0.61
51:E:128:MET:HE2	51:E:135:VAL:HG12	1.83	0.60
60:N:74:LEU:HA	79:g:150:VAL:HG21	1.84	0.60
63:Q:123:TYR:OH	66:T:126:ARG:NH1	2.34	0.60
6:k:71:GLU:OE2	26:7:1:MET:N	2.33	0.60
19:x:165:GLN:N	19:x:165:GLN:NE2	2.49	0.60
52:F:199:GLU:OE2	52:F:201:HIS:NE2	2.24	0.60
53:G:57:SER:HA	76:d:53:ILE:HB	1.83	0.60
58:L:80:LEU:HB3	58:L:82:ILE:HG23	1.83	0.60
1:1:3:U:H3	3:4:155:G:H22	1.48	0.60
1:1:617:A:H5'	1:1:619:A:H1'	1.82	0.60
1:1:2134:U:OP2	5:j:241:ARG:NH2	2.35	0.60
48:B:48:ILE:HD12	48:B:149:MET:HE3	1.84	0.60
1:1:2347:G:H2'	1:1:2348:G:C8	2.37	0.60
1:1:3233:A:OP1	9:n:45:ARG:NH2	2.33	0.60
47:A:1230:G:N1	47:A:1234:U:O4	2.34	0.60
1:1:3260:A:H2'	1:1:3261:A:C8	2.36	0.60
41:AM:24:PRO:HG2	41:AM:27:ILE:HD12	1.84	0.60
47:A:739:A:H5''	47:A:740:A:H5'	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1469:A:H2'	47:A:1470:G:C8	2.37	0.60
1:1:1951:U:H2'	1:1:1952:G:H8	1.66	0.60
9:n:65:SER:HB2	9:n:75:LEU:HD23	1.83	0.60
24:5:22:PRO:HB2	24:5:28:PHE:HB2	1.83	0.60
47:A:327:G:H5''	56:J:98:LYS:HB3	1.82	0.60
47:A:538:G:N2	78:f:25:GLU:OE2	2.29	0.60
54:H:161:GLU:HB3	54:H:170:THR:HG22	1.82	0.60
1:1:660:U:H2'	1:1:661:C:C6	2.36	0.60
1:1:1108:A:OP2	15:t:5:LYS:NZ	2.17	0.60
47:A:127:G:N7	54:H:202:ARG:NH2	2.46	0.60
47:A:1474:G:O2'	47:A:1481:C:O2	2.18	0.60
1:1:2650:A:H8	46:i:47:ASP:HB3	1.67	0.60
46:i:31:LYS:HE2	46:i:33:ASN:HB2	1.84	0.60
30:AB:24:LYS:O	30:AB:26:ARG:HG2	2.02	0.60
37:AI:14:LYS:NZ	37:AI:62:GLN:OE1	2.21	0.60
47:A:78:A:C8	54:H:154:ARG:HG3	2.37	0.60
64:R:21:VAL:HG22	64:R:64:ILE:HG12	1.83	0.60
1:1:511:C:H5''	7:l:344:LYS:HD2	1.82	0.59
47:A:1265:C:H2'	47:A:1266:G:H8	1.67	0.59
47:A:952:A:OP2	61:O:124:ARG:NH2	2.35	0.59
3:4:52:A:H62	41:AM:27:ILE:HD13	1.67	0.59
47:A:1220:C:H3'	47:A:1221:A:H8	1.66	0.59
60:N:81:GLU:HG3	79:g:156:VAL:HG12	1.83	0.59
68:V:68:LYS:O	77:e:44:ARG:NH1	2.34	0.59
1:1:896:G:H1'	1:1:1585:A:N6	2.17	0.59
11:p:42:GLN:OE1	11:p:45:ARG:NH2	2.33	0.59
20:y:123:THR:OG1	20:y:125:ASP:OD1	2.20	0.59
29:AA:103:GLU:HB2	29:AA:106:GLN:HB2	1.84	0.59
1:1:1199:A:H2'	1:1:1200:A:C8	2.36	0.59
12:q:110:ASP:HB3	12:q:128:ILE:HD12	1.84	0.59
26:7:60:LYS:HA	26:7:63:ILE:HD12	1.84	0.59
47:A:352:C:H5''	56:J:16:ALA:HB2	1.85	0.59
48:B:6:SER:O	48:B:191:ARG:NH1	2.36	0.59
1:1:1562:G:C2	1:1:1563:A:H1'	2.38	0.59
56:J:76:THR:HG21	56:J:104:ILE:HD12	1.85	0.59
1:1:1268:C:H3'	1:1:1269:A:H4'	1.84	0.59
1:1:2384:C:H2'	1:1:2385:C:C6	2.38	0.59
14:s:32:ARG:NH1	14:s:120:ILE:O	2.36	0.59
15:t:158:LEU:HB3	30:AB:98:ALA:HB1	1.85	0.59
50:D:36:LEU:HD21	50:D:51:ILE:HD12	1.83	0.59
1:1:2873:G:O2'	1:1:2996:A:N1	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3357:U:H5'	19:x:56:ARG:HH22	1.66	0.59
47:A:12:U:H2'	47:A:13:C:C6	2.37	0.59
47:A:1160:U:H2'	47:A:1161:G:H8	1.68	0.59
68:V:18:ILE:HD11	68:V:93:GLN:HB3	1.84	0.59
1:1:3287:A:H2'	1:1:3288:A:C8	2.37	0.59
47:A:1523:G:H5''	73:a:34:ASP:HA	1.85	0.59
47:A:1578:C:H2'	47:A:1579:A:C8	2.38	0.59
65:S:25:THR:HG23	65:S:27:ASP:H	1.67	0.59
80:h:96:GLU:HG2	80:h:97:THR:HG23	1.84	0.59
35:AG:16:TYR:OH	35:AG:89:LEU:O	2.17	0.59
47:A:4:C:H5	47:A:20:G:H1	1.50	0.59
47:A:815:U:HO2'	47:A:816:U:H6	1.51	0.59
47:A:1131:G:H2'	47:A:1132:A:C8	2.38	0.59
48:B:35:PRO:O	48:B:52:LYS:NZ	2.32	0.59
71:Y:69:ARG:HG3	71:Y:117:ILE:HG12	1.85	0.59
1:1:1043:A:N3	1:1:2605:U:O2'	2.34	0.58
1:1:1895:G:O2'	1:1:2312:U:O4	2.21	0.58
24:5:34:VAL:HG13	24:5:56:ILE:HG22	1.84	0.58
1:1:730:A:H4'	1:1:730:A:OP1	2.03	0.58
28:9:116:LYS:NZ	28:9:127:GLU:OE1	2.34	0.58
1:1:1795:A:H2'	1:1:1796:A:C8	2.37	0.58
5:j:80:GLU:HG3	45:AQ:66:GLY:HA2	1.86	0.58
55:I:5:ILE:HG21	55:I:10:PRO:HB3	1.84	0.58
58:L:16:PHE:O	58:L:17:GLN:HG3	2.03	0.58
66:T:69:ILE:HG22	66:T:73:MET:HE2	1.85	0.58
27:8:103:TYR:O	27:8:138:ARG:NH2	2.37	0.58
47:A:1452:G:O2'	47:A:1589:C:OP1	2.22	0.58
52:F:126:VAL:HG13	52:F:139:VAL:HG13	1.86	0.58
71:Y:107:PHE:HE1	71:Y:123:LYS:HB3	1.68	0.58
80:h:90:LEU:HD11	80:h:125:SER:HB3	1.85	0.58
1:1:2932:C:H2'	1:1:2933:G:H8	1.68	0.58
47:A:446:C:OP2	52:F:49:ARG:NH1	2.25	0.58
47:A:829:A:H2'	47:A:830:G:C8	2.39	0.58
1:1:1611:U:H2'	1:1:1612:U:C6	2.39	0.58
1:1:2669:A:H2'	1:1:2670:G:C8	2.39	0.58
19:x:32:THR:HG21	19:x:87:SER:HB3	1.84	0.58
22:0:92:LYS:HE2	22:0:109:ASP:OD2	2.04	0.58
28:9:39:LEU:HD22	28:9:43:TYR:HE2	1.67	0.58
60:N:96:LEU:O	60:N:99:GLU:HG3	2.04	0.58
1:1:3245:A:HO2'	1:1:3246:C:H6	1.52	0.58
13:r:42:THR:O	13:r:139:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:z:134:HIS:CE1	21:z:136:ARG:HB3	2.39	0.58
25:6:23:MET:HE1	25:6:78:VAL:HG22	1.86	0.58
44:AP:24[B]:LYS:HE2	44:AP:75:VAL:HG12	1.85	0.58
47:A:138:C:OP2	54:H:187:LYS:NZ	2.27	0.58
65:S:96:THR:HG23	65:S:98:GLY:H	1.68	0.58
1:1:1228:C:H42	1:1:1253:C:H42	1.51	0.58
59:M:7:VAL:HG23	59:M:8:GLN:HG2	1.84	0.58
61:O:54:LEU:HB3	61:O:60:VAL:HB	1.85	0.58
71:Y:87:VAL:HG21	71:Y:93:LEU:HD13	1.85	0.58
39:AK:21:ARG:HD3	39:AK:44:MET:SD	2.44	0.58
48:B:30:GLN:NE2	48:B:151:SER:O	2.37	0.58
14:s:46:VAL:HG12	46:i:25:PRO:HG2	1.86	0.58
19:x:103:GLU:OE2	19:x:109:SER:OG	2.22	0.58
36:AH:54:ILE:HD11	36:AH:78:GLY:HA2	1.86	0.58
71:Y:107:PHE:CD2	71:Y:114:LYS:HB3	2.39	0.58
1:1:1275:C:H2'	1:1:1276:C:C6	2.39	0.57
1:1:2780:A:N6	1:1:2926:U:H5'	2.19	0.57
6:k:372:THR:HG22	6:k:374:ALA:H	1.69	0.57
47:A:815:U:O2'	47:A:816:U:O5'	2.22	0.57
47:A:1400:U:H5''	65:S:3:ARG:HE	1.69	0.57
47:A:1592:G:OP2	64:R:126:LYS:NZ	2.33	0.57
55:I:109:PRO:HG2	55:I:112:ARG:HD3	1.86	0.57
1:1:1400:G:N2	1:1:1403:A:OP2	2.33	0.57
47:A:1431:G:HO2'	79:g:127:TYR:HH	1.47	0.57
47:A:1742:A:OP1	71:Y:63:GLN:HG2	2.04	0.57
65:S:99:GLN:N	65:S:99:GLN:OE1	2.36	0.57
1:1:443:G:C2	1:1:487:C:O2	2.57	0.57
1:1:1218:G:N2	1:1:1281:G:O2'	2.37	0.57
47:A:652:C:H5''	47:A:653:G:C8	2.38	0.57
78:f:43:ARG:HD3	78:f:56:MET:HE1	1.84	0.57
1:1:795:G:O2'	15:t:18:TRP:NE1	2.30	0.57
30:AB:36:GLY:HA3	30:AB:40:HIS:CE1	2.38	0.57
47:A:1776:G:OP2	62:P:127:ARG:NH2	2.33	0.57
65:S:89:SER:C	65:S:91:LEU:H	2.11	0.57
1:1:25:A:H2'	1:1:26:C:H6	1.70	0.57
1:1:3064:C:O2'	25:6:12:ARG:NH2	2.37	0.57
46:i:129:LEU:HD21	51:E:129:GLY:HA3	1.86	0.57
47:A:2:A:OP1	50:D:171:LYS:NZ	2.33	0.57
52:F:19:MET:HE2	52:F:108:LYS:HG2	1.87	0.57
1:1:443:G:N1	1:1:487:C:N3	2.51	0.57
3:4:52:A:OP1	41:AM:21[B]:ARG:NH1	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:103:G:OP2	3:4:105:A:O2'	2.21	0.57
47:A:811:U:O2	47:A:831:G:O6	2.23	0.57
58:L:88:PRO:O	58:L:89:LEU:HD22	2.03	0.57
63:Q:94:VAL:HG21	63:Q:116:LEU:HD11	1.85	0.57
40:AL:44:LYS:HB3	40:AL:51:GLN:HE21	1.68	0.57
68:V:21:ILE:HD13	68:V:99:VAL:HG21	1.86	0.57
1:1:619:A:H2'	1:1:620:A:C8	2.39	0.57
21:z:176:ARG:NH2	47:A:838:G:OP2	2.38	0.57
48:B:197:VAL:HG13	48:B:201:LEU:HD23	1.87	0.57
52:F:139:VAL:HG23	52:F:150:PRO:HG3	1.87	0.57
1:1:158:A:H2'	1:1:159:A:C8	2.40	0.57
1:1:444:U:H3	1:1:485:A:H61	1.53	0.57
1:1:1022:A:H8	1:1:1022:A:OP2	1.88	0.57
6:k:58:ARG:HD2	6:k:354:VAL:HG13	1.85	0.57
47:A:457:G:OP1	72:Z:109:LYS:NZ	2.27	0.57
47:A:1600:U:OP1	53:G:169:ASN:HB2	2.04	0.57
80:h:202:SER:HA	80:h:242:PHE:HD2	1.69	0.57
1:1:782:A:H4'	1:1:783:G:H5'	1.86	0.57
1:1:2740:U:H2'	1:1:2741:A:H8	1.69	0.57
3:4:8:C:H2'	3:4:9:A:C8	2.40	0.57
22:0:8:GLN:HG3	22:0:26:ARG:HD2	1.86	0.57
47:A:829:A:H2'	47:A:830:G:H8	1.70	0.57
1:1:1152:C:OP2	10:o:92:LYS:NZ	2.38	0.56
1:1:1662:G:H2'	1:1:1663:A:C8	2.39	0.56
28:9:51:ARG:HG2	28:9:52:GLN:H	1.69	0.56
47:A:518:A:H2'	47:A:519:A:C8	2.39	0.56
1:1:428:U:H2'	1:1:429:U:C6	2.40	0.56
1:1:1021:A:N6	63:Q:74:ALA:HA	2.20	0.56
1:1:1260:G:H8	1:1:1260:G:O5'	1.87	0.56
1:1:1635:C:OP2	36:AH:74:ARG:NH1	2.38	0.56
63:Q:81:ARG:NH2	63:Q:117:GLY:O	2.38	0.56
1:1:248:U:H2'	1:1:249:G:H4'	1.87	0.56
1:1:365:A:OP1	7:l:85:ARG:NH1	2.38	0.56
1:1:2603:U:OP2	23:2:4:SER:OG	2.22	0.56
1:1:2655:U:H2'	1:1:2656:C:C6	2.39	0.56
3:4:141:C:O3'	17:v:62:TYR:OH	2.22	0.56
21:z:160:GLU:OE1	21:z:163:ARG:NH1	2.38	0.56
26:7:37:ALA:O	26:7:41:GLN:HG2	2.05	0.56
47:A:1463:G:H2'	47:A:1464:G:C8	2.38	0.56
47:A:1479:A:H4'	47:A:1480:G:O5'	2.05	0.56
51:E:48:GLU:HG2	51:E:88:TYR:HE2	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2090:U:H4'	1:1:2091:A:O5'	2.04	0.56
46:i:135:GLU:OE1	51:E:95:ARG:NH2	2.38	0.56
47:A:728:U:OP1	55:I:104:LYS:N	2.38	0.56
47:A:821:U:H2'	47:A:822:G:C8	2.41	0.56
47:A:924:A:H2'	47:A:925:A:C8	2.40	0.56
58:L:17:GLN:N	58:L:88:PRO:HB3	2.21	0.56
1:1:2385:C:H2'	1:1:2386:U:H6	1.71	0.56
8:m:60:ILE:HB	8:m:80:ALA:HB2	1.87	0.56
25:6:13:MET:HE1	25:6:54:ALA:HB3	1.88	0.56
73:a:42:LEU:HD21	73:a:47:TYR:HD1	1.71	0.56
1:1:72:A:N7	15:t:66:ASN:HB3	2.21	0.56
1:1:1662:G:H2'	1:1:1663:A:H8	1.71	0.56
1:1:2634:G:H2'	1:1:2635:A:C8	2.40	0.56
52:F:253:ARG:HD2	52:F:257:ARG:HH21	1.71	0.56
9:n:39:LEU:HD13	9:n:83:VAL:HG11	1.87	0.56
20:y:67:ILE:HG12	20:y:81:ILE:HG21	1.87	0.56
47:A:1214:G:O2'	47:A:1240:G:N2	2.31	0.56
1:1:1242:G:O4'	1:1:1260:G:OP2	2.24	0.56
1:1:1970:A:H2'	1:1:1971:C:H6	1.70	0.56
6:k:211:GLN:NE2	6:k:283:TYR:O	2.38	0.56
17:v:96:LYS:NZ	17:v:104:GLU:OE2	2.37	0.56
21:z:98:ARG:HD2	21:z:133:LYS:O	2.05	0.56
47:A:1145:A:H2'	47:A:1146:C:C6	2.41	0.56
47:A:1665:C:OP1	56:J:59:ARG:NH2	2.38	0.56
80:h:20:VAL:HG11	80:h:307:ILE:HG12	1.87	0.56
1:1:164:U:H2'	1:1:165:C:H6	1.71	0.56
1:1:2210:A:H2'	1:1:2211:A:C8	2.41	0.56
1:1:2335:A:H2'	1:1:2336:A:C8	2.40	0.56
15:t:57:VAL:HG22	15:t:69:VAL:HG22	1.88	0.56
47:A:1245:U:H2'	47:A:1246:G:C8	2.40	0.56
1:1:2941:A:N7	5:j:215:ASN:ND2	2.54	0.56
47:A:940:A:H4'	47:A:1058:G:O2'	2.05	0.56
47:A:1174:A:N3	47:A:1179:A:O2'	2.30	0.56
68:V:26:THR:HG22	68:V:87:LYS:HG3	1.87	0.56
80:h:132:VAL:HB	80:h:145:LEU:HB2	1.87	0.56
1:1:1018:U:O5'	1:1:1018:U:H6	1.89	0.55
1:1:1556:G:N7	27:8:36:LYS:HE2	2.21	0.55
1:1:3040:U:OP2	21:z:62:ARG:NH2	2.40	0.55
43:AO:11:ARG:NH2	47:A:1762:U:OP1	2.37	0.55
47:A:824:U:H5''	47:A:824:U:O2	2.06	0.55
47:A:1214:G:N2	47:A:1240:G:O2'	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:Z:87:PRO:HD2	72:Z:90:ARG:HD2	1.88	0.55
79:g:124:LYS:NZ	79:g:125:LYS:O	2.39	0.55
79:g:172:ILE:HG12	79:g:185:LYS:HD3	1.87	0.55
80:h:76:ALA:HB3	80:h:120:LEU:HD11	1.86	0.55
80:h:126:ALA:HB1	80:h:152:VAL:HG23	1.88	0.55
20:y:89:ASP:OD1	20:y:113[B]:ARG:NH1	2.39	0.55
47:A:78:A:H8	54:H:154:ARG:HG3	1.71	0.55
47:A:336:C:H5''	56:J:10:LYS:HD2	1.87	0.55
47:A:1399:U:OP2	65:S:3:ARG:NH2	2.39	0.55
68:V:57:MET:HB2	68:V:87:LYS:HB3	1.87	0.55
1:1:976:A:H2'	1:1:977:U:H5'	1.88	0.55
1:1:3064:C:O2'	1:1:3066:A:OP2	2.22	0.55
11:p:163:LEU:HA	17:v:7:LEU:HD21	1.88	0.55
47:A:826:U:H3'	47:A:826:U:C6	2.41	0.55
53:G:26:ALA:HB2	64:R:25:LYS:HB3	1.88	0.55
1:1:40:G:N7	81:1:3401:SPD:N10	2.54	0.55
1:1:1021:A:OP1	1:1:1021:A:H3'	2.06	0.55
8:m:123:GLU:OE2	8:m:248:ARG:NH1	2.40	0.55
47:A:847:A:O2'	47:A:948:A:N1	2.36	0.55
47:A:1413:A:O2'	47:A:1414:G:OP1	2.25	0.55
71:Y:70:LYS:HB3	71:Y:93:LEU:HD22	1.88	0.55
1:1:1782:G:H2'	1:1:1783:A:C8	2.41	0.55
1:1:1965:U:H2'	1:1:1966:G:C4	2.41	0.55
47:A:309:U:OP2	71:Y:20:ARG:HD3	2.06	0.55
1:1:654:A:H2'	1:1:655:A:H8	1.72	0.55
1:1:1228:C:H41	1:1:1257:G:H22	1.55	0.55
1:1:1493:C:H2'	1:1:1494:A:C8	2.41	0.55
12:q:84:LYS:HD3	12:q:190:GLU:HG3	1.88	0.55
47:A:1460:G:H2'	47:A:1461:A:C8	2.41	0.55
65:S:77:GLU:O	65:S:80:ARG:NH1	2.40	0.55
76:d:63:ALA:O	76:d:64:ARG:NE	2.36	0.55
1:1:269:G:H5''	17:v:14:LYS:HE2	1.89	0.55
1:1:1937:C:O2'	1:1:3309:A:N6	2.40	0.55
1:1:2196:G:OP1	38:AJ:67:ARG:NH2	2.40	0.55
18:w:125:LEU:HD13	22:0:168:PRO:HG3	1.88	0.55
22:0:96:ASP:OD1	22:0:97:VAL:N	2.33	0.55
47:A:1276:G:H22	47:A:1309:G:H22	1.53	0.55
49:C:31:ASP:OD1	49:C:45:LYS:NZ	2.39	0.55
54:H:163:THR:HA	54:H:168:THR:HG22	1.87	0.55
73:a:60:VAL:HG23	73:a:101:TYR:HB2	1.89	0.55
1:1:412:G:OP1	19:x:62:ARG:NH1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1177:U:O4	18:w:22:SER:OG	2.22	0.55
1:1:1559:C:O2'	1:1:1560:U:OP1	2.25	0.55
1:1:2138:G:H2'	1:1:2139:G:H8	1.72	0.55
8:m:178:ASN:HA	8:m:183:TRP:CD2	2.42	0.55
47:A:563:C:O2'	47:A:575:G:N2	2.39	0.55
47:A:965:G:H4'	47:A:1763:A:H4'	1.88	0.55
55:I:29:ASP:OD1	55:I:30:LEU:N	2.40	0.55
1:1:3192:A:O3'	16:u:126:LYS:NZ	2.40	0.55
24:5:19:VAL:O	24:5:21:ALA:N	2.38	0.55
47:A:330:U:P	56:J:56:ARG:HH22	2.30	0.55
47:A:1739:U:H2'	47:A:1740:A:H8	1.72	0.55
68:V:24:THR:HB	68:V:114:GLU:HG2	1.89	0.55
1:1:172:C:O2'	1:1:173:C:OP1	2.22	0.55
1:1:358:G:N2	1:1:361:A:OP2	2.39	0.55
1:1:729:C:H3'	1:1:730:A:H5''	1.89	0.55
1:1:3179:U:OP2	16:u:121:ARG:NH2	2.40	0.55
19:x:122:ALA:HB3	19:x:143:PRO:HB2	1.89	0.55
47:A:189:G:N7	56:J:143:ARG:NH2	2.45	0.55
49:C:24:PHE:HZ	62:P:34:ILE:HA	1.72	0.55
52:F:141:THR:OG1	52:F:143:ASP:OD1	2.24	0.55
1:1:712:G:HO2'	1:1:749:C:HO2'	1.51	0.54
47:A:165:U:H2'	47:A:166:A:H5''	1.89	0.54
47:A:469:A:H5''	57:K:10:LYS:HG3	1.89	0.54
47:A:869:A:OP1	49:C:136:ARG:NH2	2.40	0.54
47:A:903:U:H2'	47:A:904:A:C8	2.43	0.54
47:A:1637:U:H2'	47:A:1638:A:C8	2.42	0.54
1:1:3060:G:OP1	6:k:313:ARG:NH1	2.39	0.54
8:m:119:TYR:OH	8:m:139:PRO:O	2.16	0.54
32:AD:57:GLU:HB2	36:AH:94:LEU:HD11	1.88	0.54
47:A:110:U:OP1	47:A:738:A:O2'	2.23	0.54
1:1:1269:A:H3'	1:1:1270:A:C8	2.38	0.54
1:1:3014:U:OP2	1:1:3064:C:N4	2.40	0.54
47:A:52:U:H2'	47:A:53:G:C8	2.43	0.54
47:A:784:U:H2'	47:A:785:G:C8	2.42	0.54
1:1:2236:U:C2	1:1:2237:A:C8	2.95	0.54
1:1:2808:OMC:H5	1:1:2824:C:N4	2.00	0.54
50:D:111:LYS:HG2	50:D:122:ALA:HB3	1.90	0.54
53:G:91:GLU:HA	53:G:94:THR:HG22	1.89	0.54
58:L:26:ASP:O	58:L:39:ASN:ND2	2.40	0.54
60:N:29:LYS:HE2	60:N:100:TRP:CD2	2.43	0.54
67:U:57:ARG:NH2	67:U:101:ASN:OD1	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:d:25:VAL:HG11	76:d:66:LEU:HD22	1.89	0.54
24:5:86:TYR:O	24:5:90:ASN:ND2	2.40	0.54
78:f:55:LYS:HB2	78:f:58:PRO:HG3	1.88	0.54
1:1:1218:G:HO2'	1:1:1219:A:P	2.30	0.54
1:1:2244:U:H2'	1:1:2245:C:H6	1.72	0.54
1:1:3147:G:OP1	18:w:6:LYS:NZ	2.35	0.54
16:u:25:GLU:OE2	16:u:44:LYS:HB2	2.07	0.54
47:A:778:U:O2'	47:A:779:U:O2	2.21	0.54
47:A:1399:U:O2'	47:A:1400:U:OP1	2.25	0.54
1:1:2138:G:H2'	1:1:2139:G:C8	2.43	0.54
6:k:284:ARG:HH11	6:k:356:LEU:HD12	1.72	0.54
47:A:827:C:O2	47:A:827:C:H2'	2.08	0.54
79:g:144:VAL:HA	79:g:147:TYR:CD2	2.43	0.54
1:1:1199:A:H2'	1:1:1200:A:H8	1.73	0.54
1:1:1436:G:OP1	7:l:84:HIS:NE2	2.27	0.54
1:1:2260:U:OP1	1:1:2945:G:O2'	2.25	0.54
17:v:177:GLY:O	17:v:184:LYS:NZ	2.41	0.54
45:AQ:28:LYS:O	45:AQ:32:GLN:HG3	2.08	0.54
47:A:144:U:H5	47:A:166:A:N7	2.05	0.54
47:A:1648:U:H2'	47:A:1649:G:H8	1.72	0.54
52:F:100:ARG:NH1	52:F:118:GLU:OE2	2.41	0.54
1:1:638:U:OP1	30:AB:21:ARG:NH1	2.37	0.54
1:1:1042:A:H2'	1:1:1045:C:C5	2.43	0.54
1:1:1080:A:H2'	1:1:1081:A:C8	2.43	0.54
1:1:2183:U:O2'	1:1:2184:G:OP1	2.26	0.54
1:1:3207:G:OP1	18:w:160:LYS:NZ	2.41	0.54
3:4:155:G:H5'	11:p:186:ARG:HD2	1.90	0.54
9:n:146:LEU:O	9:n:150:LYS:HG2	2.08	0.54
47:A:446:C:OP1	52:F:29:PRO:HD3	2.08	0.54
58:L:52:LYS:HG3	58:L:54:TYR:CD2	2.43	0.54
1:1:541:U:N3	1:1:543:C:O2'	2.41	0.54
9:n:39:LEU:HB3	9:n:83:VAL:HG13	1.89	0.54
66:T:63:GLN:O	66:T:67:GLU:HG3	2.08	0.54
1:1:843:A:H2'	1:1:844:A:C8	2.43	0.53
1:1:2054:C:H2'	1:1:2055:G:C8	2.43	0.53
1:1:2933:G:H2'	1:1:2934:U:C6	2.43	0.53
2:3:19:C:H2'	2:3:20:A:C8	2.43	0.53
47:A:815:U:O2'	47:A:816:U:H6	1.91	0.53
47:A:1168:A:N3	47:A:1195:C:O2'	2.37	0.53
55:I:135:ARG:HB3	70:X:51:GLU:OE2	2.08	0.53
80:h:155:VAL:O	80:h:156:ARG:NH1	2.35	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:826:U:C6	47:A:826:U:C3'	2.91	0.53
47:A:1659:G:H2'	47:A:1660:G:C8	2.43	0.53
80:h:261:LYS:HZ2	80:h:268:LEU:HD13	1.73	0.53
1:1:1110:U:OP1	30:AB:23:GLY:N	2.34	0.53
1:1:1115:C:H2'	1:1:1116:A:H8	1.73	0.53
8:m:94:ASN:HB2	8:m:97:ALA:H	1.73	0.53
20:y:76:ALA:HA	20:y:79:LYS:HG3	1.91	0.53
34:AF:22:HIS:CE1	34:AF:25:ARG:HE	2.26	0.53
47:A:1218:G:H1	47:A:1237:C:H5	1.56	0.53
47:A:1670:U:O2'	47:A:1671:G:O5'	2.27	0.53
71:Y:70:LYS:O	71:Y:87:VAL:HG22	1.97	0.53
1:1:772:U:H5	1:1:2691:U:O2	1.92	0.53
1:1:1106:U:H2'	1:1:1107:U:C6	2.44	0.53
1:1:2634:G:H2'	1:1:2635:A:H8	1.73	0.53
6:k:217:VAL:HG11	6:k:328:ILE:HB	1.91	0.53
46:i:101:LYS:NZ	47:A:579:U:OP1	2.39	0.53
47:A:15:U:H2'	47:A:16:G:O4'	2.09	0.53
47:A:1187:A:H1'	47:A:1192:C:N4	2.24	0.53
70:X:28:ARG:HD3	70:X:60:LYS:HE2	1.89	0.53
1:1:93:G:H2'	1:1:94:A:C8	2.43	0.53
1:1:429:U:H2'	1:1:430:G:H8	1.72	0.53
1:1:1530:A:H2'	1:1:1531:A:C8	2.42	0.53
24:5:19:VAL:HG12	24:5:108:LEU:HG	1.91	0.53
47:A:1584:A:C8	77:e:14:PHE:HD1	2.26	0.53
47:A:1602:C:P	53:G:81:ARG:HE	2.32	0.53
49:C:56:ASN:OD1	49:C:57:ALA:N	2.41	0.53
65:S:24:LEU:HD23	65:S:34:LEU:HD23	1.91	0.53
68:V:32:GLN:N	68:V:32:GLN:OE1	2.42	0.53
1:1:173:C:H2'	1:1:174:C:C6	2.44	0.53
1:1:429:U:H5''	35:AG:87:LYS:HE3	1.90	0.53
1:1:1655:U:H2'	1:1:1656:C:C6	2.43	0.53
1:1:2084:A:H2'	1:1:2085:A:C8	2.44	0.53
18:w:76:ALA:HB3	18:w:79:ARG:HG2	1.91	0.53
22:0:171:PHE:O	22:0:172:TYR:HB2	2.08	0.53
47:A:1140:G:H2'	47:A:1141:C:C6	2.44	0.53
47:A:1145:A:H2'	47:A:1146:C:H6	1.73	0.53
47:A:1396:A:O2'	47:A:1397:A:OP1	2.25	0.53
1:1:62:A:N3	1:1:77:U:O2'	2.37	0.53
1:1:2233:A:N1	47:A:1631:C:O2'	2.39	0.53
1:1:3093:U:H1'	1:1:3094:A:H5''	1.90	0.53
47:A:676:G:N3	47:A:677:G:N2	2.55	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1573:A:H2'	47:A:1574:A:O4'	2.09	0.53
55:I:85:HIS:CD2	55:I:161:LYS:HG2	2.42	0.53
58:L:73:VAL:HG21	58:L:91:ARG:HH12	1.72	0.53
1:1:3039:C:H3'	21:z:62:ARG:NH2	2.24	0.53
1:1:3319:U:O2'	56:J:77:ARG:NH1	2.41	0.53
16:u:57:LEU:HG	22:0:172:TYR:OH	2.08	0.53
47:A:1398:G:H4'	47:A:1399:U:O5'	2.09	0.53
80:h:123:ILE:O	80:h:135:TRP:N	2.39	0.53
1:1:527:G:H2'	1:1:528:A:C8	2.44	0.53
2:3:19:C:H2'	2:3:20:A:H8	1.73	0.53
9:n:170:ARG:HB3	9:n:172:HIS:CE1	2.44	0.53
47:A:217:A:H5''	47:A:217:A:C8	2.41	0.53
47:A:413:C:O2'	47:A:416:G:O6	2.26	0.53
47:A:786:G:H21	70:X:107:SER:HB3	1.74	0.53
47:A:1205:C:H2'	47:A:1206:A:C8	2.44	0.53
47:A:1302:C:O2'	47:A:1386:A:N3	2.35	0.53
47:A:1543:A:OP1	63:Q:115:TYR:OH	2.19	0.53
71:Y:107:PHE:CE1	71:Y:123:LYS:HB3	2.43	0.53
1:1:437:G:O2'	1:1:438:A:OP1	2.25	0.53
1:1:486:C:H2'	1:1:487:C:C6	2.43	0.53
15:t:122:LYS:HB3	37:AI:119:LYS:H	1.72	0.53
47:A:63:G:O2'	47:A:168:U:OP1	2.26	0.53
47:A:878:U:H5'	47:A:879:U:OP2	2.09	0.53
47:A:1468:C:H5''	47:A:1508:G:H22	1.74	0.53
80:h:214:ASP:N	80:h:214:ASP:OD1	2.42	0.53
1:1:1787:U:H2'	1:1:1788:C:C6	2.44	0.52
1:1:1911:A:H2'	1:1:1912:U:C6	2.45	0.52
7:l:36:VAL:HG21	7:l:245:LEU:HD21	1.91	0.52
47:A:1301:G:OP1	65:S:7:LYS:N	2.35	0.52
47:A:1353:G:H5''	67:U:69:LYS:HE3	1.91	0.52
47:A:1458:C:OP1	53:G:102:ARG:NH2	2.42	0.52
80:h:240:LEU:HD22	80:h:249:LEU:HD11	1.90	0.52
1:1:1241:A:N6	1:1:1268:C:O2'	2.40	0.52
1:1:2206:A:H2'	1:1:2207:A:C8	2.44	0.52
1:1:2492:U:H5'	11:p:69:ARG:HG3	1.91	0.52
1:1:2850:G:H5''	6:k:5:LYS:HE2	1.91	0.52
18:w:151:GLU:O	18:w:155:GLU:HG2	2.09	0.52
47:A:184:C:H2'	47:A:185:G:O4'	2.09	0.52
47:A:1487:C:OP1	67:U:122:ARG:NH2	2.36	0.52
48:B:56:LYS:NZ	69:W:70:ASN:OD1	2.38	0.52
58:L:15:LEU:O	58:L:19:GLY:HA2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:g:162:GLU:HA	79:g:173:PHE:HA	1.90	0.52
1:1:169:G:C6	1:1:249:G:H1'	2.44	0.52
1:1:2498:A:H2'	1:1:2499:U:C6	2.44	0.52
9:n:39:LEU:HD11	9:n:53:TYR:HB2	1.91	0.52
47:A:511:U:O4	57:K:171:ARG:NH2	2.43	0.52
47:A:1566:U:H2'	47:A:1567:C:C6	2.43	0.52
47:A:1602:C:N4	53:G:80:LYS:O	2.42	0.52
55:I:155:SER:HB2	55:I:181:ILE:HD13	1.91	0.52
63:Q:81:ARG:NH1	63:Q:98:ASN:HA	2.24	0.52
1:1:357:A:O4'	7:l:82:GLY:HA3	2.10	0.52
1:1:716:G:O2'	1:1:717:A:OP1	2.25	0.52
1:1:2184:G:H1'	1:1:2186:A:N6	2.24	0.52
1:1:2184:G:O2'	1:1:2187:U:O4	2.22	0.52
7:l:140:GLY:O	7:l:142:ARG:NH1	2.42	0.52
20:y:89:ASP:OD1	20:y:113[A]:ARG:NH1	2.42	0.52
46:i:136:ASN:OD1	46:i:137:ASP:N	2.43	0.52
47:A:1241:A:H5'	47:A:1242:U:C5	2.44	0.52
47:A:1380:G:OP1	80:h:281:ALA:N	2.41	0.52
51:E:128:MET:HE1	51:E:134:GLY:HA2	1.91	0.52
52:F:123:LEU:HD23	52:F:159:THR:HG21	1.91	0.52
63:Q:16:SER:HA	63:Q:21:ASP:HA	1.90	0.52
68:V:26:THR:OG1	68:V:112:ASP:OD1	2.26	0.52
1:1:438:A:N1	1:1:489:G:O2'	2.30	0.52
1:1:2408:A:H2'	1:1:2409:C:C6	2.45	0.52
1:1:2734:A:H2'	1:1:2735:U:H6	1.74	0.52
6:k:74:GLU:OE1	6:k:325:LYS:HE3	2.09	0.52
11:p:98:TYR:OH	11:p:208:ASP:OD2	2.23	0.52
44:AP:8:ARG:HG2	44:AP:10:THR:HG23	1.90	0.52
47:A:1263:G:H1	47:A:1416:U:H5	1.57	0.52
47:A:1521:G:N7	73:a:77:ARG:NH2	2.50	0.52
47:A:1615:U:H2'	47:A:1616:G:C8	2.44	0.52
1:1:2385:C:H2'	1:1:2386:U:C6	2.45	0.52
1:1:3159:A:O2'	1:1:3160:C:OP1	2.25	0.52
1:1:3256:G:H2'	1:1:3257:A:C8	2.44	0.52
2:3:112:G:H2'	2:3:113:C:C6	2.45	0.52
8:m:290:ILE:HG13	13:r:206:LEU:HD21	1.91	0.52
47:A:103:A:H4'	47:A:105:A:C8	2.45	0.52
47:A:151:G:H2'	47:A:152:G:C8	2.45	0.52
47:A:364:A:OP1	47:A:743:U:O2'	2.24	0.52
47:A:1715:U:H2'	47:A:1716:C:C6	2.45	0.52
1:1:158:A:H2'	1:1:159:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:10:4:A:H2'	4:10:5:G:C8	2.45	0.52
32:AD:11:ASN:O	32:AD:14:SER:OG	2.24	0.52
47:A:108:A:H2'	47:A:109:G:C8	2.44	0.52
54:H:57:ASP:HA	54:H:106:LEU:HA	1.90	0.52
60:N:104:CYS:HB2	60:N:115:VAL:HG13	1.92	0.52
1:1:1104:U:H2'	1:1:1105:U:C6	2.45	0.52
47:A:239:U:OP1	54:H:220:LYS:NZ	2.43	0.52
47:A:839:U:O4	47:A:840:A:N6	2.43	0.52
47:A:1181:A:OP2	47:A:1450:G:N2	2.37	0.52
47:A:1369:G:O2'	47:A:1370:A:H8	1.92	0.52
75:c:33:MET:HE1	75:c:73:LEU:HD21	1.90	0.52
1:1:1172:C:H4'	18:w:90:PRO:HD3	1.92	0.52
1:1:1810:A:H4'	1:1:1811:U:O4'	2.10	0.52
21:z:134:HIS:HE1	21:z:136:ARG:NE	2.07	0.52
47:A:216:A:N3	47:A:216:A:C2'	2.73	0.52
47:A:458:A:O2'	52:F:27:TYR:OH	2.21	0.52
47:A:770:C:OP1	47:A:770:C:H6	1.92	0.52
47:A:784:U:H2'	47:A:785:G:H8	1.74	0.52
47:A:1393:U:H2'	47:A:1394:G:C8	2.45	0.52
63:Q:81:ARG:HB2	63:Q:117:GLY:HA3	1.91	0.52
1:1:480:G:H2'	1:1:480:G:N3	2.25	0.52
1:1:1451:U:H1'	33:AE:25:LYS:HE3	1.91	0.52
1:1:1617:A:H2'	1:1:1618:U:H6	1.74	0.52
7:l:3:SER:OG	7:l:4:ARG:N	2.35	0.52
14:s:82:ARG:HA	14:s:85:LYS:HE2	1.91	0.52
56:J:57:ALA:HB2	56:J:183:GLY:HA2	1.92	0.52
60:N:67:THR:O	60:N:68:GLU:HG3	2.10	0.52
71:Y:89:ASN:HB3	71:Y:136:TRP:CE2	2.45	0.52
76:d:32:PHE:HZ	76:d:59:SER:HG	1.56	0.52
1:1:385:A:H2'	1:1:386:A:C8	2.45	0.51
1:1:623:A:H2'	1:1:624:U:C6	2.44	0.51
1:1:833:A:OP2	45:AQ:4:ARG:NH1	2.43	0.51
1:1:892:A:H5'	5:j:183:GLY:HA2	1.91	0.51
1:1:1225:G:H2'	1:1:1226:G:H8	1.74	0.51
3:4:156:U:H2'	3:4:157:U:C6	2.46	0.51
47:A:156:U:O2'	47:A:158:C:OP2	2.27	0.51
47:A:739:A:H5''	47:A:740:A:C5'	2.40	0.51
47:A:1160:U:H2'	47:A:1161:G:C8	2.45	0.51
47:A:1575:G:O6	47:A:1595:U:O4	2.28	0.51
48:B:63:ILE:HG12	69:W:36:ILE:HG12	1.92	0.51
51:E:171:ILE:HG12	51:E:188:LYS:HG3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:J:38:ILE:HG12	56:J:96:LEU:HD11	1.91	0.51
1:1:627:U:H2'	1:1:628:A:C8	2.44	0.51
8:m:41:LYS:HB2	23:2:68:THR:O	2.10	0.51
44:AP:15:LYS:HG2	44:AP:18:ARG:HH21	1.75	0.51
1:1:797:A:OP1	30:AB:27:LYS:HE3	2.10	0.51
1:1:1029:U:H2'	1:1:1030:U:C6	2.46	0.51
1:1:1258:G:H1'	1:1:1274:A:N6	2.26	0.51
1:1:2130:A:H2'	1:1:2131:U:C6	2.45	0.51
1:1:2345:A:H2'	1:1:2346:A:C8	2.45	0.51
37:AI:83:LYS:HG3	37:AI:83:LYS:O	2.10	0.51
47:A:1155:G:C2	47:A:1156:A:C8	2.98	0.51
1:1:58:G:H2'	3:4:33:A:O2'	2.10	0.51
1:1:453:U:H2'	1:1:454:G:H8	1.75	0.51
2:3:3:U:H2'	2:3:4:U:C6	2.45	0.51
10:o:10:LEU:HD12	10:o:13:LYS:HE3	1.92	0.51
24:5:92:ILE:HD12	24:5:96:ILE:HD13	1.92	0.51
47:A:736:G:H2'	47:A:737:A:H8	1.76	0.51
1:1:1747:G:H5'	40:AL:26:LYS:HE2	1.93	0.51
1:1:1827:U:O2'	3:4:114:G:OP1	2.17	0.51
14:s:109:HIS:CD2	14:s:114:ILE:HD11	2.35	0.51
50:D:133:PRO:HB2	50:D:217:TYR:HE2	1.75	0.51
56:J:113:TYR:OH	56:J:156:ALA:O	2.24	0.51
1:1:88:G:N7	20:y:171:LYS:NZ	2.59	0.51
1:1:164:U:H2'	1:1:165:C:C6	2.46	0.51
1:1:411:U:H2'	1:1:412:G:H8	1.75	0.51
1:1:671:U:H2'	1:1:672:G:C8	2.46	0.51
1:1:939:U:H3'	30:AB:13:GLY:HA2	1.92	0.51
1:1:1261:U:H2'	1:1:1262:G:C8	2.46	0.51
1:1:1631:G:N2	1:1:1634:A:OP2	2.39	0.51
1:1:2852:U:H1'	6:k:250:ALA:HB3	1.93	0.51
1:1:2974:C:O2'	6:k:180:GLU:OE2	2.22	0.51
44:AP:6:LYS:NZ	44:AP:93:LEU:O	2.43	0.51
47:A:1582:U:H5'	47:A:1583:C:OP2	2.10	0.51
73:a:78:VAL:HG12	73:a:81:ARG:NH2	2.25	0.51
1:1:2126:U:H2'	1:1:2127:A:C8	2.46	0.51
1:1:2322:U:H2'	1:1:2323:A:C8	2.45	0.51
3:4:94:C:OP1	39:AK:75:LYS:NZ	2.42	0.51
3:4:156:U:H2'	3:4:157:U:C5	2.46	0.51
17:v:46:ASP:OD2	17:v:50:ARG:NH2	2.42	0.51
17:v:159:ARG:HB2	17:v:164:LEU:HB2	1.92	0.51
37:AI:22:VAL:O	37:AI:26:GLN:HG3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:736:G:H2'	47:A:737:A:C8	2.46	0.51
53:G:32:ASP:OD1	53:G:33:VAL:N	2.43	0.51
71:Y:65:ASN:ND2	71:Y:116:ASP:OD2	2.26	0.51
80:h:5:GLU:OE1	80:h:246:ARG:NH2	2.40	0.51
1:1:1172:C:H2'	1:1:1173:G:N2	2.26	0.51
1:1:2790:U:H5''	31:AC:1:MET:HA	1.93	0.51
3:4:21:C:OP1	7:l:194:LYS:NZ	2.31	0.51
7:l:359:GLU:OE2	22:0:26:ARG:HD3	2.11	0.51
22:0:99:ARG:NH1	22:0:126:VAL:O	2.42	0.51
32:AD:45:ILE:HD12	32:AD:92:LEU:HD11	1.92	0.51
47:A:17:C:O2'	47:A:1122:A:N1	2.38	0.51
47:A:638:U:H2'	47:A:639:G:O4'	2.11	0.51
47:A:648:U:H2'	47:A:649:G:H8	1.74	0.51
47:A:1315:G:H21	65:S:8:THR:HG21	1.74	0.51
48:B:23:HIS:HA	48:B:48:ILE:HB	1.93	0.51
60:N:33:ARG:O	60:N:37:VAL:HG23	2.11	0.51
1:1:2603:U:OP1	1:1:2729:U:O2'	2.27	0.51
1:1:3277:U:H4'	6:k:25:GLN:OE1	2.11	0.51
45:AQ:84:ARG:O	45:AQ:88:GLU:HG2	2.10	0.51
47:A:685:C:O2'	47:A:686:G:OP1	2.28	0.51
1:1:2116:A:C4	39:AK:3:LYS:HB3	2.46	0.51
1:1:2557:G:C6	27:8:24:LEU:HD21	2.46	0.51
8:m:85:ARG:NH2	8:m:250:ASP:OD2	2.44	0.51
17:v:65:ARG:HG2	17:v:127:TYR:CD1	2.46	0.51
47:A:16:G:H2'	47:A:17:C:C6	2.46	0.51
49:C:180:THR:HG23	49:C:183:GLN:H	1.76	0.51
54:H:161:GLU:HA	54:H:170:THR:HA	1.91	0.51
60:N:132:GLU:OE2	60:N:136:LEU:HB2	2.11	0.51
1:1:941:C:H2'	1:1:942:U:C6	2.47	0.50
1:1:1951:U:H2'	1:1:1952:G:C8	2.46	0.50
1:1:2749:G:C2	30:AB:60:TYR:CE2	2.99	0.50
47:A:1548:U:H2'	47:A:1549:G:H8	1.76	0.50
48:B:200:ASP:OD2	65:S:89:SER:HA	2.11	0.50
50:D:96:VAL:HG22	50:D:110:ILE:HG12	1.93	0.50
55:I:81:PHE:HB3	55:I:84:ARG:HG3	1.92	0.50
1:1:422:A:C2	1:1:2341:A:H4'	2.46	0.50
1:1:1190:G:H2'	1:1:1191:A:C8	2.46	0.50
1:1:2244:U:H2'	1:1:2245:C:C6	2.46	0.50
1:1:2919:G:N3	6:k:250:ALA:HB1	2.27	0.50
3:4:52:A:OP1	41:AM:21[A]:ARG:NH1	2.44	0.50
47:A:302:U:H2'	47:A:303:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1211:A:O2'	47:A:1241:A:N1	2.39	0.50
47:A:1302:C:H2'	47:A:1303:G:O4'	2.10	0.50
50:D:165:ILE:HB	50:D:192:TYR:HB2	1.94	0.50
56:J:155:ALA:O	59:M:24:LYS:NZ	2.34	0.50
1:1:102:G:OP1	15:t:61:PRO:HD2	2.11	0.50
1:1:1060:A:H4'	1:1:1061:A:O5'	2.11	0.50
1:1:1576:A:H5''	1:1:1577:C:C5	2.46	0.50
1:1:2740:U:H2'	1:1:2741:A:C8	2.45	0.50
1:1:2919:G:C2	6:k:250:ALA:HB1	2.47	0.50
6:k:260:VAL:HG11	6:k:266:ARG:NH1	2.25	0.50
29:AA:101:LEU:O	29:AA:107:ARG:NH2	2.44	0.50
47:A:1198:G:H1	47:A:1436:U:H3	1.58	0.50
55:I:137:ARG:HG2	70:X:51:GLU:OE1	2.10	0.50
73:a:56:THR:HA	73:a:103:ARG:HH21	1.76	0.50
1:1:1762:G:O2'	1:1:1763:C:OP1	2.27	0.50
1:1:3136:C:H2'	1:1:3137:A:C8	2.47	0.50
25:6:15:LEU:HD13	25:6:51:ALA:HB3	1.94	0.50
47:A:1127:A:H5''	74:b:2:PRO:HB3	1.93	0.50
47:A:1635:A:H2'	47:A:1636:C:C6	2.46	0.50
48:B:92:HIS:ND1	48:B:202:TYR:OH	2.36	0.50
52:F:129:VAL:HG22	52:F:139:VAL:HG22	1.94	0.50
1:1:559:C:H2'	1:1:560:C:H6	1.76	0.50
1:1:730:A:H2'	1:1:731:U:H2'	1.94	0.50
1:1:1007:A:H2'	1:1:1008:A:C8	2.46	0.50
1:1:1115:C:H2'	1:1:1116:A:C8	2.47	0.50
1:1:1258:G:H1'	1:1:1274:A:H61	1.76	0.50
1:1:1452:A:N1	1:1:1472:G:O2'	2.43	0.50
1:1:2196:G:H2'	1:1:2197:A:H8	1.76	0.50
1:1:2196:G:H2'	1:1:2197:A:C8	2.46	0.50
1:1:2646:A:H5''	14:s:105:GLY:HA3	1.93	0.50
47:A:1149:G:H2'	47:A:1150:G:H8	1.77	0.50
47:A:1659:G:H2'	47:A:1660:G:H8	1.77	0.50
62:P:73:ALA:HB2	62:P:106:ARG:HB2	1.93	0.50
80:h:263:GLN:O	80:h:264:GLU:HG2	2.11	0.50
1:1:2404:U:H2'	1:1:2405:U:C6	2.47	0.50
1:1:2525:A:H2'	1:1:2526:C:O4'	2.12	0.50
14:s:20:ASN:HB3	14:s:126:ASP:HB3	1.94	0.50
47:A:152:G:OP1	54:H:2:LYS:HD2	2.11	0.50
47:A:822:G:O2'	47:A:823:G:N3	2.44	0.50
47:A:1367:U:O4	47:A:1368:A:N6	2.44	0.50
1:1:411:U:H2'	1:1:412:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:694:C:H2'	1:1:695:G:C8	2.47	0.50
1:1:989:G:N3	1:1:2609:A:H2'	2.27	0.50
1:1:1960:C:N4	1:1:1961:C:H41	2.10	0.50
1:1:3022:U:O2'	26:7:16:GLY:O	2.29	0.50
2:3:113:C:H2'	2:3:114:U:O4'	2.12	0.50
35:AG:68:TRP:O	35:AG:86[B]:LYS:HG2	2.12	0.50
47:A:10:G:O2'	50:D:82:GLN:OE1	2.28	0.50
47:A:644:U:H2'	47:A:645:G:H8	1.76	0.50
47:A:1551:U:H2'	47:A:1552:C:C6	2.46	0.50
76:d:35:ASP:O	76:d:37:SER:N	2.45	0.50
1:1:243:G:H2'	1:1:244:G:H8	1.76	0.50
1:1:2107:U:H2'	1:1:2108:G:C8	2.46	0.50
2:3:3:U:H2'	2:3:4:U:H6	1.77	0.50
9:n:20:THR:HG22	9:n:22:LYS:H	1.77	0.50
54:H:64:LYS:HB2	54:H:97:VAL:HG21	1.93	0.50
1:1:538:G:H1	1:1:547:U:H3	1.59	0.50
1:1:1021:A:N3	1:1:1021:A:C2'	2.73	0.50
1:1:2050:U:H2'	1:1:2051:G:C8	2.47	0.50
1:1:2079:C:HO2'	1:1:2080:U:H6	1.58	0.50
1:1:2155:G:OP2	5:j:128:ARG:NH1	2.38	0.50
1:1:3318:G:H5''	1:1:3319:U:H4'	1.92	0.50
9:n:50:ARG:O	9:n:71:ASN:ND2	2.40	0.50
19:x:47:TYR:CD1	19:x:56:ARG:HD2	2.47	0.50
44:AP:61:LYS:NZ	44:AP:63:LYS:O	2.45	0.50
47:A:29:U:H2'	47:A:30:G:H8	1.76	0.50
47:A:74:U:O2'	47:A:76:A:OP1	2.28	0.50
47:A:485:G:H1	47:A:499:U:H3	0.63	0.50
47:A:871:U:O2'	62:P:116:VAL:O	2.29	0.50
47:A:1072:A:H2'	47:A:1073:A:C8	2.47	0.50
47:A:1237:C:H5'	79:g:147:TYR:OH	2.12	0.50
47:A:1486:G:OP2	67:U:73:VAL:HG12	2.12	0.50
55:I:4:LYS:NZ	55:I:34:LEU:O	2.45	0.50
65:S:7:LYS:O	65:S:11:ARG:HG2	2.12	0.50
1:1:726:G:H5''	20:y:43:PRO:HB2	1.94	0.49
1:1:2587:G:H2'	1:1:2588:C:H6	1.77	0.49
1:1:2888:U:H5	1:1:2907:U:HO2'	1.58	0.49
3:4:9:A:H2'	3:4:10:A:C8	2.47	0.49
47:A:904:A:H2'	47:A:905:C:C6	2.47	0.49
47:A:1149:G:H2'	47:A:1150:G:C8	2.47	0.49
47:A:1265:C:H2'	47:A:1266:G:C8	2.45	0.49
47:A:1326:A:H1'	80:h:66:SER:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1431:G:O5'	79:g:131:LYS:NZ	2.43	0.49
1:1:581:A:H5''	35:AG:106:ASN:ND2	2.23	0.49
6:k:25:GLN:HE21	6:k:334:ARG:HD3	1.77	0.49
6:k:92:TYR:HB2	6:k:157:VAL:HB	1.94	0.49
19:x:47:TYR:HD1	19:x:56:ARG:HD2	1.78	0.49
46:i:65:LYS:HE2	63:Q:125:PRO:HB2	1.93	0.49
47:A:418:A:OP1	54:H:96:SER:OG	2.23	0.49
48:B:29:VAL:HG23	48:B:149:MET:HB3	1.93	0.49
57:K:31:ALA:HB2	57:K:42:ILE:HD11	1.93	0.49
1:1:600:U:C2	1:1:602:A:H1'	2.46	0.49
1:1:1030:U:H2'	1:1:1031:A:H8	1.78	0.49
1:1:3199:G:H1	1:1:3218:U:H3	1.60	0.49
5:j:79:ASN:ND2	5:j:165:VAL:HG12	2.27	0.49
39:AK:39:TYR:CD1	39:AK:40:PRO:HA	2.48	0.49
42:AN:23:CYS:HB2	42:AN:38:LYS:HD2	1.92	0.49
47:A:484:G:H2'	47:A:485:G:C8	2.48	0.49
51:E:196:ASN:O	51:E:201:ARG:NH1	2.45	0.49
62:P:76:ILE:HG21	62:P:97:LEU:HD13	1.94	0.49
1:1:117:U:O2	1:1:120:A:H5''	2.11	0.49
1:1:1239:G:H21	1:1:1240:A:H62	1.60	0.49
1:1:1936:G:N2	1:1:3327:A:H8	2.02	0.49
20:y:96:PHE:CD1	20:y:97:PRO:HD2	2.47	0.49
24:5:61:ASP:OD1	24:5:61:ASP:N	2.41	0.49
47:A:1453:C:O2'	67:U:88:PHE:O	2.26	0.49
47:A:1523:G:O2'	47:A:1524:C:OP1	2.25	0.49
48:B:200:ASP:HB2	65:S:85:VAL:HG23	1.94	0.49
49:C:59:ASP:OD1	49:C:60:GLY:N	2.45	0.49
58:L:55:VAL:HG12	58:L:68:LEU:HA	1.94	0.49
64:R:98:GLU:HG3	64:R:101:LYS:HE3	1.95	0.49
1:1:292:U:OP2	17:v:68:ARG:NH2	2.45	0.49
1:1:907:C:N4	5:j:3:ARG:HD3	2.28	0.49
1:1:3318:G:OP1	56:J:77:ARG:NH2	2.44	0.49
3:4:8:C:H2'	3:4:9:A:H8	1.77	0.49
8:m:55:PHE:H	8:m:151:GLN:HE22	1.59	0.49
20:y:125:ASP:OD1	20:y:126:GLN:N	2.45	0.49
47:A:283:G:H2'	47:A:284:C:C6	2.48	0.49
47:A:1341:U:H2'	47:A:1342:A:C8	2.48	0.49
59:M:66:ILE:HG13	59:M:140:LEU:HD21	1.94	0.49
66:T:4:VAL:HG22	73:a:82:GLN:OE1	2.12	0.49
1:1:407:A:C2	3:4:17:A:H1'	2.48	0.49
1:1:1108:A:P	15:t:5:LYS:HZ2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2084:A:H2'	1:1:2085:A:H8	1.78	0.49
1:1:2853:C:H2'	1:1:2854:U:C6	2.48	0.49
1:1:3153:A:H2'	1:1:3154:A:C8	2.48	0.49
15:t:62:THR:C	15:t:64:LYS:H	2.21	0.49
17:v:113:LEU:HB2	17:v:134:LEU:HD23	1.94	0.49
20:y:83:VAL:O	20:y:103:ALA:HA	2.12	0.49
47:A:721:C:O2'	47:A:722:A:H8	1.94	0.49
47:A:1335:U:H2'	47:A:1336:G:H8	1.74	0.49
52:F:103:TYR:CD1	52:F:189:LEU:HD21	2.47	0.49
58:L:89:LEU:HA	58:L:92:LEU:HD23	1.94	0.49
65:S:37:GLU:CD	80:h:151:TRP:HE1	2.20	0.49
79:g:163:CYS:HA	79:g:174:MET:HE2	1.94	0.49
1:1:1029:U:O2'	1:1:1030:U:OP1	2.27	0.49
1:1:1576:A:H5''	1:1:1577:C:H5	1.77	0.49
47:A:558:U:H2'	47:A:559:G:H8	1.77	0.49
47:A:769:U:O2'	47:A:770:C:OP2	2.27	0.49
47:A:1648:U:H2'	47:A:1649:G:C8	2.47	0.49
52:F:181:VAL:HG11	52:F:225:VAL:HG13	1.94	0.49
58:L:18:GLU:N	58:L:89:LEU:HD23	2.28	0.49
64:R:27:LEU:HD11	64:R:29:LYS:HE3	1.94	0.49
1:1:374:A:N3	1:1:376:G:H5''	2.28	0.49
1:1:972:U:H2'	1:1:973:C:O4'	2.12	0.49
1:1:1303:G:C4	18:w:61:LYS:HD3	2.48	0.49
1:1:2869:A:OP2	42:AN:48:LYS:NZ	2.44	0.49
47:A:677:G:H2'	47:A:678:A:C8	2.48	0.49
47:A:1298:A:N3	47:A:1300:U:H5'	2.27	0.49
47:A:1457:A:H5'	53:G:185:ARG:HG2	1.92	0.49
47:A:1520:C:OP2	73:a:77:ARG:NH1	2.41	0.49
64:R:28:ILE:HG22	64:R:35:ILE:HG21	1.94	0.49
1:1:716:G:H3'	1:1:717:A:H5''	1.95	0.49
1:1:907:C:H42	5:j:3:ARG:HD3	1.77	0.49
1:1:1006:G:OP1	13:r:39:LYS:NZ	2.33	0.49
1:1:2678:G:O2'	46:i:32:LYS:HG2	2.13	0.49
2:3:23:A:H2'	2:3:24:A:C8	2.47	0.49
39:AK:25:ARG:O	39:AK:25:ARG:HG2	2.13	0.49
47:A:932:U:H2'	47:A:933:A:C8	2.48	0.49
47:A:1029:U:H2'	47:A:1030:C:C6	2.47	0.49
47:A:1129:U:H2'	47:A:1130:U:C6	2.48	0.49
47:A:1669:U:HO2'	47:A:1670:U:H6	1.59	0.49
50:D:138:TYR:OH	50:D:144:GLY:O	2.30	0.49
60:N:60:CYS:HB2	60:N:122:VAL:HG22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:431:A:H2'	1:1:432:G:C8	2.47	0.49
1:1:1273:C:O2'	1:1:1274:A:H2'	2.12	0.49
1:1:2191:A:H2'	1:1:2192:A:H8	1.77	0.49
2:3:84:A:H2'	2:3:85:G:C8	2.47	0.49
6:k:35:ASP:OD2	6:k:191:LYS:NZ	2.28	0.49
12:q:12:ILE:HD11	12:q:53:ILE:HG13	1.94	0.49
12:q:109:GLN:HB3	12:q:127:LYS:HE2	1.93	0.49
47:A:1593:C:H2'	47:A:1594:G:C8	2.48	0.49
47:A:1647:A:H2'	47:A:1648:U:C6	2.48	0.49
47:A:1668:A:H2'	47:A:1669:U:H5'	1.94	0.49
47:A:1716:C:H2'	47:A:1717:A:O4'	2.12	0.49
51:E:21:GLU:OE2	51:E:77:ARG:NH2	2.40	0.49
51:E:214:ASP:CG	51:E:215:GLU:H	2.21	0.49
1:1:172:C:HO2'	1:1:173:C:P	2.34	0.48
1:1:541:U:O4	1:1:546:C:N4	2.46	0.48
1:1:1663:A:H2'	1:1:1664:G:H8	1.76	0.48
1:1:2810:A:H4'	13:r:74:LYS:HD3	1.95	0.48
5:j:112:ILE:HG13	45:AQ:79:VAL:HG22	1.95	0.48
6:k:62:ARG:HG2	6:k:65:SER:HB2	1.95	0.48
12:q:129:HIS:H	12:q:157:ASN:HD21	1.59	0.48
25:6:77:ILE:HD12	25:6:103:VAL:HG11	1.95	0.48
47:A:66:U:H5'	54:H:173:PRO:HA	1.95	0.48
47:A:415:A:H4'	47:A:416:G:O5'	2.13	0.48
55:I:30:LEU:HD12	55:I:30:LEU:O	2.12	0.48
1:1:46:C:OP2	1:1:47:A:O2'	2.26	0.48
1:1:417:A:H2'	1:1:418:A:C8	2.47	0.48
1:1:2339:A:H2'	1:1:2340:C:H6	1.78	0.48
1:1:2694:U:O2'	23:2:88:ARG:O	2.27	0.48
1:1:3294:U:H5''	6:k:308:MET:HE2	1.95	0.48
32:AD:18:LEU:HB3	32:AD:100:SER:HB2	1.96	0.48
47:A:391:C:H2'	47:A:392:C:C6	2.48	0.48
51:E:65:ARG:HD3	58:L:91:ARG:HE	1.77	0.48
60:N:55:ARG:NH1	60:N:81:GLU:OE1	2.46	0.48
1:1:1491:U:H5	1:1:1831:A:N1	2.10	0.48
1:1:1556:G:O2'	1:1:1557:U:H5'	2.14	0.48
1:1:3005:A:H2'	1:1:3006:C:H6	1.79	0.48
16:u:62:LEU:HD22	16:u:65:LEU:HB2	1.95	0.48
22:0:42:TRP:O	22:0:46:GLN:HG3	2.14	0.48
34:AF:67:LEU:HD23	34:AF:73:LYS:HG3	1.94	0.48
44:AP:25:VAL:HG22	44:AP:72:LEU:HD22	1.94	0.48
47:A:1226:G:H4'	63:Q:78:THR:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1478:A:O2'	47:A:1479:A:O4'	2.25	0.48
53:G:103:ASN:HA	53:G:106:LYS:HD2	1.94	0.48
63:Q:73:PRO:HD2	63:Q:93:VAL:HG23	1.94	0.48
1:1:662:U:H2'	1:1:663:A:H8	1.75	0.48
1:1:1239:G:N2	1:1:1240:A:H62	2.11	0.48
1:1:1396:U:H2'	1:1:1397:G:O4'	2.13	0.48
7:l:32:ARG:HG3	7:l:121:TYR:HE2	1.78	0.48
12:q:86:TYR:CE2	12:q:151:LEU:HB2	2.48	0.48
38:AJ:60:ILE:HG21	38:AJ:90:THR:HG22	1.94	0.48
50:D:135:ARG:HB3	50:D:216:THR:HB	1.94	0.48
52:F:194:VAL:HG11	52:F:232:ALA:HB2	1.96	0.48
80:h:92:LEU:HB2	80:h:104:PHE:HE1	1.77	0.48
1:1:92:C:OP2	1:1:2736:C:O2'	2.27	0.48
1:1:1576:A:C8	1:1:1576:A:C5'	2.97	0.48
1:1:2942:C:H4'	1:1:2943:A:C6	2.49	0.48
32:AD:43:LEU:HD23	32:AD:94:ILE:HD12	1.95	0.48
41:AM:23:LEU:HD12	41:AM:24:PRO:HD2	1.96	0.48
47:A:870:G:H2'	47:A:871:U:C6	2.49	0.48
47:A:876:A:H2'	47:A:877:G:H8	1.78	0.48
47:A:1064:U:H2'	47:A:1065:U:C6	2.49	0.48
47:A:1083:U:OP1	50:D:154:THR:OG1	2.23	0.48
47:A:1201:C:OP2	79:g:134:LYS:NZ	2.46	0.48
54:H:159:ARG:NH1	54:H:170:THR:OG1	2.45	0.48
58:L:73:VAL:HG21	58:L:91:ARG:NH1	2.28	0.48
60:N:95:LYS:HB2	60:N:117:GLY:HA3	1.95	0.48
1:1:396:A:O2'	1:1:399:A:OP1	2.26	0.48
1:1:788:G:H2'	1:1:789:C:C6	2.47	0.48
6:k:293:ASN:HB2	6:k:304:THR:HA	1.95	0.48
7:l:360:VAL:HG22	22:0:64:ILE:HG12	1.95	0.48
28:9:32:SER:HA	28:9:49:PRO:HA	1.95	0.48
28:9:51:ARG:HG2	28:9:52:GLN:N	2.29	0.48
47:A:1092:G:O2'	47:A:1093:G:H5'	2.13	0.48
47:A:1141:C:H2'	47:A:1142:A:C8	2.49	0.48
48:B:47:ILE:HD12	65:S:106:THR:HG22	1.96	0.48
51:E:74:ILE:HD12	51:E:87:ILE:HD11	1.96	0.48
66:T:134:ARG:HB2	66:T:136:GLN:NE2	2.25	0.48
73:a:65:LEU:O	73:a:69:LEU:HB2	2.14	0.48
1:1:157:G:H2'	1:1:158:A:H8	1.79	0.48
1:1:406:G:H1'	3:4:16:G:N2	2.29	0.48
1:1:583:A:H2'	1:1:584:C:C6	2.49	0.48
1:1:1493:C:H2'	1:1:1494:A:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3244:A:O2'	1:1:3245:A:H5'	2.14	0.48
3:4:37:A:H5''	3:4:39:G:O4'	2.12	0.48
5:j:129:THR:OG1	5:j:132:ASN:ND2	2.38	0.48
11:p:134:LYS:HD2	11:p:139:HIS:HE1	1.78	0.48
15:t:83:VAL:HG23	15:t:85:ILE:HG13	1.96	0.48
47:A:139:U:OP1	54:H:149:LYS:NZ	2.46	0.48
47:A:215:A:H62	47:A:830:G:H1'	1.79	0.48
47:A:598:U:OP2	71:Y:108:GLY:HA2	2.12	0.48
52:F:87:MET:HE1	52:F:237:VAL:HG21	1.95	0.48
1:1:156:A:N7	38:AJ:25:ILE:HG12	2.28	0.48
1:1:252:U:H5'	1:1:253:A:C8	2.49	0.48
1:1:990:G:N2	1:1:991:U:O4	2.39	0.48
1:1:1794:A:H2'	1:1:1795:A:C8	2.48	0.48
1:1:2391:A:H2'	1:1:2392:G:H8	1.79	0.48
12:q:34:LEU:HB3	12:q:78:LEU:HD22	1.96	0.48
18:w:122:PRO:HA	18:w:125:LEU:HD12	1.96	0.48
25:6:36:VAL:HG22	25:6:58:VAL:HG11	1.96	0.48
62:P:15:PHE:HB3	62:P:22:PHE:HB2	1.95	0.48
1:1:486:C:O5'	1:1:486:C:H6	1.95	0.48
1:1:848:U:C6	45:AQ:2:THR:HG22	2.49	0.48
1:1:951:U:H2'	1:1:952:U:C6	2.48	0.48
1:1:1069:U:H2'	1:1:1070:U:C6	2.49	0.48
1:1:3313:G:H1	1:1:3322:U:H3	1.62	0.48
3:4:75:G:OP2	28:9:74:TYR:OH	2.30	0.48
30:AB:112:VAL:HB	30:AB:130:VAL:HG12	1.96	0.48
47:A:261:C:O2'	47:A:262:G:H5'	2.13	0.48
47:A:932:U:H2'	47:A:933:A:H8	1.79	0.48
47:A:1610:C:H2'	47:A:1611:C:H6	1.79	0.48
80:h:67:HIS:CG	80:h:68:ILE:H	2.31	0.48
1:1:2583:U:H2'	1:1:2584:U:C6	2.49	0.48
1:1:3019:U:O2'	1:1:3020:A:H5'	2.13	0.48
24:5:15:PHE:HB2	24:5:66:VAL:HB	1.96	0.48
47:A:58:U:OP1	47:A:454:G:O2'	2.31	0.48
47:A:184:C:OP1	56:J:152:ARG:NH2	2.39	0.48
47:A:560:G:H2'	47:A:561:U:O2	2.14	0.48
47:A:881:U:O2	62:P:36:ARG:NH1	2.42	0.48
47:A:1216:U:OP1	79:g:136:LYS:NZ	2.39	0.48
55:I:44:GLU:OE2	55:I:52:LYS:HB3	2.13	0.48
60:N:59:LEU:HD13	60:N:133:ARG:NH1	2.29	0.48
62:P:98:ARG:HD2	74:b:49:ALA:HB2	1.95	0.48
1:1:290:G:H1'	17:v:93:LYS:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1208:A:O3'	22:0:92:LYS:NZ	2.47	0.47
1:1:2370:C:H1'	6:k:266:ARG:HH21	1.78	0.47
1:1:2557:G:H2'	1:1:2557:G:N3	2.29	0.47
33:AE:71:ARG:NH1	33:AE:103:LEU:HB3	2.29	0.47
47:A:17:C:H2'	47:A:18:C:C6	2.48	0.47
47:A:122:U:C2'	47:A:123:G:H5''	2.44	0.47
47:A:1219:A:O2'	79:g:182:TYR:OH	2.30	0.47
52:F:15:PRO:HG3	52:F:39:ARG:HD3	1.95	0.47
63:Q:41:VAL:HG13	63:Q:84:ILE:HD13	1.96	0.47
65:S:75:GLU:HA	65:S:78:ARG:HB3	1.95	0.47
80:h:19:TRP:HB2	80:h:38:ARG:HD2	1.96	0.47
1:1:907:C:OP1	5:j:14:SER:OG	2.30	0.47
1:1:1058:A:O2'	23:2:108:ARG:NH2	2.47	0.47
1:1:1363:G:OP1	34:AF:46:ARG:NH2	2.47	0.47
1:1:1754:G:H2'	1:1:1755:U:O4'	2.14	0.47
1:1:2145:A:H2'	1:1:2146:A:C8	2.49	0.47
1:1:2696:U:OP2	1:1:2698:C:N4	2.47	0.47
1:1:2790:U:H5'	1:1:2790:U:H6	1.79	0.47
1:1:2814:U:O2	1:1:2814:U:H2'	2.13	0.47
3:4:37:A:OP2	37:AI:86:ARG:HD2	2.13	0.47
11:p:160:PRO:HB2	11:p:162:GLU:OE1	2.15	0.47
12:q:80:THR:HA	12:q:83:THR:HG22	1.96	0.47
27:8:108:LEU:N	27:8:125:ARG:O	2.47	0.47
33:AE:45:THR:HG22	33:AE:47:ASP:N	2.27	0.47
37:AI:118:ILE:HG22	37:AI:119:LYS:N	2.29	0.47
47:A:873:U:H2'	47:A:874:U:C6	2.49	0.47
47:A:938:G:H2'	47:A:939:G:C8	2.49	0.47
47:A:1628:C:H2'	47:A:1629:G:C8	2.50	0.47
52:F:185:GLY:HA2	52:F:189:LEU:HD12	1.95	0.47
56:J:136:VAL:O	56:J:141:ARG:NH2	2.46	0.47
73:a:50:ILE:HG12	73:a:69:LEU:HD13	1.95	0.47
1:1:307:A:H2'	1:1:308:A:H8	1.77	0.47
1:1:1163:U:H2'	1:1:1164:U:O4'	2.14	0.47
1:1:1476:G:O2'	1:1:1867:U:O4	2.27	0.47
13:r:77:THR:HG22	13:r:82:ARG:HA	1.95	0.47
41:AM:49:LEU:HB3	41:AM:51:ILE:HG12	1.96	0.47
47:A:1099:G:O2'	47:A:1115:G:O6	2.29	0.47
67:U:135:ILE:O	67:U:139:THR:OG1	2.26	0.47
80:h:242:PHE:CE1	80:h:249:LEU:HD13	2.48	0.47
1:1:1011:C:H4'	1:1:1012:U:H6	1.80	0.47
1:1:1576:A:H3'	1:1:1577:C:H6	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2985:U:H2'	1:1:2986:U:C6	2.49	0.47
1:1:3261:A:H2'	1:1:3262:U:H6	1.78	0.47
14:s:47:GLN:OE1	14:s:64:LYS:HD3	2.13	0.47
21:z:134:HIS:CE1	21:z:136:ARG:HE	2.26	0.47
22:0:132:THR:O	22:0:141:LYS:NZ	2.46	0.47
47:A:137:A:O4'	47:A:139:U:H5'	2.14	0.47
47:A:217:A:N1	47:A:828:U:O2'	2.48	0.47
47:A:605:G:H5'	47:A:611:G:N2	2.29	0.47
47:A:810:U:H2'	47:A:811:U:O4'	2.14	0.47
47:A:1173:G:O2'	47:A:1416:U:OP1	2.32	0.47
47:A:1277:G:H21	48:B:111:ILE:HD11	1.80	0.47
48:B:57:ILE:HG23	48:B:177:LEU:HD23	1.96	0.47
58:L:77:ARG:HH22	58:L:86:ILE:N	2.11	0.47
1:1:1116:A:H2'	1:1:1117:U:H6	1.80	0.47
1:1:1870:A:OP2	21:z:21:LYS:NZ	2.42	0.47
15:t:138:PHE:HE1	37:AI:120:ALA:HB2	1.80	0.47
47:A:30:G:H2'	47:A:31:C:C6	2.49	0.47
47:A:457:G:P	72:Z:105:ARG:HH22	2.37	0.47
47:A:1551:U:H2'	47:A:1552:C:H6	1.78	0.47
1:1:496:A:H2'	1:1:497:U:C6	2.49	0.47
1:1:591:C:O2	10:o:24:ARG:NH1	2.47	0.47
1:1:1172:C:H2'	1:1:1173:G:H21	1.80	0.47
1:1:1571:G:H2'	1:1:1572:G:C8	2.50	0.47
1:1:1761:U:C5	21:z:43:LYS:HE3	2.49	0.47
1:1:3256:G:H2'	1:1:3257:A:H8	1.79	0.47
6:k:95:THR:OG1	6:k:98:GLY:O	2.32	0.47
9:n:6:PRO:HB3	34:AF:93:TYR:CE1	2.50	0.47
18:w:187:ALA:O	18:w:188:GLU:HG3	2.15	0.47
22:0:125:LYS:HG2	22:0:127:VAL:HG23	1.96	0.47
24:5:96:ILE:HG21	24:5:108:LEU:HD13	1.97	0.47
47:A:78:A:H2'	47:A:79:C:H6	1.78	0.47
47:A:116:U:H2'	47:A:117:U:C6	2.49	0.47
47:A:1276:G:N2	47:A:1309:G:H22	2.12	0.47
47:A:1757:U:H2'	47:A:1758:U:C6	2.49	0.47
63:Q:80:LEU:O	63:Q:80:LEU:HD12	2.14	0.47
67:U:65:ILE:HG12	67:U:71:VAL:CG2	2.44	0.47
79:g:148:TYR:HE1	79:g:158:ARG:HD3	1.80	0.47
1:1:62:A:H5''	17:v:174:ILE:HG21	1.96	0.47
1:1:246:U:H2'	1:1:247:C:C6	2.50	0.47
1:1:498:C:H2'	1:1:499:G:H8	1.80	0.47
1:1:830:U:H2'	1:1:831:G:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:983:U:H2'	1:1:984:U:C6	2.49	0.47
1:1:1045:C:H2'	1:1:1046:U:C6	2.50	0.47
1:1:1093:G:H4'	23:2:129:LYS:HG2	1.97	0.47
1:1:1113:G:OP1	31:AC:4:SER:HB2	2.14	0.47
1:1:1221:A:H2'	1:1:1222:G:C8	2.49	0.47
1:1:1286:A:H2'	1:1:1287:A:C8	2.49	0.47
1:1:1456:A:H2'	1:1:1457:A:C8	2.49	0.47
1:1:2381:G:O6	82:1:3403:ANM:H16	2.15	0.47
1:1:2669:A:H2'	1:1:2670:G:H8	1.80	0.47
1:1:2672:G:H5''	23:2:17:ARG:HG2	1.97	0.47
1:1:2683:C:O2'	1:1:2716:U:OP1	2.32	0.47
82:1:3403:ANM:C13	82:1:3403:ANM:N1	2.73	0.47
3:4:40:A:H2'	3:4:41:A:C8	2.50	0.47
9:n:59:ASP:HB2	9:n:102:VAL:HG22	1.97	0.47
13:r:38:ARG:NH1	13:r:45:GLU:OE1	2.45	0.47
24:5:19:VAL:C	24:5:21:ALA:H	2.23	0.47
27:8:99:VAL:HG11	27:8:124:ILE:HD13	1.97	0.47
47:A:788:A:C8	70:X:107:SER:HA	2.49	0.47
47:A:1300:U:O2'	47:A:1301:G:H8	1.97	0.47
51:E:24:GLU:OE1	58:L:61:TRP:NE1	2.31	0.47
51:E:141:GLY:HA3	51:E:183:LEU:HD23	1.96	0.47
55:I:44:GLU:OE2	55:I:52:LYS:HE3	2.14	0.47
55:I:72:ARG:HG2	55:I:75:ARG:HH21	1.79	0.47
65:S:89:SER:C	65:S:91:LEU:N	2.73	0.47
67:U:42:GLY:HA2	67:U:84:LYS:HG3	1.96	0.47
69:W:4:ASP:OD1	69:W:5:LYS:N	2.48	0.47
72:Z:10:ARG:NH1	72:Z:26:ASP:OD2	2.47	0.47
76:d:8:THR:HG21	76:d:59:SER:HB2	1.96	0.47
1:1:28:C:H4'	1:1:61:A:H4'	1.97	0.47
1:1:631:U:H2'	1:1:632:C:C6	2.50	0.47
1:1:2068:U:N3	21:z:113:GLY:O	2.48	0.47
1:1:2351:A:N3	1:1:2796:G:O2'	2.40	0.47
1:1:2978:A:H2'	1:1:2979:U:O4'	2.14	0.47
1:1:3044:C:H2'	1:1:3045:A:O4'	2.14	0.47
1:1:3259:A:H2'	1:1:3260:A:O4'	2.14	0.47
2:3:27:A:H2'	2:3:28:C:C6	2.50	0.47
3:4:26:U:O2'	7:l:52:ALA:O	2.32	0.47
7:l:139:ARG:HH21	7:l:241:PRO:HG2	1.80	0.47
19:x:29:THR:HA	19:x:32:THR:HG22	1.96	0.47
27:8:73:MET:HE2	27:8:142:ILE:HD13	1.96	0.47
34:AF:97:ILE:HG21	34:AF:106:ARG:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:165:U:C2'	47:A:166:A:H5''	2.45	0.47
47:A:366:U:H2'	47:A:367:A:O4'	2.15	0.47
47:A:1355:A:O2'	47:A:1358:G:OP1	2.32	0.47
1:1:437:G:O2'	1:1:438:A:H5''	2.15	0.47
1:1:1221:A:H2'	1:1:1222:G:H8	1.80	0.47
1:1:3112:G:N7	6:k:28:ARG:NH2	2.60	0.47
13:r:43:VAL:HG21	13:r:197:VAL:HG13	1.96	0.47
47:A:1258:G:N7	47:A:1416:U:H3'	2.30	0.47
47:A:1481:C:H2'	47:A:1482:C:C6	2.50	0.47
52:F:100:ARG:HG2	52:F:102:VAL:HG13	1.96	0.47
55:I:67:ARG:HD2	55:I:127:PHE:CE1	2.49	0.47
1:1:612:U:H2'	1:1:613:U:C6	2.49	0.47
1:1:1180:A:H2'	1:1:1181:C:C6	2.50	0.47
1:1:2794:U:H5'	1:1:2914:C:C5	2.50	0.47
6:k:256:HIS:HA	6:k:257:PRO:C	2.40	0.47
11:p:162:GLU:CD	17:v:26:ARG:HH22	2.23	0.47
42:AN:22:LYS:HG3	42:AN:42:THR:HG21	1.97	0.47
47:A:680:C:H2'	47:A:681:C:C6	2.50	0.47
72:Z:57:VAL:HB	72:Z:60:PHE:HE2	1.80	0.47
1:1:249:G:H2'	1:1:251:G:OP2	2.15	0.46
1:1:436:A:H2'	1:1:437:G:C8	2.50	0.46
1:1:546:C:H2'	1:1:547:U:O4'	2.15	0.46
1:1:1218:G:O2'	1:1:1219:A:OP2	2.28	0.46
1:1:1965:U:H2'	1:1:1966:G:N9	2.31	0.46
3:4:126:A:O2'	3:4:128:U:OP2	2.26	0.46
13:r:19:LYS:HE2	13:r:19:LYS:HB3	1.62	0.46
16:u:19:VAL:HG11	16:u:55:ILE:HD12	1.98	0.46
47:A:176:U:O2'	47:A:177:A:OP2	2.32	0.46
47:A:974:U:H2'	47:A:975:C:C6	2.50	0.46
47:A:1316:A:H61	51:E:162:GLY:HA3	1.80	0.46
48:B:164:ASN:O	48:B:170:ILE:HD11	2.15	0.46
53:G:41:LYS:HD3	53:G:47:SER:HB3	1.96	0.46
64:R:45:PHE:HA	64:R:48:TYR:HB2	1.97	0.46
76:d:11:LYS:N	76:d:31:GLU:O	2.48	0.46
1:1:792:U:H2'	1:1:793:U:C6	2.51	0.46
1:1:3261:A:H2'	1:1:3262:U:C6	2.50	0.46
49:C:66:PHE:CE1	62:P:29:SER:HB3	2.50	0.46
51:E:105:ALA:O	51:E:109:LYS:HG2	2.15	0.46
53:G:145:ASP:OD1	53:G:146:SER:N	2.48	0.46
55:I:18:ALA:HA	55:I:21:PHE:HB2	1.97	0.46
60:N:30:VAL:O	60:N:34:THR:HG23	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:S:35:THR:HG21	65:S:51:ALA:HB2	1.97	0.46
66:T:91:ASP:OD1	66:T:92:GLN:N	2.48	0.46
76:d:42:ARG:NH1	76:d:58:GLU:O	2.48	0.46
1:1:498:C:H2'	1:1:499:G:C8	2.50	0.46
1:1:859:C:H2'	1:1:860:G:O4'	2.15	0.46
1:1:1358:C:H2'	1:1:1359:A:C8	2.50	0.46
1:1:1593:C:H2'	1:1:1594:G:C8	2.51	0.46
1:1:1852:C:H2'	1:1:1853:C:H6	1.80	0.46
1:1:3316:U:O2'	1:1:3317:U:OP1	2.33	0.46
21:z:176:ARG:NH1	47:A:837:C:OP1	2.45	0.46
28:9:5:SER:HB3	28:9:8:VAL:HG23	1.97	0.46
47:A:55:A:OP1	72:Z:112:LYS:NZ	2.32	0.46
47:A:378:U:C4	57:K:5:PRO:HB3	2.50	0.46
47:A:874:U:H2'	47:A:875:C:C6	2.50	0.46
47:A:988:A:H2'	47:A:990:A:N7	2.30	0.46
47:A:1219:A:HO2'	79:g:187:HIS:CE1	2.33	0.46
48:B:200:ASP:O	48:B:203:PHE:HB2	2.14	0.46
55:I:33:GLU:HG2	55:I:34:LEU:HD12	1.97	0.46
60:N:64:ASP:OD1	60:N:72:ILE:HD12	2.15	0.46
1:1:638:U:H2'	1:1:639:C:C6	2.51	0.46
1:1:745:C:H5''	31:AC:32:LEU:HD12	1.98	0.46
1:1:844:A:C5	1:1:845:C:H1'	2.50	0.46
1:1:912:G:H5'	1:1:913:A:OP1	2.16	0.46
1:1:1229:G:H2'	1:1:1229:G:N3	2.31	0.46
1:1:1852:C:H2'	1:1:1853:C:C6	2.49	0.46
3:4:5:U:H2'	3:4:6:U:C6	2.51	0.46
11:p:261:SER:HB3	49:C:225:LEU:HD23	1.98	0.46
12:q:94:TYR:HA	12:q:177:ASP:OD1	2.14	0.46
28:9:109:LEU:HD22	28:9:115:ARG:NH2	2.30	0.46
32:AD:101:ASP:OD1	32:AD:101:ASP:N	2.48	0.46
47:A:504:A:H2'	47:A:505:U:C6	2.51	0.46
47:A:518:A:O2'	47:A:519:A:OP1	2.30	0.46
47:A:1002:U:H2'	47:A:1003:U:H6	1.80	0.46
51:E:210:ALA:O	65:S:19:ARG:NH1	2.48	0.46
80:h:33:LEU:HB3	80:h:45:TRP:HB2	1.95	0.46
1:1:65:A:N6	1:1:75:G:H1'	2.31	0.46
1:1:547:U:H2'	1:1:548:G:H8	1.80	0.46
1:1:912:G:N1	5:j:207:VAL:HG11	2.30	0.46
1:1:981:U:H2'	1:1:982:U:H6	1.80	0.46
1:1:1655:U:H2'	1:1:1656:C:H6	1.81	0.46
1:1:2041:A:H2'	1:1:2042:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2713:C:O2	44:AP:20:HIS:HE1	1.98	0.46
1:1:3241:G:O6	19:x:169:ASN:ND2	2.49	0.46
7:l:6:GLN:HB3	7:l:20:GLN:HB3	1.98	0.46
28:9:80:ILE:HG23	28:9:101:PRO:HG3	1.97	0.46
47:A:985:C:H5	47:A:988:A:H5''	1.80	0.46
47:A:1464:G:OP1	67:U:43:ASN:ND2	2.49	0.46
47:A:1529:G:H22	47:A:1555:C:H1'	1.81	0.46
64:R:49:GLU:OE1	64:R:81:ARG:NH2	2.34	0.46
1:1:314:U:H2'	1:1:315:C:C6	2.51	0.46
1:1:649:G:O2'	1:1:1431:A:OP1	2.33	0.46
1:1:713:A:N1	1:1:777:G:O2'	2.36	0.46
1:1:796:G:O6	7:l:105:LYS:NZ	2.33	0.46
1:1:1746:A:OP1	40:AL:44:LYS:NZ	2.29	0.46
2:3:77:G:H3'	22:0:46:GLN:O	2.15	0.46
13:r:82:ARG:NH1	13:r:83:ASP:OD1	2.48	0.46
14:s:101:ASN:HD22	14:s:131:MET:H	1.63	0.46
18:w:9:VAL:HG12	18:w:118:ARG:HG3	1.97	0.46
25:6:108:GLU:HG2	25:6:128[B]:ARG:HG3	1.97	0.46
30:AB:94:SER:HB3	30:AB:121:VAL:HG13	1.97	0.46
35:AG:49:ILE:HG12	35:AG:100:ILE:HD13	1.98	0.46
47:A:4:C:H5	47:A:20:G:N1	2.12	0.46
47:A:199:G:O6	47:A:200:A:N6	2.48	0.46
47:A:504:A:O2'	47:A:505:U:OP1	2.34	0.46
47:A:1282:G:N2	47:A:1285:A:OP2	2.33	0.46
47:A:1739:U:H2'	47:A:1740:A:C8	2.49	0.46
80:h:46:LYS:HB2	80:h:59:LYS:HG2	1.97	0.46
1:1:538:G:H2'	1:1:539:G:C8	2.50	0.46
1:1:1079:G:H2'	1:1:1080:A:C8	2.51	0.46
1:1:2405:U:H2'	1:1:2406:U:C6	2.50	0.46
1:1:2678:G:H21	46:i:32:LYS:HZ1	1.63	0.46
13:r:53:VAL:HG21	13:r:166:ILE:HD12	1.97	0.46
32:AD:26:THR:HG23	32:AD:95:LEU:HD11	1.96	0.46
47:A:335:G:O2'	56:J:10:LYS:NZ	2.48	0.46
63:Q:68:GLU:N	63:Q:69:PRO:HD3	2.31	0.46
68:V:68:LYS:HE2	68:V:79:ASP:OD1	2.15	0.46
69:W:73:ALA:HB1	69:W:78:LEU:HB2	1.97	0.46
1:1:624:U:H2'	1:1:625:C:C6	2.51	0.46
1:1:1007:A:H2'	1:1:1008:A:H8	1.80	0.46
1:1:2653:U:H2'	1:1:2654:C:H6	1.81	0.46
7:l:4:ARG:NH1	7:l:25:ALA:HA	2.31	0.46
12:q:105:LYS:HE3	12:q:108:GLY:HA2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1012:A:OP1	47:A:1776:G:O2'	2.28	0.46
47:A:1243:U:C6	47:A:1244:U:H5	2.33	0.46
47:A:1248:G:H2'	47:A:1249:G:O4'	2.15	0.46
47:A:1672:G:H2'	47:A:1674:U:C4	2.50	0.46
54:H:135:PRO:HB2	54:H:141:ILE:HG12	1.97	0.46
71:Y:92:CYS:HG	71:Y:136:TRP:CD1	2.34	0.46
1:1:1807:G:H2'	1:1:1808:G:O4'	2.15	0.46
1:1:2061:G:H2'	1:1:2062:G:C4	2.50	0.46
1:1:2587:G:H2'	1:1:2588:C:C6	2.51	0.46
3:4:57:C:H4'	3:4:63:G:N7	2.31	0.46
10:o:39:ARG:HA	10:o:42:ILE:HG12	1.97	0.46
12:q:134:MET:SD	12:q:146:VAL:HG22	2.56	0.46
46:i:115:LEU:O	46:i:119:VAL:HG22	2.15	0.46
63:Q:15:PHE:CE1	63:Q:110:GLU:HG3	2.51	0.46
1:1:258:U:OP1	15:t:81:LYS:HE3	2.15	0.46
1:1:1017:G:H2'	1:1:1018:U:C6	2.51	0.46
1:1:1891:A:O2'	1:1:3025:G:H4'	2.16	0.46
8:m:187:ALA:O	8:m:189:GLU:N	2.45	0.46
17:v:94:TYR:CE2	17:v:96:LYS:HB2	2.51	0.46
25:6:10:LYS:NZ	25:6:54:ALA:O	2.45	0.46
47:A:811:U:H3	47:A:831:G:H1	1.62	0.46
47:A:1242:U:H2'	47:A:1242:U:O2	2.15	0.46
67:U:127:ASN:HB3	67:U:130:ARG:HH21	1.81	0.46
1:1:432:G:OP1	35:AG:57:LYS:HB2	2.16	0.45
1:1:538:G:O2'	1:1:539:G:OP1	2.31	0.45
1:1:999:A:N1	1:1:1045:C:O2'	2.46	0.45
1:1:1035:U:H2'	1:1:1036:A:C8	2.51	0.45
1:1:1715:G:N7	21:z:121:HIS:HE1	2.15	0.45
1:1:1762:G:HO2'	1:1:1763:C:P	2.39	0.45
1:1:3166:A:H2'	1:1:3167:G:C8	2.51	0.45
6:k:66:LYS:NZ	25:6:9:ASN:H	2.13	0.45
47:A:64:U:O2'	47:A:166:A:N3	2.39	0.45
47:A:824:U:O2	47:A:824:U:H3'	2.16	0.45
47:A:1357:A:H61	68:V:20:LYS:NZ	2.14	0.45
47:A:1472:G:N2	47:A:1509:U:O4	2.50	0.45
48:B:62:ARG:HD3	69:W:37:ALA:O	2.16	0.45
55:I:69:VAL:HG12	55:I:72:ARG:HH21	1.80	0.45
61:O:5:HIS:HB2	61:O:121:ARG:HH21	1.80	0.45
76:d:14:LYS:HB3	76:d:29:ARG:HB3	1.97	0.45
76:d:33:LEU:HD21	76:d:53:ILE:HG23	1.97	0.45
1:1:208:A:H4'	1:1:210:A:N7	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:451:C:H2'	1:1:452:A:C5	2.51	0.45
1:1:1275:C:H2'	1:1:1276:C:H6	1.81	0.45
1:1:1474:C:H2'	1:1:1475:U:C6	2.51	0.45
1:1:1801:C:H2'	1:1:1802:A:H8	1.82	0.45
1:1:2058:C:H3'	1:1:2059:G:H8	1.81	0.45
1:1:2632:G:OP1	1:1:2722:U:O2'	2.31	0.45
1:1:3000:G:H2'	1:1:3001:A:C8	2.51	0.45
13:r:50:ILE:HD13	13:r:149:ILE:HG13	1.98	0.45
13:r:86:HIS:HB3	13:r:139:ARG:CG	2.46	0.45
20:y:64:VAL:HG22	20:y:96:PHE:CE1	2.51	0.45
30:AB:104:THR:OG1	30:AB:126:LYS:O	2.28	0.45
47:A:180:A:H2'	47:A:181:U:C6	2.50	0.45
47:A:290:U:H2'	47:A:291:U:C6	2.50	0.45
47:A:1701:A:H2'	47:A:1702:A:O4'	2.16	0.45
54:H:219:ARG:HB3	54:H:223:ARG:NH1	2.31	0.45
61:O:31:ASP:O	61:O:34:VAL:N	2.49	0.45
63:Q:60:LEU:HD21	63:Q:94:VAL:HG12	1.98	0.45
75:c:57:ASP:OD1	75:c:58:SER:N	2.49	0.45
1:1:911:A:H8	1:1:2114:C:O2'	1.99	0.45
1:1:1020:G:H3'	1:1:1021:A:H5''	1.97	0.45
1:1:1218:G:H1'	1:1:1282:A:N6	2.31	0.45
1:1:1494:A:H2'	1:1:1495:U:C6	2.51	0.45
6:k:48:GLY:HA3	6:k:81:THR:HG22	1.99	0.45
7:l:35:LEU:HD22	7:l:121:TYR:HD2	1.82	0.45
25:6:70:ARG:HG2	25:6:71:LYS:HG3	1.98	0.45
32:AD:55:LYS:O	32:AD:59:GLU:HG2	2.16	0.45
47:A:1259:C:O2	47:A:1413:A:O2'	2.24	0.45
60:N:64:ASP:N	60:N:92:SER:OG	2.47	0.45
79:g:182:TYR:OH	79:g:187:HIS:ND1	2.40	0.45
1:1:1832:C:O2'	1:1:1838:A:N1	2.42	0.45
1:1:1970:A:H2'	1:1:1971:C:C6	2.50	0.45
1:1:2913:A:H8	1:1:2913:A:OP2	1.99	0.45
8:m:95:TRP:CE3	8:m:198:TYR:HB3	2.52	0.45
11:p:141:VAL:HG22	11:p:167:LEU:HD21	1.99	0.45
47:A:182:C:H2'	47:A:183:C:C6	2.50	0.45
47:A:254:A:H2'	47:A:255:A:O4'	2.16	0.45
47:A:472:A:H5''	57:K:144:PRO:HD2	1.98	0.45
47:A:874:U:H2'	47:A:875:C:H6	1.80	0.45
47:A:1189:A:N3	77:e:10:HIS:HE1	2.15	0.45
47:A:1317:C:O2'	51:E:163:GLN:HB3	2.16	0.45
47:A:1355:A:O2'	47:A:1356:U:OP1	2.33	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1396:A:HO2'	47:A:1397:A:P	2.39	0.45
47:A:1581:G:H2'	47:A:1582:U:O4'	2.17	0.45
64:R:93:GLN:HB2	64:R:101:LYS:HG3	1.97	0.45
1:1:662:U:H5'	7:l:108:ARG:HA	1.98	0.45
1:1:1755:U:H2'	1:1:1756:A:H5''	1.98	0.45
1:1:2342:G:H22	1:1:2374:G:H1'	1.81	0.45
1:1:2646:A:C2	14:s:124:GLY:HA3	2.51	0.45
1:1:2660:U:OP1	8:m:12:TYR:OH	2.26	0.45
1:1:2967:A:H2'	1:1:2968:U:O4'	2.17	0.45
1:1:3193:C:H4'	1:1:3194:G:O5'	2.15	0.45
1:1:3285:A:H2'	1:1:3286:C:C6	2.51	0.45
7:l:299:VAL:HG21	20:y:133:LYS:HG3	1.97	0.45
40:AL:14:LEU:HD21	40:AL:52:TYR:CG	2.51	0.45
47:A:82:U:H2'	47:A:83:G:O4'	2.16	0.45
47:A:148:C:H42	47:A:162:A:H61	1.64	0.45
47:A:182:C:H2'	47:A:183:C:H6	1.81	0.45
47:A:975:C:H2'	47:A:976:G:O4'	2.17	0.45
47:A:1316:A:N6	51:E:162:GLY:HA3	2.31	0.45
47:A:1783:C:O2	74:b:92:ARG:HB3	2.15	0.45
48:B:118:PRO:HG2	48:B:141:ILE:HD13	1.99	0.45
51:E:158:MET:HE2	51:E:158:MET:HB2	1.83	0.45
54:H:180:THR:HG23	54:H:183:THR:H	1.82	0.45
65:S:77:GLU:O	65:S:81:LYS:HB2	2.16	0.45
80:h:152:VAL:HG12	80:h:170:SER:HB2	1.98	0.45
1:1:2058:C:H3'	1:1:2059:G:C8	2.51	0.45
1:1:2260:U:O2	1:1:2288:U:H4'	2.17	0.45
1:1:2668:A:H2'	1:1:2669:A:C8	2.52	0.45
8:m:51:LEU:HB2	8:m:144:VAL:HG12	1.98	0.45
8:m:95:TRP:CD1	8:m:158:ARG:HA	2.51	0.45
15:t:83:VAL:O	15:t:120:LYS:NZ	2.48	0.45
22:0:40:ARG:HD2	22:0:40:ARG:HA	1.84	0.45
33:AE:54:LEU:HA	33:AE:94:PRO:HG3	1.98	0.45
40:AL:24:ILE:HB	40:AL:44:LYS:HB2	1.99	0.45
47:A:154:A:H2'	47:A:155:A:O4'	2.17	0.45
47:A:470:U:O2'	47:A:754:A:N3	2.42	0.45
47:A:1158:C:H2'	47:A:1159:C:H6	1.82	0.45
47:A:1262:G:O2'	51:E:175:HIS:ND1	2.46	0.45
49:C:123:ALA:HB2	49:C:165:ARG:HG3	1.99	0.45
52:F:31:PRO:HG3	52:F:43:PRO:HG3	1.99	0.45
53:G:192:GLU:OE2	73:a:63:SER:OG	2.31	0.45
70:X:111:MET:SD	70:X:115:GLU:HG2	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:229:C:H2'	1:1:230:G:O4'	2.16	0.45
1:1:266:C:OP1	17:v:5:LYS:NZ	2.38	0.45
1:1:371:G:N1	1:1:374:A:OP2	2.36	0.45
1:1:1639:A:H2'	1:1:1640:C:C2	2.52	0.45
1:1:2185:A:H62	47:A:898:G:H21	1.65	0.45
14:s:37:LEU:HD23	14:s:37:LEU:HA	1.82	0.45
29:AA:24:VAL:HG21	29:AA:87:LEU:HB3	1.99	0.45
47:A:93:A:O2'	52:F:4:GLY:HA3	2.16	0.45
47:A:944:U:H5'	61:O:15:ALA:O	2.16	0.45
47:A:1043:U:O4	47:A:1046:A:N6	2.50	0.45
47:A:1239:U:OP2	60:N:46:ARG:NH1	2.45	0.45
53:G:98:MET:HB2	53:G:103:ASN:O	2.17	0.45
1:1:481:G:C8	1:1:482:U:C4	3.05	0.45
1:1:502:U:H2'	1:1:503:U:C6	2.52	0.45
1:1:757:A:H2'	1:1:758:U:C6	2.52	0.45
1:1:1198:A:C2	1:1:2829:C:H5'	2.52	0.45
1:1:1478:A:H4'	1:1:1479:G:OP2	2.17	0.45
1:1:2648:A:H5'	1:1:2649:G:C8	2.52	0.45
1:1:2739:U:H2'	1:1:2740:U:C6	2.51	0.45
1:1:3135:A:H2'	1:1:3136:C:C6	2.52	0.45
1:1:3163:U:H1'	1:1:3165:U:O4	2.17	0.45
7:l:157:PHE:CD1	7:l:169:VAL:HG11	2.51	0.45
18:w:60:ARG:HE	18:w:60:ARG:HB3	1.62	0.45
34:AF:39:ILE:O	34:AF:44:ARG:NH2	2.50	0.45
47:A:68:A:N6	54:H:132:ARG:HG2	2.31	0.45
47:A:1323:C:H1'	47:A:1396:A:C5	2.51	0.45
47:A:1335:U:O2'	47:A:1336:G:OP1	2.32	0.45
47:A:1375:C:O2'	65:S:52:GLY:HA3	2.17	0.45
48:B:52:LYS:HD3	69:W:82:VAL:HG23	1.99	0.45
49:C:36:THR:HA	49:C:41:ARG:HD2	1.99	0.45
50:D:78:ILE:HD11	50:D:120:ILE:HD11	1.99	0.45
67:U:131:ASP:O	67:U:135:ILE:HG12	2.17	0.45
1:1:37:U:H2'	1:1:38:A:O4'	2.17	0.45
1:1:1303:G:H4'	1:1:1304:A:O5'	2.16	0.45
1:1:1637:U:O2'	1:1:1638:A:H3'	2.17	0.45
1:1:2335:A:H2'	1:1:2336:A:H8	1.79	0.45
7:l:182:VAL:HG11	7:l:225:GLY:HA3	1.99	0.45
10:o:130:PRO:HG2	10:o:131:TYR:CE2	2.52	0.45
19:x:42:GLU:HG2	19:x:43:LYS:N	2.32	0.45
22:0:27:MET:HE2	22:0:27:MET:HB3	1.87	0.45
27:8:67:ILE:HD12	27:8:121:LYS:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AO:1:MET:HB2	47:A:1770:C:OP2	2.17	0.45
47:A:119:A:H1'	47:A:395:A:C5	2.52	0.45
47:A:151:G:H2'	47:A:152:G:H8	1.80	0.45
47:A:265:U:H2'	47:A:266:C:H6	1.82	0.45
47:A:1609:G:H2'	47:A:1610:C:C6	2.52	0.45
47:A:1664:C:H42	47:A:1711:C:H42	1.64	0.45
49:C:34:ALA:O	49:C:41:ARG:NH1	2.50	0.45
57:K:148:VAL:HG11	57:K:156:ILE:HD11	1.99	0.45
65:S:37:GLU:OE1	80:h:151:TRP:NE1	2.40	0.45
66:T:15:LEU:HB2	66:T:22:ILE:HB	1.99	0.45
66:T:30:TYR:O	66:T:33:THR:OG1	2.31	0.45
71:Y:88:PRO:O	71:Y:92:CYS:HB2	2.17	0.45
77:e:19:ARG:HD2	77:e:32:ARG:HD3	1.98	0.45
1:1:1218:G:H1'	1:1:1282:A:H62	1.82	0.45
1:1:1338:G:H2'	1:1:1339:A:O4'	2.17	0.45
1:1:1616:U:H2'	1:1:1617:A:C8	2.52	0.45
3:4:81:A:H2'	3:4:82:U:C6	2.52	0.45
3:4:157:U:O2'	3:4:158:U:O4'	2.24	0.45
5:j:77:ILE:HD13	5:j:128:ARG:HB3	1.99	0.45
47:A:397:A:H4'	52:F:3:ARG:HG2	1.99	0.45
47:A:445:U:H2'	47:A:446:C:O4'	2.17	0.45
47:A:767:G:O2'	47:A:768:C:H6	1.99	0.45
47:A:1150:G:H2'	47:A:1151:A:C8	2.52	0.45
47:A:1459:U:OP1	53:G:183:SER:OG	2.35	0.45
47:A:1548:U:H4'	47:A:1586:C:H4'	1.98	0.45
60:N:62:LEU:HD13	60:N:75:VAL:HG11	1.99	0.45
1:1:1021:A:OP2	1:1:1021:A:C8	2.70	0.44
82:1:3403:ANM:N1	82:1:3403:ANM:H13	2.31	0.44
5:j:49:ILE:HD11	5:j:60:LYS:HE2	2.00	0.44
8:m:51:LEU:HB2	8:m:144:VAL:CG1	2.47	0.44
17:v:36:ILE:HG12	17:v:64:ILE:HG13	1.99	0.44
22:0:78:TRP:CE3	22:0:125:LYS:HE3	2.52	0.44
24:5:29:ASP:HB3	24:5:32:SER:OG	2.17	0.44
43:AO:1:MET:HB3	47:A:1629:G:H5'	1.98	0.44
46:i:107:TRP:HB3	51:E:151:GLN:HE22	1.82	0.44
47:A:590:A:O2'	47:A:594:C:OP1	2.35	0.44
47:A:953:U:H2'	47:A:954:C:O4'	2.17	0.44
47:A:1016:U:H4'	47:A:1017:G:OP2	2.17	0.44
47:A:1062:C:H2'	47:A:1063:C:H6	1.82	0.44
47:A:1332:U:OP1	68:V:22:ARG:NH2	2.40	0.44
55:I:48:ASN:ND2	55:I:167:GLN:OE1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:J:49:ARG:O	56:J:52:ASN:ND2	2.50	0.44
65:S:75:GLU:O	65:S:79:GLU:HG3	2.17	0.44
80:h:88:ARG:HA	80:h:111:VAL:HG23	1.99	0.44
1:1:1660:G:H2'	1:1:1661:U:C6	2.52	0.44
1:1:2370:C:O2'	6:k:266:ARG:NH2	2.51	0.44
1:1:2391:A:H2'	1:1:2392:G:C8	2.52	0.44
15:t:194:GLU:O	15:t:198:GLU:HB3	2.18	0.44
30:AB:60:TYR:CE1	30:AB:63:LYS:HA	2.52	0.44
47:A:156:U:O2'	47:A:157:U:H3'	2.17	0.44
47:A:1002:U:H2'	47:A:1003:U:C6	2.51	0.44
47:A:1222:G:H2'	47:A:1223:A:H8	1.82	0.44
54:H:149:LYS:HB3	54:H:149:LYS:HE2	1.73	0.44
1:1:2564:G:H4'	1:1:2566:C:C2	2.53	0.44
1:1:2719:A:H2'	1:1:2720:A:C8	2.53	0.44
5:j:20:THR:HA	5:j:23:ARG:HG3	1.98	0.44
25:6:38:ALA:HB3	25:6:59:MET:HB2	1.99	0.44
29:AA:46:ILE:HG23	29:AA:68:VAL:HG13	1.99	0.44
47:A:872:A:H5''	62:P:115:PRO:HB2	2.00	0.44
47:A:1452:G:OP1	64:R:131:ARG:NH2	2.40	0.44
50:D:93:MET:HG3	50:D:116:VAL:HG23	1.99	0.44
53:G:63:GLN:HE22	53:G:66:ASN:HB2	1.83	0.44
60:N:28:LEU:HA	60:N:31:VAL:HG22	1.98	0.44
63:Q:80:LEU:HD12	63:Q:83:MET:HB2	2.00	0.44
64:R:89:VAL:HG13	64:R:101:LYS:HG2	1.99	0.44
1:1:619:A:H2'	1:1:620:A:N7	2.31	0.44
1:1:814:C:H2'	1:1:815:U:O4'	2.18	0.44
1:1:948:A:H4'	1:1:964:G:N2	2.32	0.44
1:1:1568:U:C4	1:1:1569:C:H1'	2.52	0.44
1:1:2126:U:H2'	1:1:2127:A:C5	2.53	0.44
1:1:2384:C:H2'	1:1:2385:C:H6	1.82	0.44
1:1:2915:G:H2'	1:1:2916:U:O4'	2.18	0.44
2:3:26:C:H2'	2:3:27:A:O4'	2.17	0.44
17:v:62:TYR:CD2	17:v:106:VAL:HG13	2.47	0.44
22:0:24:LEU:HD21	23:2:141:ILE:HG21	1.99	0.44
23:2:51:GLY:HA3	23:2:92:ARG:HG3	1.98	0.44
47:A:29:U:H2'	47:A:30:G:C8	2.53	0.44
47:A:740:A:HO2'	47:A:741:A:P	2.38	0.44
47:A:1339:G:O6	47:A:1354:U:C2	2.70	0.44
47:A:1487:C:P	67:U:122:ARG:HH22	2.40	0.44
47:A:1709:A:H2'	47:A:1710:G:O4'	2.18	0.44
48:B:88:LYS:HA	48:B:88:LYS:HD3	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:C:36:THR:HG23	49:C:231:LEU:O	2.16	0.44
65:S:93:LEU:HD23	65:S:93:LEU:H	1.82	0.44
68:V:32:GLN:HB3	68:V:108:GLU:HG2	1.99	0.44
80:h:200:THR:HG21	80:h:242:PHE:H	1.83	0.44
1:1:565:A:H2'	1:1:566:C:O4'	2.18	0.44
1:1:2273:A:C4	25:6:37:LEU:HD22	2.53	0.44
1:1:2370:C:H1'	6:k:266:ARG:NH2	2.33	0.44
1:1:2958:U:H2'	1:1:2959:A:C8	2.52	0.44
1:1:3240:U:H5'	35:AG:66:VAL:HG21	1.99	0.44
10:o:147:TYR:OH	10:o:180:GLU:OE2	2.23	0.44
15:t:55:ARG:NH1	15:t:73:ARG:O	2.44	0.44
17:v:73:ARG:HG2	17:v:75:VAL:HG13	1.99	0.44
17:v:193:LYS:HB3	17:v:193:LYS:HE2	1.68	0.44
47:A:393:U:H2'	47:A:394:G:O4'	2.17	0.44
47:A:933:A:H2'	47:A:934:C:C6	2.52	0.44
47:A:1333:A:H2'	47:A:1334:G:C8	2.53	0.44
60:N:24:ILE:HG13	60:N:25:GLU:N	2.33	0.44
67:U:77:ASN:HB3	67:U:95:ASP:HB3	1.99	0.44
1:1:1157:G:O2'	34:AF:55:ASN:OD1	2.36	0.44
1:1:1779:U:H2'	1:1:1780:A:C8	2.53	0.44
1:1:2186:A:O2'	1:1:2187:U:H5'	2.17	0.44
1:1:3104:C:H2'	1:1:3105:C:C6	2.52	0.44
1:1:3218:U:H2'	1:1:3219:G:C8	2.53	0.44
20:y:165:ILE:HD11	20:y:172:PHE:HB3	2.00	0.44
26:7:57:ARG:HE	26:7:63:ILE:HD11	1.81	0.44
28:9:85:LEU:HD23	28:9:85:LEU:HA	1.77	0.44
40:AL:46:ARG:HD3	40:AL:47:GLY:O	2.16	0.44
47:A:286:A:H2'	47:A:287:U:O4'	2.17	0.44
47:A:1437:C:OP1	77:e:12:ARG:NH1	2.44	0.44
49:C:168:MET:O	49:C:172:MET:HG3	2.17	0.44
54:H:85:ARG:O	54:H:87:ARG:NH1	2.51	0.44
66:T:6:GLN:OE1	66:T:6:GLN:N	2.50	0.44
70:X:77:PRO:HD2	70:X:79:PHE:CZ	2.53	0.44
1:1:539:G:H2'	1:1:540:C:C6	2.52	0.44
1:1:1263:U:H3'	1:1:1264:G:H8	1.82	0.44
1:1:3287:A:H2'	1:1:3288:A:H8	1.82	0.44
2:3:4:U:H2'	2:3:5:G:C8	2.53	0.44
10:o:79:PRO:HG2	10:o:136:TYR:CE2	2.53	0.44
10:o:143[B]:ARG:HG3	10:o:183:ILE:HD13	2.00	0.44
47:A:804:U:H2'	47:A:805:U:H5	1.83	0.44
47:A:1219:A:OP2	47:A:1230:G:O2'	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1431:G:N2	79:g:129:THR:O	2.40	0.44
51:E:214:ASP:OD1	51:E:215:GLU:N	2.47	0.44
72:Z:63:GLN:NE2	72:Z:68:LYS:HD3	2.32	0.44
79:g:161:ARG:HH12	79:g:164:PRO:HG3	1.83	0.44
1:1:672:G:O6	20:y:56:LYS:NZ	2.50	0.44
1:1:964:G:H2'	1:1:965:C:C6	2.53	0.44
1:1:1945:A:H2'	1:1:1946:U:C6	2.52	0.44
1:1:2063:C:H2'	1:1:2064:A:O4'	2.18	0.44
2:3:4:U:H2'	2:3:5:G:H8	1.82	0.44
6:k:117:ARG:HD2	6:k:176:ALA:O	2.18	0.44
8:m:290:ILE:HG21	13:r:218:TYR:CD2	2.53	0.44
18:w:76:ALA:HB1	18:w:107:GLU:OE2	2.18	0.44
29:AA:70:PRO:HG3	29:AA:115:LYS:HB2	2.00	0.44
47:A:451:C:O2	47:A:451:C:H2'	2.17	0.44
47:A:479:A:H2'	47:A:480:U:C6	2.53	0.44
47:A:485:G:N3	47:A:485:G:H2'	2.33	0.44
47:A:1002:U:C2	47:A:1003:U:C5	3.05	0.44
47:A:1026:G:H2'	47:A:1027:G:H8	1.81	0.44
47:A:1206:A:H2'	47:A:1207:C:O4'	2.18	0.44
47:A:1240:G:H2'	60:N:47:GLU:OE2	2.18	0.44
47:A:1571:G:O2'	47:A:1597:G:O6	2.31	0.44
48:B:43:ASP:OD1	48:B:44:GLY:N	2.51	0.44
1:1:1690:U:O2'	1:1:1691:U:H5'	2.18	0.44
1:1:1760:U:P	21:z:43:LYS:HE2	2.58	0.44
1:1:1965:U:H2'	1:1:1966:G:C8	2.53	0.44
1:1:2902:A:H2'	1:1:2903:C:C6	2.53	0.44
12:q:41:ILE:HG22	12:q:43:VAL:HG13	2.00	0.44
47:A:12:U:H2'	47:A:13:C:H6	1.82	0.44
47:A:988:A:H2'	47:A:990:A:C8	2.53	0.44
51:E:135:VAL:HG23	51:E:189:ILE:HG12	1.99	0.44
55:I:69:VAL:HG12	55:I:72:ARG:NH2	2.32	0.44
58:L:56:LYS:NZ	58:L:69:THR:HG22	2.33	0.44
63:Q:26:VAL:HG23	63:Q:27:GLU:OE1	2.17	0.44
66:T:49:LYS:HD3	66:T:49:LYS:HA	1.77	0.44
70:X:23:ARG:HG3	75:c:4:VAL:HG22	2.00	0.44
80:h:65:HIS:NE2	80:h:83:SER:OG	2.41	0.44
1:1:299:G:C8	38:AJ:30:GLY:HA3	2.52	0.43
1:1:708:A:H2'	1:1:709:A:C8	2.53	0.43
1:1:2545:C:O2'	1:1:2546:U:OP1	2.32	0.43
1:1:2782:C:OP1	1:1:2927:U:O2'	2.33	0.43
1:1:2917:G:O2'	1:1:2920:C:OP2	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:w:42:LEU:HD11	18:w:81:LEU:HD22	2.00	0.43
26:7:4:GLU:HB2	26:7:13:ILE:HB	1.99	0.43
55:I:8:GLU:OE1	55:I:9:ASN:ND2	2.51	0.43
1:1:559:C:H2'	1:1:560:C:C6	2.52	0.43
1:1:788:G:H2'	1:1:789:C:H6	1.83	0.43
1:1:1319:G:H4'	22:0:2:SER:HA	2.01	0.43
1:1:1576:A:C8	1:1:1576:A:O5'	2.71	0.43
1:1:3297:U:H2'	1:1:3298:G:O4'	2.18	0.43
12:q:137:SER:HB3	12:q:143:GLU:HB3	2.00	0.43
47:A:822:G:O2'	47:A:823:G:H5''	2.18	0.43
50:D:53:LEU:HA	69:W:12:TYR:CE1	2.48	0.43
55:I:60:PRO:N	55:I:61:PRO:HD2	2.33	0.43
57:K:63:ASP:OD1	57:K:64:GLU:N	2.50	0.43
61:O:46:THR:OG1	61:O:49:GLN:HG3	2.18	0.43
70:X:115:GLU:O	70:X:119:LYS:HG2	2.18	0.43
79:g:175:ALA:N	79:g:182:TYR:O	2.51	0.43
1:1:1015:G:H1	1:1:1029:U:H3	1.65	0.43
1:1:1153:G:H2'	1:1:1154:A:O4'	2.18	0.43
1:1:1466:U:H2'	1:1:1467:U:C6	2.53	0.43
1:1:1713:U:H2'	1:1:1714:G:H8	1.82	0.43
1:1:1777:C:H2'	1:1:1778:U:C6	2.53	0.43
3:4:10:A:H2'	3:4:11:C:C6	2.53	0.43
3:4:106:C:H4'	3:4:107:G:H5''	1.99	0.43
11:p:65:ILE:O	11:p:69:ARG:HG2	2.18	0.43
11:p:76:ILE:HD11	17:v:18:VAL:HG13	2.00	0.43
47:A:871:U:OP2	49:C:216:LYS:NZ	2.51	0.43
49:C:51:SER:HB2	49:C:57:ALA:H	1.82	0.43
55:I:134:LYS:C	55:I:135:ARG:HD2	2.42	0.43
63:Q:125:PRO:HB3	66:T:129:TRP:CH2	2.54	0.43
79:g:160:ARG:HH11	79:g:176:ASN:HB2	1.82	0.43
1:1:48:A:N7	17:v:187:ARG:HD2	2.33	0.43
1:1:849:G:OP2	45:AQ:2:THR:HG21	2.18	0.43
1:1:1099:A:N3	1:1:1099:A:H2'	2.33	0.43
1:1:1263:U:H3'	1:1:1264:G:C8	2.54	0.43
1:1:1496:G:H2'	1:1:1497:U:O4'	2.17	0.43
1:1:2251:G:O2'	1:1:2289:G:O6	2.34	0.43
1:1:2515:G:H1'	1:1:2516:U:O4'	2.18	0.43
8:m:235:ASP:OD1	8:m:235:ASP:N	2.47	0.43
9:n:58:GLU:H	9:n:58:GLU:CD	2.26	0.43
24:5:107:LYS:HB2	24:5:107:LYS:HE3	1.88	0.43
47:A:71:A:H2'	47:A:72:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:273:C:H2'	47:A:274:C:O4'	2.19	0.43
47:A:1502:A:O2'	47:A:1504:U:OP2	2.26	0.43
47:A:1602:C:C4	53:G:81:ARG:HA	2.54	0.43
50:D:40:VAL:HG21	50:D:63:ILE:HG23	2.00	0.43
57:K:92:LYS:C	57:K:94:ASP:H	2.26	0.43
61:O:87:ASP:OD1	61:O:87:ASP:N	2.51	0.43
80:h:60:LYS:NZ	80:h:97:THR:HA	2.32	0.43
1:1:165:C:H2'	1:1:166:U:C6	2.54	0.43
1:1:2846:G:O6	1:1:2917:G:C2'	2.65	0.43
1:1:3318:G:C6	1:1:3321:G:C5	3.07	0.43
10:o:182:LEU:HD21	10:o:200:LEU:HD11	1.99	0.43
29:AA:12:ILE:HB	29:AA:81:MET:HB3	1.99	0.43
35:AG:42:LYS:HA	35:AG:45:LEU:HG	2.00	0.43
36:AH:67:LYS:O	36:AH:71:THR:HG22	2.17	0.43
47:A:678:A:H2'	47:A:679:C:O4'	2.18	0.43
47:A:811:U:C2	47:A:812:C:C5	3.07	0.43
47:A:813:U:O2'	47:A:814:A:O5'	2.37	0.43
47:A:1265:C:O2'	68:V:69:THR:HG22	2.18	0.43
47:A:1293:G:H2'	47:A:1294:C:C6	2.53	0.43
47:A:1410:A:OP2	51:E:152:LYS:NZ	2.49	0.43
64:R:76:GLN:O	64:R:80:ILE:HG13	2.18	0.43
1:1:212:A:O4'	28:9:2:ALA:HA	2.19	0.43
1:1:561:U:H2'	1:1:562:C:C6	2.54	0.43
1:1:628:A:H2'	1:1:629:A:H8	1.79	0.43
1:1:762:U:H4'	1:1:763:U:O4'	2.18	0.43
1:1:1468:U:H5''	21:z:24:LEU:HD12	2.00	0.43
1:1:1791:U:H2'	5:j:50:HIS:CD2	2.53	0.43
1:1:2793:C:H1'	82:1:3403:ANM:C9	2.48	0.43
1:1:2876:U:H2'	1:1:2877:U:C6	2.52	0.43
1:1:3208:A:H4'	6:k:95:THR:HG22	2.01	0.43
14:s:136:ALA:HA	14:s:148:ILE:HD11	2.01	0.43
17:v:146:ALA:HA	17:v:149:ASN:OD1	2.18	0.43
18:w:189:SER:O	18:w:193:GLN:HG2	2.18	0.43
22:0:164:GLN:HG2	22:0:166:THR:H	1.84	0.43
47:A:770:C:P	47:A:770:C:O4'	2.76	0.43
47:A:1237:C:O2'	79:g:184:GLY:N	2.45	0.43
47:A:1265:C:H5'	77:e:44:ARG:HH12	1.83	0.43
47:A:1580:A:O2'	47:A:1581:G:H5'	2.18	0.43
47:A:1604:U:H2'	47:A:1605:C:C6	2.54	0.43
47:A:1700:G:H2'	47:A:1701:A:C5	2.52	0.43
58:L:35:ILE:HG22	58:L:37:THR:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:N:38:HIS:ND1	60:N:127:GLY:HA3	2.34	0.43
65:S:99:GLN:HB2	65:S:118:PRO:O	2.19	0.43
80:h:102:GLN:NE2	80:h:139:GLY:HA3	2.32	0.43
1:1:696:U:H2'	1:1:697:A:O4'	2.19	0.43
1:1:1705:C:H2'	1:1:1706:C:H6	1.84	0.43
1:1:2627:U:H4'	1:1:2628:A:O4'	2.19	0.43
3:4:156:U:O2'	3:4:157:U:OP1	2.31	0.43
10:o:108:GLN:HG3	10:o:111:ALA:HB2	2.00	0.43
20:y:67:ILE:HG23	20:y:81:ILE:HG13	2.01	0.43
34:AF:17[B]:LYS:HE3	34:AF:19:LYS:HG2	2.00	0.43
47:A:520:U:H2'	47:A:521:G:O4'	2.19	0.43
47:A:529:C:O2'	47:A:530:U:OP1	2.31	0.43
47:A:1306:A:H4'	47:A:1307:A:O5'	2.18	0.43
47:A:1634:U:H2'	47:A:1635:A:C8	2.54	0.43
51:E:41:ARG:HG3	68:V:109:PRO:HB3	1.99	0.43
53:G:200:ASN:CB	53:G:208:SER:HB3	2.45	0.43
60:N:97:LEU:HA	60:N:100:TRP:CZ2	2.54	0.43
63:Q:81:ARG:HB2	63:Q:117:GLY:CA	2.48	0.43
65:S:11:ARG:O	65:S:15:VAL:HG23	2.18	0.43
66:T:88:ARG:NH1	66:T:108:LYS:HE3	2.32	0.43
1:1:225:C:H2'	1:1:226:G:O4'	2.18	0.43
1:1:1322:A:H2'	1:1:1323:C:O4'	2.19	0.43
1:1:2161:A:H5''	5:j:7:ASN:OD1	2.19	0.43
1:1:2339:A:H2'	1:1:2340:C:C6	2.54	0.43
1:1:2807:U:H2'	1:1:2808:OMC:O2	2.18	0.43
1:1:3005:A:H2'	1:1:3006:C:C6	2.54	0.43
1:1:3038:U:H2'	1:1:3039:C:C6	2.54	0.43
9:n:91:ASN:O	9:n:148:GLU:HG2	2.18	0.43
10:o:52:GLU:OE2	10:o:184:HIS:NE2	2.51	0.43
24:5:90:ASN:O	24:5:92:ILE:HG23	2.19	0.43
45:AQ:28:LYS:HZ3	45:AQ:28:LYS:HG2	1.61	0.43
47:A:583:A:OP1	78:f:15:LYS:NZ	2.51	0.43
47:A:613:A:O2'	47:A:619:A:N1	2.47	0.43
47:A:1279:G:O2'	47:A:1306:A:N1	2.51	0.43
47:A:1719:A:H2'	47:A:1720:C:C6	2.54	0.43
74:b:24:LEU:HD22	74:b:71:LEU:HD22	1.99	0.43
76:d:18:ARG:HD2	76:d:26:THR:HG22	2.01	0.43
79:g:178:LYS:O	79:g:180:ARG:HG2	2.18	0.43
80:h:42:LEU:HD21	80:h:69:VAL:HG11	2.01	0.43
80:h:84:ALA:HA	80:h:90:LEU:HD23	2.01	0.43
1:1:92:C:C2	30:AB:55:LYS:HE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:108:A:N1	1:1:322:U:O2'	2.49	0.43
1:1:179:C:H2'	1:1:180:U:H6	1.84	0.43
1:1:1124:U:OP1	13:r:4:ARG:NH1	2.38	0.43
1:1:1795:A:H2'	1:1:1796:A:H8	1.80	0.43
1:1:2785:A:H2'	1:1:2786:G:O4'	2.19	0.43
1:1:2883:A:H4'	1:1:2884:G:C8	2.54	0.43
3:4:7:U:H2'	3:4:8:C:C6	2.53	0.43
6:k:122:TRP:CE2	6:k:127:LYS:HE3	2.54	0.43
15:t:62:THR:C	15:t:64:LYS:N	2.75	0.43
29:AA:23:VAL:HG12	29:AA:45:GLY:HA3	2.01	0.43
34:AF:77:VAL:HG13	34:AF:82:ASP:HB2	2.00	0.43
35:AG:58:GLU:HG3	35:AG:63:LYS:HE3	2.01	0.43
47:A:78:A:H2'	47:A:79:C:C6	2.54	0.43
47:A:1066:A:O2'	47:A:1068:G:N7	2.46	0.43
47:A:1105:U:H2'	47:A:1106:C:C6	2.54	0.43
47:A:1486:G:O6	47:A:1496:C:N4	2.51	0.43
47:A:1589:C:H2'	47:A:1590:U:C6	2.54	0.43
53:G:99:MET:HB2	53:G:180:ARG:CZ	2.49	0.43
53:G:121:ILE:HA	53:G:199:ILE:HD11	2.01	0.43
57:K:110:GLN:OE1	57:K:126:ARG:NH2	2.51	0.43
58:L:50:THR:HB	58:L:55:VAL:HG23	2.00	0.43
66:T:23:ASP:HB3	66:T:26:ILE:HG13	1.99	0.43
74:b:41:ILE:HG12	74:b:68:TYR:CD2	2.54	0.43
79:g:160:ARG:NH1	79:g:176:ASN:HB2	2.34	0.43
1:1:377:A:H1'	1:1:392:G:N2	2.33	0.43
1:1:1011:C:N4	1:1:1031:A:H61	2.16	0.43
1:1:1220:C:C2	1:1:1221:A:C8	3.06	0.43
1:1:2796:G:H2'	1:1:2797:C:H6	1.84	0.43
4:10:70:G:H2'	4:10:71:C:C6	2.54	0.43
16:u:20:LEU:HD21	16:u:87:TRP:CZ2	2.54	0.43
17:v:51:LEU:HD22	17:v:117:ASN:ND2	2.34	0.43
18:w:126:ARG:HG2	18:w:130:LEU:HD12	2.00	0.43
39:AK:69:HIS:O	39:AK:73:ARG:HG3	2.18	0.43
47:A:544:U:H2'	47:A:545:U:C6	2.54	0.43
47:A:553:A:H2'	47:A:554:A:C8	2.54	0.43
47:A:1188:A:C2	47:A:1543:A:C4	3.07	0.43
47:A:1626:C:H2'	47:A:1627:C:O4'	2.18	0.43
47:A:1647:A:H2'	47:A:1648:U:H6	1.83	0.43
54:H:22:HIS:HA	54:H:25:ARG:NH1	2.34	0.43
54:H:126:ASP:OD1	54:H:127:THR:N	2.52	0.43
62:P:81:THR:HG21	62:P:85:LYS:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:W:71:ARG:O	69:W:75:GLN:HG3	2.19	0.43
1:1:96:U:H2'	1:1:97:G:C8	2.54	0.42
1:1:277:G:H2'	1:1:278:U:C6	2.54	0.42
1:1:943:G:H2'	1:1:944:C:C6	2.54	0.42
1:1:1275:C:H2'	1:1:1276:C:O4'	2.19	0.42
1:1:1328:A:H2'	1:1:1329:C:C6	2.55	0.42
1:1:2262:C:N4	1:1:2286:C:OP2	2.49	0.42
1:1:2296:U:H2'	1:1:2297:U:O4'	2.19	0.42
1:1:2354:G:H2'	1:1:2355:G:C8	2.54	0.42
1:1:2485:U:H2'	1:1:2486:U:C6	2.53	0.42
1:1:3153:A:H2'	1:1:3154:A:H8	1.83	0.42
2:3:56:A:H4'	14:s:152:HIS:HB2	2.01	0.42
3:4:156:U:O2'	3:4:157:U:P	2.77	0.42
6:k:123:TYR:CZ	6:k:124:LYS:HG3	2.54	0.42
47:A:25:C:H4'	47:A:26:A:O5'	2.18	0.42
47:A:1580:A:H2'	47:A:1581:G:H8	1.84	0.42
50:D:96:VAL:HG21	50:D:203:GLU:HG3	2.00	0.42
53:G:34:GLN:HG2	64:R:56:LEU:HD11	2.01	0.42
63:Q:60:LEU:HD22	63:Q:92:SER:HB3	2.01	0.42
67:U:108:LEU:HA	67:U:111:ILE:HG22	2.00	0.42
69:W:11:LEU:HD12	69:W:12:TYR:HB3	2.01	0.42
76:d:38:ARG:O	76:d:40:ILE:HG13	2.18	0.42
80:h:123:ILE:HB	80:h:135:TRP:HB2	2.00	0.42
1:1:25:A:H2'	1:1:26:C:C6	2.52	0.42
1:1:79:G:OP1	17:v:189:HIS:NE2	2.45	0.42
1:1:673:C:O2'	1:1:677:U:OP1	2.33	0.42
1:1:783:G:H2'	1:1:784:C:C6	2.54	0.42
1:1:868:U:H2'	1:1:869:C:C6	2.54	0.42
1:1:872:A:H5''	1:1:1886:U:H5''	2.01	0.42
1:1:1909:A:N3	1:1:2098:A:H2'	2.34	0.42
1:1:2649:G:H2'	1:1:2649:G:N3	2.34	0.42
1:1:3300:A:H2'	1:1:3301:A:C8	2.53	0.42
3:4:29:U:H5''	15:t:27:ASP:HB3	2.01	0.42
15:t:2:ALA:HB3	30:AB:41:HIS:CE1	2.55	0.42
24:5:102:LYS:HD3	24:5:105:GLN:OE1	2.20	0.42
38:AJ:66:LYS:HE2	38:AJ:70:LYS:HD2	2.00	0.42
47:A:52:U:H2'	47:A:53:G:H8	1.83	0.42
47:A:125:U:OP1	54:H:201:GLN:NE2	2.29	0.42
47:A:852:G:OP2	61:O:3:ARG:NH2	2.32	0.42
47:A:1241:A:H5'	47:A:1242:U:H5	1.83	0.42
47:A:1277:G:H2'	47:A:1278:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1495:U:H2'	47:A:1496:C:C6	2.54	0.42
58:L:10:LYS:HA	58:L:13:GLN:NE2	2.34	0.42
1:1:122:A:OP1	11:p:106:LYS:NZ	2.50	0.42
1:1:630:G:H2'	1:1:631:U:C6	2.54	0.42
1:1:757:A:C2	1:1:767:A:H1'	2.54	0.42
1:1:1023:A:N6	1:1:1025:G:N3	2.67	0.42
1:1:1580:U:H2'	1:1:1581:C:H6	1.84	0.42
1:1:2201:A:H2'	1:1:2202:A:C8	2.55	0.42
3:4:104:A:C8	3:4:105:A:C8	3.07	0.42
32:AD:26:THR:OG1	32:AD:93:SER:OG	2.37	0.42
37:AI:49:LYS:HA	37:AI:49:LYS:HD3	1.93	0.42
47:A:244:G:N2	59:M:38:VAL:O	2.50	0.42
47:A:583:A:H2'	47:A:584:G:C8	2.54	0.42
48:B:84:ARG:HD3	48:B:203:PHE:O	2.18	0.42
62:P:34:ILE:HD13	62:P:71:ILE:HG13	2.01	0.42
80:h:135:TRP:C	80:h:142:MET:HE1	2.45	0.42
1:1:485:A:H3'	1:1:486:C:C5	2.55	0.42
1:1:592:U:H2'	1:1:607:G:O6	2.19	0.42
1:1:624:U:H2'	1:1:625:C:H6	1.84	0.42
1:1:1762:G:N7	21:z:46:LYS:HE2	2.34	0.42
1:1:2780:A:H61	1:1:2926:U:H5'	1.84	0.42
1:1:3061:C:H2'	1:1:3062:U:O4'	2.19	0.42
1:1:3101:A:H2'	1:1:3102:A:H5''	2.02	0.42
1:1:3284:U:O2'	1:1:3285:A:OP1	2.35	0.42
3:4:155:G:C5	3:4:156:U:C4	3.07	0.42
8:m:41:LYS:HA	8:m:41:LYS:HD3	1.86	0.42
21:z:162:ARG:NH1	47:A:799:G:N3	2.66	0.42
22:0:3:ARG:NH1	22:0:104:GLU:OE2	2.53	0.42
22:0:23:LYS:HA	22:0:23:LYS:HD3	1.81	0.42
28:9:58:VAL:HA	28:9:104:VAL:HG12	2.02	0.42
39:AK:84:LYS:HB2	39:AK:84:LYS:HE3	1.71	0.42
47:A:69:G:P	72:Z:123:ARG:HH12	2.42	0.42
47:A:94:U:H2'	47:A:95:G:O4'	2.19	0.42
47:A:1503:A:H8	68:V:57:MET:HE1	1.85	0.42
47:A:1580:A:H2'	47:A:1581:G:C8	2.54	0.42
58:L:54:TYR:CE1	58:L:75:PHE:HB2	2.55	0.42
65:S:93:LEU:HD12	65:S:99:GLN:HA	2.00	0.42
80:h:231:LEU:HD23	80:h:231:LEU:H	1.84	0.42
1:1:823:A:H5''	36:AH:14:ASN:O	2.19	0.42
1:1:1321:U:H2'	1:1:1322:A:O4'	2.20	0.42
1:1:1943:G:HO2'	1:1:1944:G:P	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2185:A:H2'	47:A:898:G:H4'	2.00	0.42
1:1:2902:A:H2'	1:1:2903:C:H6	1.84	0.42
2:3:90:A:H2'	2:3:91:G:O4'	2.19	0.42
14:s:61:ARG:NH1	46:i:34:THR:O	2.37	0.42
37:AI:62:GLN:O	37:AI:66:VAL:HG23	2.20	0.42
37:AI:70:TYR:HA	37:AI:73:LYS:HG3	2.01	0.42
47:A:147:C:H2'	47:A:148:C:C6	2.54	0.42
47:A:203:U:C2	47:A:204:A:C8	3.06	0.42
47:A:654:G:O3'	47:A:676:G:N1	2.45	0.42
47:A:1334:G:H2'	47:A:1335:U:C6	2.54	0.42
47:A:1552:C:H5''	66:T:41:ARG:HG2	2.01	0.42
47:A:1703:C:HO2'	47:A:1704:C:H6	1.67	0.42
48:B:201:LEU:O	48:B:202:TYR:HB2	2.18	0.42
54:H:136:LYS:NZ	54:H:174:LYS:O	2.44	0.42
60:N:40:GLY:O	60:N:124:LYS:HB2	2.19	0.42
61:O:100:LYS:O	61:O:103:GLU:HG2	2.19	0.42
63:Q:110:GLU:OE2	66:T:118:LYS:NZ	2.40	0.42
73:a:54:VAL:N	73:a:55:PRO:HD2	2.34	0.42
79:g:124:LYS:HD2	79:g:124:LYS:HA	1.87	0.42
1:1:243:G:H2'	1:1:244:G:C8	2.53	0.42
1:1:496:A:H4'	9:n:27:GLN:HG3	2.01	0.42
1:1:563:U:H2'	1:1:564:G:C8	2.55	0.42
1:1:1949:G:O6	1:1:2070:A:H2'	2.20	0.42
1:1:3042:A:OP1	21:z:62:ARG:NH1	2.53	0.42
5:j:107:CYS:HB2	5:j:136:ILE:HD12	2.01	0.42
33:AE:95:VAL:HG12	33:AE:97:VAL:HG13	2.01	0.42
36:AH:104:VAL:O	36:AH:108:GLN:HG2	2.20	0.42
47:A:178:A:H2'	47:A:179:A:O4'	2.19	0.42
47:A:260:U:O2'	47:A:261:C:H5'	2.20	0.42
47:A:514:G:H2'	47:A:515:U:O4'	2.19	0.42
47:A:1415:G:H2'	47:A:1416:U:O2	2.18	0.42
47:A:1425:C:H2'	47:A:1426:C:H6	1.84	0.42
57:K:65:LYS:HA	57:K:70:LEU:HD11	2.02	0.42
60:N:79:CYS:SG	60:N:88:LEU:HD21	2.60	0.42
62:P:11:VAL:HG12	62:P:13:ARG:HG3	2.00	0.42
76:d:9:LEU:HD23	76:d:53:ILE:HG22	2.02	0.42
80:h:62:PHE:HB3	80:h:93:TRP:CE3	2.55	0.42
1:1:147:G:OP2	17:v:4:TYR:OH	2.20	0.42
1:1:629:A:H2'	1:1:630:G:C8	2.55	0.42
1:1:755:U:H2'	1:1:756:G:O4'	2.18	0.42
1:1:2086:C:H1'	1:1:3309:A:H8	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2695:U:H2'	1:1:2696:U:C6	2.54	0.42
3:4:36:G:C5	37:AI:86:ARG:HD3	2.55	0.42
14:s:110:ILE:HG21	14:s:116:TYR:HD2	1.85	0.42
17:v:45:PRO:O	17:v:49:ARG:HG3	2.20	0.42
22:0:8:GLN:HB2	22:0:64:ILE:HD11	2.02	0.42
46:i:41:ALA:C	46:i:43:PRO:HD3	2.45	0.42
47:A:872:A:H2'	47:A:873:U:H6	1.84	0.42
47:A:1213:G:C6	60:N:66:VAL:HG23	2.54	0.42
51:E:92:VAL:HG11	51:E:101:VAL:HG21	2.01	0.42
53:G:108:LEU:HD21	64:R:43:LEU:HD11	2.01	0.42
74:b:100:ARG:HG2	74:b:101:LYS:HD3	2.02	0.42
1:1:71:C:H4'	15:t:66:ASN:HD21	1.85	0.42
1:1:154:G:H5''	1:1:155:A:H2'	2.02	0.42
1:1:533:G:H2'	1:1:534:G:O4'	2.20	0.42
1:1:1469:G:OP2	21:z:8:LYS:NZ	2.36	0.42
1:1:1714:G:H2'	1:1:1715:G:C8	2.54	0.42
1:1:2658:A:H2'	1:1:2659:G:O4'	2.20	0.42
1:1:3082:C:H2'	1:1:3083:U:C6	2.55	0.42
7:l:32:ARG:HG3	7:l:121:TYR:CE2	2.54	0.42
18:w:62:ALA:HA	18:w:71:PRO:HD2	2.01	0.42
40:AL:27:VAL:HG13	40:AL:39:LYS:HG3	2.00	0.42
47:A:119:A:H1'	47:A:395:A:C8	2.54	0.42
47:A:820:U:O2'	47:A:821:U:OP1	2.33	0.42
47:A:871:U:H2'	47:A:872:A:H8	1.84	0.42
47:A:886:G:H2'	47:A:887:G:C8	2.55	0.42
47:A:1148:A:H2'	47:A:1149:G:O4'	2.19	0.42
47:A:1167:U:O2'	47:A:1169:A:N7	2.45	0.42
47:A:1377:A:H2'	47:A:1378:U:C6	2.55	0.42
48:B:50:ILE:HA	48:B:53:THR:HB	2.02	0.42
53:G:146:SER:OG	53:G:157:ARG:NH2	2.53	0.42
68:V:101:ARG:O	68:V:105:ILE:HG12	2.19	0.42
1:1:88:G:H21	1:1:281:G:H4'	1.84	0.42
1:1:208:A:H4'	1:1:210:A:C8	2.55	0.42
1:1:777:G:OP1	20:y:151:ARG:HD2	2.20	0.42
1:1:1231:U:H1'	1:1:1233:G:OP2	2.20	0.42
1:1:1642:G:H1'	1:1:1805:A:N6	2.35	0.42
1:1:2397:A:H2'	1:1:2398:C:C6	2.54	0.42
1:1:2718:A:H2'	1:1:2719:A:O4'	2.20	0.42
1:1:2790:U:C5'	31:AC:1:MET:HA	2.49	0.42
1:1:3240:U:H5''	35:AG:68:TRP:HZ2	1.85	0.42
3:4:142:C:H2'	3:4:143:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:k:159:ARG:HG2	6:k:182:GLN:HA	2.01	0.42
12:q:57:VAL:HG13	12:q:64:HIS:CE1	2.54	0.42
40:AL:11:PHE:CZ	40:AL:45:VAL:HG23	2.55	0.42
40:AL:32:ASN:C	40:AL:34:ASN:H	2.27	0.42
46:i:42:ALA:N	46:i:43:PRO:HD3	2.35	0.42
47:A:189:G:H1'	47:A:193:G:C2	2.55	0.42
47:A:740:A:O2'	47:A:741:A:OP1	2.31	0.42
47:A:1354:U:H2'	47:A:1355:A:C8	2.55	0.42
48:B:79:ARG:O	48:B:83:GLN:HG3	2.20	0.42
52:F:104:ASP:HB3	52:F:110:ALA:HB2	2.02	0.42
53:G:116:HIS:O	53:G:120:ILE:HG13	2.20	0.42
60:N:54:LYS:HB2	60:N:56:GLU:HG2	2.00	0.42
80:h:50:GLY:H	80:h:55:TYR:HA	1.84	0.42
1:1:1099:A:N6	1:1:1359:A:H1'	2.34	0.42
1:1:1591:U:C2	1:1:1592:C:C5	3.08	0.42
1:1:1611:U:H2'	1:1:1612:U:H6	1.83	0.42
1:1:1824:A:H2'	1:1:1825:A:C8	2.54	0.42
1:1:2330:A:H5''	19:x:83:TRP:O	2.20	0.42
1:1:3079:U:H2'	1:1:3080:G:C8	2.54	0.42
1:1:3219:G:H2'	1:1:3220:C:C6	2.54	0.42
1:1:3247:A:H2'	1:1:3248:U:C6	2.55	0.42
5:j:150:LEU:HD11	5:j:156:LYS:HD2	2.02	0.42
11:p:144:ILE:HG23	11:p:176:VAL:HG21	2.02	0.42
44:AP:28:TYR:HB3	44:AP:69:VAL:HB	2.01	0.42
47:A:97:C:H2'	47:A:98:U:C6	2.55	0.42
47:A:857:G:H2'	47:A:858:U:O4'	2.20	0.42
47:A:1215:A:H2	47:A:1243:U:C2	2.38	0.42
47:A:1623:C:O2	47:A:1752:A:N6	2.53	0.42
52:F:95:THR:HG22	72:Z:16:PRO:HG2	2.02	0.42
58:L:44:LYS:HD3	58:L:44:LYS:HA	1.91	0.42
60:N:55:ARG:HH11	60:N:82:PRO:HB3	1.85	0.42
61:O:33:VAL:HG21	61:O:66:VAL:HG11	2.01	0.42
76:d:53:ILE:HG22	76:d:53:ILE:O	2.19	0.42
1:1:163:A:H2'	1:1:164:U:O4'	2.19	0.41
1:1:364:G:OP1	7:l:61:THR:HG23	2.20	0.41
1:1:1065:C:H2'	1:1:1066:U:C6	2.55	0.41
1:1:1308:C:H2'	1:1:1309:G:O4'	2.20	0.41
1:1:1606:G:H2'	1:1:1607:G:O4'	2.20	0.41
1:1:1841:G:H5''	1:1:1842:C:H5'	2.03	0.41
1:1:1923:G:C8	45:AQ:16:VAL:HG12	2.55	0.41
1:1:2077:A:O2'	1:1:2078:A:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2855:U:H2'	1:1:2856:C:C6	2.55	0.41
1:1:3090:C:H2'	1:1:3091:U:O4'	2.20	0.41
3:4:85:G:H4'	3:4:86:U:OP1	2.20	0.41
6:k:67:MET:SD	6:k:70:ARG:HD2	2.59	0.41
10:o:233:ILE:HD12	10:o:233:ILE:HA	1.92	0.41
21:z:172:ARG:HH21	47:A:837:C:P	2.42	0.41
38:AJ:54:ARG:O	38:AJ:58:GLU:HG2	2.20	0.41
47:A:280:C:H2'	47:A:281:U:O4'	2.20	0.41
47:A:504:A:O2'	47:A:505:U:P	2.78	0.41
47:A:1529:G:H5''	67:U:87:GLY:O	2.20	0.41
50:D:44:LYS:HA	50:D:44:LYS:HD3	1.70	0.41
51:E:65:ARG:HD3	58:L:91:ARG:NE	2.35	0.41
53:G:58:LEU:HD22	53:G:168:VAL:HG23	2.02	0.41
53:G:102:ARG:HG3	53:G:103:ASN:OD1	2.19	0.41
53:G:122:HIS:HB2	53:G:129:PRO:HG3	2.02	0.41
65:S:75:GLU:O	65:S:79:GLU:N	2.49	0.41
80:h:134:VAL:HG23	80:h:142:MET:HB2	2.02	0.41
1:1:234:A:H2'	1:1:235:G:O4'	2.21	0.41
1:1:756:G:H1'	1:1:767:A:N6	2.35	0.41
1:1:803:A:H61	1:1:930:G:H22	1.68	0.41
1:1:1184:U:OP1	1:1:1206:U:O2'	2.21	0.41
1:1:1330:U:H2'	1:1:1331:U:C6	2.55	0.41
1:1:1344:U:OP1	20:y:39:ARG:NH2	2.53	0.41
1:1:1434:U:H2'	1:1:1435:U:C6	2.55	0.41
1:1:2546:U:H5'	1:1:2547:G:O4'	2.20	0.41
10:o:71:ASN:O	23:2:143:THR:OG1	2.29	0.41
14:s:13:ARG:HH12	14:s:15:GLU:CD	2.29	0.41
16:u:65:LEU:HD12	16:u:77:LYS:HD2	2.02	0.41
39:AK:21:ARG:HD2	39:AK:37:CYS:SG	2.60	0.41
43:AO:14:LYS:HB3	43:AO:14:LYS:HE2	1.83	0.41
47:A:449:G:H2'	47:A:451:C:C5	2.55	0.41
47:A:642:C:H2'	47:A:643:U:C6	2.55	0.41
47:A:740:A:H2'	47:A:741:A:H8	1.84	0.41
48:B:3:LEU:HD12	48:B:3:LEU:HA	1.85	0.41
52:F:181:VAL:CG1	52:F:225:VAL:HG13	2.50	0.41
54:H:2:LYS:HE3	54:H:2:LYS:HB2	1.84	0.41
58:L:52:LYS:HG3	58:L:54:TYR:HD2	1.85	0.41
58:L:74:GLU:HA	58:L:77:ARG:HB2	2.02	0.41
72:Z:12:VAL:HG22	72:Z:23:PHE:HB3	2.01	0.41
76:d:34:GLU:OE1	76:d:34:GLU:N	2.41	0.41
1:1:345:G:O2'	3:4:25:G:N3	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1139:A:H5'	1:1:1364:U:H1'	2.03	0.41
1:1:1459:U:H2'	1:1:1460:G:O4'	2.20	0.41
1:1:1468:U:H5'	21:z:4:LEU:HB2	2.02	0.41
1:1:2367:C:H2'	1:1:2368:A:C8	2.54	0.41
1:1:2623:G:H5''	1:1:2624:U:O4'	2.20	0.41
3:4:5:U:H2'	3:4:6:U:H6	1.85	0.41
3:4:26:U:H2'	3:4:27:U:C6	2.54	0.41
7:l:287:VAL:HG11	20:y:31[B]:LYS:HD3	2.02	0.41
7:l:326:LEU:O	10:o:39:ARG:NH2	2.50	0.41
8:m:38:THR:O	8:m:48:LYS:NZ	2.49	0.41
15:t:63:VAL:HA	15:t:66:ASN:ND2	2.35	0.41
20:y:176:ARG:N	30:AB:51:GLY:HA2	2.35	0.41
34:AF:33:TRP:HH2	34:AF:53:GLN:HG2	1.84	0.41
47:A:876:A:H2'	47:A:877:G:C8	2.54	0.41
47:A:1503:A:O2'	47:A:1504:U:H5'	2.20	0.41
47:A:1539:U:O2'	47:A:1584:A:N3	2.47	0.41
47:A:1610:C:H2'	47:A:1611:C:C6	2.55	0.41
50:D:148:SER:OG	50:D:149:LEU:N	2.54	0.41
62:P:12:ALA:HB3	62:P:76:ILE:HD13	2.00	0.41
63:Q:52:LYS:HB2	63:Q:53:PRO:HD3	2.01	0.41
67:U:86:ARG:NH1	67:U:90:PRO:O	2.39	0.41
1:1:648:C:H2'	1:1:649:G:C8	2.56	0.41
1:1:1202:G:OP1	13:r:157:TYR:OH	2.34	0.41
1:1:2128:G:O2'	1:1:2167:U:OP1	2.32	0.41
1:1:3110:U:OP2	6:k:30:LYS:HG3	2.20	0.41
1:1:3216:U:H2'	1:1:3217:G:C8	2.55	0.41
2:3:47:C:OP2	8:m:158:ARG:HD3	2.20	0.41
8:m:179:ARG:HA	8:m:179:ARG:HD3	1.82	0.41
15:t:192:LYS:NZ	15:t:196:GLU:OE2	2.51	0.41
19:x:4:TYR:OH	19:x:18:ARG:HG3	2.21	0.41
21:z:134:HIS:HE1	21:z:136:ARG:HB3	1.83	0.41
27:8:46:TYR:CD1	37:AI:75:TYR:HB3	2.55	0.41
27:8:142:ILE:HD12	27:8:142:ILE:HA	1.90	0.41
36:AH:58:ARG:CD	36:AH:59:PRO:HD2	2.35	0.41
36:AH:106[A]:LYS:HB3	36:AH:106[A]:LYS:HE2	1.86	0.41
37:AI:114:ARG:HD3	37:AI:114:ARG:HA	1.84	0.41
47:A:811:U:C2	47:A:831:G:O6	2.73	0.41
47:A:1157:G:H2'	47:A:1158:C:C6	2.55	0.41
47:A:1656:U:H2'	47:A:1657:G:O4'	2.20	0.41
47:A:1741:A:H2'	47:A:1742:A:C8	2.54	0.41
53:G:146:SER:OG	53:G:146:SER:O	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:K:88:GLU:OE1	57:K:88:GLU:N	2.53	0.41
58:L:59:PHE:CZ	58:L:62:GLN:HA	2.55	0.41
73:a:36:ALA:HB1	73:a:38:HIS:CE1	2.55	0.41
1:1:827:G:O2'	1:1:1860:A:N3	2.42	0.41
1:1:1250:C:H41	1:1:1259:A:P	2.44	0.41
1:1:1301:U:C2	6:k:257:PRO:HG3	2.55	0.41
1:1:1502:A:H1'	1:1:1844:G:O6	2.21	0.41
1:1:1684:U:H2'	1:1:1685:U:C6	2.56	0.41
1:1:2394:U:H2'	1:1:2395:U:C6	2.55	0.41
6:k:292:ALA:HB1	6:k:295:ALA:HB3	2.01	0.41
21:z:162:ARG:HA	21:z:165:ARG:HD3	2.02	0.41
24:5:13:LYS:HD2	24:5:15:PHE:CE1	2.55	0.41
46:i:58:THR:HG23	63:Q:121:ILE:HG22	2.01	0.41
47:A:217:A:P	47:A:217:A:O4'	2.79	0.41
47:A:577:A:H61	51:E:144:ARG:H	1.69	0.41
47:A:779:U:N3	47:A:780:A:N7	2.69	0.41
47:A:1579:A:HO2'	47:A:1580:A:P	2.42	0.41
56:J:34:ALA:HB2	56:J:56:ARG:HD2	2.02	0.41
59:M:66:ILE:HG21	59:M:140:LEU:HD11	2.02	0.41
65:S:59:LYS:HE3	65:S:59:LYS:HB2	1.98	0.41
72:Z:63:GLN:CD	72:Z:68:LYS:HD3	2.46	0.41
73:a:54:VAL:HA	73:a:57:TYR:CD2	2.55	0.41
73:a:89:ILE:CG2	73:a:101:TYR:HB3	2.50	0.41
1:1:87:A:H2'	1:1:88:G:O4'	2.20	0.41
1:1:482:U:H2'	1:1:483:U:C4	2.54	0.41
1:1:1124:U:H2'	1:1:1125:A:O4'	2.20	0.41
1:1:1209:G:H5'	22:0:137:ARG:HH21	1.84	0.41
1:1:2854:U:H2'	1:1:2855:U:C6	2.55	0.41
1:1:2862:A:O2'	1:1:2905:A:N3	2.46	0.41
1:1:3175:A:OP1	16:u:102:ARG:NH1	2.51	0.41
5:j:101:ILE:HG13	5:j:165:VAL:HG22	2.03	0.41
7:l:303:ALA:HB2	20:y:39:ARG:HH12	1.86	0.41
22:0:46:GLN:HG2	22:0:51:VAL:O	2.19	0.41
28:9:11:SER:HB3	28:9:14:LYS:HB2	2.03	0.41
47:A:79:C:OP1	54:H:172:ALA:HB3	2.21	0.41
47:A:577:A:C6	51:E:144:ARG:HG2	2.55	0.41
47:A:1588:G:C2	67:U:88:PHE:HB3	2.55	0.41
51:E:139:ILE:HG12	51:E:185:ILE:HG22	2.01	0.41
55:I:67:ARG:HA	55:I:67:ARG:HD3	1.86	0.41
65:S:71:PHE:CE2	65:S:73:LEU:HB3	2.55	0.41
1:1:406:G:H1'	3:4:16:G:H22	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:851:U:H5''	21:z:95:TRP:CG	2.56	0.41
1:1:1135:G:O6	31:AC:10:HIS:NE2	2.54	0.41
1:1:2053:C:H2'	1:1:2054:C:C2	2.55	0.41
1:1:2061:G:H2'	1:1:2062:G:N9	2.35	0.41
1:1:3133:G:H2'	1:1:3134:C:O4'	2.20	0.41
6:k:106:TRP:HB2	6:k:133:TYR:CE1	2.56	0.41
13:r:73:ASN:O	13:r:77:THR:HG23	2.20	0.41
30:AB:24:LYS:O	30:AB:25:HIS:C	2.63	0.41
34:AF:33:TRP:CH2	34:AF:53:GLN:HG2	2.56	0.41
35:AG:53:TYR:CZ	35:AG:65:ARG:HB2	2.56	0.41
47:A:512:G:N3	47:A:513:A:C8	2.88	0.41
47:A:1323:C:H1'	47:A:1396:A:C4	2.56	0.41
47:A:1602:C:OP1	53:G:81:ARG:NH2	2.46	0.41
48:B:84:ARG:NH1	48:B:205:ARG:HG3	2.36	0.41
49:C:83:LYS:NZ	49:C:105:PHE:O	2.54	0.41
55:I:11:THR:HG23	55:I:14:GLU:H	1.85	0.41
58:L:3:ILE:HB	58:L:8:ARG:NH1	2.35	0.41
67:U:124:ILE:HD11	67:U:132:LEU:HD12	2.01	0.41
68:V:98:THR:O	68:V:102:ILE:HG13	2.20	0.41
1:1:1260:G:O5'	1:1:1260:G:C8	2.70	0.41
1:1:1297:A:H4'	1:1:1298:A:O5'	2.21	0.41
1:1:1329:C:C2	1:1:1330:U:C5	3.09	0.41
1:1:1561:U:H2'	1:1:1562:G:H8	1.82	0.41
1:1:2134:U:P	5:j:241:ARG:HH22	2.42	0.41
1:1:3196:U:H2'	1:1:3197:G:H8	1.85	0.41
11:p:229:GLU:OE2	11:p:232:LYS:NZ	2.42	0.41
17:v:27:CYS:HB2	17:v:122:ASN:ND2	2.35	0.41
37:AI:34:GLN:O	37:AI:38:ARG:HG2	2.21	0.41
40:AL:17:ARG:NE	40:AL:19:ASP:OD2	2.48	0.41
40:AL:30[B]:LYS:HB3	40:AL:30[B]:LYS:HE3	1.75	0.41
47:A:189:G:H1'	47:A:193:G:N2	2.36	0.41
47:A:809:G:H2'	47:A:810:U:H6	1.85	0.41
47:A:907:G:O2'	47:A:908:A:H5'	2.21	0.41
47:A:1485:G:H2'	47:A:1486:G:H8	1.86	0.41
47:A:1669:U:O2'	47:A:1670:U:O5'	2.39	0.41
53:G:164:PRO:HD3	76:d:54:LEU:HB3	2.03	0.41
55:I:25:GLU:HG3	55:I:35:ARG:HH12	1.85	0.41
80:h:97:THR:C	80:h:99:GLU:H	2.29	0.41
1:1:63:G:OP2	17:v:169:LYS:NZ	2.43	0.41
1:1:165:C:C2	1:1:166:U:C5	3.09	0.41
1:1:171:G:H2'	1:1:172:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:291:C:H2'	1:1:292:U:C6	2.56	0.41
1:1:393:U:H2'	1:1:394:G:O4'	2.19	0.41
1:1:501:U:H2'	1:1:502:U:O4'	2.21	0.41
1:1:602:A:H2'	1:1:603:C:C6	2.56	0.41
1:1:707:A:H2'	1:1:708:A:O4'	2.21	0.41
1:1:730:A:H8	1:1:733:A:N6	2.13	0.41
1:1:1093:G:H2'	1:1:1093:G:N3	2.36	0.41
1:1:1149:A:O2'	1:1:1150:A:H5'	2.20	0.41
1:1:1287:A:H2'	1:1:1288:C:O4'	2.21	0.41
1:1:1516:G:H2'	1:1:1517:G:O4'	2.21	0.41
1:1:1921:U:O2'	1:1:1923:G:N7	2.53	0.41
1:1:2239:G:H21	1:1:2240:A:N6	2.18	0.41
1:1:2331:G:H5''	19:x:86:LYS:HB2	2.02	0.41
1:1:2407:G:H2'	1:1:2408:A:C8	2.56	0.41
1:1:2516:U:O2'	1:1:2520:A:N1	2.52	0.41
1:1:2584:U:H2'	1:1:2585:U:O4'	2.21	0.41
1:1:3038:U:H2'	1:1:3039:C:H6	1.85	0.41
1:1:3344:U:H4'	6:k:315:GLY:HA2	2.03	0.41
6:k:67:MET:HE2	25:6:88:ARG:HB2	2.02	0.41
6:k:83:PRO:HB2	6:k:202:GLU:HB3	2.03	0.41
7:l:4:ARG:HH12	7:l:25:ALA:HA	1.85	0.41
7:l:17:GLY:O	7:l:18:SER:OG	2.33	0.41
7:l:300:VAL:HB	20:y:39:ARG:CG	2.50	0.41
11:p:125:ASP:OD1	11:p:126:VAL:N	2.54	0.41
16:u:17:ARG:O	16:u:28:THR:HA	2.21	0.41
20:y:147:ARG:HB3	20:y:150:VAL:HG23	2.03	0.41
23:2:39:ILE:HG12	23:2:63:ILE:HD13	2.03	0.41
26:7:18:GLY:HA3	26:7:31:PHE:O	2.21	0.41
27:8:106:ASP:HB2	27:8:130:TYR:HE2	1.86	0.41
28:9:69:LYS:HE2	28:9:69:LYS:HB3	1.76	0.41
29:AA:50:PRO:HD3	29:AA:68:VAL:HG22	2.02	0.41
34:AF:98:ALA:HB3	34:AF:101:VAL:HG23	2.01	0.41
46:i:58:THR:HG22	63:Q:103:ASN:ND2	2.35	0.41
47:A:167:A:OP2	47:A:167:A:H8	2.04	0.41
47:A:188:U:H2'	47:A:189:G:C8	2.55	0.41
47:A:481:A:H2	47:A:504:A:C6	2.39	0.41
47:A:806:A:OP1	47:A:806:A:H3'	2.21	0.41
47:A:1500:G:H1'	47:A:1505:C:O2	2.21	0.41
47:A:1555:C:H4'	47:A:1556:A:O5'	2.21	0.41
47:A:1579:A:O2'	47:A:1580:A:OP1	2.35	0.41
47:A:1595:U:O3'	64:R:72:GLY:HA3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:A:1636:C:H2'	47:A:1637:U:C6	2.56	0.41
49:C:62:LYS:HA	49:C:88:VAL:HG13	2.03	0.41
50:D:138:TYR:CD1	50:D:142:ASN:HA	2.56	0.41
52:F:48:LEU:HD11	52:F:70:VAL:HG21	2.03	0.41
56:J:39:GLY:O	56:J:61:GLU:HG3	2.21	0.41
56:J:107:THR:OG1	56:J:108:PRO:HD3	2.21	0.41
63:Q:121:ILE:HD11	63:Q:123:TYR:CZ	2.56	0.41
71:Y:71:CYS:HA	71:Y:87:VAL:HG22	2.03	0.41
73:a:54:VAL:HG12	73:a:89:ILE:HD11	2.03	0.41
80:h:40:LYS:HG2	80:h:67:HIS:O	2.21	0.41
1:1:15:A:H2'	1:1:16:G:O4'	2.21	0.41
1:1:3084:G:O6	1:1:3092:C:H5''	2.21	0.41
1:1:3111:A:H2'	1:1:3112:G:O4'	2.21	0.41
1:1:3264:C:H2'	1:1:3265:U:C6	2.56	0.41
3:4:71:A:N1	3:4:82:U:O2'	2.45	0.41
8:m:94:ASN:ND2	8:m:204:VAL:HG21	2.35	0.41
11:p:162:GLU:OE2	17:v:22:LEU:HD13	2.21	0.41
12:q:90:MET:HE3	12:q:181:VAL:HG23	2.03	0.41
13:r:41:ALA:HB3	13:r:139:ARG:HH12	1.86	0.41
22:0:73:LYS:HD2	22:0:75:PHE:CZ	2.56	0.41
32:AD:27:LEU:HD11	32:AD:85:LYS:HE3	2.03	0.41
41:AM:41:ARG:HD2	41:AM:41:ARG:HA	1.80	0.41
46:i:47:ASP:OD2	46:i:50:LYS:NZ	2.54	0.41
47:A:103:A:H4'	47:A:105:A:N7	2.35	0.41
47:A:260:U:C2'	47:A:261:C:H5'	2.51	0.41
47:A:578:A:O2'	47:A:580:U:OP1	2.38	0.41
47:A:644:U:H2'	47:A:645:G:C8	2.56	0.41
47:A:1168:A:O2'	47:A:1169:A:OP1	2.35	0.41
47:A:1535:G:O2'	66:T:89:GLN:NE2	2.54	0.41
54:H:88:ARG:HG3	54:H:91:GLU:HB2	2.03	0.41
54:H:159:ARG:HB3	54:H:172:ALA:HB2	2.02	0.41
55:I:43:LYS:HB3	55:I:57:PHE:HE2	1.86	0.41
55:I:137:ARG:NH2	70:X:49:GLU:OE1	2.45	0.41
1:1:293:C:H2'	1:1:294:U:O4'	2.21	0.40
1:1:1464:A:N1	1:1:1876:U:O2'	2.35	0.40
1:1:1620:G:O2'	1:1:1639:A:N1	2.50	0.40
1:1:1705:C:H2'	1:1:1706:C:C6	2.55	0.40
1:1:2661:A:N3	1:1:2661:A:H2'	2.36	0.40
8:m:40:HIS:CE1	23:2:69:LYS:HA	2.55	0.40
15:t:194:GLU:O	15:t:198:GLU:CB	2.69	0.40
24:5:56:ILE:HG13	24:5:66:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:8:84:PHE:HD2	27:8:124:ILE:HD12	1.86	0.40
31:AC:56:LYS:O	31:AC:60:GLU:HG2	2.21	0.40
44:AP:10:THR:O	44:AP:20:HIS:HA	2.21	0.40
47:A:278:U:H4'	47:A:279:G:O5'	2.20	0.40
47:A:1151:A:H2'	47:A:1152:G:O4'	2.21	0.40
47:A:1301:G:O2'	47:A:1387:A:O2'	2.34	0.40
47:A:1508:G:O2'	47:A:1510:G:OP2	2.33	0.40
47:A:1669:U:O2'	47:A:1670:U:H6	2.03	0.40
60:N:55:ARG:NH1	60:N:82:PRO:HB3	2.36	0.40
62:P:119:IAS:OD1	62:P:119:IAS:N	2.55	0.40
64:R:30:ILE:CG1	64:R:35:ILE:HG22	2.48	0.40
64:R:72:GLY:H	64:R:75:SER:HB3	1.86	0.40
66:T:114:GLU:O	66:T:118:LYS:N	2.35	0.40
80:h:42:LEU:HD11	80:h:83:SER:HB3	2.03	0.40
80:h:180:LEU:HD23	80:h:180:LEU:HA	1.89	0.40
1:1:1576:A:O5'	1:1:1576:A:H8	2.05	0.40
1:1:3322:U:H2'	1:1:3323:U:C6	2.56	0.40
6:k:260:VAL:HG11	6:k:266:ARG:HH11	1.86	0.40
7:l:35:LEU:HD13	7:l:121:TYR:CE2	2.55	0.40
11:p:147:LYS:HG3	11:p:174:MET:HE3	2.03	0.40
47:A:30:G:H4'	71:Y:131:SER:HB2	2.04	0.40
47:A:98:U:H2'	47:A:99:C:C6	2.56	0.40
47:A:800:G:C2	47:A:801:A:C8	3.08	0.40
47:A:830:G:H2'	47:A:831:G:O4'	2.21	0.40
47:A:1193:A:H4'	47:A:1255:G:P	2.61	0.40
47:A:1378:U:H2'	47:A:1379:C:C6	2.57	0.40
54:H:48:TYR:CD2	54:H:117:GLY:HA3	2.56	0.40
56:J:70:GLU:HB3	56:J:112:TRP:CH2	2.56	0.40
57:K:106:GLU:O	57:K:112:GLN:NE2	2.48	0.40
64:R:46:LYS:HD2	64:R:46:LYS:HA	1.87	0.40
80:h:123:ILE:N	80:h:135:TRP:O	2.48	0.40
1:1:150:A:H4'	37:AI:102:GLU:OE1	2.22	0.40
1:1:1313:A:O2'	1:1:1314:A:H3'	2.21	0.40
1:1:1434:U:H4'	7:l:89:ALA:HB3	2.03	0.40
1:1:1601:A:O2'	1:1:1603:U:OP2	2.33	0.40
1:1:1612:U:H2'	1:1:1613:G:C8	2.56	0.40
1:1:1967:U:H3'	1:1:1968:A:C8	2.57	0.40
1:1:2386:U:H5'	31:AC:1:MET:SD	2.61	0.40
1:1:2857:C:O2'	1:1:2858:U:H5'	2.20	0.40
1:1:3233:A:H5''	9:n:45:ARG:NH1	2.35	0.40
1:1:3323:U:H2'	1:1:3324:A:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:l:17:GLY:C	7:l:19:SER:H	2.29	0.40
16:u:14:GLU:HB3	22:0:149:LYS:HG2	2.03	0.40
27:8:105:VAL:HG23	27:8:130:TYR:CG	2.56	0.40
30:AB:70:ARG:HD2	30:AB:129:PHE:CD2	2.57	0.40
38:AJ:98:ARG:HD3	38:AJ:98:ARG:H	1.87	0.40
47:A:112:A:O2'	47:A:113:U:H5'	2.22	0.40
47:A:512:G:O2'	47:A:513:A:H8	2.04	0.40
47:A:649:G:O6	47:A:682:A:N6	2.55	0.40
47:A:1219:A:H5''	47:A:1230:G:H2'	2.02	0.40
47:A:1527:G:OP2	66:T:40:ARG:NH2	2.54	0.40
58:L:7:ASP:HA	58:L:10:LYS:NZ	2.36	0.40
63:Q:30:THR:O	63:Q:34:THR:HG23	2.22	0.40
70:X:51:GLU:O	70:X:61:ILE:HA	2.21	0.40
79:g:156:VAL:HG22	79:g:158:ARG:HG2	2.04	0.40
79:g:177:MET:SD	79:g:180:ARG:NE	2.94	0.40
80:h:299:PHE:HD1	80:h:309:VAL:HG22	1.85	0.40
1:1:829:G:OP1	21:z:86:ASP:HB3	2.22	0.40
1:1:1309:G:O2'	1:1:1314:A:N1	2.41	0.40
1:1:2738:U:H2'	1:1:2739:U:C6	2.57	0.40
1:1:3162:U:N3	1:1:3165:U:O4	2.54	0.40
1:1:3197:G:H2'	1:1:3198:C:C6	2.56	0.40
5:j:68:LYS:HE3	5:j:68:LYS:HB2	1.98	0.40
28:9:106:ILE:HG21	28:9:109:LEU:HD23	2.03	0.40
30:AB:19:LYS:HB3	30:AB:25:HIS:HB2	2.02	0.40
47:A:655:U:P	47:A:676:G:H1	2.44	0.40
47:A:1165:C:O2'	63:Q:128:HIS:ND1	2.41	0.40
47:A:1204:A:N3	58:L:51:SER:OG	2.52	0.40
47:A:1238:U:H2'	47:A:1239:U:H6	1.85	0.40
47:A:1255:G:H4'	79:g:122:ARG:HH12	1.86	0.40
47:A:1337:C:H2'	47:A:1338:U:O4'	2.22	0.40
48:B:33:ASN:HB3	48:B:149:MET:SD	2.62	0.40
51:E:8:LYS:HD3	51:E:8:LYS:HA	1.80	0.40
52:F:65:MET:HE1	52:F:79:ASP:O	2.22	0.40
65:S:89:SER:O	65:S:91:LEU:N	2.54	0.40
66:T:87:ASN:HB2	66:T:99:HIS:CE1	2.57	0.40
68:V:64:ILE:HD12	77:e:52:PHE:CE2	2.56	0.40
69:W:55:LEU:HD11	69:W:69:LEU:CD2	2.50	0.40
1:1:671:U:H2'	1:1:672:G:H8	1.85	0.40
1:1:1537:G:H1'	1:1:1553:A:C5	2.57	0.40
1:1:2655:U:H2'	1:1:2656:C:H6	1.83	0.40
1:1:3013:U:H2'	1:1:3014:U:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:3264:C:H2'	1:l:3265:U:H6	1.87	0.40
4:10:71:C:H2'	4:10:72:U:H6	1.87	0.40
7:l:258:SER:O	7:l:262:VAL:HG23	2.22	0.40
13:r:19:LYS:HG2	13:r:26:VAL:HG21	2.02	0.40
14:s:94[B]:LYS:HE3	14:s:94[B]:LYS:HB3	1.59	0.40
23:2:56:TYR:CZ	23:2:78:LYS:HG3	2.57	0.40
29:AA:103:GLU:HG3	29:AA:106:GLN:OE1	2.21	0.40
47:A:326:A:H2'	47:A:327:G:O4'	2.21	0.40
47:A:908:A:H2'	47:A:909:A:C8	2.56	0.40
47:A:1772:U:P	62:P:128:ARG:HH22	2.45	0.40
48:B:84:ARG:NH1	48:B:203:PHE:O	2.51	0.40
48:B:88:LYS:HD2	48:B:201:LEU:HD11	2.04	0.40
51:E:194:ALA:O	51:E:201:ARG:NH2	2.55	0.40
53:G:225:ARG:HD2	76:d:58:GLU:HG2	2.03	0.40
56:J:87:ASN:HB3	56:J:90:LEU:HG	2.03	0.40
58:L:6:GLU:OE1	58:L:10:LYS:NZ	2.54	0.40
74:b:15:ARG:CZ	74:b:15:ARG:HB2	2.52	0.40
74:b:88:SER:O	74:b:92:ARG:HG3	2.22	0.40
80:h:152:VAL:HA	80:h:170:SER:HA	2.03	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%)	240 (97%)	8 (3%)	0	100	100
6	k	385/389 (99%)	373 (97%)	12 (3%)	0	100	100
7	l	359/363 (99%)	349 (97%)	10 (3%)	0	100	100
8	m	290/298 (97%)	279 (96%)	11 (4%)	0	100	100
9	n	152/176 (86%)	150 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	o	233/241 (97%)	226 (97%)	7 (3%)	0	100	100
11	p	236/262 (90%)	231 (98%)	5 (2%)	0	100	100
12	q	188/191 (98%)	183 (97%)	5 (3%)	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	198/202 (98%)	194 (98%)	3 (2%)	1 (0%)	24	52
16	u	128/131 (98%)	125 (98%)	3 (2%)	0	100	100
17	v	201/204 (98%)	198 (98%)	3 (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
23	2	159/160 (99%)	157 (99%)	2 (1%)	0	100	100
24	5	103/124 (83%)	97 (94%)	5 (5%)	1 (1%)	12	35
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	124/127 (98%)	123 (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	62/63 (98%)	61 (98%)	1 (2%)	0	100	100
32	AD	94/106 (89%)	93 (99%)	1 (1%)	0	100	100
33	AE	107/112 (96%)	106 (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	97/99 (98%)	96 (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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	22/25 (88%)	22 (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
46	i	109/267 (41%)	102 (94%)	7 (6%)	0	100	100
48	B	206/261 (79%)	201 (98%)	5 (2%)	0	100	100
49	C	212/256 (83%)	207 (98%)	5 (2%)	0	100	100
50	D	214/249 (86%)	209 (98%)	5 (2%)	0	100	100
51	E	221/251 (88%)	214 (97%)	7 (3%)	0	100	100
52	F	258/262 (98%)	254 (98%)	4 (2%)	0	100	100
53	G	204/225 (91%)	197 (97%)	7 (3%)	0	100	100
54	H	224/236 (95%)	221 (99%)	3 (1%)	0	100	100
55	I	180/186 (97%)	174 (97%)	6 (3%)	0	100	100
56	J	201/206 (98%)	200 (100%)	1 (0%)	0	100	100
57	K	176/189 (93%)	175 (99%)	1 (1%)	0	100	100
58	L	91/118 (77%)	84 (92%)	6 (7%)	1 (1%)	11	32
59	M	139/155 (90%)	136 (98%)	3 (2%)	0	100	100
60	N	114/143 (80%)	96 (84%)	18 (16%)	0	100	100
61	O	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
62	P	123/132 (93%)	119 (97%)	4 (3%)	0	100	100
63	Q	116/142 (82%)	107 (92%)	9 (8%)	0	100	100
64	R	138/142 (97%)	134 (97%)	4 (3%)	0	100	100
65	S	123/137 (90%)	120 (98%)	3 (2%)	0	100	100
66	T	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
67	U	139/145 (96%)	136 (98%)	3 (2%)	0	100	100
68	V	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
69	W	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
70	X	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
71	Y	141/145 (97%)	139 (99%)	1 (1%)	1 (1%)	18	44
72	Z	130/135 (96%)	130 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	a	70/105 (67%)	69 (99%)	1 (1%)	0	100	100
74	b	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
75	c	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
76	d	60/67 (90%)	55 (92%)	5 (8%)	0	100	100
77	e	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
78	f	54/63 (86%)	52 (96%)	2 (4%)	0	100	100
79	g	68/193 (35%)	61 (90%)	7 (10%)	0	100	100
80	h	309/317 (98%)	291 (94%)	18 (6%)	0	100	100
All	All	11010/12138 (91%)	10713 (97%)	293 (3%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	L	88	PRO
24	5	20	ALA
71	Y	90	ASP
15	t	63	VAL

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	199/204 (98%)	199 (100%)	0	100	100
11	p	198/216 (92%)	198 (100%)	0	100	100
12	q	169/170 (99%)	169 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	r	178/186 (96%)	178 (100%)	0	100	100
14	s	148/149 (99%)	148 (100%)	0	100	100
15	t	166/168 (99%)	165 (99%)	1 (1%)	78	91
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	90
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	95/112 (85%)	93 (98%)	2 (2%)	47	76
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	111/112 (99%)	111 (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	50/49 (102%)	50 (100%)	0	100	100
32	AD	81/90 (90%)	81 (100%)	0	100	100
33	AE	98/100 (98%)	98 (100%)	0	100	100
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	79/79 (100%)	79 (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	23/24 (96%)	23 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	AP	88/89 (99%)	88 (100%)	0	100	100
45	AQ	72/73 (99%)	72 (100%)	0	100	100
46	i	92/212 (43%)	92 (100%)	0	100	100
48	B	176/215 (82%)	176 (100%)	0	100	100
49	C	194/229 (85%)	194 (100%)	0	100	100
50	D	174/198 (88%)	174 (100%)	0	100	100
51	E	174/196 (89%)	174 (100%)	0	100	100
52	F	218/220 (99%)	218 (100%)	0	100	100
53	G	178/197 (90%)	178 (100%)	0	100	100
54	H	195/204 (96%)	195 (100%)	0	100	100
55	I	163/167 (98%)	163 (100%)	0	100	100
56	J	157/160 (98%)	157 (100%)	0	100	100
57	K	153/160 (96%)	153 (100%)	0	100	100
58	L	87/104 (84%)	87 (100%)	0	100	100
59	M	122/134 (91%)	122 (100%)	0	100	100
60	N	98/123 (80%)	98 (100%)	0	100	100
61	O	129/130 (99%)	129 (100%)	0	100	100
62	P	96/101 (95%)	96 (100%)	0	100	100
63	Q	102/121 (84%)	102 (100%)	0	100	100
64	R	114/116 (98%)	114 (100%)	0	100	100
65	S	112/122 (92%)	112 (100%)	0	100	100
66	T	126/129 (98%)	126 (100%)	0	100	100
67	U	113/117 (97%)	113 (100%)	0	100	100
68	V	90/105 (86%)	90 (100%)	0	100	100
69	W	71/71 (100%)	71 (100%)	0	100	100
70	X	112/113 (99%)	112 (100%)	0	100	100
71	Y	116/118 (98%)	115 (99%)	1 (1%)	70	87
72	Z	109/112 (97%)	109 (100%)	0	100	100
73	a	64/85 (75%)	64 (100%)	0	100	100
74	b	86/102 (84%)	86 (100%)	0	100	100
75	c	72/73 (99%)	72 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
76	d	54/58 (93%)	54 (100%)	0	100	100
77	e	47/48 (98%)	47 (100%)	0	100	100
78	f	48/54 (89%)	48 (100%)	0	100	100
79	g	62/175 (35%)	62 (100%)	0	100	100
80	h	259/263 (98%)	259 (100%)	0	100	100
All	All	9443/10220 (92%)	9438 (100%)	5 (0%)	100	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	t	63	VAL
19	x	165	GLN
24	5	31[A]	GLU
24	5	31[B]	GLU
71	Y	87	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
6	k	25	GLN
6	k	182	GLN
6	k	316	ASN
7	l	6	GLN
7	l	321	ASN
7	l	323	GLN
8	m	17	GLN
8	m	151	GLN
8	m	242	ASN
10	o	50	GLN
10	o	91	ASN
10	o	198	ASN
10	o	239	GLN
10	o	241	ASN
11	p	146	ASN
12	q	129	HIS
13	r	92	HIS
13	r	212	GLN
14	s	43	GLN
16	u	112	GLN

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Mol	Chain	Res	Type
17	v	95	GLN
18	w	51	ASN
19	x	50	GLN
21	z	134	HIS
22	0	13	ASN
22	0	62	ASN
23	2	77	ASN
24	5	30	GLN
25	6	9	ASN
27	8	93	HIS
28	9	81	GLN
28	9	86	GLN
28	9	98	ASN
29	AA	122	HIS
31	AC	48	HIS
32	AD	73	GLN
34	AF	36	GLN
35	AG	24	ASN
36	AH	33	GLN
36	AH	64	GLN
37	AI	16	GLN
37	AI	59	ASN
40	AL	77	ASN
44	AP	22	GLN
44	AP	99	GLN
45	AQ	32	GLN
46	i	66	ASN
48	B	21	ASN
48	B	30	GLN
49	C	124	ASN
49	C	209	ASN
50	D	54	HIS
52	F	157	ASN
55	I	19	GLN
55	I	48	ASN
58	L	58	GLN
58	L	62	GLN
59	M	92	HIS
59	M	127	GLN
61	O	62	GLN
61	O	78	ASN
63	Q	79	HIS

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Mol	Chain	Res	Type
63	Q	103	ASN
65	S	83	GLN
66	T	89	GLN
66	T	92	GLN
70	X	42	GLN
73	a	44	GLN
80	h	102	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3205/3359 (95%)	563 (17%)	38 (1%)
2	3	120/121 (99%)	9 (7%)	0
3	4	157/158 (99%)	24 (15%)	3 (1%)
4	10	12/77 (15%)	2 (16%)	0
47	A	1685/1787 (94%)	390 (23%)	47 (2%)
All	All	5179/5502 (94%)	988 (19%)	88 (1%)

All (988) 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	135	G
1	1	155	A

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Mol	Chain	Res	Type
1	1	156	A
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	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	452	A
1	1	453	U
1	1	454	G
1	1	479	C
1	1	481	G
1	1	482	U
1	1	485	A
1	1	506	A
1	1	517	A
1	1	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

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Mol	Chain	Res	Type
1	1	635	C
1	1	647	A
1	1	658	A
1	1	675	A
1	1	679	U
1	1	688	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

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Mol	Chain	Res	Type
1	1	956	U
1	1	959	G
1	1	976	A
1	1	977	U
1	1	990	G
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	1019	U
1	1	1020	G
1	1	1021	A
1	1	1022	A
1	1	1023	A
1	1	1024	U
1	1	1025	G
1	1	1027	C
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

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Mol	Chain	Res	Type
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
1	1	1205	G
1	1	1215	C
1	1	1218	G
1	1	1223	C
1	1	1224	C
1	1	1225	G
1	1	1228	C
1	1	1229	G
1	1	1230	G
1	1	1231	U
1	1	1232	G
1	1	1234	C
1	1	1238	G
1	1	1239	G
1	1	1241	A
1	1	1242	G
1	1	1243	U
1	1	1244	C
1	1	1245	G
1	1	1247	A
1	1	1249	U
1	1	1251	C
1	1	1252	G
1	1	1253	C
1	1	1255	A
1	1	1258	G
1	1	1259	A
1	1	1262	G
1	1	1264	G

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Mol	Chain	Res	Type
1	1	1265	U
1	1	1266	A
1	1	1267	A
1	1	1268	C
1	1	1269	A
1	1	1270	A
1	1	1273	C
1	1	1278	G
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

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Mol	Chain	Res	Type
1	1	1556	G
1	1	1558	G
1	1	1559	C
1	1	1560	U
1	1	1561	U
1	1	1562	G
1	1	1563	A
1	1	1565	U
1	1	1566	U
1	1	1567	U
1	1	1568	U
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

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Mol	Chain	Res	Type
1	1	1763	C
1	1	1776	G
1	1	1793	A
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	1950	G
1	1	1958	G
1	1	1961	C
1	1	1968	A
1	1	1973	C
1	1	2043	G
1	1	2045	C
1	1	2054	C
1	1	2055	G
1	1	2066	G
1	1	2067	U
1	1	2068	U
1	1	2069	U
1	1	2070	A
1	1	2071	A
1	1	2078	A
1	1	2088	G
1	1	2089	G

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Mol	Chain	Res	Type
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
1	1	2222	A
1	1	2227	G
1	1	2233	A
1	1	2234	A
1	1	2235	C
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

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Mol	Chain	Res	Type
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	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

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Mol	Chain	Res	Type
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	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	2780	A
1	1	2782	C
1	1	2786	G
1	1	2789	A
1	1	2790	U
1	1	2793	C
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	2848	C
1	1	2859	A
1	1	2861	C
1	1	2866	C
1	1	2870	G
1	1	2871	C

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	2	G
4	10	76	A
47	A	17	C
47	A	25	C
47	A	26	A
47	A	27	U
47	A	34	G
47	A	47	A
47	A	57	G
47	A	66	U
47	A	74	U
47	A	75	U

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Mol	Chain	Res	Type
47	A	76	A
47	A	78	A
47	A	79	C
47	A	81	G
47	A	84	A
47	A	104	A
47	A	114	C
47	A	115	G
47	A	123	G
47	A	126	A
47	A	127	G
47	A	128	U
47	A	129	A
47	A	138	C
47	A	139	U
47	A	142	G
47	A	143	A
47	A	150	U
47	A	151	G
47	A	152	G
47	A	154	A
47	A	159	U
47	A	166	A
47	A	168	U
47	A	173	G
47	A	176	U
47	A	177	A
47	A	179	A
47	A	190	U
47	A	191	U
47	A	193	G
47	A	199	G
47	A	200	A
47	A	202	G
47	A	206	U
47	A	211	A
47	A	214	U
47	A	215	A
47	A	216	A
47	A	217	A
47	A	218	A
47	A	247	U

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Mol	Chain	Res	Type
47	A	255	A
47	A	259	U
47	A	260	U
47	A	261	C
47	A	262	G
47	A	266	C
47	A	269	A
47	A	270	U
47	A	274	C
47	A	276	U
47	A	277	G
47	A	278	U
47	A	279	G
47	A	283	G
47	A	285	G
47	A	297	A
47	A	312	C
47	A	314	A
47	A	318	U
47	A	320	G
47	A	335	G
47	A	336	C
47	A	350	A
47	A	357	A
47	A	358	A
47	A	359	C
47	A	388	G
47	A	398	A
47	A	400	C
47	A	402	G
47	A	414	A
47	A	416	G
47	A	421	G
47	A	422	C
47	A	423	A
47	A	424	G
47	A	432	G
47	A	437	U
47	A	442	C
47	A	446	C
47	A	452	A
47	A	458	A

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Mol	Chain	Res	Type
47	A	466	A
47	A	475	A
47	A	480	U
47	A	482	C
47	A	483	A
47	A	485	G
47	A	501	G
47	A	502	U
47	A	503	A
47	A	504	A
47	A	505	U
47	A	506	U
47	A	509	A
47	A	512	G
47	A	513	A
47	A	515	U
47	A	518	A
47	A	519	A
47	A	525	A
47	A	530	U
47	A	534	C
47	A	536	A
47	A	537	G
47	A	539	A
47	A	540	A
47	A	547	G
47	A	553	A
47	A	554	A
47	A	555	G
47	A	556	U
47	A	557	C
47	A	563	C
47	A	566	G
47	A	575	G
47	A	576	U
47	A	580	U
47	A	592	A
47	A	593	G
47	A	604	A
47	A	609	U
47	A	617	A
47	A	618	A

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Mol	Chain	Res	Type
47	A	620	A
47	A	621	A
47	A	639	G
47	A	648	U
47	A	650	G
47	A	652	C
47	A	653	G
47	A	654	G
47	A	656	C
47	A	675	U
47	A	682	A
47	A	686	G
47	A	687	A
47	A	688	G
47	A	694	C
47	A	695	C
47	A	696	U
47	A	701	G
47	A	721	C
47	A	722	A
47	A	723	G
47	A	729	U
47	A	739	A
47	A	740	A
47	A	741	A
47	A	750	G
47	A	751	U
47	A	756	A
47	A	759	A
47	A	760	G
47	A	762	C
47	A	764	U
47	A	765	U
47	A	766	U
47	A	767	G
47	A	768	C
47	A	770	C
47	A	771	G
47	A	773	A
47	A	775	A
47	A	778	U
47	A	779	U

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Mol	Chain	Res	Type
47	A	796	A
47	A	798	A
47	A	799	G
47	A	802	C
47	A	803	G
47	A	804	U
47	A	805	U
47	A	807	U
47	A	808	G
47	A	814	A
47	A	815	U
47	A	816	U
47	A	818	U
47	A	819	G
47	A	820	U
47	A	821	U
47	A	823	G
47	A	824	U
47	A	825	U
47	A	827	C
47	A	828	U
47	A	831	G
47	A	840	A
47	A	842	U
47	A	848	A
47	A	856	G
47	A	857	G
47	A	869	A
47	A	871	U
47	A	875	C
47	A	877	G
47	A	878	U
47	A	879	U
47	A	881	U
47	A	891	A
47	A	909	A
47	A	910	G
47	A	911	A
47	A	918	A
47	A	920	U
47	A	945	U
47	A	951	A

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Mol	Chain	Res	Type
47	A	973	A
47	A	975	C
47	A	977	A
47	A	988	A
47	A	989	U
47	A	997	U
47	A	998	A
47	A	1004	A
47	A	1005	A
47	A	1011	A
47	A	1013	C
47	A	1017	G
47	A	1024	A
47	A	1025	G
47	A	1039	U
47	A	1042	U
47	A	1043	U
47	A	1044	U
47	A	1047	U
47	A	1055	A
47	A	1056	U
47	A	1057	C
47	A	1058	G
47	A	1059	G
47	A	1060	C
47	A	1061	A
47	A	1067	C
47	A	1077	A
47	A	1081	C
47	A	1085	G
47	A	1123	A
47	A	1135	G
47	A	1143	C
47	A	1145	A
47	A	1152	G
47	A	1168	A
47	A	1169	A
47	A	1170	U
47	A	1179	A
47	A	1181	A
47	A	1184	G
47	A	1185	G

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Mol	Chain	Res	Type
47	A	1186	G
47	A	1187	A
47	A	1193	A
47	A	1202	A
47	A	1203	G
47	A	1206	A
47	A	1207	C
47	A	1212	A
47	A	1215	A
47	A	1219	A
47	A	1220	C
47	A	1221	A
47	A	1229	A
47	A	1230	G
47	A	1231	C
47	A	1236	U
47	A	1243	U
47	A	1250	G
47	A	1270	U
47	A	1284	G
47	A	1299	U
47	A	1300	U
47	A	1301	G
47	A	1306	A
47	A	1325	U
47	A	1330	A
47	A	1336	G
47	A	1339	G
47	A	1342	A
47	A	1343	G
47	A	1345	A
47	A	1346	U
47	A	1348	U
47	A	1349	G
47	A	1352	G
47	A	1355	A
47	A	1356	U
47	A	1357	A
47	A	1359	U
47	A	1360	C
47	A	1364	U
47	A	1365	C

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Mol	Chain	Res	Type
47	A	1369	G
47	A	1370	A
47	A	1376	U
47	A	1380	G
47	A	1381	A
47	A	1382	U
47	A	1384	U
47	A	1385	C
47	A	1392	A
47	A	1397	A
47	A	1398	G
47	A	1399	U
47	A	1400	U
47	A	1401	U
47	A	1410	A
47	A	1413	A
47	A	1414	G
47	A	1415	G
47	A	1422	A
47	A	1431	G
47	A	1433	C
47	A	1445	C
47	A	1446	A
47	A	1455	A
47	A	1457	A
47	A	1458	C
47	A	1461	A
47	A	1462	C
47	A	1463	G
47	A	1468	C
47	A	1476	A
47	A	1477	U
47	A	1480	G
47	A	1483	U
47	A	1485	G
47	A	1491	G
47	A	1502	A
47	A	1503	A
47	A	1508	G
47	A	1510	G
47	A	1511	A
47	A	1523	G

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Mol	Chain	Res	Type
47	A	1524	C
47	A	1529	G
47	A	1530	A
47	A	1541	U
47	A	1544	U
47	A	1546	G
47	A	1556	A
47	A	1560	A
47	A	1561	G
47	A	1571	G
47	A	1574	A
47	A	1575	G
47	A	1577	G
47	A	1580	A
47	A	1582	U
47	A	1584	A
47	A	1588	G
47	A	1621	C
47	A	1644	U
47	A	1645	G
47	A	1665	C
47	A	1667	G
47	A	1670	U
47	A	1671	G
47	A	1672	G
47	A	1673	U
47	A	1674	U
47	A	1677	G
47	A	1700	G
47	A	1704	C
47	A	1737	A
47	A	1743	A
47	A	1747	G
47	A	1749	A
47	A	1753	A
47	A	1756	U
47	A	1767	G
47	A	1769	A
47	A	1770	C
47	A	1779	G
47	A	1780	G
47	A	1781	A

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Mol	Chain	Res	Type
47	A	1782	U
47	A	1783	C

All (88) 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	1957	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	2780	A
1	1	2789	A
1	1	2790	U
1	1	2847	U
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

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Mol	Chain	Res	Type
1	1	3315	C
1	1	3317	U
3	4	85	G
3	4	125	U
3	4	156	U
47	A	25	C
47	A	78	A
47	A	137	A
47	A	151	G
47	A	176	U
47	A	214	U
47	A	259	U
47	A	265	U
47	A	278	U
47	A	415	A
47	A	451	C
47	A	502	U
47	A	504	A
47	A	505	U
47	A	514	G
47	A	518	A
47	A	529	C
47	A	533	A
47	A	553	A
47	A	556	U
47	A	638	U
47	A	685	C
47	A	740	A
47	A	763	C
47	A	769	U
47	A	817	U
47	A	820	U
47	A	824	U
47	A	855	C
47	A	874	U
47	A	876	A
47	A	1168	A
47	A	1335	U
47	A	1355	A
47	A	1359	U
47	A	1369	G
47	A	1396	A

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Mol	Chain	Res	Type
47	A	1398	G
47	A	1457	A
47	A	1467	C
47	A	1479	A
47	A	1484	U
47	A	1523	G
47	A	1555	C
47	A	1573	A
47	A	1579	A
47	A	1581	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	1	2808	1	19,22,23	2.97	8 (42%)	25,31,34	1.21	3 (12%)
44	MLZ	AP	40	44	8,9,10	0.72	0	4,9,11	0.94	0
44	MLZ	AP	55	44	8,9,10	0.68	0	4,9,11	0.81	0
1	OMG	1	2765	1	23,26,27	2.35	9 (39%)	32,38,41	1.86	9 (28%)
25	MLZ	6	110	25	8,9,10	0.73	0	4,9,11	0.90	0
62	IAS	P	119	62	6,7,8	1.05	0	3,8,10	1.66	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
44	MLZ	AP	40	44	-	0/7/8/10	-
44	MLZ	AP	55	44	-	3/7/8/10	-
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	-
62	IAS	P	119	62	-	1/7/7/8	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2808	OMC	C2-N3	6.33	1.48	1.36
1	1	2765	OMG	C4-N3	6.29	1.48	1.34
1	1	2808	OMC	C6-C5	5.80	1.48	1.35
1	1	2765	OMG	C2-N3	5.34	1.46	1.33
1	1	2808	OMC	C2-N1	4.86	1.50	1.40
1	1	2808	OMC	C4-N3	4.77	1.44	1.34
1	1	2808	OMC	C4-N4	4.70	1.45	1.33
1	1	2765	OMG	C2-N2	4.05	1.43	1.34
1	1	2808	OMC	O2-C2	-3.22	1.17	1.23
1	1	2765	OMG	O6-C6	-2.98	1.17	1.23
1	1	2808	OMC	C6-N1	2.94	1.45	1.38
1	1	2765	OMG	C5-N7	-2.69	1.33	1.39
1	1	2765	OMG	C2-N1	2.51	1.43	1.37
1	1	2765	OMG	C6-N1	2.43	1.43	1.38
1	1	2765	OMG	C5-C6	2.38	1.53	1.44
1	1	2808	OMC	C5-C4	2.20	1.48	1.42
1	1	2765	OMG	C4-N9	-2.19	1.32	1.38

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2765	OMG	C5-C4-N3	-4.68	120.94	128.39
1	1	2765	OMG	C2-N3-C4	4.58	120.19	112.30
1	1	2765	OMG	N9-C8-N7	-3.24	107.39	113.40
1	1	2808	OMC	O2-C2-N3	-3.17	117.34	122.33
1	1	2765	OMG	C2-N1-C6	-2.89	119.87	125.11
1	1	2765	OMG	C5-C6-N1	2.74	120.22	113.25
1	1	2765	OMG	N9-C4-N3	2.60	131.16	125.95
1	1	2808	OMC	C1'-N1-C2	2.51	123.99	118.44
1	1	2765	OMG	O6-C6-C5	-2.44	120.08	126.53
1	1	2808	OMC	C6-C5-C4	2.23	121.18	117.53
1	1	2765	OMG	C8-N7-C5	2.15	108.10	104.26
1	1	2765	OMG	N1-C2-N3	-2.03	119.60	123.32

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	6	110	MLZ	N-CA-CB-CG
25	6	110	MLZ	C-CA-CB-CG
25	6	110	MLZ	CD-CE-NZ-CM
1	1	2808	OMC	O4'-C1'-N1-C2
1	1	2808	OMC	O4'-C1'-N1-C6
44	AP	55	MLZ	CG-CD-CE-NZ
44	AP	55	MLZ	CE-CD-CG-CB
44	AP	55	MLZ	CA-CB-CG-CD
1	1	2808	OMC	C1'-C2'-O2'-CM2
62	P	119	IAS	CA-CB-CG-OD1

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	2808	OMC	3	0
62	P	119	IAS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 8 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	SPD	1	3401	-	9,9,9	0.31	0	8,8,8	0.83	0
82	ANM	1	3403	-	20,20,20	1.17	2 (10%)	24,27,27	1.64	3 (12%)
81	SPD	1	3402	-	9,9,9	0.16	0	8,8,8	0.20	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	SPD	1	3401	-	-	1/7/7/7	-
82	ANM	1	3403	-	-	6/10/23/23	0/2/2/2
81	SPD	1	3402	-	-	4/7/7/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	1	3403	ANM	C4-C3	-3.40	1.48	1.53
82	1	3403	ANM	O2-C2	-2.28	1.41	1.44

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	1	3403	ANM	C15-C16-N1	-5.23	104.50	111.21
82	1	3403	ANM	O2-C2-C3	-4.98	97.41	109.49
82	1	3403	ANM	C12-C15-C16	-2.57	109.05	113.40

There are no chirality outliers.

All (11) torsion outliers are listed below:

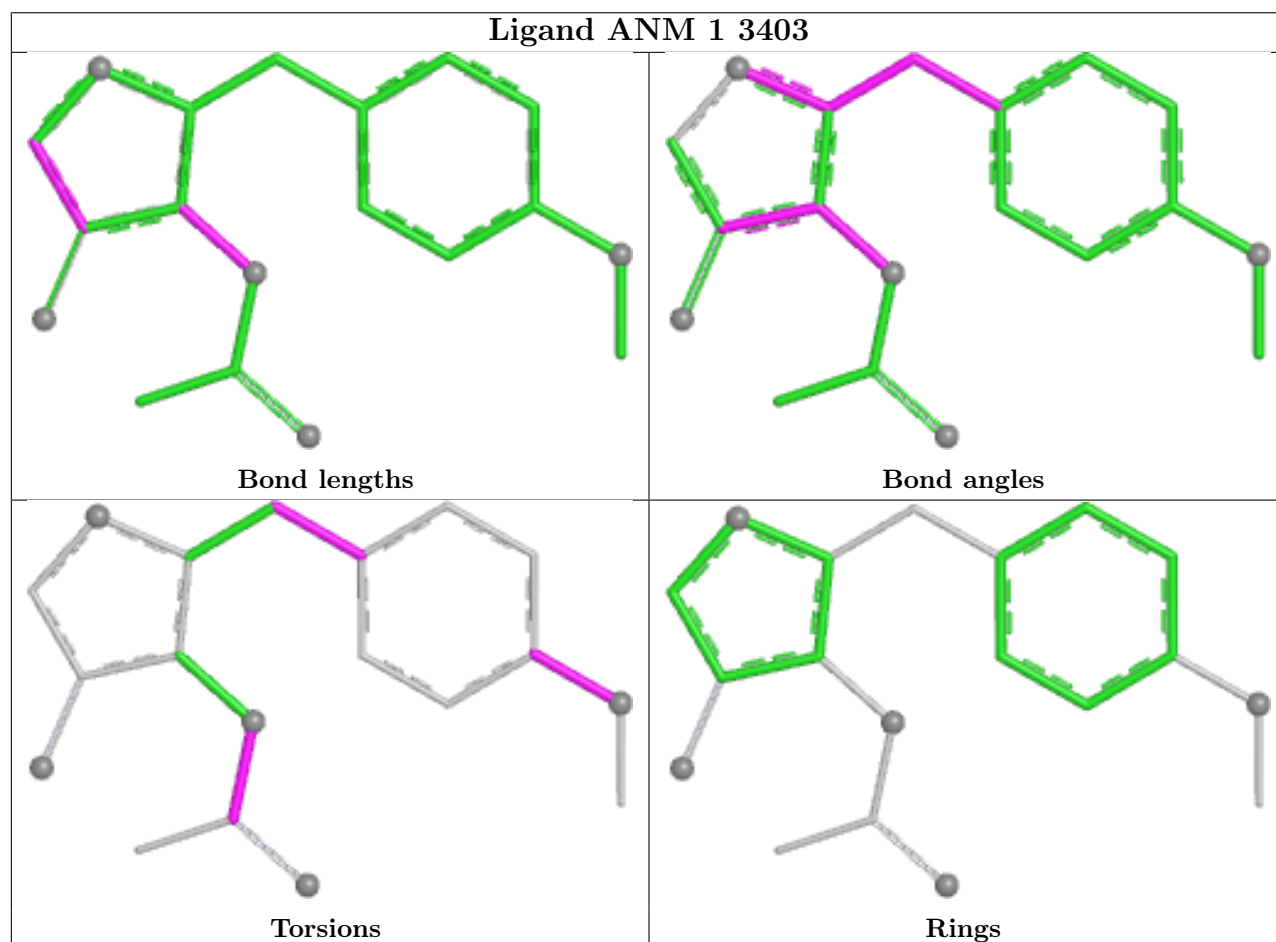
Mol	Chain	Res	Type	Atoms
82	1	3403	ANM	C1-C9-O1-C14
82	1	3403	ANM	C10-C9-O1-C14
81	1	3402	SPD	C4-C5-N6-C7
82	1	3403	ANM	C13-C12-C15-C16
82	1	3403	ANM	C6-C5-O2-C2
82	1	3403	ANM	C11-C12-C15-C16
82	1	3403	ANM	O3-C5-O2-C2
81	1	3402	SPD	C7-C8-C9-N10
81	1	3402	SPD	N6-C7-C8-C9
81	1	3402	SPD	C8-C7-N6-C5
81	1	3401	SPD	C7-C8-C9-N10

There are no ring outliers.

2 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	1	3401	SPD	1	0
82	1	3403	ANM	12	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

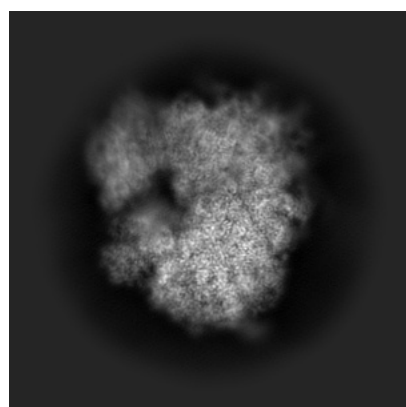
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13749. These allow visual inspection of the internal detail of the map and identification of artifacts.

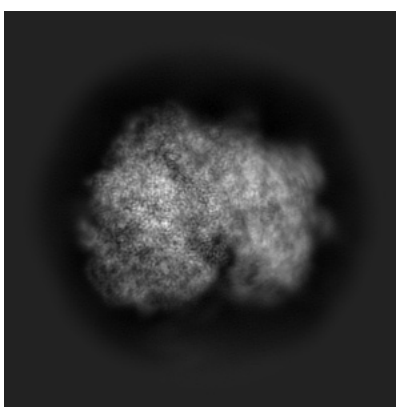
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

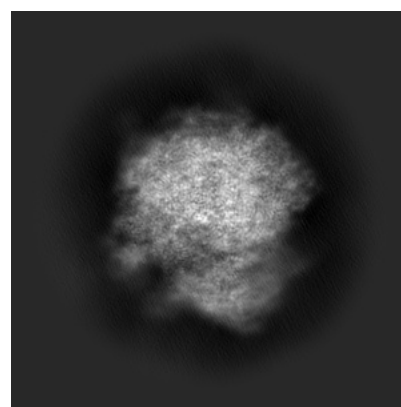
6.1.1 Primary map



X



Y

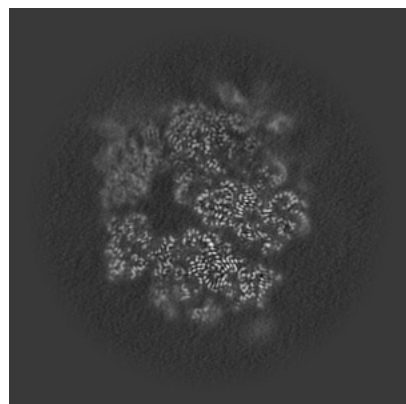


Z

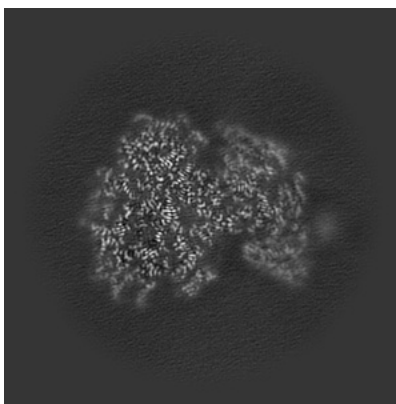
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

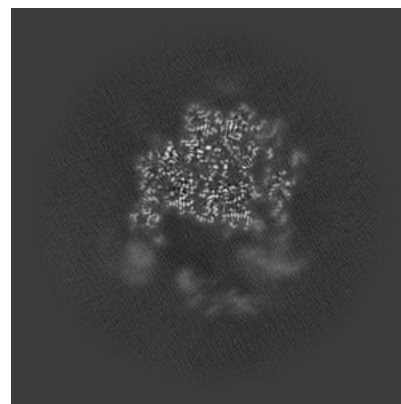
6.2.1 Primary map



X Index: 255



Y Index: 255

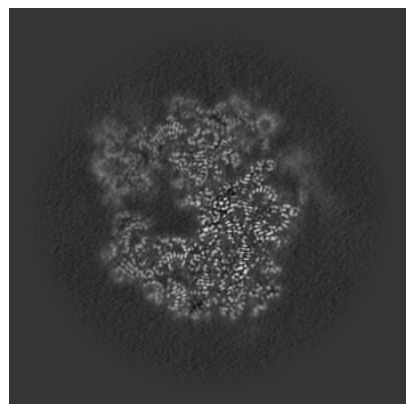


Z Index: 255

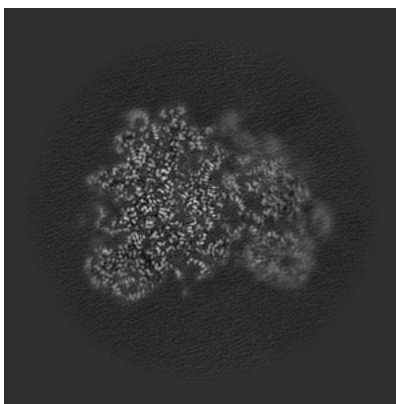
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

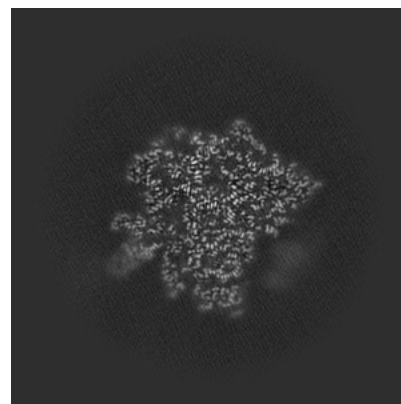
6.3.1 Primary map



X Index: 274



Y Index: 268

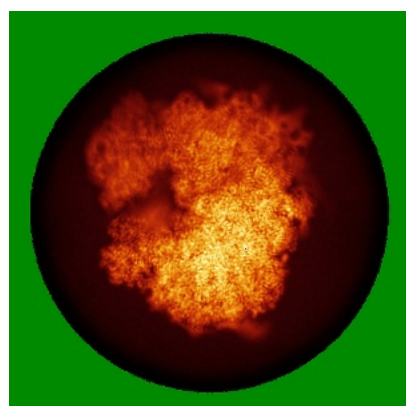


Z Index: 207

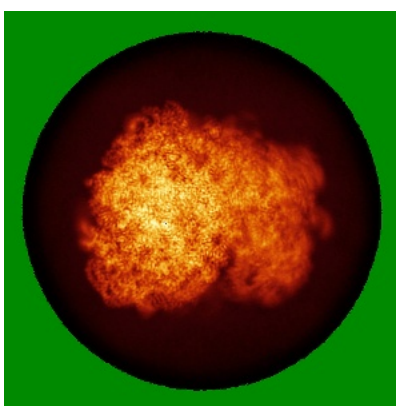
The images above show the largest variance slices of the map in three orthogonal directions.

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

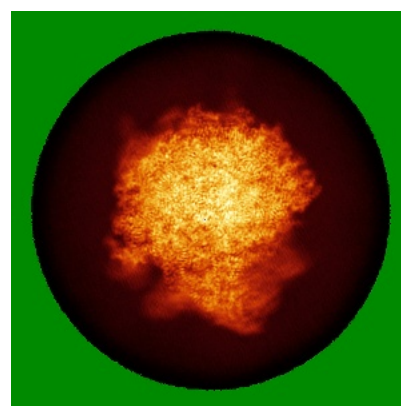
6.4.1 Primary map



X



Y

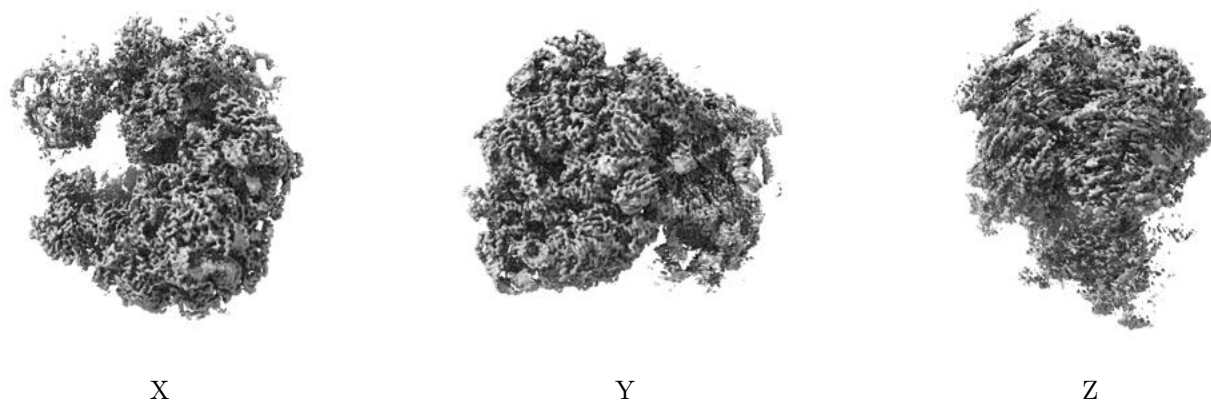


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.55. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

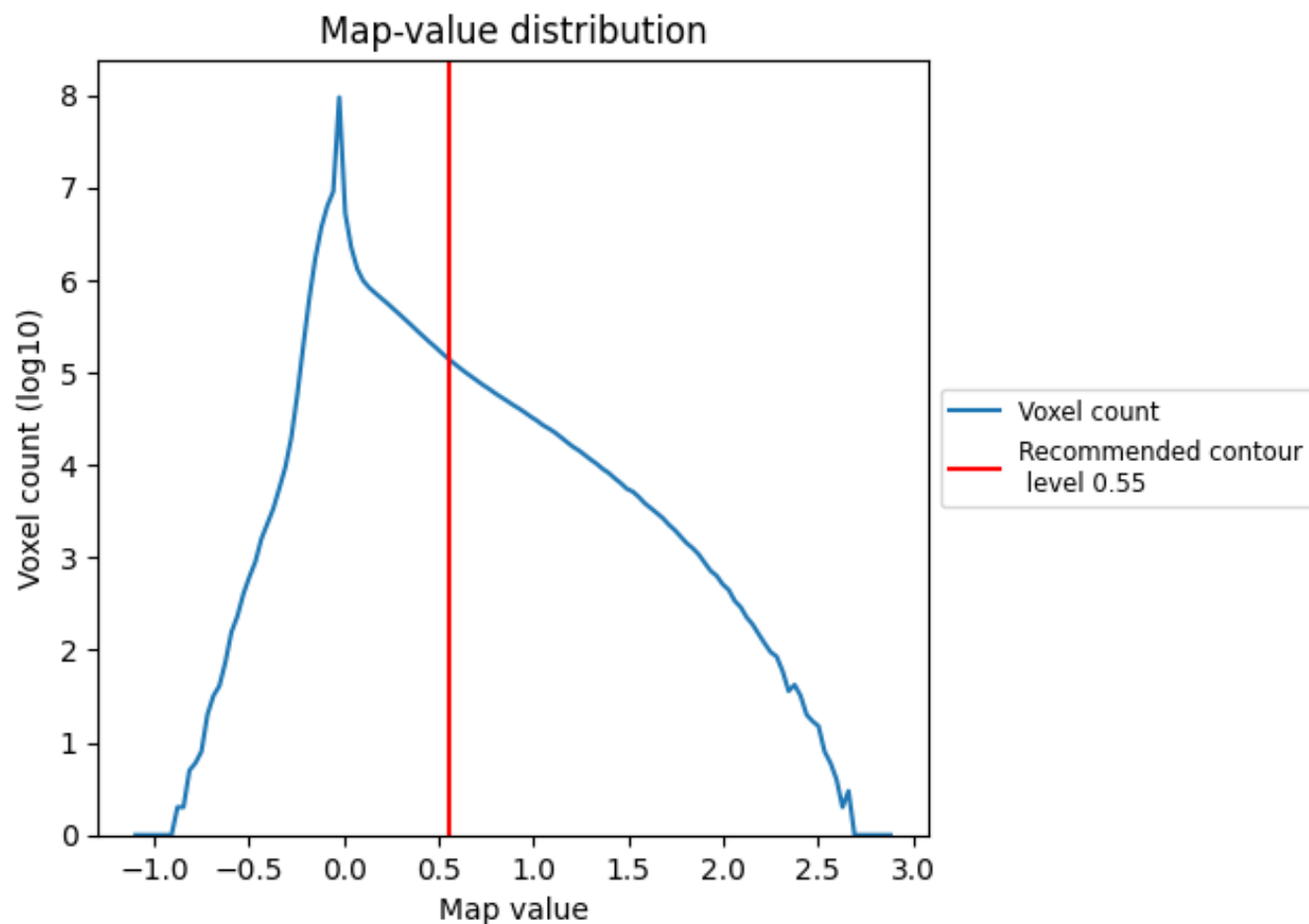
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

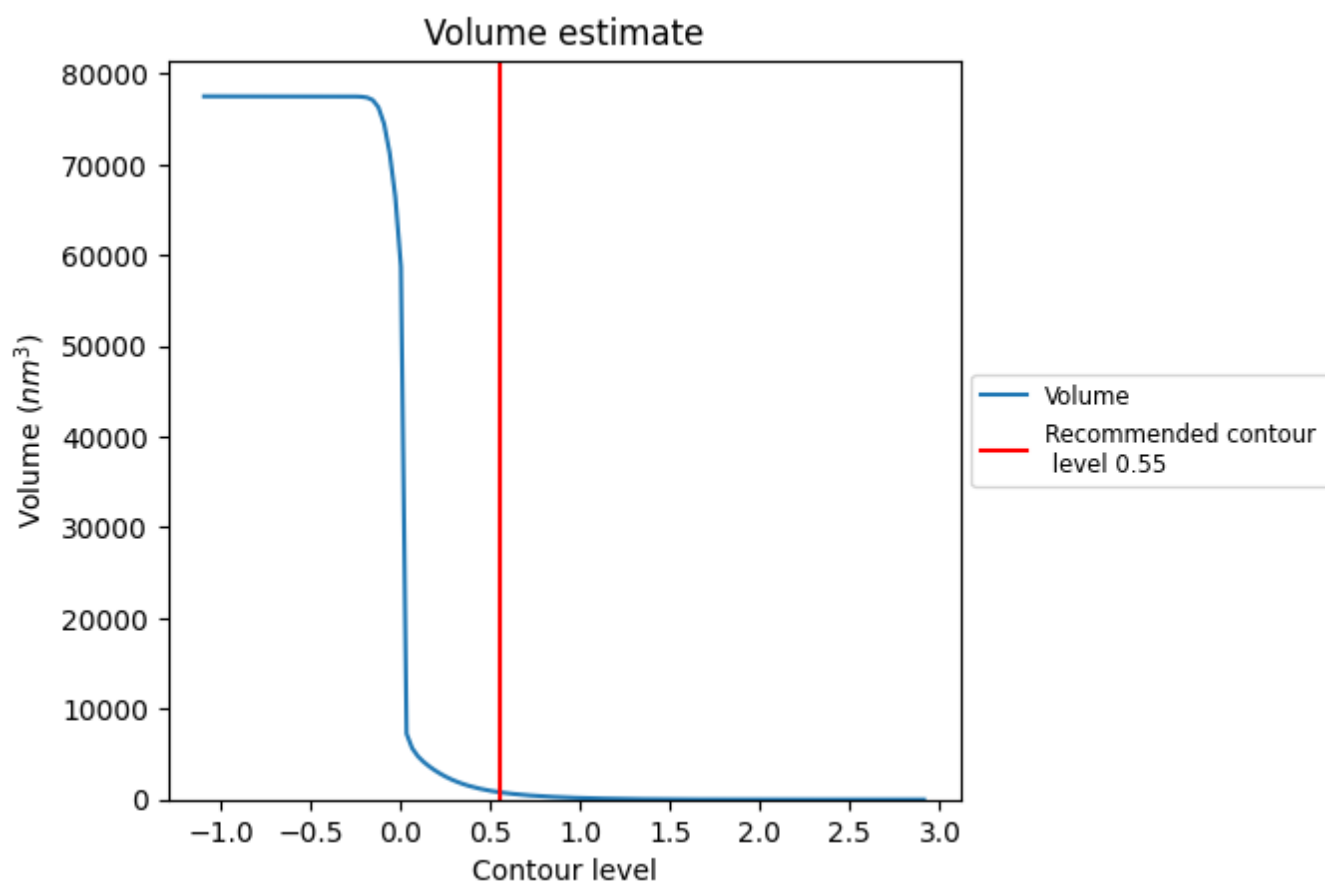
This section contains the results of statistical analysis of the map.

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.

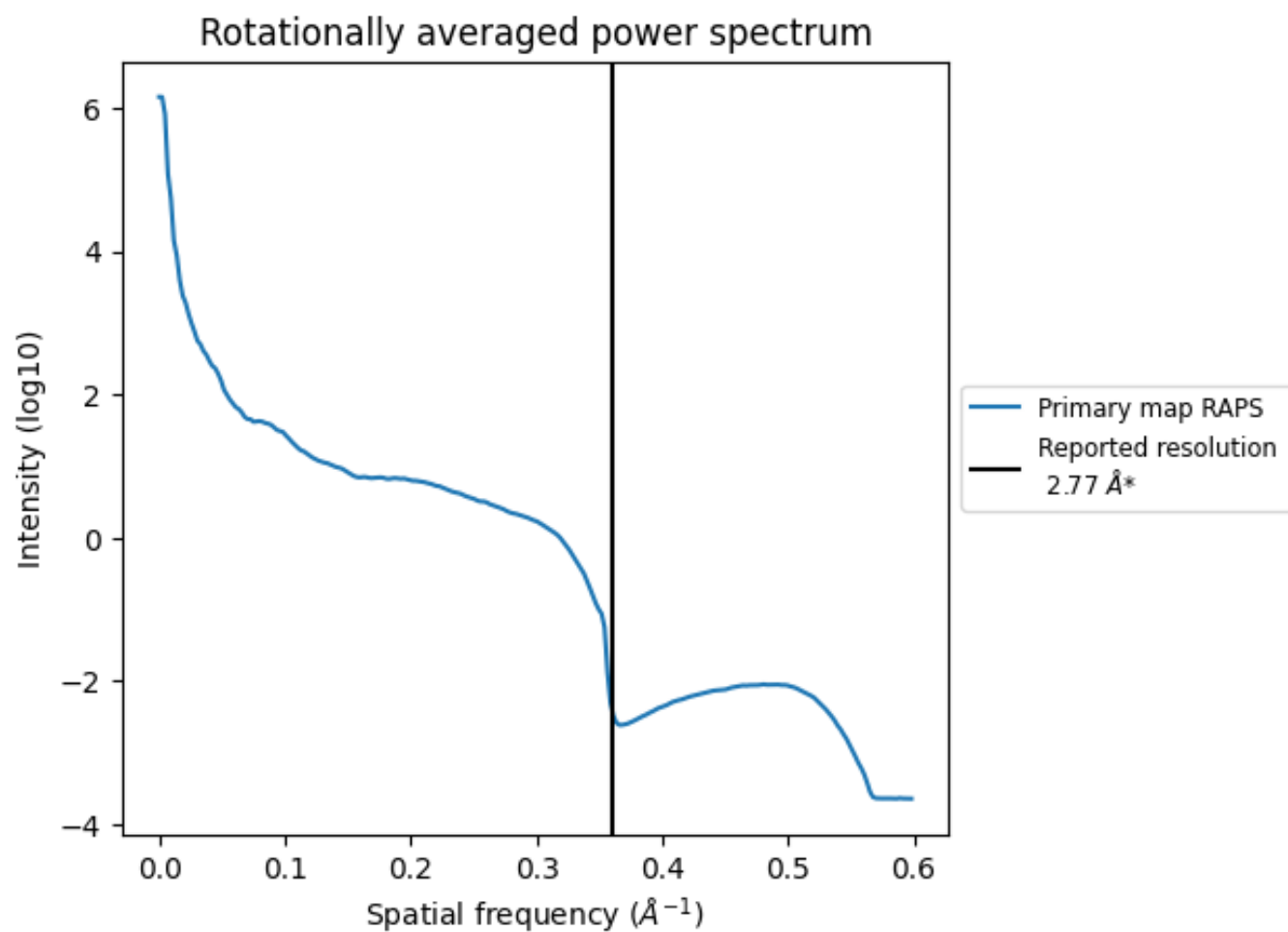
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 804 nm³; this corresponds to an approximate mass of 726 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 ⓘ

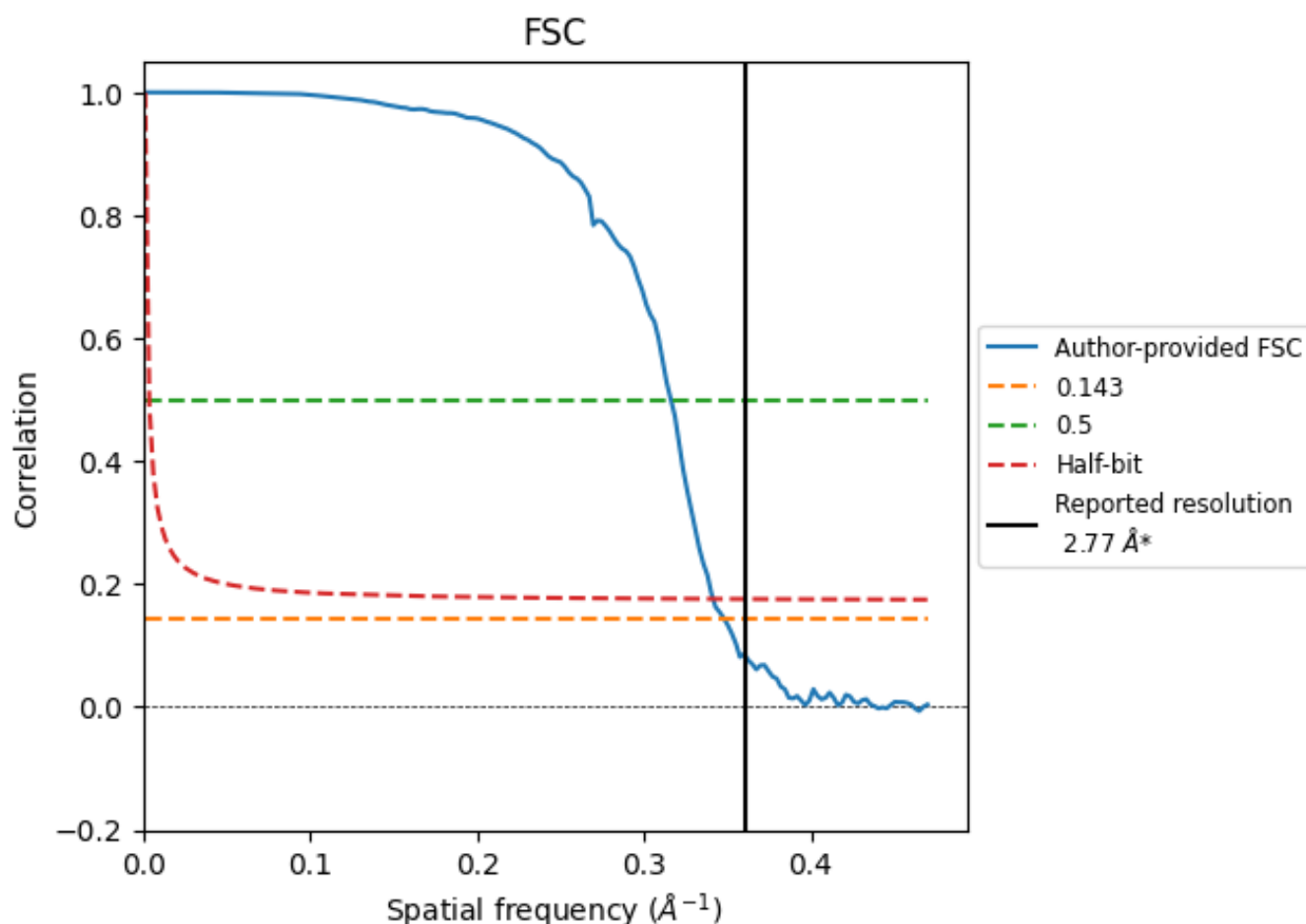


*Reported resolution corresponds to spatial frequency of 0.361 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.361 Å⁻¹

8.2 Resolution estimates [i](#)

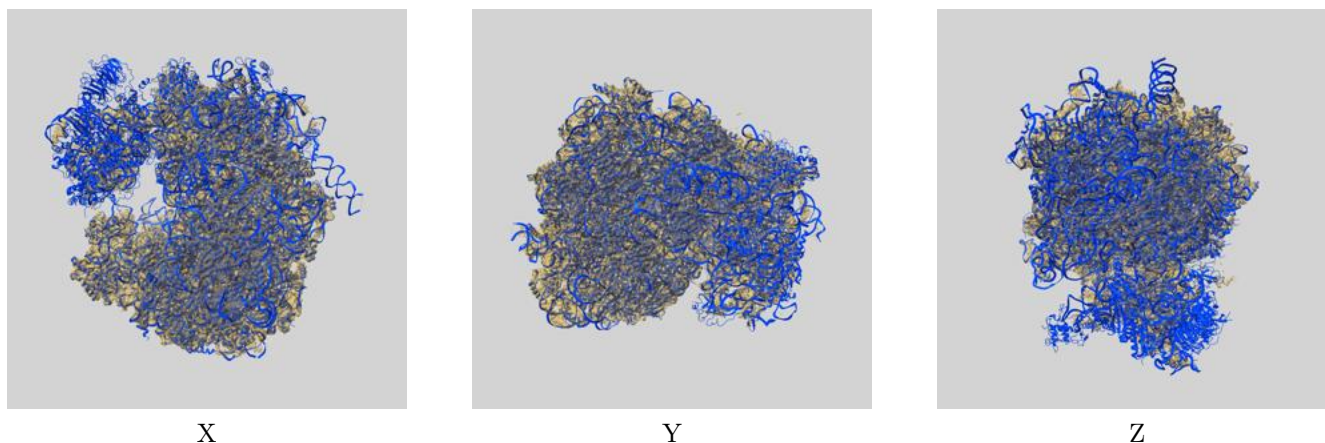
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.77	-	-
Author-provided FSC curve	2.87	3.16	2.93
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

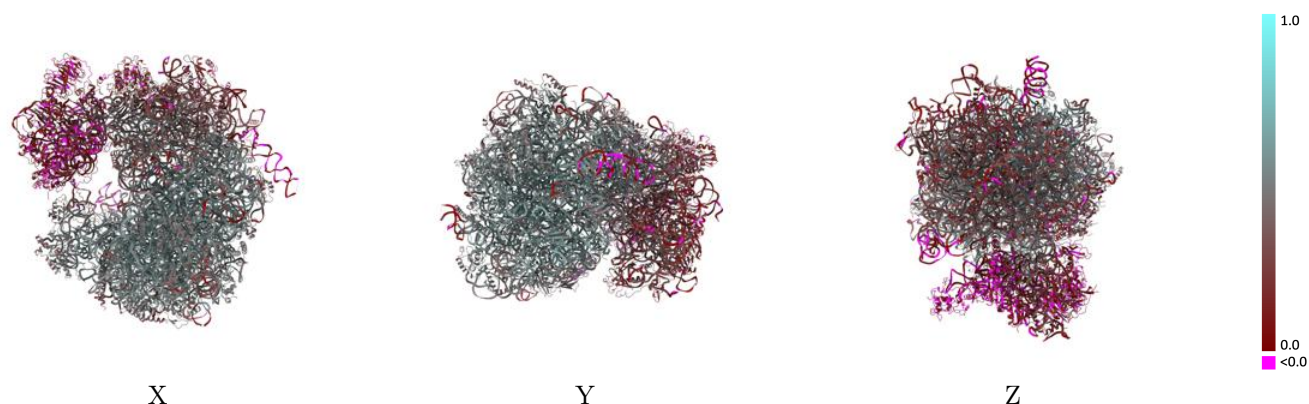
This section contains information regarding the fit between EMDB map EMD-13749 and PDB model 7Q0P. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



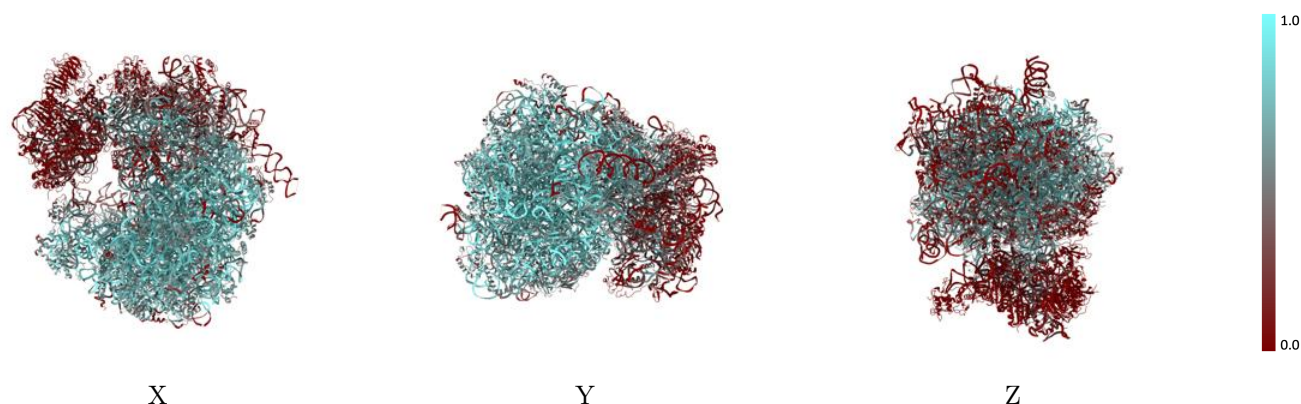
The images above show the 3D surface view of the map at the recommended contour level 0.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



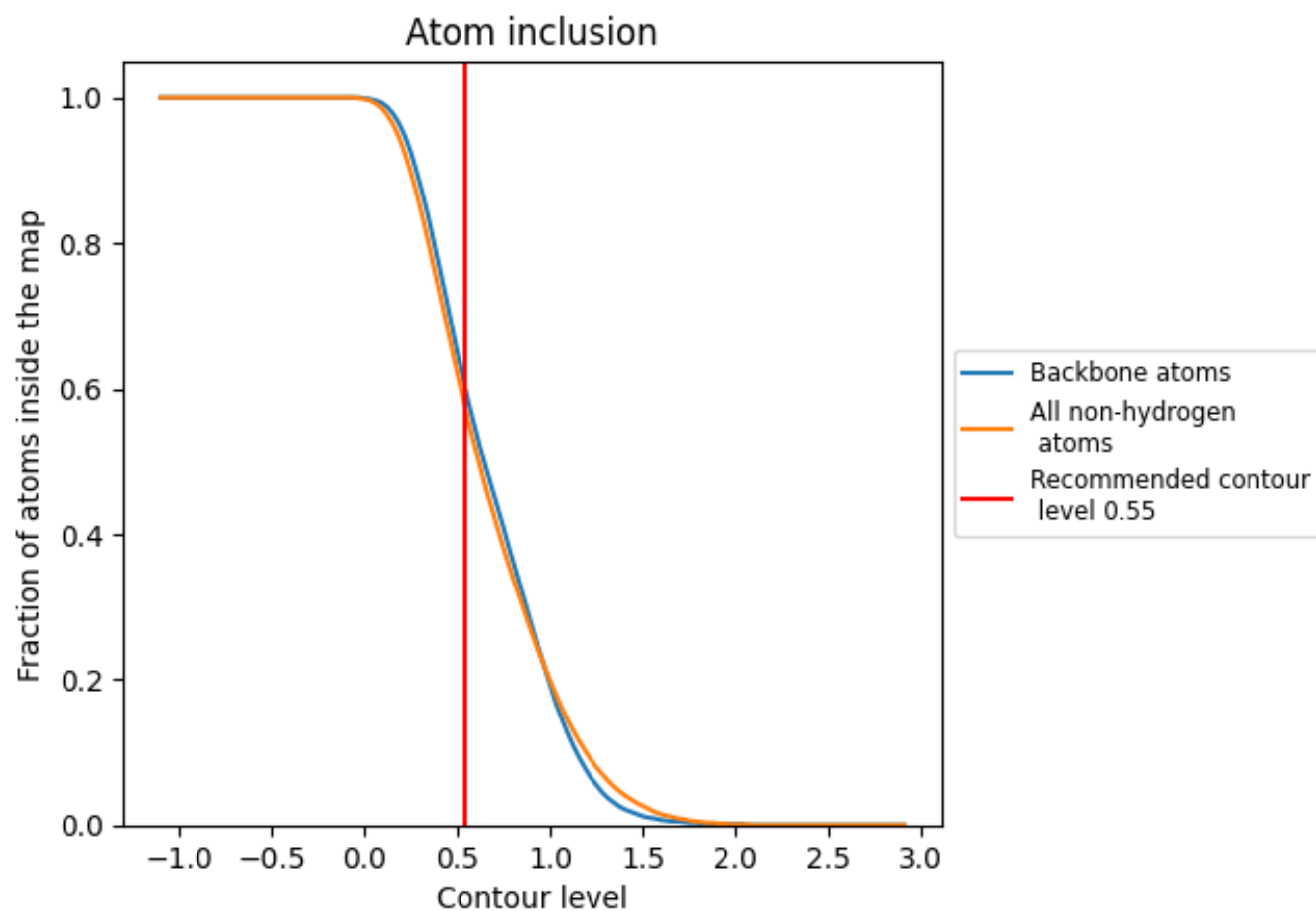
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.55).

9.4 Atom inclusion [i](#)



At the recommended contour level, 60% of all backbone atoms, 57% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5680	 0.4100
0	 0.6680	 0.5150
1	 0.8160	 0.5110
10	 0.0600	 0.3550
2	 0.6400	 0.5060
3	 0.8660	 0.5200
4	 0.8490	 0.5230
5	 0.5120	 0.4370
6	 0.6200	 0.5190
7	 0.6340	 0.5070
8	 0.6490	 0.4990
9	 0.6380	 0.4880
A	 0.4230	 0.2930
AA	 0.6060	 0.4870
AB	 0.7160	 0.5270
AC	 0.5820	 0.4590
AD	 0.6280	 0.4720
AE	 0.6400	 0.5230
AF	 0.6900	 0.5410
AG	 0.7040	 0.5520
AH	 0.6620	 0.5110
AI	 0.6140	 0.4710
AJ	 0.5270	 0.4760
AK	 0.7490	 0.5510
AL	 0.5390	 0.4480
AM	 0.7050	 0.5300
AN	 0.5860	 0.4840
AO	 0.1750	 0.4400
AP	 0.6260	 0.5160
AQ	 0.6670	 0.5130
B	 0.2020	 0.2300
C	 0.2470	 0.3560
D	 0.2630	 0.2860
E	 0.0320	 0.1040
F	 0.1410	 0.2420



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Chain	Atom inclusion	Q-score
G	 0.0180	 0.0760
H	 0.1020	 0.2580
I	 0.1550	 0.2460
J	 0.1900	 0.2510
K	 0.1690	 0.2860
L	 0.0230	 0.0450
M	 0.1380	 0.2300
N	 0.0000	 0.0320
O	 0.3640	 0.3730
P	 0.3030	 0.3920
Q	 0.0190	 0.0710
R	 0.0110	 0.1710
S	 0.0510	 0.1950
T	 0.0230	 0.0840
U	 0.0420	 0.1420
V	 0.0150	 0.1130
W	 0.1930	 0.2390
X	 0.2370	 0.2910
Y	 0.2400	 0.3090
Z	 0.1170	 0.2570
a	 0.0050	 0.0360
b	 0.4580	 0.4080
c	 0.2560	 0.3250
d	 0.0210	 0.0620
e	 0.0780	 0.0630
f	 0.1530	 0.2370
g	 0.0000	 -0.0010
h	 0.0010	 0.1090
i	 0.0040	 0.1240
j	 0.7170	 0.5560
k	 0.7010	 0.5400
l	 0.6690	 0.5040
m	 0.5880	 0.4540
n	 0.5710	 0.4820
o	 0.6390	 0.5050
p	 0.5500	 0.4560
q	 0.5720	 0.4510
r	 0.6100	 0.4970
s	 0.4580	 0.4170
t	 0.6030	 0.4770
u	 0.6150	 0.4730
v	 0.7530	 0.5490

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Chain	Atom inclusion	Q-score
w	 0.6580	 0.5220
x	 0.7490	 0.5460
y	 0.7040	 0.5210
z	 0.5980	 0.4670