



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 11:25 PM UTC

PDB ID : 5LZY / pdb_00005lzy
EMDB ID : EMD-4136
Title : Structure of the mammalian rescue complex with Pelota and Hbs1l assembled on a polyadenylated mRNA.
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.
Deposited on : 2016-10-02
Resolution : 3.99 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

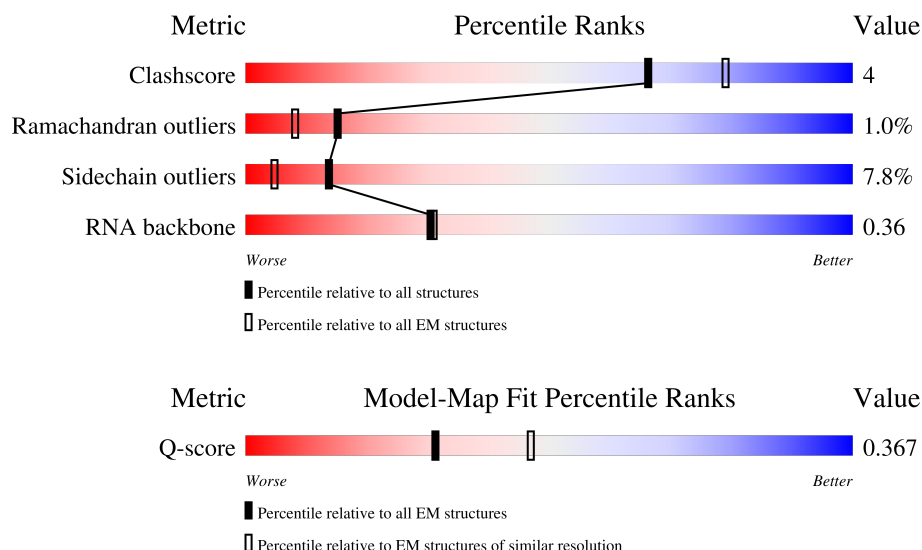
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.99 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



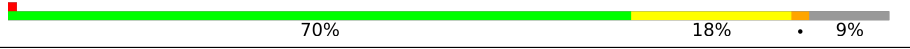
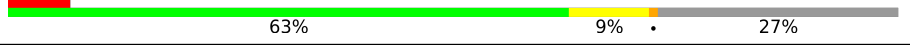
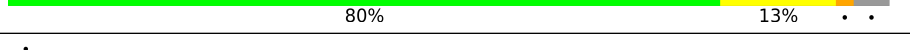
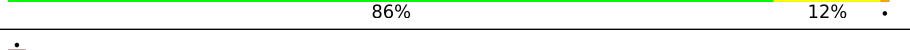
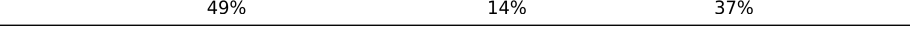
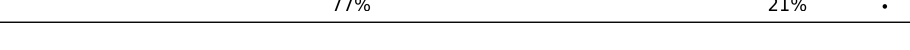
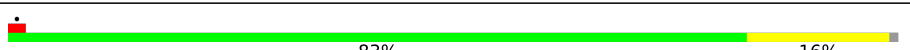
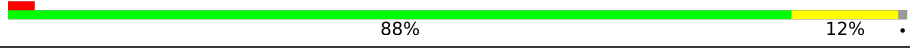
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7463 (3.49 - 4.49)

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	A	257	
2	B	403	
3	C	425	

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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	247	
7	G	319	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	245	
28	c	115	

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Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	102	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	318	
44	t	165	
45	2	75	
45	3	75	
46	5	3543	
47	7	120	
48	8	156	
49	9	1869	
50	AA	295	
51	BB	264	
52	CC	293	

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Mol	Chain	Length	Quality of chain
53	DD	243	
54	EE	263	
55	FF	204	
56	GG	249	
57	HH	194	
58	II	208	
59	JJ	194	
60	KK	165	
61	LL	158	
62	MM	132	
63	NN	151	
64	OO	168	
65	PP	145	
66	QQ	146	
67	RR	135	
68	SS	152	
69	TT	145	
70	UU	119	
71	VV	83	
72	WW	130	
73	XX	143	
74	YY	130	
75	ZZ	125	
76	aa	115	
77	bb	84	

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Mol	Chain	Length	Quality of chain
78	cc	69	
79	dd	56	
80	ee	133	
81	ff	156	
82	gg	317	
83	hh	8	
84	ii	403	
85	jj	710	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	ZN	m	200	-	-	X	-
87	ZN	p	100	-	-	X	-

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 221912 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	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	B	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
B	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	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	D	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
D	1	MET	-	initiating methionine	UNP G1SYJ6

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	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	F	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
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

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

- Molecule 9 is a protein called Ribosomal protein L10 (Predicted).

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

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	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	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	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	N	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	O	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	P	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	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 17 is a protein called eL19.

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

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	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	T	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	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 21 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	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	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 23 is a protein called eL23.

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

- Molecule 24 is a protein called uL24.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	GLN	conflict	UNP G1SNY0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	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	c	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	d	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	e	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	f	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	g	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	h	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	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called eL37.

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

- Molecule 37 is a protein called eL39.

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

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	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	o	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	p	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	r	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	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called uL11.

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

- Molecule 45 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		
45	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5	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	7	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	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	9	1698	Total	C	N	O	P	0	0
			36249	16180	6508	11864	1697		

- Molecule 50 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AA	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 52 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 53 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DD	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 54 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 55 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	FF	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 57 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	HH	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 58 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 59 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 60 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 61 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	MM	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 63 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 64 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 65 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	PP	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 66 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 67 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 68 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 69 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	TT	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 70 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	UU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 71 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	VV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 72 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	WW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	XX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 74 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	YY	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 75 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	cc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 80 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	ee	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 81 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	ff	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 82 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 83 is a RNA chain called mRNA (polyadenylated).

Mol	Chain	Residues	Atoms					AltConf	Trace
83	hh	8	Total	C	N	O	P	0	0
			176	80	40	48	8		

- Molecule 84 is a protein called Protein pelota homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	ii	372	Total	C	N	O	S	0	0
			2947	1844	528	559	16		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	221	MET	LEU	variant	UNP Q9BRX2
ii	386	GLY	-	expression tag	UNP Q9BRX2
ii	387	SER	-	expression tag	UNP Q9BRX2
ii	388	GLU	-	expression tag	UNP Q9BRX2
ii	389	ASN	-	expression tag	UNP Q9BRX2
ii	390	LEU	-	expression tag	UNP Q9BRX2
ii	391	TYR	-	expression tag	UNP Q9BRX2
ii	392	PHE	-	expression tag	UNP Q9BRX2
ii	393	GLN	-	expression tag	UNP Q9BRX2
ii	394	GLY	-	expression tag	UNP Q9BRX2
ii	395	ALA	-	expression tag	UNP Q9BRX2
ii	396	HIS	-	expression tag	UNP Q9BRX2
ii	397	HIS	-	expression tag	UNP Q9BRX2
ii	398	HIS	-	expression tag	UNP Q9BRX2
ii	399	HIS	-	expression tag	UNP Q9BRX2
ii	400	HIS	-	expression tag	UNP Q9BRX2
ii	401	HIS	-	expression tag	UNP Q9BRX2
ii	402	SER	-	expression tag	UNP Q9BRX2
ii	403	THR	-	expression tag	UNP Q9BRX2

- Molecule 85 is a protein called HBS1-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	jj	425	Total	C	N	O	S	0	0
			3292	2100	565	609	18		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
jj	-25	MET	-	initiating methionine	UNP Q9Y450
jj	-24	ASP	-	expression tag	UNP Q9Y450
jj	-23	TYR	-	expression tag	UNP Q9Y450
jj	-22	LYS	-	expression tag	UNP Q9Y450
jj	-21	ASP	-	expression tag	UNP Q9Y450
jj	-20	HIS	-	expression tag	UNP Q9Y450
jj	-19	ASP	-	expression tag	UNP Q9Y450
jj	-18	GLY	-	expression tag	UNP Q9Y450
jj	-17	ASP	-	expression tag	UNP Q9Y450
jj	-16	TYR	-	expression tag	UNP Q9Y450
jj	-15	LYS	-	expression tag	UNP Q9Y450
jj	-14	ASP	-	expression tag	UNP Q9Y450
jj	-13	HIS	-	expression tag	UNP Q9Y450
jj	-12	ASP	-	expression tag	UNP Q9Y450

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Chain	Residue	Modelled	Actual	Comment	Reference
jj	-11	ILE	-	expression tag	UNP Q9Y450
jj	-10	ASP	-	expression tag	UNP Q9Y450
jj	-9	TYR	-	expression tag	UNP Q9Y450
jj	-8	LYS	-	expression tag	UNP Q9Y450
jj	-7	ASP	-	expression tag	UNP Q9Y450
jj	-6	ASP	-	expression tag	UNP Q9Y450
jj	-5	ASP	-	expression tag	UNP Q9Y450
jj	-4	ASP	-	expression tag	UNP Q9Y450
jj	-3	LYS	-	expression tag	UNP Q9Y450
jj	-2	ALA	-	expression tag	UNP Q9Y450
jj	-1	GLY	-	expression tag	UNP Q9Y450
jj	0	SER	-	expression tag	UNP Q9Y450

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	B	1	Total	Mg	0
			1	1	
86	I	1	Total	Mg	0
			1	1	
86	L	1	Total	Mg	0
			1	1	
86	P	1	Total	Mg	0
			1	1	
86	Q	1	Total	Mg	0
			1	1	
86	V	1	Total	Mg	0
			1	1	
86	a	1	Total	Mg	0
			1	1	
86	e	1	Total	Mg	0
			1	1	
86	j	1	Total	Mg	0
			1	1	
86	5	160	Total	Mg	0
			160	160	
86	7	5	Total	Mg	0
			5	5	
86	8	3	Total	Mg	0
			3	3	
86	9	58	Total	Mg	0
			58	58	

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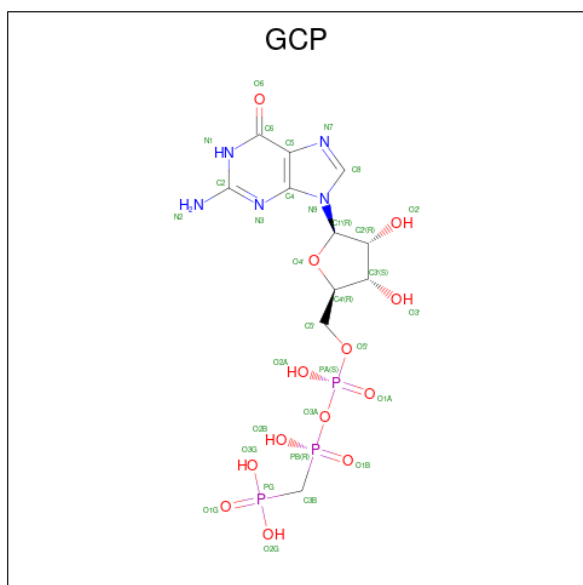
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
86	jj	1	Total	Mg	0
			1	1	

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	g	1	Total	Zn	0
			1	1	
87	j	1	Total	Zn	0
			1	1	
87	m	1	Total	Zn	0
			1	1	
87	o	1	Total	Zn	0
			1	1	
87	p	1	Total	Zn	0
			1	1	
87	aa	1	Total	Zn	0
			1	1	
87	dd	1	Total	Zn	0
			1	1	
87	ff	1	Total	Zn	0
			1	1	

- Molecule 88 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

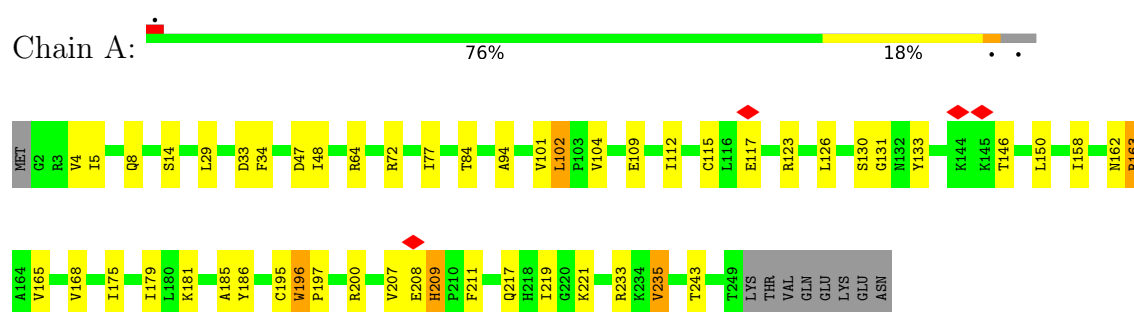


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
88	jj	1	32	11	5	13	3	0

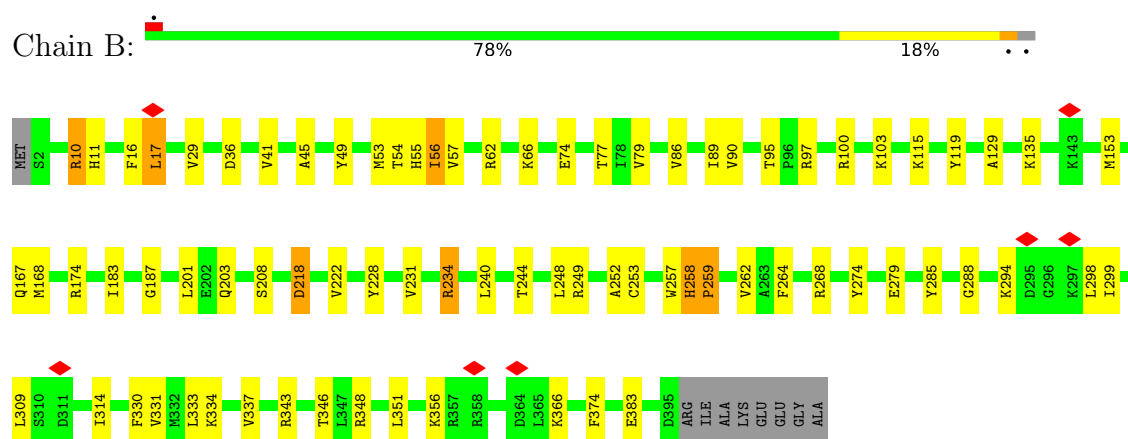
3 Residue-property plots

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.

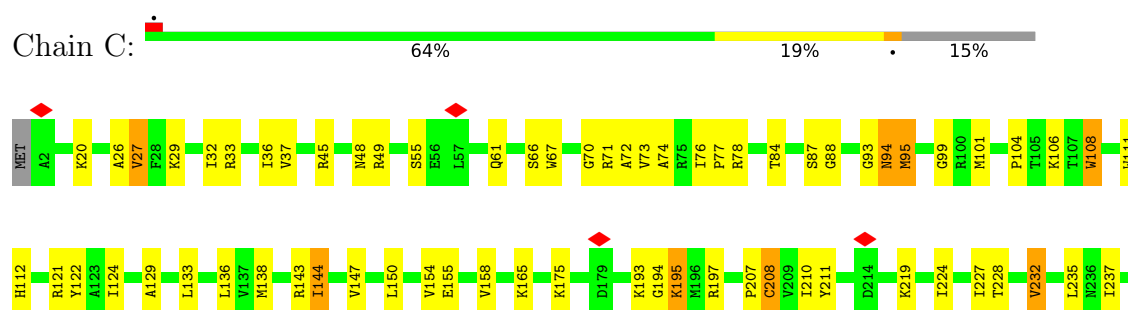
• Molecule 1: uL2



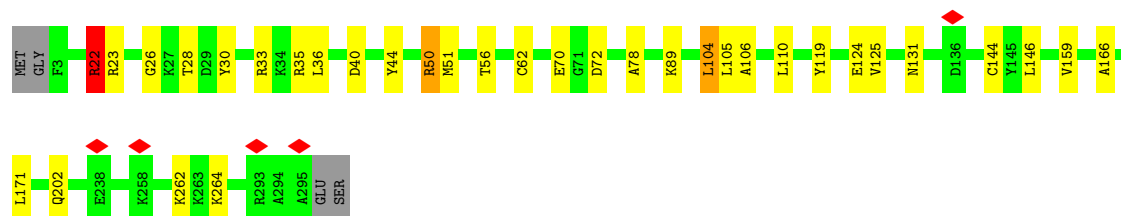
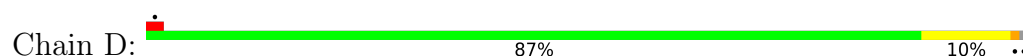
• Molecule 2: uL3



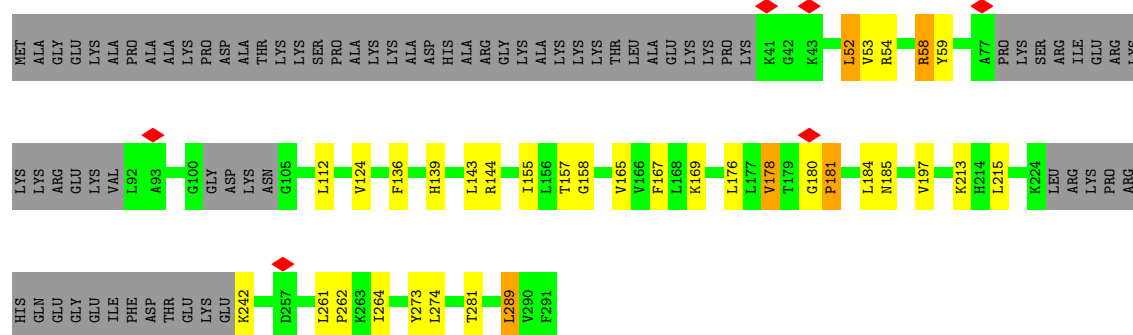
• Molecule 3: uL4



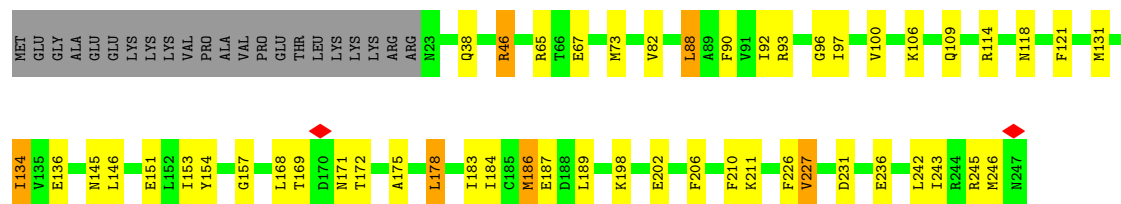
- Molecule 4: 60S ribosomal protein L5



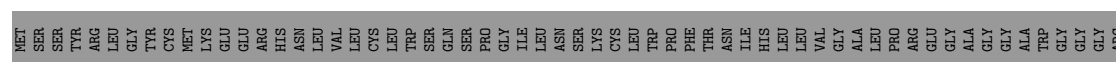
- Molecule 5: 60S ribosomal protein L6

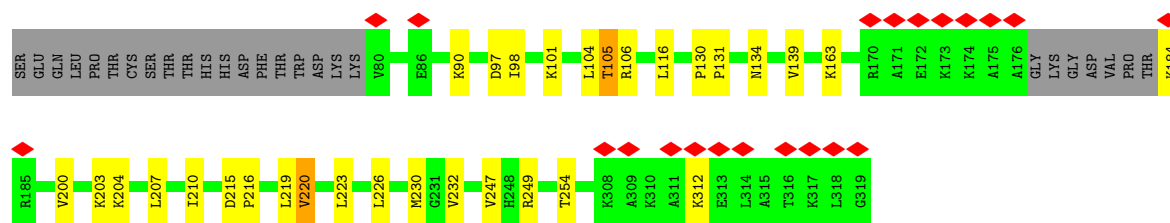


- Molecule 6: uL30

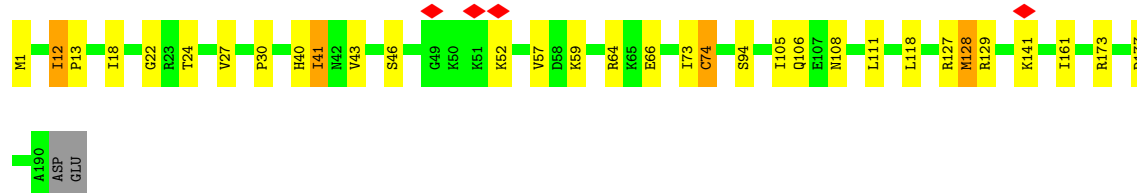
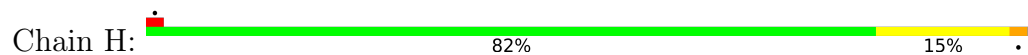


- Molecule 7: eL8

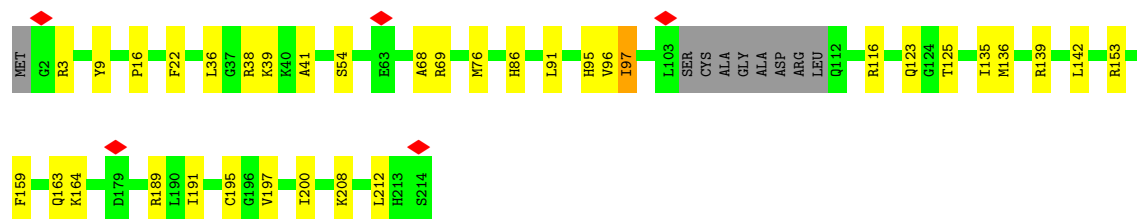
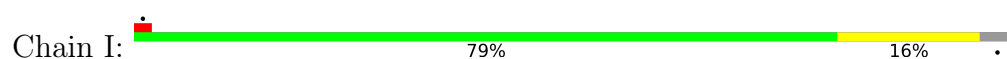




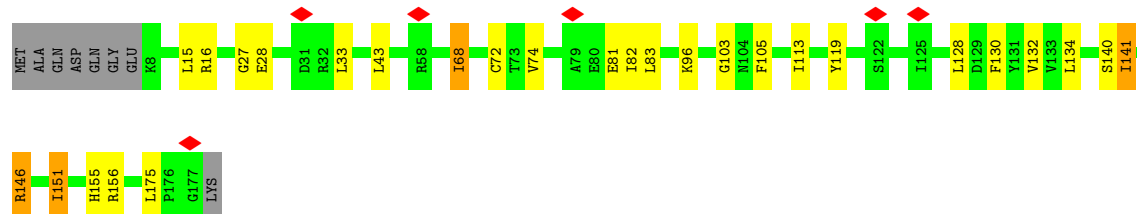
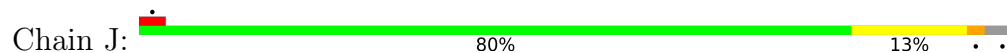
• Molecule 8: uL6



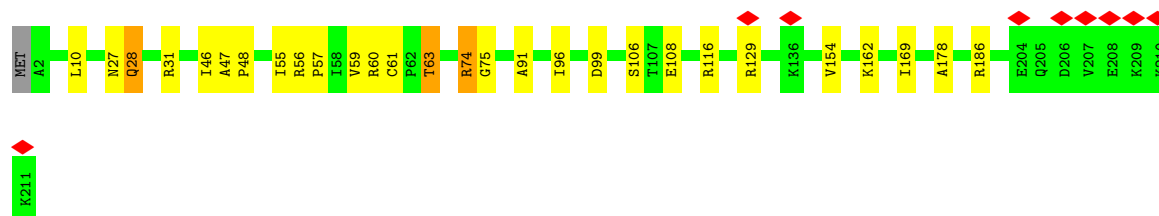
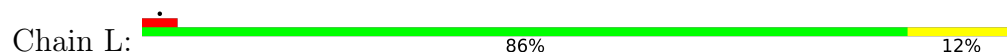
• Molecule 9: Ribosomal protein L10 (Predicted)



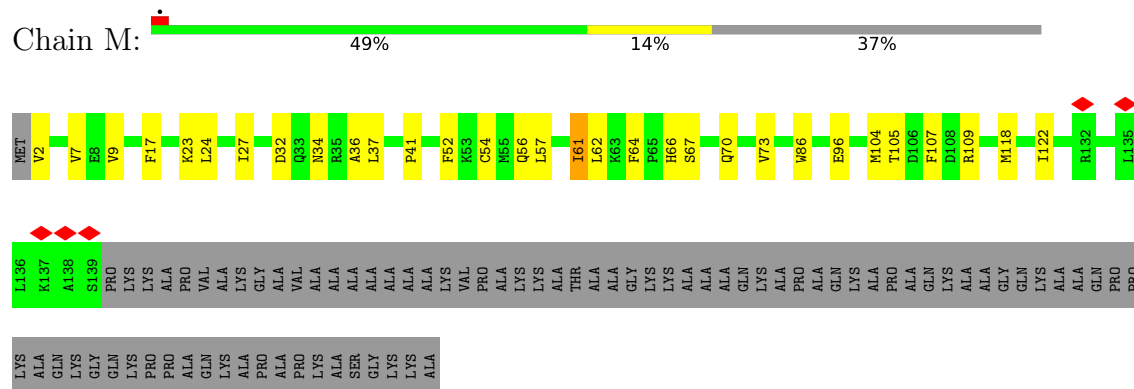
• Molecule 10: uL5



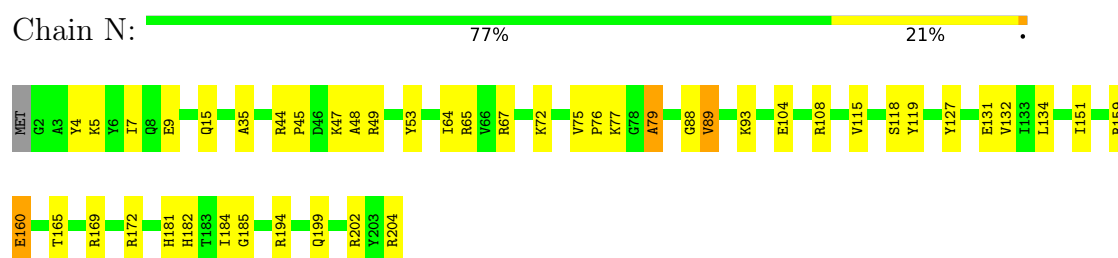
• Molecule 11: eL13



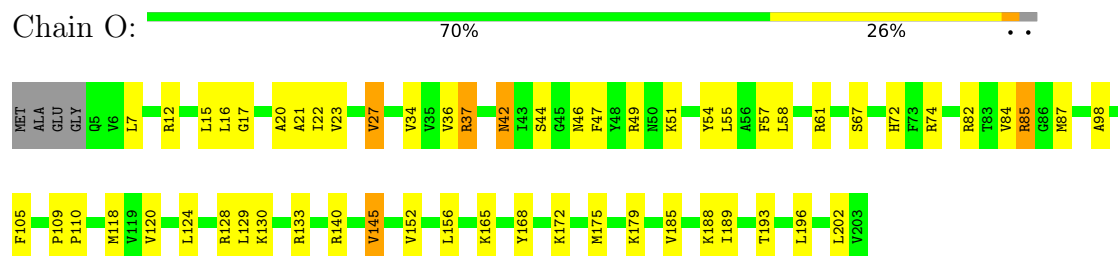
- Molecule 12: eL14



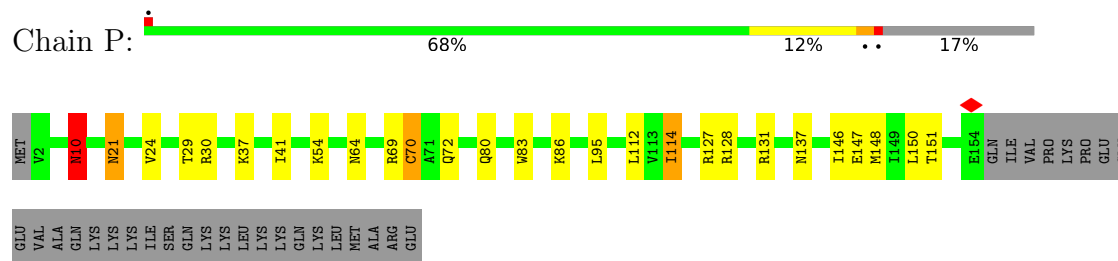
- Molecule 13: Ribosomal protein L15



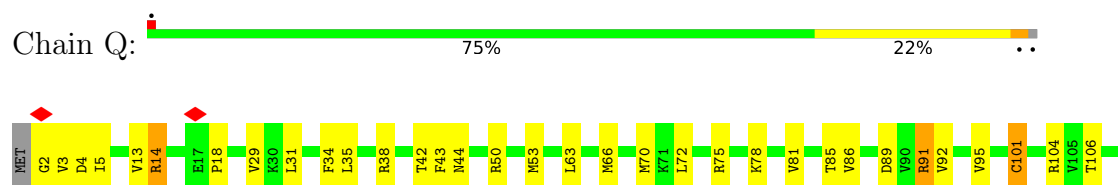
- Molecule 14: uL13



- Molecule 15: uL22

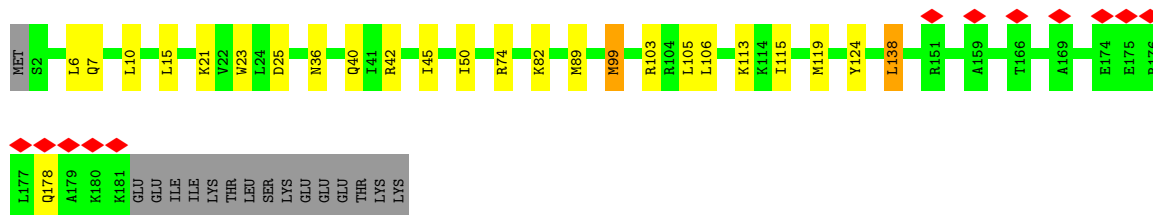
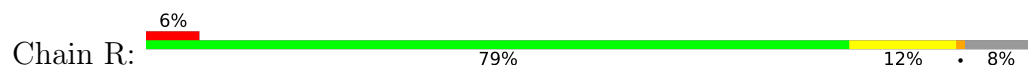


- Molecule 16: eL18

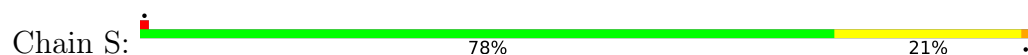




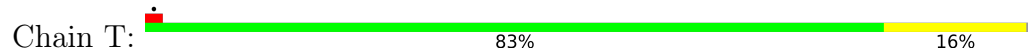
• Molecule 17: eL19



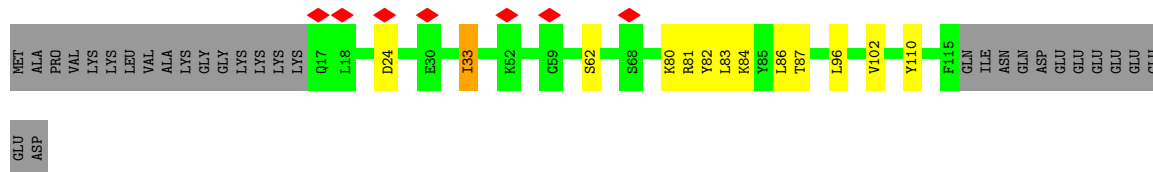
• Molecule 18: eL20



• Molecule 19: eL21



• Molecule 20: eL22

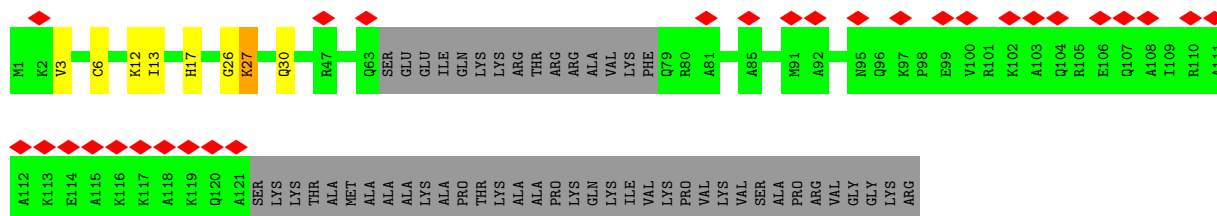


• Molecule 21: eL14

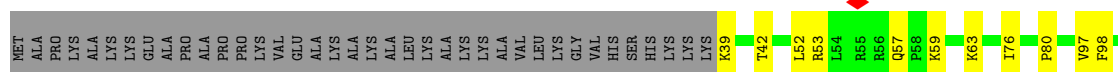




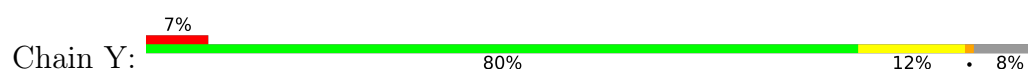
- Molecule 22: eL24



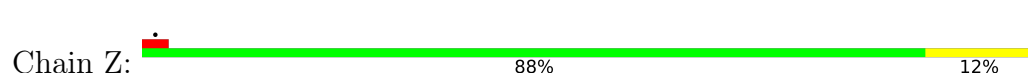
- Molecule 23: eL23



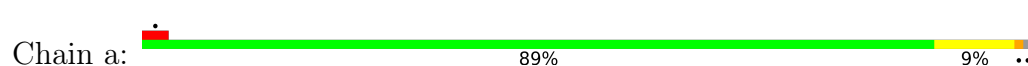
- Molecule 24: uL24



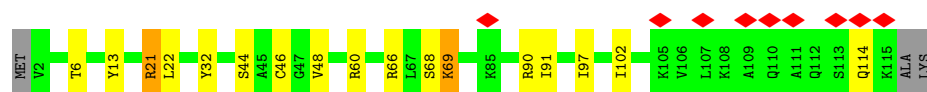
- Molecule 25: 60S ribosomal protein L27



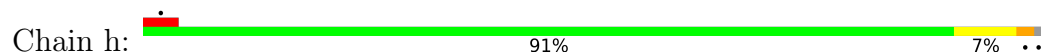
- Molecule 26: uL15



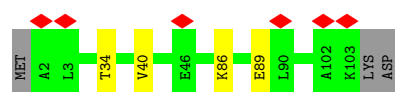
- Molecule 27: eL29



• Molecule 33: uL29



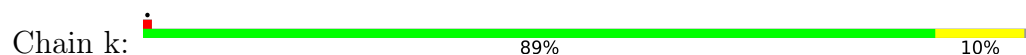
• Molecule 34: 60S ribosomal protein L36



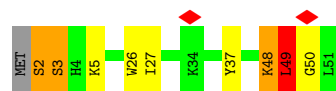
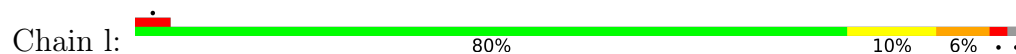
• Molecule 35: eL37



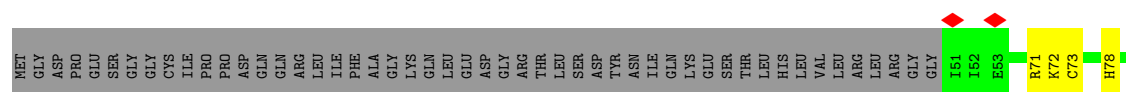
• Molecule 36: eL38



• Molecule 37: eL39

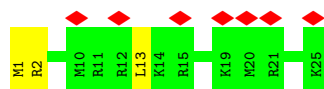
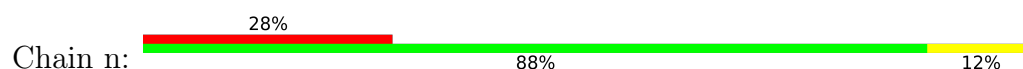


• Molecule 38: eL40

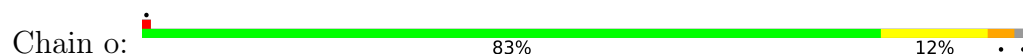




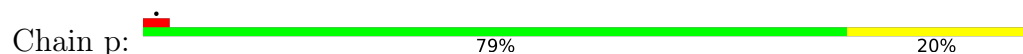
• Molecule 39: eL41



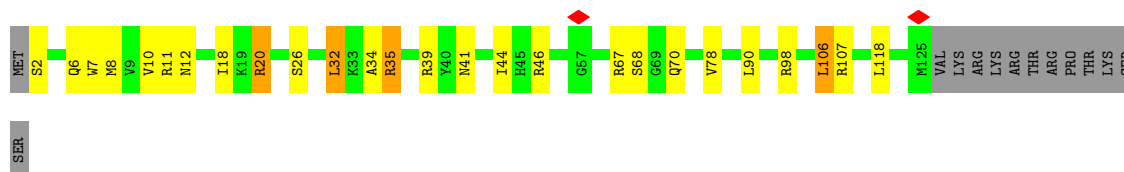
• Molecule 40: eL42



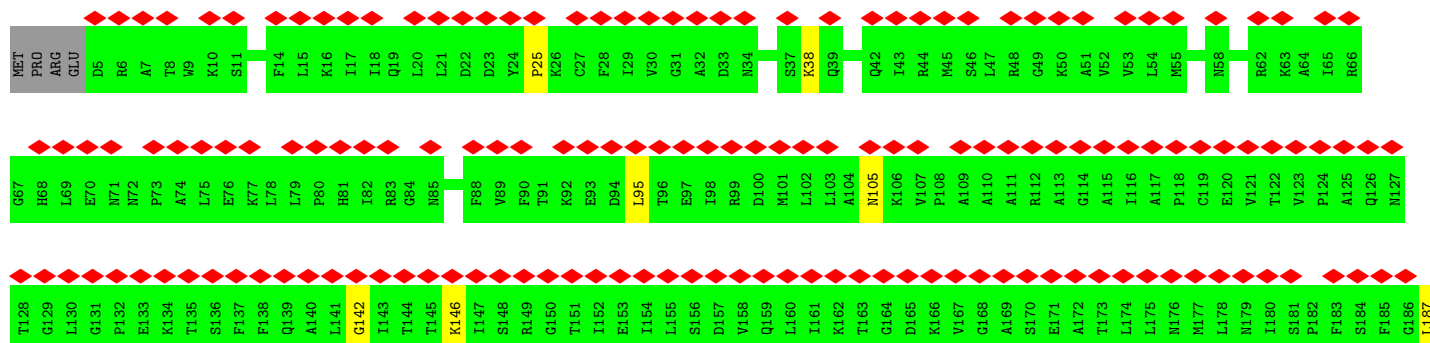
• Molecule 41: eL43

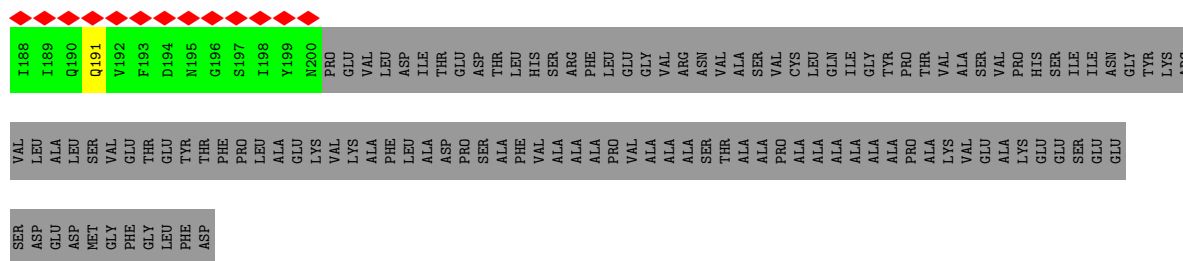


• Molecule 42: eL28

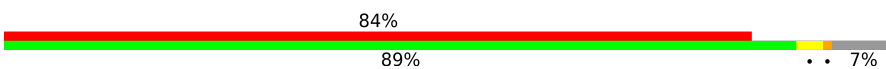


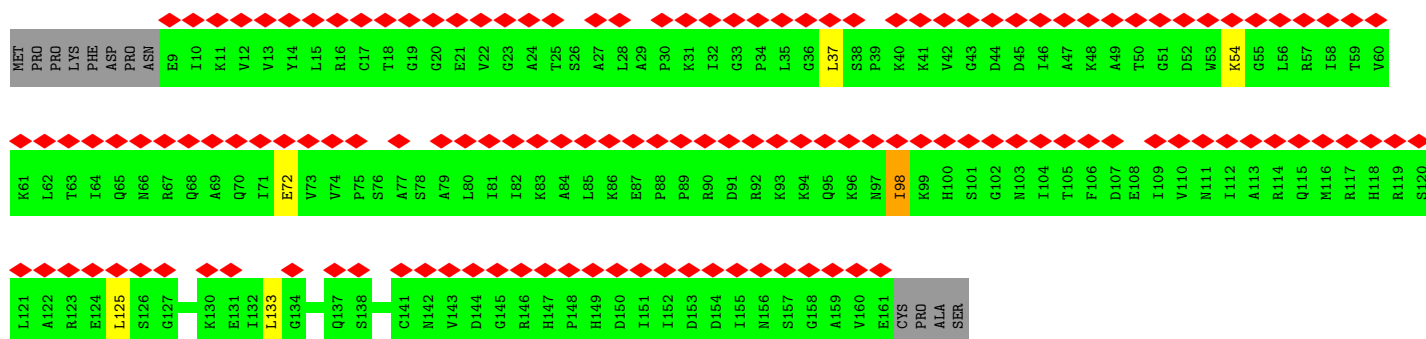
• Molecule 43: uL10



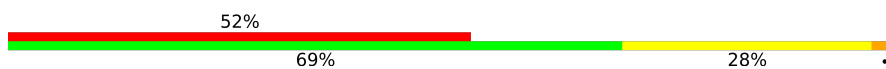


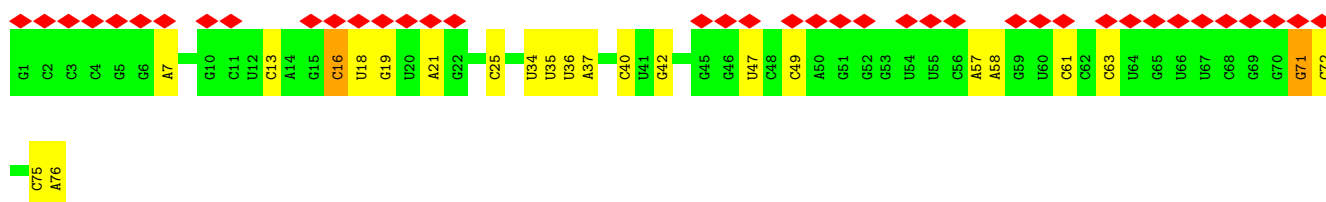
• Molecule 44: uL11

Chain t: 



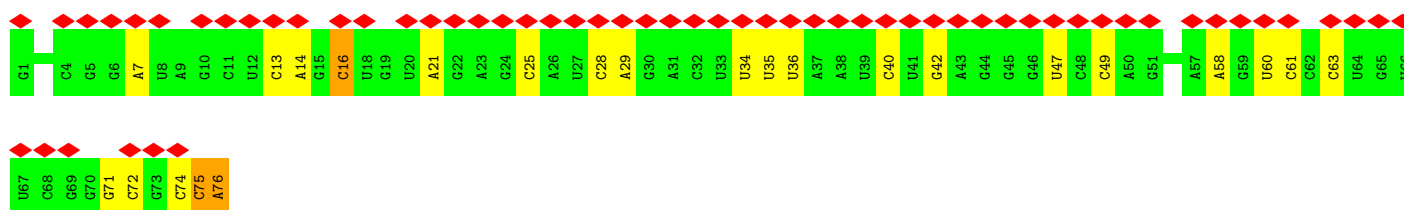
• Molecule 45: tRNA

Chain 2: 



• Molecule 45: tRNA

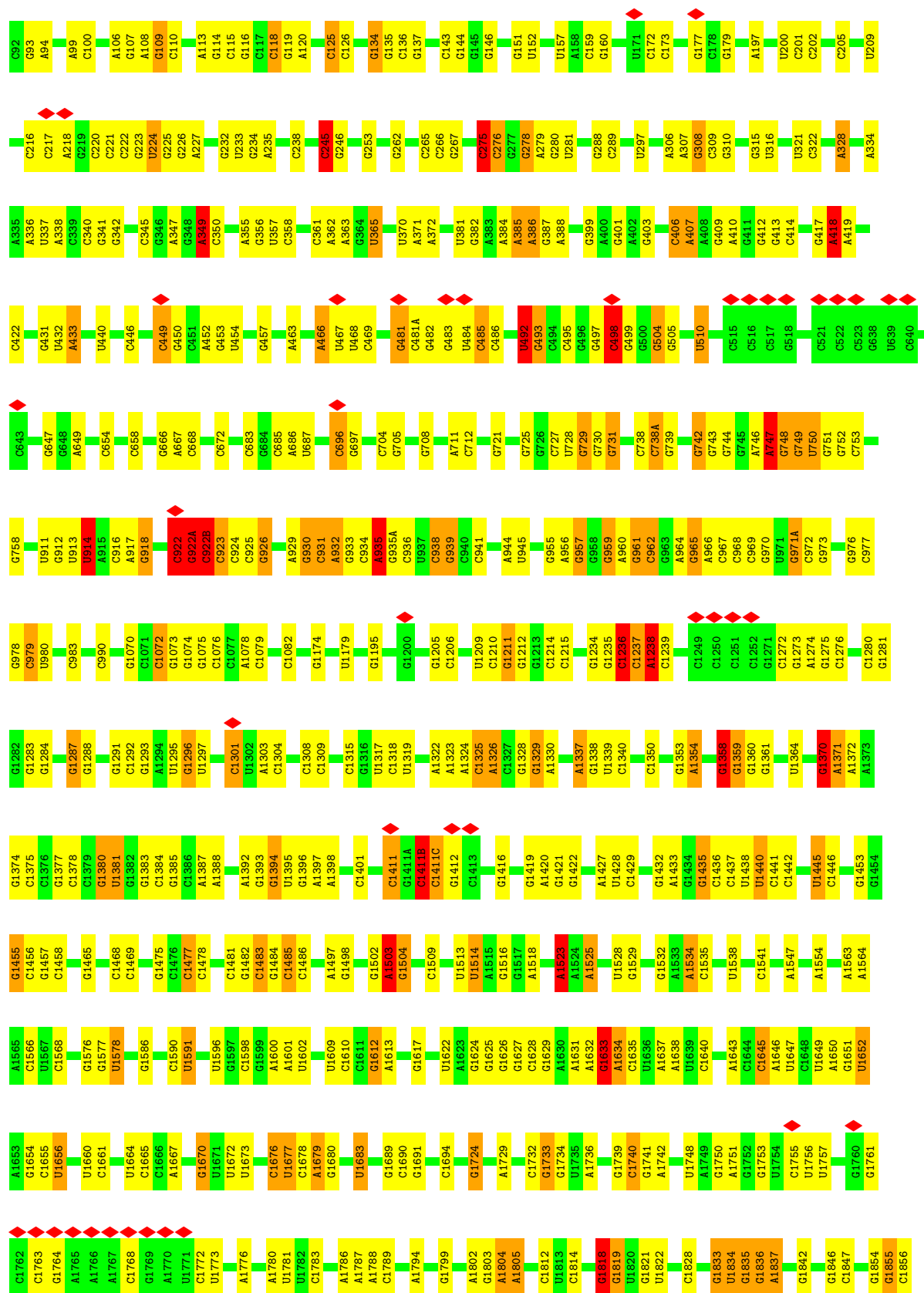
Chain 3: 

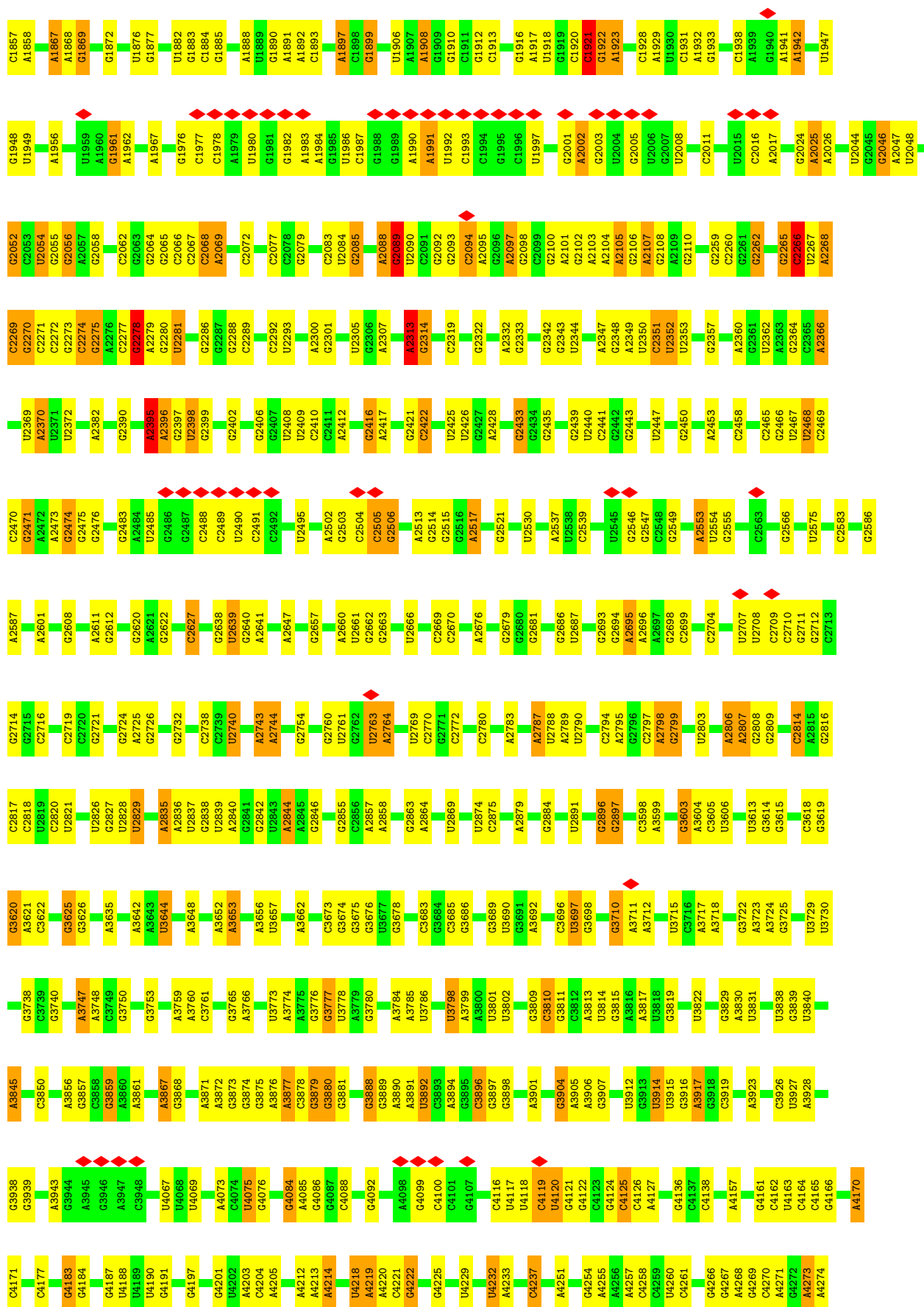


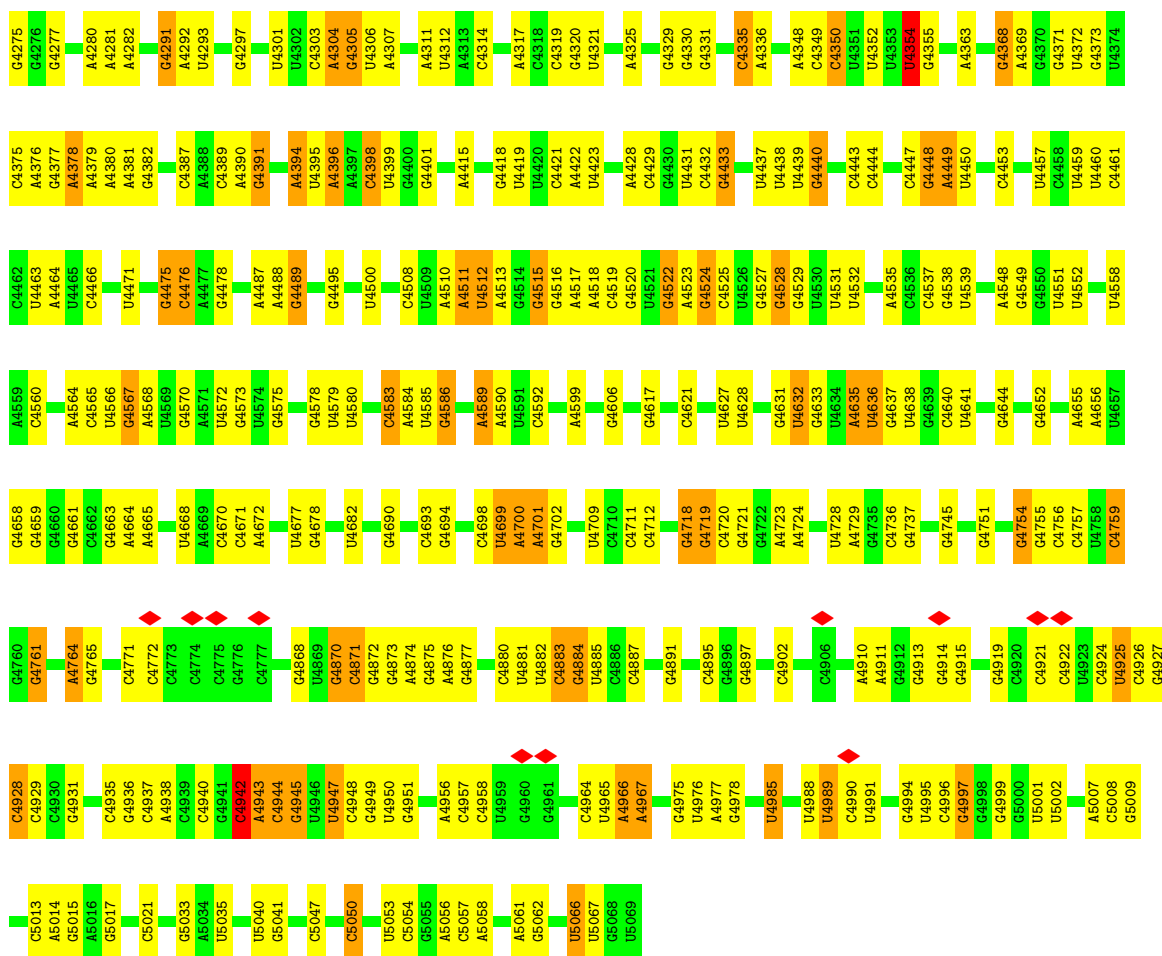
• Molecule 46: 28S ribosomal RNA

Chain 5: 

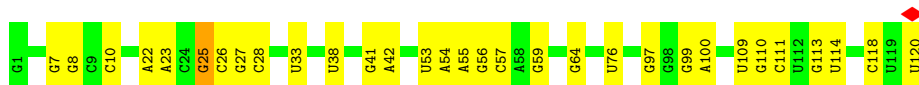








• Molecule 47: 5S ribosomal RNA

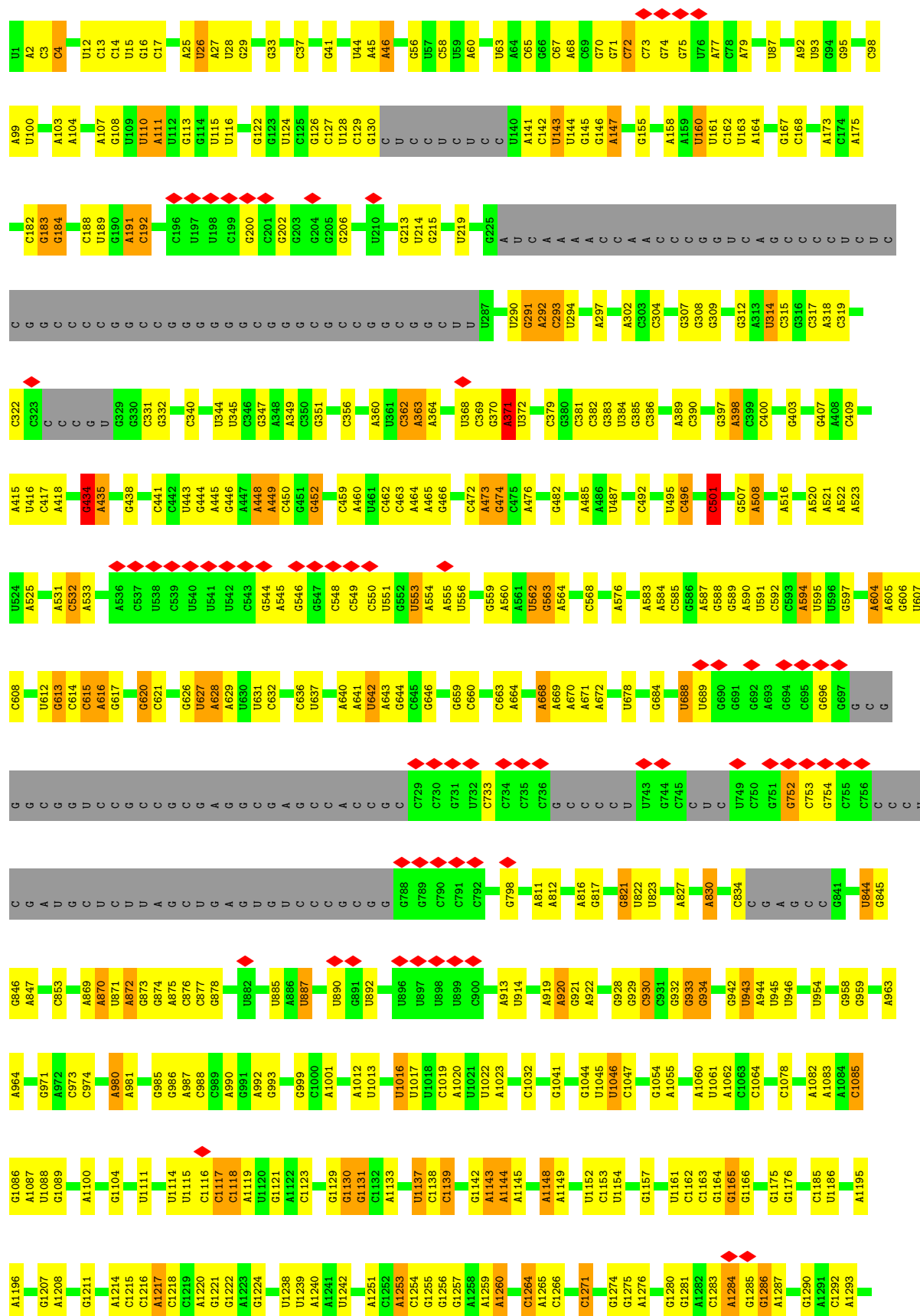


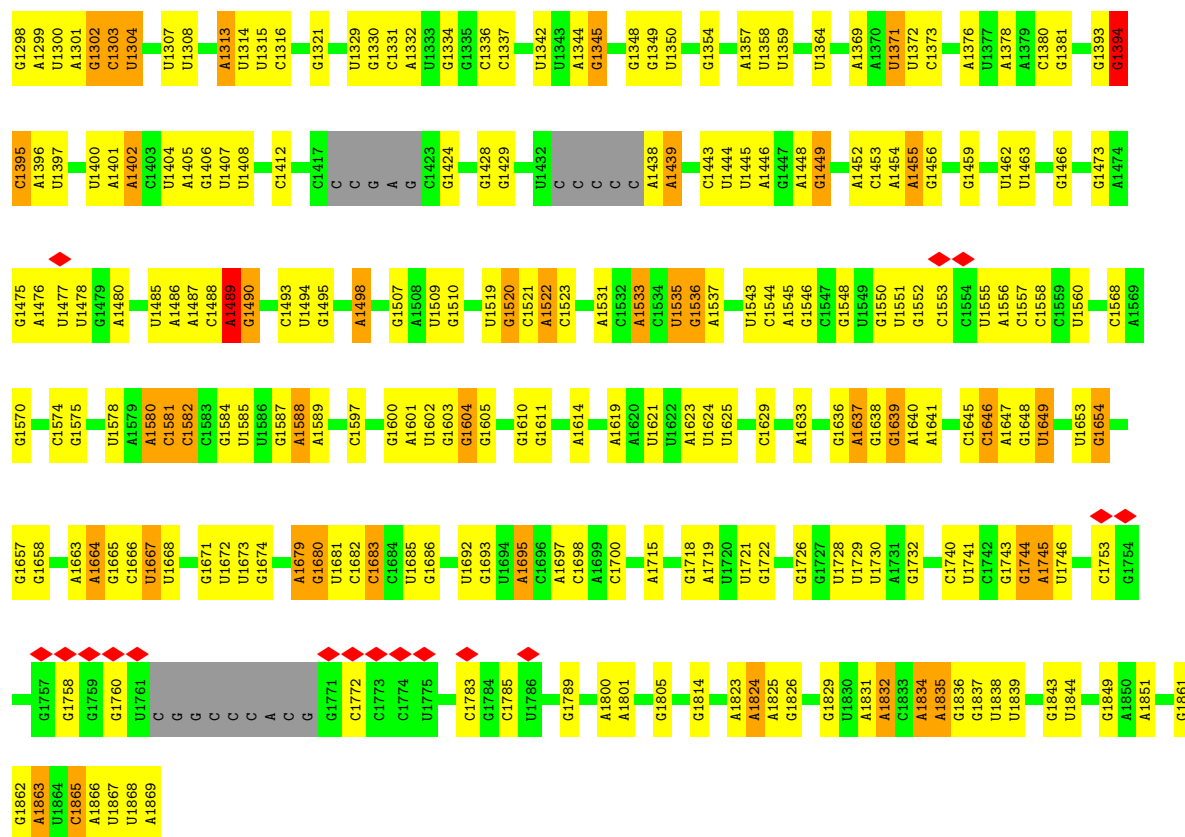
• Molecule 48: 5.8S ribosomal RNA



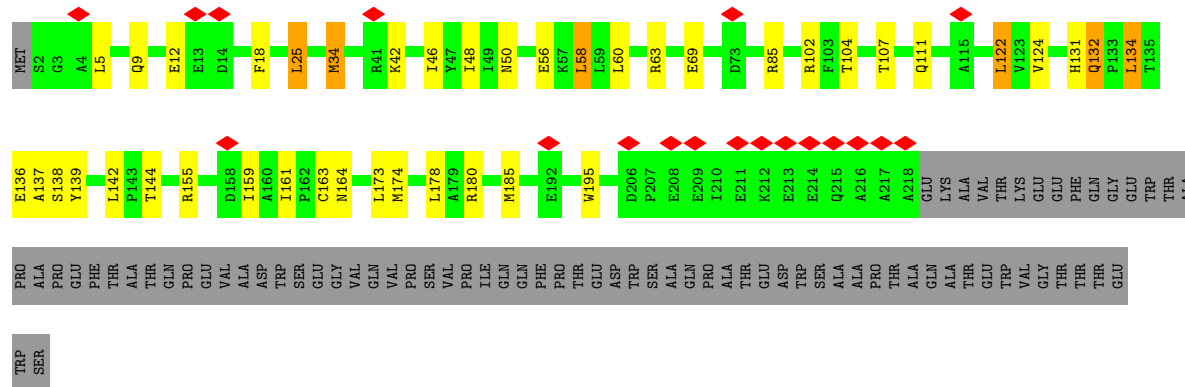
• Molecule 49: 18S ribosomal RNA



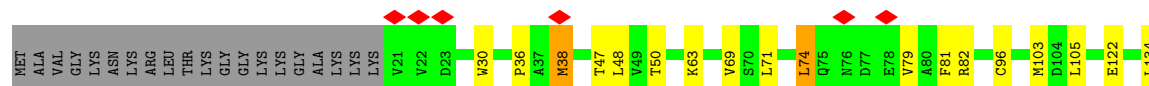


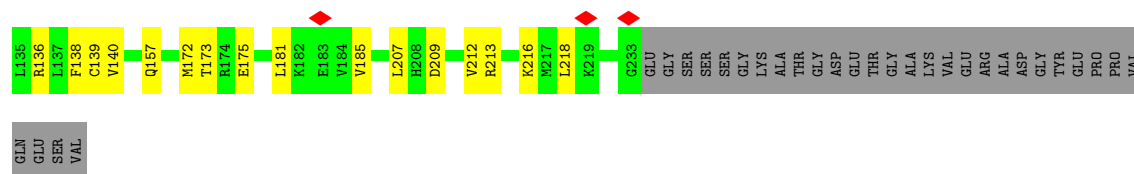


• Molecule 50: uS2

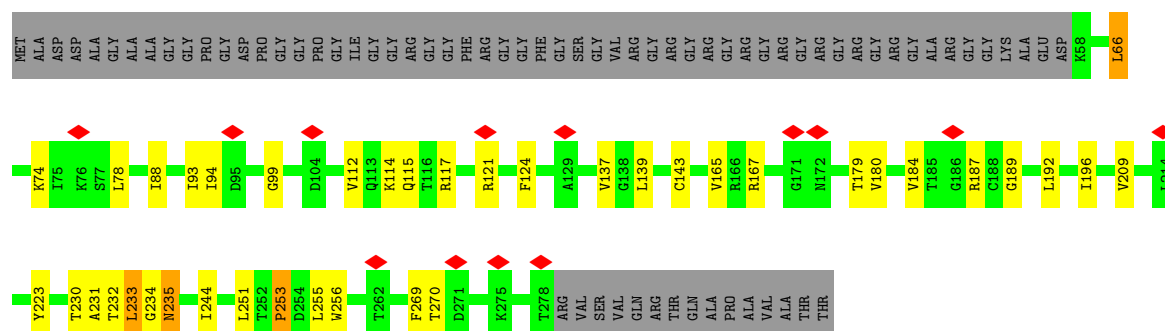


• Molecule 51: 40S ribosomal protein S3a

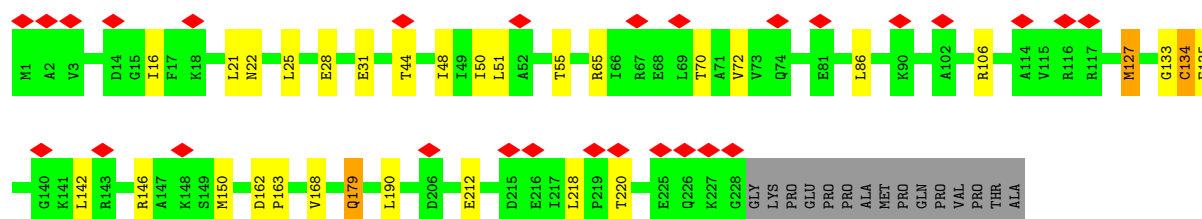
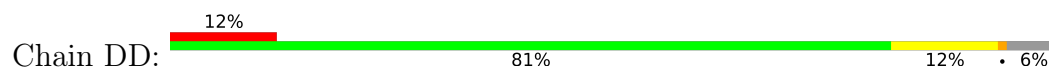




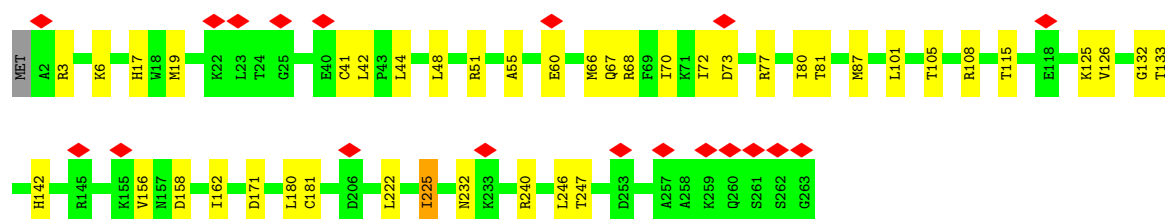
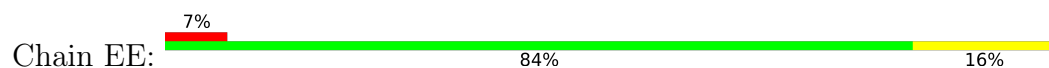
• Molecule 52: uS5



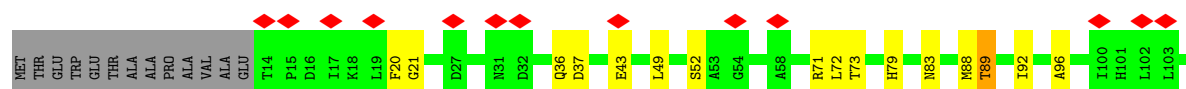
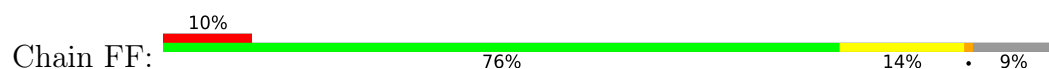
• Molecule 53: uS3

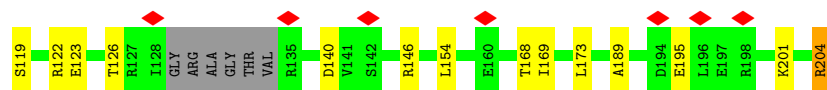


• Molecule 54: eS4



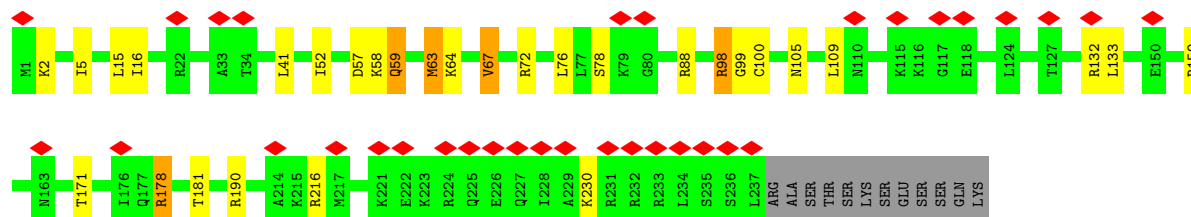
• Molecule 55: uS7





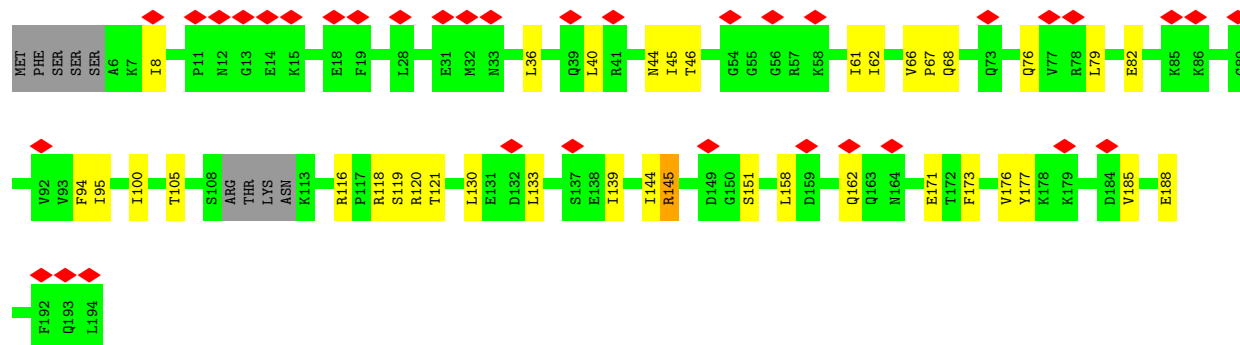
- Molecule 56: 40S ribosomal protein S6

Chain GG: 13% 83% 10% • 5%



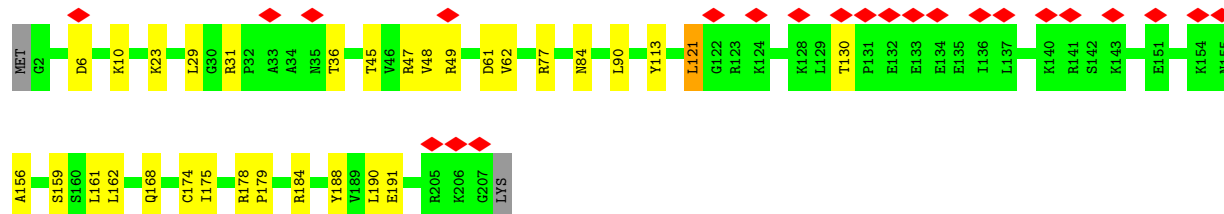
- Molecule 57: eS7

Chain HH: 18% 76% 19% • 5%



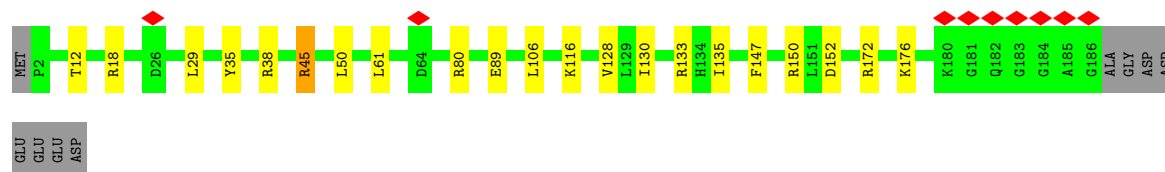
- Molecule 58: eS8

Chain II: 11% 84% 14%

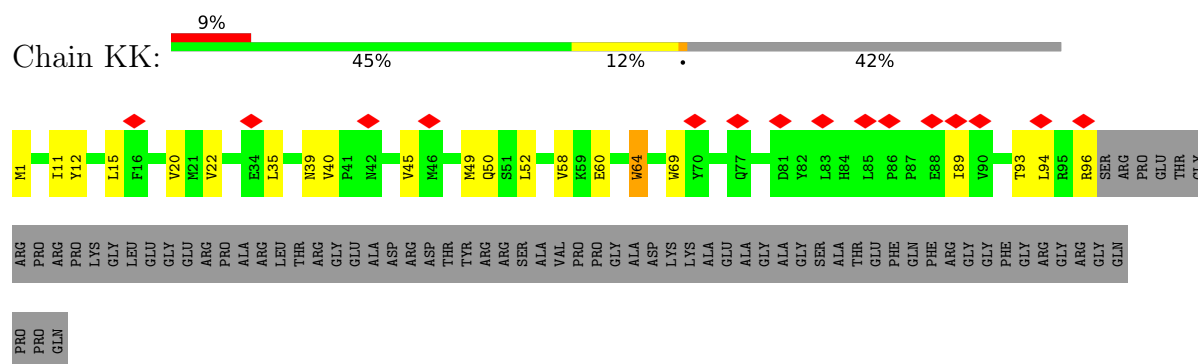


- Molecule 59: Ribosomal protein S9 (Predicted)

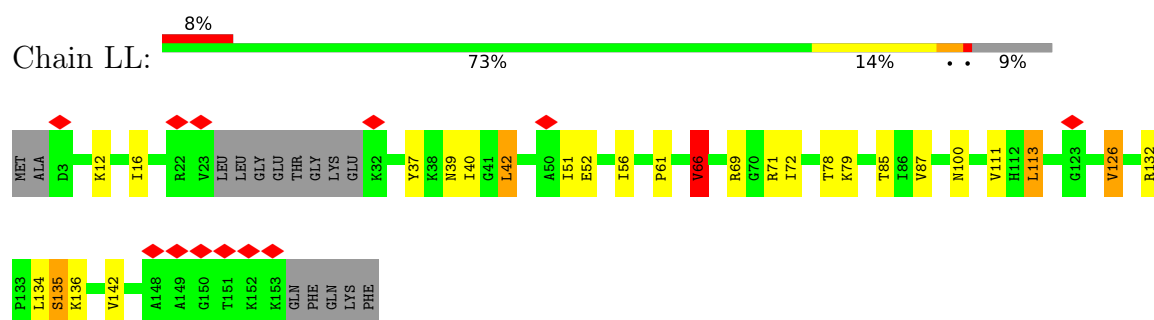
Chain JJ: 5% 85% 10% • 5%



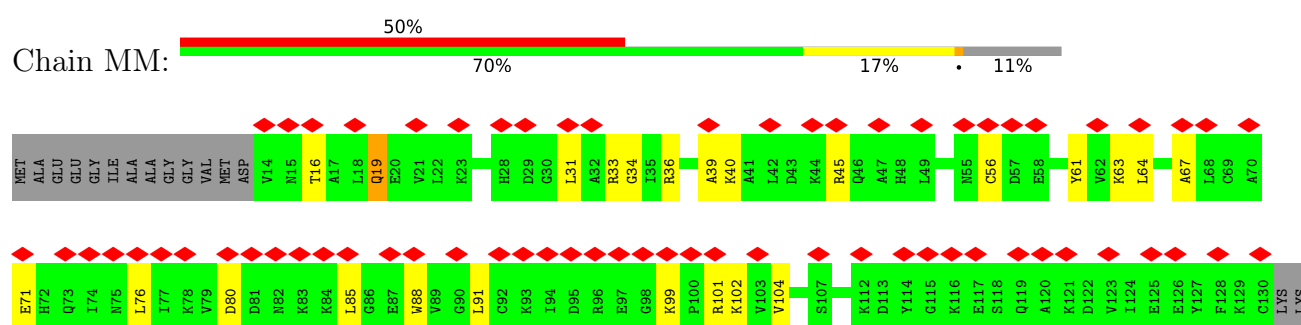
- Molecule 60: eS10



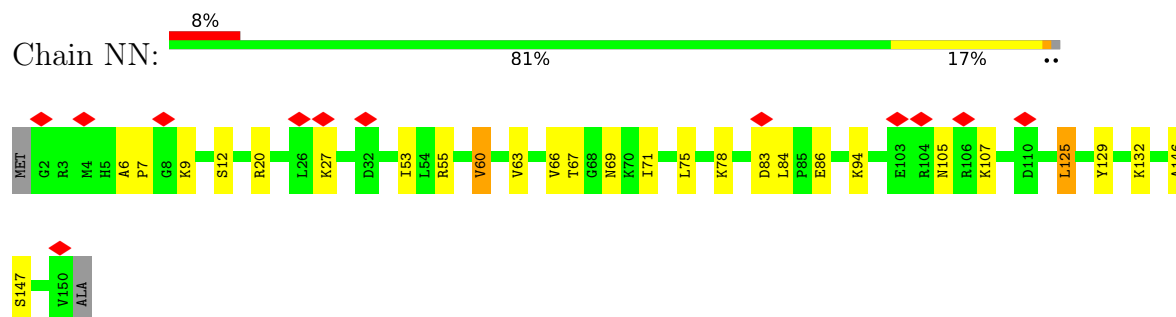
- Molecule 61: uS17



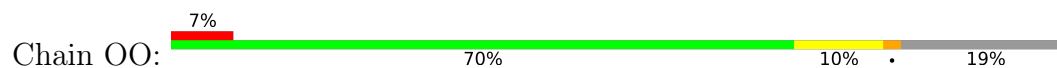
- Molecule 62: 40S ribosomal protein S12



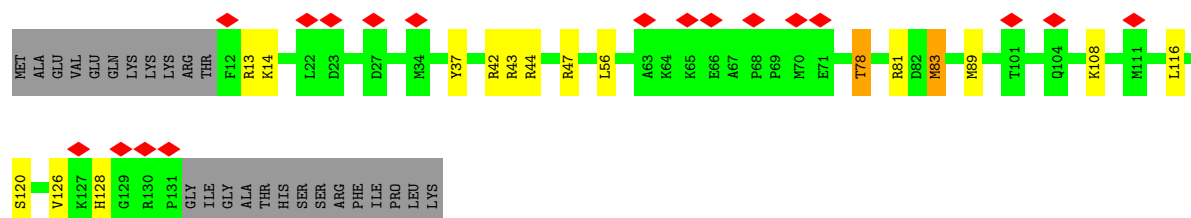
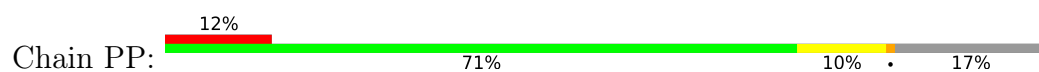
- Molecule 63: uS15



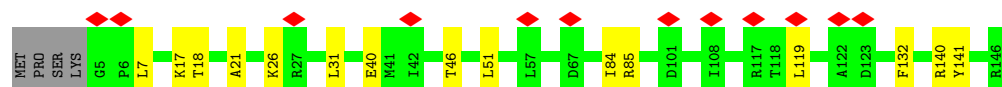
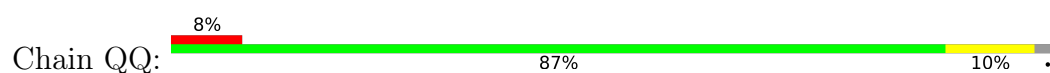
- Molecule 64: uS11



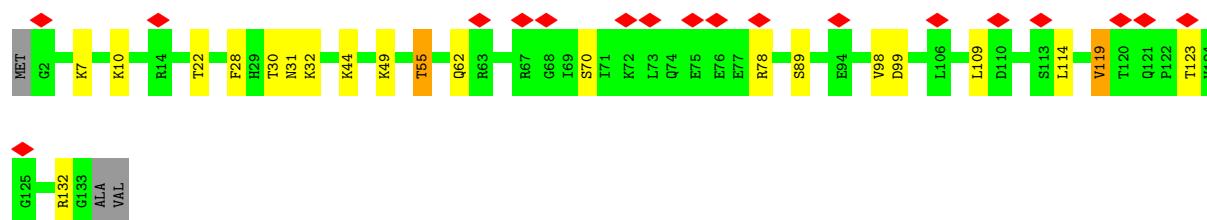
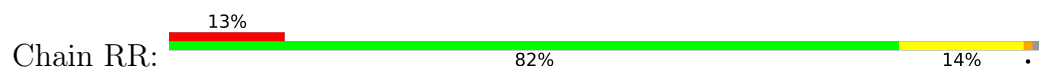
- Molecule 65: uS19



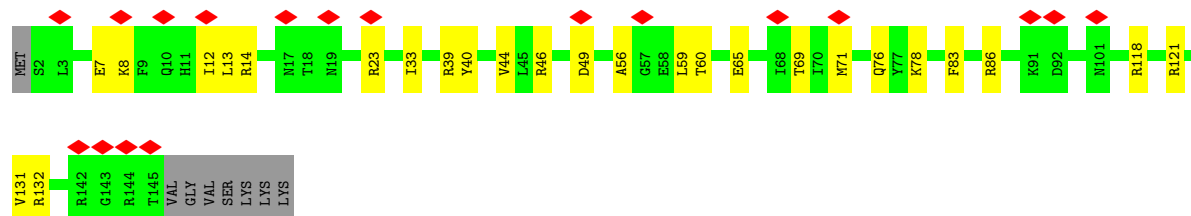
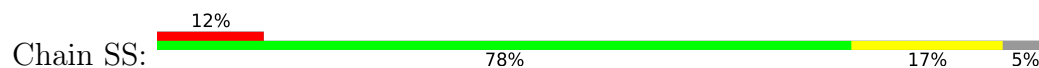
- Molecule 66: uS9



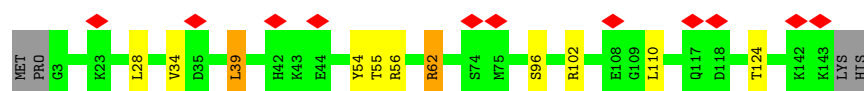
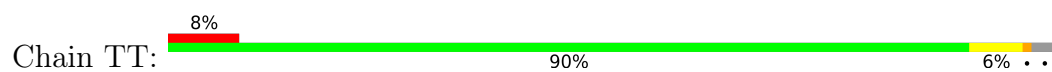
- Molecule 67: eS17



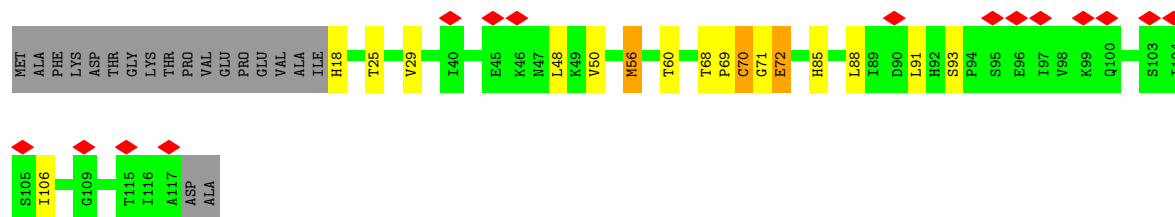
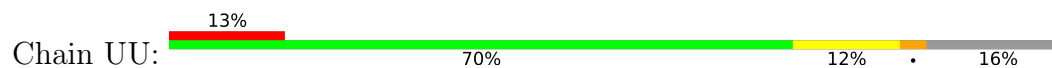
- Molecule 68: uS13



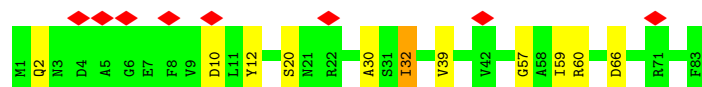
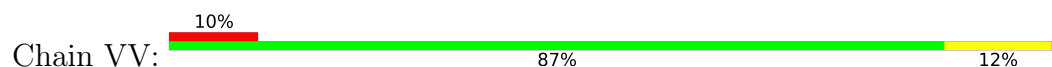
- Molecule 69: eS19



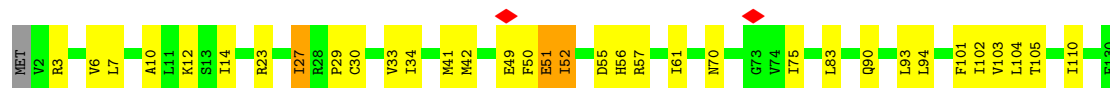
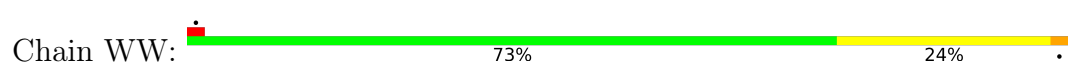
• Molecule 70: uS10



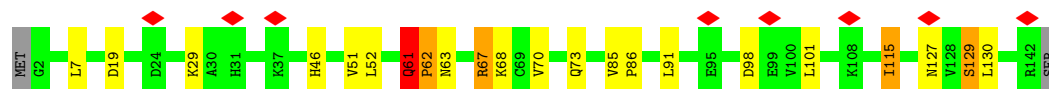
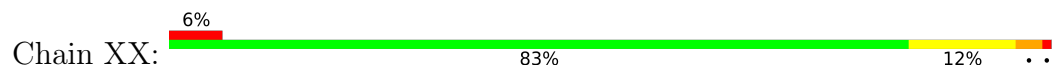
• Molecule 71: eS21



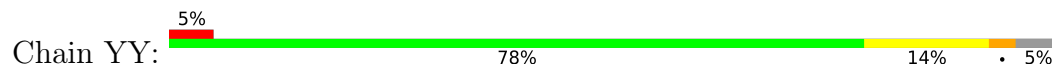
• Molecule 72: uS8



• Molecule 73: uS12

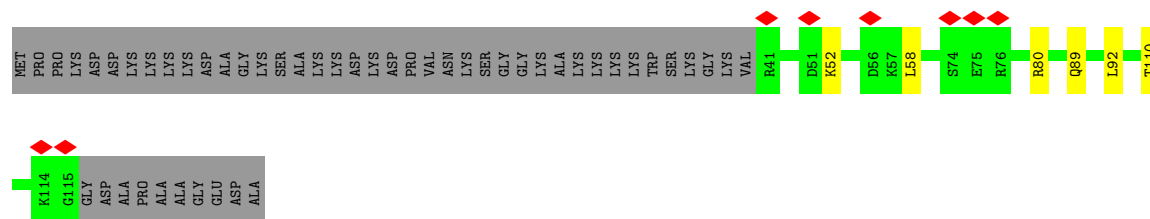


• Molecule 74: eS24

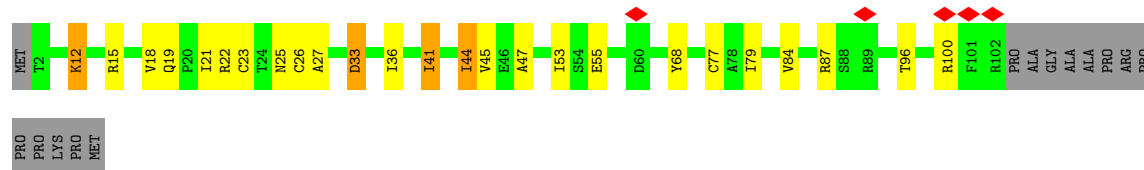


• Molecule 75: eS25

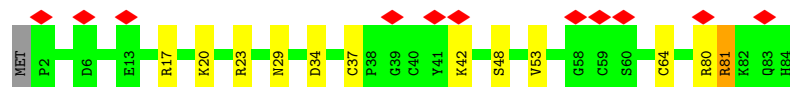
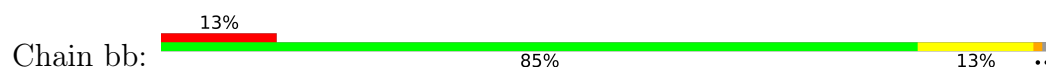




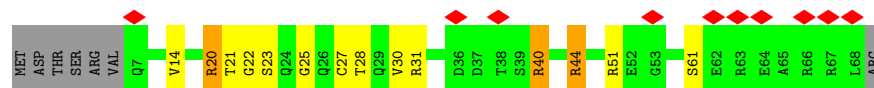
• Molecule 76: eS26



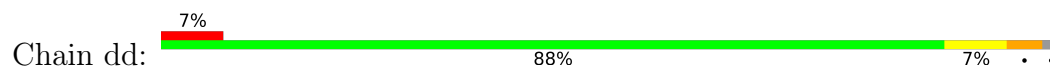
• Molecule 77: 40S ribosomal protein S27



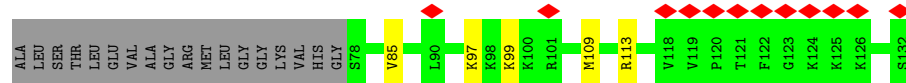
• Molecule 78: eS28



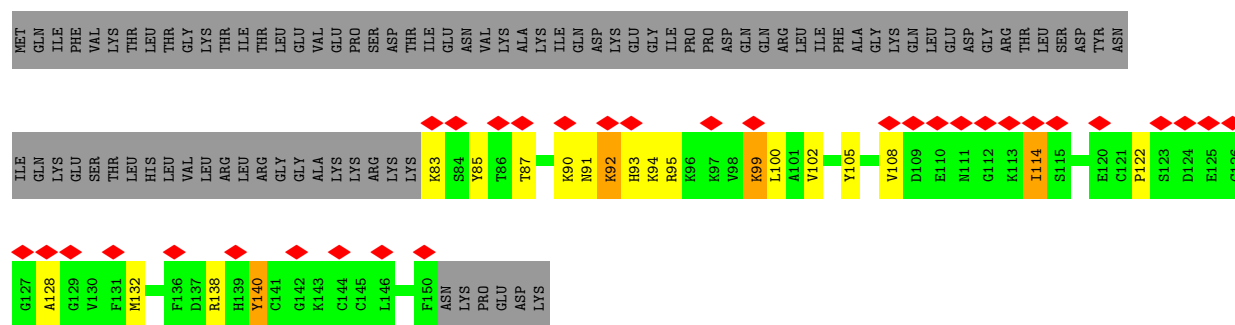
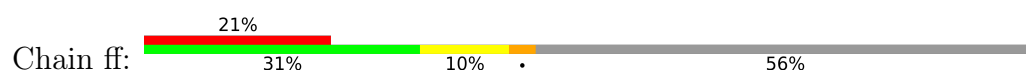
• Molecule 79: uS14



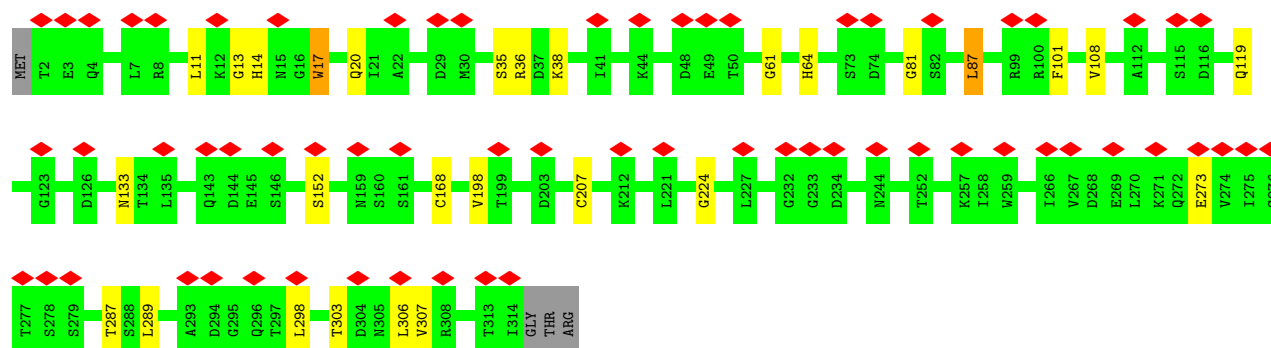
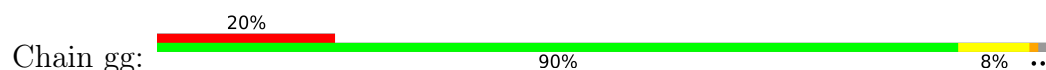
• Molecule 80: eS30



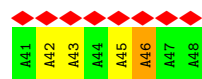
• Molecule 81: eS31



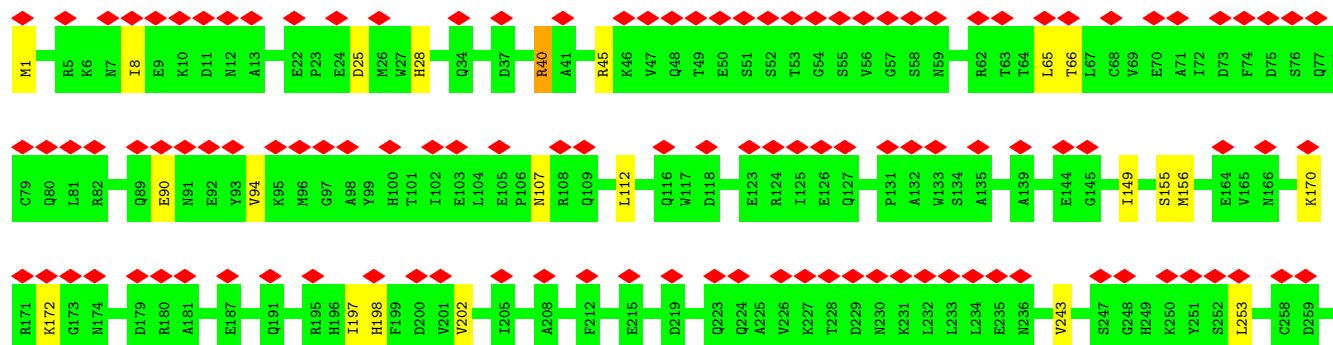
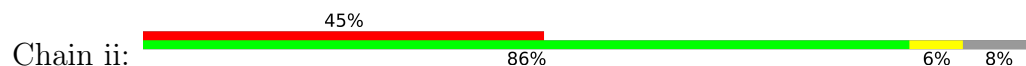
• Molecule 82: RACK1

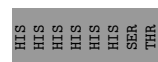


• Molecule 83: mRNA (polyadenylated)

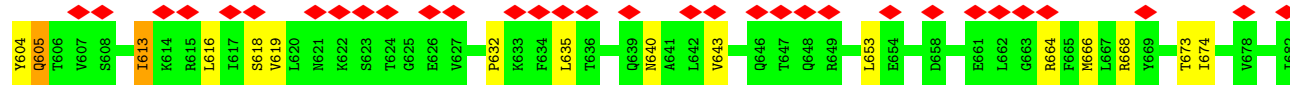
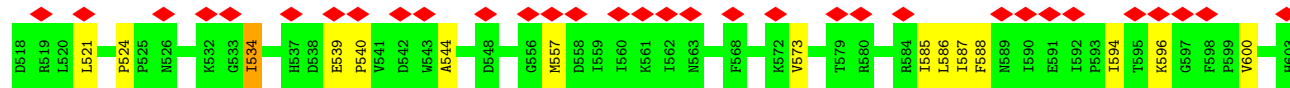
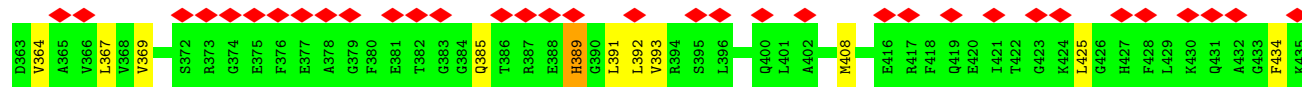
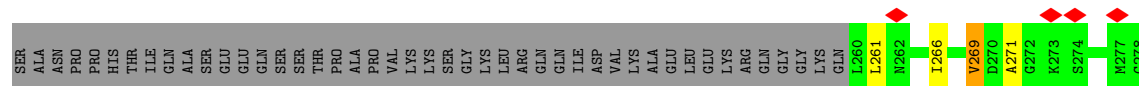
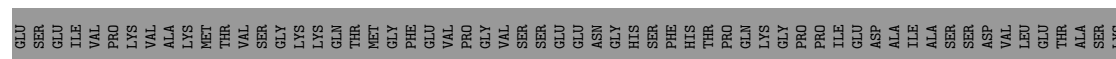


• Molecule 84: Protein pelota homolog





Chain ij: 25% 51% 7% . 40%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	20717	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.572	Depositor
Minimum map value	-0.367	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3399999, 1.3399999, 1.3399999	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A	0.59	0/1936	0.87	0/2596
2	B	0.60	0/3240	0.89	1/4339 (0.0%)
3	C	0.64	0/2937	0.93	2/3946 (0.1%)
4	D	0.51	0/2437	0.85	1/3264 (0.0%)
5	E	0.54	0/1762	0.86	0/2362
6	F	0.64	0/1911	0.92	0/2549
7	G	0.52	0/1910	0.88	2/2569 (0.1%)
8	H	0.55	0/1535	0.83	0/2063
9	I	0.56	0/1702	0.87	0/2272
10	J	0.51	0/1385	0.84	1/1852 (0.1%)
11	L	0.56	0/1733	0.90	1/2316 (0.0%)
12	M	0.56	0/1158	0.90	0/1547
13	N	0.57	0/1746	0.93	1/2338 (0.0%)
14	O	0.67	0/1662	0.97	3/2222 (0.1%)
15	P	0.61	0/1268	0.90	2/1700 (0.1%)
16	Q	0.63	0/1539	0.93	1/2054 (0.0%)
17	R	0.53	0/1524	0.88	0/2013
18	S	0.65	0/1501	0.90	1/2012 (0.0%)
19	T	0.55	0/1326	0.85	0/1770
20	U	0.51	0/823	0.80	0/1104
21	V	0.59	0/993	0.90	0/1332
22	W	0.54	0/873	0.81	0/1158
23	X	0.54	0/984	0.82	0/1323
24	Y	0.50	0/1132	0.86	1/1504 (0.1%)
25	Z	0.55	0/1130	0.81	0/1507
26	a	0.60	0/1191	0.93	1/1590 (0.1%)
27	b	0.54	0/861	0.92	0/1138
28	c	0.50	0/771	0.82	0/1034
29	d	0.58	0/903	0.87	1/1216 (0.1%)
30	e	0.65	1/1071 (0.1%)	0.90	0/1429
31	f	0.60	0/895	0.86	0/1198
32	g	0.58	0/916	0.86	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.50	0/1021	0.90	0/1348
34	i	0.50	0/841	0.87	0/1112
35	j	0.58	0/720	0.93	0/952
36	k	0.47	0/575	0.80	0/761
37	l	0.56	0/459	0.89	1/608 (0.2%)
38	m	0.53	0/435	0.86	0/575
39	n	0.47	0/240	0.85	0/305
40	o	0.50	0/864	0.80	0/1140
41	p	0.56	0/718	0.86	0/953
42	r	0.57	0/1010	0.91	0/1354
43	s	0.56	0/1530	0.74	0/2064
44	t	0.59	0/1174	0.82	0/1582
45	2	0.38	0/1777	0.73	1/2763 (0.0%)
45	3	0.37	0/1777	0.68	0/2763
46	5	0.44	3/84961 (0.0%)	0.85	182/132460 (0.1%)
47	7	0.42	0/2858	0.77	1/4455 (0.0%)
48	8	0.43	0/3581	0.82	4/5577 (0.1%)
49	9	0.42	0/40524	0.81	47/63134 (0.1%)
50	AA	0.56	0/1747	0.90	1/2374 (0.0%)
51	BB	0.47	0/1756	0.83	0/2350
52	CC	0.55	0/1753	0.93	1/2369 (0.0%)
53	DD	0.53	0/1796	0.83	0/2417
54	EE	0.53	0/2118	0.86	1/2849 (0.0%)
55	FF	0.53	0/1492	0.91	0/2005
56	GG	0.51	0/1946	0.84	0/2590
57	HH	0.52	0/1510	0.82	0/2022
58	II	0.58	0/1715	0.88	0/2287
59	JJ	0.52	0/1550	0.91	0/2069
60	KK	0.53	0/834	0.86	0/1125
61	LL	0.54	0/1195	0.82	0/1597
62	MM	0.54	0/918	0.83	0/1233
63	NN	0.52	0/1226	0.93	0/1649
64	OO	0.55	0/1029	0.97	1/1380 (0.1%)
65	PP	0.58	0/1017	0.90	0/1358
66	QQ	0.52	0/1146	0.86	0/1534
67	RR	0.53	0/1082	0.84	0/1452
68	SS	0.56	0/1208	0.89	0/1618
69	TT	0.53	0/1115	0.89	0/1493
70	UU	0.54	0/805	0.89	2/1081 (0.2%)
71	VV	0.54	0/643	0.93	0/860
72	WW	0.52	0/1051	0.91	0/1406
73	XX	0.53	0/1116	0.90	0/1490
74	YY	0.49	0/1028	0.80	0/1366

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	ZZ	0.50	0/604	0.86	0/810
76	aa	0.54	0/828	0.92	0/1109
77	bb	0.53	0/665	0.86	0/891
78	cc	0.53	0/490	0.87	0/656
79	dd	0.54	0/470	0.78	1/623 (0.2%)
80	ee	0.49	0/447	0.84	0/587
81	ff	0.53	0/567	0.74	0/753
82	gg	0.50	0/2493	0.72	0/3394
83	hh	0.39	0/199	0.80	0/308
84	ii	0.52	0/2996	0.81	0/4050
85	jj	0.53	0/3352	0.79	1/4523 (0.0%)
All	All	0.49	4/237727 (0.0%)	0.85	263/348121 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3
4	D	0	1
11	L	0	1
31	f	0	1
37	l	0	1
46	5	0	2
72	WW	0	1
73	XX	0	1
All	All	0	11

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	5	935	A	C5-C6	-7.09	1.26	1.41
46	5	922(A)	G	O3'-P	6.89	1.69	1.61
30	e	129	LEU	C-O	5.27	1.34	1.23
46	5	1411(B)	C	O3'-P	5.10	1.67	1.61

All (263) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	481	G	N1-C2-N2	-15.82	68.75	116.20
46	5	922	C	C2'-C3'-O3'	14.46	135.40	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	935	A	C5-C6-N6	-13.04	84.57	123.70
49	9	1835	A	C2'-C3'-O3'	11.37	126.56	109.50
46	5	1411	C	C2'-C3'-O3'	-10.88	97.38	113.70
46	5	2794	C	C2'-C3'-O3'	-10.03	98.66	113.70
46	5	385	A	C4'-C3'-O3'	9.99	124.39	109.40
46	5	1834	U	C2'-C3'-O3'	9.85	124.28	109.50
49	9	1664	A	C4'-C3'-O3'	9.57	123.76	109.40
46	5	47	A	C4'-C3'-O3'	9.36	123.44	109.40
46	5	2474	G	C2'-C3'-O3'	9.18	123.27	109.50
46	5	2068	C	C2'-C3'-O3'	9.12	123.18	109.50
46	5	90	G	C2'-C3'-O3'	9.08	127.32	113.70
46	5	406	C	C2'-C3'-O3'	8.70	126.74	113.70
46	5	3697	U	C2'-C3'-O3'	8.66	126.69	113.70
46	5	48	G	C2'-C3'-O3'	8.47	122.21	109.50
49	9	1394	G	C2'-C3'-O3'	8.39	126.29	113.70
49	9	1520	G	C4'-C3'-O3'	8.37	125.56	113.00
46	5	3896	C	C2'-C3'-O3'	-8.30	101.25	113.70
49	9	110	U	C2'-C3'-O3'	8.22	126.03	113.70
46	5	4335	C	C4'-C3'-O3'	-8.18	100.74	113.00
46	5	922	C	O4'-C4'-C3'	-8.05	95.95	104.00
64	OO	137	SER	N-CA-C	-8.03	102.21	110.97
46	5	2395	A	C2'-C3'-O3'	7.99	121.48	109.50
46	5	3619	G	C4'-C3'-O3'	-7.92	101.12	113.00
46	5	2313	A	C2'-C3'-O3'	7.87	121.30	109.50
46	5	971(A)	G	C4'-C3'-O3'	7.77	124.66	113.00
46	5	4925	U	C2'-C3'-O3'	7.74	121.10	109.50
46	5	4632	U	C1'-C2'-O2'	7.71	119.97	108.40
46	5	3888	G	C2'-C3'-O3'	7.64	125.17	113.70
14	O	110	PRO	N-CA-C	7.63	120.01	110.70
49	9	870	A	C4'-C3'-O3'	7.60	120.80	109.40
46	5	90	G	C4'-C3'-O3'	-7.56	101.66	113.00
46	5	449	C	C2'-C3'-O3'	7.54	120.81	109.50
46	5	2278	G	C2'-C3'-O3'	7.51	120.76	109.50
49	9	688	U	C2'-C3'-O3'	7.45	120.68	109.50
46	5	3904	G	C2'-C3'-O3'	7.44	120.66	109.50
26	a	61	TYR	N-CA-C	7.43	119.07	110.97
46	5	1683	U	C4'-C3'-O3'	-7.39	101.92	113.00
49	9	1152	U	C2'-C3'-O3'	-7.33	102.71	113.70
49	9	553	U	C2'-C3'-O3'	7.32	120.48	109.50
46	5	1211	G	C2'-C3'-O3'	7.26	124.58	113.70
46	5	1329	G	C2'-C3'-O3'	7.21	124.51	113.70
46	5	4448	G	C4'-C3'-O3'	7.18	123.77	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	935	A	N1-C6-N6	-7.16	97.12	118.60
46	5	971(A)	G	C2'-C3'-O3'	-7.12	103.02	113.70
46	5	2046	G	C4'-C3'-O3'	7.08	120.01	109.40
46	5	931	C	C4'-C3'-O3'	-7.07	102.39	113.00
46	5	2398	U	C2'-C3'-O3'	7.07	120.10	109.50
46	5	4170	A	C2'-C3'-O3'	6.98	119.97	109.50
46	5	1236	C	C4'-C3'-O3'	6.97	123.45	113.00
46	5	1323	A	C4'-C3'-O3'	-6.96	102.55	113.00
46	5	1455	G	C2'-C3'-O3'	6.96	124.14	113.70
46	5	4942	C	C4'-C3'-O3'	6.95	119.82	109.40
46	5	481	G	N3-C2-N2	-6.93	99.10	119.90
46	5	2067	C	C4'-C3'-O3'	-6.93	102.61	113.00
49	9	434	G	C2'-C3'-O3'	6.90	124.05	113.70
46	5	2695	A	C2'-C3'-O3'	6.89	119.84	109.50
46	5	4884	G	C2'-C3'-O3'	6.84	123.95	113.70
46	5	4975	G	C4'-C3'-O3'	6.81	119.61	109.40
46	5	4119	C	C2'-C3'-O3'	6.79	119.68	109.50
49	9	72	C	C4'-C3'-O3'	6.79	119.58	109.40
2	B	258	HIS	N-CA-C	6.76	124.76	109.81
49	9	1395	C	C4'-C3'-O3'	6.74	123.10	113.00
46	5	2266	C	C2'-C3'-O3'	6.72	119.58	109.50
49	9	1130	G	C4'-C3'-O3'	6.70	123.05	113.00
49	9	1253	A	C2'-C3'-O3'	6.66	119.50	109.50
46	5	1393	G	C4'-C3'-O3'	-6.66	103.02	113.00
46	5	922	C	C3'-C2'-O2'	6.64	120.67	110.70
46	5	1323	A	C3'-C2'-O2'	6.59	120.58	110.70
46	5	4449	A	C4'-C3'-O3'	6.57	119.25	109.40
3	C	232	VAL	CB-CA-C	-6.54	103.47	112.24
46	5	328	A	C4'-C3'-O3'	-6.51	103.23	113.00
46	5	492	U	C2'-C3'-O3'	6.51	119.26	109.50
49	9	1313	A	C4'-C3'-O3'	6.46	119.10	109.40
49	9	920	A	C2'-C3'-O3'	-6.46	99.81	109.50
46	5	2089	G	C2'-C3'-O3'	6.40	119.11	109.50
46	5	125	C	C2'-C3'-O3'	6.40	123.31	113.70
46	5	4638	U	C1'-C2'-O2'	6.40	118.00	108.40
49	9	594	A	C4'-C3'-O3'	6.40	119.00	109.40
70	UU	93	SER	N-CA-C	6.38	113.75	108.07
18	S	156	HIS	N-CA-C	-6.36	98.81	108.67
46	5	245	C	C2'-C3'-O3'	6.36	123.25	113.70
46	5	935	A	C6-N1-C2	-6.35	99.55	118.60
46	5	1411	C	C4'-C3'-O3'	6.35	122.53	113.00
46	5	4232	U	C4'-C3'-O3'	6.35	118.92	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	130	PRO	CA-C-N	6.33	125.82	119.24
7	G	130	PRO	C-N-CA	6.33	125.82	119.24
46	5	4312	U	C4'-C3'-O3'	-6.31	103.53	113.00
46	5	696	C	C2'-C3'-O3'	6.31	118.96	109.50
46	5	930	G	C2'-C3'-O3'	6.31	123.16	113.70
46	5	3657	U	C2'-C3'-O3'	6.29	123.14	113.70
45	2	71	G	C2'-C3'-O3'	6.29	123.13	113.70
46	5	418	A	C4'-C3'-O3'	-6.26	103.62	113.00
46	5	959	G	C4'-C3'-O3'	6.25	118.78	109.40
49	9	1679	A	C2'-C3'-O3'	6.25	118.87	109.50
46	5	4567	G	C3'-C2'-O2'	6.24	120.05	110.70
46	5	914	U	C4'-C3'-O3'	6.23	122.34	113.00
49	9	872	A	C2'-C3'-O3'	6.23	118.84	109.50
46	5	1396	G	C4'-C3'-O3'	-6.21	103.68	113.00
46	5	1818	G	C2'-C3'-O3'	6.20	123.00	113.70
46	5	3603	G	C2'-C3'-O3'	6.19	122.99	113.70
49	9	1646	C	C4'-C3'-O3'	-6.17	103.74	113.00
49	9	1646	C	C2'-C3'-O3'	6.17	122.95	113.70
49	9	434	G	C4'-C3'-O3'	6.16	122.24	113.00
46	5	4232	U	C2'-C3'-O3'	6.15	118.73	109.50
49	9	752	G	C2'-C3'-O3'	6.15	118.72	109.50
70	UU	72	GLU	N-CA-C	6.13	119.80	107.41
46	5	1072	C	C2'-C3'-O3'	6.13	118.69	109.50
46	5	371	A	C4'-C3'-O3'	-6.12	103.82	113.00
46	5	134	G	C4'-C3'-O3'	6.10	118.56	109.40
46	5	2281	U	C4'-C3'-O3'	-6.08	103.88	113.00
46	5	466	A	C2'-C3'-O3'	-6.08	104.58	113.70
46	5	3912	U	C4'-C3'-O3'	-6.07	103.90	113.00
85	jj	524	PRO	N-CA-C	6.07	118.10	110.70
46	5	1485	C	C2'-C3'-O3'	6.04	118.56	109.50
46	5	1683	U	C2'-C3'-O3'	6.04	122.75	113.70
10	J	146	ARG	N-CA-C	6.01	117.91	111.36
46	5	4517	A	C4'-C3'-O3'	-6.01	103.99	113.00
49	9	371	A	C4'-C3'-O3'	-5.99	104.01	113.00
48	8	19	C	C4'-C3'-O3'	-5.98	104.03	113.00
46	5	2695	A	C4'-C3'-O3'	5.97	118.36	109.40
11	L	74	ARG	N-CA-C	-5.95	104.42	111.03
46	5	1477	C	C2'-C3'-O3'	5.95	122.62	113.70
46	5	4947	U	C2'-C3'-O3'	5.94	122.61	113.70
46	5	1358	G	C4'-C3'-O3'	5.93	118.30	109.40
49	9	642	U	C2'-C3'-O3'	5.92	122.58	113.70
46	5	1818	G	C3'-C2'-O2'	5.92	119.58	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	922	C	C4'-C3'-C2'	-5.90	96.70	102.60
46	5	1392	A	C4'-C3'-O3'	-5.88	104.18	113.00
46	5	1236	C	C2'-C3'-O3'	5.87	122.50	113.70
46	5	2046	G	C2'-C3'-O3'	5.86	118.29	109.50
49	9	1605	G	C4'-C3'-O3'	-5.84	104.23	113.00
46	5	1428	U	C2'-C3'-O3'	5.83	122.44	113.70
46	5	1908	A	C2'-C3'-O3'	5.82	122.43	113.70
46	5	721	G	C4'-C3'-O3'	-5.82	104.27	113.00
49	9	160	U	C4'-C3'-O3'	5.82	118.13	109.40
29	d	38	PHE	N-CA-C	5.82	118.40	111.71
46	5	1428	U	C4'-C3'-O3'	-5.82	104.28	113.00
46	5	2369	U	C2'-C3'-O3'	5.80	118.20	109.50
13	N	185	GLY	N-CA-C	-5.80	103.46	112.45
46	5	922(A)	G	N9-C1'-C2'	5.80	120.70	112.00
46	5	1503	A	C4'-C3'-O3'	5.78	118.07	109.40
46	5	498	C	C4'-C3'-O3'	5.76	118.04	109.40
46	5	922(B)	C	C4'-C3'-O3'	5.74	118.00	109.40
46	5	2807	A	C2'-C3'-O3'	5.72	122.28	113.70
46	5	1633	G	C2'-C3'-O3'	-5.71	105.13	113.70
46	5	4237	C	C4'-C3'-O3'	-5.70	104.45	113.00
46	5	2517	A	C4'-C3'-O3'	-5.70	104.45	113.00
46	5	2266	C	C4'-C3'-O3'	5.70	117.94	109.40
46	5	2275	G	C4'-C3'-O3'	-5.68	104.48	113.00
46	5	727	C	C4'-C3'-O3'	-5.67	104.49	113.00
46	5	1732	C	C4'-C3'-O3'	-5.67	104.50	113.00
46	5	3603	G	C4'-C3'-O3'	-5.66	104.51	113.00
46	5	1323	A	C2'-C3'-O3'	5.66	122.19	113.70
49	9	1217	A	C4'-C3'-O3'	-5.65	104.53	113.00
46	5	3845	A	C4'-C3'-O3'	-5.64	104.53	113.00
46	5	747	A	C4'-C3'-O3'	5.64	117.86	109.40
49	9	1645	C	C4'-C3'-O3'	-5.63	104.55	113.00
49	9	980	A	C4'-C3'-O3'	-5.62	104.56	113.00
46	5	3838	U	C3'-C2'-O2'	5.62	119.14	110.70
46	5	504	G	C2'-C3'-O3'	5.62	122.13	113.70
46	5	1445	U	C2'-C3'-O3'	5.62	122.12	113.70
3	C	32	ILE	N-CA-C	-5.60	102.35	109.58
46	5	48	G	C4'-C3'-O3'	5.60	117.80	109.40
49	9	291	G	C4'-C3'-O3'	-5.58	104.62	113.00
14	O	109	PRO	CA-C-N	5.58	126.12	120.38
14	O	109	PRO	C-N-CA	5.58	126.12	120.38
79	dd	53	ILE	N-CA-C	5.58	115.20	108.06
46	5	938	C	C3'-C2'-O2'	5.57	119.06	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	9	1637	A	C2'-C3'-O3'	5.57	117.85	109.50
46	5	922	C	N1-C1'-C2'	-5.56	103.66	112.00
46	5	1523	A	C4'-C3'-O3'	-5.55	104.67	113.00
46	5	365	U	C3'-C2'-O2'	5.55	119.02	110.70
46	5	3898	G	C1'-C2'-O2'	5.53	116.70	108.40
46	5	71	C	C4'-C3'-O3'	-5.53	104.71	113.00
49	9	1085	C	C2'-C3'-O3'	-5.52	101.22	109.50
46	5	64	A	C4'-C3'-O3'	5.51	117.66	109.40
46	5	1921	C	C4'-C3'-O3'	5.51	117.66	109.40
46	5	1814	C	C4'-C3'-O3'	-5.51	104.74	113.00
46	5	2357	G	C4'-C3'-O3'	-5.50	104.74	113.00
46	5	349	A	C1'-C2'-O2'	-5.48	103.58	111.80
46	5	1890	G	C1'-C2'-O2'	-5.48	103.58	111.80
46	5	4354	U	C4'-C3'-O3'	-5.47	104.79	113.00
46	5	3710	G	C4'-C3'-O3'	5.47	117.61	109.40
48	8	124	U	C4'-C3'-O3'	5.46	117.60	109.40
46	5	3625	G	C2'-C3'-O3'	5.46	121.89	113.70
49	9	111	A	C4'-C3'-O3'	-5.45	104.82	113.00
24	Y	58	VAL	CB-CA-C	-5.44	106.08	111.30
49	9	501	C	N1-C1'-C2'	5.42	120.13	112.00
46	5	922	C	C1'-C2'-O2'	-5.42	100.28	108.40
46	5	1906	U	C4'-C3'-O3'	-5.41	104.88	113.00
46	5	2657	G	C4'-C3'-O3'	-5.40	104.90	113.00
49	9	1832	A	C4'-C3'-O3'	-5.40	104.90	113.00
49	9	1264	C	C4'-C3'-O3'	5.40	117.50	109.40
46	5	3880	G	C4'-C3'-O3'	-5.38	104.93	113.00
46	5	1287	G	C4'-C3'-O3'	5.37	121.05	113.00
46	5	1238	A	C3'-C2'-O2'	5.36	118.75	110.70
46	5	3917	A	C3'-C2'-O2'	5.35	118.73	110.70
46	5	2362	U	C3'-C2'-O2'	5.35	118.72	110.70
46	5	407	A	C4'-C3'-O3'	-5.33	105.00	113.00
54	EE	133	THR	N-CA-C	5.33	118.89	112.38
52	CC	187	ARG	N-CA-C	5.33	116.26	107.20
47	7	59	G	C1'-C2'-O2'	5.32	116.38	108.40
46	5	1440	U	C2'-C3'-O3'	5.31	121.67	113.70
49	9	532	C	C2'-C3'-O3'	5.31	121.66	113.70
46	5	38	A	C4'-C3'-O3'	-5.28	105.08	113.00
49	9	1489	A	C4'-C3'-O3'	5.27	120.90	113.00
37	1	49	LEU	N-CA-C	5.26	119.00	112.47
46	5	1942	A	C4'-C3'-O3'	-5.26	105.11	113.00
46	5	2272	C	C3'-C2'-O2'	5.24	118.56	110.70
46	5	3859	G	C4'-C3'-O3'	-5.24	105.14	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	94	A	C4'-C3'-O3'	-5.24	105.14	113.00
46	5	4522	G	C3'-C2'-O2'	5.24	118.56	110.70
15	P	10	ASN	CA-C-N	5.24	125.29	119.32
15	P	10	ASN	C-N-CA	5.24	125.29	119.32
46	5	118	C	C4'-C3'-O3'	-5.24	105.14	113.00
4	D	22	ARG	CG-CD-NE	5.23	123.51	112.00
46	5	275	C	C2'-C3'-O3'	5.23	121.55	113.70
46	5	4663	G	C4'-C3'-O3'	-5.23	105.16	113.00
46	5	2797	C	C2'-C3'-O3'	-5.22	101.66	109.50
16	Q	178	ARG	N-CA-C	5.22	117.65	111.33
46	5	2072	C	C4'-C3'-O3'	-5.22	105.17	113.00
46	5	342	G	C4'-C3'-O3'	-5.22	105.17	113.00
49	9	349	A	C4'-C3'-O3'	-5.19	105.22	113.00
46	5	3697	U	C3'-C2'-O2'	5.19	118.48	110.70
46	5	2799	G	C3'-C2'-O2'	5.17	118.46	110.70
49	9	1088	U	C2'-C3'-O3'	-5.17	101.75	109.50
46	5	1072	C	C4'-C3'-O3'	5.16	117.14	109.40
46	5	1238	A	C2'-C3'-O3'	5.16	121.44	113.70
49	9	1535	U	N1-C1'-C2'	5.15	121.72	114.00
46	5	4375	C	C2'-C3'-O3'	-5.14	105.99	113.70
46	5	1411(B)	C	C2'-C3'-O3'	-5.14	105.99	113.70
49	9	1824	A	C4'-C3'-O3'	5.14	117.11	109.40
46	5	1538	U	C3'-C2'-O2'	5.13	118.39	110.70
46	5	2274	C	C2'-C3'-O3'	-5.12	106.02	113.70
46	5	922	C	P-O5'-C5'	5.12	128.57	120.90
48	8	94	G	C2'-C3'-O3'	5.10	117.15	109.50
46	5	2286	G	C4'-C3'-O3'	-5.09	105.36	113.00
46	5	3938	G	C4'-C3'-O3'	5.08	117.03	109.40
46	5	1350	C	C3'-C2'-O2'	5.08	118.32	110.70
48	8	98	C	C3'-C2'-O2'	5.08	118.31	110.70
49	9	1022	U	C4'-C3'-O3'	-5.08	105.39	113.00
49	9	1046	U	C1'-C2'-O2'	5.07	116.00	108.40
46	5	4636	U	C3'-C2'-O2'	5.07	118.30	110.70
46	5	2836	A	C4'-C3'-O3'	-5.06	105.40	113.00
46	5	1541	C	C4'-C3'-O3'	-5.06	105.41	113.00
46	5	4075	U	C3'-C2'-O2'	5.06	118.29	110.70
46	5	3894	A	C4'-C3'-O3'	-5.05	105.42	113.00
46	5	4693	C	C4'-C3'-O3'	5.05	116.98	109.40
46	5	1427	A	C4'-C3'-O3'	-5.05	105.42	113.00
46	5	959	G	C2'-C3'-O3'	5.05	117.07	109.50
49	9	122	G	C3'-C2'-O2'	5.04	118.26	110.70
46	5	485	C	C3'-C2'-O2'	5.04	118.26	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	5	1370	G	C2'-C3'-O3'	5.04	117.06	109.50
46	5	3678	G	C2'-C3'-O3'	-5.04	101.94	109.50
46	5	345	C	C4'-C3'-O3'	-5.04	105.44	113.00
46	5	1509	C	C3'-C2'-O2'	5.04	118.25	110.70
46	5	1633	G	C4'-C3'-O3'	5.03	120.54	113.00
46	5	3738	G	C4'-C3'-O3'	-5.01	105.48	113.00
49	9	642	U	C4'-C3'-O3'	5.01	120.52	113.00
50	AA	139	TYR	N-CA-C	-5.01	107.02	113.23
46	5	3802	U	C1'-C2'-O2'	-5.00	104.30	111.80

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
46	5	481	G	Sidechain
46	5	935	A	Sidechain
2	B	16	PHE	Peptide
2	B	257	TRP	Peptide
2	B	259	PRO	Peptide
4	D	36	LEU	Peptide
11	L	46	ILE	Peptide
72	WW	27	ILE	Peptide
73	XX	61	GLN	Peptide
31	f	106	TYR	Peptide
37	l	48	LYS	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	A	1898	0	1993	28	0
2	B	3172	0	3310	34	0
3	C	2883	0	3053	55	0
4	D	2391	0	2424	15	0
5	E	1729	0	1887	18	0
6	F	1875	0	1995	27	0
7	G	1879	0	2027	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1516	0	1597	16	0
9	I	1664	0	1712	15	0
10	J	1362	0	1399	14	0
11	L	1702	0	1820	14	0
12	M	1137	0	1211	18	0
13	N	1701	0	1749	27	0
14	O	1630	0	1778	32	0
15	P	1242	0	1274	15	0
16	Q	1515	0	1634	21	0
17	R	1508	0	1664	9	0
18	S	1462	0	1508	24	0
19	T	1298	0	1366	13	0
20	U	809	0	833	9	0
21	V	979	0	1039	13	0
22	W	860	0	903	4	0
23	X	967	0	1040	4	0
24	Y	1115	0	1205	6	0
25	Z	1107	0	1182	9	0
26	a	1162	0	1209	11	0
27	b	848	0	920	3	0
28	c	761	0	794	6	0
29	d	888	0	930	19	0
30	e	1053	0	1147	17	0
31	f	876	0	912	10	0
32	g	906	0	1001	7	0
33	h	1013	0	1147	5	0
34	i	830	0	916	1	0
35	j	705	0	738	7	0
36	k	569	0	637	2	0
37	l	447	0	480	6	0
38	m	429	0	466	3	0
39	n	239	0	289	0	0
40	o	851	0	920	9	0
41	p	708	0	758	14	0
42	r	994	0	1051	11	0
43	s	1507	0	1564	0	0
44	t	1160	0	1218	1	0
45	2	1593	0	811	5	0
45	3	1593	0	811	5	0
46	5	75972	0	38399	514	0
47	7	2558	0	1296	7	0
48	8	3208	0	1629	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	9	36249	0	18316	241	0
50	AA	1710	0	1708	17	0
51	BB	1729	0	1803	14	0
52	CC	1716	0	1806	15	0
53	DD	1768	0	1866	13	0
54	EE	2076	0	2177	15	0
55	FF	1471	0	1522	9	0
56	GG	1923	0	2089	15	0
57	HH	1488	0	1582	13	0
58	II	1686	0	1772	14	0
59	JJ	1525	0	1640	9	0
60	KK	810	0	836	10	0
61	LL	1175	0	1249	11	0
62	MM	908	0	939	39	0
63	NN	1202	0	1289	7	0
64	OO	1016	0	1039	9	0
65	PP	997	0	1045	7	0
66	QQ	1128	0	1195	7	0
67	RR	1068	0	1121	4	0
68	SS	1190	0	1249	10	0
69	TT	1097	0	1132	4	0
70	UU	795	0	862	5	0
71	VV	636	0	637	4	0
72	WW	1034	0	1080	17	0
73	XX	1098	0	1167	10	0
74	YY	1011	0	1083	7	0
75	ZZ	598	0	656	0	0
76	aa	814	0	864	12	0
77	bb	651	0	672	3	0
78	cc	488	0	514	22	0
79	dd	459	0	449	5	0
80	ee	443	0	492	0	0
81	ff	555	0	566	50	0
82	gg	2436	0	2393	9	0
83	hh	176	0	89	1	0
84	ii	2947	0	2957	10	0
85	jj	3292	0	3371	19	0
86	5	160	0	0	0	0
86	7	5	0	0	0	0
86	8	3	0	0	0	0
86	9	58	0	0	0	0
86	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	I	1	0	0	0	0
86	L	1	0	0	0	0
86	P	1	0	0	0	0
86	Q	1	0	0	0	0
86	V	1	0	0	0	0
86	a	1	0	0	0	0
86	e	1	0	0	0	0
86	j	1	0	0	0	0
86	jj	1	0	0	0	0
87	aa	1	0	0	0	0
87	dd	1	0	0	0	0
87	ff	1	0	0	0	0
87	g	1	0	0	1	0
87	j	1	0	0	0	0
87	m	1	0	0	2	0
87	o	1	0	0	0	0
87	p	1	0	0	2	0
88	jj	32	0	14	0	0
All	All	221912	0	166887	1509	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 4.

All (1509) 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)
32:g:46:CYS:SG	87:g:200:ZN:ZN	1.19	1.32
46:5:3914:U:O4	46:5:4378:A:N1	1.60	1.32
49:9:1290:G:N7	81:ff:95:ARG:NH2	1.77	1.31
49:9:830:A:N1	49:9:844:U:O4	1.71	1.20
46:5:1929:A:N1	46:5:2054:U:O4	1.73	1.20
46:5:77:U:O4	46:5:336:A:N1	1.70	1.20
62:MM:36:ARG:HA	81:ff:102:VAL:HG21	1.23	1.18
46:5:922:C:C5'	46:5:922(A):G:H3'	1.74	1.17
46:5:922:C:H5'	46:5:922(A):G:H3'	1.22	1.16
78:cc:20:ARG:HD3	78:cc:28:THR:CG2	1.78	1.14
49:9:1304:U:H5'	81:ff:92:LYS:C	1.75	1.10
46:5:2468:U:O4	46:5:2473:A:N1	1.83	1.10
62:MM:36:ARG:NE	81:ff:102:VAL:HG22	1.70	1.06
62:MM:36:ARG:HD2	81:ff:102:VAL:CG2	1.84	1.05
78:cc:20:ARG:CD	78:cc:28:THR:HG22	1.87	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:1284:A:N1	62:MM:91:LEU:HD22	1.73	1.02
62:MM:36:ARG:CD	81:ff:102:VAL:HG22	1.91	0.98
62:MM:36:ARG:HE	81:ff:102:VAL:HG22	1.26	0.98
37:l:2:SER:N	46:5:2406:G:N7	2.13	0.96
46:5:922:C:H5'	46:5:922(B):C:O5'	1.64	0.96
49:9:1302:G:N2	81:ff:93:HIS:CE1	2.34	0.95
49:9:1286:G:OP1	81:ff:99:LYS:HG3	1.66	0.95
49:9:1290:G:C5	81:ff:95:ARG:NH2	2.35	0.95
78:cc:20:ARG:HD3	78:cc:28:THR:HG22	0.93	0.92
49:9:1304:U:H5'	81:ff:93:HIS:N	1.85	0.92
46:5:2409:U:C4	46:5:2783:A:N1	2.39	0.90
46:5:4699:U:N3	46:5:4701:A:N6	2.19	0.89
38:m:73:CYS:HG	87:m:200:ZN:ZN	0.56	0.87
46:5:1411:C:H4'	46:5:1411(C):C:O4'	1.74	0.87
46:5:922:C:P	46:5:922(B):C:O5'	2.32	0.87
62:MM:36:ARG:HD2	81:ff:102:VAL:HG22	1.50	0.86
49:9:1271:C:OP1	81:ff:90:LYS:HD3	1.76	0.86
46:5:2409:U:O4	46:5:2783:A:N1	2.08	0.85
62:MM:64:LEU:HD13	81:ff:108:VAL:HB	1.59	0.85
62:MM:36:ARG:CA	81:ff:102:VAL:HG21	2.07	0.84
46:5:922:C:O2'	46:5:922(B):C:O2	1.95	0.83
49:9:1283:C:H41	62:MM:102:LYS:HE3	1.42	0.83
62:MM:67:ALA:CB	81:ff:108:VAL:HG23	2.09	0.83
49:9:1283:C:N4	62:MM:102:LYS:HE3	1.94	0.82
49:9:1507:G:N2	81:ff:87:THR:O	2.12	0.82
54:EE:44:LEU:HD13	54:EE:72:ILE:HD11	1.61	0.82
8:H:41:ILE:HG21	8:H:73:ILE:HD11	1.59	0.82
62:MM:36:ARG:HD2	81:ff:102:VAL:HG23	1.60	0.81
62:MM:36:ARG:CD	81:ff:102:VAL:CG2	2.53	0.81
60:KK:35:LEU:HD12	60:KK:40:VAL:HG21	1.62	0.81
62:MM:36:ARG:HA	81:ff:102:VAL:CG2	2.06	0.81
41:p:60:CYS:SG	87:p:100:ZN:ZN	1.68	0.81
38:m:73:CYS:SG	87:m:200:ZN:ZN	1.69	0.81
14:O:12:ARG:O	18:S:171:ARG:NH2	2.14	0.80
46:5:4699:U:N3	46:5:4701:A:C6	2.50	0.79
62:MM:39:ALA:HB2	81:ff:102:VAL:HG11	1.65	0.79
46:5:4699:U:C4	46:5:4701:A:N6	2.51	0.78
46:5:922:C:O2'	46:5:922(B):C:C2	2.35	0.78
19:T:87:LYS:NZ	46:5:4301:U:OP2	2.17	0.77
46:5:922:C:H5'	46:5:922(A):G:C3'	2.11	0.76
16:Q:104:ARG:NH2	46:5:1353:G:N7	2.35	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:3914:U:C4	46:5:4378:A:N1	2.53	0.75
49:9:980:A:H2'	49:9:981:A:C8	2.21	0.75
53:DD:70:THR:HG22	53:DD:86:LEU:HD13	1.69	0.75
62:MM:67:ALA:HB2	81:ff:108:VAL:HG23	1.68	0.74
82:gg:87:LEU:HD21	82:gg:108:VAL:HG11	1.70	0.74
46:5:914:U:O4	46:5:918:G:N7	2.19	0.74
49:9:1284:A:C2	62:MM:91:LEU:HD22	2.21	0.74
46:5:1928:C:C4	46:5:2054:U:O2	2.41	0.74
49:9:1302:G:H22	81:ff:93:HIS:CE1	2.06	0.74
46:5:2395:A:O2'	46:5:2806:A:H1'	1.89	0.73
46:5:1411:C:O3'	46:5:1411(C):C:C5'	2.37	0.73
46:5:1928:C:N4	46:5:2054:U:O2	2.21	0.73
3:C:101:MET:SD	3:C:104:PRO:HA	2.29	0.72
78:cc:20:ARG:CB	78:cc:20:ARG:HH21	2.01	0.72
78:cc:20:ARG:CD	78:cc:28:THR:CG2	2.59	0.72
49:9:1304:U:C5'	81:ff:93:HIS:N	2.52	0.72
16:Q:70:MET:HE1	16:Q:137:VAL:HG21	1.71	0.71
49:9:1304:U:H4'	81:ff:91:ASN:O	1.91	0.71
13:N:202:ARG:NH2	46:5:1372:A:OP1	2.23	0.71
46:5:922:C:C2'	46:5:922(B):C:C2	2.74	0.71
3:C:341:LEU:HD21	5:E:52:LEU:HD21	1.72	0.71
49:9:1680:G:H4'	78:cc:20:ARG:NH2	2.05	0.70
85:jj:613:ILE:HD12	85:jj:643:VAL:HG21	1.72	0.70
56:GG:5:ILE:HD12	56:GG:16:ILE:HD13	1.73	0.70
71:VV:20:SER:HB3	71:VV:59:ILE:HD11	1.73	0.70
3:C:84:THR:O	3:C:87:SER:OG	2.10	0.70
46:5:77:U:C4	46:5:336:A:N1	2.60	0.70
46:5:4396:A:OP1	46:5:4443:C:O2'	2.07	0.70
53:DD:21:LEU:HD21	53:DD:48:ILE:HD11	1.73	0.69
46:5:922:C:C5'	46:5:922(B):C:O5'	2.40	0.69
46:5:1670:G:C8	46:5:1855:G:C8	2.81	0.69
46:5:922:C:H2'	46:5:922(B):C:N3	2.08	0.69
46:5:3723:A:H2'	46:5:3724:A:C8	2.28	0.69
46:5:3914:U:O4	46:5:4378:A:C2	2.46	0.69
74:YY:34:THR:HG23	74:YY:69:THR:HG21	1.74	0.69
3:C:76:ILE:HG22	3:C:77:PRO:HD2	1.74	0.68
46:5:922:C:H5''	46:5:922(B):C:P	2.33	0.68
49:9:830:A:N1	49:9:844:U:C4	2.59	0.68
4:D:62:CYS:HB3	4:D:105:LEU:HD22	1.75	0.68
46:5:922:C:O3'	46:5:922(B):C:C6	2.47	0.68
46:5:922:C:O5'	46:5:922(A):G:H3'	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:77:U:H2'	46:5:77:U:O2	1.95	0.67
46:5:742:G:C2	46:5:922(A):G:C6	2.82	0.67
14:O:72:HIS:N	46:5:4586:G:OP1	2.27	0.67
6:F:114:ARG:NH1	16:Q:4:ASP:O	2.28	0.67
46:5:3879:G:O2'	46:5:3881:G:OP2	2.12	0.67
78:cc:21:THR:OG1	78:cc:22:GLY:N	2.28	0.67
49:9:1680:G:O4'	78:cc:20:ARG:NH1	2.24	0.67
46:5:1370:G:O2'	46:5:1371:A:OP2	2.10	0.66
46:5:922:C:O5'	46:5:922(A):G:O5'	2.13	0.66
46:5:1929:A:C8	46:5:1932:A:H1'	2.30	0.66
49:9:830:A:N6	49:9:844:U:N3	2.43	0.66
49:9:1611:G:OP2	68:SS:121:ARG:NH1	2.27	0.66
62:MM:39:ALA:CB	81:ff:102:VAL:HG11	2.26	0.66
61:LL:61:PRO:HA	61:LL:66:VAL:HG13	1.76	0.66
85:jj:283:LEU:HB3	85:jj:453:ILE:HD11	1.78	0.65
49:9:929:G:H2'	49:9:930:C:O4'	1.96	0.65
3:C:316:LYS:NZ	46:5:1281:G:OP1	2.28	0.65
42:r:98:ARG:NH2	46:5:2262:G:OP2	2.29	0.65
72:WW:42:MET:HE2	72:WW:49:GLU:HA	1.79	0.65
46:5:1411:C:C5'	46:5:1411(B):C:H2'	2.27	0.65
50:AA:63:ARG:HG2	50:AA:185:MET:HE1	1.77	0.65
70:UU:50:VAL:HG23	70:UU:91:LEU:HD23	1.79	0.65
1:A:211:PHE:CD1	1:A:219:ILE:HG23	2.31	0.65
29:d:59:THR:OG1	29:d:104:THR:OG1	2.09	0.65
49:9:293:C:O2'	49:9:294:U:H3'	1.97	0.65
49:9:1284:A:C4	62:MM:91:LEU:HD13	2.31	0.65
49:9:1680:G:C2'	78:cc:20:ARG:HH22	2.10	0.65
46:5:1598:C:O2	46:5:2798:A:H2'	1.97	0.64
46:5:1929:A:N1	46:5:2054:U:C4	2.61	0.64
46:5:1854:G:N2	46:5:4394:A:O4'	2.30	0.64
46:5:2395:A:O2'	46:5:2806:A:N3	2.27	0.64
72:WW:75:ILE:HD11	72:WW:93:LEU:HD11	1.78	0.64
72:WW:42:MET:HE3	72:WW:50:PHE:CD2	2.32	0.64
49:9:1143:A:H2'	49:9:1144:A:C8	2.33	0.64
46:5:964:A:H2'	46:5:965:G:O4'	1.97	0.64
60:KK:64:TRP:CE3	79:dd:23:VAL:HG22	2.33	0.64
1:A:158:ILE:HG23	1:A:162:ASN:HD21	1.62	0.64
49:9:145:G:N7	56:GG:178:ARG:NH1	2.46	0.64
49:9:1680:G:O2'	78:cc:20:ARG:NH2	2.31	0.64
1:A:207:VAL:HG23	1:A:208:GLU:HG3	1.80	0.63
3:C:207:PRO:HB3	3:C:249:PHE:CD2	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:76:PRO:O	13:N:79:ALA:HB3	1.98	0.63
32:g:21:ARG:NH2	46:5:2641:A:OP1	2.31	0.63
18:S:68:PHE:N	46:5:729:G:O6	2.28	0.63
10:J:151:ILE:HD11	10:J:156:ARG:HG2	1.79	0.63
46:5:4291:G:H5''	46:5:4291:G:N3	2.13	0.63
46:5:2416:G:O6	46:5:2426:U:OP2	2.17	0.63
46:5:3914:U:H3	46:5:4378:A:N6	1.95	0.63
12:M:24:LEU:HD11	12:M:86:TRP:CG	2.34	0.62
49:9:1130:G:H2'	49:9:1130:G:N3	2.14	0.62
49:9:1373:C:O2'	67:RR:10:LYS:NZ	2.32	0.62
52:CC:209:VAL:HG21	52:CC:233:LEU:HD13	1.81	0.62
8:H:128:MET:HE1	8:H:161:ILE:CG2	2.30	0.62
48:8:19:C:H2'	48:8:20:A:C8	2.35	0.62
49:9:628:A:N6	49:9:1332:A:O4'	2.32	0.62
78:cc:20:ARG:HH21	78:cc:20:ARG:CG	2.12	0.62
50:AA:69:GLU:HB3	52:CC:270:THR:HG21	1.82	0.62
46:5:738:C:O2'	46:5:738(A):C:O4'	2.16	0.62
15:P:95:LEU:HD12	15:P:148:MET:HE1	1.81	0.62
46:5:1074:G:C2	46:5:1238:A:C2	2.88	0.62
46:5:4589:A:N1	46:5:4621:C:O2'	2.32	0.61
49:9:1292:C:C2	81:ff:140:TYR:CE2	2.88	0.61
49:9:1680:G:C4'	78:cc:20:ARG:HH22	2.13	0.61
31:f:20:ASN:ND2	46:5:1885:G:OP1	2.32	0.61
46:5:1818:G:O2'	46:5:1819:G:OP1	2.12	0.61
7:G:215:ASP:HB3	7:G:216:PRO:HD3	1.81	0.61
49:9:1220:A:N6	49:9:1221:G:C6	2.68	0.61
13:N:67:ARG:NH1	46:5:2458:C:OP1	2.33	0.61
46:5:922:C:C6	46:5:922(A):G:C6	2.88	0.61
46:5:3717:A:H2'	46:5:3718:A:C8	2.35	0.61
58:II:162:LEU:HD11	58:II:191:GLU:HG2	1.83	0.61
2:B:249:ARG:NH1	46:5:2837:U:OP1	2.34	0.61
46:5:1528:U:H2'	46:5:1529:G:O4'	2.01	0.61
47:7:23:A:N3	47:7:118:C:O2'	2.31	0.61
49:9:1407:U:H2'	49:9:1408:U:C6	2.35	0.61
6:F:168:LEU:HB2	6:F:186:MET:HE1	1.83	0.60
1:A:179:ILE:O	46:5:3653:A:O3'	2.19	0.60
49:9:1292:C:C2	81:ff:140:TYR:CZ	2.89	0.60
10:J:43:LEU:HD11	10:J:82:ILE:HG23	1.83	0.60
18:S:127:MET:HE1	19:T:155:PRO:HA	1.81	0.60
2:B:89:ILE:HD13	2:B:153:MET:HE1	1.84	0.60
46:5:1929:A:H3'	46:5:1929:A:N3	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:1290:G:N7	81:ff:95:ARG:CZ	2.62	0.60
33:h:58:LEU:HA	33:h:61:ILE:HD12	1.83	0.60
11:L:169:ILE:HD13	26:a:142:GLY:HA2	1.84	0.59
46:5:5057:C:H2'	46:5:5058:A:C8	2.37	0.59
46:5:922:C:O5'	46:5:922(A):G:P	2.60	0.59
49:9:615:C:H2'	49:9:616:A:O4'	2.03	0.59
49:9:1302:G:H22	81:ff:93:HIS:HE1	1.47	0.59
49:9:1302:G:H21	81:ff:93:HIS:CE1	2.20	0.59
51:BB:103:MET:HE1	51:BB:212:VAL:HG23	1.85	0.59
53:DD:16:ILE:HD11	79:dd:36:LEU:HD23	1.85	0.59
62:MM:36:ARG:HE	81:ff:102:VAL:CG2	2.09	0.59
17:R:74:ARG:NH2	46:5:2891:U:OP2	2.36	0.59
29:d:57:MET:O	29:d:59:THR:N	2.35	0.59
29:d:33:ILE:HD11	29:d:41:ARG:HB3	1.84	0.59
59:JJ:130:ILE:HG12	59:JJ:135:ILE:HD11	1.85	0.59
4:D:23:ARG:NH2	46:5:4280:A:OP2	2.36	0.58
46:5:113:A:H2'	46:5:114:G:O4'	2.02	0.58
3:C:303:ARG:O	16:Q:38:ARG:NH1	2.36	0.58
46:5:82:U:H2'	46:5:83:C:O4'	2.02	0.58
72:WW:14:ILE:HD11	72:WW:41:MET:HE1	1.85	0.58
46:5:2268:A:H4'	46:5:2269:C:H5'	1.84	0.58
46:5:4711:C:H2'	46:5:4712:C:O4'	2.04	0.58
5:E:52:LEU:HD23	5:E:58:ARG:HA	1.86	0.58
46:5:747:A:H4'	46:5:748:G:OP1	2.04	0.58
46:5:2439:G:C6	46:5:2440:U:C4	2.92	0.58
46:5:2468:U:C4	46:5:2473:A:N1	2.68	0.58
46:5:3914:U:N3	46:5:4378:A:N6	2.49	0.58
49:9:183:G:O2'	49:9:184:G:O5'	2.22	0.58
7:G:104:LEU:O	7:G:106:ARG:N	2.36	0.58
49:9:1284:A:C2	62:MM:91:LEU:CD2	2.85	0.58
49:9:1284:A:C6	62:MM:91:LEU:HD22	2.37	0.58
50:AA:18:PHE:CD1	50:AA:173:LEU:HD11	2.39	0.58
16:Q:14:ARG:NH2	46:5:2083:C:OP2	2.37	0.58
46:5:4320:G:H2'	46:5:4321:U:O4'	2.04	0.58
46:5:914:U:O4	46:5:918:G:C8	2.57	0.57
50:AA:63:ARG:CG	50:AA:185:MET:HE1	2.34	0.57
13:N:49:ARG:HH12	46:5:152:U:P	2.27	0.57
36:k:35:LYS:NZ	46:5:2693:G:OP1	2.32	0.57
46:5:4723:A:H2'	46:5:4724:A:C8	2.38	0.57
52:CC:189:GLY:HA3	52:CC:235:ASN:OD1	2.04	0.57
57:HH:133:LEU:HD21	57:HH:176:VAL:HG11	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:77:THR:HG21	2:B:337:VAL:HG22	1.85	0.57
13:N:160:GLU:N	13:N:160:GLU:OE1	2.37	0.57
42:r:41:ASN:HB3	42:r:44:ILE:HD12	1.86	0.57
49:9:1286:G:O6	62:MM:34:GLY:HA3	2.04	0.57
68:SS:33:ILE:HD13	68:SS:71:MET:HE1	1.86	0.57
9:I:54:SER:HB2	9:I:135:ILE:HD11	1.87	0.57
46:5:2409:U:O4	46:5:2783:A:C6	2.57	0.57
5:E:184:LEU:HD11	5:E:264:ILE:HD11	1.86	0.57
52:CC:196:ILE:HB	52:CC:223:TYR:HB2	1.87	0.57
59:JJ:130:ILE:CG1	59:JJ:135:ILE:HD11	2.34	0.57
8:H:128:MET:HE1	8:H:161:ILE:HG21	1.87	0.57
13:N:89:VAL:HG11	46:5:3928:A:H5'	1.86	0.57
46:5:922(B):C:N3	46:5:923:C:C5	2.73	0.57
21:V:89:ARG:HD2	21:V:95:PHE:CZ	2.39	0.57
5:E:124:VAL:HG13	30:e:7:LEU:HD11	1.87	0.56
11:L:47:ALA:HB3	11:L:48:PRO:HD3	1.87	0.56
15:P:70:CYS:SG	15:P:72:GLN:N	2.78	0.56
46:5:77:U:O2	46:5:77:U:C2'	2.50	0.56
46:5:4273:A:H2'	46:5:4274:A:C8	2.40	0.56
49:9:1667:U:H2'	49:9:1668:U:C6	2.40	0.56
49:9:1680:G:C4'	78:cc:20:ARG:NH2	2.67	0.56
26:a:61:TYR:N	46:5:4354:U:O4	2.37	0.56
49:9:1304:U:OP1	81:ff:93:HIS:N	2.30	0.56
51:BB:136:ARG:HD2	51:BB:138:PHE:CZ	2.41	0.56
73:XX:61:GLN:HB3	73:XX:62:PRO:CD	2.34	0.56
30:e:36:ARG:NH1	46:5:2322:G:OP1	2.39	0.56
45:3:16:C:O2	45:3:16:C:O4'	2.24	0.56
46:5:2468:U:H3	46:5:2473:A:N6	2.03	0.56
82:gg:17:TRP:CE3	82:gg:303:THR:HG22	2.40	0.56
16:Q:85:THR:HG22	16:Q:104:ARG:HB2	1.87	0.56
46:5:77:U:H3	46:5:336:A:N6	2.04	0.56
46:5:2468:U:C2	46:5:2506:G:N7	2.73	0.56
18:S:84:TYR:CE1	18:S:93:MET:HE3	2.40	0.56
49:9:1329:U:O2'	49:9:1332:A:OP2	2.11	0.56
55:FF:126:THR:HG21	78:cc:27:CYS:SG	2.46	0.56
49:9:928:G:H2'	49:9:929:G:C8	2.41	0.56
60:KK:15:LEU:HD22	60:KK:49:MET:HE1	1.88	0.56
60:KK:64:TRP:CZ3	79:dd:23:VAL:HG22	2.39	0.56
46:5:43:U:H2'	46:5:44:A:O5'	2.05	0.56
48:8:47:C:H1'	48:8:61:A:H2'	1.88	0.56
49:9:12:U:H2'	49:9:13:C:C6	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:4944:C:O2	46:5:4944:C:O4'	2.23	0.56
72:WW:104:LEU:O	72:WW:104:LEU:HD12	2.06	0.56
46:5:923:C:C5	46:5:926:G:O4'	2.59	0.55
46:5:4871:C:O4'	46:5:4871:C:O2	2.24	0.55
49:9:1271:C:OP1	81:ff:90:LYS:CD	2.50	0.55
46:5:922:C:C6	46:5:922:C:H3'	2.41	0.55
46:5:1337:A:C2	46:5:2349:A:C2	2.94	0.55
49:9:1139:C:O4'	49:9:1139:C:O2	2.21	0.55
49:9:1304:U:P	81:ff:93:HIS:HB2	2.46	0.55
66:QQ:51:LEU:HD22	66:QQ:84:ILE:HG13	1.88	0.55
84:ii:65:LEU:HD21	84:ii:94:VAL:HG21	1.88	0.55
15:P:37:LYS:O	15:P:114:ILE:O	2.25	0.55
35:j:14:LYS:HA	46:5:1534:A:C5	2.42	0.55
46:5:1600:A:C6	46:5:1638:A:C5	2.94	0.55
46:5:2292:C:H2'	46:5:2293:U:C6	2.41	0.55
46:5:4260:U:H2'	46:5:4261:C:C6	2.41	0.55
85:jj:619:VAL:HG23	85:jj:632:PRO:HG3	1.89	0.55
6:F:242:LEU:HD23	6:F:246:MET:HG3	1.89	0.55
29:d:26:THR:HG23	46:5:4996:C:H4'	1.87	0.55
46:5:3829:G:C2	46:5:3830:A:C8	2.95	0.55
49:9:830:A:N6	49:9:844:U:H3	2.04	0.55
60:KK:11:ILE:HD12	60:KK:45:VAL:HG22	1.87	0.55
46:5:245:C:O4'	46:5:245:C:O2	2.25	0.55
46:5:1672:U:H2'	46:5:1673:U:C6	2.41	0.55
46:5:2396:A:N6	46:5:2814:C:O2	2.40	0.55
62:MM:67:ALA:HB2	81:ff:108:VAL:CG2	2.36	0.55
6:F:153:ILE:HG22	6:F:186:MET:HE3	1.89	0.55
10:J:128:LEU:HD11	10:J:130:PHE:CE1	2.42	0.55
46:5:4537:C:H2'	46:5:4538:G:C8	2.41	0.55
68:SS:121:ARG:HG3	68:SS:131:VAL:HG21	1.87	0.55
85:jj:266:ILE:HD13	85:jj:393:VAL:HG21	1.89	0.55
2:B:228:TYR:O	46:5:2835:A:O2'	2.16	0.54
46:5:922:C:O3'	46:5:922:C:O5'	2.25	0.54
50:AA:18:PHE:CE1	50:AA:173:LEU:HD11	2.42	0.54
31:f:48:ALA:HB2	31:f:71:TRP:CZ3	2.40	0.54
40:o:81:ARG:NH2	46:5:4293:U:O2'	2.40	0.54
46:5:4942:C:H4'	46:5:4943:A:OP1	2.07	0.54
49:9:1624:U:O4'	49:9:1624:U:O2	2.23	0.54
2:B:56:ILE:HG22	2:B:74:GLU:HB3	1.89	0.54
13:N:115:VAL:HG22	13:N:134:LEU:HD21	1.90	0.54
2:B:288:GLY:HA3	2:B:330:PHE:CE1	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:5:LYS:HG2	34:i:40:VAL:HG11	1.90	0.54
14:O:193:THR:HG23	14:O:202:LEU:HD23	1.89	0.54
45:2:16:C:O4'	45:2:16:C:O2	2.24	0.54
58:II:113:TYR:OH	58:II:156:ALA:O	2.25	0.54
67:RR:28:PHE:HA	67:RR:55:THR:HG21	1.88	0.54
15:P:127:ARG:NH2	46:5:2422:C:OP1	2.40	0.54
46:5:1855:G:C6	46:5:1856:C:C4	2.95	0.54
46:5:2409:U:C4	46:5:2783:A:C2	2.95	0.54
68:SS:13:LEU:HD11	68:SS:56:ALA:O	2.08	0.54
78:cc:14:VAL:HG13	78:cc:30:VAL:HG13	1.90	0.54
9:I:3:ARG:NH2	46:5:4431:U:OP2	2.41	0.54
46:5:2627:C:O4'	46:5:2627:C:O2	2.25	0.54
7:G:219:LEU:HD21	13:N:45:PRO:HG2	1.89	0.54
41:p:60:CYS:HG	87:p:100:ZN:ZN	1.19	0.54
46:5:1872:G:O2'	46:5:4219:A:N3	2.32	0.54
49:9:1129:G:C6	49:9:1130:G:O6	2.60	0.54
10:J:141:ILE:HD11	47:7:55:A:N3	2.22	0.54
20:U:84:LYS:HG3	20:U:102:VAL:HG11	1.89	0.54
73:XX:51:VAL:HG13	73:XX:70:VAL:HG13	1.89	0.54
2:B:41:VAL:HA	2:B:187:GLY:HA3	1.90	0.54
3:C:27:VAL:HG22	3:C:264:TYR:HB2	1.90	0.54
5:E:184:LEU:O	46:5:4883:C:N4	2.41	0.54
20:U:33:ILE:HD12	20:U:96:LEU:HD22	1.89	0.54
25:Z:53:VAL:HG21	25:Z:62:ILE:HG23	1.90	0.54
3:C:253:THR:O	3:C:256:ALA:N	2.41	0.54
46:5:43:U:C2'	46:5:44:A:O5'	2.56	0.54
46:5:3810:C:O4'	46:5:3810:C:O2	2.26	0.54
49:9:1695:A:N1	49:9:1832:A:O2'	2.35	0.54
73:XX:67:ARG:HG2	73:XX:115:ILE:HG23	1.89	0.54
82:gg:152:SER:HG	82:gg:168:CYS:HG	1.55	0.54
42:r:32:LEU:HD21	42:r:106:LEU:HD12	1.89	0.53
46:5:1236:C:O2'	46:5:1238:A:OP1	2.25	0.53
48:8:94:G:H5'	48:8:94:G:C8	2.43	0.53
64:OO:95:ILE:HD13	64:OO:116:LEU:HG	1.90	0.53
46:5:77:U:O4	46:5:336:A:C2	2.57	0.53
46:5:1411:C:O2'	46:5:1411(C):C:C6	2.60	0.53
46:5:2439:G:C5	46:5:2440:U:C5	2.96	0.53
46:5:3656:A:O4'	46:5:3747:A:C2	2.61	0.53
49:9:314:U:O2	49:9:314:U:H2'	2.08	0.53
49:9:1012:A:H2'	49:9:1013:U:O4'	2.08	0.53
54:EE:44:LEU:HD21	54:EE:70:ILE:HG21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:178:LEU:HB3	6:F:183:ILE:HB	1.91	0.53
42:r:10:VAL:O	42:r:12:ASN:N	2.42	0.53
46:5:1483:C:O2	46:5:1483:C:O4'	2.24	0.53
49:9:371:A:OP2	58:II:10:LYS:HB2	2.08	0.53
49:9:501:C:H2'	49:9:501:C:O2	2.09	0.53
49:9:853:C:O4'	49:9:853:C:O2	2.27	0.53
51:BB:69:VAL:HG11	51:BB:74:LEU:HD13	1.89	0.53
46:5:2088:A:O2'	46:5:2089:G:P	2.67	0.53
49:9:143:U:N3	49:9:314:U:OP1	2.42	0.53
49:9:1452:A:OP2	67:RR:32:LYS:NZ	2.41	0.53
26:a:103:VAL:HG12	26:a:108:TYR:HB2	1.91	0.53
46:5:2505:C:O2	46:5:2505:C:O4'	2.24	0.53
48:8:137:A:H2'	48:8:138:C:C6	2.43	0.53
49:9:613:G:H2'	49:9:627:U:C6	2.44	0.53
49:9:1740:C:H2'	49:9:1741:U:C6	2.44	0.53
56:GG:52:ILE:HD11	56:GG:109:LEU:CD1	2.39	0.53
61:LL:71:ARG:C	61:LL:72:ILE:HD12	2.34	0.53
29:d:57:MET:HE1	29:d:88:LEU:O	2.08	0.53
50:AA:161:ILE:HG22	50:AA:163:CYS:SG	2.48	0.53
14:O:7:LEU:O	14:O:34:VAL:N	2.40	0.53
46:5:1411:C:O3'	46:5:1411(C):C:H5''	2.09	0.53
49:9:1315:U:O2	49:9:1315:U:O4'	2.26	0.53
10:J:27:GLY:HA2	10:J:68:ILE:HG23	1.90	0.52
11:L:74:ARG:NH2	46:5:109:G:OP2	2.42	0.52
26:a:86:THR:HG22	46:5:510:U:H5''	1.91	0.52
46:5:2693:G:C6	46:5:2694:G:C6	2.97	0.52
46:5:3873:G:H2'	46:5:3874:G:C8	2.44	0.52
45:2:37:A:C2	83:hh:46:A:N6	2.76	0.52
46:5:3891:A:H2'	46:5:3892:U:O4'	2.09	0.52
49:9:1406:G:O2'	49:9:1443:C:N3	2.42	0.52
49:9:1865:C:OP1	76:aa:87:ARG:NH2	2.41	0.52
8:H:18:ILE:HG22	8:H:27:VAL:HG22	1.90	0.52
9:I:9:TYR:CG	9:I:97:ILE:HG12	2.45	0.52
20:U:87:THR:HG23	20:U:102:VAL:HG21	1.91	0.52
41:p:39:CYS:SG	41:p:41:PHE:N	2.81	0.52
46:5:224:U:O2	46:5:224:U:O4'	2.24	0.52
49:9:1629:C:OP1	68:SS:39:ARG:NE	2.34	0.52
49:9:1863:A:H1'	76:aa:79:ILE:HD13	1.91	0.52
84:ii:197:ILE:HG23	84:ii:202:VAL:HG21	1.92	0.52
4:D:106:ALA:HB1	4:D:171:LEU:HD13	1.91	0.52
6:F:88:LEU:HD11	6:F:121:PHE:CD1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:41:ILE:CG2	8:H:73:ILE:HD11	2.36	0.52
13:N:4:TYR:OH	46:5:151:G:OP2	2.18	0.52
41:p:17:ARG:HB2	41:p:18:TYR:CE2	2.45	0.52
46:5:1411:C:O3'	46:5:1411(C):C:O5'	2.27	0.52
46:5:1667:A:H61	46:5:2280:G:H3'	1.74	0.52
46:5:1929:A:C2	46:5:2054:U:O4	2.57	0.52
49:9:1488:C:O2'	49:9:1490:G:OP2	2.26	0.52
63:NN:125:LEU:HD22	63:NN:129:TYR:CE2	2.44	0.52
40:o:41:TYR:CD1	45:3:75:C:O2	2.62	0.52
46:5:2468:U:N3	46:5:2473:A:N6	2.57	0.52
49:9:846:G:OP2	54:EE:108:ARG:NH1	2.42	0.52
54:EE:126:VAL:HG22	54:EE:158:ASP:O	2.10	0.52
17:R:105:LEU:HD12	17:R:138:LEU:HD13	1.92	0.52
21:V:65:VAL:HG21	21:V:72:LEU:HB3	1.91	0.52
2:B:119:TYR:OH	2:B:129:ALA:N	2.43	0.52
12:M:118:MET:SD	46:5:4929:C:O4'	2.68	0.52
46:5:84:A:N6	46:5:99:A:OP2	2.41	0.52
46:5:4579:U:H2'	46:5:4580:U:C6	2.45	0.52
49:9:1334:G:C4	49:9:1498:A:C2	2.97	0.52
53:DD:48:ILE:HG23	53:DD:86:LEU:HD12	1.92	0.52
46:5:2094:C:O2	46:5:2094:C:O4'	2.27	0.52
46:5:4219:A:H2'	46:5:4220:A:C8	2.45	0.52
12:M:66:HIS:CE1	12:M:67:SER:OG	2.62	0.52
31:f:88:PHE:CD2	31:f:92:LEU:HD21	2.44	0.52
49:9:95:G:HO2'	49:9:474:G:HO2'	1.58	0.52
49:9:1284:A:C5	62:MM:91:LEU:HD13	2.45	0.52
49:9:1602:U:C4	49:9:1604:G:C8	2.97	0.52
3:C:45:ARG:O	3:C:48:ASN:OD1	2.27	0.52
4:D:35:ARG:HB2	46:5:4325:A:C2	2.45	0.52
13:N:108:ARG:HH22	46:5:54:G:HO2'	1.55	0.52
14:O:84:VAL:O	14:O:85:ARG:C	2.53	0.52
31:f:28:LEU:HG	31:f:101:ILE:HD11	1.91	0.52
64:OO:99:ALA:HB3	64:OO:133:THR:HG22	1.92	0.52
21:V:87:SER:HA	21:V:97:TYR:HB3	1.91	0.51
72:WW:6:VAL:HG12	72:WW:34:ILE:HD11	1.90	0.51
46:5:307:A:C5	46:5:308:G:C6	2.98	0.51
46:5:922:C:O3'	46:5:922(B):C:C5	2.63	0.51
46:5:922:C:C6	46:5:922(A):G:C5	2.99	0.51
46:5:1961:G:O2'	46:5:2025:A:N6	2.43	0.51
49:9:434:G:H2'	49:9:435:A:C8	2.44	0.51
49:9:501:C:O2	49:9:501:C:C2'	2.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:986:G:OP2	49:9:988:C:N4	2.44	0.51
68:SS:40:TYR:O	68:SS:44:VAL:HG23	2.10	0.51
76:aa:45:VAL:HG11	76:aa:53:ILE:CD1	2.39	0.51
46:5:2809:G:O2'	46:5:4644:G:OP1	2.25	0.51
46:5:3856:A:H2'	46:5:3857:G:O4'	2.10	0.51
61:LL:113:LEU:HD23	61:LL:142:VAL:HG21	1.92	0.51
46:5:1237:C:O4'	46:5:1237:C:O2	2.28	0.51
46:5:4269:G:C6	46:5:4270:C:C4	2.98	0.51
49:9:1546:G:H5'	66:QQ:18:THR:HG21	1.92	0.51
46:5:1411:C:H5'	46:5:1411(B):C:C2'	2.40	0.51
53:DD:72:VAL:HG23	60:KK:20:VAL:HG21	1.91	0.51
58:II:113:TYR:CE1	58:II:121:LEU:HD23	2.45	0.51
3:C:129:ALA:O	3:C:133:LEU:HD13	2.10	0.51
19:T:80:VAL:HG21	19:T:85:LEU:HD12	1.91	0.51
21:V:82:ILE:HG22	21:V:83:ARG:HG3	1.93	0.51
28:c:29:LEU:HD23	28:c:94:LEU:HD13	1.92	0.51
40:o:54:PRO:O	45:3:75:C:O2'	2.26	0.51
46:5:4658:G:C6	46:5:4659:G:C5	2.97	0.51
46:5:4989:U:O2	46:5:4989:U:O4'	2.27	0.51
49:9:1117:C:O2'	49:9:1118:C:O4'	2.28	0.51
71:VV:32:ILE:HD12	71:VV:60:ARG:HD2	1.91	0.51
46:5:1679:A:N1	46:5:4391:G:O2'	2.44	0.51
31:f:18:LEU:HD23	31:f:19:ARG:NH1	2.26	0.51
36:k:35:LYS:HG2	36:k:44:THR:HG22	1.91	0.51
46:5:3723:A:C2	46:5:3724:A:C6	2.98	0.51
57:HH:116:ARG:NH2	57:HH:121:THR:OG1	2.44	0.51
46:5:1922:G:C2	46:5:1923:A:C8	2.99	0.51
46:5:4428:A:C5	46:5:4429:C:C5	2.99	0.51
49:9:1380:C:H2'	49:9:1381:G:O4'	2.11	0.51
2:B:174:ARG:NH1	46:5:4985:U:O2	2.44	0.50
18:S:78:PHE:O	18:S:96:GLU:HA	2.10	0.50
29:d:22:THR:HG22	29:d:89:SER:CB	2.40	0.50
46:5:1354:A:N1	46:5:1385:G:O2'	2.42	0.50
46:5:1655:C:H2'	46:5:1656:U:H5''	1.93	0.50
46:5:2465:C:H2'	46:5:2466:G:O4'	2.10	0.50
46:5:4476:C:O2'	46:5:4478:G:OP2	2.28	0.50
49:9:628:A:H61	49:9:1332:A:C1'	2.24	0.50
79:dd:6:LEU:O	79:dd:7:TYR:C	2.55	0.50
1:A:126:LEU:HD13	1:A:150:LEU:HD21	1.93	0.50
1:A:207:VAL:HG12	46:5:3919:C:C5'	2.41	0.50
2:B:29:VAL:HG23	2:B:346:THR:HG21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:356:G:O2'	48:8:25:G:N3	2.45	0.50
46:5:4583:C:O2'	46:5:4718:G:N2	2.44	0.50
49:9:1700:C:C2	49:9:1834:A:N6	2.79	0.50
62:MM:61:TYR:CD2	81:ff:100:LEU:HD21	2.46	0.50
46:5:3685:C:H2'	46:5:3686:G:O4'	2.12	0.50
49:9:1401:A:H2'	49:9:1402:A:C8	2.46	0.50
61:LL:37:TYR:CE2	61:LL:51:ILE:HG23	2.46	0.50
31:f:72:GLY:HA2	31:f:88:PHE:HA	1.92	0.50
46:5:932:A:H2'	46:5:939:G:O6	2.11	0.50
49:9:363:A:N1	49:9:397:G:O2'	2.32	0.50
49:9:993:G:O6	76:aa:15:ARG:HG2	2.11	0.50
49:9:1444:U:H2'	49:9:1445:U:C6	2.46	0.50
85:jj:261:LEU:HD23	85:jj:364:VAL:HG21	1.93	0.50
2:B:49:TYR:CE2	2:B:168:MET:HE1	2.46	0.50
22:W:3:VAL:HG21	22:W:12:LYS:HE2	1.92	0.50
37:l:48:LYS:O	37:l:50:GLY:N	2.45	0.50
49:9:356:C:C2'	49:9:356:C:O2	2.59	0.50
17:R:7:GLN:OE1	17:R:7:GLN:N	2.45	0.50
49:9:1551:U:O2	49:9:1551:U:O4'	2.28	0.50
58:II:159:SER:HB3	58:II:162:LEU:HD12	1.94	0.50
6:F:145:ASN:OD1	6:F:146:LEU:N	2.45	0.50
14:O:55:LEU:HD23	14:O:58:LEU:HD12	1.93	0.50
45:2:18:U:O2'	45:2:57:A:C2	2.65	0.50
46:5:1381:U:H5''	46:5:1381:U:O2	2.12	0.50
46:5:1411:C:C4'	46:5:1411(C):C:O4'	2.55	0.50
46:5:1503:A:H4'	46:5:1504:G:H5'	1.92	0.50
46:5:2366:A:N3	46:5:3850:C:O2'	2.37	0.50
46:5:2370:A:N1	46:5:2390:G:O2'	2.45	0.50
49:9:944:A:C5	49:9:945:U:C5	2.99	0.50
76:aa:36:ILE:N	76:aa:36:ILE:HD12	2.27	0.50
6:F:154:TYR:CE1	6:F:186:MET:HG2	2.46	0.50
16:Q:35:LEU:HB3	16:Q:44:ASN:ND2	2.27	0.50
18:S:35:PRO:HD2	18:S:39:VAL:HG21	1.92	0.50
31:f:88:PHE:CE1	31:f:92:LEU:HD11	2.46	0.50
46:5:1664:U:H2'	46:5:1665:C:C6	2.46	0.50
10:J:15:LEU:HD21	10:J:134:LEU:HD13	1.94	0.50
17:R:23:TRP:CH2	17:R:25:ASP:HA	2.46	0.50
27:b:13:SER:OG	46:5:1724:G:N2	2.45	0.50
30:e:50:LYS:HB2	46:5:1884:C:OP1	2.12	0.50
40:o:24:THR:OG1	40:o:25:GLN:N	2.45	0.50
46:5:106:A:H2'	46:5:107:G:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:1680:G:H2'	49:9:1681:U:C6	2.47	0.50
84:ii:65:LEU:CD2	84:ii:94:VAL:HG21	2.41	0.50
26:a:73:VAL:HB	26:a:108:TYR:CD1	2.47	0.49
46:5:2896:G:H5''	46:5:2897:G:OP2	2.12	0.49
49:9:640:A:H2'	49:9:641:A:C8	2.46	0.49
49:9:823:U:O4'	49:9:823:U:O2	2.29	0.49
49:9:1581:C:OP2	49:9:1582:C:N4	2.43	0.49
57:HH:133:LEU:HD22	57:HH:173:PHE:CD1	2.46	0.49
61:LL:12:LYS:HA	61:LL:56:ILE:HD13	1.94	0.49
82:gg:14:HIS:CE1	82:gg:35:SER:HB2	2.47	0.49
13:N:48:ALA:HB1	13:N:53:TYR:HB3	1.94	0.49
76:aa:23:CYS:SG	76:aa:25:ASN:N	2.85	0.49
2:B:259:PRO:HB3	46:5:2044:U:C2	2.48	0.49
12:M:17:PHE:CZ	12:M:54:CYS:HA	2.47	0.49
19:T:17:ARG:CD	19:T:47:THR:HG23	2.43	0.49
46:5:1380:G:H4'	46:5:1381:U:H5''	1.95	0.49
46:5:2313:A:O2'	46:5:2314:G:OP1	2.20	0.49
46:5:2608:G:C2	46:5:2732:G:C2	3.00	0.49
46:5:4305:G:C2'	46:5:4305:G:N3	2.74	0.49
46:5:4633:G:N2	46:5:4664:A:OP2	2.40	0.49
48:8:128:C:C5	48:8:129:C:C5	3.00	0.49
61:LL:100:ASN:HD22	61:LL:100:ASN:N	2.10	0.49
72:WW:90:GLN:HB3	72:WW:102:ILE:HD12	1.94	0.49
3:C:121:ARG:O	3:C:122:TYR:C	2.56	0.49
9:I:191:ILE:HD12	9:I:200:ILE:HD11	1.93	0.49
28:c:29:LEU:HD22	28:c:91:VAL:HG21	1.94	0.49
46:5:1322:A:C8	46:5:1326:A:C6	3.00	0.49
46:5:1888:A:N6	46:5:3873:G:O2'	2.46	0.49
62:MM:36:ARG:CZ	81:ff:105:TYR:CE2	2.96	0.49
73:XX:68:LYS:CG	73:XX:91:LEU:HD22	2.42	0.49
2:B:374:PHE:CE1	46:5:5050:C:H1'	2.48	0.49
12:M:41:PRO:HB3	12:M:70:GLN:HE21	1.77	0.49
16:Q:89:ASP:OD1	16:Q:91:ARG:N	2.45	0.49
18:S:160:ARG:HB2	46:5:1921:C:O2	2.12	0.49
3:C:136:LEU:HD21	42:r:6:GLN:HB2	1.94	0.49
3:C:235:LEU:HD12	3:C:264:TYR:OH	2.13	0.49
10:J:151:ILE:HD11	10:J:156:ARG:CG	2.42	0.49
49:9:1834:A:C2'	49:9:1834:A:N3	2.76	0.49
62:MM:67:ALA:HB3	81:ff:108:VAL:HG23	1.88	0.49
85:jj:392:LEU:HD23	85:jj:666:MET:HE2	1.94	0.49
3:C:211:TYR:CD1	3:C:211:TYR:C	2.90	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:281:THR:OG1	46:5:4754:G:N7	2.46	0.49
40:o:24:THR:HG23	40:o:69:ARG:HB3	1.95	0.49
46:5:1411:C:H5'	46:5:1411(B):C:H2'	1.94	0.49
49:9:1357:A:H5''	52:CC:112:VAL:HG11	1.93	0.49
49:9:1550:G:O2'	49:9:1558:C:O2	2.30	0.49
7:G:247:VAL:HG21	7:G:249:ARG:NH1	2.28	0.49
25:Z:75:TYR:CB	25:Z:80:LEU:HD21	2.43	0.49
46:5:222:C:H2'	46:5:223:G:O4'	2.13	0.49
46:5:4551:U:H2'	46:5:4552:U:C6	2.48	0.49
49:9:183:G:N3	49:9:183:G:C2'	2.75	0.49
14:O:37:ARG:NH2	46:5:4761:G:OP2	2.46	0.49
19:T:57:TYR:CD1	19:T:76:VAL:HG21	2.48	0.49
46:5:2056:G:C8	46:5:2058:G:C8	3.01	0.49
46:5:5066:U:H2'	46:5:5067:U:C6	2.48	0.49
1:A:168:VAL:HG13	41:p:79:VAL:HG21	1.94	0.48
15:P:64:ASN:O	15:P:80:GLN:NE2	2.45	0.48
46:5:1739:G:C6	46:5:1740:C:N4	2.81	0.48
46:5:2410:C:C2	46:5:2435:G:N2	2.81	0.48
46:5:3724:A:N6	46:5:3725:G:C6	2.81	0.48
51:BB:36:PRO:CG	51:BB:38:MET:HE2	2.42	0.48
3:C:49:ARG:HD3	46:5:349:A:N7	2.27	0.48
14:O:118:MET:HA	14:O:118:MET:HE2	1.95	0.48
29:d:64:ILE:HD11	29:d:68:LEU:HG	1.95	0.48
46:5:275:C:H2'	46:5:276:C:C6	2.48	0.48
46:5:4423:U:O2	46:5:4423:U:O4'	2.30	0.48
49:9:522:A:OP2	59:JJ:45:ARG:NH2	2.44	0.48
49:9:562:U:H2'	49:9:563:G:C8	2.47	0.48
1:A:77:ILE:HD12	1:A:115:CYS:SG	2.53	0.48
3:C:76:ILE:HG22	3:C:77:PRO:CD	2.42	0.48
3:C:293:LEU:HD22	16:Q:34:PHE:CD2	2.48	0.48
22:W:6:CYS:HA	22:W:13:ILE:HD11	1.94	0.48
46:5:384:A:C6	46:5:386:A:C6	3.01	0.48
46:5:1916:G:OP2	46:5:1917:A:OP2	2.31	0.48
51:BB:134:LEU:HD22	51:BB:218:LEU:HD12	1.95	0.48
69:TT:39:LEU:HD21	69:TT:56:ARG:HE	1.78	0.48
15:P:10:ASN:N	15:P:10:ASN:OD1	2.47	0.48
35:j:5:THR:OG1	46:5:1601:A:OP1	2.31	0.48
46:5:922:C:C2'	46:5:922(B):C:N3	2.76	0.48
46:5:4966:A:C2	46:5:4967:A:C2	3.01	0.48
82:gg:87:LEU:HB2	82:gg:101:PHE:HB2	1.95	0.48
1:A:29:LEU:O	1:A:123:ARG:NH1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:49:TYR:O	2:B:79:VAL:HA	2.14	0.48
2:B:95:THR:C	14:O:152:VAL:HG11	2.39	0.48
8:H:12:ILE:HD12	8:H:13:PRO:O	2.13	0.48
20:U:82:TYR:CE2	20:U:86:LEU:HD11	2.49	0.48
42:r:32:LEU:N	42:r:32:LEU:HD23	2.28	0.48
46:5:1411:C:H1'	46:5:1411(C):C:C5	2.48	0.48
51:BB:38:MET:HE3	51:BB:185:VAL:HG11	1.94	0.48
85:jj:392:LEU:CD2	85:jj:666:MET:HE2	2.43	0.48
1:A:4:VAL:HG12	1:A:8:GLN:HB2	1.95	0.48
9:I:96:VAL:HG22	9:I:125:THR:HG22	1.95	0.48
12:M:64:PHE:CE1	12:M:73:VAL:HG22	2.49	0.48
14:O:120:VAL:O	14:O:124:LEU:HD13	2.13	0.48
46:5:2471:G:C6	46:5:2473:A:C6	3.02	0.48
50:AA:42:LYS:HG3	50:AA:48:ILE:HD11	1.96	0.48
3:C:210:ILE:N	3:C:210:ILE:HD12	2.29	0.48
6:F:82:VAL:HG22	18:S:62:VAL:HA	1.96	0.48
14:O:54:TYR:O	14:O:57:PHE:N	2.47	0.48
46:5:4489:G:N2	46:5:4592:C:OP1	2.47	0.48
49:9:183:G:O2'	49:9:184:G:O4'	2.31	0.48
49:9:1507:G:C2	81:ff:85:TYR:HB2	2.49	0.48
49:9:1589:A:N3	49:9:1653:U:O2'	2.44	0.48
4:D:51:MET:HE2	4:D:166:ALA:HB3	1.96	0.48
15:P:69:ARG:NH2	46:5:4568:A:N3	2.61	0.48
19:T:17:ARG:HD3	19:T:47:THR:HG23	1.96	0.48
46:5:2816:G:C6	46:5:2817:C:C4	3.02	0.48
49:9:1290:G:C6	81:ff:95:ARG:NH2	2.65	0.48
3:C:313:VAL:CG1	6:F:169:THR:HG21	2.44	0.48
8:H:128:MET:HE1	8:H:161:ILE:HG23	1.94	0.48
13:N:93:LYS:NZ	46:5:4177:C:OP1	2.44	0.48
32:g:97:ILE:HD13	46:5:4120:U:C4	2.49	0.48
46:5:100:C:O2	46:5:100:C:O4'	2.31	0.48
46:5:1748:U:C2	46:5:1783:C:C2	3.01	0.48
49:9:830:A:C2	49:9:844:U:O4	2.60	0.48
49:9:887:U:O2	49:9:887:U:O4'	2.32	0.48
49:9:1336:C:H2'	49:9:1337:C:O4'	2.14	0.48
53:DD:134:CYS:SG	53:DD:135:GLU:N	2.86	0.48
85:jj:489:ARG:NH2	85:jj:573:VAL:O	2.47	0.48
1:A:47:ASP:HA	1:A:84:THR:HG22	1.96	0.48
2:B:56:ILE:HG23	2:B:57:VAL:N	2.28	0.48
18:S:13:VAL:HA	18:S:28:TYR:O	2.14	0.48
33:h:44:LEU:O	33:h:47:ILE:HG22	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:8:125:C:O2	48:8:125:C:O4'	2.32	0.48
49:9:980:A:C2	49:9:981:A:C6	3.02	0.48
58:II:62:VAL:HG12	58:II:77:ARG:HA	1.96	0.48
4:D:22:ARG:NH1	4:D:28:THR:OG1	2.47	0.47
46:5:979:C:C4	46:5:980:U:C4	3.02	0.47
46:5:1835:G:O2'	46:5:1836:G:OP2	2.26	0.47
46:5:1929:A:N7	46:5:1932:A:H1'	2.28	0.47
46:5:3652:A:H2'	46:5:3653:A:C5	2.47	0.47
46:5:4389:C:H2'	46:5:4390:A:H8	1.78	0.47
66:QQ:21:ALA:HB1	66:QQ:84:ILE:HG22	1.95	0.47
16:Q:70:MET:HE1	16:Q:137:VAL:CG2	2.42	0.47
41:p:52:VAL:O	41:p:54:ILE:HG22	2.14	0.47
46:5:1733:G:C4	46:5:4214:A:C2	3.02	0.47
46:5:1804:A:N6	46:5:1833:G:O4'	2.46	0.47
46:5:2698:G:H2'	46:5:2699:C:O4'	2.14	0.47
49:9:563:G:N7	59:JJ:172:ARG:NH2	2.63	0.47
49:9:1533:A:C2	49:9:1604:G:H4'	2.49	0.47
53:DD:127:MET:HE1	53:DD:133:GLY:C	2.39	0.47
3:C:33:ARG:HD2	3:C:36:ILE:HD12	1.95	0.47
8:H:106:GLN:N	8:H:106:GLN:OE1	2.47	0.47
19:T:143:THR:HG23	19:T:143:THR:O	2.14	0.47
29:d:32:ARG:HB3	29:d:48:GLU:HG2	1.94	0.47
30:e:31:ILE:HD11	46:5:2347:A:C4	2.49	0.47
46:5:1869:G:C4	46:5:3877:A:C2	3.02	0.47
49:9:29:G:H4'	73:XX:129:SER:HB2	1.95	0.47
49:9:146:G:O2'	49:9:147:A:O5'	2.30	0.47
78:cc:20:ARG:NH2	78:cc:20:ARG:CG	2.73	0.47
18:S:93:MET:HE1	18:S:117:HIS:NE2	2.29	0.47
44:t:98:ILE:HG23	44:t:98:ILE:O	2.14	0.47
46:5:922:C:P	46:5:922(B):C:C5'	3.01	0.47
46:5:2743:A:C2	46:5:2744:A:C4	3.02	0.47
57:HH:95:ILE:HD11	57:HH:133:LEU:HG	1.96	0.47
70:UU:70:CYS:SG	70:UU:72:GLU:N	2.87	0.47
2:B:234:ARG:NH2	46:5:4566:U:O3'	2.46	0.47
4:D:40:ASP:HB3	19:T:69:GLN:HA	1.96	0.47
1:A:131:GLY:HA3	46:5:3683:C:C4	2.50	0.47
3:C:73:VAL:O	46:5:2350:U:C5	2.68	0.47
20:U:80:LYS:HD3	20:U:110:TYR:CE2	2.49	0.47
41:p:42:CYS:SG	41:p:43:GLY:N	2.87	0.47
49:9:584:A:C6	49:9:585:C:C4	3.02	0.47
49:9:1393:G:C6	49:9:1394:G:C6	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:1639:G:H2'	49:9:1640:A:C8	2.50	0.47
49:9:1683:C:C6	78:cc:23:SER:O	2.68	0.47
50:AA:104:THR:O	50:AA:107:THR:HG23	2.15	0.47
1:A:72:ARG:NH2	46:5:4084:G:N7	2.62	0.47
2:B:252:ALA:HB3	46:5:4457:U:O2	2.15	0.47
10:J:119:TYR:CD2	68:SS:12:ILE:HD12	2.50	0.47
14:O:44:SER:HB3	14:O:129:LEU:HD11	1.95	0.47
14:O:133:ARG:CZ	46:5:1928:C:C4	2.97	0.47
16:Q:173:LYS:NZ	46:5:88:A:N7	2.63	0.47
18:S:83:ARG:HB2	18:S:127:MET:HE3	1.97	0.47
25:Z:24:VAL:HG23	25:Z:130:PHE:CZ	2.50	0.47
25:Z:75:TYR:HB2	25:Z:80:LEU:HD21	1.97	0.47
29:d:46:LEU:HD13	29:d:64:ILE:HD13	1.97	0.47
30:e:16:ARG:HD3	30:e:20:PHE:CE1	2.50	0.47
46:5:418:A:C2	46:5:419:A:C4	3.02	0.47
46:5:433:A:C2	46:5:3867:A:H4'	2.50	0.47
46:5:922:C:C5'	46:5:922(B):C:P	3.00	0.47
46:5:1381:U:O2	46:5:1381:U:C5'	2.62	0.47
46:5:4635:A:C2	46:5:4664:A:C5	3.02	0.47
49:9:183:G:O2'	49:9:183:G:N3	2.47	0.47
49:9:1364:U:O2	49:9:1364:U:O4'	2.31	0.47
49:9:1834:A:N3	49:9:1834:A:H2'	2.30	0.47
50:AA:122:LEU:HB3	50:AA:144:THR:HG23	1.97	0.47
58:II:61:ASP:OD2	58:II:62:VAL:HG13	2.14	0.47
78:cc:20:ARG:HH21	78:cc:20:ARG:HB3	1.78	0.47
1:A:48:ILE:HG22	41:p:54:ILE:HD12	1.97	0.47
12:M:122:ILE:HG21	14:O:189:ILE:CG2	2.45	0.47
25:Z:24:VAL:HG23	25:Z:130:PHE:CE1	2.50	0.47
49:9:1485:U:H2'	49:9:1486:A:O4'	2.15	0.47
49:9:1543:U:OP2	69:TT:62:ARG:NH1	2.48	0.47
53:DD:25:LEU:HD23	53:DD:50:ILE:HG12	1.97	0.47
55:FF:201:LYS:HA	55:FF:204:ARG:HG2	1.96	0.47
56:GG:52:ILE:HD11	56:GG:109:LEU:HD11	1.96	0.47
56:GG:52:ILE:HG23	56:GG:52:ILE:O	2.14	0.47
84:ii:40:ARG:HB3	84:ii:66:THR:HG22	1.96	0.47
84:ii:253:LEU:HD22	84:ii:351:VAL:HG21	1.97	0.47
14:O:168:TYR:CE2	14:O:172:LYS:HD2	2.50	0.47
26:a:12:ARG:HD3	46:5:1660:U:H2'	1.97	0.47
35:j:39:TYR:N	35:j:40:PRO:CD	2.78	0.47
46:5:1374:G:C6	46:5:1375:C:C4	3.03	0.47
46:5:1411:C:H3'	46:5:1411(B):C:H3'	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:3648:A:C4	46:5:3785:A:C6	3.03	0.47
46:5:3652:A:H2'	46:5:3653:A:C4	2.50	0.47
49:9:1104:G:C2	49:9:1129:G:C2	3.03	0.47
51:BB:36:PRO:HG2	51:BB:38:MET:HE2	1.95	0.47
1:A:209:HIS:CE1	1:A:235:VAL:HG11	2.50	0.47
9:I:135:ILE:HG22	9:I:136:MET:HG3	1.97	0.47
11:L:108:GLU:N	11:L:108:GLU:OE1	2.48	0.47
29:d:36:VAL:HG23	29:d:41:ARG:HG3	1.97	0.47
46:5:113:A:C2	46:5:278:G:C4	3.03	0.47
46:5:1468:C:H2'	46:5:1469:C:C6	2.50	0.47
46:5:2468:U:C5	46:5:2469:C:N4	2.83	0.47
46:5:4699:U:C2	46:5:4701:A:N6	2.83	0.47
64:OO:129:ILE:HG21	76:aa:44:ILE:HD13	1.97	0.47
3:C:195:LYS:NZ	48:8:21:C:OP1	2.47	0.46
6:F:93:ARG:NH2	6:F:96:GLY:O	2.48	0.46
8:H:118:LEU:HD21	8:H:177:ASP:HB2	1.97	0.46
29:d:36:VAL:HG23	29:d:41:ARG:CG	2.44	0.46
41:p:7:LYS:HE3	46:5:2875:C:H2'	1.97	0.46
46:5:1609:U:H2'	46:5:1610:C:O4'	2.15	0.46
46:5:2408:U:O4'	46:5:2409:U:C5	2.67	0.46
49:9:92:A:C6	49:9:446:G:C6	3.03	0.46
49:9:845:G:H2'	49:9:846:G:O4'	2.15	0.46
49:9:943:U:OP2	51:BB:216:LYS:NZ	2.40	0.46
51:BB:139:CYS:SG	51:BB:140:VAL:N	2.87	0.46
62:MM:39:ALA:CB	81:ff:102:VAL:CG1	2.93	0.46
64:OO:116:LEU:HD22	76:aa:53:ILE:HD11	1.96	0.46
70:UU:70:CYS:SG	70:UU:71:GLY:N	2.87	0.46
3:C:274:LYS:O	3:C:275:SER:C	2.58	0.46
7:G:101:LYS:HB3	23:X:42:THR:HG23	1.98	0.46
8:H:12:ILE:HG21	8:H:18:ILE:HD13	1.97	0.46
35:j:34:CYS:SG	35:j:36:LYS:N	2.87	0.46
3:C:74:ALA:HB2	46:5:2351:C:O5'	2.15	0.46
9:I:91:LEU:HD11	9:I:135:ILE:HG12	1.98	0.46
18:S:9:GLU:HG3	18:S:33:PHE:CE1	2.51	0.46
18:S:30:MET:HE1	18:S:47:PHE:CB	2.46	0.46
18:S:157:ARG:O	18:S:158:VAL:C	2.58	0.46
28:c:52:CYS:HB2	28:c:92:CYS:SG	2.55	0.46
46:5:51:A:N3	46:5:1528:U:O2'	2.46	0.46
46:5:2473:A:C2	46:5:2506:G:C2	3.03	0.46
46:5:4977:A:H2'	46:5:4978:G:O4'	2.15	0.46
49:9:520:A:H5''	59:JJ:12:THR:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:EE:55:ALA:HB1	54:EE:60:GLU:HB2	1.96	0.46
56:GG:2:LYS:HB3	56:GG:15:LEU:HD21	1.97	0.46
62:MM:19:GLN:HE22	62:MM:88:TRP:CG	2.34	0.46
5:E:136:PHE:HA	5:E:139:HIS:CE1	2.51	0.46
9:I:68:ALA:O	9:I:69:ARG:C	2.59	0.46
14:O:133:ARG:CZ	46:5:1928:C:N4	2.79	0.46
46:5:1751:A:C2	46:5:1780:A:C2	3.02	0.46
46:5:1942:A:N3	46:5:4432:C:O2'	2.46	0.46
46:5:4700:A:C4	46:5:4701:A:N7	2.82	0.46
49:9:415:A:H2'	49:9:416:U:O4'	2.14	0.46
56:GG:5:ILE:CD1	56:GG:16:ILE:HD13	2.43	0.46
3:C:26:ALA:O	3:C:27:VAL:C	2.59	0.46
6:F:153:ILE:O	6:F:157:GLY:HA3	2.15	0.46
46:5:731:G:C6	46:5:932:A:C4	3.04	0.46
46:5:4522:G:O2'	46:5:4525:C:OP2	2.33	0.46
49:9:1137:U:C4	49:9:1148:A:N1	2.84	0.46
61:LL:135:SER:OG	61:LL:136:LYS:N	2.48	0.46
65:PP:81:ARG:NH1	65:PP:120:SER:OG	2.49	0.46
3:C:36:ILE:O	3:C:37:VAL:C	2.57	0.46
6:F:202:GLU:OE1	6:F:202:GLU:N	2.48	0.46
11:L:74:ARG:HB3	11:L:99:ASP:OD2	2.16	0.46
14:O:152:VAL:HG12	14:O:156:LEU:HD12	1.97	0.46
17:R:42:ARG:HA	17:R:45:ILE:HD12	1.97	0.46
17:R:115:ILE:HG22	17:R:119:MET:HE3	1.98	0.46
19:T:54:HIS:CD2	46:5:4301:U:H4'	2.51	0.46
46:5:1308:C:H2'	46:5:1309:C:C6	2.50	0.46
46:5:4508:C:N3	46:5:4512:U:C5	2.84	0.46
49:9:1743:G:C6	49:9:1744:G:N1	2.84	0.46
74:YY:62:THR:HA	74:YY:69:THR:HG22	1.98	0.46
21:V:39:ILE:HG23	21:V:61:VAL:CG2	2.46	0.46
49:9:1303:C:O2	49:9:1303:C:O4'	2.32	0.46
49:9:1349:G:H2'	49:9:1350:U:C6	2.50	0.46
49:9:1401:A:C2	49:9:1402:A:C6	3.04	0.46
5:E:273:TYR:CE1	12:M:107:PHE:HA	2.50	0.46
13:N:184:ILE:O	13:N:194:ARG:NH1	2.49	0.46
24:Y:52:ASP:HB2	24:Y:110:LYS:HG3	1.97	0.46
55:FF:20:PHE:CD1	55:FF:20:PHE:C	2.92	0.46
56:GG:16:ILE:HD12	56:GG:16:ILE:N	2.31	0.46
57:HH:62:ILE:HG21	57:HH:94:PHE:CE1	2.51	0.46
74:YY:29:HIS:CE1	74:YY:34:THR:HA	2.51	0.46
3:C:313:VAL:HG11	6:F:169:THR:HG21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:34:ASN:OD1	12:M:34:ASN:N	2.48	0.46
18:S:9:GLU:CG	18:S:33:PHE:CE1	2.99	0.46
46:5:2763:U:O2	46:5:2763:U:O4'	2.33	0.46
49:9:389:A:H2'	49:9:390:C:C6	2.51	0.46
56:GG:59:GLN:OE1	56:GG:72:ARG:NH1	2.48	0.46
1:A:104:VAL:CG1	1:A:146:THR:HG21	2.46	0.45
4:D:50:ARG:NH2	4:D:72:ASP:OD2	2.48	0.45
5:E:184:LEU:HD11	5:E:264:ILE:CD1	2.46	0.45
12:M:122:ILE:HG21	14:O:189:ILE:HG23	1.98	0.45
29:d:22:THR:HG22	29:d:89:SER:HB2	1.98	0.45
46:5:961:G:C6	46:5:962:C:C4	3.04	0.45
46:5:1358:G:H4'	46:5:1359:G:OP1	2.15	0.45
46:5:1523:A:C8	46:5:1652:U:O4	2.69	0.45
46:5:2270:G:C6	46:5:2271:C:C4	3.04	0.45
47:7:113:G:H2'	47:7:114:U:C6	2.52	0.45
49:9:1438:A:H2'	49:9:1439:A:C8	2.50	0.45
53:DD:162:ASP:N	53:DD:163:PRO:CD	2.79	0.45
72:WW:55:ASP:O	72:WW:57:ARG:N	2.49	0.45
1:A:181:LYS:HB2	46:5:1577:G:C5	2.51	0.45
2:B:89:ILE:CD1	2:B:153:MET:HE1	2.45	0.45
12:M:23:LYS:CE	46:5:935:A:H3'	2.46	0.45
46:5:3648:A:H1'	46:5:3785:A:N6	2.31	0.45
72:WW:105:THR:HB	72:WW:110:ILE:HG12	1.97	0.45
4:D:26:GLY:O	10:J:146:ARG:O	2.35	0.45
31:f:22:ARG:NH1	46:5:2069:A:OP2	2.50	0.45
46:5:1804:A:O2'	46:5:1805:A:OP2	2.29	0.45
46:5:1846:G:H2'	46:5:1847:C:H6	1.82	0.45
46:5:4510:A:O2'	46:5:4511:A:O4'	2.33	0.45
49:9:1144:A:H2'	49:9:1145:A:C8	2.51	0.45
49:9:1718:G:C6	49:9:1814:G:C6	3.05	0.45
82:gg:38:LYS:HE2	82:gg:64:HIS:HA	1.98	0.45
2:B:86:VAL:HG12	2:B:201:LEU:HD12	1.99	0.45
3:C:224:ILE:CG2	3:C:227:ILE:HD13	2.47	0.45
13:N:119:TYR:CZ	13:N:131:GLU:HB2	2.52	0.45
21:V:26:ILE:HG22	21:V:101:ASN:HB3	1.98	0.45
46:5:5001:U:H2'	46:5:5002:U:O4'	2.15	0.45
55:FF:92:ILE:HD13	55:FF:169:ILE:HG21	1.98	0.45
76:aa:12:LYS:N	76:aa:33:ASP:OD2	2.49	0.45
82:gg:11:LEU:HB2	82:gg:307:VAL:HB	1.98	0.45
1:A:208:GLU:HG2	46:5:1629:G:H1	1.82	0.45
6:F:106:LYS:O	6:F:109:GLN:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:O:21:ALA:HA	14:O:87:MET:SD	2.57	0.45
19:T:2:THR:HG23	46:5:4220:A:OP2	2.17	0.45
46:5:2352:U:C2	46:5:2353:U:C5	3.04	0.45
46:5:2412:A:C2	46:5:2433:G:C2	3.05	0.45
46:5:4528:G:C2	46:5:4529:G:C8	3.05	0.45
63:NN:63:VAL:HG21	63:NN:71:ILE:HD11	1.99	0.45
85:jj:352:ILE:N	85:jj:353:PRO:CD	2.80	0.45
2:B:95:THR:HG21	2:B:100:ARG:HB2	1.99	0.45
9:I:135:ILE:HG21	9:I:159:PHE:CE2	2.51	0.45
12:M:17:PHE:CE2	12:M:54:CYS:HA	2.51	0.45
16:Q:18:PRO:HG3	16:Q:29:VAL:HG21	1.99	0.45
30:e:44:ARG:NH1	46:5:1315:C:OP1	2.50	0.45
31:f:43:LEU:HD22	31:f:76:ARG:HA	1.97	0.45
46:5:4699:U:C4	46:5:4702:G:C6	3.05	0.45
46:5:5008:C:H2'	46:5:5009:G:O4'	2.17	0.45
49:9:291:G:N3	61:LL:42:LEU:HD13	2.32	0.45
49:9:1286:G:C6	62:MM:34:GLY:HA3	2.52	0.45
49:9:1345:G:N7	49:9:1371:U:H2'	2.31	0.45
49:9:1489:A:H4'	49:9:1490:G:OP2	2.17	0.45
49:9:1668:U:OP2	66:QQ:141:TYR:OH	2.34	0.45
50:AA:134:LEU:HD21	50:AA:144:THR:HG21	1.98	0.45
65:PP:56:LEU:HD13	65:PP:78:THR:HG21	1.99	0.45
3:C:292:ILE:HG23	16:Q:128:LEU:HD21	1.98	0.45
18:S:93:MET:HE1	18:S:117:HIS:CE1	2.52	0.45
29:d:33:ILE:HD11	29:d:41:ARG:CB	2.46	0.45
30:e:23:HIS:HA	30:e:53:ILE:CD1	2.47	0.45
46:5:922(B):C:O2'	46:5:923:C:O5'	2.33	0.45
46:5:4564:A:C5	46:5:4565:C:C4	3.04	0.45
49:9:1304:U:C4'	81:ff:91:ASN:O	2.63	0.45
49:9:1597:C:H4'	49:9:1603:G:O6	2.16	0.45
55:FF:119:SER:OG	55:FF:189:ALA:HB1	2.17	0.45
76:aa:22:ARG:NE	76:aa:27:ALA:O	2.48	0.45
7:G:200:VAL:HG13	7:G:232:VAL:HG21	1.98	0.45
15:P:131:ARG:CD	15:P:137:ASN:ND2	2.80	0.45
33:h:52:LYS:NZ	48:8:62:A:OP1	2.50	0.45
42:r:46:ARG:HG2	42:r:70:GLN:HE22	1.82	0.45
46:5:355:A:C6	46:5:356:G:C5	3.05	0.45
46:5:422:C:C2	48:8:13:G:C2	3.05	0.45
46:5:922(B):C:H1'	46:5:923:C:O5'	2.16	0.45
46:5:1736:A:C2	46:5:1794:A:C4	3.05	0.45
46:5:3675:G:C2	46:5:3676:G:C8	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:8:112:G:C6	48:8:113:C:C4	3.05	0.45
48:8:141:C:H2'	48:8:142:U:C6	2.52	0.45
49:9:1304:U:OP2	81:ff:93:HIS:HB2	2.17	0.45
76:aa:41:ILE:HG22	76:aa:68:TYR:CD2	2.51	0.45
84:ii:40:ARG:CB	84:ii:66:THR:HG22	2.47	0.45
3:C:70:GLY:C	3:C:72:ALA:H	2.24	0.45
11:L:56:ARG:O	11:L:116:ARG:NH2	2.50	0.45
13:N:108:ARG:NH2	46:5:54:G:O2'	2.41	0.45
13:N:172:ARG:NH1	46:5:62:A:OP1	2.50	0.45
13:N:184:ILE:HG23	13:N:194:ARG:HH12	1.81	0.45
28:c:29:LEU:CD2	28:c:94:LEU:HD13	2.47	0.45
46:5:1532:G:C2	46:5:1643:A:C2	3.05	0.45
46:5:1655:C:O2'	46:5:4391:G:O2'	2.26	0.45
46:5:3777:G:N2	46:5:3815:G:H2'	2.31	0.45
49:9:92:A:O4'	54:EE:3:ARG:NH1	2.50	0.45
49:9:1260:A:C6	49:9:1619:A:C6	3.05	0.45
51:BB:69:VAL:CG1	51:BB:74:LEU:HD13	2.46	0.45
52:CC:124:PHE:O	52:CC:143:CYS:HA	2.17	0.45
63:NN:6:ALA:HB1	63:NN:7:PRO:HD2	1.99	0.45
2:B:252:ALA:HB1	46:5:4524:G:C2	2.52	0.45
30:e:104:SER:OG	46:5:2305:U:O2'	2.31	0.45
40:o:61:LYS:HD2	46:5:4372:U:OP2	2.17	0.45
46:5:2088:A:O2'	46:5:2089:G:OP2	2.33	0.45
46:5:2820:C:H2'	46:5:2821:U:H6	1.82	0.45
51:BB:79:VAL:HG21	51:BB:81:PHE:CZ	2.52	0.45
62:MM:61:TYR:HD2	81:ff:100:LEU:CD2	2.30	0.45
6:F:227:VAL:HA	18:S:39:VAL:HG12	1.98	0.44
19:T:86:ALA:HB2	27:b:24:PRO:HG3	1.98	0.44
40:o:66:ILE:HD13	40:o:91:PHE:CE1	2.52	0.44
46:5:235:A:C2	46:5:238:C:C5	3.05	0.44
46:5:1634:A:C6	46:5:1635:C:C4	3.05	0.44
49:9:604:A:C6	49:9:605:A:N1	2.85	0.44
49:9:1445:U:O4	49:9:1446:A:N6	2.49	0.44
63:NN:60:VAL:HG23	63:NN:66:VAL:HG21	1.98	0.44
4:D:78:ALA:HB1	4:D:104:LEU:HD13	2.00	0.44
14:O:51:LYS:HE2	14:O:55:LEU:HD11	1.99	0.44
21:V:98:PHE:CZ	21:V:122:ALA:HB2	2.53	0.44
29:d:46:LEU:CD1	29:d:64:ILE:HD13	2.48	0.44
33:h:88:THR:O	33:h:91:MET:N	2.51	0.44
41:p:49:ARG:CZ	41:p:51:ALA:O	2.66	0.44
46:5:26:C:O2'	46:5:338:A:N3	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:1626:G:N2	46:5:1627:G:H1'	2.32	0.44
46:5:4277:G:O2'	46:5:4282:A:N1	2.45	0.44
49:9:443:U:O4	49:9:444:G:C6	2.71	0.44
49:9:1046:U:C4	49:9:1047:C:C4	3.05	0.44
53:DD:48:ILE:CG2	53:DD:86:LEU:HD12	2.48	0.44
57:HH:44:ASN:N	57:HH:68:GLN:OE1	2.51	0.44
60:KK:93:THR:HG23	60:KK:94:LEU:HD12	1.99	0.44
62:MM:61:TYR:HD2	81:ff:100:LEU:HD21	1.81	0.44
73:XX:46:HIS:HB3	73:XX:101:LEU:HD11	1.98	0.44
14:O:27:VAL:HG12	14:O:98:ALA:HB1	1.99	0.44
15:P:29:THR:CG2	15:P:146:ILE:HD11	2.47	0.44
46:5:1318:C:H2'	46:5:1319:U:O4'	2.17	0.44
46:5:1525:A:C2	46:5:1651:G:N2	2.86	0.44
52:CC:66:LEU:HD12	52:CC:93:ILE:HD13	1.99	0.44
54:EE:80:ILE:HG13	54:EE:81:THR:HG23	1.98	0.44
65:PP:83:MET:HB3	65:PP:116:LEU:HD12	1.99	0.44
85:jj:266:ILE:CD1	85:jj:393:VAL:HG21	2.46	0.44
85:jj:503:PHE:HE1	85:jj:505:ILE:HD12	1.83	0.44
11:L:57:PRO:HG3	11:L:75:GLY:O	2.18	0.44
18:S:34:ALA:HB1	18:S:39:VAL:HG23	1.99	0.44
46:5:922:C:C6	46:5:922:C:C3'	2.99	0.44
46:5:2382:A:N1	46:5:2829:U:O2'	2.45	0.44
46:5:2443:G:N2	46:5:2780:C:C2	2.86	0.44
46:5:4515:G:C2	46:5:4516:G:C8	3.05	0.44
46:5:4583:C:O2	46:5:4719:G:O6	2.36	0.44
49:9:1162:C:H2'	49:9:1163:C:O4'	2.17	0.44
49:9:1276:A:N6	49:9:1321:G:O2'	2.51	0.44
49:9:1614:A:OP2	65:PP:42:ARG:NH1	2.51	0.44
57:HH:133:LEU:HD21	57:HH:176:VAL:CG1	2.48	0.44
85:jj:534:ILE:HD11	85:jj:544:ALA:HB3	1.99	0.44
3:C:133:LEU:N	3:C:133:LEU:HD12	2.32	0.44
4:D:144:CYS:SG	4:D:171:LEU:HD23	2.57	0.44
11:L:55:ILE:HG22	11:L:154:VAL:HG13	2.00	0.44
30:e:57:ASN:O	46:5:2319:C:H1'	2.18	0.44
46:5:20:U:O2'	48:8:37:A:N6	2.49	0.44
46:5:481(A):C:O2	46:5:481(A):C:O4'	2.35	0.44
46:5:686:A:N3	46:5:686:A:H2'	2.33	0.44
46:5:1622:U:O2'	46:5:1627:G:H4'	2.18	0.44
46:5:1786:A:H2'	46:5:1789:C:C5	2.52	0.44
48:8:142:U:H2'	48:8:143:G:O4'	2.18	0.44
49:9:356:C:O2	49:9:356:C:H2'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:362:C:C2	49:9:403:G:C2	3.05	0.44
49:9:1546:G:C5'	66:QQ:18:THR:HG21	2.48	0.44
57:HH:130:LEU:HD23	57:HH:139:ILE:HD13	1.98	0.44
82:gg:81:GLY:HA2	82:gg:87:LEU:HD23	1.99	0.44
84:ii:1:MET:HE2	84:ii:25:ASP:HB3	1.98	0.44
84:ii:28:HIS:NE2	84:ii:155:SER:OG	2.51	0.44
9:I:86:HIS:HB3	9:I:139:ARG:HG2	1.99	0.44
21:V:50:ASN:O	21:V:51:ARG:HB2	2.17	0.44
30:e:85:LEU:HD22	30:e:120:ILE:HD13	1.99	0.44
33:h:88:THR:O	33:h:89:ARG:C	2.61	0.44
35:j:12:ARG:O	35:j:13:ASN:C	2.59	0.44
37:l:26:TRP:CZ3	37:l:27:ILE:HD12	2.53	0.44
46:5:3798:U:C2	46:5:3801:U:C5	3.06	0.44
58:II:36:THR:HG21	58:II:179:PRO:HB2	1.99	0.44
1:A:33:ASP:O	1:A:34:PHE:C	2.60	0.44
1:A:117:GLU:HB2	1:A:162:ASN:HB2	2.00	0.44
3:C:106:LYS:HG2	3:C:108:TRP:CZ2	2.52	0.44
4:D:30:TYR:OH	47:7:8:G:OP2	2.20	0.44
23:X:80:PRO:HA	23:X:98:PHE:HA	1.99	0.44
29:d:46:LEU:CD2	29:d:72:VAL:HG11	2.48	0.44
46:5:3689:G:C5	46:5:3690:U:C5	3.06	0.44
46:5:4759:C:O2	46:5:4759:C:O4'	2.35	0.44
49:9:1568:C:OP1	69:TT:96:SER:OG	2.30	0.44
50:AA:134:LEU:CD2	50:AA:144:THR:HG21	2.48	0.44
52:CC:179:THR:OG1	52:CC:180:VAL:N	2.51	0.44
70:UU:56:MET:SD	70:UU:88:LEU:HD21	2.58	0.44
85:jj:587:ILE:HD11	85:jj:635:LEU:HD13	2.00	0.44
2:B:79:VAL:HB	2:B:331:VAL:HG23	2.00	0.44
12:M:23:LYS:HE2	46:5:935:A:H3'	2.00	0.44
16:Q:158:THR:O	16:Q:159:PRO:C	2.61	0.44
26:a:17:HIS:CE1	46:5:1338:G:H2'	2.52	0.44
35:j:63:ARG:NH2	48:8:58:G:N7	2.66	0.44
41:p:19:GLY:HA2	46:5:2874:U:O2	2.17	0.44
46:5:752:G:C6	46:5:753:C:C4	3.05	0.44
46:5:1296:G:C2	46:5:1297:U:C2	3.06	0.44
46:5:2514:G:C2	46:5:2515:G:C8	3.06	0.44
46:5:4303:C:O2'	46:5:4304:A:H2'	2.18	0.44
46:5:4348:A:C2	46:5:4350:C:C2	3.05	0.44
46:5:4371:G:O2'	46:5:4372:U:OP2	2.28	0.44
46:5:4564:A:H2'	46:5:4565:C:C6	2.53	0.44
46:5:4880:C:O2	46:5:4880:C:O4'	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:1344:A:H4'	49:9:1345:G:H5'	1.99	0.44
49:9:1843:G:H2'	49:9:1844:U:O4'	2.18	0.44
50:AA:185:MET:HE3	71:VV:39:VAL:HG21	1.99	0.44
56:GG:57:ASP:OD1	56:GG:58:LYS:N	2.50	0.44
76:aa:25:ASN:ND2	76:aa:77:CYS:SG	2.89	0.44
82:gg:87:LEU:CD2	82:gg:108:VAL:HG11	2.43	0.44
18:S:30:MET:HE1	18:S:47:PHE:HB3	2.00	0.44
26:a:59:ARG:NH2	26:a:61:TYR:OH	2.51	0.44
30:e:23:HIS:HB2	30:e:45:VAL:HG21	2.00	0.44
46:5:384:A:C2	46:5:386:A:C4	3.06	0.44
46:5:1876:U:H2'	46:5:1877:G:O4'	2.18	0.44
46:5:2002:A:N3	46:5:2002:A:H2'	2.33	0.44
46:5:5015:G:C2	46:5:5033:G:C2	3.05	0.44
49:9:1452:A:H4'	49:9:1453:C:O4'	2.18	0.44
49:9:1653:U:H2'	49:9:1654:G:C8	2.53	0.44
49:9:1692:U:H2'	49:9:1693:G:C8	2.52	0.44
3:C:323:ARG:NE	46:5:976:G:H21	2.16	0.43
9:I:191:ILE:HD11	9:I:212:LEU:HD11	1.99	0.43
14:O:36:VAL:HG23	14:O:105:PHE:HB2	2.00	0.43
25:Z:14:LEU:HD12	32:g:91:ILE:HG21	1.99	0.43
46:5:914:U:H3'	46:5:914:U:H6	1.83	0.43
46:5:1846:G:H2'	46:5:1847:C:C6	2.53	0.43
46:5:2079:G:N2	46:5:2278:G:C4	2.85	0.43
49:9:1045:U:C4	49:9:1046:U:C4	3.06	0.43
49:9:1685:U:C4	49:9:1686:G:N7	2.86	0.43
49:9:1719:A:N6	49:9:1814:G:O2'	2.50	0.43
54:EE:19:MET:HE3	54:EE:108:ARG:HD3	1.99	0.43
54:EE:125:LYS:HB3	54:EE:142:HIS:HB3	2.00	0.43
78:cc:40:ARG:NH1	78:cc:61:SER:OG	2.49	0.43
3:C:78:ARG:HB3	3:C:88:GLY:HA2	2.00	0.43
3:C:237:ILE:HD12	3:C:237:ILE:H	1.83	0.43
5:E:53:VAL:O	5:E:54:ARG:C	2.61	0.43
9:I:189:ARG:O	9:I:200:ILE:N	2.50	0.43
24:Y:42:TYR:CG	24:Y:119:LEU:HD23	2.53	0.43
25:Z:75:TYR:CG	25:Z:80:LEU:HD21	2.53	0.43
46:5:1646:A:C6	46:5:1647:U:C4	3.06	0.43
46:5:2639:U:O2'	46:5:2694:G:O6	2.33	0.43
49:9:398:A:H5'	49:9:398:A:C8	2.54	0.43
49:9:1657:G:C6	49:9:1658:G:C5	3.06	0.43
55:FF:96:ALA:CB	55:FF:173:LEU:HD12	2.48	0.43
2:B:54:THR:OG1	2:B:55:HIS:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:146:LEU:HD11	4:D:159:VAL:CG1	2.47	0.43
46:5:2818:C:OP1	46:5:4655:A:H4'	2.18	0.43
46:5:3829:G:N3	46:5:3829:G:H2'	2.34	0.43
49:9:1221:G:H2'	49:9:1222:G:H8	1.83	0.43
52:CC:74:LYS:HG2	52:CC:269:PHE:CE1	2.53	0.43
62:MM:36:ARG:NE	81:ff:102:VAL:CG2	2.59	0.43
66:QQ:132:PHE:CD1	66:QQ:132:PHE:C	2.96	0.43
25:Z:76:ASN:HB3	25:Z:78:ASN:OD1	2.19	0.43
42:r:35:ARG:NH1	46:5:2265:G:OP1	2.51	0.43
46:5:1676:C:N4	46:5:4378:A:C8	2.86	0.43
46:5:4928:C:O2	46:5:4928:C:O4'	2.36	0.43
49:9:449:A:O2'	49:9:452:G:N7	2.49	0.43
49:9:507:G:O2'	49:9:508:A:OP1	2.30	0.43
49:9:1649:U:C5	49:9:1674:G:N2	2.86	0.43
51:BB:136:ARG:HB2	51:BB:218:LEU:HD11	2.00	0.43
68:SS:65:GLU:O	68:SS:69:THR:HG23	2.17	0.43
72:WW:33:VAL:HG13	72:WW:110:ILE:HD13	2.00	0.43
3:C:70:GLY:O	3:C:72:ALA:N	2.50	0.43
3:C:210:ILE:HG21	3:C:252:TRP:CZ3	2.54	0.43
9:I:22:PHE:CZ	46:5:1788:A:H2'	2.54	0.43
13:N:181:HIS:O	13:N:184:ILE:HG22	2.18	0.43
30:e:23:HIS:HA	30:e:53:ILE:HD12	1.99	0.43
46:5:77:U:O2	46:5:78:U:O4'	2.37	0.43
49:9:445:A:H2'	49:9:446:G:C8	2.54	0.43
49:9:1745:A:N6	49:9:1789:G:O2'	2.51	0.43
53:DD:142:LEU:HD22	53:DD:150:MET:HG2	2.00	0.43
67:RR:119:VAL:HG13	67:RR:119:VAL:O	2.19	0.43
85:jj:266:ILE:HG23	85:jj:389:HIS:HB3	2.00	0.43
6:F:88:LEU:HD11	6:F:121:PHE:HD1	1.84	0.43
26:a:21:ARG:NH1	46:5:1317:U:OP1	2.51	0.43
28:c:50:ASN:OD1	28:c:76:GLY:C	2.61	0.43
46:5:4459:U:H2'	46:5:4460:U:C6	2.53	0.43
49:9:1164:G:C6	49:9:1165:G:O6	2.71	0.43
52:CC:88:ILE:HG21	52:CC:94:ILE:CD1	2.49	0.43
55:FF:140:ASP:OD1	78:cc:44:ARG:NH2	2.51	0.43
74:YY:20:ARG:NH2	74:YY:22:GLN:OE1	2.50	0.43
1:A:112:ILE:HG13	41:p:79:VAL:HG22	2.01	0.43
1:A:185:ALA:O	1:A:186:TYR:C	2.60	0.43
3:C:144:ILE:HD13	3:C:147:VAL:HB	2.00	0.43
21:V:82:ILE:HD12	21:V:104:VAL:HG13	2.00	0.43
24:Y:50:ARG:NH2	48:8:85:U:O4	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:a:2:PRO:HA	46:5:2342:G:OP2	2.18	0.43
29:d:85:ARG:NH2	29:d:117:LEU:HD12	2.33	0.43
46:5:384:A:N1	46:5:386:A:C4	2.87	0.43
46:5:2517:A:N3	46:5:2539:C:O2'	2.50	0.43
46:5:4371:G:C5	46:5:4372:U:C4	3.07	0.43
46:5:4398:C:C4	46:5:4399:U:C5	3.07	0.43
49:9:4:C:O2'	59:JJ:18:ARG:NH1	2.52	0.43
49:9:987:A:N6	51:BB:122:GLU:OE1	2.43	0.43
49:9:1536:G:H2'	49:9:1537:A:C8	2.53	0.43
55:FF:73:THR:O	55:FF:89:THR:HG21	2.19	0.43
3:C:154:VAL:HG11	3:C:158:VAL:HG21	2.00	0.43
3:C:208:CYS:HG	3:C:228:THR:HG1	1.61	0.43
3:C:297:GLU:OE2	3:C:297:GLU:N	2.45	0.43
8:H:40:HIS:ND1	46:5:4701:A:O2'	2.29	0.43
37:l:2:SER:O	37:l:5:LYS:NZ	2.45	0.43
46:5:492:U:O2'	46:5:493:G:P	2.76	0.43
46:5:1633:G:OP2	46:5:4535:A:OP1	2.36	0.43
46:5:1912:G:C6	46:5:1913:C:N4	2.87	0.43
46:5:1990:A:H3'	46:5:1991:A:H5''	2.01	0.43
46:5:2307:A:C8	46:5:2332:A:C6	3.06	0.43
49:9:26:U:H2'	49:9:27:A:O4'	2.19	0.43
49:9:344:U:H2'	49:9:345:U:C6	2.54	0.43
49:9:933:G:H1'	49:9:1001:A:O4'	2.19	0.43
49:9:1444:U:O2'	49:9:1580:A:N1	2.52	0.43
49:9:1522:A:C2	65:PP:128:HIS:CE1	3.06	0.43
50:AA:131:HIS:CG	50:AA:132:GLN:N	2.86	0.43
85:jj:594:ILE:HD11	85:jj:674:ILE:CG2	2.48	0.43
3:C:323:ARG:NH1	46:5:1281:G:C8	2.86	0.43
16:Q:188:ASN:N	16:Q:188:ASN:HD22	2.16	0.43
18:S:3:ALA:O	18:S:111:ARG:NH1	2.45	0.43
19:T:9:ARG:NH2	46:5:4218:U:OP2	2.50	0.43
49:9:584:A:N6	49:9:585:C:N4	2.67	0.43
49:9:1400:U:C4	49:9:1401:A:N7	2.87	0.43
49:9:1680:G:H4'	78:cc:20:ARG:CZ	2.49	0.43
2:B:285:TYR:CE1	2:B:334:LYS:HB2	2.54	0.43
9:I:38:ARG:HG2	9:I:41:ALA:HB2	2.00	0.43
13:N:159:ARG:NH2	13:N:165:THR:HG22	2.34	0.43
15:P:41:ILE:HD12	15:P:150:LEU:CD1	2.49	0.43
16:Q:43:PHE:CD2	16:Q:133:GLY:HA3	2.54	0.43
49:9:973:C:C5	49:9:974:C:C5	3.07	0.43
50:AA:58:LEU:HG	50:AA:174:MET:HE1	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:LL:78:THR:HG22	61:LL:87:VAL:O	2.18	0.43
62:MM:63:LYS:O	81:ff:108:VAL:HG21	2.19	0.43
69:TT:28:LEU:HD12	69:TT:54:TYR:CE1	2.54	0.43
3:C:93:GLY:O	3:C:94:ASN:C	2.62	0.42
3:C:112:HIS:HB2	13:N:202:ARG:O	2.19	0.42
10:J:151:ILE:HD12	10:J:155:HIS:HB3	2.01	0.42
14:O:15:LEU:HA	14:O:42:ASN:O	2.19	0.42
14:O:20:ALA:HB1	14:O:84:VAL:HG22	2.00	0.42
42:r:7:TRP:HE3	42:r:44:ILE:HD11	1.84	0.42
46:5:1667:A:N1	46:5:2281:U:OP2	2.51	0.42
46:5:1802:A:O2'	46:5:1837:A:OP1	2.37	0.42
46:5:2097:A:OP1	46:5:2107:A:N6	2.52	0.42
46:5:4352:U:C2	46:5:4363:A:C2	3.07	0.42
49:9:612:U:H2'	49:9:613:G:O4'	2.19	0.42
57:HH:177:TYR:CD2	57:HH:185:VAL:HG21	2.54	0.42
74:YY:110:ARG:NH2	74:YY:114:MET:SD	2.92	0.42
78:cc:20:ARG:NH2	78:cc:20:ARG:HG3	2.34	0.42
2:B:218:ASP:OD1	2:B:218:ASP:N	2.51	0.42
7:G:98:ILE:HG21	46:5:4125:C:H4'	2.00	0.42
46:5:115:C:O2	46:5:115:C:O4'	2.37	0.42
46:5:1667:A:N1	46:5:2280:G:H2'	2.34	0.42
46:5:2410:C:O5'	46:5:2410:C:C6	2.72	0.42
50:AA:25:LEU:O	50:AA:164:ASN:HB2	2.19	0.42
52:CC:233:LEU:HD12	52:CC:233:LEU:O	2.18	0.42
61:LL:126:VAL:HG22	61:LL:142:VAL:HG13	2.02	0.42
3:C:67:TRP:HE3	3:C:73:VAL:HG21	1.83	0.42
5:E:167:PHE:CE1	5:E:176:LEU:HD22	2.55	0.42
5:E:180:GLY:O	5:E:181:PRO:C	2.62	0.42
8:H:111:LEU:HD12	8:H:127:ARG:NH2	2.34	0.42
19:T:57:TYR:OH	46:5:4301:U:OP1	2.37	0.42
20:U:84:LYS:HA	20:U:87:THR:HG22	2.01	0.42
46:5:388:A:H1'	46:5:403:G:N2	2.33	0.42
46:5:1328:G:O2'	46:5:2349:A:OP1	2.32	0.42
46:5:3620:G:OP1	46:5:3622:C:N4	2.50	0.42
49:9:942:G:H2'	49:9:943:U:C6	2.54	0.42
49:9:1438:A:C2	49:9:1439:A:C6	3.06	0.42
49:9:1610:G:OP1	68:SS:121:ARG:NE	2.53	0.42
54:EE:126:VAL:HG23	54:EE:156:VAL:O	2.19	0.42
58:II:174:CYS:HB3	58:II:188:TYR:CE1	2.54	0.42
62:MM:71:GLU:CG	81:ff:114:ILE:HG12	2.49	0.42
2:B:298:LEU:C	2:B:299:ILE:HD12	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:92:ILE:HA	6:F:118:ASN:O	2.19	0.42
21:V:28:CYS:SG	21:V:30:ASP:OD1	2.78	0.42
37:I:37:TYR:O	46:5:362:A:N6	2.47	0.42
46:5:922:C:P	46:5:922(B):C:P	3.17	0.42
46:5:1411:C:C3'	46:5:1411(C):C:O5'	2.67	0.42
46:5:4187:G:H2'	46:5:4188:U:O4'	2.18	0.42
46:5:4303:C:O5'	46:5:4303:C:O2	2.36	0.42
46:5:4631:G:H2'	46:5:4632:U:O4'	2.20	0.42
46:5:4690:G:O6	46:5:4698:C:H5''	2.19	0.42
49:9:821:G:C5	59:JJ:150:ARG:HD2	2.54	0.42
49:9:1611:G:N2	49:9:1629:C:C2	2.88	0.42
6:F:92:ILE:HD13	6:F:242:LEU:HD22	2.02	0.42
6:F:168:LEU:CB	6:F:186:MET:HE1	2.48	0.42
14:O:44:SER:HB3	14:O:129:LEU:HD21	2.01	0.42
17:R:124:TYR:OH	46:5:2666:U:OP2	2.35	0.42
46:5:498:C:O2	46:5:498:C:O4'	2.37	0.42
46:5:2085:G:N2	46:5:2273:G:C4	2.88	0.42
46:5:2787:A:N3	46:5:2787:A:C2'	2.81	0.42
49:9:1588:A:H2'	49:9:1589:A:C8	2.55	0.42
56:GG:132:ARG:HB3	56:GG:133:LEU:HD12	2.01	0.42
64:OO:67:ASP:OD1	64:OO:67:ASP:N	2.52	0.42
4:D:51:MET:HE2	4:D:166:ALA:CB	2.49	0.42
7:G:210:ILE:HG12	7:G:254:THR:HG22	2.01	0.42
8:H:43:VAL:HA	46:5:4764:A:C2	2.55	0.42
12:M:56:GLN:HB2	46:5:4870:G:C5	2.55	0.42
13:N:35:ALA:HB2	13:N:65:ARG:CZ	2.50	0.42
14:O:22:ILE:O	14:O:23:VAL:C	2.62	0.42
20:U:80:LYS:HE2	20:U:110:TYR:CZ	2.54	0.42
45:2:18:U:O4'	45:2:58:A:C2	2.73	0.42
46:5:750:U:H2'	46:5:751:G:O4'	2.19	0.42
46:5:1411:C:H4'	46:5:1411(C):C:C1'	2.48	0.42
46:5:1411:C:C5'	46:5:1411(B):C:C2'	2.97	0.42
46:5:1411:C:C5	46:5:1411(B):C:C5	3.07	0.42
46:5:1929:A:N6	46:5:2054:U:N3	2.62	0.42
46:5:3896:C:O2	46:5:4564:A:N1	2.53	0.42
49:9:816:A:C6	49:9:817:G:C4	3.08	0.42
52:CC:180:VAL:HG11	52:CC:184:VAL:HG22	2.01	0.42
65:PP:43:ARG:NH1	65:PP:47:ARG:HD2	2.35	0.42
1:A:207:VAL:HG12	46:5:3919:C:H5''	2.00	0.42
7:G:210:ILE:HG23	7:G:220:VAL:HG11	2.01	0.42
16:Q:50:ARG:HG2	16:Q:53:MET:HE2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z:73:LYS:HG2	25:Z:75:TYR:CZ	2.54	0.42
45:3:75:C:H2'	45:3:76:A:H4'	2.00	0.42
46:5:749:G:C2	46:5:912:G:C4	3.08	0.42
46:5:1205:G:C6	46:5:1206:C:C4	3.08	0.42
46:5:1632:A:H2'	46:5:1632:A:N3	2.35	0.42
49:9:1358:U:H2'	49:9:1359:U:O4'	2.20	0.42
49:9:1834:A:H2	49:9:1837:G:N1	2.18	0.42
54:EE:87:MET:N	54:EE:101:LEU:O	2.49	0.42
63:NN:105:ASN:N	63:NN:105:ASN:HD22	2.17	0.42
84:ii:313:ILE:N	84:ii:313:ILE:HD13	2.35	0.42
3:C:49:ARG:NH1	3:C:111:TRP:O	2.47	0.42
3:C:108:TRP:O	13:N:204:ARG:NH2	2.52	0.42
5:E:261:LEU:N	5:E:262:PRO:HD2	2.35	0.42
7:G:131:PRO:HA	7:G:134:ASN:HB3	2.02	0.42
10:J:105:PHE:O	10:J:132:VAL:N	2.53	0.42
21:V:20:LEU:HD12	21:V:81:VAL:HG21	2.01	0.42
30:e:49:PHE:O	30:e:50:LYS:C	2.61	0.42
46:5:25:A:C8	46:5:341:G:C8	3.08	0.42
46:5:711:A:H2'	46:5:712:C:C6	2.54	0.42
46:5:1664:U:H2'	46:5:1665:C:H6	1.85	0.42
46:5:3874:G:C6	46:5:3875:G:C5	3.08	0.42
46:5:4220:A:H2'	46:5:4222:G:O5'	2.19	0.42
49:9:15:U:H2'	49:9:16:G:O4'	2.20	0.42
49:9:144:U:OP2	56:GG:178:ARG:HG2	2.19	0.42
49:9:521:A:OP1	59:JJ:45:ARG:NH1	2.53	0.42
49:9:945:U:H2'	49:9:946:U:C6	2.55	0.42
57:HH:144:ILE:HD12	72:WW:52:ILE:HD11	2.01	0.42
74:YY:9:THR:HG22	74:YY:23:MET:HG3	2.00	0.42
6:F:171:ASN:O	6:F:172:THR:C	2.62	0.42
6:F:175:ALA:HB2	6:F:184:ILE:HA	2.02	0.42
13:N:118:SER:HB3	13:N:132:VAL:HG22	2.02	0.42
16:Q:106:THR:HG21	46:5:1353:G:H3'	2.01	0.42
22:W:26:GLY:O	22:W:27:LYS:C	2.62	0.42
24:Y:98:GLY:O	24:Y:99:ILE:HD13	2.20	0.42
45:3:71:G:N3	46:5:3715:U:O2'	2.49	0.42
46:5:382:G:N2	46:5:384:A:H3'	2.34	0.42
46:5:1677:U:H4'	46:5:1680:G:N1	2.35	0.42
46:5:2265:G:O2'	46:5:2266:C:OP1	2.27	0.42
46:5:2408:U:C1'	46:5:2409:U:C5	3.02	0.42
46:5:4664:A:H2'	46:5:4665:A:O4'	2.20	0.42
49:9:963:A:C2	49:9:964:A:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:1142:G:N2	49:9:1145:A:OP2	2.48	0.42
57:HH:145:ARG:HA	72:WW:51:GLU:HB2	2.02	0.42
59:JJ:35:TYR:CD2	59:JJ:106:LEU:HD23	2.55	0.42
1:A:112:ILE:HG23	1:A:133:TYR:CD2	2.55	0.42
7:G:219:LEU:HD23	13:N:7:ILE:HD11	2.02	0.42
13:N:65:ARG:HD3	13:N:127:TYR:CD1	2.54	0.42
16:Q:81:VAL:HG22	16:Q:101:CYS:SG	2.60	0.42
24:Y:73:VAL:HG12	24:Y:75:ARG:HG2	2.01	0.42
46:5:106:A:H1'	46:5:336:A:N3	2.35	0.42
46:5:2693:G:C6	46:5:2694:G:N1	2.88	0.42
46:5:3867:A:H2'	46:5:3868:G:O4'	2.20	0.42
46:5:4439:U:H2'	46:5:4440:G:O4'	2.20	0.42
46:5:4524:G:OP2	46:5:4524:G:H4'	2.19	0.42
49:9:1185:C:C4	49:9:1186:U:C5	3.08	0.42
56:GG:98:ARG:HG3	56:GG:99:GLY:N	2.35	0.42
66:QQ:85:ARG:HG2	66:QQ:119:LEU:HD13	2.02	0.42
72:WW:30:CYS:SG	72:WW:61:ILE:HD11	2.60	0.42
77:bb:53:VAL:HG23	77:bb:53:VAL:O	2.19	0.42
3:C:95:MET:SD	3:C:95:MET:N	2.93	0.41
6:F:178:LEU:HD11	6:F:206:PHE:HB2	2.02	0.41
14:O:185:VAL:O	14:O:185:VAL:HG12	2.19	0.41
17:R:99:MET:N	17:R:99:MET:SD	2.93	0.41
46:5:355:A:C4	46:5:356:G:C8	3.08	0.41
46:5:976:G:C2	46:5:977:C:C5	3.08	0.41
46:5:1381:U:O2	46:5:1381:U:O4'	2.38	0.41
46:5:2839:U:C4	46:5:2840:A:N7	2.88	0.41
46:5:4944:C:H3'	46:5:4945:G:C5'	2.50	0.41
46:5:4995:U:C4	46:5:4996:C:C5	3.08	0.41
49:9:1045:U:H2'	49:9:1046:U:O4'	2.20	0.41
49:9:1217:A:H2'	49:9:1218:C:C6	2.54	0.41
51:BB:30:TRP:CH2	51:BB:48:LEU:HD23	2.55	0.41
55:FF:72:LEU:HD11	55:FF:154:LEU:HD11	2.02	0.41
60:KK:12:TYR:CZ	60:KK:52:LEU:HD21	2.54	0.41
62:MM:71:GLU:HG3	81:ff:114:ILE:HG12	2.02	0.41
72:WW:14:ILE:CD1	72:WW:41:MET:HE1	2.50	0.41
10:J:140:SER:O	10:J:141:ILE:C	2.64	0.41
15:P:54:LYS:HA	15:P:83:TRP:CD1	2.55	0.41
15:P:137:ASN:ND2	46:5:3861:A:H4'	2.35	0.41
46:5:1576:G:C2	46:5:1578:U:C2	3.08	0.41
46:5:1612:G:N3	46:5:1612:G:C2'	2.82	0.41
46:5:2857:A:N6	46:5:2858:A:C6	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:9:495:U:H2'	49:9:496:C:O4'	2.20	0.41
49:9:1016:U:OP2	77:bb:20:LYS:NZ	2.53	0.41
49:9:1284:A:C8	62:MM:104:VAL:HG21	2.55	0.41
49:9:1672:U:H2'	49:9:1673:U:C6	2.55	0.41
56:GG:64:LYS:HB3	56:GG:67:VAL:HG11	2.02	0.41
58:II:31:ARG:NH2	58:II:48:VAL:HG12	2.35	0.41
85:jj:391:LEU:HD21	85:jj:588:PHE:CD1	2.55	0.41
85:jj:668:ARG:HB3	85:jj:673:THR:HA	2.01	0.41
6:F:46:ARG:NH1	46:5:976:G:O3'	2.53	0.41
14:O:46:ASN:O	14:O:47:PHE:C	2.62	0.41
15:P:30:ARG:HD3	15:P:30:ARG:C	2.45	0.41
16:Q:66:MET:HE1	16:Q:86:VAL:HG11	2.02	0.41
46:5:76:A:C6	46:5:77:U:C5	3.08	0.41
46:5:742:G:N1	46:5:743:G:C5	2.87	0.41
46:5:1394:G:H2'	46:5:1395:U:O4'	2.21	0.41
46:5:1899:G:N7	46:5:2278:G:C6	2.89	0.41
46:5:3613:U:H2'	46:5:3614:G:C8	2.55	0.41
46:5:4183:G:N3	46:5:4183:G:H2'	2.36	0.41
49:9:27:A:H2'	49:9:28:U:O4'	2.20	0.41
49:9:107:A:H2'	49:9:108:G:C8	2.55	0.41
49:9:290:U:O2'	49:9:292:A:N7	2.50	0.41
49:9:1495:G:C4	79:dd:41:GLN:HB3	2.55	0.41
52:CC:231:ALA:O	52:CC:233:LEU:N	2.53	0.41
57:HH:66:VAL:N	57:HH:67:PRO:CD	2.84	0.41
74:YY:27:VAL:HG22	74:YY:40:ILE:HD11	2.02	0.41
3:C:61:GLN:NE2	46:5:358:C:OP1	2.53	0.41
11:L:60:ARG:NH2	46:5:72:C:N3	2.67	0.41
15:P:112:LEU:HA	15:P:151:THR:O	2.21	0.41
20:U:81:ARG:NH2	46:5:2622:G:O6	2.53	0.41
30:e:44:ARG:O	30:e:45:VAL:C	2.62	0.41
46:5:1435:G:O2'	46:5:2105:A:N1	2.46	0.41
46:5:2844:A:N1	46:5:3845:A:C6	2.89	0.41
49:9:1129:G:C6	49:9:1130:G:C6	3.09	0.41
49:9:1175:G:C6	49:9:1176:G:C5	3.08	0.41
49:9:1448:A:H2'	49:9:1449:G:O4'	2.21	0.41
64:OO:56:VAL:HG13	64:OO:77:ALA:HB1	2.02	0.41
71:VV:30:ALA:HB3	71:VV:57:GLY:HA3	2.03	0.41
72:WW:94:LEU:HD21	72:WW:101:PHE:O	2.20	0.41
84:ii:45:ARG:HD3	84:ii:94:VAL:HG22	2.03	0.41
2:B:10:ARG:HD3	2:B:11:HIS:N	2.35	0.41
2:B:222:VAL:HG11	2:B:274:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:249:PHE:CD1	3:C:249:PHE:C	2.97	0.41
5:E:157:THR:HG23	5:E:158:GLY:N	2.35	0.41
8:H:64:ARG:NH1	46:5:1949:U:OP1	2.53	0.41
11:L:91:ALA:HB1	11:L:96:ILE:HB	2.02	0.41
14:O:42:ASN:N	14:O:42:ASN:OD1	2.52	0.41
15:P:29:THR:HG21	15:P:146:ILE:HD11	2.03	0.41
28:c:30:GLY:O	28:c:34:SER:OG	2.34	0.41
45:2:19:G:C4	45:2:57:A:C2	3.09	0.41
46:5:77:U:C2	46:5:78:U:C6	3.08	0.41
46:5:1360:G:C6	46:5:1361:G:C5	3.08	0.41
46:5:4432:C:H2'	46:5:4433:G:O4'	2.21	0.41
46:5:4461:C:O2	46:5:4516:G:C2	2.74	0.41
46:5:4538:G:C6	46:5:4539:U:C4	3.08	0.41
49:9:448:A:N6	58:II:29:LEU:HD13	2.35	0.41
50:AA:180:ARG:HG2	50:AA:195:TRP:CE3	2.56	0.41
2:B:62:ARG:NH1	46:5:4617:G:OP1	2.53	0.41
7:G:90:LYS:NZ	46:5:4126:C:OP1	2.53	0.41
11:L:31:ARG:HD2	46:5:337:U:OP1	2.20	0.41
14:O:74:ARG:HG3	14:O:145:VAL:HG12	2.03	0.41
20:U:82:TYR:CZ	20:U:86:LEU:HD11	2.56	0.41
27:b:28:ARG:HD2	46:5:1805:A:C8	2.55	0.41
30:e:49:PHE:CE1	46:5:1883:G:H5'	2.56	0.41
46:5:370:U:C6	46:5:1637:A:C2	3.08	0.41
46:5:1867:A:H2'	46:5:1868:A:C8	2.56	0.41
46:5:1932:A:H2'	46:5:1933:G:C8	2.56	0.41
46:5:2065:G:C5	46:5:2066:C:C5	3.08	0.41
46:5:4627:U:H2'	46:5:4628:U:O4'	2.21	0.41
49:9:846:G:C8	54:EE:19:MET:HE1	2.55	0.41
11:L:178:ALA:HB2	26:a:144:CYS:HB2	2.02	0.41
13:N:169:ARG:NH1	46:5:63:G:OP2	2.49	0.41
16:Q:2:GLY:HA3	46:5:1897:A:O5'	2.21	0.41
18:S:147:ASP:OD1	18:S:147:ASP:C	2.64	0.41
38:m:78:HIS:CE1	38:m:81:ALA:HB2	2.55	0.41
46:5:976:G:N2	46:5:977:C:C4	2.89	0.41
49:9:1238:U:H2'	49:9:1239:U:O4'	2.20	0.41
73:XX:52:LEU:HD23	73:XX:73:GLN:HB2	2.02	0.41
73:XX:61:GLN:O	73:XX:63:ASN:N	2.54	0.41
2:B:29:VAL:HG13	2:B:348:ARG:HD3	2.02	0.41
2:B:55:HIS:HE1	22:W:17:HIS:CE1	2.38	0.41
3:C:67:TRP:CE3	3:C:73:VAL:HG21	2.56	0.41
10:J:103:GLY:O	10:J:134:LEU:HD12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L:27:ASN:O	11:L:28:GLN:C	2.63	0.41
29:d:83:ARG:NH1	46:5:4997:G:OP1	2.52	0.41
32:g:13:TYR:HA	46:5:2803:U:O2'	2.20	0.41
32:g:68:SER:O	32:g:69:LYS:C	2.64	0.41
37:l:3:SER:OG	46:5:2783:A:OP2	2.38	0.41
46:5:372:A:C2	46:5:1645:C:O4'	2.73	0.41
46:5:2738:C:O2'	46:5:2740:U:OP2	2.33	0.41
46:5:4274:A:H2'	46:5:4275:G:C8	2.56	0.41
46:5:4538:G:C5	46:5:4539:U:C4	3.09	0.41
47:7:25:G:C5	47:7:26:C:C5	3.08	0.41
49:9:297:A:H4'	54:EE:132:GLY:O	2.21	0.41
49:9:1666:C:H6	49:9:1666:C:O5'	2.04	0.41
54:EE:181:CYS:SG	54:EE:225:ILE:HG23	2.61	0.41
57:HH:118:ARG:O	57:HH:121:THR:HG22	2.21	0.41
60:KK:58:VAL:HG21	60:KK:69:TRP:HB3	2.02	0.41
64:OO:39:ASP:OD1	64:OO:40:THR:N	2.54	0.41
70:UU:29:VAL:HG22	70:UU:85:HIS:NE2	2.35	0.41
73:XX:85:VAL:HG21	73:XX:91:LEU:CD1	2.51	0.41
85:jj:539:GLU:N	85:jj:540:PRO:CD	2.84	0.41
1:A:94:ALA:HB3	1:A:102:LEU:HB3	2.03	0.41
1:A:101:VAL:HG22	1:A:163:ARG:HB3	2.03	0.41
2:B:222:VAL:HB	2:B:343:ARG:HD3	2.02	0.41
3:C:94:ASN:OD1	3:C:94:ASN:N	2.53	0.41
3:C:194:GLY:O	3:C:197:ARG:N	2.50	0.41
4:D:22:ARG:HH11	4:D:22:ARG:HG3	1.86	0.41
5:E:165:VAL:HG12	5:E:178:VAL:HG22	2.03	0.41
5:E:185:ASN:ND2	5:E:274:LEU:O	2.53	0.41
8:H:73:ILE:O	8:H:74:CYS:C	2.64	0.41
9:I:16:PRO:HA	9:I:95:HIS:CD2	2.56	0.41
11:L:75:GLY:O	11:L:99:ASP:OD1	2.39	0.41
12:M:64:PHE:CZ	12:M:73:VAL:HG22	2.56	0.41
14:O:74:ARG:NH2	46:5:4712:C:OP1	2.54	0.41
23:X:146:ALA:HA	23:X:149:VAL:HG12	2.03	0.41
30:e:47:ARG:NH1	46:5:1883:G:OP1	2.54	0.41
32:g:44:SER:OG	32:g:46:CYS:SG	2.79	0.41
40:o:82:MET:SD	40:o:82:MET:N	2.93	0.41
41:p:19:GLY:O	41:p:20:ALA:C	2.63	0.41
42:r:18:ILE:HD11	42:r:20:ARG:NH2	2.36	0.41
46:5:1325:C:O2	46:5:1325:C:O5'	2.39	0.41
46:5:1513:U:H2'	46:5:1514:U:O4'	2.21	0.41
46:5:1622:U:O2'	46:5:1627:G:O3'	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5:1929:A:N3	46:5:1929:A:C2'	2.83	0.41
46:5:3642:A:OP1	46:5:3644:U:OP1	2.39	0.41
46:5:4368:G:C6	46:5:4369:A:C5	3.09	0.41
46:5:4966:A:H2'	46:5:4967:A:C8	2.55	0.41
47:7:27:G:C2	47:7:28:C:C2	3.09	0.41
48:8:13:G:C6	48:8:14:U:C4	3.08	0.41
48:8:40:A:H2'	48:8:41:A:O4'	2.21	0.41
49:9:14:C:O2'	49:9:668:A:N1	2.41	0.41
49:9:932:G:H2'	49:9:934:G:OP2	2.20	0.41
49:9:1019:C:H2'	49:9:1020:A:O4'	2.21	0.41
49:9:1130:G:O2'	49:9:1131:G:O5'	2.39	0.41
50:AA:34:MET:HE3	50:AA:34:MET:HB3	2.01	0.41
54:EE:162:ILE:HD12	54:EE:162:ILE:C	2.46	0.41
72:WW:10:ALA:HB1	72:WW:27:ILE:HD12	2.02	0.41
73:XX:68:LYS:HG2	73:XX:91:LEU:HD22	2.03	0.41
77:bb:23:ARG:NH2	77:bb:29:ASN:OD1	2.53	0.41
5:E:289:LEU:HD12	12:M:109:ARG:CZ	2.51	0.41
6:F:131:MET:HA	6:F:134:ILE:HG22	2.03	0.41
17:R:21:LYS:NZ	46:5:2821:U:OP1	2.42	0.41
29:d:24:GLU:HB3	29:d:85:ARG:NE	2.36	0.41
42:r:106:LEU:O	42:r:107:ARG:C	2.64	0.41
46:5:23:C:H2'	46:5:24:G:O4'	2.21	0.41
46:5:957:G:C2	46:5:1283:G:H2'	2.56	0.41
46:5:1590:C:H3'	46:5:1591:U:H4'	2.03	0.41
46:5:4418:G:H2'	46:5:4475:G:N2	2.36	0.41
63:NN:67:THR:OG1	63:NN:69:ASN:O	2.38	0.41
64:OO:151:LEU:HD13	64:OO:151:LEU:N	2.36	0.41
72:WW:75:ILE:HD11	72:WW:93:LEU:CD1	2.50	0.41
1:A:196:TRP:HB3	1:A:197:PRO:HD3	2.03	0.40
2:B:45:ALA:HB3	2:B:183:ILE:HG23	2.03	0.40
18:S:7:LEU:HD12	18:S:35:PRO:HD3	2.02	0.40
21:V:89:ARG:HB2	21:V:95:PHE:CE1	2.56	0.40
29:d:59:THR:HG21	29:d:90:ARG:HG3	2.01	0.40
30:e:54:LEU:HD23	30:e:60:TYR:OH	2.21	0.40
46:5:1612:G:N3	46:5:1612:G:H2'	2.37	0.40
46:5:1857:C:H2'	46:5:1858:A:C8	2.55	0.40
46:5:2863:G:C6	46:5:2864:A:C5	3.09	0.40
46:5:4190:U:O2	46:5:4381:A:C8	2.74	0.40
49:9:46:A:C6	49:9:473:A:C2	3.09	0.40
49:9:92:A:H4'	49:9:93:U:OP2	2.20	0.40
63:NN:146:ALA:O	63:NN:147:SER:C	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SS:121:ARG:HG3	68:SS:131:VAL:CG2	2.50	0.40
6:F:90:PHE:CD2	6:F:243:ILE:HD11	2.56	0.40
10:J:74:VAL:HG11	10:J:82:ILE:HD12	2.04	0.40
18:S:68:PHE:CD2	46:5:729:G:C6	3.09	0.40
46:5:288:G:C6	46:5:289:C:C4	3.09	0.40
46:5:1590:C:H4'	46:5:2857:A:H5'	2.04	0.40
46:5:4523:A:H1'	46:5:4558:U:C4	2.56	0.40
46:5:4523:A:H5''	46:5:4524:G:H5'	2.03	0.40
49:9:191:A:C2'	49:9:192:C:OP1	2.69	0.40
49:9:636:C:C4	49:9:637:U:C4	3.09	0.40
49:9:958:G:C6	49:9:959:G:C6	3.09	0.40
49:9:1064:C:O2'	64:OO:149:ARG:NH2	2.55	0.40
53:DD:162:ASP:O	53:DD:163:PRO:C	2.64	0.40
58:II:84:ASN:OD1	58:II:90:LEU:HD12	2.21	0.40
61:LL:79:LYS:HB2	61:LL:87:VAL:HB	2.02	0.40
1:A:133:TYR:CD1	1:A:168:VAL:HG12	2.56	0.40
6:F:153:ILE:HD13	6:F:210:PHE:HZ	1.87	0.40
12:M:36:ALA:HB2	12:M:52:PHE:CZ	2.57	0.40
23:X:76:ILE:HG21	23:X:112:ALA:HB2	2.03	0.40
40:o:62:THR:HG23	40:o:63:THR:N	2.36	0.40
41:p:17:ARG:CB	41:p:18:TYR:CE2	3.05	0.40
46:5:922:C:H3'	46:5:922:C:H6	1.81	0.40
46:5:1301:C:O2	46:5:1301:C:O4'	2.37	0.40
46:5:1383:G:C5	46:5:1384:C:C4	3.10	0.40
46:5:3723:A:C2	46:5:3730:U:N3	2.88	0.40
46:5:4508:C:N3	46:5:4512:U:H5	2.19	0.40
48:8:70:G:O2'	48:8:87:G:N2	2.54	0.40
49:9:164:A:O2'	56:GG:63:MET:HE1	2.22	0.40
52:CC:233:LEU:O	52:CC:234:GLY:C	2.64	0.40
3:C:101:MET:CE	46:5:2343:G:C4	3.04	0.40
8:H:41:ILE:HG12	8:H:73:ILE:HD11	2.04	0.40
12:M:7:VAL:HG13	12:M:27:ILE:HD13	2.02	0.40
21:V:20:LEU:O	21:V:55:ALA:N	2.53	0.40
35:j:4:GLY:O	35:j:5:THR:C	2.64	0.40
46:5:1353:G:N2	46:5:1504:G:C5	2.90	0.40
46:5:1689:G:H2'	46:5:1690:C:O4'	2.22	0.40
46:5:2553:A:C2	46:5:2764:A:C6	3.10	0.40
46:5:3871:A:H2'	46:5:3872:A:O4'	2.21	0.40
46:5:3890:A:N6	46:5:4570:G:O2'	2.54	0.40
49:9:620:G:C8	49:9:621:C:C5	3.10	0.40
49:9:1455:A:C2	49:9:1456:G:C8	3.08	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:CC:253:PRO:HA	52:CC:256:TRP:CD1	2.56	0.40
53:DD:179:GLN:HA	53:DD:179:GLN:HE21	1.86	0.40
60:KK:39:ASN:O	60:KK:40:VAL:C	2.65	0.40
85:jj:604:TYR:O	85:jj:605:GLN:C	2.64	0.40
5:E:58:ARG:HB3	5:E:59:TYR:CD1	2.56	0.40
14:O:17:GLY:HA3	46:5:2052:G:O3'	2.21	0.40
18:S:154:LEU:HB3	18:S:157:ARG:HD3	2.03	0.40
24:Y:8:THR:HG23	24:Y:10:ASP:HB2	2.03	0.40
31:f:88:PHE:CZ	31:f:92:LEU:HD11	2.57	0.40
46:5:1339:U:H2'	46:5:1340:C:C6	2.55	0.40
46:5:4640:C:H2'	46:5:4641:U:O4'	2.21	0.40
47:7:56:G:C8	47:7:57:C:C5	3.09	0.40
48:8:7:U:H2'	48:8:8:U:C6	2.56	0.40
48:8:15:G:C6	48:8:16:G:N1	2.89	0.40
49:9:219:U:O4'	58:II:184:ARG:NH1	2.55	0.40
49:9:446:G:OP2	58:II:47:ARG:NH1	2.55	0.40
49:9:964:A:N3	49:9:1054:G:O2'	2.46	0.40
49:9:1238:U:O2'	65:PP:126:VAL:HG12	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	246/257 (96%)	217 (88%)	25 (10%)	4 (2%)	7	37
2	B	392/403 (97%)	343 (88%)	47 (12%)	2 (0%)	24	60
3	C	360/425 (85%)	319 (89%)	32 (9%)	9 (2%)	4	29
4	D	291/297 (98%)	270 (93%)	18 (6%)	3 (1%)	12	45
5	E	208/291 (72%)	182 (88%)	25 (12%)	1 (0%)	24	60
6	F	223/247 (90%)	199 (89%)	20 (9%)	4 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	229/319 (72%)	212 (93%)	16 (7%)	1 (0%)	30	65
8	H	188/192 (98%)	168 (89%)	18 (10%)	2 (1%)	11	44
9	I	201/214 (94%)	178 (89%)	23 (11%)	0	100	100
10	J	168/178 (94%)	156 (93%)	10 (6%)	2 (1%)	10	42
11	L	208/211 (99%)	185 (89%)	21 (10%)	2 (1%)	12	45
12	M	136/218 (62%)	126 (93%)	7 (5%)	3 (2%)	5	31
13	N	201/204 (98%)	180 (90%)	17 (8%)	4 (2%)	6	33
14	O	197/203 (97%)	176 (89%)	21 (11%)	0	100	100
15	P	151/184 (82%)	138 (91%)	11 (7%)	2 (1%)	9	41
16	Q	185/188 (98%)	163 (88%)	20 (11%)	2 (1%)	11	44
17	R	178/196 (91%)	170 (96%)	8 (4%)	0	100	100
18	S	174/176 (99%)	161 (92%)	11 (6%)	2 (1%)	11	44
19	T	157/160 (98%)	141 (90%)	16 (10%)	0	100	100
20	U	97/128 (76%)	86 (89%)	9 (9%)	2 (2%)	5	32
21	V	129/140 (92%)	117 (91%)	10 (8%)	2 (2%)	7	37
22	W	102/157 (65%)	91 (89%)	10 (10%)	1 (1%)	12	45
23	X	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
24	Y	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
25	Z	133/136 (98%)	126 (95%)	5 (4%)	2 (2%)	8	38
26	a	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
27	b	100/245 (41%)	89 (89%)	10 (10%)	1 (1%)	12	45
28	c	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d	105/125 (84%)	87 (83%)	16 (15%)	2 (2%)	6	34
30	e	126/135 (93%)	116 (92%)	9 (7%)	1 (1%)	16	52
31	f	107/110 (97%)	96 (90%)	8 (8%)	3 (3%)	4	27
32	g	112/117 (96%)	98 (88%)	12 (11%)	2 (2%)	6	34
33	h	120/123 (98%)	112 (93%)	7 (6%)	1 (1%)	16	52
34	i	100/105 (95%)	91 (91%)	9 (9%)	0	100	100
35	j	84/97 (87%)	72 (86%)	11 (13%)	1 (1%)	10	42
36	k	67/70 (96%)	61 (91%)	5 (8%)	1 (2%)	8	38
37	l	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	5	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	m	50/102 (49%)	46 (92%)	3 (6%)	1 (2%)	6	33
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	89 (87%)	11 (11%)	2 (2%)	6	33
41	p	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
42	r	122/137 (89%)	103 (84%)	16 (13%)	3 (2%)	4	29
43	s	194/318 (61%)	173 (89%)	19 (10%)	2 (1%)	12	45
44	t	151/165 (92%)	135 (89%)	14 (9%)	2 (1%)	9	41
50	AA	215/295 (73%)	189 (88%)	23 (11%)	3 (1%)	9	39
51	BB	211/264 (80%)	194 (92%)	17 (8%)	0	100	100
52	CC	219/293 (75%)	202 (92%)	14 (6%)	3 (1%)	9	39
53	DD	226/243 (93%)	207 (92%)	18 (8%)	1 (0%)	30	65
54	EE	260/263 (99%)	245 (94%)	13 (5%)	2 (1%)	16	52
55	FF	181/204 (89%)	164 (91%)	14 (8%)	3 (2%)	7	36
56	GG	235/249 (94%)	221 (94%)	13 (6%)	1 (0%)	30	65
57	HH	181/194 (93%)	170 (94%)	11 (6%)	0	100	100
58	II	204/208 (98%)	187 (92%)	17 (8%)	0	100	100
59	JJ	183/194 (94%)	172 (94%)	10 (6%)	1 (0%)	24	60
60	KK	94/165 (57%)	85 (90%)	8 (8%)	1 (1%)	11	44
61	LL	139/158 (88%)	119 (86%)	19 (14%)	1 (1%)	18	54
62	MM	115/132 (87%)	97 (84%)	18 (16%)	0	100	100
63	NN	147/151 (97%)	131 (89%)	16 (11%)	0	100	100
64	OO	134/168 (80%)	116 (87%)	17 (13%)	1 (1%)	18	54
65	PP	118/145 (81%)	103 (87%)	15 (13%)	0	100	100
66	QQ	140/146 (96%)	131 (94%)	8 (6%)	1 (1%)	18	54
67	RR	130/135 (96%)	114 (88%)	15 (12%)	1 (1%)	16	52
68	SS	142/152 (93%)	134 (94%)	6 (4%)	2 (1%)	9	39
69	TT	139/145 (96%)	130 (94%)	8 (6%)	1 (1%)	18	54
70	UU	98/119 (82%)	90 (92%)	7 (7%)	1 (1%)	12	45
71	VV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
72	WW	127/130 (98%)	112 (88%)	12 (9%)	3 (2%)	4	30
73	XX	139/143 (97%)	126 (91%)	10 (7%)	3 (2%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	YY	122/130 (94%)	116 (95%)	6 (5%)	0	100	100
75	ZZ	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
76	aa	99/115 (86%)	84 (85%)	13 (13%)	2 (2%)	6	33
77	bb	81/84 (96%)	71 (88%)	9 (11%)	1 (1%)	10	42
78	cc	60/69 (87%)	55 (92%)	4 (7%)	1 (2%)	7	36
79	dd	53/56 (95%)	44 (83%)	8 (15%)	1 (2%)	6	34
80	ee	53/133 (40%)	48 (91%)	5 (9%)	0	100	100
81	ff	66/156 (42%)	60 (91%)	4 (6%)	2 (3%)	3	26
82	gg	311/317 (98%)	281 (90%)	27 (9%)	3 (1%)	12	45
84	ii	370/403 (92%)	342 (92%)	28 (8%)	0	100	100
85	jj	423/710 (60%)	383 (90%)	35 (8%)	5 (1%)	10	42
All	All	12312/14488 (85%)	11148 (90%)	1047 (8%)	117 (1%)	15	45

All (117) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	TRP
3	C	254	GLU
7	G	105	THR
18	S	155	PRO
29	d	58	GLY
31	f	107	PRO
42	r	11	ARG
42	r	68	SER
73	XX	62	PRO
85	jj	605	GLN
1	A	14	SER
3	C	71	ARG
3	C	99	GLY
3	C	275	SER
6	F	236	GLU
11	L	63	THR
12	M	9	VAL
13	N	79	ALA
13	N	89	VAL
13	N	160	GLU
20	U	24	ASP
20	U	62	SER

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Mol	Chain	Res	Type
21	V	50	ASN
22	W	27	LYS
32	g	69	LYS
33	h	89	ARG
35	j	59	THR
43	s	142	GLY
44	t	125	LEU
52	CC	232	THR
61	LL	66	VAL
64	OO	20	GLN
68	SS	78	LYS
69	TT	34	VAL
73	XX	86	PRO
4	D	44	TYR
10	J	141	ILE
12	M	61	ILE
16	Q	14	ARG
18	S	165	PRO
25	Z	91	LEU
31	f	106	TYR
37	l	49	LEU
38	m	94	ASN
54	EE	68	ARG
55	FF	43	GLU
55	FF	79	HIS
59	JJ	147	PHE
60	KK	64	TRP
72	WW	29	PRO
76	aa	47	ALA
1	A	195	CYS
1	A	217	GLN
2	B	208	SER
4	D	119	TYR
11	L	28	GLN
12	M	104	MET
21	V	51	ARG
29	d	30	HIS
36	k	20	ALA
40	o	96	ASP
42	r	34	ALA
50	AA	137	ALA
56	GG	105	ASN

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Mol	Chain	Res	Type
66	QQ	17	LYS
68	SS	118	ARG
72	WW	3	ARG
76	aa	26	CYS
77	bb	81	ARG
79	dd	7	TYR
85	jj	618	SER
2	B	17	LEU
3	C	108	TRP
3	C	155	GLU
3	C	315	LYS
5	E	181	PRO
6	F	226	PHE
15	P	21	ASN
25	Z	90	PRO
30	e	125	PRO
50	AA	159	ILE
52	CC	99	GLY
73	XX	61	GLN
81	ff	128	ALA
85	jj	271	ALA
85	jj	596	LYS
3	C	27	VAL
3	C	94	ASN
6	F	227	VAL
43	s	25	PRO
44	t	54	LYS
50	AA	102	ARG
53	DD	44	THR
54	EE	73	ASP
72	WW	56	HIS
85	jj	269	VAL
15	P	114	ILE
82	gg	224	GLY
10	J	68	ILE
16	Q	92	VAL
32	g	48	VAL
67	RR	119	VAL
70	UU	69	PRO
78	cc	25	GLY
4	D	125	VAL
6	F	136	GLU

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Mol	Chain	Res	Type
8	H	22	GLY
27	b	102	PRO
31	f	82	GLY
40	o	50	GLY
82	gg	61	GLY
8	H	30	PRO
13	N	88	GLY
52	CC	253	PRO
55	FF	21	GLY
81	ff	122	PRO
82	gg	13	GLY

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	A	190/199 (96%)	176 (93%)	14 (7%)	13	36
2	B	342/348 (98%)	309 (90%)	33 (10%)	8	28
3	C	302/347 (87%)	278 (92%)	24 (8%)	11	35
4	D	247/250 (99%)	234 (95%)	13 (5%)	20	44
5	E	190/251 (76%)	177 (93%)	13 (7%)	14	39
6	F	196/215 (91%)	178 (91%)	18 (9%)	8	30
7	G	200/272 (74%)	186 (93%)	14 (7%)	14	38
8	H	169/171 (99%)	152 (90%)	17 (10%)	7	26
9	I	175/181 (97%)	162 (93%)	13 (7%)	13	36
10	J	143/149 (96%)	133 (93%)	10 (7%)	14	38
11	L	175/176 (99%)	167 (95%)	8 (5%)	24	47
12	M	117/161 (73%)	109 (93%)	8 (7%)	14	39
13	N	171/172 (99%)	159 (93%)	12 (7%)	14	38
14	O	171/173 (99%)	153 (90%)	18 (10%)	6	24
15	P	134/163 (82%)	127 (95%)	7 (5%)	21	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	Q	164/165 (99%)	146 (89%)	18 (11%)	6	23
17	R	159/175 (91%)	145 (91%)	14 (9%)	9	32
18	S	157/157 (100%)	146 (93%)	11 (7%)	14	38
19	T	139/140 (99%)	127 (91%)	12 (9%)	10	33
20	U	89/114 (78%)	87 (98%)	2 (2%)	45	65
21	V	101/107 (94%)	87 (86%)	14 (14%)	3	17
22	W	86/126 (68%)	85 (99%)	1 (1%)	63	73
23	X	106/134 (79%)	98 (92%)	8 (8%)	12	36
24	Y	124/135 (92%)	117 (94%)	7 (6%)	19	43
25	Z	117/118 (99%)	113 (97%)	4 (3%)	32	55
26	a	119/120 (99%)	114 (96%)	5 (4%)	26	49
27	b	84/184 (46%)	80 (95%)	4 (5%)	23	46
28	c	84/98 (86%)	77 (92%)	7 (8%)	10	33
29	d	98/110 (89%)	88 (90%)	10 (10%)	7	25
30	e	114/121 (94%)	104 (91%)	10 (9%)	9	32
31	f	88/89 (99%)	80 (91%)	8 (9%)	9	30
32	g	98/100 (98%)	89 (91%)	9 (9%)	8	30
33	h	109/110 (99%)	106 (97%)	3 (3%)	38	60
34	i	86/89 (97%)	83 (96%)	3 (4%)	32	54
35	j	73/80 (91%)	64 (88%)	9 (12%)	4	20
36	k	64/65 (98%)	60 (94%)	4 (6%)	16	41
37	l	47/48 (98%)	44 (94%)	3 (6%)	16	40
38	m	48/90 (53%)	45 (94%)	3 (6%)	16	41
39	n	24/24 (100%)	21 (88%)	3 (12%)	4	20
40	o	92/94 (98%)	87 (95%)	5 (5%)	20	44
41	p	74/75 (99%)	71 (96%)	3 (4%)	27	49
42	r	108/121 (89%)	96 (89%)	12 (11%)	6	23
43	s	164/258 (64%)	158 (96%)	6 (4%)	30	52
44	t	126/137 (92%)	122 (97%)	4 (3%)	34	56
50	AA	180/245 (74%)	159 (88%)	21 (12%)	5	21
51	BB	194/231 (84%)	177 (91%)	17 (9%)	9	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	CC	187/225 (83%)	170 (91%)	17 (9%)	9	30
53	DD	190/202 (94%)	174 (92%)	16 (8%)	10	33
54	EE	224/225 (100%)	205 (92%)	19 (8%)	10	33
55	FF	158/170 (93%)	144 (91%)	14 (9%)	9	31
56	GG	207/218 (95%)	191 (92%)	16 (8%)	12	35
57	HH	165/174 (95%)	146 (88%)	19 (12%)	5	22
58	II	178/180 (99%)	167 (94%)	11 (6%)	16	41
59	JJ	161/168 (96%)	149 (92%)	12 (8%)	12	36
60	KK	87/136 (64%)	81 (93%)	6 (7%)	14	39
61	LL	130/142 (92%)	116 (89%)	14 (11%)	6	24
62	MM	99/108 (92%)	87 (88%)	12 (12%)	5	21
63	NN	130/131 (99%)	114 (88%)	16 (12%)	4	20
64	OO	106/130 (82%)	98 (92%)	8 (8%)	12	36
65	PP	109/130 (84%)	101 (93%)	8 (7%)	13	37
66	QQ	117/121 (97%)	111 (95%)	6 (5%)	21	45
67	RR	119/121 (98%)	102 (86%)	17 (14%)	3	17
68	SS	125/132 (95%)	113 (90%)	12 (10%)	8	28
69	TT	111/115 (96%)	105 (95%)	6 (5%)	20	44
70	UU	92/107 (86%)	84 (91%)	8 (9%)	9	32
71	VV	67/67 (100%)	62 (92%)	5 (8%)	12	36
72	WW	112/113 (99%)	104 (93%)	8 (7%)	13	38
73	XX	113/115 (98%)	103 (91%)	10 (9%)	9	32
74	YY	107/112 (96%)	93 (87%)	14 (13%)	4	19
75	ZZ	66/103 (64%)	60 (91%)	6 (9%)	9	30
76	aa	88/98 (90%)	77 (88%)	11 (12%)	4	20
77	bb	75/76 (99%)	67 (89%)	8 (11%)	6	24
78	cc	55/62 (89%)	50 (91%)	5 (9%)	9	30
79	dd	48/49 (98%)	47 (98%)	1 (2%)	47	65
80	ee	46/106 (43%)	41 (89%)	5 (11%)	6	23
81	ff	61/140 (44%)	53 (87%)	8 (13%)	4	19
82	gg	272/275 (99%)	259 (95%)	13 (5%)	23	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
84	ii	326/353 (92%)	311 (95%)	15 (5%)	24	47
85	jj	358/608 (59%)	330 (92%)	28 (8%)	11	35
All	All	10727/12300 (87%)	9891 (92%)	836 (8%)	14	35

All (836) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	64	ARG
1	A	102	LEU
1	A	109	GLU
1	A	130	SER
1	A	163	ARG
1	A	165	VAL
1	A	175	ILE
1	A	200	ARG
1	A	209	HIS
1	A	221	LYS
1	A	233	ARG
1	A	235	VAL
1	A	243	THR
2	B	10	ARG
2	B	17	LEU
2	B	36	ASP
2	B	53	MET
2	B	56	ILE
2	B	66	LYS
2	B	90	VAL
2	B	97	ARG
2	B	103	LYS
2	B	115	LYS
2	B	135	LYS
2	B	167	GLN
2	B	203	GLN
2	B	218	ASP
2	B	231	VAL
2	B	234	ARG
2	B	240	LEU
2	B	244	THR
2	B	248	LEU
2	B	253	CYS

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Mol	Chain	Res	Type
2	B	258	HIS
2	B	262	VAL
2	B	264	PHE
2	B	268	ARG
2	B	279	GLU
2	B	294	LYS
2	B	309	LEU
2	B	314	ILE
2	B	333	LEU
2	B	351	LEU
2	B	356	LYS
2	B	366	LYS
2	B	383	GLU
3	C	20	LYS
3	C	29	LYS
3	C	55	SER
3	C	66	SER
3	C	95	MET
3	C	124	ILE
3	C	138	MET
3	C	143	ARG
3	C	144	ILE
3	C	150	LEU
3	C	165	LYS
3	C	175	LYS
3	C	193	LYS
3	C	195	LYS
3	C	208	CYS
3	C	219	LYS
3	C	232	VAL
3	C	246	VAL
3	C	266	THR
3	C	281	MET
3	C	284	MET
3	C	307	LYS
3	C	312	ARG
3	C	322	LEU
4	D	22	ARG
4	D	33	ARG
4	D	50	ARG
4	D	56	THR
4	D	70	GLU

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Mol	Chain	Res	Type
4	D	89	LYS
4	D	104	LEU
4	D	110	LEU
4	D	124	GLU
4	D	131	ASN
4	D	202	GLN
4	D	262	LYS
4	D	264	LYS
5	E	52	LEU
5	E	58	ARG
5	E	112	LEU
5	E	143	LEU
5	E	144	ARG
5	E	155	ILE
5	E	169	LYS
5	E	178	VAL
5	E	197	VAL
5	E	213	LYS
5	E	215	LEU
5	E	242	LYS
5	E	289	LEU
6	F	38	GLN
6	F	46	ARG
6	F	65	ARG
6	F	67	GLU
6	F	73	MET
6	F	88	LEU
6	F	97	ILE
6	F	100	VAL
6	F	134	ILE
6	F	151	GLU
6	F	178	LEU
6	F	186	MET
6	F	187	GLU
6	F	189	LEU
6	F	198	LYS
6	F	211	LYS
6	F	231	ASP
6	F	245	ARG
7	G	97	ASP
7	G	105	THR
7	G	116	LEU

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Mol	Chain	Res	Type
7	G	139	VAL
7	G	163	LYS
7	G	184	LYS
7	G	203	LYS
7	G	204	LYS
7	G	207	LEU
7	G	220	VAL
7	G	223	LEU
7	G	226	LEU
7	G	230	MET
7	G	312	LYS
8	H	1	MET
8	H	12	ILE
8	H	24	THR
8	H	41	ILE
8	H	46	SER
8	H	52	LYS
8	H	57	VAL
8	H	59	LYS
8	H	66	GLU
8	H	74	CYS
8	H	94	SER
8	H	105	ILE
8	H	108	ASN
8	H	128	MET
8	H	129	ARG
8	H	141	LYS
8	H	173	ARG
9	I	36	LEU
9	I	39	LYS
9	I	76	MET
9	I	97	ILE
9	I	116	ARG
9	I	123	GLN
9	I	142	LEU
9	I	153	ARG
9	I	163	GLN
9	I	164	LYS
9	I	195	CYS
9	I	197	VAL
9	I	208	LYS
10	J	16	ARG

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Mol	Chain	Res	Type
10	J	28	GLU
10	J	33	LEU
10	J	72	CYS
10	J	81	GLU
10	J	83	LEU
10	J	96	LYS
10	J	113	ILE
10	J	151	ILE
10	J	175	LEU
11	L	10	LEU
11	L	59	VAL
11	L	61	CYS
11	L	63	THR
11	L	106	SER
11	L	129	ARG
11	L	162	LYS
11	L	186	ARG
12	M	2	VAL
12	M	32	ASP
12	M	37	LEU
12	M	57	LEU
12	M	61	ILE
12	M	62	LEU
12	M	96	GLU
12	M	105	THR
13	N	9	GLU
13	N	15	GLN
13	N	44	ARG
13	N	47	LYS
13	N	64	ILE
13	N	72	LYS
13	N	75	VAL
13	N	77	LYS
13	N	104	GLU
13	N	151	ILE
13	N	182	HIS
13	N	199	GLN
14	O	16	LEU
14	O	27	VAL
14	O	37	ARG
14	O	42	ASN
14	O	49	ARG

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Mol	Chain	Res	Type
14	O	61	ARG
14	O	67	SER
14	O	82	ARG
14	O	85	ARG
14	O	128	ARG
14	O	130	LYS
14	O	140	ARG
14	O	145	VAL
14	O	165	LYS
14	O	175	MET
14	O	179	LYS
14	O	188	LYS
14	O	196	LEU
15	P	10	ASN
15	P	21	ASN
15	P	24	VAL
15	P	70	CYS
15	P	86	LYS
15	P	128	ARG
15	P	147	GLU
16	Q	3	VAL
16	Q	5	ILE
16	Q	13	VAL
16	Q	31	LEU
16	Q	42	THR
16	Q	63	LEU
16	Q	72	LEU
16	Q	75	ARG
16	Q	78	LYS
16	Q	91	ARG
16	Q	95	VAL
16	Q	101	CYS
16	Q	112	ARG
16	Q	115	LYS
16	Q	138	LEU
16	Q	143	ARG
16	Q	169	SER
16	Q	188	ASN
17	R	6	LEU
17	R	10	LEU
17	R	15	LEU
17	R	36	ASN

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Mol	Chain	Res	Type
17	R	40	GLN
17	R	50	ILE
17	R	82	LYS
17	R	89	MET
17	R	99	MET
17	R	103	ARG
17	R	106	LEU
17	R	113	LYS
17	R	138	LEU
17	R	178	GLN
18	S	7	LEU
18	S	9	GLU
18	S	17	LEU
18	S	70	LYS
18	S	75	VAL
18	S	92	ASN
18	S	95	ARG
18	S	102	THR
18	S	149	LYS
18	S	159	LEU
18	S	174	THR
19	T	5	LYS
19	T	33	ILE
19	T	35	LYS
19	T	52	MET
19	T	55	LYS
19	T	60	LYS
19	T	96	ILE
19	T	113	ASP
19	T	142	ARG
19	T	144	ASN
19	T	157	GLU
19	T	159	MET
20	U	33	ILE
20	U	83	LEU
21	V	15	ARG
21	V	18	LEU
21	V	25	VAL
21	V	35	LYS
21	V	45	ILE
21	V	57	VAL
21	V	60	MET

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Mol	Chain	Res	Type
21	V	69	LYS
21	V	71	GLU
21	V	80	VAL
21	V	82	ILE
21	V	91	LYS
21	V	109	LYS
21	V	123	LYS
22	W	30	GLN
23	X	39	LYS
23	X	52	LEU
23	X	53	ARG
23	X	57	GLN
23	X	59	LYS
23	X	63	LYS
23	X	97	VAL
23	X	111	GLN
24	Y	2	LYS
24	Y	8	THR
24	Y	28	LYS
24	Y	55	VAL
24	Y	72	GLN
24	Y	74	TYR
24	Y	104	VAL
25	Z	3	LYS
25	Z	11	VAL
25	Z	31	ASP
25	Z	83	THR
26	a	16	SER
26	a	56	VAL
26	a	59	ARG
26	a	84	GLU
26	a	122	VAL
27	b	9	THR
27	b	22	LYS
27	b	40	LEU
27	b	101	HIS
28	c	23	LYS
28	c	37	MET
28	c	50	ASN
28	c	78	ASN
28	c	81	LEU
28	c	83	THR

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Mol	Chain	Res	Type
28	c	92	CYS
29	d	23	ARG
29	d	26	THR
29	d	44	ARG
29	d	48	GLU
29	d	56	GLU
29	d	78	ARG
29	d	79	ASN
29	d	85	ARG
29	d	98	SER
29	d	105	LEU
30	e	9	LYS
30	e	11	LYS
30	e	21	ILE
30	e	64	LYS
30	e	78	LEU
30	e	86	GLU
30	e	87	VAL
30	e	89	LEU
30	e	106	LYS
30	e	128	ARG
31	f	5	LEU
31	f	7	CYS
31	f	23	GLU
31	f	33	VAL
31	f	52	LYS
31	f	73	LYS
31	f	76	ARG
31	f	101	ILE
32	g	6	THR
32	g	21	ARG
32	g	22	LEU
32	g	32	TYR
32	g	60	ARG
32	g	66	ARG
32	g	90	ARG
32	g	102	ILE
32	g	114	GLN
33	h	28	LEU
33	h	67	GLU
33	h	88	THR
34	i	34	THR

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Mol	Chain	Res	Type
34	i	86	LYS
34	i	89	GLU
35	j	3	LYS
35	j	15	THR
35	j	20	ARG
35	j	33	THR
35	j	34	CYS
35	j	36	LYS
35	j	58	THR
35	j	59	THR
35	j	79	ARG
36	k	37	ARG
36	k	59	SER
36	k	69	LEU
36	k	70	LYS
37	l	2	SER
37	l	3	SER
37	l	49	LEU
38	m	71	ARG
38	m	72	LYS
38	m	92	THR
39	n	1	MET
39	n	2	ARG
39	n	13	LEU
40	o	17	LYS
40	o	24	THR
40	o	28	LYS
40	o	61	LYS
40	o	82	MET
41	p	8	VAL
41	p	62	LYS
41	p	70	THR
42	r	2	SER
42	r	8	MET
42	r	20	ARG
42	r	26	SER
42	r	32	LEU
42	r	35	ARG
42	r	39	ARG
42	r	67	ARG
42	r	78	VAL
42	r	90	LEU

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Mol	Chain	Res	Type
42	r	106	LEU
42	r	118	LEU
43	s	38	LYS
43	s	95	LEU
43	s	105	ASN
43	s	146	LYS
43	s	187	LEU
43	s	191	GLN
44	t	37	LEU
44	t	72	GLU
44	t	98	ILE
44	t	133	LEU
50	AA	5	LEU
50	AA	9	GLN
50	AA	12	GLU
50	AA	25	LEU
50	AA	34	MET
50	AA	46	ILE
50	AA	50	ASN
50	AA	56	GLU
50	AA	58	LEU
50	AA	60	LEU
50	AA	85	ARG
50	AA	111	GLN
50	AA	122	LEU
50	AA	124	VAL
50	AA	132	GLN
50	AA	134	LEU
50	AA	136	GLU
50	AA	138	SER
50	AA	142	LEU
50	AA	155	ARG
50	AA	178	LEU
51	BB	38	MET
51	BB	47	THR
51	BB	50	THR
51	BB	63	LYS
51	BB	71	LEU
51	BB	74	LEU
51	BB	82	ARG
51	BB	96	CYS
51	BB	105	LEU

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Mol	Chain	Res	Type
51	BB	157	GLN
51	BB	172	MET
51	BB	173	THR
51	BB	175	GLU
51	BB	181	LEU
51	BB	207	LEU
51	BB	209	ASP
51	BB	213	ARG
52	CC	66	LEU
52	CC	78	LEU
52	CC	114	LYS
52	CC	115	GLN
52	CC	117	ARG
52	CC	121	ARG
52	CC	137	VAL
52	CC	139	LEU
52	CC	165	VAL
52	CC	167	ARG
52	CC	192	LEU
52	CC	230	THR
52	CC	233	LEU
52	CC	235	ASN
52	CC	244	ILE
52	CC	251	LEU
52	CC	255	LEU
53	DD	22	ASN
53	DD	28	GLU
53	DD	31	GLU
53	DD	51	LEU
53	DD	55	THR
53	DD	65	ARG
53	DD	106	ARG
53	DD	127	MET
53	DD	134	CYS
53	DD	146	ARG
53	DD	168	VAL
53	DD	179	GLN
53	DD	190	LEU
53	DD	212	GLU
53	DD	218	LEU
53	DD	220	THR
54	EE	6	LYS

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Mol	Chain	Res	Type
54	EE	17	HIS
54	EE	41	CYS
54	EE	42	LEU
54	EE	48	LEU
54	EE	51	ARG
54	EE	66	MET
54	EE	67	GLN
54	EE	77	ARG
54	EE	105	THR
54	EE	115	THR
54	EE	171	ASP
54	EE	180	LEU
54	EE	222	LEU
54	EE	225	ILE
54	EE	232	ASN
54	EE	240	ARG
54	EE	246	LEU
54	EE	247	THR
55	FF	36	GLN
55	FF	37	ASP
55	FF	49	LEU
55	FF	52	SER
55	FF	71	ARG
55	FF	83	ASN
55	FF	88	MET
55	FF	89	THR
55	FF	122	ARG
55	FF	123	GLU
55	FF	146	ARG
55	FF	168	THR
55	FF	195	GLU
55	FF	204	ARG
56	GG	41	LEU
56	GG	59	GLN
56	GG	63	MET
56	GG	67	VAL
56	GG	76	LEU
56	GG	78	SER
56	GG	88	ARG
56	GG	98	ARG
56	GG	100	CYS
56	GG	159	ARG

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Mol	Chain	Res	Type
56	GG	171	THR
56	GG	178	ARG
56	GG	181	THR
56	GG	190	ARG
56	GG	216	ARG
56	GG	230	LYS
57	HH	8	ILE
57	HH	36	LEU
57	HH	40	LEU
57	HH	45	ILE
57	HH	46	THR
57	HH	61	ILE
57	HH	76	GLN
57	HH	79	LEU
57	HH	82	GLU
57	HH	100	ILE
57	HH	105	THR
57	HH	119	SER
57	HH	120	ARG
57	HH	145	ARG
57	HH	151	SER
57	HH	158	LEU
57	HH	162	GLN
57	HH	171	GLU
57	HH	188	GLU
58	II	6	ASP
58	II	23	LYS
58	II	45	THR
58	II	49	ARG
58	II	121	LEU
58	II	130	THR
58	II	161	LEU
58	II	168	GLN
58	II	175	ILE
58	II	178	ARG
58	II	190	LEU
59	JJ	29	LEU
59	JJ	38	ARG
59	JJ	45	ARG
59	JJ	50	LEU
59	JJ	61	LEU
59	JJ	80	ARG

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Mol	Chain	Res	Type
59	JJ	89	GLU
59	JJ	116	LYS
59	JJ	128	VAL
59	JJ	133	ARG
59	JJ	152	ASP
59	JJ	176	LYS
60	KK	1	MET
60	KK	22	VAL
60	KK	50	GLN
60	KK	60	GLU
60	KK	89	ILE
60	KK	96	ARG
61	LL	16	ILE
61	LL	39	ASN
61	LL	40	ILE
61	LL	42	LEU
61	LL	52	GLU
61	LL	66	VAL
61	LL	69	ARG
61	LL	85	THR
61	LL	111	VAL
61	LL	113	LEU
61	LL	126	VAL
61	LL	132	ARG
61	LL	134	LEU
61	LL	135	SER
62	MM	16	THR
62	MM	19	GLN
62	MM	31	LEU
62	MM	33	ARG
62	MM	40	LYS
62	MM	45	ARG
62	MM	56	CYS
62	MM	76	LEU
62	MM	80	ASP
62	MM	85	LEU
62	MM	99	LYS
62	MM	101	ARG
63	NN	9	LYS
63	NN	12	SER
63	NN	20	ARG
63	NN	27	LYS

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Mol	Chain	Res	Type
63	NN	53	ILE
63	NN	55	ARG
63	NN	60	VAL
63	NN	75	LEU
63	NN	78	LYS
63	NN	83	ASP
63	NN	84	LEU
63	NN	86	GLU
63	NN	94	LYS
63	NN	107	LYS
63	NN	125	LEU
63	NN	132	LYS
64	OO	38	ASN
64	OO	40	THR
64	OO	51	GLU
64	OO	56	VAL
64	OO	114	SER
64	OO	146	ARG
64	OO	150	ARG
64	OO	151	LEU
65	PP	13	ARG
65	PP	14	LYS
65	PP	37	TYR
65	PP	44	ARG
65	PP	78	THR
65	PP	83	MET
65	PP	89	MET
65	PP	108	LYS
66	QQ	7	LEU
66	QQ	26	LYS
66	QQ	31	LEU
66	QQ	40	GLU
66	QQ	46	THR
66	QQ	140	ARG
67	RR	7	LYS
67	RR	22	THR
67	RR	30	THR
67	RR	31	ASN
67	RR	44	LYS
67	RR	49	LYS
67	RR	55	THR
67	RR	62	GLN

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Mol	Chain	Res	Type
67	RR	70	SER
67	RR	78	ARG
67	RR	89	SER
67	RR	98	VAL
67	RR	99	ASP
67	RR	109	LEU
67	RR	114	LEU
67	RR	123	THR
67	RR	132	ARG
68	SS	7	GLU
68	SS	8	LYS
68	SS	14	ARG
68	SS	23	ARG
68	SS	46	ARG
68	SS	49	ASP
68	SS	59	LEU
68	SS	60	THR
68	SS	76	GLN
68	SS	83	PHE
68	SS	86	ARG
68	SS	132	ARG
69	TT	39	LEU
69	TT	55	THR
69	TT	62	ARG
69	TT	102	ARG
69	TT	110	LEU
69	TT	124	THR
70	UU	18	HIS
70	UU	25	THR
70	UU	48	LEU
70	UU	56	MET
70	UU	60	THR
70	UU	68	THR
70	UU	70	CYS
70	UU	106	ILE
71	VV	2	GLN
71	VV	10	ASP
71	VV	12	TYR
71	VV	32	ILE
71	VV	66	ASP
72	WW	7	LEU
72	WW	12	LYS

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Mol	Chain	Res	Type
72	WW	23	ARG
72	WW	51	GLU
72	WW	52	ILE
72	WW	70	ASN
72	WW	83	LEU
72	WW	103	VAL
73	XX	7	LEU
73	XX	19	ASP
73	XX	29	LYS
73	XX	61	GLN
73	XX	67	ARG
73	XX	98	ASP
73	XX	115	ILE
73	XX	127	ASN
73	XX	129	SER
73	XX	130	LEU
74	YY	9	THR
74	YY	16	ARG
74	YY	17	LEU
74	YY	20	ARG
74	YY	40	ILE
74	YY	44	LEU
74	YY	47	MET
74	YY	61	ARG
74	YY	74	MET
74	YY	80	ASP
74	YY	88	LYS
74	YY	101	LYS
74	YY	114	MET
74	YY	115	LYS
75	ZZ	52	LYS
75	ZZ	58	LEU
75	ZZ	80	ARG
75	ZZ	89	GLN
75	ZZ	92	LEU
75	ZZ	110	THR
76	aa	12	LYS
76	aa	18	VAL
76	aa	19	GLN
76	aa	21	ILE
76	aa	33	ASP
76	aa	41	ILE

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Mol	Chain	Res	Type
76	aa	44	ILE
76	aa	55	GLU
76	aa	84	VAL
76	aa	96	THR
76	aa	100	ARG
77	bb	17	ARG
77	bb	34	ASP
77	bb	37	CYS
77	bb	42	LYS
77	bb	48	SER
77	bb	64	CYS
77	bb	80	ARG
77	bb	81	ARG
78	cc	20	ARG
78	cc	31	ARG
78	cc	40	ARG
78	cc	44	ARG
78	cc	51	ARG
79	dd	6	LEU
80	ee	85	VAL
80	ee	97	LYS
80	ee	99	LYS
80	ee	109	MET
80	ee	113	ARG
81	ff	83	LYS
81	ff	92	LYS
81	ff	94	LYS
81	ff	99	LYS
81	ff	114	ILE
81	ff	132	MET
81	ff	138	ARG
81	ff	140	TYR
82	gg	17	TRP
82	gg	20	GLN
82	gg	36	ARG
82	gg	87	LEU
82	gg	119	GLN
82	gg	133	ASN
82	gg	198	VAL
82	gg	207	CYS
82	gg	273	GLU
82	gg	287	THR

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Mol	Chain	Res	Type
82	gg	289	LEU
82	gg	298	LEU
82	gg	306	LEU
84	ii	8	ILE
84	ii	40	ARG
84	ii	90	GLU
84	ii	107	ASN
84	ii	112	LEU
84	ii	149	ILE
84	ii	156	MET
84	ii	170	LYS
84	ii	172	LYS
84	ii	198	HIS
84	ii	243	VAL
84	ii	311	LEU
84	ii	313	ILE
84	ii	319	ARG
84	ii	349	LEU
85	jj	269	VAL
85	jj	297	GLN
85	jj	298	GLU
85	jj	313	LEU
85	jj	330	MET
85	jj	361	GLN
85	jj	367	LEU
85	jj	369	VAL
85	jj	385	GLN
85	jj	389	HIS
85	jj	408	MET
85	jj	425	LEU
85	jj	434	PHE
85	jj	436	GLU
85	jj	489	ARG
85	jj	499	GLN
85	jj	505	ILE
85	jj	521	LEU
85	jj	534	ILE
85	jj	557	MET
85	jj	585	ILE
85	jj	586	LEU
85	jj	600	VAL
85	jj	613	ILE

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Mol	Chain	Res	Type
85	jj	616	LEU
85	jj	640	ASN
85	jj	653	LEU
85	jj	664	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (173) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	ASN
1	A	162	ASN
1	A	217	GLN
2	B	55	HIS
2	B	138	GLN
2	B	167	GLN
2	B	245	HIS
2	B	271	GLN
2	B	354	GLN
3	C	203	GLN
3	C	212	ASN
3	C	310	HIS
4	D	9	ASN
4	D	45	ASN
4	D	191	ASN
4	D	244	HIS
5	E	131	HIS
5	E	185	ASN
5	E	193	HIS
5	E	194	GLN
6	F	109	GLN
6	F	130	ASN
6	F	171	ASN
6	F	191	HIS
6	F	247	ASN
7	G	138	GLN
7	G	143	GLN
7	G	147	GLN
7	G	194	ASN
7	G	293	ASN
8	H	39	ASN
8	H	63	ASN
8	H	98	HIS
8	H	102	ASN

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Mol	Chain	Res	Type
8	H	108	ASN
9	I	95	HIS
9	I	100	ASN
9	I	123	GLN
11	L	87	HIS
11	L	104	ASN
11	L	159	ASN
12	M	66	HIS
12	M	70	GLN
13	N	182	HIS
14	O	50	ASN
14	O	199	HIS
15	P	56	GLN
15	P	97	ASN
15	P	137	ASN
16	Q	44	ASN
17	R	34	ASN
17	R	130	ASN
17	R	141	HIS
17	R	158	GLN
18	S	163	HIS
19	T	3	ASN
19	T	98	HIS
19	T	131	GLN
22	W	17	HIS
22	W	30	GLN
23	X	57	GLN
23	X	73	HIS
23	X	105	ASN
24	Y	18	HIS
24	Y	20	ASN
24	Y	56	GLN
25	Z	28	ASN
26	a	19	HIS
26	a	62	HIS
28	c	72	HIS
28	c	78	ASN
29	d	18	ASN
29	d	34	HIS
29	d	121	ASN
30	e	92	ASN
31	f	78	HIS

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Mol	Chain	Res	Type
32	g	14	ASN
32	g	110	GLN
33	h	108	GLN
34	i	20	ASN
37	l	4	HIS
40	o	19	GLN
40	o	21	HIS
40	o	102	GLN
43	s	34	ASN
43	s	126	GLN
43	s	179	ASN
44	t	65	GLN
44	t	95	GLN
50	AA	24	HIS
50	AA	29	ASN
50	AA	113	GLN
50	AA	132	GLN
51	BB	75	GLN
51	BB	163	GLN
51	BB	208	HIS
52	CC	136	HIS
53	DD	22	ASN
53	DD	159	HIS
53	DD	179	GLN
54	EE	67	GLN
54	EE	157	ASN
54	EE	161	GLN
54	EE	188	ASN
54	EE	209	HIS
55	FF	83	ASN
55	FF	95	HIS
55	FF	107	ASN
55	FF	118	ASN
56	GG	177	GLN
56	GG	186	GLN
56	GG	187	HIS
57	HH	73	GLN
57	HH	97	GLN
57	HH	126	HIS
58	II	87	ASN
58	II	99	ASN
58	II	138	ASN

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Mol	Chain	Res	Type
58	II	146	GLN
60	KK	39	ASN
60	KK	61	GLN
60	KK	84	HIS
61	LL	18	GLN
61	LL	19	ASN
61	LL	100	ASN
62	MM	19	GLN
62	MM	55	ASN
62	MM	75	ASN
63	NN	49	GLN
63	NN	105	ASN
64	OO	32	HIS
66	QQ	8	GLN
66	QQ	24	HIS
66	QQ	48	GLN
66	QQ	142	GLN
67	RR	26	ASN
67	RR	31	ASN
67	RR	121	GLN
68	SS	10	GLN
68	SS	72	GLN
69	TT	83	GLN
70	UU	18	HIS
71	VV	35	ASN
71	VV	47	ASN
71	VV	49	GLN
73	XX	77	ASN
74	YY	15	ASN
74	YY	29	HIS
75	ZZ	45	ASN
75	ZZ	89	GLN
75	ZZ	103	HIS
76	aa	8	ASN
76	aa	19	GLN
76	aa	86	ASN
77	bb	26	GLN
77	bb	49	HIS
79	dd	3	HIS
81	ff	93	HIS
82	gg	14	HIS
82	gg	76	GLN

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Mol	Chain	Res	Type
82	gg	159	ASN
82	gg	187	ASN
82	gg	196	ASN
84	ii	188	GLN
84	ii	244	HIS
84	ii	298	GLN
84	ii	358	GLN
85	jj	268	HIS
85	jj	279	HIS
85	jj	361	GLN
85	jj	481	GLN
85	jj	549	HIS
85	jj	605	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	2	72/75 (96%)	17 (23%)	1 (1%)
45	3	72/75 (96%)	23 (31%)	1 (1%)
46	5	3511/3543 (99%)	949 (27%)	179 (5%)
47	7	119/120 (99%)	19 (15%)	3 (2%)
48	8	149/156 (95%)	40 (26%)	6 (4%)
49	9	1682/1869 (89%)	456 (27%)	88 (5%)
83	hh	7/8 (87%)	4 (57%)	0
All	All	5612/5846 (95%)	1508 (26%)	278 (4%)

All (1508) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	2	7	A
45	2	13	C
45	2	16	C
45	2	21	A
45	2	25	C
45	2	34	U
45	2	35	U
45	2	36	U
45	2	40	C
45	2	42	G
45	2	47	U
45	2	49	C

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Mol	Chain	Res	Type
45	2	61	C
45	2	63	C
45	2	72	C
45	2	75	C
45	2	76	A
45	3	7	A
45	3	13	C
45	3	14	A
45	3	16	C
45	3	21	A
45	3	25	C
45	3	28	C
45	3	29	A
45	3	34	U
45	3	35	U
45	3	36	U
45	3	40	C
45	3	42	G
45	3	47	U
45	3	49	C
45	3	58	A
45	3	60	U
45	3	61	C
45	3	63	C
45	3	72	C
45	3	74	C
45	3	75	C
45	3	76	A
46	5	12	A
46	5	13	U
46	5	14	C
46	5	17	A
46	5	20	U
46	5	21	G
46	5	25	A
46	5	35	U
46	5	39	A
46	5	42	A
46	5	43	U
46	5	44	A
46	5	48	G
46	5	49	U

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Mol	Chain	Res	Type
46	5	56	A
46	5	58	G
46	5	59	A
46	5	64	A
46	5	65	A
46	5	72	C
46	5	73	A
46	5	75	G
46	5	84	A
46	5	91	G
46	5	93	G
46	5	108	A
46	5	109	G
46	5	110	C
46	5	116	G
46	5	118	C
46	5	119	G
46	5	120	A
46	5	125	C
46	5	126	C
46	5	134	G
46	5	135	G
46	5	136	C
46	5	137	G
46	5	143	C
46	5	144	G
46	5	146	G
46	5	157	U
46	5	159	C
46	5	160	G
46	5	172	C
46	5	173	C
46	5	177	G
46	5	179	G
46	5	197	A
46	5	200	U
46	5	201	C
46	5	202	C
46	5	205	C
46	5	209	U
46	5	216	C
46	5	217	C

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Mol	Chain	Res	Type
46	5	218	A
46	5	220	C
46	5	221	C
46	5	224	U
46	5	225	G
46	5	226	G
46	5	227	A
46	5	233	U
46	5	234	G
46	5	245	C
46	5	246	G
46	5	253	G
46	5	262	G
46	5	265	C
46	5	266	C
46	5	267	G
46	5	275	C
46	5	276	C
46	5	279	A
46	5	280	G
46	5	281	U
46	5	297	U
46	5	306	A
46	5	308	G
46	5	309	C
46	5	310	G
46	5	315	G
46	5	316	U
46	5	321	U
46	5	322	C
46	5	328	A
46	5	334	A
46	5	340	C
46	5	347	A
46	5	349	A
46	5	350	C
46	5	357	U
46	5	361	C
46	5	363	A
46	5	365	U
46	5	381	U
46	5	386	A

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Mol	Chain	Res	Type
46	5	387	G
46	5	399	G
46	5	401	G
46	5	406	C
46	5	407	A
46	5	409	G
46	5	410	A
46	5	412	G
46	5	413	G
46	5	414	C
46	5	417	G
46	5	418	A
46	5	431	G
46	5	432	U
46	5	433	A
46	5	440	U
46	5	446	C
46	5	449	C
46	5	450	G
46	5	452	A
46	5	453	G
46	5	454	U
46	5	457	G
46	5	463	A
46	5	466	A
46	5	467	U
46	5	468	U
46	5	469	C
46	5	482	G
46	5	483	G
46	5	484	U
46	5	485	C
46	5	486	C
46	5	492	U
46	5	493	G
46	5	495	C
46	5	497	G
46	5	498	C
46	5	499	G
46	5	505	G
46	5	510	U
46	5	647	G

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Mol	Chain	Res	Type
46	5	649	A
46	5	654	C
46	5	658	C
46	5	666	G
46	5	667	A
46	5	668	C
46	5	672	C
46	5	683	C
46	5	685	C
46	5	687	U
46	5	696	C
46	5	697	G
46	5	704	C
46	5	705	G
46	5	708	G
46	5	729	G
46	5	730	G
46	5	731	G
46	5	738(A)	C
46	5	739	G
46	5	742	G
46	5	744	G
46	5	747	A
46	5	748	G
46	5	749	G
46	5	750	U
46	5	758	G
46	5	911	U
46	5	913	U
46	5	914	U
46	5	917	A
46	5	918	G
46	5	922(A)	G
46	5	922(B)	C
46	5	923	C
46	5	924	C
46	5	925	C
46	5	926	G
46	5	929	A
46	5	931	C
46	5	932	A
46	5	933	G

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Mol	Chain	Res	Type
46	5	934	C
46	5	936	C
46	5	938	C
46	5	939	G
46	5	941	C
46	5	944	A
46	5	945	U
46	5	955	G
46	5	956	A
46	5	957	G
46	5	959	G
46	5	960	A
46	5	961	G
46	5	962	C
46	5	965	G
46	5	966	A
46	5	967	C
46	5	968	C
46	5	969	C
46	5	970	G
46	5	972	C
46	5	973	G
46	5	978	G
46	5	979	C
46	5	983	C
46	5	990	C
46	5	1070	G
46	5	1072	C
46	5	1073	G
46	5	1075	G
46	5	1076	C
46	5	1078	A
46	5	1079	C
46	5	1082	C
46	5	1174	G
46	5	1179	U
46	5	1195	G
46	5	1209	U
46	5	1210	C
46	5	1211	G
46	5	1212	G
46	5	1214	C

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Mol	Chain	Res	Type
46	5	1215	C
46	5	1234	G
46	5	1235	G
46	5	1236	C
46	5	1237	C
46	5	1238	A
46	5	1239	C
46	5	1272	C
46	5	1273	G
46	5	1274	A
46	5	1275	G
46	5	1276	C
46	5	1280	C
46	5	1284	G
46	5	1287	G
46	5	1288	G
46	5	1291	G
46	5	1292	C
46	5	1293	G
46	5	1295	U
46	5	1296	G
46	5	1301	C
46	5	1303	A
46	5	1304	C
46	5	1324	A
46	5	1325	C
46	5	1326	A
46	5	1329	G
46	5	1330	A
46	5	1337	A
46	5	1354	A
46	5	1359	G
46	5	1364	U
46	5	1370	G
46	5	1371	A
46	5	1377	G
46	5	1378	C
46	5	1380	G
46	5	1381	U
46	5	1387	A
46	5	1388	A
46	5	1394	G

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Mol	Chain	Res	Type
46	5	1397	A
46	5	1398	A
46	5	1401	C
46	5	1411(B)	C
46	5	1411(C)	C
46	5	1412	G
46	5	1416	G
46	5	1419	G
46	5	1420	A
46	5	1421	G
46	5	1422	G
46	5	1429	C
46	5	1432	G
46	5	1433	A
46	5	1435	G
46	5	1436	C
46	5	1437	C
46	5	1438	U
46	5	1441	C
46	5	1442	C
46	5	1445	U
46	5	1446	C
46	5	1453	G
46	5	1455	G
46	5	1456	C
46	5	1457	G
46	5	1458	C
46	5	1465	G
46	5	1475	G
46	5	1478	C
46	5	1481	C
46	5	1482	G
46	5	1483	C
46	5	1484	G
46	5	1485	C
46	5	1486	C
46	5	1497	A
46	5	1498	G
46	5	1502	G
46	5	1503	A
46	5	1504	G
46	5	1514	U

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Mol	Chain	Res	Type
46	5	1516	G
46	5	1518	A
46	5	1523	A
46	5	1525	A
46	5	1534	A
46	5	1535	C
46	5	1547	A
46	5	1554	A
46	5	1563	A
46	5	1564	A
46	5	1566	C
46	5	1568	C
46	5	1578	U
46	5	1586	G
46	5	1591	U
46	5	1596	U
46	5	1602	U
46	5	1612	G
46	5	1613	A
46	5	1617	G
46	5	1624	G
46	5	1625	G
46	5	1628	C
46	5	1631	A
46	5	1633	G
46	5	1634	A
46	5	1640	C
46	5	1645	C
46	5	1649	U
46	5	1650	A
46	5	1652	U
46	5	1654	G
46	5	1656	U
46	5	1661	C
46	5	1670	G
46	5	1676	C
46	5	1677	U
46	5	1678	C
46	5	1679	A
46	5	1683	U
46	5	1691	G
46	5	1694	C

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Mol	Chain	Res	Type
46	5	1724	G
46	5	1729	A
46	5	1733	G
46	5	1734	G
46	5	1740	C
46	5	1741	G
46	5	1742	A
46	5	1750	G
46	5	1753	G
46	5	1755	C
46	5	1756	U
46	5	1757	U
46	5	1761	G
46	5	1763	C
46	5	1764	G
46	5	1768	C
46	5	1772	C
46	5	1773	U
46	5	1776	A
46	5	1781	U
46	5	1787	A
46	5	1799	G
46	5	1803	G
46	5	1804	A
46	5	1805	A
46	5	1812	C
46	5	1819	G
46	5	1821	G
46	5	1822	U
46	5	1828	C
46	5	1833	G
46	5	1834	U
46	5	1835	G
46	5	1836	G
46	5	1837	A
46	5	1842	G
46	5	1855	G
46	5	1867	A
46	5	1869	G
46	5	1882	U
46	5	1891	A
46	5	1892	A

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Mol	Chain	Res	Type
46	5	1893	C
46	5	1897	A
46	5	1899	G
46	5	1910	G
46	5	1918	U
46	5	1920	C
46	5	1921	C
46	5	1922	G
46	5	1923	A
46	5	1931	C
46	5	1938	C
46	5	1941	A
46	5	1947	U
46	5	1948	G
46	5	1956	A
46	5	1961	G
46	5	1962	A
46	5	1967	A
46	5	1976	G
46	5	1977	C
46	5	1978	C
46	5	1980	U
46	5	1982	G
46	5	1983	A
46	5	1984	A
46	5	1986	U
46	5	1987	C
46	5	1991	A
46	5	1992	U
46	5	1993	C
46	5	1997	U
46	5	2001	G
46	5	2002	A
46	5	2003	G
46	5	2005	G
46	5	2008	U
46	5	2011	C
46	5	2016	C
46	5	2017	A
46	5	2024	G
46	5	2025	A
46	5	2026	A

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Mol	Chain	Res	Type
46	5	2046	G
46	5	2047	A
46	5	2048	U
46	5	2052	G
46	5	2055	G
46	5	2056	G
46	5	2062	C
46	5	2064	G
46	5	2068	C
46	5	2069	A
46	5	2077	C
46	5	2084	U
46	5	2085	G
46	5	2089	G
46	5	2090	U
46	5	2092	G
46	5	2093	G
46	5	2094	C
46	5	2095	A
46	5	2097	A
46	5	2098	G
46	5	2100	G
46	5	2101	A
46	5	2102	G
46	5	2104	A
46	5	2105	A
46	5	2106	G
46	5	2107	A
46	5	2108	G
46	5	2110	G
46	5	2259	G
46	5	2260	C
46	5	2262	G
46	5	2266	C
46	5	2267	U
46	5	2268	A
46	5	2269	C
46	5	2270	G
46	5	2274	C
46	5	2275	G
46	5	2277	C
46	5	2279	A

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Mol	Chain	Res	Type
46	5	2288	G
46	5	2289	C
46	5	2300	A
46	5	2301	G
46	5	2313	A
46	5	2314	G
46	5	2333	G
46	5	2344	U
46	5	2348	G
46	5	2351	C
46	5	2352	U
46	5	2360	A
46	5	2364	G
46	5	2366	A
46	5	2370	A
46	5	2372	U
46	5	2395	A
46	5	2396	A
46	5	2397	G
46	5	2399	G
46	5	2402	G
46	5	2416	G
46	5	2417	A
46	5	2421	G
46	5	2422	C
46	5	2425	U
46	5	2433	G
46	5	2441	C
46	5	2447	U
46	5	2450	G
46	5	2453	A
46	5	2467	U
46	5	2468	U
46	5	2470	C
46	5	2471	G
46	5	2475	G
46	5	2476	G
46	5	2483	G
46	5	2485	U
46	5	2488	C
46	5	2489	C
46	5	2490	U

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Mol	Chain	Res	Type
46	5	2491	C
46	5	2495	U
46	5	2503	G
46	5	2504	C
46	5	2505	C
46	5	2506	G
46	5	2513	A
46	5	2521	G
46	5	2530	U
46	5	2537	A
46	5	2546	G
46	5	2547	G
46	5	2549	G
46	5	2553	A
46	5	2554	U
46	5	2555	G
46	5	2566	G
46	5	2575	U
46	5	2583	C
46	5	2586	G
46	5	2587	A
46	5	2601	A
46	5	2611	A
46	5	2612	G
46	5	2620	G
46	5	2627	C
46	5	2638	G
46	5	2639	U
46	5	2640	G
46	5	2647	A
46	5	2660	A
46	5	2661	U
46	5	2662	G
46	5	2663	G
46	5	2669	C
46	5	2670	C
46	5	2676	A
46	5	2679	G
46	5	2681	G
46	5	2686	G
46	5	2687	U
46	5	2695	A

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Mol	Chain	Res	Type
46	5	2696	A
46	5	2704	C
46	5	2707	U
46	5	2708	U
46	5	2709	C
46	5	2710	C
46	5	2711	G
46	5	2712	G
46	5	2714	G
46	5	2716	C
46	5	2719	C
46	5	2721	G
46	5	2724	G
46	5	2725	A
46	5	2726	G
46	5	2740	U
46	5	2743	A
46	5	2744	A
46	5	2754	G
46	5	2760	G
46	5	2761	U
46	5	2763	U
46	5	2764	A
46	5	2769	U
46	5	2770	C
46	5	2772	C
46	5	2787	A
46	5	2788	U
46	5	2789	A
46	5	2790	U
46	5	2795	A
46	5	2798	A
46	5	2799	G
46	5	2806	A
46	5	2807	A
46	5	2808	G
46	5	2814	C
46	5	2826	U
46	5	2827	G
46	5	2828	U
46	5	2829	U
46	5	2835	A

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Mol	Chain	Res	Type
46	5	2838	G
46	5	2842	G
46	5	2844	A
46	5	2846	G
46	5	2855	G
46	5	2869	U
46	5	2879	A
46	5	2884	G
46	5	2896	G
46	5	2897	G
46	5	3598	C
46	5	3599	A
46	5	3604	A
46	5	3605	C
46	5	3606	U
46	5	3615	G
46	5	3618	C
46	5	3620	G
46	5	3621	A
46	5	3625	G
46	5	3626	G
46	5	3635	A
46	5	3644	U
46	5	3653	A
46	5	3662	A
46	5	3673	C
46	5	3674	G
46	5	3692	A
46	5	3696	C
46	5	3698	G
46	5	3711	A
46	5	3712	A
46	5	3722	G
46	5	3729	U
46	5	3740	G
46	5	3747	A
46	5	3748	A
46	5	3750	G
46	5	3753	G
46	5	3759	A
46	5	3760	A
46	5	3761	C

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Mol	Chain	Res	Type
46	5	3765	G
46	5	3766	A
46	5	3773	U
46	5	3774	A
46	5	3776	G
46	5	3777	G
46	5	3778	U
46	5	3780	G
46	5	3784	A
46	5	3786	U
46	5	3798	U
46	5	3799	A
46	5	3809	G
46	5	3810	C
46	5	3811	G
46	5	3813	A
46	5	3814	U
46	5	3817	A
46	5	3819	G
46	5	3822	U
46	5	3831	U
46	5	3839	G
46	5	3840	U
46	5	3859	G
46	5	3867	A
46	5	3876	A
46	5	3877	A
46	5	3878	C
46	5	3879	G
46	5	3880	G
46	5	3888	G
46	5	3889	G
46	5	3892	U
46	5	3897	G
46	5	3901	A
46	5	3905	A
46	5	3906	A
46	5	3907	G
46	5	3914	U
46	5	3915	U
46	5	3916	G
46	5	3917	A

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Mol	Chain	Res	Type
46	5	3923	A
46	5	3926	C
46	5	3927	U
46	5	3939	G
46	5	3943	A
46	5	4067	U
46	5	4069	U
46	5	4073	A
46	5	4076	G
46	5	4084	G
46	5	4085	A
46	5	4086	G
46	5	4088	C
46	5	4092	G
46	5	4099	G
46	5	4100	C
46	5	4116	C
46	5	4117	U
46	5	4118	U
46	5	4119	C
46	5	4120	U
46	5	4121	G
46	5	4122	G
46	5	4125	C
46	5	4127	A
46	5	4136	G
46	5	4138	C
46	5	4161	G
46	5	4162	C
46	5	4163	U
46	5	4164	C
46	5	4165	C
46	5	4166	G
46	5	4171	C
46	5	4183	G
46	5	4184	G
46	5	4191	G
46	5	4197	G
46	5	4201	G
46	5	4203	A
46	5	4205	A
46	5	4212	A

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Mol	Chain	Res	Type
46	5	4213	A
46	5	4214	A
46	5	4218	U
46	5	4219	A
46	5	4221	C
46	5	4222	G
46	5	4225	G
46	5	4229	U
46	5	4232	U
46	5	4233	A
46	5	4237	C
46	5	4251	A
46	5	4255	A
46	5	4257	A
46	5	4258	C
46	5	4266	G
46	5	4267	G
46	5	4268	A
46	5	4271	A
46	5	4273	A
46	5	4281	A
46	5	4291	G
46	5	4292	A
46	5	4297	G
46	5	4304	A
46	5	4305	G
46	5	4306	U
46	5	4307	A
46	5	4311	A
46	5	4314	C
46	5	4317	A
46	5	4319	C
46	5	4329	G
46	5	4330	G
46	5	4331	G
46	5	4335	C
46	5	4336	A
46	5	4349	C
46	5	4350	C
46	5	4354	U
46	5	4355	G
46	5	4368	G

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Mol	Chain	Res	Type
46	5	4373	G
46	5	4376	A
46	5	4377	G
46	5	4378	A
46	5	4379	A
46	5	4380	A
46	5	4382	G
46	5	4387	C
46	5	4391	G
46	5	4394	A
46	5	4395	U
46	5	4396	A
46	5	4398	C
46	5	4401	G
46	5	4415	A
46	5	4419	U
46	5	4421	C
46	5	4422	A
46	5	4433	G
46	5	4437	U
46	5	4438	U
46	5	4440	G
46	5	4444	C
46	5	4447	C
46	5	4448	G
46	5	4449	A
46	5	4450	U
46	5	4453	C
46	5	4463	U
46	5	4464	A
46	5	4466	C
46	5	4471	U
46	5	4475	G
46	5	4476	C
46	5	4487	A
46	5	4488	A
46	5	4489	G
46	5	4495	G
46	5	4500	U
46	5	4511	A
46	5	4512	U
46	5	4513	A

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Mol	Chain	Res	Type
46	5	4515	G
46	5	4518	A
46	5	4519	C
46	5	4520	G
46	5	4524	G
46	5	4527	G
46	5	4528	G
46	5	4531	U
46	5	4532	U
46	5	4548	A
46	5	4549	G
46	5	4560	C
46	5	4567	G
46	5	4572	U
46	5	4573	G
46	5	4575	G
46	5	4578	G
46	5	4583	C
46	5	4584	A
46	5	4585	U
46	5	4586	G
46	5	4589	A
46	5	4590	A
46	5	4599	A
46	5	4606	G
46	5	4635	A
46	5	4636	U
46	5	4637	G
46	5	4652	G
46	5	4656	A
46	5	4661	G
46	5	4668	U
46	5	4670	C
46	5	4671	C
46	5	4672	A
46	5	4677	U
46	5	4678	G
46	5	4682	U
46	5	4694	G
46	5	4699	U
46	5	4700	A
46	5	4701	A

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Mol	Chain	Res	Type
46	5	4709	U
46	5	4718	G
46	5	4719	G
46	5	4720	C
46	5	4721	G
46	5	4728	U
46	5	4729	A
46	5	4736	C
46	5	4737	G
46	5	4745	G
46	5	4751	G
46	5	4754	G
46	5	4755	G
46	5	4756	C
46	5	4757	C
46	5	4759	C
46	5	4761	G
46	5	4764	A
46	5	4765	G
46	5	4771	C
46	5	4772	C
46	5	4868	G
46	5	4870	G
46	5	4871	C
46	5	4872	G
46	5	4873	G
46	5	4874	A
46	5	4875	G
46	5	4876	A
46	5	4877	G
46	5	4881	U
46	5	4882	U
46	5	4883	C
46	5	4885	U
46	5	4887	C
46	5	4891	G
46	5	4895	C
46	5	4897	G
46	5	4902	C
46	5	4910	A
46	5	4911	A
46	5	4913	G

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Mol	Chain	Res	Type
46	5	4914	G
46	5	4915	G
46	5	4919	G
46	5	4921	C
46	5	4922	C
46	5	4924	C
46	5	4926	C
46	5	4927	G
46	5	4928	C
46	5	4931	G
46	5	4935	C
46	5	4937	C
46	5	4938	A
46	5	4940	C
46	5	4943	A
46	5	4944	C
46	5	4945	G
46	5	4948	C
46	5	4949	G
46	5	4950	U
46	5	4951	G
46	5	4956	A
46	5	4957	C
46	5	4958	C
46	5	4964	C
46	5	4965	U
46	5	4966	A
46	5	4967	A
46	5	4976	U
46	5	4985	U
46	5	4988	U
46	5	4989	U
46	5	4990	C
46	5	4991	U
46	5	4994	G
46	5	4997	G
46	5	4999	G
46	5	5007	A
46	5	5013	C
46	5	5014	A
46	5	5017	G
46	5	5021	C

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Mol	Chain	Res	Type
46	5	5035	U
46	5	5040	U
46	5	5041	G
46	5	5047	C
46	5	5050	C
46	5	5053	U
46	5	5054	C
46	5	5056	A
46	5	5061	A
46	5	5062	G
46	5	5066	U
47	7	7	G
47	7	10	C
47	7	22	A
47	7	25	G
47	7	33	U
47	7	38	U
47	7	41	G
47	7	42	A
47	7	53	U
47	7	54	A
47	7	64	G
47	7	76	U
47	7	97	G
47	7	99	G
47	7	100	A
47	7	109	U
47	7	110	G
47	7	111	C
47	7	120	U
48	8	2	G
48	8	3	A
48	8	22	U
48	8	23	C
48	8	24	G
48	8	32	C
48	8	34	U
48	8	35	C
48	8	49	G
48	8	51	U
48	8	52	A
48	8	57	C

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Mol	Chain	Res	Type
48	8	59	A
48	8	62	A
48	8	63	U
48	8	75	G
48	8	79	G
48	8	86	U
48	8	87	G
48	8	94	G
48	8	95	A
48	8	99	U
48	8	101	C
48	8	103	A
48	8	104	A
48	8	105	C
48	8	109	C
48	8	110	U
48	8	111	U
48	8	112	G
48	8	114	G
48	8	121	G
48	8	123	U
48	8	124	U
48	8	125	C
48	8	126	C
48	8	127	U
48	8	137	A
48	8	143	G
48	8	156	U
49	9	2	A
49	9	3	C
49	9	4	C
49	9	17	C
49	9	25	A
49	9	26	U
49	9	33	G
49	9	37	C
49	9	41	G
49	9	44	U
49	9	45	A
49	9	46	A
49	9	56	G
49	9	58	C

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Mol	Chain	Res	Type
49	9	60	A
49	9	63	U
49	9	65	C
49	9	67	C
49	9	68	A
49	9	70	G
49	9	71	G
49	9	73	C
49	9	74	G
49	9	75	G
49	9	77	A
49	9	79	A
49	9	99	A
49	9	100	U
49	9	103	A
49	9	104	A
49	9	110	U
49	9	111	A
49	9	113	G
49	9	115	U
49	9	116	U
49	9	124	U
49	9	126	G
49	9	127	C
49	9	128	U
49	9	129	C
49	9	130	G
49	9	141	A
49	9	142	C
49	9	143	U
49	9	147	A
49	9	155	G
49	9	158	A
49	9	161	U
49	9	162	C
49	9	163	U
49	9	167	G
49	9	168	C
49	9	173	A
49	9	175	A
49	9	182	C
49	9	183	G

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Mol	Chain	Res	Type
49	9	184	G
49	9	188	C
49	9	189	U
49	9	191	A
49	9	192	C
49	9	200	G
49	9	202	G
49	9	206	G
49	9	213	G
49	9	215	G
49	9	292	A
49	9	302	A
49	9	304	C
49	9	307	G
49	9	308	G
49	9	309	G
49	9	312	G
49	9	314	U
49	9	315	C
49	9	317	C
49	9	318	A
49	9	319	C
49	9	322	C
49	9	331	C
49	9	332	G
49	9	340	C
49	9	347	G
49	9	351	G
49	9	360	A
49	9	362	C
49	9	363	A
49	9	364	A
49	9	368	U
49	9	370	G
49	9	371	A
49	9	372	U
49	9	379	C
49	9	381	C
49	9	382	C
49	9	383	G
49	9	384	U
49	9	385	G

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Mol	Chain	Res	Type
49	9	386	C
49	9	398	A
49	9	400	C
49	9	407	G
49	9	409	C
49	9	417	C
49	9	418	A
49	9	434	G
49	9	435	A
49	9	438	G
49	9	441	C
49	9	448	A
49	9	449	A
49	9	450	C
49	9	452	G
49	9	459	C
49	9	460	A
49	9	462	C
49	9	463	C
49	9	464	A
49	9	465	A
49	9	466	G
49	9	472	C
49	9	473	A
49	9	474	G
49	9	476	A
49	9	482	G
49	9	485	A
49	9	487	U
49	9	492	C
49	9	496	C
49	9	501	C
49	9	508	A
49	9	523	A
49	9	525	A
49	9	531	A
49	9	532	C
49	9	533	A
49	9	544	G
49	9	545	A
49	9	546	G
49	9	548	C

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Mol	Chain	Res	Type
49	9	549	C
49	9	550	C
49	9	551	U
49	9	554	A
49	9	555	A
49	9	556	U
49	9	559	G
49	9	560	A
49	9	562	U
49	9	563	G
49	9	564	A
49	9	568	C
49	9	576	A
49	9	583	A
49	9	587	A
49	9	588	G
49	9	589	G
49	9	590	A
49	9	591	U
49	9	592	C
49	9	594	A
49	9	595	U
49	9	597	G
49	9	604	A
49	9	606	G
49	9	607	U
49	9	608	C
49	9	613	G
49	9	614	C
49	9	615	C
49	9	616	A
49	9	617	G
49	9	620	G
49	9	626	G
49	9	627	U
49	9	628	A
49	9	629	A
49	9	631	U
49	9	632	C
49	9	642	U
49	9	643	A
49	9	644	G

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Mol	Chain	Res	Type
49	9	646	G
49	9	659	G
49	9	660	C
49	9	663	C
49	9	664	A
49	9	668	A
49	9	669	A
49	9	670	A
49	9	671	A
49	9	672	A
49	9	678	U
49	9	684	G
49	9	688	U
49	9	689	U
49	9	696	G
49	9	733	C
49	9	752	G
49	9	753	C
49	9	754	G
49	9	798	G
49	9	811	A
49	9	812	A
49	9	821	G
49	9	822	U
49	9	827	A
49	9	830	A
49	9	834	C
49	9	844	U
49	9	847	A
49	9	869	A
49	9	870	A
49	9	871	U
49	9	872	A
49	9	873	G
49	9	874	G
49	9	875	A
49	9	876	C
49	9	877	C
49	9	878	G
49	9	885	U
49	9	887	U
49	9	890	U

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Mol	Chain	Res	Type
49	9	892	U
49	9	913	A
49	9	914	U
49	9	919	A
49	9	920	A
49	9	921	G
49	9	922	A
49	9	930	C
49	9	933	G
49	9	934	G
49	9	943	U
49	9	954	U
49	9	971	G
49	9	985	G
49	9	990	A
49	9	992	A
49	9	999	G
49	9	1016	U
49	9	1017	U
49	9	1023	A
49	9	1032	C
49	9	1041	G
49	9	1044	G
49	9	1055	A
49	9	1060	A
49	9	1061	U
49	9	1062	A
49	9	1078	C
49	9	1082	A
49	9	1083	A
49	9	1085	C
49	9	1086	G
49	9	1089	G
49	9	1100	A
49	9	1111	U
49	9	1114	U
49	9	1115	U
49	9	1116	C
49	9	1117	C
49	9	1118	C
49	9	1119	A
49	9	1121	G

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Mol	Chain	Res	Type
49	9	1123	C
49	9	1131	G
49	9	1133	A
49	9	1138	C
49	9	1139	C
49	9	1143	A
49	9	1144	A
49	9	1148	A
49	9	1149	A
49	9	1153	C
49	9	1154	U
49	9	1157	G
49	9	1161	U
49	9	1165	G
49	9	1166	G
49	9	1195	A
49	9	1196	A
49	9	1207	G
49	9	1208	A
49	9	1211	G
49	9	1214	A
49	9	1215	C
49	9	1216	C
49	9	1224	G
49	9	1240	A
49	9	1242	U
49	9	1251	A
49	9	1253	A
49	9	1254	C
49	9	1255	G
49	9	1256	G
49	9	1257	G
49	9	1259	A
49	9	1260	A
49	9	1265	A
49	9	1266	C
49	9	1271	C
49	9	1274	G
49	9	1275	G
49	9	1280	G
49	9	1281	G
49	9	1284	A

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Mol	Chain	Res	Type
49	9	1285	G
49	9	1286	G
49	9	1287	A
49	9	1293	A
49	9	1298	G
49	9	1299	A
49	9	1300	U
49	9	1301	A
49	9	1302	G
49	9	1303	C
49	9	1304	U
49	9	1307	U
49	9	1308	U
49	9	1313	A
49	9	1314	U
49	9	1316	C
49	9	1330	G
49	9	1331	C
49	9	1342	U
49	9	1345	G
49	9	1348	G
49	9	1354	G
49	9	1369	A
49	9	1371	U
49	9	1372	U
49	9	1376	A
49	9	1378	A
49	9	1394	G
49	9	1395	C
49	9	1396	A
49	9	1397	U
49	9	1402	A
49	9	1404	U
49	9	1405	A
49	9	1412	C
49	9	1424	G
49	9	1428	G
49	9	1429	G
49	9	1439	A
49	9	1449	G
49	9	1454	A
49	9	1455	A

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Mol	Chain	Res	Type
49	9	1459	G
49	9	1462	U
49	9	1463	U
49	9	1466	G
49	9	1473	G
49	9	1475	G
49	9	1476	A
49	9	1477	U
49	9	1478	U
49	9	1480	A
49	9	1487	A
49	9	1490	G
49	9	1494	U
49	9	1498	A
49	9	1509	U
49	9	1510	G
49	9	1519	U
49	9	1520	G
49	9	1521	C
49	9	1522	A
49	9	1523	C
49	9	1531	A
49	9	1533	A
49	9	1536	G
49	9	1544	C
49	9	1545	A
49	9	1548	G
49	9	1552	G
49	9	1553	C
49	9	1555	U
49	9	1556	A
49	9	1557	C
49	9	1560	U
49	9	1570	G
49	9	1574	C
49	9	1575	G
49	9	1580	A
49	9	1581	C
49	9	1582	C
49	9	1585	U
49	9	1587	G
49	9	1588	A

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Mol	Chain	Res	Type
49	9	1600	G
49	9	1601	A
49	9	1604	G
49	9	1621	U
49	9	1623	A
49	9	1625	U
49	9	1633	A
49	9	1637	A
49	9	1638	G
49	9	1639	G
49	9	1641	A
49	9	1647	A
49	9	1648	G
49	9	1649	U
49	9	1654	G
49	9	1663	A
49	9	1664	A
49	9	1665	G
49	9	1667	U
49	9	1671	G
49	9	1680	G
49	9	1683	C
49	9	1695	A
49	9	1698	C
49	9	1715	A
49	9	1721	U
49	9	1722	G
49	9	1726	G
49	9	1728	U
49	9	1729	U
49	9	1730	U
49	9	1732	G
49	9	1744	G
49	9	1745	A
49	9	1746	U
49	9	1753	C
49	9	1758	G
49	9	1760	G
49	9	1772	C
49	9	1783	C
49	9	1785	C
49	9	1800	A

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Mol	Chain	Res	Type
49	9	1801	A
49	9	1805	G
49	9	1823	A
49	9	1824	A
49	9	1825	A
49	9	1826	G
49	9	1829	G
49	9	1831	A
49	9	1834	A
49	9	1835	A
49	9	1836	G
49	9	1838	U
49	9	1839	U
49	9	1849	G
49	9	1851	A
49	9	1861	G
49	9	1862	G
49	9	1863	A
49	9	1865	C
49	9	1866	A
49	9	1867	U
49	9	1869	A
83	hh	42	A
83	hh	43	A
83	hh	45	A
83	hh	46	A

All (278) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	2	71	G
45	3	74	C
46	5	12	A
46	5	20	U
46	5	47	A
46	5	48	G
46	5	64	A
46	5	90	G
46	5	119	G
46	5	125	C
46	5	134	G
46	5	143	C

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Mol	Chain	Res	Type
46	5	159	C
46	5	217	C
46	5	224	U
46	5	226	G
46	5	232	G
46	5	245	C
46	5	265	C
46	5	275	C
46	5	278	G
46	5	308	G
46	5	315	G
46	5	385	A
46	5	406	C
46	5	409	G
46	5	417	G
46	5	449	C
46	5	453	G
46	5	484	U
46	5	485	C
46	5	492	U
46	5	497	G
46	5	498	C
46	5	504	G
46	5	696	C
46	5	725	G
46	5	728	U
46	5	729	G
46	5	738(A)	C
46	5	746	A
46	5	747	A
46	5	916	C
46	5	922	C
46	5	922(B)	C
46	5	930	G
46	5	935(A)	G
46	5	936	C
46	5	955	G
46	5	956	A
46	5	959	G
46	5	966	A
46	5	968	C
46	5	969	C

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Mol	Chain	Res	Type
46	5	971(A)	G
46	5	978	G
46	5	1072	C
46	5	1209	U
46	5	1211	G
46	5	1214	C
46	5	1236	C
46	5	1238	A
46	5	1287	G
46	5	1291	G
46	5	1295	U
46	5	1324	A
46	5	1329	G
46	5	1358	G
46	5	1370	G
46	5	1378	C
46	5	1432	G
46	5	1440	U
46	5	1445	U
46	5	1455	G
46	5	1477	C
46	5	1481	C
46	5	1484	G
46	5	1485	C
46	5	1497	A
46	5	1502	G
46	5	1625	G
46	5	1633	G
46	5	1654	G
46	5	1678	C
46	5	1724	G
46	5	1733	G
46	5	1740	C
46	5	1804	A
46	5	1818	G
46	5	1833	G
46	5	1834	U
46	5	1835	G
46	5	1892	A
46	5	1908	A
46	5	1921	C
46	5	1947	U

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Mol	Chain	Res	Type
46	5	1983	A
46	5	1986	U
46	5	2046	G
46	5	2054	U
46	5	2068	C
46	5	2088	A
46	5	2089	G
46	5	2090	U
46	5	2100	G
46	5	2103	A
46	5	2265	G
46	5	2266	C
46	5	2278	G
46	5	2313	A
46	5	2396	A
46	5	2398	U
46	5	2425	U
46	5	2428	A
46	5	2467	U
46	5	2474	G
46	5	2475	G
46	5	2490	U
46	5	2502	A
46	5	2530	U
46	5	2546	G
46	5	2553	A
46	5	2661	U
46	5	2695	A
46	5	2696	A
46	5	2724	G
46	5	2754	G
46	5	2769	U
46	5	2789	A
46	5	2806	A
46	5	3603	G
46	5	3625	G
46	5	3673	C
46	5	3697	U
46	5	3710	G
46	5	3759	A
46	5	3760	A
46	5	3765	G

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Mol	Chain	Res	Type
46	5	3809	G
46	5	3876	A
46	5	3888	G
46	5	3904	G
46	5	4075	U
46	5	4076	G
46	5	4084	G
46	5	4116	C
46	5	4119	C
46	5	4121	G
46	5	4124	G
46	5	4157	A
46	5	4162	C
46	5	4170	A
46	5	4204	C
46	5	4221	C
46	5	4232	U
46	5	4254	G
46	5	4266	G
46	5	4291	G
46	5	4331	G
46	5	4378	A
46	5	4379	A
46	5	4395	U
46	5	4448	G
46	5	4449	A
46	5	4463	U
46	5	4475	G
46	5	4527	G
46	5	4583	C
46	5	4635	A
46	5	4671	C
46	5	4699	U
46	5	4718	G
46	5	4719	G
46	5	4873	G
46	5	4884	G
46	5	4925	U
46	5	4936	G
46	5	4942	C
46	5	4947	U
46	5	4965	U

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Mol	Chain	Res	Type
46	5	5013	C
47	7	10	C
47	7	41	G
47	7	109	U
48	8	23	C
48	8	51	U
48	8	86	U
48	8	94	G
48	8	110	U
48	8	124	U
49	9	2	A
49	9	3	C
49	9	25	A
49	9	72	C
49	9	87	U
49	9	98	C
49	9	110	U
49	9	126	G
49	9	127	C
49	9	128	U
49	9	142	C
49	9	160	U
49	9	182	C
49	9	191	A
49	9	214	U
49	9	293	C
49	9	312	G
49	9	314	U
49	9	360	A
49	9	363	A
49	9	369	C
49	9	434	G
49	9	448	A
49	9	465	A
49	9	516	A
49	9	532	C
49	9	553	U
49	9	555	A
49	9	559	G
49	9	563	G
49	9	587	A
49	9	591	U

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Mol	Chain	Res	Type
49	9	594	A
49	9	613	G
49	9	626	G
49	9	627	U
49	9	628	A
49	9	642	U
49	9	670	A
49	9	688	U
49	9	752	G
49	9	821	G
49	9	869	A
49	9	870	A
49	9	872	A
49	9	875	A
49	9	1016	U
49	9	1087	A
49	9	1114	U
49	9	1137	U
49	9	1165	G
49	9	1253	A
49	9	1259	A
49	9	1264	C
49	9	1274	G
49	9	1284	A
49	9	1285	G
49	9	1313	A
49	9	1330	G
49	9	1394	G
49	9	1395	C
49	9	1396	A
49	9	1454	A
49	9	1476	A
49	9	1489	A
49	9	1493	C
49	9	1519	U
49	9	1520	G
49	9	1535	U
49	9	1578	U
49	9	1581	C
49	9	1584	G
49	9	1621	U
49	9	1636	G

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Mol	Chain	Res	Type
49	9	1637	A
49	9	1646	C
49	9	1663	A
49	9	1664	A
49	9	1679	A
49	9	1682	C
49	9	1697	A
49	9	1721	U
49	9	1744	G
49	9	1824	A
49	9	1825	A
49	9	1835	A
49	9	1867	U
49	9	1868	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 245 ligands modelled in this entry, 244 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	GCP	jj	700	86	32,34,34	1.40	7 (21%)	49,54,54	1.82	7 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	GCP	jj	700	86	-	3/19/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	jj	700	GCP	C5-C4	3.31	1.47	1.38
88	jj	700	GCP	PG-O2G	2.86	1.61	1.55
88	jj	700	GCP	PG-O3G	2.79	1.61	1.55
88	jj	700	GCP	C5-N7	-2.08	1.34	1.39
88	jj	700	GCP	C6-N1	-2.07	1.35	1.38
88	jj	700	GCP	PB-O2B	2.02	1.61	1.56
88	jj	700	GCP	PB-O3A	2.00	1.60	1.58

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	jj	700	GCP	C5-C4-N3	-6.19	118.54	128.39
88	jj	700	GCP	C2-N3-C4	5.22	121.30	112.30
88	jj	700	GCP	N9-C4-N3	4.45	134.86	125.95
88	jj	700	GCP	PB-O3A-PA	-3.57	120.71	132.37
88	jj	700	GCP	C6-C5-N7	3.37	136.43	130.29
88	jj	700	GCP	C4-C5-N7	-2.77	106.29	110.67
88	jj	700	GCP	O6-C6-C5	-2.12	120.95	126.53

There are no chirality outliers.

All (3) torsion outliers are listed below:

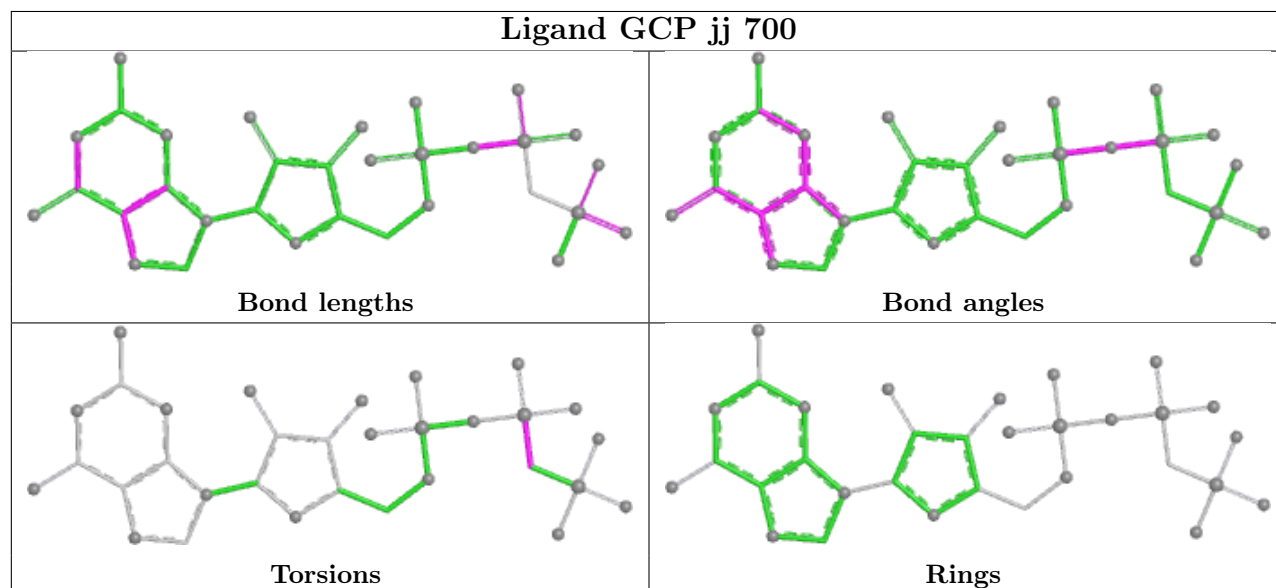
Mol	Chain	Res	Type	Atoms
88	jj	700	GCP	PG-C3B-PB-O1B
88	jj	700	GCP	PG-C3B-PB-O3A
88	jj	700	GCP	PG-C3B-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	5	42
49	9	7
45	3	2
45	2	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	40.66
1	5	1252:C	O3'	1271:G	P	36.39
1	5	1405:C	O3'	1406:G	P	23.89

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1219:G	O3'	1233:G	P	22.08
1	5	1406:G	O3'	1406(A):G	P	20.74
1	5	3948:C	O3'	4065:G	P	19.58
1	5	523:C	O3'	638:G	P	18.11
1	5	4138:C	O3'	4146:G	P	17.87
1	5	990:C	O3'	1064:G	P	17.71
1	5	4101:C	O3'	4107:G	P	17.24
1	5	4777:C	O3'	4859:C	P	16.45
1	5	5022:U	O3'	5028:G	P	15.42
1	5	760:G	O3'	904:C	P	15.08
1	5	1696:C	O3'	1720:C	P	14.92
1	5	1364:U	O3'	1368:A	P	14.40
1	5	182:G	O3'	189:G	P	13.89
1	5	2901:G	O3'	3597:G	P	13.20
1	5	1406(C):G	O3'	1411:C	P	13.13
1	5	1411:C	O3'	1411(A):G	P	12.97
1	5	481:G	O3'	481(A):C	P	12.34
1	5	921:C	O3'	922:C	P	12.33
1	5	934:C	O3'	935:A	P	10.70
1	5	970:G	O3'	971:U	P	10.66
1	5	737:C	O3'	738:C	P	10.59
1	5	971:U	O3'	971(A):G	P	9.97
1	5	512:U	O3'	515:C	P	9.68
1	5	4729:A	O3'	4735:G	P	9.50
1	5	1180:C	O3'	1183:C	P	9.31
1	5	500:G	O3'	504:G	P	7.18
1	5	1100:U	O3'	1168:G	P	6.11
1	3	19:G	O3'	20:U	P	5.51
1	2	19:G	O3'	20:U	P	5.30
1	5	4740:G	O3'	4743:G	P	5.20
1	2	16:C	O3'	18:U	P	5.18
1	5	480:C	O3'	481:G	P	5.17
1	9	322:C	O3'	323:C	P	5.05
1	3	16:C	O3'	18:U	P	4.93
1	9	304:C	O3'	305:U	P	4.29
1	9	798:G	O3'	799:U	P	4.28
1	9	309:G	O3'	310:C	P	4.21
1	5	1239:C	O3'	1244:G	P	4.20
1	5	935:A	O3'	935(A):G	P	4.08
1	5	170:C	O3'	171:U	P	3.84
1	5	1438:U	O3'	1440:U	P	3.64
1	5	4899:G	O3'	4902:C	P	3.41

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	9	902:G	O3'	903:A	P	3.38
1	5	738:C	O3'	738(A):C	P	3.34
1	9	903:A	O3'	904:A	P	3.30
1	9	1295:A	O3'	1296:U	P	3.19
1	5	267:G	O3'	268:G	P	3.10
1	5	5020:G	O3'	5021:C	P	3.05
1	5	751:G	O3'	752:G	P	3.02
1	5	2031:C	O3'	2032:U	P	2.80

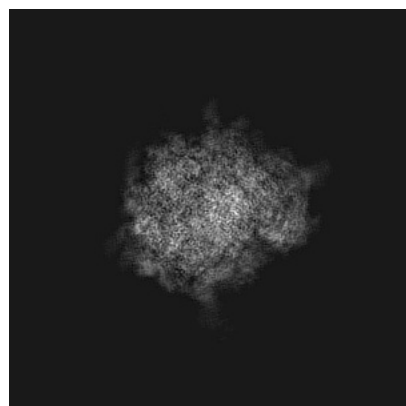
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4136. These allow visual inspection of the internal detail of the map and identification of artifacts.

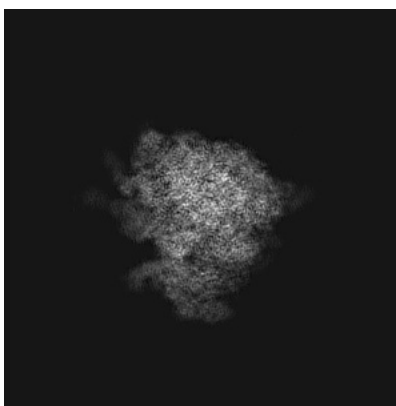
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

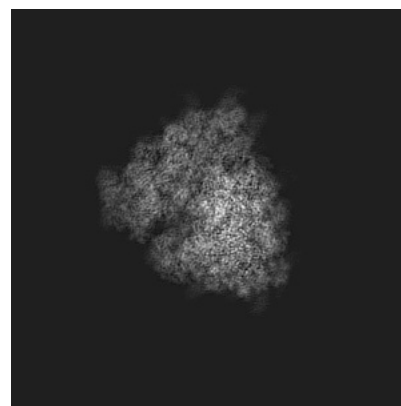
6.1.1 Primary map



X

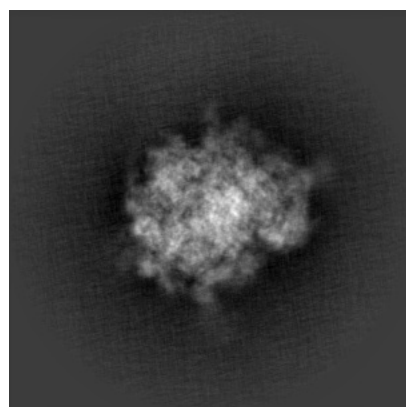


Y

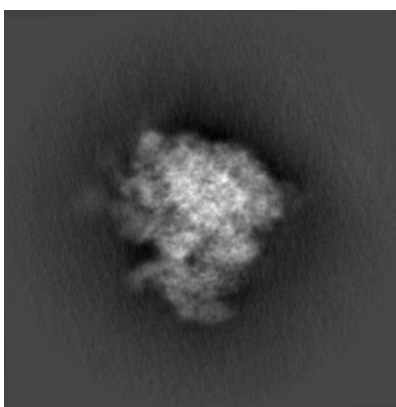


Z

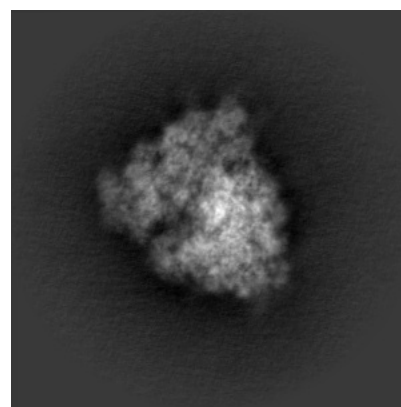
6.1.2 Raw map



X



Y

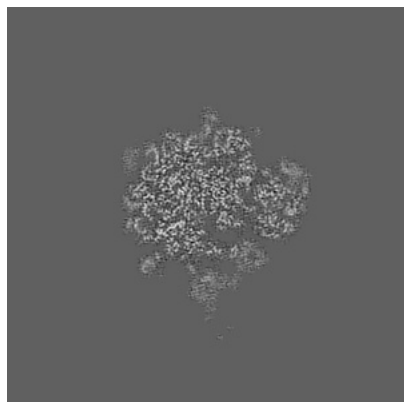


Z

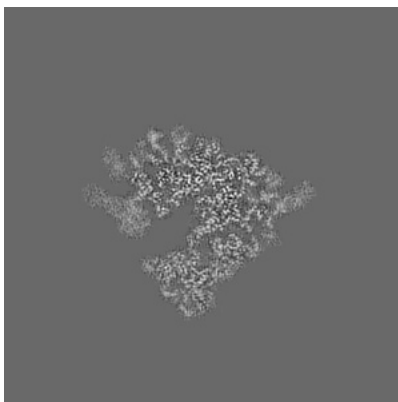
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

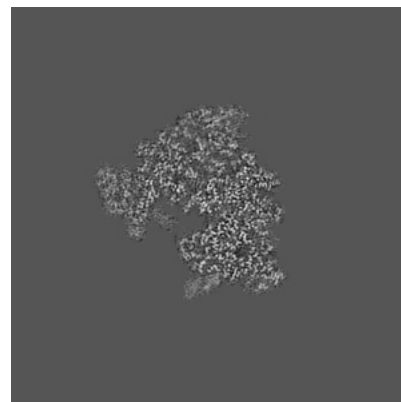
6.2.1 Primary map



X Index: 210

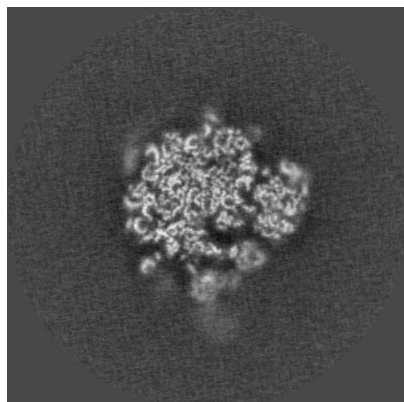


Y Index: 210

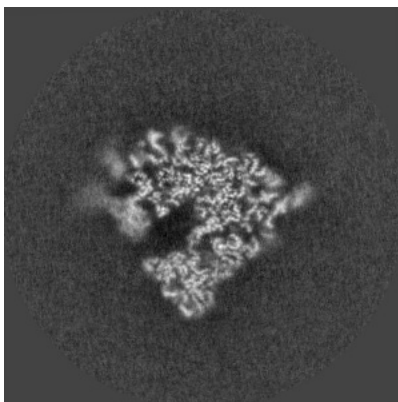


Z Index: 210

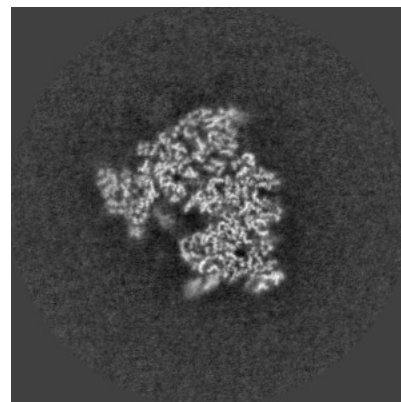
6.2.2 Raw map



X Index: 210



Y Index: 210

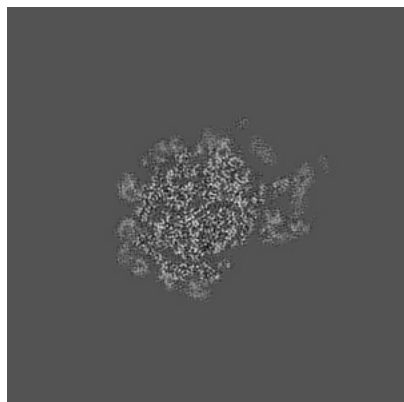


Z Index: 210

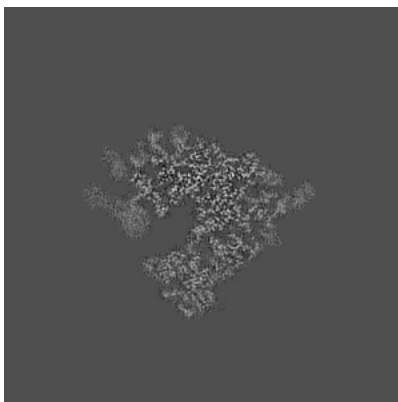
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

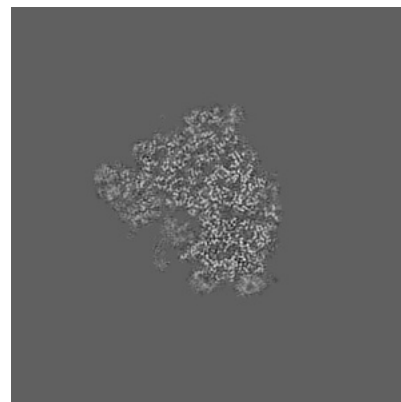
6.3.1 Primary map



X Index: 241

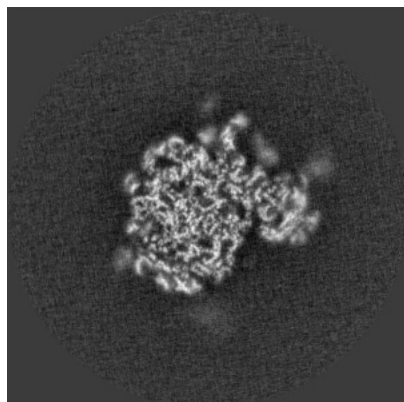


Y Index: 211

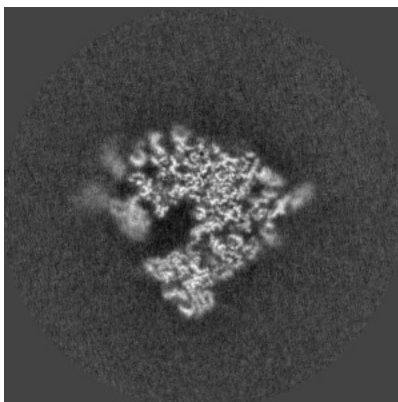


Z Index: 219

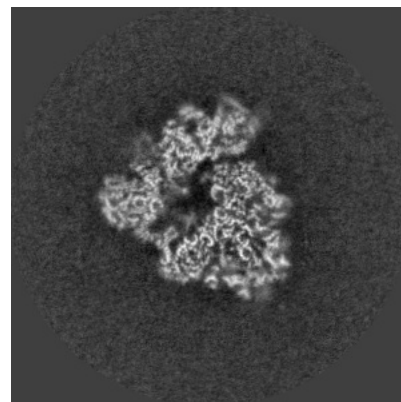
6.3.2 Raw map



X Index: 233



Y Index: 212

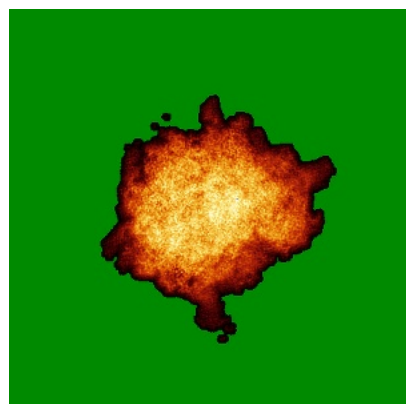


Z Index: 188

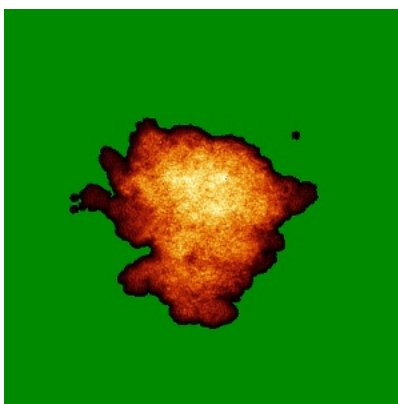
The images above show the largest variance slices of the map in three orthogonal directions.

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

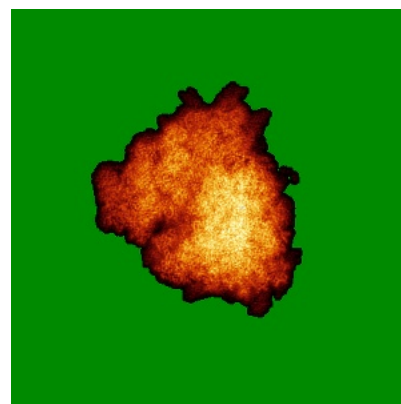
6.4.1 Primary map



X

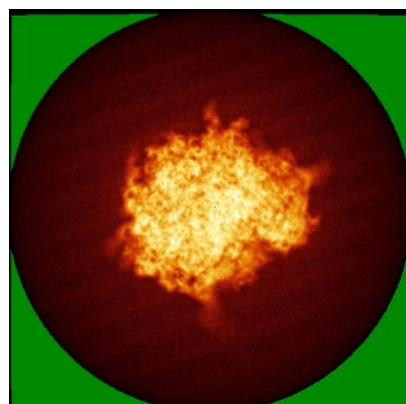


Y

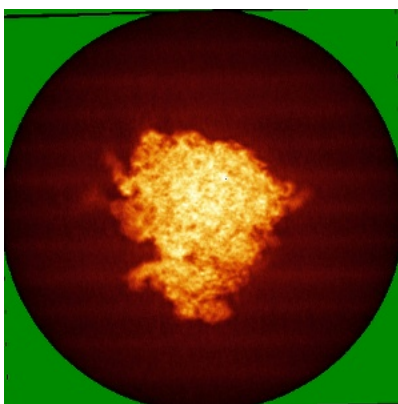


Z

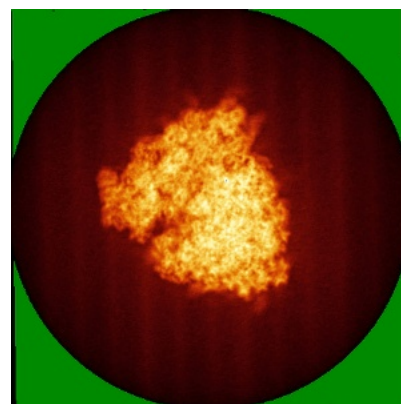
6.4.2 Raw map



X



Y

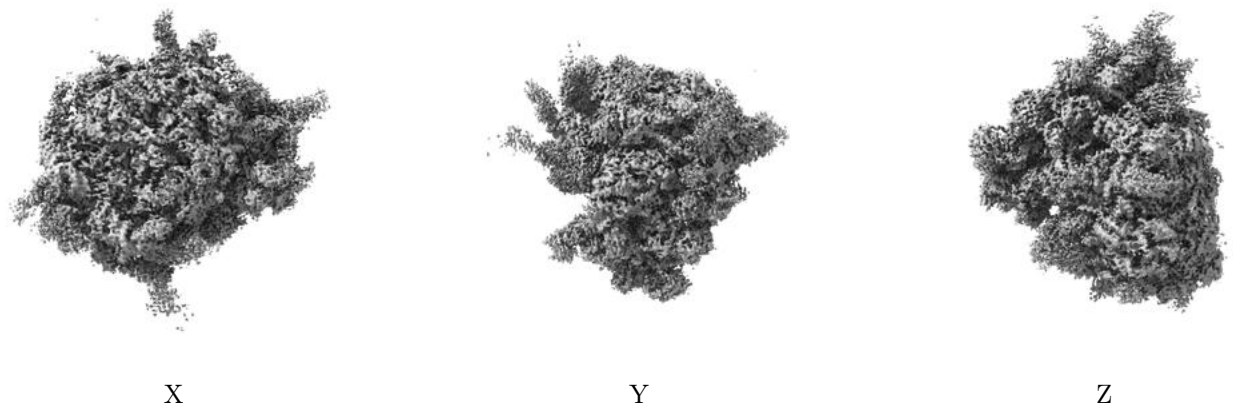


Z

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.

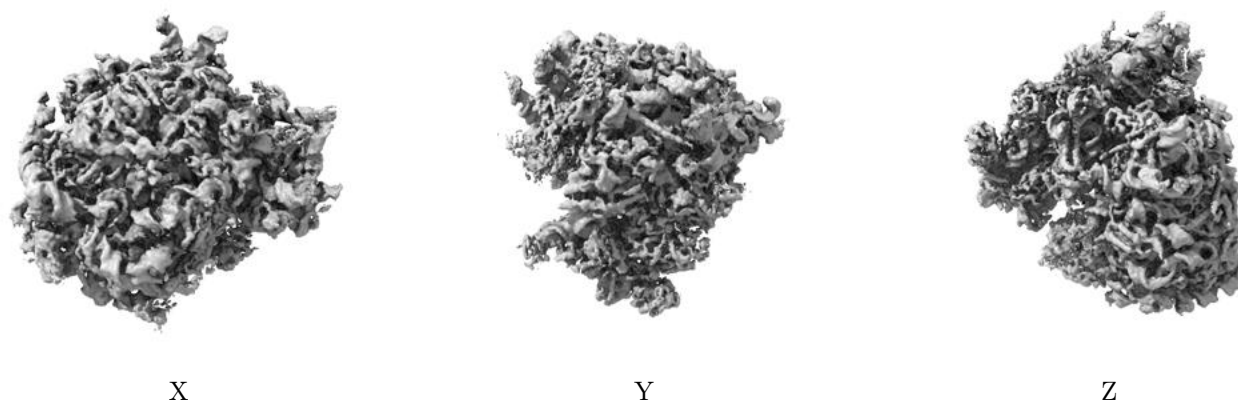
6.5 Orthogonal surface views [i](#)

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.

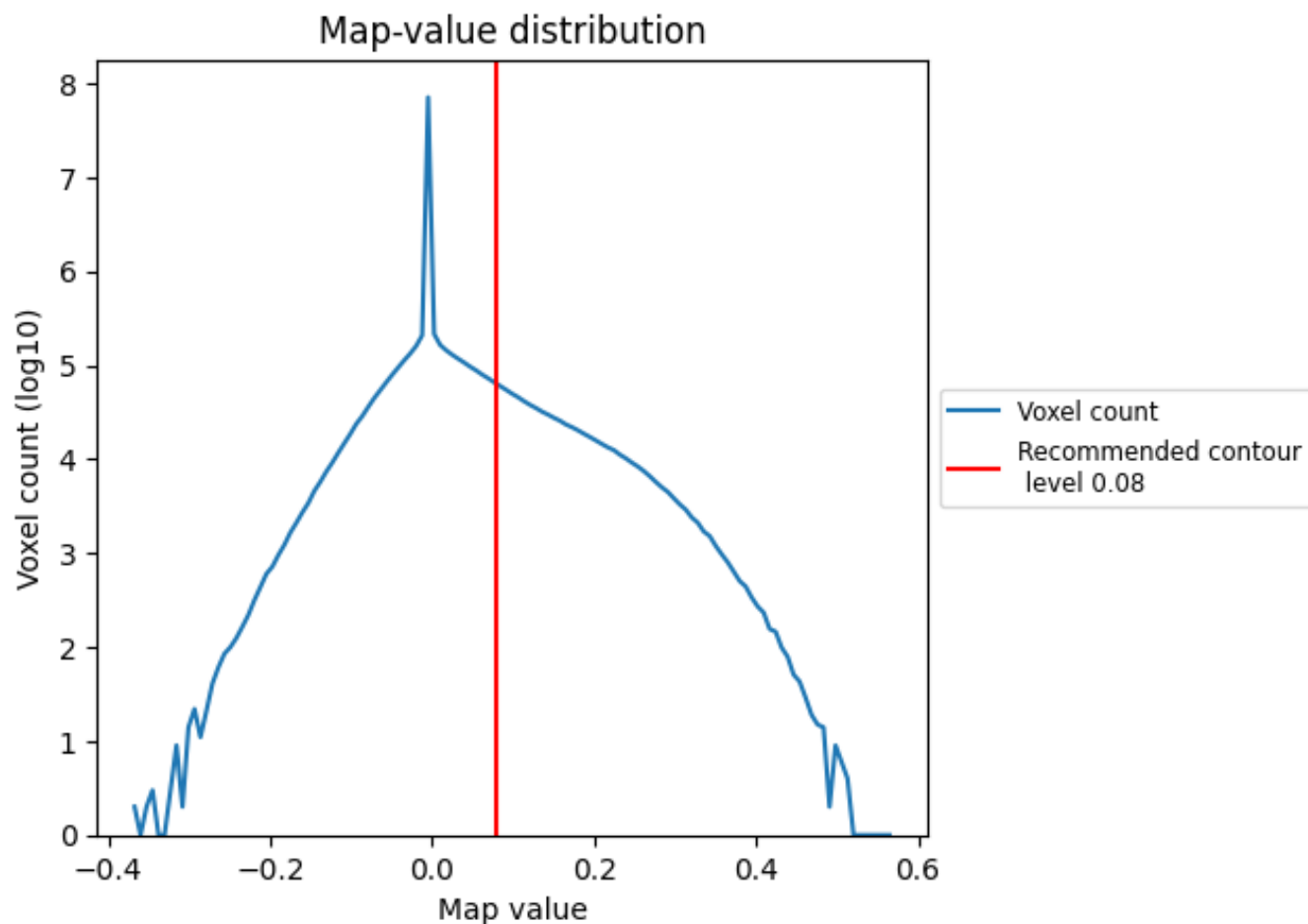
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

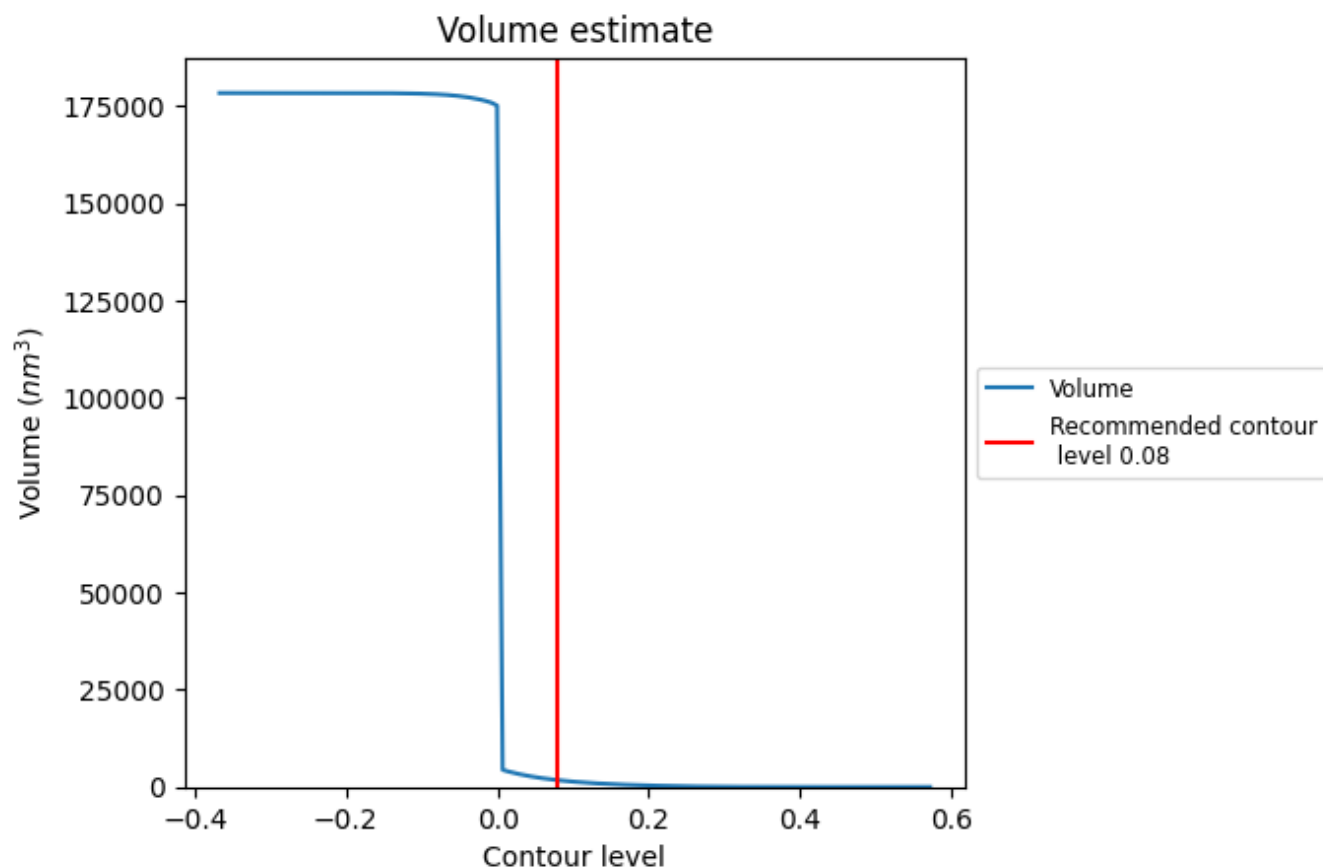
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

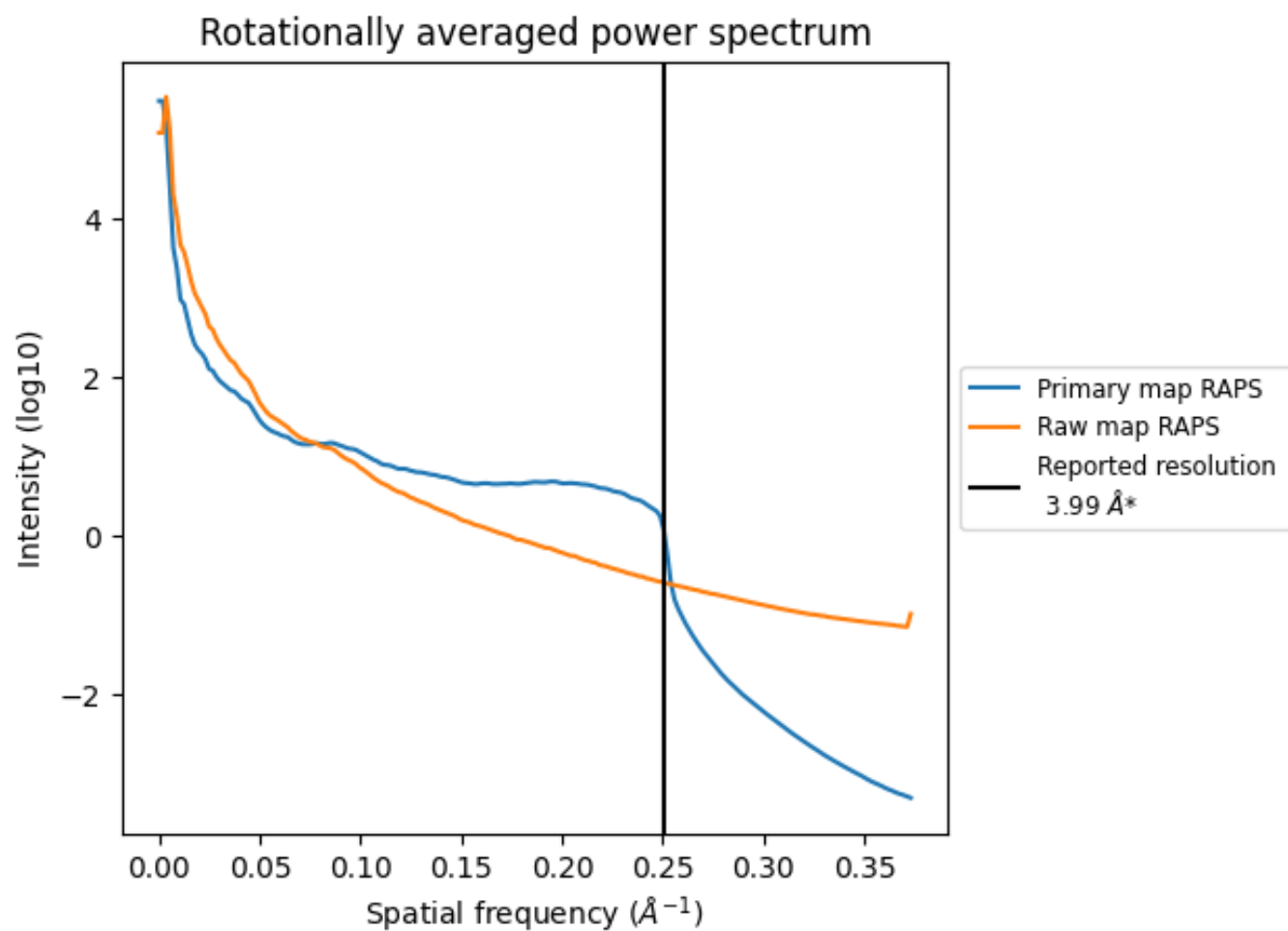
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1742 nm³; this corresponds to an approximate mass of 1573 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 ⓘ

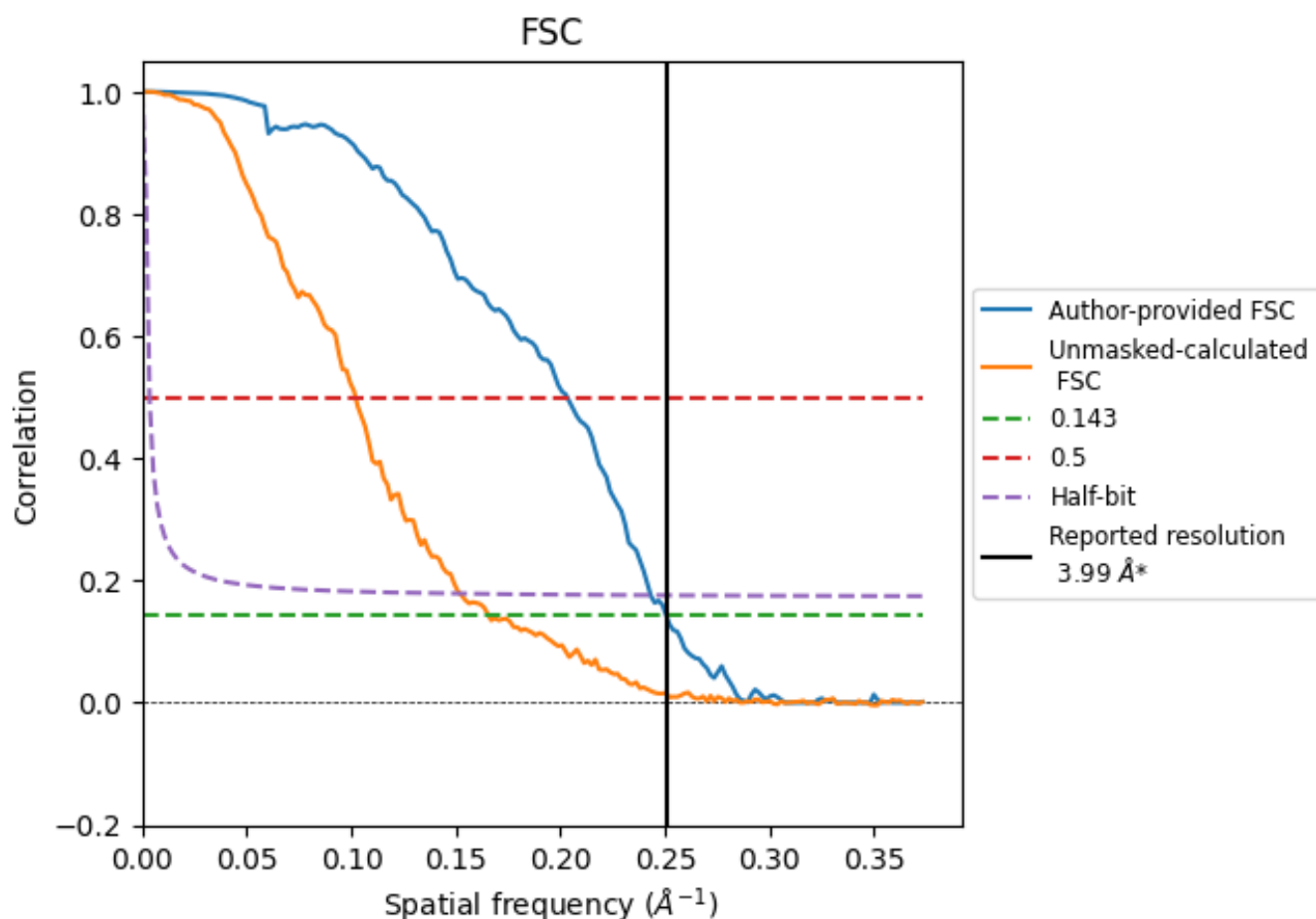


*Reported resolution corresponds to spatial frequency of 0.251 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.251 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

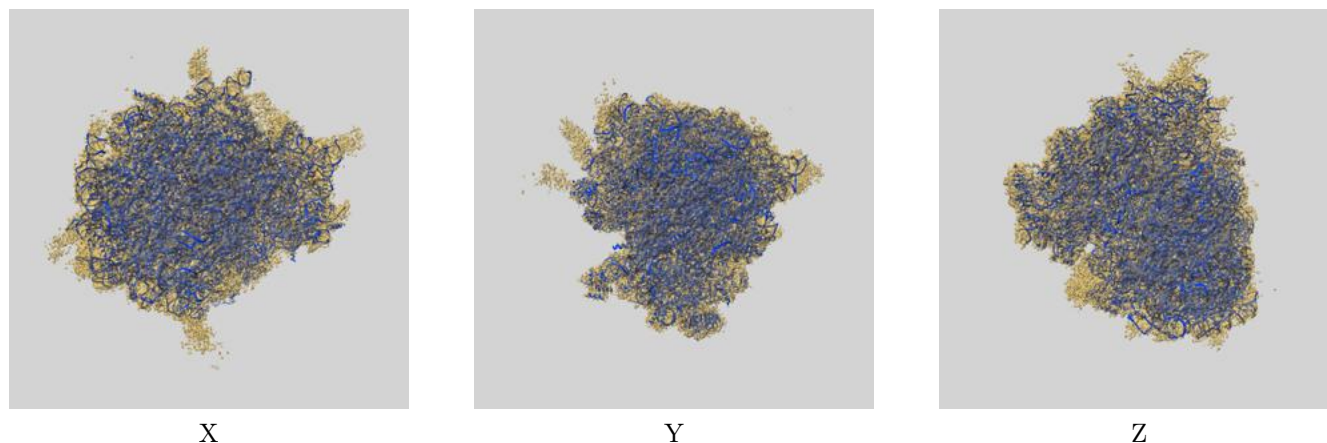
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.99	-	-
Author-provided FSC curve	3.99	4.92	4.11
Unmasked-calculated*	6.04	9.80	6.57

*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 6.04 differs from the reported value 3.99 by more than 10 %

9 Map-model fit [i](#)

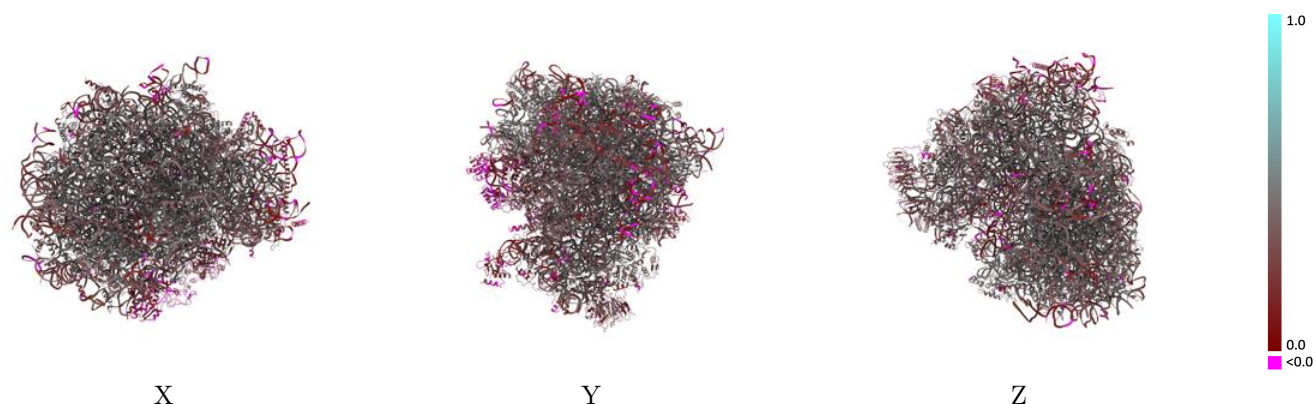
This section contains information regarding the fit between EMDB map EMD-4136 and PDB model 5LZY. Per-residue inclusion information can be found in [section 3](#) on [page 24](#).

9.1 Map-model overlay [i](#)



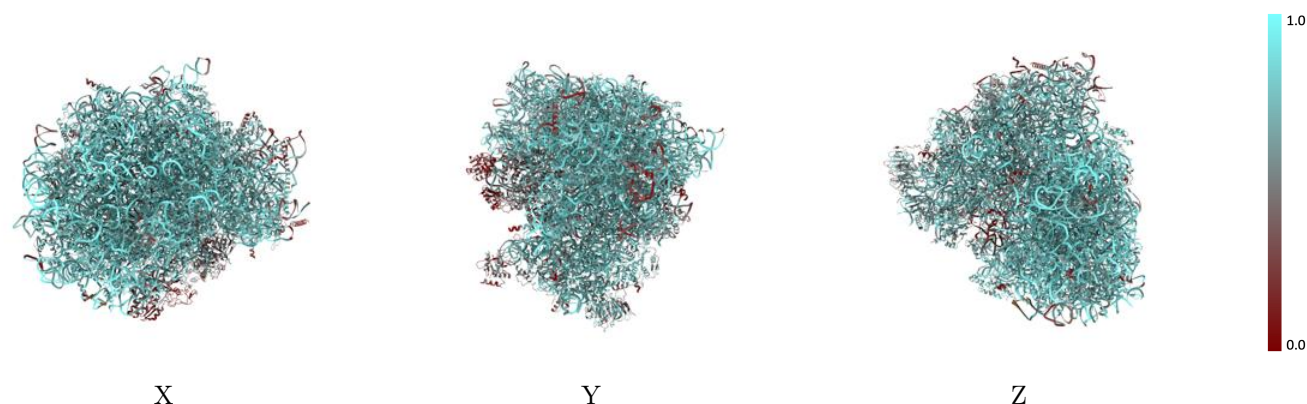
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



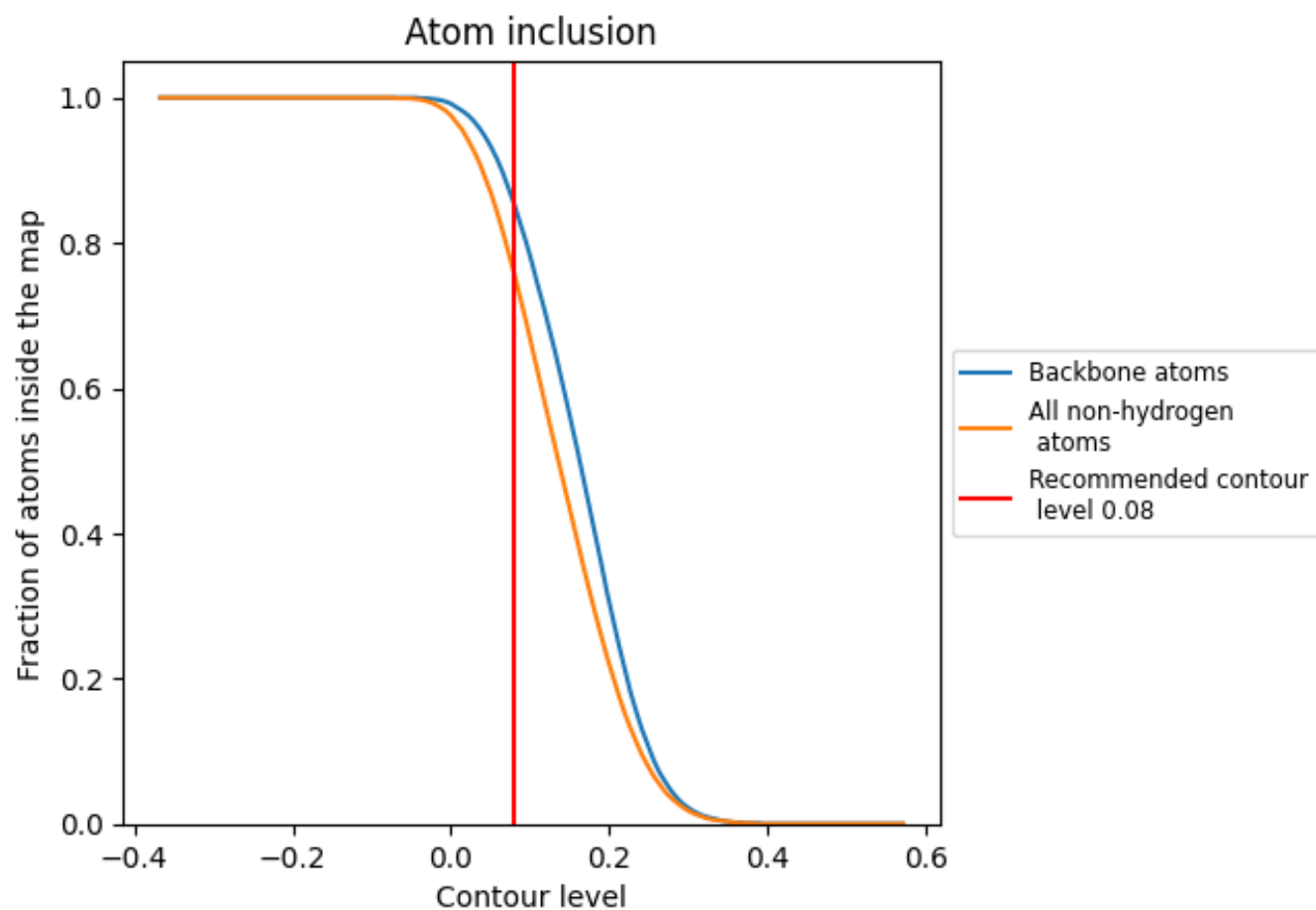
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 85% of all backbone atoms, 76% 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	 0.7590	 0.3670
2	 0.3860	 0.2510
3	 0.2810	 0.1410
5	 0.8450	 0.3750
7	 0.9170	 0.4170
8	 0.8630	 0.3820
9	 0.8180	 0.3540
A	 0.7560	 0.4430
AA	 0.6960	 0.3780
B	 0.7750	 0.4410
BB	 0.6840	 0.3840
C	 0.7700	 0.4310
CC	 0.7090	 0.3900
D	 0.7710	 0.3980
DD	 0.6230	 0.3390
E	 0.7560	 0.3940
EE	 0.6940	 0.3890
F	 0.7670	 0.4270
FF	 0.6580	 0.3620
G	 0.6990	 0.3670
GG	 0.6360	 0.3120
H	 0.7450	 0.4130
HH	 0.5930	 0.3230
I	 0.7430	 0.4230
II	 0.6720	 0.3650
J	 0.7140	 0.3820
JJ	 0.7110	 0.3740
KK	 0.6220	 0.2990
L	 0.7500	 0.4020
LL	 0.6920	 0.4060
M	 0.7640	 0.4050
MM	 0.3470	 0.1410
N	 0.7990	 0.4460
NN	 0.6870	 0.3910
O	 0.7840	 0.4380



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Chain	Atom inclusion	Q-score
OO	 0.7010	 0.3980
P	 0.7640	 0.4290
PP	 0.6240	 0.2960
Q	 0.7640	 0.4340
QQ	 0.6650	 0.3480
R	 0.7120	 0.3880
RR	 0.6360	 0.3440
S	 0.7810	 0.4380
SS	 0.6440	 0.3310
T	 0.7620	 0.4290
TT	 0.6540	 0.3400
U	 0.7000	 0.3690
UU	 0.6360	 0.3370
V	 0.7350	 0.4330
VV	 0.6860	 0.3800
W	 0.6010	 0.3290
WW	 0.7330	 0.4210
X	 0.7330	 0.4090
XX	 0.6960	 0.4160
Y	 0.7510	 0.3960
YY	 0.6760	 0.3510
Z	 0.7470	 0.4000
ZZ	 0.6360	 0.3230
a	 0.7900	 0.4340
aa	 0.7160	 0.4070
b	 0.6850	 0.3560
bb	 0.6510	 0.3640
c	 0.7330	 0.4000
cc	 0.6380	 0.3680
d	 0.7420	 0.4170
dd	 0.7290	 0.4040
e	 0.7620	 0.4390
ee	 0.6170	 0.3110
f	 0.7860	 0.4500
ff	 0.4310	 0.1380
g	 0.7300	 0.4080
gg	 0.5810	 0.2930
h	 0.7180	 0.3790
hh	 0.1420	 0.2150
i	 0.7440	 0.3980
ii	 0.4000	 0.2570
j	 0.8180	 0.4460

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Chain	Atom inclusion	Q-score
jj	 0.4570	 0.2400
k	 0.6930	 0.3710
l	 0.7490	 0.4290
m	 0.7520	 0.4210
n	 0.5870	 0.3820
o	 0.7410	 0.4220
p	 0.7270	 0.4160
r	 0.7950	 0.4450
s	 0.1820	 0.0620
t	 0.1330	 0.0300