



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 12:09 PM UTC

PDB ID : 7QWS / pdb_00007qws
EMDB ID : EMD-14193
Title : Structure of ribosome translating beta-tubulin in complex with TTC5 and NAC
Authors : Jomaa, A.; Gamerdinger, M.; Hsieh, H.; Wallisch, A.; Chandrasekaran, V.; Ulusoy, Z.; Scaiola, A.; Hegde, R.; Shan, S.; Ban, N.; Deuerling, E.
Deposited on : 2022-01-25
Resolution : 3.40 Å (reported)
Based on initial model : 7OBR

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

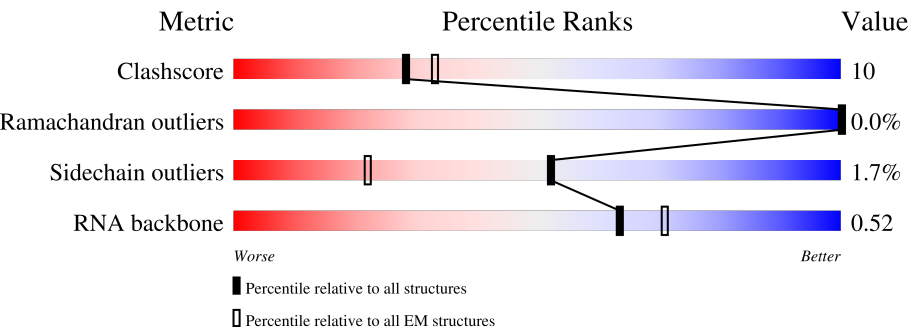
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	s	24	100% 100%
2	t	215	30% 28% 69%
3	u	162	65% 52% 14% 33%
4	A	245	87% 72% 27%
5	b	223	25% 28% 5% 66%
6	B	403	78% 70% 26% ..
7	c	115	63% 66% 16% 18%

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Mol	Chain	Length	Quality of chain
8	C	413	
9	d	125	
10	D	297	
11	e	157	
12	E	291	
13	f	110	
14	F	225	
15	g	129	
16	G	319	
17	h	123	
18	H	192	
19	i	102	
20	I	214	
21	j	97	
22	J	178	
23	k	69	
24	L	210	
25	l	51	
26	M	218	
27	m	128	
28	N	204	
29	n	25	
30	O	500	
31	o	141	
32	P	153	

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Mol	Chain	Length	Quality of chain
33	p	92	75% 86%13%
34	Q	187	83% 75%24%
35	r	137	73% 66%25%9%
36	R	196	73% 67%24%8%
37	S	175	79% 75%25%
38	T	160	82% 84%15%
39	U	105	68% 82%15%
40	V	140	82% 75%18%6%
41	W	157	34% 33%7%60%
42	5	4754	47% 33%33%7%27%
43	X	156	62% 69%8%24%
44	7	120	35% 58%36%7%
45	Y	145	74% 75%17%8%
46	8	156	68% 46%46%8%
47	K	440	88% 81%16%
48	Z	136	71% 77%22%
49	a	148	76% 72%27%

2 Entry composition [i](#)

There are 51 unique types of molecules in this entry. The entry contains 137913 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Nascent chain tubulin beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	s	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 2 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	t	67	Total	C	N	O	S	0	0
			531	335	97	98	1		

- Molecule 3 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	u	108	Total	C	N	O	S	0	0
			837	523	155	156	3		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	LYS	-	insertion	UNP A0A5F9D5B2
A	47	ASP	-	insertion	UNP A0A5F9D5B2
A	48	ILE	-	insertion	UNP A0A5F9D5B2
A	49	ILE	-	insertion	UNP A0A5F9D5B2
A	50	HIS	-	insertion	UNP A0A5F9D5B2
A	51	ASP	-	insertion	UNP A0A5F9D5B2
A	52	PRO	-	insertion	UNP A0A5F9D5B2
A	53	GLY	-	insertion	UNP A0A5F9D5B2
A	54	ARG	-	insertion	UNP A0A5F9D5B2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	55	GLY	-	insertion	UNP A0A5F9D5B2
A	56	ALA	-	insertion	UNP A0A5F9D5B2
A	57	PRO	-	insertion	UNP A0A5F9D5B2
A	58	LEU	-	insertion	UNP A0A5F9D5B2
A	59	ALA	-	insertion	UNP A0A5F9D5B2
A	60	LYS	-	insertion	UNP A0A5F9D5B2
A	61	VAL	-	insertion	UNP A0A5F9D5B2
A	62	VAL	-	insertion	UNP A0A5F9D5B2
A	63	PHE	-	insertion	UNP A0A5F9D5B2
A	64	ARG	-	insertion	UNP A0A5F9D5B2
A	65	ASP	-	insertion	UNP A0A5F9D5B2
A	66	PRO	-	insertion	UNP A0A5F9D5B2
A	67	TYR	-	insertion	UNP A0A5F9D5B2
A	68	ARG	-	insertion	UNP A0A5F9D5B2
A	69	PHE	-	insertion	UNP A0A5F9D5B2

- Molecule 5 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b	75	Total	C	N	O	S	0	0
			609	378	130	98	3		

- Molecule 6 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	394	Total	C	N	O	S	0	0
			3148	2007	591	537	13		

- Molecule 7 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	34	THR	SER	conflict	UNP G1TDL2

- Molecule 8 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 9 is a protein called Ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 10 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	292	Total	C	N	O	S	0	0
			2386	1509	437	426	14		

- Molecule 11 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 12 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	236	Total	C	N	O	S	0	0
			1898	1215	362	318	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	126	ARG	LYS	conflict	UNP G1SKF7
E	217	GLN	LYS	conflict	UNP G1SKF7

- Molecule 13 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 14 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	175	ALA	THR	conflict	UNP G1SV32
F	185	GLY	ASN	conflict	UNP G1SV32
F	202	ARG	HIS	conflict	UNP G1SV32
F	233	GLU	GLY	conflict	UNP G1SV32

- Molecule 15 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 16 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	241	Total	C	N	O	S	0	0
			1934	1233	371	326	4		

- Molecule 17 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 18 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 19 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 20 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	I	204	Total	C	N	O	S	0	0
			1655	1051	319	272	13		

- Molecule 21 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 22 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	J	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 23 is a protein called Ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 24 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	210	Total	C	N	O	S	0	0
			1703	1065	354	280	4		

- Molecule 25 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 26 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 27 is a protein called Ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 28 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 29 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 30 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	O	199	Total	C	N	O	S	0	0
			1638	1056	321	256	5		

- Molecule 31 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 32 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 33 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 34 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 35 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	r	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 36 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 37 is a protein called Ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 38 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 39 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	U	105	Total	C	N	O	S	0	0
			859	547	150	160	2		

- Molecule 40 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 41 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 42 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5	3493	Total	C	N	O	P	0	0
			74854	33335	13681	24346	3492		

- Molecule 43 is a protein called Ribosomal_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 44 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 45 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 46 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 47 is a protein called Tetratricopeptide repeat protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	K	426	Total	C	N	O	S	0	0
			3337	2097	580	647	13		

- Molecule 48 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 49 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	-	initiating methionine	UNP G1SNY0

- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
50	g	1	Total	Zn	0
			1	1	
50	j	1	Total	Zn	0
			1	1	
50	m	1	Total	Zn	0
			1	1	
50	o	1	Total	Zn	0
			1	1	
50	p	1	Total	Zn	0
			1	1	

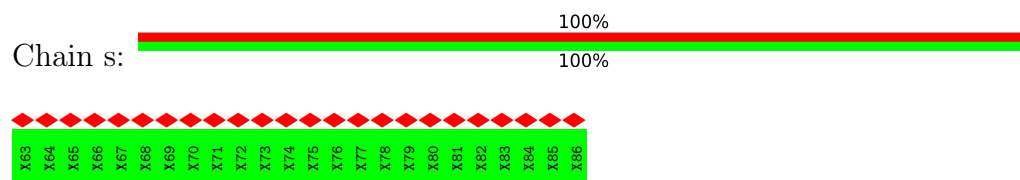
- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	5	97	Total	Mg	0
			97	97	

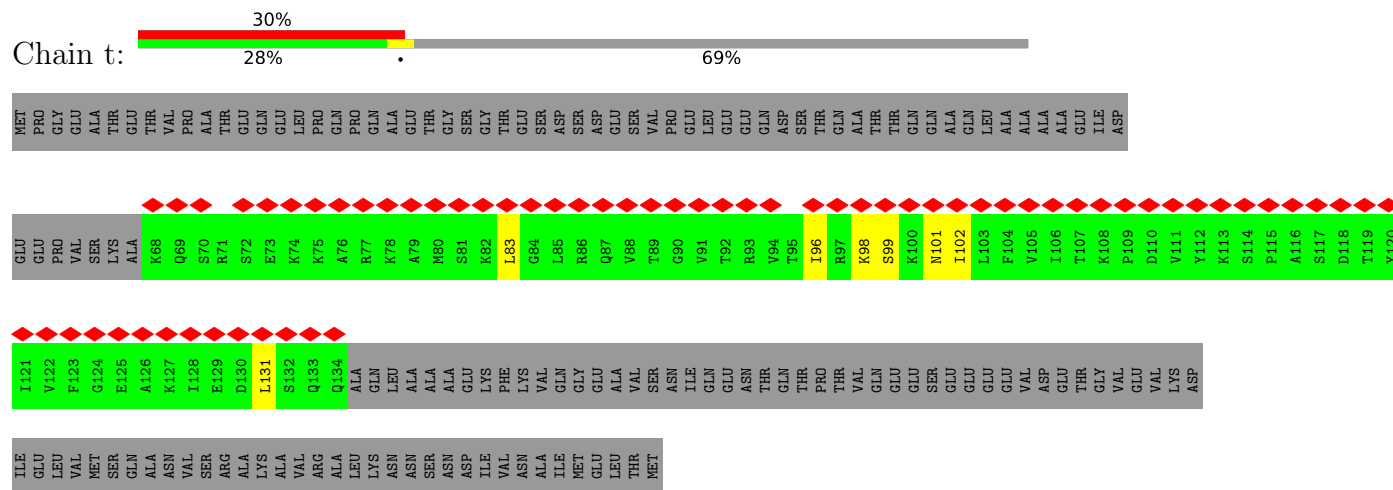
3 Residue-property plots

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.

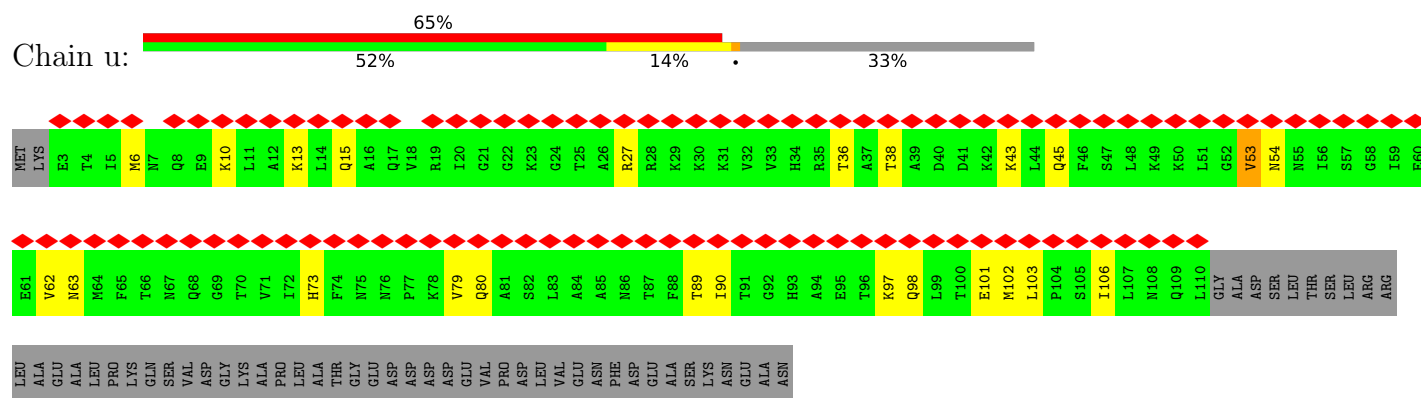
- Molecule 1: Nascent chain tubulin beta



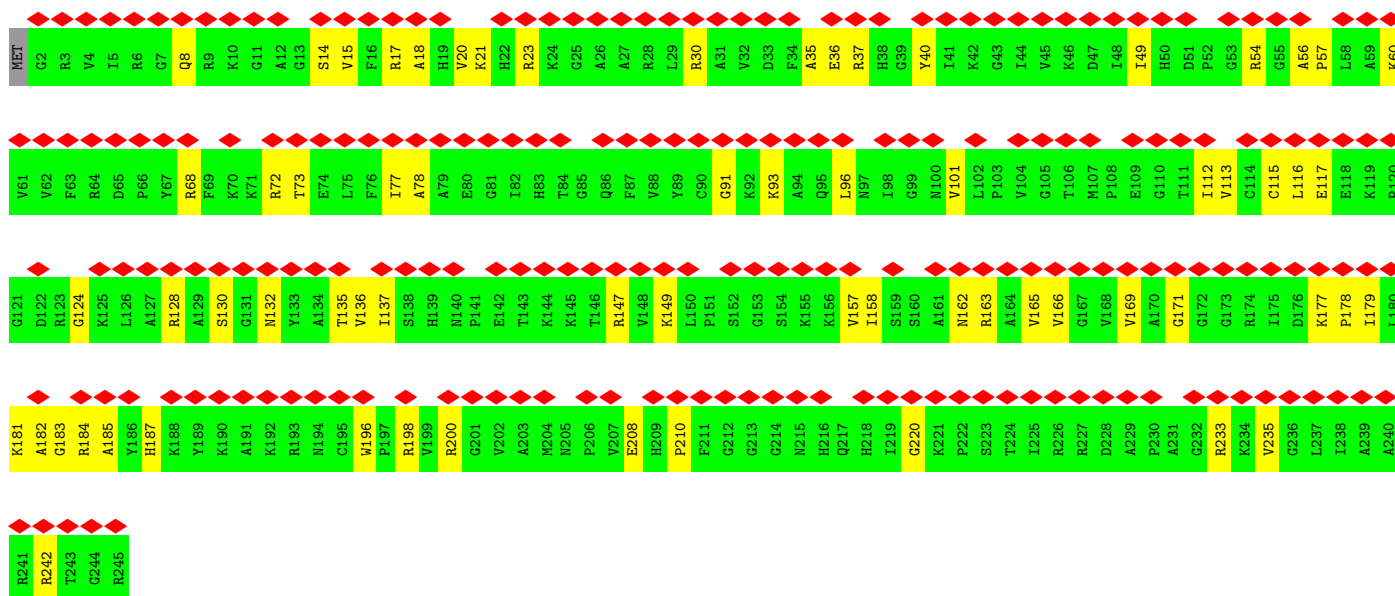
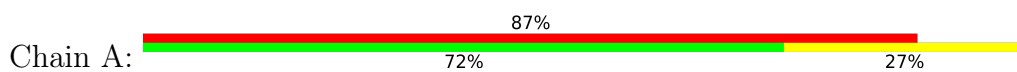
- Molecule 2: Nascent polypeptide-associated complex subunit alpha



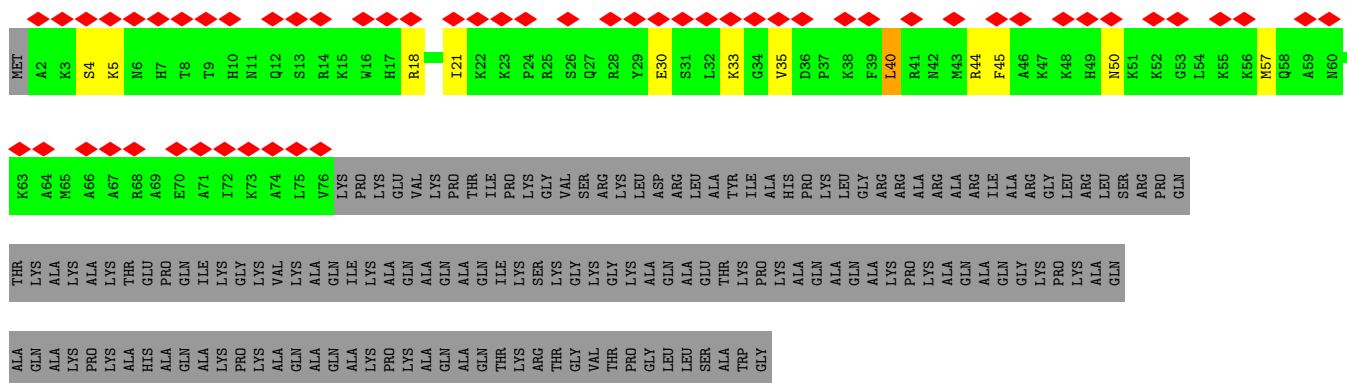
- Molecule 3: Transcription factor BTF3



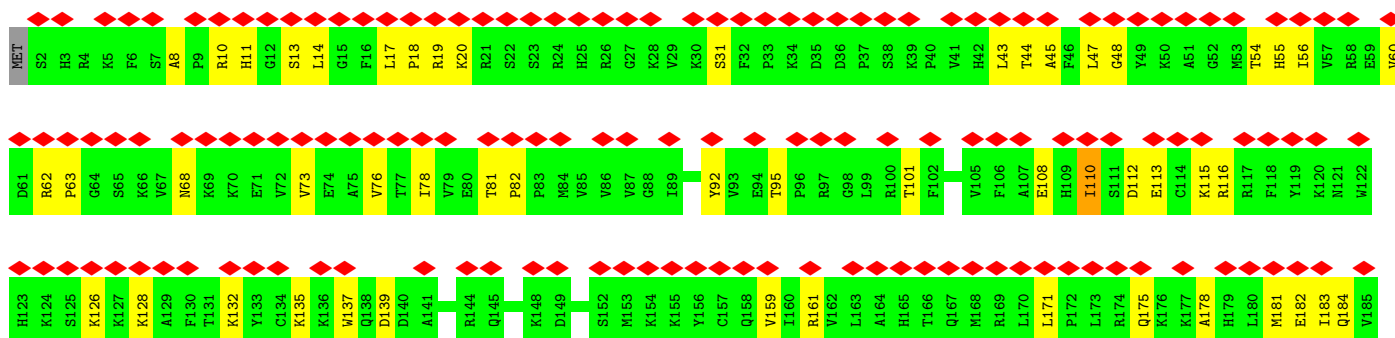
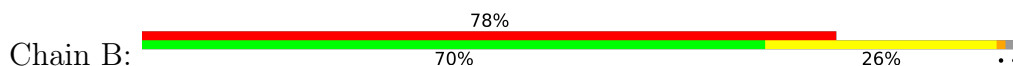
- Molecule 4: 60S ribosomal protein L8

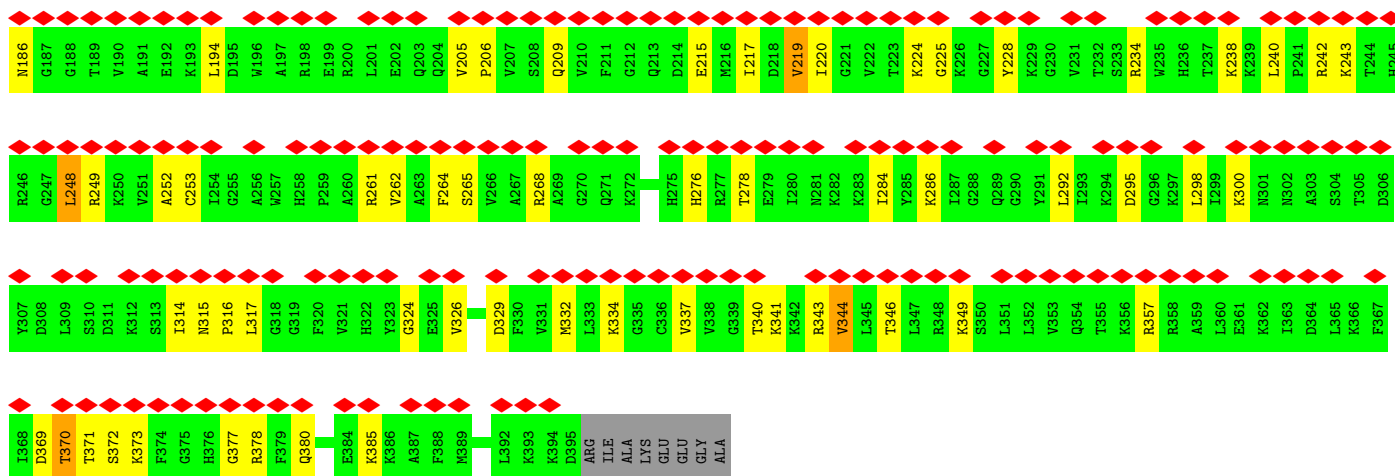


• Molecule 5: 60S ribosomal protein L29

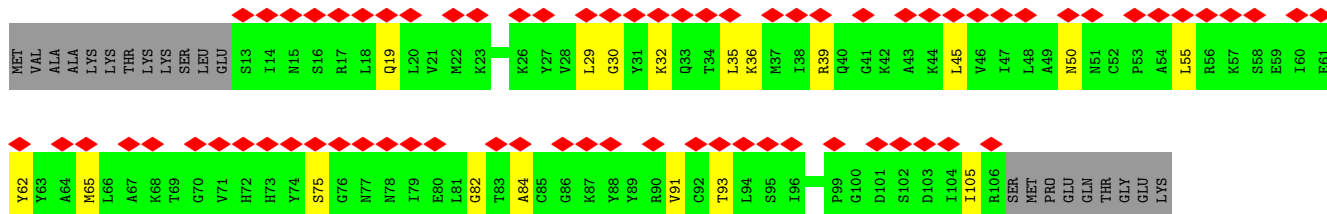


• Molecule 6: Ribosomal protein L3

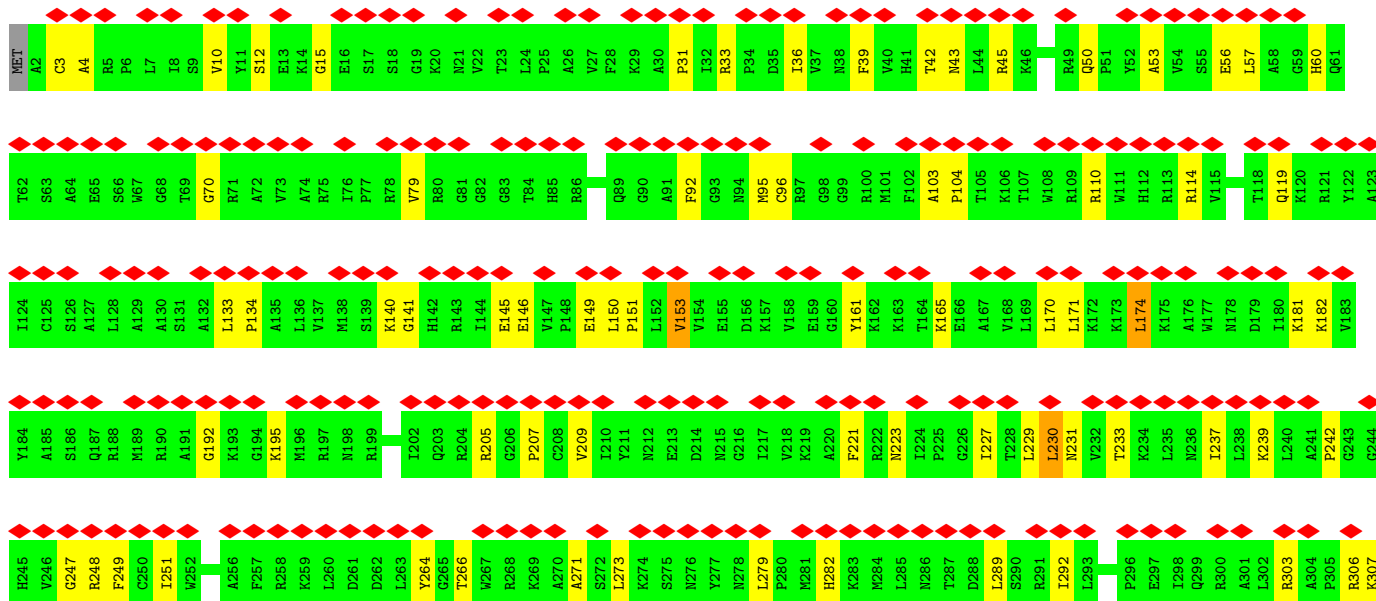


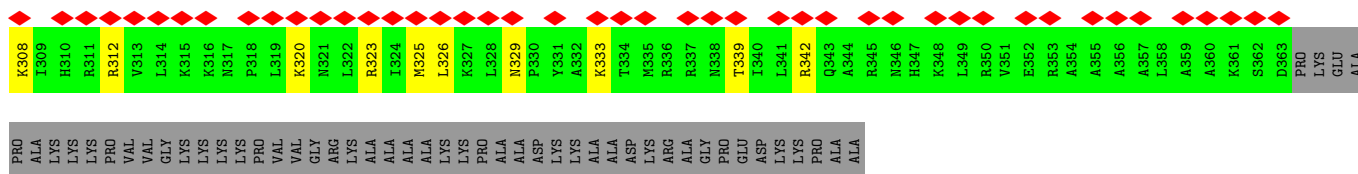


• Molecule 7: 60S ribosomal protein L30



• Molecule 8: 60S ribosomal protein L4

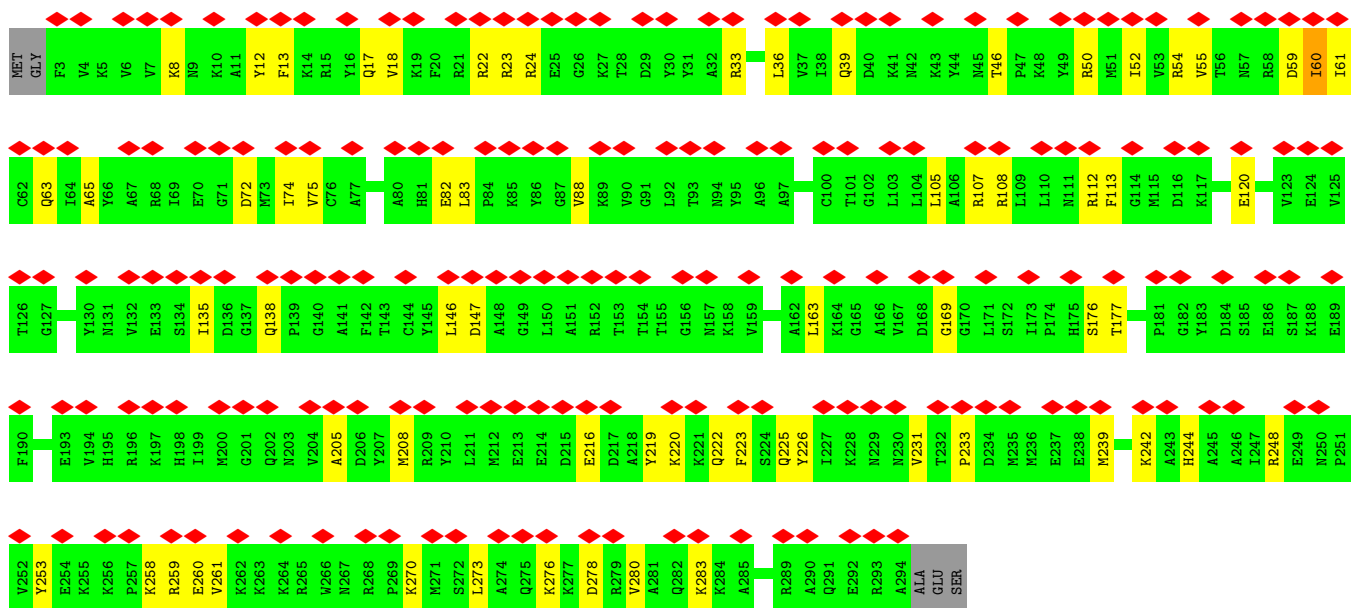
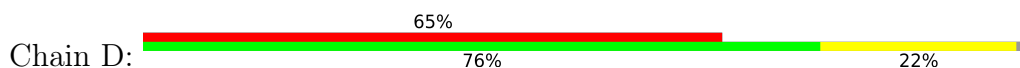




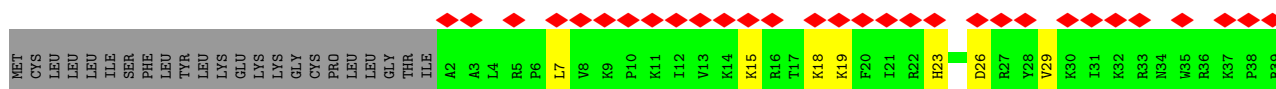
• Molecule 9: Ribosomal protein L31

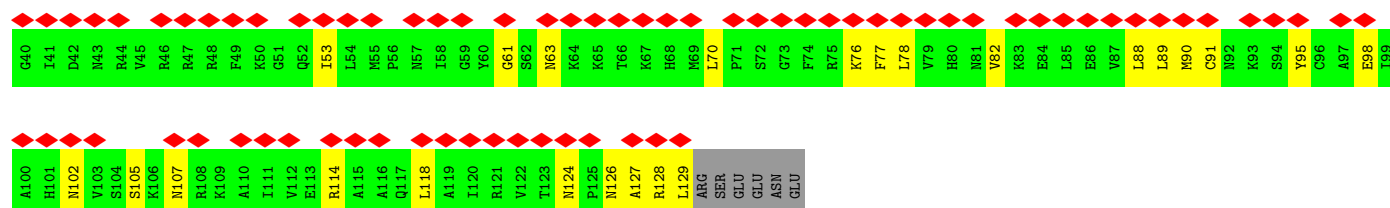


• Molecule 10: Ribosomal_L18_c domain-containing protein

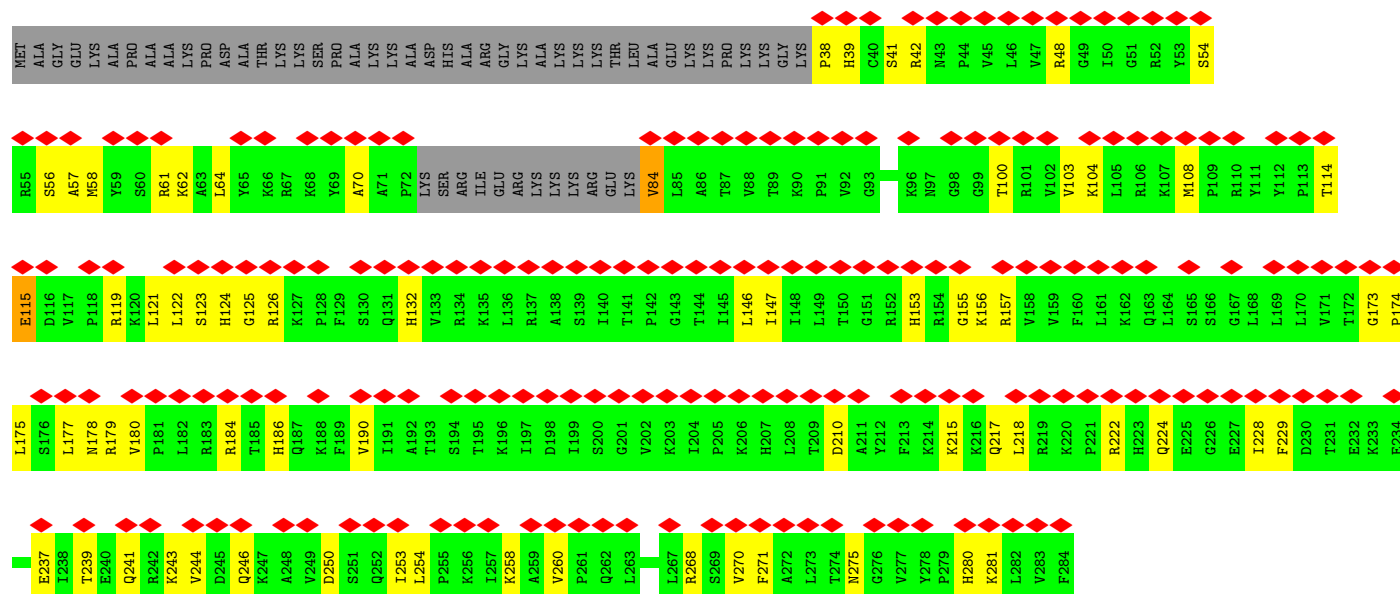


• Molecule 11: Ribosomal protein L32

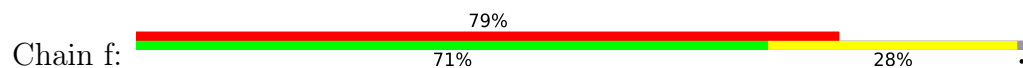




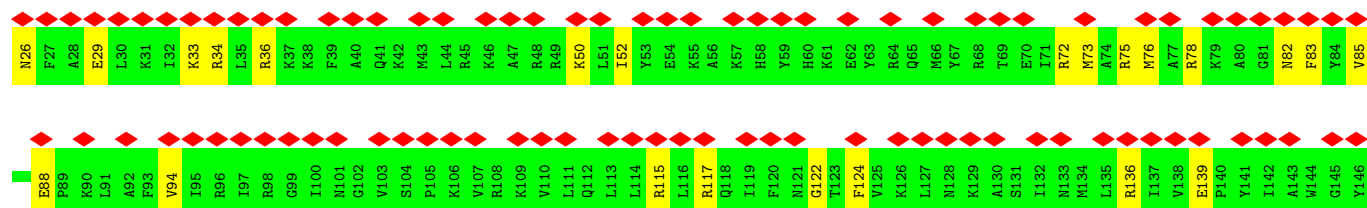
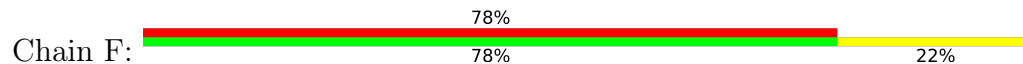
• Molecule 12: 60S ribosomal protein L6

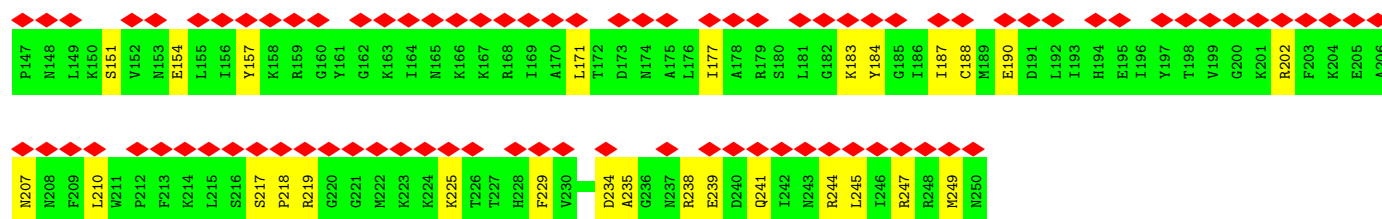


• Molecule 13: 60S ribosomal protein L35a

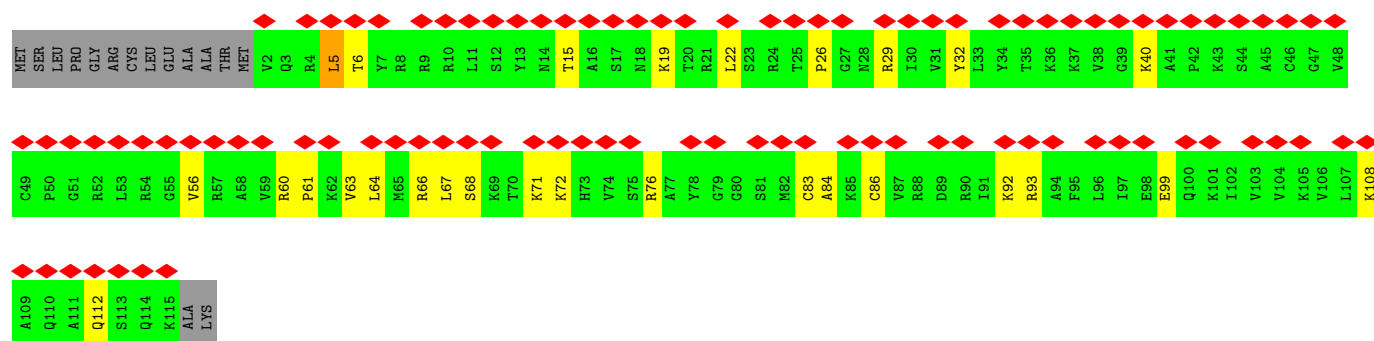
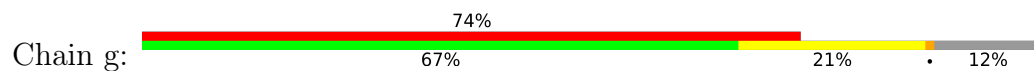


• Molecule 14: uL30

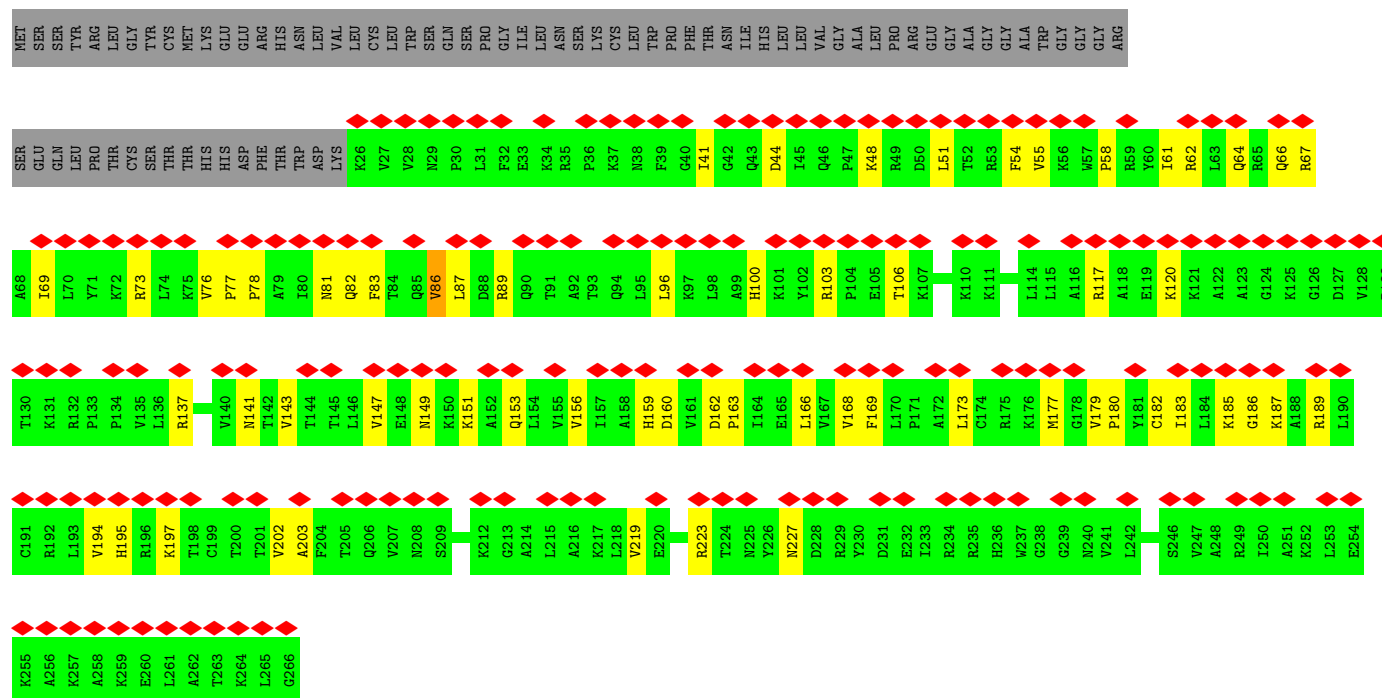




• Molecule 15: 60S ribosomal protein L34

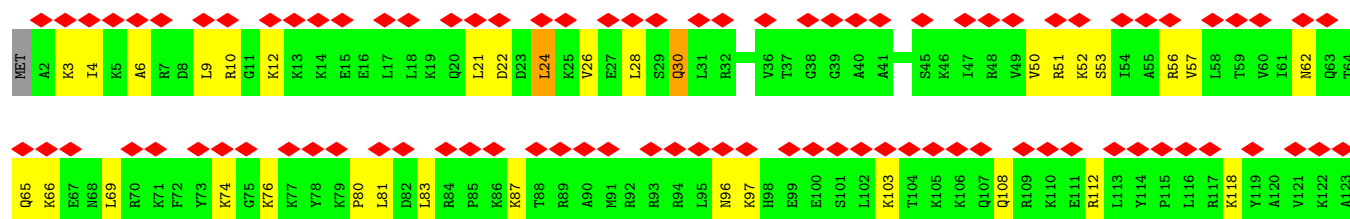


• Molecule 16: 60S ribosomal protein L7a

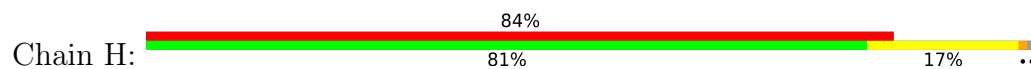


• Molecule 17: 60S ribosomal protein L35

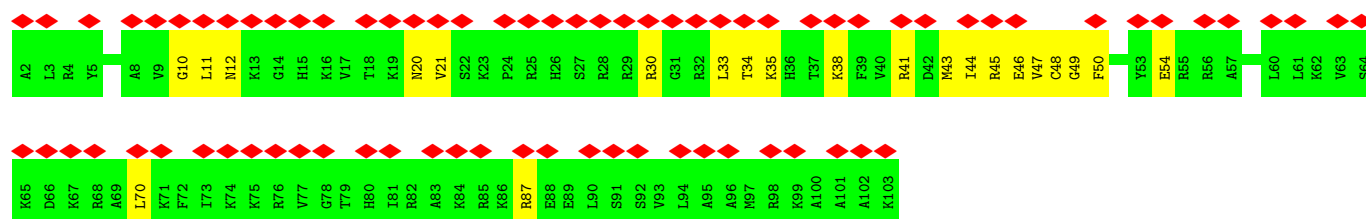
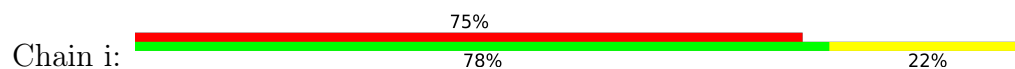




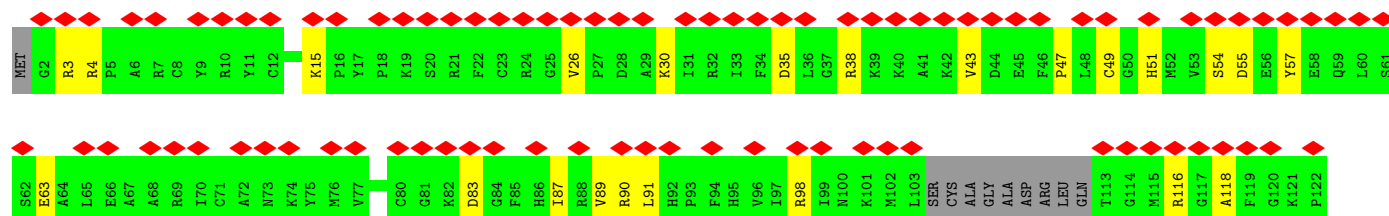
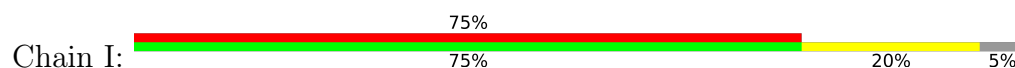
• Molecule 18: 60S ribosomal protein L9

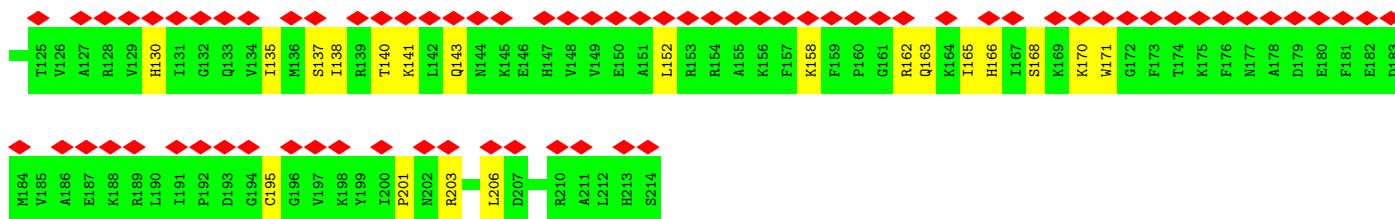


• Molecule 19: 60S ribosomal protein L36

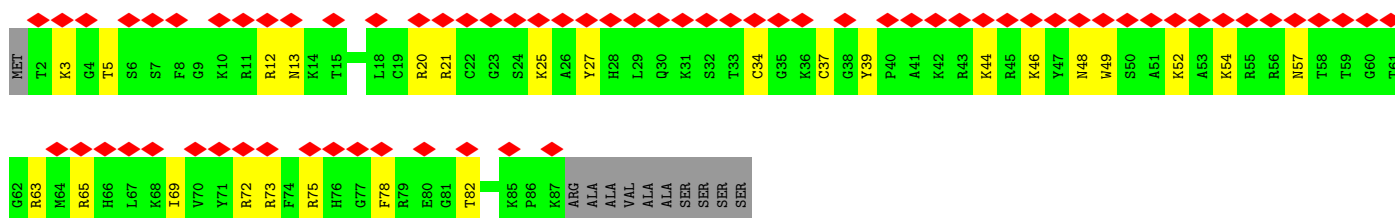


• Molecule 20: 60S ribosomal protein L10

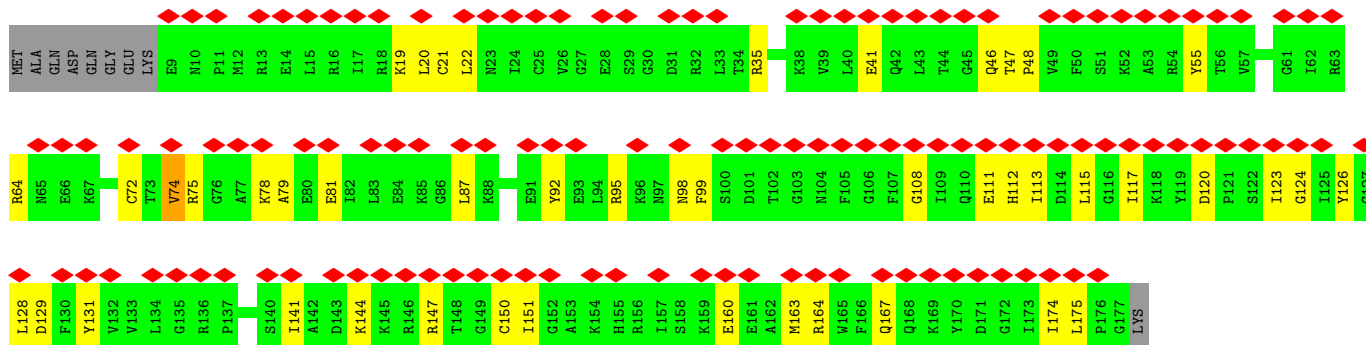




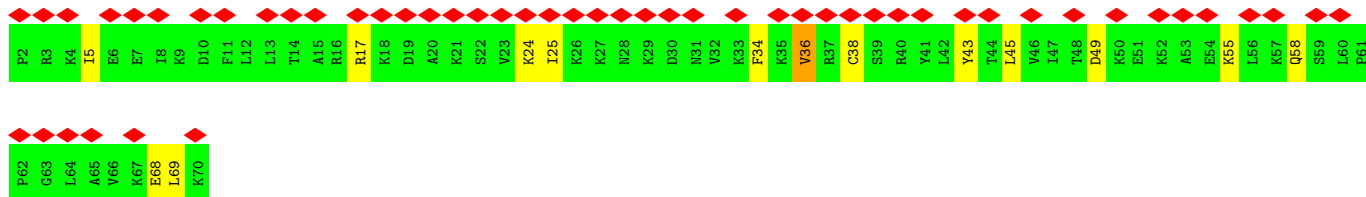
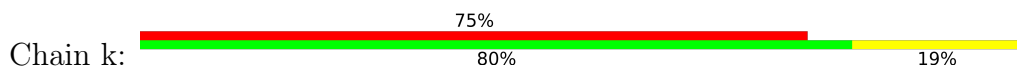
• Molecule 21: Ribosomal protein L37



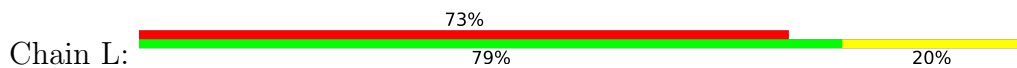
• Molecule 22: Ribosomal protein L11

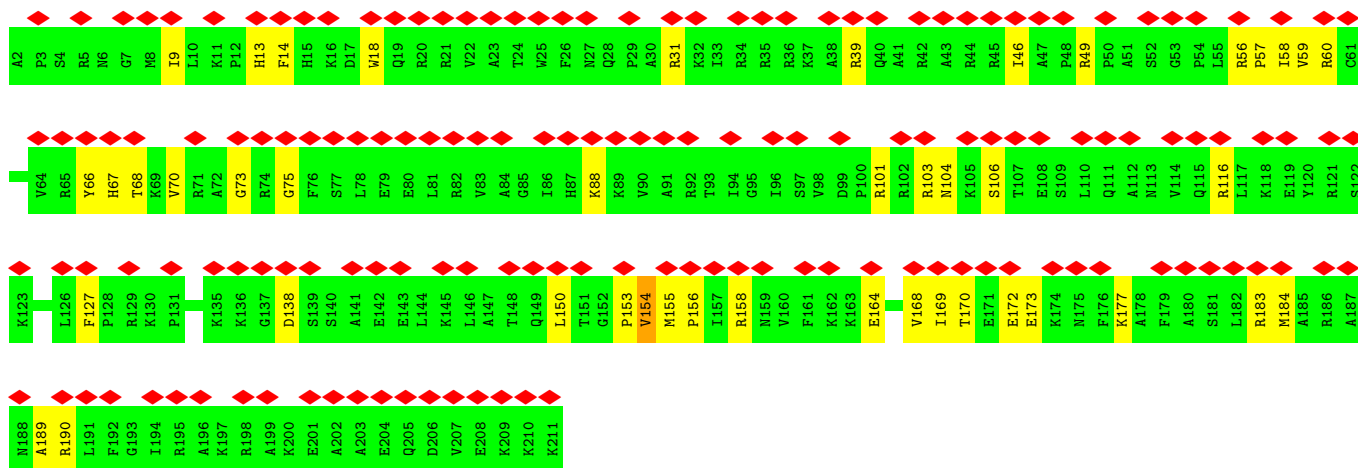


• Molecule 23: Ribosomal protein L38

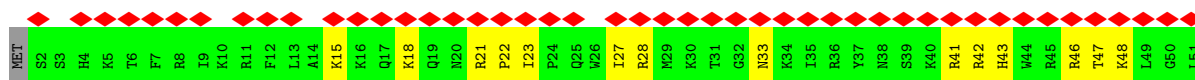
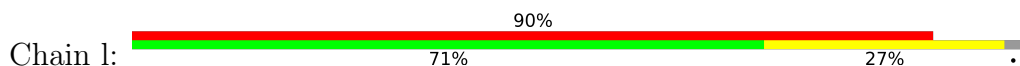


• Molecule 24: Ribosomal protein L13

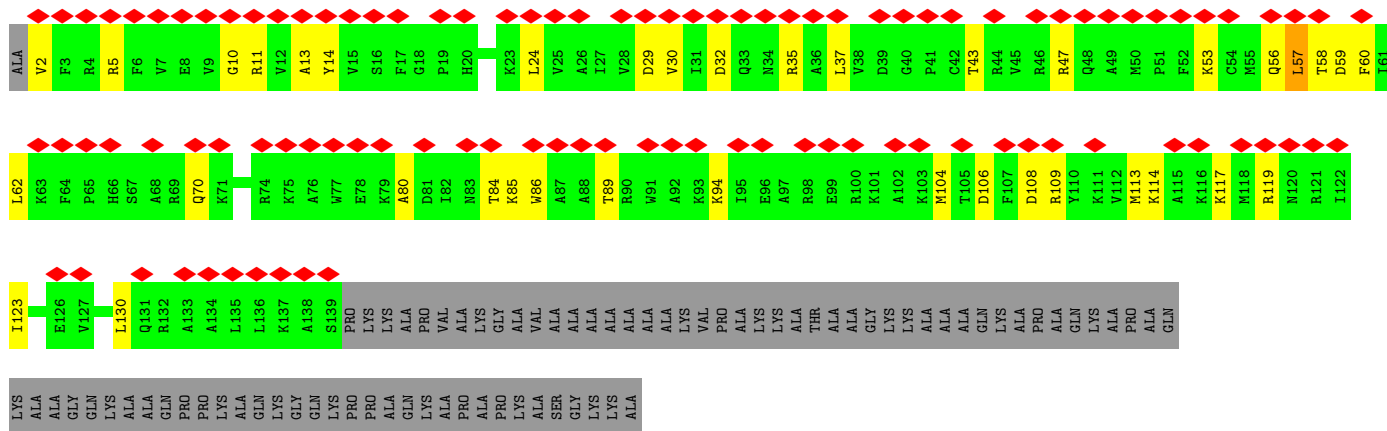




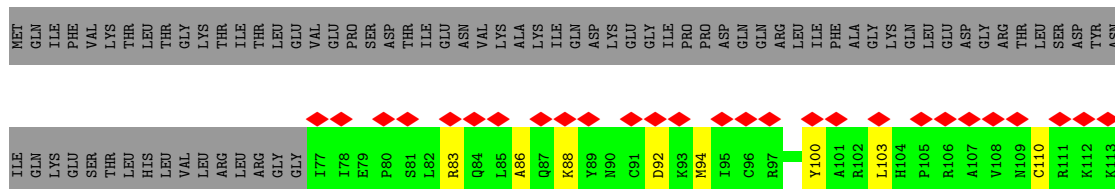
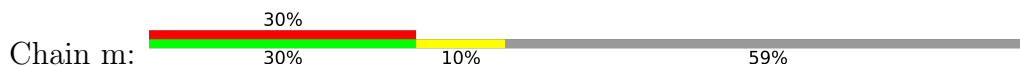
- Molecule 25: Ribosomal protein L39

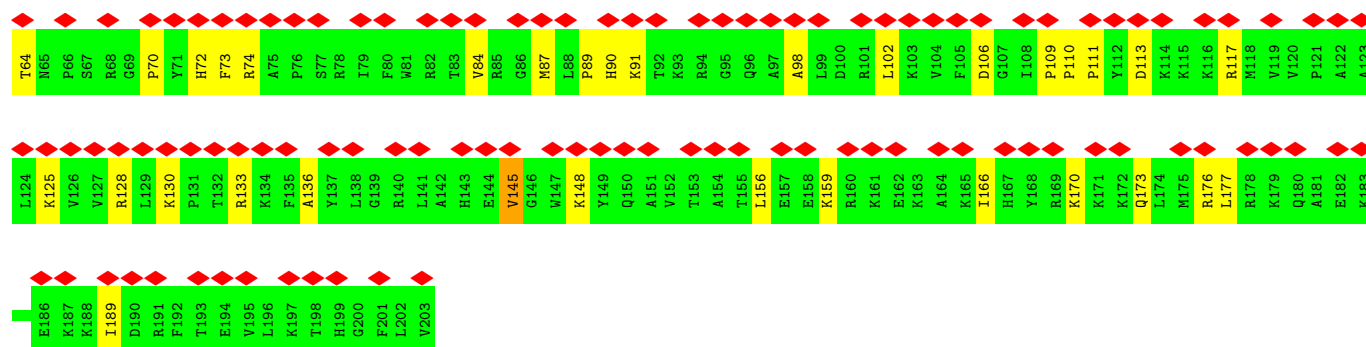


- Molecule 26: 60S ribosomal protein L14

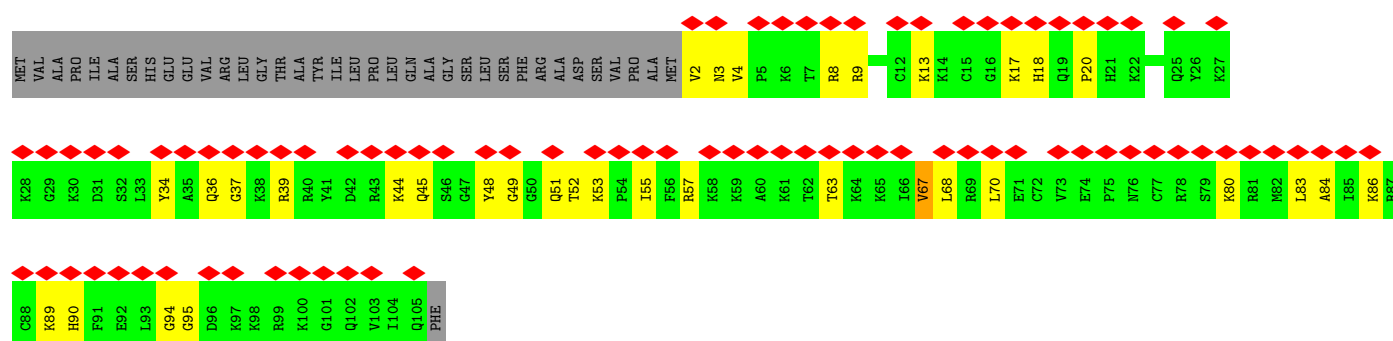


- Molecule 27: Ribosomal protein L40

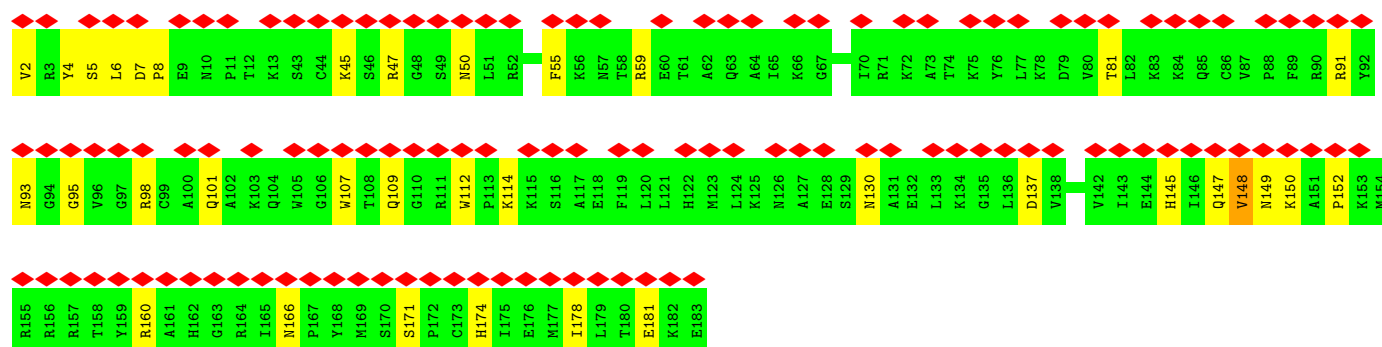
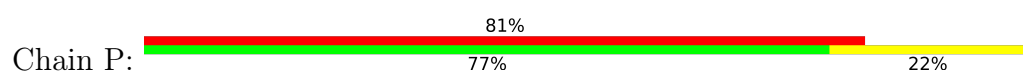




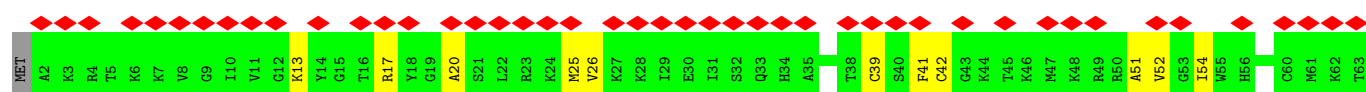
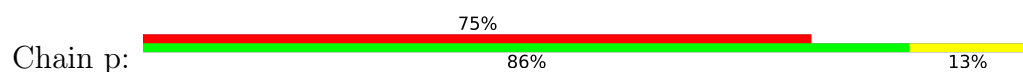
• Molecule 31: eL42

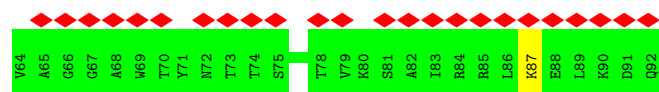


• Molecule 32: 60S ribosomal protein L17

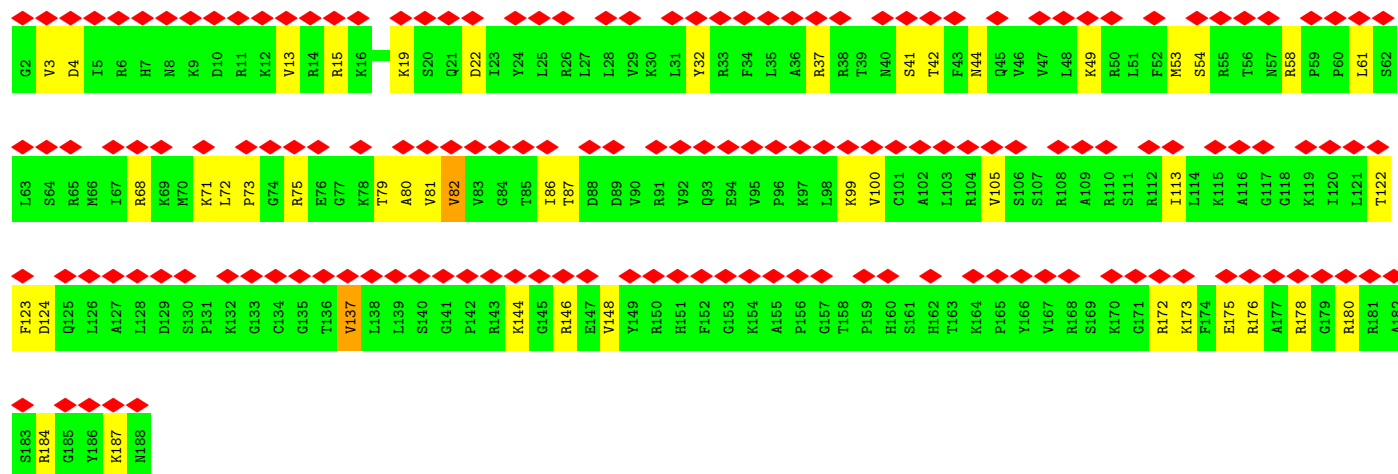
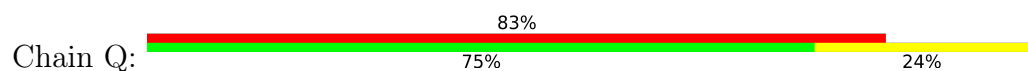


• Molecule 33: eL43

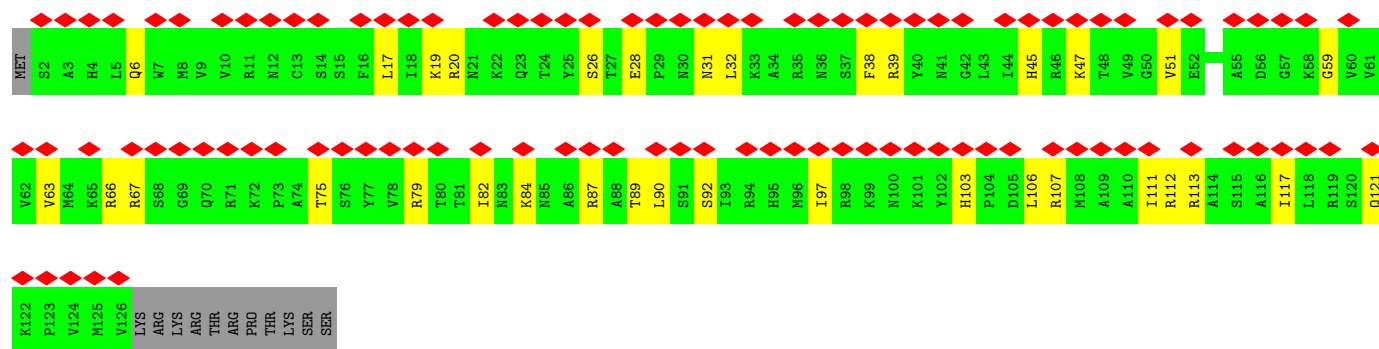




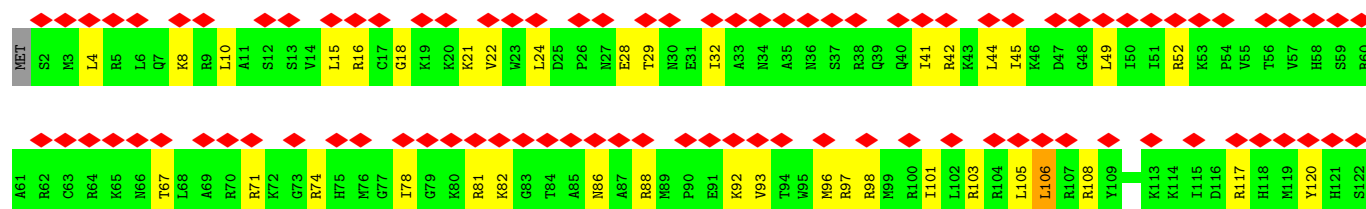
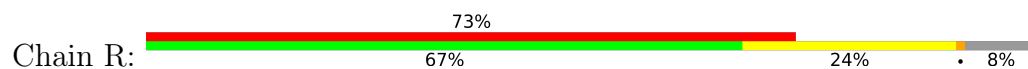
• Molecule 34: Ribosomal protein L18

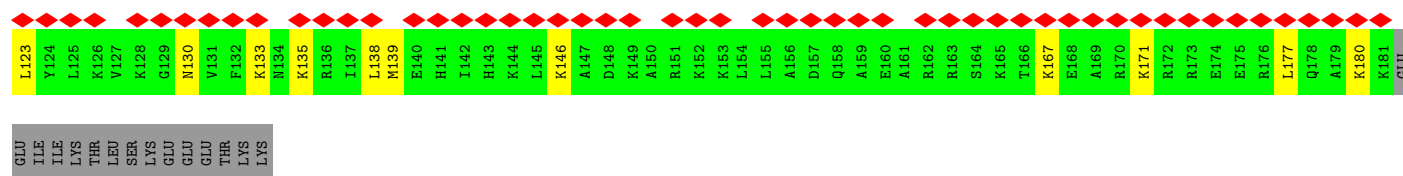


• Molecule 35: 60S ribosomal protein L28

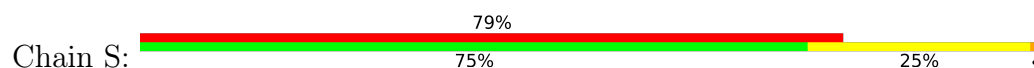


• Molecule 36: 60S ribosomal protein L19

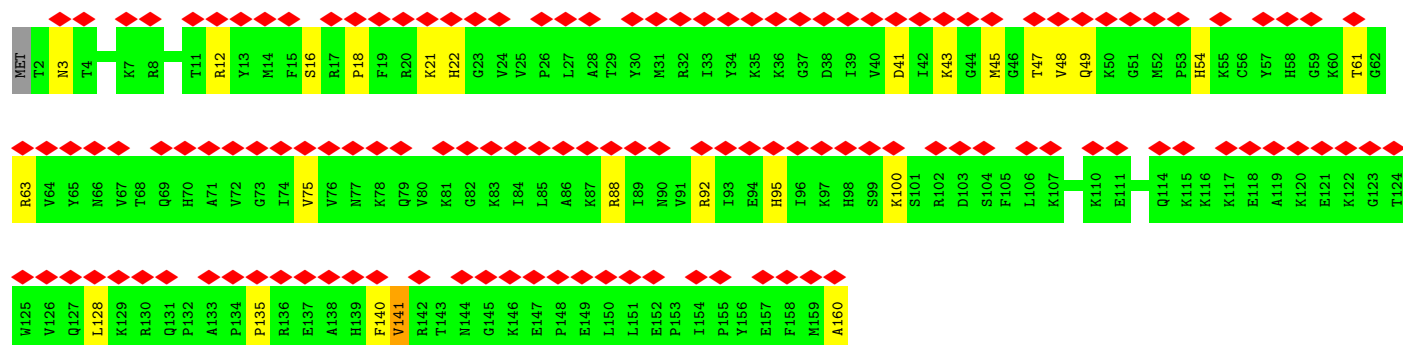
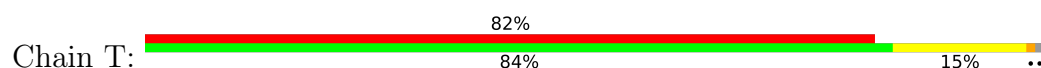




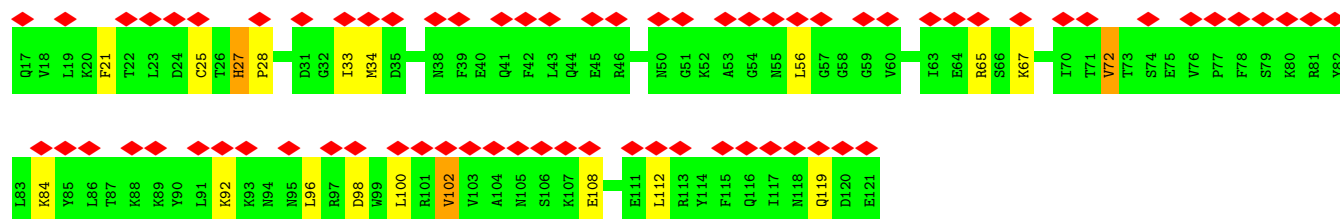
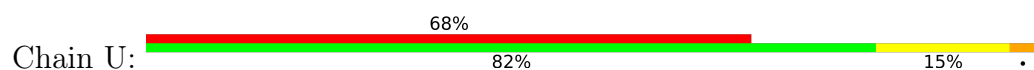
• Molecule 37: Ribosomal protein L18a



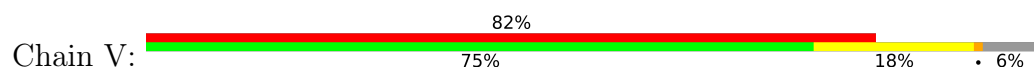
• Molecule 38: 60S ribosomal protein L21

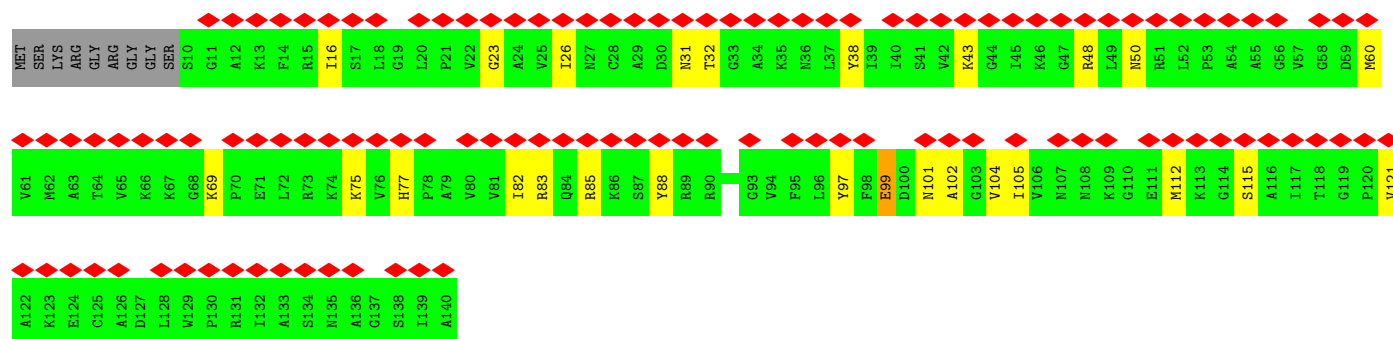


• Molecule 39: Ribosomal protein L22

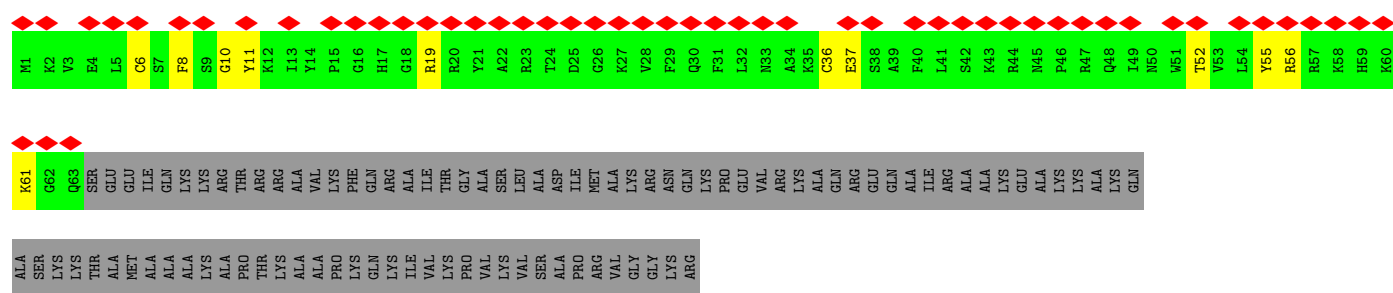
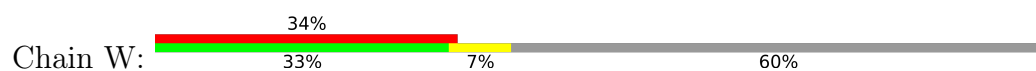


• Molecule 40: Ribosomal protein L23

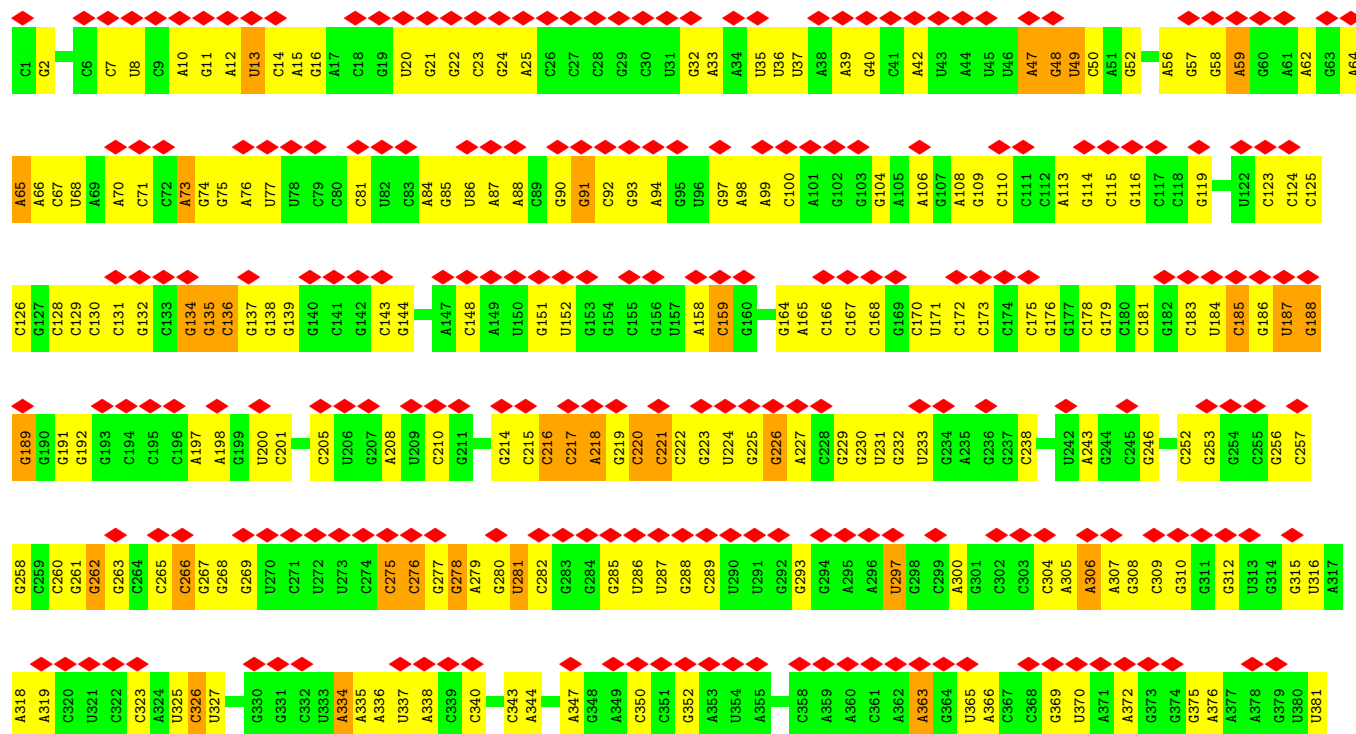




• Molecule 41: Ribosomal protein L24



• Molecule 42: 28S rRNA





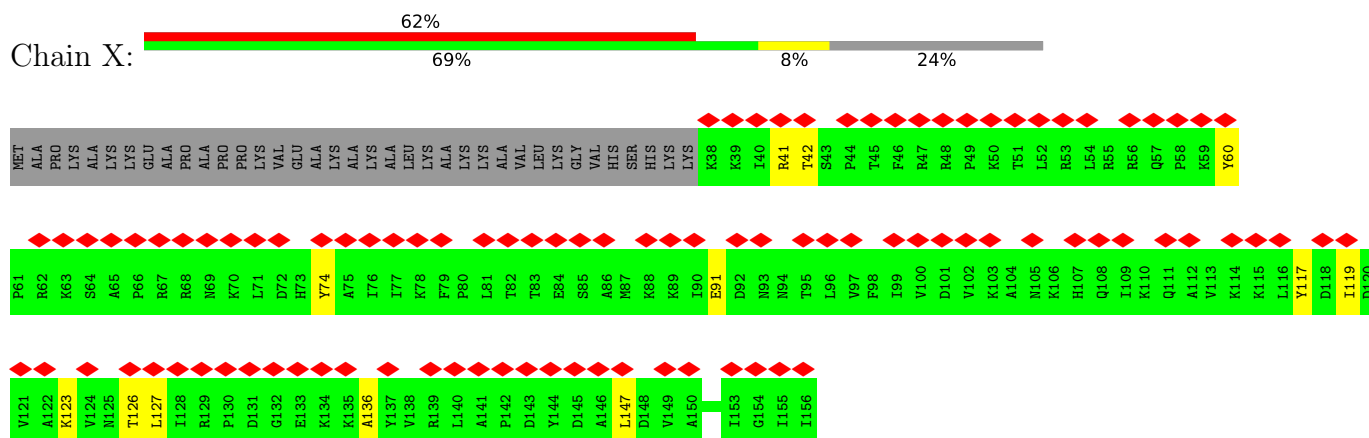




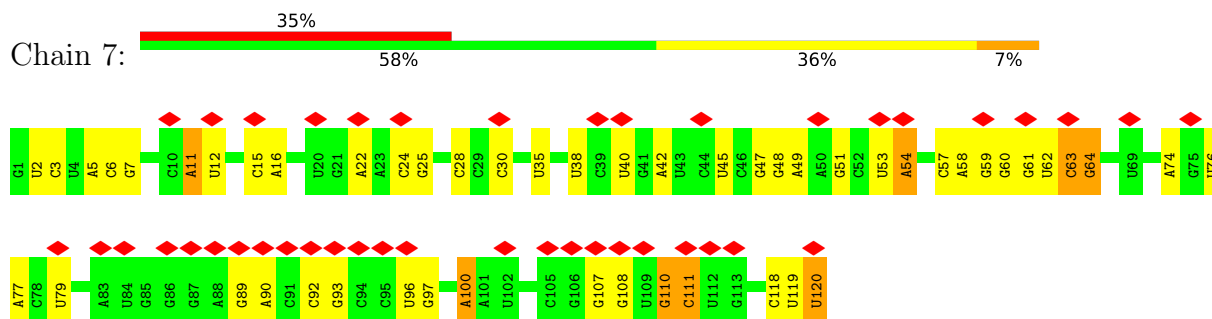
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U4227	G4166	G	C	C3911	U3848	C3788	C3666	U3606	U	C
G4228	G4167	A	C	U3912	A3849	C3789	C3667	U3607	C	C
U4229	G4168	G	C	G3913	C3850	C3790	C3668	A3608	C	C
C4230	G4169	G	C	U3914	U3851	U3729	C3669	C3609	C	D
C4231	A4170	C	U	U3915	A3852	U3730	C3670	A3610	C	C
U4232	C4171	C	G	G3916	U3853	C3731	C3671	A3611	C	C
A4233	A4172	A	A	A3917	C3854	A3732	C3672	C3612	C	C
A4234	G4173	A	G	G3918	C3855	A3733	C3673	U3613	C	C
C4237	U4174	U	U	C3919	A3856	U3734	C3674	G3614	C	C
G4238	G4175	A	C	U3920	G3857	G3735	C3675	G3615	C	C
A4239	C4176	C	C	U3921	A3862	A3736	C3676	U3616	C	C
G4240	U4177	C	U	G3922	C3863	A3737	C3677	G3617	C	C
C4241	U4118	U	C	A3923	A3864	G3738	C3678	C3618	C	C
U4242	U4119	U	C	C3924	A3865	C3739	C3679	G3619	C	C
C4243	U4120	U	C	U3925	C3866	G3740	U3680	G3620	C	C
A4251	G4121	G	C	C3926	A3867	C3741	G3681	A3621	U	C
C4252	G4122	C	C	A3928	G3868	G3742	A3682	C3622	U	C
A4253	C4123	C	C	U3932	C3869	G3743	C3683	C3623	U	C
G4254	G4124	U	C	G3933	C3870	U3745	C3684	A3624	C	C
A4255	U4125	U	C	C3934	A3871	A3746	C3685	G3625	C	C
A4256	C4126	U	C	G3935	A3872	G3747	C3686	G3626	C	C
C4259	U4127	U	C	A3936	G3873	A3748	C3687	G3627	C	C
U4260	U4128	C	C	G3937	G3874	G3750	U3688	G3628	C	C
C4261	G4131	G	C	C3938	G3875	G3751	C3689	A3629	C	C
C4262	C4132	C	C	G3939	A3877	G3752	C3691	U3631	C	C
C4263	U4133	U	C	U3940	C3878	C3753	A3692	C3632	C	C
G4264	C4134	G	C	G3944	G3879	G3754	U3693	C3633	C	C
U4265	G4135	G	C	A3945	C3880	G3755	U3694	G3634	C	C
G4266	U4136	C	C	G3946	C3881	C3757	C3695	A3635	C	C
C4267	C4137	C	C	A3947	C3882	G3758	C3696	C3636	C	C
A4268	U4138	U	C	C3948	U3883	U3759	C3697	U3637	C	C
A4271	C4139	C	C	A3949	C3884	A3760	C3698	G3638	C	C
G4272	U4140	U	C	U3950	G3885	C3761	C3699	U3639	C	C
A4273	G4141	C	C	G	C3886	C3762	C3700	U3640	C	C
A4274	C4142	C	C	A	C3887	A3763	C3701	U3641	C	C
G4275	G4143	C	C	G	G3888	U3764	A3702	A3642	C	C
C4278	C4144	C	C	A	C3889	G3765	G3703	U3643	C	C
A4279	U4145	C	C	G	A3890	A3766	U3704	U3644	C	C
G4280	G4146	C	C	G	C3891	C3767	G3705	U3645	C	C
A4281	C4147	C	C	U	U3892	U3768	C3706	A3646	C	C
C4282	U4148	U	U	C	A3894	C3769	U3707	A3647	C	C
U4285	C4149	C	C	A	G3895	U3770	C3708	C3593	C	C
C4286	G4150	C	C	G	C3896	C3771	G3709	A3649	C	C
G4287	U4151	C	C	A	G3897	U3772	A3711	A3651	C	C
U4290	C4152	C	C	U	C3898	U3773	A3712	A3652	C	C
A4291	G4153	A	A	A	G3899	A3774	U3713	A3653	C	C
A4292	U4154	G	C	G	U3900	A3775	G3714	G3654	C	C
U4293	C4155	C	C	U	A3901	G3776	U3715	C3655	C	C
C4294	U4156	C	C	G	A3902	G3777	C3716	A3656	C	C
U4295	A4157	C	C	C	G3903	U3778	A3717	U3657	C	C
U4296	C4160	C	C	A	G3904	A3718	C3658	C3602	C	C
G4297	G4161	C	C	G	A3905	G3719	G3659	G3603	C	C
	C4162	C	C	U	A3906	U3720	C3660	A3604	C	C
	U4163	C	C	G	G3907	G3721	G3661			
	C4164	C	C	C	A3908	G3722	A3662			
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		C	C	C		A3724	G3664			



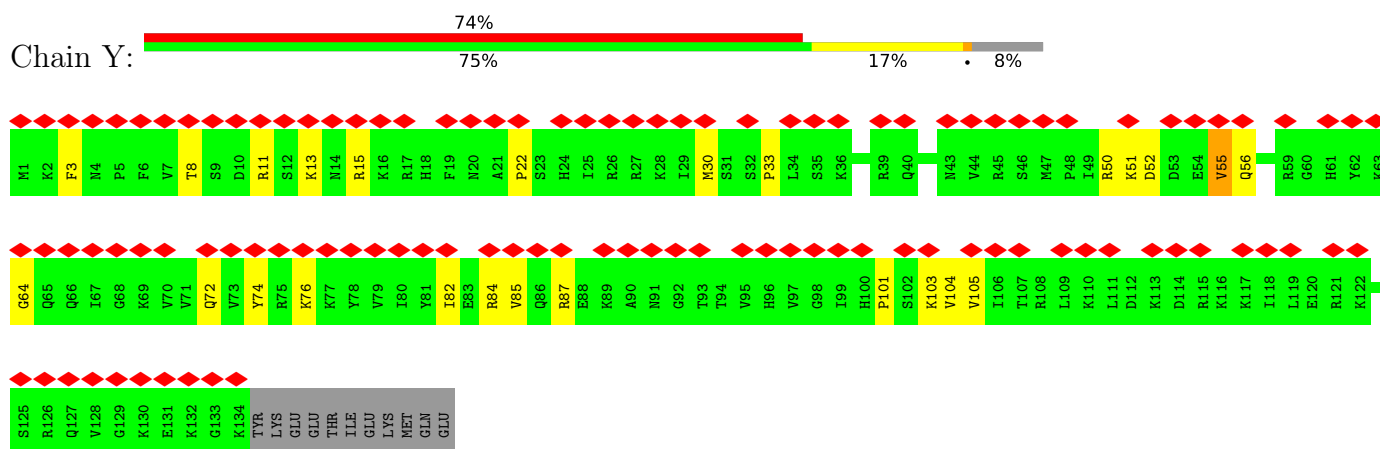
- Molecule 43: Ribosomal_L23eN domain-containing protein



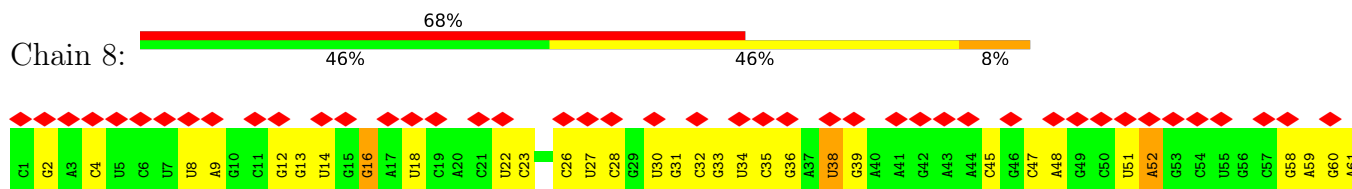
- Molecule 44: 5S rRNA

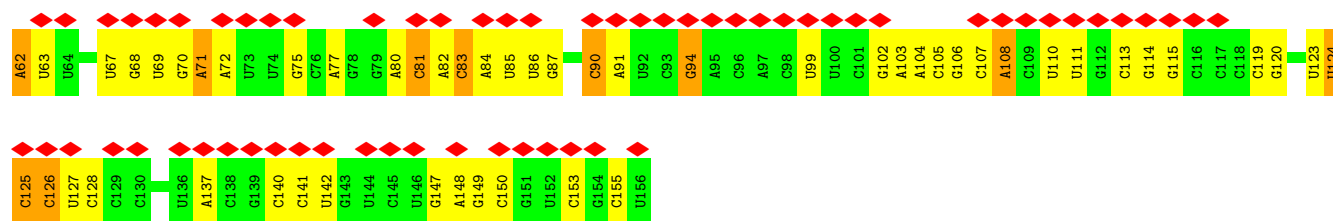


- Molecule 45: Ribosomal protein L26

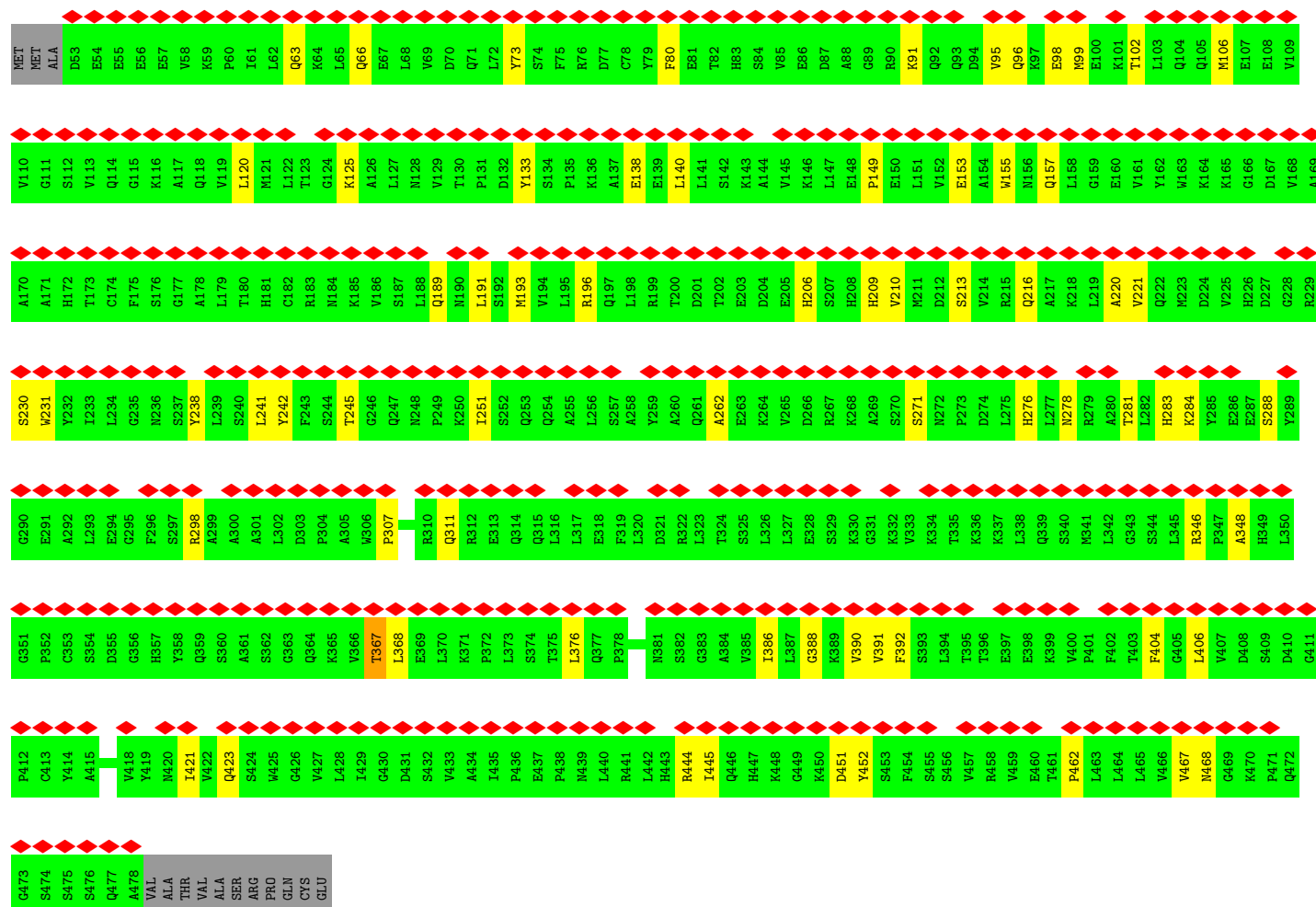
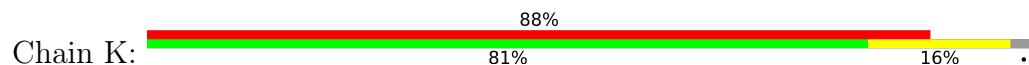


- Molecule 46: 5.8S rRNA

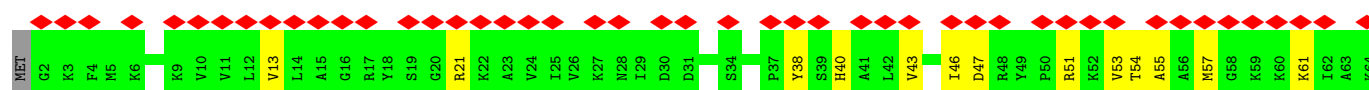


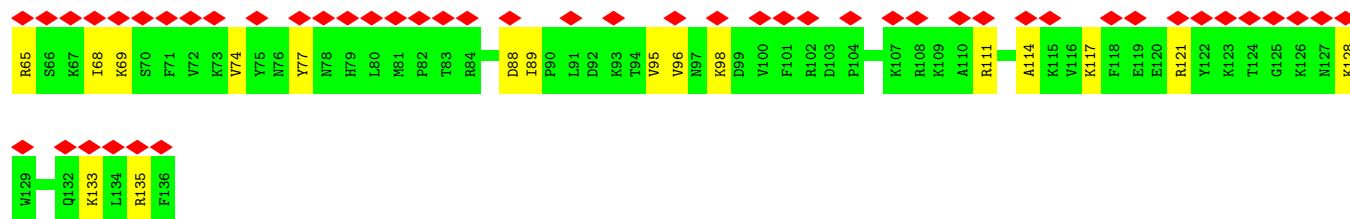


• Molecule 47: Tetratricopeptide repeat protein 5

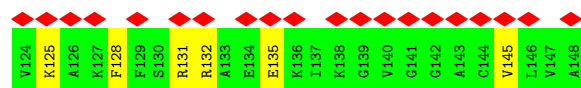
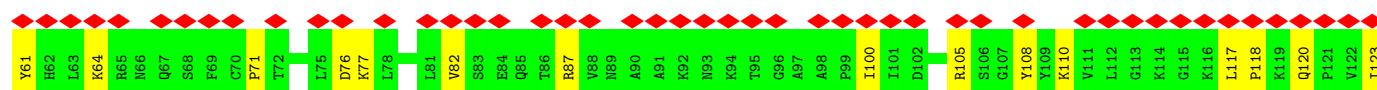
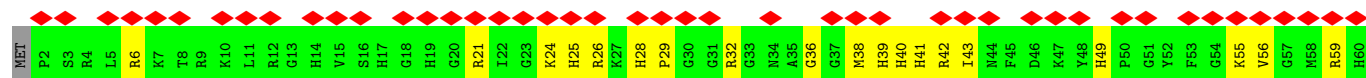
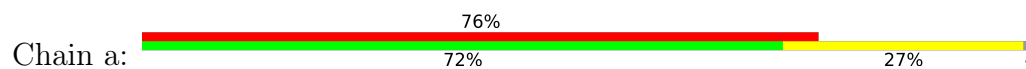


• Molecule 48: 60S ribosomal protein L27





• Molecule 49: 60S ribosomal protein L27a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83053	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.381	Depositor
Minimum map value	-0.210	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	535.6, 535.6, 535.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.339, 1.339, 1.339	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
2	t	0.07	0/536	0.19	0/715
3	u	0.10	0/845	0.25	0/1134
4	A	0.12	0/1906	0.27	0/2556
5	b	0.08	0/619	0.19	0/818
6	B	0.11	0/3216	0.27	0/4311
7	c	0.08	0/742	0.19	0/996
8	C	0.10	0/2937	0.25	0/3946
9	d	0.10	0/903	0.23	0/1216
10	D	0.10	0/2432	0.25	0/3257
11	e	0.09	0/1071	0.26	0/1429
12	E	0.12	0/1936	0.34	0/2600
13	f	0.11	0/895	0.28	0/1198
14	F	0.10	0/1905	0.25	0/2539
15	g	0.10	0/916	0.24	0/1220
16	G	0.11	0/1967	0.25	0/2647
17	h	0.09	0/1021	0.25	0/1348
18	H	0.09	0/1535	0.24	0/2063
19	i	0.12	0/841	0.24	0/1112
20	I	0.09	0/1693	0.22	0/2260
21	j	0.09	0/720	0.22	0/952
22	J	0.09	0/1376	0.24	0/1841
23	k	0.11	0/575	0.27	0/761
24	L	0.10	0/1734	0.24	0/2317
25	l	0.14	0/454	0.33	0/599
26	M	0.10	0/1158	0.24	0/1547
27	m	0.14	0/435	0.34	0/575
28	N	0.10	0/1746	0.24	0/2338
29	n	0.09	0/223	0.19	0/284
30	O	0.11	0/1671	0.25	0/2234
31	o	0.11	0/864	0.28	0/1140
32	P	0.08	0/1268	0.24	0/1700
33	p	0.09	0/718	0.23	0/953

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	Q	0.10	0/1530	0.24	0/2041
35	r	0.11	0/1017	0.31	0/1364
36	R	0.10	0/1524	0.23	0/2013
37	S	0.12	0/1493	0.26	0/2002
38	T	0.10	0/1326	0.24	0/1770
39	U	0.10	0/873	0.30	0/1172
40	V	0.11	0/993	0.27	0/1332
41	W	0.09	0/541	0.25	0/720
42	5	0.10	0/83726	0.23	1/130593 (0.0%)
43	X	0.08	0/993	0.23	0/1334
44	7	0.08	0/2858	0.19	0/4455
45	Y	0.10	0/1132	0.21	0/1504
46	8	0.09	0/3701	0.22	0/5766
47	K	0.09	0/3402	0.24	0/4603
48	Z	0.10	0/1130	0.26	0/1507
49	a	0.10	0/1191	0.26	0/1590
All	All	0.10	0/148288	0.24	1/218372 (0.0%)

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
13	f	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	5	5061	A	P-O3'-C3'	5.30	128.15	120.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	f	106	TYR	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	s	120	0	30	0	0
2	t	531	0	573	5	0
3	u	837	0	880	17	0
4	A	1868	0	1959	53	0
5	b	609	0	650	11	0
6	B	3148	0	3267	87	0
7	c	732	0	766	11	0
8	C	2883	0	3053	61	0
9	d	888	0	930	20	0
10	D	2386	0	2419	46	0
11	e	1053	0	1147	25	0
12	E	1898	0	2035	56	0
13	f	876	0	912	23	0
14	F	1870	0	1994	44	0
15	g	906	0	998	21	0
16	G	1934	0	2085	38	0
17	h	1013	0	1147	27	0
18	H	1516	0	1597	29	0
19	i	830	0	916	14	0
20	I	1655	0	1704	31	0
21	j	705	0	737	25	0
22	J	1353	0	1386	32	0
23	k	569	0	637	7	0
24	L	1703	0	1820	39	0
25	l	444	0	483	14	0
26	M	1137	0	1211	29	0
27	m	429	0	465	11	0
28	N	1701	0	1749	55	0
29	n	222	0	264	5	0
30	O	1638	0	1777	37	0
31	o	851	0	920	28	0
32	P	1242	0	1274	28	0
33	p	708	0	756	9	0
34	Q	1506	0	1623	30	0
35	r	1001	0	1060	26	0
36	R	1508	0	1664	41	0
37	S	1454	0	1496	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	T	1298	0	1366	21	0
39	U	859	0	874	14	0
40	V	979	0	1039	15	0
41	W	528	0	541	7	0
42	5	74854	0	37826	1380	0
43	X	976	0	1053	8	0
44	7	2558	0	1296	39	0
45	Y	1115	0	1205	22	0
46	8	3314	0	1683	66	0
47	K	3337	0	3320	39	0
48	Z	1107	0	1182	19	0
49	a	1162	0	1209	31	0
50	g	1	0	0	0	0
50	j	1	0	0	0	0
50	m	1	0	0	0	0
50	o	1	0	0	0	0
50	p	1	0	0	0	0
51	5	97	0	0	0	0
All	All	137913	0	100978	2217	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 10.

All (2217) 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)
42:5:1444:G:N2	42:5:2100:A:H62	1.53	1.07
42:5:2845:A:H61	42:5:3843:C:N4	1.54	1.05
42:5:1444:G:H21	42:5:2100:A:N6	1.58	1.00
42:5:2845:A:N6	42:5:3843:C:H42	1.59	0.99
42:5:1555:G:H1	42:5:1572:U:H3	1.04	0.97
42:5:2557:G:H1	42:5:2570:U:H3	0.90	0.85
42:5:2520:C:O2	42:5:2640:G:N2	2.08	0.85
42:5:1444:G:H21	42:5:2100:A:H62	0.86	0.83
42:5:2845:A:H61	42:5:3843:C:H42	0.84	0.82
42:5:1802:A:H5''	42:5:1803:G:H5'	1.62	0.82
30:O:176:ARG:HD3	42:5:4768:G:H5'	1.63	0.81
42:5:4260:U:H2'	42:5:4261:C:H6	1.43	0.80
42:5:704:C:H2'	42:5:705:G:H8	1.47	0.80
8:C:312:ARG:NH2	42:5:2075:G:OP1	2.15	0.80
44:7:28:C:H1'	44:7:54:A:H61	1.48	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:R:18:GLY:HA3	42:5:2822:G:H5''	1.64	0.78
37:S:72:PRO:HG2	42:5:731:G:H21	1.49	0.78
42:5:2638:G:H1	42:5:2697:A:H61	1.32	0.77
42:5:184:U:H3	42:5:253:G:H1	0.82	0.77
40:V:31:ASN:HD21	40:V:115:SER:H	1.32	0.76
6:B:63:PRO:HA	6:B:68:ASN:HD21	1.51	0.75
42:5:734:G:N2	42:5:930:G:O2'	2.20	0.75
9:d:118:GLN:HE22	42:5:5055:G:H21	1.34	0.73
18:H:129:ARG:HH22	42:5:4704:C:H4'	1.52	0.73
41:W:56:ARG:HG3	41:W:61:LYS:HB2	1.68	0.73
42:5:704:C:H2'	42:5:705:G:C8	2.23	0.73
4:A:101:VAL:HG22	4:A:165:VAL:HG12	1.69	0.73
35:r:19:LYS:HB2	42:5:2337:C:H4'	1.71	0.73
16:G:58:PRO:HD2	16:G:61:ILE:HD12	1.71	0.72
42:5:1332:C:H2'	42:5:1333:A:H8	1.54	0.72
16:G:67:ARG:HD3	28:N:29:GLN:HG3	1.71	0.72
14:F:75:ARG:NH1	42:5:729:G:N3	2.36	0.72
42:5:3904:G:H3'	42:5:3905:A:H5''	1.70	0.72
28:N:12:ARG:NH2	42:5:278:G:OP2	2.22	0.72
42:5:2483:G:H22	42:5:2495:U:H3	1.38	0.72
42:5:658:C:H2'	42:5:659:G:H8	1.53	0.72
40:V:16:ILE:HB	40:V:88:TYR:HB2	1.72	0.72
42:5:1468:C:OP1	49:a:132:ARG:NH2	2.23	0.71
42:5:3830:A:H4'	42:5:4552:U:H4'	1.72	0.71
42:5:422:C:H2'	42:5:423:G:H8	1.55	0.71
10:D:113:PHE:HB3	42:5:1819:G:H22	1.55	0.71
42:5:1172:C:N4	42:5:1173:G:O6	2.24	0.71
8:C:308:LYS:HD3	42:5:2093:A:H61	1.56	0.71
16:G:149:ASN:HD22	16:G:151:LYS:HZ2	1.37	0.71
42:5:1426:G:H22	42:5:1458:C:H5''	1.55	0.71
20:I:158:LYS:NZ	42:5:4429:C:N3	2.38	0.70
42:5:2889:G:H21	42:5:5034:A:H1'	1.56	0.70
42:5:961:G:O6	42:5:967:C:N4	2.24	0.70
12:E:121:LEU:H	42:5:959:G:H21	1.36	0.70
8:C:323:ARG:NH2	42:5:974:C:N3	2.37	0.70
8:C:339:THR:HG22	8:C:342:ARG:HH12	1.57	0.70
9:d:83:ARG:NH1	42:5:5046:U:OP2	2.25	0.69
6:B:19:ARG:NH2	42:5:4623:G:OP1	2.25	0.69
6:B:13:SER:HB2	42:5:4622:A:H4'	1.74	0.69
42:5:2411:C:H2'	42:5:2412:A:H8	1.57	0.69
10:D:83:LEU:HB3	10:D:88:VAL:HB	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:j:27:TYR:HA	21:j:34:CYS:HA	1.75	0.69
6:B:10:ARG:HH12	6:B:265:SER:HB2	1.58	0.69
31:o:51:GLN:HG2	31:o:55:ILE:HD11	1.75	0.69
42:5:2627:C:H42	42:5:4649:G:H1	1.39	0.69
26:M:80:ALA:O	26:M:85:LYS:NZ	2.26	0.69
8:C:195:LYS:HE3	42:5:2333:G:H5'	1.75	0.69
40:V:50:ASN:ND2	42:5:4457:U:OP1	2.24	0.69
42:5:67:C:OP2	42:5:312:G:N2	2.24	0.69
16:G:153:GLN:HE22	16:G:219:VAL:HG21	1.58	0.68
35:r:66:ARG:NH2	42:5:479:G:OP1	2.27	0.68
34:Q:173:LYS:NZ	42:5:88:A:N7	2.41	0.68
42:5:4944:C:O2	42:5:4945:G:N2	2.27	0.68
21:j:52:LYS:NZ	42:5:375:G:OP2	2.25	0.68
35:r:107:ARG:NH2	42:5:963:G:OP2	2.26	0.68
20:I:4:ARG:NH1	42:5:1866:U:OP1	2.26	0.68
42:5:1397:A:HO2'	42:5:1467:C:HO2'	1.38	0.68
4:A:242:ARG:HG3	42:5:3745:U:H4'	1.75	0.68
13:f:45:LYS:HD3	13:f:107:PRO:HD2	1.76	0.68
15:g:26:PRO:HD2	42:5:2521:G:H4'	1.76	0.68
31:o:34:TYR:O	31:o:39:ARG:NH1	2.27	0.68
42:5:1326:A:OP2	42:5:4445:U:O2'	2.11	0.68
37:S:118:ARG:NH1	42:5:2059:C:O2'	2.27	0.68
42:5:2309:G:O2'	46:8:18:U:O2	2.12	0.68
42:5:2905:C:H2'	42:5:2906:G:C8	2.29	0.68
42:5:2418:A:N1	42:5:2429:A:O2'	2.26	0.68
42:5:4453:C:O2	42:5:4529:G:N2	2.25	0.68
16:G:77:PRO:HG3	28:N:18:VAL:HA	1.75	0.67
42:5:2745:A:H2'	42:5:2746:A:H8	1.59	0.67
28:N:63:ARG:NH1	28:N:131:GLU:OE2	2.28	0.67
17:h:81:LEU:HD13	46:8:38:U:H5'	1.76	0.67
36:R:93:VAL:HG21	42:5:2725:A:H1'	1.76	0.67
42:5:419:A:N3	42:5:1332:C:O2'	2.25	0.67
14:F:88:GLU:HB3	38:T:135:PRO:HB3	1.75	0.67
35:r:59:GLY:H	35:r:121:GLN:HE22	1.42	0.67
42:5:2590:G:H21	42:5:2755:A:H62	1.43	0.67
36:R:97:ARG:NH2	42:5:2725:A:OP1	2.28	0.67
42:5:2557:G:N2	42:5:2570:U:O2	2.24	0.67
6:B:324:GLY:HA2	42:5:5051:C:H4'	1.76	0.66
42:5:2439:G:H1	42:5:2538:U:H3	1.43	0.66
10:D:176:SER:HB3	42:5:4323:A:H4'	1.77	0.66
18:H:173:ARG:NH2	42:5:4474:A:OP1	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Q:87:THR:OG1	42:5:1503:A:N6	2.29	0.66
42:5:4272:G:N2	42:5:4272:G:OP2	2.28	0.66
48:Z:47:ASP:HB3	48:Z:69:LYS:HG3	1.78	0.66
30:O:37:ARG:HH12	42:5:4759:C:H5''	1.61	0.66
47:K:189:GLN:HE21	47:K:220:ALA:HB3	1.61	0.66
18:H:176:LEU:HD22	27:m:83:ARG:HD2	1.77	0.66
42:5:1541:C:H1'	42:5:2448:G:H21	1.61	0.66
10:D:75:VAL:O	10:D:112:ARG:NH1	2.29	0.66
42:5:5047:C:O2'	42:5:5050:C:OP2	2.14	0.66
47:K:444:ARG:HH12	47:K:451:ASP:HB3	1.59	0.66
17:h:80:PRO:HG2	17:h:83:LEU:HD13	1.77	0.66
19:i:30:ARG:NH1	42:5:327:U:O2'	2.29	0.66
14:F:244:ARG:NH2	42:5:941:C:OP1	2.29	0.66
17:h:62:ASN:ND2	46:8:60:G:O6	2.29	0.66
42:5:4740:G:H22	42:5:4959:U:H3	1.42	0.66
4:A:117:GLU:HG2	4:A:124:GLY:H	1.62	0.65
33:p:39:CYS:HB3	33:p:42:CYS:SG	2.35	0.65
42:5:3868:G:H22	42:5:3900:G:H1'	1.60	0.65
42:5:4894:A:O2'	42:5:4896:G:OP1	2.11	0.65
48:Z:57:MET:HG2	48:Z:61:LYS:HD2	1.78	0.65
10:D:280:VAL:HG23	20:I:206:LEU:HD11	1.77	0.65
38:T:100:LYS:HB2	42:5:1730:U:H4'	1.77	0.65
42:5:3945:A:H2'	42:5:3946:G:H8	1.61	0.65
9:d:38:PHE:HB3	9:d:78:ARG:HG2	1.79	0.65
34:Q:49:LYS:NZ	42:5:1693:U:OP2	2.29	0.65
42:5:447:C:N4	42:5:448:G:O6	2.29	0.65
42:5:2330:G:H2'	42:5:2331:G:N3	2.12	0.65
42:5:2590:G:N2	42:5:2755:A:H62	1.93	0.65
17:h:103:LYS:HE2	17:h:108:GLN:HG2	1.78	0.65
42:5:1787:A:N3	42:5:4210:U:O2'	2.28	0.65
42:5:1315:C:N4	42:5:1316:G:O6	2.28	0.65
42:5:2457:G:H21	42:5:3672:G:H21	1.44	0.65
42:5:2590:G:H21	42:5:2755:A:N6	1.94	0.65
42:5:4260:U:H2'	42:5:4261:C:C6	2.30	0.65
24:L:158:ARG:NH1	42:5:1377:G:N7	2.44	0.65
42:5:1523:A:N3	42:5:4389:C:O2'	2.30	0.65
42:5:2777:G:H5''	42:5:2778:G:H5'	1.77	0.65
42:5:4088:C:H2'	42:5:4089:G:H8	1.61	0.65
6:B:253:CYS:SG	42:5:4520:G:N2	2.70	0.65
13:f:79:GLY:HA3	42:5:1917:A:H4'	1.78	0.65
14:F:75:ARG:HH21	42:5:726:G:H5''	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:307:LYS:NZ	42:5:2089:G:N3	2.42	0.65
28:N:90:ASN:ND2	42:5:3928:A:OP1	2.29	0.65
42:5:751:G:N2	42:5:752:G:O6	2.30	0.65
8:C:103:ALA:HA	42:5:1517:G:H22	1.63	0.65
42:5:1494:U:H2'	42:5:1495:G:H8	1.62	0.65
40:V:32:THR:O	40:V:69:LYS:NZ	2.30	0.64
42:5:3873:G:H2'	42:5:3874:G:C8	2.33	0.64
3:u:6:MET:SD	3:u:10:LYS:NZ	2.70	0.64
42:5:4598:C:H2'	42:5:4611:A:H61	1.62	0.64
42:5:4635:A:H2	42:5:4663:G:H21	1.45	0.64
24:L:177:LYS:NZ	42:5:1479:G:O2'	2.31	0.64
28:N:179:LYS:O	42:5:297:U:O2'	2.16	0.64
36:R:92:LYS:NZ	42:5:1573:G:OP1	2.31	0.64
42:5:712:C:H42	42:5:956:A:H61	1.45	0.64
42:5:453:G:H1	42:5:1294:A:H62	1.46	0.64
26:M:106:ASP:OD1	26:M:109:ARG:NH2	2.30	0.64
37:S:69:GLU:HB2	37:S:72:PRO:HG3	1.79	0.64
42:5:33:A:H3'	42:5:47:A:H61	1.63	0.64
36:R:4:LEU:HD11	36:R:29:THR:HG23	1.80	0.64
14:F:139:GLU:OE1	44:7:96:U:O2'	2.14	0.64
44:7:92:C:H2'	44:7:93:G:H8	1.63	0.64
19:i:45:ARG:NH2	19:i:54:GLU:OE1	2.30	0.64
19:i:45:ARG:HH22	19:i:50:PHE:HA	1.61	0.64
28:N:2:GLY:N	42:5:115:C:OP1	2.31	0.64
42:5:114:G:H1	42:5:158:A:H61	1.45	0.64
42:5:1743:A:N1	42:5:1789:C:O2'	2.30	0.64
8:C:239:LYS:O	8:C:248:ARG:NH1	2.31	0.64
32:P:150:LYS:NZ	42:5:2357:G:OP1	2.28	0.64
42:5:81:C:H1'	42:5:1359:G:H21	1.62	0.64
42:5:938:C:H2'	42:5:939:G:C8	2.33	0.64
42:5:3799:A:N3	42:5:4506:C:O2'	2.26	0.64
42:5:1739:G:N3	42:5:1742:A:N6	2.47	0.63
45:Y:84:ARG:NH2	47:K:423:GLN:O	2.32	0.63
27:m:100:TYR:O	42:5:4472:G:O2'	2.16	0.63
42:5:2757:A:H2'	42:5:2758:G:C4	2.33	0.63
42:5:4541:G:N2	42:5:4544:A:OP2	2.29	0.63
10:D:52:ILE:HD13	44:7:6:C:H4'	1.80	0.63
12:E:41:SER:HA	42:5:978:G:H5''	1.80	0.63
42:5:1760:G:O6	42:5:1773:U:O2	2.15	0.63
42:5:3809:G:N2	42:5:3809:G:OP2	2.32	0.63
49:a:39:HIS:O	49:a:40:HIS:ND1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:g:76:ARG:NH1	42:5:2583:C:OP2	2.32	0.63
30:O:130:LYS:HB2	30:O:133:ARG:HG2	1.80	0.63
20:I:49:CYS:SG	20:I:168:SER:OG	2.56	0.63
42:5:1199:G:H2'	42:5:1200:G:H8	1.64	0.63
42:5:1850:A:N3	42:5:2283:G:O2'	2.30	0.63
42:5:3641:U:OP2	42:5:3646:A:N6	2.30	0.63
15:g:66:ARG:HD3	42:5:2539:C:H5''	1.79	0.63
24:L:169:ILE:HD11	49:a:123:ILE:HD11	1.81	0.63
42:5:2258:C:O2'	42:5:2260:C:N4	2.30	0.63
42:5:35:U:O2'	42:5:1525:A:N1	2.29	0.63
42:5:230:G:OP1	45:Y:15:ARG:NH1	2.32	0.63
42:5:468:U:H3	42:5:688:U:H3	1.45	0.63
42:5:2459:G:N2	42:5:2462:C:OP2	2.31	0.63
42:5:4594:U:H2'	42:5:4595:G:H8	1.63	0.63
10:D:17:GLN:NE2	38:T:22:HIS:O	2.31	0.63
42:5:187:U:H5''	42:5:188:G:H5'	1.81	0.62
6:B:132:LYS:HA	6:B:135:LYS:HE3	1.80	0.62
7:c:55:LEU:HD11	15:g:92:LYS:HG3	1.80	0.62
30:O:72:HIS:N	42:5:4586:G:OP1	2.31	0.62
32:P:171:SER:OG	42:5:2361:G:O6	2.17	0.62
42:5:2489:C:O2'	42:5:2491:C:N4	2.32	0.62
12:E:184:ARG:NH1	12:E:210:ASP:OD1	2.32	0.62
32:P:98:ARG:NH2	42:5:4980:C:N3	2.45	0.62
34:Q:144:LYS:HG2	42:5:1460:C:H5''	1.82	0.62
42:5:369:G:N2	42:5:372:A:OP2	2.26	0.62
42:5:2740:U:O2'	42:5:2742:G:N2	2.31	0.62
42:5:4522:G:O2'	42:5:4525:C:OP2	2.17	0.62
20:I:49:CYS:HG	20:I:168:SER:HG	1.43	0.62
20:I:116:ARG:NH2	42:5:4194:U:O2'	2.32	0.62
42:5:4888:U:O2	42:5:4931:G:O6	2.18	0.62
14:F:26:ASN:N	42:5:2248:C:OP2	2.32	0.62
20:I:55:ASP:HB3	20:I:162:ARG:HG3	1.82	0.62
24:L:18:TRP:NE1	42:5:1516:G:O2'	2.28	0.62
28:N:125:SER:HB3	42:5:3937:C:H1'	1.80	0.62
4:A:21:LYS:HG2	42:5:1541:C:H5''	1.82	0.62
42:5:2411:C:O2'	42:5:2526:C:O2	2.18	0.62
42:5:4454:G:H1	42:5:4526:U:H3	1.47	0.62
23:k:24:LYS:HD3	23:k:69:LEU:HD11	1.82	0.62
32:P:152:PRO:HG3	46:8:14:U:H5''	1.82	0.62
42:5:1552:G:O2'	42:5:1574:G:N2	2.33	0.62
46:8:106:G:H4'	46:8:137:A:H5'	1.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:E:108:MET:O	35:r:87:ARG:NH1	2.33	0.62
10:D:33:ARG:NH1	44:7:7:G:OP1	2.32	0.62
35:r:38:PHE:O	35:r:45:HIS:NE2	2.33	0.62
42:5:933:G:H2'	42:5:940:C:H41	1.65	0.62
42:5:2551:A:H61	42:5:2766:A:H62	1.48	0.62
42:5:4528:G:H2'	42:5:4529:G:C8	2.35	0.62
42:5:4604:G:N2	42:5:4607:A:OP2	2.33	0.62
14:F:238:ARG:HB3	14:F:241:GLN:HB2	1.82	0.61
35:r:17:LEU:HD21	35:r:19:LYS:HE3	1.81	0.61
35:r:39:ARG:NH1	42:5:2266:C:O2'	2.33	0.61
42:5:963:G:H22	42:5:2255:C:H42	1.48	0.61
18:H:128:MET:HE3	18:H:157:SER:HB3	1.81	0.61
19:i:33:LEU:HD21	19:i:38:LYS:HD3	1.82	0.61
42:5:709:C:H2'	42:5:710:G:H8	1.64	0.61
42:5:1376:C:OP2	42:5:1379:C:N4	2.32	0.61
46:8:107:C:N3	46:8:108:A:N6	2.48	0.61
42:5:5057:C:H2'	42:5:5058:A:C8	2.34	0.61
45:Y:72:GLN:HE22	45:Y:74:TYR:HB2	1.64	0.61
42:5:673:C:H2'	42:5:674:G:H8	1.64	0.61
42:5:969:C:O2'	42:5:970:G:N3	2.33	0.61
42:5:2467:U:H4'	42:5:2468:U:H5'	1.82	0.61
42:5:2832:A:H2'	42:5:2833:A:C8	2.35	0.61
42:5:4392:G:N2	42:5:4395:U:O2	2.32	0.61
24:L:46:ILE:HB	24:L:49:ARG:HB2	1.83	0.61
28:N:115:VAL:HG21	28:N:160:GLU:HB3	1.82	0.61
42:5:1503:A:H4'	42:5:1504:G:H5'	1.83	0.61
42:5:2759:G:O2'	42:5:2762:G:N2	2.31	0.61
31:o:3:ASN:ND2	31:o:95:GLY:O	2.33	0.61
46:8:47:C:H1'	46:8:61:A:H2'	1.83	0.61
46:8:107:C:H2'	46:8:108:A:C8	2.36	0.61
18:H:41:ILE:HG12	18:H:73:ILE:HD11	1.82	0.61
23:k:34:PHE:HB2	23:k:45:LEU:HB3	1.83	0.61
27:m:110:CYS:O	27:m:117:HIS:ND1	2.32	0.61
42:5:1857:C:H2'	42:5:1858:A:H8	1.66	0.61
6:B:234:ARG:HH12	42:5:4566:U:HO2'	1.47	0.61
17:h:9:LEU:HD23	17:h:12:LYS:HZ1	1.65	0.61
25:l:21:ARG:HG2	25:l:22:PRO:HD2	1.83	0.61
42:5:2411:C:H2'	42:5:2412:A:C8	2.36	0.61
21:j:20:ARG:NH1	21:j:39:TYR:OH	2.34	0.61
42:5:2859:G:N2	42:5:3837:C:O2	2.33	0.61
45:Y:74:TYR:OH	46:8:75:G:OP2	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:h:112:ARG:NH1	42:5:266:C:O2	2.34	0.61
42:5:4527:G:OP2	42:5:4527:G:N2	2.30	0.61
12:E:119:ARG:O	42:5:959:G:O2'	2.18	0.60
20:I:166:HIS:NE2	38:T:160:ALA:O	2.34	0.60
36:R:78:ILE:HD13	36:R:81:ARG:HH21	1.65	0.60
42:5:2591:A:N6	42:5:2754:G:H21	1.99	0.60
30:O:42:ASN:HD22	30:O:125:LYS:HD3	1.65	0.60
42:5:2330:G:H2'	42:5:2331:G:C4	2.36	0.60
8:C:56:GLU:HG3	8:C:57:LEU:HD22	1.83	0.60
42:5:1174:G:H22	42:5:1187:G:H21	1.46	0.60
6:B:17:LEU:HG	6:B:18:PRO:HD3	1.82	0.60
9:d:41:ARG:NH1	42:5:4636:U:OP1	2.34	0.60
11:e:107:ASN:ND2	42:5:2303:C:OP1	2.34	0.60
13:f:21:GLN:NE2	42:5:1309:C:O2	2.34	0.60
24:L:88:LYS:NZ	42:5:159:C:O2	2.35	0.60
34:Q:79:THR:HG23	34:Q:99:LYS:HG2	1.84	0.60
4:A:200:ARG:NH2	42:5:3650:C:OP1	2.35	0.60
11:e:7:LEU:HD22	12:E:115:GLU:HG3	1.83	0.60
19:i:45:ARG:NH1	19:i:48:CYS:SG	2.74	0.60
35:r:28:GLU:OE2	35:r:31:ASN:ND2	2.34	0.60
4:A:147:ARG:HG2	4:A:157:VAL:HG22	1.83	0.60
42:5:1284:G:N1	42:5:2076:G:OP1	2.33	0.60
42:5:1332:C:H2'	42:5:1333:A:C8	2.36	0.60
42:5:1494:U:H2'	42:5:1495:G:C8	2.36	0.60
42:5:1645:C:H2'	42:5:1646:A:C8	2.37	0.60
42:5:2318:G:N2	42:5:2321:G:OP2	2.24	0.60
45:Y:56:GLN:NE2	45:Y:64:GLY:O	2.32	0.60
2:t:98:LYS:HB3	2:t:102:ILE:HB	1.82	0.60
15:g:6:THR:HG22	42:5:2400:G:H21	1.66	0.60
42:5:3648:A:H1'	42:5:3785:A:H61	1.66	0.60
47:K:96:GLN:HA	47:K:99:MET:HE2	1.83	0.60
32:P:109:GLN:NE2	42:5:3892:U:O2'	2.34	0.60
37:S:174:THR:HG1	42:5:4762:A:HO2'	1.45	0.60
42:5:960:A:N6	42:5:1283:G:O6	2.35	0.60
42:5:3823:G:H21	42:5:3824:A:H62	1.48	0.60
12:E:146:LEU:HD13	12:E:190:VAL:HG11	1.84	0.60
12:E:179:ARG:NH2	42:5:4937:C:O2	2.35	0.60
17:h:26:VAL:HG12	17:h:30:GLN:HE22	1.67	0.60
42:5:710:G:H2'	42:5:711:A:C8	2.37	0.60
47:K:153:GLU:HG3	47:K:157:GLN:HG2	1.83	0.60
36:R:108:ARG:NH2	42:5:2899:C:OP1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:U:25:CYS:HB3	39:U:112:LEU:HD13	1.83	0.59
42:5:32:G:H21	42:5:50:C:H5	1.50	0.59
42:5:669:C:H2'	42:5:670:G:H8	1.65	0.59
42:5:3786:U:OP1	42:5:4550:G:O2'	2.20	0.59
42:5:4232:U:H4'	42:5:4233:A:O5'	2.02	0.59
45:Y:33:PRO:HG2	45:Y:105:VAL:HG12	1.84	0.59
5:b:5:LYS:NZ	42:5:1873:A:OP2	2.34	0.59
6:B:315:ASN:HD21	6:B:326:VAL:H	1.49	0.59
9:d:85:ARG:HG3	9:d:109:VAL:HB	1.85	0.59
42:5:2601:A:N6	42:5:2744:A:OP2	2.35	0.59
8:C:95:MET:O	42:5:1335:G:N2	2.35	0.59
14:F:124:PHE:O	14:F:207:ASN:ND2	2.35	0.59
16:G:62:ARG:NH2	16:G:66:GLN:OE1	2.34	0.59
47:K:231:TRP:HB2	47:K:262:ALA:HB2	1.84	0.59
6:B:228:TYR:O	42:5:2835:A:O2'	2.19	0.59
42:5:56:A:H2'	42:5:57:G:C8	2.36	0.59
42:5:115:C:O2'	42:5:275:C:O2'	2.20	0.59
42:5:417:G:N2	46:8:16:G:O2'	2.32	0.59
42:5:3944:G:H2'	42:5:3945:A:C8	2.37	0.59
42:5:4153:C:H2'	42:5:4154:G:H8	1.67	0.59
4:A:158:ILE:HB	4:A:162:ASN:HD21	1.67	0.59
9:d:36:VAL:HG21	9:d:44:ARG:HG2	1.84	0.59
24:L:101:ARG:NH1	42:5:75:G:O2'	2.31	0.59
28:N:38:ARG:NH2	46:8:142:U:OP1	2.34	0.59
36:R:21:LYS:NZ	42:5:2822:G:OP2	2.35	0.59
42:5:308:G:OP2	42:5:308:G:N2	2.21	0.59
42:5:1503:A:H1'	42:5:1504:G:C8	2.38	0.59
42:5:3700:C:H2'	42:5:3746:A:H61	1.68	0.59
44:7:28:C:O2'	44:7:54:A:N1	2.35	0.59
12:E:132:HIS:HE1	42:5:710:G:H21	1.49	0.59
42:5:3717:A:OP2	42:5:3735:G:N2	2.36	0.59
5:b:44:ARG:NH2	42:5:1466:G:OP2	2.36	0.59
10:D:120:GLU:O	10:D:248:ARG:NH2	2.36	0.59
24:L:13:HIS:NE2	42:5:97:G:N7	2.47	0.59
30:O:89:PRO:HD3	42:5:1914:C:H4'	1.82	0.59
42:5:1371:A:N6	46:8:28:C:O2'	2.36	0.59
15:g:26:PRO:O	42:5:2638:G:N2	2.35	0.59
26:M:119:ARG:HE	26:M:123:ILE:HD11	1.68	0.59
5:b:30:GLU:OE1	38:T:63:ARG:NH1	2.33	0.59
6:B:261:ARG:HB2	30:O:64:THR:HG21	1.84	0.59
10:D:270:LYS:HD2	44:7:60:G:H5''	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:E:42:ARG:O	12:E:61:ARG:NH2	2.35	0.59
18:H:23:ARG:NH1	42:5:4764:A:OP1	2.32	0.59
8:C:149:GLU:HG2	8:C:151:PRO:HD2	1.83	0.59
30:O:10:ASP:OD2	30:O:37:ARG:NH2	2.35	0.59
42:5:1086:C:H2'	42:5:1087:A:H8	1.68	0.59
42:5:4421:C:H42	42:5:4475:G:N2	2.00	0.59
32:P:130:ASN:HD21	42:5:399:G:H21	1.50	0.58
42:5:215:C:H2'	42:5:220:C:H5'	1.84	0.58
42:5:703:G:N2	42:5:705:G:OP2	2.36	0.58
42:5:1480:C:O2'	42:5:1482:G:N2	2.36	0.58
42:5:4552:U:H2'	42:5:4553:A:C8	2.37	0.58
14:F:151:SER:HA	14:F:247:ARG:HH22	1.68	0.58
42:5:4128:A:H5'	48:Z:54:THR:HB	1.85	0.58
9:d:24:GLU:HA	9:d:87:ARG:HA	1.85	0.58
17:h:51:ARG:NH2	46:8:62:A:OP1	2.36	0.58
38:T:3:ASN:ND2	42:5:4219:A:OP2	2.37	0.58
12:E:222:ARG:HB2	12:E:229:PHE:HD1	1.68	0.58
26:M:119:ARG:HA	30:O:189:ILE:HD11	1.84	0.58
8:C:110:ARG:NH1	42:5:1508:A:OP1	2.33	0.58
12:E:228:ILE:HG13	12:E:229:PHE:H	1.68	0.58
42:5:70:A:OP2	49:a:64:LYS:NZ	2.34	0.58
42:5:1317:U:OP1	49:a:21:ARG:NH1	2.36	0.58
42:5:404:U:O2'	45:Y:87:ARG:NH2	2.36	0.58
42:5:1433:A:N6	42:5:1451:G:O2'	2.36	0.58
42:5:1669:A:N3	42:5:1852:U:O2'	2.35	0.58
42:5:2502:G:O2'	42:5:2503:G:O5'	2.20	0.58
4:A:183:GLY:HA2	42:5:1613:A:H5''	1.85	0.58
8:C:333:LYS:NZ	42:5:975:C:O2'	2.28	0.58
42:5:1278:C:H3'	42:5:1279:A:H4'	1.84	0.58
42:5:2811:G:H22	42:5:2813:A:H3'	1.68	0.58
42:5:4274:A:H2'	42:5:4275:G:H8	1.68	0.58
44:7:12:U:O4'	44:7:108:G:N2	2.32	0.58
42:5:713:C:H2'	42:5:714:G:H8	1.68	0.58
42:5:4967:A:H2'	42:5:4968:A:H8	1.69	0.58
48:Z:89:ILE:HD11	48:Z:117:LYS:HB3	1.86	0.58
7:c:50:ASN:ND2	7:c:75:SER:O	2.37	0.58
18:H:155:SER:HG	42:5:4688:C:HO2'	1.52	0.58
21:j:69:ILE:HG23	21:j:72:ARG:HH12	1.68	0.58
35:r:84:LYS:NZ	35:r:92:SER:OG	2.35	0.58
42:5:930:G:H4'	42:5:931:C:O5'	2.04	0.58
42:5:3709:U:HO2'	42:5:3710:G:H8	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:J:55:TYR:HH	42:5:4256:A:HO2'	1.49	0.58
42:5:491:G:H1'	42:5:665:C:H42	1.69	0.58
44:7:15:C:H2'	44:7:16:A:H8	1.69	0.58
12:E:215:LYS:NZ	42:5:4941:G:OP1	2.35	0.57
27:m:94:MET:HG2	27:m:121:LEU:HD23	1.85	0.57
38:T:75:VAL:HG22	38:T:88:ARG:HG2	1.86	0.57
42:5:660:A:H2'	42:5:661:C:C6	2.39	0.57
42:5:1645:C:H2'	42:5:1646:A:H8	1.68	0.57
12:E:70:ALA:HA	42:5:1273:G:H1'	1.85	0.57
12:E:84:VAL:HG23	42:5:2252:G:H3'	1.85	0.57
17:h:4:ILE:HD11	17:h:53:SER:HB3	1.85	0.57
42:5:2045:G:O6	42:5:3870:C:O2'	2.20	0.57
42:5:4126:C:H5''	42:5:4127:A:H5''	1.86	0.57
12:E:42:ARG:NH1	42:5:1070:G:N7	2.49	0.57
28:N:7:ILE:HA	28:N:10:LEU:HD12	1.85	0.57
30:O:148:LYS:NZ	42:5:4712:C:O3'	2.37	0.57
42:5:65:A:H61	42:5:75:G:H1'	1.70	0.57
47:K:281:THR:HA	47:K:284:LYS:HE3	1.86	0.57
4:A:117:GLU:HB2	4:A:162:ASN:HB2	1.84	0.57
19:i:45:ARG:NH1	19:i:49:GLY:O	2.37	0.57
32:P:107:TRP:CD1	32:P:109:GLN:H	2.23	0.57
42:5:1333:A:H2'	42:5:1334:A:H8	1.69	0.57
49:a:110:LYS:HB3	49:a:128:PHE:HB2	1.87	0.57
6:B:357:ARG:HD2	42:5:4615:C:H5''	1.85	0.57
36:R:28:GLU:HG3	36:R:49:LEU:HD11	1.87	0.57
42:5:1461:C:H2'	42:5:1462:A:H8	1.68	0.57
42:5:4635:A:H8	42:5:5048:A:H61	1.50	0.57
42:5:4891:G:O6	42:5:4929:C:N4	2.37	0.57
8:C:209:VAL:HG22	8:C:251:ILE:HD11	1.87	0.57
11:e:127:ALA:HB1	42:5:2326:G:H5''	1.86	0.57
16:G:83:PHE:HB3	16:G:159:HIS:HB2	1.84	0.57
30:O:54:TYR:OH	30:O:73:PHE:O	2.23	0.57
42:5:4454:G:O6	42:5:4526:U:O4	2.23	0.57
12:E:103:VAL:HG22	42:5:687:U:H4'	1.87	0.57
42:5:1916:G:N3	42:5:2067:C:O2'	2.38	0.57
12:E:126:ARG:NH2	42:5:712:C:O2	2.37	0.57
13:f:93:PRO:HB2	13:f:95:LYS:HG2	1.86	0.57
42:5:4890:G:H2'	42:5:4891:G:H8	1.70	0.57
8:C:104:PRO:HD2	42:5:1517:G:H1	1.69	0.57
13:f:61:GLY:N	42:5:1293:G:OP2	2.31	0.57
42:5:279:A:H61	42:5:308:G:H1	1.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:1198:G:H2'	42:5:1199:G:H8	1.69	0.57
42:5:2335:C:H2'	42:5:2336:G:H8	1.69	0.57
42:5:1329:G:H2'	42:5:3865:A:H5'	1.86	0.57
32:P:149:ASN:HB3	46:8:13:G:H1'	1.86	0.56
42:5:1321:G:O4'	42:5:1891:A:N6	2.39	0.56
42:5:4650:G:H4'	42:5:5008:C:H4'	1.86	0.56
9:d:64:ILE:HG23	9:d:68:LEU:HD23	1.86	0.56
10:D:22:ARG:NH2	44:7:6:C:OP2	2.38	0.56
18:H:21:LYS:NZ	42:5:4864:U:OP1	2.38	0.56
42:5:350:C:OP1	42:5:2294:G:O2'	2.23	0.56
42:5:1320:U:O2'	42:5:1891:A:N1	2.31	0.56
42:5:4301:U:OP2	42:5:4303:C:N4	2.38	0.56
42:5:4949:G:N2	42:5:4950:U:H2'	2.20	0.56
2:t:101:ASN:HB3	2:t:131:LEU:HB3	1.86	0.56
6:B:316:PRO:HA	6:B:370:THR:HG22	1.87	0.56
8:C:329:ASN:ND2	14:F:157:TYR:OH	2.37	0.56
12:E:54:SER:HG	12:E:57:ALA:H	1.47	0.56
13:f:45:LYS:HD2	13:f:105:LEU:HA	1.86	0.56
16:G:197:LYS:NZ	42:5:148:C:OP2	2.33	0.56
18:H:72:THR:HG21	42:5:4700:A:N1	2.20	0.56
21:j:49:TRP:O	42:5:1646:A:O2'	2.20	0.56
28:N:120:TRP:HE1	28:N:123:GLU:HB3	1.70	0.56
37:S:80:ILE:HD11	37:S:126:ILE:HD12	1.86	0.56
42:5:2730:U:H2'	42:5:2731:C:H6	1.70	0.56
42:5:4866:C:H2'	42:5:4867:G:H8	1.70	0.56
42:5:4912:G:N7	42:5:4913:G:N2	2.53	0.56
43:X:91:GLU:HG3	43:X:147:LEU:HD21	1.88	0.56
6:B:161:ARG:NH1	6:B:182:GLU:OE2	2.38	0.56
6:B:370:THR:H	6:B:380:GLN:HE22	1.52	0.56
36:R:15:LEU:O	36:R:52:ARG:NH2	2.38	0.56
36:R:130:ASN:HD21	42:5:1571:G:H1'	1.68	0.56
42:5:4967:A:H2'	42:5:4968:A:C8	2.41	0.56
5:b:18:ARG:NH1	42:5:1686:C:O2'	2.38	0.56
8:C:3:CYS:SG	8:C:4:ALA:N	2.78	0.56
8:C:96:CYS:HA	42:5:2352:U:H1'	1.87	0.56
9:d:44:ARG:NH1	42:5:2833:A:OP1	2.38	0.56
10:D:23:ARG:NH1	42:5:4280:A:OP2	2.34	0.56
30:O:26:GLN:HE21	30:O:31:ARG:HD3	1.71	0.56
37:S:174:THR:OG1	42:5:4762:A:O2'	2.15	0.56
41:W:52:THR:HG23	41:W:55:TYR:H	1.71	0.56
42:5:3848:U:H2'	42:5:3849:A:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4413:C:H41	42:5:4429:C:H42	1.53	0.56
4:A:17:ARG:NH2	42:5:2450:G:OP1	2.37	0.56
4:A:54:ARG:HG2	4:A:56:ALA:H	1.70	0.56
6:B:286:LYS:HG2	6:B:332:MET:HE2	1.88	0.56
8:C:12:SER:OG	8:C:15:GLY:O	2.23	0.56
10:D:273:LEU:HD22	44:7:107:G:H5''	1.86	0.56
26:M:113:MET:O	26:M:117:LYS:HG2	2.06	0.56
34:Q:146:ARG:HG2	34:Q:148:VAL:H	1.70	0.56
38:T:3:ASN:ND2	42:5:4212:A:N1	2.50	0.56
42:5:3689:G:O2'	42:5:3818:U:OP2	2.24	0.56
42:5:4729:A:OP2	42:5:5068:G:N1	2.29	0.56
12:E:153:HIS:HB3	12:E:156:LYS:HD2	1.88	0.56
30:O:7:LEU:HB2	30:O:33:VAL:HG12	1.88	0.56
42:5:2399:G:O2'	42:5:2822:G:O2'	2.17	0.56
42:5:2557:G:O6	42:5:2570:U:O4	2.24	0.56
8:C:39:PHE:O	8:C:43:ASN:ND2	2.33	0.56
42:5:90:G:OP2	42:5:92:C:N4	2.39	0.56
42:5:93:G:H2'	42:5:94:A:C8	2.40	0.56
42:5:114:G:N2	42:5:277:G:O4'	2.38	0.56
42:5:700:G:H2'	42:5:701:G:C8	2.41	0.56
4:A:30:ARG:O	4:A:163:ARG:NH1	2.36	0.56
14:F:239:GLU:HG2	37:S:38:VAL:HG22	1.87	0.56
15:g:40:LYS:NZ	42:5:2601:A:OP1	2.33	0.56
28:N:143:ARG:HG2	28:N:152:THR:HG21	1.88	0.56
30:O:87:MET:SD	42:5:1912:G:N2	2.78	0.56
46:8:67:U:H2'	46:8:68:G:H8	1.71	0.56
8:C:223:ASN:ND2	42:5:223:G:N3	2.49	0.56
16:G:141:ASN:HD22	28:N:2:GLY:HA3	1.71	0.56
24:L:31:ARG:NH1	42:5:337:U:OP1	2.30	0.56
39:U:100:LEU:HD11	39:U:112:LEU:HB3	1.87	0.55
42:5:3835:C:H2'	42:5:3836:A:C8	2.41	0.55
9:d:19:GLU:OE1	9:d:92:ARG:NH1	2.40	0.55
31:o:2:VAL:N	31:o:90:HIS:O	2.39	0.55
32:P:137:ASP:N	32:P:181:GLU:OE2	2.38	0.55
42:5:1414:C:N4	42:5:1415:G:O6	2.40	0.55
42:5:3839:G:N2	42:5:3843:C:O2'	2.39	0.55
8:C:140:LYS:NZ	8:C:247:GLY:O	2.38	0.55
14:F:245:LEU:O	14:F:249:MET:HB2	2.06	0.55
25:l:48:LYS:NZ	42:5:2406:G:O2'	2.39	0.55
30:O:130:LYS:NZ	42:5:2055:G:O5'	2.38	0.55
42:5:4739:C:H2'	42:5:4740:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:252:ALA:HB1	42:5:4524:G:C2	2.42	0.55
6:B:371:THR:HB	6:B:377:GLY:HA3	1.87	0.55
17:h:96:ASN:ND2	42:5:137:G:OP1	2.39	0.55
18:H:113:GLU:HG2	18:H:125:ARG:HG2	1.88	0.55
25:l:46:ARG:HG2	25:l:47:THR:HG22	1.89	0.55
28:N:172:ARG:NH1	42:5:62:A:OP1	2.39	0.55
37:S:41:LYS:HD2	37:S:61:ILE:HG13	1.88	0.55
42:5:725:G:H2'	42:5:726:G:C8	2.41	0.55
42:5:1676:C:H41	42:5:4378:A:H5''	1.71	0.55
49:a:87:ARG:HG3	49:a:120:GLN:HE22	1.71	0.55
19:i:20:ASN:HD21	24:L:104:ASN:HD21	1.54	0.55
28:N:73:ARG:NH1	42:5:32:G:OP1	2.40	0.55
31:o:57:ARG:HH12	42:5:3924:C:H4'	1.70	0.55
38:T:43:LYS:HD3	42:5:1732:C:H5''	1.88	0.55
42:5:662:C:H2'	42:5:663:G:H8	1.71	0.55
42:5:1886:G:HO2'	42:5:1909:G:HO2'	1.52	0.55
42:5:4093:G:N2	42:5:4093:G:OP2	2.38	0.55
14:F:72:ARG:NH2	42:5:1211:G:OP1	2.40	0.55
16:G:87:LEU:HD11	16:G:182:CYS:HB2	1.88	0.55
18:H:47:LEU:HG	18:H:52:LYS:HD2	1.88	0.55
21:j:46:LYS:HD2	21:j:54:LYS:HE3	1.88	0.55
42:5:487:G:H2'	42:5:488:G:C8	2.42	0.55
42:5:2905:C:H2'	42:5:2906:G:H8	1.71	0.55
42:5:4537:C:N4	42:5:4538:G:O6	2.40	0.55
42:5:4870:G:H4'	42:5:4872:G:H4'	1.89	0.55
49:a:24:LYS:HD3	49:a:26:ARG:HH21	1.72	0.55
6:B:20:LYS:HD3	42:5:4717:A:H4'	1.88	0.55
6:B:215:GLU:OE2	6:B:349:LYS:NZ	2.27	0.55
17:h:66:LYS:HD3	17:h:69:LEU:HD11	1.88	0.55
42:5:181:C:N3	42:5:256:G:N2	2.55	0.55
42:5:2599:G:N2	42:5:2747:U:O4	2.39	0.55
42:5:4239:A:H2'	42:5:4240:G:C8	2.41	0.55
42:5:4871:C:H4'	42:5:4872:G:H5'	1.89	0.55
8:C:165:LYS:NZ	42:5:223:G:N7	2.44	0.55
28:N:94:PHE:O	42:5:300:A:O2'	2.20	0.55
39:U:21:PHE:HA	39:U:108:GLU:HG2	1.87	0.55
42:5:2738:C:O2'	42:5:2740:U:O2	2.25	0.55
42:5:3835:C:H2'	42:5:3836:A:H8	1.71	0.55
3:u:62:VAL:HG11	3:u:90:ILE:HD13	1.89	0.55
11:e:15:LYS:NZ	11:e:61:GLY:O	2.37	0.55
20:I:3:ARG:NH1	42:5:4431:U:OP2	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:O:106:ASP:O	42:5:4910:G:N2	2.40	0.55
42:5:2327:G:H2'	42:5:2328:G:H8	1.72	0.55
42:5:2407:G:OP2	42:5:2407:G:N2	2.32	0.55
42:5:1933:G:H2'	42:5:1934:A:C8	2.42	0.55
42:5:2869:U:O2'	42:5:2881:A:N7	2.36	0.55
10:D:8:LYS:NZ	42:5:4264:G:OP1	2.37	0.54
24:L:150:LEU:HD23	24:L:154:VAL:HG12	1.89	0.54
36:R:88:ARG:O	42:5:2725:A:N6	2.39	0.54
42:5:1398:A:O2'	42:5:1399:G:O5'	2.25	0.54
42:5:1505:C:H2'	42:5:1506:G:H8	1.72	0.54
42:5:3904:G:O2'	42:5:3905:A:OP1	2.23	0.54
42:5:4122:G:N2	48:Z:135:ARG:O	2.28	0.54
14:F:115:ARG:NH2	14:F:210:LEU:O	2.41	0.54
16:G:159:HIS:CD2	16:G:186:GLY:H	2.25	0.54
42:5:1637:A:OP1	42:5:1640:C:N4	2.36	0.54
42:5:1786:A:O2'	42:5:1788:A:OP2	2.16	0.54
42:5:5061:A:O2'	42:5:5062:G:OP2	2.21	0.54
49:a:71:PRO:HG2	49:a:108:TYR:HA	1.88	0.54
31:o:53:LYS:HE2	42:5:91:G:H4'	1.89	0.54
31:o:63:THR:HG22	31:o:89:LYS:HB3	1.90	0.54
42:5:2486:G:H2'	42:5:2487:G:C8	2.43	0.54
42:5:4925:U:O2	42:5:4926:C:N4	2.40	0.54
42:5:4992:G:H2'	42:5:4993:G:C8	2.42	0.54
7:c:29:LEU:HD12	7:c:91:VAL:HG21	1.89	0.54
12:E:250:ASP:HA	12:E:253:ILE:HG22	1.89	0.54
14:F:217:SER:OG	42:5:1905:U:O2	2.21	0.54
20:I:54:SER:HB3	20:I:135:ILE:HD11	1.89	0.54
30:O:156:LEU:HD13	30:O:159:LYS:HD2	1.88	0.54
42:5:65:A:N6	42:5:75:G:H1'	2.23	0.54
42:5:1382:G:H2'	42:5:1383:G:H8	1.72	0.54
42:5:4552:U:H2'	42:5:4553:A:H8	1.72	0.54
44:7:15:C:H2'	44:7:16:A:C8	2.41	0.54
11:e:98:GLU:OE1	42:5:2324:C:O2'	2.25	0.54
22:J:35:ARG:NH2	22:J:124:GLY:H	2.06	0.54
21:j:21:ARG:NH2	21:j:37:CYS:O	2.40	0.54
42:5:1188:C:H2'	42:5:1189:G:H8	1.71	0.54
42:5:1604:G:H2'	42:5:1605:G:C8	2.43	0.54
47:K:221:VAL:HG22	47:K:230:SER:HB3	1.90	0.54
11:e:105:SER:HB3	11:e:128:ARG:HG2	1.90	0.54
42:5:281:U:H2'	42:5:282:C:H6	1.72	0.54
42:5:1211:G:HO2'	42:5:1212:G:P	2.30	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:1775:A:H3'	42:5:1776:A:H8	1.73	0.54
17:h:87:LYS:HA	21:j:73:ARG:HH12	1.73	0.54
24:L:60:ARG:NH1	24:L:68:THR:O	2.41	0.54
31:o:67:VAL:HA	31:o:84:ALA:HA	1.90	0.54
42:5:1240:G:OP2	42:5:1271:G:O2'	2.23	0.54
44:7:110:G:H2'	44:7:111:C:C6	2.43	0.54
6:B:217:ILE:HD13	6:B:284:ILE:HD11	1.90	0.54
34:Q:122:THR:OG1	34:Q:124:ASP:OD1	2.21	0.54
42:5:62:A:N3	42:5:77:U:O2'	2.40	0.54
42:5:306:A:H2'	42:5:307:A:C8	2.43	0.54
42:5:3658:C:H2'	42:5:3659:G:C8	2.42	0.54
42:5:3823:G:N2	42:5:3824:A:H62	2.05	0.54
42:5:5002:U:H3	42:5:5045:G:H1	1.56	0.54
36:R:16:ARG:NH2	42:5:2523:G:OP1	2.41	0.54
42:5:92:C:C2	49:a:55:LYS:HD3	2.42	0.54
42:5:1865:G:N2	42:5:1868:A:OP2	2.32	0.54
42:5:2727:C:C2	42:5:2728:U:C5	2.96	0.54
8:C:221:PHE:HB3	8:C:227:ILE:HG21	1.90	0.53
11:e:78:LEU:O	35:r:20:ARG:NH2	2.38	0.53
18:H:115:ARG:HG2	18:H:123:ILE:HG22	1.89	0.53
18:H:176:LEU:HD21	27:m:86:ALA:HB3	1.90	0.53
32:P:8:PRO:HD3	32:P:178:ILE:HD13	1.90	0.53
35:r:63:VAL:HG12	35:r:79:ARG:HG2	1.90	0.53
39:U:65:ARG:HE	39:U:67:LYS:HA	1.72	0.53
42:5:208:A:N3	42:5:232:G:O2'	2.39	0.53
42:5:1741:G:N2	42:5:1781:U:OP1	2.35	0.53
6:B:92:TYR:HB2	6:B:159:VAL:HB	1.91	0.53
12:E:58:MET:SD	12:E:58:MET:N	2.66	0.53
25:l:41:ARG:NH1	42:5:2431:A:OP1	2.23	0.53
31:o:13:LYS:NZ	42:5:4294:C:H4'	2.22	0.53
42:5:4524:G:OP1	42:5:4559:A:N6	2.40	0.53
42:5:4661:G:N2	42:5:5004:C:O3'	2.41	0.53
42:5:4860:G:H2'	42:5:4861:G:H8	1.73	0.53
47:K:278:ASN:O	47:K:281:THR:OG1	2.24	0.53
12:E:174:PRO:HB2	12:E:177:LEU:HB2	1.90	0.53
28:N:74:PRO:HA	42:5:3670:C:C2	2.44	0.53
44:7:57:C:H2'	44:7:58:A:H8	1.71	0.53
47:K:445:ILE:HB	47:K:452:TYR:HB2	1.89	0.53
4:A:179:ILE:HG21	4:A:185:ALA:HB2	1.90	0.53
11:e:124:ASN:HB2	11:e:127:ALA:HB2	1.90	0.53
30:O:54:TYR:CD2	30:O:145:VAL:HG21	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:325:U:H2'	42:5:326:C:C6	2.44	0.53
42:5:487:G:H2'	42:5:488:G:H8	1.72	0.53
42:5:2704:C:H2'	42:5:2705:G:H8	1.72	0.53
42:5:4188:U:H2'	42:5:4189:U:C6	2.43	0.53
42:5:4730:C:O5'	42:5:4731:G:N2	2.41	0.53
8:C:192:GLY:O	8:C:195:LYS:NZ	2.41	0.53
29:n:10:MET:HE2	29:n:14:LYS:HE2	1.89	0.53
42:5:7:C:H42	46:8:149:G:H1	1.57	0.53
42:5:178:C:H2'	42:5:179:G:C8	2.44	0.53
42:5:436:C:H2'	42:5:437:G:H8	1.73	0.53
42:5:1241:C:OP1	42:5:1242:G:N2	2.41	0.53
42:5:2028:C:H2'	42:5:2029:A:H8	1.73	0.53
42:5:4964:C:H2'	42:5:4965:U:C2	2.44	0.53
11:e:7:LEU:O	42:5:701:G:O2'	2.27	0.53
17:h:3:LYS:NZ	46:8:81:C:OP1	2.41	0.53
42:5:1074:G:N2	42:5:1238:A:N1	2.57	0.53
42:5:2647:A:H62	42:5:2686:G:H8	1.57	0.53
15:g:108:LYS:HE2	15:g:112:GLN:HE21	1.74	0.53
36:R:82:LYS:O	42:5:2863:G:O2'	2.25	0.53
42:5:86:U:H2'	42:5:87:A:C8	2.44	0.53
42:5:4170:A:H4'	42:5:4171:C:O5'	2.07	0.53
45:Y:50:ARG:NH1	46:8:71:A:OP2	2.42	0.53
48:Z:21:ARG:NH1	48:Z:47:ASP:O	2.41	0.53
6:B:329:ASP:OD1	6:B:329:ASP:N	2.41	0.53
6:B:385:LYS:NZ	42:5:5002:U:OP2	2.40	0.53
42:5:1870:C:H2'	42:5:1871:A:H8	1.74	0.53
42:5:2902:G:H22	42:5:3597:G:H1	1.57	0.53
20:I:43:VAL:O	20:I:171:TRP:NE1	2.36	0.53
42:5:673:C:H2'	42:5:674:G:C8	2.44	0.53
42:5:2447:U:H2'	42:5:2448:G:H8	1.74	0.53
42:5:2730:U:H2'	42:5:2731:C:C6	2.44	0.53
42:5:2735:G:H2'	42:5:2736:G:H8	1.74	0.53
42:5:4239:A:H2'	42:5:4240:G:H8	1.74	0.53
42:5:4914:C:H2'	42:5:4915:G:C8	2.43	0.53
6:B:243:LYS:NZ	42:5:2854:G:O6	2.40	0.53
11:e:19:LYS:NZ	42:5:2318:G:O6	2.42	0.53
13:f:45:LYS:HA	13:f:107:PRO:HG2	1.91	0.53
42:5:1233:G:H2'	42:5:1234:G:C8	2.44	0.53
42:5:2395:A:O2'	42:5:2806:A:H1'	2.08	0.53
8:C:33:ARG:HG2	8:C:36:ILE:HD12	1.91	0.52
24:L:103:ARG:NH2	42:5:74:G:O6	2.36	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:M:70:GLN:HG3	42:5:733:A:O2'	2.09	0.52
42:5:496:G:H2'	42:5:497:G:C8	2.43	0.52
42:5:4123:C:N4	42:5:4124:G:O6	2.42	0.52
12:E:224:GLN:HA	12:E:229:PHE:HB2	1.92	0.52
42:5:48:G:H4'	42:5:49:U:O5'	2.09	0.52
42:5:2102:G:H2'	42:5:2103:G:C8	2.44	0.52
42:5:2848:G:O2'	42:5:3838:U:O4	2.22	0.52
8:C:141:GLY:O	8:C:182:LYS:NZ	2.43	0.52
12:E:39:HIS:HB3	42:5:979:C:H5''	1.90	0.52
17:h:24:LEU:HD21	17:h:53:SER:HB2	1.91	0.52
30:O:54:TYR:HD2	30:O:145:VAL:HG21	1.74	0.52
39:U:92:LYS:HG3	42:5:2626:U:H2'	1.90	0.52
42:5:422:C:H2'	42:5:423:G:C8	2.42	0.52
42:5:1436:C:O2'	42:5:2096:G:O3'	2.27	0.52
42:5:1475:G:H2'	42:5:1476:C:C6	2.44	0.52
42:5:2266:C:H5'	42:5:2270:G:N3	2.24	0.52
42:5:2568:C:H2'	42:5:2569:G:H8	1.74	0.52
42:5:3635:A:C4	42:5:3692:A:H1'	2.45	0.52
42:5:4642:U:H2'	42:5:4643:G:H8	1.75	0.52
42:5:4922:C:H2'	42:5:4923:C:C6	2.44	0.52
48:Z:53:VAL:HG12	48:Z:55:ALA:H	1.75	0.52
10:D:259:ARG:HG3	10:D:260:GLU:H	1.75	0.52
16:G:64:GLN:HE22	46:8:149:G:H21	1.57	0.52
28:N:76:PRO:HG2	28:N:79:ALA:HB2	1.91	0.52
42:5:976:G:N2	42:5:1280:C:OP1	2.42	0.52
42:5:2839:U:O4	42:5:2840:A:N6	2.42	0.52
42:5:229:G:H2'	42:5:230:G:H8	1.75	0.52
42:5:1356:U:H1'	42:5:1505:C:H1'	1.92	0.52
42:5:1818:G:OP2	42:5:1818:G:N2	2.37	0.52
42:5:2520:C:H1'	42:5:2640:G:H21	1.75	0.52
42:5:3732:A:H2'	42:5:3733:A:C8	2.44	0.52
42:5:4593:C:H2'	42:5:4594:U:H6	1.75	0.52
4:A:181:LYS:HB2	4:A:184:ARG:HG2	1.91	0.52
6:B:248:LEU:HD12	6:B:249:ARG:HG3	1.91	0.52
15:g:67:LEU:HB2	15:g:72:LYS:HE3	1.92	0.52
42:5:1556:C:O2'	42:5:2669:C:OP1	2.20	0.52
42:5:2622:G:H2'	42:5:2623:A:H8	1.75	0.52
42:5:4923:C:H2'	42:5:4924:C:C6	2.45	0.52
46:8:8:U:H2'	46:8:9:A:H8	1.74	0.52
8:C:264:TYR:HB3	8:C:279:LEU:HD21	1.90	0.52
28:N:114:ARG:HG2	28:N:137:PRO:HG3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:S:11:LYS:HE2	37:S:29:ARG:HE	1.72	0.52
37:S:95:ARG:NH1	42:5:1951:G:O2'	2.43	0.52
38:T:41:ASP:HB3	38:T:61:THR:HG22	1.91	0.52
42:5:1188:C:H2'	42:5:1189:G:C8	2.45	0.52
42:5:4260:U:C2	42:5:4261:C:C5	2.98	0.52
4:A:178:PRO:HD2	33:p:26:VAL:HG12	1.91	0.52
10:D:205:ALA:HB1	10:D:233:PRO:HB3	1.92	0.52
15:g:60:ARG:HB2	15:g:63:VAL:HG23	1.92	0.52
17:h:76:LYS:O	42:5:136:C:N4	2.42	0.52
40:V:26:ILE:HG22	40:V:101:ASN:HB3	1.92	0.52
42:5:68:U:O2'	42:5:100:C:O3'	2.28	0.52
42:5:86:U:H2'	42:5:87:A:H8	1.75	0.52
42:5:4274:A:H2'	42:5:4275:G:C8	2.44	0.52
42:5:4396:A:N6	42:5:4447:C:O2	2.43	0.52
10:D:135:ILE:HG23	10:D:138:GLN:HB2	1.91	0.52
13:f:68:ARG:NH1	42:5:442:G:OP1	2.38	0.52
20:I:38:ARG:HD3	20:I:83:ASP:HB2	1.90	0.52
24:L:14:PHE:HE2	42:5:1342:A:H1'	1.74	0.52
42:5:386:A:O2'	45:Y:87:ARG:NH1	2.43	0.52
42:5:1236:C:O2'	42:5:1237:C:O5'	2.24	0.52
49:a:38:MET:HB3	49:a:42:ARG:HH21	1.74	0.52
34:Q:175:GLU:HB2	42:5:1497:A:H61	1.73	0.52
42:5:268:G:H2'	42:5:269:G:H8	1.75	0.52
42:5:407:A:O2'	42:5:410:A:OP1	2.28	0.52
42:5:2503:G:N2	42:5:2505:C:H41	2.08	0.52
42:5:3911:C:H2'	42:5:3912:U:H6	1.74	0.52
8:C:231:ASN:ND2	8:C:233:THR:OG1	2.43	0.51
20:I:57:TYR:HD1	20:I:130:HIS:HA	1.75	0.51
42:5:175:C:H2'	42:5:176:G:H8	1.76	0.51
42:5:3658:C:H2'	42:5:3659:G:H8	1.75	0.51
6:B:31:SER:OG	42:5:4714:C:OP1	2.23	0.51
6:B:175:GLN:HG3	42:5:4985:U:H4'	1.92	0.51
11:e:124:ASN:ND2	42:5:2325:C:O2'	2.43	0.51
26:M:37:LEU:HD21	26:M:47:ARG:HD3	1.92	0.51
36:R:105:LEU:HD23	36:R:138:LEU:HD23	1.91	0.51
42:5:4238:G:H2'	42:5:4239:A:H8	1.75	0.51
14:F:34:ARG:NH2	42:5:2258:C:OP2	2.42	0.51
22:J:41:GLU:HG2	22:J:47:THR:HA	1.93	0.51
24:L:183:ARG:NH1	42:5:1488:G:OP1	2.43	0.51
28:N:116:LEU:HD22	28:N:135:ILE:HD11	1.92	0.51
42:5:1461:C:H2'	42:5:1462:A:C8	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:1939:A:H5'	42:5:1940:G:H4'	1.92	0.51
42:5:1954:U:H2'	42:5:1955:G:C8	2.44	0.51
42:5:2611:A:H2'	42:5:2612:G:H8	1.75	0.51
45:Y:50:ARG:NH2	46:8:83:C:O2	2.43	0.51
16:G:169:PHE:HZ	28:N:3:ALA:HB1	1.76	0.51
17:h:21:LEU:HB2	17:h:57:VAL:HG11	1.92	0.51
42:5:953:C:H2'	42:5:954:C:C6	2.45	0.51
42:5:1504:G:H2'	42:5:1505:C:H6	1.75	0.51
42:5:2519:U:O2'	42:5:2530:U:O2	2.22	0.51
46:8:12:G:C2	46:8:13:G:C8	2.98	0.51
11:e:126:ASN:HB2	11:e:129:LEU:HD11	1.93	0.51
18:H:8:GLN:HE22	18:H:71:ARG:HD2	1.74	0.51
28:N:8:GLN:OE1	28:N:12:ARG:NH2	2.44	0.51
31:o:8:ARG:NH2	42:5:4292:A:O2'	2.39	0.51
32:P:101:GLN:NE2	32:P:112:TRP:HE1	2.09	0.51
42:5:2415:U:H2'	42:5:2416:G:C8	2.45	0.51
42:5:4737:G:H5''	42:5:5069:U:H2'	1.93	0.51
4:A:113:VAL:HG12	4:A:166:VAL:HA	1.92	0.51
15:g:29:ARG:NH2	42:5:2522:G:OP1	2.44	0.51
18:H:47:LEU:HD11	18:H:52:LYS:HB3	1.92	0.51
42:5:430:G:H1	46:8:4:C:H42	1.59	0.51
42:5:1838:A:H2'	42:5:1839:U:C6	2.45	0.51
42:5:2052:G:O2'	42:5:2057:A:N1	2.41	0.51
42:5:4569:U:OP1	42:5:4982:A:O2'	2.29	0.51
42:5:4688:C:H2'	42:5:4689:U:C6	2.45	0.51
6:B:116:ARG:HH22	42:5:4987:C:P	2.33	0.51
9:d:18:ASN:O	9:d:90:ARG:NH2	2.43	0.51
16:G:185:LYS:O	16:G:189:ARG:NH1	2.43	0.51
42:5:1198:G:H2'	42:5:1199:G:C8	2.45	0.51
42:5:1333:A:H2'	42:5:1334:A:C8	2.46	0.51
42:5:1727:U:H2'	42:5:1728:U:C6	2.46	0.51
42:5:1937:C:OP2	42:5:1938:C:O2'	2.27	0.51
42:5:3890:A:N6	42:5:4571:A:O4'	2.44	0.51
42:5:4413:C:H41	42:5:4429:C:N4	2.09	0.51
4:A:8:GLN:NE2	42:5:3668:C:OP1	2.41	0.51
6:B:234:ARG:NH1	42:5:4566:U:O2'	2.34	0.51
14:F:229:PHE:N	14:F:235:ALA:O	2.41	0.51
32:P:50:ASN:H	32:P:174:HIS:HD2	1.57	0.51
37:S:23:ARG:NH1	42:5:1199:G:O4'	2.43	0.51
42:5:3944:G:H2'	42:5:3945:A:H8	1.76	0.51
42:5:4434:C:H2'	42:5:4435:U:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4563:U:C2	42:5:4564:A:C8	2.99	0.51
6:B:373:LYS:HD2	42:5:4627:U:H4'	1.91	0.51
12:E:114:THR:HG23	12:E:115:GLU:HG2	1.92	0.51
14:F:244:ARG:NE	42:5:942:G:OP2	2.35	0.51
16:G:143:VAL:HG22	16:G:203:ALA:HB2	1.93	0.51
22:J:55:TYR:OH	42:5:4256:A:O2'	2.22	0.51
22:J:108:GLY:HA2	22:J:129:ASP:HA	1.93	0.51
31:o:18:HIS:N	42:5:4318:C:O2'	2.43	0.51
37:S:115:ALA:HB2	42:5:2060:G:N2	2.26	0.51
42:5:184:U:O4	42:5:253:G:O6	2.28	0.51
42:5:2699:C:H2'	42:5:2700:G:H8	1.75	0.51
42:5:3867:A:H2'	42:5:3868:G:C8	2.46	0.51
42:5:4153:C:H2'	42:5:4154:G:C8	2.46	0.51
47:K:133:TYR:OH	47:K:138:GLU:OE1	2.26	0.51
35:r:26:SER:OG	35:r:31:ASN:ND2	2.43	0.51
39:U:84:LYS:HG3	39:U:102:VAL:HG21	1.92	0.51
42:5:1565:A:C5	42:5:1566:C:H1'	2.46	0.51
16:G:162:ASP:HB3	16:G:163:PRO:HD3	1.93	0.50
31:o:70:LEU:HD13	31:o:83:LEU:HD13	1.93	0.50
36:R:4:LEU:HB2	42:5:2386:U:H5'	1.93	0.50
40:V:75:LYS:HG3	40:V:77:HIS:CE1	2.46	0.50
42:5:661:C:H2'	42:5:662:C:C6	2.45	0.50
42:5:1940:G:N2	42:5:4434:C:OP1	2.38	0.50
42:5:2539:C:H2'	42:5:2540:C:C6	2.45	0.50
42:5:3722:G:H2'	42:5:3723:A:H8	1.76	0.50
42:5:3853:U:O2'	42:5:4979:A:N3	2.44	0.50
42:5:4135:G:H2'	42:5:4136:G:H8	1.76	0.50
42:5:4730:C:H5''	42:5:4965:U:C4	2.46	0.50
45:Y:8:THR:HG21	45:Y:13:LYS:HB2	1.93	0.50
47:K:149:PRO:O	47:K:155:TRP:NE1	2.35	0.50
4:A:132:ASN:ND2	42:5:3683:C:OP1	2.43	0.50
6:B:60:VAL:HG12	6:B:62:ARG:HG2	1.93	0.50
13:f:36:ARG:HB2	13:f:80:ASN:HA	1.92	0.50
20:I:195:CYS:N	42:5:1750:G:O2'	2.43	0.50
20:I:201:PRO:HB2	20:I:203:ARG:HG2	1.92	0.50
21:j:48:ASN:N	42:5:52:G:OP1	2.40	0.50
36:R:117:ARG:HD2	42:5:2663:G:H4'	1.94	0.50
42:5:961:G:H22	42:5:969:C:H5'	1.76	0.50
42:5:2607:C:H2'	42:5:2608:G:H8	1.76	0.50
46:8:119:C:H2'	46:8:120:G:H8	1.77	0.50
32:P:91:ARG:NH1	42:5:423:G:OP1	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:184:U:O2	42:5:253:G:N2	2.27	0.50
42:5:231:U:O2	45:Y:103:LYS:NZ	2.31	0.50
42:5:1340:C:OP2	49:a:6:ARG:NH1	2.42	0.50
42:5:1542:U:H5''	42:5:2743:A:C6	2.46	0.50
42:5:3855:C:H2'	42:5:3856:A:H8	1.75	0.50
17:h:22:ASP:OD1	43:X:74:TYR:OH	2.27	0.50
32:P:93:ASN:ND2	42:5:3891:A:O2'	2.44	0.50
35:r:51:VAL:HB	35:r:113:ARG:HD3	1.93	0.50
42:5:1669:A:H4'	42:5:1685:G:H21	1.75	0.50
42:5:1918:U:O2	42:5:2064:G:O6	2.29	0.50
10:D:225:GLN:HG2	44:7:49:A:H5''	1.94	0.50
42:5:1484:G:O2'	42:5:1486:C:OP2	2.29	0.50
42:5:1760:G:C6	42:5:1773:U:O2	2.65	0.50
42:5:2386:U:H2'	42:5:2387:G:H8	1.76	0.50
42:5:3833:C:H2'	42:5:3834:C:H6	1.76	0.50
22:J:74:VAL:HG22	22:J:79:ALA:HB2	1.93	0.50
36:R:117:ARG:HH11	42:5:2663:G:H4'	1.75	0.50
39:U:27:HIS:CD2	39:U:28:PRO:HD3	2.46	0.50
41:W:8:PHE:HB3	41:W:36:CYS:SG	2.51	0.50
42:5:657:C:H2'	42:5:658:C:C6	2.46	0.50
42:5:287:U:H2'	42:5:288:G:C8	2.46	0.50
42:5:3664:G:H2'	42:5:3665:G:H8	1.77	0.50
47:K:391:VAL:HG23	47:K:392:PHE:HD2	1.77	0.50
4:A:72:ARG:NH2	42:5:4084:G:N7	2.60	0.50
6:B:44:THR:OG1	6:B:184:GLN:O	2.26	0.50
18:H:44:GLU:OE2	26:M:2:VAL:N	2.45	0.50
34:Q:82:VAL:HG11	34:Q:86:ILE:HD11	1.93	0.50
42:5:696:C:H5''	42:5:697:G:H5'	1.93	0.50
42:5:1177:U:H2'	42:5:1178:G:C8	2.47	0.50
42:5:1920:C:H3'	42:5:1921:C:H5''	1.93	0.50
42:5:3808:C:H2'	42:5:3809:G:C4	2.47	0.50
42:5:4421:C:N4	42:5:4475:G:H22	2.10	0.50
42:5:5063:G:H2'	42:5:5064:G:H8	1.76	0.50
44:7:63:C:H5'	44:7:64:G:H5''	1.94	0.50
31:o:44:LYS:NZ	42:5:91:G:O5'	2.44	0.50
42:5:2409:U:H4'	42:5:2428:A:H4'	1.94	0.50
42:5:3927:U:H2'	42:5:3928:A:H8	1.77	0.50
42:5:4870:G:OP2	42:5:4870:G:N2	2.41	0.50
22:J:112:HIS:CE1	22:J:126:TYR:H	2.30	0.49
26:M:13:ALA:HA	26:M:57:LEU:HA	1.93	0.49
34:Q:86:ILE:HB	34:Q:105:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:953:C:H2'	42:5:954:C:H6	1.76	0.49
42:5:1504:G:H2'	42:5:1505:C:C6	2.47	0.49
42:5:1688:G:H2'	42:5:1689:G:C8	2.47	0.49
42:5:4135:G:H2'	42:5:4136:G:C8	2.47	0.49
14:F:190:GLU:OE1	42:5:944:A:N6	2.45	0.49
26:M:130:LEU:HD22	30:O:177:LEU:HG	1.93	0.49
28:N:182:HIS:HD2	28:N:183:THR:HG23	1.76	0.49
42:5:1739:G:H2'	42:5:1740:C:C6	2.46	0.49
42:5:2622:G:H2'	42:5:2623:A:C8	2.47	0.49
42:5:4069:U:O2'	42:5:4070:U:OP1	2.27	0.49
42:5:5005:G:N2	42:5:5041:G:O2'	2.45	0.49
3:u:45:GLN:HE22	3:u:80:GLN:HE22	1.60	0.49
24:L:58:ILE:HG23	24:L:70:VAL:HG11	1.94	0.49
42:5:16:G:H5''	43:X:60:TYR:HE1	1.77	0.49
42:5:67:C:N4	42:5:325:U:O2'	2.36	0.49
42:5:1655:C:OP2	49:a:26:ARG:NH1	2.46	0.49
42:5:2038:U:H2'	42:5:2039:G:O4'	2.13	0.49
42:5:2362:U:H2'	42:5:2363:A:H8	1.78	0.49
42:5:4407:G:H2'	42:5:4408:G:C8	2.47	0.49
16:G:69:ILE:HG23	16:G:73:ARG:HE	1.78	0.49
16:G:137:ARG:HB2	16:G:203:ALA:HB3	1.94	0.49
27:m:94:MET:N	27:m:103:LEU:O	2.41	0.49
42:5:115:C:O2'	42:5:276:C:OP1	2.31	0.49
42:5:710:G:H2'	42:5:711:A:H8	1.78	0.49
42:5:1810:G:H2'	42:5:1811:G:H8	1.77	0.49
42:5:2260:C:H2'	42:5:2261:G:C8	2.48	0.49
42:5:2906:G:H2'	42:5:2907:G:C8	2.47	0.49
42:5:4263:C:H2'	42:5:4264:G:O4'	2.13	0.49
42:5:4291:G:H5''	42:5:4293:U:C6	2.47	0.49
42:5:4492:U:H5''	42:5:4493:U:H5'	1.94	0.49
6:B:48:GLY:HA3	6:B:81:THR:HG22	1.94	0.49
6:B:220:ILE:HG23	6:B:278:THR:HG22	1.93	0.49
17:h:28:LEU:HB2	17:h:50:VAL:HG11	1.93	0.49
34:Q:73:PRO:O	42:5:1456:C:O2'	2.28	0.49
42:5:1233:G:H2'	42:5:1234:G:H8	1.77	0.49
42:5:1804:A:H4'	42:5:1805:A:O5'	2.13	0.49
42:5:2535:G:H2'	42:5:2536:A:C8	2.47	0.49
42:5:2745:A:H2'	42:5:2746:A:C8	2.45	0.49
42:5:4458:C:H2'	42:5:4459:U:C6	2.47	0.49
42:5:4704:C:H2'	42:5:4705:A:H8	1.77	0.49
47:K:80:PHE:HD2	47:K:271:SER:HB3	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:b:35:VAL:HB	5:b:40:LEU:HD23	1.94	0.49
13:f:71:TRP:HE1	42:5:4945:G:N2	2.11	0.49
42:5:1795:A:N3	44:7:79:U:O2'	2.43	0.49
42:5:2457:G:O2'	42:5:3672:G:O2'	2.28	0.49
42:5:2520:C:H2'	42:5:2521:G:H8	1.77	0.49
42:5:3916:G:H2'	42:5:3917:A:H8	1.77	0.49
42:5:4759:C:H2'	42:5:4760:G:O4'	2.13	0.49
46:8:30:U:H2'	46:8:31:G:H8	1.77	0.49
6:B:82:PRO:HG3	6:B:171:LEU:HD21	1.94	0.49
20:I:118:ALA:O	42:5:1864:G:O2'	2.22	0.49
28:N:93:LYS:HG3	42:5:300:A:C2	2.47	0.49
36:R:8:LYS:HG3	36:R:22:VAL:HG21	1.93	0.49
42:5:138:G:H2'	42:5:139:G:C8	2.47	0.49
42:5:909:A:H2'	42:5:910:G:C8	2.47	0.49
42:5:1190:C:H2'	42:5:1191:C:C6	2.47	0.49
42:5:1193:C:H2'	42:5:1194:G:H8	1.78	0.49
42:5:1380:G:O2'	42:5:1382:G:O6	2.23	0.49
42:5:4594:U:H2'	42:5:4595:G:C8	2.45	0.49
46:8:30:U:H2'	46:8:31:G:C8	2.48	0.49
6:B:268:ARG:HH21	42:5:3896:C:H1'	1.78	0.49
13:f:40:GLU:O	13:f:109:ARG:NH2	2.46	0.49
16:G:223:ARG:HD2	16:G:227:ASN:HD22	1.78	0.49
35:r:82:ILE:HD11	35:r:89:THR:HA	1.94	0.49
38:T:92:ARG:NH2	42:5:4313:A:OP1	2.42	0.49
42:5:709:C:H2'	42:5:710:G:C8	2.45	0.49
42:5:2490:U:H3'	42:5:2491:C:C6	2.48	0.49
42:5:2638:G:N7	42:5:2718:U:H2'	2.28	0.49
42:5:4592:C:H2'	42:5:4593:C:C6	2.48	0.49
10:D:36:LEU:HD23	42:5:4325:A:H1'	1.94	0.49
42:5:475:G:H2'	42:5:476:G:H8	1.78	0.49
42:5:1241:C:H3'	42:5:1242:G:H5''	1.95	0.49
42:5:2753:G:H2'	42:5:2754:G:C4	2.48	0.49
49:a:36:GLY:O	49:a:41:HIS:HB2	2.13	0.49
49:a:82:VAL:HG12	49:a:105:ARG:HH22	1.77	0.49
8:C:45:ARG:NH1	42:5:2295:C:O2'	2.39	0.49
8:C:230:LEU:HD23	8:C:239:LYS:HD2	1.95	0.49
28:N:4:TYR:HA	28:N:7:ILE:HG22	1.94	0.49
37:S:19:THR:HG23	37:S:22:CYS:H	1.78	0.49
42:5:229:G:H5''	45:Y:11:ARG:HG3	1.94	0.49
42:5:2607:C:H2'	42:5:2608:G:C8	2.47	0.49
42:5:3584:C:H2'	42:5:3585:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4312:U:H2'	42:5:4313:A:H8	1.77	0.49
42:5:5006:U:H4'	42:5:5007:A:H5'	1.94	0.49
48:Z:88:ASP:OD1	48:Z:121:ARG:NH1	2.45	0.49
6:B:184:GLN:HE21	6:B:186:ASN:HD21	1.61	0.48
16:G:160:ASP:OD1	16:G:187:LYS:N	2.43	0.48
16:G:166:LEU:HD21	28:N:45:PRO:HG2	1.94	0.48
30:O:23:VAL:HG13	30:O:33:VAL:HG21	1.95	0.48
31:o:17:LYS:HA	42:5:4318:C:H4'	1.94	0.48
35:r:97:ILE:HD13	35:r:107:ARG:HA	1.94	0.48
42:5:1340:C:H2'	42:5:1341:U:C6	2.48	0.48
42:5:2517:A:N3	42:5:2539:C:O2'	2.44	0.48
16:G:76:VAL:O	16:G:81:ASN:ND2	2.46	0.48
25:l:43:HIS:NE2	42:5:2429:A:OP1	2.40	0.48
42:5:676:C:H2'	42:5:677:G:C8	2.48	0.48
42:5:2502:G:HO2'	42:5:2503:G:P	2.36	0.48
42:5:2894:A:H2'	42:5:2895:A:C8	2.49	0.48
42:5:4875:G:C5	42:5:4878:C:H4'	2.48	0.48
14:F:78:ARG:NH1	42:5:729:G:OP2	2.46	0.48
14:F:83:PHE:HB2	38:T:141:VAL:HG23	1.94	0.48
26:M:24:LEU:HD11	26:M:86:TRP:CG	2.47	0.48
32:P:81:THR:HG23	32:P:114:LYS:HE3	1.95	0.48
41:W:19:ARG:NH1	42:5:4629:U:O2'	2.46	0.48
42:5:469:C:H3'	42:5:683:C:H42	1.77	0.48
42:5:978:G:H2'	42:5:979:C:C6	2.48	0.48
42:5:2578:G:H2'	42:5:2579:G:C8	2.48	0.48
3:u:36:THR:HG22	3:u:38:THR:H	1.78	0.48
6:B:11:HIS:NE2	42:5:4458:C:OP1	2.44	0.48
6:B:224:LYS:HD3	6:B:340:THR:HB	1.95	0.48
8:C:271:ALA:O	8:C:273:LEU:N	2.47	0.48
18:H:41:ILE:HG23	18:H:43:VAL:HG13	1.95	0.48
26:M:104:MET:HG2	26:M:109:ARG:HG3	1.95	0.48
28:N:187:SER:H	28:N:190:ALA:HB3	1.77	0.48
32:P:7:ASP:OD1	32:P:7:ASP:N	2.45	0.48
35:r:47:LYS:O	35:r:103:HIS:ND1	2.47	0.48
42:5:491:G:H21	42:5:663:G:H1	1.61	0.48
42:5:1514:U:H2'	42:5:1515:A:C8	2.48	0.48
42:5:1655:C:O2	42:5:4390:A:O2'	2.31	0.48
42:5:1942:A:H2'	42:5:1943:A:C8	2.48	0.48
42:5:1950:U:H2'	42:5:1951:G:H8	1.78	0.48
42:5:2521:G:H2'	42:5:2522:G:H8	1.77	0.48
42:5:3736:A:H2'	42:5:3737:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:3916:G:H2'	42:5:3917:A:C8	2.48	0.48
47:K:388:GLY:HA3	47:K:406:LEU:HG	1.96	0.48
16:G:86:VAL:HG13	16:G:183:ILE:HG22	1.95	0.48
30:O:8:VAL:HG12	30:O:117:ARG:HG3	1.95	0.48
31:o:68:LEU:N	31:o:83:LEU:O	2.33	0.48
42:5:185:C:O2'	42:5:189:G:OP1	2.25	0.48
42:5:1524:A:H61	42:5:1651:G:H22	1.60	0.48
42:5:2809:G:O2'	42:5:4644:G:OP1	2.31	0.48
42:5:2810:U:H2'	42:5:2811:G:O4'	2.13	0.48
42:5:3720:G:H22	42:5:3733:A:H2	1.61	0.48
42:5:4477:A:O2'	42:5:4603:C:O2'	2.27	0.48
42:5:4918:C:N4	42:5:4919:G:O6	2.46	0.48
42:5:5061:A:H4'	42:5:5062:G:H5''	1.96	0.48
22:J:20:LEU:HB3	22:J:74:VAL:HG13	1.93	0.48
28:N:67:ARG:HE	42:5:2458:C:H5''	1.77	0.48
40:V:97:TYR:OH	41:W:37:GLU:OE2	2.23	0.48
42:5:1396:G:O2'	42:5:1468:C:O2'	2.25	0.48
42:5:1617:G:H1'	42:5:2513:A:N6	2.27	0.48
42:5:4421:C:O2'	42:5:4422:A:H5'	2.13	0.48
21:j:82:THR:OG1	46:8:94:G:N2	2.43	0.48
34:Q:3:VAL:HG21	42:5:2277:C:H5''	1.96	0.48
42:5:13:U:O4	46:8:115:G:N2	2.39	0.48
42:5:58:G:H4'	42:5:59:A:H4'	1.96	0.48
42:5:167:C:H2'	42:5:168:C:C6	2.48	0.48
42:5:658:C:H2'	42:5:659:G:C8	2.43	0.48
42:5:1687:U:H2'	42:5:1688:G:C8	2.49	0.48
42:5:1895:G:O2'	42:5:1907:A:N3	2.35	0.48
42:5:3633:C:H2'	42:5:3634:G:C8	2.48	0.48
45:Y:30:MET:HB3	45:Y:101:PRO:HG2	1.96	0.48
4:A:130:SER:OG	4:A:171:GLY:O	2.32	0.48
6:B:95:THR:HG22	42:5:4910:G:H4'	1.94	0.48
8:C:205:ARG:HG3	42:5:2297:G:H5'	1.95	0.48
17:h:52:LYS:O	17:h:56:ARG:HD3	2.13	0.48
22:J:21:CYS:HB2	22:J:131:TYR:HB3	1.95	0.48
25:l:21:ARG:NH1	46:8:51:U:OP2	2.42	0.48
36:R:105:LEU:HD22	36:R:135:LYS:HE3	1.96	0.48
42:5:676:C:H2'	42:5:677:G:H8	1.78	0.48
42:5:1398:A:H5'	42:5:1420:A:N1	2.29	0.48
42:5:1440:U:H2'	42:5:1441:C:C6	2.49	0.48
42:5:1505:C:H2'	42:5:1506:G:C8	2.49	0.48
42:5:1593:A:H5''	42:5:2839:U:H5''	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:1812:C:H2'	42:5:1813:U:C6	2.49	0.48
42:5:2734:U:H2'	42:5:2735:G:H8	1.79	0.48
42:5:3783:A:H4'	42:5:3784:A:H5''	1.94	0.48
42:5:4404:U:O2'	42:5:4406:U:O4	2.22	0.48
42:5:4453:C:H2'	42:5:4454:G:O4'	2.14	0.48
4:A:54:ARG:NH2	42:5:3680:U:OP1	2.32	0.48
6:B:224:LYS:NZ	42:5:4626:A:OP2	2.38	0.48
8:C:133:LEU:HB3	35:r:6:GLN:HE21	1.79	0.48
11:e:26:ASP:OD2	42:5:435:A:O2'	2.28	0.48
19:i:41:ARG:NH1	28:N:9:GLU:OE2	2.46	0.48
32:P:59:ARG:HA	32:P:148:VAL:HG11	1.95	0.48
42:5:1079:C:H2'	42:5:1080:C:H6	1.77	0.48
42:5:1191:C:H2'	42:5:1192:C:C6	2.49	0.48
42:5:2823:G:H2'	42:5:2824:C:C6	2.49	0.48
42:5:3911:C:H2'	42:5:3912:U:C6	2.48	0.48
44:7:35:U:O2	44:7:45:U:O2'	2.31	0.48
47:K:193:MET:SD	47:K:196:ARG:NH2	2.86	0.48
6:B:300:LYS:H	6:B:300:LYS:HD2	1.78	0.48
10:D:17:GLN:O	42:5:4265:U:N3	2.47	0.48
10:D:260:GLU:HG2	44:7:120:U:H3'	1.96	0.48
42:5:1872:G:O2'	42:5:4219:A:N3	2.45	0.48
44:7:60:G:H2'	44:7:61:G:H8	1.78	0.48
8:C:325:MET:O	8:C:329:ASN:N	2.35	0.47
12:E:268:ARG:HH12	42:5:4884:G:H3'	1.78	0.47
17:h:97:LYS:HD3	42:5:135:G:C6	2.49	0.47
21:j:44:LYS:N	42:5:22:G:OP1	2.46	0.47
21:j:75:ARG:HH21	42:5:344:A:H5'	1.79	0.47
25:l:27:ILE:HD13	46:8:52:A:N6	2.29	0.47
27:m:88:LYS:HA	27:m:92:ASP:HB2	1.96	0.47
42:5:702:U:H2'	42:5:703:G:H4'	1.96	0.47
42:5:713:C:H2'	42:5:714:G:C8	2.49	0.47
42:5:1199:G:H2'	42:5:1200:G:C8	2.46	0.47
42:5:1804:A:HO2'	42:5:1833:G:H1	1.61	0.47
42:5:1931:C:N4	42:5:2040:A:O2'	2.33	0.47
42:5:2330:G:H2'	42:5:2331:G:C2	2.49	0.47
47:K:206:HIS:HA	47:K:209:HIS:CE1	2.49	0.47
20:I:35:ASP:N	20:I:35:ASP:OD1	2.47	0.47
24:L:106:SER:OG	42:5:73:A:OP1	2.24	0.47
36:R:135:LYS:O	36:R:139:MET:HG2	2.14	0.47
42:5:1411:C:H2'	42:5:1412:G:H8	1.77	0.47
42:5:1662:C:H2'	42:5:1663:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:2083:C:H4'	42:5:2084:C:OP2	2.14	0.47
42:5:4586:G:O6	42:5:4717:A:N6	2.48	0.47
6:B:161:ARG:HB3	6:B:182:GLU:HB2	1.96	0.47
16:G:51:LEU:HD21	42:5:4086:G:C4	2.49	0.47
22:J:19:LYS:HB3	22:J:75:ARG:NH1	2.29	0.47
42:5:716:C:HO2'	42:5:1904:G:HO2'	1.51	0.47
42:5:1084:C:H42	42:5:1215:C:H42	1.62	0.47
42:5:1380:G:N2	42:5:1381:U:O4	2.45	0.47
42:5:2448:G:H2'	42:5:2449:A:C8	2.49	0.47
42:5:4648:A:H2'	42:5:4649:G:H8	1.79	0.47
24:L:101:ARG:HH11	42:5:75:G:HO2'	1.57	0.47
36:R:42:ARG:NH2	42:5:2524:U:OP1	2.48	0.47
36:R:101:ILE:HD13	42:5:2897:G:H4'	1.96	0.47
38:T:45:MET:H	38:T:95:HIS:HD2	1.62	0.47
42:5:957:G:H4'	42:5:958:G:O5'	2.13	0.47
42:5:4421:C:H42	42:5:4475:G:H22	1.61	0.47
42:5:4459:U:H2'	42:5:4460:U:C6	2.49	0.47
42:5:4538:G:H2'	42:5:4539:U:H6	1.79	0.47
42:5:4708:A:C2	42:5:4709:U:H5'	2.49	0.47
4:A:182:ALA:HB2	42:5:3652:A:O2'	2.15	0.47
8:C:50:GLN:NE2	42:5:347:A:O2'	2.47	0.47
18:H:173:ARG:HH21	27:m:124:LYS:HG2	1.78	0.47
25:l:28:ARG:HA	25:l:33:ASN:HD22	1.79	0.47
42:5:2465:C:N4	42:5:2466:G:O6	2.48	0.47
42:5:2734:U:H2'	42:5:2735:G:C8	2.49	0.47
4:A:137:ILE:HD11	4:A:149:LYS:HB3	1.95	0.47
12:E:104:LYS:NZ	42:5:965:G:OP2	2.47	0.47
14:F:73:MET:HA	14:F:76:MET:HG2	1.94	0.47
18:H:44:GLU:HG2	26:M:2:VAL:HG22	1.96	0.47
20:I:30:LYS:HD3	20:I:63:GLU:HA	1.97	0.47
24:L:170:THR:HG23	24:L:172:GLU:H	1.80	0.47
24:L:190:ARG:NH2	42:5:1393:G:O2'	2.47	0.47
33:p:17:ARG:NH2	42:5:1577:G:OP1	2.42	0.47
42:5:492:U:H2'	42:5:493:G:C8	2.50	0.47
42:5:951:G:H2'	42:5:952:G:H8	1.79	0.47
42:5:1427:A:H1'	42:5:1694:C:OP1	2.14	0.47
42:5:1514:U:H2'	42:5:1515:A:H8	1.80	0.47
42:5:1662:C:H2'	42:5:1663:C:H6	1.78	0.47
42:5:1758:G:H2'	42:5:1759:G:C8	2.50	0.47
42:5:1758:G:H2'	42:5:1759:G:H8	1.80	0.47
42:5:2906:G:N1	42:5:3589:G:O6	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4186:A:H2'	42:5:4187:G:H8	1.79	0.47
42:5:4770:U:H2'	42:5:4772:C:H41	1.79	0.47
44:7:76:U:H2'	44:7:77:A:H8	1.80	0.47
49:a:24:LYS:H	49:a:24:LYS:HD2	1.80	0.47
4:A:112:ILE:HG12	4:A:135:THR:HG22	1.95	0.47
4:A:220:GLY:O	42:5:4542:U:O2'	2.32	0.47
8:C:242:PRO:HB2	42:5:2297:G:H4'	1.96	0.47
8:C:289:LEU:HA	8:C:292:ILE:HG12	1.95	0.47
12:E:157:ARG:O	12:E:178:ASN:ND2	2.48	0.47
14:F:50:LYS:NZ	42:5:1237:C:O2'	2.42	0.47
19:i:44:ILE:HA	19:i:47:VAL:HG12	1.97	0.47
25:l:15:LYS:HD3	46:8:45:C:P	2.55	0.47
27:m:94:MET:O	27:m:103:LEU:N	2.44	0.47
28:N:93:LYS:HG3	42:5:300:A:H2	1.80	0.47
31:o:13:LYS:HZ2	42:5:4294:C:H4'	1.79	0.47
32:P:4:TYR:OH	42:5:400:A:OP1	2.23	0.47
35:r:66:ARG:HD2	35:r:75:THR:O	2.15	0.47
42:5:106:A:H1'	42:5:336:A:H8	1.80	0.47
42:5:134:G:H4'	42:5:135:G:O5'	2.14	0.47
42:5:262:G:H2'	42:5:263:G:H8	1.80	0.47
42:5:308:G:H8	42:5:310:G:H1'	1.79	0.47
42:5:1075:G:H2'	42:5:1076:C:H6	1.79	0.47
42:5:1361:G:H2'	42:5:1362:G:H8	1.79	0.47
42:5:1368:A:O2'	42:5:1369:C:OP1	2.31	0.47
42:5:2264:C:H2'	42:5:2265:G:C2	2.50	0.47
42:5:2581:A:O2'	42:5:2654:C:O2'	2.16	0.47
42:5:2693:G:H2'	42:5:2694:G:C8	2.50	0.47
42:5:3870:C:H2'	42:5:3871:A:H8	1.80	0.47
42:5:4914:C:H2'	42:5:4915:G:H8	1.80	0.47
4:A:117:GLU:HG2	4:A:124:GLY:N	2.29	0.47
6:B:126:LYS:HG3	42:5:4966:A:H5''	1.96	0.47
23:k:25:ILE:HB	23:k:68:GLU:HG3	1.97	0.47
26:M:5:ARG:NE	26:M:59:ASP:OD1	2.48	0.47
26:M:11:ARG:NH1	26:M:58:THR:O	2.48	0.47
39:U:34:MET:HE3	39:U:96:LEU:HD22	1.97	0.47
42:5:52:G:H4'	42:5:1529:G:H4'	1.97	0.47
42:5:85:G:O2'	42:5:97:G:O6	2.30	0.47
42:5:1326:A:H2'	42:5:1327:C:C6	2.50	0.47
42:5:1740:C:O2	42:5:1786:A:N6	2.48	0.47
42:5:2028:C:H2'	42:5:2029:A:C8	2.50	0.47
42:5:2654:C:H2'	42:5:2655:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:5061:A:C4'	42:5:5062:G:H5''	2.45	0.47
46:8:90:C:H2'	46:8:91:A:C8	2.50	0.47
47:K:238:TYR:HD2	47:K:251:ILE:HG23	1.79	0.47
48:Z:74:VAL:HG11	48:Z:98:LYS:HE3	1.96	0.47
14:F:234:ASP:HA	14:F:238:ARG:HH21	1.80	0.47
20:I:49:CYS:SG	20:I:170:LYS:HB2	2.55	0.47
28:N:103:GLU:OE2	28:N:118:SER:OG	2.30	0.47
36:R:93:VAL:HA	36:R:96:MET:HE2	1.96	0.47
42:5:229:G:H2'	42:5:230:G:C8	2.50	0.47
42:5:444:G:H2'	42:5:445:U:C6	2.50	0.47
42:5:2430:C:H2'	42:5:2431:A:H8	1.79	0.47
42:5:2492:C:H2'	42:5:2493:G:C8	2.50	0.47
42:5:3670:C:H2'	42:5:3671:G:C4	2.49	0.47
42:5:3932:U:H2'	42:5:3933:G:H8	1.79	0.47
42:5:4088:C:H2'	42:5:4089:G:C8	2.45	0.47
42:5:4507:A:H2'	42:5:4508:C:C6	2.49	0.47
4:A:187:HIS:NE2	42:5:1613:A:OP2	2.40	0.47
4:A:233:ARG:HB2	42:5:4184:G:H5'	1.96	0.47
6:B:43:LEU:HG	6:B:183:ILE:HG21	1.97	0.47
8:C:307:LYS:HG2	42:5:2087:C:H4'	1.96	0.47
13:f:81:SER:OG	42:5:1918:U:OP1	2.27	0.47
20:I:140:THR:OG1	20:I:141:LYS:N	2.47	0.47
31:o:45:GLN:HE22	31:o:51:GLN:HA	1.80	0.47
34:Q:176:ARG:HA	34:Q:180:ARG:HD2	1.97	0.47
42:5:1358:G:O2'	42:5:1359:G:H8	1.98	0.47
42:5:4460:U:H2'	42:5:4461:C:C6	2.49	0.47
7:c:62:TYR:O	7:c:65:MET:HG3	2.15	0.46
11:e:29:VAL:HB	42:5:1332:C:H5''	1.96	0.46
12:E:48:ARG:NH2	42:5:1281:G:O5'	2.47	0.46
13:f:71:TRP:HZ3	13:f:104:MET:HE3	1.80	0.46
14:F:218:PRO:O	42:5:1905:U:O2'	2.30	0.46
16:G:48:LYS:HB3	43:X:42:THR:HG23	1.97	0.46
21:j:73:ARG:HG2	21:j:78:PHE:HA	1.97	0.46
42:5:352:G:O2'	46:8:22:U:O4	2.26	0.46
42:5:453:G:H2'	42:5:453:G:N3	2.30	0.46
42:5:1211:G:H2'	42:5:1212:G:C8	2.50	0.46
42:5:1280:C:H2'	42:5:1281:G:H5''	1.96	0.46
46:8:67:U:H2'	46:8:68:G:C8	2.49	0.46
46:8:124:U:H4'	46:8:125:C:O5'	2.15	0.46
2:t:98:LYS:HG2	2:t:99:SER:H	1.80	0.46
6:B:225:GLY:N	42:5:4977:A:OP1	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:292:LEU:HD21	6:B:298:LEU:HD23	1.96	0.46
9:d:41:ARG:HB2	9:d:77:ILE:O	2.15	0.46
9:d:46:LEU:HD22	42:5:2373:C:H5'	1.96	0.46
12:E:54:SER:OG	12:E:56:SER:N	2.49	0.46
13:f:25:THR:HG22	13:f:87:LYS:HG2	1.97	0.46
20:I:98:ARG:NH2	42:5:1865:G:OP2	2.38	0.46
28:N:8:GLN:NE2	42:5:278:G:OP1	2.42	0.46
34:Q:41:SER:OG	34:Q:44:ASN:OD1	2.33	0.46
42:5:705:G:H2'	42:5:706:C:C6	2.50	0.46
42:5:1670:G:O2'	42:5:1853:G:H4'	2.16	0.46
42:5:3707:U:H2'	42:5:3708:C:C6	2.50	0.46
42:5:4192:A:H2'	42:5:4193:C:C6	2.50	0.46
42:5:4716:C:H2'	42:5:4717:A:H8	1.80	0.46
45:Y:74:TYR:CE2	45:Y:76:LYS:HB3	2.51	0.46
5:b:4:SER:HB2	42:5:1855:G:OP1	2.15	0.46
6:B:240:LEU:HD21	6:B:252:ALA:HB2	1.97	0.46
8:C:303:ARG:HH12	8:C:306:ARG:HG2	1.80	0.46
8:C:312:ARG:HB2	42:5:2274:C:H5'	1.97	0.46
10:D:239:MET:HA	10:D:242:LYS:HG2	1.97	0.46
20:I:54:SER:HA	20:I:163:GLN:HG3	1.96	0.46
38:T:18:PRO:HG2	38:T:21:LYS:HB2	1.96	0.46
42:5:3721:U:H2'	42:5:3722:G:C8	2.51	0.46
42:5:4681:A:H2'	42:5:4682:U:O4'	2.16	0.46
3:u:79:VAL:HG13	3:u:90:ILE:HG12	1.97	0.46
14:F:183:LYS:HG3	14:F:184:TYR:CE2	2.50	0.46
14:F:219:ARG:NE	42:5:717:U:OP1	2.44	0.46
30:O:110:PRO:N	30:O:111:PRO:HD2	2.30	0.46
32:P:5:SER:OG	32:P:147:GLN:OE1	2.33	0.46
40:V:82:ILE:HB	40:V:121:VAL:HG13	1.98	0.46
42:5:1218:G:H3'	42:5:1219:G:H5''	1.98	0.46
42:5:1551:C:H2'	42:5:1552:G:O4'	2.15	0.46
42:5:2811:G:N2	42:5:2813:A:H3'	2.30	0.46
42:5:2844:A:O2'	42:5:4631:G:H4'	2.16	0.46
42:5:3721:U:H2'	42:5:3722:G:H8	1.80	0.46
42:5:3848:U:H2'	42:5:3849:A:H8	1.78	0.46
42:5:3871:A:H2'	42:5:3872:A:C8	2.50	0.46
2:t:96:ILE:HG23	3:u:62:VAL:HG22	1.97	0.46
18:H:48:LEU:HG	18:H:54:ARG:NH2	2.31	0.46
22:J:99:PHE:CD1	22:J:163:MET:HE1	2.51	0.46
28:N:49:ARG:HH21	42:5:114:G:P	2.39	0.46
34:Q:22:ASP:N	34:Q:22:ASP:OD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Q:32:TYR:HE2	34:Q:123:PHE:HB3	1.81	0.46
35:r:90:LEU:HD22	35:r:111:ILE:HG23	1.97	0.46
42:5:123:C:H2'	42:5:124:C:H6	1.80	0.46
42:5:260:C:H2'	42:5:261:G:C8	2.50	0.46
42:5:318:A:H2'	42:5:319:A:H8	1.81	0.46
42:5:323:C:H1'	42:5:4355:G:N2	2.30	0.46
42:5:693:C:O2'	42:5:694:C:OP1	2.32	0.46
42:5:1393:G:O2'	42:5:4352:U:OP1	2.32	0.46
42:5:2591:A:H2'	42:5:2592:U:H6	1.79	0.46
42:5:3920:U:H2'	42:5:3921:U:C6	2.51	0.46
46:8:102:G:OP2	46:8:104:A:O2'	2.26	0.46
6:B:315:ASN:ND2	6:B:326:VAL:H	2.12	0.46
10:D:244:HIS:O	10:D:248:ARG:HG2	2.16	0.46
22:J:167:GLN:HE21	22:J:174:ILE:HD11	1.80	0.46
36:R:96:MET:HG2	42:5:2667:C:O4'	2.16	0.46
38:T:3:ASN:OD1	42:5:4211:C:N4	2.45	0.46
42:5:197:A:N3	42:5:222:C:O2'	2.44	0.46
42:5:964:A:N6	42:5:966:A:N7	2.62	0.46
42:5:1682:A:H2	49:a:43:ILE:HD12	1.80	0.46
42:5:2562:G:N2	42:5:2565:A:OP2	2.25	0.46
42:5:3878:C:N4	42:5:4518:A:O4'	2.48	0.46
42:5:4348:A:O2'	42:5:4350:C:H5'	2.16	0.46
42:5:4460:U:H2'	42:5:4461:C:H6	1.81	0.46
42:5:4704:C:H2'	42:5:4705:A:C8	2.51	0.46
42:5:5022:U:O2'	42:5:5024:C:OP2	2.28	0.46
3:u:80:GLN:O	3:u:89:THR:N	2.45	0.46
4:A:15:VAL:HG21	42:5:1628:C:H5''	1.98	0.46
9:d:67:ARG:HA	9:d:70:LYS:HE3	1.98	0.46
21:j:75:ARG:NH2	42:5:343:C:O2'	2.48	0.46
28:N:180:PHE:C	28:N:182:HIS:H	2.23	0.46
28:N:181:HIS:HB2	42:5:293:G:H1	1.78	0.46
29:n:23:ARG:NE	42:5:3807:A:OP1	2.41	0.46
36:R:177:LEU:HA	36:R:180:LYS:HE3	1.97	0.46
42:5:2385:U:H2'	42:5:2386:U:H6	1.81	0.46
42:5:2457:G:N2	42:5:3672:G:H21	2.11	0.46
42:5:2624:G:H1	42:5:2632:U:H3	1.62	0.46
42:5:2906:G:H2'	42:5:2907:G:H8	1.79	0.46
42:5:3927:U:H2'	42:5:3928:A:C8	2.50	0.46
42:5:4591:U:H2'	42:5:4592:C:C6	2.50	0.46
47:K:242:TYR:HD1	47:K:251:ILE:HB	1.81	0.46
4:A:177:LYS:O	42:5:2739:C:N4	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:113:GLU:HG3	6:B:178:ALA:HB2	1.98	0.46
11:e:23:HIS:HA	11:e:53:ILE:HD12	1.98	0.46
11:e:102:ASN:OD1	42:5:2302:C:O2'	2.29	0.46
21:j:63:ARG:NH2	46:8:58:G:N7	2.62	0.46
22:J:129:ASP:OD1	22:J:129:ASP:N	2.49	0.46
26:M:86:TRP:O	26:M:89:THR:OG1	2.27	0.46
36:R:92:LYS:O	36:R:96:MET:HG3	2.15	0.46
37:S:2:LYS:HD3	37:S:43:ARG:HH11	1.81	0.46
42:5:1663:C:H2'	42:5:1664:U:H6	1.80	0.46
47:K:63:GLN:HA	47:K:66:GLN:HG2	1.97	0.46
4:A:181:LYS:HE2	4:A:184:ARG:HE	1.81	0.46
8:C:329:ASN:ND2	14:F:190:GLU:OE2	2.49	0.46
10:D:63:GLN:NE2	44:7:5:A:O2'	2.48	0.46
28:N:104:GLU:HA	28:N:160:GLU:HG3	1.97	0.46
28:N:181:HIS:CD2	42:5:99:A:H4'	2.51	0.46
42:5:980:U:H2'	42:5:981:C:C6	2.51	0.46
42:5:4538:G:H2'	42:5:4539:U:C6	2.51	0.46
42:5:4736:C:H2'	42:5:4737:G:C8	2.51	0.46
47:K:346:ARG:HG2	47:K:348:ALA:H	1.80	0.46
6:B:252:ALA:HB1	42:5:4524:G:N3	2.31	0.46
10:D:223:PHE:HB3	10:D:226:TYR:HB2	1.98	0.46
12:E:62:LYS:HE2	12:E:64:LEU:HD21	1.97	0.46
36:R:106:LEU:HD11	36:R:123:LEU:HD23	1.97	0.46
42:5:675:C:H2'	42:5:676:C:H6	1.81	0.46
42:5:1213:G:H5''	42:5:1214:C:H5''	1.98	0.46
42:5:2502:G:H4'	42:5:2503:G:OP1	2.15	0.46
42:5:3880:G:H2'	42:5:3881:G:C8	2.51	0.46
47:K:390:VAL:HG13	47:K:404:PHE:HB2	1.97	0.46
4:A:14:SER:OG	4:A:15:VAL:N	2.45	0.45
11:e:63:ASN:HD22	42:5:2077:C:H4'	1.81	0.45
22:J:108:GLY:HA3	42:5:4251:A:H5''	1.97	0.45
31:o:4:VAL:O	31:o:94:GLY:N	2.47	0.45
32:P:50:ASN:H	32:P:174:HIS:CD2	2.33	0.45
32:P:160:ARG:HG3	32:P:166:ASN:ND2	2.30	0.45
34:Q:72:LEU:HB2	34:Q:75:ARG:HD2	1.99	0.45
42:5:130:C:H2'	42:5:131:C:C6	2.50	0.45
42:5:216:C:O2'	42:5:217:C:OP1	2.34	0.45
42:5:223:G:H4'	42:5:225:G:N7	2.31	0.45
42:5:2539:C:H2'	42:5:2540:C:H6	1.79	0.45
42:5:2729:C:C4	42:5:2730:U:C4	3.04	0.45
42:5:4448:G:H5''	42:5:4449:A:H5'	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4600:G:O2'	42:5:4609:G:O6	2.30	0.45
42:5:4642:U:H2'	42:5:4643:G:C8	2.51	0.45
42:5:5051:C:H2'	42:5:5052:C:C6	2.51	0.45
46:8:69:U:H2'	46:8:70:G:O4'	2.16	0.45
3:u:97:LYS:HD2	3:u:102:MET:HE3	1.99	0.45
6:B:78:ILE:HD12	6:B:314:ILE:HD11	1.98	0.45
8:C:119:GLN:NE2	42:5:1350:C:O2	2.49	0.45
10:D:59:ASP:OD1	10:D:60:ILE:N	2.49	0.45
10:D:278:ASP:OD1	42:5:1185:G:N2	2.34	0.45
12:E:58:MET:HA	12:E:61:ARG:HB2	1.98	0.45
18:H:103:VAL:HG22	18:H:114:ILE:HG12	1.97	0.45
22:J:55:TYR:HA	22:J:64:ARG:HD2	1.99	0.45
22:J:78:LYS:O	22:J:81:GLU:HG3	2.16	0.45
24:L:9:ILE:HG12	49:a:49:HIS:CE1	2.51	0.45
30:O:74:ARG:N	42:5:4585:U:OP1	2.49	0.45
30:O:90:HIS:CE1	30:O:91:LYS:HE3	2.52	0.45
37:S:5:GLY:O	37:S:111:ARG:NH2	2.48	0.45
42:5:1501:C:H4'	42:5:1502:G:H5'	1.98	0.45
42:5:1884:C:H2'	42:5:1885:G:H8	1.81	0.45
42:5:2751:G:N1	42:5:2752:G:O6	2.49	0.45
42:5:3620:G:OP1	42:5:3622:C:N4	2.48	0.45
47:K:209:HIS:O	47:K:213:SER:N	2.47	0.45
47:K:467:VAL:HG22	47:K:468:ASN:ND2	2.32	0.45
48:Z:95:VAL:HG23	48:Z:96:VAL:HG23	1.98	0.45
3:u:63:ASN:OD1	3:u:73:HIS:ND1	2.43	0.45
6:B:14:LEU:O	42:5:4587:G:O2'	2.30	0.45
26:M:56:GLN:HA	37:S:157:ARG:HH12	1.81	0.45
29:n:2:ARG:HB3	29:n:5:TRP:CD1	2.52	0.45
36:R:10:LEU:HB3	36:R:41:ILE:HD12	1.98	0.45
37:S:45:TRP:CZ3	37:S:54:MET:HE2	2.51	0.45
42:5:365:U:H2'	42:5:366:A:H8	1.82	0.45
42:5:2492:C:H2'	42:5:2493:G:H8	1.81	0.45
42:5:2778:G:N1	46:8:113:C:OP1	2.50	0.45
42:5:2890:C:H42	42:5:3611:A:H61	1.63	0.45
42:5:2902:G:N7	42:5:2903:G:N2	2.64	0.45
42:5:3648:A:H1'	42:5:3785:A:N6	2.30	0.45
42:5:3700:C:O2'	42:5:3774:A:H1'	2.16	0.45
42:5:4528:G:H2'	42:5:4529:G:N7	2.31	0.45
42:5:5032:C:H2'	42:5:5033:G:O4'	2.16	0.45
4:A:116:LEU:HD21	4:A:158:ILE:HD13	1.97	0.45
6:B:76:VAL:HG12	6:B:334:LYS:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:e:70:LEU:HD11	11:e:76:LYS:HB2	1.97	0.45
16:G:180:PRO:HA	16:G:227:ASN:HD21	1.80	0.45
24:L:67:HIS:NE2	42:5:71:C:O3'	2.50	0.45
39:U:21:PHE:HB2	39:U:72:VAL:HG13	1.97	0.45
42:5:1358:G:N2	42:5:1359:G:O6	2.49	0.45
42:5:1509:C:H2'	42:5:1510:G:H8	1.82	0.45
42:5:1555:G:O6	42:5:1572:U:O4	2.34	0.45
42:5:3690:U:H2'	42:5:3691:G:O4'	2.16	0.45
42:5:3736:A:H2'	42:5:3737:A:H8	1.81	0.45
42:5:4165:C:C2	42:5:4166:G:C8	3.05	0.45
42:5:4510:A:N1	42:5:4592:C:H4'	2.32	0.45
42:5:4716:C:H2'	42:5:4717:A:C8	2.51	0.45
46:8:27:U:H2'	46:8:28:C:H6	1.81	0.45
5:b:18:ARG:NH1	42:5:1668:A:O3'	2.33	0.45
12:E:237:GLU:HG2	12:E:239:THR:H	1.81	0.45
36:R:24:LEU:HD23	36:R:32:ILE:HG21	1.98	0.45
42:5:1190:C:H2'	42:5:1191:C:H6	1.82	0.45
42:5:1633:G:H5'	42:5:1634:A:OP1	2.16	0.45
45:Y:55:VAL:HG13	45:Y:104:VAL:HB	1.98	0.45
47:K:276:HIS:CE1	47:K:298:ARG:HE	2.35	0.45
6:B:112:ASP:O	6:B:116:ARG:HG3	2.16	0.45
11:e:89:LEU:HD13	11:e:118:LEU:HD22	1.98	0.45
18:H:71:ARG:HG2	42:5:4691:A:H4'	1.98	0.45
20:I:47:PRO:HB3	20:I:171:TRP:CE2	2.52	0.45
22:J:87:LEU:HD12	22:J:92:TYR:HA	1.99	0.45
42:5:158:A:N1	42:5:276:C:O2'	2.43	0.45
42:5:1933:G:H8	42:5:1933:G:O5'	2.00	0.45
42:5:2459:G:H4'	42:5:3671:G:H21	1.81	0.45
42:5:2514:G:O2'	42:5:2743:A:N6	2.49	0.45
42:5:4208:U:H2'	42:5:4209:G:C8	2.52	0.45
42:5:4592:C:H2'	42:5:4593:C:H6	1.82	0.45
44:7:76:U:H2'	44:7:77:A:C8	2.51	0.45
4:A:210:PRO:HG2	4:A:235:VAL:HG21	1.99	0.45
5:b:57:MET:HE3	42:5:1811:G:H21	1.80	0.45
12:E:175:LEU:HD22	12:E:246:GLN:HG2	1.99	0.45
15:g:15:THR:O	15:g:19:LYS:NZ	2.50	0.45
15:g:83:CYS:SG	15:g:86:CYS:HB2	2.57	0.45
26:M:60:PHE:HE1	26:M:85:LYS:HE2	1.82	0.45
32:P:45:LYS:HG2	32:P:178:ILE:HG12	1.97	0.45
36:R:97:ARG:HH21	42:5:2725:A:H5''	1.82	0.45
37:S:147:ASP:N	37:S:147:ASP:OD1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:1432:G:O2'	42:5:1452:A:N6	2.50	0.45
42:5:2654:C:H2'	42:5:2655:C:H6	1.81	0.45
42:5:3871:A:H2'	42:5:3872:A:H8	1.82	0.45
3:u:80:GLN:N	3:u:89:THR:O	2.40	0.45
6:B:8:ALA:HB1	40:V:48:ARG:HH12	1.82	0.45
7:c:19:GLN:NE2	7:c:84:ALA:O	2.50	0.45
9:d:60:PRO:HD2	9:d:100:ASN:ND2	2.31	0.45
12:E:175:LEU:HD12	12:E:179:ARG:HA	1.99	0.45
13:f:20:ASN:ND2	42:5:1885:G:OP1	2.42	0.45
19:i:10:GLY:O	19:i:12:ASN:N	2.49	0.45
19:i:70:LEU:HD22	19:i:87:ARG:HH22	1.81	0.45
22:J:112:HIS:HD2	22:J:117:ILE:HB	1.82	0.45
26:M:53:LYS:NZ	42:5:1923:A:OP1	2.38	0.45
30:O:47:PHE:HA	30:O:136:ALA:HB2	1.99	0.45
42:5:220:C:H2'	42:5:221:C:C6	2.52	0.45
42:5:223:G:H4'	42:5:225:G:C8	2.52	0.45
42:5:1300:G:O2'	42:5:1302:U:O4	2.26	0.45
42:5:1311:G:H2'	42:5:1312:A:O4'	2.17	0.45
42:5:2611:A:H2'	42:5:2612:G:C8	2.52	0.45
42:5:4145:C:H2'	42:5:4146:G:H8	1.82	0.45
42:5:4478:G:O2'	42:5:4602:A:N1	2.44	0.45
42:5:4635:A:O2'	42:5:4637:G:OP1	2.31	0.45
48:Z:51:ARG:HB2	48:Z:65:ARG:HE	1.82	0.45
2:t:83:LEU:HD13	3:u:43:LYS:HE2	1.99	0.45
10:D:108:ARG:HH11	10:D:253:TYR:HD2	1.64	0.45
15:g:5:LEU:HD21	15:g:22:LEU:HD11	1.99	0.45
26:M:24:LEU:O	26:M:43:THR:HG21	2.17	0.45
31:o:86:LYS:NZ	42:5:4330:G:N7	2.62	0.45
37:S:99:ASP:OD1	37:S:100:LEU:N	2.46	0.45
42:5:1193:C:H2'	42:5:1194:G:C8	2.52	0.45
42:5:1338:G:H22	49:a:25:HIS:CD2	2.35	0.45
42:5:1577:G:H3'	42:5:1577:G:N3	2.32	0.45
42:5:2601:A:N6	42:5:2743:A:H3'	2.32	0.45
42:5:3709:U:O2'	42:5:3710:G:H5'	2.16	0.45
42:5:4178:A:H2'	42:5:4179:G:C8	2.52	0.45
8:C:320:LYS:O	42:5:1281:G:N2	2.50	0.45
9:d:70:LYS:HD3	42:5:2388:A:O2'	2.17	0.45
12:E:54:SER:OG	12:E:57:ALA:N	2.30	0.45
12:E:275:ASN:H	42:5:4753:U:H5	1.65	0.45
14:F:154:GLU:OE1	14:F:247:ARG:NH2	2.50	0.45
42:5:15:A:H61	46:8:142:U:H3	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:1533:A:O5'	42:5:1623:A:N6	2.50	0.45
42:5:2049:G:H2'	42:5:2050:G:C8	2.51	0.45
42:5:2832:A:H2'	42:5:2833:A:H8	1.81	0.45
42:5:3717:A:H2'	42:5:3718:A:C8	2.52	0.45
42:5:3717:A:H2'	42:5:3718:A:H8	1.81	0.45
42:5:3917:A:H2'	42:5:3918:G:H8	1.82	0.45
42:5:4094:G:H2'	42:5:4095:G:C8	2.51	0.45
42:5:4192:A:H2'	42:5:4193:C:H6	1.82	0.45
42:5:4455:G:H2'	42:5:4456:C:H6	1.82	0.45
6:B:92:TYR:CE1	6:B:101:THR:HG22	2.52	0.44
20:I:89:VAL:HG12	20:I:91:LEU:H	1.82	0.44
22:J:95:ARG:HH21	22:J:175:LEU:H	1.65	0.44
22:J:160:GLU:O	22:J:164:ARG:HG2	2.18	0.44
28:N:74:PRO:HA	42:5:3670:C:O2	2.17	0.44
30:O:128:ARG:NH2	42:5:2057:A:OP1	2.50	0.44
36:R:106:LEU:HB3	36:R:120:TYR:HE1	1.82	0.44
37:S:15:ARG:HD2	37:S:25:PRO:HG2	1.99	0.44
39:U:33:ILE:HG13	39:U:34:MET:HG2	1.98	0.44
42:5:426:A:H61	46:8:8:U:H3	1.65	0.44
42:5:1822:U:H3'	42:5:1823:G:H8	1.82	0.44
42:5:2263:A:N7	42:5:2266:C:N4	2.65	0.44
42:5:3937:C:H2'	42:5:3938:G:C2	2.52	0.44
42:5:4477:A:H2'	42:5:4478:G:H8	1.83	0.44
42:5:4699:U:H4'	42:5:4700:A:OP1	2.16	0.44
44:7:38:U:H1'	44:7:42:A:H61	1.83	0.44
47:K:376:LEU:HD11	47:K:386:ILE:HG21	1.99	0.44
4:A:40:TYR:HD2	4:A:93:LYS:HB3	1.82	0.44
4:A:187:HIS:HB3	42:5:2740:U:O4'	2.18	0.44
4:A:208:GLU:OE1	42:5:1629:G:N1	2.36	0.44
16:G:180:PRO:HG3	16:G:219:VAL:HG13	1.99	0.44
22:J:22:LEU:HD22	22:J:128:LEU:HD12	1.98	0.44
22:J:35:ARG:HH22	22:J:124:GLY:H	1.63	0.44
24:L:39:ARG:CZ	42:5:1362:G:H5''	2.47	0.44
26:M:14:TYR:HD2	26:M:56:GLN:HE21	1.65	0.44
28:N:84:PRO:HA	28:N:87:HIS:CD2	2.51	0.44
38:T:12:ARG:O	38:T:16:SER:OG	2.34	0.44
38:T:54:HIS:CE1	42:5:4301:U:H4'	2.51	0.44
42:5:460:C:H2'	42:5:461:G:H8	1.82	0.44
42:5:1758:G:O6	42:5:1775:A:N6	2.50	0.44
42:5:2387:G:H2'	42:5:2388:A:H8	1.82	0.44
42:5:4601:U:O2	42:5:4602:A:C8	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4922:C:H2'	42:5:4923:C:H6	1.83	0.44
42:5:5057:C:H2'	42:5:5058:A:H8	1.79	0.44
4:A:36:GLU:HG3	4:A:91:GLY:HA2	1.98	0.44
6:B:47:LEU:HD23	6:B:181:MET:HE2	2.00	0.44
6:B:242:ARG:NH1	42:5:2856:C:O2	2.50	0.44
6:B:262:VAL:HG11	6:B:268:ARG:NH1	2.32	0.44
7:c:39:ARG:NE	48:Z:77:TYR:HB3	2.32	0.44
14:F:225:LYS:HE3	42:5:1907:A:H4'	2.00	0.44
14:F:239:GLU:OE2	37:S:37:HIS:ND1	2.48	0.44
17:h:3:LYS:HZ2	46:8:81:C:P	2.40	0.44
24:L:31:ARG:NH2	42:5:338:A:OP1	2.50	0.44
34:Q:187:LYS:NZ	42:5:1495:G:O3'	2.49	0.44
36:R:44:LEU:HD11	36:R:49:LEU:HD13	1.98	0.44
42:5:285:G:H2'	42:5:286:U:C6	2.53	0.44
42:5:2735:G:H2'	42:5:2736:G:C8	2.52	0.44
47:K:191:LEU:HD23	47:K:216:GLN:HG3	1.98	0.44
4:A:200:ARG:HG2	42:5:3651:A:OP1	2.17	0.44
16:G:89:ARG:NH1	46:8:155:C:OP1	2.50	0.44
28:N:157:LYS:HD2	42:5:56:A:H4'	1.98	0.44
42:5:693:C:H2'	42:5:694:C:C6	2.52	0.44
42:5:1088:C:H2'	42:5:1089:G:C8	2.52	0.44
42:5:1088:C:H2'	42:5:1089:G:H8	1.82	0.44
42:5:1874:A:O4'	42:5:4213:A:N6	2.50	0.44
42:5:3920:U:H2'	42:5:3921:U:H6	1.82	0.44
4:A:20:VAL:HG12	4:A:23:ARG:HD2	1.98	0.44
11:e:91:CYS:HB3	11:e:95:TYR:HD2	1.82	0.44
12:E:124:HIS:ND1	42:5:971:U:O4	2.50	0.44
12:E:173:GLY:HA3	12:E:180:VAL:HB	2.00	0.44
24:L:164:GLU:HB3	49:a:100:ILE:HD12	1.98	0.44
32:P:112:TRP:O	42:5:3856:A:H5''	2.18	0.44
35:r:51:VAL:HG12	35:r:117:ILE:HD12	2.00	0.44
37:S:164:LYS:O	37:S:165:PRO:C	2.60	0.44
42:5:243:A:H5''	45:Y:3:PHE:HB2	1.98	0.44
42:5:287:U:H2'	42:5:288:G:H8	1.82	0.44
42:5:4173:G:H2'	42:5:4174:U:H6	1.82	0.44
42:5:4414:A:P	42:5:4422:A:H61	2.40	0.44
42:5:5004:C:H2'	42:5:5005:G:O4'	2.17	0.44
42:5:5060:A:O2'	42:5:5061:A:OP1	2.31	0.44
6:B:317:LEU:HB2	6:B:372:SER:HB2	1.99	0.44
14:F:85:VAL:HG12	37:S:62:VAL:HA	2.00	0.44
15:g:93:ARG:HH11	42:5:4122:G:H5'	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:H:173:ARG:HH22	27:m:125:LYS:HB2	1.83	0.44
20:I:57:TYR:O	44:7:90:A:O2'	2.35	0.44
22:J:150:CYS:SG	22:J:151:ILE:N	2.91	0.44
35:r:59:GLY:H	35:r:121:GLN:NE2	2.13	0.44
42:5:1340:C:H2'	42:5:1341:U:H6	1.83	0.44
42:5:2456:G:H2'	42:5:2457:G:C8	2.53	0.44
42:5:3589:G:H2'	42:5:3590:G:N9	2.32	0.44
44:7:118:C:H2'	44:7:119:U:C6	2.53	0.44
45:Y:51:LYS:HB2	46:8:72:A:P	2.57	0.44
7:c:45:LEU:HD11	7:c:105:ILE:HA	2.00	0.44
7:c:62:TYR:HE1	15:g:99:GLU:HG2	1.83	0.44
10:D:216:GLU:O	10:D:220:LYS:HG2	2.17	0.44
14:F:29:GLU:HG3	14:F:33:LYS:HE3	1.99	0.44
26:M:94:LYS:NZ	42:5:4872:G:H5''	2.32	0.44
28:N:4:TYR:OH	42:5:151:G:OP2	2.25	0.44
30:O:173:GLN:NE2	30:O:176:ARG:HH22	2.16	0.44
34:Q:54:SER:O	34:Q:58:ARG:HG2	2.17	0.44
40:V:23:GLY:HA2	40:V:38:TYR:CZ	2.52	0.44
42:5:420:A:N6	46:8:14:U:H3	2.15	0.44
42:5:748:G:H8	42:5:749:G:H5'	1.82	0.44
42:5:1418:C:H2'	42:5:1419:G:O4'	2.18	0.44
42:5:1870:C:H2'	42:5:1871:A:C8	2.52	0.44
42:5:3661:G:N2	42:5:3681:G:O2'	2.49	0.44
42:5:3795:A:H2'	42:5:3796:U:C6	2.53	0.44
42:5:3883:U:H2'	42:5:3884:U:C6	2.53	0.44
42:5:4435:U:H2'	42:5:4436:U:C2	2.53	0.44
6:B:55:HIS:HB2	6:B:369:ASP:HB2	2.00	0.44
16:G:55:VAL:HG21	43:X:41:ARG:HD2	1.99	0.44
18:H:43:VAL:O	42:5:4763:U:O2'	2.30	0.44
31:o:44:LYS:HE2	31:o:52:THR:HB	1.99	0.44
32:P:150:LYS:O	46:8:13:G:O2'	2.25	0.44
42:5:40:G:N2	42:5:4380:A:H62	2.16	0.44
42:5:2049:G:H2'	42:5:2050:G:H8	1.83	0.44
42:5:2555:G:H2'	42:5:2556:G:C8	2.53	0.44
44:7:24:C:H2'	44:7:25:G:O4'	2.17	0.44
49:a:76:ASP:OD1	49:a:77:LYS:N	2.50	0.44
4:A:96:LEU:HB2	33:p:87:LYS:HD3	2.00	0.44
6:B:108:GLU:HG3	6:B:137:TRP:HB2	1.98	0.44
18:H:59:LYS:NZ	18:H:66:GLU:OE2	2.42	0.44
33:p:41:PHE:O	42:5:2674:A:N6	2.45	0.44
34:Q:178:ARG:HA	34:Q:184:ARG:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:138:G:H2'	42:5:139:G:H8	1.83	0.44
42:5:717:U:H3	42:5:951:G:H22	1.66	0.44
42:5:1449:C:H2'	42:5:1450:C:C6	2.52	0.44
42:5:4888:U:O2'	42:5:4889:G:O5'	2.35	0.44
42:5:5059:C:H2'	42:5:5060:A:H8	1.82	0.44
43:X:123:LYS:HE3	43:X:123:LYS:HB3	1.89	0.44
44:7:119:U:OP2	44:7:120:U:O2'	2.35	0.44
4:A:49:ILE:HD13	4:A:60:LYS:HE3	2.00	0.43
10:D:222:GLN:HE22	44:7:47:G:H21	1.65	0.43
12:E:239:THR:HG22	12:E:241:GLN:HG2	1.99	0.43
23:k:5:ILE:HD11	23:k:43:TYR:HB3	1.99	0.43
30:O:84:VAL:HG11	30:O:102:LEU:HD22	2.00	0.43
31:o:9:ARG:HB3	42:5:4290:U:OP1	2.18	0.43
31:o:9:ARG:HA	31:o:20:PRO:HA	1.99	0.43
36:R:74:ARG:NE	42:5:2891:U:OP2	2.47	0.43
41:W:6:CYS:HB3	41:W:10:GLY:H	1.83	0.43
42:5:731:G:C6	42:5:732:A:N1	2.86	0.43
42:5:2456:G:H2'	42:5:2457:G:H8	1.83	0.43
42:5:3597:G:H2'	42:5:3598:C:H6	1.83	0.43
42:5:3653:A:N6	42:5:3691:G:H1'	2.32	0.43
42:5:3845:A:H4'	42:5:4668:U:H4'	2.00	0.43
42:5:4719:G:O2'	42:5:4720:C:O5'	2.26	0.43
4:A:35:ALA:HA	16:G:41:ILE:HD13	1.99	0.43
4:A:37:ARG:NH2	42:5:4087:G:OP2	2.50	0.43
8:C:134:PRO:HA	8:C:150:LEU:HD22	1.99	0.43
8:C:223:ASN:O	42:5:226:G:O2'	2.27	0.43
25:l:23:ILE:HG22	46:8:52:A:C4	2.53	0.43
42:5:20:U:P	46:8:36:G:H1	2.42	0.43
42:5:288:G:H2'	42:5:289:C:C6	2.54	0.43
42:5:926:G:O2'	42:5:927:G:H5'	2.18	0.43
42:5:1079:C:H2'	42:5:1080:C:C6	2.53	0.43
42:5:1080:C:N4	42:5:1221:G:O6	2.51	0.43
42:5:1574:G:H5''	42:5:2605:G:O2'	2.19	0.43
42:5:1855:G:O6	42:5:1880:G:N2	2.51	0.43
42:5:2262:G:O2'	42:5:2263:A:OP1	2.31	0.43
42:5:2758:G:H2'	42:5:2759:G:C4	2.53	0.43
45:Y:22:PRO:HB2	46:8:90:C:O2'	2.19	0.43
6:B:45:ALA:HB3	6:B:183:ILE:HG23	1.99	0.43
6:B:220:ILE:HB	6:B:346:THR:HB	2.00	0.43
8:C:171:LEU:HD12	8:C:174:LEU:HD11	2.00	0.43
10:D:54:ARG:NH2	10:D:147:ASP:OD2	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:I:143:GLN:OE1	20:I:143:GLN:N	2.47	0.43
22:J:48:PRO:HB3	22:J:72:CYS:HB2	1.99	0.43
42:5:727:C:H3'	42:5:728:U:H3'	2.00	0.43
42:5:978:G:H2'	42:5:979:C:H6	1.81	0.43
42:5:1075:G:H2'	42:5:1076:C:C6	2.53	0.43
42:5:1738:A:H2'	42:5:1739:G:C8	2.53	0.43
42:5:4405:G:N1	42:5:4440:G:H1'	2.33	0.43
42:5:4991:U:H2'	42:5:4992:G:C8	2.53	0.43
3:u:98:GLN:HB2	3:u:101:GLU:HG3	2.00	0.43
4:A:68:ARG:NH2	42:5:2503:G:OP2	2.51	0.43
6:B:56:ILE:O	6:B:73:VAL:HA	2.18	0.43
8:C:150:LEU:HB3	8:C:151:PRO:HD3	2.01	0.43
12:E:54:SER:HG	12:E:57:ALA:N	2.14	0.43
14:F:33:LYS:HE2	14:F:33:LYS:HB3	1.81	0.43
16:G:117:ARG:HE	16:G:120:LYS:HD3	1.84	0.43
17:h:74:LYS:HE3	17:h:74:LYS:HB3	1.92	0.43
26:M:32:ASP:OD1	26:M:35:ARG:HB2	2.19	0.43
32:P:95:GLY:HA3	42:5:2362:U:H5''	2.00	0.43
36:R:67:THR:O	36:R:71:ARG:HG2	2.19	0.43
42:5:62:A:N6	42:5:334:A:OP2	2.50	0.43
42:5:381:U:H4'	42:5:415:G:H5'	2.01	0.43
42:5:425:U:C2	42:5:426:A:C8	3.06	0.43
42:5:1191:C:H2'	42:5:1192:C:H6	1.84	0.43
42:5:1204:C:H2'	42:5:1205:G:H8	1.81	0.43
42:5:1448:G:H2'	42:5:1449:C:C6	2.54	0.43
42:5:1507:C:C2	42:5:1508:A:C8	3.05	0.43
42:5:1510:G:H2'	42:5:1511:U:H6	1.83	0.43
42:5:2386:U:C2	42:5:2387:G:C8	3.06	0.43
42:5:3788:C:N4	42:5:3812:C:O4'	2.51	0.43
42:5:4208:U:H2'	42:5:4209:G:H8	1.83	0.43
42:5:4347:G:H2'	42:5:4348:A:C8	2.53	0.43
48:Z:47:ASP:N	48:Z:69:LYS:O	2.45	0.43
6:B:110:ILE:HG23	6:B:115:LYS:HE3	2.01	0.43
7:c:32:LYS:HG2	7:c:36:LYS:HE3	1.98	0.43
8:C:181:LYS:HE2	42:5:218:A:H5'	1.99	0.43
14:F:187:ILE:HG21	42:5:2094:G:C6	2.54	0.43
17:h:118:LYS:HG2	24:L:127:PHE:HD2	1.84	0.43
21:j:3:LYS:HG2	42:5:3643:A:N7	2.32	0.43
26:M:58:THR:OG1	26:M:59:ASP:N	2.51	0.43
28:N:135:ILE:HG21	28:N:151:ILE:HG21	2.01	0.43
37:S:15:ARG:HB3	37:S:27:LEU:HD23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:S:132:ILE:HG23	37:S:136:LYS:HG3	2.01	0.43
42:5:1846:G:H2'	42:5:1847:C:H6	1.83	0.43
42:5:2694:G:H5''	42:5:2696:A:C8	2.54	0.43
42:5:3834:C:C2	42:5:3835:C:C5	3.07	0.43
42:5:4467:A:O2'	42:5:4510:A:N3	2.47	0.43
42:5:4935:C:O2'	42:5:4936:G:OP1	2.34	0.43
47:K:307:PRO:O	47:K:311:GLN:HG2	2.19	0.43
9:d:64:ILE:O	42:5:2374:A:H5'	2.18	0.43
18:H:174:LYS:NZ	42:5:4604:G:OP1	2.47	0.43
34:Q:68:ARG:HA	34:Q:71:LYS:HE2	2.00	0.43
35:r:32:LEU:HD12	35:r:106:LEU:HD23	2.00	0.43
40:V:104:VAL:HB	40:V:112:MET:HE1	2.00	0.43
42:5:1077:C:C4	42:5:1078:A:H1'	2.54	0.43
42:5:1810:G:H2'	42:5:1811:G:C8	2.53	0.43
42:5:4679:G:H2'	42:5:4680:G:C8	2.53	0.43
6:B:47:LEU:HD13	6:B:344:VAL:HG23	1.99	0.43
24:L:39:ARG:NH1	42:5:1362:G:OP1	2.43	0.43
28:N:50:ARG:HA	42:5:113:A:H1'	1.99	0.43
34:Q:80:ALA:HA	34:Q:137:VAL:HG13	2.01	0.43
34:Q:100:VAL:HG11	34:Q:113:ILE:HD13	1.99	0.43
36:R:167:LYS:O	36:R:171:LYS:HG2	2.18	0.43
42:5:214:G:OP2	42:5:219:G:N2	2.52	0.43
42:5:1320:U:H2'	42:5:1891:A:H61	1.83	0.43
42:5:1338:G:H4'	42:5:1339:U:H6	1.82	0.43
42:5:1654:G:H5''	49:a:29:PRO:HA	2.00	0.43
42:5:4414:A:H2'	42:5:4422:A:C2	2.54	0.43
43:X:117:TYR:HB2	43:X:119:ILE:HG12	2.00	0.43
45:Y:82:ILE:HB	45:Y:85:VAL:HB	1.99	0.43
47:K:283:HIS:HB3	47:K:288:SER:HB2	2.00	0.43
10:D:107:ARG:NH2	10:D:169:GLY:O	2.50	0.43
12:E:123:SER:OG	12:E:126:ARG:HD3	2.19	0.43
12:E:280:HIS:CE1	12:E:281:LYS:HG2	2.53	0.43
42:5:2263:A:H1'	42:5:2264:C:C5	2.54	0.43
42:5:2299:G:H2'	42:5:2301:G:O4'	2.18	0.43
42:5:2362:U:H2'	42:5:2363:A:C8	2.52	0.43
42:5:3653:A:C2	42:5:3692:A:H4'	2.54	0.43
42:5:3707:U:H2'	42:5:3708:C:H6	1.84	0.43
42:5:4313:A:H3'	42:5:4314:C:H5''	2.00	0.43
42:5:4412:C:H2'	42:5:4413:C:O2	2.19	0.43
46:8:8:U:H2'	46:8:9:A:C8	2.53	0.43
49:a:117:LEU:HD12	49:a:118:PRO:HD2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:196:TRP:O	4:A:198:ARG:N	2.52	0.43
10:D:12:TYR:OH	42:5:4265:U:OP1	2.36	0.43
15:g:68:SER:OG	15:g:71:LYS:NZ	2.52	0.43
20:I:90:ARG:HH12	20:I:137:SER:HB2	1.82	0.43
21:j:5:THR:OG1	42:5:1601:A:OP1	2.34	0.43
28:N:80:THR:HB	28:N:87:HIS:CD2	2.54	0.43
40:V:43:LYS:HB2	40:V:60:MET:O	2.18	0.43
42:5:197:A:H2'	42:5:198:A:C8	2.54	0.43
42:5:1942:A:H2'	42:5:1943:A:H8	1.83	0.43
42:5:2610:G:H2'	42:5:2611:A:H8	1.84	0.43
42:5:4234:A:H2	42:5:4271:A:C6	2.36	0.43
42:5:4293:U:OP2	42:5:4329:G:O2'	2.30	0.43
42:5:4888:U:O2'	42:5:4889:G:H2'	2.19	0.43
5:b:50:ASN:HD21	42:5:1827:C:H1'	1.84	0.43
6:B:219:VAL:HG11	6:B:337:VAL:HG12	2.00	0.43
6:B:370:THR:H	6:B:380:GLN:NE2	2.17	0.43
7:c:82:GLY:HA2	7:c:91:VAL:HG12	2.01	0.43
10:D:65:ALA:HB2	10:D:74:ILE:HG13	1.99	0.43
13:f:54:LYS:NZ	42:5:4747:C:O3'	2.50	0.43
14:F:76:MET:HE1	42:5:1088:C:O2	2.19	0.43
14:F:82:ASN:HD21	38:T:140:PHE:HB3	1.83	0.43
28:N:85:VAL:HA	31:o:49:GLY:HA2	2.01	0.43
32:P:2:VAL:HG21	32:P:47:ARG:HH11	1.84	0.43
42:5:1557:C:H2'	42:5:1558:A:C8	2.54	0.43
42:5:1734:G:N2	42:5:1735:U:O4	2.40	0.43
42:5:1813:U:H2'	42:5:1814:C:C6	2.54	0.43
42:5:2043:A:O2'	42:5:4461:C:O2	2.36	0.43
42:5:2073:C:H2'	42:5:2074:C:C6	2.54	0.43
42:5:2081:C:H2'	42:5:2082:G:C8	2.54	0.43
42:5:2522:G:H2'	42:5:2523:G:H8	1.84	0.43
42:5:2844:A:N6	42:5:3839:G:O2'	2.52	0.43
42:5:3610:A:H2'	42:5:3611:A:H8	1.84	0.43
42:5:4163:U:H5'	42:5:4164:C:H5''	2.01	0.43
42:5:4186:A:H2'	42:5:4187:G:C8	2.54	0.43
42:5:4537:C:H2'	42:5:4538:G:C8	2.54	0.43
42:5:4540:C:N4	42:5:4541:G:O6	2.52	0.43
42:5:4901:G:H2'	42:5:4902:C:C6	2.54	0.43
6:B:378:ARG:HD2	41:W:11:TYR:CG	2.54	0.42
10:D:18:VAL:HG13	10:D:24:ARG:HD3	2.00	0.42
14:F:117:ARG:NH2	34:Q:4:ASP:O	2.48	0.42
16:G:156:VAL:HB	16:G:202:VAL:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:j:63:ARG:NH1	46:8:58:G:N7	2.65	0.42
28:N:78:GLY:O	28:N:80:THR:HG23	2.19	0.42
31:o:80:LYS:O	42:5:4346:U:O2'	2.37	0.42
42:5:257:C:H2'	42:5:258:G:C8	2.53	0.42
42:5:308:G:C8	42:5:310:G:H1'	2.54	0.42
42:5:947:C:H2'	42:5:948:C:H6	1.84	0.42
42:5:1211:G:O2'	42:5:1212:G:OP1	2.23	0.42
42:5:1308:C:H2'	42:5:1309:C:C6	2.53	0.42
42:5:1361:G:H2'	42:5:1362:G:C8	2.53	0.42
42:5:1876:U:H2'	42:5:1877:G:C8	2.54	0.42
42:5:2683:C:H2'	42:5:2684:C:C6	2.53	0.42
42:5:3907:G:O6	42:5:4397:A:N1	2.52	0.42
44:7:60:G:H2'	44:7:61:G:C8	2.54	0.42
6:B:194:LEU:HD23	6:B:194:LEU:HA	1.90	0.42
11:e:82:VAL:HG13	11:e:114:ARG:HG2	2.01	0.42
12:E:254:LEU:HG	12:E:258:LYS:HE2	2.00	0.42
17:h:62:ASN:HA	17:h:65:GLN:HG2	2.01	0.42
19:i:35:LYS:HE3	19:i:35:LYS:HB3	1.84	0.42
21:j:65:ARG:NH1	46:8:99:U:O4	2.52	0.42
22:J:111:GLU:HB3	22:J:113:ILE:HG22	2.00	0.42
25:l:42:ARG:NH2	42:5:2408:U:OP2	2.52	0.42
29:n:23:ARG:HH22	42:5:3782:C:P	2.42	0.42
36:R:86:ASN:HB3	42:5:1550:G:OP1	2.18	0.42
42:5:396:A:H2'	42:5:397:G:C8	2.54	0.42
42:5:1309:C:H2'	42:5:1310:C:C6	2.54	0.42
42:5:1458:C:H3'	42:5:1459:A:H8	1.84	0.42
42:5:1823:G:H2'	42:5:1825:A:C8	2.55	0.42
42:5:1837:A:H2'	42:5:1838:A:C8	2.54	0.42
42:5:2413:U:C2	42:5:2414:G:C8	3.07	0.42
42:5:2548:C:H2'	42:5:2549:G:C8	2.54	0.42
42:5:4196:G:C8	42:5:4396:A:H4'	2.54	0.42
42:5:4562:C:H2'	42:5:4563:U:H6	1.83	0.42
11:e:76:LYS:NZ	42:5:2324:C:O2	2.51	0.42
15:g:64:LEU:O	15:g:72:LYS:NZ	2.31	0.42
24:L:57:PRO:HG2	24:L:73:GLY:HA3	2.00	0.42
28:N:49:ARG:NH1	42:5:152:U:OP2	2.39	0.42
28:N:119:TYR:CZ	28:N:131:GLU:HB2	2.54	0.42
29:n:10:MET:O	29:n:14:LYS:HG2	2.19	0.42
34:Q:49:LYS:O	34:Q:53:MET:HG3	2.19	0.42
39:U:92:LYS:CG	42:5:2626:U:H2'	2.49	0.42
42:5:260:C:H2'	42:5:261:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:318:A:H2'	42:5:319:A:C8	2.54	0.42
42:5:441:G:H2'	42:5:442:G:H8	1.84	0.42
42:5:675:C:H2'	42:5:676:C:C6	2.54	0.42
42:5:1389:U:O2'	42:5:1469:C:O2	2.36	0.42
42:5:1580:C:H2'	42:5:1581:G:O4'	2.19	0.42
42:5:2073:C:H2'	42:5:2074:C:H6	1.85	0.42
42:5:2092:G:O2'	42:5:2093:A:OP2	2.31	0.42
42:5:3794:C:H2'	42:5:3795:A:H8	1.83	0.42
48:Z:38:TYR:CE2	48:Z:40:HIS:HB3	2.54	0.42
14:F:136:ARG:NH1	44:7:97:G:OP1	2.52	0.42
16:G:100:HIS:CD2	16:G:103:ARG:HH22	2.37	0.42
18:H:94:SER:HA	18:H:179:ILE:HG22	2.01	0.42
19:i:10:GLY:HA2	24:L:189:ALA:HB2	2.00	0.42
23:k:55:LYS:HA	23:k:58:GLN:HE21	1.85	0.42
34:Q:172:ARG:NH1	49:a:56:VAL:O	2.45	0.42
42:5:1196:G:H2'	42:5:1197:C:C6	2.54	0.42
42:5:1812:C:H2'	42:5:1813:U:H6	1.85	0.42
42:5:3938:G:H4'	42:5:3939:G:O5'	2.18	0.42
42:5:4230:C:H1'	42:5:4271:A:N1	2.33	0.42
42:5:4238:G:H2'	42:5:4239:A:C8	2.53	0.42
43:X:126:THR:HA	43:X:136:ALA:HA	2.01	0.42
44:7:62:U:O2'	44:7:64:G:O4'	2.36	0.42
4:A:242:ARG:O	42:5:3658:C:H5''	2.20	0.42
6:B:340:THR:OG1	6:B:341:LYS:N	2.53	0.42
8:C:42:THR:HG23	42:5:2340:C:H4'	2.01	0.42
12:E:155:GLY:O	12:E:271:PHE:N	2.43	0.42
14:F:52:ILE:HD12	14:F:188:CYS:HB3	2.02	0.42
28:N:178:HIS:HA	28:N:181:HIS:CD2	2.54	0.42
32:P:6:LEU:HD23	32:P:145:HIS:HB2	2.01	0.42
34:Q:79:THR:OG1	34:Q:99:LYS:HE3	2.20	0.42
42:5:128:C:H2'	42:5:129:C:H6	1.85	0.42
42:5:191:G:H2'	42:5:192:G:H8	1.85	0.42
42:5:325:U:H2'	42:5:326:C:H6	1.84	0.42
42:5:1074:G:H2'	42:5:1075:G:C8	2.54	0.42
42:5:1486:C:H2'	42:5:1487:G:C8	2.54	0.42
42:5:2368:A:N6	42:5:2827:G:O2'	2.51	0.42
42:5:2376:A:H2'	42:5:2377:C:C6	2.54	0.42
42:5:2486:G:H2'	42:5:2487:G:H8	1.83	0.42
42:5:2522:G:H2'	42:5:2523:G:C8	2.54	0.42
42:5:2555:G:H2'	42:5:2556:G:H8	1.84	0.42
42:5:3633:C:H2'	42:5:3634:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4417:C:H2'	42:5:4418:G:O4'	2.19	0.42
42:5:4583:C:H2'	42:5:4584:A:C8	2.55	0.42
49:a:131:ARG:NH1	49:a:135:GLU:OE2	2.53	0.42
3:u:103:LEU:HA	3:u:106:ILE:HG22	2.01	0.42
5:b:33:LYS:HE3	5:b:33:LYS:HB3	1.80	0.42
6:B:19:ARG:HB2	6:B:234:ARG:HH21	1.84	0.42
6:B:238:LYS:HG2	42:5:4457:U:H5''	2.02	0.42
8:C:70:GLY:HA2	42:5:3905:A:O2'	2.19	0.42
8:C:161:TYR:HE2	8:C:170:LEU:HD22	1.85	0.42
10:D:146:LEU:HD12	10:D:163:LEU:HB2	2.01	0.42
12:E:122:LEU:HD11	42:5:970:G:N2	2.34	0.42
21:j:25:LYS:NZ	42:5:370:U:O3'	2.45	0.42
42:5:1516:G:P	49:a:32:ARG:HH21	2.42	0.42
42:5:2102:G:H2'	42:5:2103:G:H8	1.84	0.42
42:5:2521:G:H2'	42:5:2522:G:C8	2.54	0.42
42:5:4493:U:H2'	42:5:4494:G:C8	2.53	0.42
42:5:4493:U:H2'	42:5:4494:G:H8	1.84	0.42
47:K:102:THR:O	47:K:106:MET:N	2.48	0.42
4:A:18:ALA:HB2	42:5:3677:U:H5''	2.00	0.42
6:B:206:PRO:HG2	6:B:209:GLN:HG2	2.01	0.42
8:C:207:PRO:HB3	8:C:249:PHE:CD2	2.55	0.42
10:D:13:PHE:O	44:7:11:A:N6	2.40	0.42
13:f:14:TYR:OH	13:f:92:LEU:O	2.34	0.42
20:I:87:ILE:HG12	20:I:138:ILE:HG12	2.02	0.42
23:k:36:VAL:HG13	23:k:43:TYR:HB2	2.01	0.42
24:L:170:THR:N	24:L:173:GLU:OE2	2.40	0.42
26:M:10:GLY:O	26:M:62:LEU:N	2.39	0.42
28:N:97:SER:HB3	42:5:300:A:H5'	2.00	0.42
42:5:664:G:N2	42:5:665:C:H41	2.16	0.42
42:5:741:C:H42	42:5:923:C:H42	1.68	0.42
42:5:944:A:OP2	42:5:944:A:H4'	2.19	0.42
42:5:1177:U:H2'	42:5:1178:G:H8	1.84	0.42
42:5:1328:G:H2'	42:5:1329:G:C8	2.54	0.42
42:5:1669:A:H62	42:5:1881:C:H5	1.68	0.42
42:5:2402:G:C2	42:5:2403:A:C8	3.08	0.42
42:5:2448:G:OP2	42:5:2510:G:N1	2.34	0.42
42:5:3702:A:C6	42:5:3703:G:N7	2.87	0.42
42:5:3787:G:H1'	42:5:3789:C:H41	1.84	0.42
42:5:4312:U:H2'	42:5:4313:A:C8	2.54	0.42
42:5:4486:C:H2'	42:5:4487:A:O4'	2.20	0.42
42:5:4659:G:H2'	42:5:4660:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4719:G:H2'	42:5:4721:G:C8	2.55	0.42
46:8:141:C:H2'	46:8:142:U:C6	2.53	0.42
48:Z:128:LYS:HE2	48:Z:128:LYS:HB3	1.92	0.42
6:B:262:VAL:HG11	6:B:268:ARG:HH11	1.85	0.42
10:D:113:PHE:HB3	42:5:1819:G:N2	2.29	0.42
10:D:258:LYS:NZ	10:D:259:ARG:O	2.53	0.42
12:E:217:GLN:HG3	12:E:218:LEU:H	1.85	0.42
16:G:96:LEU:HD11	16:G:189:ARG:HD3	2.02	0.42
19:i:43:MET:O	19:i:46:GLU:HG3	2.19	0.42
20:I:49:CYS:SG	20:I:51:HIS:NE2	2.91	0.42
22:J:120:ASP:HB3	22:J:123:ILE:HB	2.01	0.42
24:L:116:ARG:CZ	24:L:155:MET:HE3	2.50	0.42
27:m:114:LYS:HZ1	42:5:4685:U:P	2.42	0.42
37:S:45:TRP:CE2	37:S:56:LYS:HG3	2.55	0.42
42:5:405:U:H5'	45:Y:87:ARG:NH2	2.35	0.42
42:5:1238:A:H4'	42:5:1239:C:OP1	2.18	0.42
42:5:1384:C:C2	42:5:1385:G:C8	3.08	0.42
42:5:1411:C:H2'	42:5:1412:G:C8	2.54	0.42
42:5:1440:U:O2'	42:5:1441:C:OP1	2.34	0.42
42:5:1890:G:O2'	42:5:1891:A:H5'	2.19	0.42
42:5:2536:A:O2'	42:5:2641:A:N1	2.39	0.42
42:5:2752:G:H2'	42:5:2753:G:C8	2.55	0.42
42:5:4689:U:H2'	42:5:4690:G:O4'	2.20	0.42
42:5:4740:G:N2	42:5:4959:U:H3	2.14	0.42
42:5:4765:G:H22	42:5:4869:U:H3	1.68	0.42
4:A:57:PRO:HG2	4:A:78:ALA:HB3	2.01	0.42
4:A:68:ARG:HH22	42:5:2503:G:P	2.43	0.42
10:D:82:GLU:OE1	10:D:82:GLU:N	2.52	0.42
12:E:186:HIS:HE1	42:5:709:C:O3'	2.02	0.42
22:J:141:ILE:HA	22:J:144:LYS:HD3	2.01	0.42
31:o:36:GLN:HB2	42:5:4363:A:H5''	2.01	0.42
33:p:13:LYS:HA	42:5:1575:A:H2	1.84	0.42
42:5:475:G:H2'	42:5:476:G:C8	2.54	0.42
42:5:657:C:O2'	42:5:658:C:O4'	2.29	0.42
42:5:672:C:H2'	42:5:673:C:C6	2.55	0.42
42:5:909:A:H2'	42:5:910:G:H8	1.84	0.42
42:5:1202:C:H2'	42:5:1203:G:H8	1.84	0.42
42:5:1811:G:H2'	42:5:1812:C:H6	1.83	0.42
42:5:2509:C:H4'	46:8:108:A:O2'	2.19	0.42
42:5:2591:A:N6	42:5:2754:G:N2	2.66	0.42
42:5:3738:G:H2'	42:5:3739:C:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4420:U:O2	42:5:4420:U:H2'	2.20	0.42
42:5:4601:U:H2'	42:5:4602:A:H8	1.84	0.42
42:5:4898:G:H2'	42:5:4899:G:C8	2.55	0.42
48:Z:61:LYS:HG2	48:Z:65:ARG:HG2	2.02	0.42
12:E:38:PRO:N	42:5:979:C:H4'	2.35	0.42
14:F:36:ARG:HH22	42:5:1438:U:H5''	1.84	0.42
23:k:17:ARG:NH2	23:k:38:CYS:SG	2.93	0.42
24:L:66:TYR:C	24:L:68:THR:H	2.28	0.42
42:5:84:A:N1	42:5:98:A:H5''	2.35	0.42
42:5:496:G:H2'	42:5:497:G:H8	1.84	0.42
42:5:5027:C:H1'	42:5:5028:G:OP2	2.19	0.42
48:Z:111:ARG:HA	48:Z:114:ALA:HB3	2.01	0.42
4:A:77:ILE:HD11	4:A:115:CYS:HB2	2.02	0.41
9:d:24:GLU:HG2	9:d:87:ARG:HB3	2.02	0.41
12:E:122:LEU:HD11	42:5:970:G:H22	1.85	0.41
12:E:241:GLN:HA	12:E:244:VAL:HG12	2.01	0.41
15:g:76:ARG:HH12	15:g:84:ALA:HB2	1.85	0.41
22:J:144:LYS:HZ2	22:J:147:ARG:H	1.68	0.41
24:L:153:PRO:HG2	24:L:156:PRO:HG3	2.02	0.41
34:Q:178:ARG:HG3	42:5:4340:U:H5'	2.00	0.41
40:V:85:ARG:NH1	40:V:99:GLU:O	2.51	0.41
42:5:432:U:H4'	42:5:433:A:H5''	2.02	0.41
42:5:1307:A:H2'	42:5:1308:C:C6	2.55	0.41
42:5:1339:U:H2'	42:5:1340:C:C6	2.55	0.41
42:5:1431:C:H2'	42:5:1432:G:O4'	2.19	0.41
42:5:1688:G:H2'	42:5:1689:G:H8	1.85	0.41
42:5:2520:C:H2'	42:5:2521:G:C8	2.54	0.41
42:5:2535:G:H2'	42:5:2536:A:H8	1.84	0.41
42:5:3714:G:H2'	42:5:3715:U:C6	2.55	0.41
42:5:3794:C:H2'	42:5:3795:A:C8	2.55	0.41
42:5:4424:A:H1'	42:5:4474:A:O2'	2.19	0.41
42:5:4500:U:H2'	42:5:4501:U:C6	2.55	0.41
42:5:4637:G:H2'	42:5:4638:U:C6	2.55	0.41
42:5:4641:U:H3	42:5:4658:G:H1	1.68	0.41
42:5:4674:C:H2'	42:5:4675:U:C6	2.55	0.41
44:7:16:A:N6	44:7:64:G:O6	2.52	0.41
44:7:30:C:C2	44:7:48:G:N2	2.88	0.41
11:e:90:MET:HE3	35:r:113:ARG:HB2	2.02	0.41
13:f:94:ALA:O	42:5:1308:C:O2'	2.38	0.41
21:j:13:ASN:OD1	21:j:13:ASN:N	2.52	0.41
39:U:92:LYS:HE2	42:5:2626:U:P	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:23:C:H2'	42:5:24:G:O4'	2.19	0.41
42:5:252:C:H2'	42:5:253:G:H8	1.85	0.41
42:5:705:G:H2'	42:5:706:C:H6	1.86	0.41
42:5:1068:G:H2'	42:5:1069:G:H8	1.85	0.41
42:5:1234:G:C4	42:5:1235:G:C8	3.08	0.41
42:5:3764:U:H2'	42:5:3765:G:O4'	2.19	0.41
42:5:4890:G:H2'	42:5:4891:G:C8	2.54	0.41
44:7:58:A:H2'	44:7:59:G:H8	1.85	0.41
47:K:120:LEU:HD22	47:K:140:LEU:HD22	2.02	0.41
6:B:139:ASP:N	6:B:139:ASP:OD1	2.52	0.41
8:C:114:ARG:NH1	42:5:1358:G:H4'	2.34	0.41
15:g:61:PRO:HB3	42:5:2598:A:N3	2.35	0.41
18:H:68:ALA:O	18:H:72:THR:HG23	2.19	0.41
24:L:56:ARG:HD2	24:L:73:GLY:O	2.21	0.41
31:o:48:TYR:HE1	42:5:3927:U:H5''	1.85	0.41
31:o:80:LYS:HB2	42:5:4346:U:O3'	2.21	0.41
33:p:51:ALA:HB3	33:p:54:ILE:HD13	2.01	0.41
40:V:77:HIS:HB3	40:V:105:ILE:HG23	2.02	0.41
42:5:1455:G:H4'	42:5:1456:C:OP1	2.20	0.41
42:5:1822:U:H3'	42:5:1823:G:C8	2.55	0.41
42:5:2277:C:H2'	42:5:2278:G:C8	2.54	0.41
42:5:2587:A:O2'	42:5:2588:C:O4'	2.33	0.41
42:5:4237:C:O2	42:5:4321:U:O2'	2.39	0.41
42:5:4237:C:OP1	42:5:4327:C:O2'	2.38	0.41
42:5:4319:C:H2'	42:5:4320:G:H8	1.85	0.41
44:7:74:A:N1	44:7:100:A:H5'	2.35	0.41
45:Y:8:THR:CG2	45:Y:13:LYS:HB2	2.50	0.41
8:C:145:GLU:HG3	8:C:146:GLU:CD	2.46	0.41
12:E:243:LYS:HD3	42:5:4937:C:H41	1.85	0.41
13:f:47:CYS:HA	13:f:103:VAL:HA	2.02	0.41
14:F:94:VAL:O	14:F:122:GLY:HA2	2.21	0.41
14:F:184:TYR:HB3	14:F:202:ARG:HG3	2.01	0.41
21:j:39:TYR:HE1	46:8:102:G:H5''	1.85	0.41
24:L:57:PRO:HG3	24:L:75:GLY:O	2.20	0.41
42:5:499:G:H2'	42:5:499:G:N3	2.34	0.41
42:5:1338:G:H4'	42:5:1339:U:C6	2.56	0.41
42:5:2743:A:H2'	42:5:2744:A:C8	2.55	0.41
42:5:2780:C:H2'	42:5:2781:G:C8	2.55	0.41
42:5:3584:C:H2'	42:5:3585:G:H8	1.84	0.41
42:5:3697:U:O2'	42:5:3698:G:OP2	2.33	0.41
42:5:3734:U:H2'	42:5:3735:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:3809:G:O2'	42:5:3810:C:H5''	2.21	0.41
42:5:3904:G:HO2'	42:5:3905:A:P	2.43	0.41
42:5:4230:C:H2'	42:5:4231:C:C6	2.55	0.41
47:K:210:VAL:HG22	47:K:241:LEU:HD23	2.03	0.41
48:Z:46:ILE:HG21	48:Z:68:ILE:HD12	2.03	0.41
49:a:28:HIS:CD2	49:a:32:ARG:HG2	2.55	0.41
3:u:13:LYS:HE3	39:U:119:GLN:HB3	2.02	0.41
6:B:343:ARG:NH2	42:5:4977:A:OP1	2.53	0.41
16:G:78:PRO:O	16:G:82:GLN:HG3	2.20	0.41
16:G:147:VAL:O	16:G:177:MET:HG2	2.20	0.41
20:I:152:LEU:HB3	20:I:165:ILE:HD12	2.03	0.41
26:M:29:ASP:OD1	26:M:30:VAL:N	2.50	0.41
33:p:20:ALA:HB2	42:5:2874:U:H1'	2.02	0.41
42:5:166:C:H2'	42:5:167:C:C6	2.56	0.41
42:5:1460:C:C2	42:5:1461:C:C5	3.09	0.41
42:5:1538:U:H2'	42:5:1539:G:H8	1.85	0.41
42:5:2478:C:H2'	42:5:2479:G:O4'	2.20	0.41
42:5:2594:C:H2'	42:5:2595:C:C6	2.56	0.41
42:5:2723:U:H2'	42:5:2724:G:C8	2.56	0.41
42:5:2894:A:H2'	42:5:2895:A:H8	1.84	0.41
42:5:3693:U:H2'	42:5:3694:U:H6	1.86	0.41
42:5:4467:A:O2'	42:5:4510:A:H1'	2.20	0.41
49:a:59:ARG:NH2	49:a:61:TYR:OH	2.53	0.41
3:u:53:VAL:HG13	3:u:54:ASN:H	1.86	0.41
6:B:264:PHE:N	30:O:64:THR:O	2.53	0.41
7:c:30:GLY:HA2	42:5:2673:G:O3'	2.21	0.41
8:C:10:VAL:HG13	8:C:153:VAL:HG22	2.03	0.41
10:D:50:ARG:NH2	10:D:72:ASP:OD2	2.53	0.41
15:g:22:LEU:HD12	15:g:22:LEU:HA	1.86	0.41
22:J:95:ARG:H	22:J:98:ASN:HD22	1.68	0.41
42:5:37:U:H4'	49:a:32:ARG:HD3	2.03	0.41
42:5:222:C:H2'	42:5:223:G:O4'	2.21	0.41
42:5:423:G:H2'	42:5:424:U:H6	1.85	0.41
42:5:1276:C:H2'	42:5:1277:G:H8	1.85	0.41
42:5:1322:A:H1'	42:5:1324:A:OP2	2.21	0.41
42:5:1616:U:H2'	42:5:1617:G:H8	1.84	0.41
42:5:1806:G:H2'	42:5:1807:C:H6	1.86	0.41
42:5:2625:U:H2'	42:5:2626:U:C6	2.55	0.41
42:5:3594:C:H2'	42:5:3595:U:H5'	2.03	0.41
42:5:4564:A:C5	42:5:4565:C:C5	3.09	0.41
42:5:4566:U:C2	42:5:4567:G:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4870:G:H21	42:5:4870:G:P	2.44	0.41
42:5:4915:G:H2'	42:5:4916:G:C8	2.55	0.41
46:8:32:C:H2'	46:8:33:G:O4'	2.20	0.41
8:C:209:VAL:HB	8:C:229:LEU:HD13	2.01	0.41
24:L:46:ILE:HG22	24:L:49:ARG:HE	1.86	0.41
24:L:138:ASP:N	24:L:138:ASP:OD1	2.53	0.41
30:O:27:VAL:HG13	30:O:98:ALA:HB1	2.02	0.41
34:Q:15:ARG:HH21	34:Q:19:LYS:HG3	1.84	0.41
37:S:161:ARG:HA	37:S:161:ARG:HD3	1.85	0.41
42:5:286:U:H2'	42:5:287:U:C6	2.56	0.41
42:5:1455:G:H2'	42:5:1456:C:C6	2.55	0.41
42:5:1624:G:C5	42:5:1643:A:C8	3.09	0.41
42:5:1889:U:O2'	42:5:3873:G:N2	2.51	0.41
42:5:2694:G:H5''	42:5:2696:A:N7	2.36	0.41
42:5:3684:G:H2'	42:5:3685:C:C6	2.55	0.41
42:5:3700:C:H2'	42:5:3746:A:N6	2.33	0.41
42:5:3873:G:H2'	42:5:3874:G:H8	1.84	0.41
42:5:4593:C:H2'	42:5:4594:U:C6	2.55	0.41
42:5:5019:A:H2'	42:5:5020:G:H8	1.86	0.41
3:u:27:ARG:NH1	42:5:2624:G:OP1	2.53	0.41
8:C:31:PRO:HD3	8:C:282:HIS:CD2	2.55	0.41
9:d:28:ASN:ND2	9:d:31:LYS:HB2	2.36	0.41
10:D:208:MET:HB2	10:D:219:TYR:HE1	1.85	0.41
10:D:283:LYS:HD3	10:D:283:LYS:HA	1.73	0.41
13:f:23:GLU:HG2	42:5:439:G:H1'	2.03	0.41
13:f:43:LEU:HD22	13:f:76:ARG:HA	2.02	0.41
17:h:6:ALA:HB1	17:h:10:ARG:HH12	1.86	0.41
18:H:122:TYR:HB2	42:5:4613:C:O4'	2.21	0.41
24:L:66:TYR:O	24:L:68:THR:N	2.54	0.41
25:l:21:ARG:NH1	46:8:52:A:OP1	2.54	0.41
26:M:114:LYS:HD3	26:M:114:LYS:HA	1.92	0.41
30:O:61:ARG:HA	30:O:70:PRO:HD2	2.01	0.41
34:Q:61:LEU:HB3	34:Q:86:ILE:HD13	2.02	0.41
38:T:128:LEU:HD23	38:T:128:LEU:H	1.86	0.41
42:5:947:C:H2'	42:5:948:C:C6	2.55	0.41
42:5:1300:G:H4'	42:5:1301:C:O2	2.20	0.41
42:5:1382:G:C2	42:5:1383:G:N7	2.89	0.41
42:5:1472:C:H2'	42:5:1473:U:C6	2.55	0.41
42:5:1644:C:C2	42:5:1645:C:C5	3.09	0.41
42:5:1669:A:H4'	42:5:1685:G:N2	2.35	0.41
42:5:1735:U:H2'	42:5:1736:A:H8	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:1811:G:H2'	42:5:1812:C:C6	2.56	0.41
42:5:2485:U:H2'	42:5:2486:G:C8	2.56	0.41
42:5:2688:G:H2'	42:5:2689:C:C6	2.56	0.41
42:5:2753:G:H5''	48:Z:133:LYS:NZ	2.36	0.41
42:5:3893:C:H2'	42:5:3894:A:H8	1.86	0.41
42:5:4066:U:H2'	42:5:4067:U:C6	2.56	0.41
42:5:4382:G:H2'	42:5:4383:U:C6	2.56	0.41
42:5:4582:C:H2'	42:5:4583:C:O4'	2.20	0.41
42:5:4674:C:H2'	42:5:4675:U:H6	1.86	0.41
42:5:5059:C:H2'	42:5:5060:A:C8	2.55	0.41
4:A:128:ARG:HA	4:A:169:VAL:HG21	2.03	0.41
10:D:280:VAL:HG21	44:7:63:C:H1'	2.03	0.41
11:e:77:PHE:HD2	11:e:88:LEU:HD11	1.86	0.41
12:E:125:GLY:C	12:E:126:ARG:HD2	2.46	0.41
17:h:6:ALA:HB1	17:h:10:ARG:NH1	2.36	0.41
21:j:3:LYS:HG2	42:5:3643:A:C5	2.56	0.41
21:j:12:ARG:HH21	42:5:2403:A:H2	1.69	0.41
22:J:87:LEU:HB3	22:J:92:TYR:CD1	2.56	0.41
24:L:101:ARG:HG2	42:5:75:G:C2	2.56	0.41
25:l:27:ILE:HD13	46:8:52:A:H62	1.85	0.41
28:N:204:ARG:NH1	42:5:1341:U:O3'	2.54	0.41
32:P:55:PHE:HZ	42:5:423:G:H5'	1.86	0.41
36:R:103:ARG:HH22	42:5:2668:G:P	2.43	0.41
38:T:49:GLN:NE2	42:5:4282:A:N1	2.67	0.41
40:V:83:ARG:HG2	40:V:102:ALA:HB3	2.03	0.41
42:5:220:C:H2'	42:5:221:C:H6	1.85	0.41
42:5:304:C:H2'	42:5:305:A:O4'	2.20	0.41
42:5:363:A:N1	42:5:376:A:H5''	2.36	0.41
42:5:752:G:O6	42:5:911:U:N3	2.54	0.41
42:5:1076:C:H2'	42:5:1077:C:H6	1.86	0.41
42:5:1201:U:H2'	42:5:1202:C:H6	1.85	0.41
42:5:1217:G:N1	42:5:1219:G:N7	2.68	0.41
42:5:1318:C:OP1	49:a:21:ARG:HB2	2.21	0.41
42:5:1406:G:O6	42:5:1408:G:O2'	2.33	0.41
42:5:1468:C:H2'	42:5:1469:C:C6	2.56	0.41
42:5:1621:A:H2'	42:5:1622:U:C6	2.55	0.41
42:5:1664:U:H2'	42:5:1665:C:C6	2.56	0.41
42:5:1794:A:H5''	42:5:4214:A:H61	1.85	0.41
42:5:2256:C:H4'	42:5:2257:C:H6	1.84	0.41
42:5:2571:C:H2'	42:5:2572:C:C6	2.56	0.41
42:5:2723:U:H2'	42:5:2724:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4272:G:H3'	42:5:4273:A:H5''	2.02	0.41
42:5:4495:G:H2'	42:5:4496:A:H8	1.85	0.41
42:5:4580:U:H2'	42:5:4581:G:O4'	2.21	0.41
49:a:125:LYS:HA	49:a:145:VAL:O	2.21	0.41
6:B:276:HIS:ND1	42:5:4716:C:OP1	2.48	0.41
11:e:18:LYS:HA	42:5:1302:U:H4'	2.03	0.41
17:h:51:ARG:HH12	46:8:48:A:H5''	1.86	0.41
30:O:110:PRO:HA	30:O:113:ASP:CG	2.46	0.41
31:o:37:GLY:HA3	42:5:4342:C:O3'	2.21	0.41
42:5:275:C:H2'	42:5:276:C:C6	2.56	0.41
42:5:281:U:H2'	42:5:282:C:C6	2.53	0.41
42:5:282:C:C2	42:5:306:A:N6	2.89	0.41
42:5:716:C:O2'	42:5:1904:G:O2'	2.24	0.41
42:5:725:G:C6	42:5:942:G:C2	3.09	0.41
42:5:956:A:H3'	42:5:957:G:C5	2.55	0.41
42:5:972:C:H2'	42:5:973:G:H8	1.86	0.41
42:5:983:C:H2'	42:5:984:C:O4'	2.21	0.41
42:5:2340:C:H2'	42:5:2341:A:C8	2.56	0.41
42:5:2394:G:O4'	42:5:2397:G:N2	2.53	0.41
42:5:2684:C:H2'	42:5:2685:C:C6	2.55	0.41
42:5:3619:G:H22	42:5:3624:A:H1'	1.85	0.41
42:5:3714:G:H2'	42:5:3715:U:H6	1.86	0.41
42:5:4563:U:N3	42:5:4564:A:N7	2.69	0.41
4:A:183:GLY:CA	42:5:1613:A:H5''	2.49	0.40
5:b:45:PHE:HD2	42:5:1814:C:H4'	1.87	0.40
6:B:295:ASP:OD1	6:B:295:ASP:N	2.54	0.40
13:f:104:MET:N	13:f:104:MET:SD	2.94	0.40
14:F:171:LEU:HG	14:F:177:ILE:HD11	2.03	0.40
21:j:57:ASN:OD1	21:j:57:ASN:N	2.55	0.40
22:J:46:GLN:NE2	22:J:72:CYS:SG	2.91	0.40
30:O:109:PRO:HB2	30:O:111:PRO:HG2	2.03	0.40
35:r:66:ARG:O	35:r:67:ARG:HB3	2.21	0.40
38:T:47:THR:O	42:5:4282:A:N6	2.54	0.40
42:5:1327:C:N4	42:5:1328:G:O6	2.55	0.40
42:5:1328:G:O2'	42:5:2349:A:OP1	2.39	0.40
42:5:1450:C:H2'	42:5:1451:G:O4'	2.21	0.40
42:5:1867:A:H2'	42:5:1868:A:C8	2.56	0.40
42:5:1940:G:H1	42:5:4434:C:H5''	1.85	0.40
42:5:2032:U:H2'	42:5:2033:A:C8	2.56	0.40
42:5:2309:G:O6	42:5:2330:G:C2	2.74	0.40
42:5:2357:G:H2'	42:5:2358:G:C8	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5:4075:U:H1'	42:5:4076:G:H2'	2.03	0.40
46:8:125:C:H4'	46:8:126:C:H5'	2.02	0.40
46:8:147:G:H2'	46:8:148:A:H8	1.86	0.40
8:C:60:HIS:HA	8:C:92:PHE:HE1	1.86	0.40
12:E:114:THR:O	35:r:112:ARG:HD3	2.21	0.40
20:I:15:LYS:NZ	42:5:4212:A:OP2	2.39	0.40
25:l:15:LYS:HA	25:l:18:LYS:HG2	2.03	0.40
28:N:124:ASP:N	28:N:127:TYR:O	2.52	0.40
33:p:25:MET:HE2	33:p:25:MET:HB2	1.98	0.40
42:5:10:A:N6	42:5:11:G:O6	2.54	0.40
42:5:36:U:H5''	42:5:1652:U:O4'	2.21	0.40
42:5:973:G:H1	42:5:1282:G:HO2'	1.68	0.40
42:5:2550:G:C2	42:5:2551:A:N7	2.89	0.40
42:5:3723:A:H2'	42:5:3724:A:H8	1.86	0.40
42:5:3725:G:N2	42:5:3728:A:OP2	2.39	0.40
44:7:2:U:H2'	44:7:3:C:C6	2.55	0.40
3:u:15:GLN:NE2	39:U:98:ASP:OD2	2.54	0.40
6:B:56:ILE:HD13	6:B:56:ILE:HA	1.96	0.40
8:C:53:ALA:O	46:8:26:C:O2'	2.33	0.40
9:d:37:GLY:O	9:d:41:ARG:HG2	2.22	0.40
10:D:273:LEU:HA	10:D:276:LYS:HE2	2.03	0.40
16:G:106:THR:HB	16:G:195:HIS:CD2	2.56	0.40
26:M:104:MET:HG3	26:M:108:ASP:HB2	2.04	0.40
30:O:166:ILE:HG22	30:O:170:LYS:HE2	2.03	0.40
36:R:146:LYS:NZ	42:5:3595:U:O2'	2.44	0.40
42:5:343:C:C2	42:5:344:A:C8	3.10	0.40
42:5:425:U:N3	42:5:426:A:N7	2.70	0.40
42:5:948:C:H2'	42:5:949:G:C8	2.57	0.40
42:5:1460:C:H2'	42:5:1461:C:H6	1.85	0.40
42:5:4576:U:H2'	42:5:4577:U:C6	2.56	0.40
42:5:4643:G:H2'	42:5:4644:G:C8	2.56	0.40
42:5:4866:C:H2'	42:5:4867:G:C8	2.54	0.40
47:K:73:TYR:CE2	47:K:125:LYS:HE2	2.56	0.40
47:K:95:VAL:O	47:K:98:GLU:HG3	2.21	0.40
47:K:95:VAL:O	47:K:99:MET:HG3	2.21	0.40
47:K:367:THR:O	47:K:368:LEU:HD13	2.22	0.40
6:B:128:LYS:HE3	6:B:128:LYS:HB3	1.92	0.40
8:C:36:ILE:HD11	42:5:1351:G:H5'	2.03	0.40
10:D:39:GLN:NE2	10:D:46:THR:OG1	2.54	0.40
12:E:258:LYS:NZ	42:5:4931:G:H5'	2.37	0.40
26:M:30:VAL:HG21	37:S:150:ILE:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:N:183:THR:HG22	28:N:188:ARG:N	2.37	0.40
30:O:9:LEU:HB2	30:O:35:VAL:HG12	2.02	0.40
36:R:15:LEU:HD21	36:R:45:ILE:HD13	2.04	0.40
36:R:98:ARG:NH2	36:R:133:LYS:HA	2.37	0.40
42:5:1923:A:H2'	42:5:1924:C:C6	2.57	0.40
42:5:3877:A:OP2	42:5:3877:A:H2'	2.22	0.40
42:5:4146:G:H2'	42:5:4147:G:H8	1.87	0.40
42:5:4188:U:H2'	42:5:4189:U:H6	1.85	0.40
42:5:4684:A:H2'	42:5:4685:U:O4'	2.22	0.40
42:5:4710:C:H2'	42:5:4711:C:C6	2.55	0.40
47:K:281:THR:O	47:K:284:LYS:HG2	2.21	0.40
47:K:421:ILE:HG22	47:K:462:PRO:HG3	2.03	0.40
6:B:54:THR:OG1	6:B:55:HIS:N	2.55	0.40
13:f:54:LYS:HB3	42:5:443:G:H5''	2.03	0.40
16:G:44:ASP:N	16:G:44:ASP:OD1	2.54	0.40
22:J:112:HIS:HB2	22:J:115:LEU:HD12	2.02	0.40
28:N:135:ILE:HG23	28:N:142:ILE:HD13	2.03	0.40
30:O:87:MET:HE2	42:5:2051:C:H2'	2.03	0.40
42:5:33:A:H5''	42:5:47:A:N1	2.36	0.40
42:5:961:G:N3	42:5:961:G:H2'	2.37	0.40
42:5:1306:C:H2'	42:5:1307:A:C8	2.56	0.40
42:5:1569:U:H2'	42:5:1570:G:C8	2.57	0.40
42:5:1699:A:N6	42:5:2094:G:H1'	2.36	0.40
42:5:2315:G:H2'	42:5:2316:G:O4'	2.20	0.40
42:5:2375:A:H2'	42:5:2376:A:H8	1.86	0.40
46:8:107:C:C4	46:8:108:A:N6	2.90	0.40
46:8:140:C:H2'	46:8:141:C:C6	2.56	0.40
46:8:148:A:H2'	46:8:149:G:C8	2.56	0.40
47:K:91:LYS:HE3	47:K:91:LYS:HB3	1.86	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	
2	t	65/215 (30%)	63 (97%)	2 (3%)	0	100	100
3	u	106/162 (65%)	102 (96%)	4 (4%)	0	100	100
4	A	242/245 (99%)	223 (92%)	19 (8%)	0	100	100
5	b	73/223 (33%)	72 (99%)	1 (1%)	0	100	100
6	B	392/403 (97%)	384 (98%)	8 (2%)	0	100	100
7	c	92/115 (80%)	91 (99%)	1 (1%)	0	100	100
8	C	360/413 (87%)	347 (96%)	13 (4%)	0	100	100
9	d	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
10	D	290/297 (98%)	280 (97%)	10 (3%)	0	100	100
11	e	126/157 (80%)	121 (96%)	5 (4%)	0	100	100
12	E	232/291 (80%)	205 (88%)	27 (12%)	0	100	100
13	f	107/110 (97%)	101 (94%)	6 (6%)	0	100	100
14	F	223/225 (99%)	218 (98%)	5 (2%)	0	100	100
15	g	112/129 (87%)	111 (99%)	1 (1%)	0	100	100
16	G	239/319 (75%)	225 (94%)	14 (6%)	0	100	100
17	h	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
18	H	188/192 (98%)	181 (96%)	7 (4%)	0	100	100
19	i	100/102 (98%)	97 (97%)	2 (2%)	1 (1%)	12	40
20	I	200/214 (94%)	193 (96%)	7 (4%)	0	100	100
21	j	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
22	J	167/178 (94%)	159 (95%)	8 (5%)	0	100	100
23	k	67/69 (97%)	62 (92%)	5 (8%)	0	100	100
24	L	208/210 (99%)	196 (94%)	12 (6%)	0	100	100
25	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
26	M	136/218 (62%)	128 (94%)	8 (6%)	0	100	100
27	m	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
28	N	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
29	n	21/25 (84%)	21 (100%)	0	0	100	100
30	O	197/500 (39%)	196 (100%)	1 (0%)	0	100	100
31	o	102/141 (72%)	96 (94%)	6 (6%)	0	100	100
32	P	151/153 (99%)	150 (99%)	1 (1%)	0	100	100
33	p	89/92 (97%)	87 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Q	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
35	r	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
36	R	178/196 (91%)	175 (98%)	3 (2%)	0	100	100
37	S	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
38	T	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
39	U	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
40	V	129/140 (92%)	127 (98%)	2 (2%)	0	100	100
41	W	61/157 (39%)	61 (100%)	0	0	100	100
43	X	117/156 (75%)	115 (98%)	2 (2%)	0	100	100
45	Y	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
47	K	424/440 (96%)	417 (98%)	7 (2%)	0	100	100
48	Z	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
49	a	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
All	All	6953/8408 (83%)	6697 (96%)	255 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	i	11	LEU

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	
2	t	60/183 (33%)	60 (100%)	0	100	100
3	u	92/136 (68%)	91 (99%)	1 (1%)	65	74
4	A	187/188 (100%)	185 (99%)	2 (1%)	65	74
5	b	62/170 (36%)	60 (97%)	2 (3%)	34	58
6	B	336/348 (97%)	330 (98%)	6 (2%)	51	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	c	79/98 (81%)	77 (98%)	2 (2%)	42	62
8	C	302/337 (90%)	295 (98%)	7 (2%)	44	63
9	d	98/110 (89%)	95 (97%)	3 (3%)	35	59
10	D	247/250 (99%)	240 (97%)	7 (3%)	38	60
11	e	114/141 (81%)	114 (100%)	0	100	100
12	E	208/251 (83%)	202 (97%)	6 (3%)	37	60
13	f	88/89 (99%)	86 (98%)	2 (2%)	44	63
14	F	194/195 (100%)	194 (100%)	0	100	100
15	g	98/109 (90%)	95 (97%)	3 (3%)	35	59
16	G	206/273 (76%)	200 (97%)	6 (3%)	37	60
17	h	109/110 (99%)	107 (98%)	2 (2%)	51	67
18	H	169/171 (99%)	164 (97%)	5 (3%)	36	59
19	i	86/86 (100%)	84 (98%)	2 (2%)	44	63
20	I	174/181 (96%)	173 (99%)	1 (1%)	78	80
21	j	73/80 (91%)	73 (100%)	0	100	100
22	J	142/149 (95%)	141 (99%)	1 (1%)	76	78
23	k	64/64 (100%)	62 (97%)	2 (3%)	35	59
24	L	176/176 (100%)	172 (98%)	4 (2%)	44	63
25	l	47/48 (98%)	47 (100%)	0	100	100
26	M	117/160 (73%)	115 (98%)	2 (2%)	53	67
27	m	48/116 (41%)	48 (100%)	0	100	100
28	N	171/172 (99%)	170 (99%)	1 (1%)	78	80
29	n	22/24 (92%)	22 (100%)	0	100	100
30	O	171/433 (40%)	169 (99%)	2 (1%)	63	72
31	o	92/121 (76%)	91 (99%)	1 (1%)	65	74
32	P	134/134 (100%)	133 (99%)	1 (1%)	76	78
33	p	74/75 (99%)	73 (99%)	1 (1%)	59	70
34	Q	163/163 (100%)	157 (96%)	6 (4%)	30	55
35	r	109/121 (90%)	109 (100%)	0	100	100
36	R	159/175 (91%)	158 (99%)	1 (1%)	78	80
37	S	156/156 (100%)	149 (96%)	7 (4%)	24	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	T	139/140 (99%)	137 (99%)	2 (1%)	59	70
39	U	95/95 (100%)	91 (96%)	4 (4%)	26	52
40	V	101/107 (94%)	100 (99%)	1 (1%)	68	75
41	W	55/126 (44%)	55 (100%)	0	100	100
43	X	107/134 (80%)	106 (99%)	1 (1%)	70	76
45	Y	124/135 (92%)	122 (98%)	2 (2%)	55	68
47	K	370/381 (97%)	368 (100%)	2 (0%)	81	81
48	Z	117/118 (99%)	115 (98%)	2 (2%)	53	67
49	a	119/120 (99%)	119 (100%)	0	100	100
All	All	6054/7149 (85%)	5954 (98%)	100 (2%)	52	67

All (100) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	u	53	VAL
4	A	73	THR
4	A	136	VAL
5	b	21	ILE
5	b	40	LEU
6	B	110	ILE
6	B	205	VAL
6	B	219	VAL
6	B	248	LEU
6	B	344	VAL
6	B	370	THR
7	c	35	LEU
7	c	93	THR
8	C	79	VAL
8	C	153	VAL
8	C	174	LEU
8	C	230	LEU
8	C	237	ILE
8	C	266	THR
8	C	326	LEU
9	d	20	VAL
9	d	46	LEU
9	d	102	LEU
10	D	55	VAL
10	D	60	ILE

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Mol	Chain	Res	Type
10	D	61	ILE
10	D	105	LEU
10	D	177	THR
10	D	231	VAL
10	D	261	VAL
12	E	84	VAL
12	E	100	THR
12	E	115	GLU
12	E	147	ILE
12	E	260	VAL
12	E	270	VAL
13	f	18	LEU
13	f	33	VAL
15	g	5	LEU
15	g	32	TYR
15	g	56	VAL
16	G	54	PHE
16	G	86	VAL
16	G	168	VAL
16	G	173	LEU
16	G	179	VAL
16	G	194	VAL
17	h	24	LEU
17	h	30	GLN
18	H	26	ILE
18	H	59	LYS
18	H	86	LEU
18	H	95	VAL
18	H	179	ILE
19	i	21	VAL
19	i	34	THR
20	I	26	VAL
22	J	74	VAL
23	k	36	VAL
23	k	49	ASP
24	L	59	VAL
24	L	154	VAL
24	L	168	VAL
24	L	184	MET
26	M	57	LEU
26	M	84	THR
28	N	18	VAL

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Mol	Chain	Res	Type
30	O	27	VAL
30	O	145	VAL
31	o	67	VAL
32	P	148	VAL
33	p	52	VAL
34	Q	13	VAL
34	Q	37	ARG
34	Q	42	THR
34	Q	81	VAL
34	Q	82	VAL
34	Q	137	VAL
36	R	106	LEU
37	S	24	THR
37	S	51	LEU
37	S	96	GLU
37	S	101	THR
37	S	102	THR
37	S	158	VAL
37	S	164	LYS
38	T	48	VAL
38	T	141	VAL
39	U	27	HIS
39	U	56	LEU
39	U	72	VAL
39	U	102	VAL
40	V	99	GLU
43	X	127	LEU
45	Y	52	ASP
45	Y	55	VAL
47	K	245	THR
47	K	367	THR
48	Z	13	VAL
48	Z	43	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (123) such sidechains are listed below:

Mol	Chain	Res	Type
3	u	45	GLN
3	u	80	GLN
4	A	86	GLN
4	A	97	ASN
4	A	162	ASN

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Mol	Chain	Res	Type
4	A	215	ASN
5	b	7	HIS
5	b	17	HIS
5	b	49	HIS
5	b	50	ASN
5	b	58	GLN
5	b	61	ASN
6	B	68	ASN
6	B	184	GLN
6	B	271	GLN
6	B	281	ASN
6	B	315	ASN
6	B	354	GLN
6	B	380	GLN
7	c	19	GLN
8	C	41	HIS
8	C	50	GLN
8	C	198	ASN
8	C	231	ASN
8	C	299	GLN
8	C	329	ASN
8	C	346	ASN
8	C	347	HIS
9	d	18	ASN
9	d	28	ASN
9	d	34	HIS
9	d	118	GLN
10	D	63	GLN
10	D	138	GLN
10	D	250	ASN
10	D	282	GLN
11	e	124	ASN
12	E	132	HIS
12	E	163	GLN
12	E	186	HIS
12	E	187	GLN
12	E	280	HIS
14	F	112	GLN
15	g	100	GLN
16	G	29	ASN
16	G	64	GLN
16	G	100	HIS

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Mol	Chain	Res	Type
16	G	141	ASN
16	G	149	ASN
16	G	153	GLN
16	G	159	HIS
16	G	227	ASN
16	G	236	HIS
17	h	30	GLN
18	H	8	GLN
18	H	79	ASN
20	I	73	ASN
20	I	86	HIS
20	I	92	HIS
22	J	42	GLN
22	J	98	ASN
23	k	31	ASN
23	k	58	GLN
24	L	28	GLN
24	L	87	HIS
24	L	104	ASN
24	L	149	GLN
25	l	33	ASN
26	M	33	GLN
26	M	125	ASN
27	m	119	ASN
28	N	87	HIS
28	N	117	ASN
30	O	26	GLN
30	O	42	ASN
30	O	63	ASN
30	O	96	GLN
30	O	184	ASN
31	o	36	GLN
31	o	51	GLN
31	o	102	GLN
32	P	54	HIS
32	P	63	GLN
32	P	85	GLN
32	P	101	GLN
32	P	109	GLN
32	P	130	ASN
32	P	145	HIS
32	P	166	ASN

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Mol	Chain	Res	Type
32	P	174	HIS
33	p	72	ASN
34	Q	21	GLN
35	r	31	ASN
35	r	121	GLN
36	R	130	ASN
36	R	141	HIS
37	S	156	HIS
37	S	162	GLN
38	T	54	HIS
38	T	58	HIS
38	T	95	HIS
40	V	31	ASN
40	V	101	ASN
41	W	59	HIS
43	X	73	HIS
45	Y	4	ASN
45	Y	14	ASN
45	Y	24	HIS
45	Y	65	GLN
45	Y	72	GLN
47	K	66	GLN
47	K	118	GLN
47	K	128	ASN
47	K	189	GLN
47	K	248	ASN
47	K	276	HIS
47	K	311	GLN
47	K	439	ASN
47	K	443	HIS
47	K	468	ASN
49	a	17	HIS
49	a	60	HIS
49	a	66	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
42	5	3477/4754 (73%)	684 (19%)	65 (1%)
44	7	119/120 (99%)	13 (10%)	0
46	8	155/156 (99%)	36 (23%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	3751/5030 (74%)	733 (19%)	66 (1%)

All (733) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
42	5	2	G
42	5	8	U
42	5	12	A
42	5	13	U
42	5	14	C
42	5	21	G
42	5	25	A
42	5	39	A
42	5	42	A
42	5	48	G
42	5	49	U
42	5	59	A
42	5	64	A
42	5	65	A
42	5	66	A
42	5	73	A
42	5	76	A
42	5	91	G
42	5	104	G
42	5	108	A
42	5	109	G
42	5	110	C
42	5	116	G
42	5	119	G
42	5	126	C
42	5	132	G
42	5	134	G
42	5	135	G
42	5	136	C
42	5	143	C
42	5	144	G
42	5	159	C
42	5	164	G
42	5	165	A
42	5	171	U
42	5	172	C
42	5	173	C

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Mol	Chain	Res	Type
42	5	183	C
42	5	185	C
42	5	186	G
42	5	188	G
42	5	189	G
42	5	200	U
42	5	201	C
42	5	205	C
42	5	210	C
42	5	216	C
42	5	217	C
42	5	218	A
42	5	220	C
42	5	221	C
42	5	224	U
42	5	226	G
42	5	227	A
42	5	233	U
42	5	238	C
42	5	246	G
42	5	262	G
42	5	265	C
42	5	266	C
42	5	267	G
42	5	276	C
42	5	278	G
42	5	280	G
42	5	281	U
42	5	297	U
42	5	306	A
42	5	309	C
42	5	315	G
42	5	316	U
42	5	326	C
42	5	334	A
42	5	335	A
42	5	340	C
42	5	363	A
42	5	386	A
42	5	387	G
42	5	390	C
42	5	407	A

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Mol	Chain	Res	Type
42	5	409	G
42	5	412	G
42	5	413	G
42	5	431	G
42	5	444	G
42	5	446	C
42	5	451	C
42	5	452	A
42	5	453	G
42	5	454	U
42	5	455	C
42	5	468	U
42	5	485	C
42	5	486	C
42	5	487	G
42	5	654	C
42	5	664	G
42	5	666	G
42	5	667	A
42	5	669	C
42	5	683	C
42	5	684	G
42	5	685	C
42	5	686	A
42	5	694	C
42	5	696	C
42	5	697	G
42	5	703	G
42	5	704	C
42	5	707	C
42	5	718	C
42	5	729	G
42	5	730	G
42	5	732	A
42	5	737	C
42	5	746	A
42	5	748	G
42	5	749	G
42	5	914	U
42	5	918	G
42	5	920	C
42	5	927	G

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Mol	Chain	Res	Type
42	5	928	C
42	5	929	A
42	5	930	G
42	5	931	C
42	5	932	A
42	5	933	G
42	5	934	C
42	5	936	C
42	5	939	G
42	5	940	C
42	5	942	G
42	5	944	A
42	5	945	U
42	5	946	C
42	5	957	G
42	5	958	G
42	5	960	A
42	5	961	G
42	5	962	C
42	5	963	G
42	5	964	A
42	5	965	G
42	5	966	A
42	5	967	C
42	5	968	C
42	5	969	C
42	5	970	G
42	5	971	U
42	5	976	G
42	5	978	G
42	5	982	U
42	5	984	C
42	5	1072	C
42	5	1210	C
42	5	1211	G
42	5	1212	G
42	5	1219	G
42	5	1233	G
42	5	1236	C
42	5	1237	C
42	5	1238	A
42	5	1239	C

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Mol	Chain	Res	Type
42	5	1242	G
42	5	1272	C
42	5	1273	G
42	5	1274	A
42	5	1275	G
42	5	1276	C
42	5	1279	A
42	5	1280	C
42	5	1281	G
42	5	1285	U
42	5	1286	C
42	5	1288	G
42	5	1289	C
42	5	1293	G
42	5	1295	C
42	5	1296	G
42	5	1297	U
42	5	1302	U
42	5	1304	C
42	5	1314	C
42	5	1326	A
42	5	1330	A
42	5	1344	C
42	5	1354	A
42	5	1358	G
42	5	1366	G
42	5	1367	C
42	5	1369	C
42	5	1370	G
42	5	1371	A
42	5	1377	G
42	5	1378	C
42	5	1379	C
42	5	1380	G
42	5	1387	A
42	5	1394	G
42	5	1397	A
42	5	1399	G
42	5	1407	C
42	5	1408	G
42	5	1409	C
42	5	1410	U

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Mol	Chain	Res	Type
42	5	1415	G
42	5	1420	A
42	5	1429	C
42	5	1437	C
42	5	1440	U
42	5	1441	C
42	5	1445	U
42	5	1456	C
42	5	1457	G
42	5	1475	G
42	5	1478	C
42	5	1481	C
42	5	1482	G
42	5	1483	C
42	5	1497	A
42	5	1498	G
42	5	1501	C
42	5	1514	U
42	5	1516	G
42	5	1523	A
42	5	1534	A
42	5	1547	A
42	5	1553	A
42	5	1563	A
42	5	1566	C
42	5	1574	G
42	5	1578	U
42	5	1591	U
42	5	1596	U
42	5	1602	U
42	5	1612	G
42	5	1613	A
42	5	1624	G
42	5	1625	G
42	5	1631	A
42	5	1633	G
42	5	1634	A
42	5	1638	A
42	5	1641	G
42	5	1654	G
42	5	1661	C
42	5	1676	C

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Mol	Chain	Res	Type
42	5	1677	U
42	5	1691	G
42	5	1696	C
42	5	1697	G
42	5	1698	C
42	5	1720	C
42	5	1721	G
42	5	1724	G
42	5	1729	A
42	5	1734	G
42	5	1741	G
42	5	1742	A
42	5	1751	A
42	5	1754	U
42	5	1755	C
42	5	1756	U
42	5	1757	U
42	5	1761	G
42	5	1764	G
42	5	1769	G
42	5	1772	C
42	5	1776	A
42	5	1777	C
42	5	1780	A
42	5	1787	A
42	5	1803	G
42	5	1804	A
42	5	1805	A
42	5	1815	G
42	5	1819	G
42	5	1821	G
42	5	1822	U
42	5	1828	C
42	5	1833	G
42	5	1834	U
42	5	1835	G
42	5	1836	G
42	5	1840	G
42	5	1848	C
42	5	1855	G
42	5	1869	G
42	5	1882	U

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Mol	Chain	Res	Type
42	5	1890	G
42	5	1897	A
42	5	1910	G
42	5	1916	G
42	5	1918	U
42	5	1919	G
42	5	1920	C
42	5	1921	C
42	5	1922	G
42	5	1923	A
42	5	1928	C
42	5	1931	C
42	5	1945	G
42	5	1948	G
42	5	1956	A
42	5	1958	A
42	5	1961	G
42	5	1962	A
42	5	2026	A
42	5	2047	A
42	5	2048	U
42	5	2055	G
42	5	2056	G
42	5	2062	C
42	5	2064	G
42	5	2084	C
42	5	2089	G
42	5	2092	G
42	5	2093	A
42	5	2094	G
42	5	2095	A
42	5	2097	U
42	5	2107	C
42	5	2248	C
42	5	2250	C
42	5	2251	G
42	5	2252	G
42	5	2253	A
42	5	2254	G
42	5	2255	C
42	5	2257	C
42	5	2259	G

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Mol	Chain	Res	Type
42	5	2260	C
42	5	2261	G
42	5	2263	A
42	5	2264	C
42	5	2265	G
42	5	2266	C
42	5	2267	U
42	5	2268	A
42	5	2269	C
42	5	2270	G
42	5	2275	G
42	5	2289	C
42	5	2300	A
42	5	2301	G
42	5	2306	G
42	5	2313	A
42	5	2314	G
42	5	2316	G
42	5	2331	G
42	5	2333	G
42	5	2348	G
42	5	2351	C
42	5	2360	A
42	5	2395	A
42	5	2396	A
42	5	2409	U
42	5	2422	C
42	5	2425	U
42	5	2432	U
42	5	2433	G
42	5	2441	C
42	5	2443	G
42	5	2469	C
42	5	2471	G
42	5	2475	G
42	5	2488	C
42	5	2489	C
42	5	2490	U
42	5	2491	C
42	5	2503	G
42	5	2504	C
42	5	2505	C

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Mol	Chain	Res	Type
42	5	2506	G
42	5	2512	A
42	5	2513	A
42	5	2529	A
42	5	2536	A
42	5	2537	A
42	5	2544	G
42	5	2546	G
42	5	2547	G
42	5	2552	G
42	5	2554	U
42	5	2555	G
42	5	2575	U
42	5	2582	A
42	5	2583	C
42	5	2586	G
42	5	2587	A
42	5	2589	C
42	5	2620	G
42	5	2623	A
42	5	2625	U
42	5	2627	C
42	5	2662	G
42	5	2686	G
42	5	2687	U
42	5	2695	A
42	5	2696	A
42	5	2707	U
42	5	2708	U
42	5	2710	C
42	5	2711	G
42	5	2713	C
42	5	2714	G
42	5	2725	A
42	5	2726	G
42	5	2740	U
42	5	2744	A
42	5	2753	G
42	5	2754	G
42	5	2756	G
42	5	2758	G
42	5	2762	G

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Mol	Chain	Res	Type
42	5	2767	U
42	5	2768	C
42	5	2769	U
42	5	2770	C
42	5	2772	C
42	5	2787	A
42	5	2788	U
42	5	2790	U
42	5	2794	C
42	5	2798	A
42	5	2806	A
42	5	2814	C
42	5	2826	U
42	5	2828	U
42	5	2833	A
42	5	2838	G
42	5	2842	G
42	5	2855	G
42	5	2905	C
42	5	3593	C
42	5	3594	C
42	5	3595	U
42	5	3596	A
42	5	3597	G
42	5	3602	C
42	5	3605	C
42	5	3625	G
42	5	3626	G
42	5	3635	A
42	5	3643	A
42	5	3662	A
42	5	3664	G
42	5	3672	G
42	5	3673	C
42	5	3680	U
42	5	3692	A
42	5	3698	G
42	5	3710	G
42	5	3711	A
42	5	3714	G
42	5	3727	A
42	5	3748	A

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Mol	Chain	Res	Type
42	5	3753	G
42	5	3759	A
42	5	3760	A
42	5	3773	U
42	5	3776	G
42	5	3777	G
42	5	3778	U
42	5	3784	A
42	5	3786	U
42	5	3791	C
42	5	3809	G
42	5	3810	C
42	5	3811	G
42	5	3812	C
42	5	3814	U
42	5	3817	A
42	5	3819	G
42	5	3839	G
42	5	3840	U
42	5	3877	A
42	5	3878	C
42	5	3879	G
42	5	3889	G
42	5	3892	U
42	5	3897	G
42	5	3901	A
42	5	3905	A
42	5	3906	A
42	5	3907	G
42	5	3915	U
42	5	3917	A
42	5	3926	C
42	5	3938	G
42	5	3939	G
42	5	4069	U
42	5	4070	U
42	5	4076	G
42	5	4085	A
42	5	4086	G
42	5	4088	C
42	5	4090	G
42	5	4094	G

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Mol	Chain	Res	Type
42	5	4097	G
42	5	4114	C
42	5	4115	G
42	5	4116	C
42	5	4117	U
42	5	4120	U
42	5	4125	C
42	5	4127	A
42	5	4128	A
42	5	4143	G
42	5	4144	C
42	5	4145	C
42	5	4162	C
42	5	4163	U
42	5	4165	C
42	5	4166	G
42	5	4171	C
42	5	4183	G
42	5	4184	G
42	5	4191	G
42	5	4203	A
42	5	4212	A
42	5	4225	G
42	5	4229	U
42	5	4233	A
42	5	4241	C
42	5	4243	C
42	5	4251	A
42	5	4254	G
42	5	4255	A
42	5	4267	G
42	5	4268	A
42	5	4271	A
42	5	4273	A
42	5	4280	A
42	5	4291	G
42	5	4297	G
42	5	4303	C
42	5	4304	A
42	5	4305	G
42	5	4306	U
42	5	4314	C

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Mol	Chain	Res	Type
42	5	4318	C
42	5	4319	C
42	5	4330	G
42	5	4332	C
42	5	4336	A
42	5	4337	C
42	5	4349	C
42	5	4350	C
42	5	4354	U
42	5	4355	G
42	5	4376	A
42	5	4377	G
42	5	4378	A
42	5	4387	C
42	5	4394	A
42	5	4395	U
42	5	4398	C
42	5	4401	G
42	5	4415	A
42	5	4419	U
42	5	4421	C
42	5	4422	A
42	5	4436	U
42	5	4437	U
42	5	4440	G
42	5	4444	C
42	5	4448	G
42	5	4449	A
42	5	4453	C
42	5	4464	A
42	5	4466	C
42	5	4471	U
42	5	4472	G
42	5	4473	A
42	5	4476	C
42	5	4500	U
42	5	4512	U
42	5	4513	A
42	5	4518	A
42	5	4528	G
42	5	4529	G
42	5	4531	U

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Mol	Chain	Res	Type
42	5	4548	A
42	5	4549	G
42	5	4560	C
42	5	4570	G
42	5	4575	G
42	5	4577	U
42	5	4581	G
42	5	4586	G
42	5	4590	A
42	5	4599	A
42	5	4617	G
42	5	4627	U
42	5	4636	U
42	5	4637	G
42	5	4647	G
42	5	4652	G
42	5	4656	A
42	5	4657	U
42	5	4667	C
42	5	4670	C
42	5	4671	C
42	5	4672	A
42	5	4677	U
42	5	4682	U
42	5	4691	A
42	5	4695	C
42	5	4697	U
42	5	4700	A
42	5	4709	U
42	5	4719	G
42	5	4720	C
42	5	4730	C
42	5	4731	G
42	5	4732	G
42	5	4744	A
42	5	4745	G
42	5	4746	C
42	5	4750	G
42	5	4753	U
42	5	4756	C
42	5	4758	U
42	5	4761	G

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Mol	Chain	Res	Type
42	5	4764	A
42	5	4770	U
42	5	4869	U
42	5	4871	C
42	5	4873	G
42	5	4876	U
42	5	4883	C
42	5	4884	G
42	5	4886	C
42	5	4889	G
42	5	4890	G
42	5	4895	C
42	5	4896	G
42	5	4901	G
42	5	4902	C
42	5	4903	G
42	5	4904	G
42	5	4906	C
42	5	4910	G
42	5	4911	A
42	5	4913	G
42	5	4919	G
42	5	4927	G
42	5	4930	C
42	5	4933	C
42	5	4936	G
42	5	4937	C
42	5	4944	C
42	5	4945	G
42	5	4948	C
42	5	4949	G
42	5	4951	G
42	5	4959	U
42	5	4963	G
42	5	4964	C
42	5	4965	U
42	5	4966	A
42	5	4976	U
42	5	4988	U
42	5	4989	U
42	5	4990	C
42	5	4991	U

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Mol	Chain	Res	Type
42	5	5006	U
42	5	5007	A
42	5	5013	C
42	5	5017	G
42	5	5023	C
42	5	5024	C
42	5	5026	U
42	5	5027	C
42	5	5028	G
42	5	5041	G
42	5	5047	C
42	5	5050	C
42	5	5052	C
42	5	5054	C
42	5	5060	A
42	5	5061	A
42	5	5062	G
44	7	11	A
44	7	22	A
44	7	40	U
44	7	51	G
44	7	53	U
44	7	54	A
44	7	63	C
44	7	64	G
44	7	89	G
44	7	100	A
44	7	110	G
44	7	111	C
44	7	120	U
46	8	2	G
46	8	16	G
46	8	23	C
46	8	34	U
46	8	35	C
46	8	38	U
46	8	39	G
46	8	52	A
46	8	59	A
46	8	62	A
46	8	63	U
46	8	71	A

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Mol	Chain	Res	Type
46	8	77	A
46	8	80	A
46	8	81	C
46	8	82	A
46	8	83	C
46	8	84	A
46	8	85	U
46	8	86	U
46	8	87	G
46	8	90	C
46	8	94	G
46	8	103	A
46	8	105	C
46	8	108	A
46	8	110	U
46	8	111	U
46	8	114	G
46	8	123	U
46	8	125	C
46	8	126	C
46	8	127	U
46	8	128	C
46	8	150	C
46	8	153	C

All (66) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
42	5	12	A
42	5	47	A
42	5	48	G
42	5	125	C
42	5	134	G
42	5	170	C
42	5	187	U
42	5	216	C
42	5	226	G
42	5	265	C
42	5	275	C
42	5	385	A
42	5	406	C
42	5	451	C

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Mol	Chain	Res	Type
42	5	454	U
42	5	684	G
42	5	693	C
42	5	917	A
42	5	930	G
42	5	932	A
42	5	957	G
42	5	965	G
42	5	1211	G
42	5	1232	G
42	5	1236	C
42	5	1238	A
42	5	1296	G
42	5	1329	G
42	5	1357	C
42	5	1368	A
42	5	1407	C
42	5	1440	U
42	5	1455	G
42	5	1633	G
42	5	1804	A
42	5	2046	G
42	5	2083	C
42	5	2093	A
42	5	2260	C
42	5	2262	G
42	5	2502	G
42	5	2695	A
42	5	2712	G
42	5	3625	G
42	5	3697	U
42	5	3888	G
42	5	4069	U
42	5	4119	C
42	5	4170	A
42	5	4232	U
42	5	4448	G
42	5	4528	G
42	5	4656	A
42	5	4699	U
42	5	4719	G
42	5	4885	U

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Mol	Chain	Res	Type
42	5	4888	U
42	5	4889	G
42	5	4935	C
42	5	4948	C
42	5	5022	U
42	5	5027	C
42	5	5059	C
42	5	5060	A
42	5	5061	A
46	8	124	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 102 ligands modelled in this entry, 102 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.

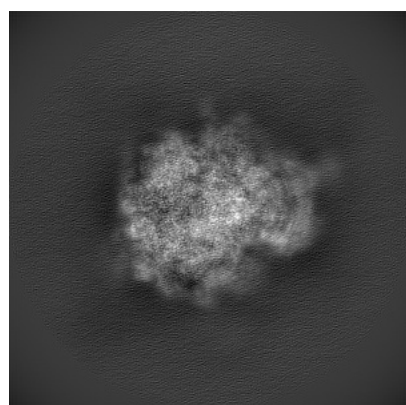
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14193. These allow visual inspection of the internal detail of the map and identification of artifacts.

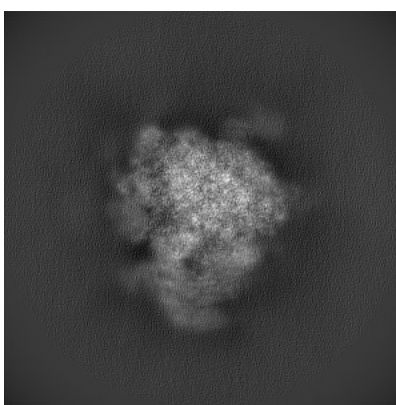
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

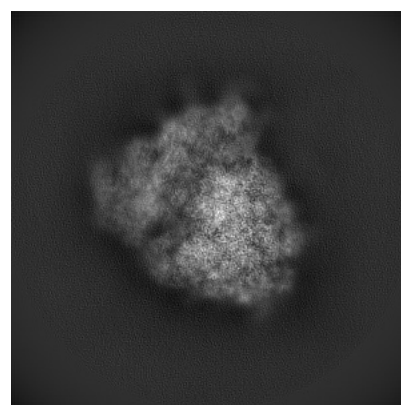
6.1.1 Primary map



X



Y

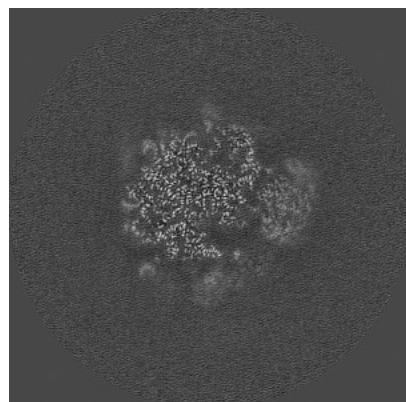


Z

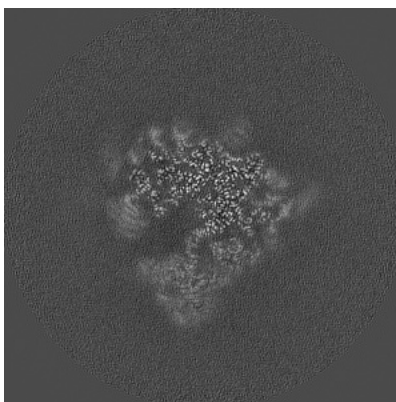
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

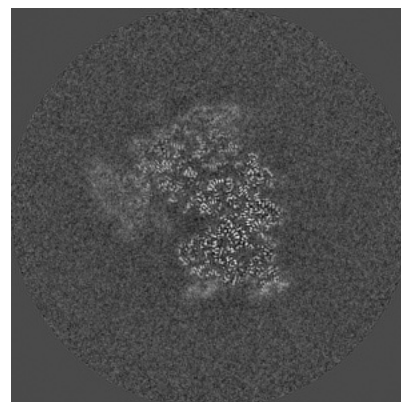
6.2.1 Primary map



X Index: 200



Y Index: 200

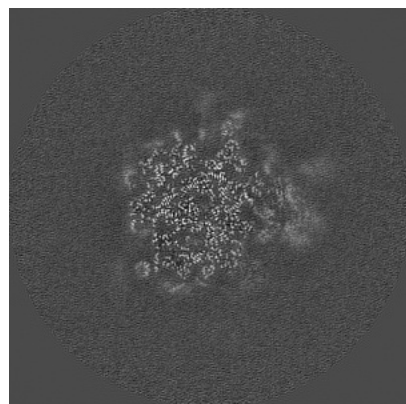


Z Index: 200

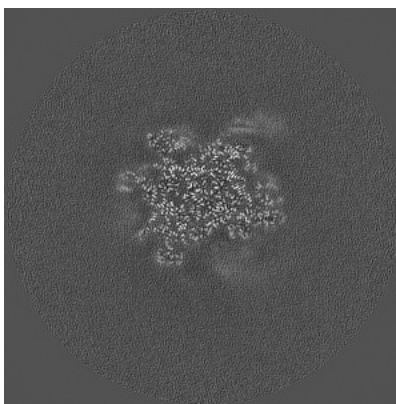
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

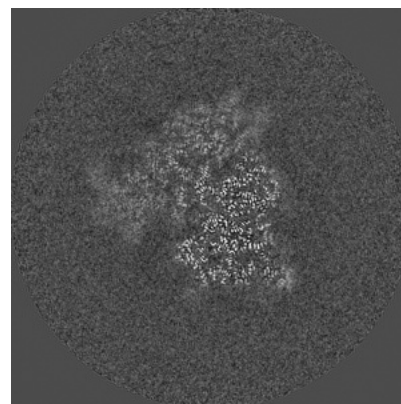
6.3.1 Primary map



X Index: 216



Y Index: 160

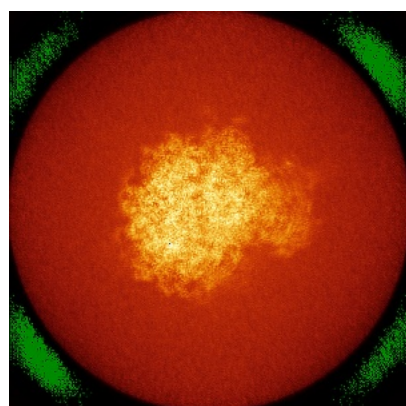


Z Index: 191

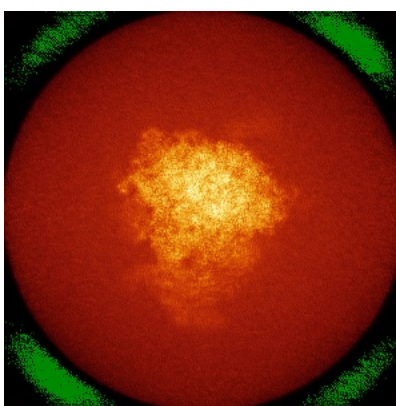
The images above show the largest variance slices of the map in three orthogonal directions.

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

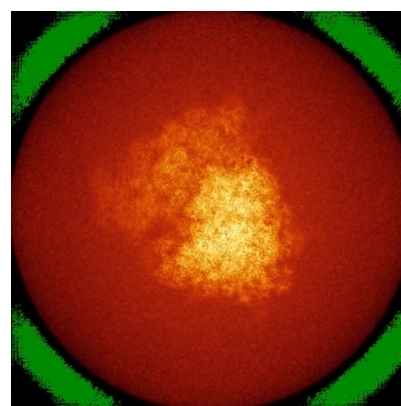
6.4.1 Primary map



X



Y

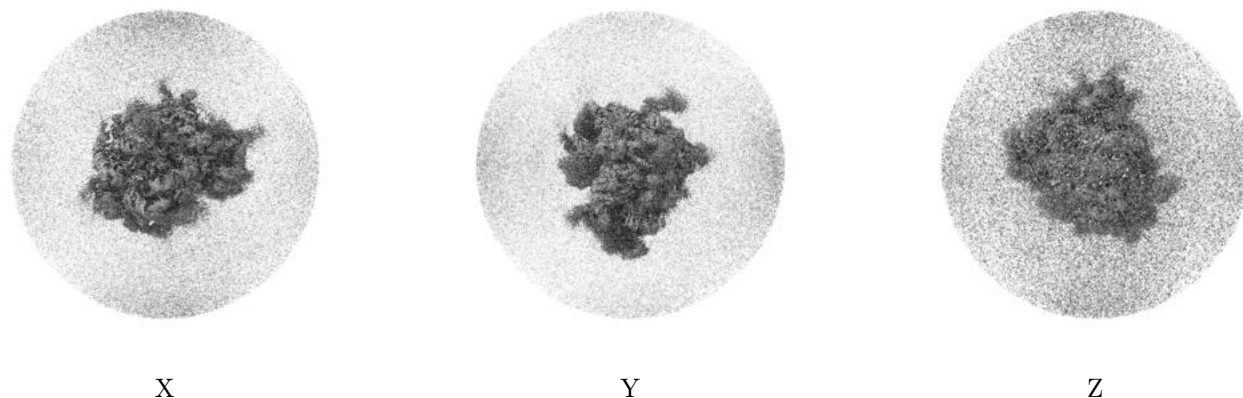


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

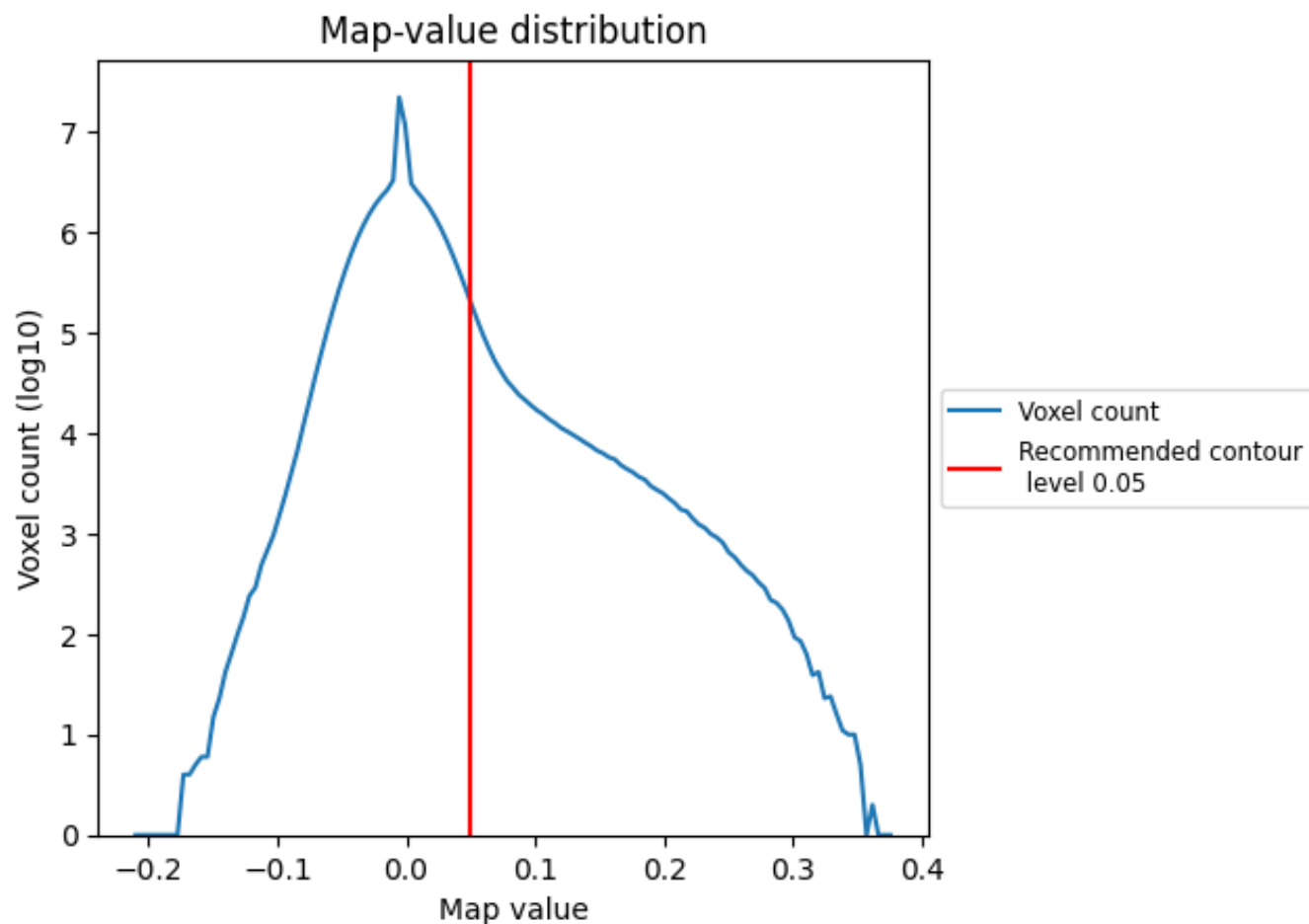
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

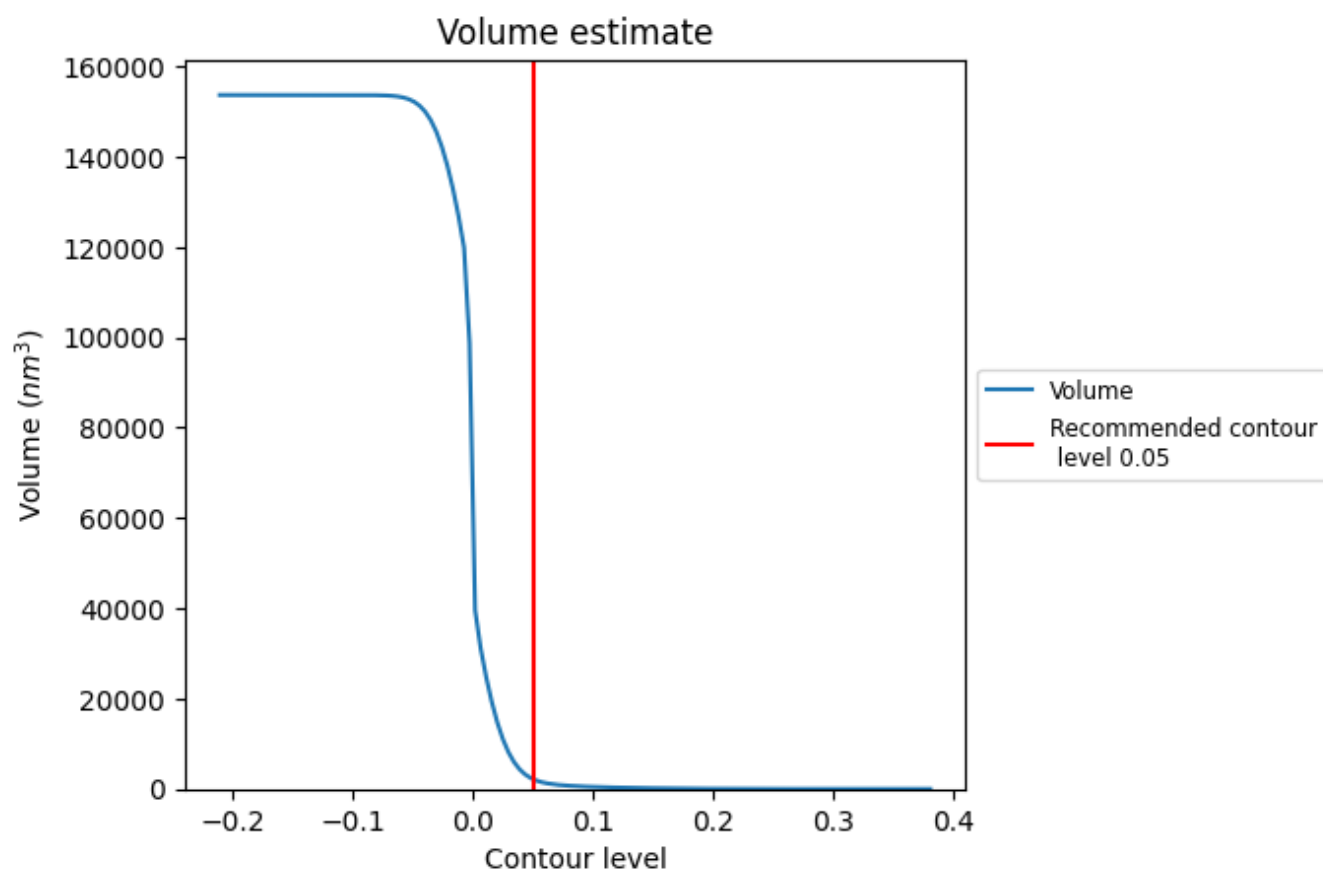
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

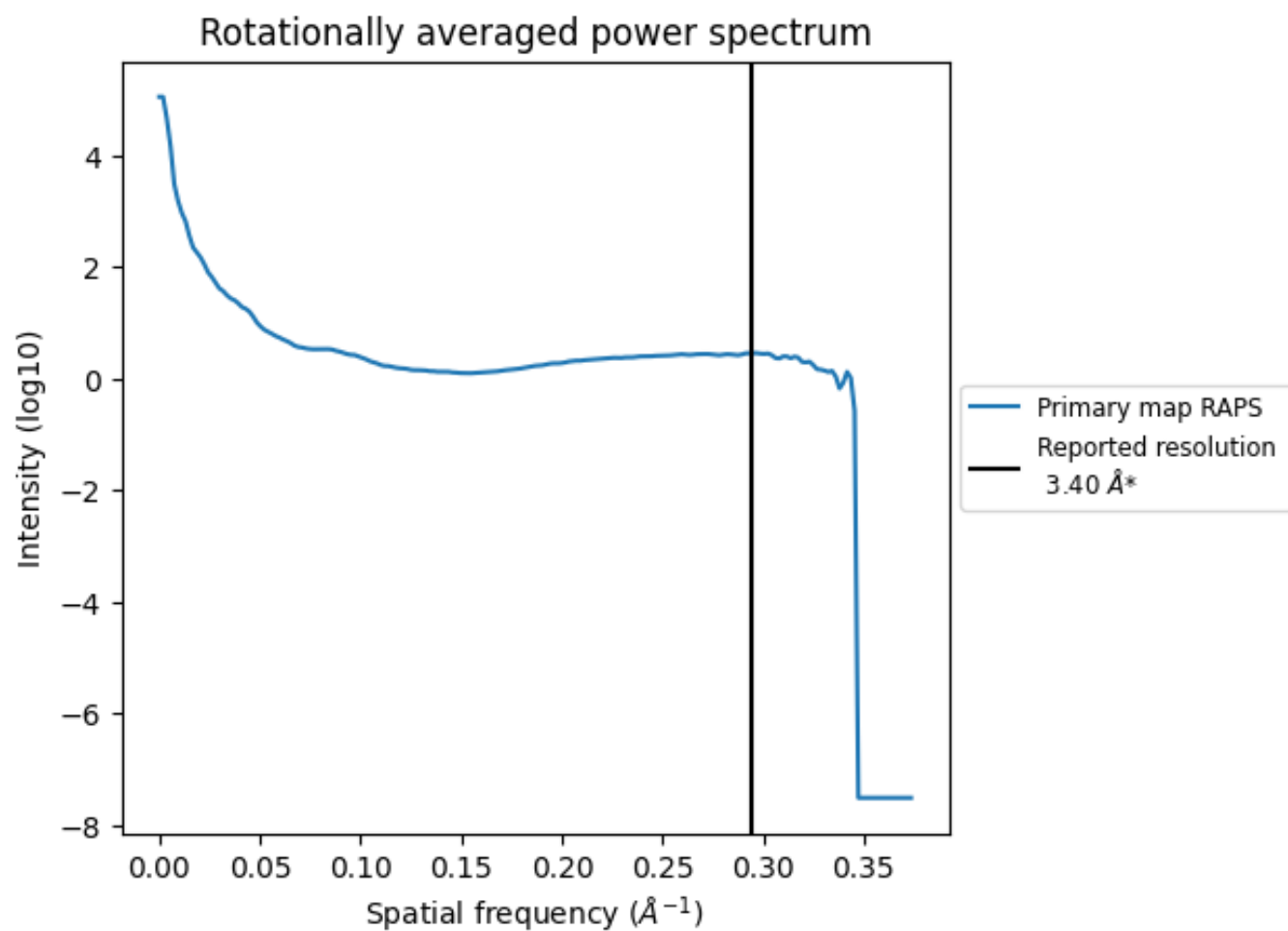
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2230 nm³; this corresponds to an approximate mass of 2015 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

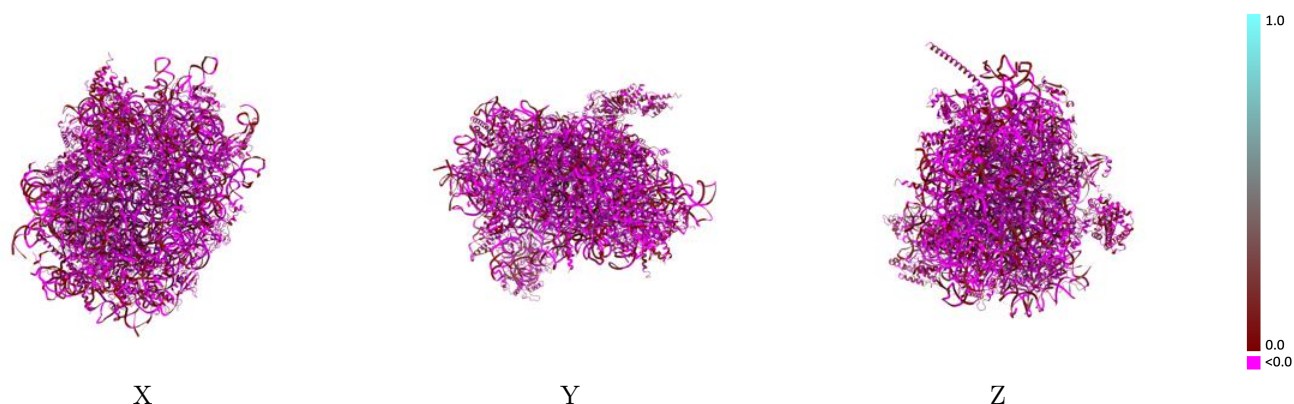
This section contains information regarding the fit between EMDB map EMD-14193 and PDB model 7QWS. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



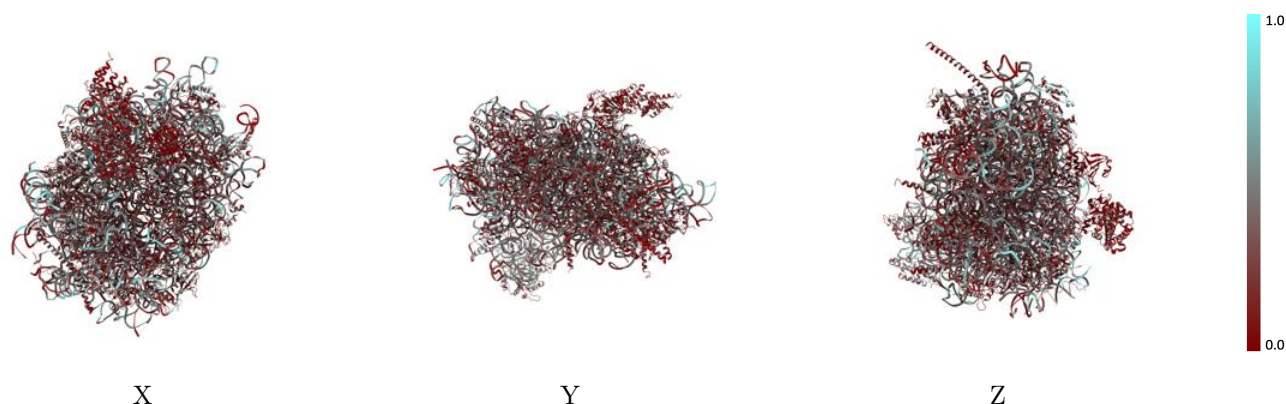
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



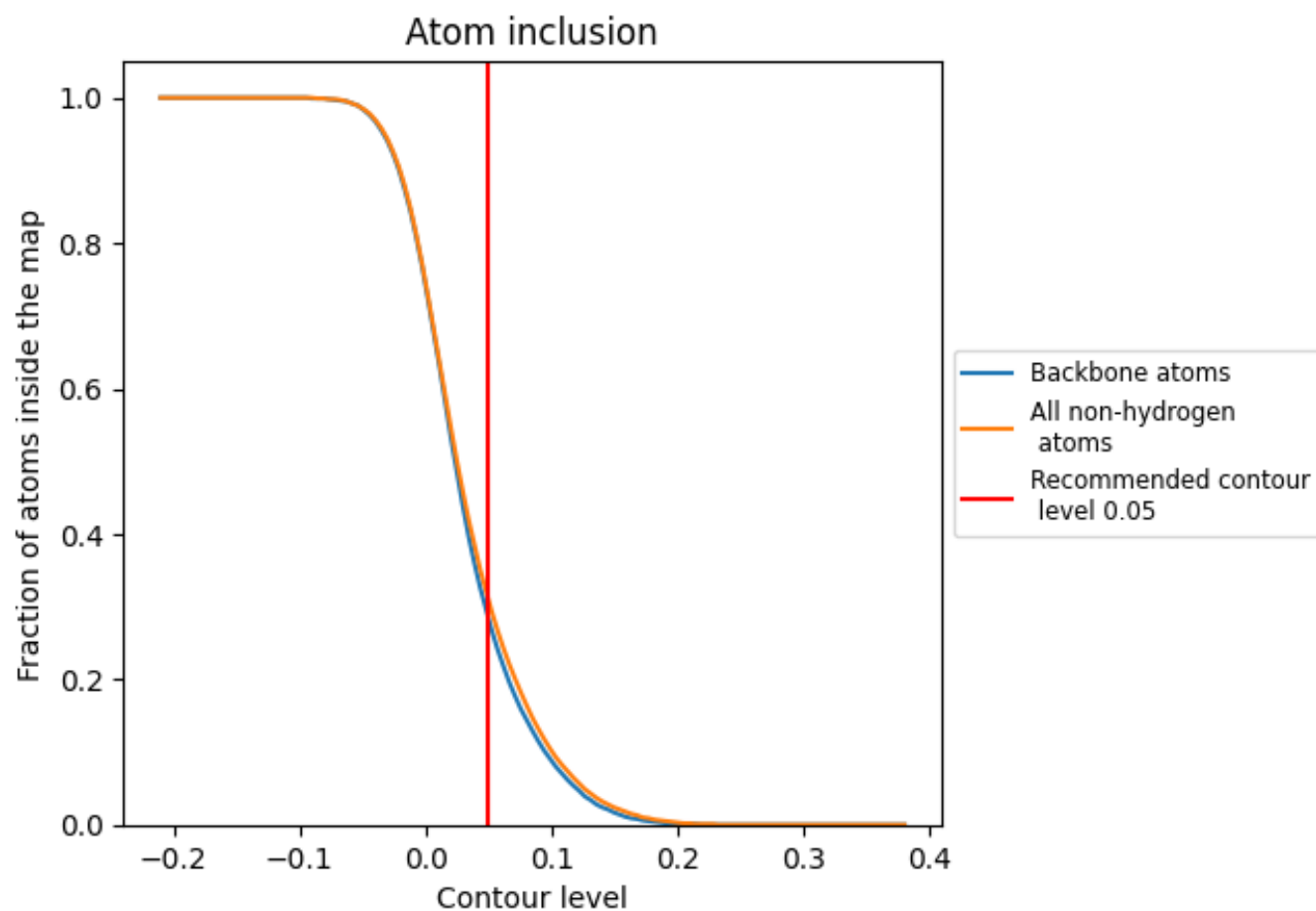
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 29% of all backbone atoms, 31% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3110	 -0.0540
5	 0.3640	 -0.0470
7	 0.4800	 -0.0430
8	 0.3490	 -0.0470
A	 0.1850	 -0.1200
B	 0.2390	 -0.0850
C	 0.2460	 -0.0870
D	 0.3320	 -0.0080
E	 0.2240	 -0.0540
F	 0.2520	 -0.0690
G	 0.2300	 -0.0470
H	 0.2020	 -0.0740
I	 0.2350	 -0.0640
J	 0.2660	 -0.0140
K	 0.1280	 0.0050
L	 0.2650	 -0.0490
M	 0.2820	 -0.0520
N	 0.2230	 -0.1060
O	 0.2550	 -0.0560
P	 0.2270	 -0.0920
Q	 0.2150	 -0.0930
R	 0.2220	 -0.0910
S	 0.2450	 -0.0600
T	 0.2210	 -0.0440
U	 0.3290	 0.0040
V	 0.1770	 -0.0990
W	 0.2120	 -0.0840
X	 0.2520	 -0.0870
Y	 0.2350	 -0.1150
Z	 0.2730	 -0.0520
a	 0.2430	 -0.0830
b	 0.2460	 -0.0350
c	 0.2460	 -0.0670
d	 0.2240	 -0.0750
e	 0.2160	 -0.1000



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Chain	Atom inclusion	Q-score
f	 0.2370	 -0.0820
g	 0.2070	 -0.0920
h	 0.2820	 -0.0570
i	 0.2550	 -0.0630
j	 0.2390	 -0.1050
k	 0.2530	 -0.0690
l	 0.1630	 -0.1180
m	 0.2070	 -0.0700
n	 0.1740	 -0.0650
o	 0.2200	 -0.0770
p	 0.2350	 -0.0670
r	 0.2400	 -0.1050
s	 0.0750	 0.0350
t	 0.0410	 0.0100
u	 0.0580	 0.0090