



Full wwPDB EM Validation Report ⓘ

Jun 27, 2026 – 04:24 PM EDT

PDB ID : 6VZ7 / pdb_00006vz7
EMDB ID : EMD-21486
Title : Escherichia coli transcription-translation complex C1 (TTC-C1) containing a 27 nt long mRNA spacer, NusG, and fMet-tRNAs at P-site and E-site
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on : 2020-02-27
Resolution : 7.00 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:

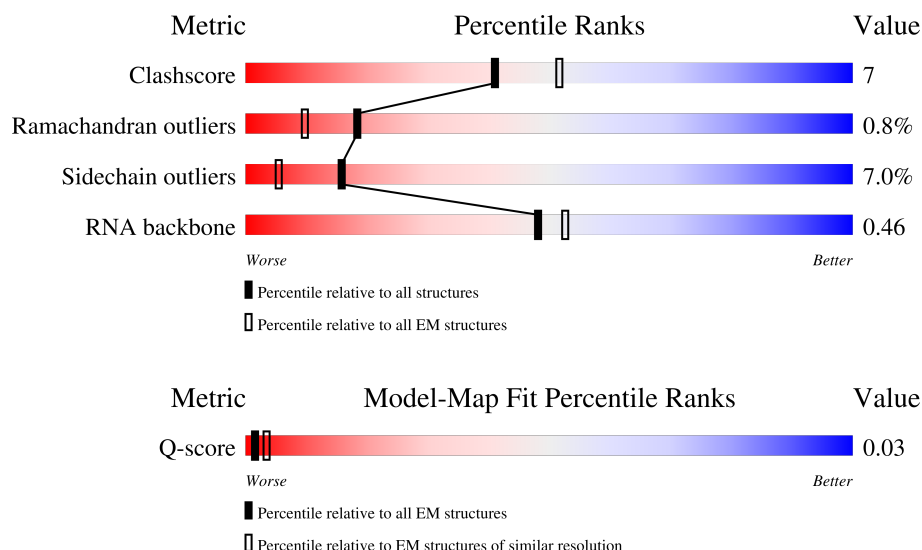
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 7.00 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	483 (6.50 - 7.50)

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	0	103	100% 84% 15% •
2	1	110	100% 75% 25%
3	2	94	100% 91% 6% •

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Mol	Chain	Length	Quality of chain
4	3	103	
5	4	94	
6	5	27	
7	6	27	
8	7	16	
9	A	76	
9	B	76	
10	AA	1341	
11	AB	112	
12	AC	230	
12	AD	230	
13	AE	1358	
14	AF	83	
15	C	66	
16	D	1542	
17	E	86	
18	F	70	
19	G	225	
20	H	557	
21	I	208	
22	J	205	
23	K	156	
24	L	104	
25	M	151	
26	N	129	

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Mol	Chain	Length	Quality of chain
27	O	127	
28	P	99	
29	Q	117	
30	R	123	
31	S	100	
32	T	88	
33	U	82	
34	V	80	
35	W	83	
36	X	116	
37	Y	3	
38	a	2903	
39	b	76	
40	c	77	
41	d	120	
42	e	62	
43	f	58	
44	g	66	
45	h	271	
46	i	56	
47	j	209	
48	k	52	
49	l	201	
50	m	46	
51	n	177	

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Mol	Chain	Length	Quality of chain
52	o	64	
53	p	175	
54	q	38	
55	r	149	
56	s	142	
57	t	123	
58	u	144	
59	v	136	
60	w	119	
61	x	116	
62	y	114	
63	z	117	

2 Entry composition [i](#)

There are 65 unique types of molecules in this entry. The entry contains 299447 atoms, of which 125488 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	94	Total	C	H	N	O	S	0	0
			1557	470	811	140	134	2		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	103	Total	C	H	N	O	0	0
			1632	498	844	148	142		

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			732	225	260	87	137	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			848	259	306	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 27 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	16	Total	C	H	N	O	P	0	0
			515	154	168	62	115	16		

- Molecule 9 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
9	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
9	B	76	Total	C	H	N	O	P	0	0
			2433	723	813	295	527	75		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	U	deletion	GB 1848954948
B	?	-	U	deletion	GB 1848954948

- Molecule 10 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	AA	1322	Total	C	H	N	O	S	0	0
			20852	6539	10427	1817	2026	43		

- Molecule 11 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AB	98	Total	C	H	N	O	S	0	0
			1573	505	783	139	140	6		

- Molecule 12 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AC	230	Total	C	H	N	O	S	0	0
			3599	1112	1813	317	351	6		

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Mol	Chain	Residues	Atoms						AltConf	Trace
12	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	1335	Total	C	H	N	O	S	0	0
			20999	6526	10611	1854	1958	50		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AF	83	Total	C	H	N	O	S	0	0
			1318	399	663	123	132	1		

- Molecule 15 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	C	66	Total	C	H	N	O	S	0	0
			1103	344	559	102	97	1		

- Molecule 16 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	D	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- Molecule 17 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	E	86	Total	C	H	N	O	S	0	0
			1388	414	719	138	114	3		

- Molecule 18 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	F	70	Total	C	H	N	O	S	0	0
			1218	366	629	125	97	1		

- Molecule 19 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 20 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 21 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 22 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 23 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 24 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 25 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 26 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 27 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

- Molecule 28 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

- Molecule 29 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

- Molecule 30 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

- Molecule 31 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 32 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 33 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 34 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 35 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 36 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 37 is a RNA chain called mRNA in the ribosomal RNA entrance pore.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	Y	3	Total	C	H	N	O	P	0	0
			90	27	30	6	24	3		

- Molecule 38 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

- Molecule 39 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

- Molecule 40 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 41 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

- Molecule 44 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 45 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

- Molecule 46 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

- Molecule 47 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

- Molecule 49 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

- Molecule 50 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

- Molecule 52 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 53 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 55 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 56 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 57 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 58 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 59 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 60 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 61 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	x	116	Total	C	H	N	O	0	0
			1815	552	923	178	162		

- Molecule 62 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 63 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	z	117	Total	C	H	N	O	0	0
			1967	604	1020	192	151		

- Molecule 64 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
64	7	1	Total	Mg	0
			1	1	

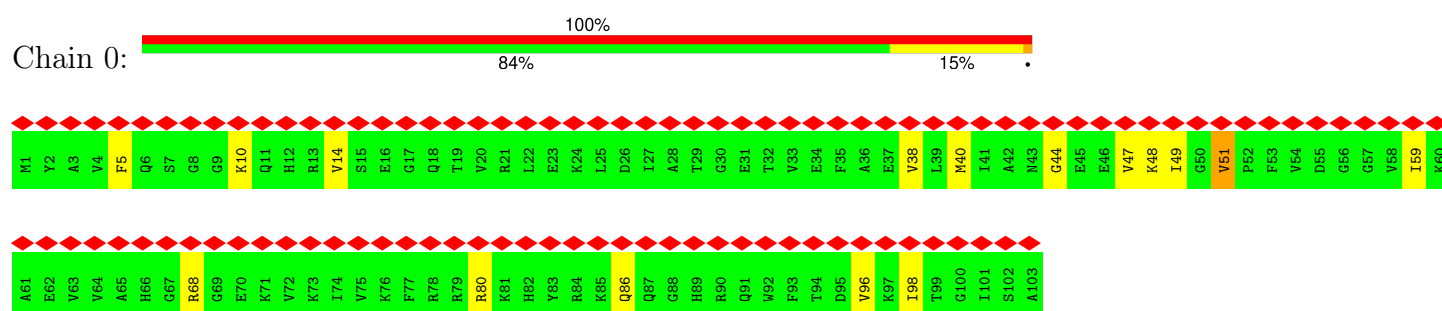
- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
65	AA	2	Total	Zn	0
			2	2	

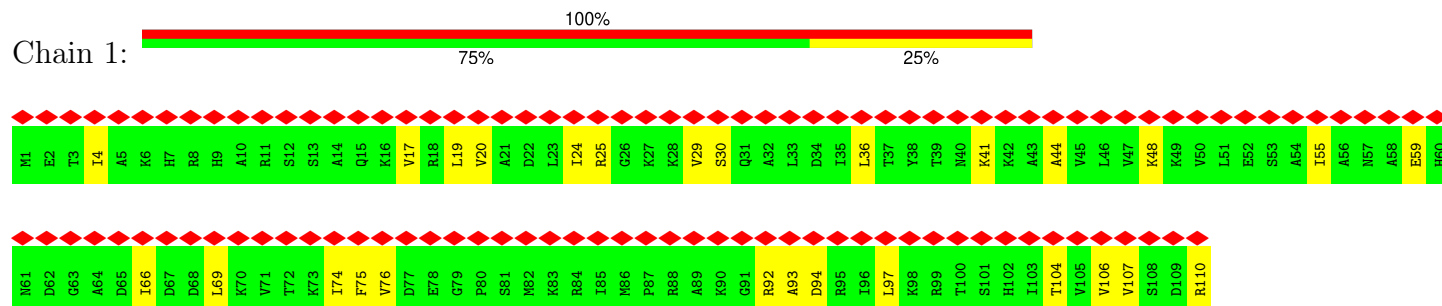
3 Residue-property plots

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

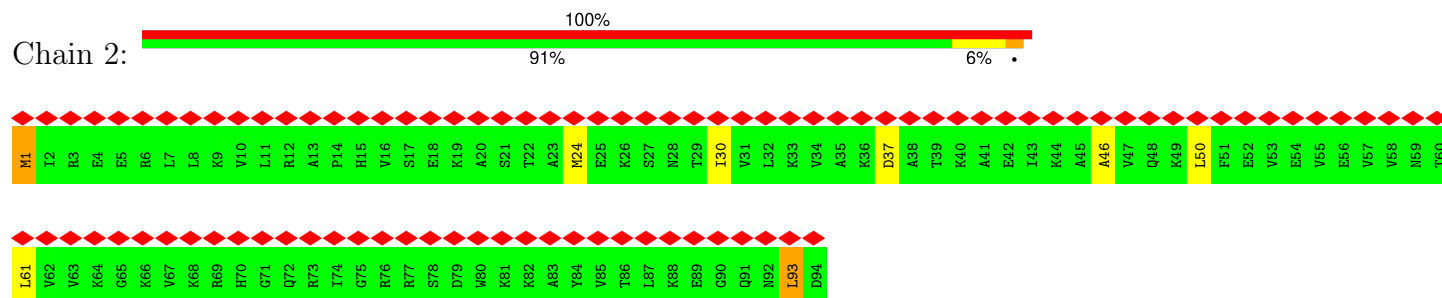
• Molecule 1: 50S ribosomal protein L21



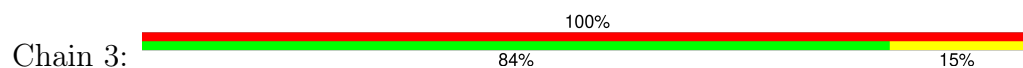
• Molecule 2: 50S ribosomal protein L22

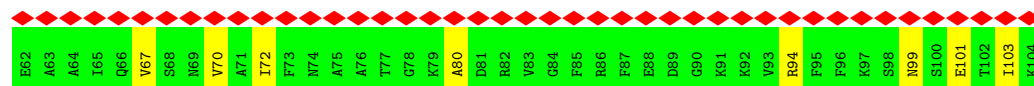


• Molecule 3: 50S ribosomal protein L23

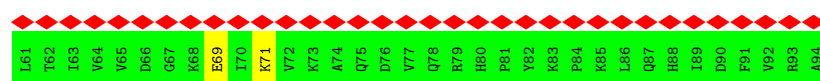
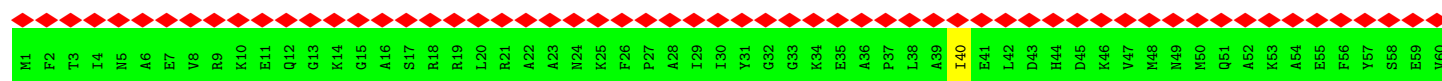


• Molecule 4: 50S ribosomal protein L24

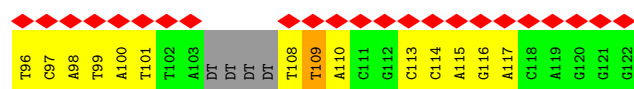
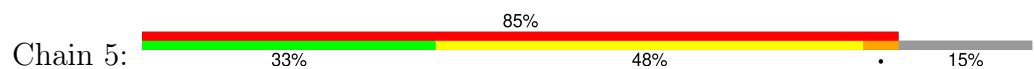




• Molecule 5: 50S ribosomal protein L25



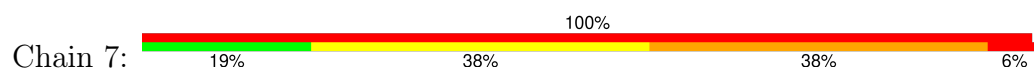
• Molecule 6: NT DNA



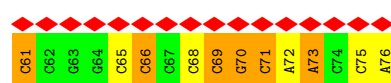
• Molecule 7: T DNA



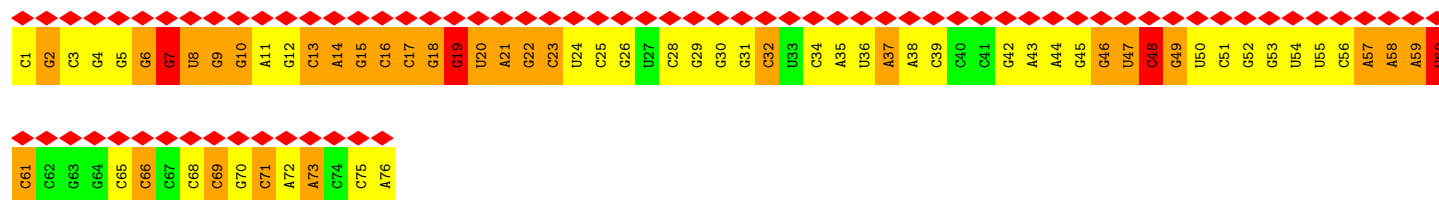
• Molecule 8: mRNA with 27 nt long spacer



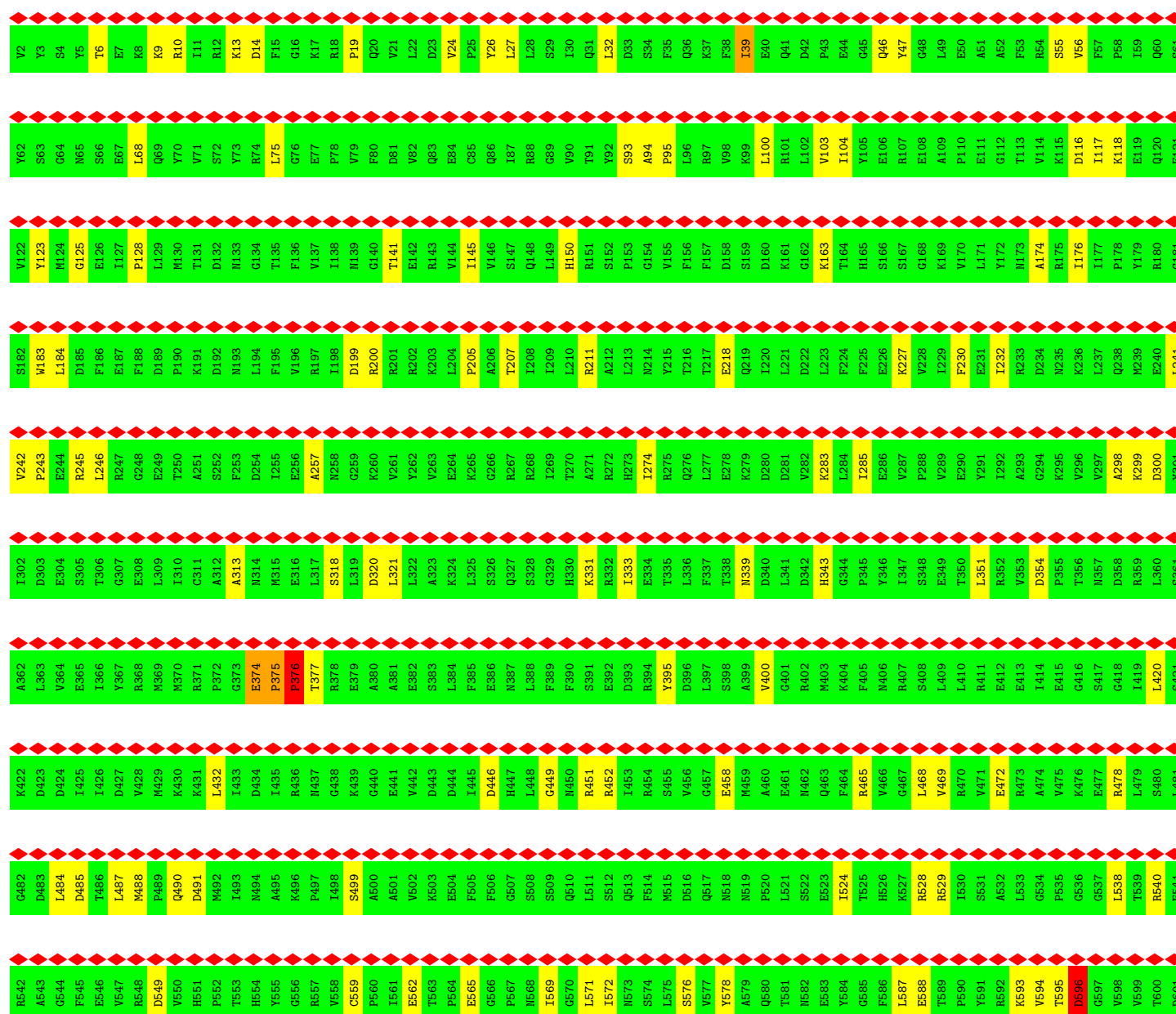
• Molecule 9: E-site and P-site tRNA (fMet)



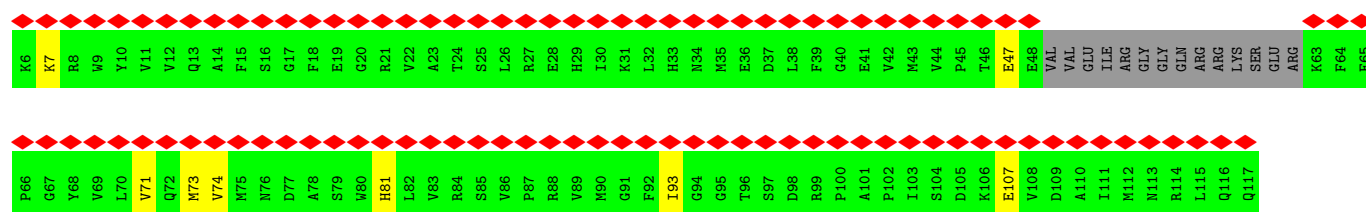
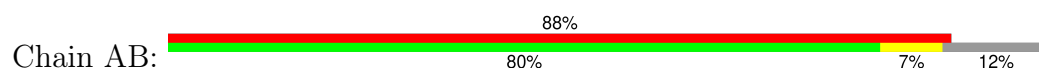
● Molecule 9: E-site and P-site tRNA (fMet)



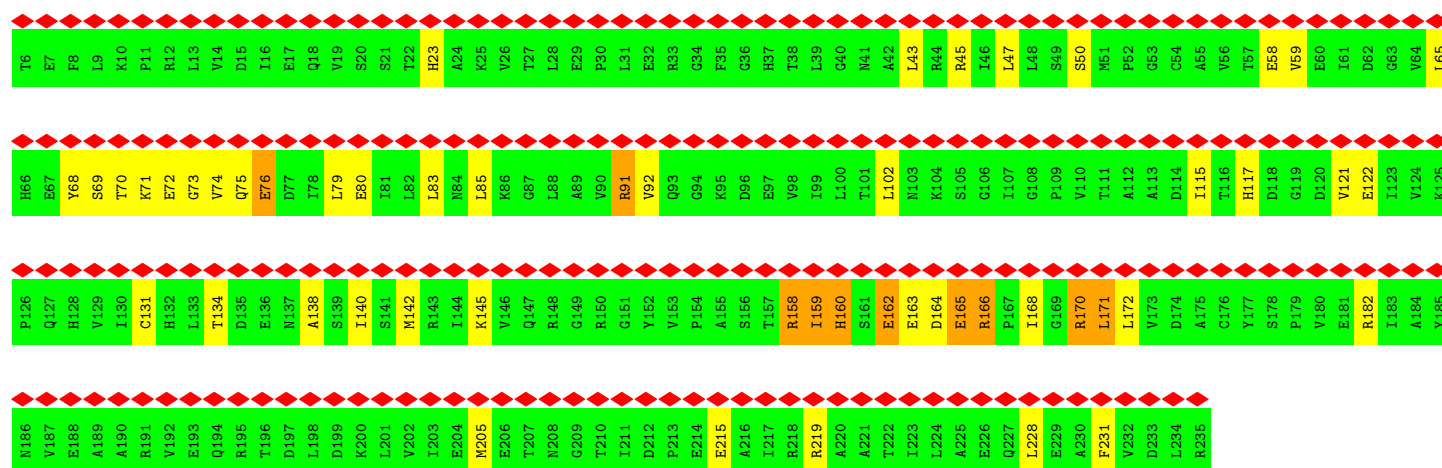
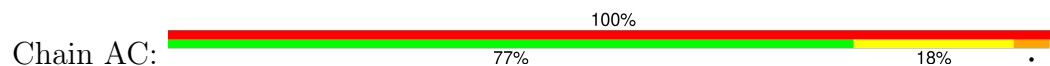
● Molecule 10: DNA-directed RNA polymerase subunit beta



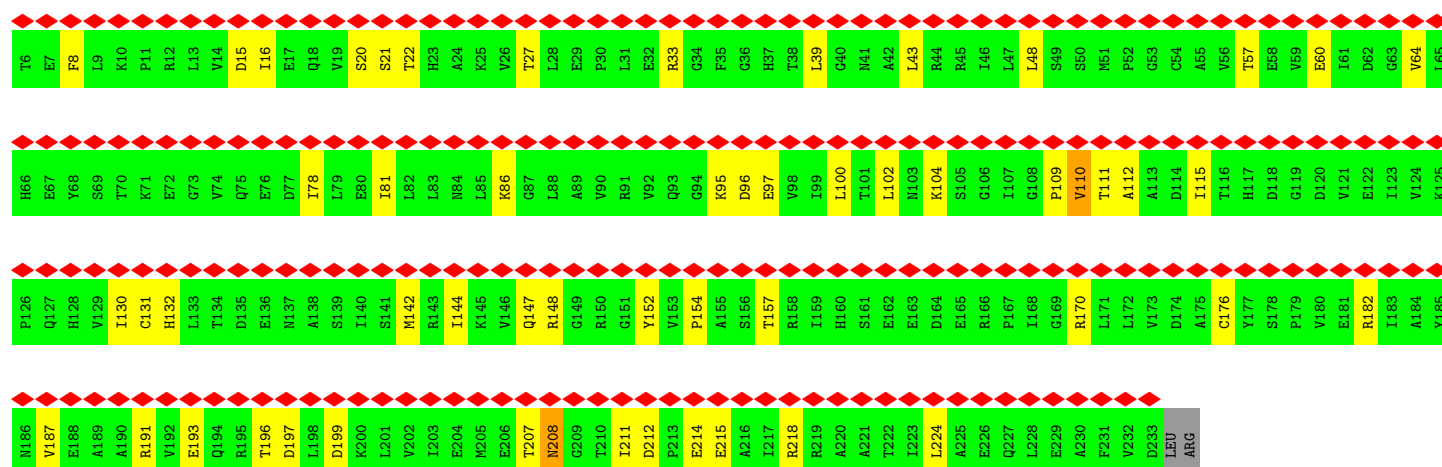
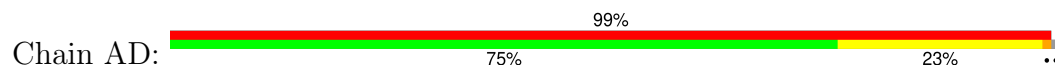
- Molecule 11: Transcription termination/antitermination protein NusG



- Molecule 12: DNA-directed RNA polymerase subunit alpha



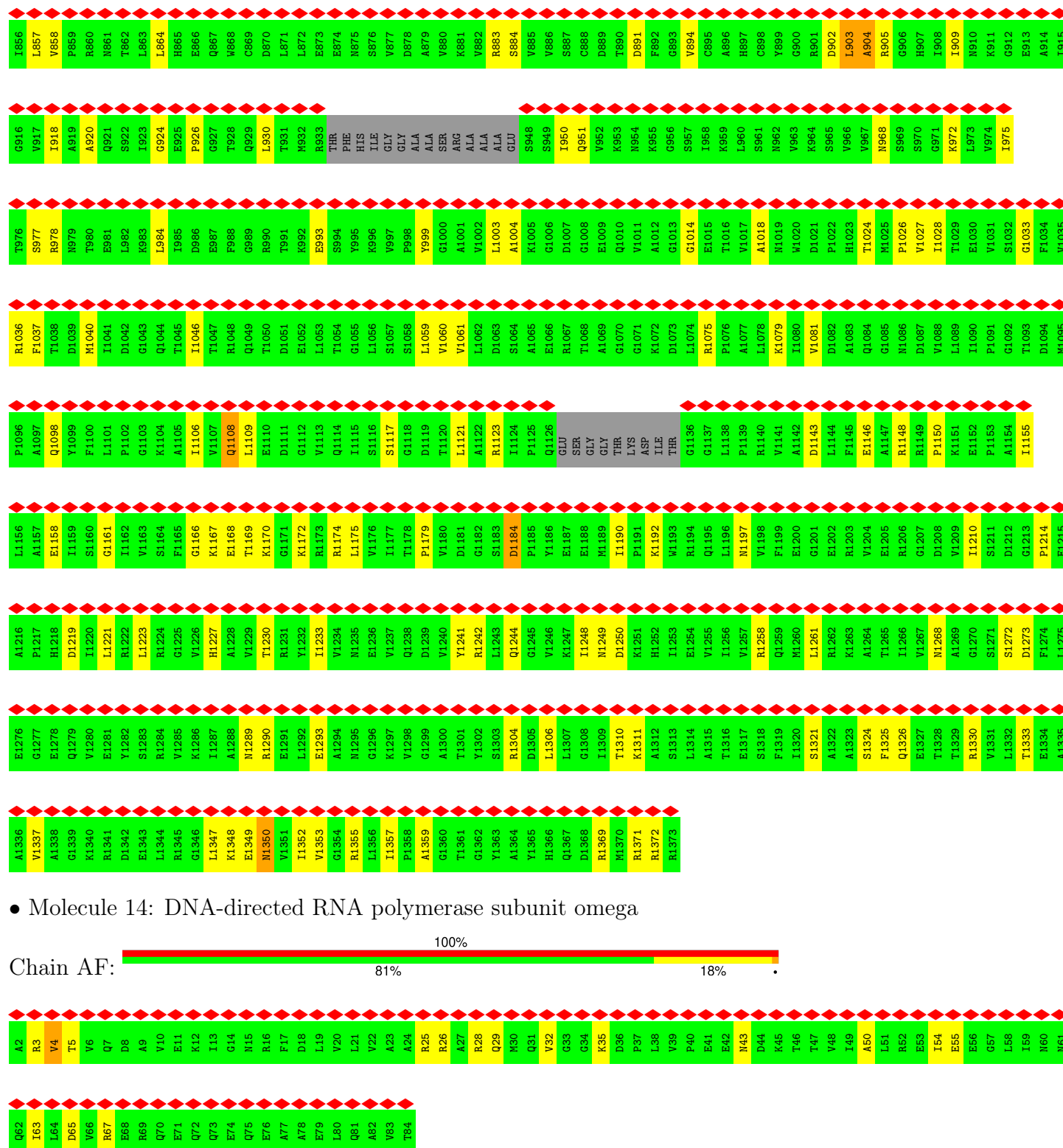
- Molecule 12: DNA-directed RNA polymerase subunit alpha

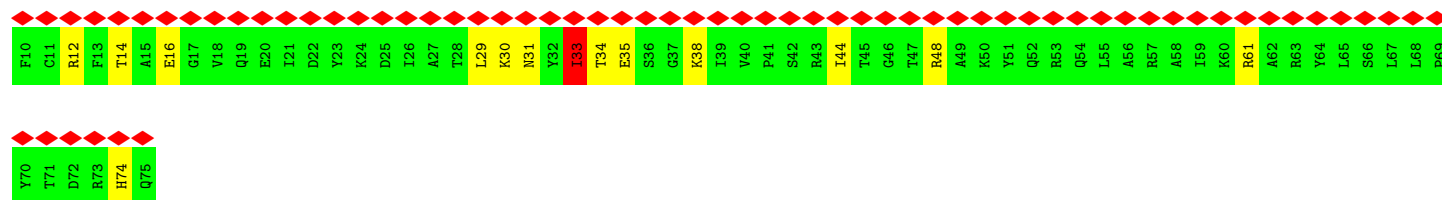


- Molecule 13: DNA-directed RNA polymerase subunit

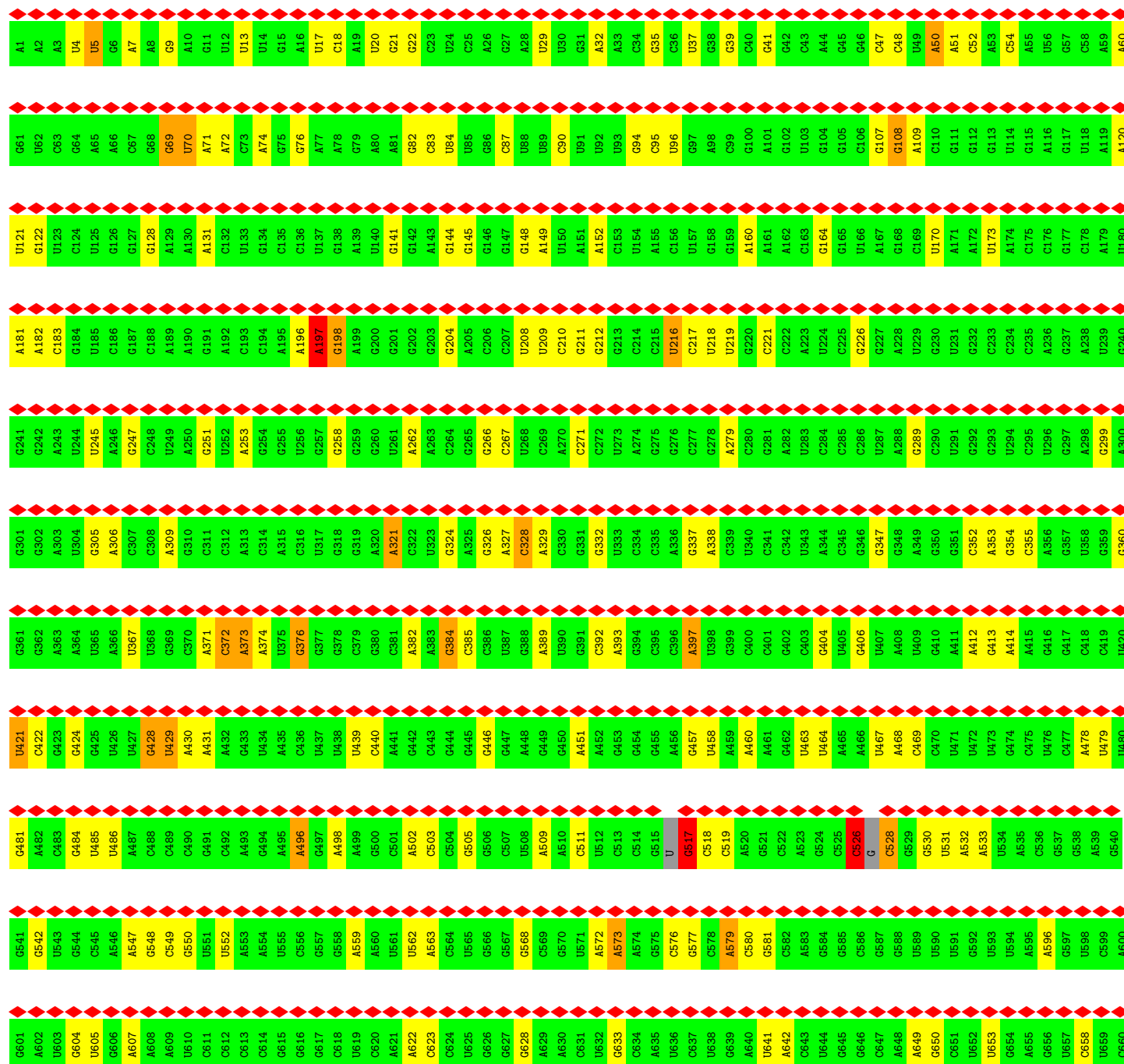


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E16	F17	D18	A19	I20	K21	I22	A23	L24	A25	S26	P27	D28	N29	I30	R31	S32	V33	S34	F35	G36	E37	V38	K39	K40	P41	E42	T43	I44	I45	Y46	R47	T48	F49	K50	P51	E52	R53	D54	O55	L56	F57	C58	A59	R60	T61	F62	O63	P64	V65	K66	D67	V68	E69	C70	L71	C72	G73	K74	Y75	

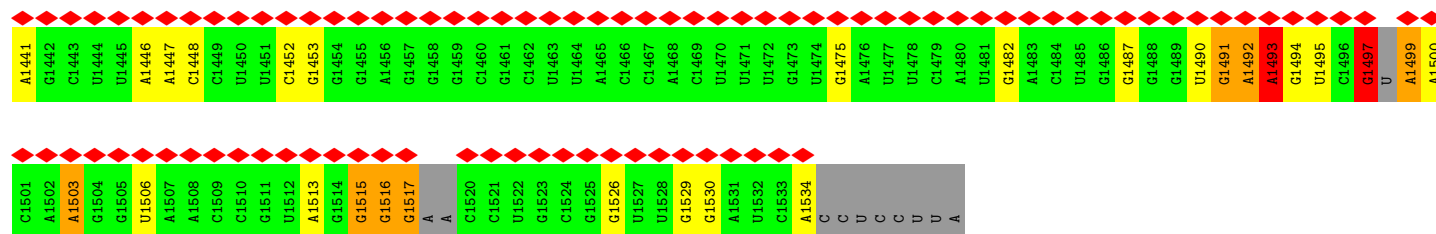




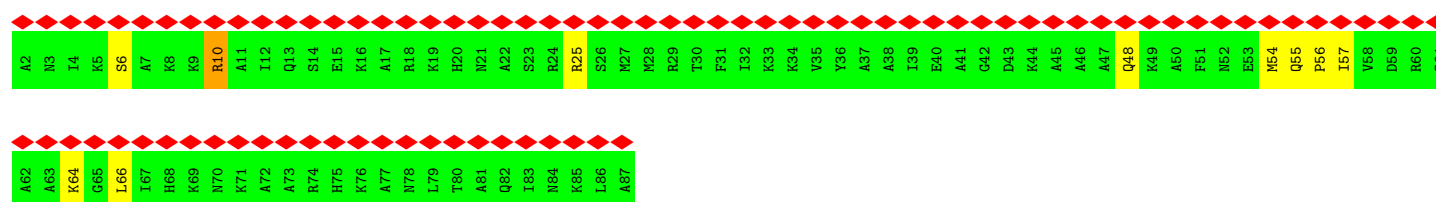
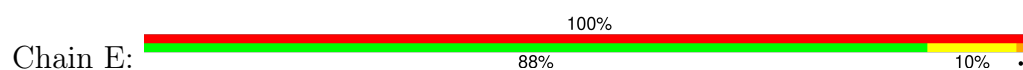
● Molecule 16: 16S rRNA



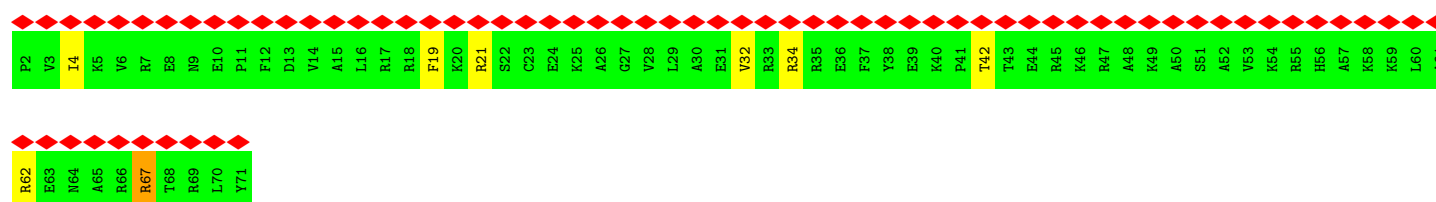
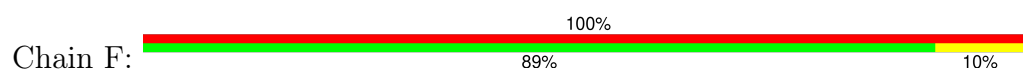
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G721	G722	U723	G724	G725	C726	G727	A728	A729	G730	G731	C732	G733	G734	C735	C736	C737	C738	C739	U740	G741	G742	A743	G744	G745	A746	A747	G748	A749	C750	U751	G752	A753	C754	G755	C756	U757	G758	C759	G760	G761	U762	G763	G764	G765	A766	A767	A768	G769	C770	G771	U772	G773	G774	G775	G776	A777	G778	C779	A780
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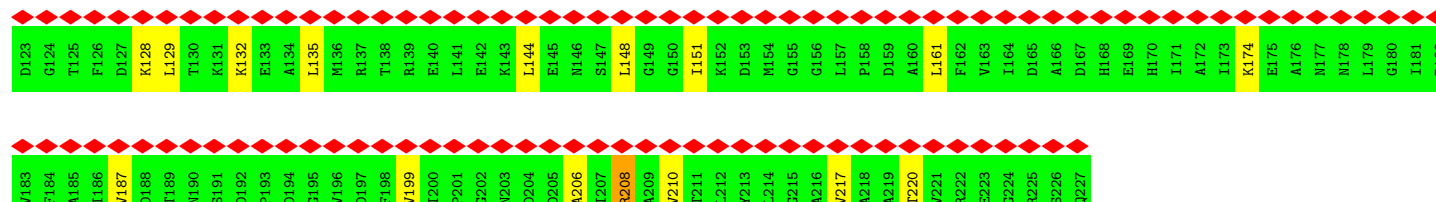
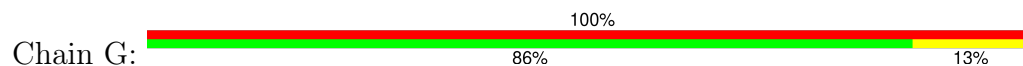
• Molecule 17: 30S ribosomal protein S20



• Molecule 18: 30S ribosomal protein S21

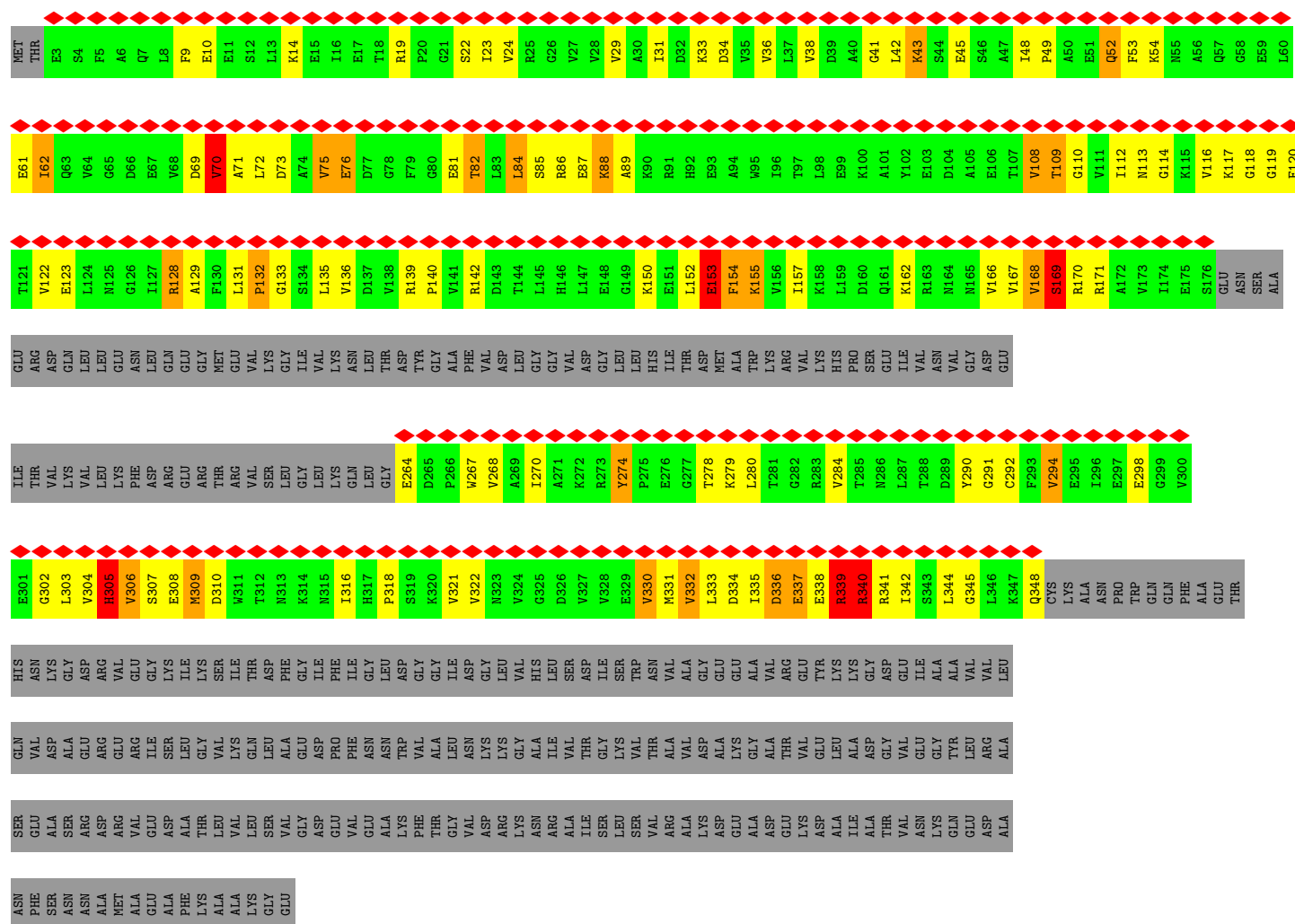


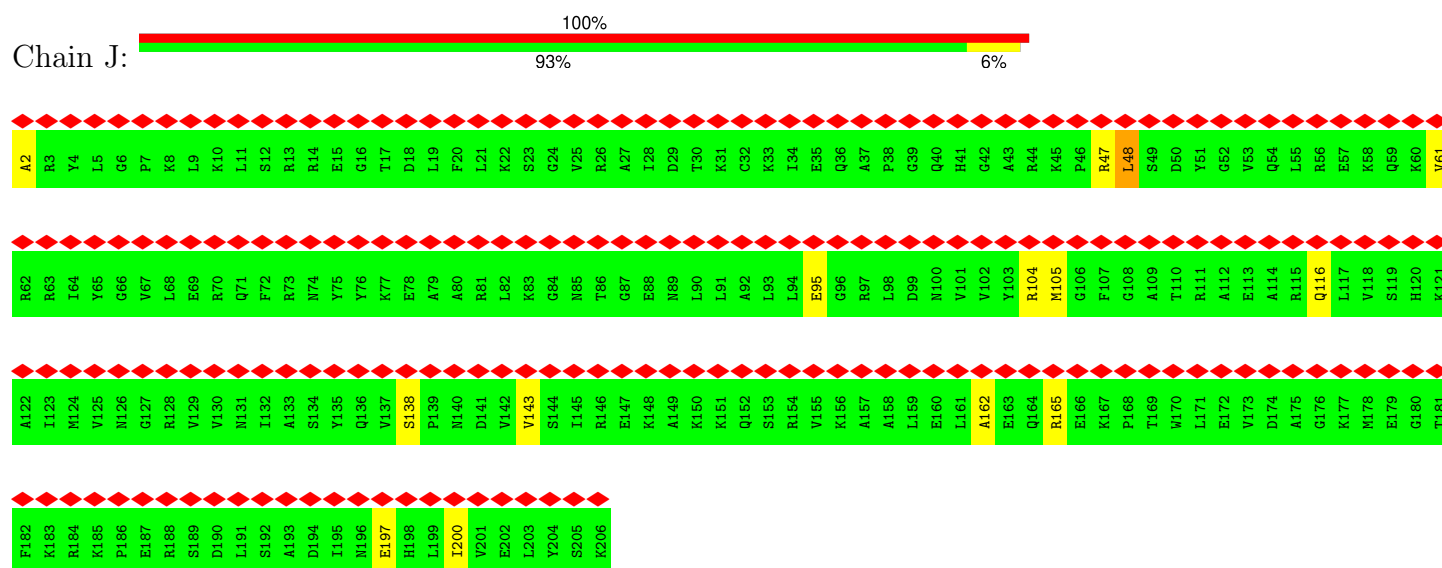
• Molecule 19: 30S ribosomal protein S2



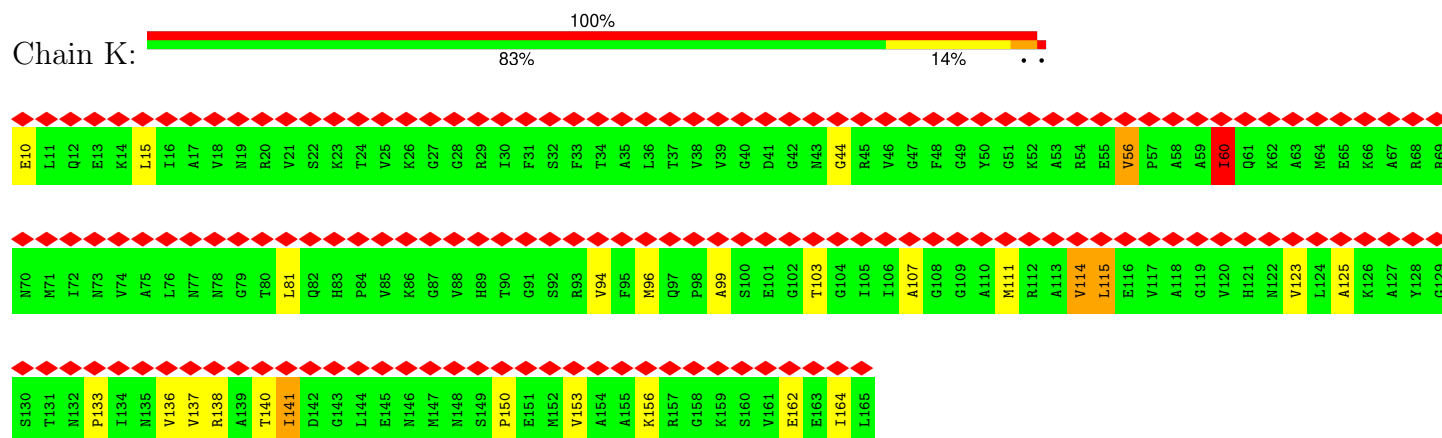
• Molecule 20: 30S ribosomal protein S1



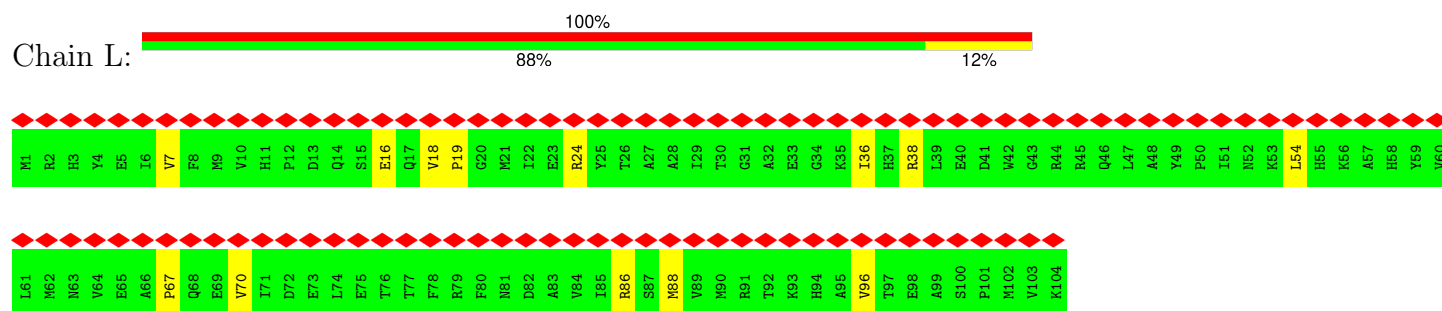




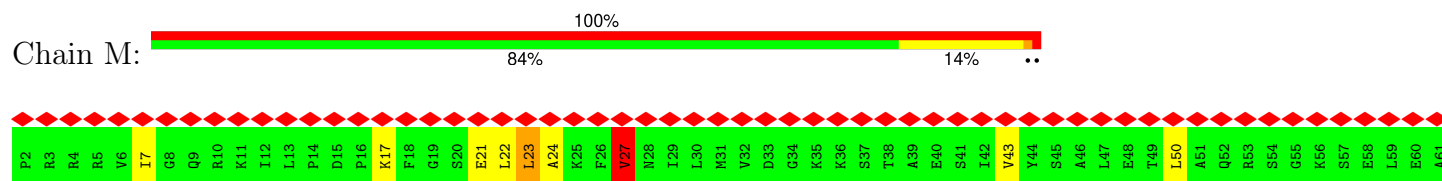
- Molecule 23: 30S ribosomal protein S5



- Molecule 24: 30S ribosomal protein S6

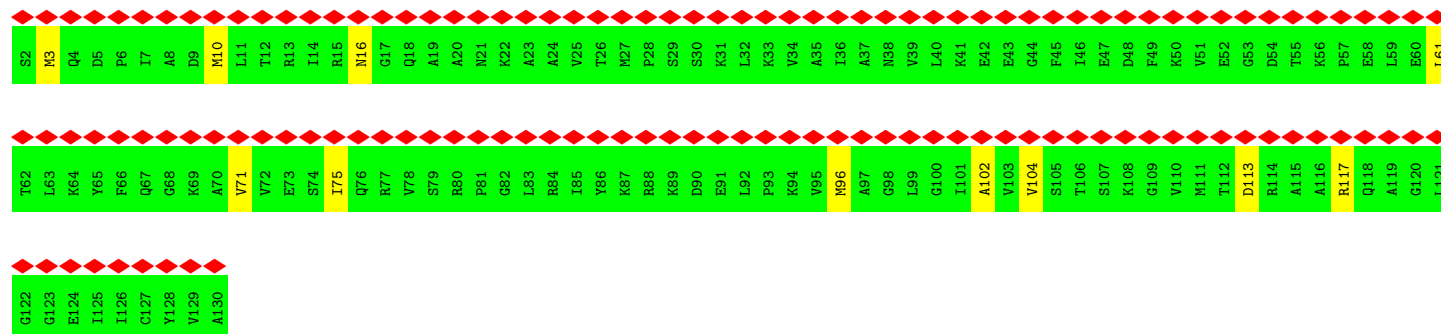
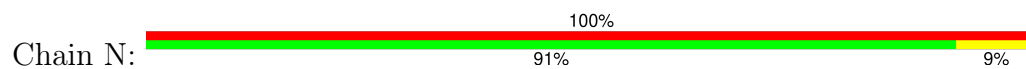


- Molecule 25: 30S ribosomal protein S7

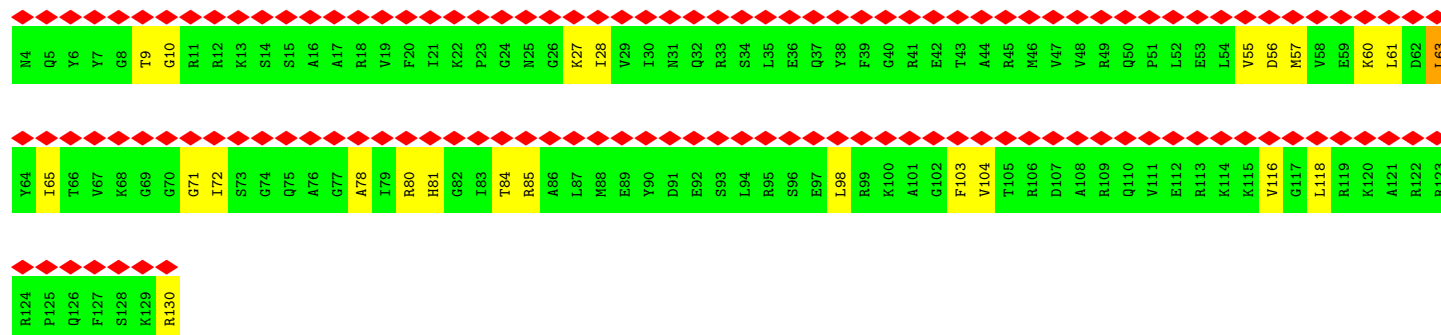
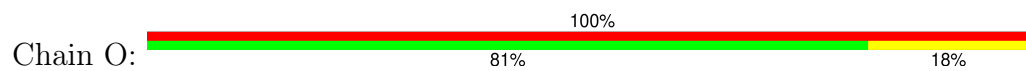




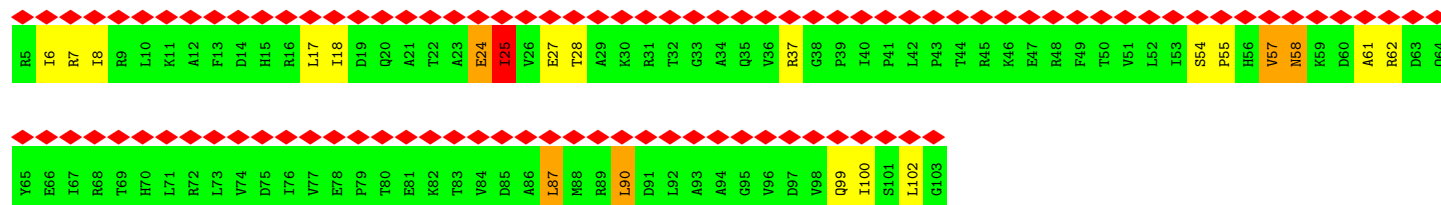
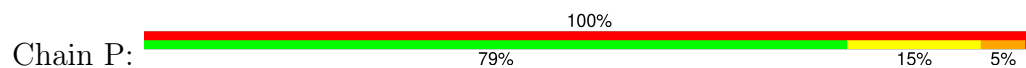
• Molecule 26: 30S ribosomal protein S8



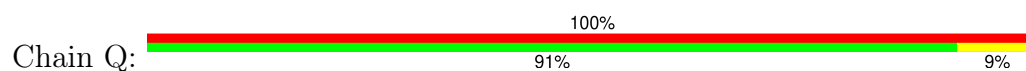
• Molecule 27: 30S ribosomal protein S9



• Molecule 28: 30S ribosomal protein S10

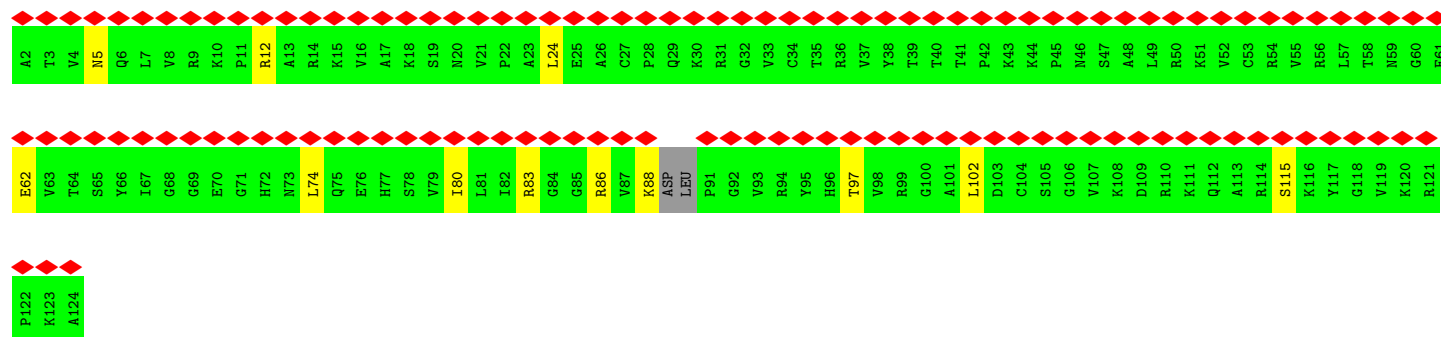
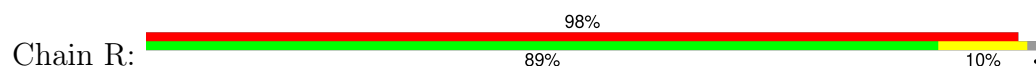


• Molecule 29: 30S ribosomal protein S11

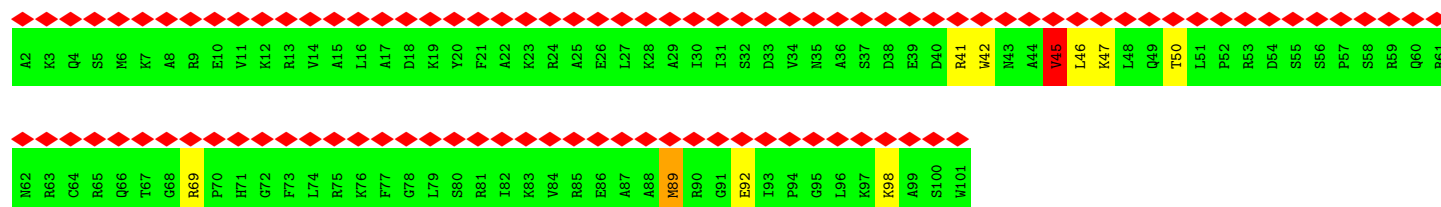
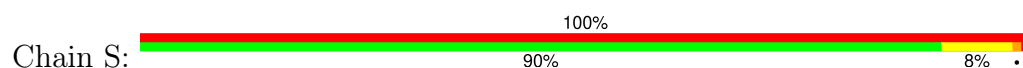




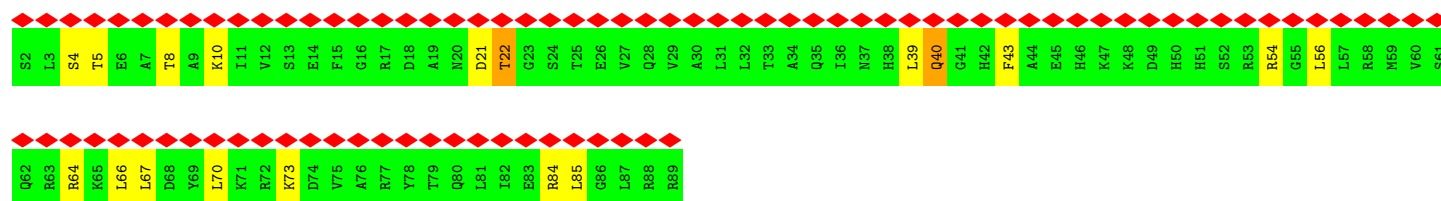
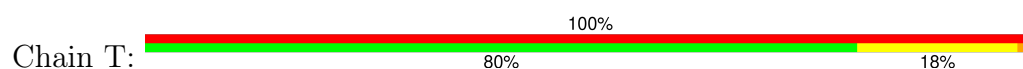
• Molecule 30: 30S ribosomal protein S12



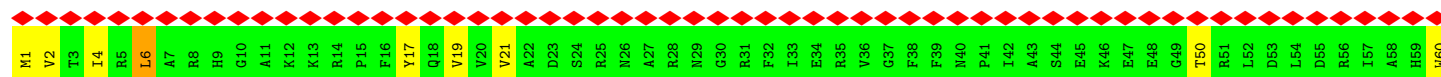
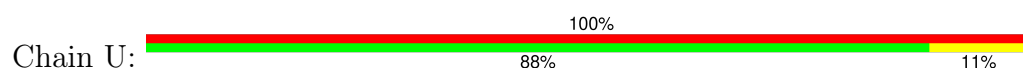
• Molecule 31: 30S ribosomal protein S14



• Molecule 32: 30S ribosomal protein S15

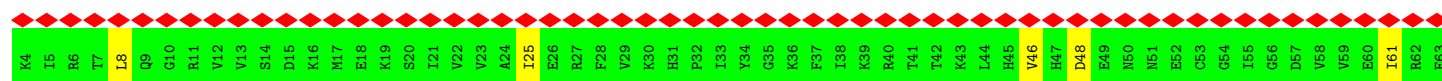
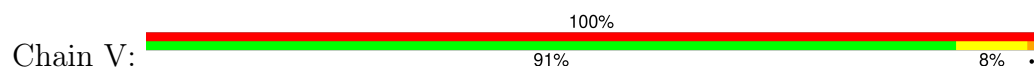


• Molecule 33: 30S ribosomal protein S16

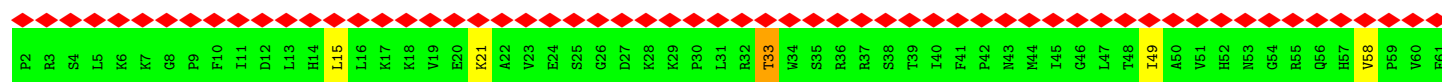
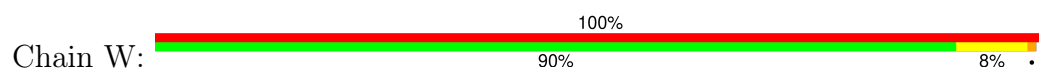




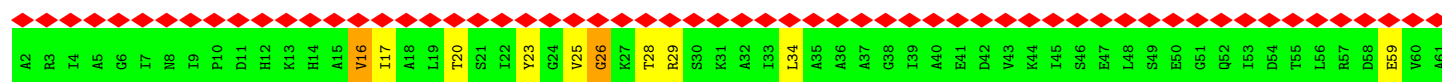
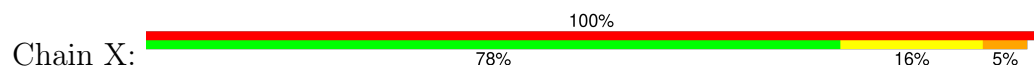
• Molecule 34: 30S ribosomal protein S17



• Molecule 35: 30S ribosomal protein S19



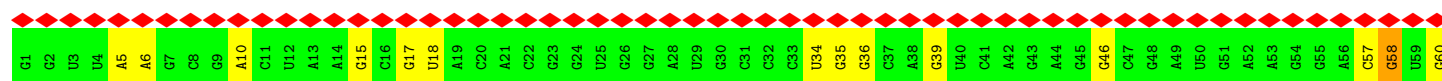
• Molecule 36: 30S ribosomal protein S13



• Molecule 37: mRNA in the ribosomal RNA entrance pore



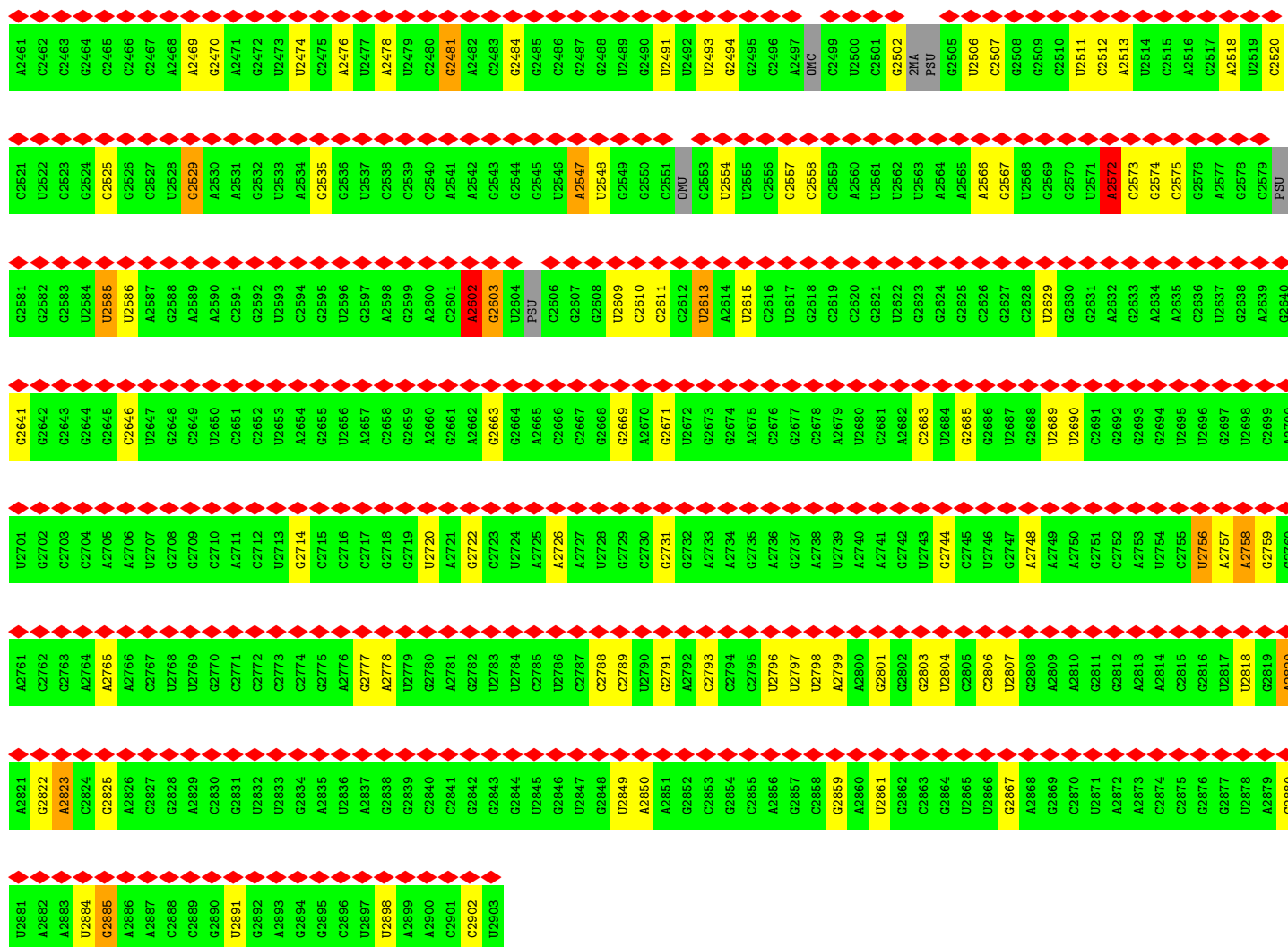
• Molecule 38: 23S rRNA



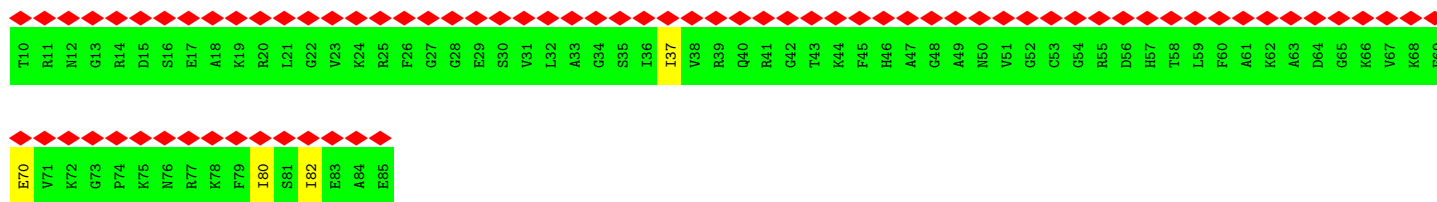
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G1673	G1613	U1553	C1493	A1433	A1373	U1313	A1253	G1193	A1133	G1073	C1013	G953
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C1675	C1615	G1555	A1495	G1435	U1375	C1315	U1255	G1195	C1135	C1075	U1015	PSD
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A1678	6VZ	C1558	U1498	U1438	A1378	U1318	U1258	U1198	G1138	U1078	U1018	U958
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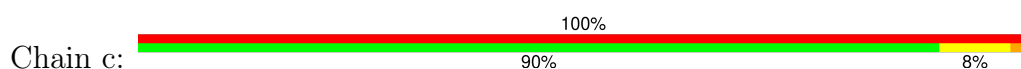
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C1741	U1742	G1743	A1744	C1745	A1746	U1747	C1748	A1749	A1750	U1751	C1752	G1753	A1754	A1755	G1756	A1757	U1758	A1759	C1760	A1761	A1762	G1763	C1764	U1765	G1766	G1767	C1768	U1769	G1770	A1771	C1772	A1773	C1774	U1775	G1776	A1777	U1778	U1779	A1780	U1781	U1782	G1783	A1784	A1785	A1786	A1787	C1788	A1789	C1790	A1791	G1792	C1793	A1794	C1795	U1796	U1797	U1798	A1799	C1800		
A1801	A1802	A1803	C1804	A1805	C1806	G1807	A1808	A1809	A1810	U1811	U1812	G1813	G1814	A1815	C1816	U1817	U1818	A1819	U1820	A1821	C1822	G1823	G1824	U1825	G1826	U1827	G1828	A1829	C1830	G1831	C1832	C1833	U1834	2MG	C1836	C1837	C1838	G1839	G1840	U1841	G1842	C1843	C1844	G1845	G1846	A1847	A1848	G1849	G1850	U1851	U1852	A1853	A1854	U1855	U1856	G1857	A1858	U1859	G1860		
G1861	G1862	G1863	U1864	U1865	A1866	G1867	C1868	G1869	C1870	A1871	A1872	G1873	C1874	G1875	A1876	A1877	G1878	C1879	U1880	C1881	U1882	U1883	G1884	A1885	U1886	C1887	G1888	A1889	A1890	G1891	C1892	C1893	C1894	C1895	G1896	G1897	C1898	A1899	A1900	A1901	C1902	G1903	G1904	C1905	G1906	G1907	C1908	C1909	G1910	PSU	U1912	A1913	C1914	3TD	A1916	PSU	A1918	A1919	C1920		
G1921	G1922	U1923	C1924	C1925	U1926	A1927	A1928	G1929	G1930	U1931	A1932	G1933	C1934	G1935	A1936	A1937	A1938	5MG	U1940	C1941	C1942	U1943	U1944	G1945	U1946	C1947	G1948	G1949	G1950	U1951	A1952	A1953	G1954	U1955	U1956	C1957	C1958	G1959	A1960	C1961	5MC	U1963	G1964	C1965	A1966	C1967	G1968	A1969	U1970	U1971	G1972	G1973	C1974	G1975	U1976	A1977	U1978	U1979	G1980		
A1981	U1982	G1983	G1984	C1985	C1986	A1987	G1988	G1989	C1990	U1991	G1992	U1993	C1994	U1995	C1996	C1997	A1998	C1999	C2000	C2001	C2002	A2003	G2004	A2005	C2006	U2007	C2008	A2009	G2010	U2011	G2012	A2013	A2014	A2015	U2016	U2017	G2018	A2019	A2020	C2021	U2022	C2023	G2024	C2025	U2026	G2027	U2028	G2029	6MZ	A2031	A2032	A2033	U2034	G2035	C2036	A2037	G2038	U2039	G2040		
U2041	A2042	C2043	C2044	C2045	G2046	C2047	G2048	G2049	C2050	A2051	A2052	G2053	A2054	C2055	G2056	G2057	A2058	A2059	A2060	G2061	A2062	C2063	C2064	C2065	C2066	G2067	U2068	GTN	A2070	A2071	C2072	C2073	U	U2075	U2076	A2077	C2078	U2079	A2080	U2081	A2082	G2083	C2084	U2085	U2086	G2087	A2088	C2089	A2090	C2091	U2092	G2093	A2094	A2095	C2096	A2097	U2098	U2099	G2100		
A2101	G2102	C2103	C2104	U2105	U2106	G2107	A2108	U2109	G2110	U2111	G2112	U2113	A2114	G2115	G2116	A2117	U2118	A2119	G2120	G2121	U2122	G2123	G2124	G2125	A2126	G2127	G2128	C2129	U2130	U2131	U2132	G2133	A2134	U2075	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	C2143	G2144	C2145	C2146	A2147	G2148	U2149	C2150	U2151	G2152	C2153	A2154	U2155	G2156	G2157	A2158	U2159	C2160	
C2161	G2162	A2163	C2164	C2165	U2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174	C2175	A2176	C2177	C2178	C2179	U2180	U2181	U2182	A2183	A2184	U2185	G2186	G2187	U2188	U2189	G2190	A2191	U2192	G2193	U2194	U2195	C2196	U2197	A2198	A2199	C2200	G2201	U2202	U2203	G2204	A2205	C2206	C2207	C2208	G2209	U2210	A2211	G2212	U2213	C2214	C2215	G2216	G2217	G2218	U2219	U2220		
G2221	C2222	G2223	G2224	A2225	C2226	A2227	G2228	U2229	G2230	U2231	C2232	U2233	G2234	G2235	U2236	G2237	G2238	G2239	U2240	A2241	G2242	U2243	U2244	U2245	G2246	A2247	C2248	U2249	C2250	DMG	G2252	G2253	C2254	G2255	G2256	U2257	C2258	U2259	C2260	C2261	U2262	C2263	C2264	U2265	A2266	A2267	A2268	G2269	A2270	G2271	U2272	A2273	A2274	C2275	G2276	G2277	G2278	G2279	G2280		
A2281	G2282	C2283	A2284	C2285	G2286	A2287	A2288	G2289	G2290	U2291	U2292	G2293	G2294	C2295	U2296	A2297	A2298	U2299	C2300	C2301	U2302	G2303	G2304	U2305	C2306	G2307	G2308	A2309	C2310	A2311	U2312	C2313	C2314	G2315	G2316	A2317	G2318	G2319	U2320	U2321	A2322	G2323	U2324	G2325	G2326	A2327	A2328	U2329	G2330	G2331	C2332	A2333	U2334	A2335	A2336	G2337	C2338	C2339	A2340		
G2341	C2342	U2343	U2344	G2345	A2346	C2347	U2348	G2349	C2350	G2351	A2352	G2353	C2354	G2355	U2356	A2357	A2358	C2359	G2360	G2361	G2362	C2363	C2364	G2365	A2366	G2367	C2368	G2369	A2370	G2371	U2372	G2373	C2374	G2375	A2376	A2377	U2378	G2379	C2380	A2381	C2382	G2383	U2384	C2385	A2386	U2387	C2388	G2389	U2390	G2391	A2392	U2393	C2394	C2395	C2396	U2397	PSU	G2458	A2459	G2399	G2400
U2401	U2402	C2403	U2404	G2405	A2406	A2407	U2408	G2409	G2410	A2411	A2412	G2413	G2414	G2415	C2416	C2417	A2418	U2419	C2420	G2421	U2422	U2423	C2424	A2425	A2426	C2427	G2428	G2429	A2430	U2431	A2432	A2433	A2434	A2435	C2436	G2437	U2438	A2439	C2440	U2441	C2442	C2443	C2444	2MG	G2446	G2447	A2448	U2449	U2450	A2451	C2452	A2453	G2454	C2455	C2456	PSU	G2458	A2459	G2399	G2460	

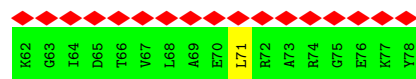


• Molecule 39: 50S ribosomal protein L27

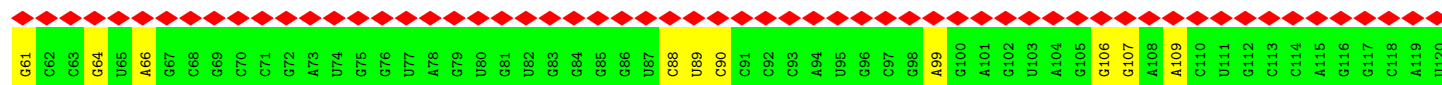
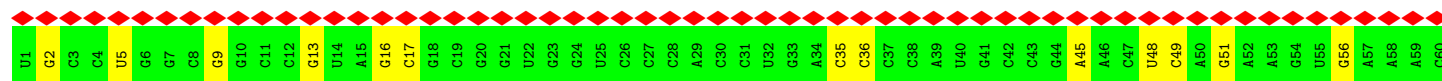
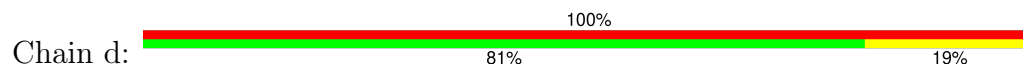


• Molecule 40: 50S ribosomal protein L28

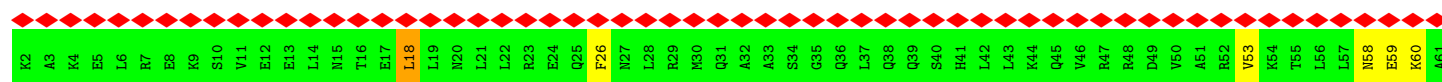
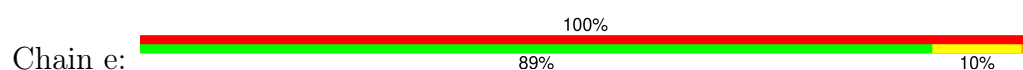




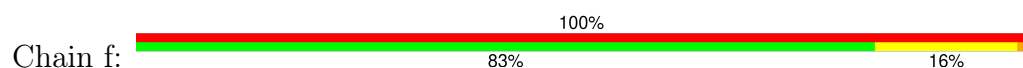
• Molecule 41: 5S rRNA



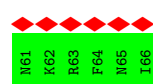
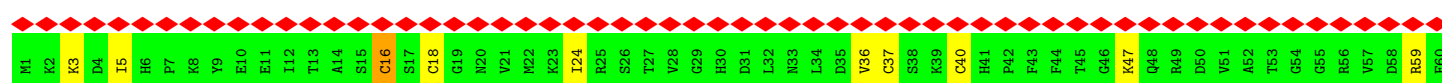
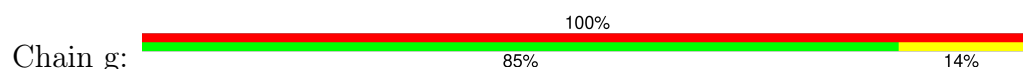
• Molecule 42: 50S ribosomal protein L29



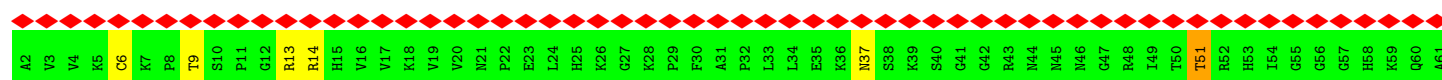
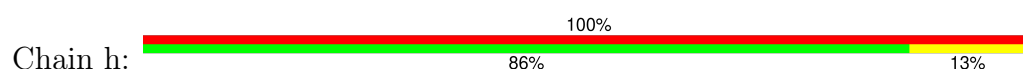
• Molecule 43: 50S ribosomal protein L30

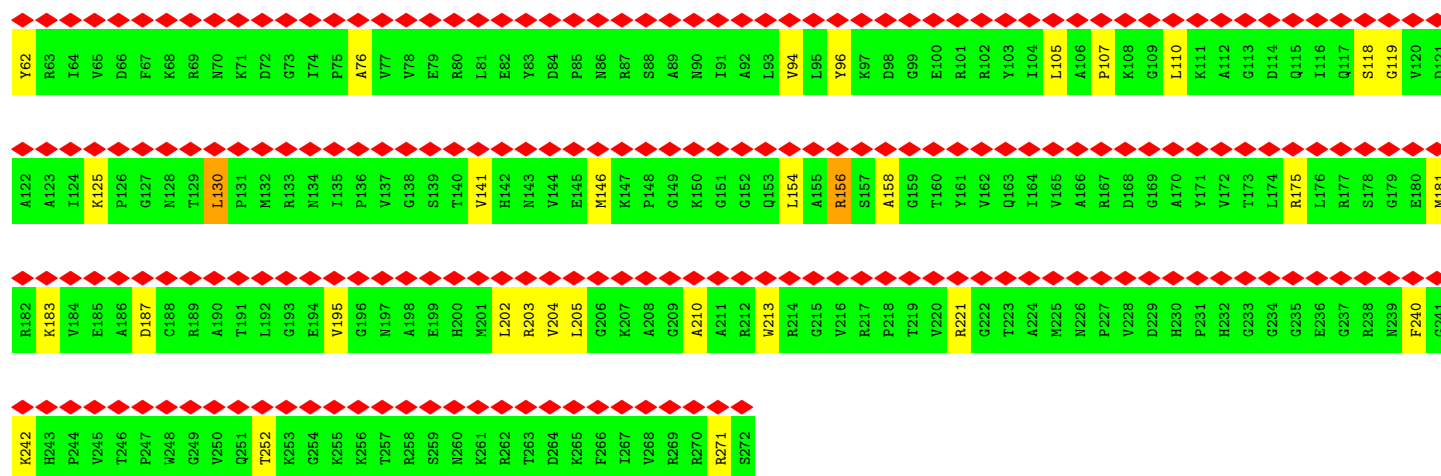


• Molecule 44: 50S ribosomal protein L31

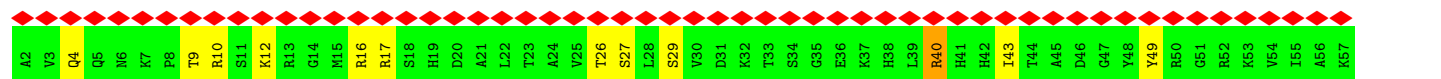
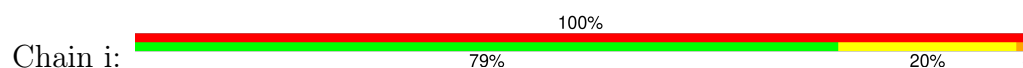


• Molecule 45: 50S ribosomal protein L2

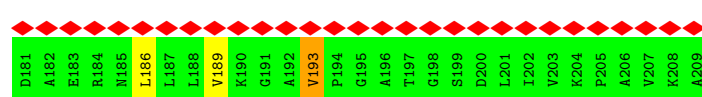
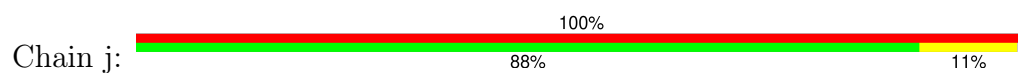




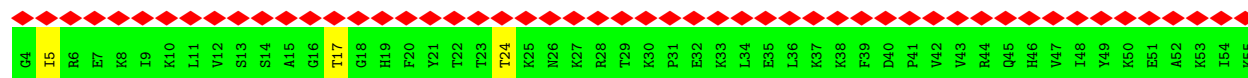
• Molecule 46: 50S ribosomal protein L32



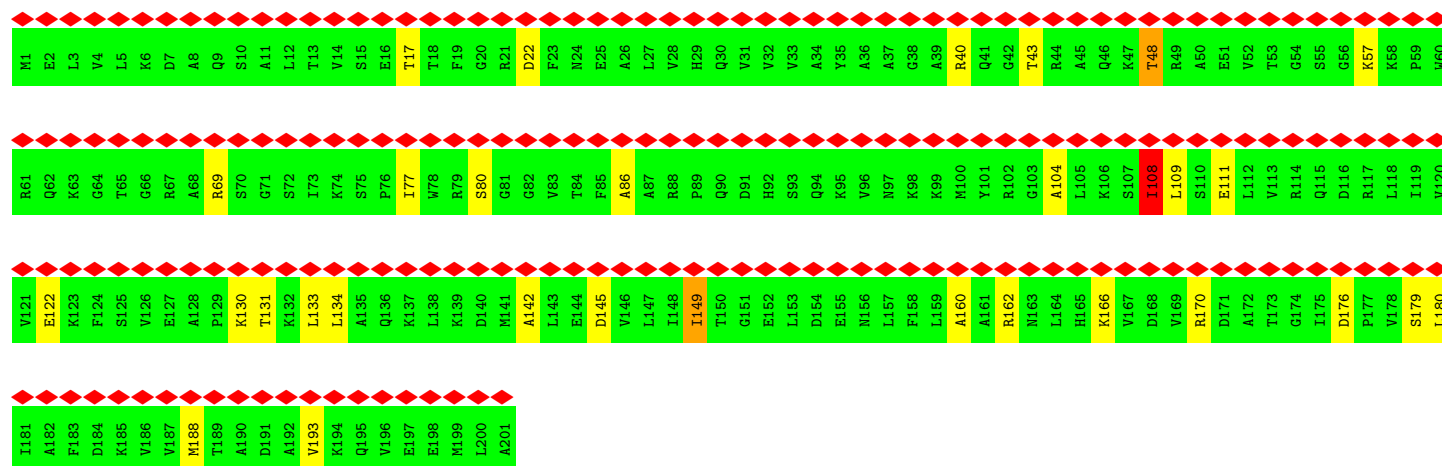
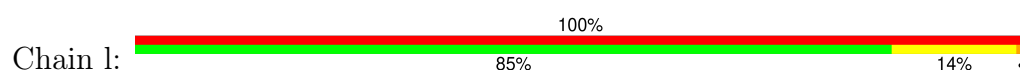
• Molecule 47: 50S ribosomal protein L3



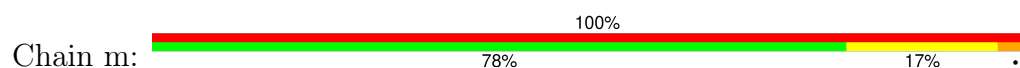
• Molecule 48: 50S ribosomal protein L33



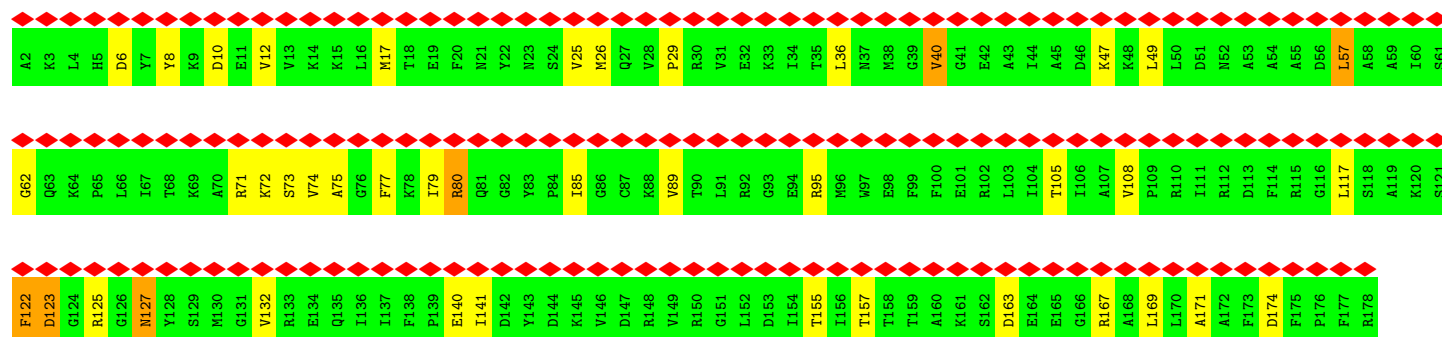
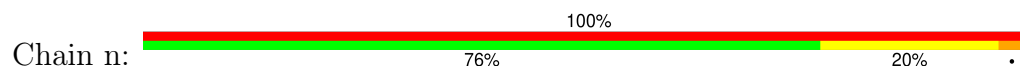
• Molecule 49: 50S ribosomal protein L4



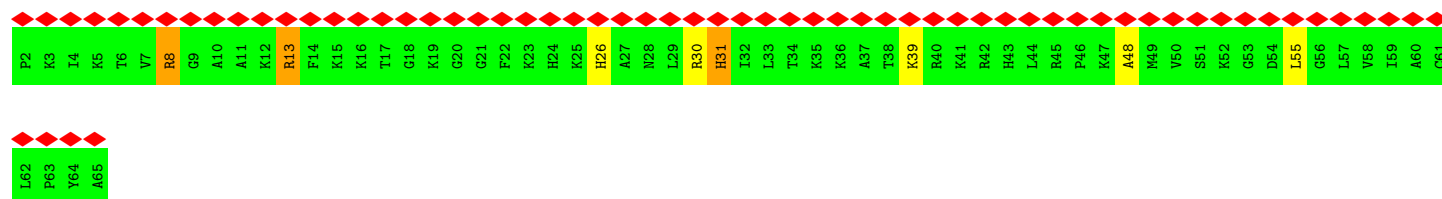
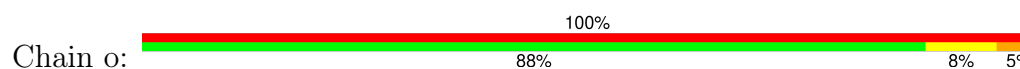
• Molecule 50: 50S ribosomal protein L34



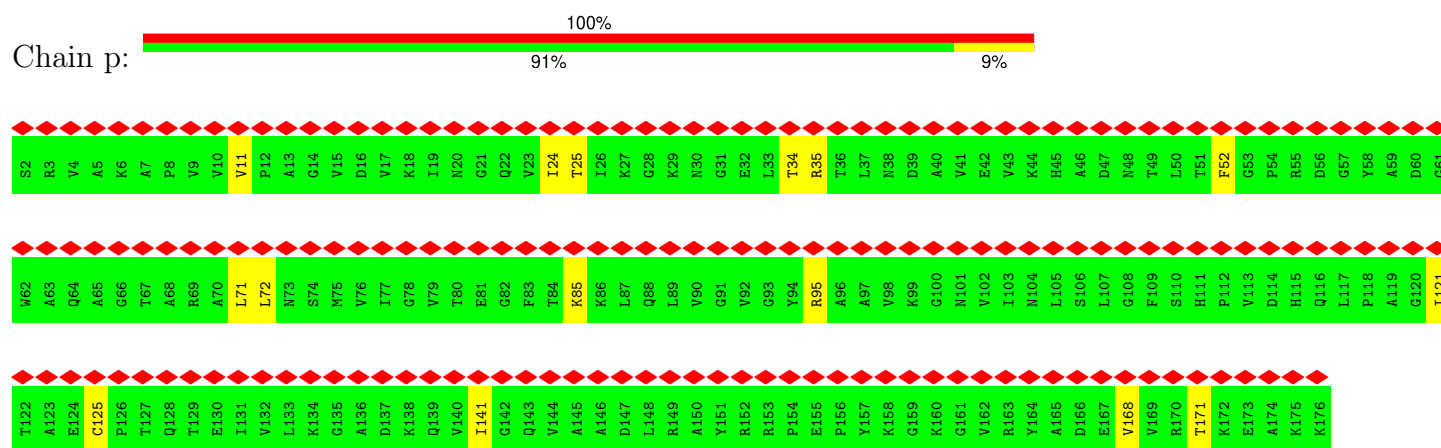
• Molecule 51: 50S ribosomal protein L5



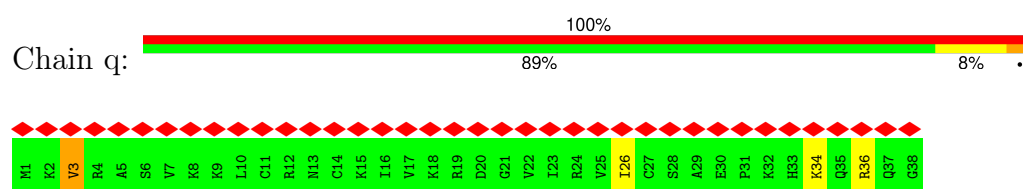
• Molecule 52: 50S ribosomal protein L35



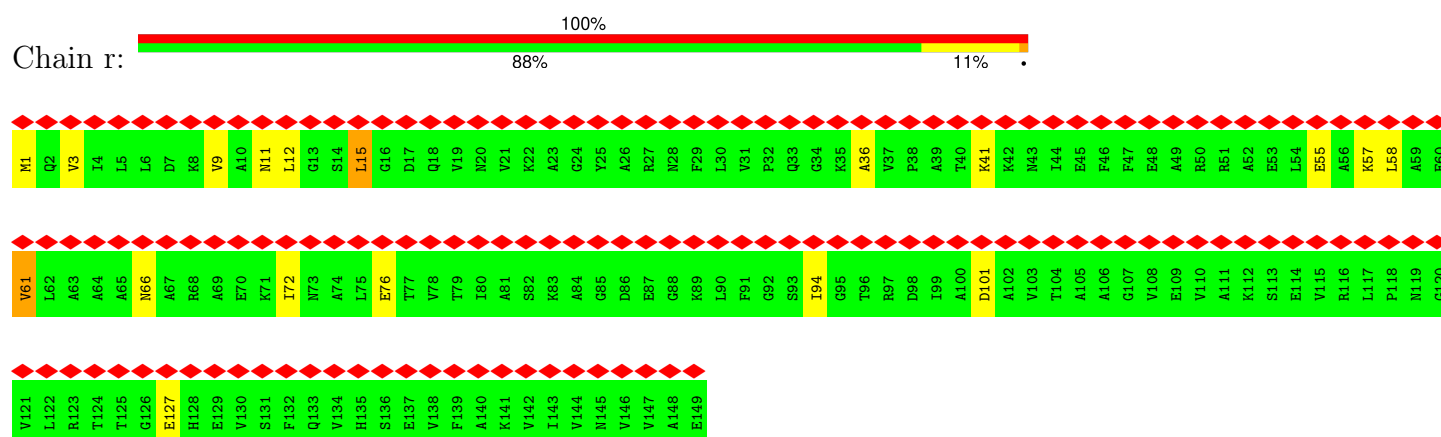
• Molecule 53: 50S ribosomal protein L6



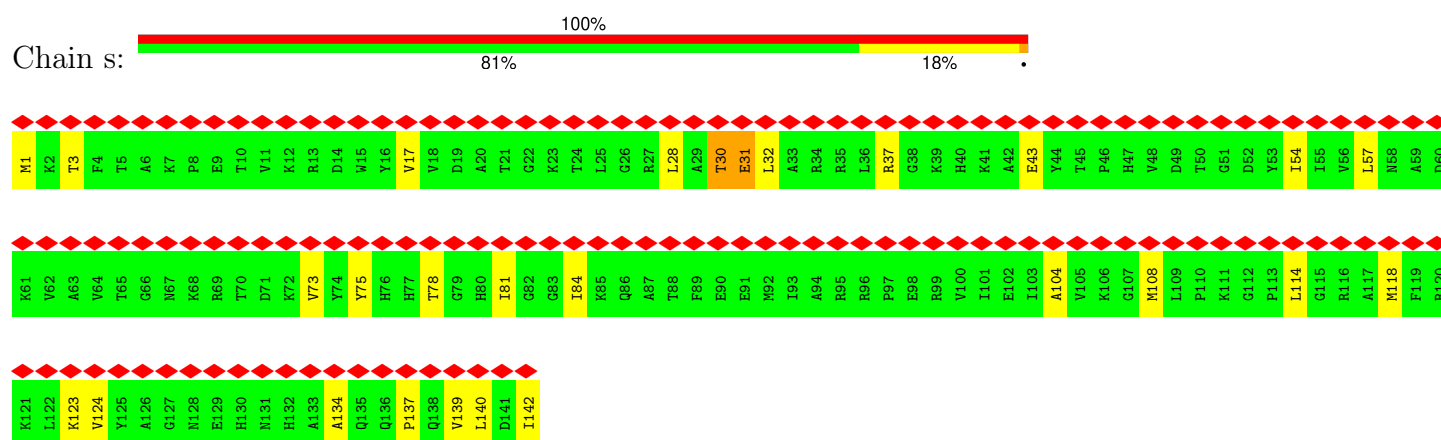
- Molecule 54: 50S ribosomal protein L36



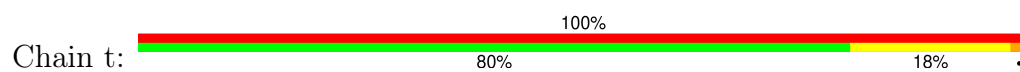
- Molecule 55: 50S ribosomal protein L9



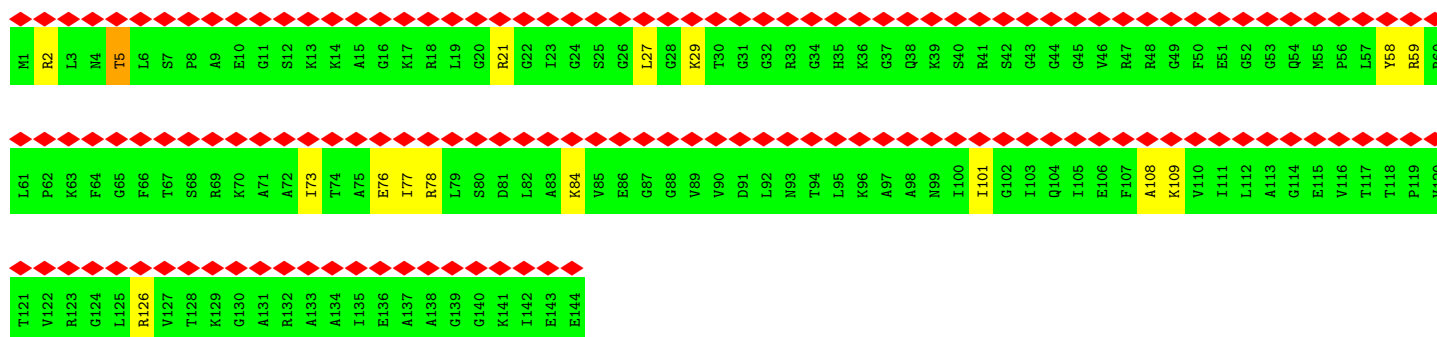
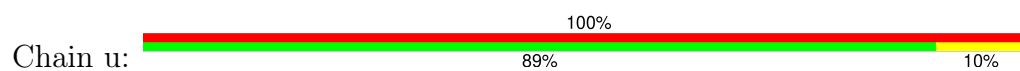
- Molecule 56: 50S ribosomal protein L13



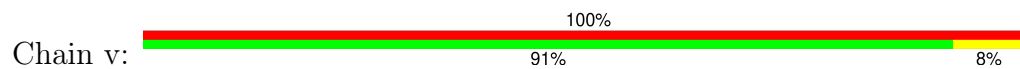
- Molecule 57: 50S ribosomal protein L14



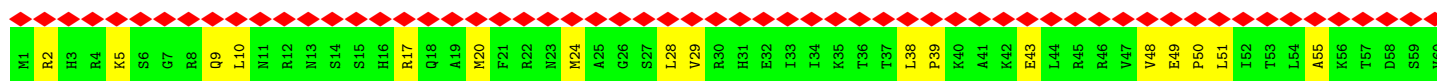
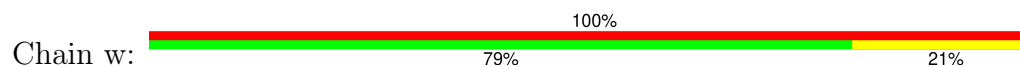
• Molecule 58: 50S ribosomal protein L15

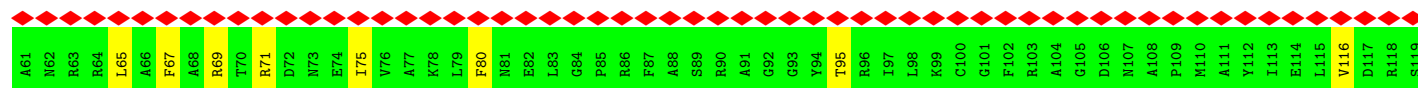


• Molecule 59: 50S ribosomal protein L16

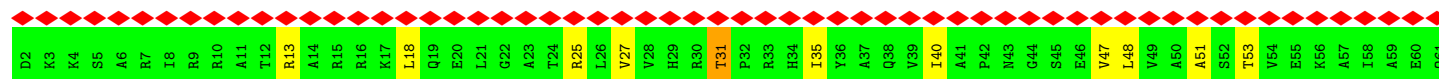
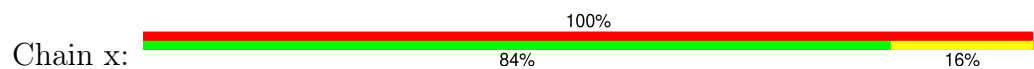


• Molecule 60: 50S ribosomal protein L17

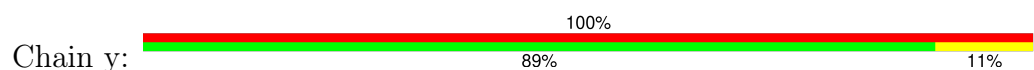




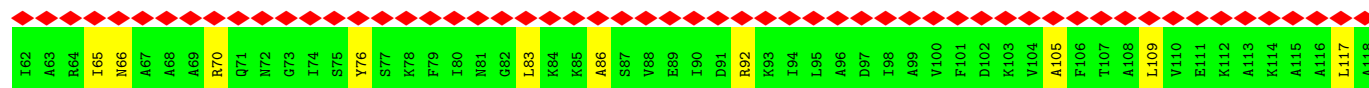
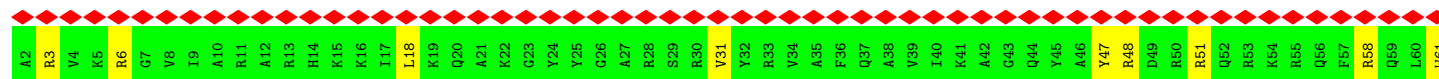
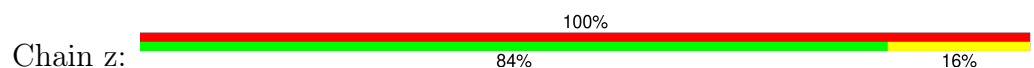
• Molecule 61: 50S ribosomal protein L18



• Molecule 62: 50S ribosomal protein L19



• Molecule 63: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5979	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.080	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	564.48, 564.48, 564.48	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.016, 2.016, 2.016	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.49	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.89	0/1005
4	3	0.47	0/796	0.78	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.76	4/388 (1.0%)	0.55	0/604
9	A	0.36	0/1810	0.72	2/2821 (0.1%)
9	B	0.43	0/1810	0.87	9/2821 (0.3%)
10	AA	0.67	14/10591 (0.1%)	0.98	56/14289 (0.4%)
11	AB	0.42	0/808	0.70	2/1088 (0.2%)
12	AC	0.58	4/1808 (0.2%)	0.70	9/2450 (0.4%)
12	AD	0.39	0/1789	0.55	0/2425
13	AE	0.54	8/10545 (0.1%)	0.74	25/14236 (0.2%)
14	AF	0.47	0/657	0.73	0/886
15	C	0.66	0/553	1.14	2/743 (0.3%)
16	D	0.40	9/36610 (0.0%)	0.75	40/57091 (0.1%)
17	E	0.76	0/675	1.32	0/895
18	F	0.71	0/597	1.20	0/792
19	G	0.65	0/1791	1.08	1/2413 (0.0%)
20	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
21	I	0.58	0/1663	0.98	0/2241
22	J	0.63	0/1665	1.08	0/2227
23	K	0.64	0/1165	1.06	2/1568 (0.1%)
24	L	0.58	0/867	0.94	0/1171
25	M	0.68	0/1195	1.19	3/1602 (0.2%)
26	N	0.55	0/989	0.91	0/1326
27	O	0.58	0/1034	1.02	1/1375 (0.1%)
28	P	0.60	0/800	1.10	4/1082 (0.4%)
29	Q	0.55	0/893	0.91	0/1205
30	R	0.49	0/952	0.81	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.64	0/817	1.11	1/1088 (0.1%)
32	T	0.69	0/722	1.21	0/964
33	U	0.57	0/659	0.99	0/884
34	V	0.46	0/657	0.73	0/881
35	W	0.51	0/680	0.83	0/915
36	X	0.67	0/909	1.21	3/1215 (0.2%)
37	Y	0.42	0/65	0.86	0/98
38	a	0.40	3/69247 (0.0%)	0.75	56/107985 (0.1%)
39	b	0.51	0/589	0.76	0/779
40	c	0.63	0/635	0.97	0/848
41	d	0.38	0/2872	0.69	0/4478
42	e	0.69	0/502	1.19	0/667
43	f	0.62	0/452	1.02	0/605
44	g	0.55	0/531	0.99	1/709 (0.1%)
45	h	0.54	0/2121	0.85	0/2852
46	i	0.52	0/450	0.94	0/599
47	j	0.60	0/1586	0.87	0/2134
48	k	0.47	0/433	0.80	0/576
49	l	0.61	0/1571	1.03	1/2113 (0.0%)
50	m	0.68	0/380	1.22	0/498
51	n	0.62	0/1434	1.18	10/1926 (0.5%)
52	o	0.63	0/513	1.10	1/676 (0.1%)
53	p	0.58	0/1333	0.89	0/1805
54	q	0.51	0/303	0.88	0/397
55	r	0.63	0/1122	0.97	1/1515 (0.1%)
56	s	0.68	0/1152	1.02	2/1551 (0.1%)
57	t	0.57	0/955	0.88	0/1279
58	u	0.55	0/1062	0.95	1/1413 (0.1%)
59	v	0.60	0/1093	0.97	0/1460
60	w	0.68	0/964	1.13	0/1289
61	x	0.61	0/902	1.09	0/1209
62	y	0.53	0/929	0.79	0/1242
63	z	0.80	0/960	1.25	0/1278
All	All	0.49	48/187139 (0.0%)	0.83	267/276026 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	A	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	B	0	2
10	AA	0	12
13	AE	0	5
14	AF	0	1
20	H	0	3
36	X	0	1
All	All	0	26

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	AA	374	GLU	C-N	17.47	1.53	1.33
10	AA	850	ILE	N-CA	-13.10	1.29	1.46
13	AE	93	THR	CA-C	12.26	1.69	1.52
20	H	169	SER	N-CA	11.74	1.61	1.46
16	D	1516	G	O3'-P	-10.78	1.45	1.61
13	AE	70	CYS	CA-CB	-8.73	1.41	1.53
16	D	1339	A	O3'-P	8.47	1.73	1.61
10	AA	869	GLY	C-N	7.60	1.44	1.33
20	H	88	LYS	N-CA	7.04	1.55	1.46
12	AC	76	GLU	N-CA	-7.00	1.37	1.46
8	7	69	G	C1'-N9	-6.97	1.37	1.48
6	5	109	DT	O3'-P	6.87	1.71	1.61
16	D	145	G	O3'-P	6.83	1.71	1.61
16	D	196	A	O3'-P	6.68	1.71	1.61
20	H	168	VAL	C-N	6.53	1.42	1.33
8	7	59	U	C1'-N1	6.30	1.57	1.48
16	D	1275	A	O3'-P	6.19	1.70	1.61
12	AC	75	GLN	CA-C	-6.14	1.45	1.53
10	AA	1008	GLN	N-CA	6.10	1.54	1.46
38	a	2434	A	O3'-P	5.98	1.70	1.61
8	7	60	U	C1'-N1	5.91	1.57	1.48
16	D	1515	G	O3'-P	-5.84	1.52	1.61
20	H	88	LYS	CA-C	5.76	1.60	1.52
16	D	1395	C	O3'-P	5.74	1.69	1.61
13	AE	90	VAL	CA-C	5.70	1.60	1.52
10	AA	996	ARG	N-CA	-5.69	1.38	1.45
8	7	64	U	C1'-N1	5.59	1.56	1.48
10	AA	885	GLY	C-O	-5.53	1.16	1.23
16	D	1490	U	O3'-P	5.50	1.69	1.61
7	6	10	DG	C1'-N9	-5.36	1.35	1.46
38	a	1905	C	O3'-P	5.28	1.69	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	AA	604	HIS	ND1-CE1	5.27	1.37	1.32
13	AE	1350	ASN	CG-ND2	-5.27	1.22	1.33
12	AC	160	HIS	CD2-NE2	-5.25	1.32	1.37
16	D	1492	A	O3'-P	5.24	1.69	1.61
10	AA	1257	GLN	CD-OE1	5.22	1.33	1.23
38	a	2167	U	O3'-P	5.19	1.69	1.61
13	AE	424	ASN	CG-ND2	-5.15	1.22	1.33
10	AA	1116	HIS	CD2-NE2	-5.14	1.32	1.37
10	AA	1157	GLN	CD-NE2	-5.14	1.22	1.33
10	AA	604	HIS	CD2-NE2	-5.13	1.32	1.37
10	AA	1256	GLN	CD-OE1	5.12	1.33	1.23
10	AA	1116	HIS	ND1-CE1	5.10	1.37	1.32
13	AE	777	HIS	ND1-CE1	5.10	1.37	1.32
12	AC	23	HIS	CD2-NE2	-5.07	1.32	1.37
13	AE	1108	GLN	CD-OE1	5.05	1.33	1.23
10	AA	760	ASN	CG-ND2	-5.05	1.22	1.33
13	AE	1268	ASN	CG-OD1	5.00	1.33	1.23

All (267) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	O3'-P-O5'	17.45	130.17	104.00
10	AA	1007	LYS	O-C-N	-17.26	101.87	122.58
10	AA	727	VAL	N-CA-C	-17.24	95.05	110.74
20	H	88	LYS	CA-C-N	16.93	143.58	120.38
20	H	88	LYS	C-N-CA	16.93	143.58	120.38
9	B	29	G	C3'-C2'-O2'	15.96	134.63	110.70
16	D	1516	G	P-O3'-C3'	-15.51	96.94	120.20
10	AA	374	GLU	CA-C-N	15.01	135.84	120.38
10	AA	374	GLU	C-N-CA	15.01	135.84	120.38
10	AA	1250	SER	CA-C-N	14.99	149.69	123.01
10	AA	1250	SER	C-N-CA	14.99	149.69	123.01
20	H	332	VAL	N-CA-C	13.62	124.51	110.62
20	H	169	SER	N-CA-C	12.72	137.90	110.80
20	H	330	VAL	N-CA-C	12.21	126.96	109.51
20	H	305	HIS	N-CA-C	11.90	131.01	111.37
10	AA	1008	GLN	CB-CA-C	11.77	130.94	112.00
13	AE	90	VAL	N-CA-C	9.92	122.23	107.75
38	a	2244	U	C1'-C2'-O2'	-9.86	93.61	108.40
10	AA	995	ASP	O-C-N	-9.80	109.55	122.59
10	AA	375	PRO	CA-N-CD	-9.70	98.42	112.00
51	n	73	SER	N-CA-CB	-9.60	94.54	110.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1206	G	C4'-C3'-O3'	9.55	127.33	113.00
10	AA	935	THR	CA-CB-OG1	-9.44	95.44	109.60
28	P	54	SER	CA-C-N	9.31	128.99	118.85
28	P	54	SER	C-N-CA	9.31	128.99	118.85
38	a	2250	G	C4'-C3'-O3'	-9.20	95.60	109.40
10	AA	376	PRO	N-CA-CB	-9.08	93.72	103.25
10	AA	864	LYS	N-CA-C	-8.98	102.42	112.57
16	D	1401	G	C4'-C3'-O3'	8.82	126.23	113.00
16	D	428	G	C4'-C3'-O3'	8.73	122.49	109.40
20	H	339	ARG	CA-C-N	8.59	137.95	121.54
20	H	339	ARG	C-N-CA	8.59	137.95	121.54
31	S	45	VAL	N-CA-CB	8.42	120.41	110.55
10	AA	375	PRO	N-CA-C	8.41	120.96	110.70
16	D	1515	G	O3'-P-O5'	-8.41	91.39	104.00
38	a	2296	U	C4'-C3'-O3'	8.40	122.00	109.40
38	a	404	A	C2'-C3'-O3'	8.39	122.08	109.50
10	AA	849	GLU	CA-C-N	8.34	136.98	121.97
10	AA	849	GLU	C-N-CA	8.34	136.98	121.97
28	P	57	VAL	N-CA-C	8.30	120.05	107.77
38	a	2252	G	N9-C1'-C2'	-8.18	99.74	112.00
16	D	197	A	C2'-C3'-O3'	8.16	121.75	109.50
16	D	1401	G	N9-C1'-C2'	-7.96	100.06	112.00
10	AA	859	GLU	CA-C-N	7.96	133.70	121.53
10	AA	859	GLU	C-N-CA	7.96	133.70	121.53
10	AA	855	PRO	N-CA-CB	-7.90	94.95	103.25
10	AA	1048	LYS	CA-C-N	-7.90	115.46	122.96
10	AA	1048	LYS	C-N-CA	-7.90	115.46	122.96
38	a	2425	A	C2'-C3'-O3'	7.84	121.27	109.50
20	H	155	LYS	CA-C-N	-7.80	110.89	121.66
20	H	155	LYS	C-N-CA	-7.80	110.89	121.66
38	a	2071	A	C4'-C3'-O3'	-7.69	101.46	113.00
10	AA	1010	GLN	N-CA-CB	-7.67	97.53	110.49
20	H	168	VAL	CA-C-N	7.67	136.18	121.54
20	H	168	VAL	C-N-CA	7.67	136.18	121.54
51	n	75	ALA	CA-C-N	7.64	129.69	120.14
51	n	75	ALA	C-N-CA	7.64	129.69	120.14
20	H	52	GLN	N-CA-C	-7.63	104.12	113.50
36	X	102	THR	CB-CA-C	7.61	123.48	110.84
13	AE	903	LEU	CA-C-N	7.61	136.07	121.54
13	AE	903	LEU	C-N-CA	7.61	136.07	121.54
16	D	1493	A	C2'-C3'-O3'	7.59	125.09	113.70
20	H	84	LEU	N-CA-C	7.56	120.90	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1499	A	N9-C1'-C2'	-7.55	100.68	112.00
23	K	60	ILE	N-CA-CB	7.54	119.37	110.55
16	D	1339	A	P-O3'-C3'	7.53	131.50	120.20
16	D	528	C	N1-C1'-C2'	-7.52	100.72	112.00
51	n	108	VAL	O-C-N	7.45	125.36	120.07
20	H	336	ASP	CB-CA-C	-7.43	98.68	110.79
23	K	56	VAL	O-C-N	7.38	125.14	120.42
51	n	73	SER	CB-CA-C	7.38	122.81	110.79
9	B	28	C	P-O3'-C3'	7.32	131.19	120.20
38	a	2602	A	C4'-C3'-O3'	7.26	120.30	109.40
38	a	783	A	C4'-C3'-O3'	7.24	123.86	113.00
9	B	29	G	N9-C1'-C2'	-7.20	101.21	112.00
10	AA	751	TYR	CA-C-N	7.19	132.15	121.72
10	AA	751	TYR	C-N-CA	7.19	132.15	121.72
19	G	47	VAL	O-C-N	7.17	125.00	120.42
16	D	1497	G	C1'-C2'-O2'	-7.14	97.69	108.40
38	a	2162	G	C4'-C3'-O3'	7.12	120.08	109.40
10	AA	375	PRO	CB-CA-C	-7.12	102.24	110.92
16	D	196	A	P-O3'-C3'	7.11	130.86	120.20
38	a	2225	A	C4'-C3'-O3'	7.05	119.98	109.40
38	a	896	A	C4'-C3'-O3'	7.04	119.97	109.40
38	a	1379	U	C2'-C3'-O3'	7.03	124.24	113.70
10	AA	1010	GLN	CB-CA-C	6.99	124.33	110.42
25	M	27	VAL	N-CA-CB	6.95	118.68	110.55
20	H	140	PRO	N-CA-CB	6.92	110.52	103.25
38	a	2244	U	C4'-C3'-O3'	6.88	123.31	113.00
20	H	340	ARG	CA-C-N	-6.82	112.52	123.23
20	H	340	ARG	C-N-CA	-6.82	112.52	123.23
38	a	2252	G	C4'-C3'-O3'	6.80	123.20	113.00
12	AC	160	HIS	CB-CG-CD2	-6.78	122.38	131.20
10	AA	728	ASP	N-CA-C	6.76	125.21	110.80
10	AA	604	HIS	CB-CG-CD2	-6.75	122.43	131.20
51	n	71	ARG	CA-C-N	6.73	133.95	122.37
51	n	71	ARG	C-N-CA	6.73	133.95	122.37
10	AA	855	PRO	CB-CA-C	-6.71	100.49	111.56
16	D	517	G	C5'-C4'-C3'	6.67	125.20	115.20
20	H	170	ARG	N-CA-C	6.67	119.64	110.24
38	a	2243	U	C4'-C3'-O3'	6.66	122.99	113.00
12	AC	117	HIS	CB-CA-C	-6.63	97.91	109.64
20	H	87	GLU	N-CA-C	-6.58	104.11	111.28
38	a	2189	U	C1'-C2'-O2'	-6.57	101.94	111.80
10	AA	1116	HIS	CB-CG-CD2	-6.57	122.66	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	AA	869	GLY	CA-C-O	-6.56	109.15	120.57
20	H	303	LEU	N-CA-C	6.56	121.11	112.13
20	H	112	ILE	N-CA-C	6.55	117.14	106.72
27	O	72	ILE	N-CA-C	-6.55	105.33	111.48
51	n	127	ASN	CB-CA-C	6.55	121.70	110.77
38	a	2167	U	P-O3'-C3'	6.54	130.02	120.20
38	a	894	U	C2'-C3'-O3'	6.54	119.32	109.50
20	H	155	LYS	N-CA-C	-6.54	98.24	108.90
20	H	132	PRO	N-CA-CB	6.52	110.22	103.38
16	D	526	C	C4'-C3'-O3'	6.51	122.76	113.00
55	r	61	VAL	N-CA-CB	6.50	118.16	110.55
52	o	13	ARG	N-CA-C	6.49	121.03	113.18
16	D	526	C	N1-C1'-C2'	-6.48	102.28	112.00
51	n	127	ASN	CA-CB-CG	-6.48	106.12	112.60
16	D	1340	A	C1'-C2'-O2'	6.47	118.11	108.40
10	AA	1009	ASN	CA-C-N	6.45	133.87	121.54
10	AA	1009	ASN	C-N-CA	6.45	133.87	121.54
13	AE	450	HIS	CB-CG-CD2	-6.44	122.83	131.20
11	AB	81	HIS	CB-CG-CD2	-6.43	122.84	131.20
12	AC	23	HIS	CB-CG-CD2	-6.41	122.86	131.20
38	a	754	U	N1-C1'-C2'	6.41	121.62	112.00
13	AE	93	THR	CA-C-N	6.33	132.96	121.06
13	AE	93	THR	C-N-CA	6.33	132.96	121.06
10	AA	150	HIS	CB-CG-CD2	-6.32	122.98	131.20
13	AE	61	ILE	CA-C-N	-6.31	114.06	121.64
13	AE	61	ILE	C-N-CA	-6.31	114.06	121.64
16	D	69	G	C4'-C3'-O3'	-6.30	103.55	113.00
38	a	2434	A	P-O3'-C3'	6.28	129.62	120.20
15	C	33	ILE	CA-C-O	-6.28	114.89	121.93
16	D	1208	C	N1-C1'-C2'	-6.26	102.60	112.00
10	AA	1009	ASN	N-CA-C	-6.26	104.45	111.28
20	H	153	GLU	N-CA-C	-6.26	97.47	110.80
13	AE	777	HIS	CB-CG-CD2	-6.25	123.08	131.20
10	AA	888	THR	CB-CA-C	-6.22	99.39	108.91
10	AA	850	ILE	N-CA-CB	6.21	121.48	111.23
9	B	28	C	O3'-P-O5'	-6.19	94.71	104.00
38	a	2425	A	C4'-C3'-O3'	6.18	118.67	109.40
20	H	113	ASN	N-CA-C	6.17	118.09	111.36
13	AE	70	CYS	CB-CA-C	6.12	120.33	110.29
10	AA	861	ALA	CA-C-N	6.11	133.22	121.54
10	AA	861	ALA	C-N-CA	6.11	133.22	121.54
16	D	1206	G	N9-C1'-C2'	-6.09	102.87	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	a	271	G	C4'-C3'-O3'	6.07	118.50	109.40
16	D	1516	G	OP1-P-O3'	-6.05	89.83	108.00
38	a	2210	U	C4'-C3'-O3'	6.04	118.46	109.40
16	D	1408	A	C4'-C3'-O3'	6.04	122.05	113.00
16	D	550	G	C3'-C2'-O2'	6.03	119.75	110.70
38	a	2820	A	C4'-C3'-O3'	-5.97	104.04	113.00
13	AE	90	VAL	CA-C-O	-5.96	114.19	120.39
38	a	1913	A	C2'-C3'-O3'	5.95	118.42	109.50
49	l	108	ILE	N-CA-CB	5.93	118.60	110.54
10	AA	1009	ASN	CB-CA-C	5.92	120.61	110.79
12	AC	74	VAL	N-CA-C	5.92	117.36	108.96
12	AC	75	GLN	N-CA-CB	5.90	119.33	110.19
20	H	150	LYS	N-CA-C	5.87	118.27	110.53
38	a	2308	G	C2'-C3'-O3'	-5.86	104.91	113.70
10	AA	604	HIS	CB-CG-ND1	5.86	131.49	122.70
20	H	75	VAL	N-CA-C	5.86	116.55	108.12
25	M	92	ARG	CA-C-N	5.85	125.33	119.24
25	M	92	ARG	C-N-CA	5.85	125.33	119.24
20	H	109	THR	N-CA-C	-5.85	99.12	109.06
51	n	72	LYS	N-CA-C	-5.84	99.14	109.06
10	AA	936	ARG	CA-C-O	-5.83	114.00	120.70
36	X	26	GLY	N-CA-C	-5.82	104.33	112.13
38	a	2756	U	C4'-C3'-O3'	5.81	118.12	109.40
10	AA	1116	HIS	CB-CG-ND1	5.80	131.40	122.70
16	D	1275	A	P-O3'-C3'	5.80	128.90	120.20
38	a	1905	C	P-O3'-C3'	5.80	128.90	120.20
9	B	29	G	O5'-C5'-C4'	-5.79	102.81	111.50
12	AC	76	GLU	N-CA-C	-5.79	101.71	110.28
10	AA	732	ILE	CB-CA-C	-5.78	103.64	111.15
38	a	70	G	C4'-C3'-O3'	5.78	118.06	109.40
9	B	48	C	N1-C1'-C2'	5.75	120.63	112.00
12	AC	160	HIS	CB-CG-ND1	5.75	131.33	122.70
13	AE	91	GLU	N-CA-C	5.74	123.03	110.80
16	D	1492	A	P-O3'-C3'	5.73	128.79	120.20
16	D	976	G	C4'-C3'-O3'	-5.72	104.42	113.00
16	D	1490	U	P-O3'-C3'	5.72	128.78	120.20
16	D	1406	U	N1-C1'-C2'	-5.71	103.43	112.00
38	a	2168	G	C4'-C3'-O3'	-5.71	104.43	113.00
38	a	1757	A	C4'-C3'-O3'	-5.71	104.44	113.00
9	A	48	C	N1-C1'-C2'	5.70	120.55	112.00
16	D	1340	A	C5'-C4'-C3'	5.69	124.54	116.00
38	a	2017	U	C2'-C3'-O3'	-5.65	105.23	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	AB	81	HIS	CB-CG-ND1	5.59	131.09	122.70
38	a	1568	G	C4'-C3'-O3'	-5.59	104.61	113.00
10	AA	853	ASP	CA-C-N	5.58	130.40	120.70
10	AA	853	ASP	C-N-CA	5.58	130.40	120.70
20	H	114	GLY	N-CA-C	5.57	121.17	111.14
10	AA	868	SER	N-CA-C	5.57	119.32	112.03
10	AA	996	ARG	N-CA-C	-5.57	101.20	109.94
12	AC	23	HIS	CB-CG-ND1	5.56	131.03	122.70
16	D	780	A	C4'-C3'-O3'	-5.56	104.67	113.00
13	AE	450	HIS	CB-CG-ND1	5.55	131.03	122.70
38	a	2731	G	C4'-C3'-O3'	-5.53	104.71	113.00
38	a	2447	G	C2'-C3'-O3'	-5.52	101.22	109.50
10	AA	150	HIS	CB-CG-ND1	5.49	130.93	122.70
13	AE	69	GLU	CA-C-N	-5.45	113.82	121.72
13	AE	69	GLU	C-N-CA	-5.45	113.82	121.72
9	B	35	A	P-O3'-C3'	5.40	128.30	120.20
38	a	2572	A	C4'-C3'-O3'	-5.40	101.30	109.40
13	AE	93	THR	CB-CA-C	5.39	121.15	110.42
38	a	944	C	C4'-C3'-O3'	-5.39	104.91	113.00
10	AA	375	PRO	N-CA-CB	5.38	108.29	103.08
16	D	1499	A	C4'-C3'-O3'	5.37	121.06	113.00
38	a	375	G	C2'-C3'-O3'	5.37	121.75	113.70
38	a	2481	G	C4'-C3'-O3'	-5.36	104.97	113.00
16	D	1145	A	C4'-C3'-O3'	-5.36	104.97	113.00
16	D	864	A	N9-C1'-C2'	5.35	120.03	112.00
38	a	2068	U	C4'-C3'-O3'	-5.35	104.98	113.00
13	AE	777	HIS	CB-CG-ND1	5.34	130.72	122.70
13	AE	70	CYS	N-CA-C	-5.34	101.07	109.25
44	g	5	ILE	N-CA-C	5.32	117.70	111.05
38	a	1270	C	C2'-C3'-O3'	-5.31	105.73	113.70
10	AA	1158	LYS	CA-C-N	5.31	131.53	121.97
10	AA	1158	LYS	C-N-CA	5.31	131.53	121.97
16	D	517	G	C4'-C3'-O3'	-5.31	101.44	109.40
16	D	145	G	P-O3'-C3'	5.29	128.14	120.20
38	a	2231	U	C1'-C2'-O2'	5.29	116.33	108.40
13	AE	73	GLY	N-CA-C	5.27	125.67	113.18
13	AE	90	VAL	O-C-N	-5.27	117.61	123.20
38	a	2020	A	C4'-C3'-O3'	-5.26	105.11	113.00
10	AA	934	PHE	N-CA-C	-5.26	103.71	111.81
10	AA	732	ILE	N-CA-CB	5.25	116.25	110.53
38	a	2529	G	C4'-C3'-O3'	-5.25	105.12	113.00
36	X	102	THR	CA-C-O	-5.25	114.88	121.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	AE	88	CYS	N-CA-C	5.25	120.34	113.88
16	D	1395	C	P-O3'-C3'	5.24	128.06	120.20
10	AA	859	GLU	O-C-N	5.22	129.53	122.59
9	A	60	U	C2'-C3'-O3'	5.19	117.28	109.50
9	B	60	U	C2'-C3'-O3'	5.18	117.27	109.50
38	a	2245	U	N1-C1'-C2'	-5.18	104.23	112.00
38	a	528	A	C4'-C3'-O3'	-5.17	105.25	113.00
38	a	1834	U	C4'-C3'-O3'	-5.17	105.25	113.00
20	H	128	ARG	CA-C-N	-5.16	114.14	122.81
20	H	128	ARG	C-N-CA	-5.16	114.14	122.81
38	a	423	A	C2'-C3'-O3'	-5.16	105.96	113.70
20	H	154	PHE	N-CA-C	-5.14	100.32	109.06
56	s	28	LEU	CA-C-N	5.10	127.08	120.44
56	s	28	LEU	C-N-CA	5.10	127.08	120.44
28	P	25	ILE	N-CA-CB	5.09	117.47	110.54
16	D	1335	U	C4'-C3'-O3'	-5.09	105.36	113.00
58	u	101	ILE	N-CA-C	5.09	116.40	112.12
38	a	328	U	C4'-C3'-O3'	-5.09	105.37	113.00
38	a	1025	G	C4'-C3'-O3'	5.09	117.03	109.40
38	a	479	A	C4'-C3'-O3'	5.08	117.03	109.40
38	a	1864	U	C4'-C3'-O3'	-5.07	105.39	113.00
12	AC	117	HIS	N-CA-C	5.07	116.83	110.24
13	AE	89	GLY	CA-C-N	5.07	129.84	123.10
13	AE	89	GLY	C-N-CA	5.07	129.84	123.10
13	AE	1184	ASP	N-CA-C	5.06	121.00	109.81
15	C	35	GLU	N-CA-C	-5.05	105.96	111.82
16	D	70	U	C2'-C3'-O3'	5.05	117.08	109.50
38	a	126	A	C4'-C3'-O3'	-5.05	105.42	113.00
38	a	2193	G	C2'-C3'-O3'	5.05	121.27	113.70
16	D	573	A	C4'-C3'-O3'	-5.02	105.47	113.00
9	B	19	G	N9-C1'-C2'	5.02	119.53	112.00
20	H	108	VAL	N-CA-C	-5.01	98.92	109.34
13	AE	61	ILE	CA-C-O	-5.01	115.74	120.95
10	AA	377	THR	CA-C-N	5.00	126.94	120.44
10	AA	377	THR	C-N-CA	5.00	126.94	120.44
38	a	1078	U	C2'-C3'-O3'	-5.00	106.20	113.70

There are no chirality outliers.

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	A	19	G	Sidechain

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Mol	Chain	Res	Type	Group
9	A	7	G	Sidechain
10	AA	1007	LYS	Mainchain
10	AA	1134	GLN	Peptide
10	AA	1157	GLN	Peptide
10	AA	1158	LYS	Peptide
10	AA	205	PRO	Peptide
10	AA	594	VAL	Peptide
10	AA	595	THR	Peptide
10	AA	596	ASP	Mainchain
10	AA	696	ASP	Peptide
10	AA	746	ALA	Peptide
10	AA	853	ASP	Mainchain
10	AA	859	GLU	Mainchain
13	AE	1184	ASP	Peptide
13	AE	1326	GLN	Peptide
13	AE	313	GLY	Peptide
13	AE	416	ILE	Peptide
13	AE	804	ALA	Peptide
14	AF	32	VAL	Peptide
9	B	19	G	Sidechain
9	B	7	G	Sidechain
20	H	274	TYR	Peptide
20	H	81	GLU	Peptide
20	H	82	THR	Peptide
36	X	100	GLN	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	6	0
4	3	788	844	844	10	0
5	4	753	780	780	0	0
6	5	472	260	261	23	0
7	6	542	306	306	15	0
8	7	347	168	169	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	A	1620	826	826	174	0
9	B	1620	813	827	139	0
10	AA	10425	10427	10430	354	0
11	AB	790	783	783	7	0
12	AC	1786	1813	1813	44	0
12	AD	1767	1789	1789	47	0
13	AE	10388	10611	10611	364	0
14	AF	655	663	663	14	0
15	C	544	559	560	24	0
16	D	32703	16423	16460	189	0
17	E	669	719	719	4	0
18	F	589	629	629	8	0
19	G	1760	1785	1785	47	0
20	H	1730	1454	1454	211	0
21	I	1636	1710	1710	7	0
22	J	1643	1707	1707	15	0
23	K	1152	1196	1196	16	0
24	L	848	846	846	3	0
25	M	1181	1235	1235	34	0
26	N	979	1031	1031	5	0
27	O	1022	1070	1070	11	0
28	P	790	831	831	22	0
29	Q	877	887	887	4	0
30	R	939	1001	1001	6	0
31	S	805	844	844	6	0
32	T	714	734	734	8	0
33	U	649	666	666	3	0
34	V	648	691	691	4	0
35	W	663	688	688	2	0
36	X	900	964	964	57	0
37	Y	60	30	31	2	0
38	a	61841	31077	31124	277	0
39	b	582	599	599	2	0
40	c	625	652	652	4	0
41	d	2569	1301	1301	3	0
42	e	501	531	531	4	0
43	f	448	488	488	6	0
44	g	522	520	520	11	0
45	h	2082	2154	2154	18	0
46	i	444	459	458	6	0
47	j	1565	1617	1616	15	0
48	k	426	464	464	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	l	1552	1619	1619	14	0
50	m	377	418	418	10	0
51	n	1410	1443	1444	28	0
52	o	504	572	572	5	0
53	p	1313	1358	1358	7	0
54	q	302	343	343	1	0
55	r	1111	1148	1148	5	0
56	s	1129	1162	1162	15	0
57	t	946	1023	1023	12	0
58	u	1053	1129	1129	8	0
59	v	1074	1157	1157	5	0
60	w	951	994	994	10	0
61	x	892	923	923	8	0
62	y	917	962	962	4	0
63	z	947	1020	1019	13	0
64	7	1	0	0	0	0
65	AA	2	0	0	0	0
All	All	173959	125488	125591	2065	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 (2065) 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)
20:H:131:LEU:CB	20:H:167:VAL:CA	1.78	1.56
15:C:12:ARG:HG3	20:H:264:GLU:CB	1.30	1.54
20:H:131:LEU:CB	20:H:167:VAL:HA	1.03	1.48
20:H:71:ALA:C	20:H:72:LEU:HD12	1.49	1.35
16:D:1358:U:O4	16:D:1363:A:N1	1.60	1.34
20:H:118:GLY:O	20:H:133:GLY:CA	1.74	1.34
38:a:1839:G:H1'	38:a:1927:A:C8	1.62	1.33
38:a:1021:A:N1	38:a:1141:U:O4	1.63	1.31
20:H:118:GLY:O	20:H:133:GLY:HA3	1.27	1.26
16:D:948:C:OP2	36:X:105:ASN:OD1	1.53	1.26
16:D:1308:U:H3'	36:X:98:ARG:CZ	1.43	1.25
16:D:1308:U:H2'	36:X:98:ARG:NH2	1.48	1.24
15:C:12:ARG:CG	20:H:264:GLU:CB	2.15	1.24
9:A:32:C:O4'	25:M:144:MET:HE1	1.09	1.24
9:B:18:G:N7	9:B:57:A:N6	1.87	1.21
16:D:563:A:N1	16:D:884:U:O4	1.73	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:267:TRP:CZ2	20:H:340:ARG:HG2	1.75	1.21
9:A:18:G:N7	9:A:57:A:N6	1.87	1.21
16:D:1308:U:C2'	36:X:98:ARG:NH2	2.03	1.20
16:D:1227:A:OP2	36:X:110:LYS:HE3	1.35	1.19
9:B:70:G:H2'	9:B:71:C:H5''	1.23	1.19
19:G:19:GLN:CD	20:H:76:GLU:HB3	1.67	1.18
16:D:1329:A:OP1	36:X:28:THR:HB	1.47	1.14
20:H:119:GLY:HA2	20:H:133:GLY:HA2	1.14	1.13
19:G:19:GLN:CD	20:H:76:GLU:CB	2.19	1.13
20:H:135:LEU:CB	20:H:167:VAL:CB	2.27	1.13
15:C:44:ILE:HD13	20:H:339:ARG:CG	1.78	1.13
20:H:267:TRP:CE2	20:H:340:ARG:HG2	1.84	1.10
9:A:32:C:O4'	25:M:144:MET:CE	1.97	1.10
16:D:1308:U:C3'	36:X:98:ARG:CZ	2.31	1.09
16:D:1308:U:C3'	36:X:98:ARG:NH2	2.16	1.09
22:J:162:ALA:HA	22:J:165:ARG:CZ	1.83	1.09
38:a:1839:G:C8	38:a:1927:A:H1'	1.87	1.08
9:A:70:G:H2'	9:A:71:C:H5''	1.23	1.08
20:H:267:TRP:CH2	20:H:340:ARG:HG2	1.86	1.08
15:C:44:ILE:HD13	20:H:339:ARG:HG2	1.18	1.07
19:G:19:GLN:CG	20:H:75:VAL:HG22	1.84	1.07
16:D:1308:U:C2'	36:X:98:ARG:HH21	1.63	1.07
20:H:71:ALA:O	20:H:72:LEU:HD12	1.54	1.07
19:G:19:GLN:HG3	20:H:75:VAL:HG22	1.38	1.05
20:H:162:LYS:CB	20:H:298:GLU:CD	2.30	1.05
9:A:18:G:N2	9:A:55:U:O2	1.90	1.04
9:A:56:C:H2'	9:A:57:A:H5''	1.38	1.04
13:AE:24:LEU:HG	13:AE:232:ASN:HD21	1.17	1.04
20:H:19:ARG:O	20:H:72:LEU:HB2	1.58	1.03
9:B:56:C:O4'	51:n:80:ARG:NH2	1.91	1.03
9:B:70:G:C2'	9:B:71:C:H5''	1.89	1.03
9:A:70:G:C2'	9:A:71:C:H5''	1.89	1.02
10:AA:992:LEU:HD22	10:AA:992:LEU:H	1.21	1.02
16:D:1227:A:OP2	36:X:110:LYS:CE	2.06	1.02
9:B:18:G:N2	9:B:55:U:O2	1.90	1.02
9:B:56:C:H5'	51:n:80:ARG:CZ	1.90	1.02
19:G:38:VAL:CG2	20:H:75:VAL:HG21	1.90	1.01
20:H:290:TYR:O	20:H:305:HIS:O	1.77	1.01
16:D:1329:A:OP1	36:X:28:THR:CB	2.07	1.01
16:D:1308:U:H3'	36:X:98:ARG:NH2	1.76	1.00
38:a:2297:A:N1	38:a:2321:U:C4	2.29	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:56:C:H2'	9:B:57:A:H5''	1.39	1.00
13:AE:111:THR:HG23	13:AE:300:GLN:CD	1.86	1.00
16:D:13:U:N3	16:D:915:A:C6	2.29	1.00
20:H:131:LEU:CB	20:H:167:VAL:CB	2.40	0.99
38:a:1839:G:C1'	38:a:1927:A:C8	2.47	0.98
9:A:32:C:O2'	25:M:86:GLN:CG	2.12	0.98
16:D:13:U:O4	16:D:20:U:O4	1.79	0.98
19:G:38:VAL:HG22	20:H:75:VAL:HG21	1.44	0.97
9:A:32:C:C4'	25:M:144:MET:HE1	1.93	0.97
38:a:1839:G:O4'	38:a:1927:A:O4'	1.82	0.97
20:H:118:GLY:O	20:H:133:GLY:HA2	1.63	0.96
20:H:119:GLY:CA	20:H:133:GLY:HA2	1.95	0.96
8:7:60:U:OP1	13:AE:256:ASP:CG	2.09	0.95
13:AE:68:TYR:O	13:AE:75:TYR:CE2	2.20	0.95
7:6:15:DC:N4	7:6:16:DC:N4	2.15	0.95
12:AC:158:ARG:HB3	12:AC:158:ARG:HH11	1.32	0.95
9:B:72:A:H2'	9:B:73:A:H5''	1.49	0.94
16:D:13:U:C4	16:D:915:A:N6	2.36	0.94
38:a:1839:G:O4'	38:a:1927:A:C1'	2.15	0.94
16:D:13:U:N3	16:D:915:A:N6	2.16	0.93
20:H:135:LEU:HA	20:H:157:ILE:CB	1.98	0.93
38:a:67:U:N3	38:a:74:A:C6	2.36	0.93
9:A:32:C:O2'	25:M:86:GLN:HG3	1.68	0.93
20:H:71:ALA:C	20:H:72:LEU:CD1	2.42	0.93
10:AA:870:ILE:HG23	10:AA:884:VAL:HG13	1.51	0.93
9:A:72:A:H2'	9:A:73:A:H5''	1.49	0.92
20:H:119:GLY:HA3	20:H:131:LEU:O	1.68	0.92
9:B:75:C:OP1	38:a:2602:A:C8	2.22	0.92
10:AA:878:THR:O	10:AA:920:VAL:HG11	1.68	0.92
10:AA:768:MET:CE	12:AC:80:GLU:OE1	2.17	0.92
38:a:2013:A:N6	38:a:2613:U:H3	1.68	0.91
16:D:13:U:C4	16:D:20:U:O4	2.23	0.91
38:a:1406:U:O2'	38:a:1407:G:C5'	2.19	0.91
13:AE:202:ARG:HG2	13:AE:202:ARG:HH11	1.35	0.91
9:A:68:C:H2'	9:A:69:C:H5''	1.51	0.91
9:B:68:C:H2'	9:B:69:C:H5''	1.51	0.90
6:5:113:DC:OP2	10:AA:163:LYS:HD3	1.71	0.90
9:A:18:G:N2	9:A:58:A:N7	2.19	0.90
13:AE:68:TYR:C	13:AE:75:TYR:HE2	1.80	0.90
9:A:56:C:H1'	38:a:2112:G:C6	2.06	0.90
10:AA:728:ASP:OD1	10:AA:769:PRO:HG2	1.71	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:24:LEU:HB2	13:AE:232:ASN:OD1	1.72	0.90
16:D:1308:U:H2'	36:X:98:ARG:HH21	1.06	0.90
9:B:18:G:N2	9:B:58:A:N7	2.19	0.90
20:H:279:LYS:HA	20:H:331:MET:HB3	1.54	0.89
6:5:109:DT:H2''	10:AA:200:ARG:HG3	1.53	0.89
38:a:2314:A:H1'	51:n:155:THR:HG21	1.54	0.89
9:A:33:U:H5''	25:M:84:THR:HG21	1.55	0.89
20:H:162:LYS:N	20:H:298:GLU:OE2	2.06	0.88
13:AE:136:GLU:OE1	13:AE:312:ARG:NH1	2.04	0.88
11:AB:107:GLU:CD	13:AE:288:PRO:HB3	1.99	0.88
6:5:114:DC:H5''	13:AE:1148:ARG:NH2	1.87	0.88
11:AB:107:GLU:OE1	13:AE:288:PRO:HB3	1.72	0.88
12:AC:91:ARG:NE	12:AC:122:GLU:OE2	2.07	0.87
44:g:16:CYS:CB	44:g:37:CYS:HB3	2.05	0.87
20:H:131:LEU:CB	20:H:167:VAL:N	2.37	0.87
38:a:783:A:N3	38:a:783:A:H2'	1.89	0.87
10:AA:1090:ASN:O	12:AC:182:ARG:NH1	2.08	0.86
20:H:119:GLY:HA2	20:H:133:GLY:CA	2.01	0.86
20:H:332:VAL:HG11	20:H:335:ILE:HG13	1.57	0.86
13:AE:68:TYR:O	13:AE:75:TYR:HE2	1.58	0.86
20:H:348:GLN:N	20:H:348:GLN:OE1	2.08	0.86
15:C:31:ASN:OD1	20:H:268:VAL:HG22	1.74	0.86
6:5:110:DA:N7	10:AA:183:TRP:CH2	2.43	0.86
16:D:197:A:C6	16:D:221:C:H4'	2.11	0.86
22:J:162:ALA:HB2	22:J:165:ARG:NH2	1.90	0.86
13:AE:425:ARG:NH1	13:AE:458:ASN:O	2.09	0.86
10:AA:980:VAL:HA	10:AA:984:VAL:HB	1.58	0.85
9:A:16:C:O2	38:a:2181:U:H5'	1.76	0.85
10:AA:967:LEU:O	10:AA:967:LEU:HD12	1.76	0.85
9:B:18:G:N7	9:B:57:A:C6	2.44	0.85
14:AF:3:ARG:NH1	14:AF:55:GLU:OE2	2.09	0.85
13:AE:24:LEU:HG	13:AE:232:ASN:ND2	1.90	0.85
10:AA:975:ILE:HG13	10:AA:1014:LEU:HD23	1.57	0.85
19:G:18:HIS:HA	20:H:43:LYS:HD2	1.55	0.84
38:a:67:U:N3	38:a:74:A:N6	2.25	0.84
10:AA:953:LEU:HA	10:AA:1036:ILE:HD13	1.59	0.84
13:AE:26:SER:HB2	13:AE:236:TRP:CZ2	2.12	0.84
15:C:12:ARG:HH22	20:H:268:VAL:CG2	1.90	0.84
19:G:16:PHE:HB3	20:H:43:LYS:HA	1.59	0.84
20:H:131:LEU:CB	20:H:166:VAL:O	2.26	0.84
20:H:267:TRP:CZ3	20:H:340:ARG:HG2	2.12	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:J:61:VAL:HG21	22:J:200:ILE:HD11	1.57	0.84
38:a:2303:G:C2	38:a:2314:A:C2	2.66	0.84
4:3:34:VAL:HG13	4:3:67:VAL:HG22	1.58	0.84
9:A:68:C:C2'	9:A:69:C:H5''	2.08	0.84
13:AE:68:TYR:HB3	13:AE:75:TYR:OH	1.76	0.84
9:B:56:C:H5'	51:n:80:ARG:NE	1.93	0.84
20:H:267:TRP:CD2	20:H:340:ARG:HG2	2.11	0.84
23:K:111:MET:HE2	23:K:125:ALA:HB1	1.59	0.84
9:A:18:G:N7	9:A:57:A:C6	2.44	0.84
9:B:68:C:C2'	9:B:69:C:H5''	2.08	0.83
20:H:135:LEU:CB	20:H:167:VAL:C	2.50	0.83
20:H:267:TRP:CH2	20:H:340:ARG:CG	2.60	0.83
16:D:1227:A:H5'	36:X:110:LYS:NZ	1.93	0.83
9:B:72:A:C2'	9:B:73:A:H5''	2.08	0.83
6:5:110:DA:N7	10:AA:183:TRP:HH2	1.77	0.83
20:H:162:LYS:CA	20:H:298:GLU:OE2	2.16	0.82
12:AD:86:LYS:CE	13:AE:528:THR:HB	2.09	0.82
10:AA:1314:GLN:HB2	14:AF:28:ARG:HH12	1.43	0.82
10:AA:1043:ALA:HB1	10:AA:1044:PRO:HD2	1.61	0.82
19:G:19:GLN:OE1	20:H:75:VAL:O	1.85	0.82
9:A:54:U:H3	9:A:58:A:N6	1.77	0.82
38:a:1839:G:C1'	38:a:1927:A:N9	2.43	0.82
38:a:1406:U:O2'	38:a:1407:G:H5''	1.79	0.82
20:H:267:TRP:CZ3	20:H:340:ARG:CG	2.63	0.81
9:A:72:A:C2'	9:A:73:A:H5''	2.09	0.81
10:AA:883:LEU:HD11	10:AA:920:VAL:HG22	1.59	0.81
10:AA:886:LYS:HE3	10:AA:886:LYS:O	1.80	0.81
13:AE:141:PHE:HE2	13:AE:296:LYS:HB2	1.44	0.81
16:D:37:U:N3	16:D:397:A:N6	2.28	0.81
16:D:972:C:O2'	28:P:57:VAL:CG2	2.29	0.81
38:a:1021:A:N6	38:a:1141:U:H3	1.77	0.81
9:B:54:U:H3	9:B:58:A:N6	1.77	0.81
20:H:155:LYS:CB	20:H:169:SER:CB	2.58	0.81
38:a:585:G:N7	63:z:6:ARG:NH1	2.29	0.81
9:B:56:C:C2'	9:B:57:A:H5''	2.11	0.81
16:D:1397:C:OP1	16:D:1397:C:H2'	1.81	0.81
13:AE:1169:THR:OG1	13:AE:1192:LYS:NZ	2.13	0.81
15:C:12:ARG:CB	20:H:264:GLU:CB	2.59	0.81
38:a:1019:U:H3	38:a:1142:A:N6	1.77	0.81
22:J:162:ALA:CB	22:J:165:ARG:NH2	2.44	0.81
10:AA:611:GLU:OE2	10:AA:637:ARG:NH2	2.13	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:305:HIS:CD2	20:H:306:VAL:H	1.98	0.80
9:A:22:G:H2'	9:A:23:C:C6	2.16	0.80
9:A:58:A:O2'	9:A:59:A:H3'	1.81	0.80
13:AE:37:GLU:O	13:AE:61:ILE:HD11	1.81	0.80
9:B:22:G:H2'	9:B:23:C:C6	2.16	0.80
9:B:76:A:H1'	38:a:2494:G:P	2.20	0.80
22:J:162:ALA:CA	22:J:165:ARG:NH2	2.44	0.80
13:AE:141:PHE:CE2	13:AE:296:LYS:HB2	2.15	0.80
20:H:123:GLU:HA	20:H:128:ARG:HA	1.63	0.80
9:A:56:C:C2'	9:A:57:A:H5''	2.10	0.80
13:AE:90:VAL:HG13	13:AE:90:VAL:O	1.82	0.80
44:g:18:CYS:HB3	44:g:40:CYS:CB	2.12	0.80
38:a:1021:A:H61	38:a:1141:U:H3	1.29	0.80
10:AA:724:VAL:CG1	10:AA:774:GLY:H	1.93	0.80
20:H:270:ILE:CG2	20:H:337:GLU:HB3	2.12	0.80
38:a:1019:U:H3	38:a:1142:A:H61	1.28	0.80
13:AE:111:THR:HG23	13:AE:300:GLN:OE1	1.81	0.80
8:7:70:G:O2'	13:AE:425:ARG:NH2	2.15	0.80
13:AE:144:TYR:HE1	13:AE:162:GLU:OE2	1.64	0.80
16:D:1329:A:P	36:X:28:THR:HB	2.22	0.80
9:B:70:G:H2'	9:B:71:C:C5'	2.11	0.80
22:J:162:ALA:HA	22:J:165:ARG:NH2	1.95	0.79
38:a:2298:A:C4	38:a:2321:U:C5	2.70	0.79
51:n:125:ARG:O	51:n:127:ASN:ND2	2.14	0.79
10:AA:118:LYS:NZ	10:AA:487:LEU:O	2.14	0.79
9:A:18:G:N2	9:A:58:A:C5	2.50	0.79
38:a:2297:A:N1	38:a:2321:U:O4	2.14	0.79
9:B:18:G:N2	9:B:58:A:C5	2.50	0.79
9:A:7:G:H4'	9:A:8:U:OP1	1.81	0.79
9:B:58:A:O2'	9:B:59:A:H3'	1.82	0.79
20:H:122:VAL:O	20:H:129:ALA:N	2.13	0.79
13:AE:87:LYS:HA	13:AE:87:LYS:HE3	1.64	0.79
19:G:16:PHE:CZ	20:H:41:GLY:O	2.36	0.78
20:H:19:ARG:HD3	20:H:73:ASP:CG	2.09	0.78
38:a:1406:U:O2'	38:a:1407:G:O5'	2.01	0.78
9:A:76:A:H2'	38:a:2394:C:H42	1.48	0.78
38:a:2189:U:OP1	38:a:2189:U:O4'	2.01	0.78
13:AE:1075:ARG:NH2	13:AE:1168:GLU:OE2	2.17	0.78
9:B:7:G:H4'	9:B:8:U:OP1	1.81	0.78
9:B:15:G:N1	9:B:20:U:O2	2.17	0.78
19:G:35:ARG:HD2	20:H:14:LYS:HD3	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:1406:U:O2'	38:a:1407:G:P	2.42	0.78
38:a:2756:U:N3	38:a:2758:A:N6	2.32	0.78
44:g:16:CYS:HB2	44:g:37:CYS:HB3	1.63	0.78
9:A:5:G:H2'	9:A:6:G:H5'	1.66	0.78
9:A:15:G:N1	9:A:20:U:O2	2.17	0.78
9:B:5:G:H2'	9:B:6:G:H5'	1.66	0.77
9:A:33:U:O3'	25:M:84:THR:OG1	2.01	0.77
10:AA:964:LEU:HD12	10:AA:964:LEU:O	1.84	0.77
9:A:68:C:C3'	9:A:69:C:H5''	2.15	0.77
10:AA:1257:GLN:HE22	13:AE:345:LYS:HA	1.48	0.77
13:AE:186:GLN:HG3	13:AE:238:ILE:HG13	1.65	0.77
38:a:2756:U:N3	38:a:2758:A:C6	2.53	0.77
47:j:4:LEU:HD23	47:j:29:VAL:HG11	1.65	0.77
10:AA:858:GLY:O	10:AA:860:ALA:N	2.17	0.77
15:C:44:ILE:CD1	20:H:339:ARG:CG	2.63	0.77
10:AA:1024:GLU:HA	10:AA:1027:LYS:HE3	1.66	0.77
10:AA:1257:GLN:OE1	13:AE:345:LYS:CG	2.32	0.77
9:A:18:G:C5	9:A:57:A:C6	2.72	0.77
10:AA:943:LYS:HD3	10:AA:943:LYS:N	1.97	0.77
9:B:68:C:C3'	9:B:69:C:H5''	2.15	0.77
12:AC:76:GLU:CD	12:AC:131:CYS:HA	2.09	0.76
13:AE:123:ARG:HG3	13:AE:1337:VAL:HG11	1.67	0.76
10:AA:871:VAL:N	10:AA:883:LEU:O	2.18	0.76
9:B:18:G:C5	9:B:57:A:C6	2.72	0.76
10:AA:992:LEU:HD21	10:AA:999:GLU:OE2	1.86	0.76
19:G:19:GLN:CD	20:H:76:GLU:HB2	2.08	0.76
20:H:305:HIS:CD2	20:H:306:VAL:N	2.53	0.76
22:J:162:ALA:HB2	22:J:165:ARG:HH22	1.47	0.76
10:AA:954:LYS:HZ2	10:AA:954:LYS:C	1.93	0.76
6:5:108:DT:H72	10:AA:199:ASP:HB3	1.67	0.76
10:AA:1026:GLU:HA	10:AA:1026:GLU:OE2	1.84	0.76
10:AA:1034:ARG:HG2	10:AA:1034:ARG:HH11	1.51	0.76
7:6:15:DC:C4	7:6:16:DC:N4	2.53	0.76
10:AA:955:GLN:OE1	10:AA:955:GLN:HA	1.83	0.76
16:D:197:A:N6	16:D:221:C:H4'	2.01	0.75
10:AA:1272:GLU:OE2	13:AE:798:ARG:NH1	2.19	0.75
9:A:41:C:O4'	25:M:143:ARG:NH1	2.20	0.75
12:AD:196:THR:HB	13:AE:443:GLU:HG3	1.68	0.75
20:H:109:THR:HA	20:H:153:GLU:HA	1.68	0.75
44:g:18:CYS:CB	44:g:40:CYS:HB3	2.16	0.75
16:D:1358:U:C4	16:D:1363:A:N1	2.53	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AA:985:GLU:HG2	10:AA:988:LYS:HE3	1.68	0.75
38:a:2298:A:C4	38:a:2321:U:H5	2.05	0.75
9:A:6:G:O2'	9:A:7:G:O5'	2.05	0.75
9:A:41:C:H1'	25:M:143:ARG:HH12	1.52	0.75
10:AA:1246:ARG:HH11	10:AA:1266:GLY:HA2	1.50	0.75
12:AC:158:ARG:HB3	12:AC:158:ARG:NH1	2.02	0.75
28:P:24:GLU:OE2	28:P:90:LEU:HD11	1.87	0.75
61:x:31:THR:O	61:x:102:ARG:NH1	2.19	0.75
19:G:35:ARG:HG3	20:H:10:GLU:OE2	1.86	0.74
4:3:36:VAL:HG11	4:3:39:ILE:HD12	1.68	0.74
20:H:131:LEU:CB	20:H:166:VAL:C	2.60	0.74
9:B:70:G:C3'	9:B:71:C:H5''	2.17	0.74
38:a:1021:A:N1	38:a:1141:U:C4	2.55	0.74
20:H:109:THR:CA	20:H:153:GLU:HA	2.17	0.74
9:A:70:G:C3'	9:A:71:C:H5''	2.18	0.74
13:AE:68:TYR:C	13:AE:75:TYR:CE2	2.65	0.74
9:B:76:A:H2'	9:B:76:A:N3	2.02	0.74
9:A:18:G:H1'	9:A:58:A:C2	2.23	0.74
10:AA:941:LYS:NZ	10:AA:944:ARG:NH2	2.35	0.74
23:K:137:VAL:O	23:K:140:THR:OG1	2.04	0.74
9:A:32:C:C1'	25:M:144:MET:HE1	2.16	0.74
10:AA:991:LYS:HD2	10:AA:991:LYS:N	2.03	0.74
13:AE:44:ILE:HD12	13:AE:252:LEU:CD2	2.18	0.74
9:B:6:G:O2'	9:B:7:G:O5'	2.05	0.74
20:H:304:VAL:HG12	20:H:309:MET:SD	2.28	0.74
13:AE:395:LYS:HZ2	13:AE:399:LYS:CD	2.00	0.74
16:D:1228:C:OP1	36:X:107:ARG:NH1	2.21	0.74
6:5:115:DA:OP1	13:AE:1148:ARG:NE	2.21	0.73
9:A:18:G:O2'	9:A:60:U:C2	2.41	0.73
9:A:70:G:H2'	9:A:71:C:C5'	2.11	0.73
13:AE:210:SER:HB3	13:AE:213:LYS:HB2	1.71	0.73
9:B:18:G:H1'	9:B:58:A:C2	2.23	0.73
16:D:517:G:O2'	16:D:530:G:H4'	1.89	0.73
20:H:110:GLY:CA	20:H:153:GLU:O	2.36	0.73
9:A:33:U:H5''	25:M:84:THR:CG2	2.19	0.73
10:AA:964:LEU:HD12	10:AA:964:LEU:C	2.13	0.73
10:AA:1047:LEU:O	10:AA:1049:ILE:HD12	1.89	0.73
13:AE:120:LEU:O	13:AE:1330:ARG:NH1	2.21	0.73
13:AE:211:GLU:HG2	13:AE:215:LYS:HE3	1.70	0.73
9:B:18:G:O2'	9:B:60:U:C2	2.41	0.73
10:AA:1043:ALA:HB1	10:AA:1044:PRO:CD	2.19	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:G:19:GLN:CG	20:H:76:GLU:HB2	2.18	0.73
13:AE:44:ILE:HD12	13:AE:252:LEU:HD21	1.71	0.72
10:AA:972:PHE:HA	10:AA:975:ILE:HD12	1.71	0.72
13:AE:110:PRO:HG2	13:AE:183:GLU:HG3	1.68	0.72
9:B:76:A:H1'	38:a:2494:G:OP1	1.88	0.72
20:H:267:TRP:CE3	20:H:340:ARG:CG	2.72	0.72
38:a:1913:A:OP2	38:a:1913:A:H3'	1.89	0.72
10:AA:1253:LEU:HD12	13:AE:253:VAL:CG1	2.19	0.72
9:A:46:G:H1'	9:A:47:U:C5	2.25	0.72
13:AE:107:LEU:HD11	13:AE:242:LEU:HB2	1.70	0.72
20:H:19:ARG:HB2	20:H:73:ASP:OD2	1.88	0.72
38:a:1839:G:H1'	38:a:1927:A:N9	2.03	0.72
38:a:1839:G:C1'	38:a:1927:A:C1'	2.67	0.72
19:G:16:PHE:CB	20:H:43:LYS:HA	2.20	0.72
10:AA:956:ALA:HB1	10:AA:1032:LYS:HG3	1.70	0.72
10:AA:1257:GLN:OE1	13:AE:345:LYS:HD3	1.89	0.72
30:R:86:ARG:HG3	30:R:86:ARG:O	1.89	0.71
15:C:12:ARG:HB2	20:H:264:GLU:CB	2.20	0.71
16:D:827:U:H3	16:D:872:A:N6	1.88	0.71
20:H:70:VAL:HA	20:H:85:SER:CB	2.20	0.71
38:a:67:U:C4	38:a:74:A:N6	2.57	0.71
9:B:72:A:C3'	9:B:73:A:H5''	2.20	0.71
16:D:1308:U:O5'	36:X:98:ARG:HG3	1.90	0.71
20:H:267:TRP:CE3	20:H:340:ARG:HG2	2.25	0.71
9:B:46:G:H1'	9:B:47:U:C5	2.25	0.71
38:a:742:A:H2'	38:a:743:A:C8	2.26	0.71
44:g:18:CYS:CB	44:g:40:CYS:CB	2.68	0.71
10:AA:839:VAL:O	10:AA:886:LYS:HD3	1.90	0.71
15:C:44:ILE:HD13	20:H:339:ARG:HG3	1.70	0.71
10:AA:878:THR:HA	10:AA:925:SER:HA	1.73	0.71
9:B:18:G:C5	9:B:57:A:N6	2.59	0.71
9:A:72:A:C3'	9:A:73:A:H5''	2.20	0.71
13:AE:142:GLU:HG3	13:AE:142:GLU:O	1.89	0.71
27:O:84:THR:HG21	27:O:103:PHE:HB3	1.71	0.70
9:A:18:G:C5	9:A:57:A:N6	2.59	0.70
9:A:32:C:C4'	25:M:144:MET:CE	2.66	0.70
9:B:76:A:H2'	38:a:2493:U:H5''	1.72	0.70
38:a:2314:A:C1'	51:n:155:THR:HG21	2.21	0.70
9:A:15:G:H2'	9:A:15:G:N3	2.06	0.70
10:AA:207:THR:OG1	10:AA:354:ASP:OD2	2.09	0.70
10:AA:839:VAL:HA	10:AA:1048:LYS:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:86:ARG:O	20:H:89:ALA:HB3	1.91	0.70
13:AE:157:GLN:OE1	13:AE:157:GLN:HA	1.88	0.70
9:A:32:C:C1'	25:M:144:MET:CE	2.69	0.70
16:D:972:C:O2'	28:P:57:VAL:HG23	1.92	0.70
16:D:1309:G:H8	36:X:98:ARG:NH2	1.89	0.70
10:AA:859:GLU:OE2	10:AA:859:GLU:N	2.21	0.70
12:AD:86:LYS:HE3	13:AE:528:THR:HB	1.72	0.70
13:AE:105:ILE:HD12	13:AE:242:LEU:HD22	1.71	0.70
9:A:16:C:O2	38:a:2181:U:C5'	2.40	0.70
10:AA:878:THR:O	10:AA:920:VAL:CG1	2.40	0.70
13:AE:220:ARG:HG2	13:AE:220:ARG:HH11	1.55	0.70
13:AE:1143:ASP:OD1	13:AE:1148:ARG:NH1	2.21	0.70
36:X:96:PRO:HG2	36:X:102:THR:CG2	2.21	0.70
45:h:146:MET:HE3	45:h:154:LEU:HD21	1.74	0.70
10:AA:935:THR:HA	10:AA:1049:ILE:HD12	1.74	0.69
13:AE:128:LEU:HD11	13:AE:189:LEU:HG	1.73	0.69
9:A:41:C:C1'	25:M:143:ARG:NH1	2.55	0.69
10:AA:883:LEU:HD11	10:AA:920:VAL:CG2	2.21	0.69
20:H:19:ARG:HD3	20:H:73:ASP:OD1	1.92	0.69
13:AE:54:ASP:OD1	13:AE:54:ASP:N	2.24	0.69
16:D:915:A:N6	16:D:916:U:C4	2.60	0.69
38:a:2310:C:O2'	51:n:74:VAL:CG1	2.40	0.69
9:B:15:G:H2'	9:B:15:G:N3	2.06	0.69
13:AE:202:ARG:HG2	13:AE:202:ARG:NH1	1.99	0.69
20:H:70:VAL:HA	20:H:85:SER:CA	2.22	0.69
38:a:1596:A:H2'	38:a:1597:A:C8	2.28	0.69
20:H:267:TRP:CE2	20:H:340:ARG:CG	2.73	0.69
1:0:80:ARG:NH2	38:a:572:A:OP2	2.25	0.69
10:AA:992:LEU:CD2	10:AA:999:GLU:OE2	2.40	0.69
9:B:11:A:H2'	9:B:12:G:O4'	1.92	0.69
38:a:927:A:H2'	38:a:928:A:C8	2.28	0.69
38:a:1021:A:H3'	38:a:1021:A:N3	2.07	0.69
38:a:1839:G:C4	38:a:1927:A:C4	2.81	0.69
9:A:11:A:H2'	9:A:12:G:O4'	1.92	0.69
16:D:37:U:H3	16:D:397:A:N6	1.90	0.69
38:a:2756:U:C4	38:a:2758:A:N6	2.61	0.69
10:AA:728:ASP:OD1	10:AA:769:PRO:CG	2.41	0.68
10:AA:1047:LEU:O	10:AA:1049:ILE:CD1	2.40	0.68
10:AA:339:ASN:HB3	10:AA:343:HIS:H	1.58	0.68
13:AE:832:LYS:C	13:AE:1242:ARG:HH12	2.01	0.68
16:D:1308:U:C3'	36:X:98:ARG:HH21	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:110:GLY:HA3	20:H:153:GLU:O	1.93	0.68
36:X:96:PRO:CG	36:X:102:THR:CG2	2.71	0.68
38:a:2013:A:H61	38:a:2613:U:H3	1.31	0.68
7:6:8:DC:C2'	7:6:9:DT:H71	2.24	0.68
12:AC:76:GLU:OE1	12:AC:131:CYS:HA	1.92	0.68
13:AE:39:LYS:O	13:AE:273:ILE:CG2	2.41	0.68
16:D:13:U:O4	16:D:21:G:C2	2.46	0.68
20:H:19:ARG:HD3	20:H:73:ASP:OD2	1.92	0.68
38:a:1153:C:OP1	63:z:92:ARG:NH1	2.27	0.68
38:a:1839:G:H8	38:a:1927:A:H1'	1.54	0.68
10:AA:19:PRO:HA	10:AA:1156:ARG:HD3	1.73	0.68
20:H:267:TRP:CD2	20:H:340:ARG:CG	2.76	0.68
13:AE:141:PHE:CD2	13:AE:293:ARG:O	2.47	0.68
13:AE:161:THR:HG22	13:AE:164:GLN:HB2	1.76	0.68
10:AA:802:VAL:HA	10:AA:1096:ILE:O	1.93	0.68
13:AE:395:LYS:HZ2	13:AE:399:LYS:HD3	1.59	0.68
20:H:117:LYS:CB	20:H:279:LYS:O	2.41	0.68
38:a:2310:C:O2'	51:n:74:VAL:HG12	1.94	0.68
13:AE:117:LEU:HD12	13:AE:117:LEU:O	1.94	0.68
9:B:5:G:H2'	9:B:6:G:C5'	2.24	0.68
38:a:1920:C:O5'	38:a:1920:C:H6	1.77	0.68
10:AA:958:LYS:HB3	10:AA:958:LYS:NZ	2.08	0.67
15:C:44:ILE:CD1	20:H:339:ARG:HG2	2.12	0.67
19:G:16:PHE:HZ	20:H:41:GLY:O	1.77	0.67
13:AE:108:ALA:CB	13:AE:279:LEU:HD22	2.25	0.67
13:AE:1355:ARG:NH1	13:AE:1369:ARG:HH12	1.93	0.67
10:AA:768:MET:HE3	12:AC:80:GLU:OE1	1.95	0.67
10:AA:768:MET:HE1	12:AC:80:GLU:CD	2.19	0.67
10:AA:992:LEU:HD22	10:AA:992:LEU:N	2.04	0.67
16:D:1227:A:H5'	36:X:110:LYS:HZ1	1.58	0.67
10:AA:1253:LEU:HD12	13:AE:253:VAL:HG11	1.77	0.67
36:X:96:PRO:CG	36:X:102:THR:HG22	2.25	0.67
9:B:66:C:H5'	9:B:66:C:H6	1.60	0.67
38:a:2013:A:N6	38:a:2613:U:N3	2.33	0.67
9:A:66:C:H6	9:A:66:C:H5'	1.60	0.67
20:H:110:GLY:N	20:H:153:GLU:C	2.53	0.67
38:a:1779:U:H5	38:a:1784:A:N7	1.93	0.67
10:AA:960:LEU:HD13	10:AA:1029:LEU:HB2	1.77	0.67
13:AE:108:ALA:HB3	13:AE:279:LEU:HD22	1.77	0.67
34:V:25:ILE:HD11	34:V:61:ILE:HD11	1.77	0.67
9:A:56:C:C5	38:a:2168:G:C6	2.84	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:94:GLN:HB2	13:AE:97:VAL:HG23	1.76	0.66
16:D:1329:A:P	36:X:28:THR:CB	2.83	0.66
9:A:5:G:H2'	9:A:6:G:C5'	2.24	0.66
9:A:21:A:H4'	9:A:21:A:OP1	1.95	0.66
20:H:110:GLY:H	20:H:153:GLU:CA	2.08	0.66
10:AA:9:LYS:HG2	10:AA:1171:ARG:NH1	2.11	0.66
13:AE:111:THR:CG2	13:AE:300:GLN:CD	2.66	0.66
9:B:21:A:H4'	9:B:21:A:OP1	1.95	0.66
9:B:56:C:H5'	51:n:80:ARG:NH2	2.10	0.66
20:H:70:VAL:HA	20:H:85:SER:HA	1.77	0.66
10:AA:852:ALA:O	10:AA:854:ILE:N	2.28	0.66
10:AA:963:GLU:HA	10:AA:966:ILE:HD12	1.77	0.66
10:AA:1251:TYR:C	10:AA:1259:LEU:CD1	2.69	0.66
13:AE:984:LEU:HB3	13:AE:993:GLU:HB2	1.77	0.66
21:I:75:ILE:O	21:I:75:ILE:HD13	1.95	0.66
10:AA:995:ASP:OD1	10:AA:995:ASP:N	2.29	0.66
20:H:270:ILE:HG23	20:H:337:GLU:HB3	1.78	0.66
12:AC:76:GLU:OE2	12:AC:131:CYS:HA	1.95	0.66
13:AE:978:ARG:HG2	13:AE:1197:ASN:HD21	1.60	0.66
56:s:114:LEU:HG	56:s:118:MET:HE3	1.78	0.66
10:AA:839:VAL:O	10:AA:886:LYS:CD	2.44	0.66
10:AA:1257:GLN:OE1	13:AE:345:LYS:CD	2.44	0.66
10:AA:1257:GLN:OE1	13:AE:345:LYS:HG2	1.96	0.66
13:AE:84:ILE:O	13:AE:84:ILE:HG13	1.96	0.66
10:AA:9:LYS:HG2	10:AA:1171:ARG:HH12	1.61	0.66
7:6:16:DC:H1'	13:AE:426:ALA:HB1	1.76	0.66
9:A:19:G:N2	38:a:2112:G:C8	2.62	0.65
20:H:162:LYS:CB	20:H:298:GLU:OE1	2.44	0.65
38:a:1839:G:C8	38:a:1927:A:C1'	2.74	0.65
9:B:22:G:H2'	9:B:23:C:H6	1.62	0.65
16:D:1308:U:H5''	36:X:98:ARG:HG2	1.78	0.65
10:AA:768:MET:HE1	12:AC:80:GLU:OE1	1.94	0.65
13:AE:193:ASP:HB3	13:AE:196:GLN:HB2	1.78	0.65
9:B:18:G:C8	9:B:57:A:C6	2.85	0.65
9:B:37:A:H3'	9:B:37:A:OP2	1.96	0.65
16:D:563:A:N1	16:D:884:U:C4	2.60	0.65
53:p:24:ILE:HD13	53:p:72:LEU:HD21	1.77	0.65
11:AB:93:ILE:HG22	13:AE:290:ILE:CG2	2.27	0.65
12:AC:71:LYS:HZ1	12:AC:140:ILE:HB	1.60	0.65
10:AA:529:ARG:HH11	10:AA:572:ILE:HG22	1.62	0.65
10:AA:964:LEU:HD21	10:AA:1022:LYS:HD2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AD:102:LEU:HB2	12:AD:115:ILE:HG13	1.77	0.65
13:AE:1037:PHE:HB3	13:AE:1040:MET:HB2	1.78	0.65
9:B:75:C:OP1	38:a:2602:A:N9	2.30	0.65
19:G:38:VAL:HG22	20:H:75:VAL:CG2	2.24	0.65
20:H:267:TRP:CE3	20:H:340:ARG:HG3	2.32	0.65
13:AE:162:GLU:OE1	13:AE:162:GLU:HA	1.97	0.65
38:a:1923:U:H2'	38:a:1923:U:OP2	1.96	0.65
13:AE:67:ASP:OD1	13:AE:95:THR:OG1	2.15	0.65
13:AE:975:ILE:HG22	13:AE:977:SER:H	1.62	0.65
16:D:197:A:C6	16:D:221:C:C4'	2.80	0.65
20:H:52:GLN:O	20:H:53:PHE:CD1	2.50	0.65
9:A:41:C:C4'	25:M:143:ARG:NH1	2.60	0.65
12:AD:86:LYS:HE3	13:AE:528:THR:CG2	2.26	0.65
19:G:18:HIS:HA	20:H:43:LYS:CD	2.28	0.65
19:G:19:GLN:CG	20:H:75:VAL:CG2	2.70	0.65
20:H:135:LEU:CA	20:H:157:ILE:CB	2.74	0.65
31:S:47:LYS:O	31:S:50:THR:OG1	2.12	0.65
36:X:96:PRO:HG3	36:X:102:THR:HG22	1.77	0.65
16:D:827:U:N3	16:D:872:A:N6	2.45	0.64
16:D:1308:U:O5'	36:X:98:ARG:CG	2.45	0.64
19:G:19:GLN:CG	20:H:76:GLU:CB	2.76	0.64
20:H:332:VAL:HG12	20:H:334:ASP:H	1.62	0.64
22:J:162:ALA:CB	22:J:165:ARG:HH22	2.08	0.64
9:A:18:G:C8	9:A:57:A:C6	2.85	0.64
38:a:2303:G:N3	38:a:2314:A:C2	2.65	0.64
10:AA:962:GLU:OE1	10:AA:962:GLU:HA	1.97	0.64
10:AA:1257:GLN:HE22	13:AE:345:LYS:CA	2.09	0.64
13:AE:141:PHE:HD2	13:AE:293:ARG:O	1.80	0.64
9:B:3:C:H2'	9:B:4:G:H8	1.62	0.64
9:B:6:G:HO2'	9:B:7:G:H8	1.46	0.64
19:G:35:ARG:HH21	20:H:10:GLU:HG2	1.62	0.64
20:H:85:SER:O	20:H:88:LYS:CB	2.45	0.64
52:o:26:HIS:CE1	52:o:48:ALA:HB2	2.32	0.64
9:A:3:C:H2'	9:A:4:G:H8	1.62	0.64
9:B:76:A:H1'	38:a:2493:U:O3'	1.97	0.64
20:H:118:GLY:C	20:H:133:GLY:CA	2.68	0.64
16:D:1227:A:OP2	36:X:110:LYS:NZ	2.29	0.64
2:1:36:LEU:HD13	2:1:48:LYS:HA	1.80	0.64
13:AE:245:LEU:HG	13:AE:246:PRO:HD2	1.79	0.64
10:AA:988:LYS:NZ	10:AA:988:LYS:HB3	2.13	0.64
16:D:1227:A:H5'	36:X:110:LYS:HZ2	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:267:TRP:CZ2	20:H:340:ARG:CG	2.68	0.64
9:B:50:U:H2'	9:B:51:C:C6	2.33	0.64
16:D:1358:U:N3	16:D:1363:A:N6	2.46	0.64
38:a:2885:G:N7	46:i:40:ARG:NH2	2.46	0.64
9:A:31:G:O2'	25:M:144:MET:SD	2.56	0.63
13:AE:68:TYR:HB3	13:AE:75:TYR:CE2	2.32	0.63
38:a:1082:U:N3	38:a:1086:A:N6	2.45	0.63
8:7:60:U:OP1	13:AE:256:ASP:N	2.31	0.63
38:a:2297:A:C2	38:a:2321:U:C4	2.86	0.63
6:5:98:DA:C2'	6:5:99:DT:H72	2.28	0.63
14:AF:29:GLN:HB3	14:AF:35:LYS:HD2	1.80	0.63
16:D:1309:G:C8	36:X:98:ARG:NH2	2.66	0.63
20:H:119:GLY:CA	20:H:131:LEU:O	2.46	0.63
6:5:101:DT:OP2	13:AE:275:ARG:NH2	2.31	0.63
7:6:15:DC:N4	7:6:16:DC:H41	1.96	0.63
9:A:50:U:H2'	9:A:51:C:C6	2.33	0.63
10:AA:724:VAL:HG23	10:AA:734:ILE:HD13	1.80	0.63
20:H:270:ILE:HG21	20:H:337:GLU:HB3	1.80	0.63
38:a:1909:C:O5'	38:a:1909:C:H6	1.81	0.63
9:A:69:C:H2'	9:A:70:G:O4'	1.99	0.63
9:B:69:C:H2'	9:B:70:G:O4'	1.99	0.63
16:D:1358:U:H3	16:D:1363:A:N6	1.96	0.63
13:AE:44:ILE:CD1	13:AE:252:LEU:HD21	2.29	0.63
13:AE:144:TYR:CE1	13:AE:162:GLU:OE2	2.51	0.63
20:H:110:GLY:N	20:H:153:GLU:O	2.32	0.63
38:a:2189:U:O4'	38:a:2189:U:P	2.57	0.63
9:A:6:G:HO2'	9:A:7:G:H8	1.46	0.62
10:AA:992:LEU:N	10:AA:992:LEU:HD13	2.14	0.62
20:H:162:LYS:CB	20:H:298:GLU:OE2	2.45	0.62
53:p:121:ILE:HD12	53:p:141:ILE:HG22	1.79	0.62
9:A:37:A:O2'	9:A:38:A:H5'	1.99	0.62
10:AA:13:LYS:HB2	10:AA:1180:MET:HE2	1.81	0.62
10:AA:941:LYS:HZ3	10:AA:944:ARG:HH22	1.45	0.62
20:H:49:PRO:CD	20:H:84:LEU:HD11	2.29	0.62
12:AD:176:CYS:SG	13:AE:535:ARG:NH2	2.72	0.62
16:D:1059:C:O2	28:P:55:PRO:HG3	1.99	0.62
10:AA:850:ILE:O	10:AA:850:ILE:HG22	1.98	0.62
13:AE:128:LEU:HA	13:AE:192:MET:HE1	1.81	0.62
10:AA:1251:TYR:C	10:AA:1259:LEU:HD13	2.24	0.62
13:AE:201:LEU:HB2	13:AE:221:ILE:HD13	1.80	0.62
20:H:19:ARG:O	20:H:72:LEU:CB	2.41	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AA:1328:LYS:HD2	13:AE:102:MET:SD	2.40	0.62
13:AE:111:THR:CG2	13:AE:300:GLN:NE2	2.63	0.62
20:H:270:ILE:CG2	20:H:337:GLU:CB	2.77	0.62
25:M:23:LEU:O	25:M:27:VAL:HG13	1.99	0.62
38:a:1998:A:OP2	47:j:141:ARG:NH2	2.32	0.62
9:A:22:G:H2'	9:A:23:C:H6	1.62	0.62
9:A:33:U:H4'	25:M:84:THR:HB	1.82	0.62
9:A:56:C:O2	38:a:2112:G:C4	2.52	0.62
16:D:13:U:O4	16:D:20:U:C4	2.52	0.62
1:O:40:MET:HE1	63:z:105:ALA:HB1	1.80	0.62
6:5:108:DT:O4	10:AA:199:ASP:OD2	2.18	0.62
13:AE:136:GLU:CD	13:AE:312:ARG:HH22	2.06	0.62
15:C:29:LEU:O	15:C:33:ILE:HG23	2.00	0.62
9:A:41:C:C1'	25:M:143:ARG:HH12	2.12	0.62
36:X:101:ARG:O	36:X:101:ARG:HD3	2.00	0.62
38:a:1789:A:OP2	45:h:221:ARG:NH1	2.32	0.62
9:A:42:G:H2'	9:A:43:A:H8	1.65	0.62
9:A:54:U:N3	9:A:58:A:N6	2.47	0.62
13:AE:1355:ARG:NH1	13:AE:1369:ARG:NH1	2.47	0.62
10:AA:941:LYS:HZ3	10:AA:944:ARG:NH2	1.98	0.61
20:H:305:HIS:O	20:H:306:VAL:HB	2.00	0.61
9:A:34:C:P	25:M:84:THR:HG1	2.23	0.61
9:B:3:C:H2'	9:B:4:G:C8	2.35	0.61
16:D:37:U:O2	16:D:548:G:C2	2.52	0.61
16:D:1358:U:O4	16:D:1363:A:C2	2.47	0.61
20:H:304:VAL:HG12	20:H:304:VAL:O	1.99	0.61
15:C:44:ILE:CD1	20:H:339:ARG:HG3	2.28	0.61
38:a:754:U:H2'	38:a:755:U:C6	2.35	0.61
38:a:1839:G:O4'	38:a:1927:A:H1'	1.97	0.61
13:AE:92:VAL:O	13:AE:92:VAL:HG12	1.99	0.61
28:P:57:VAL:O	28:P:58:ASN:CG	2.43	0.61
19:G:19:GLN:HG3	20:H:75:VAL:CG2	2.23	0.61
38:a:1839:G:N9	38:a:1927:A:N9	2.48	0.61
10:AA:374:GLU:HG3	10:AA:374:GLU:O	2.01	0.61
10:AA:660:VAL:HG13	10:AA:661:VAL:HG13	1.82	0.61
38:a:84:A:N1	38:a:98:G:O2'	2.33	0.61
13:AE:154:LEU:HD21	13:AE:160:LEU:HD21	1.83	0.61
13:AE:416:ILE:HG13	13:AE:441:LEU:HD11	1.83	0.61
16:D:1308:U:H2'	36:X:98:ARG:HH22	1.61	0.61
33:U:21:VAL:HG21	33:U:60:TRP:CD1	2.36	0.61
10:AA:941:LYS:HD2	10:AA:941:LYS:C	2.26	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:67:ASP:OD1	13:AE:67:ASP:N	2.34	0.61
16:D:658:C:H1'	32:T:22:THR:HG21	1.83	0.61
20:H:84:LEU:HD22	20:H:84:LEU:N	2.16	0.61
9:A:3:C:H2'	9:A:4:G:C8	2.36	0.61
10:AA:478:ARG:NH1	10:AA:491:ASP:O	2.34	0.61
13:AE:90:VAL:O	13:AE:90:VAL:CG1	2.48	0.61
9:B:42:G:H2'	9:B:43:A:H8	1.65	0.61
16:D:13:U:C5	16:D:20:U:O4	2.53	0.61
38:a:2297:A:C2	38:a:2321:U:C5	2.89	0.61
9:A:65:C:H2'	9:A:66:C:H5'	1.82	0.60
10:AA:118:LYS:NZ	10:AA:485:ASP:OD1	2.25	0.60
9:B:65:C:H2'	9:B:66:C:H5'	1.82	0.60
3:2:50:LEU:HD23	42:e:26:PHE:CE1	2.35	0.60
7:6:15:DC:C4	7:6:16:DC:C4	2.88	0.60
13:AE:68:TYR:HB3	13:AE:75:TYR:CZ	2.35	0.60
13:AE:342:LEU:HD23	13:AE:1352:ILE:HG23	1.83	0.60
38:a:1921:G:O5'	38:a:1921:G:H8	1.85	0.60
38:a:2683:C:OP1	62:y:51:ARG:NH2	2.31	0.60
13:AE:201:LEU:HD11	13:AE:220:ARG:HH11	1.67	0.60
13:AE:395:LYS:NZ	13:AE:399:LYS:HD3	2.15	0.60
9:B:56:C:C4'	51:n:80:ARG:NH2	2.64	0.60
10:AA:1223:ARG:NH2	13:AE:721:SER:OG	2.34	0.60
13:AE:951:GLN:NE2	13:AE:1014:GLY:O	2.35	0.60
9:A:41:C:H4'	25:M:143:ARG:CZ	2.31	0.60
10:AA:941:LYS:HZ1	10:AA:944:ARG:NH2	1.99	0.60
19:G:19:GLN:CD	20:H:75:VAL:HG22	2.25	0.60
10:AA:528:ARG:NH2	10:AA:576:SER:O	2.34	0.60
10:AA:943:LYS:HD3	10:AA:943:LYS:H	1.64	0.60
16:D:1218:C:H2'	16:D:1219:A:C8	2.36	0.60
20:H:284:VAL:HG12	20:H:294:VAL:HB	1.84	0.60
9:A:34:C:P	25:M:84:THR:OG1	2.60	0.60
10:AA:861:ALA:HA	10:AA:882:ILE:HD13	1.83	0.60
13:AE:370:LYS:HG2	13:AE:441:LEU:HD23	1.84	0.60
19:G:19:GLN:HG3	20:H:76:GLU:HB2	1.82	0.60
20:H:331:MET:N	20:H:331:MET:SD	2.75	0.60
23:K:107:ALA:HB2	23:K:125:ALA:HB3	1.82	0.60
13:AE:926:PRO:HG2	13:AE:1248:ILE:HD11	1.84	0.60
13:AE:1161:GLY:HA3	13:AE:1179:PRO:HA	1.83	0.60
16:D:404:G:N7	22:J:2:ALA:HB3	2.17	0.60
19:G:18:HIS:CA	20:H:43:LYS:HD2	2.29	0.60
38:a:2720:U:OP1	62:y:53:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:305:HIS:CD2	20:H:307:SER:H	2.20	0.59
50:m:31:LEU:HD22	50:m:42:LEU:HD13	1.84	0.59
9:B:47:U:O2'	9:B:50:U:P	2.61	0.59
20:H:117:LYS:CB	20:H:278:THR:HG23	2.32	0.59
20:H:118:GLY:C	20:H:133:GLY:HA2	2.27	0.59
14:AF:26:ARG:NH1	14:AF:67:ARG:HH12	2.00	0.59
25:M:69:VAL:HG23	25:M:100:ALA:HB1	1.83	0.59
9:A:47:U:O2'	9:A:50:U:P	2.61	0.59
10:AA:376:PRO:O	10:AA:376:PRO:HG2	2.02	0.59
10:AA:1184:THR:HG23	10:AA:1190:ALA:H	1.67	0.59
43:f:24:LEU:HD11	43:f:54:MET:HE2	1.84	0.59
10:AA:888:THR:OG1	10:AA:889:PRO:HD2	2.02	0.59
10:AA:941:LYS:NZ	10:AA:944:ARG:HH22	1.97	0.59
10:AA:967:LEU:HD12	10:AA:967:LEU:C	2.25	0.59
13:AE:118:LYS:HD2	13:AE:312:ARG:NH2	2.17	0.59
13:AE:223:LEU:HG	13:AE:223:LEU:O	2.00	0.59
16:D:13:U:C2	16:D:915:A:N6	2.70	0.59
12:AD:86:LYS:HE3	13:AE:528:THR:CB	2.32	0.59
13:AE:412:LEU:HD22	13:AE:441:LEU:HD21	1.84	0.59
9:B:54:U:N3	9:B:58:A:N6	2.47	0.59
17:E:25:ARG:HA	17:E:66:LEU:HD21	1.85	0.59
10:AA:1142:ARG:NH2	10:AA:1166:ASP:OD1	2.36	0.59
16:D:563:A:N6	16:D:884:U:N3	2.51	0.59
20:H:270:ILE:HG21	20:H:337:GLU:CB	2.32	0.59
20:H:280:LEU:N	20:H:330:VAL:O	2.32	0.59
12:AD:81:ILE:HD13	12:AD:131:CYS:HB2	1.83	0.59
19:G:217:VAL:O	19:G:220:THR:HG22	2.02	0.59
10:AA:976:ARG:HG3	10:AA:989:LEU:HD13	1.85	0.59
11:AB:93:ILE:HG22	13:AE:290:ILE:HG22	1.85	0.59
16:D:1225:A:H4'	35:W:78:ARG:NH1	2.18	0.59
18:F:4:ILE:CD1	18:F:19:PHE:HA	2.33	0.59
20:H:305:HIS:HD2	20:H:306:VAL:H	1.49	0.59
13:AE:161:THR:HG23	13:AE:164:GLN:H	1.68	0.58
20:H:72:LEU:HD12	20:H:72:LEU:N	2.11	0.58
13:AE:99:ARG:HG3	13:AE:99:ARG:NH1	2.18	0.58
13:AE:275:ARG:NH1	13:AE:278:ARG:NH1	2.51	0.58
19:G:35:ARG:HD2	20:H:14:LYS:CD	2.32	0.58
10:AA:1014:LEU:HA	10:AA:1017:GLN:HG2	1.85	0.58
13:AE:24:LEU:CG	13:AE:232:ASN:ND2	2.64	0.58
20:H:119:GLY:HA3	20:H:132:PRO:C	2.28	0.58
47:j:33:ARG:NH1	47:j:53:GLY:O	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AA:954:LYS:O	10:AA:954:LYS:NZ	2.33	0.58
10:AA:963:GLU:HA	10:AA:963:GLU:OE1	2.01	0.58
12:AC:76:GLU:OE1	12:AC:131:CYS:CA	2.51	0.58
38:a:70:G:H4'	38:a:71:A:OP1	2.02	0.58
13:AE:438:GLU:HG3	13:AE:485:MET:HE1	1.85	0.58
13:AE:491:LEU:HB2	13:AE:904:ALA:HA	1.86	0.58
13:AE:514:THR:HG21	13:AE:596:LEU:HD12	1.84	0.58
16:D:321:A:N7	16:D:328:C:O2'	2.34	0.58
7:6:8:DC:H2'	7:6:9:DT:H71	1.86	0.58
9:B:58:A:H1'	9:B:60:U:C5	2.38	0.58
6:5:115:DA:OP2	13:AE:1148:ARG:HG3	2.04	0.58
8:7:70:G:H21	13:AE:427:PRO:HD3	1.68	0.58
16:D:1308:U:C5'	36:X:98:ARG:HG2	2.32	0.58
16:D:1526:G:OP2	18:F:42:THR:HG23	2.04	0.58
38:a:1590:A:H2'	38:a:1591:A:C8	2.38	0.58
2:1:20:VAL:HG11	2:1:44:ALA:HA	1.86	0.58
10:AA:1034:ARG:NH1	10:AA:1034:ARG:O	2.37	0.58
13:AE:124:ILE:HG22	13:AE:124:ILE:O	2.04	0.58
33:U:4:ILE:HG12	33:U:21:VAL:HG22	1.84	0.58
9:A:58:A:H1'	9:A:60:U:C5	2.38	0.58
13:AE:24:LEU:CG	13:AE:232:ASN:HD21	2.05	0.58
13:AE:97:VAL:HG11	13:AE:101:ARG:NH2	2.18	0.58
16:D:439:U:O2	16:D:440:C:C6	2.56	0.58
20:H:291:GLY:HA2	20:H:305:HIS:HA	1.86	0.58
38:a:2314:A:O2'	51:n:155:THR:CG2	2.51	0.58
8:7:63:G:H2'	8:7:64:U:C6	2.39	0.58
9:A:35:A:H2'	9:A:36:U:C6	2.38	0.58
9:A:60:U:P	9:A:61:C:H41	2.27	0.58
20:H:36:VAL:HB	20:H:48:ILE:HB	1.84	0.58
32:T:5:THR:O	32:T:8:THR:OG1	2.18	0.58
9:A:76:A:H2'	38:a:2394:C:N4	2.11	0.57
16:D:496:A:N3	16:D:496:A:H2'	2.19	0.57
19:G:19:GLN:NE2	20:H:75:VAL:HG22	2.19	0.57
38:a:2572:A:C8	47:j:149:ASN:OD1	2.56	0.57
8:7:60:U:OP2	13:AE:255:LEU:HA	2.04	0.57
9:A:76:A:C2'	38:a:2394:C:H42	2.16	0.57
19:G:148:LEU:HD22	19:G:151:ILE:HD11	1.87	0.57
9:A:50:U:H2'	9:A:51:C:H6	1.69	0.57
20:H:267:TRP:CH2	20:H:340:ARG:CB	2.86	0.57
28:P:6:ILE:HG23	28:P:100:ILE:HG23	1.87	0.57
10:AA:400:VAL:HG11	10:AA:452:ARG:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:1046:ILE:HD12	13:AE:1059:LEU:HB3	1.86	0.57
9:B:60:U:P	9:B:61:C:H41	2.27	0.57
9:A:11:A:H2'	9:A:12:G:C8	2.40	0.57
9:B:56:C:C5'	51:n:80:ARG:NH2	2.67	0.57
16:D:1329:A:P	36:X:28:THR:OG1	2.62	0.57
29:Q:67:ALA:HB2	29:Q:96:THR:HG23	1.86	0.57
10:AA:914:LYS:H	10:AA:914:LYS:HD3	1.68	0.57
10:AA:1072:ASN:ND2	10:AA:1111:GLN:OE1	2.37	0.57
12:AD:15:ASP:HB3	12:AD:27:THR:HB	1.87	0.57
23:K:56:VAL:O	23:K:60:ILE:HG23	2.04	0.57
38:a:2245:U:O2'	38:a:2436:G:OP2	2.22	0.57
4:3:36:VAL:CG1	4:3:39:ILE:HD12	2.32	0.57
10:AA:974:ARG:HD2	10:AA:1014:LEU:HD11	1.85	0.57
38:a:1021:A:C2	38:a:1141:U:O4	2.51	0.57
38:a:1818:U:OP2	45:h:156:ARG:NH1	2.38	0.57
13:AE:37:GLU:O	13:AE:61:ILE:CD1	2.52	0.57
13:AE:241:VAL:HG12	13:AE:241:VAL:O	2.04	0.57
20:H:71:ALA:O	20:H:72:LEU:CD1	2.42	0.57
20:H:110:GLY:N	20:H:153:GLU:CA	2.67	0.57
20:H:290:TYR:C	20:H:305:HIS:O	2.47	0.57
20:H:330:VAL:HB	20:H:344:LEU:HD23	1.86	0.57
13:AE:741:ALA:O	13:AE:762:ASN:ND2	2.38	0.57
6:5:99:DT:H2''	6:5:100:DA:H5''	1.85	0.56
10:AA:10:ARG:NH1	10:AA:697:LYS:HD3	2.19	0.56
13:AE:74:LYS:HD2	13:AE:85:CYS:SG	2.45	0.56
13:AE:99:ARG:HH11	13:AE:99:ARG:CG	2.18	0.56
20:H:110:GLY:H	20:H:153:GLU:C	2.11	0.56
26:N:10:MET:HE3	26:N:61:LEU:HD11	1.87	0.56
38:a:1839:G:N9	38:a:1927:A:C4	2.72	0.56
49:l:104:ALA:O	49:l:108:ILE:HG23	2.05	0.56
10:AA:449:GLY:HA3	10:AA:609:ILE:HG23	1.88	0.56
10:AA:855:PRO:O	10:AA:855:PRO:HG2	2.04	0.56
10:AA:1005:GLU:OE1	10:AA:1005:GLU:HA	2.05	0.56
10:AA:1256:GLN:OE1	10:AA:1256:GLN:HA	2.03	0.56
13:AE:198:CYS:HA	13:AE:221:ILE:HD11	1.86	0.56
36:X:104:THR:O	36:X:104:THR:HG22	2.03	0.56
10:AA:1257:GLN:OE1	13:AE:345:LYS:HB3	2.05	0.56
12:AD:81:ILE:HD11	12:AD:130:ILE:HG22	1.87	0.56
13:AE:247:PRO:HA	13:AE:250:ARG:HG3	1.87	0.56
9:B:11:A:H2'	9:B:12:G:C8	2.40	0.56
9:B:32:C:OP2	27:O:130:ARG:NH2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:119:GLY:CA	20:H:133:GLY:CA	2.74	0.56
58:u:77:ILE:HD11	58:u:108:ALA:HB1	1.87	0.56
10:AA:1084:ASP:OD1	12:AC:45:ARG:NH1	2.32	0.56
13:AE:638:SER:OG	13:AE:639:VAL:N	2.36	0.56
40:c:31:PRO:HG2	40:c:33:LEU:HD13	1.87	0.56
10:AA:958:LYS:HB3	10:AA:958:LYS:HZ1	1.69	0.56
10:AA:1046:VAL:HG22	10:AA:1049:ILE:HG13	1.88	0.56
9:B:50:U:H2'	9:B:51:C:H6	1.69	0.56
38:a:580:U:O3'	63:z:31:VAL:HG13	2.05	0.56
2:1:93:ALA:HB2	38:a:1614:A:C2	2.40	0.56
13:AE:903:LEU:HD21	13:AE:1249:ASN:HD22	1.70	0.56
20:H:49:PRO:HD3	20:H:84:LEU:HD11	1.87	0.56
9:A:56:C:C6	38:a:2168:G:C6	2.94	0.56
13:AE:343:LEU:HD11	13:AE:1324:SER:HB3	1.87	0.56
10:AA:39:ILE:HD12	10:AA:75:LEU:HD22	1.88	0.56
10:AA:174:ALA:HB2	10:AA:432:LEU:HD13	1.88	0.56
10:AA:218:GLU:OE2	10:AA:300:ASP:N	2.28	0.56
10:AA:880:GLY:O	10:AA:919:ARG:HD3	2.06	0.56
10:AA:1251:TYR:C	10:AA:1259:LEU:HD11	2.31	0.56
10:AA:1257:GLN:NE2	13:AE:346:ARG:H	2.04	0.56
12:AC:69:SER:OG	12:AC:70:THR:N	2.38	0.56
36:X:17:ILE:O	36:X:20:THR:OG1	2.22	0.56
10:AA:1246:ARG:NH1	10:AA:1266:GLY:HA2	2.20	0.56
13:AE:144:TYR:HE1	13:AE:162:GLU:CD	2.14	0.56
13:AE:1175:LEU:HD22	13:AE:1190:ILE:HD11	1.88	0.56
9:B:11:A:H8	9:B:11:A:O5'	1.89	0.56
16:D:927:G:O2'	16:D:1503:A:N7	2.36	0.56
9:A:11:A:O5'	9:A:11:A:H8	1.89	0.56
10:AA:859:GLU:O	10:AA:859:GLU:HG2	2.06	0.56
13:AE:160:LEU:HD22	13:AE:164:GLN:HB3	1.86	0.56
13:AE:510:LEU:HD22	13:AE:601:ILE:HD12	1.86	0.56
9:B:60:U:O2'	9:B:61:C:OP1	2.23	0.56
38:a:2303:G:C4	38:a:2314:A:C2	2.94	0.56
10:AA:241:LEU:HD21	10:AA:246:LEU:HD11	1.88	0.55
10:AA:801:ARG:HG2	10:AA:1094:VAL:HG23	1.87	0.55
12:AC:91:ARG:HD2	12:AC:122:GLU:HB3	1.88	0.55
10:AA:227:LYS:NZ	10:AA:298:ALA:HB1	2.21	0.55
10:AA:724:VAL:CG1	10:AA:774:GLY:N	2.68	0.55
10:AA:818:VAL:HG22	10:AA:1096:ILE:HG12	1.87	0.55
10:AA:976:ARG:HG3	10:AA:976:ARG:HH11	1.71	0.55
13:AE:1166:GLY:HA3	13:AE:1174:ARG:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:51:VAL:HG23	63:z:86:ALA:O	2.05	0.55
10:AA:1070:HIS:NE2	10:AA:1114:GLU:OE1	2.36	0.55
13:AE:39:LYS:O	13:AE:273:ILE:HG21	2.06	0.55
13:AE:130:MET:HE2	13:AE:135:ILE:HG12	1.87	0.55
13:AE:171:GLU:HA	13:AE:171:GLU:OE1	2.05	0.55
38:a:2000:C:OP1	60:w:5:LYS:NZ	2.36	0.55
12:AD:142:MET:N	12:AD:142:MET:SD	2.80	0.55
9:B:18:G:C8	9:B:57:A:N6	2.70	0.55
16:D:528:C:H6	16:D:528:C:H5''	1.71	0.55
38:a:811:U:H2'	58:u:21:ARG:HA	1.89	0.55
38:a:2249:U:H3'	38:a:2250:G:C5'	2.36	0.55
20:H:154:PHE:CB	20:H:168:VAL:CB	2.85	0.55
20:H:332:VAL:CG1	20:H:335:ILE:HG13	2.33	0.55
10:AA:1252:SER:N	10:AA:1259:LEU:CD1	2.70	0.55
11:AB:107:GLU:OE1	13:AE:288:PRO:CB	2.52	0.55
16:D:769:G:H4'	16:D:1513:A:H4'	1.88	0.55
44:g:18:CYS:HB3	44:g:40:CYS:HB2	1.88	0.55
20:H:267:TRP:CH2	20:H:340:ARG:HB3	2.41	0.55
9:A:38:A:H2'	9:A:39:C:H5'	1.88	0.55
13:AE:102:MET:HG2	13:AE:246:PRO:HG3	1.87	0.55
61:x:27:VAL:HG21	61:x:40:ILE:HD12	1.89	0.55
13:AE:58:CYS:SG	13:AE:59:ALA:N	2.80	0.55
49:l:108:ILE:HD11	49:l:180:LEU:HD13	1.89	0.55
49:l:130:LYS:HB2	49:l:133:LEU:HD12	1.89	0.55
9:A:60:U:O2'	9:A:61:C:OP1	2.23	0.55
10:AA:1246:ARG:NH1	10:AA:1258:PRO:HB3	2.22	0.55
13:AE:833:GLU:HB2	13:AE:1242:ARG:NH1	2.22	0.55
16:D:13:U:C4	16:D:915:A:C6	2.92	0.55
16:D:563:A:N6	16:D:884:U:H3	2.05	0.55
3:2:50:LEU:HD23	42:e:26:PHE:CZ	2.42	0.54
9:A:32:C:O2'	25:M:86:GLN:CD	2.31	0.54
13:AE:136:GLU:OE1	13:AE:312:ARG:CZ	2.55	0.54
20:H:45:GLU:OE1	20:H:45:GLU:N	2.40	0.54
27:O:81:HIS:O	27:O:84:THR:OG1	2.23	0.54
20:H:279:LYS:HA	20:H:331:MET:CB	2.33	0.54
55:r:58:LEU:O	55:r:61:VAL:HG22	2.08	0.54
10:AA:699:LEU:HG	10:AA:799:ASN:HD22	1.72	0.54
10:AA:840:SER:HA	10:AA:886:LYS:HD2	1.90	0.54
10:AA:991:LYS:HB2	10:AA:992:LEU:HD22	1.88	0.54
38:a:2314:A:O2'	51:n:155:THR:HG21	2.06	0.54
8:7:58:A:H3'	8:7:58:A:N3	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:124:ILE:HG23	13:AE:128:LEU:HD12	1.89	0.54
13:AE:1155:ILE:HG13	13:AE:1210:ILE:HB	1.89	0.54
16:D:439:U:O2	16:D:440:C:C5	2.61	0.54
7:6:26:DT:H2''	7:6:27:DG:H5'	1.88	0.54
12:AD:215:GLU:OE1	12:AD:218:ARG:NH1	2.40	0.54
10:AA:452:ARG:HH12	10:AA:458:GLU:CD	2.15	0.54
13:AE:145:VAL:HG23	13:AE:159:ILE:HG22	1.89	0.54
14:AF:26:ARG:HH12	14:AF:67:ARG:HH12	1.56	0.54
20:H:52:GLN:OE1	20:H:86:ARG:CB	2.55	0.54
28:P:8:ILE:HD12	28:P:25:ILE:HD11	1.89	0.54
10:AA:1275:VAL:HG13	10:AA:1287:LEU:HD11	1.90	0.54
12:AC:140:ILE:HD11	12:AC:142:MET:HE3	1.89	0.54
13:AE:26:SER:HB2	13:AE:236:TRP:CE2	2.42	0.54
13:AE:746:LEU:HG	13:AE:758:PRO:HG3	1.90	0.54
20:H:116:VAL:C	20:H:279:LYS:HB2	2.33	0.54
10:AA:738:GLU:HA	10:AA:741:MET:HE2	1.90	0.54
10:AA:858:GLY:C	10:AA:860:ALA:H	2.14	0.54
12:AD:22:THR:OG1	12:AD:207:THR:O	2.26	0.54
13:AE:814:CYS:SG	13:AE:883:ARG:NH2	2.81	0.54
38:a:1906:G:H5''	38:a:1906:G:H8	1.73	0.54
59:v:66:ARG:NH1	59:v:104:GLU:OE1	2.39	0.54
10:AA:724:VAL:HG12	10:AA:774:GLY:H	1.72	0.54
10:AA:985:GLU:HB2	10:AA:988:LYS:HB2	1.90	0.54
13:AE:205:LEU:HG	13:AE:217:LEU:HB3	1.90	0.54
16:D:13:U:C4	16:D:21:G:C2	2.96	0.54
16:D:961:U:O4	16:D:974:A:N1	2.40	0.54
20:H:321:VAL:HG13	20:H:322:VAL:HG23	1.90	0.54
38:a:523:C:O2	38:a:554:U:O2'	2.25	0.54
9:A:18:G:C2	9:A:58:A:C5	2.96	0.54
10:AA:835:GLU:OE2	10:AA:1051:LYS:HD3	2.08	0.54
20:H:135:LEU:CB	20:H:167:VAL:CA	2.86	0.54
35:W:15:LEU:HD13	35:W:33:THR:HG21	1.88	0.54
20:H:84:LEU:HD22	20:H:84:LEU:H	1.72	0.53
28:P:24:GLU:OE2	28:P:90:LEU:CD1	2.56	0.53
41:d:5:U:OP1	41:d:61:G:O2'	2.26	0.53
10:AA:946:LEU:HD23	10:AA:946:LEU:N	2.23	0.53
13:AE:68:TYR:CA	13:AE:75:TYR:HE2	2.22	0.53
13:AE:78:LEU:O	13:AE:78:LEU:HD13	2.08	0.53
9:B:76:A:N3	38:a:2493:U:H4'	2.24	0.53
16:D:945:G:C2	16:D:946:A:C8	2.96	0.53
38:a:2192:U:H2'	38:a:2193:G:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:13:VAL:CG2	4:3:39:ILE:HD13	2.39	0.53
9:A:56:C:C2	38:a:2112:G:C8	2.96	0.53
10:AA:1010:GLN:O	10:AA:1010:GLN:NE2	2.41	0.53
12:AD:196:THR:HB	13:AE:443:GLU:CG	2.36	0.53
9:B:18:G:C2	9:B:58:A:C5	2.97	0.53
23:K:94:VAL:HG13	23:K:111:MET:HE1	1.91	0.53
23:K:99:ALA:HB1	23:K:103:THR:HG21	1.89	0.53
38:a:1056:G:O2'	38:a:1103:A:N6	2.41	0.53
7:6:2:DC:H2''	7:6:3:DC:C5	2.43	0.53
10:AA:994:ARG:HD2	10:AA:994:ARG:O	2.09	0.53
12:AC:215:GLU:OE2	12:AC:219:ARG:NH2	2.41	0.53
13:AE:209:ASN:HA	13:AE:214:ARG:HH21	1.74	0.53
13:AE:759:ILE:HG23	13:AE:771:GLN:HB3	1.89	0.53
13:AE:785:ASP:O	13:AE:789:LYS:HB2	2.08	0.53
16:D:1329:A:OP1	36:X:28:THR:N	2.41	0.53
61:x:35:ILE:HG21	61:x:71:ALA:HA	1.90	0.53
10:AA:992:LEU:H	10:AA:992:LEU:CD2	1.95	0.53
13:AE:56:LEU:CD1	13:AE:273:ILE:HD12	2.39	0.53
13:AE:975:ILE:HD11	13:AE:1003:LEU:HD11	1.91	0.53
9:B:56:C:C5'	51:n:80:ARG:CZ	2.76	0.53
57:t:7:MET:HE1	57:t:44:LYS:HD2	1.91	0.53
9:A:12:G:H2'	9:A:13:C:OP1	2.08	0.53
10:AA:1287:LEU:HD13	13:AE:1357:ILE:HD11	1.90	0.53
13:AE:46:TYR:CD1	13:AE:46:TYR:C	2.86	0.53
9:B:12:G:H2'	9:B:13:C:OP1	2.07	0.53
16:D:767:A:H2'	16:D:768:A:O4'	2.08	0.53
16:D:1227:A:P	36:X:110:LYS:HZ2	2.32	0.53
20:H:332:VAL:O	20:H:334:ASP:N	2.40	0.53
44:g:16:CYS:HB3	44:g:37:CYS:HB3	1.86	0.53
13:AE:30:ILE:HG21	13:AE:241:VAL:O	2.08	0.53
16:D:13:U:C2	16:D:915:A:C6	2.95	0.53
16:D:1228:C:OP2	36:X:110:LYS:NZ	2.41	0.53
39:b:37:ILE:HD11	39:b:82:ILE:HD11	1.90	0.53
2:1:59:GLU:CG	2:1:66:ILE:HD11	2.38	0.53
9:A:18:G:C8	9:A:57:A:N6	2.69	0.53
13:AE:99:ARG:HG3	13:AE:99:ARG:HH11	1.74	0.53
13:AE:832:LYS:HB3	13:AE:1242:ARG:NH1	2.24	0.53
38:a:1839:G:N9	38:a:1927:A:H1'	2.23	0.53
10:AA:227:LYS:HZ2	10:AA:298:ALA:HB1	1.72	0.53
10:AA:726:TYR:HD2	10:AA:726:TYR:O	1.92	0.53
10:AA:953:LEU:HD13	10:AA:1036:ILE:HG21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AD:109:PRO:HA	12:AD:132:HIS:HA	1.91	0.53
20:H:22:SER:N	20:H:69:ASP:OD2	2.40	0.53
20:H:84:LEU:H	20:H:84:LEU:CD2	2.21	0.53
10:AA:524:ILE:HG21	10:AA:708:VAL:HG13	1.91	0.53
13:AE:201:LEU:HD12	13:AE:224:LEU:HD12	1.91	0.53
15:C:61:ARG:NH2	16:D:736:C:OP1	2.43	0.53
38:a:2315:G:O2'	51:n:125:ARG:HD3	2.09	0.53
49:l:131:THR:HG22	49:l:160:ALA:O	2.08	0.53
10:AA:1069:ARG:NH2	10:AA:1114:GLU:OE2	2.30	0.52
13:AE:112:ALA:HA	13:AE:238:ILE:HA	1.91	0.52
20:H:24:VAL:HG12	20:H:69:ASP:H	1.74	0.52
21:I:77:ILE:HA	21:I:84:VAL:HG23	1.91	0.52
30:R:80:ILE:HD12	30:R:97:THR:HG22	1.90	0.52
38:a:523:C:H4'	38:a:540:C:O2	2.10	0.52
38:a:2328:A:H2'	38:a:2329:U:C6	2.45	0.52
9:A:17:C:O2	9:A:17:C:H2'	2.08	0.52
9:A:38:A:C2'	9:A:39:C:H5'	2.39	0.52
10:AA:628:HIS:HB3	10:AA:647:ARG:HH21	1.73	0.52
13:AE:111:THR:HG22	13:AE:300:GLN:NE2	2.23	0.52
9:B:6:G:O2'	9:B:7:G:H8	1.92	0.52
27:O:98:LEU:HB3	27:O:104:VAL:HG13	1.91	0.52
9:A:12:G:C2'	9:A:13:C:OP1	2.57	0.52
9:A:22:G:O2'	9:A:23:C:P	2.68	0.52
13:AE:39:LYS:O	13:AE:273:ILE:HG23	2.08	0.52
13:AE:215:LYS:HA	13:AE:218:THR:HG22	1.91	0.52
20:H:19:ARG:O	20:H:72:LEU:HD22	2.09	0.52
2:1:93:ALA:HB2	38:a:1614:A:N1	2.25	0.52
7:6:8:DC:H2''	7:6:9:DT:H71	1.91	0.52
9:A:16:C:O2	9:A:16:C:H2'	2.09	0.52
9:A:72:A:H2'	9:A:73:A:C5'	2.32	0.52
10:AA:1034:ARG:HH11	10:AA:1034:ARG:CG	2.20	0.52
13:AE:99:ARG:HA	13:AE:248:ASP:HB2	1.92	0.52
15:C:30:LYS:HA	15:C:33:ILE:HD13	1.91	0.52
16:D:1515:G:H2'	16:D:1516:G:H8	1.72	0.52
20:H:135:LEU:CB	20:H:157:ILE:CB	2.87	0.52
51:n:8:TYR:HA	51:n:12:VAL:HB	1.91	0.52
57:t:71:ARG:NH2	57:t:123:LEU:O	2.42	0.52
10:AA:242:VAL:HB	10:AA:245:ARG:NH1	2.25	0.52
10:AA:813:GLU:HB2	13:AE:461:PHE:HD2	1.74	0.52
9:B:15:G:N3	9:B:15:G:C2'	2.73	0.52
9:B:22:G:O2'	9:B:23:C:P	2.67	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:J:61:VAL:HG21	22:J:200:ILE:CD1	2.35	0.52
44:g:16:CYS:CB	44:g:37:CYS:CB	2.82	0.52
10:AA:840:SER:O	10:AA:840:SER:OG	2.19	0.52
10:AA:862:LEU:HD23	10:AA:862:LEU:H	1.74	0.52
10:AA:1257:GLN:OE1	13:AE:345:LYS:CB	2.57	0.52
13:AE:144:TYR:CE1	13:AE:162:GLU:CD	2.88	0.52
16:D:673:A:H2'	16:D:674:G:C8	2.44	0.52
16:D:864:A:C2	16:D:865:A:C2	2.98	0.52
23:K:81:LEU:HD13	23:K:123:VAL:HG12	1.92	0.52
60:w:38:LEU:N	60:w:39:PRO:CD	2.73	0.52
10:AA:960:LEU:HB3	10:AA:1025:PHE:CE1	2.45	0.52
13:AE:1167:LYS:HZ2	13:AE:1170:LYS:HB2	1.74	0.52
16:D:1276:G:O5'	16:D:1276:G:H8	1.93	0.52
38:a:1814:G:H4'	45:h:51:THR:HG21	1.92	0.52
63:z:58:ARG:HA	63:z:61:TRP:CE3	2.45	0.52
4:3:94:ARG:HB3	4:3:103:ILE:HD12	1.91	0.52
9:A:18:G:C2	9:A:58:A:C6	2.98	0.52
9:A:41:C:H4'	25:M:143:ARG:NH1	2.25	0.52
13:AE:395:LYS:HZ2	13:AE:399:LYS:CE	2.23	0.52
9:B:16:C:O2	9:B:16:C:H2'	2.09	0.52
38:a:639:U:H2'	38:a:640:C:C6	2.45	0.52
38:a:1693:U:O2'	45:h:14:ARG:NH2	2.43	0.52
12:AC:171:LEU:HD23	12:AC:171:LEU:N	2.24	0.51
9:B:5:G:C2'	9:B:6:G:H5'	2.40	0.51
38:a:1266:G:OP2	46:i:17:ARG:NE	2.43	0.51
53:p:121:ILE:HD12	53:p:141:ILE:CG2	2.40	0.51
4:3:12:ILE:HG21	4:3:80:ALA:HB2	1.92	0.51
9:A:56:C:H2'	9:A:57:A:C5'	2.27	0.51
10:AA:808:ASN:H	13:AE:633:ALA:HB2	1.74	0.51
9:B:17:C:O2	9:B:17:C:H2'	2.08	0.51
38:a:929:U:H1'	43:f:26:GLY:O	2.10	0.51
38:a:2298:A:C5	38:a:2321:U:O4	2.62	0.51
9:A:6:G:O2'	9:A:7:G:H8	1.92	0.51
10:AA:991:LYS:N	10:AA:991:LYS:CD	2.73	0.51
12:AC:158:ARG:NH1	12:AC:158:ARG:CB	2.73	0.51
20:H:49:PRO:HD2	20:H:84:LEU:CD1	2.39	0.51
10:AA:884:VAL:HG11	10:AA:1050:VAL:HG11	1.90	0.51
9:B:12:G:C2'	9:B:13:C:OP1	2.57	0.51
16:D:1499:A:O2'	16:D:1500:A:H5'	2.10	0.51
20:H:308:GLU:O	20:H:310:ASP:N	2.43	0.51
37:Y:72:U:H6	37:Y:72:U:H3'	1.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:118:A:C8	38:a:119:A:C8	2.99	0.51
38:a:1910:G:O5'	38:a:1910:G:H8	1.93	0.51
38:a:1980:G:O2'	38:a:1982:U:OP2	2.28	0.51
10:AA:1045:GLY:O	10:AA:1047:LEU:HD13	2.10	0.51
9:A:56:C:H1'	38:a:2112:G:C5	2.46	0.51
9:A:56:C:C3'	9:A:57:A:H5''	2.40	0.51
10:AA:873:ILE:HG12	12:AC:65:LEU:HD13	1.93	0.51
12:AD:95:LYS:O	12:AD:148:ARG:NH2	2.42	0.51
18:F:4:ILE:HD12	18:F:19:PHE:HA	1.93	0.51
20:H:332:VAL:C	20:H:334:ASP:H	2.18	0.51
9:A:28:C:H2'	9:A:29:G:H8	1.76	0.51
10:AA:657:THR:HG21	10:AA:1188:ASP:HB2	1.92	0.51
10:AA:859:GLU:H	10:AA:859:GLU:CD	2.15	0.51
12:AD:33:ARG:HD3	12:AD:197:ASP:HB2	1.91	0.51
12:AD:182:ARG:CD	13:AE:581:MET:HE1	2.39	0.51
50:m:31:LEU:HD22	50:m:42:LEU:CD1	2.40	0.51
57:t:113:MET:O	57:t:116:ILE:HG13	2.11	0.51
10:AA:862:LEU:HD23	10:AA:862:LEU:N	2.25	0.51
10:AA:1252:SER:CA	10:AA:1259:LEU:HD11	2.41	0.51
13:AE:275:ARG:HH12	13:AE:278:ARG:NH1	2.09	0.51
19:G:35:ARG:NH2	20:H:10:GLU:HG2	2.25	0.51
20:H:267:TRP:CZ3	20:H:340:ARG:HG3	2.43	0.51
38:a:587:C:OP2	58:u:21:ARG:NH1	2.43	0.51
38:a:1869:G:N2	38:a:1871:A:O2'	2.44	0.51
6:5:101:DT:H72	13:AE:271:ARG:CZ	2.41	0.51
9:A:76:A:O2'	38:a:2395:C:C2	2.64	0.51
12:AD:182:ARG:HD3	13:AE:581:MET:HE1	1.92	0.51
13:AE:437:PHE:HZ	13:AE:453:VAL:HG11	1.76	0.51
2:1:59:GLU:HG3	2:1:66:ILE:HD11	1.92	0.51
9:A:56:C:C5	38:a:2168:G:O6	2.64	0.51
10:AA:694:ARG:NH2	12:AC:83:LEU:HD13	2.26	0.51
13:AE:972:LYS:HD2	13:AE:1004:ALA:HA	1.93	0.51
9:B:15:G:H22	9:B:20:U:H3	1.59	0.51
16:D:1228:C:OP1	36:X:107:ARG:CZ	2.58	0.51
16:D:1404:C:H2'	16:D:1404:C:O2	2.10	0.51
16:D:1410:A:C2	16:D:1491:G:C2	2.99	0.51
38:a:1964:G:H4'	38:a:1965:C:OP2	2.11	0.51
38:a:2243:U:H2'	38:a:2244:U:C6	2.46	0.51
2:1:24:ILE:HD13	2:1:36:LEU:HD11	1.93	0.50
10:AA:689:ALA:HB2	10:AA:1233:LEU:HD23	1.92	0.50
10:AA:733:VAL:HG22	10:AA:750:ILE:HG12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AA:984:VAL:O	10:AA:984:VAL:HG22	2.10	0.50
13:AE:850:LYS:HB2	13:AE:857:LEU:HB2	1.91	0.50
9:B:34:C:O2	9:B:34:C:H2'	2.11	0.50
28:P:57:VAL:O	28:P:57:VAL:HG13	2.11	0.50
32:T:40:GLN:CA	32:T:40:GLN:HE21	2.23	0.50
10:AA:14:ASP:HA	10:AA:1183:ALA:HB3	1.94	0.50
13:AE:88:CYS:HB3	13:AE:90:VAL:HG12	1.92	0.50
16:D:1308:U:OP1	36:X:100:GLN:OE1	2.23	0.50
32:T:21:ASP:O	32:T:22:THR:HG22	2.12	0.50
38:a:1141:U:O2	38:a:1142:A:N6	2.44	0.50
38:a:2557:G:H2'	38:a:2558:C:C6	2.46	0.50
57:t:43:ILE:HD12	57:t:56:ASP:HB2	1.93	0.50
10:AA:880:GLY:C	10:AA:919:ARG:HD3	2.36	0.50
10:AA:1253:LEU:HD12	13:AE:253:VAL:HG13	1.90	0.50
9:B:18:G:C2	9:B:58:A:C6	2.99	0.50
63:z:47:TYR:CD1	63:z:47:TYR:C	2.90	0.50
9:A:48:C:H2'	9:A:48:C:O2	2.11	0.50
10:AA:988:LYS:NZ	10:AA:988:LYS:CB	2.73	0.50
10:AA:1244:HIS:NE2	10:AA:1266:GLY:O	2.35	0.50
10:AA:1252:SER:HA	10:AA:1259:LEU:HD11	1.93	0.50
13:AE:390:LEU:N	13:AE:390:LEU:CD1	2.73	0.50
13:AE:1371:ARG:HE	13:AE:1372:ARG:NH1	2.10	0.50
16:D:1308:U:P	36:X:98:ARG:HG3	2.50	0.50
41:d:106:G:H2'	41:d:107:G:O4'	2.10	0.50
53:p:35:ARG:HD3	53:p:71:LEU:HD13	1.94	0.50
10:AA:817:LEU:HD12	10:AA:1078:LYS:HB3	1.93	0.50
9:B:56:C:C3'	9:B:57:A:H5''	2.40	0.50
38:a:1209:U:O2'	38:a:1237:A:N1	2.40	0.50
9:A:15:G:N3	9:A:15:G:C2'	2.73	0.50
13:AE:804:ALA:O	13:AE:806:ASP:N	2.41	0.50
16:D:1356:G:H2'	16:D:1357:A:C8	2.47	0.50
20:H:117:LYS:CB	20:H:278:THR:CG2	2.90	0.50
45:h:107:PRO:HD2	45:h:110:LEU:HD22	1.94	0.50
9:B:24:U:O2'	38:a:1922:G:O3'	2.29	0.50
9:B:48:C:O2	9:B:48:C:H2'	2.11	0.50
19:G:35:ARG:CD	20:H:14:LYS:HD3	2.40	0.50
20:H:49:PRO:HD2	20:H:84:LEU:HD11	1.92	0.50
56:s:32:LEU:CD2	56:s:54:ILE:HG21	2.42	0.50
9:A:37:A:H2'	9:A:38:A:H8	1.77	0.50
9:B:39:C:O5'	9:B:39:C:H6	1.95	0.50
16:D:108:G:H5''	16:D:108:G:N3	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:D:872:A:H2'	16:D:872:A:N3	2.27	0.50
16:D:1366:C:O2'	28:P:62:ARG:NH2	2.44	0.50
47:j:25:THR:HG21	47:j:193:VAL:HG22	1.94	0.50
6:5:96:DT:H2''	6:5:97:DC:C5	2.46	0.50
6:5:98:DA:N9	6:5:99:DT:H72	2.26	0.50
10:AA:125:GLY:HA2	10:AA:499:SER:HB2	1.94	0.50
14:AF:26:ARG:NH1	14:AF:67:ARG:NH1	2.59	0.50
19:G:38:VAL:CG2	20:H:75:VAL:CG2	2.77	0.50
56:s:17:VAL:HG23	56:s:137:PRO:HB2	1.93	0.50
10:AA:728:ASP:HA	10:AA:731:ARG:O	2.12	0.49
10:AA:1314:GLN:CB	14:AF:28:ARG:HH12	2.22	0.49
16:D:50:A:O2'	16:D:360:G:N2	2.45	0.49
16:D:1208:C:H2'	16:D:1209:C:C6	2.47	0.49
20:H:132:PRO:N	20:H:167:VAL:CB	2.75	0.49
38:a:742:A:C2	38:a:743:A:C6	3.00	0.49
38:a:2646:C:O5'	38:a:2646:C:H6	1.95	0.49
9:A:47:U:H2'	9:A:48:C:H4'	1.94	0.49
9:A:59:A:H2'	9:A:60:U:H5'	1.94	0.49
10:AA:232:ILE:HD12	10:AA:331:LYS:HA	1.94	0.49
10:AA:632:ASP:HA	10:AA:647:ARG:HB2	1.94	0.49
9:B:25:C:H2'	9:B:26:G:H5'	1.95	0.49
16:D:1329:A:OP1	36:X:28:THR:OG1	2.31	0.49
26:N:3:MET:HA	26:N:3:MET:HE3	1.94	0.49
43:f:24:LEU:HD11	43:f:54:MET:CE	2.42	0.49
10:AA:935:THR:HA	10:AA:1049:ILE:CD1	2.41	0.49
13:AE:24:LEU:CB	13:AE:232:ASN:OD1	2.54	0.49
9:B:49:G:O5'	9:B:49:G:H8	1.95	0.49
20:H:52:GLN:O	20:H:53:PHE:HD1	1.95	0.49
23:K:114:VAL:HG21	23:K:141:ILE:HD12	1.94	0.49
32:T:4:SER:O	32:T:8:THR:HG23	2.12	0.49
38:a:2297:A:C6	38:a:2321:U:O4	2.65	0.49
51:n:127:ASN:ND2	51:n:127:ASN:N	2.60	0.49
55:r:3:VAL:HG22	55:r:36:ALA:HB1	1.95	0.49
13:AE:145:VAL:HG12	13:AE:184:ALA:HB1	1.94	0.49
13:AE:421:VAL:O	13:AE:436:ALA:HA	2.11	0.49
38:a:464:U:O3'	50:m:12:ARG:NH2	2.45	0.49
38:a:2038:G:H2'	38:a:2039:U:O4'	2.13	0.49
42:e:18:LEU:HB2	42:e:53:VAL:HG11	1.94	0.49
1:0:14:VAL:HG21	1:0:98:ILE:HG13	1.94	0.49
2:1:55:ILE:HG23	2:1:66:ILE:HD12	1.93	0.49
10:AA:1013:GLN:N	10:AA:1013:GLN:NE2	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:59:A:H2'	9:B:60:U:H5'	1.95	0.49
38:a:1824:G:O2'	45:h:252:THR:HG21	2.11	0.49
38:a:2303:G:C6	38:a:2314:A:N1	2.81	0.49
50:m:22:MET:O	50:m:28:ARG:NH1	2.45	0.49
50:m:24:THR:HG23	50:m:27:GLY:H	1.78	0.49
9:A:11:A:H2'	9:A:12:G:C1'	2.42	0.49
10:AA:529:ARG:HH22	10:AA:687:ARG:NH1	2.11	0.49
11:AB:71:VAL:HG12	11:AB:73:MET:HB2	1.93	0.49
12:AC:71:LYS:NZ	12:AC:140:ILE:CG1	2.76	0.49
13:AE:749:LYS:HB3	13:AE:755:ILE:HD11	1.94	0.49
9:B:11:A:C2'	9:B:12:G:O4'	2.60	0.49
16:D:60:A:N1	16:D:107:G:O2'	2.42	0.49
56:s:30:THR:HG22	56:s:31:GLU:N	2.27	0.49
60:w:55:ALA:HA	60:w:80:PHE:CE1	2.47	0.49
61:x:51:ALA:HB3	61:x:78:VAL:HB	1.94	0.49
9:A:5:G:C2'	9:A:6:G:H5'	2.40	0.49
9:A:42:G:H2'	9:A:43:A:C8	2.47	0.49
9:A:49:G:H8	9:A:49:G:O5'	1.96	0.49
40:c:3:ARG:HD2	40:c:30:LEU:HD22	1.95	0.49
1:0:14:VAL:CG2	1:0:98:ILE:HG13	2.43	0.49
12:AD:60:GLU:OE2	12:AD:170:ARG:NE	2.45	0.49
13:AE:102:MET:HG2	13:AE:246:PRO:HD3	1.95	0.49
13:AE:115:TRP:O	13:AE:1333:THR:HG21	2.13	0.49
13:AE:799:ARG:HG2	13:AE:1325:PHE:HZ	1.78	0.49
13:AE:802:ASP:OD1	13:AE:1348:LYS:NZ	2.31	0.49
9:B:56:C:H2'	9:B:57:A:C5'	2.27	0.49
38:a:404:A:O2'	38:a:405:U:OP2	2.22	0.49
38:a:2298:A:N3	38:a:2321:U:C5	2.80	0.49
9:A:18:G:C5	9:A:57:A:C5	3.01	0.49
10:AA:943:LYS:O	10:AA:943:LYS:NZ	2.34	0.49
13:AE:683:ILE:HD12	13:AE:754:ILE:HG21	1.93	0.49
9:B:47:U:H2'	9:B:48:C:H4'	1.94	0.49
20:H:120:PHE:CB	20:H:136:VAL:CB	2.91	0.49
24:L:18:VAL:N	24:L:19:PRO:CD	2.76	0.49
38:a:1412:U:C4	38:a:1413:A:N7	2.81	0.49
60:w:67:PHE:O	60:w:71:ARG:N	2.46	0.49
10:AA:1102:GLY:HA2	10:AA:1106:ARG:NH1	2.28	0.49
16:D:1017:U:O2'	16:D:1018:G:O4'	2.31	0.49
16:D:1169:A:H2'	16:D:1170:A:C8	2.48	0.49
20:H:318:PRO:HA	20:H:321:VAL:HG12	1.95	0.49
38:a:1067:A:O2'	38:a:1068:G:O4'	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:15:G:H22	9:A:20:U:H3	1.59	0.48
10:AA:943:LYS:C	10:AA:943:LYS:CE	2.86	0.48
13:AE:114:ILE:HG12	13:AE:311:ARG:HD2	1.95	0.48
9:B:42:G:H2'	9:B:43:A:C8	2.48	0.48
23:K:99:ALA:CB	23:K:103:THR:HG21	2.43	0.48
9:A:15:G:C2	9:A:20:U:O2	2.66	0.48
10:AA:866:ASP:OD2	10:AA:869:GLY:O	2.31	0.48
10:AA:936:ARG:O	10:AA:936:ARG:HD3	2.13	0.48
10:AA:943:LYS:NZ	10:AA:947:GLU:HB2	2.28	0.48
9:B:18:G:C5	9:B:57:A:C5	3.01	0.48
16:D:1311:A:OP1	44:g:59:ARG:NH1	2.45	0.48
34:V:48:ASP:HB3	34:V:75:LEU:HD23	1.94	0.48
1:0:40:MET:HE3	1:0:49:ILE:CD1	2.44	0.48
10:AA:24:VAL:HG22	10:AA:578:TYR:HE1	1.78	0.48
13:AE:800:LEU:HB3	13:AE:920:ALA:HB1	1.95	0.48
16:D:13:U:O4	16:D:21:G:N3	2.46	0.48
16:D:974:A:OP1	31:S:69:ARG:NH1	2.46	0.48
38:a:560:C:O2	63:z:48:ARG:NH1	2.41	0.48
12:AD:100:LEU:O	12:AD:144:ILE:N	2.39	0.48
16:D:1174:G:H2'	16:D:1175:G:H5'	1.95	0.48
38:a:2585:U:O2	38:a:2585:U:O4'	2.32	0.48
53:p:24:ILE:CD1	53:p:72:LEU:HD21	2.44	0.48
10:AA:1029:LEU:C	10:AA:1029:LEU:HD23	2.39	0.48
12:AD:96:ASP:OD1	12:AD:96:ASP:N	2.46	0.48
12:AD:191:ARG:NH2	12:AD:193:GLU:O	2.47	0.48
13:AE:141:PHE:HE2	13:AE:296:LYS:CB	2.22	0.48
14:AF:4:VAL:HG22	14:AF:5:THR:HG23	1.96	0.48
38:a:1588:G:C6	38:a:1589:U:O4	2.67	0.48
38:a:1839:G:N9	38:a:1927:A:C1'	2.77	0.48
2:1:4:ILE:HG12	2:1:106:VAL:HG22	1.95	0.48
2:1:29:VAL:HB	2:1:55:ILE:HD11	1.96	0.48
10:AA:641:GLU:OE2	13:AE:749:LYS:NZ	2.47	0.48
10:AA:857:VAL:CG1	10:AA:861:ALA:HB2	2.43	0.48
10:AA:1314:GLN:HA	14:AF:28:ARG:HH22	1.78	0.48
12:AC:102:LEU:HB2	12:AC:115:ILE:HG12	1.95	0.48
34:V:75:LEU:C	34:V:75:LEU:HD12	2.38	0.48
45:h:210:ALA:HA	45:h:213:TRP:CE3	2.48	0.48
47:j:156:PHE:CE1	56:s:81:ILE:HD13	2.48	0.48
2:1:25:ARG:NH1	2:1:74:ILE:O	2.46	0.48
9:A:18:G:N3	9:A:58:A:C6	2.82	0.48
9:A:76:A:N6	38:a:2422:C:O4'	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AA:1032:LYS:HZ1	10:AA:1036:ILE:HD11	1.79	0.48
13:AE:220:ARG:HG2	13:AE:220:ARG:NH1	2.26	0.48
13:AE:968:ASN:HA	13:AE:1117:SER:HB2	1.96	0.48
16:D:604:G:H2'	16:D:605:U:O4'	2.14	0.48
16:D:1064:G:O2'	16:D:1190:G:N2	2.47	0.48
16:D:1499:A:H3'	16:D:1499:A:OP2	2.12	0.48
61:x:27:VAL:CG2	61:x:40:ILE:HD12	2.44	0.48
8:7:60:U:OP1	13:AE:256:ASP:CB	2.62	0.48
10:AA:103:VAL:HG12	10:AA:117:ILE:HG22	1.94	0.48
10:AA:1101:LEU:HD21	13:AE:508:LEU:HD22	1.95	0.48
13:AE:117:LEU:HG	13:AE:118:LYS:HG3	1.95	0.48
13:AE:201:LEU:HD11	13:AE:220:ARG:HG2	1.95	0.48
9:A:19:G:C5	38:a:2112:G:H4'	2.45	0.48
9:A:25:C:H2'	9:A:26:G:H5'	1.95	0.48
12:AD:48:LEU:HD22	13:AE:535:ARG:HG3	1.96	0.48
13:AE:47:ARG:CZ	13:AE:47:ARG:HB2	2.44	0.48
13:AE:103:GLY:H	13:AE:244:VAL:HG22	1.79	0.48
13:AE:809:VAL:HG21	13:AE:909:ILE:HG12	1.95	0.48
9:B:15:G:C2	9:B:20:U:O2	2.66	0.48
9:B:58:A:C8	9:B:58:A:OP2	2.67	0.48
16:D:5:U:O2	16:D:5:U:O4'	2.29	0.48
38:a:565:C:H2'	38:a:566:U:O4'	2.13	0.48
38:a:1993:U:H4'	47:j:133:THR:HG22	1.96	0.48
56:s:84:ILE:HG23	56:s:84:ILE:O	2.14	0.48
10:AA:958:LYS:NZ	10:AA:958:LYS:CB	2.73	0.48
10:AA:991:LYS:HA	10:AA:991:LYS:HE3	1.95	0.48
13:AE:152:THR:HB	13:AE:172:PHE:CZ	2.48	0.48
13:AE:550:VAL:O	13:AE:569:LEU:HA	2.13	0.48
13:AE:891:ASP:OD2	13:AE:1290:ARG:NH2	2.47	0.48
14:AF:25:ARG:NH2	14:AF:65:ASP:OD1	2.44	0.48
9:B:11:A:H2'	9:B:12:G:C1'	2.43	0.48
20:H:23:ILE:N	20:H:69:ASP:OD2	2.47	0.48
39:b:37:ILE:HG21	39:b:80:ILE:HG21	1.95	0.48
4:3:7:ARG:HB2	38:a:85:G:OP2	2.13	0.47
10:AA:845:LEU:HD23	10:AA:845:LEU:N	2.28	0.47
12:AC:43:LEU:O	12:AC:47:LEU:HB2	2.14	0.47
13:AE:1027:VAL:HB	13:AE:1121:LEU:HB2	1.96	0.47
3:2:61:LEU:C	3:2:61:LEU:HD12	2.39	0.47
9:A:68:C:C4	9:A:69:C:C5	3.02	0.47
10:AA:1047:LEU:O	10:AA:1049:ILE:HD11	2.13	0.47
13:AE:395:LYS:NZ	13:AE:399:LYS:CD	2.74	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:68:C:C4	9:B:69:C:C5	3.02	0.47
28:P:6:ILE:HG23	28:P:100:ILE:CG2	2.43	0.47
47:j:121:THR:HB	47:j:127:PHE:CD2	2.49	0.47
9:A:58:A:OP2	9:A:58:A:C8	2.67	0.47
12:AC:71:LYS:NZ	12:AC:140:ILE:HB	2.27	0.47
12:AC:162:GLU:HG2	12:AC:162:GLU:O	2.04	0.47
13:AE:395:LYS:NZ	13:AE:399:LYS:CE	2.77	0.47
13:AE:1150:PRO:HG3	13:AE:1214:PRO:HB2	1.96	0.47
14:AF:26:ARG:HH12	14:AF:67:ARG:NH1	2.12	0.47
9:B:9:G:H5''	9:B:10:G:OP2	2.14	0.47
16:D:911:U:H2'	16:D:912:C:C6	2.49	0.47
38:a:2685:G:OP1	57:t:78:ARG:NH2	2.47	0.47
6:5:109:DT:H2''	10:AA:200:ARG:CG	2.37	0.47
9:A:14:A:H2'	9:A:14:A:N3	2.29	0.47
9:A:33:U:H2'	9:A:35:A:OP2	2.14	0.47
9:A:37:A:H2'	9:A:38:A:C8	2.48	0.47
10:AA:1023:HIS:ND1	10:AA:1023:HIS:C	2.73	0.47
13:AE:1221:LEU:HD22	13:AE:1306:LEU:HB2	1.96	0.47
22:J:162:ALA:O	22:J:165:ARG:O	2.33	0.47
38:a:1433:A:H2'	38:a:1434:A:O4'	2.13	0.47
10:AA:562:GLU:OE1	10:AA:662:SER:OG	2.31	0.47
10:AA:941:LYS:HZ3	10:AA:941:LYS:HG3	1.39	0.47
10:AA:1010:GLN:NE2	10:AA:1010:GLN:C	2.72	0.47
10:AA:1034:ARG:NH1	10:AA:1034:ARG:C	2.73	0.47
12:AD:104:LYS:HG2	12:AD:110:VAL:HB	1.97	0.47
16:D:371:A:H2'	16:D:372:C:O4'	2.14	0.47
16:D:526:C:P	30:R:88:LYS:HE3	2.54	0.47
28:P:6:ILE:CG2	28:P:100:ILE:HG23	2.43	0.47
38:a:1814:G:C4'	45:h:51:THR:HG21	2.44	0.47
47:j:152:PRO:HG3	47:j:156:PHE:CZ	2.50	0.47
9:A:18:G:C6	9:A:57:A:N7	2.83	0.47
10:AA:243:PRO:HB2	10:AA:274:ILE:HG23	1.96	0.47
10:AA:559:CYS:HB2	10:AA:662:SER:HB3	1.97	0.47
12:AD:20:SER:OG	12:AD:21:SER:N	2.46	0.47
13:AE:902:ASP:OD2	13:AE:905:ARG:HB2	2.15	0.47
13:AE:1347:LEU:HG	13:AE:1357:ILE:HG23	1.96	0.47
16:D:552:U:O2'	30:R:83:ARG:O	2.27	0.47
16:D:1103:C:O2	19:G:106:THR:HG21	2.15	0.47
20:H:290:TYR:O	20:H:305:HIS:C	2.56	0.47
20:H:330:VAL:HG12	20:H:345:GLY:O	2.14	0.47
22:J:61:VAL:CG2	22:J:200:ILE:HD11	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:995:C:O2	56:s:3:THR:OG1	2.24	0.47
44:g:18:CYS:HB2	44:g:40:CYS:HB3	1.96	0.47
10:AA:957:LYS:HA	10:AA:1029:LEU:HD12	1.97	0.47
12:AC:166:ARG:HB3	12:AC:166:ARG:NH1	2.30	0.47
13:AE:842:ARG:HH22	13:AE:1250:ASP:HB2	1.80	0.47
13:AE:1036:ARG:HE	13:AE:1081:VAL:HG11	1.79	0.47
13:AE:1261:LEU:HD12	13:AE:1304:ARG:HH21	1.79	0.47
9:B:18:G:C6	9:B:57:A:N7	2.83	0.47
9:B:18:G:N3	9:B:58:A:C6	2.82	0.47
15:C:33:ILE:O	15:C:33:ILE:HG12	2.14	0.47
17:E:54:MET:O	17:E:57:ILE:HG22	2.15	0.47
24:L:67:PRO:O	24:L:70:VAL:HG22	2.15	0.47
26:N:102:ALA:HB3	26:N:113:ASP:HB3	1.96	0.47
38:a:686:U:O4	50:m:12:ARG:HB2	2.14	0.47
38:a:783:A:N3	38:a:783:A:C2'	2.70	0.47
38:a:2168:G:H8	38:a:2168:G:OP1	1.97	0.47
44:g:37:CYS:N	44:g:40:CYS:SG	2.78	0.47
1:O:5:PHE:HB3	1:O:59:ILE:HD12	1.96	0.47
9:A:41:C:H5'	25:M:143:ARG:HD2	1.95	0.47
10:AA:618:GLN:HG3	13:AE:770:LEU:HD13	1.96	0.47
10:AA:914:LYS:NZ	10:AA:914:LYS:HB2	2.29	0.47
10:AA:1119:MET:HG3	10:AA:1204:LEU:HD13	1.97	0.47
13:AE:128:LEU:HD21	13:AE:188:LEU:HB3	1.97	0.47
13:AE:1060:VAL:HG13	13:AE:1106:ILE:HG12	1.96	0.47
13:AE:1146:GLU:OE2	13:AE:1310:THR:HG22	2.14	0.47
10:AA:318:SER:H	10:AA:321:LEU:HD12	1.80	0.47
10:AA:549:ASP:OD2	13:AE:750:PRO:HB3	2.15	0.47
10:AA:588:GLU:HA	10:AA:606:LEU:O	2.15	0.47
10:AA:685:MET:SD	10:AA:1073:LYS:HG2	2.55	0.47
10:AA:948:ILE:HA	10:AA:951:MET:SD	2.55	0.47
10:AA:1032:LYS:CA	10:AA:1032:LYS:CE	2.92	0.47
12:AD:109:PRO:HB3	12:AD:132:HIS:CD2	2.50	0.47
16:D:13:U:O2	16:D:915:A:N7	2.47	0.47
16:D:1175:G:N3	16:D:1176:A:C8	2.83	0.47
16:D:1228:C:P	36:X:107:ARG:HH12	2.38	0.47
23:K:96:MET:CE	23:K:115:LEU:HD11	2.45	0.47
23:K:111:MET:CE	23:K:125:ALA:HB1	2.39	0.47
36:X:16:VAL:HG23	36:X:17:ILE:HD12	1.97	0.47
38:a:2315:G:H5'	51:n:157:THR:HG23	1.97	0.47
38:a:2756:U:C4	38:a:2759:G:C6	3.03	0.47
9:A:11:A:C2'	9:A:12:G:O4'	2.60	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AA:735:LYS:HA	10:AA:748:ILE:HG22	1.96	0.47
10:AA:1007:LYS:HD3	10:AA:1009:ASN:OD1	2.14	0.47
13:AE:87:LYS:HE3	13:AE:87:LYS:CA	2.41	0.47
13:AE:526:VAL:HG12	13:AE:549:LYS:HB2	1.96	0.47
13:AE:833:GLU:N	13:AE:1242:ARG:HH12	2.12	0.47
16:D:35:G:N3	30:R:115:SER:OG	2.47	0.47
16:D:373:A:C2	16:D:374:A:C8	3.03	0.47
16:D:868:C:H2'	16:D:869:G:O4'	2.15	0.47
16:D:915:A:C8	16:D:915:A:H3'	2.50	0.47
38:a:517:C:OP2	46:i:10:ARG:NH2	2.48	0.47
10:AA:719:LYS:H	10:AA:751:TYR:HH	1.61	0.46
10:AA:756:TYR:CD2	12:AC:68:TYR:O	2.68	0.46
10:AA:965:GLN:HA	10:AA:968:GLU:HB3	1.98	0.46
10:AA:976:ARG:HG3	10:AA:976:ARG:NH1	2.30	0.46
13:AE:1321:SER:OG	13:AE:1349:GLU:OE2	2.22	0.46
9:B:60:U:H4'	9:B:61:C:OP2	2.14	0.46
16:D:526:C:OP2	30:R:88:LYS:HE3	2.15	0.46
20:H:291:GLY:HA2	20:H:305:HIS:O	2.15	0.46
21:I:75:ILE:HD13	21:I:75:ILE:C	2.40	0.46
34:V:8:LEU:HD23	34:V:25:ILE:HG21	1.97	0.46
59:v:96:ILE:HG21	59:v:126:ILE:HD12	1.97	0.46
3:2:30:ILE:HD13	3:2:93:LEU:HD12	1.97	0.46
10:AA:318:SER:OG	10:AA:320:ASP:OD1	2.31	0.46
10:AA:1020:GLU:HA	10:AA:1023:HIS:HD2	1.81	0.46
13:AE:141:PHE:CE2	13:AE:296:LYS:CB	2.94	0.46
9:B:5:G:C2'	9:B:6:G:C5'	2.93	0.46
9:B:14:A:N3	9:B:14:A:H2'	2.29	0.46
20:H:69:ASP:O	20:H:85:SER:CB	2.63	0.46
36:X:96:PRO:HG2	36:X:102:THR:HG23	1.97	0.46
38:a:1020:A:C6	38:a:1141:U:O2	2.68	0.46
9:A:60:U:H4'	9:A:61:C:OP2	2.14	0.46
10:AA:1280:ALA:HB1	13:AE:918:ILE:HG22	1.96	0.46
9:B:76:A:N3	9:B:76:A:C2'	2.74	0.46
38:a:1695:G:N7	45:h:14:ARG:NH2	2.64	0.46
51:n:36:LEU:HB3	51:n:57:LEU:HD21	1.97	0.46
1:0:51:VAL:HG22	1:0:51:VAL:O	2.15	0.46
10:AA:93:SER:HA	10:AA:128:PRO:HA	1.97	0.46
10:AA:1257:GLN:CD	13:AE:345:LYS:HB3	2.40	0.46
13:AE:190:LYS:HE3	13:AE:190:LYS:HB2	1.41	0.46
16:D:429:U:N3	16:D:431:A:N6	2.64	0.46
16:D:1225:A:OP1	36:X:101:ARG:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:316:ILE:HD11	20:H:321:VAL:HG11	1.96	0.46
28:P:99:GLN:O	28:P:99:GLN:HG2	2.16	0.46
10:AA:538:LEU:HD11	10:AA:571:LEU:HD22	1.98	0.46
10:AA:724:VAL:HG13	10:AA:774:GLY:H	1.76	0.46
10:AA:1018:TYR:CD1	10:AA:1018:TYR:C	2.94	0.46
13:AE:43:THR:HG22	13:AE:57:PHE:HE1	1.80	0.46
16:D:946:A:H2'	16:D:947:G:C8	2.50	0.46
38:a:1406:U:H3	38:a:1596:A:H2	1.59	0.46
38:a:2303:G:C2	38:a:2314:A:N3	2.82	0.46
47:j:4:LEU:HD23	47:j:29:VAL:CG1	2.39	0.46
52:o:13:ARG:HD3	58:u:58:TYR:O	2.14	0.46
10:AA:618:GLN:OE1	10:AA:635:THR:OG1	2.32	0.46
10:AA:841:ARG:HB2	10:AA:841:ARG:NH1	2.30	0.46
10:AA:844:LYS:HD3	10:AA:844:LYS:HA	1.48	0.46
10:AA:940:GLU:HG3	10:AA:945:ALA:H	1.81	0.46
10:AA:1034:ARG:NH1	10:AA:1034:ARG:CG	2.77	0.46
10:AA:1252:SER:N	10:AA:1259:LEU:HD11	2.30	0.46
13:AE:198:CYS:HA	13:AE:221:ILE:CD1	2.45	0.46
13:AE:417:ARG:HH12	14:AF:43:ASN:HB2	1.79	0.46
16:D:1308:U:P	36:X:98:ARG:CG	3.03	0.46
16:D:1517:G:H1'	38:a:1919:A:O2'	2.15	0.46
19:G:16:PHE:CD2	20:H:42:LEU:O	2.69	0.46
38:a:742:A:C2	38:a:755:U:N3	2.81	0.46
38:a:998:C:OP2	63:z:58:ARG:NH2	2.49	0.46
38:a:2168:G:OP1	38:a:2168:G:C8	2.69	0.46
60:w:28:LEU:HD23	60:w:48:VAL:HG21	1.98	0.46
9:A:29:G:H2'	9:A:30:G:O4'	2.15	0.46
9:B:68:C:H3'	9:B:69:C:H5''	1.96	0.46
20:H:309:MET:HE2	20:H:318:PRO:HB3	1.97	0.46
38:a:2291:U:H2'	38:a:2292:U:C6	2.51	0.46
38:a:2298:A:C6	38:a:2299:U:C2	3.04	0.46
6:5:113:DC:P	10:AA:163:LYS:HD3	2.55	0.46
8:7:58:A:N3	8:7:58:A:H5''	2.31	0.46
9:A:5:G:C2'	9:A:6:G:C5'	2.93	0.46
9:A:9:G:H5''	9:A:10:G:OP2	2.14	0.46
10:AA:446:ASP:HA	10:AA:451:ARG:HH21	1.81	0.46
13:AE:1167:LYS:NZ	13:AE:1170:LYS:HB2	2.30	0.46
16:D:1308:U:O5'	36:X:98:ARG:HG2	2.16	0.46
29:Q:34:ILE:HG12	29:Q:70:CYS:SG	2.56	0.46
8:7:60:U:C5	8:7:61:U:N3	2.84	0.46
9:A:14:A:H1'	9:A:22:G:N2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:18:G:C8	9:A:57:A:N1	2.83	0.46
9:A:32:C:HO2'	25:M:86:GLN:HG3	1.78	0.46
13:AE:1219:ASP:O	13:AE:1223:LEU:HB2	2.15	0.46
9:B:18:G:C8	9:B:57:A:N1	2.83	0.46
9:B:72:A:H2'	9:B:73:A:C5'	2.32	0.46
16:D:17:U:H2'	16:D:18:C:C6	2.51	0.46
19:G:114:LEU:HD13	19:G:144:LEU:CB	2.46	0.46
20:H:135:LEU:CB	20:H:167:VAL:O	2.63	0.46
20:H:332:VAL:HG13	20:H:342:ILE:HG23	1.98	0.46
28:P:8:ILE:HD12	28:P:25:ILE:CD1	2.46	0.46
38:a:784:G:H5'	38:a:785:G:OP1	2.16	0.46
10:AA:933:VAL:O	10:AA:933:VAL:HG12	2.16	0.46
10:AA:994:ARG:C	10:AA:994:ARG:CD	2.89	0.46
12:AD:131:CYS:SG	12:AD:132:HIS:N	2.89	0.46
13:AE:201:LEU:HD11	13:AE:220:ARG:NH1	2.31	0.46
13:AE:420:PRO:HA	13:AE:437:PHE:O	2.15	0.46
20:H:19:ARG:O	20:H:72:LEU:HD13	2.16	0.46
25:M:24:ALA:O	25:M:27:VAL:HG22	2.16	0.46
25:M:27:VAL:HG12	25:M:43:VAL:HG11	1.98	0.46
38:a:2006:C:O2'	38:a:2823:A:N3	2.47	0.46
47:j:186:LEU:HD21	62:y:4:ILE:HG21	1.98	0.46
9:A:41:C:C5'	25:M:143:ARG:HD2	2.46	0.45
10:AA:829:THR:HG23	10:AA:1059:ARG:HA	1.97	0.45
9:B:58:A:C1'	9:B:60:U:C5	2.99	0.45
51:n:57:LEU:HD22	51:n:89:VAL:CG2	2.47	0.45
57:t:18:ARG:HB2	57:t:45:GLU:HB3	1.97	0.45
4:3:94:ARG:CB	4:3:103:ILE:HD12	2.45	0.45
10:AA:988:LYS:HB3	10:AA:988:LYS:HZ1	1.81	0.45
13:AE:209:ASN:HA	13:AE:214:ARG:NH2	2.31	0.45
13:AE:1158:GLU:HA	13:AE:1223:LEU:HD21	1.99	0.45
16:D:1340:A:H8	16:D:1340:A:O5'	1.99	0.45
18:F:67:ARG:HD3	18:F:67:ARG:N	2.31	0.45
38:a:1394:U:H4'	38:a:1603:A:H4'	1.97	0.45
45:h:76:ALA:HB2	45:h:96:TYR:CD1	2.51	0.45
10:AA:27:LEU:O	10:AA:528:ARG:NH1	2.42	0.45
12:AC:59:VAL:O	12:AC:171:LEU:HG	2.17	0.45
13:AE:385:LEU:HD23	13:AE:390:LEU:HB2	1.98	0.45
13:AE:847:ASP:N	13:AE:847:ASP:OD1	2.49	0.45
13:AE:926:PRO:HB2	13:AE:1241:TYR:HE1	1.82	0.45
9:B:37:A:N3	9:B:37:A:H5''	2.32	0.45
9:B:48:C:N4	9:B:59:A:C5	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C:61:ARG:HG2	24:L:88:MET:HE1	1.98	0.45
36:X:106:ALA:HB3	36:X:110:LYS:HD2	1.98	0.45
8:7:56:U:O2	8:7:56:U:H2'	2.17	0.45
9:A:58:A:C1'	9:A:60:U:C5	2.99	0.45
12:AC:73:GLY:HA3	12:AC:138:ALA:CB	2.46	0.45
12:AD:199:ASP:N	12:AD:199:ASP:OD1	2.47	0.45
13:AE:109:SER:HB2	13:AE:296:LYS:HG2	1.98	0.45
13:AE:506:VAL:HG23	13:AE:628:GLY:HA3	1.99	0.45
16:D:1176:A:H2'	16:D:1177:G:O4'	2.16	0.45
27:O:63:LEU:HD13	27:O:65:ILE:HD11	1.97	0.45
28:P:28:THR:HG21	28:P:87:LEU:CD1	2.46	0.45
38:a:68:G:N2	38:a:74:A:OP2	2.49	0.45
38:a:645:C:H2'	38:a:647:G:C8	2.52	0.45
8:7:66:A:OP2	10:AA:540:ARG:NH2	2.49	0.45
9:A:6:G:O2'	9:A:7:G:C5'	2.64	0.45
9:A:18:G:O2'	9:A:60:U:N3	2.48	0.45
10:AA:967:LEU:HD23	10:AA:1021:LEU:HD21	1.98	0.45
10:AA:1046:VAL:CG2	10:AA:1049:ILE:HG13	2.46	0.45
12:AD:96:ASP:HB3	12:AD:148:ARG:HE	1.81	0.45
13:AE:53:ARG:HA	13:AE:54:ASP:HA	1.55	0.45
13:AE:115:TRP:HB3	13:AE:1333:THR:CG2	2.46	0.45
13:AE:395:LYS:NZ	13:AE:399:LYS:HE2	2.32	0.45
38:a:1047:G:N2	38:a:1110:G:O2'	2.50	0.45
38:a:1720:U:H2'	38:a:1721:G:O4'	2.16	0.45
38:a:2093:G:O2'	38:a:2198:A:N1	2.41	0.45
10:AA:914:LYS:HD3	10:AA:914:LYS:N	2.31	0.45
12:AC:92:VAL:HG12	12:AC:121:VAL:HG12	1.98	0.45
12:AC:159:ILE:HD13	12:AC:159:ILE:HA	1.69	0.45
13:AE:201:LEU:CD1	13:AE:224:LEU:HD12	2.46	0.45
13:AE:319:SER:HA	13:AE:320:ASN:HA	1.64	0.45
16:D:1397:C:O5'	16:D:1397:C:C6	2.70	0.45
21:I:117:ALA:HB2	21:I:200:VAL:CG1	2.46	0.45
28:P:28:THR:HG21	28:P:87:LEU:HD12	1.99	0.45
38:a:39:G:H1'	49:l:43:THR:HG21	1.99	0.45
38:a:930:G:H1'	43:f:25:LEU:HD11	1.98	0.45
51:n:17:MET:HE2	51:n:25:VAL:HA	1.98	0.45
51:n:29:PRO:HB2	51:n:169:LEU:HD22	1.99	0.45
7:6:15:DC:C4	7:6:16:DC:C5	3.05	0.45
7:6:15:DC:N3	7:6:16:DC:C4	2.84	0.45
10:AA:46:GLN:HA	10:AA:47:TYR:HA	1.77	0.45
9:B:6:G:O2'	9:B:7:G:C5'	2.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C:12:ARG:CZ	20:H:264:GLU:HA	2.46	0.45
20:H:72:LEU:CD1	20:H:72:LEU:N	2.73	0.45
38:a:1906:G:H4'	38:a:1906:G:OP1	2.16	0.45
43:f:25:LEU:C	43:f:25:LEU:HD13	2.41	0.45
58:u:2:ARG:H	58:u:5:THR:HG1	1.64	0.45
9:A:48:C:C5	9:A:59:A:C8	3.05	0.45
10:AA:724:VAL:HG12	10:AA:774:GLY:N	2.31	0.45
9:B:48:C:C5	9:B:59:A:C8	3.05	0.45
19:G:114:LEU:HA	19:G:144:LEU:HD13	1.98	0.45
19:G:208:ARG:HH12	20:H:29:VAL:HG11	1.82	0.45
20:H:294:VAL:HG21	20:H:330:VAL:HG21	1.99	0.45
38:a:340:A:O2'	49:l:162:ARG:NH1	2.50	0.45
38:a:1266:G:OP1	46:i:16:ARG:NE	2.45	0.45
55:r:15:LEU:HD13	55:r:15:LEU:C	2.42	0.45
61:x:18:LEU:HD23	61:x:25:ARG:HD2	1.99	0.45
9:A:76:A:C2	52:o:31:HIS:NE2	2.85	0.45
10:AA:1032:LYS:CE	10:AA:1032:LYS:HA	2.46	0.45
12:AD:81:ILE:HD12	12:AD:81:ILE:HA	1.85	0.45
12:AD:86:LYS:HE3	13:AE:528:THR:HG21	1.97	0.45
22:J:165:ARG:NH1	22:J:165:ARG:HB2	2.32	0.45
38:a:1327:A:H2'	38:a:1328:A:O4'	2.17	0.45
56:s:30:THR:CG2	56:s:31:GLU:N	2.79	0.45
9:B:14:A:H1'	9:B:22:G:N2	2.31	0.45
9:B:34:C:C5	9:B:34:C:OP1	2.70	0.45
16:D:198:G:OP2	16:D:198:G:C8	2.70	0.45
16:D:1255:G:O2'	16:D:1258:G:N3	2.47	0.45
17:E:55:GLN:N	17:E:56:PRO:HD2	2.32	0.45
36:X:75:MET:HA	36:X:75:MET:HE3	1.99	0.45
13:AE:245:LEU:CG	13:AE:246:PRO:HD2	2.47	0.44
19:G:108:ARG:HD3	19:G:108:ARG:HA	1.74	0.44
20:H:38:VAL:HG22	20:H:48:ILE:HD11	1.99	0.44
20:H:84:LEU:N	20:H:84:LEU:CD2	2.78	0.44
49:l:149:ILE:CD1	49:l:188:MET:HE3	2.46	0.44
9:A:48:C:N4	9:A:59:A:C5	2.84	0.44
10:AA:524:ILE:HB	10:AA:712:SER:HB2	1.99	0.44
10:AA:859:GLU:N	10:AA:859:GLU:CD	2.73	0.44
10:AA:976:ARG:NH2	10:AA:989:LEU:HB3	2.32	0.44
9:B:22:G:H2'	9:B:23:C:C5	2.52	0.44
9:B:34:C:O5'	9:B:34:C:C6	2.70	0.44
9:B:49:G:O5'	9:B:49:G:C8	2.71	0.44
16:D:13:U:C2	16:D:915:A:C5	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:2070:A:H2'	38:a:2071:A:O4'	2.16	0.44
38:a:2547:A:H2'	38:a:2548:U:C6	2.52	0.44
55:r:55:GLU:HA	55:r:58:LEU:HD12	1.99	0.44
10:AA:857:VAL:HG11	10:AA:861:ALA:HB2	1.99	0.44
12:AC:228:LEU:HD11	12:AD:224:LEU:HD23	1.97	0.44
13:AE:62:PHE:CD1	13:AE:62:PHE:N	2.86	0.44
13:AE:1079:LYS:HD3	13:AE:1098:GLN:HB3	2.00	0.44
9:B:49:G:C2'	9:B:50:U:H5'	2.47	0.44
16:D:376:G:C2	16:D:389:A:C2	3.05	0.44
16:D:915:A:H8	16:D:915:A:O5'	2.00	0.44
19:G:206:ALA:O	19:G:210:VAL:HG23	2.18	0.44
22:J:197:GLU:HA	22:J:200:ILE:HD12	1.99	0.44
45:h:6:CYS:SG	45:h:13:ARG:NH1	2.89	0.44
8:7:69:G:C6	8:7:70:G:C5	3.05	0.44
9:A:25:C:C2'	9:A:26:G:H5'	2.48	0.44
9:A:57:A:O5'	9:A:58:A:P	2.76	0.44
10:AA:943:LYS:C	10:AA:943:LYS:HE3	2.42	0.44
10:AA:974:ARG:HD2	10:AA:1014:LEU:CD1	2.46	0.44
13:AE:76:LYS:HB3	13:AE:76:LYS:NZ	2.32	0.44
16:D:1240:U:OP1	25:M:116:MET:HB2	2.16	0.44
38:a:74:A:N7	38:a:88:G:C5	2.86	0.44
38:a:1007:C:OP1	56:s:37:ARG:NH2	2.50	0.44
41:d:48:U:H2'	41:d:49:C:C6	2.52	0.44
2:1:17:VAL:HG12	2:1:76:VAL:HG21	1.98	0.44
10:AA:1029:LEU:HD11	10:AA:1033:ARG:HH21	1.82	0.44
12:AD:212:ASP:O	12:AD:215:GLU:N	2.48	0.44
13:AE:108:ALA:HB1	13:AE:279:LEU:HD22	1.96	0.44
13:AE:126:LEU:HD12	13:AE:223:LEU:HD22	1.99	0.44
13:AE:213:LYS:HA	13:AE:213:LYS:HE3	1.99	0.44
13:AE:850:LYS:HB3	13:AE:855:ASP:HB2	1.99	0.44
13:AE:1227:HIS:HA	13:AE:1230:THR:HG22	1.99	0.44
15:C:12:ARG:HD3	15:C:16:GLU:OE1	2.18	0.44
27:O:80:ARG:O	27:O:84:THR:HG23	2.17	0.44
38:a:214:G:N2	38:a:216:A:N3	2.66	0.44
38:a:954:G:OP2	59:v:16:ARG:NH2	2.50	0.44
9:A:1:C:C5	9:A:2:G:N7	2.86	0.44
9:A:49:G:C2'	9:A:50:U:H5'	2.47	0.44
10:AA:933:VAL:HG22	10:AA:935:THR:CG2	2.47	0.44
10:AA:939:VAL:HG12	10:AA:939:VAL:O	2.17	0.44
10:AA:971:LEU:HG	10:AA:1014:LEU:HG	2.00	0.44
12:AD:211:ILE:HD11	12:AD:215:GLU:HG3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:75:TYR:CD2	13:AE:75:TYR:O	2.70	0.44
13:AE:128:LEU:CD2	13:AE:188:LEU:HB3	2.48	0.44
13:AE:515:ARG:NH2	13:AE:718:SER:O	2.48	0.44
16:D:107:G:N7	17:E:10:ARG:NH2	2.60	0.44
16:D:337:G:H2'	16:D:338:A:C8	2.52	0.44
16:D:684:U:H2'	16:D:685:G:O4'	2.18	0.44
16:D:1493:A:C8	16:D:1493:A:OP1	2.70	0.44
18:F:21:ARG:HH22	20:H:341:ARG:HD2	1.82	0.44
19:G:76:ALA:CB	19:G:210:VAL:HG11	2.47	0.44
9:A:22:G:HO2'	9:A:23:C:P	2.41	0.44
10:AA:850:ILE:HD12	10:AA:1048:LYS:HG2	1.99	0.44
10:AA:870:ILE:HG12	10:AA:884:VAL:HG12	1.99	0.44
10:AA:1032:LYS:CA	10:AA:1032:LYS:HE2	2.47	0.44
12:AC:58:GLU:HB3	12:AC:170:ARG:HG2	1.99	0.44
13:AE:107:LEU:HA	13:AE:276:ASN:ND2	2.33	0.44
13:AE:222:LYS:HA	13:AE:222:LYS:HD2	1.32	0.44
13:AE:1026:PRO:HB2	13:AE:1028:ILE:HG23	2.00	0.44
9:B:60:U:OP2	9:B:61:C:N4	2.45	0.44
16:D:109:A:C6	16:D:326:G:C6	3.05	0.44
21:I:155:GLY:HA2	21:I:163:ALA:HB1	1.99	0.44
36:X:23:TYR:CD2	36:X:69:LEU:HD23	2.53	0.44
36:X:106:ALA:HB3	36:X:110:LYS:CD	2.47	0.44
38:a:813:U:H2'	38:a:814:C:C6	2.53	0.44
38:a:2365:G:N7	52:o:39:LYS:NZ	2.59	0.44
56:s:73:VAL:HG11	56:s:75:TYR:CZ	2.53	0.44
6:5:115:DA:P	13:AE:1148:ARG:HG3	2.58	0.44
9:A:9:G:O2'	9:A:45:G:H2'	2.18	0.44
9:A:22:G:O2'	9:A:23:C:O5'	2.36	0.44
13:AE:1108:GLN:HG3	13:AE:1109:LEU:HD12	1.99	0.44
9:B:9:G:O2'	9:B:45:G:H2'	2.18	0.44
63:z:76:TYR:OH	63:z:92:ARG:NH1	2.51	0.44
6:5:98:DA:C2'	6:5:99:DT:C7	2.96	0.44
6:5:116:DG:C6	6:5:117:DA:C6	3.06	0.44
9:A:56:C:OP1	38:a:2168:G:C4	2.71	0.44
10:AA:176:ILE:HD12	10:AA:184:LEU:HD23	1.99	0.44
10:AA:596:ASP:N	10:AA:596:ASP:OD1	2.49	0.44
10:AA:960:LEU:HB3	10:AA:1025:PHE:CD1	2.53	0.44
10:AA:1029:LEU:HA	10:AA:1032:LYS:HB2	1.99	0.44
10:AA:1117:LEU:HD12	10:AA:1195:ILE:HG12	2.00	0.44
13:AE:161:THR:H	13:AE:164:GLN:HB2	1.82	0.44
13:AE:978:ARG:HD3	13:AE:999:TYR:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:1357:ILE:HG22	13:AE:1359:ALA:H	1.83	0.44
9:B:22:G:O2'	9:B:23:C:O5'	2.36	0.44
16:D:397:A:H3'	16:D:397:A:N3	2.32	0.44
20:H:61:GLU:HG2	20:H:62:ILE:HG23	2.00	0.44
20:H:136:VAL:HA	20:H:168:VAL:O	2.18	0.44
23:K:153:VAL:HG23	23:K:164:ILE:HD13	2.00	0.44
38:a:631:A:N3	38:a:2415:G:O2'	2.48	0.44
38:a:1589:U:C2	38:a:1590:A:C8	3.06	0.44
50:m:12:ARG:HG3	50:m:44:VAL:HG11	2.00	0.44
10:AA:726:TYR:O	10:AA:726:TYR:CD2	2.69	0.43
13:AE:824:PRO:HD3	13:AE:835:LEU:HD12	2.00	0.43
13:AE:1033:GLY:HA3	13:AE:1081:VAL:O	2.18	0.43
16:D:1417:G:C6	16:D:1482:G:C6	3.06	0.43
32:T:21:ASP:OD1	32:T:22:THR:N	2.49	0.43
40:c:37:ARG:HG2	40:c:48:THR:HG23	2.00	0.43
57:t:24:VAL:HG13	57:t:33:ALA:HB2	2.00	0.43
7:6:12:DC:O5'	7:6:12:DC:H6	2.01	0.43
10:AA:95:PRO:HB3	10:AA:123:TYR:HE1	1.83	0.43
16:D:197:A:C5	16:D:221:C:H4'	2.53	0.43
20:H:33:LYS:HA	20:H:34:ASP:HA	1.61	0.43
23:K:156:LYS:HG2	26:N:71:VAL:HG13	2.00	0.43
38:a:1095:A:H2'	38:a:1096:A:C8	2.53	0.43
38:a:1925:C:C5	38:a:1925:C:OP2	2.71	0.43
43:f:27:LEU:O	43:f:38:ARG:NE	2.46	0.43
9:A:18:G:N3	9:A:58:A:C5	2.87	0.43
10:AA:800:MET:HB2	10:AA:800:MET:HE3	1.60	0.43
33:U:6:LEU:HG	33:U:17:TYR:HB3	2.01	0.43
38:a:705:A:O4'	45:h:9:THR:HG21	2.19	0.43
38:a:1927:A:C8	38:a:1927:A:O5'	2.70	0.43
59:v:35:ALA:HB2	59:v:102:LEU:HD11	2.00	0.43
10:AA:469:VAL:HA	10:AA:472:GLU:HG2	2.00	0.43
10:AA:953:LEU:HA	10:AA:953:LEU:HD13	1.83	0.43
12:AC:205:MET:HE3	12:AC:205:MET:HB2	1.87	0.43
13:AE:26:SER:CB	13:AE:236:TRP:CZ2	2.95	0.43
13:AE:201:LEU:CB	13:AE:221:ILE:HD13	2.47	0.43
13:AE:388:ARG:HG2	13:AE:388:ARG:NH1	2.32	0.43
13:AE:568:SER:HB3	13:AE:570:LYS:NZ	2.34	0.43
9:B:1:C:C5	9:B:2:G:N7	2.86	0.43
9:B:46:G:O2'	9:B:47:U:H5''	2.19	0.43
9:B:57:A:O5'	9:B:58:A:P	2.76	0.43
16:D:976:G:C8	16:D:1358:U:O2	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:280:LEU:HB2	20:H:330:VAL:O	2.18	0.43
38:a:1082:U:H3	38:a:1086:A:N6	2.15	0.43
38:a:2252:G:O2'	38:a:2253:G:H5'	2.18	0.43
8:7:60:U:H2'	8:7:61:U:O4'	2.19	0.43
9:A:34:C:OP1	25:M:84:THR:OG1	2.35	0.43
10:AA:830:THR:HG22	10:AA:1234:LYS:NZ	2.34	0.43
10:AA:1018:TYR:HA	10:AA:1021:LEU:HD12	2.00	0.43
12:AD:16:ILE:HD13	12:AD:214:GLU:HG2	1.99	0.43
13:AE:126:LEU:CD1	13:AE:223:LEU:HD22	2.49	0.43
13:AE:388:ARG:HG2	13:AE:388:ARG:HH11	1.84	0.43
16:D:1515:G:H2'	16:D:1516:G:C8	2.52	0.43
19:G:16:PHE:CG	20:H:43:LYS:HA	2.53	0.43
19:G:35:ARG:CG	20:H:10:GLU:OE2	2.63	0.43
20:H:302:GLY:HA3	20:H:344:LEU:HD13	2.00	0.43
20:H:335:ILE:HG12	20:H:342:ILE:HG23	2.00	0.43
38:a:57:C:H2'	38:a:58:G:O4'	2.18	0.43
6:5:116:DG:OP1	13:AE:1311:LYS:NZ	2.46	0.43
10:AA:488:MET:O	10:AA:490:GLN:N	2.47	0.43
10:AA:565:GLU:HA	10:AA:569:ILE:HG12	2.01	0.43
10:AA:873:ILE:O	10:AA:928:VAL:HB	2.18	0.43
10:AA:991:LYS:HD2	10:AA:991:LYS:H	1.80	0.43
12:AC:50:SER:HB3	12:AD:8:PHE:HZ	1.84	0.43
12:AC:71:LYS:NZ	12:AC:140:ILE:HG13	2.32	0.43
12:AD:57:THR:HG21	12:AD:147:GLN:HB2	1.99	0.43
12:AD:207:THR:OG1	12:AD:208:ASN:N	2.52	0.43
13:AE:51:PRO:HB2	13:AE:52:GLU:H	1.65	0.43
13:AE:515:ARG:HH12	13:AE:724:MET:HG2	1.83	0.43
9:B:18:G:N3	9:B:58:A:C5	2.87	0.43
20:H:76:GLU:HA	20:H:76:GLU:OE2	2.19	0.43
20:H:109:THR:C	20:H:153:GLU:HA	2.43	0.43
38:a:2133:G:O2'	38:a:2157:G:N2	2.51	0.43
38:a:2469:A:N6	38:a:2481:G:O2'	2.52	0.43
9:A:53:G:C2	9:A:54:U:C5	3.07	0.43
9:A:60:U:OP2	9:A:61:C:N4	2.45	0.43
10:AA:623:LEU:HD13	10:AA:627:GLY:HA2	2.01	0.43
11:AB:7:LYS:HG2	11:AB:74:VAL:HG13	2.01	0.43
12:AD:86:LYS:NZ	13:AE:528:THR:HB	2.33	0.43
13:AE:111:THR:CG2	13:AE:300:GLN:HA	2.48	0.43
13:AE:395:LYS:HZ2	13:AE:399:LYS:HE2	1.84	0.43
13:AE:559:ALA:HB3	13:AE:562:GLU:HB3	2.01	0.43
16:D:324:G:N2	16:D:327:A:C8	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:G:114:LEU:HD13	19:G:144:LEU:HB3	1.99	0.43
29:Q:88:GLY:H	29:Q:114:THR:HG22	1.84	0.43
38:a:637:A:N1	38:a:651:G:O2'	2.51	0.43
38:a:973:A:O4'	38:a:1188:U:C6	2.72	0.43
57:t:107:LEU:HD21	57:t:115:ILE:HG21	2.01	0.43
6:5:114:DC:H5''	13:AE:1148:ARG:CZ	2.46	0.43
9:A:26:G:N2	9:A:45:G:N2	2.66	0.43
9:A:49:G:O5'	9:A:49:G:C8	2.71	0.43
9:A:68:C:H3'	9:A:69:C:H5''	1.95	0.43
10:AA:529:ARG:HH22	10:AA:687:ARG:HH11	1.66	0.43
10:AA:803:ALA:HB2	10:AA:1094:VAL:HG21	1.99	0.43
10:AA:839:VAL:O	10:AA:886:LYS:HD2	2.19	0.43
13:AE:24:LEU:CD1	13:AE:232:ASN:ND2	2.82	0.43
13:AE:894:VAL:HG22	13:AE:1258:ARG:HH11	1.83	0.43
9:B:26:G:N2	9:B:45:G:N2	2.66	0.43
16:D:384:G:H2'	16:D:385:C:C6	2.54	0.43
16:D:826:C:O2	26:N:16:ASN:ND2	2.52	0.43
16:D:1333:A:H2'	16:D:1334:G:O4'	2.19	0.43
20:H:152:LEU:CB	20:H:171:ARG:H	2.32	0.43
22:J:48:LEU:HD13	22:J:48:LEU:N	2.33	0.43
38:a:2252:G:H2'	38:a:2253:G:H8	1.84	0.43
38:a:2395:C:H2'	38:a:2396:G:O4'	2.18	0.43
42:e:59:GLU:O	42:e:63:ALA:HB3	2.17	0.43
51:n:123:ASP:C	51:n:123:ASP:OD1	2.62	0.43
9:A:58:A:HO2'	9:A:60:U:H5	1.62	0.43
13:AE:26:SER:HB2	13:AE:236:TRP:CH2	2.51	0.43
13:AE:58:CYS:SG	13:AE:60:ARG:HG2	2.59	0.43
13:AE:123:ARG:HD3	13:AE:123:ARG:HA	1.49	0.43
13:AE:244:VAL:HA	13:AE:269:TYR:OH	2.19	0.43
13:AE:513:MET:HG3	13:AE:544:LEU:HD11	2.01	0.43
9:B:25:C:C2'	9:B:26:G:H5'	2.48	0.43
16:D:842:U:H3'	16:D:843:U:C5'	2.48	0.43
16:D:1126:U:OP1	28:P:7:ARG:NH2	2.51	0.43
16:D:1499:A:O2'	16:D:1500:A:C5'	2.66	0.43
38:a:879:G:H2'	38:a:880:G:O4'	2.19	0.43
38:a:1142:A:H2'	38:a:1142:A:N3	2.34	0.43
54:q:3:VAL:HA	54:q:36:ARG:O	2.19	0.43
10:AA:395:TYR:HE2	10:AA:420:LEU:HG	1.84	0.43
10:AA:805:MET:HE3	10:AA:805:MET:HB2	1.87	0.43
13:AE:417:ARG:NH1	14:AF:43:ASN:O	2.51	0.43
16:D:429:U:O2	16:D:430:A:C8	2.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:1021:A:N3	38:a:1021:A:C3'	2.78	0.43
38:a:1386:C:H2'	38:a:1387:A:C8	2.53	0.43
10:AA:796:LEU:N	10:AA:1231:TYR:OH	2.52	0.42
10:AA:1329:GLU:HA	13:AE:245:LEU:HD13	2.00	0.42
12:AC:79:LEU:HD23	12:AC:79:LEU:HA	1.86	0.42
12:AD:64:VAL:HG11	12:AD:78:ILE:HG21	1.99	0.42
13:AE:111:THR:HG21	13:AE:303:VAL:HB	2.00	0.42
9:B:53:G:C2	9:B:54:U:C5	3.07	0.42
16:D:622:A:C8	16:D:623:C:C6	3.07	0.42
38:a:819:A:C4	38:a:1189:A:C2	3.07	0.42
38:a:2602:A:H5''	38:a:2603:G:C5'	2.49	0.42
9:A:76:A:C2'	38:a:2394:C:N4	2.75	0.42
10:AA:300:ASP:OD1	10:AA:313:ALA:N	2.52	0.42
10:AA:452:ARG:NH1	10:AA:458:GLU:OE2	2.52	0.42
10:AA:1010:GLN:NE2	10:AA:1010:GLN:CA	2.82	0.42
12:AC:231:PHE:HE2	12:AD:39:LEU:HD13	1.84	0.42
13:AE:395:LYS:HB3	13:AE:395:LYS:HE3	1.45	0.42
14:AF:50:ALA:O	14:AF:54:ILE:HG12	2.19	0.42
19:G:47:VAL:N	19:G:48:PRO:HD2	2.34	0.42
20:H:274:TYR:HD1	20:H:335:ILE:HD12	1.84	0.42
38:a:126:A:O5'	50:m:19:ARG:HG3	2.19	0.42
38:a:1394:U:C4	38:a:1395:A:C6	3.07	0.42
38:a:2615:U:C2	46:i:4:GLN:HA	2.55	0.42
38:a:2803:G:H2'	38:a:2804:U:C5	2.55	0.42
60:w:49:GLU:HB2	60:w:50:PRO:HD3	2.00	0.42
4:3:12:ILE:CG2	4:3:80:ALA:HB2	2.49	0.42
10:AA:75:LEU:HD23	10:AA:94:ALA:HB3	2.00	0.42
10:AA:1034:ARG:HG2	10:AA:1034:ARG:NH1	2.25	0.42
13:AE:1024:THR:HG23	13:AE:1123:ARG:HA	2.00	0.42
19:G:208:ARG:NH1	20:H:29:VAL:HG11	2.34	0.42
38:a:1020:A:C2	38:a:1141:U:C2	3.07	0.42
38:a:1385:A:O2'	38:a:1396:U:O2	2.35	0.42
38:a:2511:U:O4	38:a:2575:C:N3	2.52	0.42
49:l:170:ARG:NH2	49:l:176:ASP:OD1	2.49	0.42
56:s:32:LEU:HD23	56:s:54:ILE:HD13	2.01	0.42
58:u:109:LYS:HG2	58:u:126:ARG:HB2	2.02	0.42
10:AA:666:SER:HB2	10:AA:1186:VAL:HG21	2.00	0.42
12:AD:43:LEU:HD23	12:AD:43:LEU:HA	1.88	0.42
13:AE:586:GLY:HA3	13:AE:612:LEU:HD11	2.01	0.42
13:AE:609:TYR:HD2	13:AE:610:ARG:NH1	2.17	0.42
13:AE:950:ILE:HB	13:AE:1018:ALA:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:1350:ASN:HA	13:AE:1353:VAL:HG12	2.02	0.42
16:D:1371:G:O3'	27:O:71:GLY:HA3	2.19	0.42
20:H:332:VAL:HG11	20:H:335:ILE:CG1	2.38	0.42
38:a:567:U:OP2	58:u:29:LYS:NZ	2.53	0.42
38:a:1028:A:N6	38:a:1125:G:H2'	2.34	0.42
38:a:1082:U:N3	38:a:1086:A:C6	2.87	0.42
38:a:1925:C:OP2	38:a:1925:C:C6	2.73	0.42
47:j:172:VAL:HG11	47:j:175:LEU:HD21	2.01	0.42
4:3:39:ILE:HG22	4:3:40:ASN:N	2.34	0.42
9:A:15:G:H1	9:A:20:U:H3	1.68	0.42
9:A:56:C:C2	38:a:2112:G:C5	3.07	0.42
10:AA:241:LEU:N	10:AA:283:LYS:O	2.51	0.42
13:AE:68:TYR:O	13:AE:75:TYR:CD2	2.70	0.42
13:AE:242:LEU:C	13:AE:242:LEU:HD23	2.44	0.42
13:AE:797:THR:HG22	13:AE:924:GLY:HA3	2.01	0.42
23:K:150:PRO:O	23:K:153:VAL:HG22	2.19	0.42
38:a:126:A:OP1	50:m:45:SER:OG	2.38	0.42
38:a:1932:A:H2'	38:a:1933:G:O4'	2.19	0.42
60:w:9:GLN:O	60:w:17:ARG:NH2	2.51	0.42
10:AA:400:VAL:HG21	10:AA:452:ARG:HE	1.84	0.42
10:AA:587:LEU:HD23	10:AA:587:LEU:HA	1.89	0.42
13:AE:211:GLU:CG	13:AE:215:LYS:HE3	2.44	0.42
20:H:342:ILE:HG22	20:H:344:LEU:HD12	2.01	0.42
37:Y:72:U:C3'	37:Y:72:U:C6	3.03	0.42
38:a:2756:U:C4	38:a:2759:G:O6	2.72	0.42
49:l:145:ASP:HA	49:l:166:LYS:HB3	2.02	0.42
63:z:65:ILE:CD1	63:z:92:ARG:HB2	2.49	0.42
3:2:1:MET:N	38:a:142:A:O2'	2.47	0.42
9:A:36:U:H2'	9:A:37:A:O4'	2.19	0.42
10:AA:68:LEU:HD11	10:AA:100:LEU:HB3	2.01	0.42
10:AA:943:LYS:HZ1	10:AA:947:GLU:HB2	1.84	0.42
10:AA:959:ASP:HA	10:AA:962:GLU:HB2	2.01	0.42
10:AA:976:ARG:HA	10:AA:979:LEU:HB2	2.02	0.42
10:AA:979:LEU:HD13	10:AA:979:LEU:HA	1.74	0.42
13:AE:102:MET:HG2	13:AE:246:PRO:CG	2.49	0.42
13:AE:144:TYR:CE1	13:AE:162:GLU:OE1	2.73	0.42
13:AE:246:PRO:HA	13:AE:247:PRO:HD3	1.96	0.42
16:D:502:A:H2'	16:D:503:C:O4'	2.20	0.42
16:D:1329:A:OP1	36:X:28:THR:CA	2.66	0.42
38:a:1406:U:HO2'	38:a:1407:G:C5'	2.28	0.42
46:i:43:ILE:HG22	46:i:49:TYR:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:s:114:LEU:HD12	56:s:114:LEU:HA	1.87	0.42
61:x:99:TYR:OH	61:x:111:ARG:NH1	2.53	0.42
10:AA:104:ILE:HD11	10:AA:116:ASP:HB2	2.01	0.42
10:AA:257:ALA:HB2	10:AA:285:ILE:HG22	2.02	0.42
10:AA:914:LYS:C	10:AA:914:LYS:HE3	2.44	0.42
13:AE:820:ILE:HD11	13:AE:822:MET:HE2	2.02	0.42
13:AE:1046:ILE:HG22	13:AE:1061:VAL:HA	2.00	0.42
15:C:44:ILE:HG21	20:H:339:ARG:HA	2.01	0.42
16:D:309:A:O2'	16:D:607:A:N1	2.51	0.42
19:G:19:GLN:OE1	20:H:76:GLU:HB3	2.12	0.42
20:H:292:CYS:SG	20:H:304:VAL:HB	2.60	0.42
27:O:28:ILE:HD12	27:O:28:ILE:N	2.35	0.42
38:a:67:U:C4	38:a:74:A:C6	3.04	0.42
38:a:1548:A:H2'	38:a:1549:A:C8	2.55	0.42
45:h:240:PHE:CD2	45:h:240:PHE:O	2.73	0.42
7:6:27:DG:H1'	7:6:28:DA:C5	2.55	0.42
9:A:58:A:OP2	9:A:58:A:H8	2.02	0.42
10:AA:717:VAL:HG22	10:AA:782:VAL:HG12	2.00	0.42
13:AE:213:LYS:HE3	13:AE:213:LYS:CA	2.47	0.42
13:AE:848:VAL:HB	13:AE:858:VAL:HG22	2.02	0.42
16:D:1323:G:H2'	16:D:1324:A:C8	2.55	0.42
20:H:110:GLY:H	20:H:153:GLU:N	2.17	0.42
20:H:119:GLY:CA	20:H:132:PRO:C	2.92	0.42
21:I:50:ALA:HB2	21:I:75:ILE:HD12	2.00	0.42
27:O:55:VAL:O	27:O:57:MET:N	2.52	0.42
38:a:493:G:H2'	38:a:494:G:O4'	2.20	0.42
38:a:1275:A:N1	38:a:1295:C:O2'	2.46	0.42
38:a:1921:G:C2'	38:a:1922:G:H5'	2.49	0.42
51:n:77:PHE:CD1	51:n:77:PHE:N	2.82	0.42
57:t:113:MET:HE3	57:t:116:ILE:HD11	2.01	0.42
8:7:63:G:H2'	8:7:64:U:H6	1.81	0.42
10:AA:55:SER:CB	10:AA:465:ARG:HH12	2.32	0.42
10:AA:1253:LEU:CD1	13:AE:253:VAL:CG1	2.95	0.42
13:AE:68:TYR:HB3	13:AE:75:TYR:HE2	1.81	0.42
13:AE:647:PRO:HG3	13:AE:697:MET:HB3	2.01	0.42
9:B:26:G:H1	9:B:44:A:N6	2.18	0.42
18:F:32:VAL:HG11	29:Q:89:PRO:HG3	2.01	0.42
19:G:187:VAL:HG21	19:G:199:VAL:HG23	2.02	0.42
21:I:9:GLY:HA3	31:S:89:MET:HE3	2.01	0.42
25:M:22:LEU:HD13	25:M:97:ASN:ND2	2.35	0.42
38:a:548:G:H3'	38:a:549:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:a:2311:A:C2	51:n:85:ILE:HD11	2.55	0.42
45:h:37:ASN:HB2	45:h:62:TYR:HB2	2.01	0.42
57:t:76:VAL:HG12	62:y:73:VAL:HB	2.00	0.42
63:z:83:LEU:HD23	63:z:83:LEU:HA	1.93	0.42
9:A:22:G:H2'	9:A:23:C:C5	2.52	0.41
10:AA:888:THR:HG22	10:AA:914:LYS:HD2	2.02	0.41
10:AA:933:VAL:O	10:AA:933:VAL:CG1	2.68	0.41
12:AC:145:LYS:HB2	12:AC:145:LYS:HE3	1.83	0.41
13:AE:515:ARG:HG2	13:AE:516:ASP:H	1.85	0.41
13:AE:839:VAL:HG12	13:AE:864:LEU:HD12	2.01	0.41
9:B:47:U:O2'	9:B:50:U:OP1	2.37	0.41
16:D:1061:G:H5'	28:P:61:ALA:HB2	2.02	0.41
23:K:133:PRO:HA	23:K:136:VAL:HG12	2.02	0.41
38:a:851:C:H2'	38:a:852:U:C6	2.55	0.41
38:a:1250:G:OP2	58:u:21:ARG:NH2	2.52	0.41
38:a:2273:A:H2'	38:a:2274:A:C8	2.55	0.41
49:l:149:ILE:HD11	49:l:188:MET:HE3	2.02	0.41
50:m:12:ARG:CG	50:m:44:VAL:HG11	2.50	0.41
8:7:55:U:O5'	8:7:55:U:H6	2.03	0.41
9:A:26:G:C2	9:A:45:G:N2	2.89	0.41
10:AA:218:GLU:HG2	10:AA:299:LYS:HA	2.02	0.41
13:AE:47:ARG:CA	13:AE:47:ARG:NE	2.83	0.41
13:AE:120:LEU:HA	13:AE:121:PRO:HA	1.84	0.41
13:AE:820:ILE:HG12	13:AE:884:SER:HB2	2.02	0.41
15:C:12:ARG:O	15:C:16:GLU:HG3	2.19	0.41
28:P:57:VAL:O	28:P:58:ASN:ND2	2.52	0.41
38:a:1082:U:C4	38:a:1086:A:N6	2.88	0.41
38:a:2788:C:H2'	38:a:2789:C:C6	2.55	0.41
51:n:171:ALA:O	51:n:174:ASP:N	2.54	0.41
9:A:34:C:H41	25:M:83:SER:HA	1.86	0.41
9:A:46:G:O2'	9:A:47:U:H5''	2.19	0.41
13:AE:105:ILE:HD12	13:AE:242:LEU:CD2	2.44	0.41
9:B:15:G:H1	9:B:20:U:H3	1.69	0.41
16:D:404:G:O2'	16:D:498:A:N1	2.50	0.41
16:D:429:U:O2	16:D:430:A:N7	2.53	0.41
16:D:915:A:C6	16:D:916:U:C4	3.08	0.41
32:T:43:PHE:CE2	32:T:56:LEU:HD22	2.55	0.41
38:a:320:A:H2'	49:l:131:THR:HG21	2.01	0.41
38:a:742:A:N1	38:a:755:U:O4	2.53	0.41
38:a:948:C:H1'	38:a:984:A:C8	2.55	0.41
49:l:134:LEU:HB2	49:l:160:ALA:HB1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:p:25:THR:HG22	53:p:34:THR:HG23	2.02	0.41
57:t:38:ILE:HD11	57:t:112:PHE:CZ	2.54	0.41
2:l:92:ARG:NE	2:l:94:ASP:OD1	2.53	0.41
10:AA:593:LYS:HB3	10:AA:602:GLU:HG3	2.02	0.41
10:AA:858:GLY:C	10:AA:860:ALA:N	2.75	0.41
13:AE:385:LEU:CD2	13:AE:390:LEU:HB2	2.50	0.41
16:D:37:U:O2	16:D:548:G:N2	2.53	0.41
31:S:41:ARG:O	31:S:45:VAL:HG12	2.20	0.41
38:a:17:G:H2'	38:a:18:U:C6	2.56	0.41
38:a:1406:U:O2'	38:a:1407:G:OP2	2.39	0.41
49:l:48:THR:HG23	49:l:86:ALA:HB3	2.02	0.41
10:AA:230:PHE:HB2	10:AA:333:ILE:HB	2.01	0.41
10:AA:963:GLU:CA	10:AA:966:ILE:HD12	2.49	0.41
10:AA:1029:LEU:HD21	10:AA:1033:ARG:CZ	2.50	0.41
10:AA:1251:TYR:CE2	10:AA:1301:ARG:NH1	2.88	0.41
13:AE:136:GLU:OE1	13:AE:312:ARG:NH2	2.53	0.41
13:AE:141:PHE:CD2	13:AE:297:ARG:HB2	2.54	0.41
13:AE:144:TYR:N	13:AE:144:TYR:CD1	2.88	0.41
13:AE:220:ARG:NH1	13:AE:220:ARG:CG	2.82	0.41
16:D:563:A:C2	16:D:884:U:O4	2.62	0.41
16:D:1235:U:H2'	16:D:1236:A:O4'	2.20	0.41
38:a:2602:A:H5''	38:a:2603:G:H5''	2.02	0.41
38:a:2683:C:O2	57:t:70:ARG:NH2	2.52	0.41
9:A:8:U:OP2	9:A:8:U:H6	2.04	0.41
10:AA:56:VAL:HG11	10:AA:468:LEU:HD13	2.02	0.41
13:AE:47:ARG:NE	13:AE:47:ARG:HA	2.34	0.41
13:AE:109:SER:CB	13:AE:296:LYS:HG2	2.51	0.41
13:AE:239:LEU:N	13:AE:239:LEU:HD23	2.36	0.41
9:B:26:G:C2	9:B:45:G:N2	2.89	0.41
16:D:421:U:O2	16:D:421:U:O4'	2.37	0.41
20:H:155:LYS:O	20:H:169:SER:CB	2.68	0.41
28:P:90:LEU:HD22	28:P:90:LEU:HA	1.86	0.41
38:a:1182:G:H2'	38:a:1183:U:O4'	2.21	0.41
38:a:1839:G:C4	38:a:1927:A:C5	3.08	0.41
45:h:76:ALA:HB2	45:h:96:TYR:CE1	2.55	0.41
6:5:108:DT:C7	10:AA:199:ASP:HB3	2.45	0.41
9:A:47:U:O2'	9:A:50:U:OP1	2.38	0.41
9:A:56:C:OP1	38:a:2168:G:N3	2.53	0.41
10:AA:1252:SER:N	10:AA:1259:LEU:HD13	2.35	0.41
10:AA:1340:GLU:HB3	10:AA:1341:ASP:H	1.58	0.41
12:AC:158:ARG:HH12	12:AC:172:LEU:HD23	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:576:ARG:HD3	13:AE:593:ASN:HA	2.03	0.41
15:C:14:THR:CG2	15:C:48:ARG:HE	2.33	0.41
38:a:36:G:N3	38:a:450:G:O2'	2.53	0.41
49:l:188:MET:HE2	49:l:193:VAL:HA	2.03	0.41
59:v:73:ILE:HG21	59:v:91:TYR:CZ	2.55	0.41
9:A:46:G:H2'	9:A:47:U:OP2	2.21	0.41
10:AA:960:LEU:HD21	10:AA:1028:LYS:HB3	2.02	0.41
13:AE:616:PRO:HA	13:AE:619:ILE:HG22	2.02	0.41
16:D:216:U:H2'	16:D:217:C:C6	2.55	0.41
16:D:548:G:C6	16:D:549:C:C4	3.08	0.41
16:D:860:A:H2'	16:D:861:G:O4'	2.21	0.41
16:D:1330:U:OP2	36:X:26:GLY:HA3	2.21	0.41
20:H:19:ARG:CD	20:H:73:ASP:OD1	2.66	0.41
27:O:10:GLY:HA3	27:O:78:ALA:O	2.21	0.41
38:a:5:A:H2'	38:a:6:A:C8	2.56	0.41
38:a:299:A:N1	38:a:322:A:O2'	2.47	0.41
38:a:2898:U:O2'	56:s:134:ALA:O	2.28	0.41
9:A:26:G:H1	9:A:44:A:N6	2.18	0.41
9:A:75:C:HO2'	9:A:76:A:H8	1.68	0.41
10:AA:484:LEU:HA	10:AA:485:ASP:HA	1.81	0.41
10:AA:775:GLU:HA	10:AA:776:PRO:HD3	1.96	0.41
10:AA:801:ARG:HH12	10:AA:1119:MET:HE1	1.86	0.41
10:AA:968:GLU:HG3	10:AA:972:PHE:CZ	2.56	0.41
12:AC:71:LYS:HZ1	12:AC:140:ILE:HD12	1.85	0.41
13:AE:68:TYR:CB	13:AE:75:TYR:HE2	2.34	0.41
13:AE:394:ILE:O	13:AE:394:ILE:HG13	2.18	0.41
13:AE:1289:ASN:O	13:AE:1293:GLU:HB2	2.20	0.41
9:B:7:G:O6	9:B:49:G:O6	2.39	0.41
9:B:58:A:OP2	9:B:58:A:H8	2.02	0.41
16:D:977:A:H1'	16:D:982:U:O4	2.20	0.41
16:D:1225:A:H2'	16:D:1226:C:C5	2.55	0.41
23:K:136:VAL:O	23:K:140:THR:HG23	2.20	0.41
28:P:87:LEU:HD12	28:P:87:LEU:HA	1.87	0.41
38:a:207:A:H2'	38:a:208:C:O4'	2.21	0.41
38:a:244:A:OP2	52:o:8:ARG:NH2	2.50	0.41
38:a:2822:G:OP1	47:j:164:GLN:NE2	2.47	0.41
45:h:119:GLY:O	45:h:130:LEU:HB3	2.20	0.41
53:p:52:PHE:CZ	53:p:72:LEU:HD22	2.56	0.41
56:s:104:ALA:O	56:s:108:MET:HG3	2.21	0.41
60:w:29:VAL:HG11	60:w:75:ILE:HG23	2.03	0.41
3:2:46:ALA:O	3:2:50:LEU:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AA:998:LEU:HD13	10:AA:998:LEU:C	2.46	0.41
10:AA:1046:VAL:HG22	10:AA:1049:ILE:CG1	2.50	0.41
12:AD:97:GLU:HG3	12:AD:147:GLN:HG2	2.03	0.41
13:AE:1272:SER:OG	13:AE:1273:ASP:N	2.53	0.41
16:D:580:C:H2'	16:D:581:G:O4'	2.21	0.41
16:D:1370:G:C2	16:D:1371:G:C8	3.09	0.41
16:D:1526:G:P	18:F:42:THR:HG23	2.61	0.41
27:O:9:THR:O	27:O:85:ARG:HD2	2.21	0.41
36:X:16:VAL:O	36:X:20:THR:HG23	2.21	0.41
38:a:67:U:C2	38:a:74:A:N6	2.89	0.41
38:a:1095:A:O2'	38:a:1096:A:O4'	2.33	0.41
38:a:1406:U:C2'	38:a:1407:G:OP2	2.69	0.41
45:h:175:ARG:NH1	45:h:181:MET:HE2	2.36	0.41
10:AA:812:PHE:HZ	13:AE:503:SER:HB2	1.85	0.40
10:AA:855:PRO:O	10:AA:857:VAL:N	2.54	0.40
10:AA:1102:GLY:HA2	10:AA:1106:ARG:HH11	1.85	0.40
13:AE:930:LEU:HA	13:AE:1244:GLN:HG3	2.02	0.40
9:B:8:U:H6	9:B:8:U:OP2	2.04	0.40
9:B:18:G:O2'	9:B:60:U:N3	2.48	0.40
16:D:791:G:N2	16:D:1497:G:O3'	2.53	0.40
38:a:458:G:O2'	38:a:469:G:O6	2.38	0.40
38:a:476:G:H4'	38:a:502:A:N1	2.35	0.40
38:a:984:A:H2'	38:a:984:A:N3	2.35	0.40
38:a:1570:A:H2'	38:a:1571:A:C8	2.55	0.40
40:c:33:LEU:O	40:c:34:HIS:CG	2.75	0.40
51:n:122:PHE:CZ	51:n:167:ARG:HA	2.56	0.40
61:x:53:THR:HG23	61:x:74:VAL:HG21	2.03	0.40
10:AA:6:THR:OG1	10:AA:781:ASP:OD1	2.34	0.40
12:AC:85:LEU:HA	12:AC:85:LEU:HD23	1.80	0.40
12:AD:111:THR:OG1	12:AD:112:ALA:N	2.54	0.40
13:AE:390:LEU:N	13:AE:390:LEU:HD13	2.35	0.40
13:AE:805:GLN:HG3	13:AE:1348:LYS:HD3	2.03	0.40
20:H:348:GLN:N	20:H:348:GLN:CD	2.79	0.40
36:X:16:VAL:HG13	36:X:34:LEU:CD1	2.51	0.40
38:a:871:U:H2'	38:a:872:U:C6	2.56	0.40
63:z:66:ASN:OD1	63:z:70:ARG:NE	2.54	0.40
12:AD:152:TYR:HE2	13:AE:535:ARG:HH21	1.68	0.40
12:AD:154:PRO:HG2	12:AD:157:THR:HG22	2.04	0.40
15:C:12:ARG:NH2	20:H:268:VAL:CG2	2.71	0.40
16:D:218:U:H2'	16:D:219:U:O4'	2.21	0.40
20:H:305:HIS:CG	20:H:306:VAL:N	2.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:P:99:GLN:O	28:P:99:GLN:CG	2.70	0.40
31:S:42:TRP:HA	31:S:45:VAL:HG13	2.04	0.40
38:a:1169:A:H5''	38:a:1169:A:N3	2.36	0.40
38:a:2315:G:C5'	51:n:157:THR:HG23	2.52	0.40
38:a:2572:A:N7	47:j:150:GLN:NE2	2.69	0.40
38:a:2641:G:OP1	56:s:78:THR:HG22	2.21	0.40
38:a:2806:C:H2'	38:a:2807:U:O4'	2.22	0.40
47:j:175:LEU:CD1	47:j:193:VAL:HG12	2.51	0.40
2:1:75:PHE:CZ	2:1:104:THR:HG21	2.56	0.40
7:6:21:DA:H5''	10:AA:141:THR:HG21	2.03	0.40
10:AA:26:TYR:HE2	10:AA:32:LEU:HD12	1.86	0.40
10:AA:211:ARG:HH21	10:AA:351:LEU:HD22	1.86	0.40
10:AA:1105:SER:OG	13:AE:731:ARG:NH2	2.54	0.40
13:AE:92:VAL:O	13:AE:92:VAL:CG1	2.69	0.40
13:AE:108:ALA:HB2	13:AE:276:ASN:OD1	2.22	0.40
13:AE:144:TYR:OH	13:AE:162:GLU:OE1	2.34	0.40
13:AE:279:LEU:HD13	13:AE:299:LEU:HD13	2.02	0.40
13:AE:351:GLY:O	13:AE:467:ALA:HA	2.21	0.40
9:B:46:G:H2'	9:B:47:U:OP2	2.21	0.40
16:D:152:A:N6	16:D:170:U:C2	2.89	0.40
16:D:579:A:O2'	32:T:54:ARG:NH1	2.54	0.40
16:D:712:A:H2'	16:D:713:G:O4'	2.21	0.40
16:D:1189:U:OP1	31:S:98:LYS:NZ	2.55	0.40
16:D:1389:C:H2'	16:D:1390:U:O4'	2.22	0.40
18:F:67:ARG:HD3	18:F:67:ARG:H	1.85	0.40
38:a:221:A:N1	38:a:265:A:O2'	2.54	0.40
38:a:1421:G:C2	38:a:1422:G:C8	3.09	0.40
38:a:2298:A:C5	38:a:2321:U:C4	3.09	0.40
55:r:57:LYS:O	55:r:61:VAL:HG13	2.21	0.40
60:w:67:PHE:O	60:w:71:ARG:HG2	2.21	0.40
10:AA:850:ILE:HG21	10:AA:870:ILE:HD11	2.03	0.40
10:AA:936:ARG:HH21	10:AA:936:ARG:HG3	1.86	0.40
13:AE:113:HIS:ND1	13:AE:115:TRP:HB2	2.37	0.40
13:AE:390:LEU:HD13	13:AE:390:LEU:H	1.86	0.40
9:B:25:C:H2'	9:B:26:G:C5'	2.51	0.40
9:B:37:A:H5''	9:B:37:A:C4	2.56	0.40
15:C:34:THR:N	15:C:38:LYS:O	2.55	0.40
16:D:1208:C:H2'	16:D:1209:C:H6	1.85	0.40
20:H:332:VAL:HG12	20:H:334:ASP:N	2.33	0.40
60:w:10:LEU:HD11	60:w:43:GLU:HG3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	48
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
4	3	101/103 (98%)	96 (95%)	4 (4%)	1 (1%)	12	48
5	4	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
10	AA	1318/1341 (98%)	1145 (87%)	140 (11%)	33 (2%)	4	26
11	AB	94/112 (84%)	88 (94%)	6 (6%)	0	100	100
12	AC	228/230 (99%)	214 (94%)	12 (5%)	2 (1%)	14	51
12	AD	226/230 (98%)	212 (94%)	14 (6%)	0	100	100
13	AE	1329/1358 (98%)	1198 (90%)	122 (9%)	9 (1%)	18	56
14	AF	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
15	C	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
17	E	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
18	F	68/70 (97%)	68 (100%)	0	0	100	100
19	G	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
20	H	255/557 (46%)	189 (74%)	54 (21%)	12 (5%)	2	16
21	I	206/208 (99%)	196 (95%)	9 (4%)	1 (0%)	24	63
22	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
23	K	154/156 (99%)	146 (95%)	7 (4%)	1 (1%)	21	59
24	L	102/104 (98%)	97 (95%)	4 (4%)	1 (1%)	12	48
25	M	149/151 (99%)	144 (97%)	4 (3%)	1 (1%)	18	56
26	N	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	16	54
27	O	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	54
28	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	12	48
29	Q	115/117 (98%)	104 (90%)	9 (8%)	2 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	R	117/123 (95%)	116 (99%)	1 (1%)	0	100	100
31	S	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
32	T	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	42
34	V	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
35	W	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
36	X	114/116 (98%)	107 (94%)	5 (4%)	2 (2%)	6	34
39	b	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
40	c	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
42	e	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
43	f	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
44	g	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
45	h	269/271 (99%)	259 (96%)	9 (3%)	1 (0%)	30	67
46	i	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
47	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
48	k	50/52 (96%)	50 (100%)	0	0	100	100
49	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	63
50	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
51	n	175/177 (99%)	162 (93%)	11 (6%)	2 (1%)	11	46
52	o	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
53	p	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
54	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
55	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
56	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
57	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
58	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
59	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
60	w	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
61	x	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
62	y	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
63	z	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	9136/9618 (95%)	8457 (93%)	604 (7%)	75 (1%)	18	54

All (75) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	AA	596	ASP
10	AA	853	ASP
10	AA	859	GLU
10	AA	862	LEU
10	AA	937	ASP
10	AA	993	PRO
10	AA	1010	GLN
20	H	139	ARG
20	H	153	GLU
20	H	169	SER
20	H	306	VAL
20	H	340	ARG
27	O	56	ASP
36	X	103	LYS
10	AA	375	PRO
10	AA	856	ASN
10	AA	870	ILE
10	AA	873	ILE
10	AA	985	GLU
10	AA	1005	GLU
10	AA	1158	LYS
13	AE	175	GLU
20	H	108	VAL
20	H	309	MET
20	H	333	LEU
45	h	158	ALA
49	l	142	ALA
63	z	3	ARG
10	AA	376	PRO
10	AA	723	VAL
10	AA	728	ASP
10	AA	935	THR
10	AA	980	VAL
10	AA	1045	GLY
12	AC	164	ASP
12	AC	165	GLU
13	AE	51	PRO

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Mol	Chain	Res	Type
13	AE	805	GLN
20	H	76	GLU
20	H	142	ARG
25	M	130	ASN
28	P	58	ASN
29	Q	119	ASN
10	AA	850	ILE
10	AA	940	GLU
10	AA	941	LYS
10	AA	943	LYS
10	AA	991	LYS
10	AA	995	ASP
13	AE	174	ASP
13	AE	193	ASP
21	I	80	LYS
36	X	105	ASN
51	n	40	VAL
10	AA	917	SER
10	AA	1003	THR
10	AA	1044	PRO
13	AE	91	GLU
20	H	70	VAL
20	H	82	THR
4	3	39	ILE
13	AE	49	PHE
13	AE	73	GLY
13	AE	904	ALA
24	L	96	VAL
1	0	44	GLY
10	AA	697	LYS
10	AA	1159	VAL
23	K	44	GLY
10	AA	1317	PRO
29	Q	74	VAL
33	U	64	GLY
51	n	62	GLY
10	AA	933	VAL
26	N	75	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	76 (90%)	8 (10%)	8	25
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	33
3	2	81/81 (100%)	77 (95%)	4 (5%)	22	43
4	3	84/84 (100%)	79 (94%)	5 (6%)	17	39
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	50
10	AA	1140/1156 (99%)	1027 (90%)	113 (10%)	7	24
11	AB	86/98 (88%)	85 (99%)	1 (1%)	63	75
12	AC	198/198 (100%)	185 (93%)	13 (7%)	15	37
12	AD	196/198 (99%)	193 (98%)	3 (2%)	57	72
13	AE	1120/1134 (99%)	1046 (93%)	74 (7%)	15	37
14	AF	70/70 (100%)	68 (97%)	2 (3%)	37	58
15	C	57/57 (100%)	55 (96%)	2 (4%)	32	53
17	E	65/65 (100%)	61 (94%)	4 (6%)	16	38
18	F	60/60 (100%)	57 (95%)	3 (5%)	22	43
19	G	187/187 (100%)	174 (93%)	13 (7%)	14	35
20	H	137/461 (30%)	124 (90%)	13 (10%)	8	25
21	I	171/171 (100%)	163 (95%)	8 (5%)	23	45
22	J	172/172 (100%)	164 (95%)	8 (5%)	23	45
23	K	119/119 (100%)	111 (93%)	8 (7%)	15	36
24	L	91/91 (100%)	84 (92%)	7 (8%)	12	32
25	M	124/124 (100%)	113 (91%)	11 (9%)	9	28
26	N	104/104 (100%)	101 (97%)	3 (3%)	37	58
27	O	105/105 (100%)	99 (94%)	6 (6%)	18	40
28	P	86/86 (100%)	77 (90%)	9 (10%)	6	21
29	Q	90/90 (100%)	88 (98%)	2 (2%)	45	64
30	R	101/103 (98%)	95 (94%)	6 (6%)	18	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	S	83/83 (100%)	79 (95%)	4 (5%)	23	44
32	T	76/76 (100%)	65 (86%)	11 (14%)	3	13
33	U	65/65 (100%)	60 (92%)	5 (8%)	12	32
34	V	74/74 (100%)	71 (96%)	3 (4%)	27	48
35	W	72/72 (100%)	66 (92%)	6 (8%)	10	30
36	X	94/94 (100%)	87 (93%)	7 (7%)	13	33
39	b	58/58 (100%)	57 (98%)	1 (2%)	53	69
40	c	67/67 (100%)	64 (96%)	3 (4%)	24	46
42	e	54/54 (100%)	51 (94%)	3 (6%)	19	40
43	f	48/48 (100%)	43 (90%)	5 (10%)	7	22
44	g	59/59 (100%)	54 (92%)	5 (8%)	10	29
45	h	216/216 (100%)	199 (92%)	17 (8%)	11	32
46	i	47/47 (100%)	41 (87%)	6 (13%)	4	15
47	j	164/164 (100%)	156 (95%)	8 (5%)	22	43
48	k	47/47 (100%)	44 (94%)	3 (6%)	16	37
49	l	165/165 (100%)	151 (92%)	14 (8%)	10	29
50	m	38/38 (100%)	36 (95%)	2 (5%)	20	41
51	n	148/148 (100%)	130 (88%)	18 (12%)	5	17
52	o	51/51 (100%)	47 (92%)	4 (8%)	11	32
53	p	136/136 (100%)	130 (96%)	6 (4%)	25	47
54	q	34/34 (100%)	31 (91%)	3 (9%)	9	28
55	r	114/114 (100%)	102 (90%)	12 (10%)	6	21
56	s	116/116 (100%)	106 (91%)	10 (9%)	10	29
57	t	104/104 (100%)	97 (93%)	7 (7%)	15	36
58	u	103/103 (100%)	96 (93%)	7 (7%)	14	36
59	v	109/109 (100%)	105 (96%)	4 (4%)	30	51
60	w	99/99 (100%)	91 (92%)	8 (8%)	11	31
61	x	86/86 (100%)	80 (93%)	6 (7%)	14	35
62	y	99/99 (100%)	91 (92%)	8 (8%)	11	31
63	z	89/89 (100%)	85 (96%)	4 (4%)	24	46
All	All	7614/7984 (95%)	7078 (93%)	536 (7%)	16	35

All (536) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	10	LYS
1	0	38	VAL
1	0	47	VAL
1	0	48	LYS
1	0	51	VAL
1	0	68	ARG
1	0	86	GLN
1	0	96	VAL
2	1	19	LEU
2	1	30	SER
2	1	41	LYS
2	1	69	LEU
2	1	97	LEU
2	1	107	VAL
2	1	110	ARG
3	2	1	MET
3	2	24	MET
3	2	37	ASP
3	2	93	LEU
4	3	52	LEU
4	3	70	VAL
4	3	72	ILE
4	3	99	ASN
4	3	101	GLU
5	4	40	ILE
5	4	69	GLU
5	4	71	LYS
10	AA	39	ILE
10	AA	145	ILE
10	AA	376	PRO
10	AA	615	VAL
10	AA	723	VAL
10	AA	727	VAL
10	AA	728	ASP
10	AA	731	ARG
10	AA	732	ILE
10	AA	752	ASN
10	AA	753	LEU
10	AA	802	VAL
10	AA	817	LEU
10	AA	840	SER
10	AA	844	LYS

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Mol	Chain	Res	Type
10	AA	845	LEU
10	AA	851	THR
10	AA	854	ILE
10	AA	855	PRO
10	AA	857	VAL
10	AA	862	LEU
10	AA	864	LYS
10	AA	865	LEU
10	AA	866	ASP
10	AA	867	GLU
10	AA	868	SER
10	AA	871	VAL
10	AA	872	TYR
10	AA	873	ILE
10	AA	884	VAL
10	AA	886	LYS
10	AA	887	VAL
10	AA	890	LYS
10	AA	911	SER
10	AA	913	VAL
10	AA	914	LYS
10	AA	918	LEU
10	AA	933	VAL
10	AA	936	ARG
10	AA	939	VAL
10	AA	941	LYS
10	AA	942	ASP
10	AA	943	LYS
10	AA	944	ARG
10	AA	946	LEU
10	AA	947	GLU
10	AA	949	GLU
10	AA	950	GLU
10	AA	951	MET
10	AA	952	GLN
10	AA	953	LEU
10	AA	954	LYS
10	AA	955	GLN
10	AA	957	LYS
10	AA	958	LYS
10	AA	959	ASP
10	AA	960	LEU

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Mol	Chain	Res	Type
10	AA	962	GLU
10	AA	963	GLU
10	AA	964	LEU
10	AA	965	GLN
10	AA	967	LEU
10	AA	968	GLU
10	AA	971	LEU
10	AA	973	SER
10	AA	974	ARG
10	AA	979	LEU
10	AA	980	VAL
10	AA	985	GLU
10	AA	988	LYS
10	AA	989	LEU
10	AA	991	LYS
10	AA	992	LEU
10	AA	994	ARG
10	AA	995	ASP
10	AA	997	TRP
10	AA	999	GLU
10	AA	1004	ASP
10	AA	1005	GLU
10	AA	1007	LYS
10	AA	1010	GLN
10	AA	1013	GLN
10	AA	1014	LEU
10	AA	1019	ASP
10	AA	1020	GLU
10	AA	1023	HIS
10	AA	1024	GLU
10	AA	1025	PHE
10	AA	1026	GLU
10	AA	1027	LYS
10	AA	1029	LEU
10	AA	1030	GLU
10	AA	1032	LYS
10	AA	1034	ARG
10	AA	1035	LYS
10	AA	1037	THR
10	AA	1038	GLN
10	AA	1041	ASP
10	AA	1042	LEU

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Mol	Chain	Res	Type
10	AA	1046	VAL
10	AA	1047	LEU
10	AA	1048	LYS
10	AA	1076	ILE
10	AA	1151	LEU
10	AA	1159	VAL
10	AA	1248	THR
10	AA	1250	SER
10	AA	1252	SER
10	AA	1253	LEU
10	AA	1254	VAL
10	AA	1256	GLN
10	AA	1259	LEU
10	AA	1298	VAL
11	AB	47	GLU
12	AC	72	GLU
12	AC	91	ARG
12	AC	134	THR
12	AC	158	ARG
12	AC	159	ILE
12	AC	160	HIS
12	AC	162	GLU
12	AC	163	GLU
12	AC	165	GLU
12	AC	166	ARG
12	AC	168	ILE
12	AC	170	ARG
12	AC	171	LEU
12	AD	110	VAL
12	AD	187	VAL
12	AD	208	ASN
13	AE	40	LYS
13	AE	42	GLU
13	AE	44	ILE
13	AE	46	TYR
13	AE	47	ARG
13	AE	49	PHE
13	AE	50	LYS
13	AE	52	GLU
13	AE	53	ARG
13	AE	54	ASP
13	AE	56	LEU

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Mol	Chain	Res	Type
13	AE	60	ARG
13	AE	66	LYS
13	AE	67	ASP
13	AE	70	CYS
13	AE	74	LYS
13	AE	76	LYS
13	AE	78	LEU
13	AE	80	HIS
13	AE	81	ARG
13	AE	87	LYS
13	AE	88	CYS
13	AE	91	GLU
13	AE	94	GLN
13	AE	95	THR
13	AE	96	LYS
13	AE	99	ARG
13	AE	100	GLU
13	AE	114	ILE
13	AE	117	LEU
13	AE	119	SER
13	AE	123	ARG
13	AE	132	LEU
13	AE	135	ILE
13	AE	142	GLU
13	AE	144	TYR
13	AE	145	VAL
13	AE	146	VAL
13	AE	147	ILE
13	AE	152	THR
13	AE	154	LEU
13	AE	157	GLN
13	AE	159	ILE
13	AE	175	GLU
13	AE	180	MET
13	AE	190	LYS
13	AE	193	ASP
13	AE	196	GLN
13	AE	210	SER
13	AE	212	THR
13	AE	216	LYS
13	AE	222	LYS
13	AE	223	LEU

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Mol	Chain	Res	Type
13	AE	227	PHE
13	AE	233	LYS
13	AE	237	MET
13	AE	238	ILE
13	AE	239	LEU
13	AE	240	THR
13	AE	244	VAL
13	AE	271	ARG
13	AE	324	LEU
13	AE	385	LEU
13	AE	386	GLU
13	AE	387	LEU
13	AE	390	LEU
13	AE	393	THR
13	AE	394	ILE
13	AE	395	LYS
13	AE	506	VAL
13	AE	514	THR
13	AE	839	VAL
13	AE	1172	LYS
13	AE	1233	ILE
14	AF	4	VAL
14	AF	63	ILE
15	C	33	ILE
15	C	74	HIS
17	E	6	SER
17	E	10	ARG
17	E	48	GLN
17	E	64	LYS
18	F	34	ARG
18	F	62	ARG
18	F	67	ARG
19	G	8	ASP
19	G	45	LYS
19	G	59	LYS
19	G	105	LYS
19	G	108	ARG
19	G	117	LEU
19	G	128	LYS
19	G	129	LEU
19	G	132	LYS
19	G	135	LEU

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Mol	Chain	Res	Type
19	G	161	LEU
19	G	174	LYS
19	G	208	ARG
20	H	9	PHE
20	H	31	ILE
20	H	43	LYS
20	H	54	LYS
20	H	62	ILE
20	H	70	VAL
20	H	294	VAL
20	H	305	HIS
20	H	336	ASP
20	H	337	GLU
20	H	338	GLU
20	H	339	ARG
20	H	340	ARG
21	I	14	ILE
21	I	21	THR
21	I	33	LEU
21	I	75	ILE
21	I	89	LYS
21	I	175	LEU
21	I	178	LEU
21	I	200	VAL
22	J	47	ARG
22	J	48	LEU
22	J	95	GLU
22	J	104	ARG
22	J	105	MET
22	J	116	GLN
22	J	138	SER
22	J	143	VAL
23	K	10	GLU
23	K	15	LEU
23	K	60	ILE
23	K	114	VAL
23	K	115	LEU
23	K	138	ARG
23	K	141	ILE
23	K	162	GLU
24	L	7	VAL
24	L	16	GLU

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Mol	Chain	Res	Type
24	L	24	ARG
24	L	36	ILE
24	L	38	ARG
24	L	54	LEU
24	L	86	ARG
25	M	7	ILE
25	M	17	LYS
25	M	21	GLU
25	M	23	LEU
25	M	27	VAL
25	M	50	LEU
25	M	79	ARG
25	M	91	VAL
25	M	109	ARG
25	M	130	ASN
25	M	146	GLU
26	N	96	MET
26	N	104	VAL
26	N	117	ARG
27	O	27	LYS
27	O	60	LYS
27	O	61	LEU
27	O	63	LEU
27	O	116	VAL
27	O	118	LEU
28	P	17	LEU
28	P	18	ILE
28	P	24	GLU
28	P	25	ILE
28	P	27	GLU
28	P	37	ARG
28	P	87	LEU
28	P	90	LEU
28	P	102	LEU
29	Q	15	GLN
29	Q	107	ILE
30	R	5	ASN
30	R	12	ARG
30	R	24	LEU
30	R	62	GLU
30	R	74	LEU
30	R	102	LEU

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Mol	Chain	Res	Type
31	S	45	VAL
31	S	46	LEU
31	S	89	MET
31	S	92	GLU
32	T	10	LYS
32	T	22	THR
32	T	39	LEU
32	T	40	GLN
32	T	64	ARG
32	T	66	LEU
32	T	67	LEU
32	T	70	LEU
32	T	73	LYS
32	T	84	ARG
32	T	85	LEU
33	U	1	MET
33	U	2	VAL
33	U	6	LEU
33	U	19	VAL
33	U	50	THR
34	V	46	VAL
34	V	75	LEU
34	V	81	LYS
35	W	21	LYS
35	W	33	THR
35	W	49	ILE
35	W	58	VAL
35	W	79	THR
35	W	81	ARG
36	X	16	VAL
36	X	25	VAL
36	X	29	ARG
36	X	59	GLU
36	X	93	ARG
36	X	101	ARG
36	X	117	LYS
39	b	70	GLU
40	c	33	LEU
40	c	48	THR
40	c	71	LEU
42	e	18	LEU
42	e	58	ASN

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Mol	Chain	Res	Type
42	e	60	LYS
43	f	3	LYS
43	f	11	ARG
43	f	25	LEU
43	f	45	ARG
43	f	55	VAL
44	g	3	LYS
44	g	16	CYS
44	g	24	ILE
44	g	36	VAL
44	g	47	LYS
45	h	51	THR
45	h	94	VAL
45	h	105	LEU
45	h	118	SER
45	h	125	LYS
45	h	130	LEU
45	h	141	VAL
45	h	156	ARG
45	h	183	LYS
45	h	187	ASP
45	h	195	VAL
45	h	202	LEU
45	h	203	ARG
45	h	204	VAL
45	h	205	LEU
45	h	242	LYS
45	h	271	ARG
46	i	9	THR
46	i	12	LYS
46	i	26	THR
46	i	27	SER
46	i	29	SER
46	i	40	ARG
47	j	13	ARG
47	j	18	ASP
47	j	91	THR
47	j	99	GLU
47	j	104	VAL
47	j	177	VAL
47	j	189	VAL
47	j	193	VAL

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Mol	Chain	Res	Type
48	k	5	ILE
48	k	17	THR
48	k	24	THR
49	l	17	THR
49	l	22	ASP
49	l	40	ARG
49	l	48	THR
49	l	57	LYS
49	l	69	ARG
49	l	77	ILE
49	l	80	SER
49	l	108	ILE
49	l	109	LEU
49	l	111	GLU
49	l	122	GLU
49	l	149	ILE
49	l	179	SER
50	m	22	MET
50	m	42	LEU
51	n	6	ASP
51	n	10	ASP
51	n	26	MET
51	n	40	VAL
51	n	47	LYS
51	n	49	LEU
51	n	57	LEU
51	n	79	ILE
51	n	80	ARG
51	n	95	ARG
51	n	105	THR
51	n	117	LEU
51	n	122	PHE
51	n	123	ASP
51	n	132	VAL
51	n	140	GLU
51	n	141	ILE
51	n	163	ASP
52	o	8	ARG
52	o	30	ARG
52	o	31	HIS
52	o	55	LEU
53	p	11	VAL

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Mol	Chain	Res	Type
53	p	85	LYS
53	p	95	ARG
53	p	125	CYS
53	p	168	VAL
53	p	171	THR
54	q	3	VAL
54	q	26	ILE
54	q	34	LYS
55	r	1	MET
55	r	9	VAL
55	r	11	ASN
55	r	12	LEU
55	r	15	LEU
55	r	41	LYS
55	r	66	ASN
55	r	72	ILE
55	r	76	GLU
55	r	94	ILE
55	r	101	ASP
55	r	127	GLU
56	s	1	MET
56	s	30	THR
56	s	31	GLU
56	s	43	GLU
56	s	57	LEU
56	s	123	LYS
56	s	124	VAL
56	s	139	VAL
56	s	140	LEU
56	s	142	ILE
57	t	7	MET
57	t	35	VAL
57	t	49	ARG
57	t	67	LYS
57	t	70	ARG
57	t	80	ASP
57	t	104	THR
58	u	5	THR
58	u	27	LEU
58	u	59	ARG
58	u	73	ILE
58	u	76	GLU

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Mol	Chain	Res	Type
58	u	78	ARG
58	u	84	LYS
59	v	110	GLU
59	v	126	ILE
59	v	127	LYS
59	v	128	THR
60	w	2	ARG
60	w	20	MET
60	w	24	MET
60	w	51	LEU
60	w	65	LEU
60	w	69	ARG
60	w	95	THR
60	w	116	VAL
61	x	13	ARG
61	x	31	THR
61	x	47	VAL
61	x	48	LEU
61	x	91	SER
61	x	116	GLN
62	y	8	LEU
62	y	10	GLN
62	y	27	GLU
62	y	40	LEU
62	y	81	VAL
62	y	85	SER
62	y	102	GLU
62	y	114	LEU
63	z	18	LEU
63	z	51	ARG
63	z	109	LEU
63	z	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (65) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	86	GLN
2	1	61	ASN
3	2	28	ASN
3	2	59	ASN
4	3	54	GLN
10	AA	273	HIS

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Mol	Chain	Res	Type
10	AA	761	GLN
10	AA	808	ASN
10	AA	824	GLN
10	AA	965	GLN
10	AA	1010	GLN
10	AA	1013	GLN
10	AA	1157	GLN
10	AA	1236	ASN
12	AC	41	ASN
12	AC	66	HIS
12	AC	132	HIS
12	AD	41	ASN
12	AD	93	GLN
12	AD	103	ASN
13	AE	196	GLN
13	AE	469	HIS
13	AE	865	HIS
13	AE	1195	GLN
13	AE	1238	GLN
13	AE	1249	ASN
14	AF	29	GLN
14	AF	62	GLN
17	E	55	GLN
17	E	61	GLN
19	G	18	HIS
19	G	58	ASN
19	G	94	HIS
21	I	6	HIS
21	I	25	ASN
21	I	123	GLN
22	J	36	GLN
22	J	40	GLN
22	J	41	HIS
23	K	97	GLN
24	L	11	HIS
24	L	63	ASN
24	L	94	HIS
25	M	148	ASN
27	O	81	HIS
28	P	58	ASN
29	Q	15	GLN
30	R	72	HIS

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Mol	Chain	Res	Type
32	T	40	GLN
33	U	59	HIS
36	X	12	HIS
36	X	105	ASN
44	g	41	HIS
45	h	25	HIS
46	i	5	GLN
48	k	26	ASN
51	n	63	GLN
52	o	28	ASN
53	p	88	GLN
54	q	35	GLN
55	r	11	ASN
55	r	20	ASN
55	r	133	GLN
57	t	88	ASN
62	y	15	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	D	1515/1542 (98%)	290 (19%)	35 (2%)
37	Y	2/3 (66%)	2 (100%)	0
38	a	2859/2903 (98%)	540 (18%)	0
41	d	119/120 (99%)	17 (14%)	0
8	7	15/16 (93%)	7 (46%)	0
9	A	75/76 (98%)	29 (38%)	6 (8%)
9	B	75/76 (98%)	35 (46%)	6 (8%)
All	All	4660/4736 (98%)	920 (19%)	47 (1%)

All (920) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	56	U
8	7	57	G
8	7	58	A
8	7	59	U
8	7	60	U
8	7	62	G
8	7	63	G
9	A	2	G

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Mol	Chain	Res	Type
9	A	6	G
9	A	7	G
9	A	8	U
9	A	10	G
9	A	13	C
9	A	14	A
9	A	15	G
9	A	16	C
9	A	17	C
9	A	18	G
9	A	19	G
9	A	20	U
9	A	21	A
9	A	22	G
9	A	23	C
9	A	46	G
9	A	47	U
9	A	48	C
9	A	49	G
9	A	52	G
9	A	57	A
9	A	58	A
9	A	59	A
9	A	61	C
9	A	66	C
9	A	69	C
9	A	71	C
9	A	73	A
9	B	2	G
9	B	6	G
9	B	7	G
9	B	8	U
9	B	10	G
9	B	13	C
9	B	14	A
9	B	15	G
9	B	16	C
9	B	17	C
9	B	18	G
9	B	19	G
9	B	20	U
9	B	21	A

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Mol	Chain	Res	Type
9	B	22	G
9	B	23	C
9	B	30	G
9	B	31	G
9	B	32	C
9	B	36	U
9	B	37	A
9	B	38	A
9	B	46	G
9	B	47	U
9	B	48	C
9	B	49	G
9	B	52	G
9	B	57	A
9	B	58	A
9	B	59	A
9	B	61	C
9	B	66	C
9	B	69	C
9	B	71	C
9	B	73	A
16	D	4	U
16	D	5	U
16	D	9	G
16	D	22	G
16	D	29	U
16	D	32	A
16	D	39	G
16	D	41	G
16	D	47	C
16	D	48	C
16	D	50	A
16	D	51	A
16	D	52	C
16	D	54	C
16	D	69	G
16	D	70	U
16	D	71	A
16	D	72	A
16	D	74	A
16	D	76	G
16	D	82	G

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Mol	Chain	Res	Type
16	D	83	C
16	D	84	U
16	D	87	C
16	D	90	C
16	D	94	G
16	D	95	C
16	D	96	U
16	D	108	G
16	D	120	A
16	D	122	G
16	D	128	G
16	D	131	A
16	D	141	G
16	D	144	G
16	D	148	G
16	D	149	A
16	D	160	A
16	D	164	G
16	D	173	U
16	D	181	A
16	D	182	A
16	D	197	A
16	D	198	G
16	D	204	G
16	D	208	U
16	D	209	U
16	D	210	C
16	D	211	G
16	D	212	G
16	D	216	U
16	D	226	G
16	D	245	U
16	D	247	G
16	D	251	G
16	D	253	A
16	D	258	G
16	D	262	A
16	D	266	G
16	D	267	C
16	D	271	C
16	D	279	A
16	D	289	G

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Mol	Chain	Res	Type
16	D	299	G
16	D	306	A
16	D	321	A
16	D	328	C
16	D	329	A
16	D	332	G
16	D	347	G
16	D	352	C
16	D	353	A
16	D	354	G
16	D	355	C
16	D	367	U
16	D	372	C
16	D	373	A
16	D	376	G
16	D	382	A
16	D	384	G
16	D	392	C
16	D	393	A
16	D	397	A
16	D	406	G
16	D	412	A
16	D	413	G
16	D	414	A
16	D	421	U
16	D	422	C
16	D	424	G
16	D	429	U
16	D	446	G
16	D	451	A
16	D	457	G
16	D	458	U
16	D	460	A
16	D	463	U
16	D	464	U
16	D	467	U
16	D	468	A
16	D	469	C
16	D	478	A
16	D	479	U
16	D	481	G
16	D	484	G

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Mol	Chain	Res	Type
16	D	485	U
16	D	486	U
16	D	505	G
16	D	509	A
16	D	511	C
16	D	518	C
16	D	519	C
16	D	526	C
16	D	531	U
16	D	532	A
16	D	533	A
16	D	542	G
16	D	547	A
16	D	559	A
16	D	562	U
16	D	568	G
16	D	572	A
16	D	573	A
16	D	576	C
16	D	577	G
16	D	579	A
16	D	596	A
16	D	628	G
16	D	633	G
16	D	641	U
16	D	642	A
16	D	649	A
16	D	650	G
16	D	653	U
16	D	665	A
16	D	666	G
16	D	687	A
16	D	700	G
16	D	723	U
16	D	724	G
16	D	731	G
16	D	734	G
16	D	747	A
16	D	748	G
16	D	755	G
16	D	760	G
16	D	777	A

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Mol	Chain	Res	Type
16	D	793	U
16	D	794	A
16	D	815	A
16	D	817	C
16	D	828	U
16	D	829	G
16	D	832	G
16	D	841	C
16	D	844	G
16	D	845	A
16	D	849	G
16	D	874	G
16	D	887	G
16	D	902	G
16	D	914	A
16	D	916	U
16	D	926	G
16	D	934	C
16	D	935	A
16	D	954	G
16	D	960	U
16	D	963	G
16	D	969	A
16	D	972	C
16	D	975	A
16	D	976	G
16	D	991	U
16	D	992	U
16	D	993	G
16	D	996	A
16	D	999	C
16	D	1004	A
16	D	1008	U
16	D	1009	U
16	D	1017	U
16	D	1018	G
16	D	1021	A
16	D	1024	G
16	D	1026	G
16	D	1028	C
16	D	1030	U
16	D	1031	C

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Mol	Chain	Res	Type
16	D	1037	C
16	D	1043	G
16	D	1044	A
16	D	1046	A
16	D	1065	U
16	D	1085	U
16	D	1086	U
16	D	1094	G
16	D	1095	U
16	D	1099	G
16	D	1101	A
16	D	1124	G
16	D	1133	G
16	D	1135	U
16	D	1136	C
16	D	1137	C
16	D	1139	G
16	D	1140	C
16	D	1141	C
16	D	1142	G
16	D	1143	G
16	D	1145	A
16	D	1146	A
16	D	1151	A
16	D	1152	A
16	D	1158	C
16	D	1159	U
16	D	1167	A
16	D	1171	A
16	D	1174	G
16	D	1175	G
16	D	1176	A
16	D	1184	G
16	D	1196	A
16	D	1197	A
16	D	1206	G
16	D	1211	U
16	D	1212	U
16	D	1213	A
16	D	1214	C
16	D	1215	G
16	D	1226	C

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Mol	Chain	Res	Type
16	D	1227	A
16	D	1228	C
16	D	1238	A
16	D	1256	A
16	D	1257	A
16	D	1260	G
16	D	1275	A
16	D	1276	G
16	D	1278	G
16	D	1279	G
16	D	1280	A
16	D	1285	A
16	D	1286	U
16	D	1287	A
16	D	1299	A
16	D	1300	G
16	D	1302	C
16	D	1305	G
16	D	1312	G
16	D	1317	C
16	D	1320	C
16	D	1323	G
16	D	1329	A
16	D	1338	G
16	D	1340	A
16	D	1346	A
16	D	1347	G
16	D	1353	G
16	D	1363	A
16	D	1370	G
16	D	1378	C
16	D	1379	G
16	D	1381	U
16	D	1391	U
16	D	1396	A
16	D	1397	C
16	D	1398	A
16	D	1404	C
16	D	1419	G
16	D	1429	A
16	D	1441	A
16	D	1446	A

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Mol	Chain	Res	Type
16	D	1447	A
16	D	1448	C
16	D	1452	C
16	D	1453	G
16	D	1475	G
16	D	1487	G
16	D	1492	A
16	D	1493	A
16	D	1494	G
16	D	1495	U
16	D	1497	G
16	D	1503	A
16	D	1506	U
16	D	1517	G
16	D	1529	G
16	D	1530	G
16	D	1534	A
37	Y	72	U
37	Y	73	U
38	a	10	A
38	a	15	G
38	a	34	U
38	a	35	G
38	a	46	G
38	a	58	G
38	a	60	G
38	a	63	A
38	a	71	A
38	a	74	A
38	a	75	G
38	a	83	A
38	a	84	A
38	a	85	G
38	a	93	G
38	a	96	C
38	a	102	U
38	a	103	A
38	a	110	G
38	a	114	U
38	a	118	A
38	a	119	A
38	a	120	U

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Mol	Chain	Res	Type
38	a	122	G
38	a	131	A
38	a	136	G
38	a	139	U
38	a	140	C
38	a	141	G
38	a	145	C
38	a	163	C
38	a	165	A
38	a	181	A
38	a	196	A
38	a	199	A
38	a	200	U
38	a	215	G
38	a	216	A
38	a	222	A
38	a	225	C
38	a	248	G
38	a	249	C
38	a	261	G
38	a	264	C
38	a	265	A
38	a	266	G
38	a	267	C
38	a	271	G
38	a	272	A
38	a	275	C
38	a	276	U
38	a	278	A
38	a	285	G
38	a	311	A
38	a	324	A
38	a	329	G
38	a	330	A
38	a	353	C
38	a	359	G
38	a	361	G
38	a	362	A
38	a	371	A
38	a	372	G
38	a	373	U
38	a	375	G

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Mol	Chain	Res	Type
38	a	383	C
38	a	386	G
38	a	396	G
38	a	405	U
38	a	411	G
38	a	412	A
38	a	420	C
38	a	424	G
38	a	435	C
38	a	451	U
38	a	456	C
38	a	457	A
38	a	477	A
38	a	481	G
38	a	491	G
38	a	501	A
38	a	503	A
38	a	504	A
38	a	505	A
38	a	509	C
38	a	522	A
38	a	529	A
38	a	532	A
38	a	543	G
38	a	546	U
38	a	547	A
38	a	548	G
38	a	549	G
38	a	551	G
38	a	563	A
38	a	569	U
38	a	573	U
38	a	575	A
38	a	588	U
38	a	603	A
38	a	609	A
38	a	613	A
38	a	614	A
38	a	615	U
38	a	616	A
38	a	618	G
38	a	620	G

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Mol	Chain	Res	Type
38	a	621	A
38	a	627	A
38	a	637	A
38	a	645	C
38	a	647	G
38	a	654	A
38	a	664	G
38	a	668	A
38	a	685	A
38	a	686	U
38	a	710	U
38	a	717	C
38	a	730	A
38	a	738	G
38	a	757	G
38	a	764	A
38	a	765	C
38	a	775	G
38	a	776	G
38	a	782	A
38	a	784	G
38	a	785	G
38	a	800	A
38	a	802	A
38	a	805	G
38	a	812	C
38	a	819	A
38	a	827	U
38	a	828	U
38	a	845	A
38	a	846	U
38	a	858	G
38	a	859	G
38	a	869	G
38	a	878	A
38	a	881	G
38	a	883	G
38	a	884	U
38	a	885	C
38	a	888	C
38	a	891	G
38	a	892	A

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Mol	Chain	Res	Type
38	a	893	C
38	a	895	U
38	a	896	A
38	a	897	C
38	a	899	A
38	a	907	G
38	a	910	A
38	a	914	G
38	a	915	C
38	a	931	U
38	a	941	A
38	a	945	A
38	a	946	C
38	a	953	G
38	a	961	C
38	a	974	G
38	a	983	A
38	a	984	A
38	a	985	C
38	a	995	C
38	a	996	A
38	a	999	U
38	a	1005	C
38	a	1012	U
38	a	1013	C
38	a	1022	G
38	a	1023	U
38	a	1026	G
38	a	1033	U
38	a	1041	G
38	a	1042	G
38	a	1045	C
38	a	1046	A
38	a	1047	G
38	a	1060	U
38	a	1061	U
38	a	1062	G
38	a	1063	G
38	a	1064	C
38	a	1065	U
38	a	1066	U
38	a	1067	A

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Mol	Chain	Res	Type
38	a	1068	G
38	a	1069	A
38	a	1070	A
38	a	1071	G
38	a	1073	A
38	a	1074	G
38	a	1076	C
38	a	1079	C
38	a	1080	A
38	a	1081	U
38	a	1082	U
38	a	1083	U
38	a	1084	A
38	a	1087	G
38	a	1088	A
38	a	1090	A
38	a	1095	A
38	a	1096	A
38	a	1107	G
38	a	1110	G
38	a	1111	A
38	a	1112	G
38	a	1119	U
38	a	1122	G
38	a	1132	U
38	a	1134	A
38	a	1135	C
38	a	1142	A
38	a	1143	A
38	a	1169	A
38	a	1170	C
38	a	1173	U
38	a	1174	U
38	a	1175	A
38	a	1176	U
38	a	1177	G
38	a	1178	C
38	a	1179	G
38	a	1180	U
38	a	1186	G
38	a	1238	G
38	a	1248	G

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Mol	Chain	Res	Type
38	a	1253	A
38	a	1256	G
38	a	1266	G
38	a	1271	G
38	a	1272	A
38	a	1273	U
38	a	1301	A
38	a	1321	A
38	a	1345	C
38	a	1352	U
38	a	1365	A
38	a	1368	G
38	a	1378	A
38	a	1379	U
38	a	1380	G
38	a	1383	A
38	a	1387	A
38	a	1395	A
38	a	1406	U
38	a	1407	G
38	a	1408	G
38	a	1411	U
38	a	1414	C
38	a	1415	U
38	a	1416	G
38	a	1417	C
38	a	1419	A
38	a	1420	A
38	a	1428	C
38	a	1452	G
38	a	1453	A
38	a	1460	U
38	a	1478	G
38	a	1482	G
38	a	1490	A
38	a	1491	G
38	a	1497	U
38	a	1503	A
38	a	1508	A
38	a	1509	A
38	a	1510	G
38	a	1515	A

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Mol	Chain	Res	Type
38	a	1529	G
38	a	1534	U
38	a	1535	A
38	a	1536	C
38	a	1537	G
38	a	1554	U
38	a	1559	U
38	a	1566	A
38	a	1569	A
38	a	1578	U
38	a	1580	A
38	a	1581	G
38	a	1582	C
38	a	1583	A
38	a	1584	U
38	a	1589	U
38	a	1590	A
38	a	1608	A
38	a	1609	A
38	a	1610	A
38	a	1647	U
38	a	1648	U
38	a	1649	G
38	a	1651	G
38	a	1674	G
38	a	1677	A
38	a	1703	G
38	a	1714	U
38	a	1715	G
38	a	1718	G
38	a	1729	U
38	a	1730	C
38	a	1732	C
38	a	1738	G
38	a	1750	G
38	a	1755	A
38	a	1758	U
38	a	1764	C
38	a	1773	A
38	a	1791	A
38	a	1800	C
38	a	1801	A

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Mol	Chain	Res	Type
38	a	1808	A
38	a	1811	G
38	a	1816	C
38	a	1829	A
38	a	1833	C
38	a	1847	A
38	a	1848	A
38	a	1858	A
38	a	1859	U
38	a	1862	G
38	a	1864	U
38	a	1869	G
38	a	1870	C
38	a	1872	A
38	a	1873	G
38	a	1905	C
38	a	1906	G
38	a	1907	G
38	a	1913	A
38	a	1914	C
38	a	1919	A
38	a	1920	C
38	a	1922	G
38	a	1923	U
38	a	1924	C
38	a	1925	C
38	a	1926	U
38	a	1928	A
38	a	1929	G
38	a	1930	G
38	a	1936	A
38	a	1938	A
38	a	1955	U
38	a	1965	C
38	a	1967	C
38	a	1970	A
38	a	1971	U
38	a	1972	G
38	a	1987	A
38	a	1991	U
38	a	1992	G
38	a	1993	U

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Mol	Chain	Res	Type
38	a	1997	C
38	a	2002	G
38	a	2022	U
38	a	2023	C
38	a	2027	G
38	a	2033	A
38	a	2043	C
38	a	2051	A
38	a	2052	A
38	a	2055	C
38	a	2056	G
38	a	2060	A
38	a	2061	G
38	a	2062	A
38	a	2063	C
38	a	2077	A
38	a	2097	A
38	a	2099	U
38	a	2100	G
38	a	2108	A
38	a	2110	G
38	a	2111	U
38	a	2113	U
38	a	2115	G
38	a	2116	G
38	a	2117	A
38	a	2118	U
38	a	2121	G
38	a	2122	U
38	a	2124	G
38	a	2125	G
38	a	2126	A
38	a	2127	G
38	a	2128	G
38	a	2131	U
38	a	2132	U
38	a	2133	G
38	a	2134	A
38	a	2139	U
38	a	2141	G
38	a	2146	C
38	a	2147	A

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Mol	Chain	Res	Type
38	a	2154	A
38	a	2157	G
38	a	2158	A
38	a	2159	G
38	a	2162	G
38	a	2163	A
38	a	2164	C
38	a	2165	C
38	a	2169	A
38	a	2171	A
38	a	2172	U
38	a	2178	C
38	a	2182	U
38	a	2183	A
38	a	2185	U
38	a	2188	U
38	a	2189	U
38	a	2190	G
38	a	2191	A
38	a	2193	G
38	a	2194	U
38	a	2198	A
38	a	2204	G
38	a	2210	U
38	a	2211	A
38	a	2212	A
38	a	2213	U
38	a	2225	A
38	a	2226	C
38	a	2229	U
38	a	2238	G
38	a	2239	G
38	a	2244	U
38	a	2250	G
38	a	2268	A
38	a	2278	A
38	a	2283	C
38	a	2287	A
38	a	2297	A
38	a	2305	U
38	a	2308	G
38	a	2309	A

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Mol	Chain	Res	Type
38	a	2315	G
38	a	2322	A
38	a	2325	G
38	a	2327	A
38	a	2333	A
38	a	2339	C
38	a	2345	G
38	a	2347	C
38	a	2350	C
38	a	2361	G
38	a	2372	U
38	a	2376	A
38	a	2383	G
38	a	2385	C
38	a	2402	U
38	a	2403	C
38	a	2406	A
38	a	2423	U
38	a	2424	C
38	a	2425	A
38	a	2426	A
38	a	2429	G
38	a	2430	A
38	a	2431	U
38	a	2434	A
38	a	2435	A
38	a	2441	U
38	a	2447	G
38	a	2448	A
38	a	2470	G
38	a	2474	U
38	a	2476	A
38	a	2478	A
38	a	2484	G
38	a	2491	U
38	a	2502	G
38	a	2506	U
38	a	2507	C
38	a	2512	C
38	a	2513	A
38	a	2518	A
38	a	2520	C

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Mol	Chain	Res	Type
38	a	2525	G
38	a	2529	G
38	a	2535	G
38	a	2547	A
38	a	2554	U
38	a	2566	A
38	a	2567	G
38	a	2572	A
38	a	2573	C
38	a	2574	G
38	a	2585	U
38	a	2586	U
38	a	2602	A
38	a	2603	G
38	a	2609	U
38	a	2610	C
38	a	2611	C
38	a	2613	U
38	a	2629	U
38	a	2663	G
38	a	2669	G
38	a	2671	G
38	a	2689	U
38	a	2690	U
38	a	2714	G
38	a	2722	G
38	a	2726	A
38	a	2744	G
38	a	2748	A
38	a	2757	A
38	a	2758	A
38	a	2765	A
38	a	2777	G
38	a	2778	A
38	a	2791	G
38	a	2793	C
38	a	2796	U
38	a	2797	U
38	a	2798	U
38	a	2799	A
38	a	2801	G
38	a	2818	U

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Mol	Chain	Res	Type
38	a	2820	A
38	a	2823	A
38	a	2825	G
38	a	2849	U
38	a	2850	A
38	a	2859	G
38	a	2861	U
38	a	2867	G
38	a	2880	C
38	a	2884	U
38	a	2885	G
38	a	2891	U
38	a	2902	C
41	d	2	G
41	d	9	G
41	d	13	G
41	d	16	G
41	d	17	C
41	d	35	C
41	d	36	C
41	d	45	A
41	d	51	G
41	d	56	G
41	d	64	G
41	d	66	A
41	d	88	C
41	d	89	U
41	d	90	C
41	d	99	A
41	d	109	A

All (47) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	6	G
9	A	7	G
9	A	9	G
9	A	22	G
9	A	60	U
9	A	70	G
9	B	6	G
9	B	7	G

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Mol	Chain	Res	Type
9	B	9	G
9	B	22	G
9	B	37	A
9	B	60	U
16	D	7	A
16	D	70	U
16	D	121	U
16	D	181	A
16	D	183	C
16	D	197	A
16	D	209	U
16	D	305	G
16	D	328	C
16	D	428	G
16	D	496	A
16	D	517	G
16	D	531	U
16	D	532	A
16	D	562	U
16	D	641	U
16	D	722	G
16	D	793	U
16	D	991	U
16	D	992	U
16	D	1109	C
16	D	1145	A
16	D	1196	A
16	D	1211	U
16	D	1212	U
16	D	1213	A
16	D	1214	C
16	D	1225	A
16	D	1299	A
16	D	1396	A
16	D	1432	G
16	D	1447	A
16	D	1491	G
16	D	1492	A
16	D	1493	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

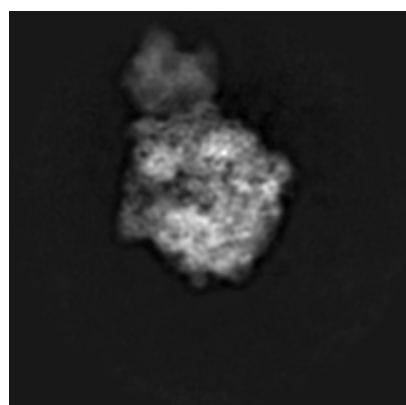
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21486. These allow visual inspection of the internal detail of the map and identification of artifacts.

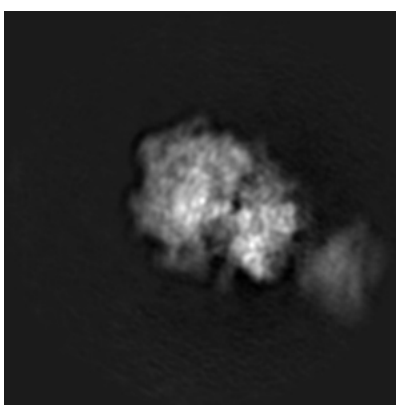
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

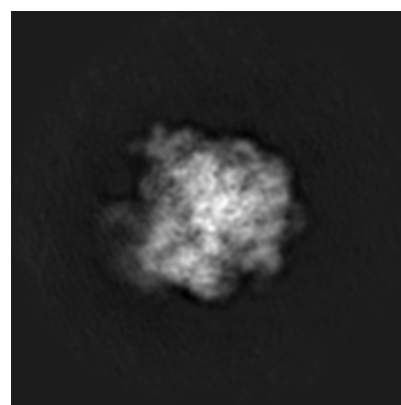
6.1.1 Primary map



X



Y

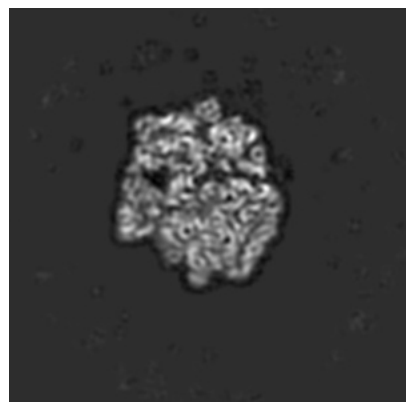


Z

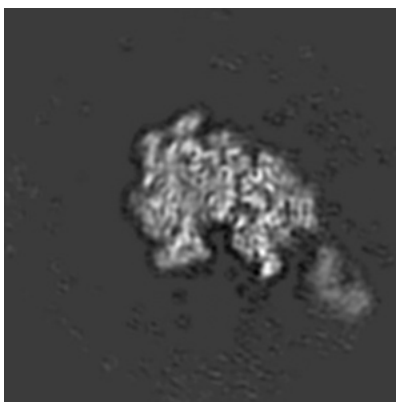
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

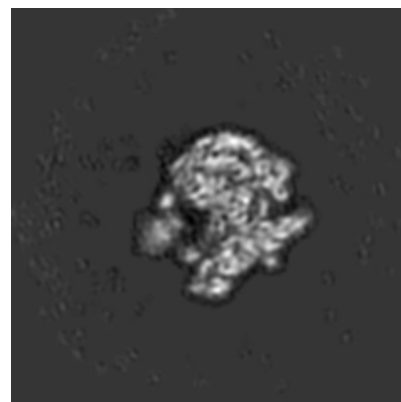
6.2.1 Primary map



X Index: 140



Y Index: 140

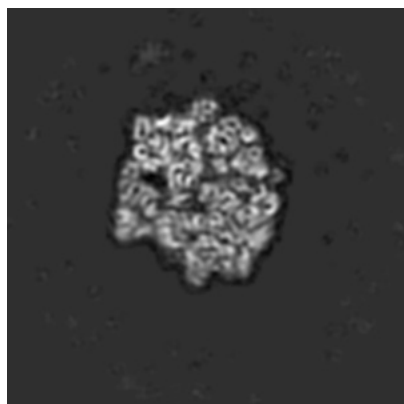


Z Index: 140

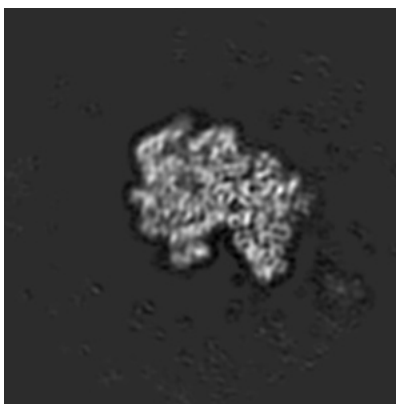
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

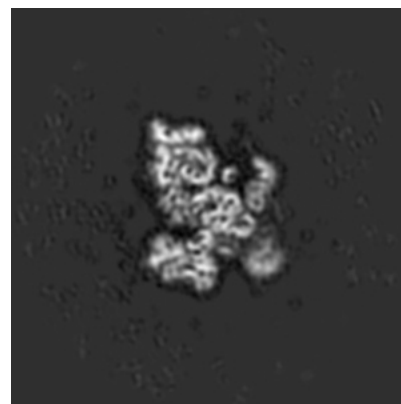
6.3.1 Primary map



X Index: 137



Y Index: 147

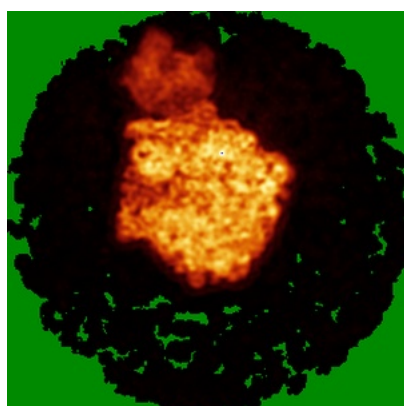


Z Index: 169

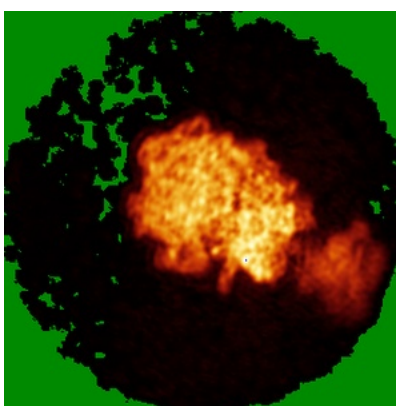
The images above show the largest variance slices of the map in three orthogonal directions.

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

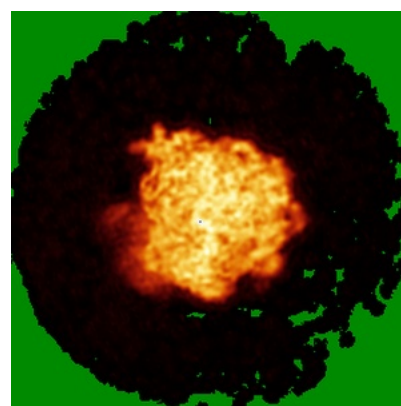
6.4.1 Primary map



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

6.5.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

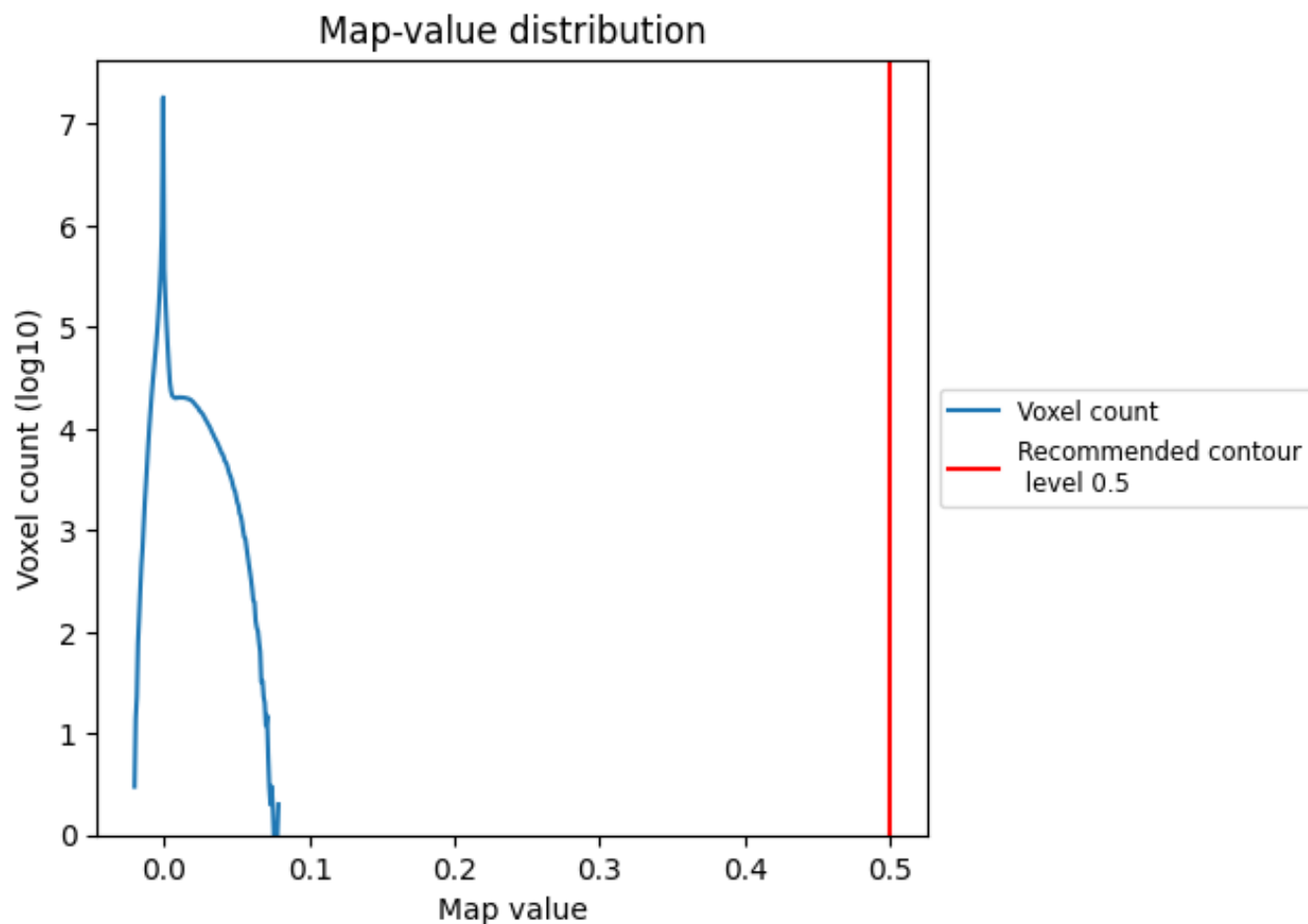
6.6 Mask visualisation

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

7 Map analysis [i](#)

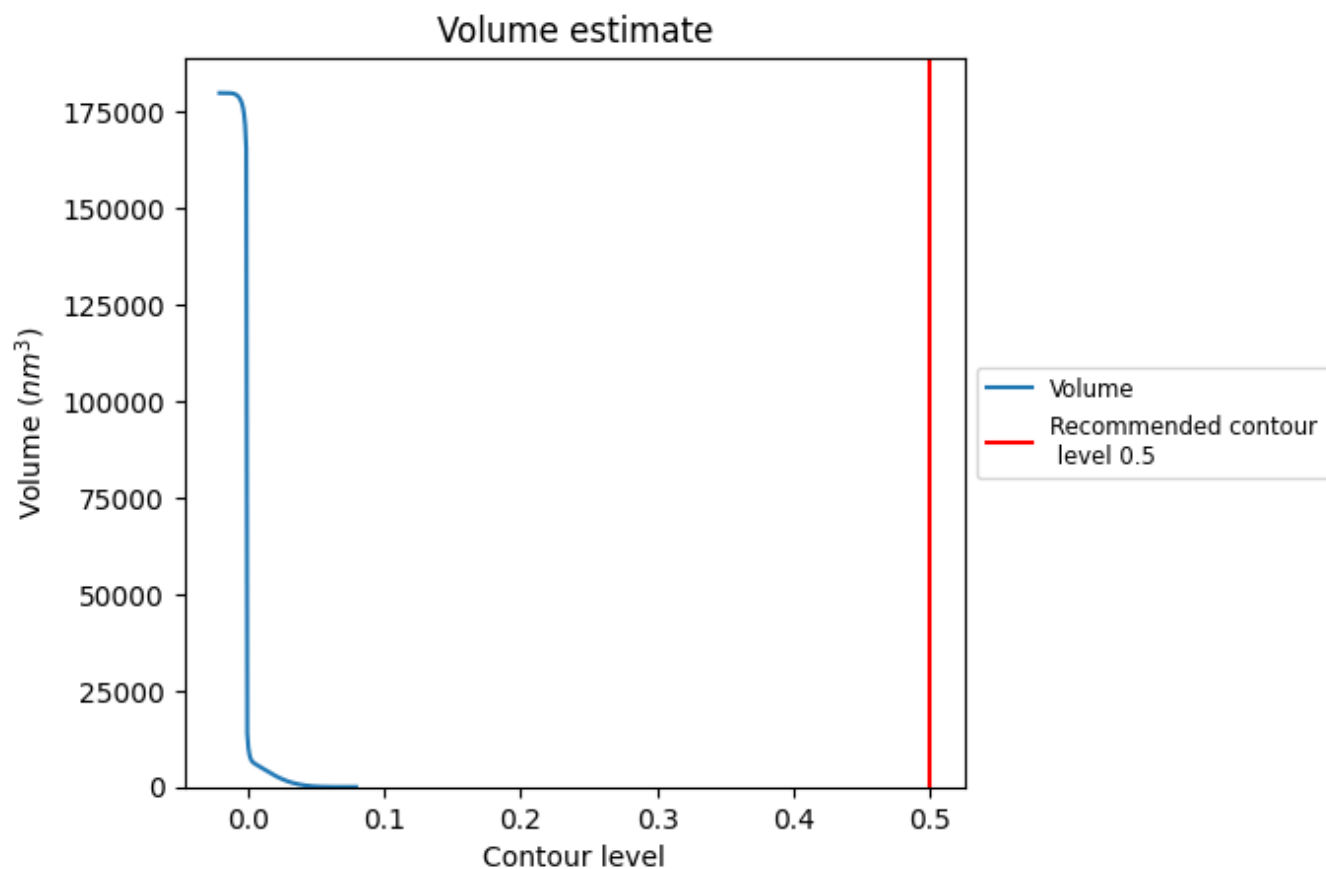
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



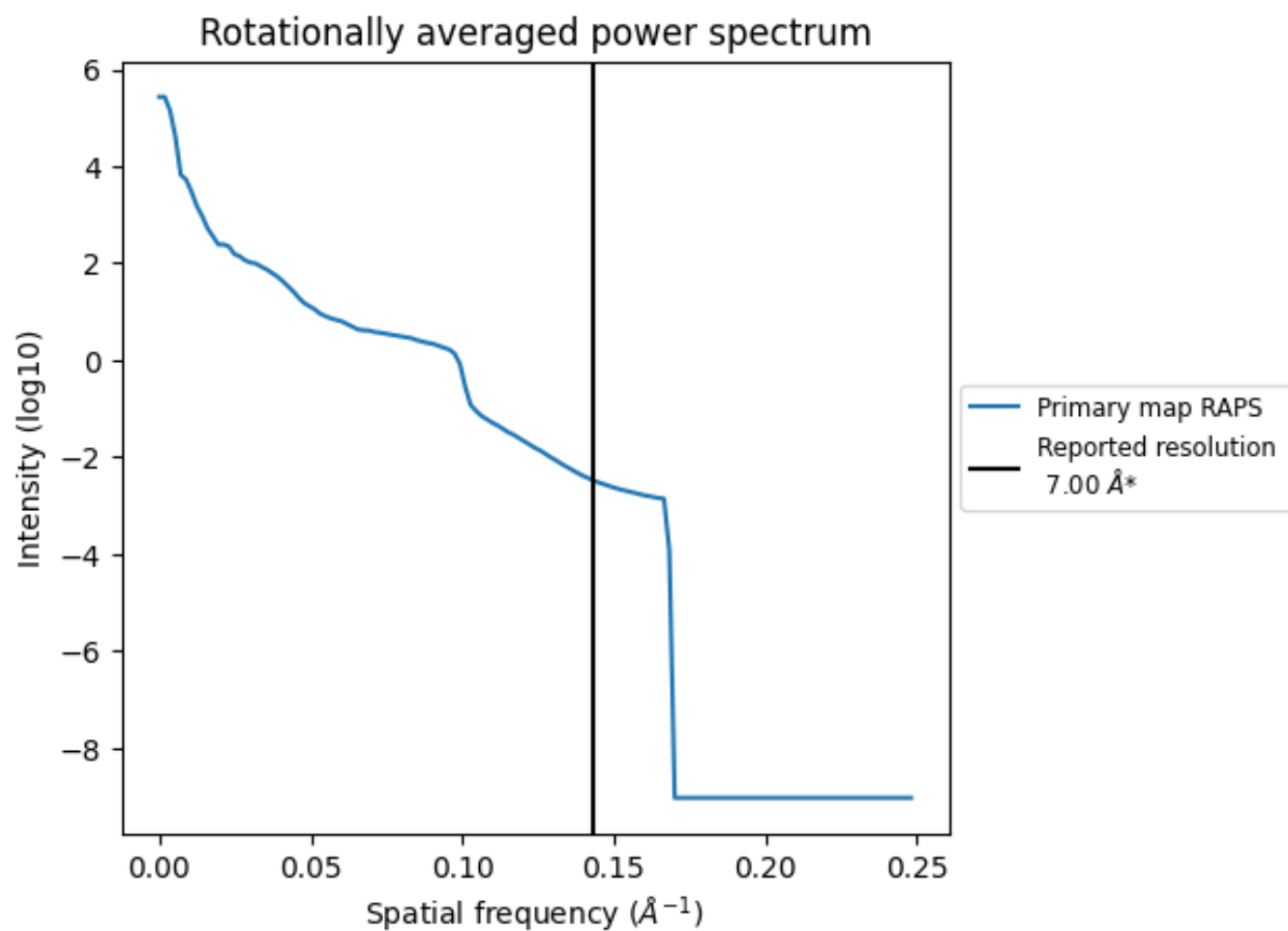
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate [i](#)



The volume 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 0.143 Å⁻¹

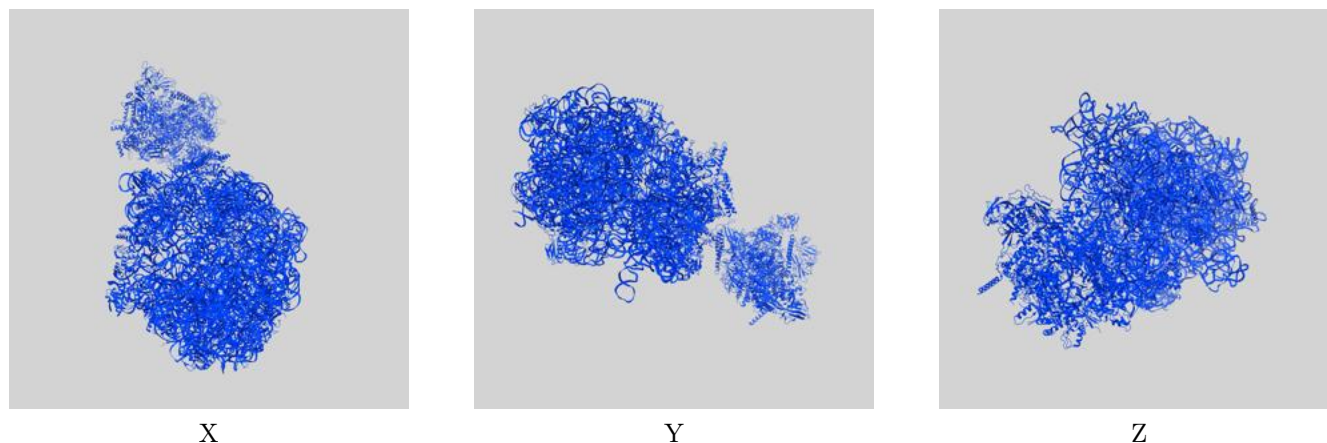
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

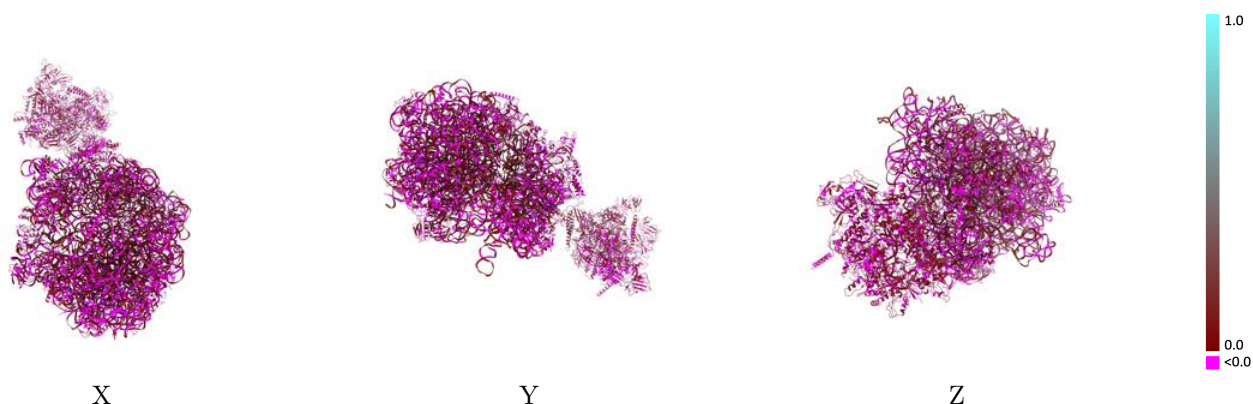
This section contains information regarding the fit between EMDB map EMD-21486 and PDB model 6VZ7. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



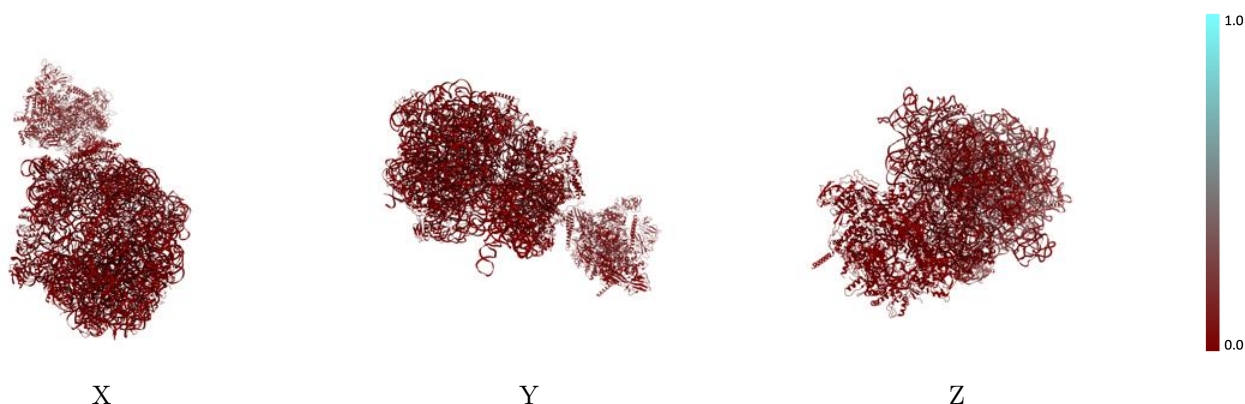
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



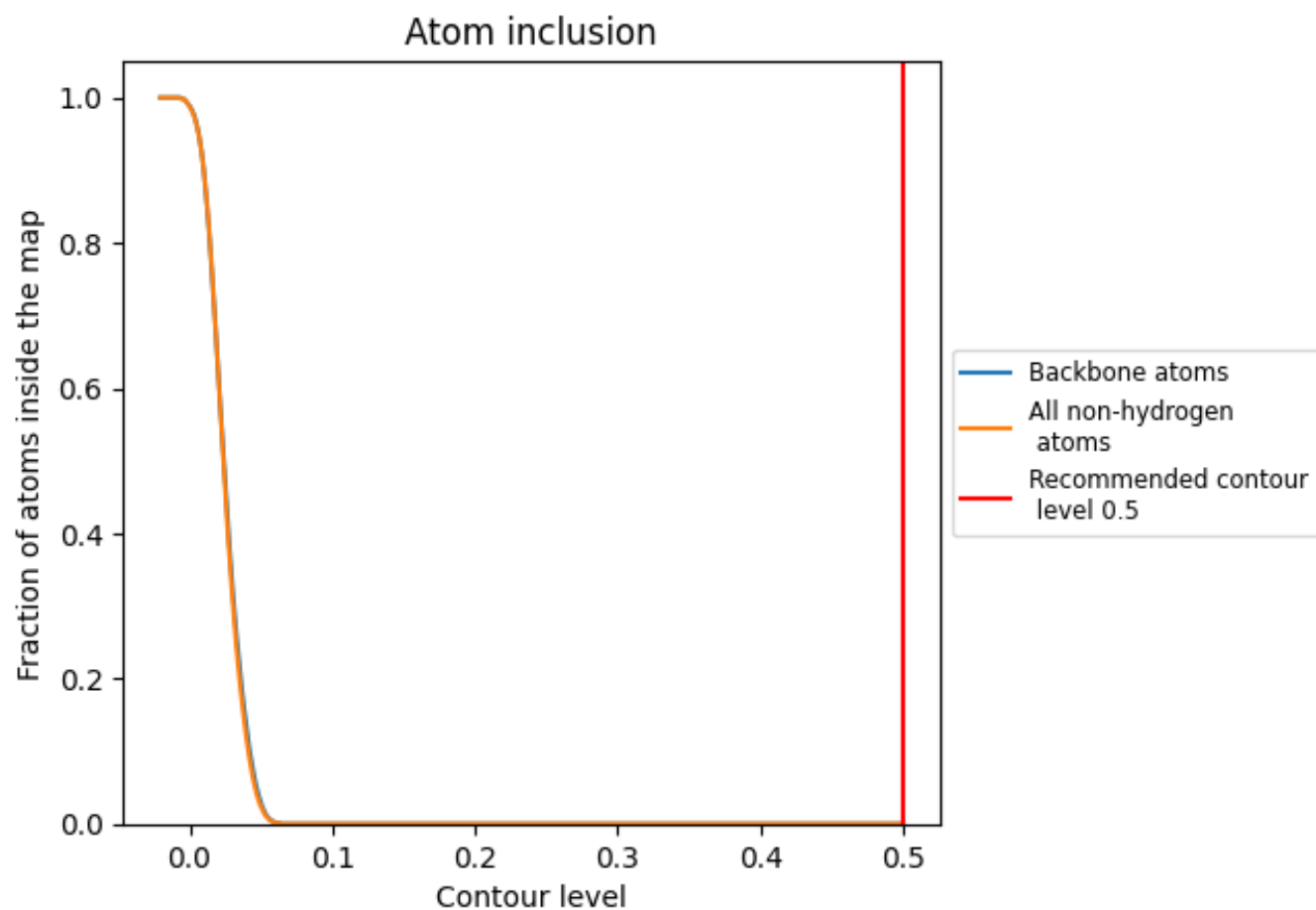
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 0% of all backbone atoms, 0% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0000	0.0300
0	0.0000	0.0020
1	0.0000	0.0080
2	0.0000	-0.0330
3	0.0000	-0.0130
4	0.0000	-0.0030
5	0.0000	0.0950
6	0.0000	0.0900
7	0.0000	0.0580
A	0.0000	0.0900
AA	0.0000	0.0590
AB	0.0000	-0.0250
AC	0.0000	0.0180
AD	0.0000	-0.0080
AE	0.0000	0.0240
AF	0.0000	0.0100
B	0.0000	0.0390
C	0.0000	-0.0340
D	0.0000	0.0480
E	0.0000	-0.0150
F	0.0000	0.0690
G	0.0000	-0.0150
H	0.0000	0.0120
I	0.0000	-0.0090
J	0.0000	-0.0300
K	0.0000	0.0230
L	0.0000	0.0250
M	0.0000	-0.0080
N	0.0000	-0.0380
O	0.0000	-0.0220
P	0.0000	0.0170
Q	0.0000	0.0100
R	0.0000	0.0630
S	0.0000	-0.0070
T	0.0000	0.0160



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Chain	Atom inclusion	Q-score
U	 0.0000	 -0.0240
V	 0.0000	 0.0350
W	 0.0000	 -0.0100
X	 0.0000	 -0.0140
Y	 0.0000	 0.1350
a	 0.0000	 0.0430
b	 0.0000	 -0.0530
c	 0.0000	 0.0060
d	 0.0000	 0.0100
e	 0.0000	 -0.0190
f	 0.0000	 -0.0020
g	 0.0000	 0.0100
h	 0.0000	 0.0360
i	 0.0000	 -0.0340
j	 0.0000	 -0.0180
k	 0.0000	 -0.0000
l	 0.0000	 -0.0020
m	 0.0000	 -0.0210
n	 0.0000	 0.0070
o	 0.0000	 -0.0420
p	 0.0000	 0.0130
q	 0.0000	 -0.0130
r	 0.0000	 -0.0370
s	 0.0000	 -0.0310
t	 0.0000	 0.0190
u	 0.0000	 -0.0080
v	 0.0000	 0.0330
w	 0.0000	 -0.0340
x	 0.0000	 -0.0130
y	 0.0000	 -0.0280
z	 0.0000	 -0.0350