



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 07:52 AM UTC

PDB ID : 6T59 / pdb_00006t59
EMDB ID : EMD-10380
Title : Structure of rabbit 80S ribosome translating beta-tubulin in complex with tetratricopeptide protein 5 and nascent chain-associated complex
Authors : Lin, Z.; Gasic, I.; Chandrasekaran, V.; Peters, N.; Shao, S.; Ramakrishnan, V.; Mitchison, T.J.; Hegde, R.S.
Deposited on : 2019-10-15
Resolution : 3.11 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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

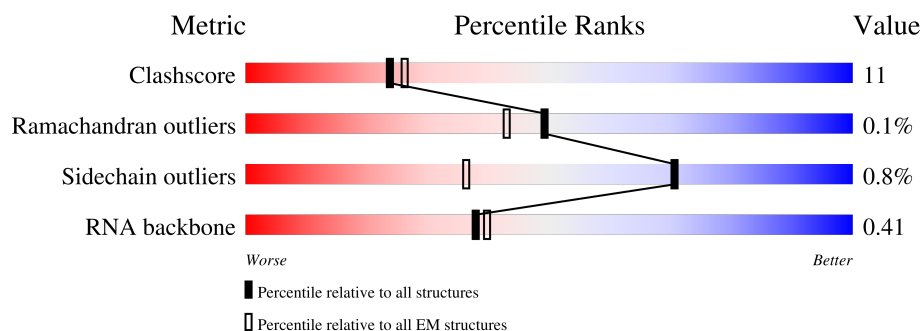
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.11 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	A3	257	85% 67% 30% .
2	B3	403	79% 68% 29% .
3	C3	425	68% 62% 23% 15%
4	D3	297	70% 75% 24% .
5	E3	291	62% 53% 21% 26%
6	F3	247	75% 68% 23% 9%
7	G3	319	57% 54% 19% 27%

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Mol	Chain	Length	Quality of chain
8	H3	192	
9	I3	214	
10	J3	178	
11	L3	211	
12	M3	218	
13	N3	204	
14	O3	203	
15	P3	184	
16	Q3	188	
17	R3	196	
18	S3	176	
19	T3	160	
20	U3	128	
21	V3	140	
22	W3	157	
23	X3	156	
24	Y3	145	
25	Z3	136	
26	a3	148	
27	b3	226	
28	c3	115	
29	d3	125	
30	e3	135	
31	f3	110	
32	g3	116	

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Mol	Chain	Length	Quality of chain
33	h3	123	
34	i3	105	
35	j3	97	
36	k3	70	
37	l3	51	
38	m3	102	
39	n3	25	
40	o3	106	
41	p3	92	
42	r3	137	
43	s3	318	
44	t3	165	
45	23	76	
46	54	3543	
47	74	120	
48	84	156	
49	NI	29	
50	NA	215	
51	NB	206	
52	TT	440	
53	1	64	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 143047 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 Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A3	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B3	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B3	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D3	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D3	1	MET	-	initiating methionine	UNP G1SYJ6

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E3	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 6 is a protein called Ul30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F3	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F3	61	ARG	GLY	conflict	UNP G1TUB1
F3	93	ARG	GLY	conflict	UNP G1TUB1
F3	131	MET	VAL	conflict	UNP G1TUB1
F3	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G3	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H3	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I3	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J3	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L3	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M3	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N3	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O3	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P3	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q3	187	Total	C	N	O	S	0	0
			1514	946	315	249	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R3	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S3	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T3	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U3	102	Total	C	N	O	S	0	0
			834	534	146	152	2		

- Molecule 21 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V3	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W3	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X3	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y3	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z3	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a3	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
a3	1	MET	-	initiating methionine	UNP G1SNY0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b3	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c3	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d3	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e3	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f3	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g3	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h3	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i3	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j3	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k3	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k3	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l3	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m3	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n3	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o3	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p3	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r3	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s3	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t3	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	23	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 46 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	54	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 47 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	74	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 48 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	84	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 49 is a protein called Nascent polypeptide-associated complex subunit alpha N-terminal region.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	NI	29	Total	C	N	O	0	0
			150	92	29	29		

- Molecule 50 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	NA	54	Total	C	N	O	S	0	0
			420	270	71	78	1		

- Molecule 51 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NB	58	Total	C	N	O	S	0	0
			444	278	76	88	2		

- Molecule 52 is a protein called Tetratricopeptide repeat protein 5.

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

- Molecule 53 is a protein called Tubulin Beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	36	Total	C	N	O	S	0	0
			292	184	51	55	2		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	P3	2	Total	Mg	0
			2	2	
54	V3	1	Total	Mg	0
			1	1	
54	a3	1	Total	Mg	0
			1	1	
54	g3	1	Total	Mg	0
			1	1	
54	j3	1	Total	Mg	0
			1	1	
54	54	201	Total	Mg	0
			201	201	
54	74	7	Total	Mg	0
			7	7	
54	84	6	Total	Mg	0
			6	6	

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	g3	1	Total	Zn	0
			1	1	
55	j3	1	Total	Zn	0
			1	1	

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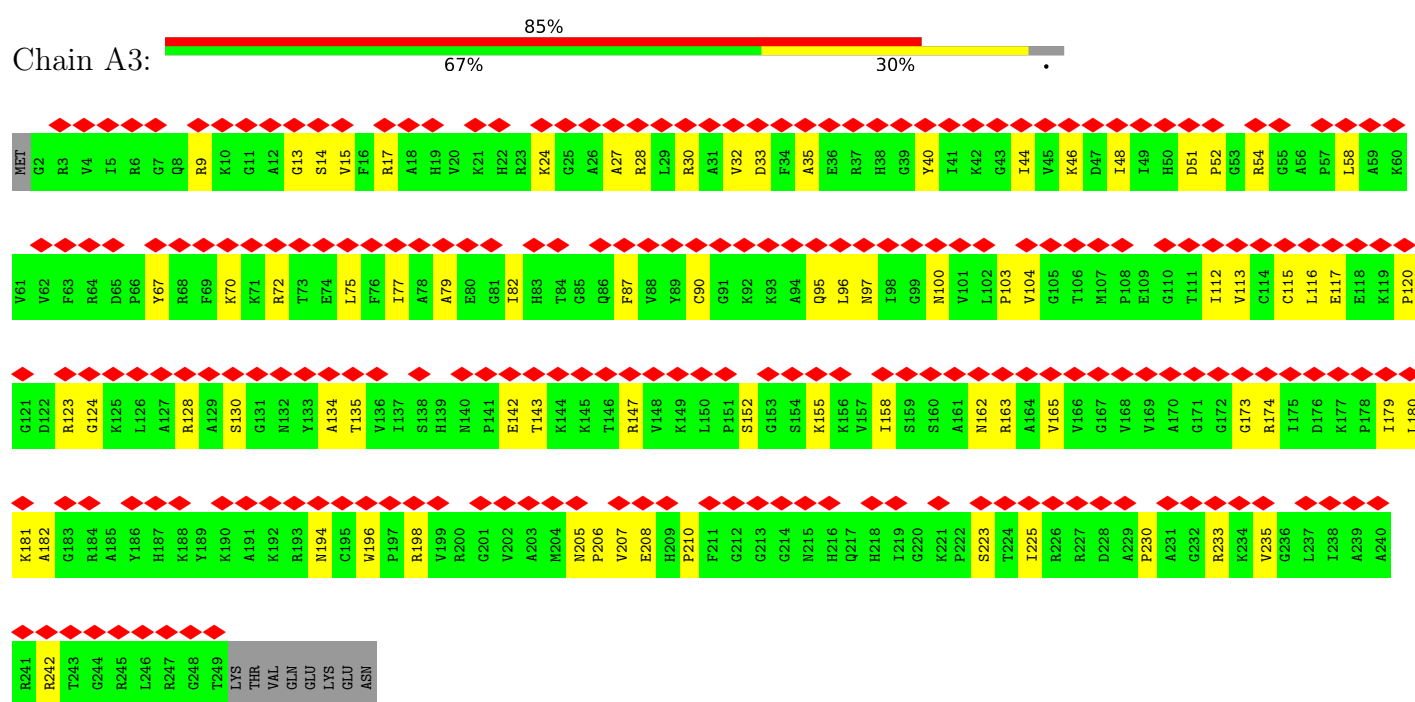
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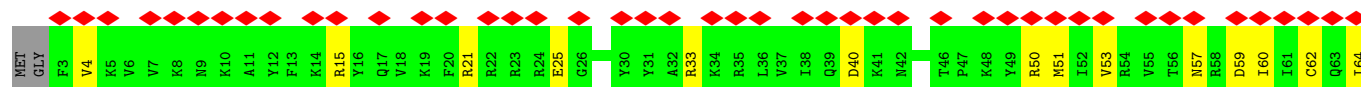
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55	m3	1	Total 1	Zn 1	0
55	o3	1	Total 1	Zn 1	0
55	p3	1	Total 1	Zn 1	0

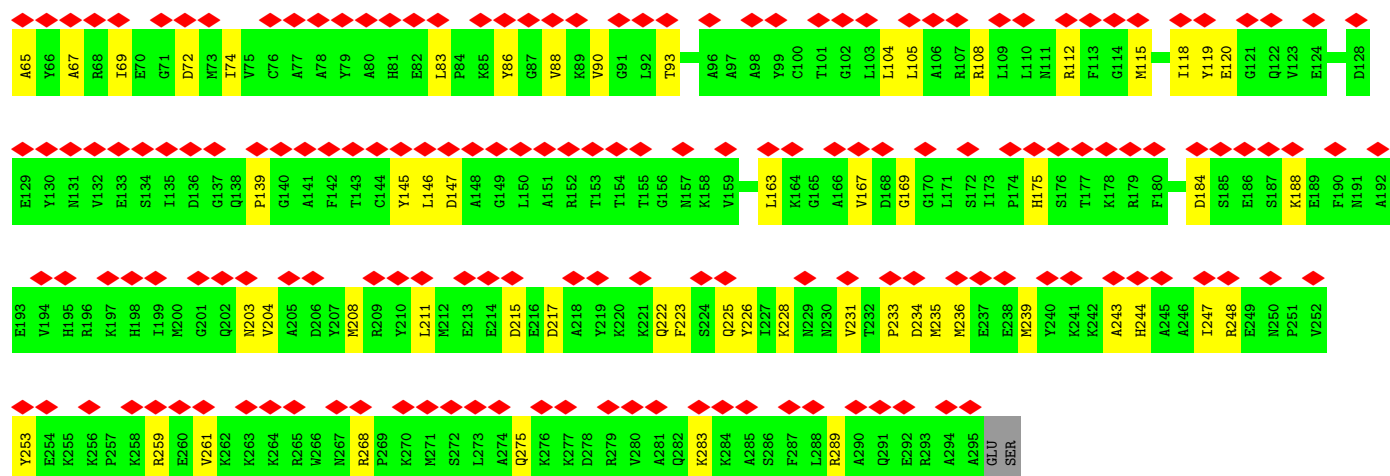
3 Residue-property plots

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

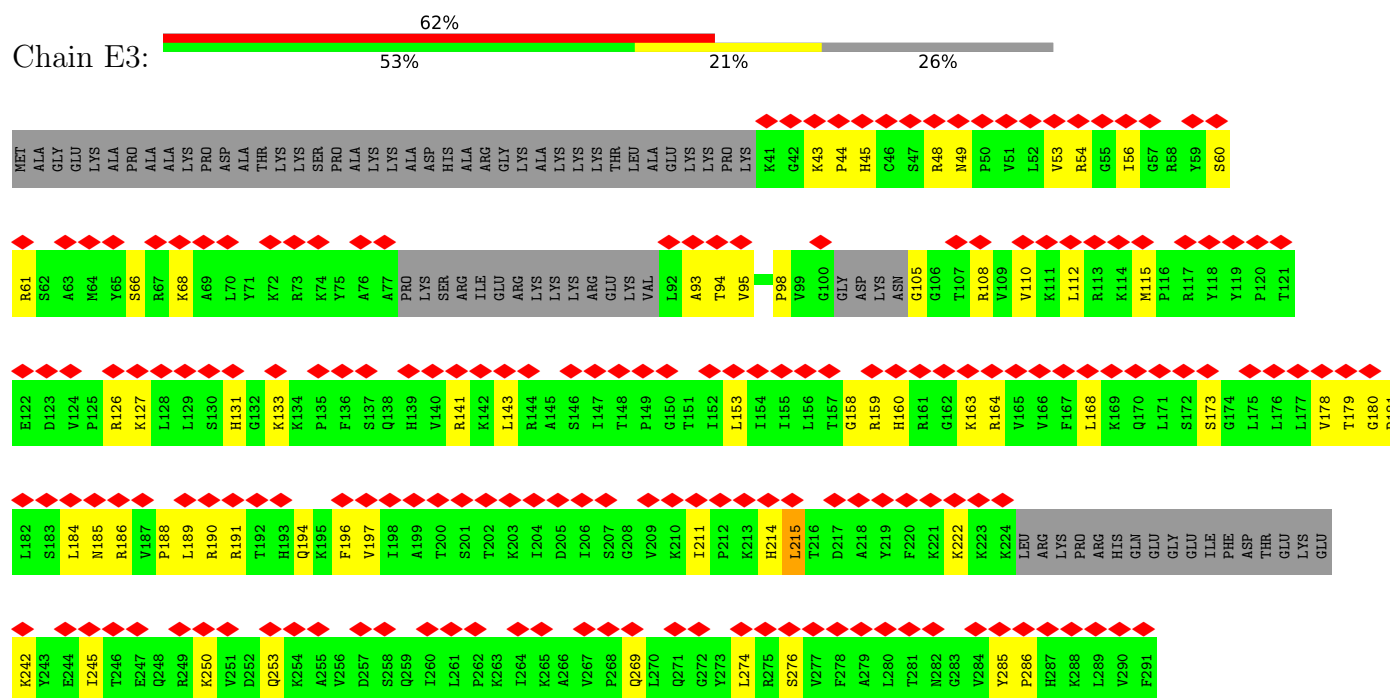
• Molecule 1: Ribosomal protein L8



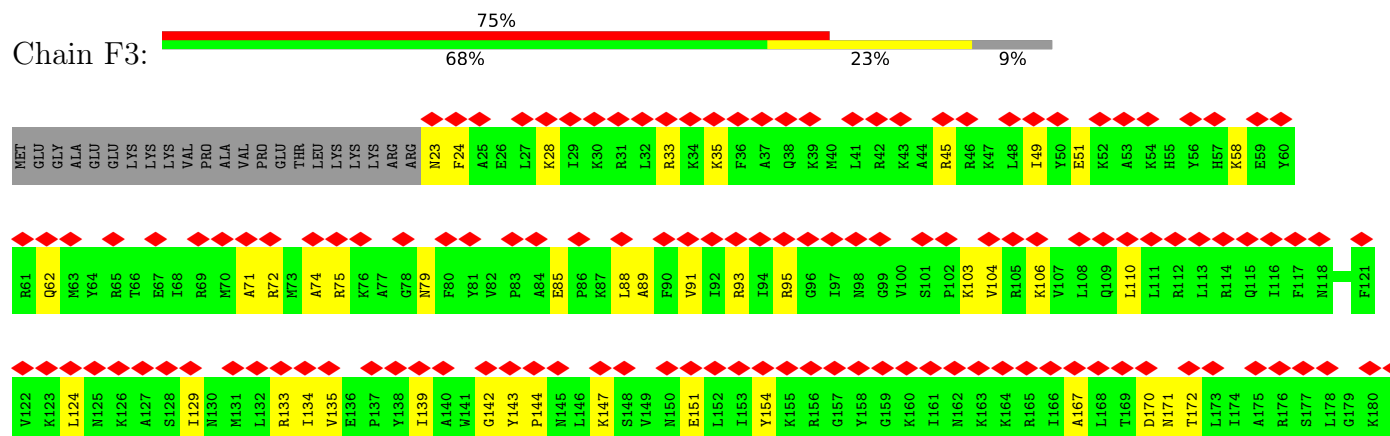


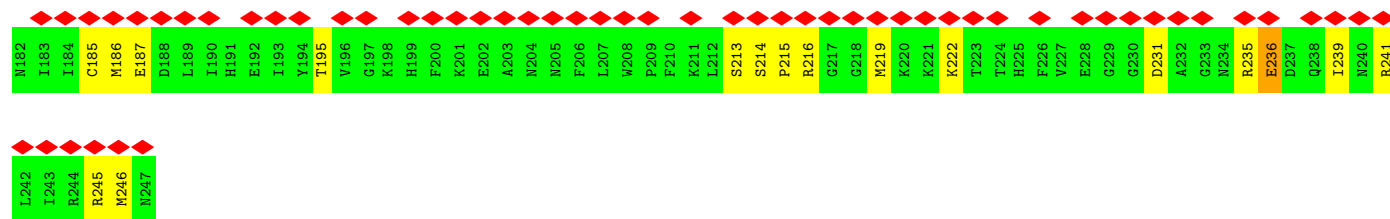


• Molecule 5: 60S ribosomal protein L6

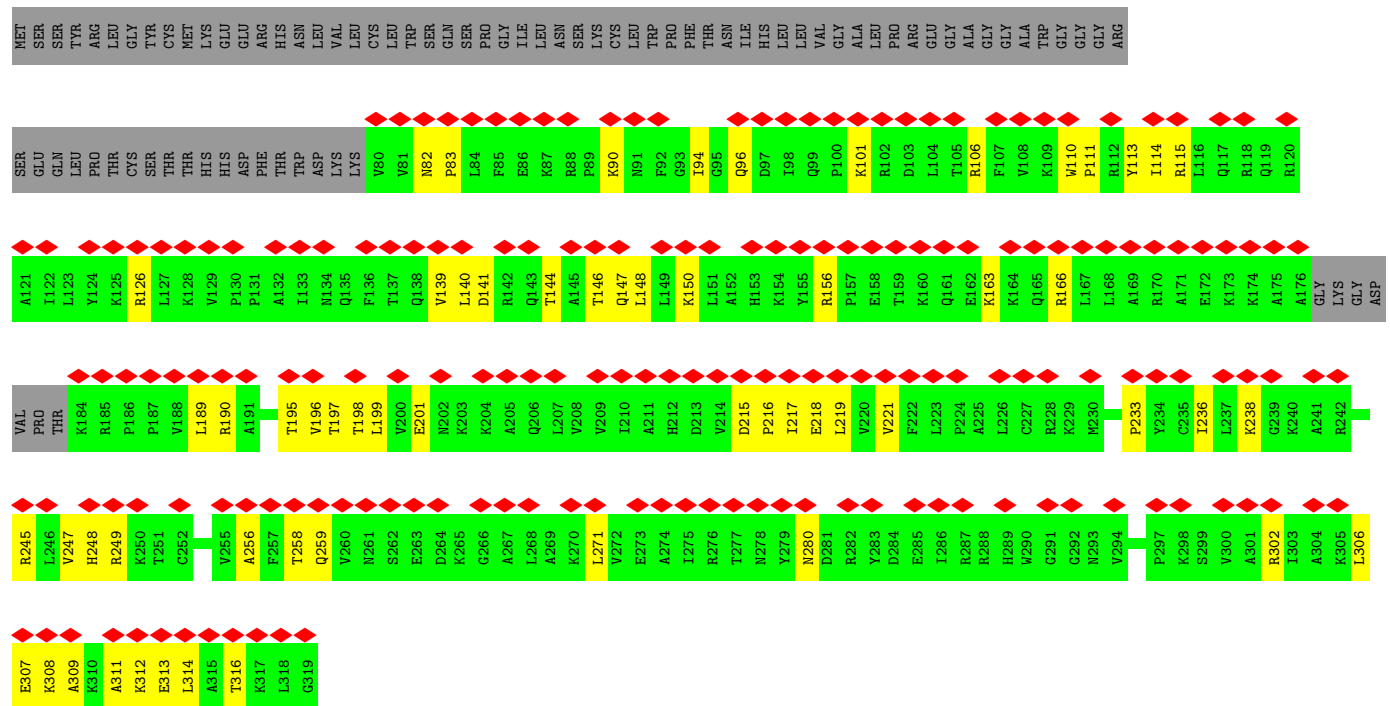


• Molecule 6: U130

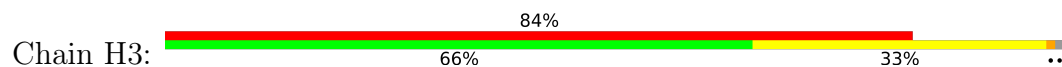




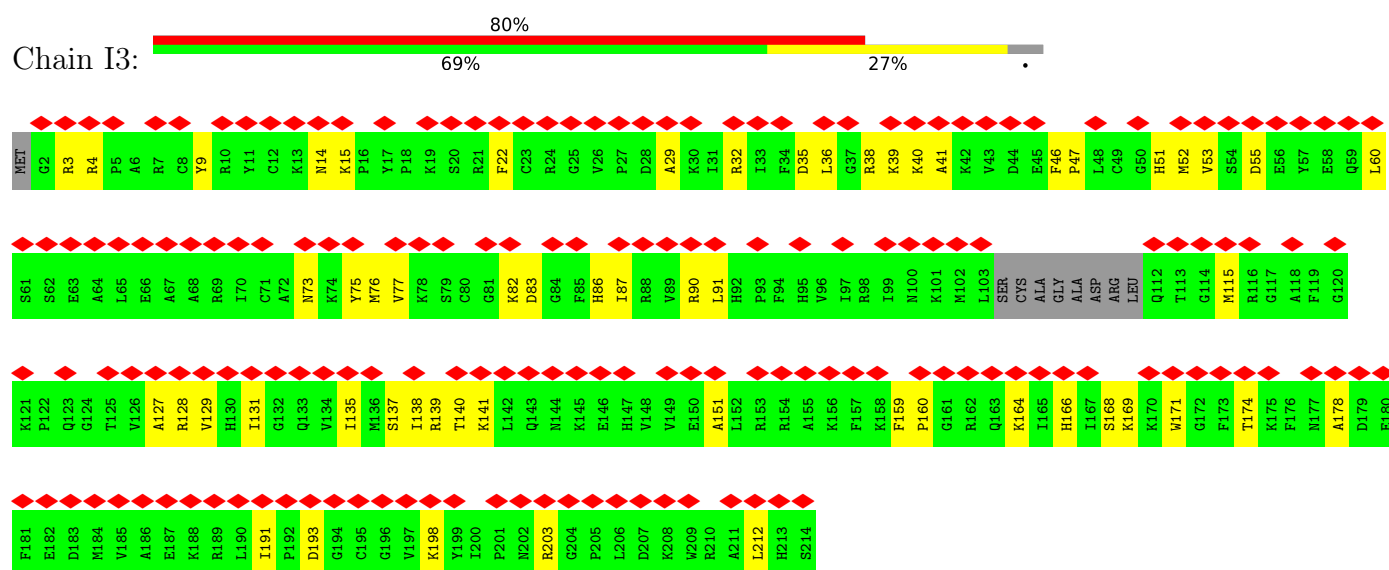
• Molecule 7: eL8



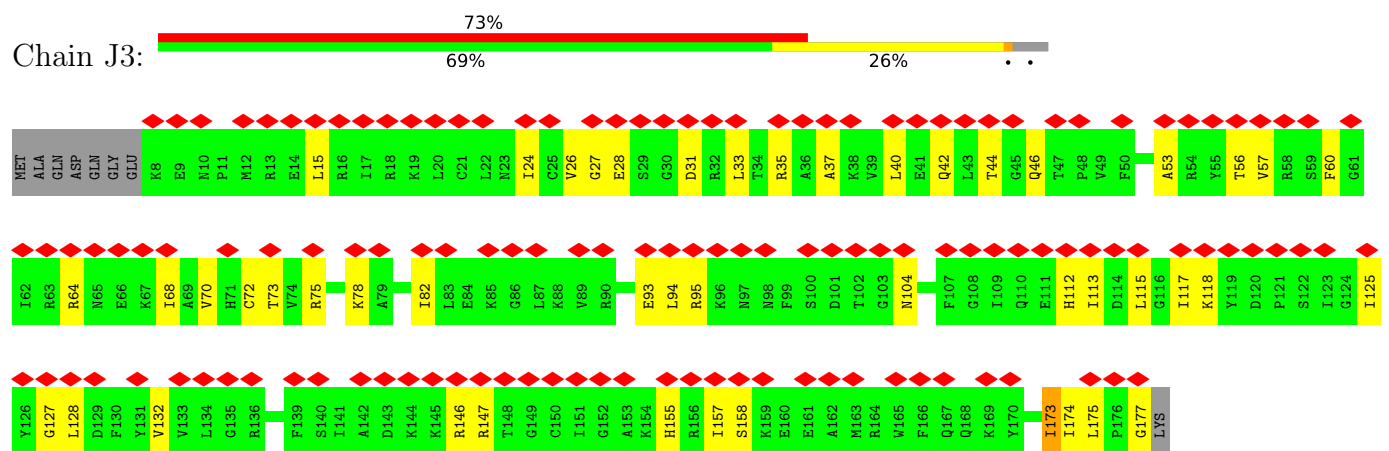
• Molecule 8: uL6



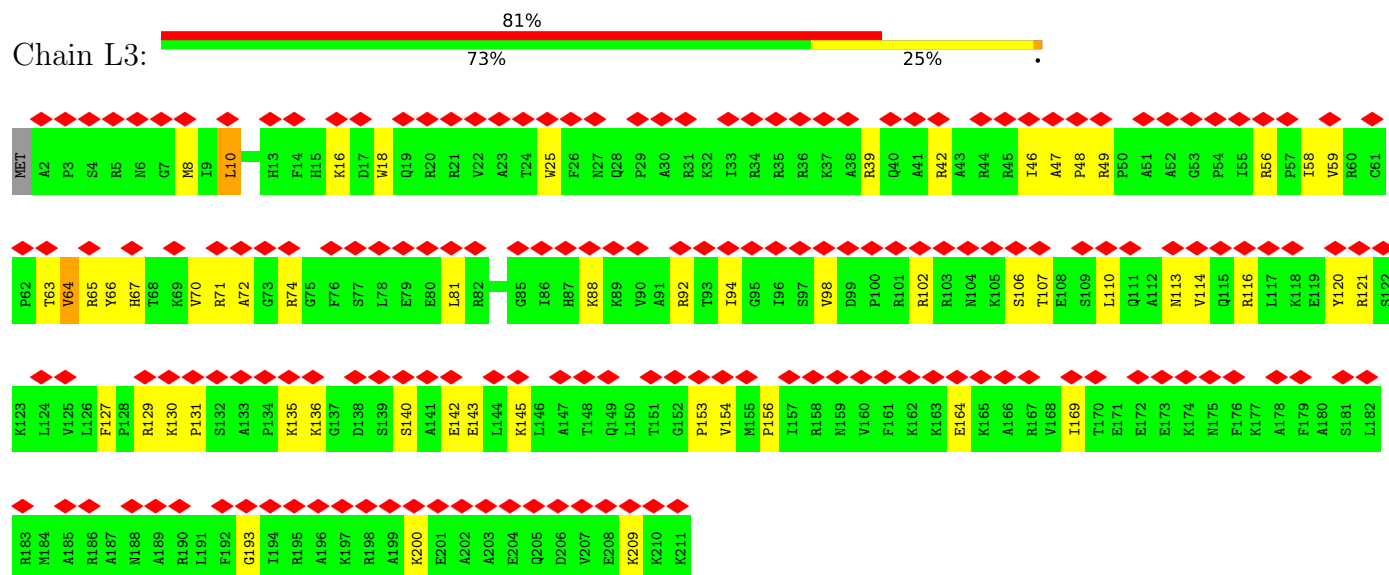
• Molecule 9: 60S ribosomal protein L10



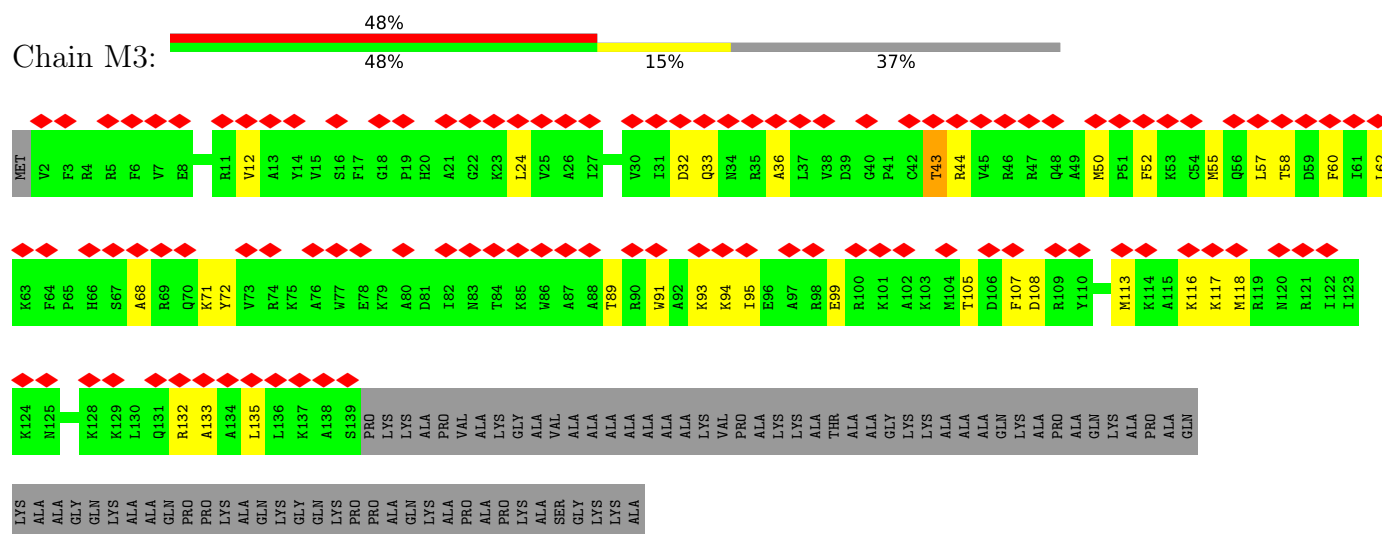
• Molecule 10: Ribosomal protein L11



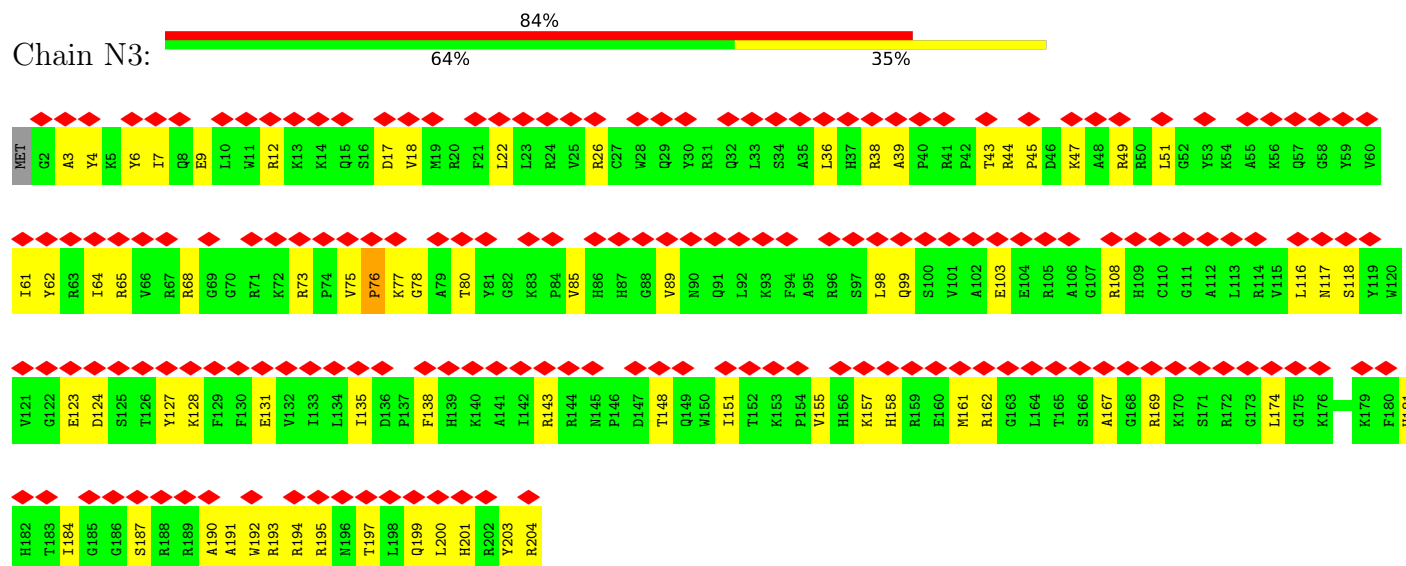
• Molecule 11: eL13



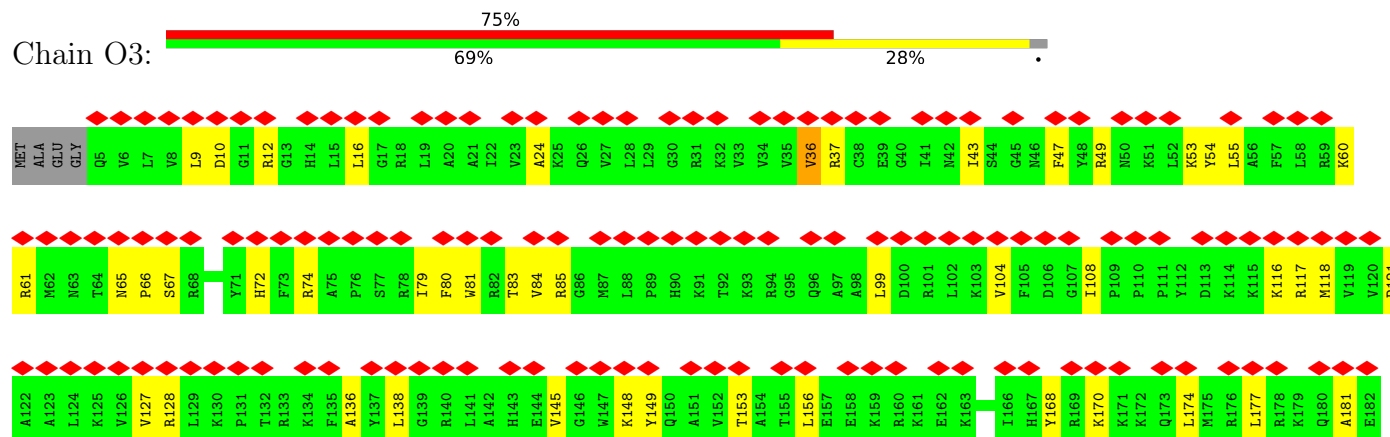
• Molecule 12: Ribosomal protein L14

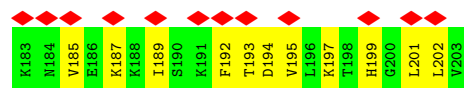


- Molecule 13: Ribosomal protein L15

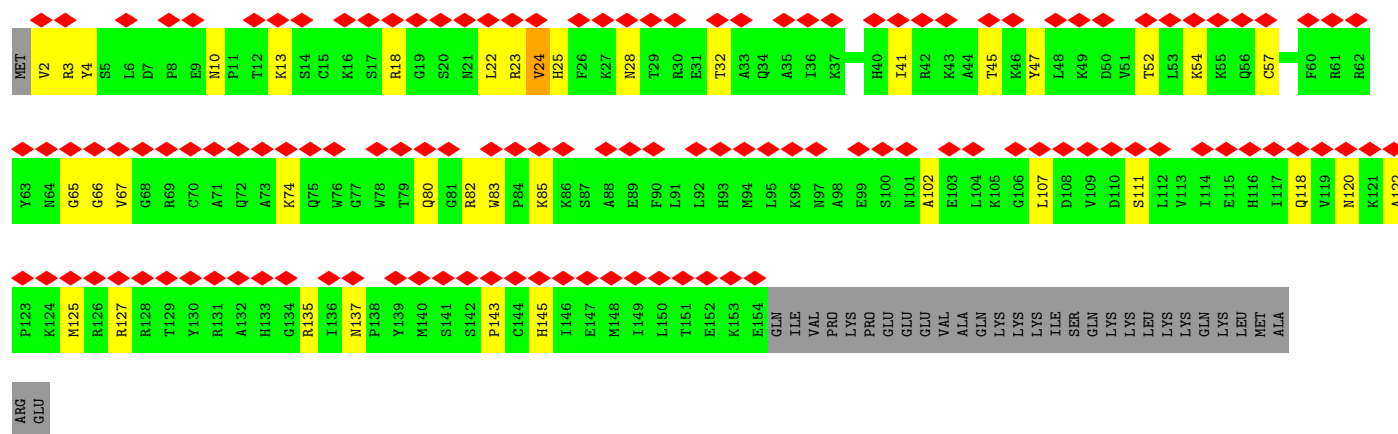


- Molecule 14: uL13

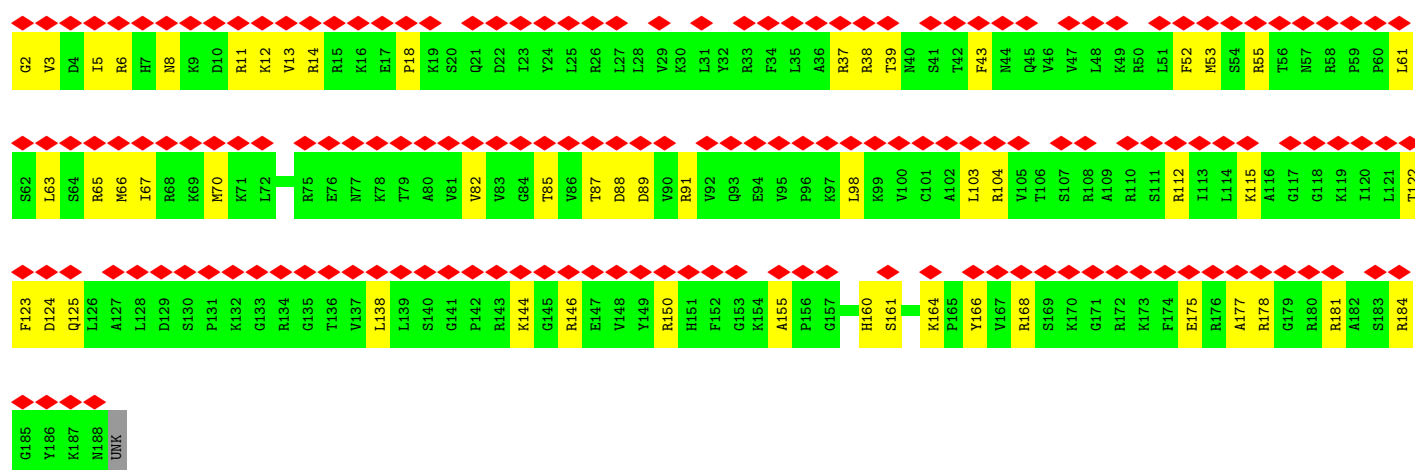
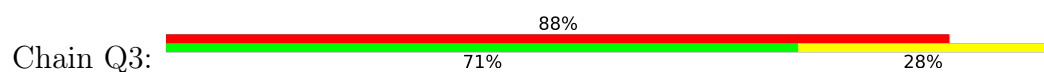




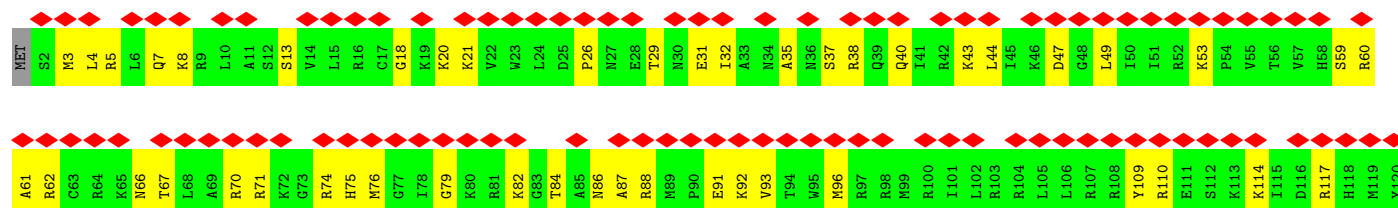
• Molecule 15: uL22



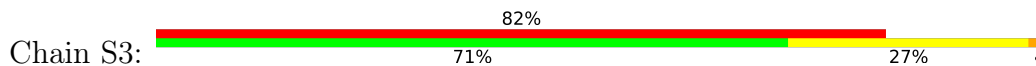
• Molecule 16: eL18



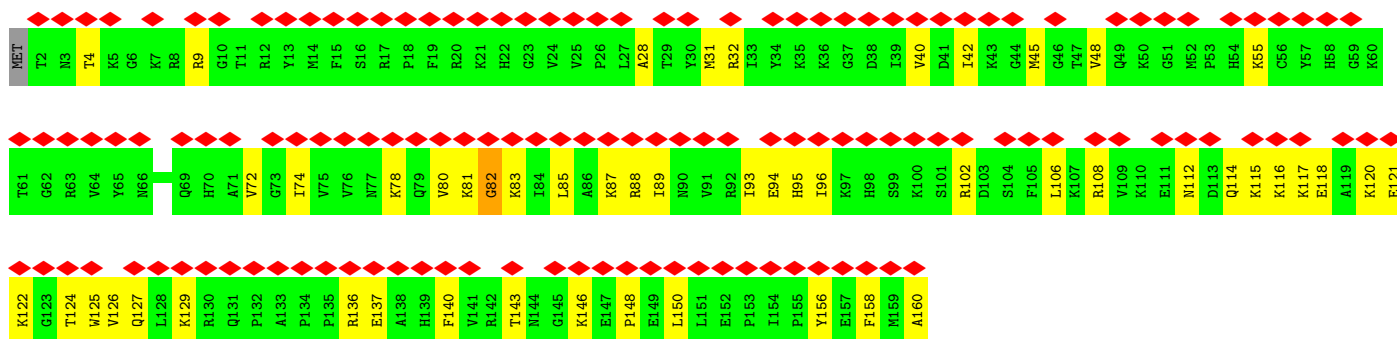
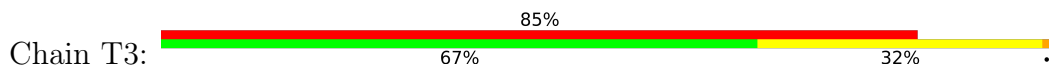
• Molecule 17: eL19



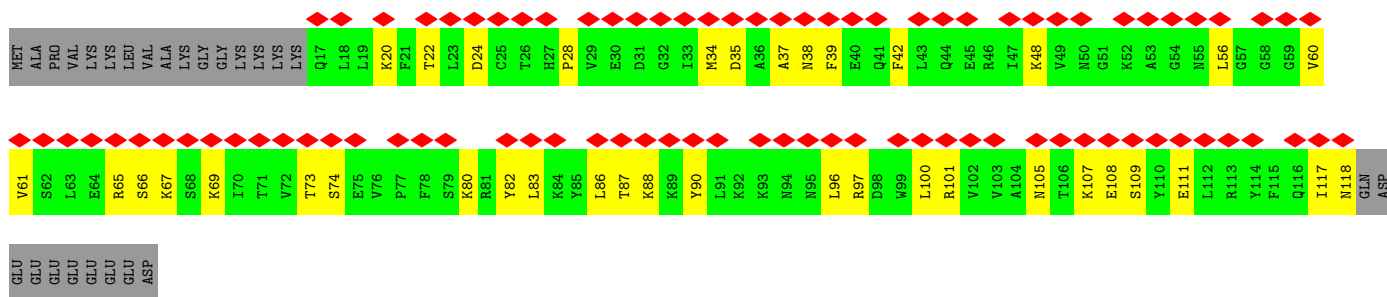
- Molecule 18: eL20



- Molecule 19: eL21

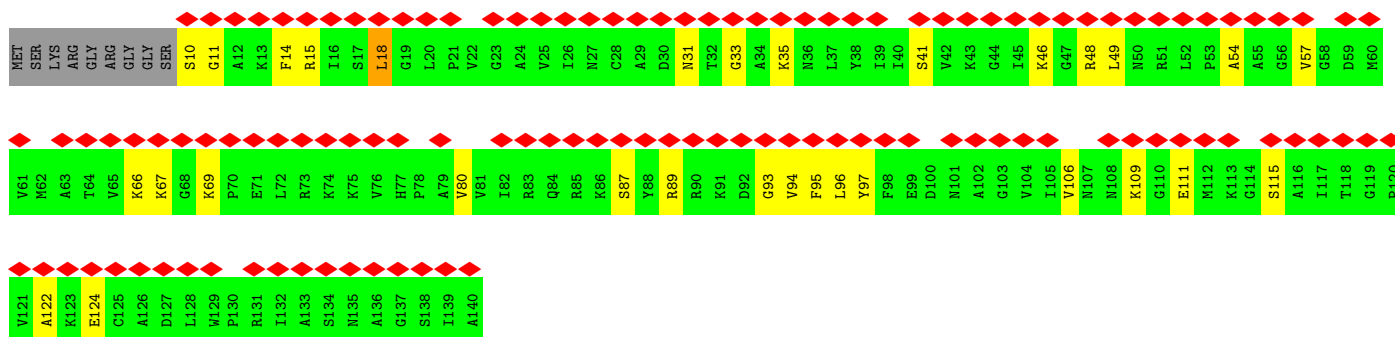


- Molecule 20: eL22



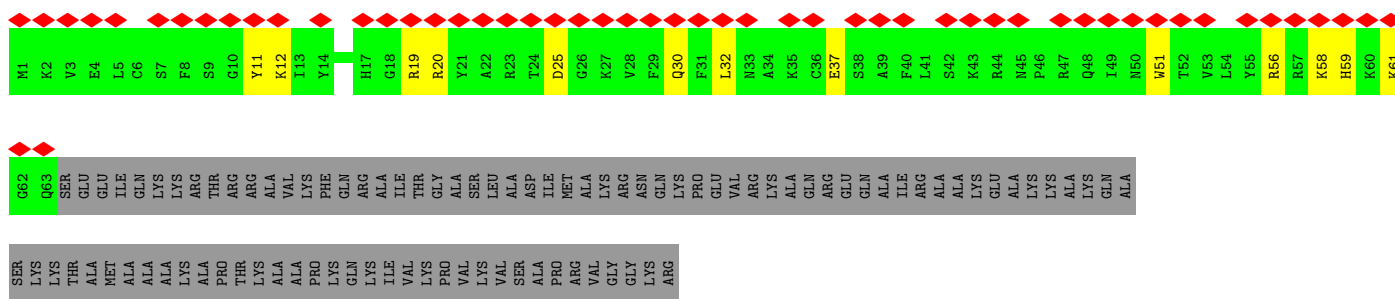
- Molecule 21: Ribosomal protein L23

Frequency	Percentage
Very often	85%
Often	71%
Sometimes	21%
Never	6%



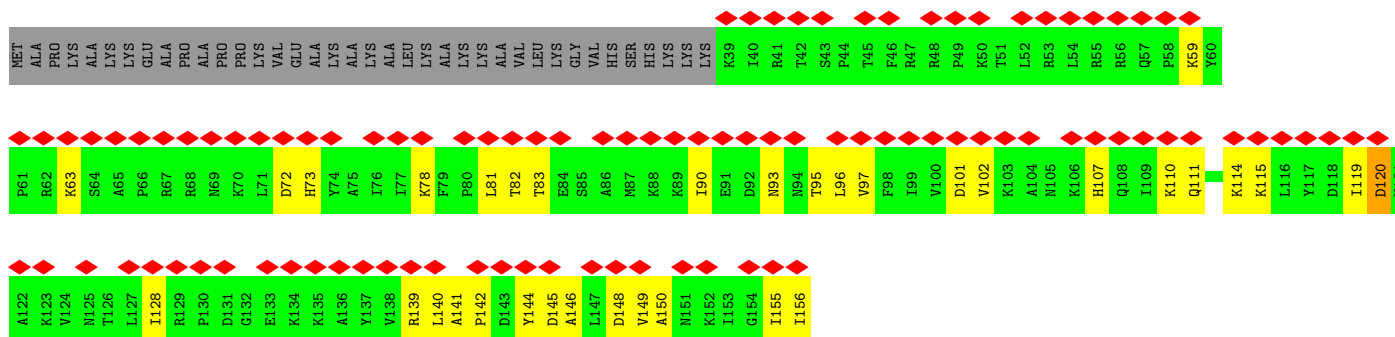
- Molecule 22: eL24

Category	Percentage
Very bad	34%
Bad	32%
Good	8%
Very good	60%



- Molecule 23: uL23

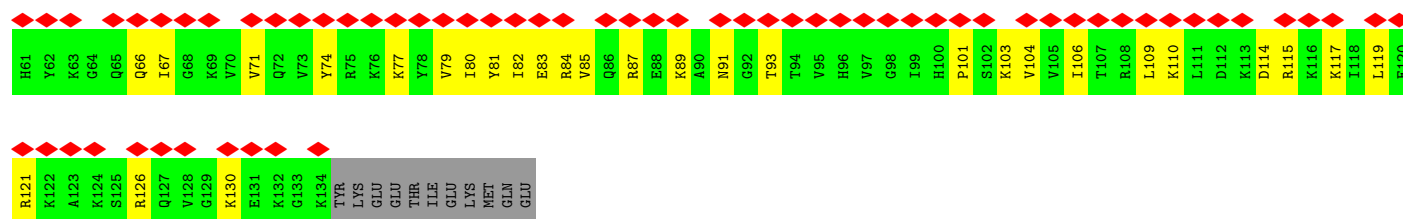
Category	Percentage
Very bad	63%
Bad	53%
Good	22%
Very good	24%



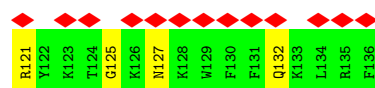
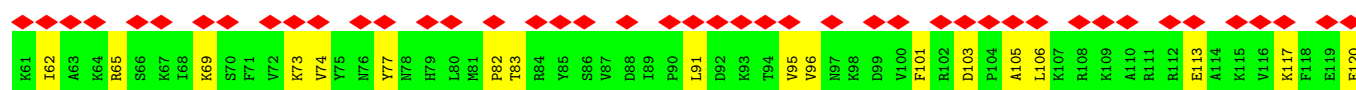
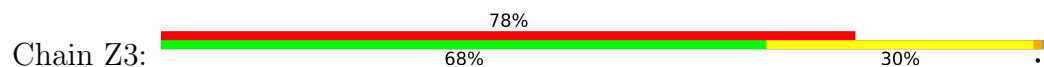
- Molecule 24: Ribosomal protein L26

Category	Percentage
Very bad	78%
Bad	60%

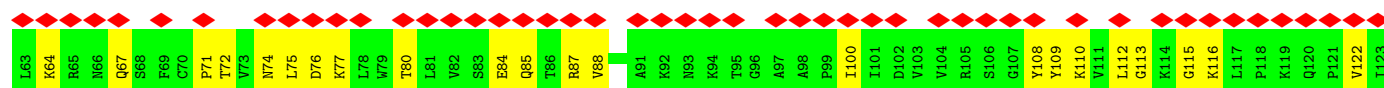
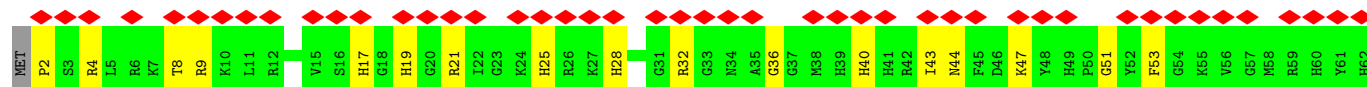
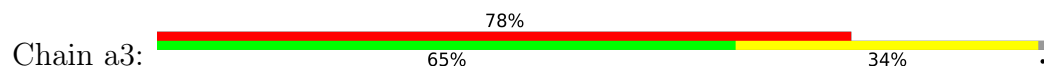




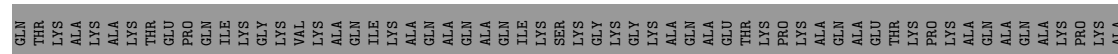
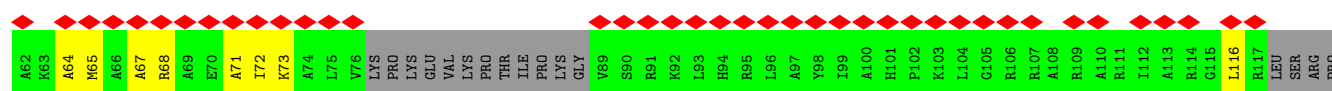
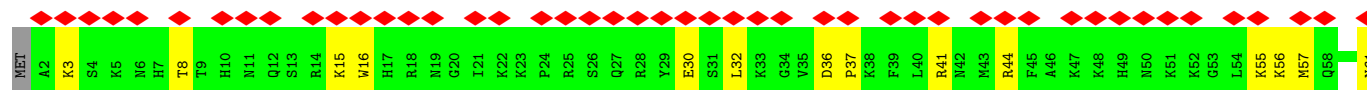
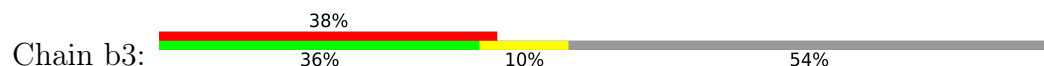
• Molecule 25: 60S ribosomal protein L27

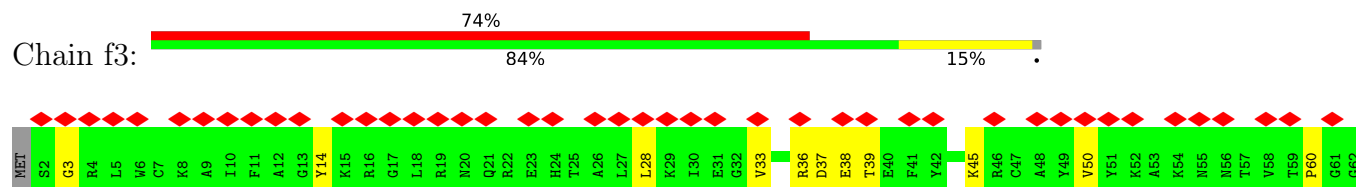


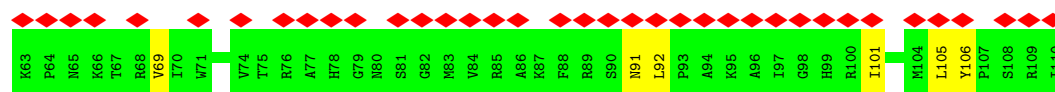
• Molecule 26: uL15



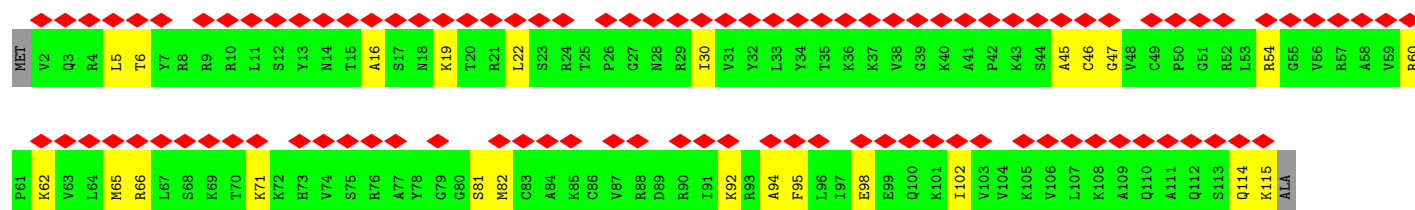
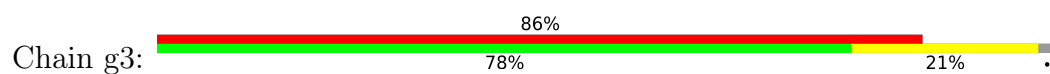
• Molecule 27: eL29



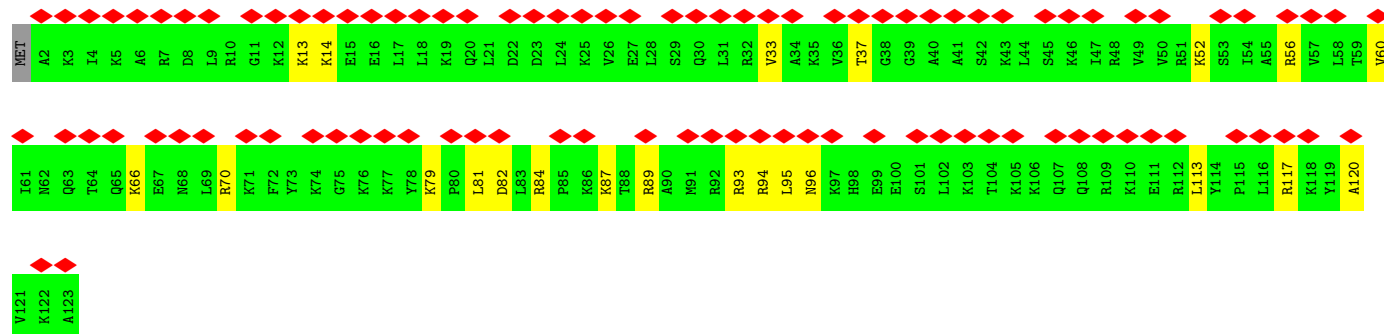
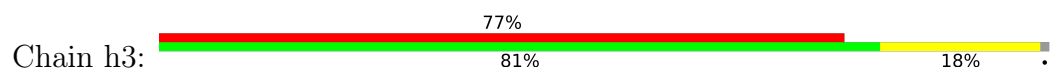




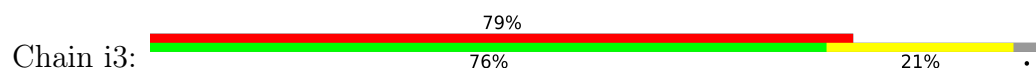
- Molecule 32: eL34



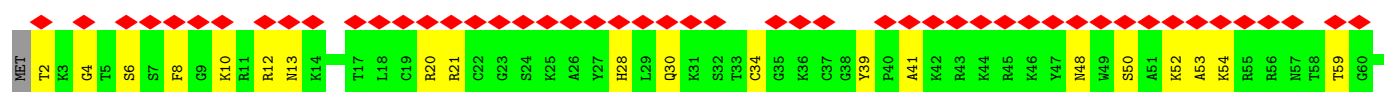
- Molecule 33: uL29



- Molecule 34: 60S ribosomal protein L36

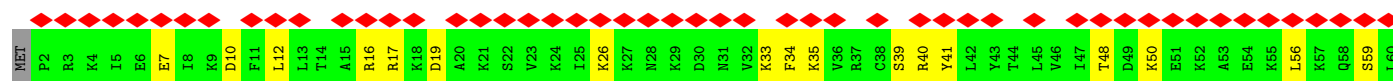
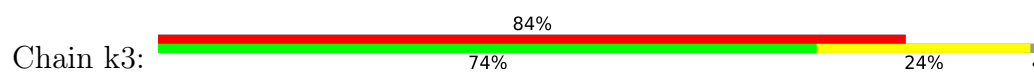


- Molecule 35: Ribosomal protein L37





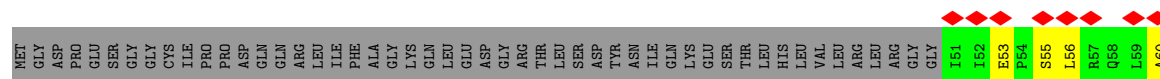
• Molecule 36: eL38



• Molecule 37: eL39



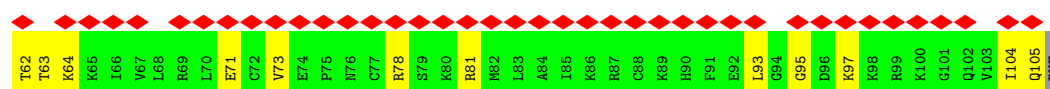
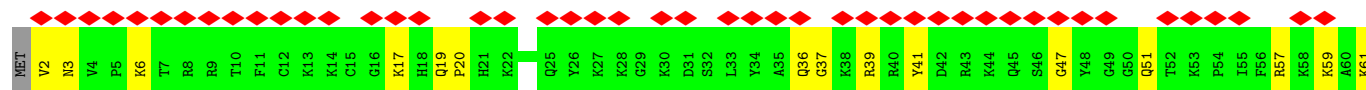
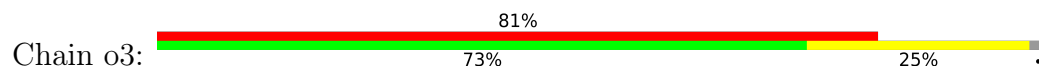
• Molecule 38: eL40



• Molecule 39: 60s ribosomal protein l41

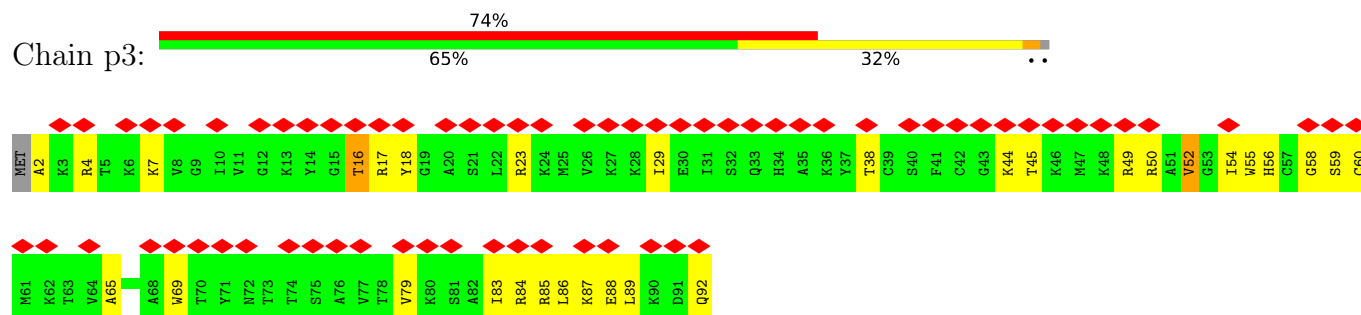


• Molecule 40: eL42



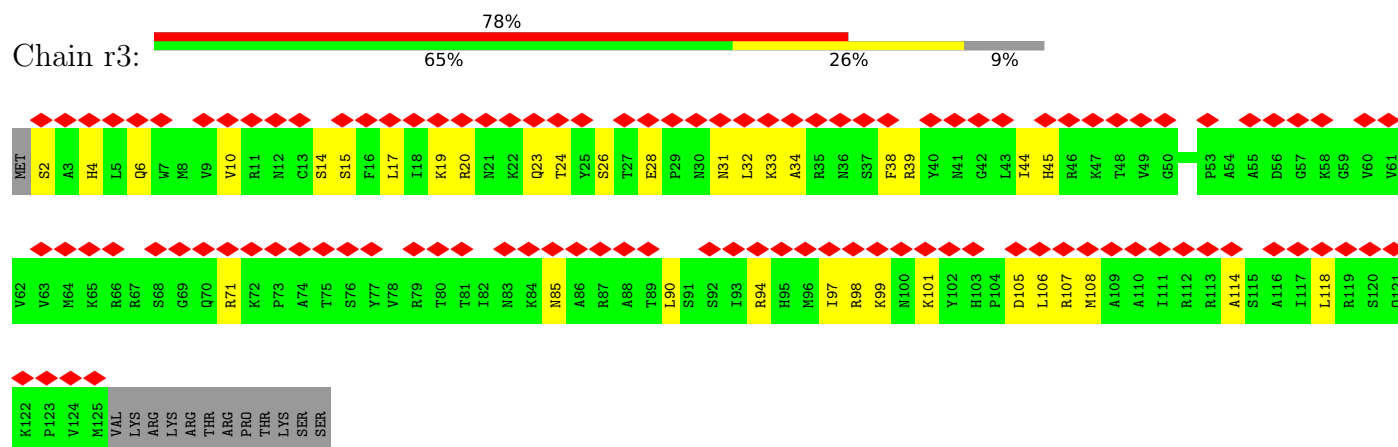
- Molecule 41: eL43

Chain p3:



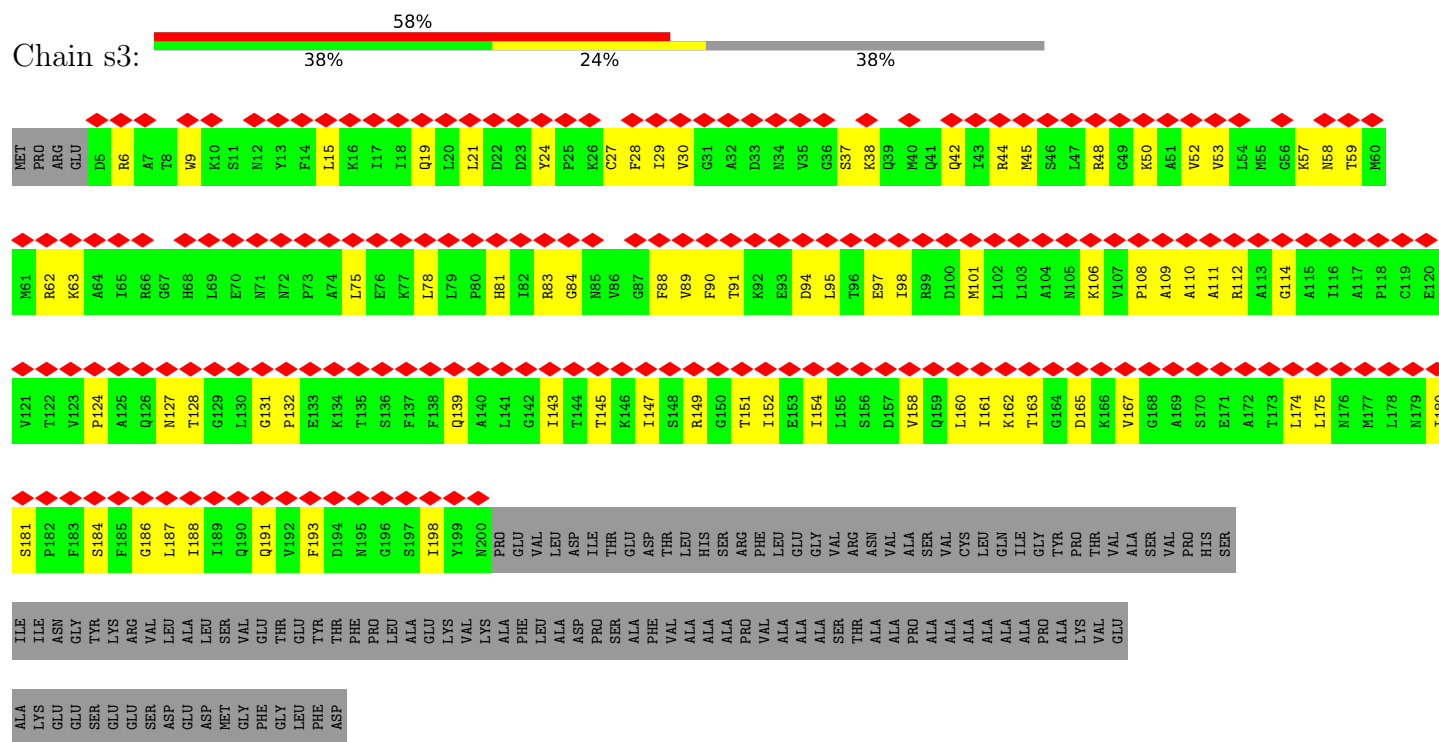
- Molecule 42: eL28

Chain r3:

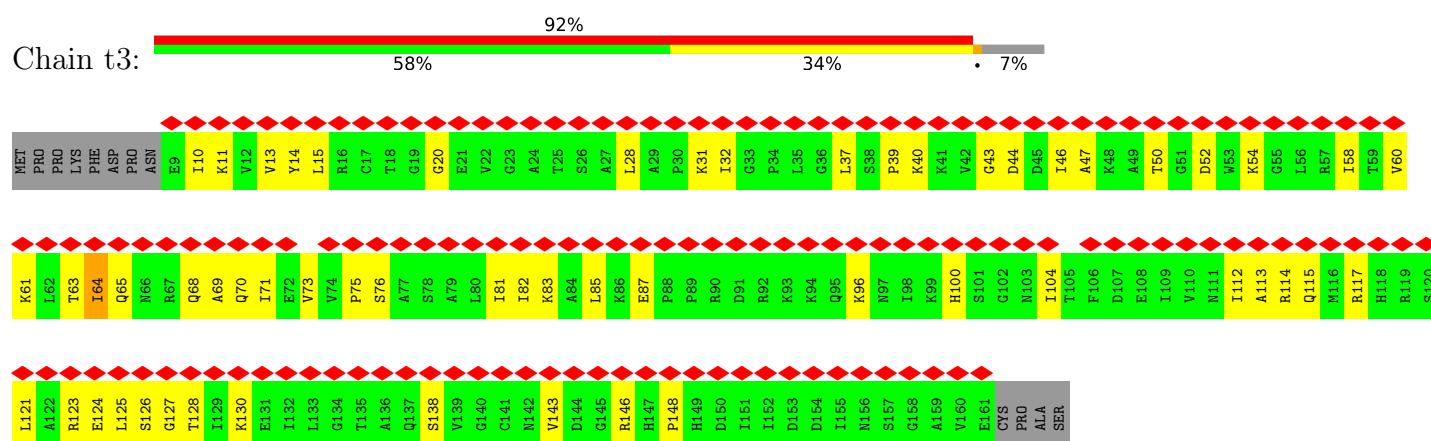


- Molecule 43: uL10

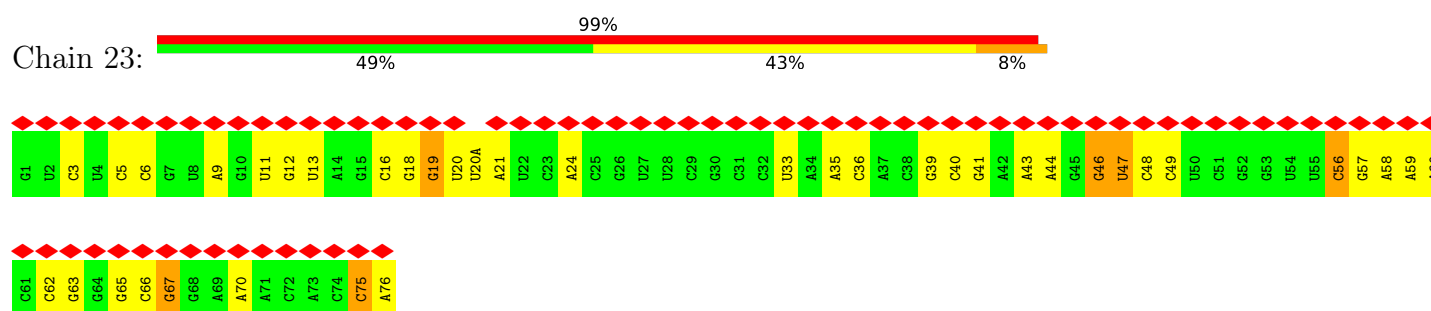
Chain s3:



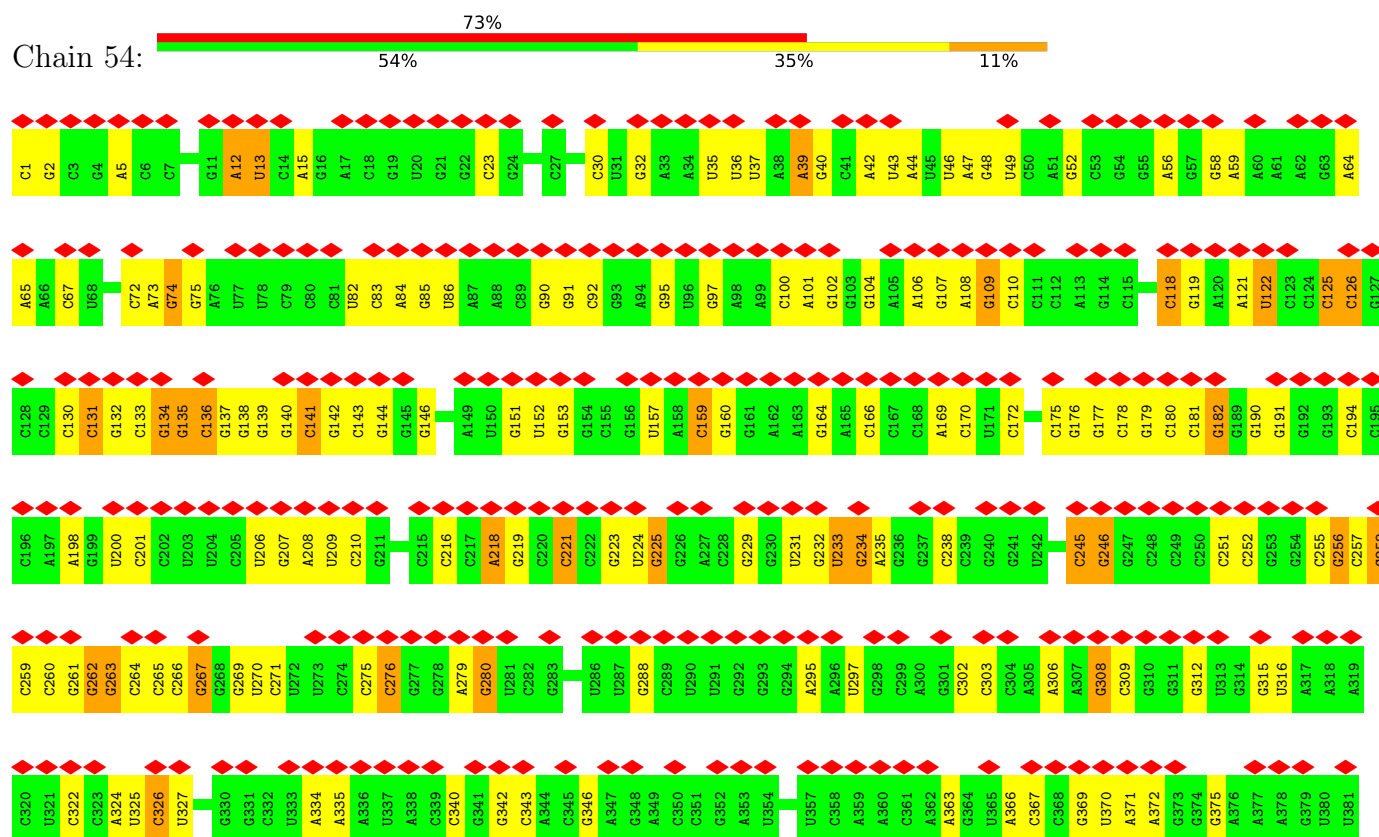
- Molecule 44: Ribosomal protein L12

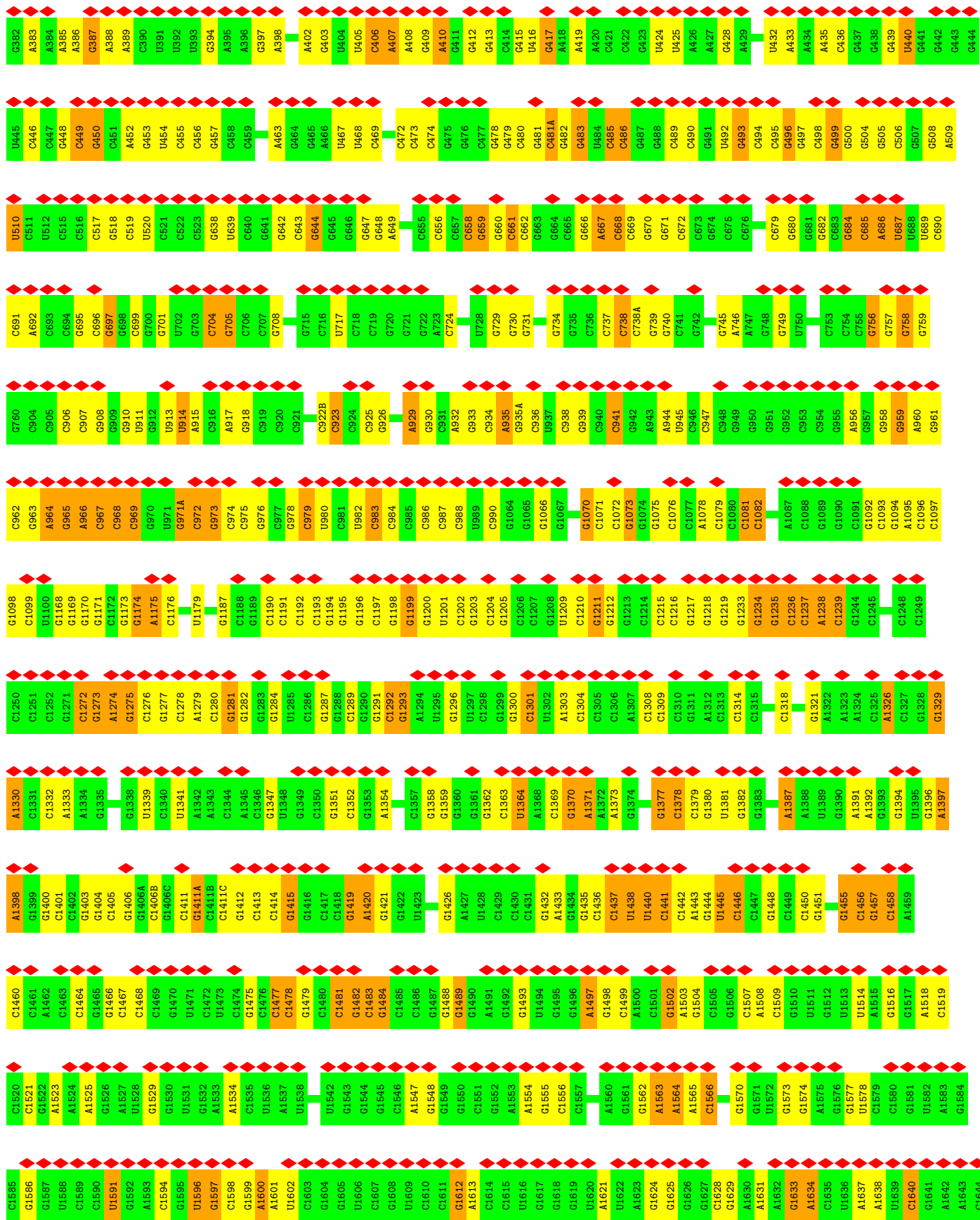


• Molecule 45: P-site tRNA



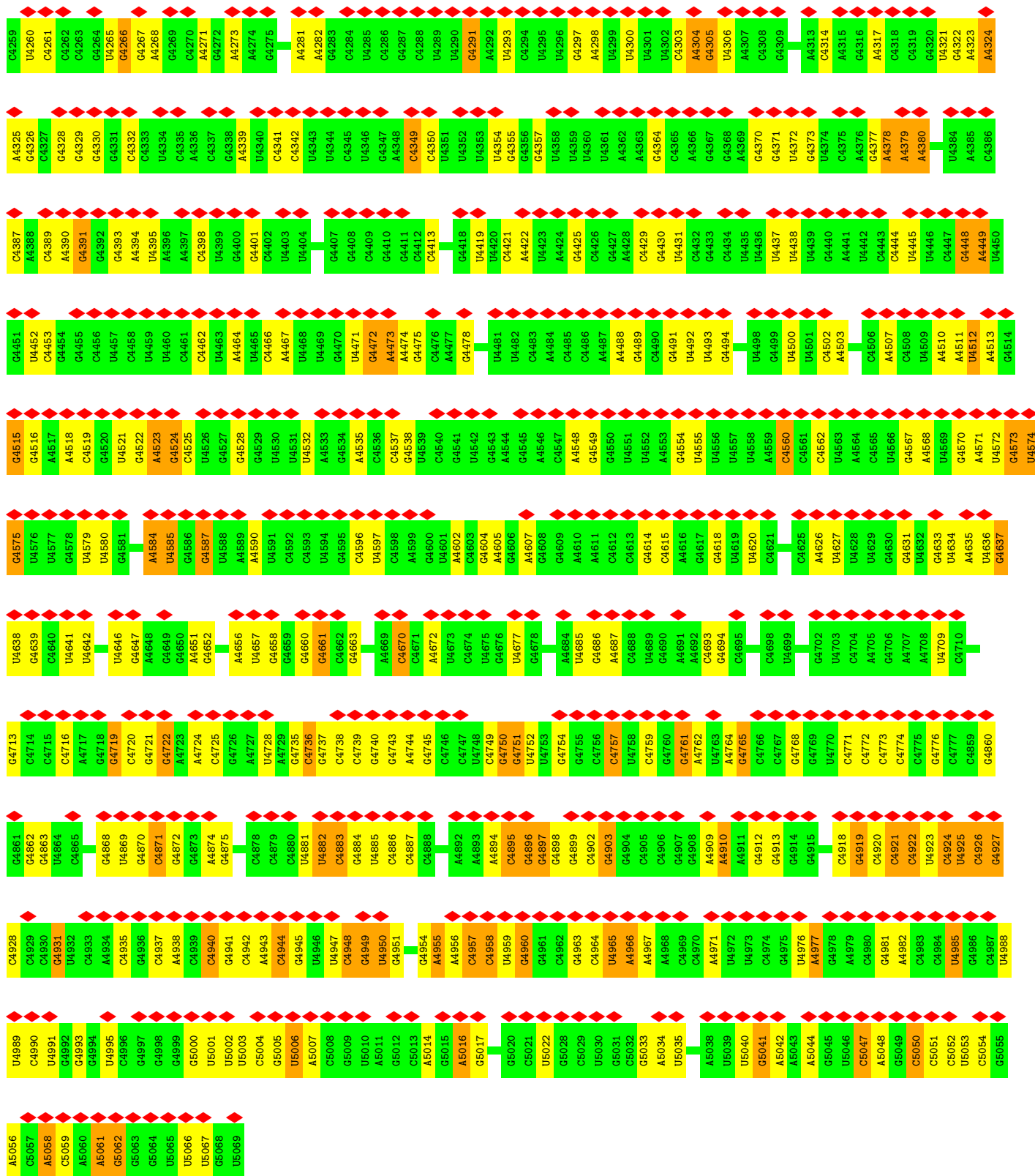
• Molecule 46: 28S ribosomal RNA







C4193	U4194	C4195	U4196	C4197	C4198	C4199	C4200	C4201	U4202	A4203	C4204	A4205	C4206	C4207	U4208	C4211	A4212	C4215	C4216	C4217	U4218	A4219	C4220	C4221	C4222	C4223	A4224	C4225	C4226	U4227	C4228	U4229	C4230	C4231	U4232	A4233	C4234	C4235	C4236	C4237	U4242	C4243	A4244	C4245	C4246	C4247	U4250	A4251	C4252	A4253	C4254	A4255	A4256	C4257	C4258										
G4124	C4125	C4126	A4127	A4128	G4129	C4130	C4131	C4132	C4133	C4134	C4135	C4136	C4137	C4138	G4139	G4140	C4141	C4142	C4143	C4144	C4145	C4146	U4147	U4148	C4149	U4150	U4151	U4152	C4153	C4154	C4155	C4156	A4157	C4158	C4159	C4160	C4161	C4162	U4163	C4164	C4165	C4166	C4167	U4168	C4169	A4170	C4171	A4172	C4173	U4174	C4175	C4176	C4177	A4178	U4182	C4183	C4184	C4185	C4186	C4187	U4188	U4189	U4190	C4191	A4192
G3880	G3881	C3882	U3883	U3884	C3885	G3886	C3887	G3888	G3889	A3890	A3891	U3892	C3893	A3894	G3895	C3896	G3897	G3898	C3899	G3900	A3901	A3902	A3903	A3904	A3905	A3906	G3907	A3908	C3909	C3910	C3911	U3914	U3915	C3916	A3917	C3918	C3919	U3920	U3921	C3922	A3923	U3924	U3925	C3926	U3927	A3928	C3929	U3930	C3931	U3932	C3933	G3934	C3937	C3938	C3939	U3940	G3941								
A3942	A3943	G3946	A3947	C3948	C4005	U4006	U4007	U4008	U4009	U4070	U4071	C4072	A4073	C4074	U4075	C4076	A4077	C4078	C4079	C4080	C4081	C4082	U4083	C4084	A4085	C4086	C4087	C4088	C4089	C4090	C4091	C4092	C4093	C4094	C4095	C4096	C4097	A4098	C4099	C4100	C4101	C4102	C4103	C4104	C4105	C4106	U4111	C4112	C4113	C4114	C4115	C4116	U4117	U4118	C4119	U4120	C4121	C4122	C4123						
C2627	U2628	C2629	U2630	U2631	U2632	U2633	C2634	U2637	C2638	U2639	C2640	A2641	A2642	U2643	U2644	C2645	A2647	U2648	U2649	C2650	C2651	C2652	C2653	C2654	C2655	U2656	C2657	U2658	A2660	U2661	C2662	C2663	C2664	U2665	U2666	C2667	C2668	C2669	C2670	C2671	C2672	C2673	A2674	U2675	A2676	C2677	U2678	A2679	U2680	C2681	C2682	C2683	C2684	C2685	U2686	U2687									
G2688	C2689	C2690	U2691	U2692	U2693	C2694	A2695	A2696	A2697	C2698	C2702	U2703	A2704	C2705	U2706	U2707	U2708	C2709	C2710	C2711	C2712	C2713	C2714	C2715	C2716	C2717	U2718	C2719	C2720	C2721	C2722	A2725	C2726	C2727	U2728	C2729	U2730	C2731	C2732	C2733	U2734	C2738	C2739	U2740	U2741	C2742	A2743	U2744	A2745	U2746	U2747	C2748	C2749	C2750	C2751	C2752									
C2753	C2754	A2755	C2759	C2760	U2761	U2762	U2763	A2764	A2765	C2768	U2769	C2770	C2771	C2772	C2773	C2774	C2775	C2776	C2777	C2778	C2779	C2780	C2781	C2782	U2783	C2784	C2785	C2786	U2787	C2788	A2789	U2790	C2791	C2792	C2793	C2794	A2795	C2796	C2797	A2798	C2799	U2800	U2801	C2802	U2803	C2804	C2805	A2806	U2807	C2808	C2809	U2810	C2811	C2812	A2813	C2814	A2815								
G2816	C2817	C2818	U2819	C2820	U2821	C2822	C2823	C2824	A2825	U2826	C2827	U2828	U2829	C2830	C2831	A2832	C2833	C2834	U2837	A2840	C2841	C2842	U2843	A2844	A2845	C2846	C2847	C2848	A2849	C2850	U2851	C2852	C2853	C2854	C2855	C2856	C2859	C2860	C2861	C2862	C2863	A2864	C2865	C2866	C2867	C2868	U2869	A2870	A2871	C2872	U2873	U2874	C2875	C2876	C2877	C2878									
A2879	U2880	A2881	A2882	U2883	C2884	A2885	U2886	C2890	U2891	C2892	U2893	A2894	A2895	C2896	C2899	U2900	C2901	C3597	C3598	A3599	C3600	C3601	C3602	C3603	A3604	C3605	U3606	U3607	A3608	C3609	A3610	A3611	C3612	U3613	C3614	C3615	U3616	C3617	C3618	C3619	C3620	A3621	C3622	C3623	A3624	C3625	C3626	C3627	C3628	A3629	A3630	U3631	C3632	C3633	C3634	A3635	C3636								
U3637	C3638	U3639	U3640	U3641	U3642	A3643	U3644	U3645	U3646	A3647	A3648	A3649	C3650	A3651	A3652	A3653	C3654	C3655	A3656	U3657	C3658	C3659	C3660	C3661	A3662	C3663	C3664	C3665	C3666	C3667	C3668	C3669	C3670	C3671	C3672	C3673	C3674	C3675	C3676	U3677	C3678	U3679	C3680	C3681	C3682	C3683	C3684	C3685	C3686	A3687	U3688	U3689	C3690	C3691	A3692	U3693	U3694	C3696							
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U3758	A3759	A3760	C3761	U3762	A3763	U3764	C3765	A3766	C3767	U3768	C3769	U3770	C3771	U3772	U3773	A3774	A3775	C3776	C3777	U3778	A3779	C3780	C3781	C3782	A3783	A3784	A3785	U3786	C3787	C3788	C3789	U3790	C3791	C3792	U3793	C3794	A3795	U3796	C3797	U3798	A3799	A3800	U3801	U3802	A3803	C3804	U3805	C3806	A3807	C3808	C3809	C3810	C3811	C3812	A3813	U3814	C3815	A3816	A3817						
U3818	C3819	C3820	A3821	U3822	C3823	A3824	A3825	C3826	C3827	A3828	C3829	C3830	U3831	U3832	C3833	C3834	C3835	A3836	C3837	U3838	C3839	A3901	A3902	A3903	C3904	A3905	A3906	G3907	A3908	C3909	C3910	C3911	U3914	U3915	C3916	A3917	C3918	C3919	U3920	U3921	C3922	A3923	U3924	U3925	C3926	U3927	A3928	C3929	U3930	C3931	U3932	C3933	G3934	C3937	C3938	C3939	U3940	G3941							
A3942	A3943	G3946	A3947	C3948	C4005	U4006	U4007	U4008	U4009	U4070	U4071	C4072	A4073	C4074	U4075	C4076	A4077	C4078	C4079	C4080	C4081	C4082	U4083	C4084	A4085	C4086	C4087	C4088	C4089	C4090	C4091	C4092	C4093	C4094	C4095	C4096	C4097	A4098	C4099	C4100	C4101	C4102	C4103	C4104	C4105	C4106	U4111	C4112	C4113	C4114	C4115	C4116	U4117	U4118	C4119	U4120	C4121	C4122	C4123						



• Molecule 47: 5S ribosomal RNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	49626	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 ($e^-/\text{\AA}^2$)	48.36	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.694	Depositor
Minimum map value	-0.371	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	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	$\# Z > 5$
1	A3	0.56	0/1936	0.52	0/2596
2	B3	0.57	0/3240	0.50	0/4339
3	C3	0.59	1/2937 (0.0%)	0.54	0/3946
4	D3	0.49	0/2437	0.45	0/3264
5	E3	0.48	0/1762	0.49	0/2362
6	F3	0.61	0/1911	0.49	0/2549
7	G3	0.45	0/1910	0.45	0/2569
8	H3	0.49	0/1535	0.48	0/2063
9	I3	0.53	0/1702	0.47	0/2272
10	J3	0.39	0/1385	0.46	0/1852
11	L3	0.50	0/1733	0.49	0/2316
12	M3	0.54	0/1158	0.45	0/1547
13	N3	0.63	0/1746	0.54	0/2338
14	O3	0.60	0/1662	0.53	0/2222
15	P3	0.58	0/1268	0.53	0/1700
16	Q3	0.60	0/1538	0.57	0/2054
17	R3	0.50	0/1310	0.51	0/1734
18	S3	0.60	0/1501	0.52	0/2012
19	T3	0.55	0/1326	0.49	0/1770
20	U3	0.42	0/848	0.48	0/1138
21	V3	0.54	0/993	0.48	0/1332
22	W3	0.52	0/541	0.48	0/720
23	X3	0.49	0/984	0.45	0/1323
24	Y3	0.53	0/1132	0.52	0/1504
25	Z3	0.45	0/1130	0.46	0/1507
26	a3	0.62	0/1191	0.49	0/1590
27	b3	0.42	0/861	0.47	0/1138
28	c3	0.47	0/771	0.43	0/1034
29	d3	0.53	0/903	0.48	0/1216
30	e3	0.61	0/1071	0.53	0/1429
31	f3	0.64	0/895	0.61	0/1198
32	g3	0.51	0/916	0.48	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h3	0.48	0/1021	0.46	0/1348
34	i3	0.43	0/841	0.47	0/1112
35	j3	0.61	0/720	0.53	0/952
36	k3	0.41	0/575	0.43	0/761
37	l3	0.59	0/459	0.58	0/608
38	m3	0.52	0/435	0.50	0/575
39	n3	0.25	0/240	0.48	0/305
40	o3	0.50	0/864	0.49	0/1140
41	p3	0.50	0/718	0.52	0/953
42	r3	0.57	0/1010	0.53	0/1354
43	s3	0.20	0/1530	0.42	0/2064
44	t3	0.18	0/1174	0.46	0/1582
45	23	0.20	0/1805	0.32	0/2809
46	54	0.58	0/84976	0.41	0/132520
47	74	0.57	0/2858	0.36	0/4455
48	84	0.57	0/3581	0.37	0/5577
49	NI	0.30	0/150	0.76	1/209 (0.5%)
50	NA	0.20	0/425	0.45	0/572
51	NB	0.20	0/450	0.46	0/612
52	TT	0.20	0/3402	0.41	0/4603
53	1	0.53	0/295	0.79	0/394
All	All	0.55	1/153762 (0.0%)	0.44	1/226359 (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	N3	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C3	61	GLN	CA-C	-5.17	1.45	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	NI	17	ALA	N-CA-C	5.21	114.72	107.73

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	N3	76	PRO	Peptide
13	N3	78	GLY	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	A3	1898	0	1993	65	0
2	B3	3172	0	3310	91	0
3	C3	2883	0	3053	82	0
4	D3	2391	0	2424	58	0
5	E3	1729	0	1887	49	0
6	F3	1875	0	1995	44	0
7	G3	1879	0	2027	47	0
8	H3	1516	0	1597	46	0
9	I3	1664	0	1712	41	0
10	J3	1362	0	1399	33	0
11	L3	1702	0	1820	47	0
12	M3	1137	0	1211	28	0
13	N3	1701	0	1749	54	0
14	O3	1630	0	1778	46	0
15	P3	1242	0	1274	31	0
16	Q3	1514	0	1634	53	0
17	R3	1294	0	1434	46	0
18	S3	1462	0	1508	43	0
19	T3	1298	0	1366	53	0
20	U3	834	0	858	24	0
21	V3	979	0	1039	25	0
22	W3	528	0	541	13	0
23	X3	967	0	1040	24	0
24	Y3	1115	0	1205	41	0
25	Z3	1107	0	1182	33	0
26	a3	1162	0	1209	43	0
27	b3	848	0	920	19	0
28	c3	761	0	794	13	0
29	d3	888	0	930	21	0
30	e3	1053	0	1147	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	f3	876	0	912	13	0
32	g3	906	0	999	23	0
33	h3	1013	0	1147	20	0
34	i3	830	0	916	18	0
35	j3	705	0	737	22	0
36	k3	569	0	637	14	0
37	l3	447	0	480	18	0
38	m3	429	0	465	12	0
39	n3	239	0	289	10	0
40	o3	851	0	920	20	0
41	p3	708	0	757	26	0
42	r3	994	0	1051	32	0
43	s3	1507	0	1564	60	0
44	t3	1160	0	1218	43	0
45	23	1616	0	823	20	0
46	54	75972	0	38385	1073	0
47	74	2558	0	1296	23	0
48	84	3208	0	1629	40	0
49	NI	150	0	152	1	0
50	NA	420	0	450	30	0
51	NB	444	0	441	25	0
52	TT	3337	0	3318	153	0
53	1	292	0	291	28	0
54	54	201	0	0	0	0
54	74	7	0	0	0	0
54	84	6	0	0	0	0
54	P3	2	0	0	0	0
54	V3	1	0	0	0	0
54	a3	1	0	0	0	0
54	g3	1	0	0	0	0
54	j3	1	0	0	0	0
55	g3	1	0	0	0	0
55	j3	1	0	0	0	0
55	m3	1	0	0	0	0
55	o3	1	0	0	0	0
55	p3	1	0	0	0	0
All	All	143047	0	104913	2477	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 11.

All (2477) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:973:G:N2	46:54:1282:G:N7	2.03	1.07
46:54:2638:G:N2	46:54:2697:A:N1	2.11	0.98
46:54:2486:G:H1	46:54:2492:C:H42	1.16	0.92
46:54:4751:G:H1	46:54:4948:C:H5	1.14	0.91
46:54:496:G:N1	46:54:658:C:N3	2.17	0.91
46:54:178:C:N4	46:54:258:G:O6	2.06	0.88
26:a3:76:ASP:HB3	26:a3:115:GLY:HA3	1.55	0.88
5:E3:185:ASN:ND2	5:E3:274:LEU:O	2.06	0.87
43:s3:131:GLY:HA2	43:s3:151:THR:HA	1.55	0.87
46:54:4949:G:H4'	46:54:4950:U:H5'	1.56	0.86
41:p3:17:ARG:NH2	46:54:1577:G:OP1	2.09	0.86
37:l3:41:ARG:NH1	46:54:2431:A:OP1	2.10	0.85
52:TT:434:ALA:HB3	52:TT:466:VAL:HB	1.59	0.85
42:r3:98:ARG:NH2	46:54:2262:G:OP2	2.10	0.85
43:s3:94:ASP:HB3	43:s3:97:GLU:HG2	1.59	0.85
10:J3:56:THR:HG22	10:J3:64:ARG:H	1.41	0.85
46:54:976:G:H1	46:54:1279:A:H2	1.20	0.84
46:54:3943:A:N6	46:54:4070:U:O4	2.11	0.84
52:TT:377:GLN:O	52:TT:381:ASN:ND2	2.11	0.84
52:TT:274:ASP:OD1	53:1:4:ILE:HD12	1.77	0.83
46:54:495:C:N4	46:54:659:G:O6	2.10	0.83
40:o3:61:LYS:NZ	46:54:4372:U:OP2	2.11	0.83
46:54:757:G:O6	46:54:906:C:N4	2.12	0.83
50:NA:110:ASP:HB3	50:NA:123:PHE:HB2	1.60	0.82
46:54:1169:G:H1	46:54:1192:C:H42	1.27	0.82
44:t3:64:ILE:HA	44:t3:69:ALA:HA	1.61	0.82
13:N3:108:ARG:HB2	13:N3:161:MET:HE1	1.61	0.82
52:TT:274:ASP:OD1	53:1:4:ILE:CD1	2.28	0.82
11:L3:58:ILE:H	11:L3:113:ASN:HD21	1.27	0.82
42:r3:107:ARG:NH1	46:54:2263:A:OP1	2.12	0.82
41:p3:4:ARG:NH2	46:54:1555:G:N7	2.27	0.81
6:F3:231:ASP:OD1	6:F3:235:ARG:NH1	2.12	0.81
18:S3:9:GLU:HG3	18:S3:67:VAL:HG13	1.62	0.81
46:54:2395:A:O2'	46:54:2806:A:H1'	1.80	0.81
52:TT:163:TRP:CD1	53:1:1:MET:SD	2.74	0.80
16:Q3:14:ARG:NH2	46:54:2083:C:OP2	2.13	0.80
17:R3:62:ARG:NH2	46:54:4646:U:OP2	2.14	0.80
19:T3:42:ILE:HD11	19:T3:74:ILE:HD11	1.64	0.80
46:54:2416:G:N2	46:54:2427:G:O6	2.15	0.80
46:54:4596:C:N4	46:54:4614:G:O6	2.12	0.79
11:L3:59:VAL:HG13	46:54:74:G:H5'	1.64	0.79
25:Z3:22:LYS:NZ	25:Z3:132:GLN:O	2.14	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B3:224:LYS:NZ	46:54:4626:A:OP2	2.16	0.79
9:I3:40:LYS:NZ	46:54:1751:A:OP1	2.16	0.79
24:Y3:121:ARG:NH2	46:54:194:C:O2	2.16	0.78
45:23:49:C:N4	45:23:65:G:O6	2.15	0.78
10:J3:42:GLN:HE21	10:J3:117:ILE:HD11	1.49	0.78
29:d3:94:GLU:HG3	29:d3:95:ASP:H	1.47	0.78
46:54:4902:C:N4	46:54:4919:G:O6	2.16	0.78
46:54:756:G:N2	46:54:907:C:O2	2.15	0.77
46:54:2008:U:H1'	46:54:2011:C:H5	1.49	0.77
2:B3:80:GLU:OE2	2:B3:328:ASN:ND2	2.18	0.77
20:U3:101:ARG:NH2	46:54:2702:C:OP1	2.17	0.77
43:s3:44:ARG:HH12	46:54:1997:U:H4'	1.48	0.77
46:54:164:G:O6	46:54:271:C:N4	2.18	0.77
52:TT:285:TYR:O	52:TT:458:ARG:NH2	2.17	0.77
35:j3:72:ARG:NH2	48:84:94:G:OP2	2.18	0.76
46:54:1503:A:H4'	46:54:1504:G:H5'	1.67	0.76
46:54:4133:C:N3	46:54:4151:G:N1	2.30	0.76
32:g3:54:ARG:NH2	46:54:2653:C:OP1	2.19	0.76
10:J3:75:ARG:NH1	47:74:40:U:O2	2.18	0.76
41:p3:84:ARG:HG2	41:p3:85:ARG:HH21	1.49	0.76
46:54:1098:G:N2	46:54:1198:G:O6	2.13	0.76
35:j3:21:ARG:NH2	35:j3:41:ALA:O	2.17	0.76
46:54:982:U:H3	46:54:1273:G:H1	1.32	0.76
13:N3:184:ILE:O	13:N3:194:ARG:NH1	2.19	0.76
3:C3:321:ASN:OD1	46:54:1280:C:O2'	2.04	0.75
46:54:472:C:N4	46:54:682:G:O6	2.19	0.75
46:54:1562:G:N2	46:54:1565:A:OP2	2.18	0.75
46:54:1760:G:O6	46:54:1772:C:N4	2.17	0.75
46:54:3938:G:N2	46:54:4171:C:OP2	2.19	0.75
40:o3:81:ARG:NH2	46:54:4293:U:O2'	2.19	0.75
7:G3:96:GLN:O	46:54:4124:G:N2	2.19	0.75
41:p3:89:LEU:O	41:p3:92:GLN:NE2	2.19	0.75
3:C3:45:ARG:NH2	46:54:2295:C:O2'	2.19	0.75
44:t3:46:ILE:HD12	44:t3:71:ILE:HG23	1.67	0.75
5:E3:108:ARG:NH2	46:54:469:C:N3	2.32	0.75
17:R3:37:SER:HB3	17:R3:40:GLN:HB3	1.69	0.75
44:t3:126:SER:O	44:t3:130:LYS:N	2.17	0.75
46:54:1098:G:O2'	46:54:1198:G:N2	2.18	0.75
1:A3:14:SER:HA	1:A3:17:ARG:HH21	1.52	0.74
17:R3:20:LYS:NZ	46:54:2822:G:N7	2.32	0.74
5:E3:159:ARG:NH1	46:54:4940:C:OP1	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F3:124:LEU:HD12	6:F3:129:ILE:HG12	1.69	0.74
16:Q3:144:LYS:HG2	46:54:1460:C:H5'	1.69	0.74
21:V3:31:ASN:HD21	21:V3:115:SER:HB2	1.53	0.74
46:54:3756:A:N6	46:54:3768:U:O4	2.17	0.74
2:B3:17:LEU:O	2:B3:19:ARG:N	2.21	0.74
6:F3:49:ILE:HD12	6:F3:185:CYS:HB3	1.68	0.74
46:54:1406:G:N2	46:54:1411(C):C:O2	2.19	0.73
33:h3:52:LYS:NZ	48:84:63:U:O2'	2.19	0.73
46:54:517:C:H2'	46:54:518:G:H8	1.53	0.73
2:B3:174:ARG:NH1	46:54:4985:U:O2	2.21	0.73
7:G3:90:LYS:NZ	46:54:4126:C:OP1	2.22	0.73
9:I3:191:ILE:HD11	9:I3:212:LEU:HD11	1.70	0.73
3:C3:159:GLU:HB3	3:C3:215:ASN:HB2	1.69	0.73
46:54:1763:C:H42	46:54:1769:G:H1	1.36	0.73
2:B3:128:LYS:HG3	46:54:4966:A:H5'	1.70	0.73
46:54:4133:C:O2	46:54:4151:G:N2	2.18	0.73
52:TT:356:GLY:HA2	52:TT:365:LYS:HE3	1.70	0.73
46:54:2465:C:H1'	46:54:3672:G:H22	1.54	0.73
46:54:2490:U:O2'	46:54:2491:C:O4'	2.06	0.73
46:54:166:C:N4	46:54:269:G:O6	2.13	0.73
1:A3:120:PRO:HA	1:A3:162:ASN:HB3	1.69	0.72
8:H3:111:LEU:HD12	8:H3:127:ARG:HD2	1.70	0.72
24:Y3:15:ARG:NH2	48:84:23:C:OP1	2.22	0.72
52:TT:337:LYS:HE3	52:TT:341:MET:HE2	1.69	0.72
25:Z3:59:LYS:HD3	46:54:4148:C:H5'	1.71	0.72
16:Q3:37:ARG:NH1	46:54:2088:A:OP2	2.22	0.72
44:t3:123:ARG:HB3	44:t3:127:GLY:HA3	1.72	0.72
46:54:2089:G:H1	46:54:2099:C:H41	1.37	0.72
46:54:166:C:N3	46:54:269:G:N1	2.33	0.72
8:H3:12:ILE:HD13	8:H3:18:ILE:HG21	1.72	0.72
52:TT:195:LEU:HA	52:TT:198:LEU:HD13	1.70	0.72
2:B3:249:ARG:NH2	46:54:3845:A:OP2	2.23	0.72
19:T3:55:LYS:NZ	46:54:4217:G:OP1	2.22	0.72
43:s3:59:THR:HA	43:s3:62:ARG:HD2	1.71	0.72
46:54:4237:C:O2	46:54:4321:U:O2'	2.07	0.72
6:F3:241:ARG:NH1	46:54:941:C:OP2	2.21	0.71
46:54:2553:A:H2	46:54:2765:A:H62	1.38	0.71
1:A3:117:GLU:OE2	1:A3:123:ARG:N	2.23	0.71
14:O3:37:ARG:NH2	46:54:4761:G:OP2	2.20	0.71
33:h3:96:ASN:ND2	46:54:136:C:OP2	2.21	0.71
16:Q3:65:ARG:NH1	46:54:1502:G:OP1	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:S3:92:ASN:HD21	19:T3:156:TYR:H	1.37	0.71
24:Y3:83:GLU:OE1	24:Y3:84:ARG:NH1	2.23	0.71
30:e3:107:ASN:ND2	46:54:2303:C:OP1	2.23	0.71
35:j3:52:LYS:NZ	46:54:375:G:OP2	2.22	0.71
1:A3:54:ARG:NH2	46:54:3680:U:OP1	2.23	0.71
46:54:1398:A:H62	46:54:1419:G:H21	1.39	0.71
46:54:4492:U:O2'	46:54:4512:U:O2	2.08	0.71
46:54:1404:G:N2	46:54:1413:C:O2	2.18	0.71
5:E3:164:ARG:NH2	5:E3:276:SER:OG	2.23	0.71
9:I3:14:ASN:O	9:I3:128:ARG:NH2	2.23	0.71
21:V3:15:ARG:HB3	46:54:4618:G:H5''	1.71	0.71
9:I3:3:ARG:NH2	46:54:4431:U:OP2	2.24	0.70
52:TT:261:GLN:HA	52:TT:264:LYS:HG2	1.73	0.70
46:54:648:G:H2'	46:54:649:A:H8	1.56	0.70
8:H3:120:GLU:OE1	8:H3:124:ARG:NH2	2.24	0.70
46:54:1426:G:N2	46:54:1458:C:OP2	2.24	0.70
27:b3:44:ARG:NH1	46:54:1493:G:OP2	2.24	0.70
5:E3:196:PHE:HD1	31:f3:106:TYR:HB2	1.54	0.70
15:P3:66:GLY:HA3	46:54:2362:U:H5''	1.74	0.70
26:a3:47:LYS:NZ	46:54:1684:A:OP1	2.24	0.70
1:A3:208:GLU:HG2	46:54:1629:G:H1	1.57	0.70
11:L3:64:VAL:HA	11:L3:67:HIS:CD2	2.27	0.70
9:I3:203:ARG:NH2	47:74:105:C:OP2	2.25	0.70
20:U3:20:LYS:NZ	20:U3:73:THR:OG1	2.25	0.70
46:54:1756:U:OP2	46:54:1768:C:N4	2.25	0.70
46:54:4948:C:H5''	46:54:4949:G:H5''	1.73	0.70
50:NA:86:ARG:NH1	50:NA:113:LYS:O	2.24	0.70
11:L3:56:ARG:O	11:L3:116:ARG:NH2	2.22	0.70
17:R3:60:ARG:NH1	46:54:2808:G:O3'	2.25	0.70
30:e3:104:SER:HB3	46:54:2303:C:H5''	1.72	0.70
16:Q3:11:ARG:HG3	46:54:2081:C:H5''	1.74	0.69
25:Z3:48:ARG:NH1	46:54:2575:U:OP1	2.25	0.69
37:l3:2:SER:OG	37:l3:3:SER:N	2.22	0.69
46:54:2483:G:H2'	46:54:2484:A:H8	1.57	0.69
46:54:3770:U:H2'	46:54:3771:C:H6	1.56	0.69
8:H3:91:LYS:HG2	8:H3:145:VAL:HG22	1.73	0.69
24:Y3:13:LYS:NZ	46:54:346:G:OP2	2.25	0.69
44:t3:58:ILE:HG23	44:t3:60:VAL:HG23	1.73	0.69
46:54:4635:A:H2	46:54:4663:G:H21	1.40	0.69
51:NB:56:ILE:N	51:NB:79:VAL:O	2.25	0.69
13:N3:116:LEU:HD22	13:N3:135:ILE:HD11	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:3770:U:H2'	46:54:3771:C:C6	2.27	0.69
46:54:4413:C:H5	46:54:4429:C:H42	1.40	0.69
46:54:5047:C:O2'	46:54:5050:C:OP2	2.10	0.69
13:N3:4:TYR:OH	46:54:151:G:OP2	2.11	0.69
33:h3:95:LEU:O	46:54:135:G:N2	2.24	0.69
24:Y3:19:PHE:O	24:Y3:26:ARG:NH2	2.25	0.69
52:TT:319:PHE:HZ	52:TT:403:THR:HG21	1.56	0.69
52:TT:385:VAL:HG23	52:TT:436:PRO:HA	1.73	0.69
24:Y3:8:THR:OG1	46:54:346:G:OP1	2.11	0.69
13:N3:169:ARG:HE	13:N3:174:LEU:HD11	1.57	0.69
14:O3:12:ARG:O	18:S3:171:ARG:NH2	2.25	0.69
17:R3:18:GLY:HA3	46:54:2822:G:H5''	1.75	0.69
46:54:1195:G:H2'	46:54:1196:G:H8	1.59	0.68
44:t3:58:ILE:HD11	44:t3:75:PRO:HA	1.74	0.68
46:54:1481:C:O2'	46:54:1482:G:O4'	2.12	0.68
46:54:2094:C:H3'	46:54:2095:A:H5'	1.76	0.68
12:M3:108:ASP:OD2	14:O3:199:HIS:NE2	2.27	0.68
27:b3:72:ILE:HG23	27:b3:73:LYS:HD2	1.75	0.68
7:G3:126:ARG:HH12	46:54:4162:C:H5	1.38	0.68
46:54:980:U:H3	46:54:1275:G:H1	1.38	0.68
46:54:1168:G:H1	46:54:1193:C:H42	1.41	0.68
46:54:4096:C:H2'	46:54:4097:G:C8	2.29	0.68
2:B3:80:GLU:HG3	2:B3:326:VAL:HG13	1.74	0.68
46:54:3946:G:H1	46:54:4067:U:H3	1.42	0.68
4:D3:50:ARG:NH1	4:D3:72:ASP:OD2	2.27	0.68
35:j3:30:GLN:NE2	46:54:1621:A:OP2	2.27	0.68
29:d3:64:ILE:HG23	29:d3:68:LEU:HD23	1.76	0.68
46:54:2483:G:H1	46:54:2495:U:H3	1.41	0.68
5:E3:191:ARG:NH1	46:54:4941:G:OP2	2.26	0.67
10:J3:44:THR:O	10:J3:78:LYS:NZ	2.27	0.67
15:P3:127:ARG:NH2	46:54:2422:C:OP1	2.27	0.67
15:P3:10:ASN:HD22	15:P3:13:LYS:HD3	1.59	0.67
26:a3:4:ARG:NH1	46:54:2341:A:OP2	2.27	0.67
46:54:2647:A:H62	46:54:2686:G:H8	1.41	0.67
18:S3:95:ARG:NH2	18:S3:112:ASP:OD2	2.28	0.67
7:G3:302:ARG:NH2	46:54:4075:U:OP1	2.28	0.67
46:54:1757:U:O4	46:54:1775:A:N6	2.20	0.67
46:54:3717:A:OP2	46:54:3735:G:N2	2.27	0.67
16:Q3:178:ARG:H	26:a3:51:GLY:HA2	1.58	0.67
3:C3:6:PRO:HB3	46:54:668:C:H4'	1.77	0.67
52:TT:193:MET:CE	53:1:2:ARG:HA	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:s3:58:ASN:ND2	43:s3:84:GLY:O	2.28	0.67
43:s3:108:PRO:HA	43:s3:184:SER:HB2	1.77	0.67
46:54:1197:C:H2'	46:54:1198:G:C8	2.29	0.67
16:Q3:181:ARG:NH1	46:54:1391:A:OP1	2.28	0.67
38:m3:99:LYS:HG3	46:54:4474:A:H5'	1.76	0.67
42:r3:85:ASN:HD22	46:54:690:C:H4'	1.59	0.66
43:s3:27:CYS:H	43:s3:193:PHE:HB3	1.61	0.66
10:J3:31:ASP:OD2	10:J3:35:ARG:NE	2.16	0.66
1:A3:67:TYR:OH	46:54:4087:G:N7	2.24	0.66
23:X3:120:ASP:N	23:X3:120:ASP:OD1	2.26	0.66
6:F3:85:GLU:OE1	19:T3:136:ARG:NH1	2.28	0.66
13:N3:49:ARG:NH2	46:54:152:U:OP2	2.29	0.66
43:s3:37:SER:OG	46:54:1999:A:N6	2.29	0.66
46:54:85:G:O2'	46:54:97:G:O6	2.12	0.66
48:84:105:C:H4'	48:84:106:G:H5''	1.75	0.66
52:TT:358:TYR:HD1	52:TT:366:VAL:H	1.40	0.66
18:S3:80:ILE:HG23	18:S3:129:VAL:HG22	1.75	0.66
35:j3:48:ASN:OD1	35:j3:54:LYS:NZ	2.28	0.66
46:54:2601:A:N6	46:54:2744:A:OP2	2.29	0.66
46:54:3809:G:OP2	46:54:3809:G:N2	2.28	0.66
46:54:394:G:N2	46:54:397:G:OP2	2.22	0.66
46:54:2093:G:H4'	46:54:2094:C:H5'	1.78	0.66
46:54:2440:U:O2'	46:54:2441:C:OP1	2.10	0.66
46:54:3766:A:OP2	46:54:3767:C:N4	2.29	0.66
52:TT:280:ALA:HB2	52:TT:295:GLY:HA3	1.77	0.66
1:A3:117:GLU:HB2	1:A3:162:ASN:HB2	1.78	0.66
6:F3:33:ARG:NH1	46:54:1272:C:OP2	2.28	0.66
3:C3:323:ARG:HH21	46:54:976:G:N2	1.94	0.66
46:54:2042:A:N3	46:54:4462:C:O2'	2.27	0.66
46:54:2380:G:N2	46:54:2424:G:H5'	2.11	0.66
3:C3:209:VAL:HB	3:C3:229:LEU:HD13	1.77	0.66
3:C3:254:GLU:OE1	3:C3:258:ARG:NH1	2.29	0.66
10:J3:95:ARG:HD3	10:J3:177:GLY:HA3	1.76	0.66
1:A3:27:ALA:O	1:A3:128:ARG:NH2	2.28	0.65
4:D3:83:LEU:HB3	4:D3:88:VAL:HG23	1.78	0.65
12:M3:117:LYS:NZ	46:54:4882:U:OP1	2.29	0.65
46:54:5006:U:H4'	46:54:5007:A:H5'	1.77	0.65
52:TT:473:GLY:O	52:TT:476:SER:OG	2.13	0.65
33:h3:56:ARG:NH1	48:84:65:A:OP1	2.28	0.65
4:D3:90:VAL:HG11	4:D3:231:VAL:HG21	1.78	0.65
11:L3:58:ILE:H	11:L3:113:ASN:ND2	1.94	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:f3:91:ASN:O	46:54:440:U:O2'	2.13	0.65
46:54:1445:U:O4	46:54:2109:A:N6	2.17	0.65
4:D3:268:ARG:HH21	46:54:1176:C:H5''	1.62	0.65
46:54:2490:U:O2'	46:54:2491:C:O5'	2.14	0.65
53:1:2:ARG:CG	53:1:2:ARG:O	2.44	0.65
5:E3:66:SER:OG	46:54:1239:C:N4	2.30	0.65
18:S3:1:MET:HE3	18:S3:35:PRO:HD3	1.78	0.65
26:a3:2:PRO:HD2	46:54:1509:C:H5''	1.78	0.65
43:s3:63:LYS:HD2	46:54:1960:A:H5'	1.79	0.65
14:O3:10:ASP:HB2	14:O3:117:ARG:HG3	1.77	0.65
28:c3:17:ARG:HH22	28:c3:107:SER:HB2	1.61	0.65
14:O3:81:TRP:HB2	14:O3:104:VAL:HG21	1.78	0.65
15:P3:67:VAL:O	15:P3:80:GLN:NE2	2.30	0.65
46:54:1818:G:O2'	46:54:1819:G:OP1	2.14	0.65
53:1:2:ARG:O	53:1:2:ARG:HG2	1.95	0.65
46:54:4133:C:N4	46:54:4151:G:O6	2.23	0.65
52:TT:133:TYR:CZ	52:TT:165:LYS:HB2	2.31	0.65
4:D3:65:ALA:HB2	4:D3:74:ILE:HD13	1.79	0.65
46:54:734:G:H1	46:54:929:A:H62	1.45	0.65
46:54:3598:C:H2'	46:54:3599:A:H8	1.61	0.65
11:L3:127:PHE:O	33:h3:117:ARG:NH2	2.25	0.64
46:54:643:C:H2'	46:54:644:G:C8	2.32	0.64
46:54:132:G:N2	46:54:136:C:O2	2.31	0.64
46:54:369:G:N2	46:54:372:A:OP2	2.28	0.64
46:54:1886:G:HO2'	46:54:1909:G:HO2'	1.43	0.64
50:NA:111:VAL:HG11	51:NB:64:MET:HE1	1.80	0.64
2:B3:218:ASP:OD2	2:B3:348:ARG:NH2	2.29	0.64
3:C3:100:ARG:NH2	46:54:1521:C:OP1	2.30	0.64
46:54:245:C:O2'	46:54:246:G:OP2	2.14	0.64
23:X3:107:HIS:O	23:X3:111:GLN:NE2	2.29	0.64
25:Z3:36:ARG:NH1	25:Z3:38:TYR:OH	2.30	0.64
44:t3:14:TYR:HA	44:t3:61:LYS:HE3	1.78	0.64
52:TT:117:ALA:HA	52:TT:120:LEU:HD12	1.80	0.64
4:D3:120:GLU:O	4:D3:248:ARG:NH2	2.30	0.64
10:J3:27:GLY:HA2	10:J3:68:ILE:HG23	1.78	0.64
24:Y3:74:TYR:OH	48:84:75:G:OP2	2.15	0.64
3:C3:140:LYS:HE3	3:C3:245:HIS:HB2	1.80	0.64
22:W3:19:ARG:NH2	22:W3:37:GLU:OE2	2.31	0.64
28:c3:28:VAL:HG21	28:c3:37:MET:HG3	1.79	0.64
44:t3:39:PRO:O	44:t3:43:GLY:N	2.30	0.64
46:54:1414:C:N4	46:54:1415:G:O6	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:1983:A:H1'	46:54:2010:A:H5'	1.80	0.64
46:54:4237:C:O2'	46:54:4326:G:N2	2.28	0.64
40:o3:41:TYR:OH	40:o3:51:GLN:NE2	2.26	0.64
51:NB:70:THR:HA	51:NB:98:GLN:HA	1.80	0.64
1:A3:180:LEU:HD22	41:p3:18:TYR:HB3	1.79	0.64
46:54:499:G:H2'	46:54:500:G:H8	1.63	0.64
46:54:1195:G:H2'	46:54:1196:G:C8	2.32	0.63
46:54:2529:A:O2'	46:54:2531:C:OP2	2.15	0.63
46:54:4898:G:H2'	46:54:4899:G:H8	1.61	0.63
52:TT:254:GLN:O	52:TT:258:ALA:N	2.31	0.63
3:C3:195:LYS:NZ	46:54:2334:C:OP2	2.31	0.63
6:F3:216:ARG:O	6:F3:245:ARG:NH1	2.31	0.63
9:I3:36:LEU:HD13	9:I3:73:ASN:HD22	1.64	0.63
33:h3:81:LEU:HD23	33:h3:84:ARG:HD2	1.81	0.63
46:54:67:C:OP2	46:54:312:G:N2	2.30	0.63
5:E3:61:ARG:NH1	46:54:978:G:OP2	2.27	0.63
46:54:974:C:H41	46:54:1281:G:H21	1.46	0.63
46:54:1073:G:H22	46:54:1238:A:H2	1.47	0.63
6:F3:93:ARG:NH2	6:F3:95:ARG:O	2.32	0.63
11:L3:8:MET:HG2	16:Q3:166:TYR:HB3	1.80	0.63
25:Z3:14:LEU:HD21	32:g3:92:LYS:HE3	1.80	0.63
43:s3:57:LYS:NZ	46:54:1961:G:OP2	2.31	0.63
44:t3:114:ARG:HA	44:t3:117:ARG:HB3	1.81	0.63
46:54:2489:C:H4'	46:54:2490:U:H5	1.63	0.63
2:B3:252:ALA:HB1	46:54:4524:G:N3	2.12	0.63
12:M3:132:ARG:NH2	46:54:4895:C:N3	2.47	0.63
17:R3:84:THR:O	17:R3:87:ALA:N	2.29	0.63
22:W3:56:ARG:HH21	22:W3:61:LYS:HB3	1.64	0.63
46:54:4620:U:OP2	46:54:4670:C:N4	2.32	0.63
52:TT:163:TRP:O	53:1:1:MET:CG	2.46	0.63
8:H3:89:ARG:NH1	8:H3:147:GLU:OE2	2.32	0.63
44:t3:60:VAL:HG22	44:t3:73:VAL:HG13	1.79	0.63
16:Q3:168:ARG:NH1	46:54:86:U:OP1	2.31	0.63
34:i3:79:THR:HG22	34:i3:81:ILE:H	1.64	0.63
46:54:1192:C:H2'	46:54:1193:C:O4'	1.99	0.63
1:A3:97:ASN:OD1	1:A3:100:ASN:ND2	2.32	0.63
24:Y3:57:VAL:HA	24:Y3:104:VAL:HG23	1.81	0.63
35:j3:82:THR:OG1	48:84:94:G:N2	2.32	0.63
46:54:2502:A:O2'	46:54:2503:G:O5'	2.14	0.63
3:C3:293:LEU:O	3:C3:299:GLN:NE2	2.31	0.63
14:O3:85:ARG:NH2	46:54:3887:C:OP2	2.26	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r3:24:THR:OG1	46:54:2289:C:N4	2.32	0.63
44:t3:104:ILE:HB	44:t3:143:VAL:HG12	1.79	0.63
46:54:508:G:O2'	46:54:510:U:OP2	2.16	0.63
46:54:907:C:H2'	46:54:908:G:C8	2.34	0.63
46:54:1969:G:H21	46:54:2017:A:H62	1.46	0.63
46:54:3603:G:O2'	46:54:3604:A:O4'	2.16	0.63
53:1:7:ILE:HG22	53:1:7:ILE:O	1.98	0.63
6:F3:215:PRO:HD3	6:F3:246:MET:HE2	1.79	0.62
8:H3:41:ILE:HG22	8:H3:43:VAL:HG13	1.79	0.62
38:m3:98:LYS:NZ	46:54:4473:A:OP1	2.32	0.62
1:A3:28:ARG:HB3	1:A3:123:ARG:HB3	1.81	0.62
32:g3:46:CYS:SG	32:g3:47:GLY:N	2.72	0.62
46:54:2483:G:H2'	46:54:2484:A:C8	2.34	0.62
46:54:5005:G:N2	46:54:5041:G:O2'	2.31	0.62
3:C3:358:LEU:HA	3:C3:361:LYS:HZ1	1.63	0.62
7:G3:111:PRO:HD2	7:G3:114:ILE:HD12	1.82	0.62
29:d3:26:THR:HB	29:d3:85:ARG:HD2	1.81	0.62
46:54:3700:C:O2'	46:54:3774:A:N3	2.28	0.62
53:1:41:ASP:OD1	53:1:43:GLN:NE2	2.31	0.62
15:P3:74:LYS:NZ	46:54:4982:A:OP1	2.21	0.62
17:R3:13:SER:OG	17:R3:38:ARG:NH1	2.32	0.62
25:Z3:16:GLY:O	25:Z3:19:SER:OG	2.15	0.62
43:s3:44:ARG:NH1	46:54:1997:U:H4'	2.14	0.62
46:54:1435:G:O2'	46:54:2105:A:N1	2.27	0.62
46:54:1768:C:H4'	46:54:1769:G:H5''	1.81	0.62
46:54:3641:U:OP2	46:54:3646:A:N6	2.33	0.62
47:74:92:C:H2'	47:74:93:G:C8	2.34	0.62
49:NI:18:ALA:HB1	49:NI:19:PRO:HD2	1.80	0.62
52:TT:193:MET:HE1	53:1:2:ARG:HA	1.81	0.62
6:F3:28:LYS:NZ	46:54:965:G:N7	2.37	0.62
20:U3:88:LYS:HD2	20:U3:97:ARG:NH2	2.14	0.62
34:i3:54:GLU:HG2	34:i3:90:LEU:HD11	1.81	0.62
52:TT:188:LEU:HB3	52:TT:220:ALA:HB2	1.80	0.62
13:N3:103:GLU:OE1	13:N3:118:SER:OG	2.16	0.62
17:R3:117:ARG:NH1	46:54:2660:A:OP1	2.27	0.62
29:d3:32:ARG:NH2	46:54:4995:U:O3'	2.33	0.62
45:23:18:G:N2	45:23:58:A:O4'	2.33	0.62
14:O3:177:LEU:O	14:O3:181:ALA:N	2.31	0.62
16:Q3:88:ASP:OD1	16:Q3:89:ASP:N	2.33	0.62
27:b3:32:LEU:HD12	46:54:1464:C:H5''	1.81	0.62
43:s3:174:LEU:HD12	43:s3:175:LEU:HD23	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:1198:G:H2'	46:54:1199:G:H8	1.64	0.62
40:o3:39:ARG:NH1	46:54:295:A:OP2	2.32	0.62
7:G3:106:ARG:NH2	46:54:4163:U:OP2	2.32	0.62
13:N3:73:ARG:NH1	46:54:32:G:OP1	2.32	0.61
19:T3:83:LYS:HE2	19:T3:85:LEU:HD21	1.81	0.61
24:Y3:2:LYS:NZ	24:Y3:7:VAL:O	2.26	0.61
27:b3:15:LYS:NZ	46:54:1670:G:OP1	2.30	0.61
44:t3:127:GLY:HA2	44:t3:130:LYS:HB2	1.81	0.61
46:54:1326:A:OP2	46:54:4445:U:O2'	2.17	0.61
44:t3:138:SER:O	46:54:2002:A:N6	2.33	0.61
3:C3:307:LYS:NZ	46:54:2090:U:OP2	2.32	0.61
5:E3:160:HIS:HB3	5:E3:163:LYS:HD2	1.82	0.61
11:L3:66:TYR:OH	46:54:1382:G:OP1	2.12	0.61
43:s3:147:ILE:HD12	43:s3:152:ILE:HG12	1.82	0.61
3:C3:150:LEU:O	3:C3:152:LEU:N	2.33	0.61
5:E3:43:LYS:HD2	5:E3:44:PRO:HD2	1.82	0.61
6:F3:79:ASN:HA	19:T3:143:THR:HG22	1.81	0.61
23:X3:93:ASN:ND2	46:54:2532:C:O2'	2.33	0.61
24:Y3:87:ARG:HH12	46:54:405:U:P	2.23	0.61
1:A3:30:ARG:O	1:A3:163:ARG:NH2	2.29	0.61
11:L3:64:VAL:O	26:a3:109:TYR:OH	2.17	0.61
19:T3:121:GLU:HG2	19:T3:122:LYS:HD2	1.81	0.61
25:Z3:41:ALA:HB2	25:Z3:77:TYR:HE1	1.64	0.61
46:54:1444:G:H21	46:54:2110:G:H1	1.49	0.61
52:TT:119:VAL:O	52:TT:123:THR:OG1	2.16	0.61
52:TT:315:GLN:O	52:TT:319:PHE:N	2.26	0.61
16:Q3:6:ARG:HH21	16:Q3:8:ASN:HD22	1.49	0.61
27:b3:3:LYS:HD3	46:54:4194:U:H3'	1.81	0.61
3:C3:323:ARG:NH1	46:54:1280:C:OP1	2.33	0.61
24:Y3:87:ARG:NH1	46:54:405:U:OP1	2.34	0.61
39:n3:21:ARG:O	39:n3:24:SER:OG	2.19	0.61
46:54:4492:U:H5''	46:54:4493:U:H5'	1.80	0.61
51:NB:98:GLN:HB3	51:NB:101:GLU:HG2	1.82	0.61
52:TT:195:LEU:HB3	52:TT:209:HIS:HB3	1.81	0.61
52:TT:401:PRO:HG2	52:TT:403:THR:HG22	1.82	0.61
4:D3:50:ARG:NH2	4:D3:147:ASP:OD2	2.30	0.61
29:d3:46:LEU:HD12	29:d3:64:ILE:HD13	1.83	0.61
2:B3:155:LYS:HD2	2:B3:156:TYR:CZ	2.35	0.61
11:L3:47:ALA:HB3	11:L3:48:PRO:HD3	1.81	0.61
23:X3:83:THR:HG21	46:54:2434:G:H5'	1.83	0.61
38:m3:74:TYR:O	46:54:4472:G:O2'	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E3:105:GLY:N	46:54:685:C:OP1	2.33	0.61
52:TT:319:PHE:HD1	52:TT:320:LEU:HD22	1.66	0.61
2:B3:246:ARG:NH1	46:54:4525:C:OP1	2.34	0.60
2:B3:287:ILE:HG12	2:B3:331:VAL:HG12	1.83	0.60
3:C3:78:ARG:HB3	3:C3:88:GLY:HA2	1.82	0.60
15:P3:54:LYS:NZ	46:54:3855:C:O2'	2.34	0.60
18:S3:82:LEU:HB2	18:S3:93:MET:HB2	1.82	0.60
46:54:181:C:H42	46:54:255:C:H42	1.49	0.60
52:TT:221:VAL:HG22	52:TT:230:SER:HB3	1.83	0.60
19:T3:87:LYS:CE	46:54:4305:G:H22	2.14	0.60
44:t3:124:GLU:O	44:t3:127:GLY:N	2.33	0.60
46:54:1369:C:OP2	46:54:1370:G:O2'	2.14	0.60
46:54:1967:A:N6	46:54:2020:U:O4	2.34	0.60
46:54:2000:G:O2'	46:54:2001:G:N7	2.31	0.60
51:NB:62:VAL:HB	51:NB:74:PHE:HB2	1.83	0.60
4:D3:62:CYS:HB3	4:D3:105:LEU:HD22	1.82	0.60
8:H3:93:ARG:HG2	8:H3:182:SER:HB3	1.83	0.60
28:c3:105:ILE:HG13	28:c3:106:ARG:HD2	1.82	0.60
39:n3:18:ARG:HH12	39:n3:22:GLN:HB2	1.66	0.60
46:54:1235:G:O2'	46:54:1236:C:OP2	2.15	0.60
2:B3:89:ILE:HD12	2:B3:194:LEU:HD11	1.84	0.60
4:D3:236:MET:HA	4:D3:239:MET:HE3	1.84	0.60
24:Y3:82:ILE:HB	24:Y3:85:VAL:HG22	1.82	0.60
44:t3:63:THR:O	44:t3:70:GLN:N	2.31	0.60
46:54:738(A):C:O2'	46:54:740:G:OP2	2.18	0.60
26:a3:72:THR:HG22	26:a3:110:LYS:HB3	1.84	0.60
43:s3:114:GLY:H	43:s3:167:VAL:HG23	1.67	0.60
46:54:4896:G:H2'	46:54:4897:G:H8	1.66	0.60
53:1:47:ILE:HG22	53:1:49:VAL:HG13	1.84	0.60
13:N3:68:ARG:NH2	46:54:303:C:OP2	2.34	0.60
46:54:1170:G:H2'	46:54:1171:G:H8	1.67	0.60
3:C3:266:THR:HG23	3:C3:269:LYS:H	1.67	0.60
46:54:2395:A:HO2'	46:54:2806:A:H1'	1.65	0.60
48:84:111:U:H4'	48:84:112:G:H5'	1.84	0.60
22:W3:58:LYS:HE3	22:W3:59:HIS:CE1	2.37	0.60
37:l3:20:ASN:O	37:l3:41:ARG:NH2	2.32	0.60
9:I3:29:ALA:O	9:I3:32:ARG:NH1	2.33	0.60
46:54:5016:A:H2	46:54:5033:G:H21	1.49	0.60
2:B3:80:GLU:OE1	2:B3:323:TYR:OH	2.19	0.60
16:Q3:89:ASP:OD1	16:Q3:91:ARG:NH2	2.35	0.60
46:54:35:U:O2'	46:54:1525:A:N1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B3:139:ASP:OD1	2:B3:139:ASP:N	2.33	0.59
12:M3:57:LEU:HD23	12:M3:57:LEU:H	1.66	0.59
15:P3:120:ASN:HD21	48:84:12:G:H21	1.50	0.59
25:Z3:52:LYS:O	25:Z3:65:ARG:NH2	2.34	0.59
33:h3:52:LYS:NZ	48:84:61:A:OP1	2.28	0.59
46:54:1276:C:H2'	46:54:1277:G:O4'	2.02	0.59
46:54:1548:G:O2'	46:54:2812:A:N3	2.32	0.59
1:A3:112:ILE:HD13	1:A3:135:THR:HG22	1.84	0.59
11:L3:74:ARG:NH2	46:54:109:G:OP2	2.35	0.59
12:M3:71:LYS:NZ	46:54:737:C:OP2	2.34	0.59
13:N3:181:HIS:O	13:N3:195:ARG:NH2	2.32	0.59
46:54:4232:U:H4'	46:54:4233:A:O5'	2.01	0.59
6:F3:95:ARG:NH2	46:54:1895:G:OP1	2.35	0.59
7:G3:308:LYS:O	7:G3:312:LYS:N	2.26	0.59
15:P3:23:ARG:HG3	15:P3:125:MET:HE1	1.85	0.59
18:S3:13:VAL:HG22	18:S3:63:TYR:HB3	1.83	0.59
27:b3:37:PRO:O	27:b3:41:ARG:N	2.32	0.59
2:B3:215:GLU:OE2	2:B3:349:LYS:NZ	2.28	0.59
15:P3:2:VAL:HG12	15:P3:3:ARG:H	1.66	0.59
24:Y3:67:ILE:O	24:Y3:84:ARG:NH2	2.35	0.59
30:e3:86:GLU:OE1	30:e3:86:GLU:N	2.34	0.59
35:j3:28:HIS:HD2	35:j3:30:GLN:H	1.49	0.59
41:p3:59:SER:OG	41:p3:60:CYS:N	2.36	0.59
43:s3:111:ALA:O	43:s3:112:ARG:NE	2.34	0.59
46:54:269:G:H2'	46:54:270:U:H6	1.67	0.59
6:F3:89:ALA:HB2	6:F3:124:LEU:HD21	1.83	0.59
8:H3:115:ARG:HG2	8:H3:123:ILE:HG22	1.84	0.59
9:I3:87:ILE:HG12	9:I3:138:ILE:HG12	1.84	0.59
43:s3:30:VAL:HB	43:s3:187:LEU:HB3	1.83	0.59
46:54:3641:U:H5	46:54:3646:A:N7	2.00	0.59
46:54:3692:A:H62	46:54:3823:G:H21	1.48	0.59
46:54:704:C:O2'	46:54:705:G:OP1	2.18	0.59
13:N3:99:GLN:HE21	13:N3:167:ALA:HB2	1.67	0.59
14:O3:49:ARG:NH2	46:54:1932:A:OP2	2.35	0.59
46:54:495:C:H2'	46:54:496:G:O4'	2.03	0.59
24:Y3:11:ARG:NH1	46:54:229:G:OP1	2.34	0.59
50:NA:101:ASN:O	50:NA:131:LEU:N	2.32	0.59
8:H3:134:CYS:SG	8:H3:144:LEU:HD23	2.43	0.59
45:23:57:G:H2'	45:23:58:A:H5''	1.85	0.59
46:54:406:C:O2'	46:54:407:A:OP1	2.19	0.59
46:54:1397:A:HO2'	46:54:1467:C:HO2'	1.49	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:1655:C:HO2'	46:54:4391:G:HO2'	1.49	0.59
52:TT:294:GLU:O	52:TT:298:ARG:N	2.16	0.59
52:TT:425:TRP:HE1	52:TT:472:GLN:NE2	2.00	0.59
3:C3:234:LYS:NZ	46:54:1364:U:O2	2.27	0.58
13:N3:17:ASP:OD1	13:N3:18:VAL:N	2.35	0.58
28:c3:64:ALA:HB1	28:c3:69:THR:HB	1.84	0.58
39:n3:1:MET:HG2	39:n3:6:ARG:HH21	1.67	0.58
26:a3:116:LYS:NZ	46:54:1420:A:H62	2.01	0.58
43:s3:161:ILE:HD13	43:s3:167:VAL:HG11	1.85	0.58
46:54:2489:C:H4'	46:54:2490:U:C5	2.37	0.58
4:D3:259:ARG:HB3	47:74:120:U:H2'	1.85	0.58
11:L3:39:ARG:NH2	46:54:1362:G:OP1	2.36	0.58
11:L3:71:ARG:NH1	46:54:102:G:OP1	2.37	0.58
13:N3:192:TRP:NE1	46:54:48:G:OP1	2.32	0.58
36:k3:12:LEU:HB3	36:k3:16:ARG:HH12	1.68	0.58
36:k3:35:LYS:NZ	46:54:2695:A:OP1	2.33	0.58
46:54:1798:G:H2'	46:54:1799:G:H5''	1.84	0.58
46:54:2093:G:H22	46:54:2262:G:H1	1.50	0.58
3:C3:39:PHE:O	3:C3:43:ASN:ND2	2.34	0.58
6:F3:51:GLU:OE2	46:54:1237:C:O2'	2.18	0.58
38:m3:53:GLU:OE1	38:m3:55:SER:N	2.33	0.58
46:54:983:C:H2'	46:54:984:C:C6	2.38	0.58
20:U3:28:PRO:HB2	20:U3:34:MET:HG2	1.84	0.58
11:L3:88:LYS:NZ	46:54:159:C:O2'	2.36	0.58
23:X3:146:ALA:HA	23:X3:149:VAL:HG12	1.84	0.58
25:Z3:95:VAL:HG11	25:Z3:113:GLU:HG2	1.85	0.58
28:c3:14:ILE:HD13	28:c3:17:ARG:HH21	1.68	0.58
17:R3:31:GLU:N	17:R3:31:GLU:OE2	2.36	0.58
46:54:1082:C:H42	46:54:1217:G:H1	1.52	0.58
16:Q3:2:GLY:N	46:54:2072:C:OP1	2.37	0.58
17:R3:62:ARG:O	17:R3:66:ASN:ND2	2.35	0.58
46:54:175:C:H2'	46:54:176:G:H8	1.69	0.58
46:54:2639:U:H2'	46:54:2694:G:H1	1.67	0.58
2:B3:89:ILE:HG22	2:B3:162:VAL:HG23	1.85	0.58
7:G3:83:PRO:HB2	25:Z3:125:GLY:HA3	1.86	0.58
46:54:1757:U:OP1	46:54:1768:C:N4	2.36	0.58
46:54:2779:C:O2'	48:84:112:G:OP1	2.17	0.58
46:54:4322:G:N2	46:54:4325:A:OP2	2.34	0.58
46:54:4467:A:O2'	46:54:4510:A:N3	2.33	0.58
4:D3:88:VAL:HG12	4:D3:239:MET:SD	2.44	0.57
17:R3:124:TYR:OH	46:54:2666:U:OP2	2.15	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z3:121:ARG:NH2	25:Z3:127:ASN:OD1	2.37	0.57
46:54:1187:G:OP2	46:54:1187:G:N2	2.34	0.57
46:54:4635:A:H8	46:54:5048:A:H61	1.52	0.57
52:TT:232:TYR:OH	52:TT:274:ASP:OD2	2.22	0.57
52:TT:274:ASP:OD1	53:1:4:ILE:HD13	2.01	0.57
16:Q3:55:ARG:HH11	46:54:1352:C:H41	1.52	0.57
17:R3:114:LYS:O	17:R3:146:LYS:NZ	2.31	0.57
25:Z3:38:TYR:HB3	46:54:2656:U:H5''	1.86	0.57
44:t3:113:ALA:O	44:t3:117:ARG:N	2.36	0.57
2:B3:216:MET:HG3	2:B3:354:GLN:HE21	1.69	0.57
3:C3:269:LYS:NZ	3:C3:270:ALA:O	2.35	0.57
46:54:1092:G:N2	46:54:1204:C:O2	2.29	0.57
1:A3:181:LYS:HB2	46:54:1577:G:C5	2.39	0.57
11:L3:94:ILE:O	11:L3:120:TYR:OH	2.13	0.57
46:54:1942:A:H2'	46:54:1943:A:C8	2.40	0.57
46:54:2590:G:O2'	46:54:2755:A:N6	2.37	0.57
46:54:4098:A:N6	46:54:4111:U:O4	2.37	0.57
52:TT:120:LEU:HD23	52:TT:140:LEU:HD22	1.86	0.57
2:B3:268:ARG:NH1	46:54:3896:C:O2'	2.34	0.57
19:T3:112:ASN:O	19:T3:116:LYS:N	2.36	0.57
46:54:1075:G:H22	46:54:1235:G:N2	2.02	0.57
46:54:2811:G:N1	46:54:2814:C:OP2	2.36	0.57
46:54:4523:A:H5''	46:54:4524:G:H5'	1.85	0.57
10:J3:33:LEU:HD22	10:J3:70:VAL:HG23	1.86	0.57
23:X3:90:ILE:HG12	23:X3:96:LEU:HD23	1.86	0.57
40:o3:71:GLU:OE2	40:o3:78:ARG:NH1	2.38	0.57
42:r3:32:LEU:HD23	42:r3:32:LEU:H	1.70	0.57
46:54:757:G:N1	46:54:906:C:N3	2.43	0.57
46:54:1398:A:H62	46:54:1419:G:N2	2.02	0.57
48:84:85:U:H5'	48:84:87:G:H5'	1.86	0.57
43:s3:139:GLN:NE2	43:s3:143:ILE:O	2.29	0.57
44:t3:20:GLY:HA2	44:t3:47:ALA:HB1	1.86	0.57
46:54:695:G:O2'	46:54:697:G:OP2	2.22	0.57
1:A3:24:LYS:HE2	1:A3:52:PRO:HD3	1.86	0.57
9:I3:115:MET:HE3	46:54:1868:A:H61	1.70	0.57
24:Y3:84:ARG:HD2	52:TT:426:GLY:HA3	1.86	0.57
44:t3:125:LEU:O	44:t3:128:THR:OG1	2.21	0.57
46:54:910:G:H2'	46:54:911:U:H6	1.69	0.57
46:54:2793:G:C5'	46:54:2794:C:H5''	2.33	0.57
4:D3:283:LYS:NZ	47:74:63:C:OP2	2.38	0.57
46:54:2005:G:N1	46:54:2014:C:O2	2.32	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R3:7:GLN:HG2	17:R3:32:ILE:HG22	1.86	0.57
42:r3:107:ARG:NH2	42:r3:108:MET:SD	2.78	0.57
46:54:2793:G:H5'	46:54:2794:C:H5''	1.87	0.57
2:B3:114:CYS:SG	2:B3:180:LEU:HD11	2.45	0.56
6:F3:75:ARG:NE	46:54:730:G:OP2	2.38	0.56
23:X3:150:ALA:HB1	23:X3:155:ILE:HG13	1.87	0.56
46:54:1218:G:H2'	46:54:1219:G:H8	1.68	0.56
46:54:3736:A:H2'	46:54:3737:A:C8	2.40	0.56
14:O3:47:PHE:HA	14:O3:136:ALA:HB2	1.86	0.56
43:s3:127:ASN:OD1	43:s3:128:THR:N	2.39	0.56
21:V3:94:VAL:HG11	22:W3:20:ARG:HE	1.71	0.56
23:X3:82:THR:HG22	23:X3:155:ILE:HG22	1.85	0.56
41:p3:29:ILE:HG23	41:p3:69:TRP:HB3	1.87	0.56
46:54:2021:G:H2'	46:54:2022:C:C2	2.41	0.56
46:54:2459:G:N2	46:54:2462:C:OP2	2.31	0.56
46:54:2579:G:N2	46:54:2582:A:OP2	2.33	0.56
52:TT:84:SER:OG	52:TT:85:VAL:N	2.37	0.56
52:TT:126:ALA:O	52:TT:129:VAL:HG23	2.05	0.56
1:A3:30:ARG:NH2	1:A3:33:ASP:OD2	2.24	0.56
3:C3:149:GLU:OE1	42:r3:71:ARG:NE	2.38	0.56
18:S3:81:TRP:O	18:S3:127:MET:HG2	2.05	0.56
19:T3:87:LYS:NZ	46:54:4305:G:H22	2.04	0.56
36:k3:7:GLU:HG3	36:k3:10:ASP:H	1.70	0.56
44:t3:32:ILE:HD11	44:t3:37:LEU:HD12	1.87	0.56
1:A3:152:SER:OG	46:54:3661:G:N7	2.38	0.56
24:Y3:91:ASN:OD1	24:Y3:93:THR:HG22	2.06	0.56
41:p3:85:ARG:NH1	41:p3:88:GLU:OE2	2.38	0.56
46:54:1563:A:H2'	46:54:1564:A:C8	2.41	0.56
46:54:4135:G:H2'	46:54:4136:G:C8	2.39	0.56
52:TT:456:SER:OG	52:TT:457:VAL:N	2.39	0.56
1:A3:9:ARG:NH2	46:54:1629:G:N7	2.53	0.56
2:B3:81:THR:OG1	2:B3:207:VAL:HG21	2.05	0.56
34:i3:50:PHE:O	34:i3:55:ARG:NH2	2.38	0.56
46:54:4510:A:O2'	46:54:4511:A:O4'	2.24	0.56
4:D3:119:TYR:OH	4:D3:139:PRO:O	2.16	0.56
7:G3:156:ARG:HH21	7:G3:248:HIS:CE1	2.23	0.56
15:P3:82:ARG:NH2	46:54:2362:U:OP1	2.39	0.56
19:T3:87:LYS:NZ	46:54:4300:U:OP1	2.39	0.56
46:54:1755:C:O2'	46:54:1757:U:OP2	2.24	0.56
46:54:2486:G:H1	46:54:2492:C:N4	1.96	0.56
46:54:4743:G:N2	46:54:4958:C:O2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A3:28:ARG:HE	1:A3:123:ARG:NH1	2.04	0.56
46:54:910:G:H2'	46:54:911:U:C6	2.41	0.56
46:54:4862:G:H2'	46:54:4863:G:H8	1.69	0.56
11:L3:46:ILE:HB	11:L3:49:ARG:HB2	1.87	0.56
13:N3:193:ARG:O	13:N3:197:THR:OG1	2.16	0.56
46:54:1093:C:N4	46:54:1094:G:O6	2.38	0.56
46:54:1194:G:C2	46:54:1195:G:C4	2.94	0.56
52:TT:73:TYR:O	52:TT:77:ASP:N	2.35	0.56
2:B3:213:GLN:NE2	2:B3:285:TYR:O	2.35	0.56
14:O3:80:PHE:O	14:O3:83:THR:HG22	2.06	0.56
46:54:2844:A:O2'	46:54:4631:G:H4'	2.05	0.56
46:54:4743:G:H1	46:54:4957:C:H42	1.52	0.56
50:NA:119:THR:HG22	51:NB:91:THR:HG23	1.88	0.56
52:TT:121:MET:CE	52:TT:154:ALA:HA	2.36	0.56
4:D3:208:MET:HB3	4:D3:233:PRO:HG3	1.87	0.55
46:54:1766:A:H2'	46:54:1767:A:C8	2.41	0.55
46:54:1978:C:O2'	46:54:1989:G:N2	2.38	0.55
46:54:1998:A:N3	46:54:2019:C:O2'	2.38	0.55
50:NA:101:ASN:OD1	50:NA:102:ILE:N	2.39	0.55
4:D3:59:ASP:OD1	4:D3:60:ILE:N	2.39	0.55
4:D3:253:TYR:OH	47:74:117:G:OP1	2.18	0.55
14:O3:36:VAL:HG21	14:O3:108:ILE:HG23	1.88	0.55
17:R3:121:HIS:ND1	46:54:2664:G:OP2	2.39	0.55
24:Y3:91:ASN:HA	46:54:389:A:H1'	1.88	0.55
46:54:407:A:O2'	46:54:410:A:OP1	2.23	0.55
46:54:2491:C:H2'	46:54:2492:C:C6	2.41	0.55
46:54:2638:G:H22	46:54:2697:A:N6	2.04	0.55
8:H3:123:ILE:HD12	8:H3:125:ARG:HH21	1.72	0.55
26:a3:64:LYS:HG3	26:a3:67:GLN:HG3	1.87	0.55
30:e3:38:PRO:HB2	30:e3:43:ASN:ND2	2.21	0.55
39:n3:20:MET:HE1	39:n3:23:ARG:HH21	1.71	0.55
44:t3:20:GLY:H	44:t3:54:LYS:HA	1.71	0.55
46:54:914:U:H1'	46:54:915:A:C5	2.40	0.55
46:54:1637:A:OP1	46:54:1640:C:N4	2.37	0.55
52:TT:202:THR:HB	52:TT:205:GLU:HB2	1.87	0.55
2:B3:55:HIS:ND1	2:B3:369:ASP:OD2	2.39	0.55
3:C3:145:GLU:OE1	3:C3:145:GLU:N	2.39	0.55
4:D3:225:GLN:HA	4:D3:228:LYS:HB3	1.88	0.55
11:L3:63:THR:O	11:L3:65:ARG:N	2.40	0.55
26:a3:76:ASP:N	26:a3:76:ASP:OD1	2.39	0.55
36:k3:26:LYS:HE2	46:54:2696:A:H5'	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:2869:U:O2'	46:54:2881:A:N7	2.37	0.55
46:54:4067:U:H2'	46:54:4068:U:C6	2.42	0.55
47:74:11:A:O2'	47:74:13:A:OP2	2.25	0.55
13:N3:38:ARG:HB2	13:N3:62:TYR:CE1	2.41	0.55
13:N3:85:VAL:HG22	46:54:43:U:H5''	1.88	0.55
18:S3:170:LYS:NZ	46:54:4874:A:O2'	2.38	0.55
19:T3:127:GLN:HE21	19:T3:129:LYS:HB2	1.71	0.55
19:T3:137:GLU:H	19:T3:137:GLU:CD	2.14	0.55
41:p3:44:LYS:NZ	46:54:2672:C:OP1	2.39	0.55
46:54:4378:A:O2'	46:54:4379:A:H2'	2.06	0.55
51:NB:60:GLU:HG2	51:NB:61:GLU:HG2	1.89	0.55
35:j3:34:CYS:HB3	35:j3:39:TYR:H	1.72	0.55
46:54:2290:C:HO2'	46:54:2322:G:HO2'	1.55	0.55
2:B3:50:LYS:NZ	46:54:4626:A:OP1	2.36	0.55
7:G3:110:TRP:O	7:G3:115:ARG:NH2	2.38	0.55
43:s3:75:LEU:HD22	43:s3:78:LEU:HD12	1.88	0.55
46:54:2457:G:H21	46:54:3672:G:N2	2.02	0.55
46:54:3940:U:H3	46:54:4073:A:H61	1.54	0.55
50:NA:122:VAL:HB	51:NB:88:PHE:HB2	1.87	0.55
7:G3:141:ASP:OD2	7:G3:144:THR:OG1	2.20	0.55
18:S3:171:ARG:O	46:54:4871:C:N4	2.40	0.55
46:54:4584:A:C2	46:54:4585:U:H1'	2.42	0.55
52:TT:148:GLU:HB3	52:TT:151:LEU:HD13	1.89	0.55
52:TT:280:ALA:O	52:TT:284:LYS:N	2.39	0.55
1:A3:103:PRO:HA	1:A3:163:ARG:HA	1.89	0.55
7:G3:245:ARG:NH1	46:54:5:A:O2'	2.40	0.55
19:T3:108:ARG:NH2	46:54:1802:A:O2'	2.39	0.55
26:a3:125:LYS:HZ2	26:a3:145:VAL:HG11	1.70	0.55
27:b3:56:LYS:HD2	46:54:1812:C:H5''	1.87	0.55
46:54:4896:G:H2'	46:54:4897:G:C8	2.42	0.55
52:TT:106:MET:HE1	52:TT:122:LEU:HB3	1.89	0.55
52:TT:160:GLU:O	52:TT:164:LYS:HG3	2.07	0.55
9:I3:4:ARG:NH2	9:I3:9:TYR:OH	2.40	0.55
10:J3:57:VAL:HG23	10:J3:60:PHE:HB2	1.89	0.55
16:Q3:150:ARG:NH2	46:54:1499:C:OP1	2.40	0.55
18:S3:147:ASP:OD1	18:S3:149:LYS:N	2.40	0.55
23:X3:72:ASP:OD1	23:X3:73:HIS:N	2.40	0.55
44:t3:146:ARG:HB2	44:t3:148:PRO:HD2	1.87	0.55
46:54:988:C:H42	46:54:1066:G:H1	1.55	0.55
46:54:2485:U:H2'	46:54:2486:G:C8	2.41	0.55
46:54:2764:A:H2'	46:54:2765:A:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B3:119:TYR:HH	2:B3:129:ALA:H	1.54	0.54
3:C3:323:ARG:HH21	46:54:976:G:H21	1.56	0.54
4:D3:261:VAL:HG11	47:74:119:U:C2	2.42	0.54
5:E3:184:LEU:O	46:54:4883:C:N4	2.39	0.54
14:O3:148:LYS:NZ	46:54:4713:G:OP1	2.29	0.54
14:O3:193:THR:HG23	14:O3:202:LEU:HD23	1.88	0.54
25:Z3:10:VAL:O	25:Z3:83:THR:OG1	2.23	0.54
40:o3:6:LYS:HG2	40:o3:93:LEU:HB3	1.89	0.54
46:54:1377:G:H21	46:54:1380:G:H5'	1.71	0.54
46:54:1920:C:H3'	46:54:1921:C:H5''	1.88	0.54
1:A3:104:VAL:HG22	1:A3:162:ASN:O	2.07	0.54
2:B3:21:ARG:NH2	46:54:4981:G:O6	2.40	0.54
8:H3:113:GLU:OE1	8:H3:115:ARG:NH2	2.37	0.54
37:l3:48:LYS:O	37:l3:50:GLY:N	2.40	0.54
44:t3:10:ILE:HD12	44:t3:65:GLN:HA	1.89	0.54
47:74:92:C:H2'	47:74:93:G:H8	1.72	0.54
2:B3:89:ILE:HD11	2:B3:150:PHE:CE1	2.42	0.54
25:Z3:48:ARG:HB3	25:Z3:69:LYS:HB3	1.89	0.54
43:s3:28:PHE:CZ	43:s3:95:LEU:HA	2.43	0.54
4:D3:163:LEU:HD21	4:D3:175:HIS:HB3	1.90	0.54
11:L3:48:PRO:HB2	33:h3:120:ALA:HB2	1.89	0.54
21:V3:33:GLY:HA3	21:V3:69:LYS:HD2	1.88	0.54
21:V3:41:SER:OG	46:54:4507:A:O2'	2.25	0.54
21:V3:87:SER:HB2	22:W3:19:ARG:HH11	1.72	0.54
53:1:42:LEU:HD12	53:1:43:GLN:H	1.73	0.54
8:H3:88:PHE:CE2	8:H3:151:ILE:HB	2.42	0.54
27:b3:57:MET:O	27:b3:61:ASN:ND2	2.40	0.54
41:p3:38:THR:HA	41:p3:45:THR:HA	1.89	0.54
46:54:1594:C:O2'	46:54:1597:G:O2'	2.25	0.54
46:54:2561:C:N4	46:54:2562:G:O6	2.41	0.54
46:54:4448:G:O2'	46:54:4449:A:OP2	2.22	0.54
34:i3:34:THR:HG21	46:54:276:C:H5''	1.89	0.54
46:54:1405:C:H2'	46:54:1406:G:H8	1.72	0.54
46:54:4572:U:H2'	46:54:4573:G:C8	2.42	0.54
46:54:4736:C:H2'	46:54:4737:G:H8	1.72	0.54
46:54:4902:C:H42	46:54:4920:C:H42	1.56	0.54
46:54:4925:U:O2'	46:54:4926:C:OP1	2.25	0.54
16:Q3:6:ARG:HH21	16:Q3:8:ASN:ND2	2.05	0.54
16:Q3:63:LEU:O	16:Q3:67:ILE:HG12	2.07	0.54
18:S3:86:SER:OG	18:S3:91:HIS:HE1	1.91	0.54
46:54:1198:G:H2'	46:54:1199:G:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:1633:G:H5'	46:54:1634:A:OP1	2.07	0.54
51:NB:79:VAL:HG13	51:NB:90:ILE:HA	1.90	0.54
4:D3:223:PHE:HB3	4:D3:226:TYR:HB2	1.88	0.54
5:E3:53:VAL:HG11	46:54:947:C:H5''	1.88	0.54
5:E3:94:THR:OG1	5:E3:110:VAL:O	2.21	0.54
9:I3:38:ARG:HG2	9:I3:41:ALA:HB2	1.90	0.54
13:N3:9:GLU:HB2	34:i3:44:ILE:HD12	1.90	0.54
14:O3:79:ILE:HG21	14:O3:138:LEU:HD11	1.88	0.54
46:54:190:G:H2'	46:54:191:G:H8	1.72	0.54
46:54:1170:G:H2'	46:54:1171:G:C8	2.43	0.54
46:54:1193:C:H2'	46:54:1194:G:H8	1.73	0.54
17:R3:93:VAL:HG11	46:54:2725:A:H1'	1.89	0.54
46:54:978:G:N2	46:54:1277:G:H22	2.05	0.54
46:54:2718:U:H5''	46:54:2719:C:H5'	1.89	0.54
41:p3:7:LYS:HE2	46:54:2875:C:H5''	1.90	0.54
46:54:667:A:OP1	46:54:668:C:N4	2.30	0.54
46:54:1482:G:O2'	46:54:1483:C:OP2	2.25	0.54
2:B3:240:LEU:HB3	2:B3:244:THR:HG21	1.89	0.53
6:F3:195:THR:O	6:F3:195:THR:OG1	2.24	0.53
8:H3:13:PRO:HG2	8:H3:16:VAL:HG23	1.89	0.53
10:J3:56:THR:HG22	10:J3:64:ARG:N	2.18	0.53
26:a3:113:GLY:O	46:54:1397:A:H5'	2.08	0.53
28:c3:32:LYS:NZ	46:54:2657:G:O6	2.40	0.53
46:54:5061:A:H3'	46:54:5062:G:H5'	1.91	0.53
5:E3:222:LYS:NZ	46:54:4940:C:OP2	2.41	0.53
16:Q3:160:HIS:HE1	46:54:4298:A:H5''	1.73	0.53
20:U3:48:LYS:NZ	46:54:2630:U:OP1	2.30	0.53
32:g3:114:GLN:HE21	32:g3:115:LYS:HG2	1.73	0.53
2:B3:57:VAL:HG22	2:B3:73:VAL:HG22	1.89	0.53
5:E3:153:LEU:HB3	5:E3:197:VAL:HG13	1.90	0.53
5:E3:189:LEU:H	5:E3:253:GLN:NE2	2.06	0.53
15:P3:120:ASN:HB2	15:P3:145:HIS:HB2	1.90	0.53
36:k3:19:ASP:HB2	36:k3:39:SER:HB2	1.89	0.53
40:o3:105:GLN:N	40:o3:105:GLN:OE1	2.41	0.53
46:54:118:C:H42	46:54:153:G:H1	1.55	0.53
46:54:1598:C:H2'	46:54:1599:G:H8	1.73	0.53
46:54:4094:G:H1	46:54:4114:C:H42	1.55	0.53
46:54:4633:G:O2'	46:54:4635:A:OP2	2.17	0.53
2:B3:89:ILE:HD11	2:B3:150:PHE:HE1	1.73	0.53
3:C3:56:GLU:CD	3:C3:56:GLU:H	2.16	0.53
5:E3:127:LYS:HB2	46:54:958:G:N3	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N3:123:GLU:OE1	13:N3:128:LYS:NZ	2.41	0.53
43:s3:97:GLU:O	43:s3:101:MET:HG2	2.09	0.53
46:54:308:G:OP2	46:54:308:G:N2	2.32	0.53
52:TT:160:GLU:HG2	52:TT:164:LYS:HE2	1.89	0.53
52:TT:276:HIS:CE1	52:TT:298:ARG:HH11	2.26	0.53
53:1:7:ILE:O	53:1:7:ILE:CG2	2.57	0.53
1:A3:179:ILE:O	46:54:3653:A:H4'	2.08	0.53
20:U3:42:PHE:CE2	20:U3:90:TYR:HB2	2.44	0.53
35:j3:20:ARG:HD3	35:j3:39:TYR:CZ	2.44	0.53
46:54:219:G:H2'	46:54:219:G:N3	2.24	0.53
46:54:1300:G:O2'	46:54:1301:C:N4	2.41	0.53
46:54:2740:U:O2'	46:54:2742:G:N2	2.41	0.53
46:54:4660:G:H2'	46:54:4661:G:H5''	1.90	0.53
50:NA:95:THR:HG22	50:NA:105:VAL:HG22	1.90	0.53
50:NA:106:ILE:HG22	50:NA:126:ALA:HB2	1.90	0.53
2:B3:119:TYR:OH	2:B3:129:ALA:N	2.38	0.53
33:h3:13:LYS:HD3	33:h3:14:LYS:H	1.74	0.53
42:r3:19:LYS:HG2	42:r3:24:THR:HG23	1.90	0.53
46:54:35:U:H5'	46:54:36:U:OP2	2.08	0.53
50:NA:103:LEU:N	50:NA:129:GLU:O	2.42	0.53
52:TT:294:GLU:HA	52:TT:297:SER:HB2	1.91	0.53
52:TT:408:ASP:OD1	52:TT:409:SER:N	2.42	0.53
2:B3:165:HIS:ND1	2:B3:166:THR:O	2.35	0.53
21:V3:10:SER:OG	21:V3:11:GLY:N	2.39	0.53
26:a3:8:THR:HG21	46:54:1339:U:OP1	2.08	0.53
35:j3:4:GLY:O	35:j3:8:PHE:HD1	1.91	0.53
46:54:4491:G:N3	46:54:4511:A:H2	2.07	0.53
46:54:5034:A:H2'	46:54:5035:U:O4'	2.07	0.53
3:C3:44:LEU:HD22	46:54:1373:A:H5''	1.91	0.53
12:M3:94:LYS:NZ	46:54:4872:G:OP2	2.40	0.53
26:a3:116:LYS:HZ3	46:54:1420:A:H62	1.54	0.53
35:j3:21:ARG:NH2	35:j3:39:TYR:O	2.42	0.53
42:r3:39:ARG:NH2	42:r3:105:ASP:OD2	2.42	0.53
42:r3:17:LEU:HD21	42:r3:19:LYS:HD2	1.90	0.53
46:54:2538:U:H2'	46:54:2539:C:C6	2.44	0.53
4:D3:33:ARG:NH2	47:74:7:G:O3'	2.42	0.53
10:J3:42:GLN:NE2	10:J3:117:ILE:HD11	2.21	0.53
17:R3:70:ARG:HE	17:R3:75:HIS:HB2	1.73	0.53
33:h3:56:ARG:O	33:h3:60:VAL:HG23	2.09	0.53
52:TT:436:PRO:HG2	52:TT:464:LEU:HD11	1.91	0.53
2:B3:55:HIS:CE1	46:54:4627:U:HO2'	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:U3:66:SER:OG	20:U3:67:LYS:N	2.38	0.52
24:Y3:52:ASP:HB2	24:Y3:110:LYS:HG3	1.92	0.52
26:a3:9:ARG:O	46:54:1661:C:N4	2.22	0.52
26:a3:84:GLU:OE1	26:a3:87:ARG:NH2	2.42	0.52
26:a3:85:GLN:HA	26:a3:88:VAL:HG12	1.92	0.52
46:54:5001:U:H2'	46:54:5002:U:O4'	2.09	0.52
50:NA:86:ARG:HH12	50:NA:113:LYS:HG3	1.73	0.52
27:b3:44:ARG:NH2	46:54:1466:G:OP2	2.42	0.52
27:b3:64:ALA:O	27:b3:68:ARG:HG2	2.08	0.52
27:b3:68:ARG:O	27:b3:72:ILE:HG22	2.10	0.52
46:54:1563:A:O2'	46:54:1564:A:O4'	2.25	0.52
46:54:2495:U:H2'	46:54:2496:G:H8	1.73	0.52
2:B3:10:ARG:NH2	2:B3:11:HIS:O	2.42	0.52
5:E3:141:ARG:NE	5:E3:173:SER:O	2.41	0.52
7:G3:190:ARG:HD2	7:G3:195:THR:HG21	1.90	0.52
11:L3:39:ARG:NH1	46:54:1363:C:OP2	2.42	0.52
14:O3:65:ASN:OD1	14:O3:67:SER:OG	2.27	0.52
46:54:4131:G:H1	46:54:4153:C:H42	1.57	0.52
46:54:4188:U:H2'	46:54:4189:U:C6	2.45	0.52
1:A3:95:GLN:HB3	41:p3:87:LYS:HE3	1.91	0.52
1:A3:181:LYS:HB2	46:54:1577:G:C6	2.44	0.52
5:E3:60:SER:OG	5:E3:61:ARG:N	2.43	0.52
43:s3:38:LYS:NZ	46:54:1971:U:O2	2.43	0.52
46:54:638:G:O2'	46:54:639:U:O4'	2.26	0.52
46:54:2848:G:O2'	46:54:3838:U:O4	2.16	0.52
46:54:4862:G:H2'	46:54:4863:G:C8	2.44	0.52
51:NB:80:GLN:HG2	51:NB:89:THR:HB	1.91	0.52
4:D3:83:LEU:HB3	4:D3:88:VAL:CG2	2.39	0.52
9:I3:55:ASP:HB3	9:I3:164:LYS:HE3	1.91	0.52
42:r3:107:ARG:HH12	46:54:2262:G:H3'	1.75	0.52
5:E3:179:THR:O	5:E3:179:THR:HG23	2.10	0.52
8:H3:63:ASN:OD1	8:H3:66:GLU:HB2	2.10	0.52
15:P3:120:ASN:ND2	48:84:12:G:H21	2.07	0.52
34:i3:42:ASP:OD1	34:i3:43:MET:N	2.43	0.52
45:23:62:C:H2'	45:23:63:G:H8	1.75	0.52
46:54:1991:A:OP1	46:54:1991:A:H4'	2.09	0.52
46:54:4898:G:N2	46:54:4922:C:C2	2.78	0.52
12:M3:36:ALA:HB2	12:M3:52:PHE:CZ	2.45	0.52
12:M3:116:LYS:HE3	14:O3:201:LEU:HD13	1.91	0.52
14:O3:168:TYR:OH	46:54:4768:G:OP1	2.23	0.52
46:54:258:G:C5	46:54:259:C:C4	2.97	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:1405:C:H2'	46:54:1406:G:C8	2.44	0.52
46:54:1477:C:H2'	46:54:1478:C:C6	2.44	0.52
46:54:2007:G:O2'	46:54:2012:A:N6	2.34	0.52
46:54:2502:A:H4'	46:54:2503:G:OP1	2.08	0.52
46:54:3656:A:O2'	46:54:3747:A:O2'	2.28	0.52
52:TT:209:HIS:O	52:TT:213:SER:N	2.41	0.52
15:P3:122:ALA:HB3	15:P3:143:PRO:HG2	1.90	0.52
17:R3:8:LYS:NZ	46:54:2387:G:OP1	2.38	0.52
26:a3:36:GLY:HA3	26:a3:40:HIS:CE1	2.45	0.52
46:54:1093:C:H2'	46:54:1094:G:H8	1.75	0.52
46:54:4739:C:H2'	46:54:4740:G:H8	1.75	0.52
1:A3:142:GLU:O	1:A3:143:THR:OG1	2.24	0.52
7:G3:197:THR:O	7:G3:201:GLU:HG3	2.10	0.52
14:O3:121:PRO:HD3	18:S3:168:THR:HG22	1.92	0.52
16:Q3:168:ARG:HH12	46:54:86:U:P	2.32	0.52
20:U3:61:VAL:HG12	20:U3:74:SER:HB2	1.92	0.52
46:54:138:G:H2'	46:54:139:G:H8	1.75	0.52
46:54:179:G:C2	46:54:258:G:C6	2.98	0.52
46:54:1734:G:N2	46:54:1735:U:O4	2.29	0.52
46:54:2440:U:HO2'	46:54:2441:C:P	2.31	0.52
46:54:4944:C:H4'	46:54:4944:C:OP1	2.09	0.52
52:TT:218:LYS:O	52:TT:222:GLN:N	2.41	0.52
52:TT:350:LEU:HD23	52:TT:387:LEU:HD13	1.91	0.52
52:TT:358:TYR:HE2	52:TT:436:PRO:HB2	1.75	0.52
6:F3:142:GLY:HA3	6:F3:239:ILE:HB	1.92	0.52
16:Q3:124:ASP:OD1	16:Q3:125:GLN:N	2.43	0.52
24:Y3:1:MET:HG3	24:Y3:2:LYS:H	1.75	0.52
30:e3:43:ASN:O	30:e3:47:ARG:HG3	2.10	0.52
52:TT:196:ARG:NH2	53:1:3:GLU:HB2	2.25	0.52
52:TT:235:GLY:HA2	52:TT:238:TYR:HB2	1.92	0.52
4:D3:222:GLN:O	47:74:48:G:O2'	2.23	0.51
6:F3:74:ALA:HB2	19:T3:140:PHE:CE2	2.44	0.51
16:Q3:12:LYS:HB2	16:Q3:14:ARG:NH1	2.25	0.51
19:T3:89:ILE:HG22	46:54:4300:U:H4'	1.92	0.51
44:t3:87:GLU:N	44:t3:87:GLU:OE2	2.43	0.51
46:54:1094:G:H2'	46:54:1095:A:H8	1.75	0.51
46:54:2467:U:H4'	46:54:2468:U:H5'	1.92	0.51
51:NB:64:MET:HB3	51:NB:72:ILE:HB	1.92	0.51
2:B3:291:TYR:OH	2:B3:315:ASN:ND2	2.42	0.51
12:M3:113:MET:HG3	46:54:4881:U:C4	2.45	0.51
46:54:1477:C:O2'	46:54:1478:C:OP1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:TT:212:ASP:O	52:TT:216:GLN:HG2	2.10	0.51
1:A3:104:VAL:HG21	1:A3:158:ILE:HD11	1.92	0.51
10:J3:15:LEU:HD11	10:J3:157:ILE:HG12	1.92	0.51
10:J3:33:LEU:O	10:J3:37:ALA:N	2.44	0.51
11:L3:106:SER:OG	11:L3:107:THR:N	2.42	0.51
14:O3:127:VAL:HG12	14:O3:128:ARG:HD2	1.92	0.51
42:r3:28:GLU:HB2	42:r3:31:ASN:HB2	1.91	0.51
43:s3:139:GLN:HE22	43:s3:145:THR:HB	1.74	0.51
43:s3:175:LEU:HD22	43:s3:180:ILE:HG13	1.93	0.51
46:54:691:C:H2'	46:54:692:A:C8	2.45	0.51
46:54:1766:A:H2'	46:54:1767:A:H8	1.74	0.51
3:C3:94:ASN:HA	3:C3:100:ARG:O	2.10	0.51
3:C3:315:LYS:HD2	6:F3:167:ALA:HB1	1.93	0.51
6:F3:154:TYR:OH	6:F3:187:GLU:OE2	2.28	0.51
10:J3:93:GLU:HG2	10:J3:173:ILE:HG12	1.93	0.51
11:L3:110:LEU:O	11:L3:114:VAL:HG23	2.10	0.51
26:a3:77:LYS:O	26:a3:80:THR:OG1	2.27	0.51
31:f3:36:ARG:O	31:f3:39:THR:HG22	2.10	0.51
46:54:2556:G:H1	46:54:2571:C:H42	1.59	0.51
52:TT:59:LYS:O	52:TT:63:GLN:N	2.41	0.51
2:B3:60:VAL:HG11	2:B3:67:VAL:HG23	1.93	0.51
2:B3:117:ARG:HG2	2:B3:180:LEU:HD13	1.93	0.51
5:E3:49:ASN:ND2	46:54:979:C:OP1	2.43	0.51
29:d3:44:ARG:NH1	46:54:2832:A:OP1	2.41	0.51
33:h3:89:ARG:HD2	48:84:36:G:C8	2.46	0.51
40:o3:36:GLN:OE1	40:o3:39:ARG:NH1	2.44	0.51
45:23:62:C:H2'	45:23:63:G:C8	2.45	0.51
46:54:978:G:N2	46:54:1277:G:H1	2.07	0.51
7:G3:190:ARG:HG2	7:G3:199:LEU:HD21	1.93	0.51
11:L3:136:LYS:HZ3	46:54:170:C:H5'	1.76	0.51
39:n3:7:LYS:HA	39:n3:10:MET:HB2	1.92	0.51
43:s3:162:LYS:O	43:s3:165:ASP:HB2	2.11	0.51
46:54:40:G:N2	46:54:4380:A:H62	2.08	0.51
46:54:3690:U:H5'	46:54:3818:U:OP2	2.11	0.51
2:B3:48:GLY:HA3	2:B3:81:THR:HG22	1.93	0.51
12:M3:12:VAL:HB	12:M3:60:PHE:HB2	1.93	0.51
14:O3:61:ARG:NH1	14:O3:66:PRO:HG3	2.26	0.51
19:T3:28:ALA:HA	19:T3:31:MET:HG2	1.92	0.51
32:g3:6:THR:HG22	46:54:2400:G:H21	1.74	0.51
32:g3:94:ALA:O	32:g3:98:GLU:HG3	2.10	0.51
46:54:643:C:H2'	46:54:644:G:H8	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:1967:A:H61	46:54:2020:U:H3	1.56	0.51
46:54:3823:G:H8	46:54:3823:G:O5'	1.94	0.51
1:A3:230:PRO:HB3	46:54:3928:A:N1	2.25	0.51
19:T3:40:VAL:HG13	19:T3:96:ILE:HG23	1.93	0.51
19:T3:81:LYS:O	27:b3:16:TRP:CE2	2.63	0.51
46:54:4067:U:H2'	46:54:4068:U:H6	1.75	0.51
2:B3:252:ALA:HB1	46:54:4524:G:C2	2.46	0.51
46:54:1094:G:H2'	46:54:1095:A:C8	2.46	0.51
46:54:1238:A:HO2'	46:54:1239:C:P	2.34	0.51
46:54:1437:C:O2'	46:54:1438:U:O4'	2.29	0.51
52:TT:326:LEU:HD23	52:TT:331:GLY:HA2	1.93	0.51
4:D3:67:ALA:HA	4:D3:72:ASP:HB3	1.93	0.51
13:N3:89:VAL:CG2	46:54:3928:A:H5'	2.41	0.51
29:d3:90:ARG:HD3	29:d3:102:LEU:HD13	1.93	0.51
6:F3:72:ARG:HD3	46:54:730:G:C5	2.47	0.50
7:G3:215:ASP:HB2	7:G3:216:PRO:HD3	1.92	0.50
27:b3:36:ASP:N	27:b3:36:ASP:OD1	2.41	0.50
48:84:102:G:OP2	48:84:104:A:O2'	2.29	0.50
52:TT:210:VAL:HA	52:TT:213:SER:HB2	1.92	0.50
1:A3:124:GLY:O	1:A3:128:ARG:NH1	2.44	0.50
13:N3:43:THR:OG1	13:N3:131:GLU:OE2	2.26	0.50
46:54:3621:A:N7	46:54:4642:U:O2'	2.40	0.50
46:54:4389:C:H2'	46:54:4390:A:C8	2.46	0.50
46:54:4926:C:H3'	46:54:4927:G:H5''	1.93	0.50
50:NA:97:ARG:HE	51:NB:109:GLN:CD	2.18	0.50
2:B3:10:ARG:NH1	2:B3:265:SER:O	2.44	0.50
3:C3:76:ILE:HD12	3:C3:77:PRO:HD2	1.92	0.50
4:D3:215:ASP:OD1	4:D3:215:ASP:N	2.44	0.50
7:G3:233:PRO:HA	7:G3:280:ASN:OD1	2.12	0.50
10:J3:146:ARG:HG2	10:J3:147:ARG:HG3	1.94	0.50
22:W3:58:LYS:HE3	22:W3:59:HIS:HE1	1.75	0.50
23:X3:78:LYS:HE3	23:X3:101:ASP:HA	1.94	0.50
46:54:218:A:O2'	46:54:221:C:OP1	2.28	0.50
46:54:389:A:N7	46:54:402:A:H2	2.10	0.50
46:54:1565:A:C5	46:54:1566:C:H1'	2.45	0.50
46:54:4773:C:H2'	46:54:4774:C:H6	1.76	0.50
52:TT:409:SER:OG	52:TT:410:ASP:N	2.36	0.50
7:G3:82:ASN:OD1	7:G3:83:PRO:HD2	2.10	0.50
7:G3:307:GLU:O	7:G3:311:ALA:N	2.43	0.50
14:O3:16:LEU:HD21	14:O3:83:THR:HG21	1.94	0.50
17:R3:4:LEU:HD11	17:R3:29:THR:HG23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:S3:29:ARG:NH2	19:T3:150:LEU:HB2	2.27	0.50
18:S3:71:SER:O	18:S3:71:SER:OG	2.28	0.50
42:r3:101:LYS:HE3	46:54:2094:C:H5	1.75	0.50
46:54:92:C:OP2	46:54:4341:C:O2'	2.22	0.50
46:54:134:G:H4'	46:54:135:G:O5'	2.10	0.50
46:54:1168:G:H1	46:54:1193:C:N4	2.06	0.50
46:54:1203:G:C6	46:54:1204:C:C4	2.99	0.50
46:54:1971:U:N3	46:54:2000:G:N3	2.44	0.50
8:H3:95:VAL:HG22	38:m3:56:LEU:HB3	1.94	0.50
15:P3:111:SER:O	15:P3:111:SER:OG	2.26	0.50
46:54:1093:C:H2'	46:54:1094:G:C8	2.46	0.50
46:54:1478:C:H2'	46:54:1479:G:C8	2.46	0.50
46:54:2488:C:H3'	46:54:2490:U:C4	2.47	0.50
4:D3:64:ILE:HG13	4:D3:105:LEU:HD21	1.94	0.50
5:E3:94:THR:OG1	5:E3:95:VAL:N	2.44	0.50
11:L3:58:ILE:N	11:L3:113:ASN:HD21	2.05	0.50
13:N3:45:PRO:O	13:N3:49:ARG:HG3	2.12	0.50
30:e3:29:VAL:HB	46:54:1332:C:H5''	1.94	0.50
36:k3:17:ARG:NH2	46:54:2772:C:O2'	2.45	0.50
37:l3:35:ILE:HD11	48:84:53:G:N2	2.26	0.50
42:r3:32:LEU:O	42:r3:33:LYS:HB2	2.11	0.50
42:r3:114:ALA:O	42:r3:118:LEU:HD23	2.12	0.50
46:54:499:G:H2'	46:54:500:G:C8	2.45	0.50
46:54:679:C:H2'	46:54:680:G:H8	1.77	0.50
46:54:1404:G:N1	46:54:1413:C:N3	2.53	0.50
46:54:1984:A:N6	46:54:2010:A:O2'	2.45	0.50
46:54:3690:U:H2'	46:54:3691:G:O4'	2.12	0.50
2:B3:41:VAL:HA	2:B3:187:GLY:HA3	1.94	0.50
14:O3:85:ARG:HG3	14:O3:99:LEU:HD11	1.93	0.50
17:R3:88:ARG:O	46:54:2725:A:N6	2.45	0.50
20:U3:82:TYR:CZ	20:U3:86:LEU:HD11	2.46	0.50
25:Z3:91:LEU:HD12	25:Z3:96:VAL:HG21	1.94	0.50
41:p3:52:VAL:HG13	46:54:2739:C:H5'	1.93	0.50
46:54:1:C:H2'	46:54:2:G:O4'	2.11	0.50
46:54:757:G:O2'	46:54:758:G:H8	1.94	0.50
46:54:1456:C:H5'	46:54:1457:G:OP2	2.11	0.50
16:Q3:175:GLU:HA	26:a3:51:GLY:O	2.12	0.50
26:a3:75:LEU:HG	26:a3:113:GLY:HA2	1.93	0.50
30:e3:38:PRO:HG2	30:e3:46:ARG:HB3	1.94	0.50
33:h3:33:VAL:O	33:h3:37:THR:HG23	2.12	0.50
45:23:35:A:H2'	45:23:36:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:1173:G:H2'	46:54:1174:G:C8	2.47	0.50
46:54:1440:U:O2'	46:54:1441:C:OP1	2.28	0.50
50:NA:85:LEU:HD12	50:NA:112:TYR:HB3	1.94	0.50
52:TT:69:VAL:HG11	52:TT:122:LEU:HG	1.94	0.50
2:B3:15:GLY:O	46:54:4587:G:N2	2.43	0.50
20:U3:96:LEU:HB3	20:U3:100:LEU:HD12	1.94	0.50
37:I3:42:ARG:HH22	46:54:2408:U:P	2.35	0.50
43:s3:28:PHE:HZ	43:s3:95:LEU:HA	1.77	0.50
46:54:1174:G:O2'	46:54:1175:A:OP1	2.28	0.50
46:54:1400:G:H2'	46:54:1401:C:C6	2.47	0.50
46:54:2895:A:H2'	46:54:2896:G:O4'	2.12	0.50
52:TT:327:LEU:HD23	52:TT:413:CYS:SG	2.52	0.50
1:A3:225:ILE:HD12	1:A3:233:ARG:NH1	2.26	0.49
7:G3:139:VAL:HG22	7:G3:140:LEU:H	1.77	0.49
28:c3:30:GLY:O	28:c3:34:SER:OG	2.28	0.49
43:s3:106:LYS:NZ	43:s3:184:SER:O	2.44	0.49
46:54:2492:C:H2'	46:54:2493:G:H8	1.77	0.49
46:54:5050:C:H2'	46:54:5051:C:C6	2.47	0.49
1:A3:233:ARG:HB2	46:54:4184:G:H5'	1.95	0.49
18:S3:29:ARG:HB2	19:T3:148:PRO:HB2	1.94	0.49
21:V3:87:SER:HA	21:V3:97:TYR:HB3	1.94	0.49
46:54:705:G:H1	46:54:1292:C:H42	1.60	0.49
46:54:738:C:OP1	46:54:739:G:H4'	2.13	0.49
46:54:2380:G:H22	46:54:2424:G:H5'	1.76	0.49
46:54:2638:G:H22	46:54:2697:A:H61	1.60	0.49
46:54:3764:U:H2'	46:54:3765:G:O4'	2.12	0.49
47:74:83:A:O2'	47:74:85:G:OP1	2.27	0.49
52:TT:422:VAL:HG12	52:TT:425:TRP:HB2	1.95	0.49
3:C3:94:ASN:OD1	3:C3:94:ASN:N	2.41	0.49
25:Z3:103:ASP:HB3	25:Z3:106:LEU:HB2	1.94	0.49
46:54:4096:C:H2'	46:54:4097:G:H8	1.73	0.49
46:54:5007:A:N7	46:54:5042:A:O2'	2.36	0.49
52:TT:396:THR:OG1	52:TT:398:GLU:OE1	2.24	0.49
3:C3:323:ARG:HD2	46:54:976:G:H21	1.76	0.49
17:R3:7:GLN:HE21	17:R3:35:ALA:HB3	1.76	0.49
19:T3:80:VAL:O	19:T3:82:GLY:N	2.44	0.49
24:Y3:106:ILE:HG21	24:Y3:109:LEU:HD23	1.93	0.49
25:Z3:74:VAL:HG23	25:Z3:101:PHE:CE2	2.47	0.49
31:f3:14:TYR:OH	31:f3:92:LEU:O	2.22	0.49
37:I3:48:LYS:NZ	46:54:2406:G:O2'	2.45	0.49
43:s3:162:LYS:HG2	43:s3:163:THR:H	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:4114:C:H2'	46:54:4115:G:H8	1.77	0.49
52:TT:73:TYR:CE1	52:TT:129:VAL:HG22	2.47	0.49
52:TT:163:TRP:O	53:1:1:MET:HG3	2.12	0.49
8:H3:23:ARG:HH21	8:H3:42:ASN:H	1.61	0.49
12:M3:68:ALA:HB1	12:M3:72:TYR:HB2	1.94	0.49
15:P3:24:VAL:HG12	15:P3:25:HIS:H	1.77	0.49
21:V3:80:VAL:HG23	21:V3:106:VAL:HG21	1.94	0.49
25:Z3:53:VAL:HG21	25:Z3:62:ILE:HG23	1.94	0.49
30:e3:76:LYS:O	42:r3:23:GLN:NE2	2.26	0.49
31:f3:28:LEU:HG	31:f3:101:ILE:HD11	1.93	0.49
34:i3:93:VAL:O	34:i3:97:MET:HG3	2.12	0.49
40:o3:20:PRO:O	40:o3:73:VAL:HG22	2.12	0.49
46:54:190:G:H2'	46:54:191:G:C8	2.47	0.49
46:54:1846:G:H2'	46:54:1847:C:C6	2.48	0.49
46:54:4921:C:H4'	46:54:4922:C:OP1	2.12	0.49
46:54:5050:C:H2'	46:54:5051:C:H6	1.78	0.49
52:TT:205:GLU:HG3	52:TT:209:HIS:CD2	2.47	0.49
3:C3:327:LYS:NZ	46:54:975:C:O2	2.27	0.49
7:G3:258:THR:OG1	7:G3:259:GLN:N	2.46	0.49
10:J3:40:LEU:HD23	10:J3:72:CYS:HB2	1.94	0.49
46:54:2492:C:H2'	46:54:2493:G:C8	2.48	0.49
46:54:2522:G:N2	46:54:2534:C:O2	2.45	0.49
46:54:3811:G:O2'	46:54:3814:U:OP2	2.31	0.49
3:C3:322:LEU:HD21	5:E3:56:ILE:HG13	1.95	0.49
3:C3:338:ASN:C	3:C3:340:ILE:H	2.20	0.49
4:D3:208:MET:HE2	4:D3:233:PRO:HG3	1.94	0.49
15:P3:25:HIS:HE1	46:54:3859:G:OP2	1.96	0.49
21:V3:57:VAL:HG11	21:V3:122:ALA:HB3	1.95	0.49
22:W3:20:ARG:NH1	22:W3:30:GLN:HE21	2.11	0.49
26:a3:134:GLU:O	26:a3:138:LYS:HG2	2.11	0.49
46:54:1556:C:O2'	46:54:2669:C:OP1	2.24	0.49
46:54:1976:G:H22	46:54:1991:A:H8	1.61	0.49
46:54:2594:C:H2'	46:54:2595:C:H6	1.78	0.49
3:C3:6:PRO:HB3	46:54:668:C:C4'	2.43	0.49
12:M3:58:THR:HG22	12:M3:91:TRP:CZ3	2.48	0.49
17:R3:92:LYS:NZ	46:54:1573:G:OP1	2.30	0.49
42:r3:97:ILE:HG21	42:r3:107:ARG:HB3	1.94	0.49
46:54:424:U:H2'	46:54:425:U:H6	1.78	0.49
46:54:1974:U:O3'	46:54:1975:G:H3'	2.12	0.49
46:54:3695:U:H2'	46:54:3696:C:O4'	2.13	0.49
46:54:4089:G:H2'	46:54:4090:G:C8	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:4291:G:HO2'	46:54:4328:G:HO2'	1.61	0.49
46:54:4661:G:N2	46:54:5004:C:O3'	2.46	0.49
2:B3:242:ARG:NH2	46:54:2856:C:O2	2.45	0.49
3:C3:159:GLU:HG2	3:C3:213:GLU:O	2.13	0.49
24:Y3:80:ILE:HG23	24:Y3:101:PRO:HG3	1.95	0.49
31:f3:37:ASP:OD1	31:f3:37:ASP:N	2.46	0.49
46:54:518:G:H3'	46:54:519:C:C6	2.48	0.49
46:54:2065:G:H2'	46:54:2066:C:O4'	2.12	0.49
52:TT:277:LEU:HD12	52:TT:309:PRO:HB3	1.95	0.49
4:D3:115:MET:SD	46:54:1819:G:O2'	2.70	0.49
8:H3:27:VAL:O	8:H3:33:THR:HA	2.13	0.49
10:J3:33:LEU:HD21	10:J3:68:ILE:O	2.13	0.49
16:Q3:3:VAL:HG23	16:Q3:5:ILE:HG12	1.94	0.49
23:X3:95:THR:HG22	23:X3:139:ARG:HG3	1.95	0.49
43:s3:161:ILE:HG21	43:s3:167:VAL:HG12	1.94	0.49
46:54:388:A:O2'	46:54:402:A:N1	2.44	0.49
46:54:2480:G:H1	46:54:2498:C:H42	1.61	0.49
46:54:3876:A:HO2'	46:54:3877:A:P	2.35	0.49
46:54:5000:G:H2'	46:54:5001:U:O4'	2.12	0.49
52:TT:94:ASP:O	52:TT:98:GLU:HG3	2.13	0.49
52:TT:155:TRP:CD1	52:TT:155:TRP:H	2.31	0.49
3:C3:302:LEU:HD23	16:Q3:39:THR:HG22	1.95	0.48
6:F3:213:SER:OG	6:F3:214:SER:N	2.46	0.48
9:I3:86:HIS:HB3	9:I3:139:ARG:HG2	1.95	0.48
14:O3:16:LEU:HD12	14:O3:138:LEU:HD22	1.94	0.48
16:Q3:53:MET:SD	46:54:1692:C:H5''	2.52	0.48
24:Y3:10:ASP:OD1	24:Y3:11:ARG:N	2.46	0.48
24:Y3:55:VAL:HG22	24:Y3:104:VAL:HG22	1.94	0.48
34:i3:89:GLU:O	34:i3:93:VAL:HG12	2.13	0.48
46:54:179:G:H2'	46:54:180:C:C6	2.48	0.48
46:54:1381:U:H5'	46:54:1382:G:OP2	2.13	0.48
46:54:1976:G:H1'	46:54:2002:A:N7	2.27	0.48
46:54:2601:A:N6	46:54:2743:A:H3'	2.28	0.48
46:54:4244:A:H2'	46:54:4245:G:O4'	2.13	0.48
1:A3:147:ARG:NH2	1:A3:155:LYS:HD2	2.28	0.48
17:R3:43:LYS:HG2	17:R3:47:ASP:OD2	2.13	0.48
24:Y3:89:LYS:HD3	24:Y3:93:THR:HG23	1.95	0.48
25:Z3:26:VAL:HG22	25:Z3:42:LEU:O	2.12	0.48
46:54:1856:C:O2'	46:54:1892:A:N1	2.39	0.48
46:54:3751:G:H21	46:54:3775:A:H8	1.58	0.48
50:NA:126:ALA:HB3	51:NB:86:ASN:HD21	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:TT:193:MET:HE2	53:1:2:ARG:HA	1.94	0.48
7:G3:215:ASP:HB2	7:G3:216:PRO:CD	2.44	0.48
19:T3:124:THR:OG1	19:T3:125:TRP:N	2.47	0.48
26:a3:71:PRO:HG2	26:a3:108:TYR:HA	1.95	0.48
46:54:100:C:H2'	46:54:101:A:O4'	2.12	0.48
46:54:408:A:H4'	46:54:409:G:H3'	1.93	0.48
46:54:1278:C:H2'	46:54:1279:A:O4'	2.13	0.48
46:54:1591:U:N3	46:54:4555:U:OP1	2.43	0.48
46:54:1810:G:H1	46:54:1828:C:H42	1.60	0.48
46:54:2845:A:H61	46:54:3843:C:H42	1.61	0.48
52:TT:284:LYS:HD3	52:TT:296:PHE:HE2	1.78	0.48
6:F3:154:TYR:CE1	6:F3:186:MET:HG2	2.48	0.48
9:I3:140:THR:OG1	9:I3:141:LYS:N	2.47	0.48
18:S3:11:LYS:HE3	18:S3:29:ARG:HD3	1.95	0.48
37:I3:25:GLN:NE2	37:I3:28:TRP:HE1	2.11	0.48
46:54:1442:C:H2'	46:54:1443:A:C8	2.48	0.48
48:84:69:U:C4	48:84:70:G:C6	3.01	0.48
1:A3:28:ARG:HE	1:A3:123:ARG:HH11	1.60	0.48
1:A3:79:ALA:O	1:A3:82:ILE:HG12	2.13	0.48
13:N3:148:THR:O	13:N3:151:ILE:HG22	2.14	0.48
17:R3:136:ARG:O	17:R3:140:GLU:HG2	2.12	0.48
24:Y3:24:HIS:CE1	24:Y3:25:ILE:HG13	2.48	0.48
29:d3:85:ARG:NH2	29:d3:118:GLN:O	2.46	0.48
43:s3:42:GLN:HE22	44:t3:121:LEU:HD21	1.78	0.48
46:54:1413:C:H2'	46:54:1414:C:C6	2.48	0.48
46:54:2382:A:N1	46:54:2829:U:O2'	2.39	0.48
46:54:2588:C:OP1	46:54:2768:C:O2'	2.31	0.48
46:54:2764:A:H2'	46:54:2765:A:H8	1.78	0.48
2:B3:229:LYS:HG3	2:B3:272:LYS:HD3	1.94	0.48
8:H3:73:ILE:O	8:H3:77:VAL:HG23	2.13	0.48
11:L3:42:ARG:O	11:L3:46:ILE:HG12	2.14	0.48
37:I3:23:ILE:O	37:I3:23:ILE:HG13	2.13	0.48
46:54:385:A:N3	46:54:387:G:H5''	2.29	0.48
46:54:448:G:H3'	46:54:449:C:H4'	1.96	0.48
46:54:1204:C:H2'	46:54:1205:G:H8	1.77	0.48
46:54:1444:G:N2	46:54:2110:G:H1	2.09	0.48
46:54:4776:G:H1'	46:54:4860:G:N2	2.28	0.48
50:NA:92:THR:HG23	50:NA:93:ARG:H	1.78	0.48
51:NB:78:LYS:O	51:NB:78:LYS:HG3	2.13	0.48
52:TT:278:ASN:HB2	53:1:4:ILE:HD12	1.95	0.48
1:A3:225:ILE:HD11	1:A3:233:ARG:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B3:375:GLY:O	2:B3:377:GLY:N	2.46	0.48
3:C3:294:LYS:HE2	3:C3:294:LYS:HB3	1.68	0.48
5:E3:245:ILE:HB	5:E3:250:LYS:HE3	1.95	0.48
19:T3:88:ARG:HH21	27:b3:30:GLU:CD	2.21	0.48
24:Y3:66:GLN:HB3	52:TT:393:SER:HB3	1.96	0.48
35:j3:63:ARG:NH2	48:84:58:G:O6	2.46	0.48
40:o3:81:ARG:HH22	46:54:4293:U:HO2'	1.61	0.48
46:54:481(A):C:H1'	46:54:483:G:O2'	2.13	0.48
46:54:968:C:O2'	46:54:969:C:O5'	2.32	0.48
46:54:2425:U:H5''	46:54:2426:U:H5	1.78	0.48
46:54:4322:G:O2'	46:54:4324:A:N7	2.42	0.48
2:B3:73:VAL:HB	21:V3:93:GLY:HA3	1.96	0.48
3:C3:36:ILE:HD11	46:54:1351:G:H5'	1.96	0.48
13:N3:3:ALA:O	13:N3:7:ILE:HG13	2.13	0.48
29:d3:57:MET:O	29:d3:59:THR:N	2.44	0.48
42:r3:38:PHE:O	42:r3:45:HIS:HE1	1.97	0.48
43:s3:124:PRO:O	43:s3:154:ILE:HD11	2.13	0.48
44:t3:127:GLY:HA2	44:t3:130:LYS:HD2	1.96	0.48
46:54:456:C:H2'	46:54:457:G:C8	2.49	0.48
46:54:1236:C:O2'	46:54:1238:A:OP1	2.32	0.48
46:54:1808:C:H1'	46:54:1831:G:N2	2.28	0.48
46:54:3904:G:N3	53:1:59:TYR:HE1	2.12	0.48
46:54:4596:C:H2'	46:54:4597:U:O4'	2.13	0.48
51:NB:77:PRO:HB2	51:NB:91:THR:O	2.14	0.48
1:A3:9:ARG:HD2	46:54:1628:C:OP2	2.14	0.48
1:A3:30:ARG:HH12	1:A3:33:ASP:CG	2.22	0.48
2:B3:189:THR:O	2:B3:193:LYS:N	2.37	0.48
3:C3:155:GLU:HG3	3:C3:156:ASP:H	1.78	0.48
6:F3:134:ILE:HD11	46:54:1726:U:H5'	1.94	0.48
18:S3:87:ARG:HG3	46:54:2034:G:OP1	2.13	0.48
18:S3:99:ASP:OD1	18:S3:100:LEU:N	2.42	0.48
38:m3:74:TYR:OH	46:54:4425:G:OP1	2.27	0.48
44:t3:96:LYS:NZ	46:54:1979:A:O5'	2.45	0.48
46:54:1073:G:H1	46:54:1238:A:H2	1.60	0.48
46:54:4894:A:H4'	46:54:4896:G:C8	2.48	0.48
1:A3:77:ILE:HD11	1:A3:115:CYS:HB2	1.96	0.48
3:C3:108:TRP:HB2	13:N3:200:LEU:HD13	1.96	0.48
7:G3:146:THR:O	7:G3:150:LYS:N	2.42	0.48
9:I3:51:HIS:CD2	9:I3:168:SER:HB2	2.49	0.48
46:54:1378:C:H4'	46:54:1379:C:H5'	1.96	0.48
46:54:4266:G:H2'	46:54:4266:G:N3	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:TT:183:ARG:HH11	52:TT:223:MET:HB2	1.79	0.48
52:TT:205:GLU:HG3	52:TT:209:HIS:HD2	1.79	0.48
52:TT:287:GLU:HB3	52:TT:443:HIS:HE1	1.79	0.48
2:B3:285:TYR:CD1	2:B3:363:ILE:HG13	2.49	0.47
3:C3:29:LYS:HB2	3:C3:267:TRP:HH2	1.79	0.47
3:C3:285:LEU:N	16:Q3:124:ASP:OD2	2.44	0.47
7:G3:312:LYS:O	7:G3:316:THR:OG1	2.28	0.47
8:H3:50:LYS:HE2	46:54:759:G:H4'	1.96	0.47
9:I3:46:PHE:HB2	9:I3:139:ARG:HH11	1.79	0.47
10:J3:175:LEU:HD23	10:J3:175:LEU:H	1.79	0.47
16:Q3:43:PHE:HE1	16:Q3:138:LEU:HG	1.79	0.47
46:54:140:G:H2'	46:54:141:C:O4'	2.14	0.47
46:54:179:G:H1'	46:54:258:G:H22	1.79	0.47
46:54:4228:G:H4'	46:54:4229:U:OP2	2.14	0.47
46:54:5058:A:H2'	46:54:5059:C:O4'	2.14	0.47
52:TT:319:PHE:CD1	52:TT:320:LEU:HD22	2.47	0.47
3:C3:207:PRO:HB3	3:C3:249:PHE:CD2	2.49	0.47
6:F3:219:MET:SD	6:F3:222:LYS:HB2	2.54	0.47
9:I3:77:VAL:HG23	9:I3:82:LYS:HA	1.97	0.47
13:N3:65:ARG:HD2	13:N3:127:TYR:CD1	2.49	0.47
18:S3:2:LYS:O	18:S3:4:SER:N	2.46	0.47
19:T3:114:GLN:O	19:T3:118:GLU:HG2	2.14	0.47
20:U3:56:LEU:HB3	20:U3:61:VAL:HG23	1.97	0.47
24:Y3:115:ARG:O	24:Y3:119:LEU:HD13	2.14	0.47
29:d3:85:ARG:NH1	29:d3:117:LEU:HD12	2.29	0.47
30:e3:17:THR:HG21	46:54:1301:C:H2'	1.95	0.47
34:i3:58:MET:HG3	34:i3:90:LEU:HD22	1.96	0.47
46:54:966:A:O4'	46:54:968:C:N4	2.47	0.47
46:54:1445:U:H2'	46:54:1446:C:C6	2.49	0.47
51:NB:59:ILE:HG13	51:NB:79:VAL:HB	1.96	0.47
52:TT:341:MET:O	52:TT:389:LYS:HE2	2.14	0.47
2:B3:206:PRO:HG2	2:B3:209:GLN:HG2	1.97	0.47
10:J3:157:ILE:HG22	10:J3:158:SER:H	1.79	0.47
16:Q3:178:ARG:HB2	26:a3:53:PHE:O	2.15	0.47
18:S3:87:ARG:HD3	47:74:87:G:H4'	1.96	0.47
26:a3:44:ASN:ND2	46:54:1683:U:OP1	2.47	0.47
42:r3:26:SER:N	42:r3:34:ALA:O	2.40	0.47
46:54:1300:G:HO2'	46:54:1301:C:N4	2.11	0.47
46:54:2638:G:H1	46:54:2697:A:H61	1.62	0.47
46:54:3600:G:C2	46:54:3601:C:C2	3.02	0.47
46:54:4371:G:HO2'	46:54:4372:U:P	2.36	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:4898:G:N2	46:54:4922:C:N3	2.61	0.47
52:TT:273:PRO:HA	52:TT:302:LEU:HD13	1.96	0.47
4:D3:57:ASN:ND2	47:74:27:G:H5''	2.30	0.47
7:G3:195:THR:O	7:G3:198:THR:HG22	2.14	0.47
12:M3:89:THR:O	12:M3:93:LYS:HG3	2.14	0.47
18:S3:75:VAL:HA	18:S3:100:LEU:HD23	1.97	0.47
24:Y3:126:ARG:NH2	46:54:198:A:OP1	2.47	0.47
26:a3:32:ARG:HD2	46:54:37:U:H4'	1.96	0.47
26:a3:43:ILE:HG23	46:54:4304:A:C2	2.50	0.47
45:23:5:C:H2'	45:23:6:C:C6	2.49	0.47
46:54:207:G:N2	46:54:383:A:C8	2.82	0.47
46:54:2264:C:H2'	46:54:2265:G:O4'	2.14	0.47
48:84:125:C:H4'	48:84:126:C:H2'	1.95	0.47
52:TT:65:LEU:HD23	52:TT:106:MET:HG2	1.96	0.47
2:B3:96:PRO:HG3	46:54:4910:A:C2	2.50	0.47
7:G3:148:LEU:HD13	7:G3:271:LEU:HD13	1.97	0.47
8:H3:41:ILE:HG21	8:H3:73:ILE:HD11	1.96	0.47
17:R3:3:MET:HE1	17:R3:5:ARG:CZ	2.44	0.47
31:f3:33:VAL:HG23	31:f3:38:GLU:HB2	1.95	0.47
46:54:2361:G:O2'	46:54:3859:G:O6	2.33	0.47
46:54:4765:G:O6	46:54:4869:U:H5	1.98	0.47
50:NA:103:LEU:HD22	50:NA:131:LEU:HD11	1.95	0.47
1:A3:40:TYR:HA	1:A3:90:CYS:O	2.14	0.47
4:D3:211:LEU:HA	4:D3:211:LEU:HD23	1.77	0.47
5:E3:133:LYS:N	5:E3:133:LYS:HD2	2.30	0.47
8:H3:5:LEU:HD13	8:H3:60:TRP:CH2	2.50	0.47
9:I3:38:ARG:HD3	9:I3:83:ASP:HB2	1.96	0.47
17:R3:82:LYS:HB3	17:R3:82:LYS:HE3	1.68	0.47
42:r3:107:ARG:NH1	46:54:2262:G:H3'	2.30	0.47
45:23:46:G:H3'	45:23:47:U:H5''	1.96	0.47
46:54:1201:U:H2'	46:54:1202:C:H6	1.80	0.47
46:54:2455:G:H2'	46:54:2456:G:O4'	2.15	0.47
52:TT:62:LEU:HA	52:TT:65:LEU:HD12	1.97	0.47
1:A3:207:VAL:HG11	46:54:1633:G:N1	2.29	0.47
2:B3:71:GLU:OE2	2:B3:71:GLU:N	2.45	0.47
3:C3:80:ARG:HD2	3:C3:80:ARG:HA	1.71	0.47
4:D3:184:ASP:O	4:D3:188:LYS:N	2.48	0.47
5:E3:269:GLN:N	46:54:4931:G:OP1	2.42	0.47
14:O3:194:ASP:HA	14:O3:197:LYS:HB2	1.97	0.47
17:R3:21:LYS:O	17:R3:53:LYS:HE2	2.14	0.47
43:s3:29:ILE:HD12	43:s3:191:GLN:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t3:40:LYS:O	44:t3:44:ASP:N	2.43	0.47
46:54:519:C:H2'	46:54:520:U:C6	2.49	0.47
46:54:976:G:N1	46:54:1279:A:H2	1.99	0.47
46:54:1612:G:H2'	46:54:1612:G:N3	2.29	0.47
46:54:1883:G:O6	46:54:1896:A:H2	1.96	0.47
46:54:2637:U:O2'	46:54:2718:U:O2'	2.24	0.47
46:54:3722:G:H2'	46:54:3723:A:H8	1.78	0.47
46:54:4094:G:H2'	46:54:4095:G:C8	2.50	0.47
46:54:4773:C:N4	46:54:4862:G:O6	2.47	0.47
7:G3:238:LYS:HE2	48:84:153:C:OP1	2.14	0.47
17:R3:59:SER:HA	46:54:2634:C:H5'	1.97	0.47
26:a3:113:GLY:N	26:a3:133:ALA:HB2	2.29	0.47
41:p3:86:LEU:HD23	41:p3:89:LEU:HD13	1.95	0.47
45:23:3:C:H42	45:23:70:A:H61	1.63	0.47
46:54:679:C:H2'	46:54:680:G:C8	2.50	0.47
46:54:1209:U:O2'	46:54:1211:G:H5'	2.15	0.47
46:54:1982:G:H21	46:54:2010:A:P	2.38	0.47
46:54:2089:G:H22	46:54:2099:C:H5	1.63	0.47
52:TT:187:SER:O	52:TT:191:LEU:N	2.46	0.47
52:TT:413:CYS:SG	52:TT:414:TYR:N	2.88	0.47
6:F3:23:ASN:OD1	6:F3:24:PHE:N	2.45	0.47
8:H3:15:ASN:HD21	8:H3:30:PRO:HG2	1.79	0.47
11:L3:140:SER:N	11:L3:143:GLU:OE1	2.47	0.47
14:O3:12:ARG:HB2	14:O3:37:ARG:HD3	1.96	0.47
14:O3:72:HIS:O	14:O3:74:ARG:HD2	2.14	0.47
15:P3:83:TRP:O	46:54:3856:A:H5''	2.15	0.47
16:Q3:13:VAL:HG11	46:54:1690:C:C5	2.50	0.47
25:Z3:11:VAL:HG23	25:Z3:82:PRO:HA	1.97	0.47
37:l3:41:ARG:HH12	46:54:2431:A:P	2.37	0.47
43:s3:53:VAL:HG23	43:s3:89:VAL:HG22	1.96	0.47
45:23:40:C:H2'	45:23:41:G:C8	2.50	0.47
46:54:1193:C:H2'	46:54:1194:G:C8	2.49	0.47
46:54:3947:A:N6	46:54:4065:G:O6	2.48	0.47
50:NA:106:ILE:O	50:NA:106:ILE:HG13	2.15	0.47
50:NA:127:LYS:HZ3	50:NA:129:GLU:HB2	1.80	0.47
6:F3:170:ASP:OD1	6:F3:171:ASN:N	2.48	0.47
15:P3:4:TYR:CE1	15:P3:18:ARG:HD2	2.50	0.47
17:R3:26:PRO:O	17:R3:29:THR:OG1	2.32	0.47
27:b3:65:MET:O	27:b3:68:ARG:HB2	2.15	0.47
28:c3:44:LYS:HD2	28:c3:99:PRO:HD3	1.96	0.47
43:s3:160:LEU:HG	43:s3:161:ILE:HG12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:2093:G:N2	46:54:2262:G:H1	2.12	0.47
50:NA:121:ILE:HD12	51:NB:89:THR:HG23	1.95	0.47
52:TT:127:LEU:HB2	52:TT:137:ALA:HB2	1.97	0.47
53:1:43:GLN:OE1	53:1:43:GLN:N	2.47	0.47
9:I3:35:ASP:OD1	9:I3:39:LYS:HD2	2.16	0.46
24:Y3:51:LYS:HE3	24:Y3:71:VAL:O	2.15	0.46
24:Y3:103:LYS:HE3	46:54:231:U:O2'	2.15	0.46
46:54:971(A):G:H4'	46:54:972:C:H5'	1.96	0.46
46:54:1890:G:N2	46:54:1939:A:H61	2.13	0.46
46:54:2503:G:N2	46:54:4084:G:C8	2.83	0.46
52:TT:338:LEU:HA	52:TT:338:LEU:HD23	1.72	0.46
52:TT:377:GLN:HG3	52:TT:381:ASN:HD22	1.80	0.46
3:C3:89:GLN:HG2	46:54:2353:U:H5''	1.98	0.46
17:R3:96:MET:HG2	46:54:2667:C:O4'	2.15	0.46
29:d3:38:PHE:C	29:d3:40:LYS:H	2.23	0.46
30:e3:23:HIS:HA	30:e3:53:ILE:HD12	1.97	0.46
46:54:499:G:H1	46:54:656:C:H42	1.63	0.46
46:54:4115:G:O2'	46:54:4116:C:N3	2.49	0.46
46:54:4898:G:H1	46:54:4922:C:N4	2.14	0.46
48:84:91:A:H2'	48:84:92:U:O4'	2.15	0.46
52:TT:197:GLN:HE21	53:1:3:GLU:HB3	1.81	0.46
3:C3:323:ARG:CD	46:54:976:G:H21	2.28	0.46
5:E3:131:HIS:HE1	46:54:1282:G:OP2	1.98	0.46
11:L3:121:ARG:HA	11:L3:121:ARG:HD2	1.71	0.46
13:N3:157:LYS:O	13:N3:162:ARG:NH1	2.48	0.46
19:T3:137:GLU:OE1	19:T3:137:GLU:N	2.44	0.46
36:k3:33:LYS:NZ	46:54:2695:A:OP2	2.47	0.46
43:s3:143:ILE:HG23	43:s3:158:VAL:HG21	1.96	0.46
46:54:1933:G:O2'	46:54:2058:G:O2'	2.31	0.46
46:54:2483:G:N2	46:54:2495:U:O2	2.26	0.46
46:54:4291:G:N3	46:54:4291:G:H5''	2.30	0.46
46:54:4518:A:H8	46:54:4518:A:OP2	1.99	0.46
46:54:4568:A:O2'	46:54:4981:G:N7	2.47	0.46
50:NA:95:THR:HG22	50:NA:105:VAL:HG13	1.96	0.46
51:NB:64:MET:N	51:NB:72:ILE:O	2.47	0.46
2:B3:18:PRO:O	2:B3:20:LYS:HG2	2.14	0.46
2:B3:85:VAL:HG22	2:B3:204:GLN:HG2	1.97	0.46
6:F3:23:ASN:CG	6:F3:24:PHE:H	2.23	0.46
10:J3:78:LYS:O	10:J3:82:ILE:HG12	2.16	0.46
16:Q3:13:VAL:O	16:Q3:13:VAL:HG12	2.15	0.46
46:54:40:G:H21	46:54:4380:A:H62	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:82:U:H2'	46:54:83:C:O4'	2.16	0.46
48:84:122:G:H21	48:84:128:C:H5	1.59	0.46
52:TT:163:TRP:CE3	52:TT:194:VAL:HG12	2.50	0.46
52:TT:283:HIS:HB3	52:TT:288:SER:HB2	1.96	0.46
9:I3:115:MET:O	9:I3:115:MET:HG3	2.15	0.46
10:J3:112:HIS:CE1	10:J3:125:ILE:HA	2.51	0.46
13:N3:138:PHE:CZ	33:h3:93:ARG:HG2	2.51	0.46
17:R3:43:LYS:HD2	46:54:2709:C:OP2	2.15	0.46
27:b3:67:ALA:O	27:b3:71:ALA:N	2.49	0.46
32:g3:81:SER:O	32:g3:81:SER:OG	2.33	0.46
46:54:260:C:N4	46:54:261:G:O6	2.48	0.46
46:54:366:A:H2'	46:54:367:C:O4'	2.15	0.46
46:54:2503:G:H1'	46:54:4084:G:C2	2.50	0.46
46:54:4303:C:O2'	46:54:4304:A:H2'	2.14	0.46
51:NB:55:ASN:HA	51:NB:80:GLN:HB3	1.98	0.46
52:TT:93:GLN:O	52:TT:97:LYS:N	2.44	0.46
52:TT:210:VAL:O	52:TT:214:VAL:HG13	2.16	0.46
1:A3:14:SER:HA	1:A3:17:ARG:NH2	2.25	0.46
3:C3:306:ARG:N	46:54:2087:C:OP1	2.42	0.46
13:N3:47:LYS:O	13:N3:51:LEU:HG	2.15	0.46
14:O3:116:LYS:N	46:54:4757:C:OP2	2.41	0.46
25:Z3:41:ALA:HB2	25:Z3:77:TYR:CE1	2.47	0.46
30:e3:103:VAL:O	30:e3:108:ARG:NH1	2.43	0.46
35:j3:50:SER:O	35:j3:50:SER:OG	2.24	0.46
42:r3:32:LEU:HD21	42:r3:106:LEU:HD12	1.97	0.46
46:54:182:G:H22	46:54:256:G:H1'	1.80	0.46
48:84:33:G:H5''	48:84:34:U:OP1	2.16	0.46
48:84:140:C:H2'	48:84:141:C:C6	2.51	0.46
52:TT:324:THR:HA	52:TT:327:LEU:HD12	1.97	0.46
8:H3:59:LYS:HE2	8:H3:66:GLU:HB3	1.97	0.46
13:N3:68:ARG:HB3	46:54:302:C:OP1	2.14	0.46
16:Q3:155:ALA:HB1	26:a3:47:LYS:O	2.15	0.46
23:X3:156:ILE:HD12	23:X3:156:ILE:HA	1.81	0.46
30:e3:22:ARG:HB2	30:e3:34:ASN:O	2.15	0.46
34:i3:29:ARG:HH22	34:i3:34:THR:HG22	1.81	0.46
38:m3:87:LYS:HD3	38:m3:91:HIS:NE2	2.30	0.46
39:n3:1:MET:SD	39:n3:9:ARG:NH2	2.89	0.46
46:54:46:U:OP2	46:54:47:A:O2'	2.27	0.46
46:54:478:G:H2'	46:54:479:G:H8	1.79	0.46
46:54:1818:G:HO2'	46:54:1819:G:P	2.36	0.46
46:54:2523:G:H2'	46:54:2524:U:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:2553:A:O2'	46:54:2554:U:OP2	2.31	0.46
48:84:85:U:H5''	48:84:86:U:H2'	1.98	0.46
52:TT:101:LYS:O	52:TT:105:GLN:HB2	2.16	0.46
13:N3:51:LEU:HB3	13:N3:117:ASN:HD22	1.81	0.46
19:T3:78:LYS:HD2	19:T3:87:LYS:HD3	1.97	0.46
30:e3:76:LYS:NZ	30:e3:98:GLU:OE1	2.49	0.46
32:g3:22:LEU:HD12	32:g3:30:ILE:CG2	2.46	0.46
36:k3:50:LYS:N	36:k3:50:LYS:HD2	2.30	0.46
44:t3:123:ARG:HG3	44:t3:124:GLU:H	1.80	0.46
52:TT:163:TRP:CZ3	52:TT:194:VAL:HG12	2.51	0.46
6:F3:58:LYS:O	6:F3:62:GLN:HG3	2.16	0.46
6:F3:133:ARG:NH1	47:74:97:G:O5'	2.49	0.46
7:G3:216:PRO:HG2	7:G3:219:LEU:HD13	1.98	0.46
17:R3:125:LEU:O	17:R3:129:GLY:N	2.43	0.46
18:S3:13:VAL:HG23	18:S3:62:VAL:HB	1.96	0.46
18:S3:111:ARG:NH1	46:54:2062:C:O2'	2.49	0.46
19:T3:72:VAL:HG13	19:T3:93:ILE:HD11	1.98	0.46
32:g3:16:ALA:O	32:g3:19:LYS:HG2	2.15	0.46
35:j3:50:SER:OG	35:j3:53:ALA:HB3	2.16	0.46
46:54:745:G:O6	46:54:746:A:N6	2.48	0.46
46:54:1204:C:H2'	46:54:1205:G:C8	2.51	0.46
46:54:2380:G:N1	46:54:2425:U:OP1	2.46	0.46
46:54:2594:C:H2'	46:54:2595:C:C6	2.51	0.46
46:54:3787:G:H1'	46:54:3789:C:N4	2.31	0.46
46:54:4524:G:OP2	46:54:4524:G:H4'	2.15	0.46
53:1:1:MET:O	53:1:2:ARG:HG2	2.15	0.46
2:B3:195:ASP:O	2:B3:199:GLU:HG2	2.16	0.46
6:F3:147:LYS:O	6:F3:151:GLU:HG2	2.16	0.46
23:X3:63:LYS:HB3	23:X3:63:LYS:HE2	1.71	0.46
26:a3:28:HIS:ND1	26:a3:32:ARG:HG2	2.31	0.46
30:e3:109:LYS:HB3	30:e3:109:LYS:HE2	1.51	0.46
38:m3:76:ARG:NE	46:54:4473:A:OP1	2.48	0.46
41:p3:16:THR:HG21	46:54:2877:G:O2'	2.16	0.46
41:p3:49:ARG:HB2	41:p3:55:TRP:CZ3	2.51	0.46
43:s3:88:PHE:HB3	43:s3:90:PHE:HE1	1.81	0.46
43:s3:127:ASN:HD21	43:s3:151:THR:HG21	1.80	0.46
46:54:386:A:H2'	46:54:386:A:N3	2.32	0.46
48:84:125:C:H4'	48:84:126:C:C2'	2.46	0.46
50:NA:110:ASP:O	50:NA:123:PHE:N	2.43	0.46
2:B3:223:THR:O	2:B3:274:TYR:HA	2.15	0.45
3:C3:173:LYS:HD3	3:C3:173:LYS:HA	1.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C3:181:LYS:HZ1	46:54:219:G:H1	1.62	0.45
17:R3:86:ASN:ND2	17:R3:91:GLU:H	2.13	0.45
23:X3:59:LYS:HE2	23:X3:59:LYS:HB3	1.74	0.45
33:h3:52:LYS:NZ	48:84:63:U:HO2'	2.14	0.45
33:h3:96:ASN:HD21	46:54:136:C:H5'	1.81	0.45
41:p3:23:ARG:NH1	46:54:2875:C:OP1	2.37	0.45
41:p3:50:ARG:HH21	41:p3:56:HIS:CD2	2.34	0.45
42:r3:99:LYS:NZ	46:54:2260:C:O2	2.42	0.45
46:54:416:U:H2'	46:54:417:G:H5'	1.98	0.45
52:TT:217:ALA:O	52:TT:221:VAL:HG23	2.15	0.45
6:F3:72:ARG:HD3	46:54:730:G:C6	2.51	0.45
8:H3:126:VAL:HG11	8:H3:161:ILE:HG22	1.97	0.45
13:N3:36:LEU:HD12	13:N3:64:ILE:HD12	1.98	0.45
19:T3:48:VAL:HG11	19:T3:94:GLU:HB2	1.97	0.45
39:n3:23:ARG:NH1	46:54:3782:C:OP2	2.49	0.45
40:o3:62:THR:OG1	40:o3:63:THR:N	2.49	0.45
46:54:12:A:H5'	46:54:13:U:OP2	2.16	0.45
46:54:642:G:N1	46:54:643:C:O2	2.50	0.45
46:54:1440:U:H2'	46:54:1441:C:C6	2.51	0.45
46:54:1990:A:C2	46:54:1991:A:H1'	2.51	0.45
46:54:3773:U:N3	46:54:3775:A:H5''	2.30	0.45
46:54:4537:C:H2'	46:54:4538:G:C8	2.52	0.45
52:TT:183:ARG:HE	52:TT:188:LEU:HD11	1.81	0.45
52:TT:196:ARG:CZ	53:1:3:GLU:HB2	2.45	0.45
52:TT:359:GLN:HB2	52:TT:363:GLY:HA2	1.98	0.45
11:L3:64:VAL:HA	11:L3:67:HIS:HD2	1.79	0.45
16:Q3:164:LYS:HG3	46:54:1497:A:H1'	1.98	0.45
18:S3:17:LEU:HD23	18:S3:17:LEU:HA	1.84	0.45
18:S3:135:SER:O	18:S3:135:SER:OG	2.30	0.45
45:23:66:C:H2'	45:23:67:G:O4'	2.16	0.45
46:54:106:A:O2'	46:54:335:A:N3	2.39	0.45
46:54:966:A:H4'	46:54:967:C:O5'	2.16	0.45
46:54:1194:G:C6	46:54:1195:G:C6	3.05	0.45
52:TT:135:PRO:HA	52:TT:138:GLU:HB3	1.97	0.45
2:B3:67:VAL:HG13	21:V3:14:PHE:HE2	1.80	0.45
5:E3:185:ASN:O	5:E3:186:ARG:HB2	2.16	0.45
6:F3:106:LYS:NZ	6:F3:110:LEU:HD21	2.31	0.45
9:I3:171:TRP:HB2	9:I3:178:ALA:HA	1.99	0.45
35;j3:12:ARG:O	46:54:2405:G:H5'	2.16	0.45
42:r3:14:SER:OG	42:r3:15:SER:N	2.49	0.45
46:54:4633:G:O3'	46:54:4634:U:H3'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:4736:C:H2'	46:54:4737:G:C8	2.51	0.45
46:54:5002:U:H2'	46:54:5003:U:C6	2.51	0.45
52:TT:65:LEU:HB3	52:TT:106:MET:HE3	1.98	0.45
5:E3:250:LYS:HG2	46:54:4938:A:N6	2.32	0.45
8:H3:92:MET:SD	8:H3:161:ILE:HD11	2.56	0.45
12:M3:44:ARG:HB3	46:54:935:A:H1'	1.98	0.45
16:Q3:55:ARG:HH11	46:54:1352:C:N4	2.13	0.45
21:V3:48:ARG:HD3	21:V3:49:LEU:N	2.32	0.45
24:Y3:45:ARG:NH2	46:54:238:C:OP2	2.50	0.45
25:Z3:73:LYS:NZ	46:54:2580:U:H5''	2.32	0.45
42:r3:90:LEU:O	42:r3:94:ARG:NH1	2.50	0.45
43:s3:81:HIS:CE1	43:s3:198:ILE:HG21	2.51	0.45
46:54:1233:G:O2'	46:54:1234:G:OP2	2.31	0.45
46:54:1329:G:H3'	46:54:1329:G:C8	2.52	0.45
46:54:1370:G:H4'	46:54:1371:A:O5'	2.16	0.45
46:54:1759:G:N1	46:54:1774:C:O2	2.50	0.45
46:54:4638:U:OP1	46:54:5044:A:O2'	2.33	0.45
46:54:4925:U:H1'	46:54:4926:C:OP2	2.16	0.45
2:B3:219:VAL:HG11	2:B3:337:VAL:HB	1.98	0.45
4:D3:69:ILE:HD11	19:T3:32:ARG:NH2	2.31	0.45
5:E3:190:ARG:NH2	46:54:4942:C:OP1	2.49	0.45
8:H3:8:GLN:O	8:H3:56:ARG:HG2	2.16	0.45
8:H3:31:ARG:HB2	8:H3:84:VAL:O	2.17	0.45
8:H3:128:MET:HE3	8:H3:146:LEU:HD21	1.97	0.45
14:O3:60:LYS:HZ2	46:54:2046:G:H5'	1.81	0.45
15:P3:137:ASN:ND2	46:54:3861:A:H4'	2.31	0.45
18:S3:112:ASP:OD1	18:S3:116:ARG:NH1	2.49	0.45
32:g3:66:ARG:CD	46:54:2539:C:H5''	2.47	0.45
46:54:1881:C:H5'	46:54:2281:U:H1'	1.99	0.45
46:54:1999:A:HO2'	46:54:2018:C:HO2'	1.62	0.45
3:C3:290:SER:O	3:C3:294:LYS:HG2	2.16	0.45
5:E3:48:ARG:HH11	5:E3:68:LYS:HG2	1.81	0.45
10:J3:68:ILE:HD12	46:54:4258:C:H5'	1.98	0.45
15:P3:28:ASN:O	15:P3:32:THR:HG22	2.17	0.45
17:R3:67:THR:O	17:R3:71:ARG:HD3	2.17	0.45
18:S3:14:GLY:HA2	18:S3:62:VAL:HG23	1.99	0.45
29:d3:94:GLU:HG3	29:d3:95:ASP:N	2.26	0.45
42:r3:10:VAL:HG13	42:r3:14:SER:HB2	1.99	0.45
46:54:689:U:H2'	46:54:690:C:O4'	2.16	0.45
46:54:1330:A:C8	46:54:3864:C:C4	3.04	0.45
46:54:1962:A:H8	46:54:1962:A:OP2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:2518:G:H1'	46:54:2539:C:H1'	1.99	0.45
52:TT:306:TRP:HA	52:TT:307:PRO:HD3	1.80	0.45
4:D3:72:ASP:OD1	4:D3:72:ASP:N	2.49	0.45
5:E3:93:ALA:O	5:E3:112:LEU:HD12	2.16	0.45
5:E3:180:GLY:O	5:E3:181:PRO:C	2.60	0.45
11:L3:153:PRO:HG2	11:L3:156:PRO:HB3	1.99	0.45
11:L3:169:ILE:HD13	26:a3:142:GLY:HA2	1.98	0.45
29:d3:124:GLU:N	29:d3:124:GLU:OE1	2.50	0.45
46:54:121:A:H5'	46:54:122:U:OP2	2.16	0.45
46:54:1070:G:C6	46:54:1071:C:C4	3.05	0.45
46:54:4260:U:H2'	46:54:4261:C:C6	2.52	0.45
11:L3:142:GLU:O	11:L3:145:LYS:NZ	2.38	0.45
11:L3:164:GLU:HG2	26:a3:100:ILE:HD12	1.98	0.45
13:N3:44:ARG:NH2	46:54:280:G:OP1	2.21	0.45
18:S3:1:MET:HG2	18:S3:2:LYS:N	2.32	0.45
19:T3:45:MET:H	19:T3:95:HIS:CD2	2.35	0.45
21:V3:109:LYS:NZ	21:V3:111:GLU:OE2	2.48	0.45
32:g3:6:THR:HG22	46:54:2400:G:N2	2.32	0.45
34:i3:29:ARG:HH22	34:i3:34:THR:CG2	2.30	0.45
35:j3:63:ARG:HD2	35:j3:65:ARG:HB3	1.99	0.45
41:p3:2:ALA:N	46:54:1570:G:O6	2.49	0.45
43:s3:186:GLY:O	43:s3:188:ILE:N	2.50	0.45
44:t3:13:VAL:HB	44:t3:31:LYS:HG2	1.99	0.45
46:54:2686:G:H5'	46:54:2687:U:OP1	2.17	0.45
46:54:4959:U:H2'	46:54:4960:G:O4'	2.16	0.45
48:84:124:U:OP1	48:84:126:C:N4	2.40	0.45
51:NB:95:GLU:OE1	51:NB:97:LYS:HG3	2.17	0.45
1:A3:210:PRO:HG2	1:A3:235:VAL:HG21	1.98	0.45
4:D3:112:ARG:HE	4:D3:112:ARG:HB3	1.47	0.45
5:E3:45:HIS:HD2	5:E3:48:ARG:CZ	2.30	0.45
7:G3:163:LYS:NZ	7:G3:166:ARG:HH22	2.14	0.45
11:L3:16:LYS:O	11:L3:18:TRP:N	2.50	0.45
11:L3:102:ARG:HG2	46:54:75:G:N7	2.32	0.45
20:U3:65:ARG:NH2	20:U3:66:SER:O	2.50	0.45
25:Z3:5:MET:HE3	25:Z3:25:ILE:HD11	1.99	0.45
36:k3:12:LEU:HB3	36:k3:16:ARG:NH1	2.31	0.45
36:k3:59:SER:O	36:k3:59:SER:OG	2.27	0.45
43:s3:15:LEU:O	43:s3:19:GLN:HB2	2.17	0.45
43:s3:149:ARG:O	43:s3:151:THR:N	2.42	0.45
46:54:175:C:H2'	46:54:176:G:C8	2.51	0.45
46:54:956:A:H1'	46:54:2076:G:H5''	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:1273:G:H2'	46:54:1274:A:C8	2.53	0.45
46:54:1450:C:H1'	46:54:2105:A:H1'	1.99	0.45
46:54:2019:C:C4	46:54:2020:U:O4	2.70	0.45
46:54:2595:C:H2'	46:54:2596:G:O4'	2.17	0.45
46:54:3625:G:O2'	46:54:3626:G:OP1	2.35	0.45
46:54:4066:U:H2'	46:54:4067:U:O4'	2.17	0.45
46:54:4389:C:H2'	46:54:4390:A:H8	1.82	0.45
46:54:4740:G:N2	46:54:4959:U:O2	2.38	0.45
46:54:4903:G:H1	46:54:4918:C:H42	1.64	0.45
8:H3:93:ARG:HE	8:H3:143:GLU:HB3	1.81	0.44
9:I3:51:HIS:ND1	9:I3:137:SER:HB3	2.31	0.44
9:I3:193:ASP:OD2	9:I3:198:LYS:HG3	2.16	0.44
10:J3:26:VAL:HG23	10:J3:28:GLU:H	1.81	0.44
11:L3:135:LYS:HA	11:L3:135:LYS:HD3	1.83	0.44
17:R3:109:TYR:CD2	17:R3:142:ILE:HD13	2.52	0.44
18:S3:60:GLU:HB2	19:T3:136:ARG:NH2	2.31	0.44
33:h3:66:LYS:O	33:h3:70:ARG:HG2	2.16	0.44
35:j3:59:THR:HG23	46:54:23:C:H4'	2.00	0.44
37:l3:25:GLN:HE21	37:l3:28:TRP:HZ2	1.63	0.44
38:m3:69:ILE:HD12	46:54:4473:A:H5''	1.98	0.44
42:r3:6:GLN:HG3	42:r3:44:ILE:HD12	1.99	0.44
42:r3:107:ARG:HG3	42:r3:108:MET:N	2.32	0.44
46:54:132:G:H2'	46:54:133:C:O4'	2.16	0.44
46:54:433:A:C2	46:54:3867:A:H4'	2.51	0.44
46:54:1767:A:H5''	46:54:1768:C:OP2	2.16	0.44
46:54:4515:G:C2	46:54:4516:G:C8	3.05	0.44
1:A3:223:SER:OG	46:54:3748:A:O2'	2.15	0.44
3:C3:109:ARG:HA	46:54:1341:U:H5'	1.98	0.44
3:C3:114:ARG:HB3	13:N3:203:TYR:HD2	1.82	0.44
17:R3:79:GLY:O	46:54:3619:G:H4'	2.17	0.44
23:X3:145:ASP:OD1	23:X3:148:ASP:N	2.47	0.44
26:a3:2:PRO:CD	46:54:1509:C:H5''	2.47	0.44
30:e3:35:TRP:CZ2	30:e3:56:PRO:HD2	2.53	0.44
31:f3:3:GLY:O	46:54:4945:G:N1	2.49	0.44
31:f3:28:LEU:CG	31:f3:101:ILE:HD11	2.47	0.44
41:p3:52:VAL:CG1	46:54:2739:C:H5'	2.47	0.44
43:s3:161:ILE:HG21	43:s3:167:VAL:CG1	2.47	0.44
44:t3:15:LEU:HD13	44:t3:28:LEU:HG	1.98	0.44
46:54:1554:A:H2'	46:54:1555:G:O4'	2.17	0.44
46:54:1967:A:N1	46:54:2020:U:N3	2.65	0.44
46:54:2546:G:O2'	46:54:2547:G:OP1	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:4188:U:H2'	46:54:4189:U:H6	1.80	0.44
46:54:4886:C:H2'	46:54:4887:C:C6	2.52	0.44
52:TT:189:GLN:HE21	52:TT:220:ALA:HB3	1.82	0.44
52:TT:259:TYR:O	52:TT:263:GLU:HG3	2.17	0.44
1:A3:48:ILE:HD13	41:p3:65:ALA:HB2	1.98	0.44
1:A3:130:SER:OG	1:A3:174:ARG:NH2	2.37	0.44
1:A3:180:LEU:HD23	1:A3:180:LEU:HA	1.63	0.44
3:C3:133:LEU:HD23	42:r3:6:GLN:OE1	2.18	0.44
7:G3:126:ARG:NE	46:54:4076:G:OP1	2.29	0.44
10:J3:113:ILE:HG12	10:J3:125:ILE:HD12	1.98	0.44
16:Q3:66:MET:HE3	16:Q3:98:LEU:HD13	2.00	0.44
17:R3:60:ARG:HH12	46:54:2809:G:P	2.41	0.44
19:T3:9:ARG:O	19:T3:55:LYS:HE2	2.17	0.44
21:V3:35:LYS:HB2	21:V3:67:LYS:HG3	1.98	0.44
36:k3:35:LYS:NZ	46:54:2696:A:H62	2.16	0.44
38:m3:84:CYS:SG	38:m3:85:ARG:N	2.90	0.44
46:54:971(A):G:O2'	46:54:972:C:O5'	2.29	0.44
46:54:1488:G:H2'	46:54:1489:G:O4'	2.16	0.44
46:54:2259:G:H5'	46:54:2260:C:OP2	2.18	0.44
46:54:2553:A:H1'	46:54:2554:U:O4'	2.18	0.44
46:54:4168:G:H2'	46:54:4169:G:H5'	2.00	0.44
46:54:5016:A:N6	46:54:5033:G:O2'	2.51	0.44
1:A3:70:LYS:HD3	1:A3:72:ARG:NH1	2.32	0.44
2:B3:137:TRP:O	2:B3:143:LYS:NZ	2.44	0.44
2:B3:283:LYS:HD2	2:B3:285:TYR:HE1	1.82	0.44
6:F3:236:GLU:HG2	18:S3:38:VAL:HG22	1.98	0.44
14:O3:60:LYS:NZ	46:54:2046:G:H5'	2.33	0.44
14:O3:61:ARG:HH11	14:O3:66:PRO:HG3	1.82	0.44
15:P3:125:MET:SD	15:P3:143:PRO:HG3	2.57	0.44
17:R3:44:LEU:HD22	17:R3:49:LEU:HD12	1.98	0.44
19:T3:114:GLN:HE22	19:T3:117:LYS:NZ	2.15	0.44
35:j3:81:GLY:HA3	46:54:134:G:C5	2.53	0.44
36:k3:34:PHE:CZ	36:k3:56:LEU:HD23	2.53	0.44
37:l3:18:LYS:HB2	37:l3:18:LYS:HE3	1.71	0.44
46:54:432:U:H4'	46:54:433:A:H5''	1.99	0.44
46:54:489:C:H2'	46:54:490:C:C6	2.51	0.44
46:54:4097:G:N1	46:54:4111:U:O4	2.48	0.44
46:54:5061:A:H3'	46:54:5062:G:C5'	2.48	0.44
52:TT:293:LEU:HD13	52:TT:447:HIS:CG	2.52	0.44
3:C3:190:ARG:HG2	3:C3:191:ALA:H	1.82	0.44
3:C3:284:MET:HA	16:Q3:122:THR:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G3:219:LEU:HD11	13:N3:45:PRO:HG2	1.98	0.44
8:H3:176:LEU:HB3	38:m3:60:ALA:CB	2.47	0.44
14:O3:54:TYR:CD1	14:O3:145:VAL:HG21	2.53	0.44
16:Q3:12:LYS:HD2	16:Q3:14:ARG:HH12	1.82	0.44
26:a3:74:ASN:HA	26:a3:112:LEU:O	2.17	0.44
37:l3:2:SER:N	46:54:2407:G:O6	2.50	0.44
41:p3:58:GLY:O	46:54:2652:G:N1	2.36	0.44
44:t3:43:GLY:O	44:t3:46:ILE:HG22	2.17	0.44
46:54:1481:C:O2'	46:54:1482:G:O5'	2.35	0.44
46:54:1967:A:N6	46:54:2020:U:H3	2.14	0.44
46:54:2517:A:N3	46:54:2539:C:O2'	2.50	0.44
46:54:3678:G:H8	46:54:3678:G:OP1	2.00	0.44
46:54:4761:G:H2'	46:54:4762:A:C8	2.52	0.44
52:TT:289:TYR:HD1	52:TT:316:LEU:HD21	1.83	0.44
52:TT:294:GLU:HG3	52:TT:298:ARG:HG3	2.00	0.44
4:D3:53:VAL:HG22	4:D3:62:CYS:SG	2.58	0.44
4:D3:215:ASP:HB2	4:D3:217:ASP:OD1	2.18	0.44
7:G3:196:VAL:HG22	7:G3:256:ALA:HB2	1.99	0.44
8:H3:118:LEU:HA	8:H3:118:LEU:HD23	1.76	0.44
10:J3:118:LYS:HD3	10:J3:118:LYS:HA	1.82	0.44
14:O3:9:LEU:HD23	14:O3:118:MET:HB2	2.00	0.44
18:S3:19:THR:HB	18:S3:20:PRO:HD2	1.99	0.44
22:W3:56:ARG:NH1	46:54:5041:G:C5	2.86	0.44
23:X3:119:ILE:HG22	23:X3:144:TYR:CD2	2.53	0.44
28:c3:29:LEU:HD22	28:c3:91:VAL:HG21	1.99	0.44
39:n3:18:ARG:NH1	39:n3:22:GLN:HB2	2.31	0.44
44:t3:81:ILE:O	44:t3:85:LEU:HG	2.17	0.44
46:54:179:G:C2	46:54:180:C:C4	3.05	0.44
46:54:1573:G:C6	46:54:1574:G:N1	2.86	0.44
46:54:2607:C:H2'	46:54:2608:G:C8	2.53	0.44
52:TT:321:ASP:O	52:TT:325:SER:N	2.51	0.44
52:TT:401:PRO:HB2	52:TT:418:VAL:H	1.83	0.44
1:A3:72:ARG:NH2	46:54:4084:G:N7	2.66	0.44
2:B3:257:TRP:CD1	2:B3:257:TRP:C	2.94	0.44
3:C3:305:PRO:HD3	16:Q3:38:ARG:HH21	1.83	0.44
7:G3:101:LYS:HA	7:G3:101:LYS:HD3	1.56	0.44
13:N3:39:ALA:HB3	13:N3:61:ILE:HG22	1.97	0.44
16:Q3:103:LEU:HD23	16:Q3:103:LEU:HA	1.79	0.44
16:Q3:146:ARG:HH22	46:54:1347:G:P	2.40	0.44
17:R3:35:ALA:O	17:R3:40:GLN:HG2	2.17	0.44
26:a3:137:ILE:O	26:a3:140:VAL:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:h3:87:LYS:HB2	33:h3:87:LYS:HE2	1.71	0.44
46:54:39:A:O2'	46:54:1654:G:O6	2.32	0.44
46:54:493:G:H2'	46:54:494:C:H6	1.82	0.44
46:54:746:A:O2'	46:54:913:U:O4	2.13	0.44
46:54:3923:A:H2'	46:54:3924:C:C6	2.53	0.44
53:1:55:THR:HG22	53:1:55:THR:O	2.18	0.44
1:A3:13:GLY:C	1:A3:15:VAL:H	2.25	0.44
2:B3:115:LYS:HB3	2:B3:115:LYS:HE2	1.81	0.44
2:B3:244:THR:OG1	2:B3:248:LEU:HB3	2.18	0.44
3:C3:348:LYS:HB3	3:C3:348:LYS:HE2	1.70	0.44
6:F3:104:VAL:HG13	6:F3:135:VAL:HG12	1.99	0.44
8:H3:61:TRP:CZ3	12:M3:33:GLN:HG2	2.53	0.44
12:M3:95:ILE:O	12:M3:99:GLU:HG3	2.18	0.44
15:P3:102:ALA:HB1	15:P3:107:LEU:HB2	1.99	0.44
18:S3:166:ARG:NH2	46:54:1919:G:C4	2.86	0.44
20:U3:20:LYS:O	20:U3:108:GLU:HB3	2.18	0.44
29:d3:113:THR:OG1	29:d3:115:LYS:HG2	2.18	0.44
30:e3:11:LYS:HA	30:e3:11:LYS:HD2	1.81	0.44
37:l3:27:ILE:HD13	48:84:52:A:H62	1.82	0.44
44:t3:20:GLY:N	44:t3:54:LYS:HA	2.32	0.44
46:54:169:A:H1'	46:54:267:G:N2	2.33	0.44
46:54:1455:G:O2'	46:54:1456:C:OP1	2.27	0.44
46:54:2355:G:H2'	46:54:2356:U:O4'	2.18	0.44
46:54:2708:U:O2'	46:54:2709:C:H6	2.01	0.44
46:54:4349:C:H3'	46:54:4350:C:H5'	2.00	0.44
46:54:4724:A:H2'	46:54:4725:C:O4'	2.17	0.44
6:F3:103:LYS:NZ	46:54:1797:G:OP1	2.50	0.44
9:l3:166:HIS:HB2	19:T3:158:PHE:HE2	1.83	0.44
14:O3:24:ALA:HB2	14:O3:84:VAL:HG13	1.99	0.44
14:O3:83:THR:OG1	46:54:2052:G:H5'	2.18	0.44
15:P3:22:LEU:O	15:P3:24:VAL:N	2.48	0.44
19:T3:74:ILE:HG21	19:T3:74:ILE:HD13	1.74	0.44
24:Y3:130:LYS:HA	24:Y3:130:LYS:HD3	1.83	0.44
40:o3:57:ARG:O	40:o3:59:LYS:N	2.51	0.44
40:o3:64:LYS:HD2	46:54:4370:G:H5''	2.00	0.44
46:54:90:G:N7	46:54:92:C:C2	2.86	0.44
46:54:448:G:C6	46:54:450:G:C8	3.05	0.44
46:54:1481:C:O2'	46:54:1482:G:N3	2.44	0.44
46:54:1482:G:HO2'	46:54:1483:C:P	2.41	0.44
46:54:1483:C:H4'	46:54:1484:G:H5'	1.99	0.44
46:54:1772:C:H2'	46:54:1773:U:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:2548:C:H2'	46:54:2549:G:C8	2.52	0.44
46:54:3667:C:H2'	46:54:3668:C:H6	1.82	0.44
46:54:3753:G:C5	46:54:3776:G:C2	3.06	0.44
46:54:4323:A:H2'	46:54:4324:A:O4'	2.17	0.44
52:TT:125:LYS:HD3	52:TT:157:GLN:CD	2.43	0.44
52:TT:307:PRO:HA	52:TT:310:ARG:NH2	2.33	0.44
2:B3:95:THR:HG22	46:54:4910:A:H4'	1.99	0.43
14:O3:53:LYS:HE3	14:O3:53:LYS:HB2	1.70	0.43
16:Q3:70:MET:HB3	16:Q3:70:MET:HE3	1.66	0.43
24:Y3:74:TYR:CE1	24:Y3:77:LYS:HG3	2.53	0.43
32:g3:66:ARG:HD3	46:54:2539:C:H5''	1.99	0.43
43:s3:52:VAL:O	43:s3:89:VAL:HA	2.17	0.43
43:s3:161:ILE:HD13	43:s3:167:VAL:CG1	2.47	0.43
46:54:1238:A:O2'	46:54:1239:C:OP1	2.30	0.43
46:54:1411:C:H2'	46:54:1411(A):G:C8	2.53	0.43
46:54:3860:A:H61	46:54:4560:C:H5	1.65	0.43
46:54:4095:G:N2	46:54:4113:U:O2	2.49	0.43
52:TT:133:TYR:HE1	52:TT:161:VAL:O	2.01	0.43
52:TT:344:SER:O	52:TT:344:SER:OG	2.29	0.43
53:1:1:MET:HE3	53:1:1:MET:HB3	1.72	0.43
2:B3:30:LYS:HG3	46:54:4716:C:OP2	2.19	0.43
5:E3:98:PRO:HG2	46:54:687:U:C4	2.53	0.43
5:E3:153:LEU:HD13	5:E3:197:VAL:HG11	1.98	0.43
10:J3:53:ALA:HB2	10:J3:68:ILE:HD11	2.00	0.43
12:M3:50:MET:HE3	12:M3:50:MET:HB2	1.81	0.43
12:M3:62:LEU:HD23	12:M3:62:LEU:H	1.83	0.43
14:O3:54:TYR:HD1	14:O3:145:VAL:HG21	1.83	0.43
20:U3:22:THR:O	20:U3:109:SER:HA	2.17	0.43
20:U3:80:LYS:N	46:54:2620:G:OP1	2.40	0.43
20:U3:107:LYS:HB3	20:U3:107:LYS:HE2	1.82	0.43
26:a3:138:LYS:O	26:a3:141:GLY:N	2.46	0.43
45:23:19:G:H4'	45:23:20:U:OP2	2.18	0.43
46:54:493:G:H2'	46:54:494:C:C6	2.53	0.43
46:54:686:A:H2'	46:54:686:A:N3	2.33	0.43
46:54:1411(C):C:H2'	46:54:1412:G:C8	2.53	0.43
46:54:2459:G:H2'	46:54:2461:G:OP2	2.17	0.43
46:54:4371:G:O2'	46:54:4372:U:OP2	2.29	0.43
46:54:4886:C:H2'	46:54:4887:C:H6	1.82	0.43
52:TT:355:ASP:CG	52:TT:356:GLY:H	2.26	0.43
1:A3:51:ASP:HB2	1:A3:58:LEU:HG	1.99	0.43
1:A3:113:VAL:HG22	1:A3:134:ALA:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C3:70:GLY:HA2	46:54:3905:A:O3'	2.18	0.43
3:C3:181:LYS:NZ	46:54:219:G:H22	2.17	0.43
4:D3:236:MET:HG2	4:D3:239:MET:CE	2.48	0.43
8:H3:51:LYS:HG2	8:H3:53:LYS:HZ2	1.83	0.43
14:O3:55:LEU:HD23	14:O3:55:LEU:HA	1.74	0.43
17:R3:74:ARG:O	17:R3:76:MET:HG2	2.18	0.43
43:s3:6:ARG:HA	43:s3:9:TRP:HB3	2.00	0.43
46:54:125:C:O2'	46:54:126:C:O5'	2.30	0.43
46:54:758:G:C2	46:54:759:G:H1'	2.54	0.43
46:54:914:U:HO2'	46:54:915:A:C1'	2.32	0.43
46:54:1075:G:N2	46:54:1235:G:N2	2.64	0.43
46:54:2528:G:H4'	46:54:2783:A:H4'	1.99	0.43
52:TT:423:GLN:CD	52:TT:423:GLN:H	2.27	0.43
3:C3:38:ASN:O	3:C3:42:THR:HG23	2.17	0.43
4:D3:15:ARG:HE	4:D3:15:ARG:HB3	1.51	0.43
4:D3:146:LEU:HD12	4:D3:163:LEU:HD13	2.00	0.43
8:H3:174:LYS:NZ	46:54:4604:G:OP1	2.36	0.43
12:M3:105:THR:HG23	12:M3:107:PHE:H	1.83	0.43
13:N3:38:ARG:HD2	13:N3:62:TYR:HE1	1.83	0.43
13:N3:124:ASP:N	13:N3:124:ASP:OD1	2.50	0.43
13:N3:187:SER:H	13:N3:190:ALA:HB3	1.83	0.43
14:O3:170:LYS:HB3	14:O3:170:LYS:HE3	1.76	0.43
24:Y3:27:ARG:CZ	48:84:70:G:H5''	2.48	0.43
25:Z3:36:ARG:HH22	46:54:2580:U:P	2.42	0.43
25:Z3:53:VAL:HG23	25:Z3:62:ILE:HG12	2.01	0.43
46:54:181:C:N3	46:54:182:G:N1	2.66	0.43
46:54:397:G:C5	46:54:398:A:H1'	2.53	0.43
46:54:439:G:H2'	46:54:440:U:O4'	2.19	0.43
46:54:684:G:O2'	46:54:685:C:OP1	2.31	0.43
46:54:1748:U:H2'	46:54:1749:A:O4'	2.18	0.43
46:54:1973:G:H2'	46:54:1974:U:C5	2.53	0.43
46:54:2630:U:H1'	46:54:4647:G:N2	2.33	0.43
46:54:3598:C:H2'	46:54:3599:A:C8	2.48	0.43
46:54:4571:A:H2'	46:54:4572:U:H6	1.84	0.43
46:54:4945:G:N3	46:54:4945:G:H2'	2.33	0.43
50:NA:98:LYS:HA	50:NA:98:LYS:HD3	1.74	0.43
52:TT:290:GLY:N	52:TT:445:ILE:HD12	2.33	0.43
2:B3:53:MET:HE2	2:B3:53:MET:HB3	1.78	0.43
5:E3:188:PRO:HG3	46:54:4938:A:H1'	2.00	0.43
6:F3:35:LYS:HB2	6:F3:35:LYS:HE3	1.80	0.43
6:F3:45:ARG:O	6:F3:49:ILE:HG12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G3:216:PRO:HA	13:N3:26:ARG:HH21	1.83	0.43
16:Q3:61:LEU:HD12	16:Q3:82:VAL:HG21	2.00	0.43
23:X3:110:LYS:O	23:X3:114:LYS:HD3	2.18	0.43
24:Y3:89:LYS:NZ	46:54:386:A:H5'	2.33	0.43
33:h3:79:LYS:HE2	33:h3:79:LYS:HB3	1.73	0.43
34:i3:36:HIS:O	34:i3:40:VAL:HG23	2.18	0.43
46:54:302:C:O5'	46:54:302:C:H6	2.02	0.43
46:54:1218:G:H2'	46:54:1219:G:C8	2.52	0.43
46:54:1808:C:H2'	46:54:1809:C:C6	2.53	0.43
46:54:4303:C:H2'	46:54:4305:G:C8	2.54	0.43
46:54:4685:U:H2'	46:54:4686:G:C8	2.53	0.43
52:TT:259:TYR:HB3	52:TT:275:LEU:HG	2.00	0.43
52:TT:369:GLU:O	52:TT:385:VAL:HG12	2.18	0.43
52:TT:398:GLU:O	52:TT:400:VAL:HG23	2.18	0.43
3:C3:248:ARG:HG2	3:C3:249:PHE:H	1.83	0.43
3:C3:287:THR:OG1	42:r3:2:SER:OG	2.33	0.43
6:F3:88:LEU:HD23	6:F3:144:PRO:HG2	2.00	0.43
10:J3:24:ILE:HG23	10:J3:127:GLY:O	2.18	0.43
13:N3:49:ARG:HH22	46:54:152:U:P	2.38	0.43
16:Q3:67:ILE:HD13	16:Q3:98:LEU:HD11	1.99	0.43
23:X3:101:ASP:OD1	23:X3:102:VAL:N	2.52	0.43
30:e3:108:ARG:HD3	30:e3:127:ALA:HB3	2.00	0.43
38:m3:72:LYS:HD3	38:m3:89:CYS:HB2	2.00	0.43
45:23:19:G:H5''	45:23:60:A:H61	1.83	0.43
46:54:233:U:H3'	46:54:234:G:H5''	2.00	0.43
46:54:690:C:H2'	46:54:691:C:H6	1.84	0.43
46:54:1826:G:H2'	46:54:1827:C:O4'	2.18	0.43
46:54:2533:C:O5'	46:54:2533:C:H6	2.02	0.43
46:54:3611:A:H2	46:54:5016:A:H8	1.66	0.43
52:TT:184:ASN:ND2	52:TT:186:VAL:HB	2.34	0.43
52:TT:241:LEU:HD12	52:TT:245:THR:OG1	2.19	0.43
6:F3:91:VAL:HG13	6:F3:139:ILE:HD12	2.01	0.43
9:I3:15:LYS:NZ	46:54:4212:A:OP2	2.47	0.43
13:N3:12:ARG:NH2	46:54:279:A:OP2	2.46	0.43
13:N3:89:VAL:HG21	46:54:3928:A:H5'	1.99	0.43
16:Q3:161:SER:O	16:Q3:161:SER:OG	2.34	0.43
18:S3:90:THR:HG23	19:T3:156:TYR:CE2	2.54	0.43
43:s3:50:LYS:HE3	43:s3:50:LYS:HB3	1.80	0.43
44:t3:82:ILE:HD12	44:t3:100:HIS:CE1	2.53	0.43
46:54:964:A:H2'	46:54:965:G:O4'	2.19	0.43
46:54:987:C:H2'	46:54:988:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:1999:A:C4	46:54:2000:G:N7	2.87	0.43
46:54:4117:U:H6	46:54:4117:U:O5'	2.02	0.43
52:TT:121:MET:HE1	52:TT:154:ALA:HA	2.01	0.43
52:TT:150:GLU:HA	52:TT:181:HIS:ND1	2.34	0.43
52:TT:218:LYS:HA	52:TT:218:LYS:HD2	1.65	0.43
2:B3:9:PRO:HD2	21:V3:48:ARG:HH22	1.84	0.43
2:B3:18:PRO:O	2:B3:20:LYS:N	2.52	0.43
2:B3:217:ILE:HD11	2:B3:333:LEU:HD21	2.01	0.43
2:B3:356:LYS:HE3	2:B3:356:LYS:HB2	1.82	0.43
5:E3:158:GLY:HA2	46:54:4942:C:H5''	2.00	0.43
6:F3:28:LYS:HA	6:F3:28:LYS:HD2	1.83	0.43
8:H3:23:ARG:NH2	8:H3:42:ASN:H	2.16	0.43
8:H3:167:VAL:HG12	8:H3:170:LYS:HB2	2.01	0.43
11:L3:25:TRP:HE1	13:N3:199:GLN:NE2	2.16	0.43
16:Q3:61:LEU:O	16:Q3:87:THR:OG1	2.27	0.43
17:R3:37:SER:HA	46:54:2526:C:H5'	2.00	0.43
46:54:1666:C:O2'	46:54:1688:G:OP1	2.24	0.43
46:54:1984:A:N6	46:54:2010:A:HO2'	2.17	0.43
46:54:2368:A:N6	46:54:2827:G:O2'	2.48	0.43
46:54:2894:A:H2'	46:54:2895:A:C8	2.54	0.43
46:54:3714:G:H1	46:54:3739:C:H42	1.65	0.43
46:54:4111:U:H2'	46:54:4112:C:O4'	2.19	0.43
52:TT:282:LEU:HD23	52:TT:283:HIS:CD2	2.54	0.43
2:B3:23:SER:O	2:B3:23:SER:OG	2.36	0.43
2:B3:56:ILE:HD12	2:B3:365:LEU:HD22	2.01	0.43
2:B3:230:GLY:O	2:B3:234:ARG:HB2	2.18	0.43
3:C3:189:MET:HE2	3:C3:201:ARG:HG3	2.00	0.43
3:C3:331:TYR:CE2	3:C3:335:MET:HG3	2.54	0.43
7:G3:139:VAL:HG11	7:G3:238:LYS:HG3	2.01	0.43
14:O3:170:LYS:O	14:O3:174:LEU:HD23	2.18	0.43
25:Z3:51:ARG:HB2	25:Z3:65:ARG:HD2	2.01	0.43
26:a3:74:ASN:OD1	46:54:1387:A:N6	2.35	0.43
40:o3:37:GLY:HA3	46:54:4342:C:O3'	2.17	0.43
44:t3:112:ILE:HD12	44:t3:112:ILE:H	1.84	0.43
45:23:11:U:H2'	45:23:12:G:C8	2.54	0.43
45:23:43:A:H2'	45:23:44:A:C8	2.54	0.43
46:54:473:C:H2'	46:54:474:C:C6	2.53	0.43
46:54:717:U:O2'	46:54:1904:G:H4'	2.18	0.43
46:54:1292:C:H5'	46:54:1293:G:OP2	2.19	0.43
46:54:3810:C:O2'	46:54:3811:G:OP1	2.34	0.43
46:54:4502:C:H2'	46:54:4503:A:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:TT:142:SER:HA	52:TT:158:LEU:HD22	2.01	0.43
52:TT:444:ARG:HH22	52:TT:451:ASP:HB3	1.82	0.43
1:A3:173:GLY:O	41:p3:69:TRP:NE1	2.51	0.43
1:A3:242:ARG:O	46:54:3658:C:H5''	2.19	0.43
2:B3:253:CYS:SG	46:54:4521:U:H1'	2.59	0.43
3:C3:48:ASN:HB2	46:54:1370:G:OP2	2.19	0.43
5:E3:168:LEU:HD13	5:E3:211:ILE:HD13	2.01	0.43
7:G3:139:VAL:HG23	7:G3:236:ILE:HG22	2.01	0.43
13:N3:75:VAL:O	46:54:3670:C:H5'	2.18	0.43
29:d3:70:LYS:HB2	29:d3:70:LYS:HE3	1.62	0.43
32:g3:54:ARG:NH2	46:54:2651:C:O2'	2.52	0.43
35:j3:13:ASN:OD1	35:j3:13:ASN:N	2.52	0.43
46:54:255:C:H2'	46:54:256:G:H5''	2.01	0.43
46:54:1191:C:H2'	46:54:1192:C:C6	2.53	0.43
46:54:1279:A:O2'	46:54:1281:G:N7	2.40	0.43
46:54:2899:C:N4	46:54:2900:U:O4	2.52	0.43
46:54:4169:G:H4'	46:54:4171:C:C2	2.54	0.43
46:54:4735:G:HO2'	46:54:4736:C:H6	1.64	0.43
1:A3:44:ILE:HD11	1:A3:46:LYS:NZ	2.34	0.42
4:D3:222:GLN:HE22	47:74:47:G:N2	2.18	0.42
12:M3:44:ARG:HE	12:M3:44:ARG:HB2	1.43	0.42
13:N3:143:ARG:NH1	33:h3:94:ARG:O	2.51	0.42
13:N3:158:HIS:HB3	13:N3:161:MET:CG	2.48	0.42
14:O3:149:TYR:O	14:O3:153:THR:OG1	2.31	0.42
16:Q3:122:THR:HG22	16:Q3:123:PHE:H	1.83	0.42
19:T3:81:LYS:HB2	19:T3:81:LYS:HE3	1.89	0.42
21:V3:57:VAL:HG12	21:V3:124:GLU:HB2	2.00	0.42
23:X3:141:ALA:HB1	23:X3:142:PRO:HD2	2.01	0.42
24:Y3:89:LYS:HZ3	46:54:386:A:H5'	1.83	0.42
39:n3:8:LYS:HE3	39:n3:12:ARG:NH1	2.34	0.42
46:54:106:A:H2'	46:54:107:G:O4'	2.19	0.42
46:54:386:A:H3'	46:54:387:G:H5''	2.01	0.42
46:54:1600:A:H5''	46:54:1601:A:OP1	2.18	0.42
46:54:4199:C:H2'	46:54:4200:G:H5'	2.01	0.42
46:54:4719:G:C2	46:54:4721:G:H1'	2.54	0.42
51:NB:102:MET:HE2	51:NB:102:MET:HA	1.99	0.42
1:A3:116:LEU:HD12	1:A3:117:GLU:H	1.83	0.42
3:C3:358:LEU:HA	3:C3:361:LYS:NZ	2.33	0.42
5:E3:93:ALA:HB2	46:54:2259:G:H21	1.84	0.42
7:G3:146:THR:OG1	7:G3:147:GLN:N	2.52	0.42
9:I3:53:VAL:HG11	19:T3:160:ALA:HB1	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M3:55:MET:O	18:S3:157:ARG:NH2	2.52	0.42
14:O3:185:VAL:HG12	14:O3:189:ILE:HG23	2.01	0.42
19:T3:94:GLU:OE1	19:T3:94:GLU:N	2.46	0.42
21:V3:18:LEU:HD12	21:V3:18:LEU:O	2.19	0.42
22:W3:11:TYR:HB2	22:W3:32:LEU:HD22	2.00	0.42
24:Y3:1:MET:HG3	24:Y3:2:LYS:N	2.35	0.42
26:a3:19:HIS:HB3	26:a3:25:HIS:HB2	2.00	0.42
27:b3:55:LYS:HB3	27:b3:55:LYS:HE3	1.85	0.42
32:g3:22:LEU:HD12	32:g3:30:ILE:HG22	2.00	0.42
32:g3:60:ARG:HA	32:g3:60:ARG:HD2	1.77	0.42
34:i3:26:HIS:HE1	46:54:276:C:O2	2.03	0.42
43:s3:162:LYS:HE2	43:s3:162:LYS:HB3	1.76	0.42
46:54:223:G:H4'	46:54:225:G:N7	2.34	0.42
46:54:388:A:H1'	46:54:403:G:N2	2.33	0.42
46:54:2632:U:H2'	46:54:2633:U:C6	2.54	0.42
46:54:3692:A:N6	46:54:3823:G:H21	2.17	0.42
46:54:4532:U:OP2	46:54:4554:G:N1	2.45	0.42
48:84:152:U:H2'	48:84:153:C:O4'	2.18	0.42
48:84:155:C:H2'	48:84:156:U:O4'	2.19	0.42
52:TT:95:VAL:HG12	52:TT:130:THR:HB	2.00	0.42
2:B3:39:LYS:HB3	2:B3:39:LYS:HE2	1.82	0.42
6:F3:71:ALA:O	6:F3:75:ARG:HG3	2.19	0.42
7:G3:147:GLN:HA	7:G3:150:LYS:HB3	2.02	0.42
7:G3:309:ALA:HA	7:G3:312:LYS:HG2	2.00	0.42
15:P3:3:ARG:HD2	15:P3:3:ARG:HA	1.88	0.42
21:V3:89:ARG:HB2	21:V3:95:PHE:CE2	2.54	0.42
25:Z3:83:THR:HG22	32:g3:95:PHE:CZ	2.54	0.42
26:a3:127:LYS:NZ	26:a3:148:ALA:O	2.47	0.42
31:f3:60:PRO:HD2	46:54:4944:C:C4	2.54	0.42
46:54:2464:C:H2'	46:54:2465:C:H6	1.85	0.42
46:54:4651:A:H8	46:54:4651:A:O5'	2.02	0.42
47:74:23:A:N3	47:74:118:C:O2'	2.45	0.42
48:84:56:G:H2'	48:84:57:C:O4'	2.19	0.42
52:TT:196:ARG:HH22	53:1:3:GLU:HB2	1.84	0.42
52:TT:253:GLN:O	52:TT:256:LEU:HG	2.19	0.42
9:I3:36:LEU:HD13	9:I3:73:ASN:ND2	2.34	0.42
11:L3:10:LEU:H	11:L3:10:LEU:HG	1.68	0.42
12:M3:32:ASP:OD1	12:M3:33:GLN:N	2.46	0.42
17:R3:60:ARG:HG3	17:R3:60:ARG:O	2.20	0.42
20:U3:60:VAL:HG13	20:U3:61:VAL:HG22	2.02	0.42
23:X3:81:LEU:HD12	23:X3:97:VAL:HG11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:c3:29:LEU:HD13	28:c3:89:TYR:HE2	1.84	0.42
44:t3:11:LYS:HE2	44:t3:11:LYS:HB3	1.86	0.42
44:t3:64:ILE:HG23	44:t3:69:ALA:HB2	2.01	0.42
45:23:18:G:HO2'	45:23:19:G:H8	1.64	0.42
45:23:75:C:H2'	45:23:76:A:O4'	2.19	0.42
46:54:223:G:H4'	46:54:225:G:C8	2.55	0.42
46:54:978:G:N2	46:54:1277:G:N2	2.67	0.42
46:54:1412:G:H2'	46:54:1413:C:H5'	2.00	0.42
46:54:2008:U:H1'	46:54:2011:C:C5	2.40	0.42
46:54:4898:G:H2'	46:54:4899:G:C8	2.48	0.42
51:NB:103:LEU:HA	51:NB:106:ILE:HG22	2.02	0.42
52:TT:156:ASN:HD21	52:TT:187:SER:HB2	1.84	0.42
2:B3:19:ARG:O	2:B3:234:ARG:NH2	2.53	0.42
2:B3:223:THR:HA	2:B3:338:VAL:HG22	2.01	0.42
3:C3:157:LYS:H	3:C3:157:LYS:HG2	1.59	0.42
4:D3:86:TYR:CE2	4:D3:104:LEU:HD21	2.55	0.42
4:D3:203:ASN:OD1	4:D3:204:VAL:N	2.52	0.42
7:G3:306:LEU:HD23	7:G3:306:LEU:HA	1.71	0.42
9:I3:75:TYR:HD2	9:I3:151:ALA:HB2	1.85	0.42
12:M3:132:ARG:HD2	12:M3:133:ALA:N	2.35	0.42
18:S3:67:VAL:HA	46:54:729:G:H1	1.84	0.42
25:Z3:48:ARG:NH2	46:54:2576:G:OP1	2.49	0.42
26:a3:17:HIS:O	26:a3:17:HIS:ND1	2.49	0.42
43:s3:109:ALA:O	43:s3:181:SER:HB3	2.20	0.42
46:54:1396:G:HO2'	46:54:1468:C:HO2'	1.65	0.42
46:54:2099:C:H4'	46:54:2100:G:H5'	2.02	0.42
46:54:2868:G:H21	46:54:2882:A:H62	1.66	0.42
46:54:3621:A:O2'	46:54:4658:G:O2'	2.20	0.42
46:54:4122:G:H2'	46:54:4123:C:H6	1.84	0.42
46:54:4574:U:H3'	46:54:4575:G:H5''	2.01	0.42
46:54:4641:U:H2'	46:54:4642:U:C6	2.55	0.42
2:B3:193:LYS:HB2	2:B3:193:LYS:HE3	1.75	0.42
2:B3:258:HIS:O	2:B3:260:ALA:N	2.53	0.42
4:D3:234:ASP:OD1	4:D3:235:MET:N	2.52	0.42
8:H3:77:VAL:HA	8:H3:80:MET:HE2	2.00	0.42
19:T3:102:ARG:NH1	46:54:1802:A:OP1	2.53	0.42
21:V3:18:LEU:HD13	21:V3:54:ALA:HB3	2.00	0.42
30:e3:84:GLU:OE1	42:r3:20:ARG:NH2	2.53	0.42
43:s3:114:GLY:N	43:s3:167:VAL:HG23	2.34	0.42
46:54:210:C:H5'	46:54:235:A:C2	2.54	0.42
46:54:643:C:C2	46:54:644:G:N7	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:54:914:U:O2'	46:54:915:A:O4'	2.37	0.42
46:54:974:C:H41	46:54:1281:G:N2	2.13	0.42
46:54:1097:C:O2	46:54:1199:G:N1	2.49	0.42
46:54:1398:A:N6	46:54:1419:G:H21	2.13	0.42
46:54:2468:U:H4'	46:54:2469:C:OP1	2.20	0.42
46:54:3603:G:H2'	46:54:3604:A:C8	2.54	0.42
46:54:4964:C:N4	46:54:4965:U:O4	2.52	0.42
47:74:2:U:H2'	47:74:3:C:C6	2.54	0.42
52:TT:249:PRO:O	52:TT:253:GLN:HG2	2.17	0.42
52:TT:436:PRO:HD2	52:TT:464:LEU:HG	2.02	0.42
1:A3:97:ASN:OD1	1:A3:97:ASN:N	2.52	0.42
1:A3:225:ILE:CD1	1:A3:233:ARG:HG3	2.49	0.42
3:C3:114:ARG:HB3	13:N3:203:TYR:CD2	2.55	0.42
3:C3:214:ASP:OD1	3:C3:218:VAL:HG13	2.19	0.42
13:N3:98:LEU:HD12	13:N3:128:LYS:HD2	2.01	0.42
15:P3:65:GLY:C	15:P3:67:VAL:H	2.26	0.42
37:I3:37:TYR:CD1	37:I3:37:TYR:C	2.97	0.42
43:s3:24:TYR:HB2	43:s3:90:PHE:HD2	1.84	0.42
46:54:965:G:O2'	46:54:966:A:H5'	2.20	0.42
46:54:1445:U:H2'	46:54:1446:C:H6	1.84	0.42
48:84:1:C:H2'	48:84:2:G:H5'	2.02	0.42
2:B3:357:ARG:NE	46:54:4615:C:H5''	2.35	0.42
3:C3:151:PRO:O	3:C3:153:VAL:HG23	2.19	0.42
3:C3:284:MET:HE3	3:C3:284:MET:HB2	1.90	0.42
4:D3:51:MET:N	4:D3:145:TYR:O	2.44	0.42
8:H3:63:ASN:OD1	8:H3:63:ASN:N	2.49	0.42
11:L3:193:GLY:HA3	46:54:4357:G:O3'	2.20	0.42
12:M3:132:ARG:NE	46:54:4895:C:O2	2.53	0.42
17:R3:110:ARG:HE	17:R3:110:ARG:HB3	1.71	0.42
35:j3:10:LYS:O	35:j3:12:ARG:HG2	2.20	0.42
36:k3:7:GLU:OE2	36:k3:10:ASP:HB2	2.19	0.42
40:o3:3:ASN:ND2	40:o3:95:GLY:O	2.51	0.42
43:s3:131:GLY:HA3	43:s3:132:PRO:HD3	1.89	0.42
44:t3:15:LEU:CD1	44:t3:28:LEU:HG	2.49	0.42
44:t3:58:ILE:HD11	44:t3:76:SER:H	1.84	0.42
46:54:1097:C:O2	46:54:1200:G:N1	2.53	0.42
46:54:2024:G:O2'	46:54:2025:A:OP2	2.28	0.42
46:54:4194:U:H5	46:54:4198:G:OP2	2.03	0.42
51:NB:69:GLY:O	51:NB:98:GLN:HG3	2.20	0.42
2:B3:47:LEU:HD23	2:B3:166:THR:HG23	2.01	0.42
2:B3:140:ASP:OD1	2:B3:141:ALA:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D3:118:ILE:H	4:D3:118:ILE:HD12	1.85	0.42
7:G3:189:LEU:HD23	7:G3:189:LEU:HA	1.86	0.42
11:L3:209:LYS:HB3	11:L3:209:LYS:HE3	1.83	0.42
12:M3:44:ARG:HA	46:54:935:A:N3	2.35	0.42
13:N3:201:HIS:H	13:N3:201:HIS:CD2	2.38	0.42
19:T3:4:THR:O	19:T3:9:ARG:NE	2.51	0.42
19:T3:114:GLN:HG3	19:T3:118:GLU:OE1	2.19	0.42
26:a3:127:LYS:HG2	34:i3:8:ALA:HB2	2.00	0.42
26:a3:132:ARG:NH2	46:54:1468:C:OP1	2.47	0.42
35:j3:84:PRO:HD3	48:84:94:G:C5	2.54	0.42
41:p3:50:ARG:HD2	41:p3:54:ILE:HD11	2.02	0.42
44:t3:50:THR:O	44:t3:52:ASP:N	2.47	0.42
46:54:48:G:O2'	46:54:49:U:OP2	2.38	0.42
46:54:175:C:O2	46:54:262:G:N2	2.53	0.42
46:54:671:G:C6	46:54:672:C:C4	3.08	0.42
46:54:1406(B):C:N4	46:54:1411:C:H42	2.17	0.42
46:54:1438:U:O2'	46:54:1440:U:OP2	2.30	0.42
46:54:2004:U:C4	46:54:2016:C:C4	3.07	0.42
46:54:2469:C:H5''	46:54:2470:C:OP2	2.20	0.42
46:54:2544:G:C6	48:84:126:C:C4	3.07	0.42
46:54:2647:A:N6	46:54:2686:G:H8	2.15	0.42
46:54:4925:U:O2'	46:54:4926:C:P	2.78	0.42
50:NA:113:LYS:HZ1	50:NA:118:ASP:HA	1.85	0.42
52:TT:459:VAL:HG11	52:TT:465:LEU:HD21	2.02	0.42
4:D3:51:MET:HE2	4:D3:51:MET:HB3	1.85	0.42
7:G3:218:GLU:OE1	13:N3:22:LEU:HD13	2.20	0.42
13:N3:191:ALA:HA	13:N3:194:ARG:NH1	2.35	0.42
14:O3:187:LYS:HD2	14:O3:187:LYS:HA	1.67	0.42
19:T3:45:MET:H	19:T3:95:HIS:HD2	1.68	0.42
32:g3:82:MET:HB2	32:g3:82:MET:HE3	1.77	0.42
34:i3:45:ARG:HD2	34:i3:50:PHE:CZ	2.55	0.42
46:54:1094:G:C2	46:54:1095:A:C5	3.07	0.42
46:54:1168:G:C2	46:54:1169:G:C8	3.08	0.42
46:54:2528:G:H2'	46:54:2529:A:O4'	2.20	0.42
46:54:3784:A:O2'	46:54:3785:A:H3'	2.18	0.42
46:54:4155:C:H2'	46:54:4156:G:O4'	2.20	0.42
4:D3:289:ARG:H	4:D3:289:ARG:HG2	1.70	0.41
9:I3:127:ALA:O	9:I3:129:VAL:HG23	2.20	0.41
15:P3:135:ARG:NH2	46:54:1596:U:O2'	2.53	0.41
16:Q3:11:ARG:NH2	46:54:1690:C:OP2	2.52	0.41
18:S3:161:ARG:HD2	18:S3:164:LYS:HD2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z3:74:VAL:HG23	25:Z3:101:PHE:HE2	1.84	0.41
29:d3:46:LEU:HD13	29:d3:46:LEU:HA	1.92	0.41
42:r3:6:GLN:HG3	42:r3:44:ILE:HG23	2.01	0.41
43:s3:160:LEU:HD23	43:s3:160:LEU:H	1.84	0.41
46:54:1823:G:C6	46:54:1824:G:C6	3.08	0.41
46:54:2503:G:H1'	46:54:4084:G:N2	2.35	0.41
46:54:2567:G:H2'	46:54:2568:C:C6	2.55	0.41
46:54:4138:C:H1'	46:54:4147:G:H21	1.85	0.41
46:54:4493:U:O2'	46:54:4494:G:H5'	2.20	0.41
46:54:4584:A:H2'	46:54:4585:U:O4'	2.20	0.41
46:54:4923:U:H2'	46:54:4924:C:C6	2.55	0.41
46:54:4971:A:O5'	46:54:4971:A:H8	2.03	0.41
50:NA:111:VAL:HA	50:NA:121:ILE:O	2.19	0.41
50:NA:113:LYS:HA	50:NA:119:THR:O	2.20	0.41
52:TT:211:MET:HE2	52:TT:211:MET:HB3	1.90	0.41
53:1:4:ILE:O	53:1:4:ILE:HG12	2.20	0.41
1:A3:96:LEU:O	41:p3:87:LYS:HD3	2.21	0.41
1:A3:182:ALA:HB2	46:54:3652:A:O2'	2.19	0.41
1:A3:196:TRP:O	1:A3:198:ARG:N	2.53	0.41
2:B3:96:PRO:HD3	14:O3:156:LEU:CD1	2.49	0.41
2:B3:332:MET:HE1	2:B3:365:LEU:HD11	2.02	0.41
4:D3:4:VAL:HG21	46:54:4247:G:H5'	2.02	0.41
5:E3:115:MET:HE3	5:E3:115:MET:HB3	1.84	0.41
8:H3:123:ILE:O	8:H3:123:ILE:HG13	2.20	0.41
10:J3:24:ILE:HG12	10:J3:128:LEU:HB3	2.01	0.41
17:R3:88:ARG:NH1	46:54:2812:A:OP1	2.52	0.41
18:S3:82:LEU:HD13	18:S3:126:ILE:HD13	2.02	0.41
19:T3:45:MET:N	19:T3:95:HIS:HD2	2.18	0.41
22:W3:25:ASP:OD1	22:W3:25:ASP:N	2.53	0.41
26:a3:21:ARG:HD3	46:54:1318:C:OP1	2.20	0.41
46:54:178:C:H3'	46:54:179:G:H8	1.86	0.41
46:54:642:G:C6	46:54:643:C:C2	3.08	0.41
46:54:757:G:HO2'	46:54:758:G:H8	1.67	0.41
46:54:986:C:H2'	46:54:987:C:C6	2.54	0.41
46:54:1770:A:H3'	46:54:1771:U:H6	1.86	0.41
46:54:1812:C:H2'	46:54:1813:U:C6	2.54	0.41
46:54:2430:C:O2'	46:54:2431:A:H5'	2.20	0.41
46:54:2538:U:O5'	46:54:2538:U:H6	2.03	0.41
46:54:3893:C:H2'	46:54:3894:A:C8	2.56	0.41
3:C3:22:VAL:HG11	3:C3:257:PHE:HD2	1.86	0.41
3:C3:350:ARG:HD2	46:54:724:C:OP1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D3:275:GLN:HE21	46:54:1187:G:H1'	1.84	0.41
5:E3:126:ARG:HB2	46:54:959:G:C8	2.55	0.41
7:G3:217:ILE:O	7:G3:221:VAL:HG23	2.21	0.41
12:M3:118:MET:HG2	14:O3:192:PHE:CE2	2.56	0.41
16:Q3:177:ALA:O	16:Q3:184:ARG:HB2	2.20	0.41
18:S3:147:ASP:OD1	18:S3:148:SER:N	2.52	0.41
19:T3:115:LYS:HG2	19:T3:126:VAL:HG21	2.01	0.41
22:W3:56:ARG:NH1	46:54:5041:G:C6	2.88	0.41
25:Z3:103:ASP:OD1	25:Z3:105:ALA:N	2.53	0.41
30:e3:58:ILE:O	30:e3:58:ILE:HG13	2.20	0.41
46:54:508:G:O3'	46:54:509:A:H3'	2.20	0.41
46:54:2409:U:H5	46:54:2783:A:N1	2.19	0.41
46:54:3648:A:H1'	46:54:3785:A:N6	2.35	0.41
46:54:3667:C:H2'	46:54:3668:C:C6	2.56	0.41
46:54:3773:U:O2	46:54:3776:G:C5	2.73	0.41
50:NA:104:PHE:N	50:NA:104:PHE:CD1	2.87	0.41
51:NB:60:GLU:H	51:NB:60:GLU:CD	2.27	0.41
52:TT:141:LEU:HD13	52:TT:157:GLN:HB3	2.01	0.41
1:A3:15:VAL:CG1	1:A3:194:ASN:HD22	2.32	0.41
4:D3:222:GLN:HE22	47:74:47:G:H21	1.67	0.41
4:D3:275:GLN:NE2	46:54:1187:G:H1'	2.35	0.41
8:H3:167:VAL:CG1	8:H3:170:LYS:HB2	2.50	0.41
9:I3:55:ASP:HA	9:I3:131:ILE:HG23	2.03	0.41
9:I3:91:LEU:HD23	9:I3:91:LEU:HA	1.86	0.41
19:T3:146:LYS:HE2	19:T3:146:LYS:HB2	1.84	0.41
29:d3:30:HIS:HE1	46:54:4637:G:OP1	2.04	0.41
34:i3:33:LEU:HG	46:54:308:G:O2'	2.20	0.41
40:o3:2:VAL:HG22	40:o3:3:ASN:H	1.85	0.41
46:54:52:G:H4'	46:54:1529:G:H4'	2.02	0.41
46:54:324:A:H2'	46:54:325:U:O4'	2.20	0.41
46:54:3722:G:H2'	46:54:3723:A:C8	2.55	0.41
46:54:4607:A:H8	46:54:4607:A:O5'	2.03	0.41
48:84:10:G:C6	48:84:11:C:N3	2.89	0.41
50:NA:101:ASN:C	50:NA:131:LEU:H	2.24	0.41
52:TT:202:THR:HB	52:TT:205:GLU:CB	2.51	0.41
52:TT:229:ARG:HA	52:TT:232:TYR:HB3	2.02	0.41
2:B3:132:LYS:HA	2:B3:135:LYS:HE2	2.02	0.41
8:H3:51:LYS:HE2	8:H3:53:LYS:HE3	2.02	0.41
9:I3:76:MET:HE2	9:I3:138:ILE:HG21	2.03	0.41
9:I3:168:SER:OG	9:I3:169:LYS:N	2.52	0.41
11:L3:81:LEU:HD11	11:L3:98:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L3:130:LYS:NZ	11:L3:131:PRO:HD2	2.36	0.41
18:S3:165:PRO:O	18:S3:167:PHE:N	2.54	0.41
19:T3:115:LYS:HA	19:T3:118:GLU:HG3	2.02	0.41
24:Y3:89:LYS:HE3	24:Y3:89:LYS:HB3	1.88	0.41
25:Z3:117:LYS:HA	25:Z3:120:GLU:HG2	2.03	0.41
32:g3:71:LYS:HD2	32:g3:71:LYS:N	2.35	0.41
41:p3:79:VAL:O	41:p3:83:ILE:HG12	2.20	0.41
46:54:130:C:H2'	46:54:131:C:O4'	2.20	0.41
46:54:206:U:O2'	46:54:208:A:N7	2.32	0.41
46:54:1195:G:C2	46:54:1196:G:C5	3.08	0.41
46:54:2027:U:H2'	46:54:2028:C:C6	2.56	0.41
46:54:2862:G:N3	46:54:3624:A:H2'	2.36	0.41
46:54:3777:G:N2	46:54:3815:G:H2'	2.36	0.41
46:54:4390:A:H2'	46:54:4391:G:O4'	2.19	0.41
46:54:4925:U:HO2'	46:54:4926:C:P	2.43	0.41
52:TT:247:GLN:HG2	52:TT:285:TYR:OH	2.21	0.41
52:TT:289:TYR:CD1	52:TT:316:LEU:HD21	2.56	0.41
1:A3:33:ASP:OD1	1:A3:33:ASP:N	2.50	0.41
1:A3:35:ALA:HA	7:G3:94:ILE:HD13	2.02	0.41
1:A3:44:ILE:HG22	1:A3:87:PHE:CE1	2.56	0.41
10:J3:155:HIS:HB2	47:74:55:A:H4'	2.03	0.41
12:M3:135:LEU:HD12	12:M3:135:LEU:HA	1.90	0.41
13:N3:6:TYR:CE1	34:i3:40:VAL:HG13	2.55	0.41
13:N3:76:PRO:O	13:N3:77:LYS:C	2.63	0.41
16:Q3:89:ASP:OD1	16:Q3:91:ARG:HG2	2.20	0.41
18:S3:53:LYS:HD2	47:74:75:G:C4	2.56	0.41
20:U3:37:ALA:C	20:U3:39:PHE:H	2.27	0.41
23:X3:115:LYS:HB2	23:X3:115:LYS:HE2	1.77	0.41
29:d3:33:ILE:HD11	29:d3:41:ARG:O	2.21	0.41
29:d3:75:LYS:HB2	29:d3:79:ASN:O	2.21	0.41
31:f3:45:LYS:HD2	31:f3:105:LEU:HA	2.03	0.41
37:l3:42:ARG:NH2	46:54:2408:U:OP1	2.51	0.41
43:s3:110:ALA:HA	43:s3:181:SER:OG	2.20	0.41
46:54:1075:G:H1	46:54:1235:G:H1	1.69	0.41
46:54:1190:C:H2'	46:54:1191:C:H6	1.85	0.41
46:54:1886:G:C6	46:54:1887:G:C5	3.08	0.41
46:54:2279:A:H2'	46:54:2280:G:O4'	2.20	0.41
46:54:2752:G:H2'	46:54:2753:G:O4'	2.21	0.41
46:54:3753:G:H1'	46:54:3776:G:C5	2.56	0.41
46:54:4735:G:H1	46:54:4964:C:H42	1.69	0.41
50:NA:96:ILE:HB	50:NA:104:PHE:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:TT:106:MET:HE2	52:TT:123:THR:HG23	2.02	0.41
52:TT:379:GLY:N	52:TT:440:LEU:O	2.32	0.41
2:B3:162:VAL:HG12	2:B3:183:ILE:O	2.19	0.41
3:C3:70:GLY:C	3:C3:72:ALA:H	2.29	0.41
3:C3:283:LYS:HB2	3:C3:283:LYS:HE2	1.75	0.41
4:D3:244:HIS:O	4:D3:248:ARG:HG3	2.20	0.41
5:E3:143:LEU:HD12	5:E3:194:GLN:OE1	2.21	0.41
7:G3:313:GLU:OE2	7:G3:314:LEU:N	2.52	0.41
8:H3:95:VAL:O	8:H3:177:ASP:HA	2.21	0.41
9:I3:171:TRP:O	9:I3:174:THR:OG1	2.31	0.41
24:Y3:71:VAL:N	24:Y3:81:TYR:O	2.40	0.41
28:c3:102:SER:OG	28:c3:103:ASP:N	2.53	0.41
32:g3:5:LEU:HD23	32:g3:5:LEU:H	1.85	0.41
43:s3:95:LEU:H	43:s3:95:LEU:HD23	1.85	0.41
46:54:342:G:H2'	46:54:343:C:C6	2.56	0.41
46:54:406:C:HO2'	46:54:407:A:P	2.41	0.41
46:54:1082:C:N4	46:54:1217:G:H1	2.15	0.41
46:54:1321:G:OP1	46:54:1880:G:O2'	2.35	0.41
46:54:2479:G:C6	46:54:2480:G:C5	3.09	0.41
46:54:4977:A:O2'	46:54:4982:A:N1	2.48	0.41
47:74:66:G:C2	47:74:67:C:C2	3.08	0.41
52:TT:56:GLU:HG3	52:TT:56:GLU:O	2.21	0.41
7:G3:113:TYR:CZ	7:G3:114:ILE:HG13	2.55	0.41
8:H3:47:LEU:HD12	8:H3:47:LEU:HA	1.80	0.41
8:H3:105:ILE:CD1	8:H3:136:VAL:HG23	2.51	0.41
9:I3:22:PHE:CZ	46:54:1788:A:H2'	2.56	0.41
9:I3:91:LEU:HD12	9:I3:135:ILE:HG23	2.03	0.41
10:J3:94:LEU:O	10:J3:174:ILE:HA	2.21	0.41
13:N3:204:ARG:HA	13:N3:204:ARG:HD3	1.90	0.41
17:R3:59:SER:C	17:R3:61:ALA:H	2.28	0.41
19:T3:81:LYS:O	27:b3:16:TRP:NE1	2.54	0.41
25:Z3:3:LYS:HB2	25:Z3:6:LYS:NZ	2.36	0.41
30:e3:44:ARG:HB2	30:e3:49:PHE:CD2	2.56	0.41
30:e3:81:ASN:HA	30:e3:111:ILE:HD11	2.03	0.41
32:g3:65:MET:HE3	32:g3:65:MET:HB2	1.88	0.41
46:54:2425:U:H5''	46:54:2426:U:C5	2.56	0.41
46:54:3769:C:C4	46:54:3770:U:C4	3.09	0.41
46:54:4119:C:O2'	46:54:4120:U:O5'	2.31	0.41
46:54:4749:C:H2'	46:54:4750:G:O4'	2.21	0.41
46:54:4903:G:H1	46:54:4918:C:N4	2.19	0.41
52:TT:302:LEU:C	52:TT:304:PRO:HD3	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:TT:320:LEU:HD13	52:TT:323:LEU:HD23	2.02	0.41
1:A3:58:LEU:HB3	1:A3:75:LEU:HD22	2.01	0.41
2:B3:17:LEU:HB3	2:B3:18:PRO:HD3	2.01	0.41
2:B3:56:ILE:HD13	2:B3:56:ILE:HA	1.85	0.41
3:C3:140:LYS:NZ	3:C3:242:PRO:HD2	2.35	0.41
3:C3:218:VAL:O	3:C3:222:ARG:HB3	2.21	0.41
4:D3:21:ARG:O	4:D3:25:GLU:HG3	2.20	0.41
4:D3:93:THR:O	4:D3:93:THR:HG22	2.21	0.41
4:D3:104:LEU:HD22	4:D3:108:ARG:HH11	1.86	0.41
10:J3:157:ILE:HG22	10:J3:158:SER:N	2.35	0.41
11:L3:71:ARG:NH2	46:54:74:G:O3'	2.54	0.41
15:P3:10:ASN:ND2	15:P3:13:LYS:HB2	2.35	0.41
16:Q3:6:ARG:NH2	16:Q3:8:ASN:HD22	2.15	0.41
16:Q3:18:PRO:HD3	16:Q3:52:PHE:CD1	2.56	0.41
16:Q3:85:THR:HG22	16:Q3:104:ARG:HB2	2.03	0.41
17:R3:152:LYS:C	17:R3:153:LYS:HD3	2.45	0.41
18:S3:2:LYS:HG3	46:54:2062:C:OP1	2.21	0.41
19:T3:87:LYS:NZ	46:54:4305:G:N2	2.68	0.41
19:T3:93:ILE:HD13	19:T3:93:ILE:HA	1.80	0.41
20:U3:83:LEU:HD23	20:U3:83:LEU:HA	1.75	0.41
21:V3:46:LYS:H	21:V3:46:LYS:HG2	1.74	0.41
23:X3:119:ILE:HD12	23:X3:140:LEU:HD21	2.02	0.41
24:Y3:114:ASP:O	24:Y3:117:LYS:N	2.54	0.41
28:c3:81:LEU:HB3	28:c3:91:VAL:HG13	2.02	0.41
39:n3:7:LYS:O	39:n3:11:ARG:N	2.49	0.41
43:s3:45:MET:SD	43:s3:48:ARG:NH2	2.94	0.41
43:s3:91:THR:HG21	43:s3:98:ILE:HG13	2.02	0.41
44:t3:68:GLN:CG	44:t3:69:ALA:H	2.34	0.41
44:t3:83:LYS:HE3	44:t3:83:LYS:HB3	1.83	0.41
46:54:182:G:H22	46:54:256:G:C1'	2.34	0.41
46:54:326:C:N4	46:54:327:U:O4	2.53	0.41
46:54:435:A:H2'	46:54:436:C:O4'	2.20	0.41
46:54:493:G:N2	46:54:662:C:H1'	2.36	0.41
46:54:671:G:C2	46:54:672:C:C2	3.09	0.41
46:54:1597:G:O6	46:54:1600:A:H5'	2.21	0.41
46:54:2465:C:O2'	46:54:3672:G:N1	2.51	0.41
46:54:2488:C:HO2'	46:54:2489:C:P	2.44	0.41
46:54:2544:G:O6	48:84:126:C:N4	2.53	0.41
46:54:2564:G:H2'	46:54:2565:A:H8	1.86	0.41
46:54:4579:U:H2'	46:54:4580:U:C6	2.56	0.41
47:74:50:A:H2'	47:74:51:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:84:47:C:H1'	48:84:61:A:H2'	2.03	0.41
52:TT:66:GLN:HA	52:TT:122:LEU:HD23	2.03	0.41
52:TT:155:TRP:CD1	52:TT:155:TRP:N	2.89	0.41
3:C3:53:ALA:HB1	3:C3:105:THR:O	2.22	0.41
4:D3:167:VAL:C	4:D3:169:GLY:H	2.29	0.41
5:E3:215:LEU:O	5:E3:215:LEU:HD12	2.21	0.41
8:H3:82:LYS:HD2	8:H3:88:PHE:CE1	2.56	0.41
9:I3:47:PRO:HB3	9:I3:171:TRP:CZ2	2.56	0.41
9:I3:60:LEU:HD22	9:I3:160:PRO:HD2	2.03	0.41
11:L3:200:LYS:HE2	11:L3:200:LYS:HB3	1.91	0.41
12:M3:24:LEU:H	12:M3:43:THR:HG21	1.85	0.41
16:Q3:115:LYS:HB3	16:Q3:115:LYS:HE2	1.91	0.41
19:T3:118:GLU:C	19:T3:120:LYS:H	2.29	0.41
20:U3:117:ILE:HG22	20:U3:118:ASN:N	2.36	0.41
21:V3:49:LEU:HA	21:V3:49:LEU:HD12	1.87	0.41
21:V3:96:LEU:HG	21:V3:97:TYR:N	2.36	0.41
22:W3:51:TRP:CD1	22:W3:51:TRP:H	2.39	0.41
23:X3:140:LEU:HD11	23:X3:149:VAL:HG11	2.03	0.41
29:d3:121:ASN:ND2	46:54:5058:A:OP1	2.54	0.41
36:k3:40:ARG:NH2	36:k3:41:TYR:OH	2.54	0.41
43:s3:83:ARG:HH12	46:54:2023:C:P	2.44	0.41
45:23:48:C:C2	45:23:59:A:H1'	2.56	0.41
46:54:251:C:H2'	46:54:252:C:H6	1.87	0.41
46:54:2793:G:H5''	46:54:2794:C:H5''	2.01	0.41
46:54:2805:C:N4	46:54:2806:A:N6	2.69	0.41
46:54:4097:G:H22	46:54:4111:U:H3	1.69	0.41
46:54:4132:C:O2	46:54:4152:G:N1	2.50	0.41
46:54:4478:G:O2'	46:54:4602:A:N1	2.54	0.41
46:54:4926:C:H6	46:54:4926:C:H2'	1.65	0.41
1:A3:205:ASN:HB3	1:A3:206:PRO:HD2	2.02	0.40
2:B3:217:ILE:HD13	2:B3:284:ILE:HD11	2.04	0.40
4:D3:243:ALA:O	4:D3:247:ILE:HG13	2.21	0.40
7:G3:247:VAL:HG21	7:G3:249:ARG:NH1	2.36	0.40
8:H3:25:VAL:HG23	8:H3:80:MET:HE1	2.02	0.40
9:I3:52:MET:HE1	9:I3:159:PHE:HE2	1.85	0.40
10:J3:104:ASN:HB3	10:J3:132:VAL:O	2.21	0.40
11:L3:92:ARG:CZ	46:54:109:G:H5'	2.51	0.40
14:O3:43:ILE:HD12	14:O3:43:ILE:H	1.86	0.40
15:P3:47:TYR:OH	15:P3:57:CYS:O	2.30	0.40
20:U3:24:ASP:HA	20:U3:69:LYS:HA	2.03	0.40
23:X3:128:ILE:O	37:l3:10:LYS:NZ	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d3:117:LEU:HD13	29:d3:117:LEU:HA	1.95	0.40
31:f3:36:ARG:NH1	46:54:2066:C:H5''	2.36	0.40
32:g3:102:ILE:HD13	32:g3:102:ILE:HA	1.91	0.40
40:o3:97:LYS:HG3	46:54:4233:A:OP1	2.22	0.40
43:s3:21:LEU:HD22	43:s3:90:PHE:CZ	2.56	0.40
46:54:1190:C:H2'	46:54:1191:C:C6	2.57	0.40
46:54:1446:C:H42	46:54:2108:G:H1	1.68	0.40
46:54:1507:C:C2	46:54:1508:A:C8	3.09	0.40
46:54:1667:A:H5'	46:54:1688:G:OP1	2.20	0.40
46:54:2007:G:C2	46:54:2013:A:N6	2.89	0.40
46:54:2564:G:H2'	46:54:2565:A:C8	2.56	0.40
2:B3:152:SER:OG	2:B3:153:MET:N	2.54	0.40
5:E3:242:LYS:HE2	5:E3:242:LYS:HB3	1.84	0.40
6:F3:143:TYR:CE2	6:F3:236:GLU:HB2	2.57	0.40
15:P3:52:THR:HG22	15:P3:85:LYS:HG3	2.03	0.40
19:T3:106:LEU:HA	19:T3:106:LEU:HD23	1.78	0.40
20:U3:105:ASN:HB2	20:U3:111:GLU:HG2	2.03	0.40
27:b3:8:THR:HG22	46:54:1671:U:H4'	2.03	0.40
31:f3:50:VAL:HG22	31:f3:69:VAL:HG23	2.04	0.40
33:h3:113:LEU:HD23	33:h3:113:LEU:HA	1.90	0.40
35:j3:2:THR:HA	35:j3:6:SER:HB3	2.03	0.40
46:54:48:G:HO2'	46:54:49:U:P	2.44	0.40
46:54:179:G:C2	46:54:258:G:N1	2.88	0.40
46:54:256:G:C2	46:54:257:C:C2	3.10	0.40
46:54:660:G:C2	46:54:661:C:C2	3.09	0.40
46:54:1432:G:O2'	46:54:1451:G:N2	2.45	0.40
46:54:1978:C:O2	46:54:1989:G:N1	2.54	0.40
46:54:2544:G:C5	46:54:2545:U:C5	3.09	0.40
46:54:3753:G:C6	46:54:3754:G:N7	2.90	0.40
46:54:4721:G:C6	46:54:4722:G:C6	3.09	0.40
46:54:4954:G:H2'	46:54:4955:A:O4'	2.21	0.40
52:TT:371:LYS:HG2	52:TT:376:LEU:HG	2.04	0.40
3:C3:290:SER:OG	42:r3:4:HIS:NE2	2.47	0.40
4:D3:40:ASP:OD1	4:D3:40:ASP:N	2.53	0.40
5:E3:285:TYR:HA	5:E3:286:PRO:HD3	1.96	0.40
9:I3:90:ARG:HH21	46:54:1784:U:P	2.44	0.40
11:L3:46:ILE:HG13	11:L3:46:ILE:O	2.22	0.40
11:L3:107:THR:OG1	34:i3:20:ASN:HB3	2.21	0.40
14:O3:185:VAL:O	14:O3:187:LYS:N	2.54	0.40
15:P3:118:GLN:NE2	15:P3:120:ASN:OD1	2.52	0.40
17:R3:134:ASN:OD1	17:R3:134:ASN:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:U3:35:ASP:OD1	20:U3:38:ASN:HB2	2.21	0.40
25:Z3:5:MET:O	25:Z3:28:ASN:ND2	2.54	0.40
46:54:175:C:C2	46:54:262:G:N2	2.89	0.40
46:54:419:A:H61	48:84:15:G:H1'	1.87	0.40
46:54:922(B):C:H3'	46:54:923:C:H5''	2.03	0.40
46:54:962:C:C2'	46:54:963:G:H5'	2.52	0.40
46:54:1096:C:C4	46:54:1097:C:C4	3.10	0.40
46:54:1308:C:H2'	46:54:1309:C:C6	2.56	0.40
46:54:1332:C:H2'	46:54:1333:A:C8	2.57	0.40
46:54:1804:A:H5'	46:54:1806:G:O4'	2.20	0.40
46:54:2422:C:O2'	46:54:3857:G:O2'	2.38	0.40
46:54:2587:A:H3'	46:54:2588:C:C6	2.56	0.40
50:NA:92:THR:HG23	50:NA:93:ARG:N	2.36	0.40
50:NA:111:VAL:HG22	50:NA:122:VAL:HG22	2.02	0.40
52:TT:168:VAL:HA	52:TT:171:ALA:HB3	2.02	0.40
52:TT:386:ILE:HD11	52:TT:435:ILE:HB	2.03	0.40
2:B3:294:LYS:HE2	2:B3:294:LYS:HB2	1.96	0.40
3:C3:339:THR:HA	3:C3:342:ARG:HB3	2.03	0.40
9:I3:51:HIS:HD2	9:I3:168:SER:HB2	1.87	0.40
10:J3:46:GLN:NE2	10:J3:73:THR:O	2.54	0.40
11:L3:71:ARG:HG2	11:L3:72:ALA:H	1.86	0.40
16:Q3:112:ARG:H	16:Q3:112:ARG:HG2	1.67	0.40
20:U3:39:PHE:HZ	20:U3:87:THR:HG23	1.85	0.40
21:V3:66:LYS:HA	21:V3:66:LYS:HD2	1.90	0.40
28:c3:65:MET:HE3	28:c3:65:MET:HB3	1.65	0.40
32:g3:45:ALA:HB3	32:g3:82:MET:HE2	2.03	0.40
32:g3:62:LYS:HD2	46:54:2517:A:O4'	2.22	0.40
37:l3:16:LYS:HA	37:l3:16:LYS:HD3	1.95	0.40
40:o3:47:GLY:HA2	46:54:288:G:H5''	2.04	0.40
40:o3:104:ILE:HD13	45:23:56:C:C2	2.57	0.40
43:s3:106:LYS:HE3	43:s3:106:LYS:HB3	1.88	0.40
44:t3:112:ILE:HA	44:t3:115:GLN:HB3	2.03	0.40
46:54:143:C:H5''	46:54:144:G:H5''	2.03	0.40
46:54:517:C:H2'	46:54:518:G:C8	2.42	0.40
46:54:1754:U:C2	46:54:1756:U:H5	2.39	0.40
51:NB:70:THR:OG1	51:NB:71:VAL:N	2.54	0.40
52:TT:133:TYR:HD1	52:TT:164:LYS:HB2	1.86	0.40
52:TT:261:GLN:O	52:TT:265:VAL:HG12	2.21	0.40
53:1:4:ILE:O	53:1:4:ILE:HG23	2.22	0.40
2:B3:312:LYS:HD2	2:B3:370:THR:HG21	2.03	0.40
3:C3:44:LEU:HD21	3:C3:120:LYS:HE2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C3:208:CYS:SG	3:C3:230:LEU:HD12	2.62	0.40
5:E3:54:ARG:O	5:E3:54:ARG:HG3	2.20	0.40
5:E3:214:HIS:CD2	5:E3:214:HIS:H	2.38	0.40
6:F3:172:THR:O	6:F3:172:THR:OG1	2.40	0.40
11:L3:129:ARG:HA	11:L3:129:ARG:HD2	1.83	0.40
15:P3:41:ILE:O	15:P3:45:THR:HG23	2.22	0.40
21:V3:18:LEU:H	21:V3:18:LEU:HG	1.69	0.40
22:W3:12:LYS:HB2	22:W3:12:LYS:HE3	1.83	0.40
24:Y3:82:ILE:HG22	24:Y3:83:GLU:H	1.86	0.40
40:o3:17:LYS:HE2	40:o3:19:GLN:HE21	1.86	0.40
45:23:33:U:N3	45:23:36:C:OP2	2.50	0.40
46:54:263:G:N7	46:54:264:C:N4	2.69	0.40
46:54:485:C:H4'	46:54:486:C:OP1	2.22	0.40
46:54:1081:C:H5'	46:54:1082:C:OP2	2.22	0.40
46:54:5066:U:H2'	46:54:5067:U:C6	2.56	0.40
52:TT:350:LEU:HD23	52:TT:350:LEU:HA	1.88	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A3	246/257 (96%)	218 (89%)	28 (11%)	0	100	100
2	B3	392/403 (97%)	358 (91%)	34 (9%)	0	100	100
3	C3	360/425 (85%)	331 (92%)	29 (8%)	0	100	100
4	D3	291/297 (98%)	265 (91%)	26 (9%)	0	100	100
5	E3	208/291 (72%)	185 (89%)	23 (11%)	0	100	100
6	F3	223/247 (90%)	206 (92%)	17 (8%)	0	100	100
7	G3	229/319 (72%)	212 (93%)	17 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H3	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I3	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
10	J3	168/178 (94%)	155 (92%)	13 (8%)	0	100	100
11	L3	208/211 (99%)	193 (93%)	14 (7%)	1 (0%)	24	55
12	M3	136/218 (62%)	125 (92%)	11 (8%)	0	100	100
13	N3	201/204 (98%)	185 (92%)	16 (8%)	0	100	100
14	O3	197/203 (97%)	185 (94%)	12 (6%)	0	100	100
15	P3	151/184 (82%)	142 (94%)	9 (6%)	0	100	100
16	Q3	185/188 (98%)	170 (92%)	15 (8%)	0	100	100
17	R3	153/196 (78%)	142 (93%)	11 (7%)	0	100	100
18	S3	174/176 (99%)	158 (91%)	15 (9%)	1 (1%)	21	50
19	T3	157/160 (98%)	138 (88%)	18 (12%)	1 (1%)	21	50
20	U3	100/128 (78%)	89 (89%)	11 (11%)	0	100	100
21	V3	129/140 (92%)	119 (92%)	10 (8%)	0	100	100
22	W3	61/157 (39%)	54 (88%)	7 (12%)	0	100	100
23	X3	116/156 (74%)	104 (90%)	12 (10%)	0	100	100
24	Y3	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
25	Z3	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
26	a3	145/148 (98%)	131 (90%)	14 (10%)	0	100	100
27	b3	100/226 (44%)	94 (94%)	6 (6%)	0	100	100
28	c3	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d3	105/125 (84%)	92 (88%)	13 (12%)	0	100	100
30	e3	126/135 (93%)	118 (94%)	7 (6%)	1 (1%)	16	45
31	f3	107/110 (97%)	98 (92%)	9 (8%)	0	100	100
32	g3	112/116 (97%)	106 (95%)	6 (5%)	0	100	100
33	h3	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
34	i3	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
35	j3	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
36	k3	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
37	l3	48/51 (94%)	38 (79%)	10 (21%)	0	100	100
38	m3	50/102 (49%)	46 (92%)	4 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	n3	23/25 (92%)	23 (100%)	0	0	100	100
40	o3	102/106 (96%)	90 (88%)	12 (12%)	0	100	100
41	p3	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
42	r3	122/137 (89%)	111 (91%)	11 (9%)	0	100	100
43	s3	194/318 (61%)	167 (86%)	27 (14%)	0	100	100
44	t3	151/165 (92%)	121 (80%)	30 (20%)	0	100	100
49	NI	27/29 (93%)	15 (56%)	11 (41%)	1 (4%)	2	14
50	NA	52/215 (24%)	42 (81%)	10 (19%)	0	100	100
51	NB	56/206 (27%)	50 (89%)	6 (11%)	0	100	100
52	TT	424/440 (96%)	395 (93%)	29 (7%)	0	100	100
53	1	32/64 (50%)	17 (53%)	13 (41%)	2 (6%)	1	6
All	All	7271/8745 (83%)	6614 (91%)	650 (9%)	7 (0%)	49	77

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
53	1	4	ILE
11	L3	64	VAL
18	S3	166	ARG
30	e3	127	ALA
49	NI	20	ALA
19	T3	82	GLY
53	1	5	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A3	190/199 (96%)	188 (99%)	2 (1%)	65	76
2	B3	342/348 (98%)	340 (99%)	2 (1%)	78	81
3	C3	302/347 (87%)	302 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D3	247/250 (99%)	247 (100%)	0	100	100
5	E3	190/251 (76%)	188 (99%)	2 (1%)	65	76
6	F3	196/215 (91%)	195 (100%)	1 (0%)	81	83
7	G3	200/272 (74%)	200 (100%)	0	100	100
8	H3	169/171 (99%)	168 (99%)	1 (1%)	78	81
9	I3	175/181 (97%)	175 (100%)	0	100	100
10	J3	143/149 (96%)	141 (99%)	2 (1%)	59	74
11	L3	175/176 (99%)	172 (98%)	3 (2%)	53	72
12	M3	117/161 (73%)	116 (99%)	1 (1%)	70	78
13	N3	171/172 (99%)	169 (99%)	2 (1%)	63	76
14	O3	171/173 (99%)	169 (99%)	2 (1%)	63	76
15	P3	134/163 (82%)	133 (99%)	1 (1%)	76	80
16	Q3	164/164 (100%)	164 (100%)	0	100	100
17	R3	138/175 (79%)	138 (100%)	0	100	100
18	S3	157/157 (100%)	155 (99%)	2 (1%)	61	75
19	T3	139/140 (99%)	139 (100%)	0	100	100
20	U3	92/114 (81%)	92 (100%)	0	100	100
21	V3	101/107 (94%)	100 (99%)	1 (1%)	68	77
22	W3	55/126 (44%)	55 (100%)	0	100	100
23	X3	106/134 (79%)	105 (99%)	1 (1%)	70	78
24	Y3	124/135 (92%)	123 (99%)	1 (1%)	73	80
25	Z3	117/118 (99%)	115 (98%)	2 (2%)	53	72
26	a3	119/120 (99%)	118 (99%)	1 (1%)	73	80
27	b3	84/172 (49%)	83 (99%)	1 (1%)	63	76
28	c3	84/98 (86%)	83 (99%)	1 (1%)	63	76
29	d3	98/110 (89%)	96 (98%)	2 (2%)	48	70
30	e3	114/121 (94%)	114 (100%)	0	100	100
31	f3	88/89 (99%)	88 (100%)	0	100	100
32	g3	98/99 (99%)	98 (100%)	0	100	100
33	h3	109/110 (99%)	108 (99%)	1 (1%)	70	78
34	i3	86/89 (97%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	j3	73/80 (91%)	71 (97%)	2 (3%)	39	65
36	k3	64/65 (98%)	63 (98%)	1 (2%)	55	73
37	l3	47/48 (98%)	47 (100%)	0	100	100
38	m3	48/90 (53%)	48 (100%)	0	100	100
39	n3	24/24 (100%)	24 (100%)	0	100	100
40	o3	92/94 (98%)	92 (100%)	0	100	100
41	p3	74/75 (99%)	72 (97%)	2 (3%)	39	65
42	r3	108/121 (89%)	108 (100%)	0	100	100
43	s3	164/258 (64%)	164 (100%)	0	100	100
44	t3	126/137 (92%)	125 (99%)	1 (1%)	73	80
49	NI	2/2 (100%)	2 (100%)	0	100	100
50	NA	48/183 (26%)	47 (98%)	1 (2%)	47	69
51	NB	51/165 (31%)	51 (100%)	0	100	100
52	TT	370/381 (97%)	368 (100%)	2 (0%)	81	83
53	1	32/53 (60%)	25 (78%)	7 (22%)	1	4
All	All	6318/7382 (86%)	6270 (99%)	48 (1%)	70	80

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A3	32	VAL
1	A3	165	VAL
2	B3	90	VAL
2	B3	207	VAL
5	E3	178	VAL
5	E3	215	LEU
6	F3	236	GLU
8	H3	105	ILE
10	J3	115	LEU
10	J3	173	ILE
11	L3	10	LEU
11	L3	70	VAL
11	L3	154	VAL
12	M3	43	THR
13	N3	80	THR
13	N3	155	VAL
14	O3	36	VAL

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Mol	Chain	Res	Type
14	O3	195	VAL
15	P3	24	VAL
18	S3	67	VAL
18	S3	90	THR
21	V3	18	LEU
23	X3	120	ASP
24	Y3	79	VAL
25	Z3	11	VAL
25	Z3	53	VAL
26	a3	122	VAL
27	b3	116	LEU
28	c3	91	VAL
29	d3	22	THR
29	d3	86	VAL
33	h3	82	ASP
35	j3	67	LEU
35	j3	82	THR
36	k3	48	THR
41	p3	16	THR
41	p3	52	VAL
44	t3	64	ILE
50	NA	88	VAL
52	TT	204	ASP
52	TT	277	LEU
53	1	1	MET
53	1	2	ARG
53	1	3	GLU
53	1	5	VAL
53	1	6	HIS
53	1	8	GLN
53	1	49	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (131) such sidechains are listed below:

Mol	Chain	Res	Type
1	A3	86	GLN
1	A3	194	ASN
1	A3	205	ASN
2	B3	3	HIS
2	B3	245	HIS
2	B3	315	ASN
2	B3	354	GLN

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Mol	Chain	Res	Type
3	C3	50	GLN
3	C3	119	GLN
3	C3	142	HIS
3	C3	198	ASN
3	C3	215	ASN
4	D3	131	ASN
4	D3	175	HIS
4	D3	275	GLN
5	E3	45	HIS
5	E3	193	HIS
5	E3	214	HIS
5	E3	253	GLN
5	E3	287	HIS
6	F3	57	HIS
6	F3	115	GLN
6	F3	118	ASN
6	F3	125	ASN
6	F3	199	HIS
7	G3	91	ASN
7	G3	99	GLN
7	G3	138	GLN
7	G3	206	GLN
7	G3	248	HIS
9	I3	59	GLN
9	I3	73	ASN
9	I3	144	ASN
9	I3	163	GLN
10	J3	42	GLN
10	J3	97	ASN
10	J3	104	ASN
11	L3	19	GLN
11	L3	111	GLN
11	L3	113	ASN
11	L3	115	GLN
12	M3	20	HIS
12	M3	48	GLN
12	M3	131	GLN
13	N3	37	HIS
13	N3	99	GLN
13	N3	149	GLN
13	N3	156	HIS
13	N3	196	ASN

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Mol	Chain	Res	Type
13	N3	199	GLN
14	O3	50	ASN
14	O3	150	GLN
14	O3	167	HIS
15	P3	10	ASN
15	P3	21	ASN
15	P3	25	HIS
15	P3	28	ASN
15	P3	56	GLN
15	P3	75	GLN
15	P3	116	HIS
16	Q3	7	HIS
16	Q3	8	ASN
16	Q3	40	ASN
16	Q3	44	ASN
16	Q3	57	ASN
16	Q3	125	GLN
16	Q3	160	HIS
16	Q3	188	ASN
17	R3	7	GLN
17	R3	34	ASN
17	R3	58	HIS
17	R3	130	ASN
18	S3	37	HIS
18	S3	91	HIS
18	S3	92	ASN
18	S3	125	GLN
18	S3	163	HIS
19	T3	95	HIS
19	T3	114	GLN
19	T3	127	GLN
20	U3	17	GLN
20	U3	105	ASN
22	W3	50	ASN
23	X3	57	GLN
23	X3	93	ASN
23	X3	105	ASN
24	Y3	66	GLN
27	b3	10	HIS
27	b3	49	HIS
27	b3	50	ASN
27	b3	60	ASN

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Mol	Chain	Res	Type
27	b3	61	ASN
27	b3	101	HIS
29	d3	18	ASN
29	d3	79	ASN
30	e3	52	GLN
32	g3	18	ASN
32	g3	114	GLN
33	h3	63	GLN
33	h3	96	ASN
33	h3	108	GLN
34	i3	26	HIS
34	i3	36	HIS
34	i3	80	HIS
35	j3	28	HIS
35	j3	76	HIS
37	l3	25	GLN
38	m3	78	HIS
40	o3	102	GLN
42	r3	45	HIS
42	r3	103	HIS
43	s3	42	GLN
43	s3	58	ASN
43	s3	72	ASN
43	s3	81	HIS
43	s3	105	ASN
51	NB	73	HIS
51	NB	75	ASN
51	NB	108	ASN
52	TT	93	GLN
52	TT	128	ASN
52	TT	157	GLN
52	TT	172	HIS
52	TT	197	GLN
52	TT	209	HIS
52	TT	226	HIS
52	TT	278	ASN
52	TT	311	GLN
52	TT	359	GLN
52	TT	443	HIS
53	1	8	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	23	74/76 (97%)	13 (17%)	0
46	54	3518/3543 (99%)	823 (23%)	58 (1%)
47	74	119/120 (99%)	14 (11%)	0
48	84	149/156 (95%)	32 (21%)	1 (0%)
All	All	3860/3895 (99%)	882 (22%)	59 (1%)

All (882) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	23	9	A
45	23	13	U
45	23	16	C
45	23	19	G
45	23	20(A)	U
45	23	21	A
45	23	24	A
45	23	39	G
45	23	46	G
45	23	47	U
45	23	56	C
45	23	67	G
45	23	75	C
46	54	12	A
46	54	13	U
46	54	15	A
46	54	30	C
46	54	39	A
46	54	42	A
46	54	44	A
46	54	56	A
46	54	58	G
46	54	59	A
46	54	64	A
46	54	65	A
46	54	72	C
46	54	73	A
46	54	74	G
46	54	84	A
46	54	91	G
46	54	95	G
46	54	104	G
46	54	108	A
46	54	109	G

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Mol	Chain	Res	Type
46	54	110	C
46	54	118	C
46	54	119	G
46	54	122	U
46	54	126	C
46	54	131	C
46	54	134	G
46	54	135	G
46	54	136	C
46	54	137	G
46	54	141	C
46	54	142	G
46	54	146	G
46	54	157	U
46	54	159	C
46	54	160	G
46	54	172	C
46	54	177	G
46	54	182	G
46	54	200	U
46	54	201	C
46	54	209	U
46	54	216	C
46	54	218	A
46	54	221	C
46	54	224	U
46	54	225	G
46	54	232	G
46	54	233	U
46	54	234	G
46	54	246	G
46	54	256	G
46	54	258	G
46	54	262	G
46	54	263	G
46	54	265	C
46	54	266	C
46	54	267	G
46	54	276	C
46	54	280	G
46	54	297	U
46	54	306	A

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Mol	Chain	Res	Type
46	54	308	G
46	54	309	C
46	54	315	G
46	54	316	U
46	54	322	C
46	54	326	C
46	54	334	A
46	54	340	C
46	54	363	A
46	54	370	U
46	54	371	A
46	54	387	G
46	54	407	A
46	54	410	A
46	54	412	G
46	54	413	G
46	54	415	G
46	54	417	G
46	54	428	G
46	54	440	U
46	54	446	C
46	54	449	C
46	54	450	G
46	54	452	A
46	54	453	G
46	54	454	U
46	54	455	C
46	54	463	A
46	54	467	U
46	54	468	U
46	54	481	G
46	54	481(A)	C
46	54	482	G
46	54	483	G
46	54	485	C
46	54	486	C
46	54	492	U
46	54	493	G
46	54	496	G
46	54	497	G
46	54	498	C
46	54	499	G

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Mol	Chain	Res	Type
46	54	505	G
46	54	506	C
46	54	510	U
46	54	644	G
46	54	647	G
46	54	658	C
46	54	659	G
46	54	661	C
46	54	666	G
46	54	667	A
46	54	668	C
46	54	669	C
46	54	670	G
46	54	685	C
46	54	686	A
46	54	687	U
46	54	696	C
46	54	697	G
46	54	699	C
46	54	701	G
46	54	704	C
46	54	705	G
46	54	708	G
46	54	731	G
46	54	738	C
46	54	749	G
46	54	756	G
46	54	758	G
46	54	914	U
46	54	917	A
46	54	918	G
46	54	923	C
46	54	925	C
46	54	926	G
46	54	929	A
46	54	930	G
46	54	932	A
46	54	933	G
46	54	934	C
46	54	935	A
46	54	935(A)	G
46	54	936	C

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Mol	Chain	Res	Type
46	54	938	C
46	54	939	G
46	54	941	C
46	54	944	A
46	54	945	U
46	54	959	G
46	54	960	A
46	54	961	G
46	54	964	A
46	54	965	G
46	54	966	A
46	54	967	C
46	54	968	C
46	54	969	C
46	54	971(A)	G
46	54	972	C
46	54	973	G
46	54	979	C
46	54	983	C
46	54	990	C
46	54	1070	G
46	54	1072	C
46	54	1073	G
46	54	1076	C
46	54	1078	A
46	54	1079	C
46	54	1081	C
46	54	1082	C
46	54	1099	C
46	54	1175	A
46	54	1179	U
46	54	1199	G
46	54	1210	C
46	54	1211	G
46	54	1212	G
46	54	1215	C
46	54	1216	C
46	54	1234	G
46	54	1235	G
46	54	1236	C
46	54	1237	C
46	54	1238	A

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Mol	Chain	Res	Type
46	54	1239	C
46	54	1272	C
46	54	1273	G
46	54	1274	A
46	54	1275	G
46	54	1281	G
46	54	1284	G
46	54	1287	G
46	54	1289	C
46	54	1291	G
46	54	1292	C
46	54	1293	G
46	54	1296	G
46	54	1301	C
46	54	1303	A
46	54	1304	C
46	54	1314	C
46	54	1326	A
46	54	1330	A
46	54	1354	A
46	54	1358	G
46	54	1359	G
46	54	1364	U
46	54	1370	G
46	54	1371	A
46	54	1377	G
46	54	1378	C
46	54	1387	A
46	54	1392	A
46	54	1394	G
46	54	1397	A
46	54	1398	A
46	54	1403	G
46	54	1411(A)	G
46	54	1415	G
46	54	1419	G
46	54	1420	A
46	54	1421	G
46	54	1433	A
46	54	1436	C
46	54	1437	C
46	54	1438	U

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Mol	Chain	Res	Type
46	54	1440	U
46	54	1441	C
46	54	1445	U
46	54	1446	C
46	54	1448	G
46	54	1456	C
46	54	1457	G
46	54	1458	C
46	54	1475	G
46	54	1478	C
46	54	1481	C
46	54	1482	G
46	54	1483	C
46	54	1484	G
46	54	1489	G
46	54	1497	A
46	54	1498	G
46	54	1502	G
46	54	1514	U
46	54	1516	G
46	54	1518	A
46	54	1519	C
46	54	1523	A
46	54	1534	A
46	54	1547	A
46	54	1563	A
46	54	1564	A
46	54	1566	C
46	54	1578	U
46	54	1586	G
46	54	1591	U
46	54	1596	U
46	54	1597	G
46	54	1600	A
46	54	1602	U
46	54	1612	G
46	54	1613	A
46	54	1624	G
46	54	1625	G
46	54	1631	A
46	54	1633	G
46	54	1634	A

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Mol	Chain	Res	Type
46	54	1638	A
46	54	1640	C
46	54	1654	G
46	54	1658	G
46	54	1661	C
46	54	1676	C
46	54	1677	U
46	54	1696	C
46	54	1731	C
46	54	1733	G
46	54	1741	G
46	54	1742	A
46	54	1750	G
46	54	1756	U
46	54	1760	G
46	54	1761	G
46	54	1764	G
46	54	1767	A
46	54	1768	C
46	54	1769	G
46	54	1772	C
46	54	1774	C
46	54	1775	A
46	54	1780	A
46	54	1787	A
46	54	1798	G
46	54	1799	G
46	54	1804	A
46	54	1807	C
46	54	1809	C
46	54	1811	G
46	54	1815	G
46	54	1818	G
46	54	1819	G
46	54	1821	G
46	54	1822	U
46	54	1828	C
46	54	1834	U
46	54	1835	G
46	54	1836	G
46	54	1837	A
46	54	1842	G

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Mol	Chain	Res	Type
46	54	1843	A
46	54	1847	C
46	54	1855	G
46	54	1869	G
46	54	1882	U
46	54	1889	U
46	54	1892	A
46	54	1897	A
46	54	1898	C
46	54	1916	G
46	54	1918	U
46	54	1920	C
46	54	1921	C
46	54	1922	G
46	54	1931	C
46	54	1932	A
46	54	1935	C
46	54	1940	G
46	54	1945	G
46	54	1947	U
46	54	1948	G
46	54	1957	U
46	54	1958	A
46	54	1960	A
46	54	1961	G
46	54	1962	A
46	54	1963	C
46	54	1964	A
46	54	1965	G
46	54	1968	G
46	54	1969	G
46	54	1971	U
46	54	1974	U
46	54	1975	G
46	54	1976	G
46	54	1978	C
46	54	1979	A
46	54	1980	U
46	54	1984	A
46	54	1987	C
46	54	1988	G
46	54	1990	A

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Mol	Chain	Res	Type
46	54	1991	A
46	54	1997	U
46	54	1999	A
46	54	2001	G
46	54	2002	A
46	54	2003	G
46	54	2004	U
46	54	2008	U
46	54	2011	C
46	54	2018	C
46	54	2020	U
46	54	2021	G
46	54	2022	C
46	54	2024	G
46	54	2026	A
46	54	2043	A
46	54	2046	G
46	54	2047	A
46	54	2048	U
46	54	2052	G
46	54	2053	C
46	54	2055	G
46	54	2056	G
46	54	2063	G
46	54	2064	G
46	54	2069	A
46	54	2071	A
46	54	2084	U
46	54	2090	U
46	54	2092	G
46	54	2093	G
46	54	2094	C
46	54	2095	A
46	54	2097	A
46	54	2098	G
46	54	2099	C
46	54	2100	G
46	54	2101	A
46	54	2102	G
46	54	2104	A
46	54	2105	A
46	54	2107	A

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Mol	Chain	Res	Type
46	54	2108	G
46	54	2110	G
46	54	2259	G
46	54	2260	C
46	54	2267	U
46	54	2268	A
46	54	2269	C
46	54	2275	G
46	54	2277	C
46	54	2279	A
46	54	2289	C
46	54	2294	G
46	54	2299	G
46	54	2300	A
46	54	2301	G
46	54	2306	G
46	54	2313	A
46	54	2314	G
46	54	2316	G
46	54	2331	G
46	54	2333	G
46	54	2335	C
46	54	2348	G
46	54	2351	C
46	54	2364	G
46	54	2382	A
46	54	2395	A
46	54	2396	A
46	54	2398	U
46	54	2408	U
46	54	2409	U
46	54	2417	A
46	54	2422	C
46	54	2424	G
46	54	2425	U
46	54	2430	C
46	54	2431	A
46	54	2433	G
46	54	2441	C
46	54	2447	U
46	54	2450	G
46	54	2453	A

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Mol	Chain	Res	Type
46	54	2469	C
46	54	2475	G
46	54	2476	G
46	54	2487	G
46	54	2488	C
46	54	2489	C
46	54	2490	U
46	54	2491	C
46	54	2492	C
46	54	2498	C
46	54	2503	G
46	54	2504	C
46	54	2505	C
46	54	2506	G
46	54	2511	A
46	54	2512	A
46	54	2513	A
46	54	2527	A
46	54	2529	A
46	54	2530	U
46	54	2536	A
46	54	2537	A
46	54	2546	G
46	54	2547	G
46	54	2553	A
46	54	2554	U
46	54	2566	G
46	54	2568	C
46	54	2570	U
46	54	2575	U
46	54	2583	C
46	54	2586	G
46	54	2587	A
46	54	2588	C
46	54	2599	G
46	54	2600	A
46	54	2602	G
46	54	2618	G
46	54	2620	G
46	54	2621	A
46	54	2627	C
46	54	2638	G

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Mol	Chain	Res	Type
46	54	2653	C
46	54	2662	G
46	54	2669	C
46	54	2673	G
46	54	2674	A
46	54	2676	A
46	54	2677	G
46	54	2686	G
46	54	2687	U
46	54	2695	A
46	54	2696	A
46	54	2705	G
46	54	2707	U
46	54	2708	U
46	54	2709	C
46	54	2711	G
46	54	2714	G
46	54	2721	G
46	54	2725	A
46	54	2726	G
46	54	2740	U
46	54	2743	A
46	54	2760	G
46	54	2761	U
46	54	2763	U
46	54	2764	A
46	54	2769	U
46	54	2772	C
46	54	2787	A
46	54	2788	U
46	54	2790	U
46	54	2794	C
46	54	2798	A
46	54	2803	U
46	54	2807	A
46	54	2808	G
46	54	2822	G
46	54	2826	U
46	54	2827	G
46	54	2828	U
46	54	2834	C
46	54	2842	G

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Mol	Chain	Res	Type
46	54	2850	A
46	54	2855	G
46	54	2867	C
46	54	2875	C
46	54	2879	A
46	54	2895	A
46	54	3598	C
46	54	3603	G
46	54	3604	A
46	54	3605	C
46	54	3616	U
46	54	3617	G
46	54	3618	C
46	54	3622	C
46	54	3625	G
46	54	3626	G
46	54	3630	A
46	54	3635	A
46	54	3644	U
46	54	3646	A
46	54	3648	A
46	54	3649	A
46	54	3657	U
46	54	3662	A
46	54	3664	G
46	54	3672	G
46	54	3673	C
46	54	3674	G
46	54	3682	A
46	54	3692	A
46	54	3702	A
46	54	3711	A
46	54	3714	G
46	54	3728	A
46	54	3729	U
46	54	3743	G
46	54	3748	A
46	54	3750	G
46	54	3753	G
46	54	3756	A
46	54	3760	A
46	54	3763	A

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Mol	Chain	Res	Type
46	54	3767	C
46	54	3772	U
46	54	3773	U
46	54	3776	G
46	54	3777	G
46	54	3780	G
46	54	3783	A
46	54	3784	A
46	54	3786	U
46	54	3787	G
46	54	3809	G
46	54	3810	C
46	54	3811	G
46	54	3814	U
46	54	3817	A
46	54	3819	G
46	54	3822	U
46	54	3824	A
46	54	3838	U
46	54	3840	U
46	54	3876	A
46	54	3877	A
46	54	3878	C
46	54	3879	G
46	54	3880	G
46	54	3889	G
46	54	3897	G
46	54	3901	A
46	54	3904	G
46	54	3905	A
46	54	3906	A
46	54	3907	G
46	54	3908	A
46	54	3915	U
46	54	3916	G
46	54	3917	A
46	54	3923	A
46	54	3926	C
46	54	3938	G
46	54	3939	G
46	54	3943	A
46	54	3946	G

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Mol	Chain	Res	Type
46	54	4066	U
46	54	4069	U
46	54	4070	U
46	54	4076	G
46	54	4084	G
46	54	4086	G
46	54	4088	C
46	54	4097	G
46	54	4111	U
46	54	4116	C
46	54	4118	U
46	54	4119	C
46	54	4120	U
46	54	4121	G
46	54	4127	A
46	54	4128	A
46	54	4133	C
46	54	4136	G
46	54	4158	C
46	54	4162	C
46	54	4163	U
46	54	4166	G
46	54	4170	A
46	54	4171	C
46	54	4183	G
46	54	4184	G
46	54	4191	G
46	54	4203	A
46	54	4212	A
46	54	4215	C
46	54	4225	G
46	54	4229	U
46	54	4233	A
46	54	4237	C
46	54	4251	A
46	54	4254	G
46	54	4265	U
46	54	4266	G
46	54	4267	G
46	54	4268	A
46	54	4271	A
46	54	4273	A

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Mol	Chain	Res	Type
46	54	4281	A
46	54	4282	A
46	54	4291	G
46	54	4297	G
46	54	4304	A
46	54	4305	G
46	54	4306	U
46	54	4314	C
46	54	4317	A
46	54	4324	A
46	54	4329	G
46	54	4330	G
46	54	4332	C
46	54	4339	A
46	54	4349	C
46	54	4354	U
46	54	4355	G
46	54	4364	G
46	54	4373	G
46	54	4377	G
46	54	4378	A
46	54	4379	A
46	54	4380	A
46	54	4387	C
46	54	4391	G
46	54	4393	G
46	54	4394	A
46	54	4395	U
46	54	4398	C
46	54	4401	G
46	54	4419	U
46	54	4421	C
46	54	4422	A
46	54	4430	G
46	54	4437	U
46	54	4438	U
46	54	4444	C
46	54	4448	G
46	54	4449	A
46	54	4452	U
46	54	4453	C
46	54	4464	A

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Mol	Chain	Res	Type
46	54	4466	C
46	54	4471	U
46	54	4472	G
46	54	4473	A
46	54	4475	G
46	54	4488	A
46	54	4489	G
46	54	4500	U
46	54	4512	U
46	54	4513	A
46	54	4515	G
46	54	4519	C
46	54	4522	G
46	54	4523	A
46	54	4524	G
46	54	4528	G
46	54	4535	A
46	54	4548	A
46	54	4549	G
46	54	4560	C
46	54	4562	C
46	54	4567	G
46	54	4570	G
46	54	4573	G
46	54	4574	U
46	54	4575	G
46	54	4584	A
46	54	4585	U
46	54	4587	G
46	54	4590	A
46	54	4605	A
46	54	4636	U
46	54	4637	G
46	54	4639	G
46	54	4652	G
46	54	4656	A
46	54	4657	U
46	54	4661	G
46	54	4670	C
46	54	4672	A
46	54	4677	U
46	54	4687	A

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Mol	Chain	Res	Type
46	54	4693	C
46	54	4694	G
46	54	4709	U
46	54	4719	G
46	54	4720	C
46	54	4722	G
46	54	4728	U
46	54	4736	C
46	54	4738	C
46	54	4744	A
46	54	4745	G
46	54	4750	G
46	54	4751	G
46	54	4752	U
46	54	4754	G
46	54	4757	C
46	54	4759	C
46	54	4761	G
46	54	4764	A
46	54	4765	G
46	54	4771	C
46	54	4772	C
46	54	4868	G
46	54	4870	G
46	54	4871	C
46	54	4875	G
46	54	4882	U
46	54	4883	C
46	54	4885	U
46	54	4895	C
46	54	4896	G
46	54	4897	G
46	54	4903	G
46	54	4909	A
46	54	4910	A
46	54	4912	G
46	54	4913	G
46	54	4919	G
46	54	4921	C
46	54	4922	C
46	54	4924	C
46	54	4925	U

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Mol	Chain	Res	Type
46	54	4926	C
46	54	4927	G
46	54	4928	C
46	54	4931	G
46	54	4935	C
46	54	4937	C
46	54	4940	C
46	54	4943	A
46	54	4944	C
46	54	4948	C
46	54	4949	G
46	54	4950	U
46	54	4951	G
46	54	4955	A
46	54	4956	A
46	54	4957	C
46	54	4958	C
46	54	4960	G
46	54	4963	G
46	54	4965	U
46	54	4966	A
46	54	4967	A
46	54	4976	U
46	54	4977	A
46	54	4985	U
46	54	4988	U
46	54	4989	U
46	54	4990	C
46	54	4991	U
46	54	4993	G
46	54	5006	U
46	54	5014	A
46	54	5016	A
46	54	5017	G
46	54	5022	U
46	54	5040	U
46	54	5041	G
46	54	5047	C
46	54	5050	C
46	54	5052	C
46	54	5053	U
46	54	5054	C

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Mol	Chain	Res	Type
46	54	5056	A
46	54	5058	A
46	54	5061	A
46	54	5062	G
47	74	7	G
47	74	10	C
47	74	22	A
47	74	25	G
47	74	31	G
47	74	42	A
47	74	53	U
47	74	54	A
47	74	64	G
47	74	80	U
47	74	100	A
47	74	110	G
47	74	111	C
47	74	120	U
48	84	2	G
48	84	3	A
48	84	13	G
48	84	20	A
48	84	23	C
48	84	32	C
48	84	34	U
48	84	35	C
48	84	38	U
48	84	49	G
48	84	59	A
48	84	62	A
48	84	63	U
48	84	75	G
48	84	79	G
48	84	86	U
48	84	87	G
48	84	103	A
48	84	105	C
48	84	106	G
48	84	109	C
48	84	110	U
48	84	111	U
48	84	112	G

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Mol	Chain	Res	Type
48	84	114	G
48	84	123	U
48	84	125	C
48	84	126	C
48	84	127	U
48	84	128	C
48	84	153	C
48	84	156	U

All (59) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	54	12	A
46	54	125	C
46	54	134	G
46	54	245	C
46	54	265	C
46	54	275	C
46	54	406	C
46	54	449	C
46	54	480	C
46	54	485	C
46	54	498	C
46	54	504	G
46	54	684	G
46	54	685	C
46	54	696	C
46	54	704	C
46	54	935(A)	G
46	54	959	G
46	54	971(A)	G
46	54	1072	C
46	54	1174	G
46	54	1211	G
46	54	1236	C
46	54	1238	A
46	54	1329	G
46	54	1370	G
46	54	1440	U
46	54	1445	U
46	54	1455	G
46	54	1477	C

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Mol	Chain	Res	Type
46	54	1482	G
46	54	1633	G
46	54	1818	G
46	54	2046	G
46	54	2089	G
46	54	2266	C
46	54	2468	U
46	54	2488	C
46	54	2502	A
46	54	2546	G
46	54	2695	A
46	54	3603	G
46	54	3625	G
46	54	3876	A
46	54	3888	G
46	54	3904	G
46	54	4119	C
46	54	4170	A
46	54	4232	U
46	54	4354	U
46	54	4378	A
46	54	4448	G
46	54	4719	G
46	54	4884	G
46	54	4921	C
46	54	4925	U
46	54	4947	U
46	54	4989	U
48	84	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 225 ligands modelled in this entry, 225 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

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	54	27
45	23	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	54	2113:G	O3'	2258:C	P	40.63
1	54	1252:C	O3'	1271:G	P	37.10
1	54	1219:G	O3'	1233:G	P	19.39
1	54	3948:C	O3'	4065:G	P	18.92
1	54	4138:C	O3'	4146:G	P	18.16
1	54	990:C	O3'	1064:G	P	17.76
1	54	1696:C	O3'	1720:C	P	16.65
1	54	523:C	O3'	638:G	P	16.27
1	54	5022:U	O3'	5028:G	P	16.12
1	54	4777:C	O3'	4859:C	P	16.01
1	54	1406(C):G	O3'	1411:C	P	15.31
1	54	4101:C	O3'	4107:G	P	15.18
1	54	1364:U	O3'	1368:A	P	13.95
1	54	760:G	O3'	904:C	P	13.79
1	54	2901:G	O3'	3597:G	P	12.37
1	54	182:G	O3'	189:G	P	12.34
1	54	1180:C	O3'	1183:C	P	9.50
1	54	4729:A	O3'	4735:G	P	9.38
1	54	1100:U	O3'	1168:G	P	8.14

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	54	512:U	O3'	515:C	P	7.49
1	54	500:G	O3'	504:G	P	6.25
1	23	16:C	O3'	18:G	P	5.32
1	54	4740:G	O3'	4743:G	P	5.30
1	54	170:C	O3'	171:U	P	4.95
1	54	1239:C	O3'	1244:G	P	4.92
1	54	5020:G	O3'	5021:C	P	3.70
1	54	4899:G	O3'	4902:C	P	3.31
1	54	751:G	O3'	752:G	P	3.15

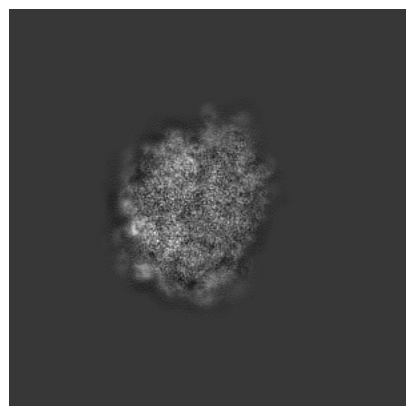
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10380. These allow visual inspection of the internal detail of the map and identification of artifacts.

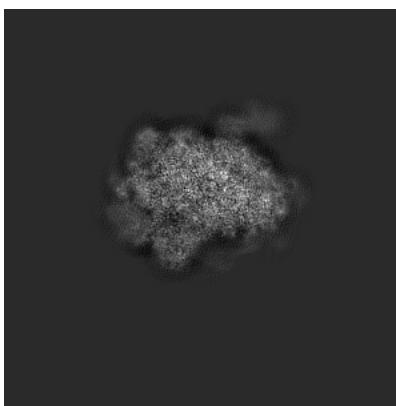
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

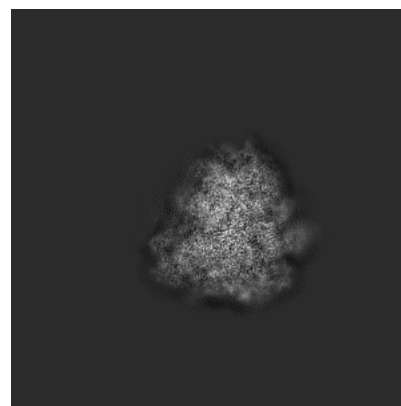
6.1.1 Primary map



X

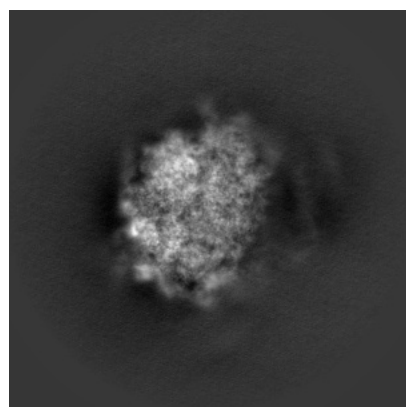


Y

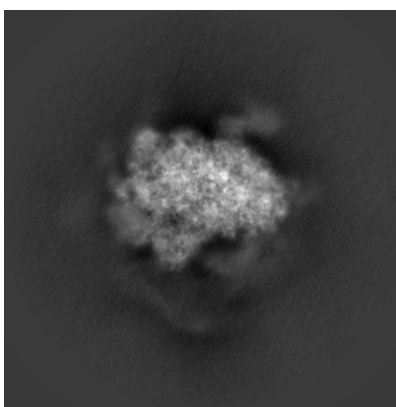


Z

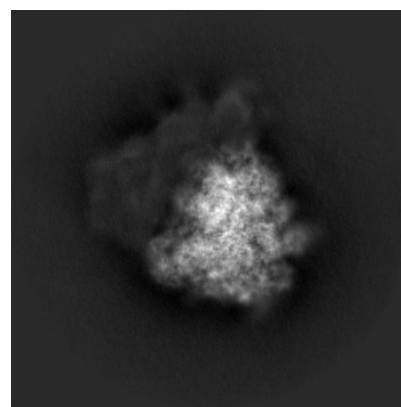
6.1.2 Raw map



X



Y

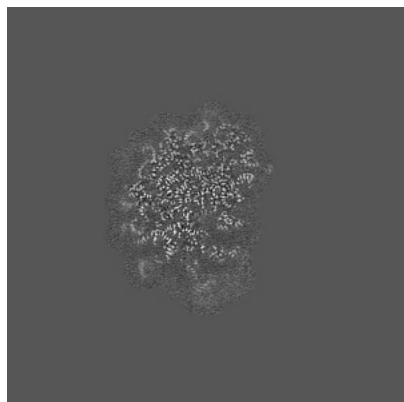


Z

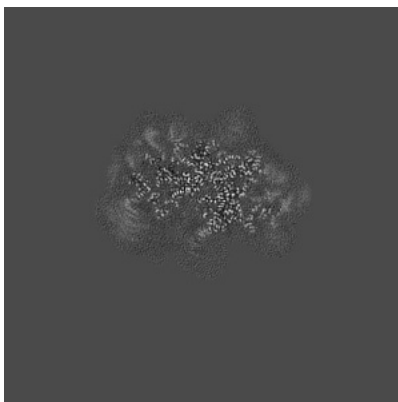
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

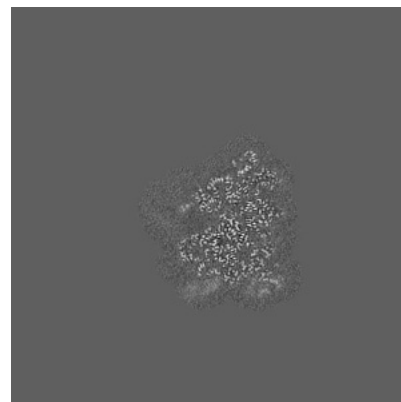
6.2.1 Primary map



X Index: 200

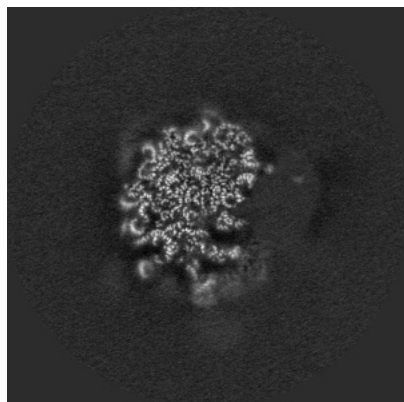


Y Index: 200

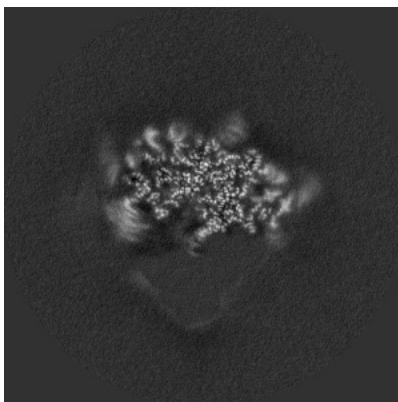


Z Index: 200

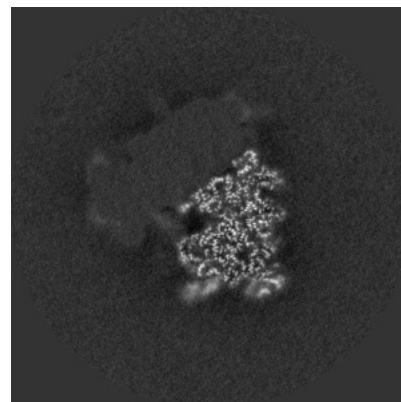
6.2.2 Raw map



X Index: 200



Y Index: 200

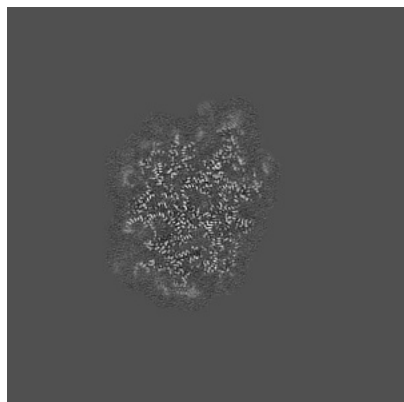


Z Index: 200

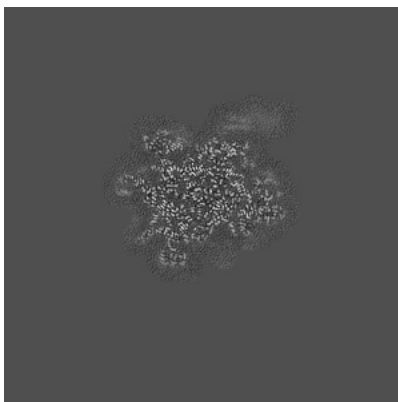
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

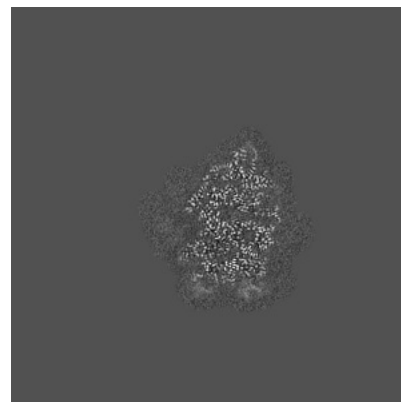
6.3.1 Primary map



X Index: 218

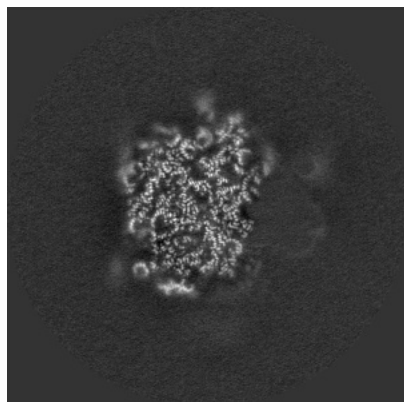


Y Index: 161

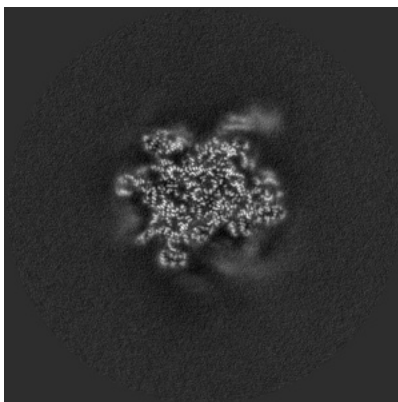


Z Index: 208

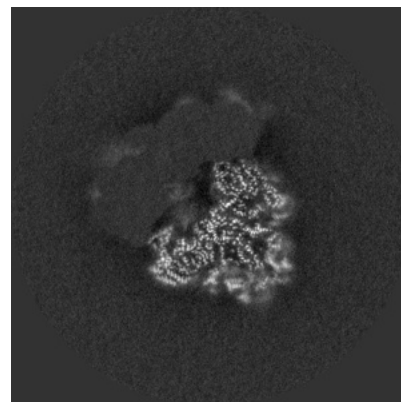
6.3.2 Raw map



X Index: 215



Y Index: 161

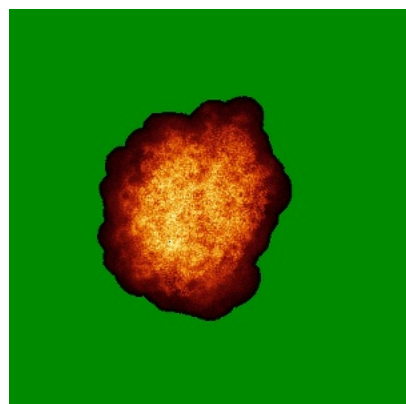


Z Index: 176

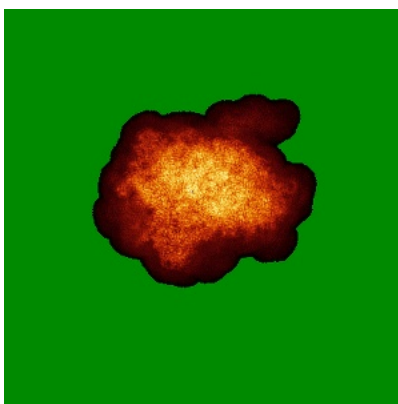
The images above show the largest variance slices of the map in three orthogonal directions.

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

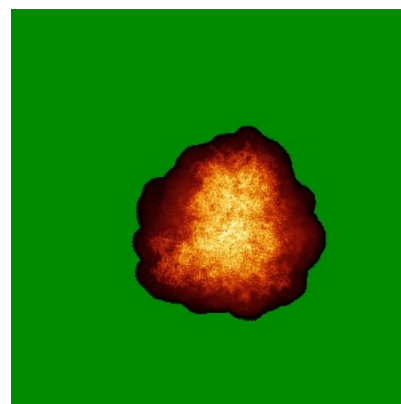
6.4.1 Primary map



X

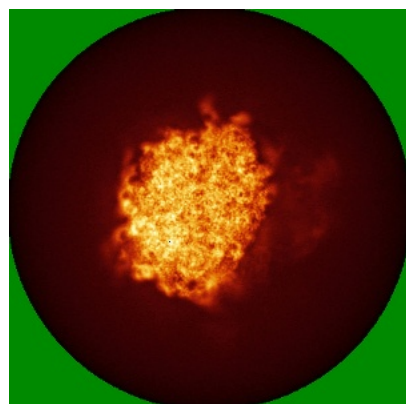


Y

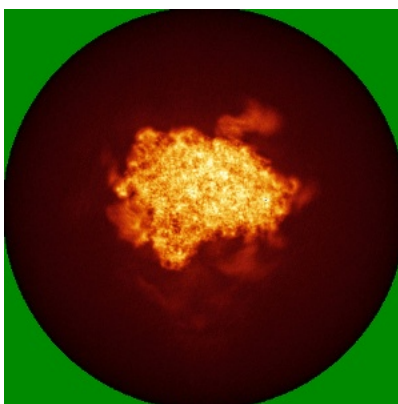


Z

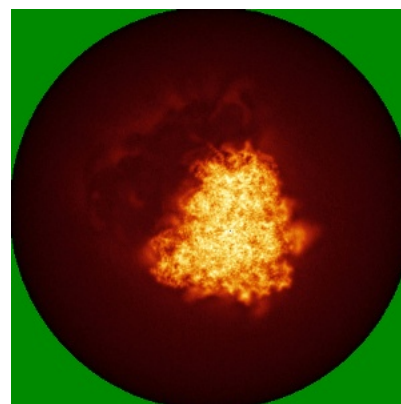
6.4.2 Raw map



X



Y

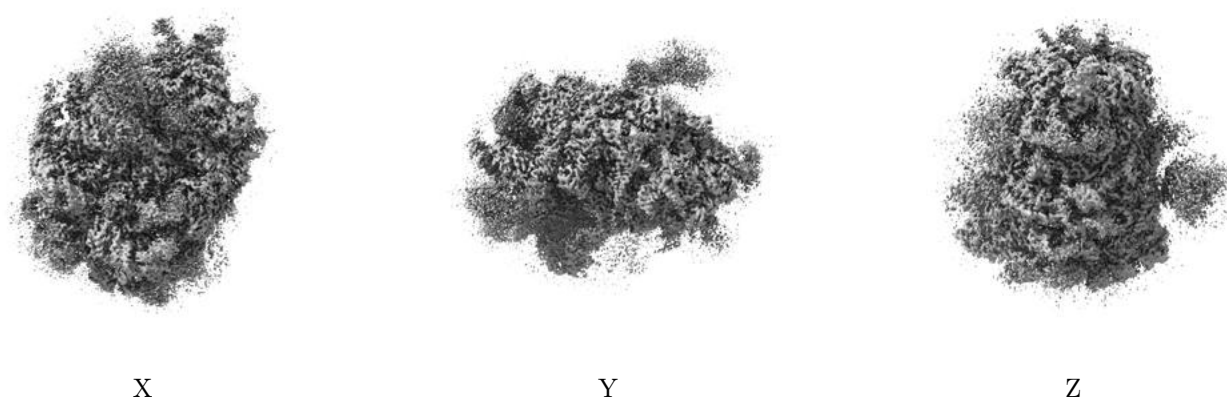


Z

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 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

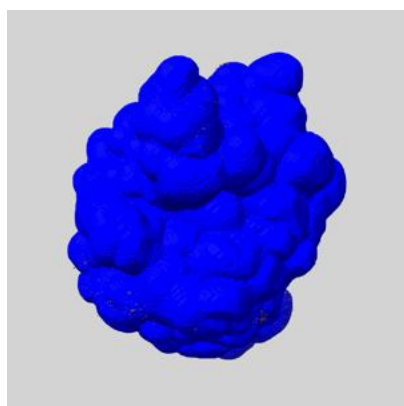
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

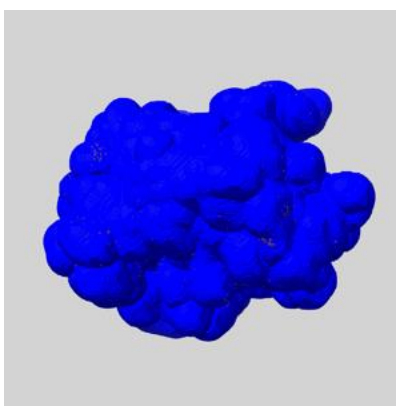
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

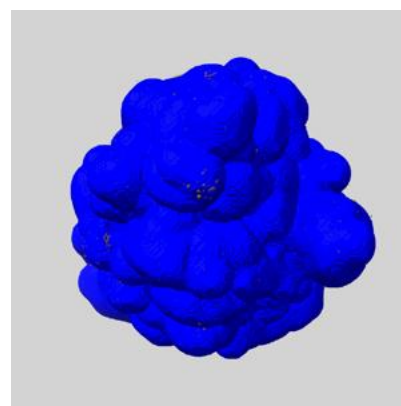
6.6.1 emd_10380_msk_1.map [i](#)



X



Y

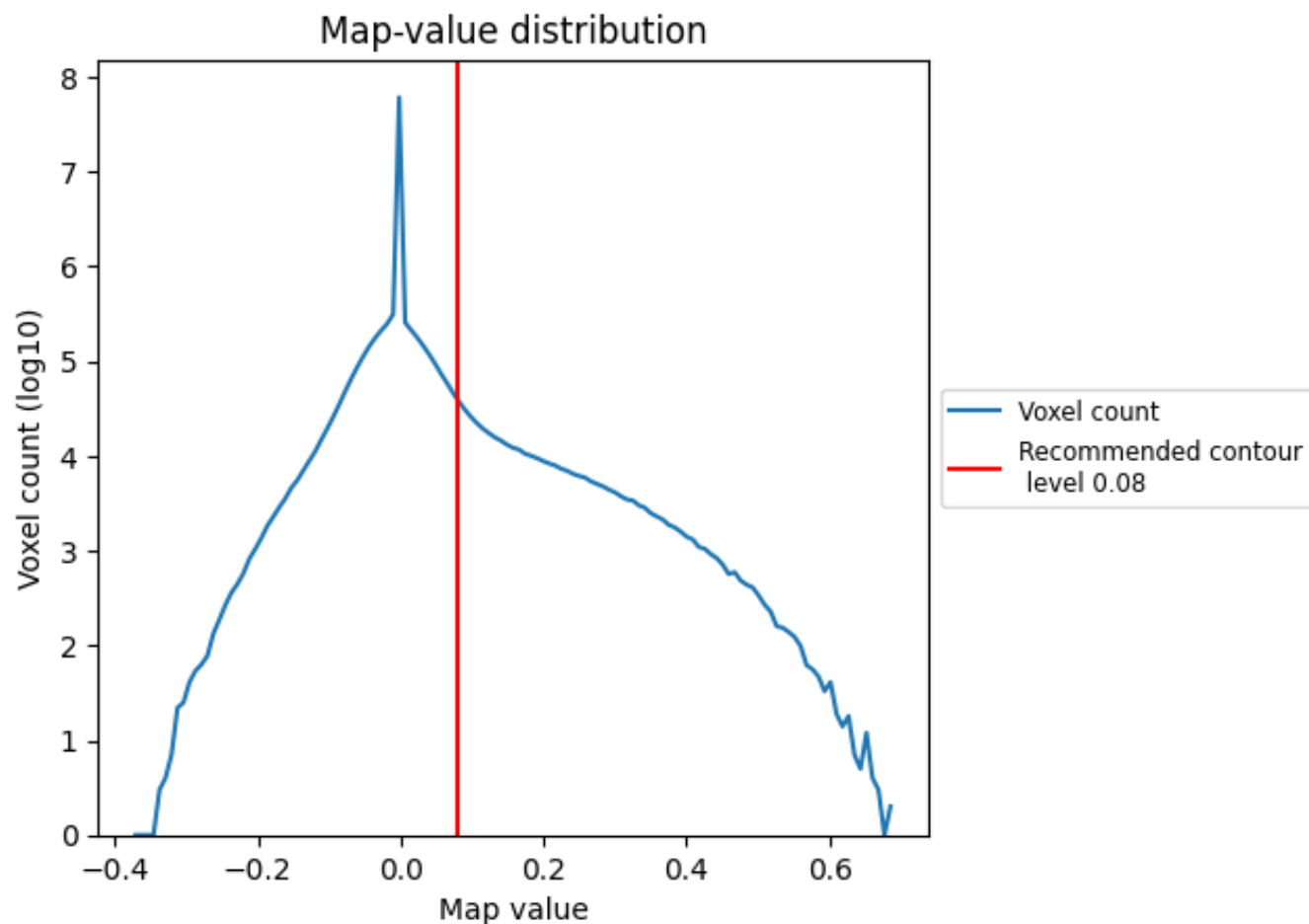


Z

7 Map analysis [i](#)

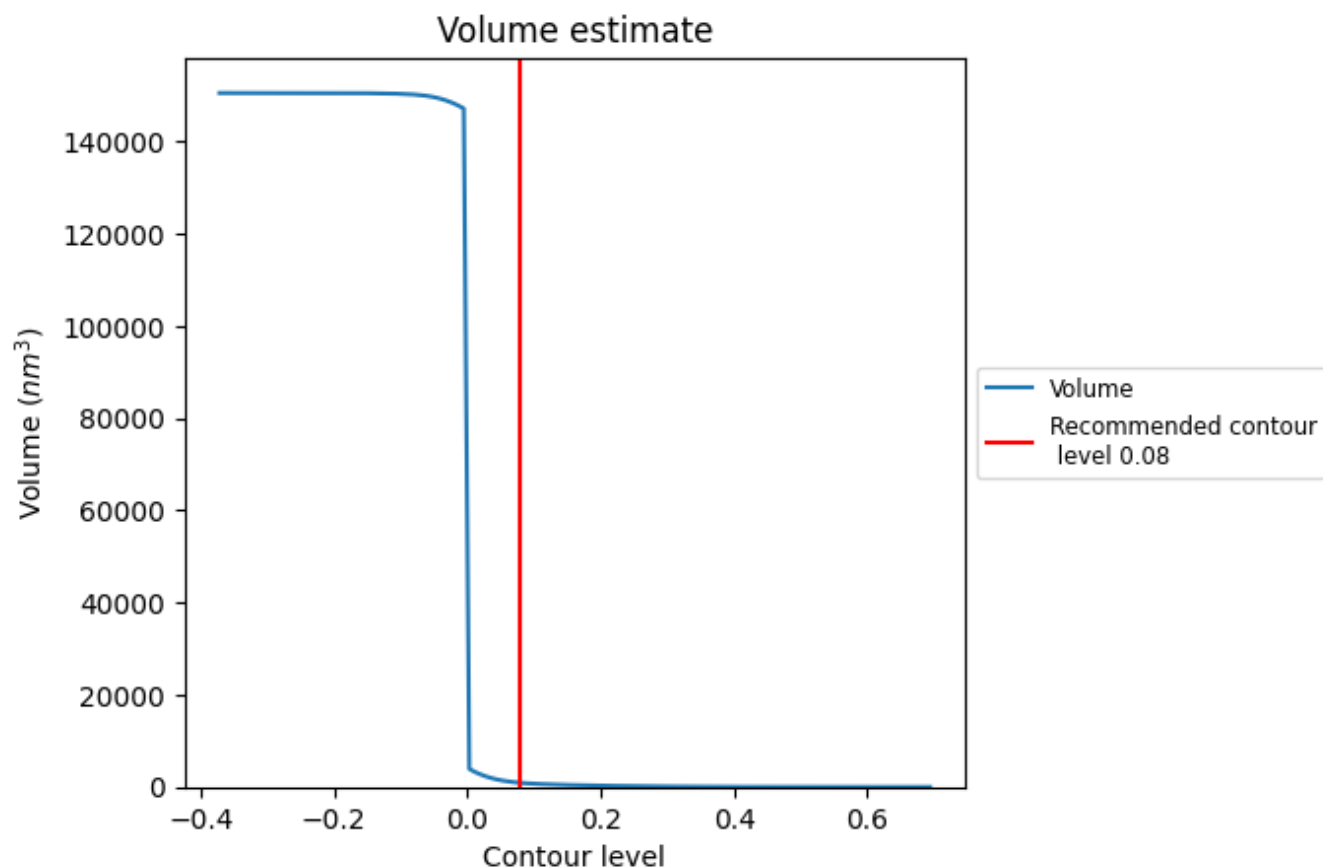
This section contains the results of statistical analysis of the map.

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.

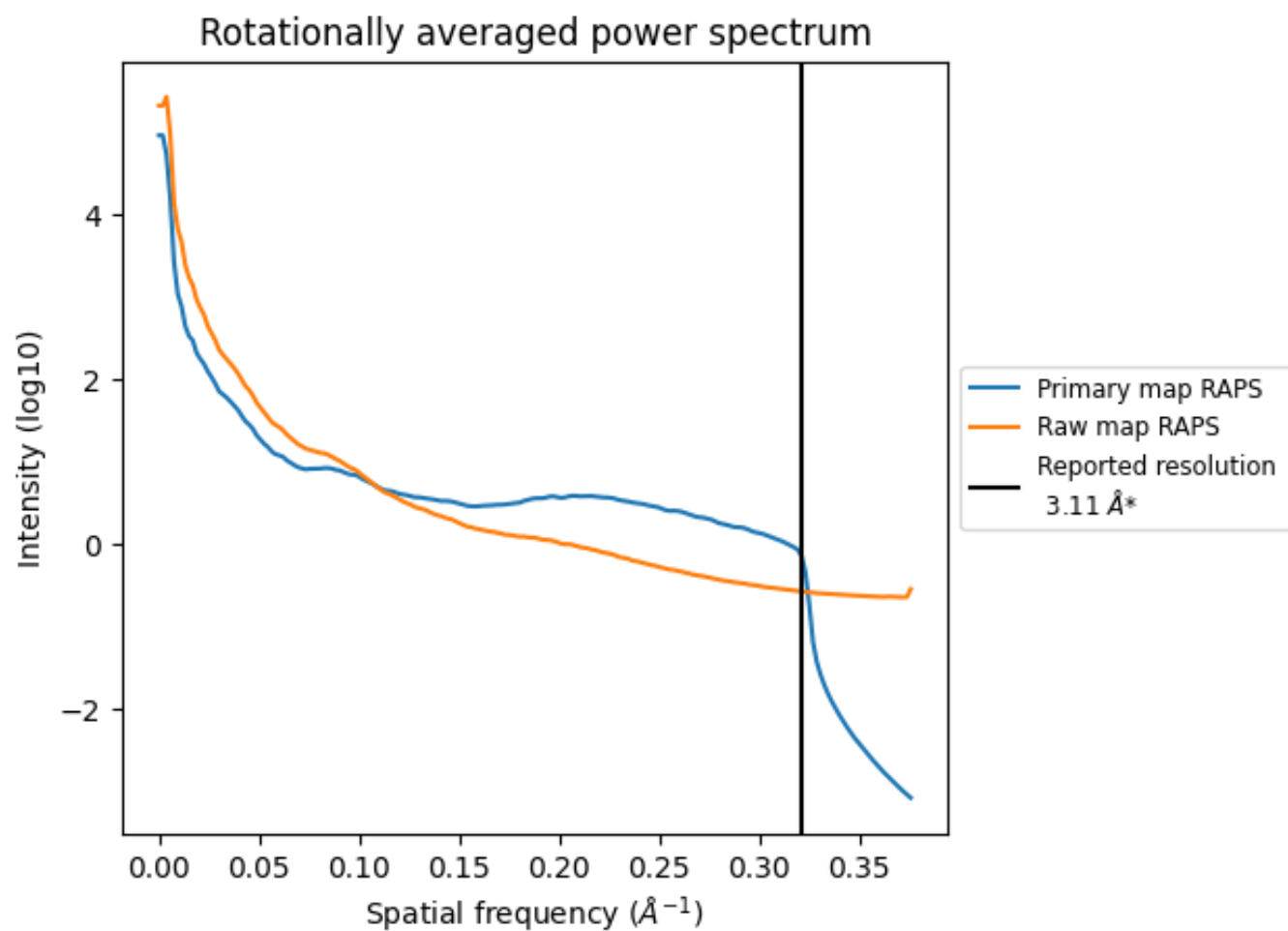
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 897 nm³; this corresponds to an approximate mass of 810 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 ⓘ

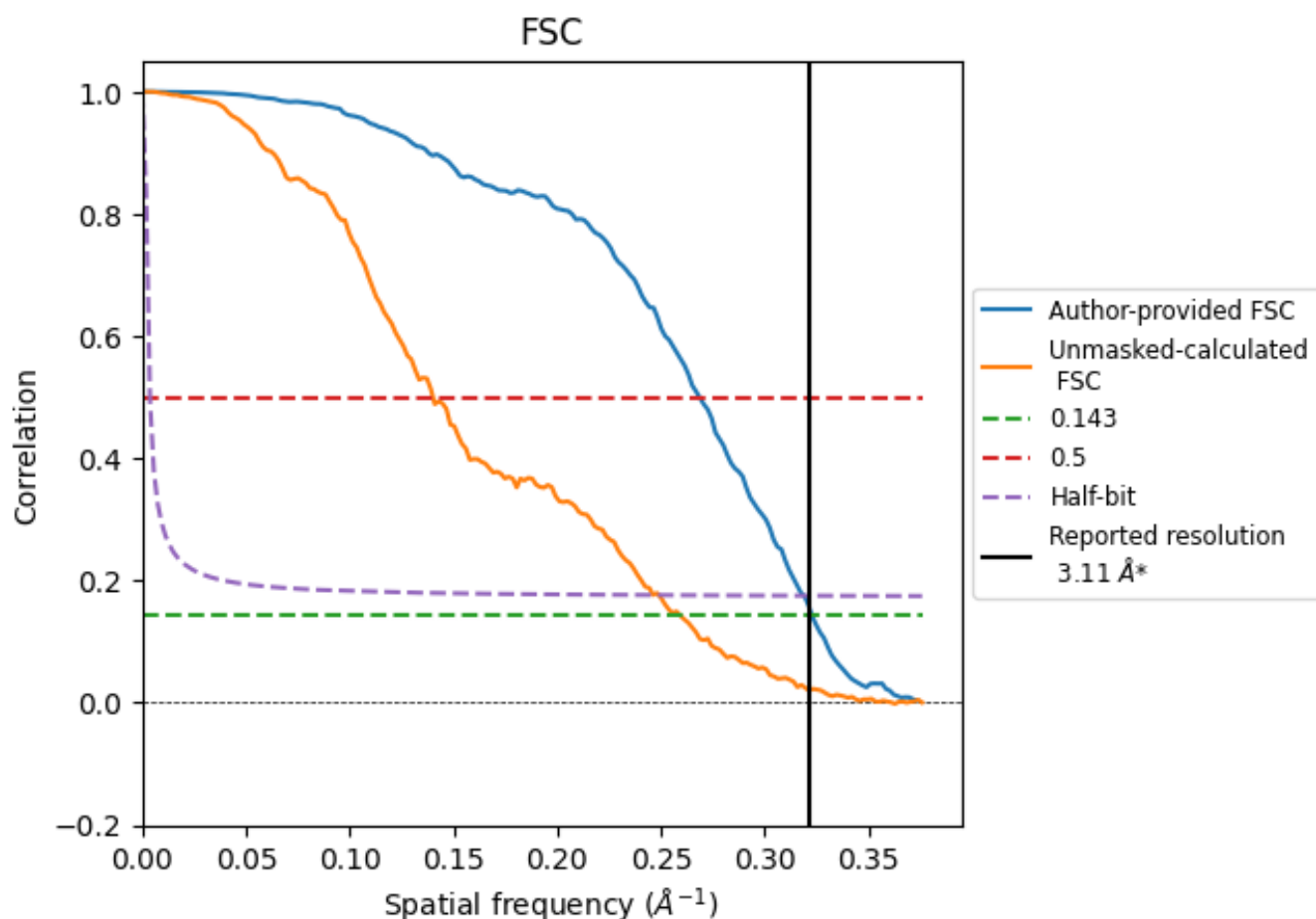


*Reported resolution corresponds to spatial frequency of 0.322 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.322 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

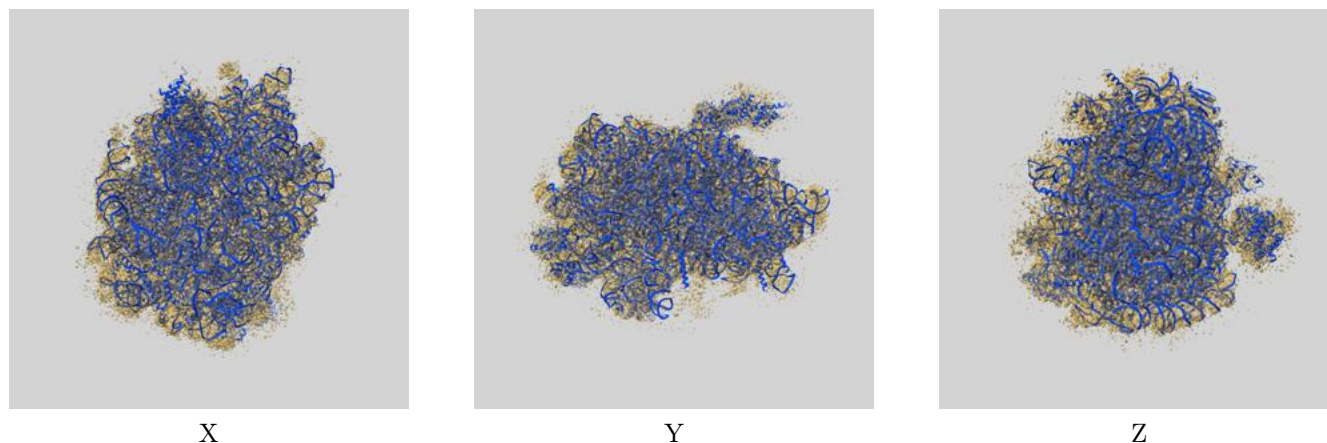
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.11	-	-
Author-provided FSC curve	3.10	3.72	3.14
Unmasked-calculated*	3.86	7.14	4.02

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.86 differs from the reported value 3.11 by more than 10 %

9 Map-model fit [i](#)

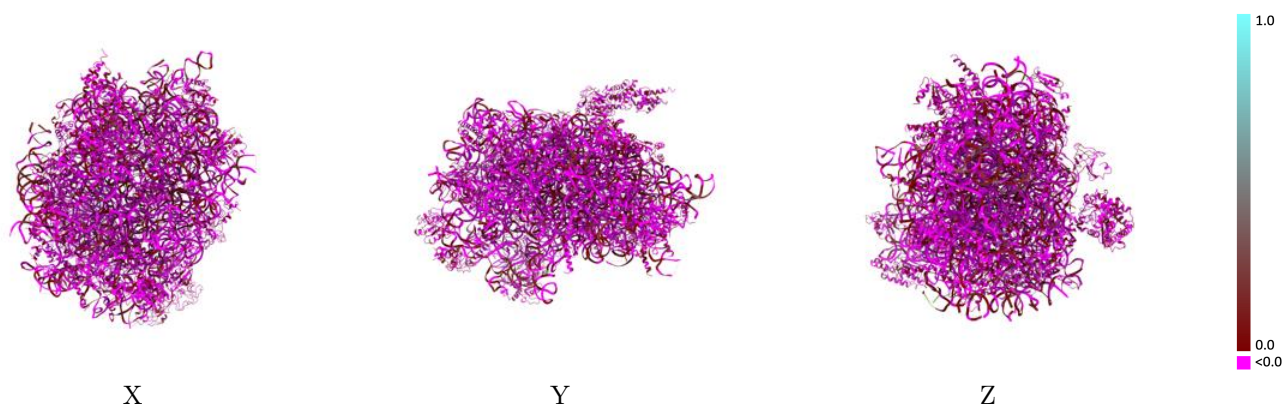
This section contains information regarding the fit between EMDB map EMD-10380 and PDB model 6T59. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



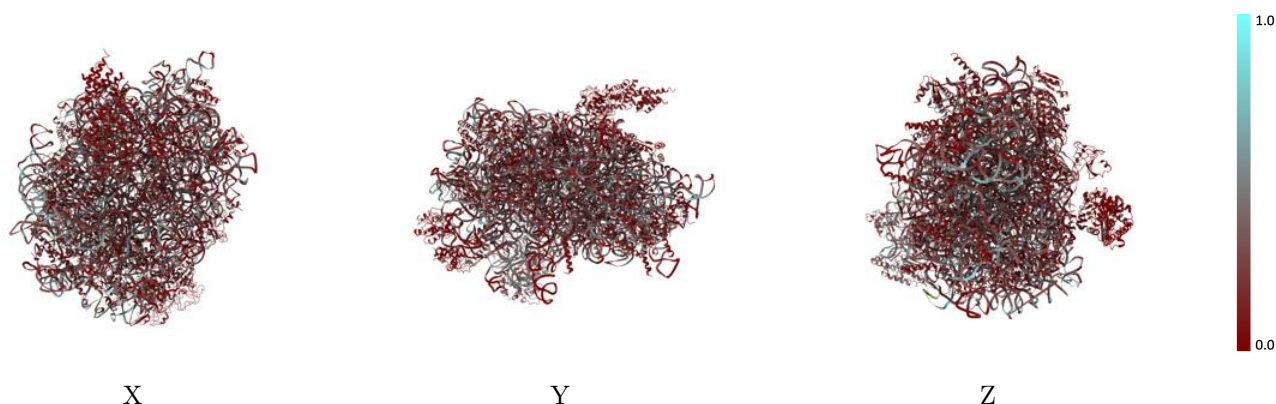
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



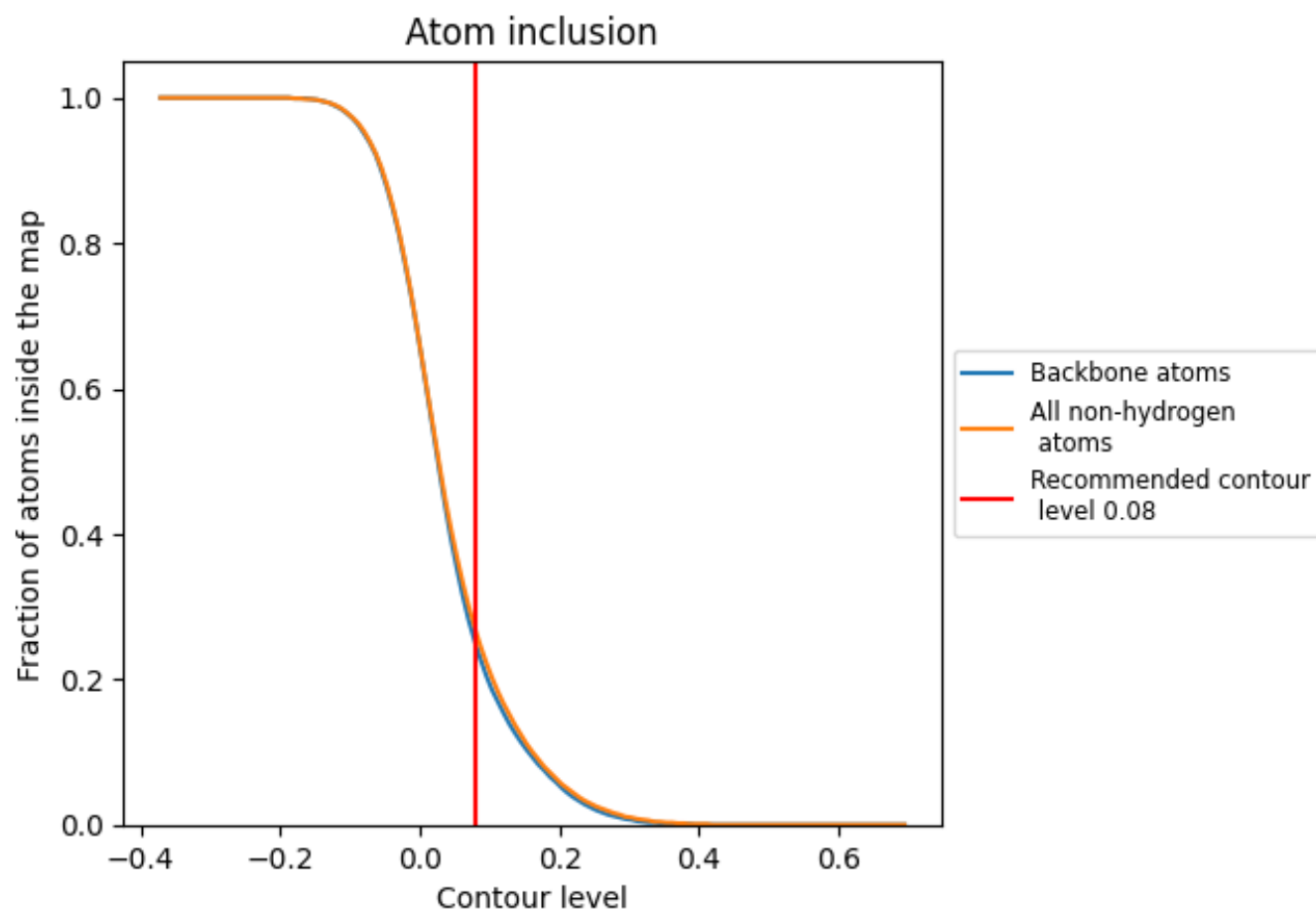
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 25% of all backbone atoms, 27% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2670	 -0.0680
1	 0.0460	 0.0020
23	 0.0730	 -0.0110
54	 0.3170	 -0.0600
74	 0.3820	 -0.1130
84	 0.3300	 -0.0320
A3	 0.1850	 -0.1380
B3	 0.2070	 -0.0910
C3	 0.2270	 -0.0980
D3	 0.2970	 -0.0630
E3	 0.2210	 -0.0940
F3	 0.2230	 -0.1080
G3	 0.2170	 -0.0680
H3	 0.1930	 -0.0940
I3	 0.2320	 -0.0920
J3	 0.2410	 -0.0470
L3	 0.2320	 -0.0770
M3	 0.2550	 -0.1010
N3	 0.2200	 -0.1120
NA	 0.0560	 0.0400
NB	 0.0220	 0.0230
NI	 0.1530	 -0.1020
O3	 0.2320	 -0.0910
P3	 0.1900	 -0.1070
Q3	 0.1930	 -0.1340
R3	 0.2200	 -0.0660
S3	 0.2570	 -0.0880
T3	 0.2250	 -0.1000
TT	 0.0900	 -0.0270
U3	 0.1740	 -0.0630
V3	 0.1680	 -0.1160
W3	 0.1850	 -0.0880
X3	 0.1820	 -0.0520
Y3	 0.1860	 -0.0900
Z3	 0.2130	 -0.0630



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Chain	Atom inclusion	Q-score
a3	 0.2390	 -0.1140
b3	 0.1890	 -0.0920
c3	 0.2510	 -0.0690
d3	 0.1770	 -0.0770
e3	 0.1940	 -0.1160
f3	 0.2200	 -0.1000
g3	 0.1850	 -0.0740
h3	 0.2060	 -0.0630
i3	 0.2410	 -0.0720
j3	 0.2370	 -0.0720
k3	 0.1690	 -0.0380
l3	 0.2180	 -0.0780
m3	 0.2020	 -0.1270
n3	 0.0320	 -0.0910
o3	 0.1900	 -0.1030
p3	 0.2470	 -0.0540
r3	 0.1910	 -0.1180
s3	 0.0700	 -0.0170
t3	 0.0580	 0.0140