



Full wwPDB EM Validation Report ⓘ

Jul 6, 2026 – 07:02 PM JST

PDB ID : 9VTI / pdb_00009vti
EMDB ID : EMD-65329
Title : cryoEM structure of tobacco mosaic virus tRNA-like structure complexed with tobacco 80S
Authors : Lu, G.; Lin, J.
Deposited on : 2025-07-10
Resolution : 2.96 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

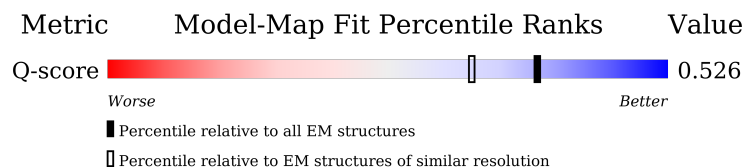
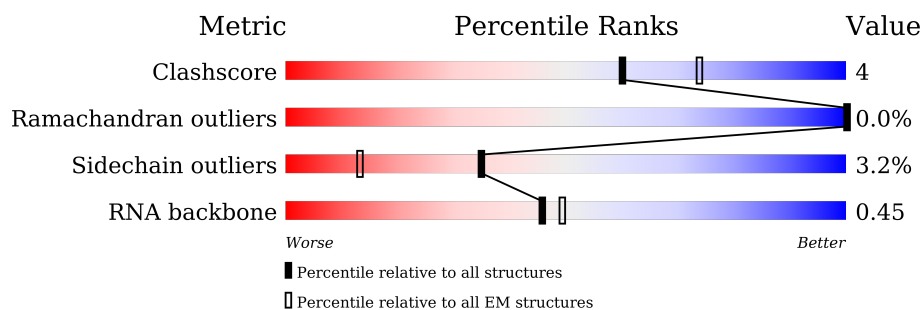
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.96 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	13155 (2.46 - 3.46)

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	SA	257	
2	SB	248	
3	SC	187	

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Mol	Chain	Length	Quality of chain
4	SD	280	
5	SE	210	
6	SF	130	
7	SG	147	
8	SH	122	
9	SI	150	
10	SJ	142	
11	SK	141	
12	SL	56	
13	SM	151	
14	SN	159	
15	SO	152	
16	SP	261	
17	SQ	264	
18	SR	249	
19	SS	191	
20	ST	212	
21	SU	118	
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23	SW	131	
24	SX	143	
25	SY	82	
26	SZ	133	
27	Sa	74	
28	Sb	113	

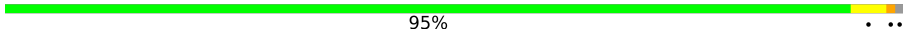
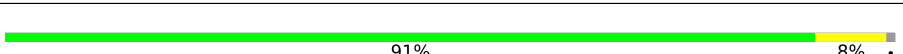
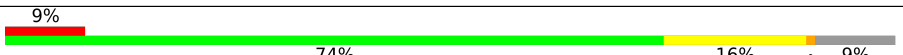
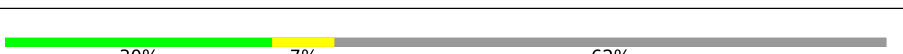
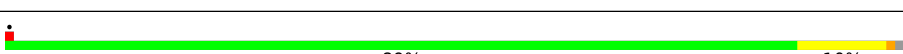
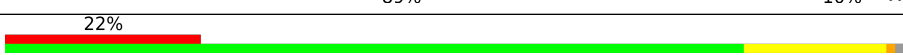
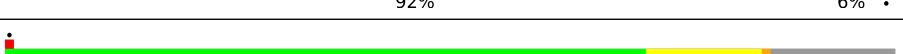
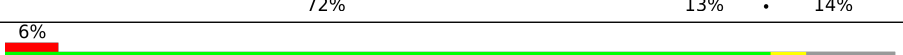
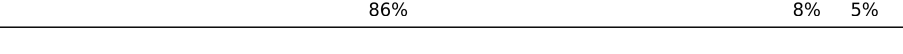
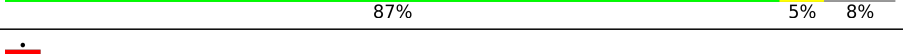
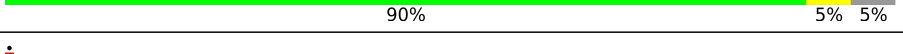
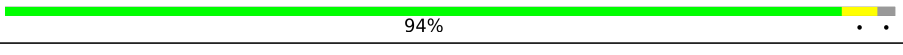
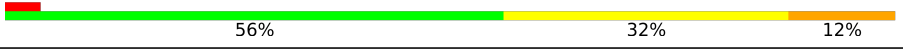
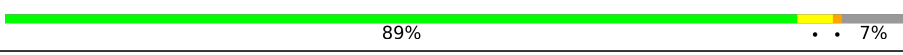
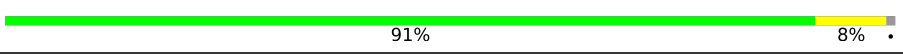
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Mol	Chain	Length	Quality of chain
29	Sc	85	
30	Sd	65	
31	Se	62	
32	Sf	156	
33	LA	217	
34	LB	260	
35	LC	389	
36	LD	405	
37	LE	181	
38	LF	194	
39	LG	206	
40	LH	140	
41	LI	148	
42	LJ	219	
43	LK	293	
44	LL	175	
45	LM	154	
46	LN	146	
47	LO	123	
48	LP	242	
49	LQ	230	
50	LR	237	
51	LS	200	
52	LT	130	
53	LU	204	

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Mol	Chain	Length	Quality of chain
54	LV	187	
55	LW	211	
56	LX	178	
57	LY	164	
58	LZ	108	
59	La	164	
60	Lb	135	
61	Lc	143	
62	Ld	50	
63	Le	113	
64	Lf	120	
65	Lg	133	
66	Lh	112	
67	Li	120	
68	Lj	110	
69	Lk	95	
70	Ll	69	
71	Lm	51	
72	Ln	128	
73	Lo	25	
74	Lp	105	
75	Lq	77	
76	10	204	
77	11	1808	
78	12	119	

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Mol	Chain	Length	Quality of chain
79	13	163	69% 28%
80	14	3390	67% 23% 7%

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 199397 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 Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	SA	202	Total	C	N	O	S	0	0
			1603	1019	286	288	10		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SA	214	GLU	GLN	conflict	UNP A0A1U7W513
SA	230	GLY	ALA	conflict	UNP A0A1U7W513

- Molecule 2 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SB	211	Total	C	N	O	S	0	0
			1645	1044	299	294	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SB	95	ASN	SER	conflict	UNP A0A1U7WQT4
SB	215	SER	PRO	conflict	UNP A0A1U7WQT4
SB	220	LYS	GLU	conflict	UNP A0A1U7WQT4

- Molecule 3 is a protein called 40S ribosomal protein S9-2-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SC	183	Total	C	N	O	S	0	0
			1501	952	291	253	5		

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SD	217	Total	C	N	O	S	0	0
			1686	1089	300	289	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SD	268	SER	PRO	conflict	UNP A0A1U7Y544
SD	269	THR	ALA	conflict	UNP A0A1U7Y544

- Molecule 5 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SE	194	Total	C	N	O	S	0	0
			1520	948	284	280	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SE	16	SER	ASN	conflict	UNP A0A1S4AYA1

- Molecule 6 is a protein called Small ribosomal subunit protein uS8c.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SF	129	Total	C	N	O	S	0	0
			1032	659	188	180	5		

- Molecule 7 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SG	141	Total	C	N	O	S	0	0
			1135	722	221	188	4		

- Molecule 8 is a protein called 40S ribosomal protein S20-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SH	102	Total	C	N	O	S	0	0
			804	505	151	145	3		

- Molecule 9 is a protein called 40S ribosomal protein S14-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SI	132	Total	C	N	O	S	0	0
			998	611	197	185	5		

- Molecule 10 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SJ	141	Total	C	N	O	S	0	0
			1100	695	215	187	3		

- Molecule 11 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SK	141	Total	C	N	O	S	0	0
			1144	712	225	201	6		

- Molecule 12 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SL	55	Total	C	N	O	S	0	0
			441	274	90	71	6		

- Molecule 13 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SM	149	Total	C	N	O	S	0	0
			1189	762	223	202	2		

- Molecule 14 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SN	145	Total	C	N	O	S	0	0
			1155	734	222	194	5		

- Molecule 15 is a protein called 40S ribosomal protein S15-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SO	131	Total	C	N	O	S	0	0
			1057	679	199	174	5		

- Molecule 16 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SP	216	Total	C	N	O	S	0	0
			1760	1118	314	320	8		

- Molecule 17 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SQ	259	Total	C	N	O	S	0	0
			2068	1320	384	357	7		

- Molecule 18 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SR	230	Total	C	N	O	S	0	0
			1826	1143	355	320	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SR	170	THR	ASN	conflict	UNP A0A1S3Z3Y7

- Molecule 19 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SS	188	Total	C	N	O	S	0	0
			1533	976	280	274	3		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SS	22	PHE	SER	conflict	UNP A0A1S3Z906
SS	29	ALA	ASP	conflict	UNP A0A1S3Z906
SS	50	MET	VAL	conflict	UNP A0A1S3Z906
SS	63	LEU	ILE	conflict	UNP A0A1S3Z906
SS	144	HIS	ARG	conflict	UNP A0A1S3Z906
SS	183	LEU	VAL	conflict	UNP A0A1S3Z906

- Molecule 20 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	ST	185	Total	C	N	O	S	0	0
			1504	938	298	264	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ST	20	SER	ALA	conflict	UNP A0A1S4CZK3
ST	40	SER	ALA	conflict	UNP A0A1S4CZK3

- Molecule 21 is a protein called 40S ribosomal protein S10-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SU	91	Total	C	N	O	S	0	0
			769	506	124	135	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SU	12	ARG	TRP	conflict	UNP A0A1S4DHU6

- Molecule 22 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SV	85	Total	C	N	O	S	0	0
			602	374	110	112	6		

- Molecule 23 is a protein called 40S ribosomal protein S17-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SW	82	Total	C	N	O	S	0	0
			675	421	134	118	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SW	93	ILE	THR	conflict	UNP A0A1S3Z9G2
SW	109	MET	LEU	conflict	UNP A0A1S3Z9G2
SW	126	VAL	ALA	conflict	UNP A0A1S3Z9G2
SW	127	MET	ILE	conflict	UNP A0A1S3Z9G2

- Molecule 24 is a protein called 40S ribosomal protein S19-3-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SX	136	Total	C	N	O	S	0	0
			1081	676	211	190	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SX	142	ALA	SER	conflict	UNP A0A1S4CYT7

- Molecule 25 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SY	82	Total	C	N	O	S	0	0
			651	401	120	126	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SY	67	GLY	ALA	conflict	UNP A0A1S4C2G0

- Molecule 26 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SZ	127	Total	C	N	O	S	0	0
			1000	638	189	170	3		

- Molecule 27 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Sa	73	Total	C	N	O	S	0	0
			574	359	107	105	3		

- Molecule 28 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Sb	98	Total	C	N	O	S	0	0
			789	491	161	129	8		

- Molecule 29 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Sc	84	Total	C	N	O	S	0	0
			650	401	122	119	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Sc	2	GLY	VAL	conflict	UNP A0A1S4BH20
Sc	9	MET	SER	conflict	UNP A0A1S4BH20

- Molecule 30 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Sd	61	Total	C	N	O	S	0	0
			493	303	102	86	2		

- Molecule 31 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Se	45	Total	C	N	O	S	0	0
			353	216	78	58	1		

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S27a-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sf	69	Total	C	N	O	S	0	0
			562	360	103	94	5		

- Molecule 33 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LA	215	Total	C	N	O	S	0	0
			1702	1086	298	307	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LA	2	SER	-	insertion	UNP A0A1S3Y379
LA	216	ILE	VAL	conflict	UNP A0A1S3Y379

- Molecule 34 is a protein called 60S ribosomal protein L8-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LB	245	Total	C	N	O	S	0	0
			1880	1174	381	315	10		

- Molecule 35 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LC	386	Total	C	N	O	S	0	0
			3107	1983	577	532	15		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LC	200	SER	GLY	conflict	UNP A0A1S3ZLI9
LC	308	GLU	ASP	conflict	UNP A0A1S3ZLI9
LC	381	GLU	GLN	conflict	UNP A0A1S3ZLI9

- Molecule 36 is a protein called 60S ribosomal protein L4-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LD	398	Total	C	N	O	S	0	0
			3087	1952	577	548	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LD	27	VAL	LEU	conflict	UNP A0A1S4BWA4

- Molecule 37 is a protein called 60S ribosomal protein L11-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LE	169	Total	C	N	O	S	0	0
			1362	862	254	239	7		

- Molecule 38 is a protein called 60S ribosomal protein L9-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LF	191	Total	C	N	O	S	0	0
			1520	966	274	275	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LF	125	LYS	ARG	conflict	UNP A0A1S4CJ62
LF	191	VAL	ALA	conflict	UNP A0A1S4CJ62

- Molecule 39 is a protein called 60S ribosomal protein L13a-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LG	205	Total	C	N	O	S	0	0
			1644	1046	320	270	8		

- Molecule 40 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LH	131	Total	C	N	O	S	0	0
			985	623	183	170	9		

- Molecule 41 is a protein called 60s ribosomal protein l27a-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LI	147	Total	C	N	O	S	0	0
			1155	735	226	191	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	94	SER	ASN	conflict	UNP A0A1J6IJF4

- Molecule 42 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LJ	209	Total	C	N	O	S	0	0
			1671	1058	329	273	11		

- Molecule 43 is a protein called 60S ribosomal protein L5-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LK	288	Total	C	N	O	S	0	0
			2339	1481	428	425	5		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LK	85	ARG	GLN	conflict	UNP A0A1S3XE16
LK	126	THR	SER	conflict	UNP A0A1S3XE16
LK	150	VAL	ILE	conflict	UNP A0A1S3XE16
LK	218	PHE	TYR	conflict	UNP A0A1S3XE16

- Molecule 44 is a protein called 60S ribosomal protein L17-1 isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LL	154	Total	C	N	O	S	0	0
			1236	769	245	217	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LL	46	LYS	ARG	conflict	UNP A0A1S4DQP0
LL	168	SER	PRO	conflict	UNP A0A1S4DQP0

- Molecule 45 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LM	117	Total	C	N	O	S	0	0
			950	609	170	169	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LM	31	PHE	LEU	conflict	UNP Q07761

- Molecule 46 is a protein called 60S ribosomal protein L26-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LN	126	Total	C	N	O	S	0	0
			1023	635	209	176	3		

- Molecule 47 is a protein called 60S ribosomal protein L35-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LO	122	Total	C	N	O	S	0	0
			997	640	191	165	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LO	100	ALA	VAL	conflict	UNP A0A1S3WY31

- Molecule 48 is a protein called 60S ribosomal protein L7-4-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LP	238	Total	C	N	O	S	0	0
			1958	1255	361	338	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LP	7	PRO	LEU	conflict	UNP A0A1U7X2X8
LP	64	ARG	GLN	conflict	UNP A0A1U7X2X8

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Chain	Residue	Modelled	Actual	Comment	Reference
LP	157	ASP	GLU	conflict	UNP A0A1U7X2X8

- Molecule 49 is a protein called 60S ribosomal protein L6-like isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LQ	207	Total	C	N	O	S	0	0
			1600	1040	285	272	3		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LQ	60	ILE	PHE	conflict	UNP A0A1U7WD54
LQ	97	LYS	ARG	conflict	UNP A0A1U7WD54
LQ	144	VAL	ILE	conflict	UNP A0A1U7WD54
LQ	148	SER	ASN	conflict	UNP A0A1U7WD54
LQ	152	PHE	ILE	conflict	UNP A0A1U7WD54
LQ	187	GLU	GLY	conflict	UNP A0A1U7WD54

- Molecule 50 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LR	233	Total	C	N	O	S	0	0
			1874	1206	343	318	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LR	108	ILE	VAL	conflict	UNP A0A1U7XNI3
LR	110	LYS	ARG	conflict	UNP A0A1U7XNI3

- Molecule 51 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LS	200	Total	C	N	O	S	0	0
			1608	1010	324	270	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LS	139	VAL	ALA	conflict	UNP A0A1S4CSN1
LS	163	GLU	ASP	conflict	UNP A0A1S4CSN1

- Molecule 52 is a protein called 60S ribosomal protein L14-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LT	129	Total	C	N	O	S	0	0
			1046	673	195	175	3		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LT	82	THR	ASN	conflict	UNP A0A1U7UYX7
LT	86	ASN	SER	conflict	UNP A0A1U7UYX7
LT	101	ALA	SER	conflict	UNP A0A1U7UYX7

- Molecule 53 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LU	203	Total	C	N	O	S	0	0
			1701	1072	350	276	3		

- Molecule 54 is a protein called 60S ribosomal protein L18-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LV	186	Total	C	N	O	S	0	0
			1462	931	283	245	3		

- Molecule 55 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LW	182	Total	C	N	O	S	0	0
			1519	940	323	247	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	190	VAL	ALA	conflict	UNP A0A1S4A7M5
LW	195	SER	PRO	conflict	UNP A0A1S4A7M5
LW	197	THR	ALA	conflict	UNP A0A1S4A7M5
LW	198	PRO	SER	conflict	UNP A0A1S4A7M5

- Molecule 56 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LX	177	Total	C	N	O	S	0	0
			1505	969	277	251	8		

- Molecule 57 is a protein called 60S ribosomal protein L21-1-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LY	163	Total	C	N	O	S	0	0
			1306	823	255	224	4		

- Molecule 58 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LZ	98	Total	C	N	O	S	0	0
			799	510	140	147	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LZ	61	ALA	THR	conflict	UNP A0A1S4BSU3
LZ	63	ALA	THR	conflict	UNP A0A1S4BSU3

- Molecule 59 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	La	62	Total	C	N	O	S	0	0
			526	341	101	81	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Lb	134	Total	C	N	O	S	0	0
			1097	707	206	182	2		

- Molecule 61 is a protein called 60S ribosomal protein L28-1-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Lc	142	Total	C	N	O	S	0	0
			1114	706	206	200	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lc	53	TYR	ASN	conflict	UNP A0A1U7WYY1
Lc	98	ALA	THR	conflict	UNP A0A1U7WYY1

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Ld	49	Total	C	N	O	S	0	0
			407	249	87	70	1		

- Molecule 63 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Le	97	Total	C	N	O	S	0	0
			745	475	130	135	5		

- Molecule 64 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Lf	108	Total	C	N	O	S	0	0
			875	549	168	156	2		

- Molecule 65 is a protein called 60S ribosomal protein L32-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Lg	126	Total	C	N	O	S	0	0
			1034	653	206	170	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lg	9	THR	LYS	conflict	UNP A0A1U7YAK1

- Molecule 66 is a protein called 60S ribosomal protein L35a-3-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Lh	103	Total	C	N	O	S	0	0
			836	534	155	142	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lh	57	VAL	ILE	conflict	UNP A0A1S4AHL7

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Chain	Residue	Modelled	Actual	Comment	Reference
Lh	91	LYS	ASN	conflict	UNP A0A1S4AHL7

- Molecule 67 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Li	114	Total	C	N	O	S	0	0
			926	579	193	153	1		

- Molecule 68 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Lj	98	Total	C	N	O	S	0	0
			784	491	162	129	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lj	45	SER	GLY	conflict	UNP A0A1U7VXX3

- Molecule 69 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Lk	86	Total	C	N	O	S	0	0
			701	429	155	112	5		

- Molecule 70 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ll	68	Total	C	N	O	S	0	0
			558	358	99	98	3		

- Molecule 71 is a protein called 60S ribosomal protein L39-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lm	50	Total	C	N	O	S	0	0
			448	286	96	64	2		

- Molecule 72 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Ln	51	Total	C	N	O	S	0	0
			420	261	88	65	6		

- Molecule 73 is a protein called 60s ribosomal protein l41-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Lo	25	Total	C	N	O	S	0	0
			233	139	64	27	3		

- Molecule 74 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Lp	98	Total	C	N	O	S	0	0
			785	493	157	131	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lp	17	GLY	CYS	conflict	UNP A0A1U7YPT7

- Molecule 75 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Lq	76	Total	C	N	O	S	0	0
			586	371	109	101	5		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lq	8	THR	ALA	conflict	UNP A0A1U7XSD1
Lq	35	ASN	SER	conflict	UNP A0A1U7XSD1
Lq	59	TYR	ASP	conflict	UNP A0A1U7XSD1
Lq	62	ASN	LYS	conflict	UNP A0A1U7XSD1
Lq	65	VAL	ALA	conflict	UNP A0A1U7XSD1
Lq	76	ASP	ALA	conflict	UNP A0A1U7XSD1

- Molecule 76 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	10	158	Total	C	N	O	P	0	0
			3359	1500	590	1111	158		

- Molecule 77 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	11	1626	Total	C	N	O	P	0	0
			34688	15501	6194	11367	1626		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
11	794	U	C	conflict	GB 806909817
11	1134	A	U	conflict	GB 806909817

- Molecule 78 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	12	119	Total	C	N	O	P	0	0
			2538	1133	457	829	119		

- Molecule 79 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	13	163	Total	C	N	O	P	0	0
			3478	1553	628	1134	163		

- Molecule 80 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	14	3142	Total	C	N	O	P	0	0
			67280	30009	12243	21886	3142		

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	10	7	Total	Mg	0
			7	7	
81	14	2	Total	Mg	0
			2	2	

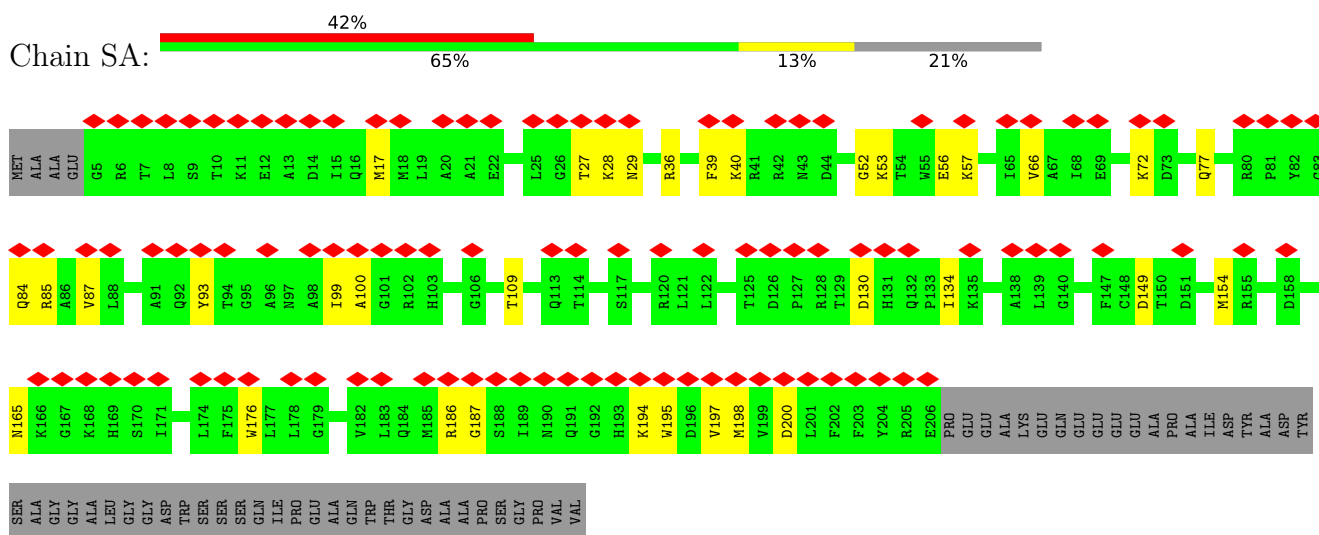
- Molecule 82 is water.

Mol	Chain	Residues	Atoms		AltConf
82	10	20	Total	O	0
			20	20	
82	14	14	Total	O	0
			14	14	

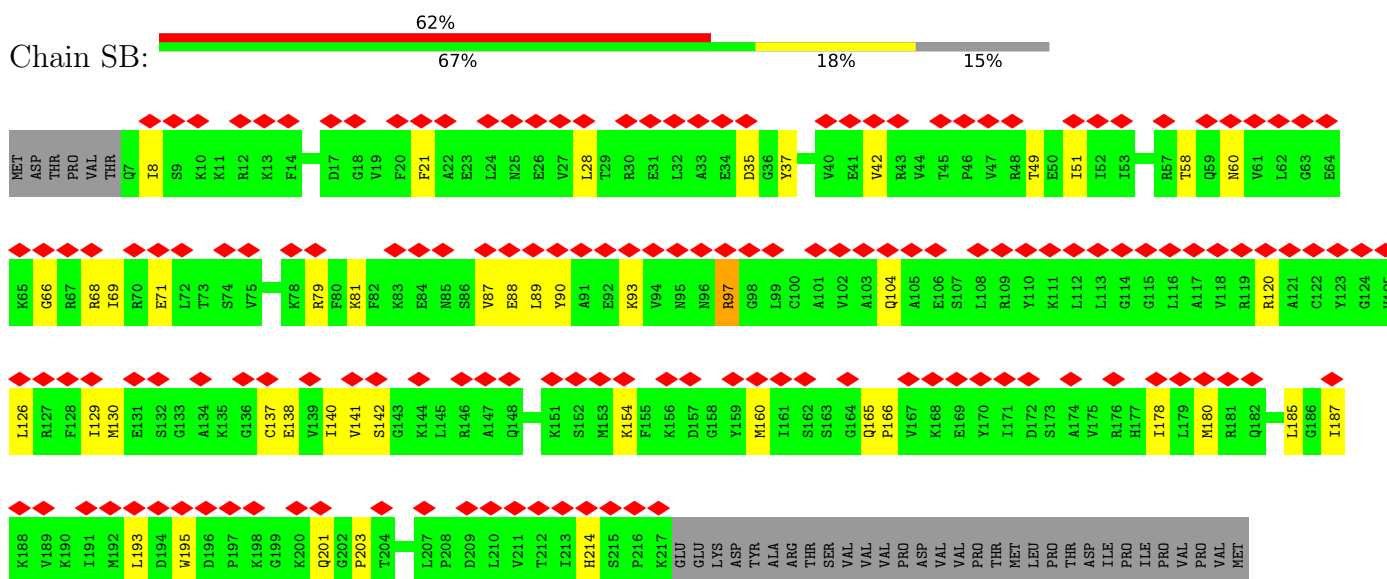
3 Residue-property plots

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.

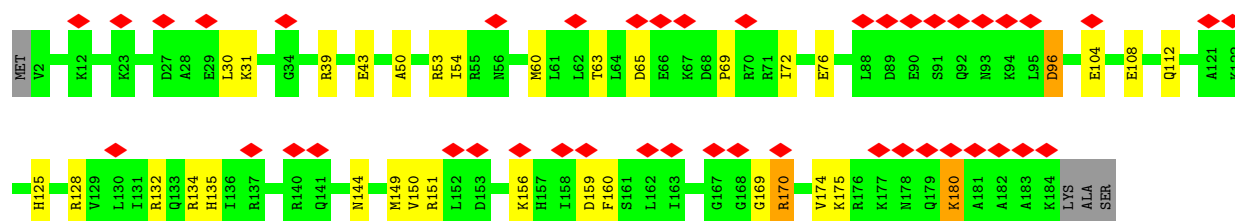
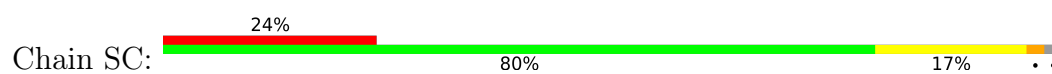
- Molecule 1: Small ribosomal subunit protein uS2



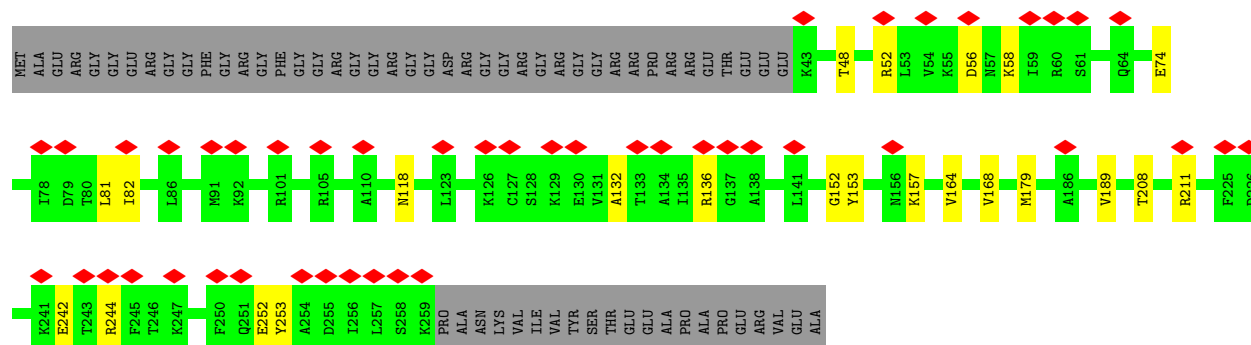
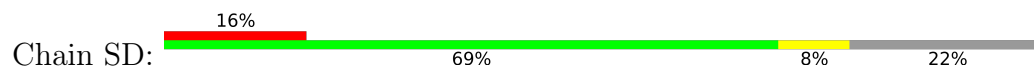
- Molecule 2: 30S ribosomal protein S3, chloroplastic



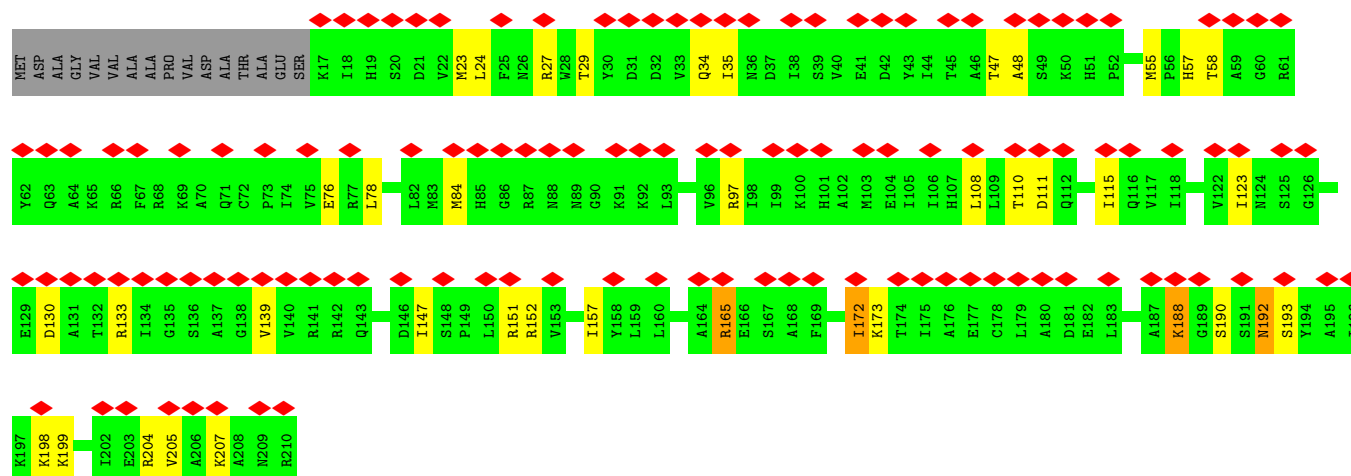
- Molecule 3: 40S ribosomal protein S9-2-like



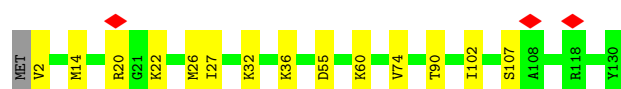
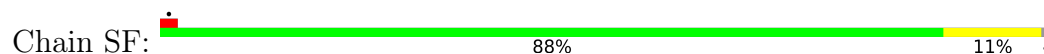
• Molecule 4: Small ribosomal subunit protein uS5



• Molecule 5: 40S ribosomal protein S5

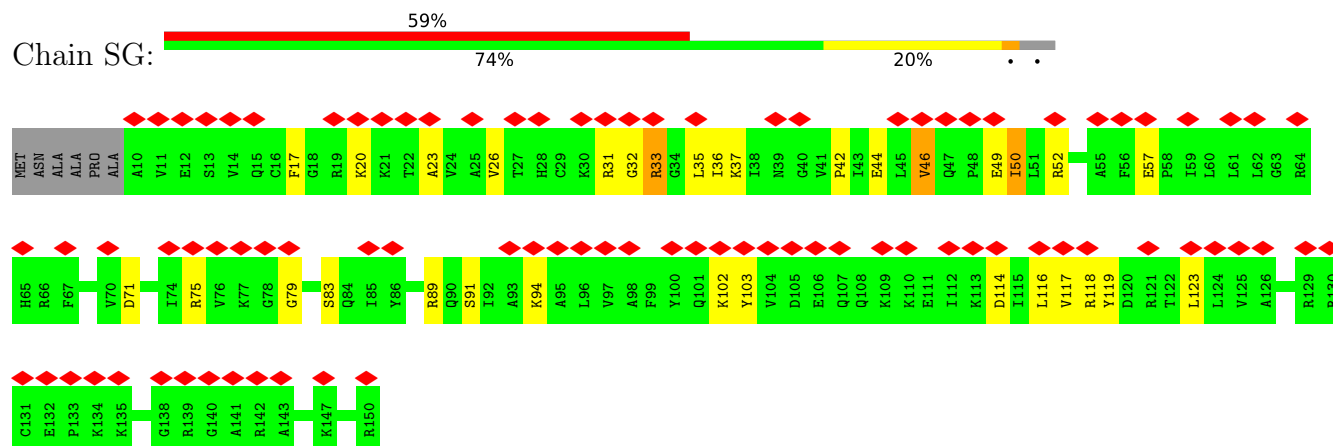


• Molecule 6: Small ribosomal subunit protein uS8c



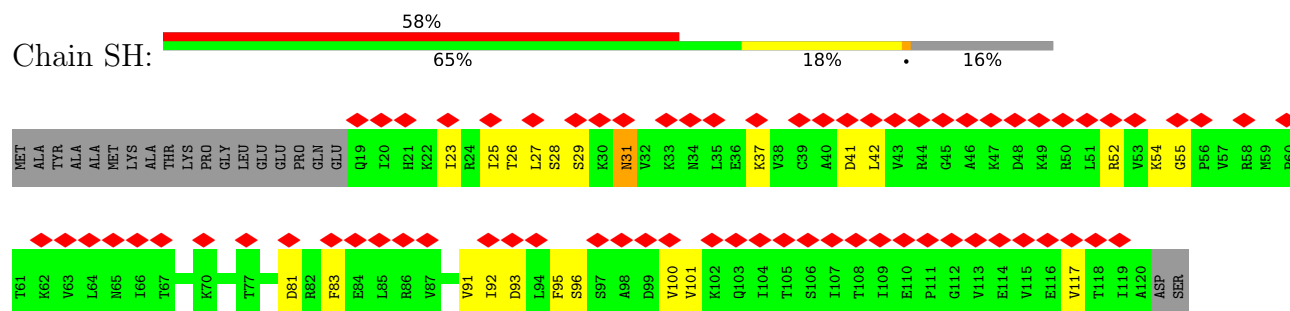
- Molecule 7: 40S ribosomal protein S16

Chain SG:



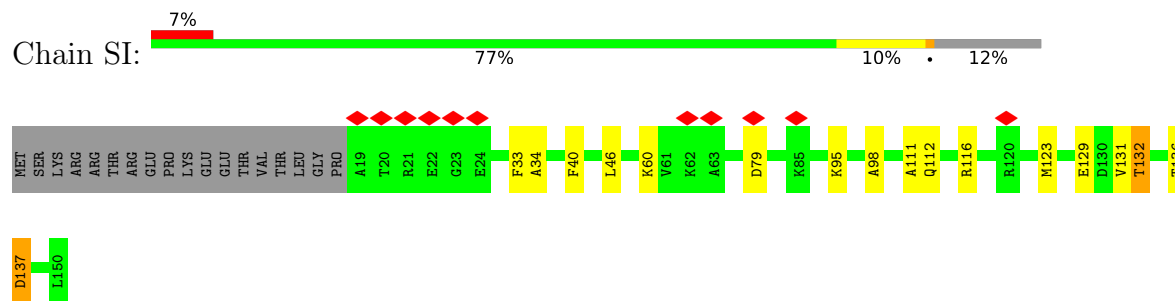
- Molecule 8: 40S ribosomal protein S20-2

Chain SH:



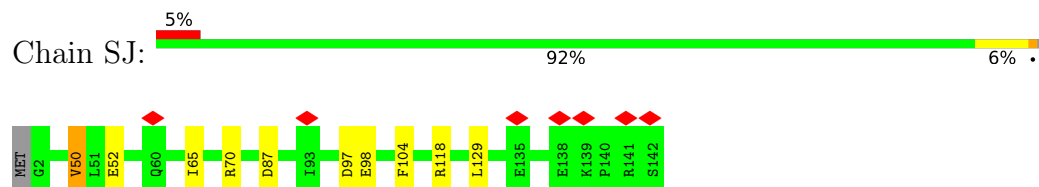
- Molecule 9: 40S ribosomal protein S14-2

Chain SI:



- Molecule 10: 40S ribosomal protein S23

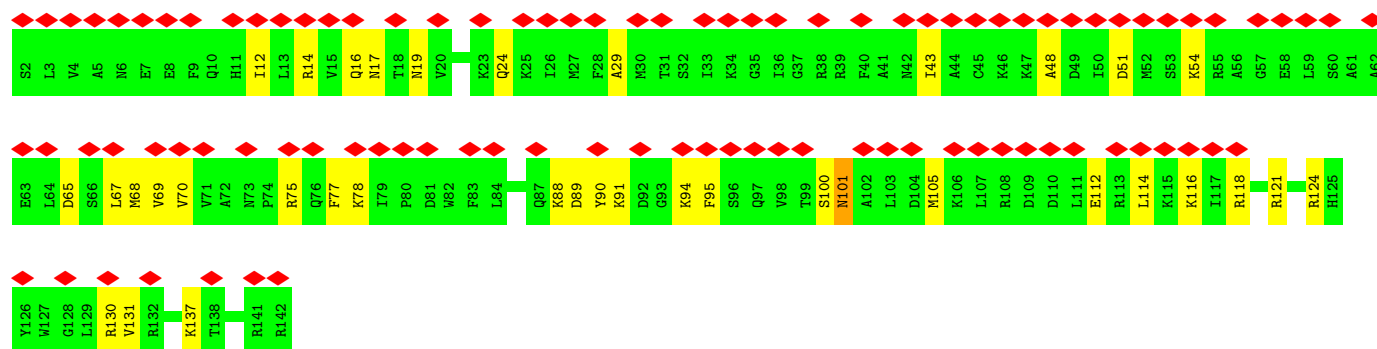
Chain SJ:



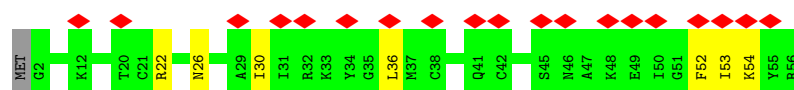
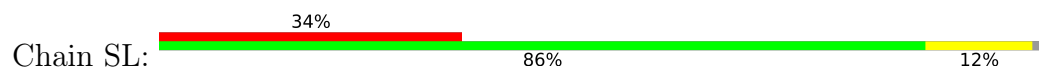
- Molecule 11: 40S ribosomal protein S18

Chain SK:

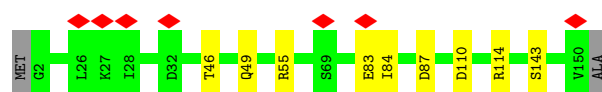




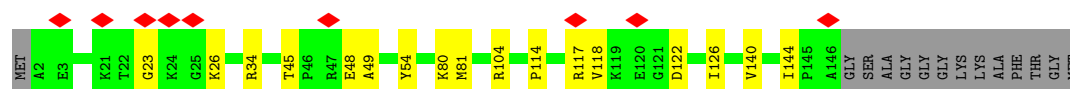
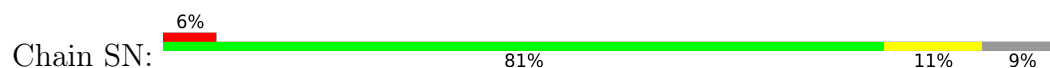
- Molecule 12: 40S ribosomal protein S29



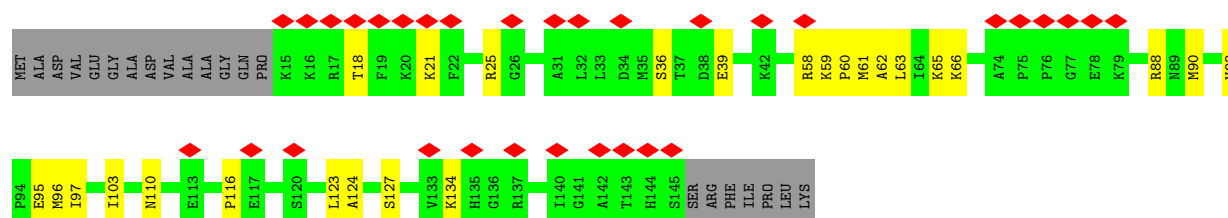
- Molecule 13: 40S ribosomal protein S13



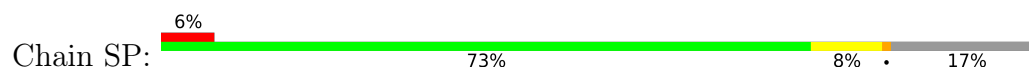
- Molecule 14: 40S ribosomal protein S11

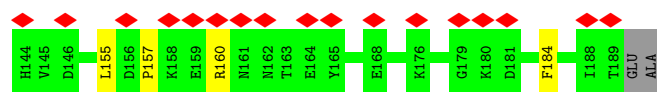


- Molecule 15: 40S ribosomal protein S15-like

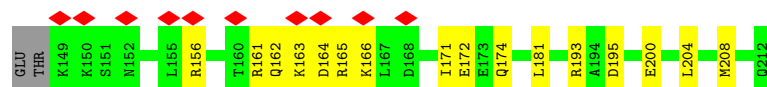
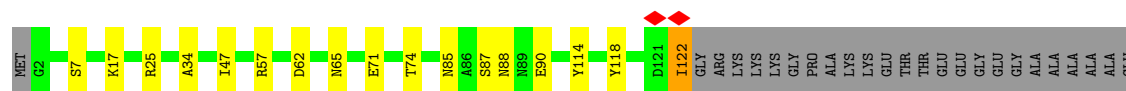
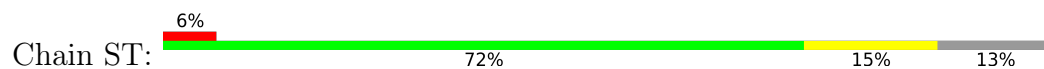


- Molecule 16: Small ribosomal subunit protein eS1

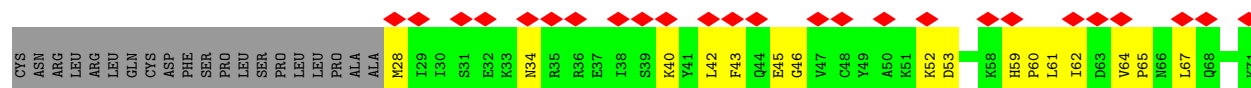




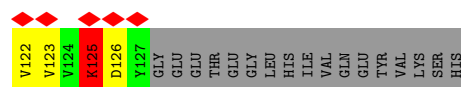
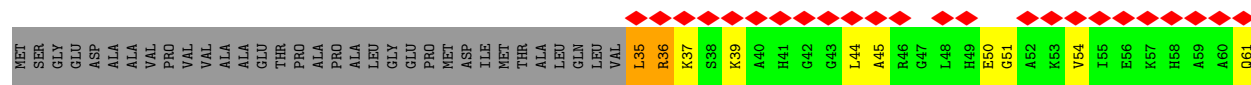
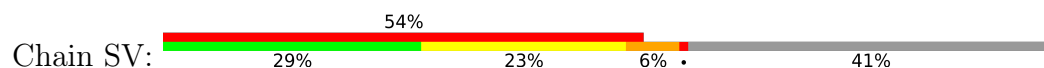
- Molecule 20: 40S ribosomal protein S8



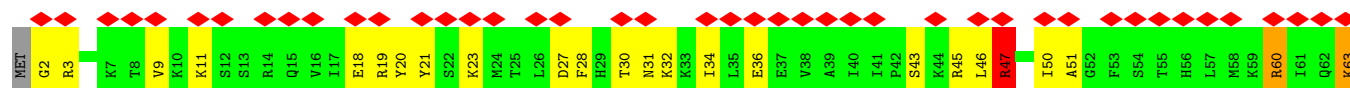
- Molecule 21: 40S ribosomal protein S10-1

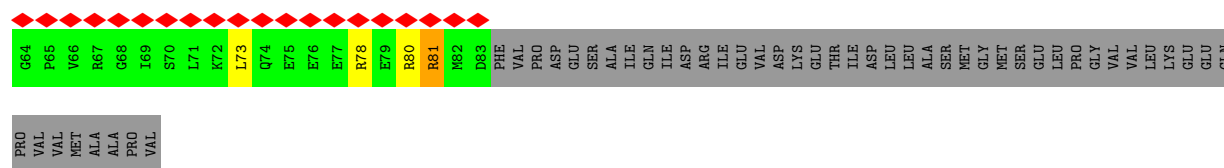


- Molecule 22: 40S ribosomal protein S12

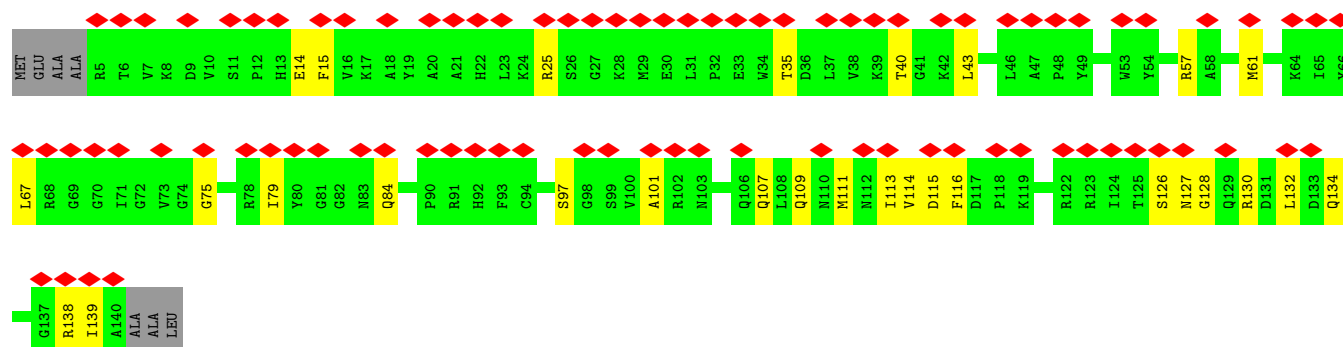


- Molecule 23: 40S ribosomal protein S17-like

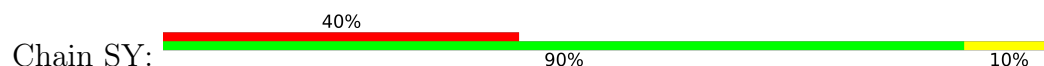




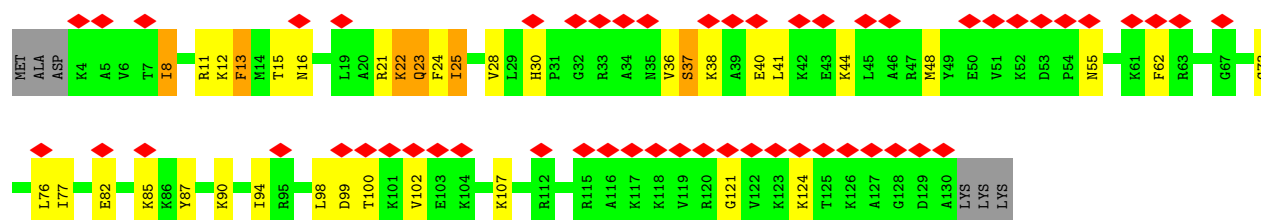
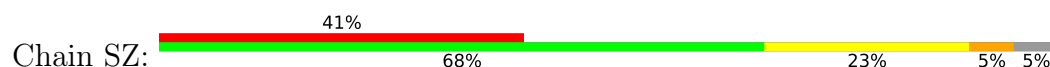
- Molecule 24: 40S ribosomal protein S19-3-like



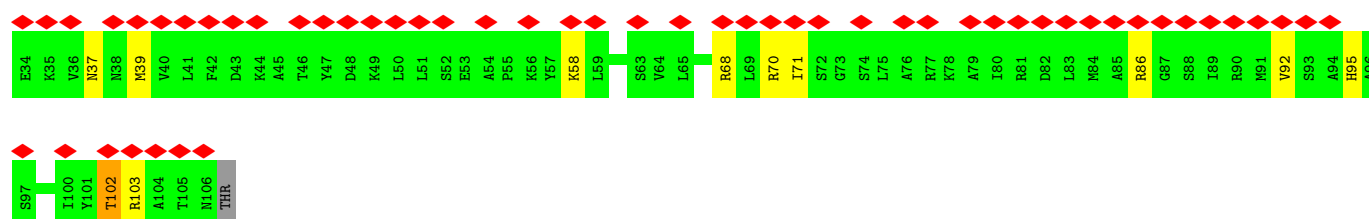
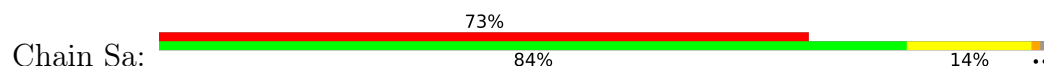
- Molecule 25: 40S ribosomal protein S21



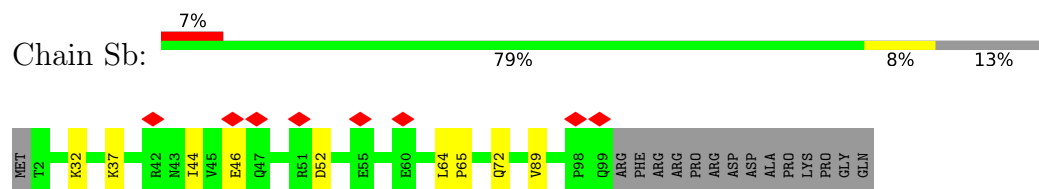
- Molecule 26: 40S ribosomal protein S24



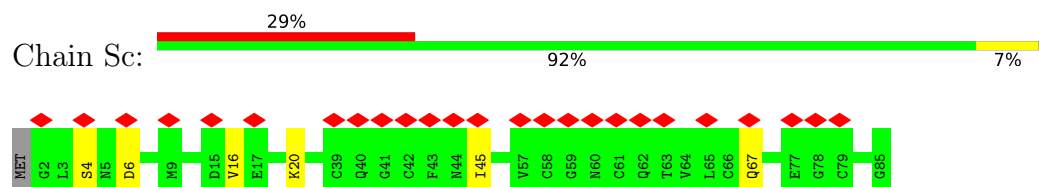
- Molecule 27: 40S ribosomal protein S25



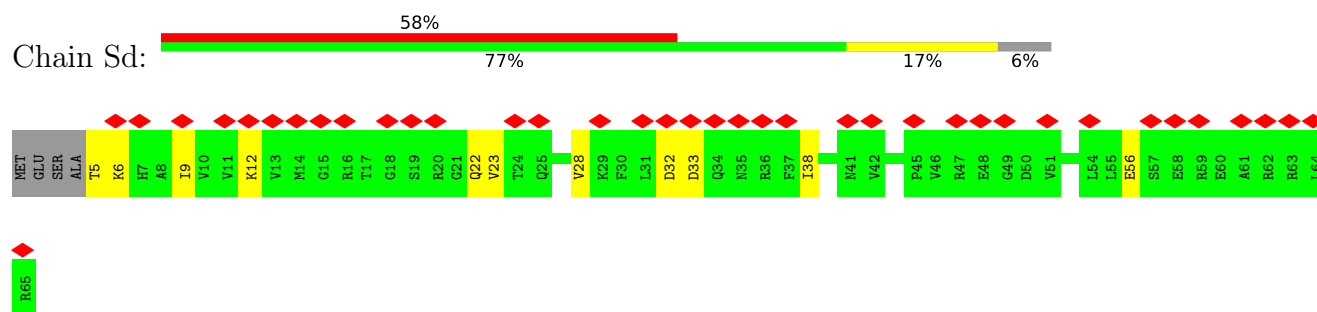
- Molecule 28: 40S ribosomal protein S26



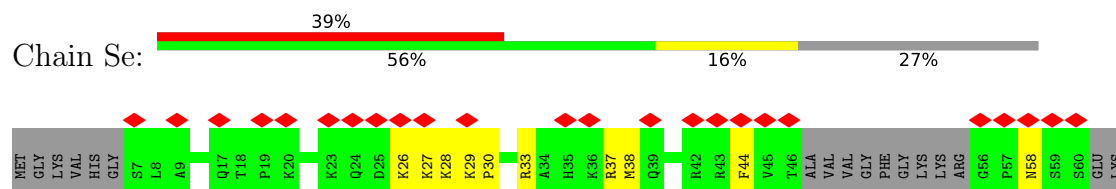
- Molecule 29: 40S ribosomal protein S27



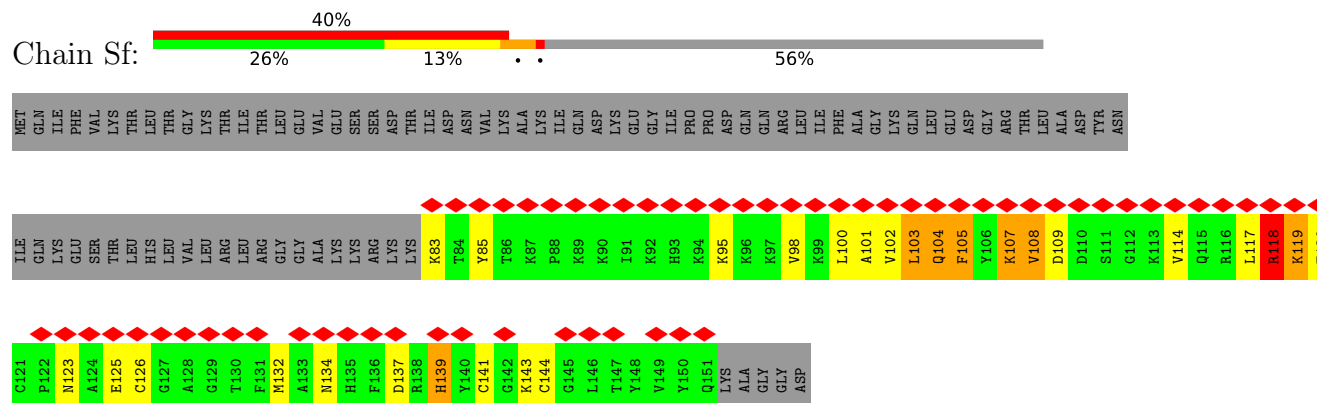
- Molecule 30: 40S ribosomal protein S28



- Molecule 31: 40S ribosomal protein S30

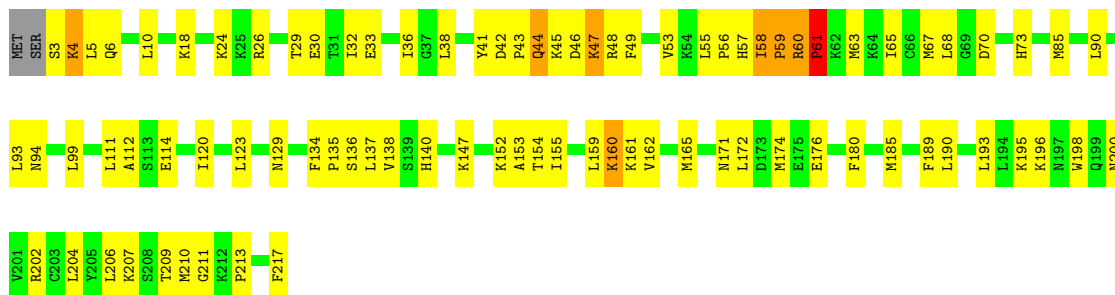


- Molecule 32: Ubiquitin-40S ribosomal protein S27a-like



- Molecule 33: Ribosomal protein





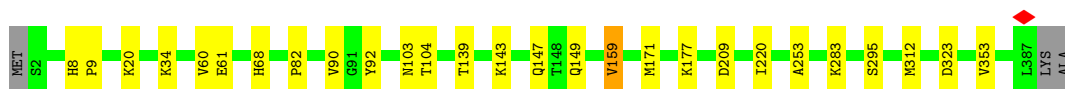
- Molecule 34: 60S ribosomal protein L8-like

Chain LB: 89% 5% 6%



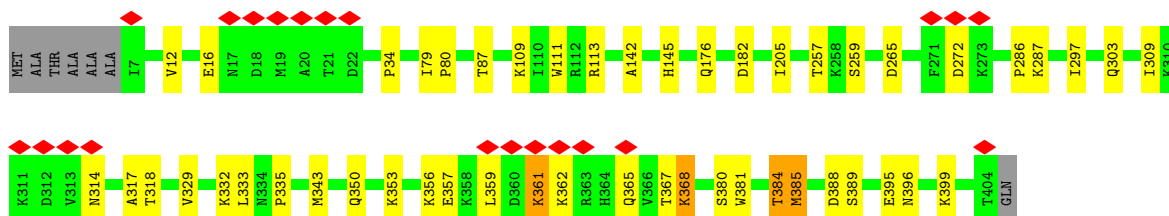
- Molecule 35: 60S ribosomal protein L3

Chain LC: 92% 7% .



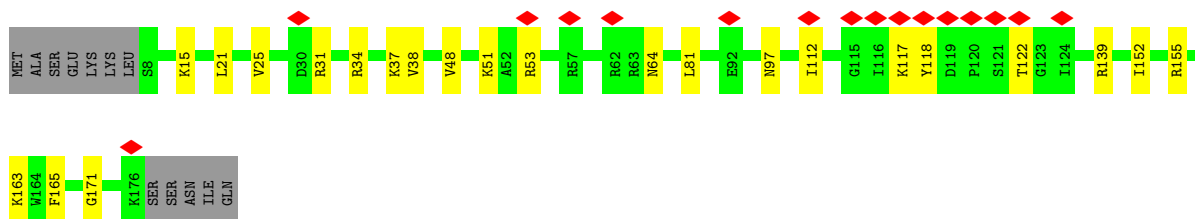
- Molecule 36: 60S ribosomal protein L4-like

Chain LD: 5% 86% 11% ..



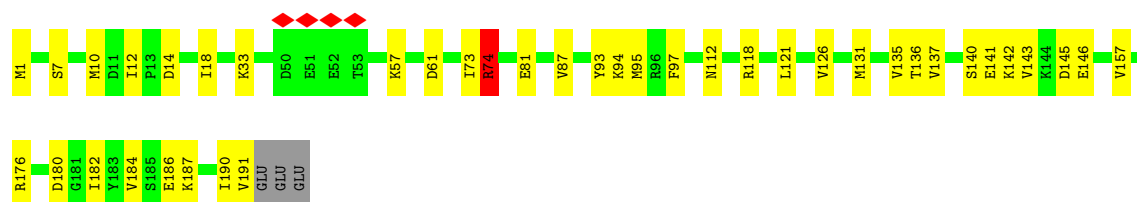
- Molecule 37: 60S ribosomal protein L11-1

Chain LE: 9% 81% 13% 7%



- Molecule 38: 60S ribosomal protein L9-1

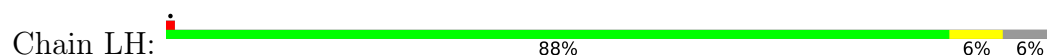
Chain LF: 78% 20% ..



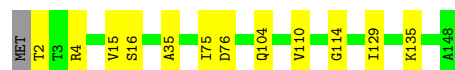
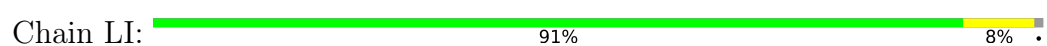
- Molecule 39: 60S ribosomal protein L13a-4



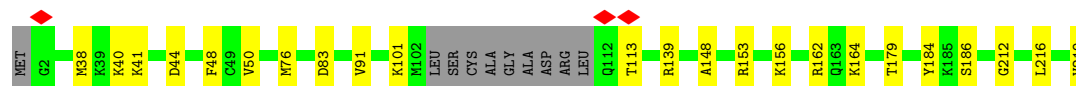
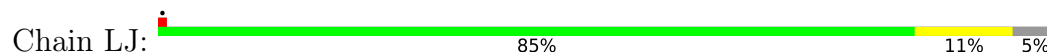
- Molecule 40: 60S ribosomal protein L23



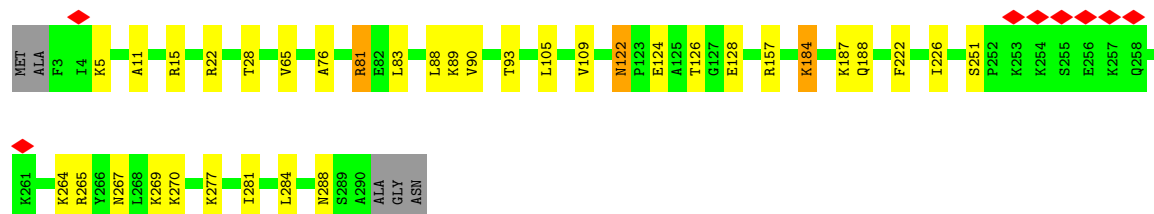
- Molecule 41: 60S ribosomal protein L27a-3



- Molecule 42: 60S ribosomal protein L10



- Molecule 43: 60S ribosomal protein L5-like



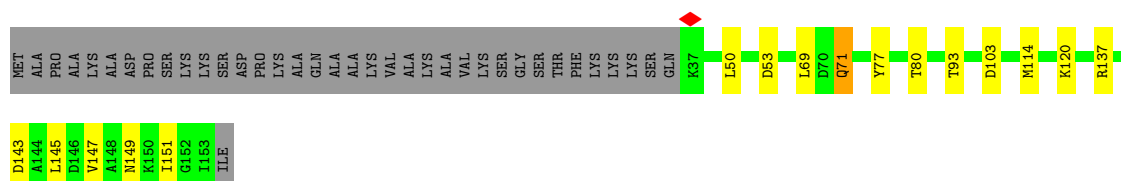
- Molecule 44: 60S ribosomal protein L17-1 isoform X2

Chain LL:  81% 7% 12%



- Molecule 45: Large ribosomal subunit protein uL23

Chain LM:  66% 10% 24%



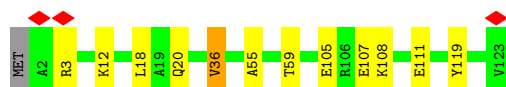
- Molecule 46: 60S ribosomal protein L26-1

Chain LN:  81% 5% 14%



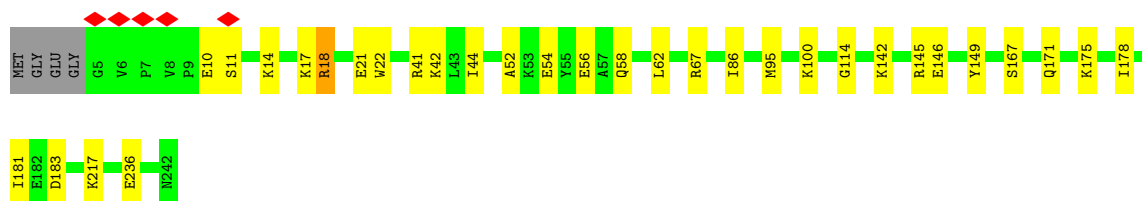
- Molecule 47: 60S ribosomal protein L35-like

Chain LO:  89% 9% ..



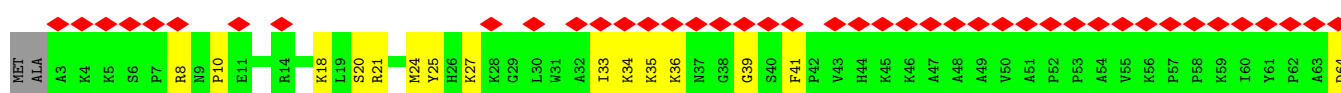
- Molecule 48: 60S ribosomal protein L7-4-like

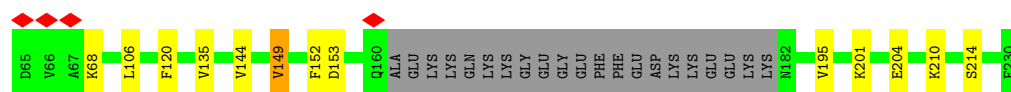
Chain LP:  85% 13% .



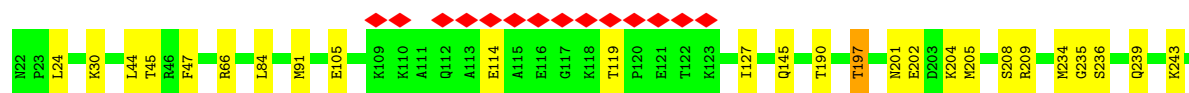
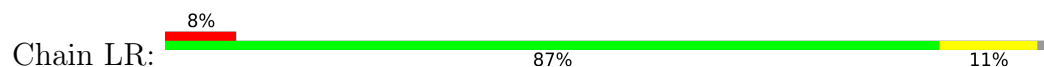
- Molecule 49: 60S ribosomal protein L6-like isoform X1

Chain LQ:  20% 78% 12% 10%





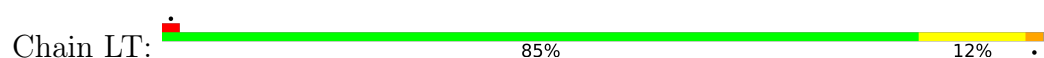
- Molecule 50: 60S ribosomal protein L7a



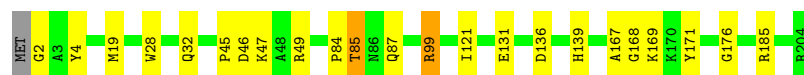
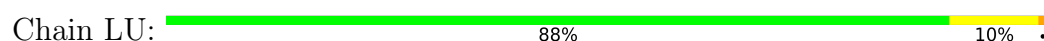
- Molecule 51: 60S ribosomal protein L13



- Molecule 52: 60S ribosomal protein L14-1



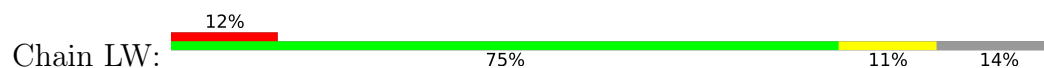
- Molecule 53: Ribosomal protein L15



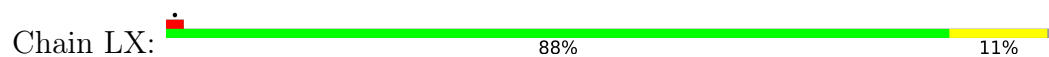
- Molecule 54: 60S ribosomal protein L18-2



- Molecule 55: Ribosomal protein L19



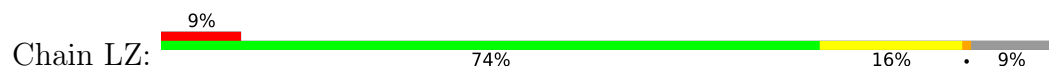
- Molecule 56: 60S ribosomal protein L18a



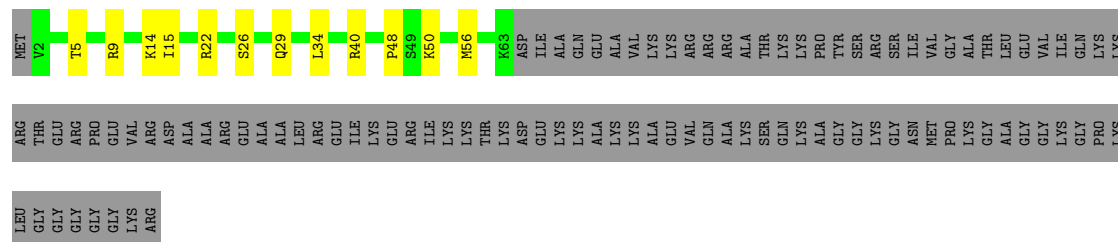
- Molecule 57: 60S ribosomal protein L21-1-like



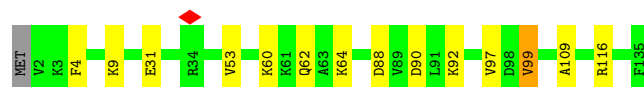
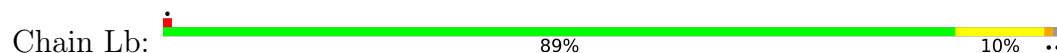
- Molecule 58: Large ribosomal subunit protein eL22



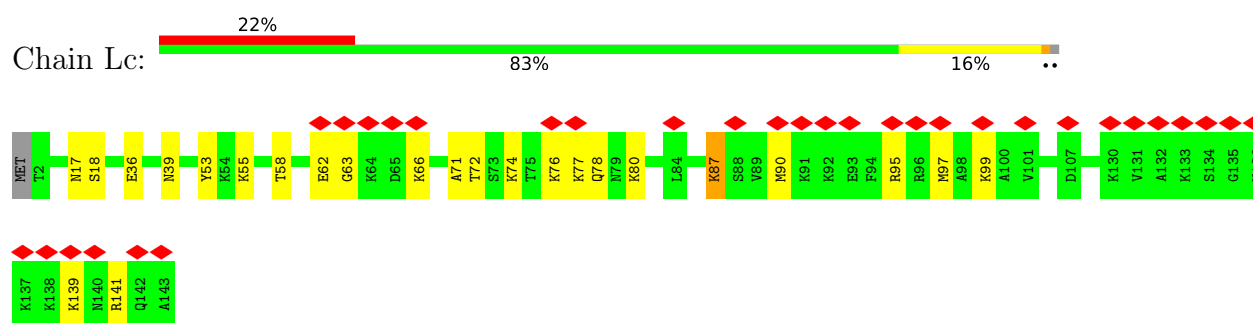
- Molecule 59: 60S ribosomal protein L24



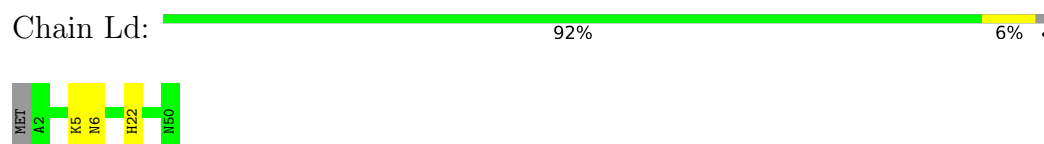
- Molecule 60: 60S ribosomal protein L27



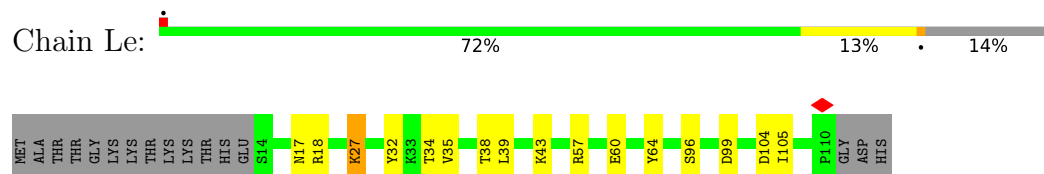
- Molecule 61: 60S ribosomal protein L28-1-like



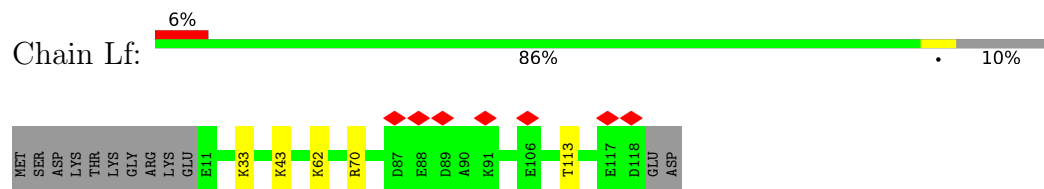
- Molecule 62: 60S ribosomal protein L29



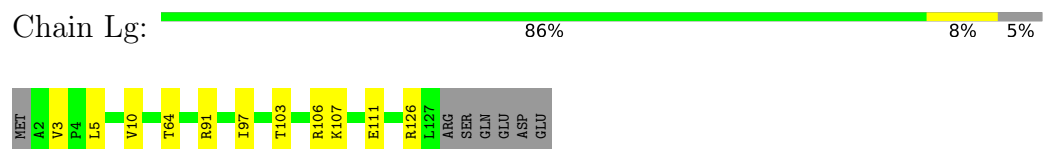
- Molecule 63: 60S ribosomal protein L30



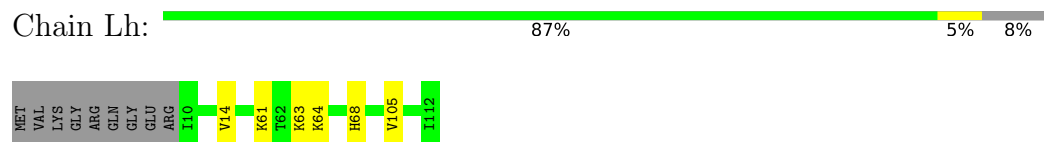
- Molecule 64: 60S ribosomal protein L31



- Molecule 65: 60S ribosomal protein L32-1

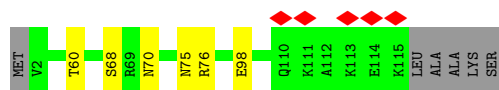


- Molecule 66: 60S ribosomal protein L35a-3-like

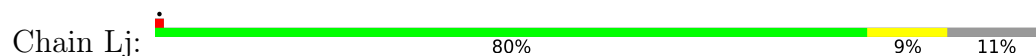


- Molecule 67: Large ribosomal subunit protein eL34





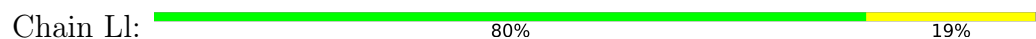
- Molecule 68: 60S ribosomal protein L36



- Molecule 69: Ribosomal protein L37



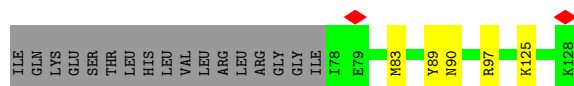
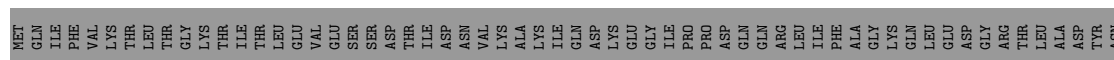
- Molecule 70: 60S ribosomal protein L38



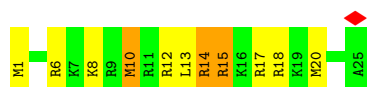
- Molecule 71: 60S ribosomal protein L39-3



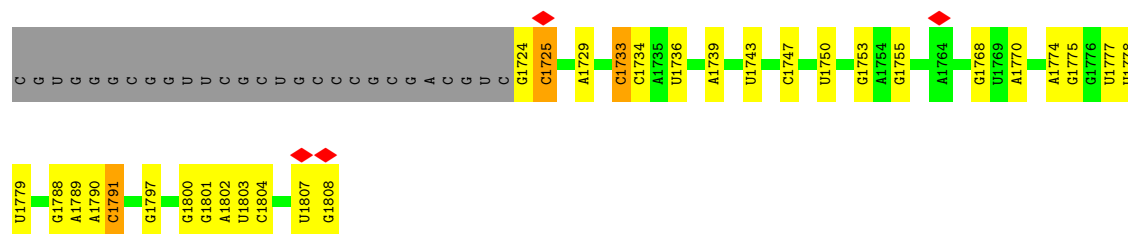
- Molecule 72: Ubiquitin-60S ribosomal protein L40



- Molecule 73: 60s ribosomal protein l41-like







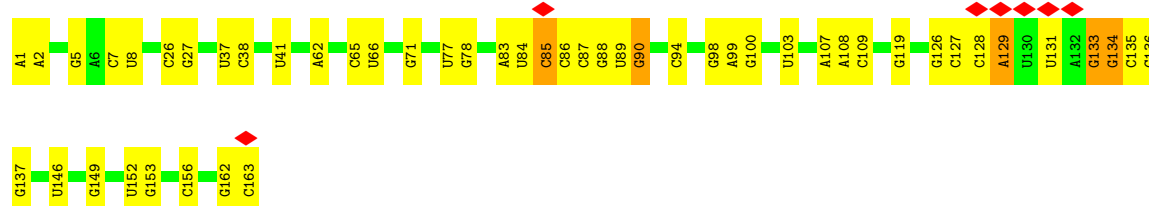
• Molecule 78: 5S rRNA

Chain 12: 84% 13% .



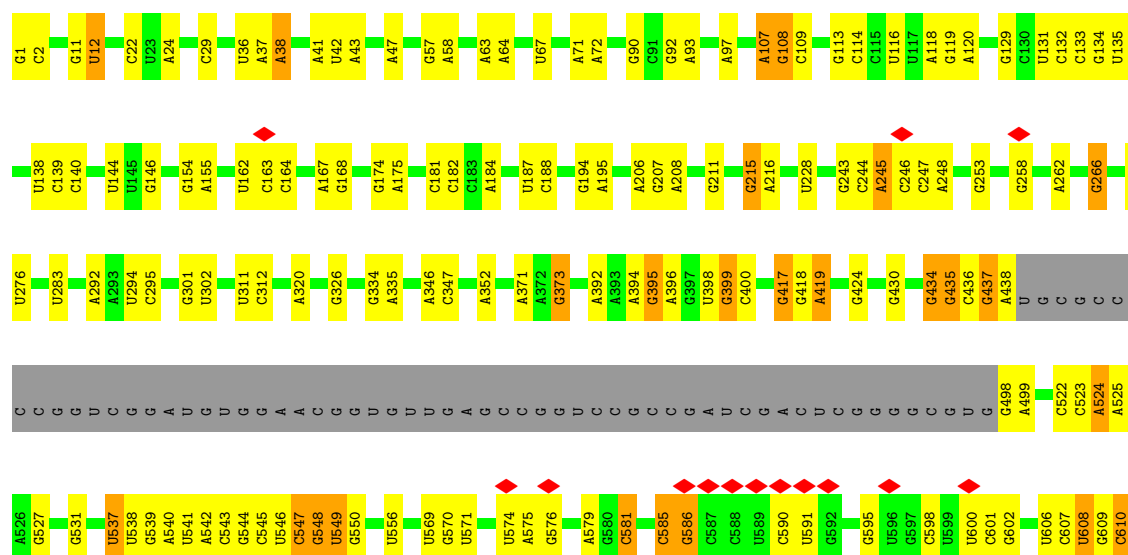
• Molecule 79: 5.8S rRNA

Chain 13: 69% 28% .

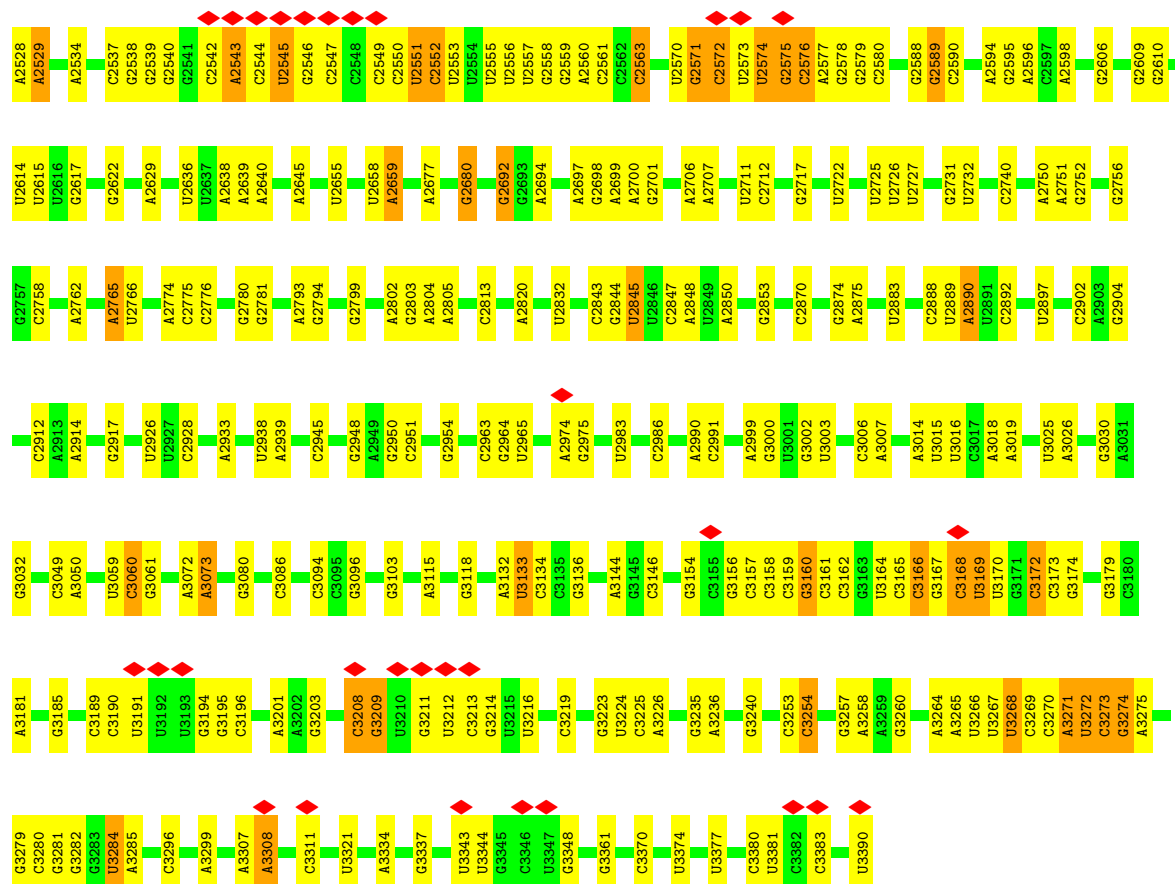


• Molecule 80: 25S rRNA

Chain 14: 67% 23% 7%







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	422599	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	2.131	Depositor
Minimum map value	-0.895	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	537.04, 537.04, 537.04	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95899993, 0.95899993, 0.95899993	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

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	SA	0.30	0/1637	0.45	0/2214
2	SB	0.34	0/1668	0.56	0/2238
3	SC	0.36	0/1528	0.52	0/2048
4	SD	0.27	0/1721	0.44	0/2320
5	SE	0.60	0/1542	0.82	0/2082
6	SF	0.26	0/1050	0.41	0/1405
7	SG	0.31	0/1154	0.49	0/1542
8	SH	0.20	0/813	0.46	0/1095
9	SI	0.36	0/1010	0.56	1/1352 (0.1%)
10	SJ	0.24	0/1119	0.40	0/1487
11	SK	0.25	0/1161	0.47	0/1550
12	SL	0.19	0/453	0.31	0/605
13	SM	0.24	0/1214	0.34	0/1632
14	SN	0.26	0/1180	0.43	0/1579
15	SO	0.26	0/1080	0.55	0/1445
16	SP	0.26	0/1790	0.41	0/2402
17	SQ	0.27	0/2108	0.44	0/2830
18	SR	0.35	0/1850	0.55	0/2465
19	SS	0.19	0/1561	0.44	0/2098
20	ST	0.29	0/1528	0.44	0/2041
21	SU	0.45	0/790	0.72	0/1069
22	SV	0.93	0/609	1.12	1/825 (0.1%)
23	SW	0.60	0/682	0.81	0/906
24	SX	0.32	0/1103	0.49	0/1480
25	SY	0.21	0/661	0.39	0/888
26	SZ	0.34	0/1015	0.58	0/1352
27	Sa	0.22	0/580	0.46	0/778
28	Sb	0.25	0/802	0.37	0/1072
29	Sc	0.19	0/661	0.30	0/888
30	Sd	0.19	0/496	0.36	0/661
31	Se	0.21	0/357	0.50	0/470
32	Sf	0.46	0/574	0.70	0/763

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LA	0.75	0/1727	1.15	1/2310 (0.0%)
34	LB	0.31	0/1924	0.51	0/2585
35	LC	0.29	0/3175	0.47	0/4253
36	LD	0.45	0/3149	0.66	0/4249
37	LE	0.25	0/1384	0.46	0/1852
38	LF	0.27	0/1539	0.47	0/2058
39	LG	0.28	0/1673	0.42	0/2241
40	LH	0.28	0/1001	0.47	0/1345
41	LI	0.38	0/1183	0.52	0/1581
42	LJ	0.25	0/1707	0.39	0/2283
43	LK	0.35	0/2384	0.50	0/3197
44	LL	0.33	0/1261	0.51	0/1693
45	LM	0.27	0/965	0.45	0/1295
46	LN	0.26	0/1037	0.42	0/1385
47	LO	0.25	0/1007	0.37	0/1340
48	LP	0.29	0/1993	0.49	0/2672
49	LQ	0.20	0/1634	0.37	0/2196
50	LR	0.24	0/1907	0.36	0/2555
51	LS	0.26	0/1638	0.42	0/2198
52	LT	0.25	0/1059	0.40	0/1415
53	LU	0.32	0/1740	0.49	0/2333
54	LV	0.29	0/1487	0.45	0/1989
55	LW	0.28	0/1538	0.45	0/2031
56	LX	0.30	0/1544	0.41	0/2071
57	LY	0.30	0/1331	0.44	0/1784
58	LZ	0.39	0/810	0.61	0/1085
59	La	0.24	0/539	0.40	0/716
60	Lb	0.26	0/1116	0.39	0/1489
61	Lc	0.33	0/1130	0.56	0/1514
62	Ld	0.40	0/417	0.61	0/555
63	Le	0.27	0/757	0.42	0/1018
64	Lf	0.27	0/885	0.38	0/1184
65	Lg	0.30	0/1051	0.49	0/1407
66	Lh	0.29	0/856	0.43	0/1149
67	Li	0.27	0/939	0.42	0/1251
68	Lj	0.24	0/793	0.45	0/1050
69	Lk	0.33	0/714	0.54	0/949
70	Ll	0.22	0/566	0.34	0/752
71	Lm	0.29	0/460	0.42	0/611
72	Ln	0.17	0/426	0.37	0/561
73	Lo	0.77	0/234	1.21	0/300
74	Lp	0.43	0/799	0.56	0/1055
75	Lq	0.33	0/595	0.48	0/791

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	10	0.67	0/3752	1.06	4/5844 (0.1%)
77	11	0.36	0/38798	0.48	2/60451 (0.0%)
78	12	0.31	0/2837	0.35	0/4420
79	13	0.37	0/3889	0.43	0/6060
80	14	0.42	0/75291	0.53	2/117423 (0.0%)
All	All	0.38	0/214138	0.53	11/314128 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	SB	0	1
5	SE	0	4
7	SG	0	1
18	SR	0	2
22	SV	0	1
23	SW	0	6
24	SX	0	1
32	Sf	0	1
33	LA	0	4
37	LE	0	1
38	LF	0	1
73	Lo	0	6
All	All	0	29

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	LA	61	PRO	N-CA-CB	-8.12	94.72	103.25
76	10	164	C	C2'-C3'-O3'	-6.79	103.52	113.70
9	SI	136	THR	N-CA-C	-6.06	103.84	111.11
80	14	1093	U	C2'-C3'-O3'	-6.05	104.62	113.70
76	10	160	A	C2'-C3'-O3'	5.97	118.46	109.50
77	11	1668	G	C4'-C3'-C2'	-5.52	97.08	102.60
77	11	128	G	O3'-P-O5'	-5.46	95.81	104.00
22	SV	125	LYS	N-CA-C	-5.21	106.83	114.39
76	10	105	C	O3'-P-O5'	-5.21	96.19	104.00
80	14	692	A	C3'-C2'-C1'	-5.13	96.37	101.50
76	10	161	A	C4'-C3'-O3'	5.04	116.95	109.40

There are no chirality outliers.

All (29) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	LA	202	ARG	Sidechain
33	LA	26	ARG	Sidechain
33	LA	48	ARG	Sidechain
33	LA	60	ARG	Sidechain
37	LE	31	ARG	Sidechain
38	LF	74	ARG	Sidechain
73	Lo	12	ARG	Sidechain
73	Lo	14	ARG	Sidechain
73	Lo	15	ARG	Sidechain
73	Lo	17	ARG	Sidechain
73	Lo	18	ARG	Sidechain
73	Lo	6	ARG	Sidechain
2	SB	97	ARG	Sidechain
5	SE	151	ARG	Sidechain
5	SE	152	ARG	Sidechain
5	SE	165	ARG	Sidechain
5	SE	27	ARG	Sidechain
7	SG	33	ARG	Sidechain
18	SR	156	ARG	Sidechain
18	SR	164	ARG	Sidechain
22	SV	114	ARG	Sidechain
23	SW	45	ARG	Sidechain
23	SW	47	ARG	Sidechain
23	SW	60	ARG	Sidechain
23	SW	78	ARG	Sidechain
23	SW	80	ARG	Sidechain
23	SW	81	ARG	Sidechain
24	SX	57	ARG	Sidechain
32	Sf	118	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	SA	1603	0	1611	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	SB	1645	0	1726	34	0
3	SC	1501	0	1551	22	0
4	SD	1686	0	1789	17	0
5	SE	1520	0	1553	21	0
6	SF	1032	0	1068	12	0
7	SG	1135	0	1198	15	0
8	SH	804	0	865	15	0
9	SI	998	0	1028	10	0
10	SJ	1100	0	1165	5	0
11	SK	1144	0	1171	23	0
12	SL	441	0	434	5	0
13	SM	1189	0	1278	6	0
14	SN	1155	0	1210	9	0
15	SO	1057	0	1127	22	0
16	SP	1760	0	1820	14	0
17	SQ	2068	0	2170	30	0
18	SR	1826	0	1929	46	0
19	SS	1533	0	1587	21	0
20	ST	1504	0	1557	19	0
21	SU	769	0	770	24	0
22	SV	602	0	586	27	0
23	SW	675	0	719	21	0
24	SX	1081	0	1091	21	0
25	SY	651	0	630	6	0
26	SZ	1000	0	1047	28	0
27	Sa	574	0	607	8	0
28	Sb	789	0	824	7	0
29	Sc	650	0	649	3	0
30	Sd	493	0	524	4	0
31	Se	353	0	376	8	0
32	Sf	562	0	584	23	0
33	LA	1702	0	1790	55	0
34	LB	1880	0	1915	9	0
35	LC	3107	0	3232	19	0
36	LD	3087	0	3207	25	0
37	LE	1362	0	1405	14	0
38	LF	1520	0	1614	25	0
39	LG	1644	0	1773	6	0
40	LH	985	0	1046	6	0
41	LI	1155	0	1197	7	0
42	LJ	1671	0	1731	14	0
43	LK	2339	0	2377	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	LL	1236	0	1262	7	0
45	LM	950	0	1029	11	0
46	LN	1023	0	1105	6	0
47	LO	997	0	1136	7	0
48	LP	1958	0	2057	21	0
49	LQ	1600	0	1731	24	0
50	LR	1874	0	2030	17	0
51	LS	1608	0	1697	13	0
52	LT	1046	0	1144	13	0
53	LU	1701	0	1771	15	0
54	LV	1462	0	1581	5	0
55	LW	1519	0	1630	16	0
56	LX	1505	0	1557	13	0
57	LY	1306	0	1367	8	0
58	LZ	799	0	836	10	0
59	La	526	0	554	10	0
60	Lb	1097	0	1182	6	0
61	Lc	1114	0	1189	15	0
62	Ld	407	0	393	2	0
63	Le	745	0	783	9	0
64	Lf	875	0	934	3	0
65	Lg	1034	0	1110	7	0
66	Lh	836	0	865	4	0
67	Li	926	0	1013	4	0
68	Lj	784	0	871	7	0
69	Lk	701	0	729	13	0
70	Ll	558	0	604	9	0
71	Lm	448	0	480	1	0
72	Ln	420	0	461	5	0
73	Lo	233	0	270	3	0
74	Lp	785	0	844	3	0
75	Lq	586	0	611	5	0
76	10	3359	0	1699	97	0
77	11	34688	0	17477	254	0
78	12	2538	0	1286	6	0
79	13	3478	0	1761	20	0
80	14	67280	0	33921	293	0
81	10	7	0	0	0	0
81	14	2	0	0	0	0
82	10	20	0	0	1	0
82	14	14	0	0	0	0
All	All	199397	0	148501	1513	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 (1513) 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)
33:LA:204:LEU:HB2	33:LA:217:PHE:HB3	1.50	0.93
77:11:1594:G:H1	77:11:1614:U:H3	1.13	0.90
57:LY:129:LYS:HB3	80:14:1109:A:H5'	1.51	0.89
33:LA:171:ASN:OD1	33:LA:174:MET:HG3	1.74	0.88
33:LA:36:ILE:HG21	33:LA:190:LEU:HD21	1.58	0.86
80:14:1031:G:H1	80:14:1045:U:H3	1.25	0.84
35:LC:34:LYS:H	35:LC:34:LYS:HD2	1.43	0.84
76:10:74:U:H2'	76:10:75:U:H2'	1.61	0.82
76:10:95:A:H3'	76:10:96:G:H8	1.43	0.82
76:10:93:G:H2'	76:10:94:A:H8	1.43	0.81
22:SV:105:CYS:HB2	22:SV:114:ARG:HH21	1.44	0.81
15:SO:60:PRO:HA	15:SO:90:MET:HE1	1.63	0.80
76:10:184:G:H1'	76:10:196:A:H5'	1.64	0.80
18:SR:193:ARG:NH1	77:11:288:G:N7	2.33	0.77
54:LV:36:LEU:O	54:LV:40:THR:HB	1.85	0.77
80:14:424:G:H22	80:14:643:U:H3	1.31	0.77
49:LQ:24:MET:HE2	49:LQ:24:MET:HA	1.66	0.77
23:SW:21:TYR:HE2	23:SW:73:LEU:HD21	1.49	0.77
80:14:2263:U:HO2'	80:14:2264:G:H8	1.32	0.77
23:SW:21:TYR:HE2	23:SW:73:LEU:CD2	1.98	0.76
80:14:3208:C:H4'	80:14:3209:G:H5'	1.68	0.76
1:SA:84:GLN:HG2	1:SA:100:ALA:HB1	1.67	0.76
36:LD:317:ALA:HB2	80:14:1373:C:H5''	1.69	0.75
8:SH:54:LYS:HA	8:SH:54:LYS:HE3	1.69	0.75
76:10:136:C:H3'	76:10:137:A:C8	2.24	0.73
18:SR:69:THR:HG22	18:SR:71:GLY:H	1.52	0.73
61:Lc:90:MET:HE2	61:Lc:97:MET:HG2	1.71	0.73
22:SV:105:CYS:HB2	22:SV:114:ARG:NH2	2.04	0.72
38:LF:74:ARG:HG2	80:14:3115:A:H4'	1.72	0.72
50:LR:234:MET:SD	80:14:2518:U:H4'	2.29	0.72
77:11:1:U:H2'	77:11:374:A:H5'	1.69	0.72
80:14:746:A:H5'	80:14:991:U:C4	2.24	0.71
79:13:85:C:H2'	79:13:88:G:H4'	1.72	0.71
8:SH:26:THR:HG22	8:SH:91:VAL:HG23	1.71	0.71
22:SV:65:LEU:HB2	22:SV:89:LEU:HD11	1.72	0.71
55:LW:67:LYS:NZ	80:14:2105:C:OP1	2.24	0.71
73:Lo:1:MET:HG3	77:11:1791:C:OP2	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:10:93:G:H2'	76:10:94:A:C8	2.25	0.71
80:14:434:G:H4'	80:14:435:G:H5''	1.73	0.71
76:10:80:C:H3'	76:10:81:U:H6	1.55	0.71
18:SR:23:LYS:HD2	18:SR:42:GLY:H	1.57	0.70
65:Lg:103:THR:HG22	65:Lg:126:ARG:HB3	1.73	0.70
8:SH:55:GLY:HA3	8:SH:92:ILE:HG23	1.72	0.70
66:Lh:61:LYS:HB2	80:14:3168:C:H42	1.56	0.70
36:LD:381:TRP:O	36:LD:385:MET:HG3	1.92	0.69
35:LC:103:ASN:HD21	35:LC:149:GLN:HG2	1.58	0.69
80:14:859:C:H2'	80:14:860:U:C6	2.26	0.69
49:LQ:68:LYS:H	49:LQ:68:LYS:HD2	1.57	0.69
2:SB:58:THR:H	2:SB:93:LYS:HZ1	1.41	0.69
55:LW:123:MET:HE2	55:LW:123:MET:HA	1.75	0.69
22:SV:96:LYS:HA	22:SV:118:GLY:HA2	1.75	0.68
21:SU:43:PHE:HB2	21:SU:103:LEU:HD21	1.76	0.68
80:14:3225:C:H2'	80:14:3226:A:H8	1.57	0.68
25:SY:9:MET:HE3	25:SY:9:MET:HA	1.76	0.68
56:LX:28:ARG:NH1	57:LY:148:THR:OG1	2.27	0.68
69:Lk:46:LYS:NZ	80:14:22:C:OP1	2.26	0.68
33:LA:114:GLU:HG2	33:LA:137:LEU:HD11	1.74	0.67
22:SV:76:LYS:HZ3	32:Sf:108:VAL:HB	1.58	0.67
18:SR:53:MET:HB3	77:11:161:G:H4'	1.76	0.67
44:LL:57:ALA:HB3	44:LL:73:VAL:HG13	1.76	0.67
2:SB:141:VAL:CG1	2:SB:185:LEU:HD11	2.24	0.67
40:LH:96:MET:HE2	59:La:22:ARG:HD2	1.77	0.67
51:LS:37:ARG:NH2	80:14:696:G:OP1	2.26	0.67
43:LK:93:THR:HG22	43:LK:157:ARG:NH1	2.08	0.67
76:10:98:G:C2	76:10:99:U:H1'	2.29	0.67
33:LA:120:ILE:HD13	33:LA:135:PRO:HG2	1.75	0.67
17:SQ:54:TYR:O	26:SZ:16:ASN:ND2	2.28	0.67
18:SR:138:LYS:NZ	18:SR:179:LYS:O	2.25	0.67
33:LA:36:ILE:HD13	33:LA:190:LEU:HD22	1.75	0.67
76:10:79:C:H2'	76:10:80:C:C6	2.29	0.67
76:10:140:U:H2'	76:10:141:A:H8	1.60	0.67
8:SH:83:PHE:HB3	12:SL:52:PHE:HB3	1.76	0.66
5:SE:35:ILE:HG23	5:SE:123:ILE:HD11	1.78	0.66
76:10:70:G:H2'	76:10:71:U:C6	2.31	0.66
77:11:104:A:H2	77:11:362:U:H3	1.43	0.66
77:11:871:G:H1	77:11:963:U:H3	1.43	0.66
80:14:764:G:H2'	80:14:765:A:H8	1.60	0.66
55:LW:162:ARG:HG2	77:11:819:G:N2	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:LW:7:GLN:NE2	55:LW:35:ALA:O	2.27	0.66
76:10:105:C:H2'	76:10:106:U:C6	2.31	0.66
11:SK:121:ARG:NH1	77:11:1552:G:OP1	2.28	0.66
59:La:5:THR:HG21	59:La:14:LYS:HG3	1.76	0.66
21:SU:46:GLY:HA2	21:SU:95:LEU:HD12	1.78	0.66
38:LF:94:LYS:NZ	38:LF:186:GLU:OE2	2.24	0.66
45:LM:93:THR:HG22	45:LM:137:ARG:HG3	1.77	0.65
77:11:647:A:N1	77:11:690:C:N4	2.43	0.65
38:LF:176:ARG:NH1	72:Ln:125:LYS:O	2.29	0.65
77:11:109:A:H2'	77:11:110:G:C8	2.32	0.65
80:14:3159:C:H2'	80:14:3160:G:C8	2.31	0.65
76:10:96:G:H3'	76:10:97:G:H8	1.62	0.65
38:LF:131:MET:HB3	38:LF:135:VAL:HG13	1.78	0.65
76:10:136:C:H3'	76:10:137:A:H8	1.60	0.65
15:SO:63:LEU:HD23	15:SO:90:MET:HE3	1.77	0.64
15:SO:65:LYS:HD2	15:SO:66:LYS:N	2.12	0.64
69:Lk:65:ARG:NH2	79:13:103:U:O4	2.23	0.64
74:Lp:6:LYS:HD3	74:Lp:94:GLY:HA3	1.79	0.64
77:11:1044:G:H2'	77:11:1045:G:C8	2.32	0.64
80:14:3280:C:H2'	80:14:3281:G:C8	2.32	0.64
27:Sa:39:MET:HE2	27:Sa:71:ILE:HG22	1.79	0.64
79:13:1:A:O2'	80:14:2999:A:N7	2.29	0.64
8:SH:54:LYS:HB2	8:SH:93:ASP:HB2	1.79	0.64
45:LM:145:LEU:O	45:LM:149:ASN:ND2	2.31	0.64
76:10:87:U:H4'	76:10:88:A:C2	2.33	0.64
38:LF:141:GLU:N	38:LF:141:GLU:OE1	2.30	0.64
50:LR:205:MET:HE1	50:LR:209:ARG:HE	1.63	0.64
9:SI:98:ALA:H	9:SI:132:THR:HB	1.63	0.64
80:14:2216:A:H2'	80:14:2217:A:C8	2.33	0.64
1:SA:77:GLN:HB3	1:SA:99:ILE:HB	1.79	0.63
80:14:2543:A:H2	80:14:2545:U:H3	1.45	0.63
17:SQ:146:THR:HG21	77:11:124:G:H21	1.63	0.63
50:LR:201:ASN:HA	50:LR:204:LYS:HG3	1.80	0.63
58:LZ:100:ARG:HD3	58:LZ:116:PHE:HB3	1.80	0.63
20:ST:204:LEU:O	20:ST:208:MET:HG3	1.98	0.63
43:LK:89:LYS:HG2	43:LK:90:VAL:HG13	1.79	0.63
2:SB:142:SER:O	2:SB:185:LEU:HD12	1.97	0.63
20:ST:163:LYS:HE3	20:ST:164:ASP:HB3	1.80	0.63
47:LO:55:ALA:O	47:LO:59:THR:HG23	1.98	0.63
77:11:1356:U:H3	77:11:1375:G:H1	1.45	0.63
79:13:133:G:H2'	79:13:134:G:C8	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SE:190:SER:HA	76:10:96:G:H4'	1.78	0.63
48:LP:217:LYS:NZ	80:14:1169:G:OP1	2.31	0.63
16:SP:91:VAL:HG22	16:SP:96:VAL:HG12	1.79	0.63
38:LF:97:PHE:HB2	38:LF:145:ASP:HB3	1.81	0.63
76:10:118:G:C4	76:10:119:G:H1'	2.33	0.63
77:11:942:A:H2'	77:11:943:A:C8	2.34	0.63
31:Se:58:ASN:ND2	77:11:591:U:O2	2.32	0.62
22:SV:100:GLU:HG2	22:SV:105:CYS:HB3	1.79	0.62
77:11:1174:A:H2'	77:11:1175:G:C8	2.33	0.62
32:Sf:108:VAL:HG23	32:Sf:114:VAL:HG12	1.82	0.62
38:LF:12:ILE:HD13	38:LF:18:ILE:HG21	1.81	0.62
6:SF:55:ASP:OD2	6:SF:60:LYS:NZ	2.31	0.62
18:SR:166:PHE:HE1	18:SR:176:LYS:HG3	1.64	0.62
2:SB:104:GLN:HG3	2:SB:129:ILE:HD11	1.80	0.62
22:SV:66:ALA:HA	22:SV:92:VAL:HG13	1.80	0.62
35:LC:82:PRO:HG2	35:LC:171:MET:HE2	1.80	0.62
18:SR:169:LYS:NZ	77:11:70:C:OP1	2.29	0.62
47:LO:3:ARG:NH2	79:13:90:G:OP2	2.32	0.62
8:SH:23:ILE:HG21	8:SH:101:VAL:HG21	1.81	0.62
77:11:128:G:H1'	77:11:177:C:H42	1.63	0.61
2:SB:68:ARG:O	2:SB:71:GLU:HB2	2.00	0.61
17:SQ:110:ARG:NH1	77:11:789:C:O2	2.33	0.61
45:LM:71:GLN:NE2	45:LM:114:MET:SD	2.73	0.61
61:Lc:53:TYR:OH	80:14:1364:G:N2	2.33	0.61
76:10:75:U:H1'	76:10:76:U:H2'	1.82	0.61
80:14:417:G:N2	80:14:2388:G:OP2	2.30	0.61
18:SR:133:ARG:NH1	77:11:164:C:OP1	2.30	0.61
41:LI:110:VAL:HB	41:LI:129:ILE:HD12	1.83	0.61
80:14:858:A:H3'	80:14:859:C:O4'	2.00	0.61
80:14:2235:A:H2'	80:14:2236:A:C8	2.36	0.61
14:SN:34:ARG:NH1	14:SN:49:ALA:O	2.33	0.61
16:SP:152:ARG:NH2	77:11:1047:U:OP1	2.28	0.61
22:SV:35:LEU:HD11	22:SV:98:LEU:HD12	1.82	0.61
80:14:692:A:N6	80:14:708:C:H2'	2.15	0.61
4:SD:82:ILE:O	4:SD:82:ILE:HG13	2.00	0.61
15:SO:110:ASN:ND2	15:SO:127:SER:OG	2.34	0.61
24:SX:25:ARG:HB2	24:SX:25:ARG:NH1	2.16	0.61
4:SD:244:ARG:CZ	4:SD:244:ARG:HA	2.30	0.61
77:11:888:G:H2'	77:11:889:U:C6	2.35	0.61
3:SC:132:ARG:NH1	3:SC:144:ASN:O	2.33	0.60
8:SH:25:ILE:HG22	8:SH:117:VAL:HG12	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:SZ:28:VAL:HG21	26:SZ:36:VAL:HG21	1.83	0.60
33:LA:4:LYS:HB2	33:LA:217:PHE:HE1	1.66	0.60
56:LX:84:GLN:HG3	56:LX:89:TYR:CE1	2.35	0.60
11:SK:105:MET:HE3	11:SK:105:MET:HA	1.82	0.60
13:SM:46:THR:H	13:SM:49:GLN:HE21	1.49	0.60
17:SQ:196:LYS:NZ	17:SQ:211:GLN:OE1	2.34	0.60
23:SW:9:VAL:HG13	23:SW:50:ILE:HA	1.83	0.60
80:14:1236:C:H41	80:14:1297:G:H21	1.49	0.60
18:SR:46:LYS:H	18:SR:46:LYS:HD2	1.66	0.60
80:14:1819:A:H2'	80:14:1820:G:C8	2.35	0.60
77:11:874:A:H2'	77:11:875:G:C8	2.37	0.60
80:14:1959:G:O4'	80:14:2096:A:N6	2.35	0.60
17:SQ:151:ASP:HB3	17:SQ:154:ILE:HG13	1.83	0.60
2:SB:178:ILE:HD11	2:SB:187:ILE:HD13	1.84	0.60
18:SR:32:ILE:HG12	18:SR:102:CYS:HB2	1.82	0.60
77:11:276:G:H2'	77:11:277:G:H8	1.66	0.60
6:SF:20:ARG:HG2	6:SF:22:LYS:HE2	1.84	0.60
24:SX:109:GLN:HE22	24:SX:116:PHE:HD1	1.50	0.60
80:14:1206:G:H2'	80:14:1207:A:C8	2.36	0.60
42:LJ:76:MET:HE2	42:LJ:148:ALA:HA	1.84	0.60
77:11:411:A:H2'	77:11:412:C:C6	2.36	0.60
80:14:673:U:H2'	80:14:674:C:C6	2.37	0.60
7:SG:116:LEU:HD22	7:SG:123:LEU:HD13	1.84	0.59
2:SB:79:ARG:NH1	2:SB:79:ARG:O	2.34	0.59
36:LD:16:GLU:H	36:LD:176:GLN:NE2	1.99	0.59
33:LA:85:MET:HE1	33:LA:93:LEU:HD11	1.83	0.59
77:11:631:G:H21	77:11:974:A:H62	1.51	0.59
76:10:118:G:C5	76:10:119:G:H1'	2.37	0.59
21:SU:106:TYR:HD1	21:SU:107:LEU:HD13	1.67	0.59
22:SV:92:VAL:HG11	22:SV:98:LEU:HD13	1.85	0.59
77:11:818:A:H1'	77:11:819:G:H3'	1.83	0.59
39:LG:179:LEU:HD11	52:LT:129:LYS:HE2	1.84	0.59
80:14:162:U:H3	80:14:253:G:H1	1.51	0.59
80:14:955:C:H2'	80:14:956:C:C6	2.37	0.59
19:SS:53:ASP:HA	19:SS:59:LYS:HG2	1.84	0.59
33:LA:213:PRO:HD3	80:14:2496:A:H4'	1.85	0.59
47:LO:107:GLU:O	47:LO:111:GLU:HG2	2.03	0.59
23:SW:21:TYR:CE2	23:SW:73:LEU:CD2	2.84	0.59
17:SQ:187:ARG:HH21	77:11:756:A:P	2.26	0.59
23:SW:21:TYR:CE2	23:SW:73:LEU:HD21	2.36	0.59
33:LA:209:THR:HG21	80:14:2470:G:H4'	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:LK:265:ARG:NH1	43:LK:267:ASN:O	2.35	0.59
80:14:692:A:H62	80:14:708:C:H2'	1.67	0.59
80:14:3049:C:O2'	80:14:3050:A:H5'	2.03	0.59
2:SB:42:VAL:HG22	2:SB:51:ILE:HG12	1.84	0.58
5:SE:133:ARG:NH2	5:SE:139:VAL:O	2.36	0.58
42:LJ:83:ASP:OD1	42:LJ:83:ASP:N	2.36	0.58
49:LQ:34:LYS:O	49:LQ:39:GLY:N	2.30	0.58
4:SD:48:THR:OG1	4:SD:74:GLU:OE1	2.21	0.58
24:SX:128:GLY:O	24:SX:132:LEU:HD12	2.03	0.58
35:LC:90:VAL:HG22	35:LC:104:THR:HG23	1.85	0.58
77:11:76:C:H2'	77:11:77:A:C4	2.37	0.58
80:14:394:A:H4'	80:14:395:G:H3'	1.85	0.58
6:SF:2:VAL:N	77:11:1037:C:HO2'	2.00	0.58
78:12:29:C:O2'	78:12:50:A:N1	2.35	0.58
8:SH:52:ARG:O	8:SH:95:PHE:HB2	2.03	0.58
77:11:789:C:N4	77:11:791:G:OP1	2.37	0.58
77:11:1061:U:H3	77:11:1065:A:H62	1.50	0.58
19:SS:106:LYS:HD3	19:SS:107:ARG:N	2.18	0.58
33:LA:210:MET:HE1	80:14:2493:A:N1	2.19	0.58
19:SS:30:MET:HE3	19:SS:30:MET:HA	1.86	0.58
32:Sf:123:ASN:HD21	32:Sf:125:GLU:HB3	1.68	0.58
80:14:1:G:H2'	80:14:2:C:C6	2.39	0.58
80:14:1818:G:H2'	80:14:1819:A:O4'	2.03	0.58
76:10:124:A:H2'	76:10:125:U:C2	2.39	0.58
5:SE:108:LEU:HD21	27:Sa:102:THR:HG22	1.85	0.58
15:SO:93:VAL:H	15:SO:96:MET:HG3	1.69	0.58
33:LA:94:ASN:HA	33:LA:123:LEU:O	2.04	0.58
22:SV:35:LEU:HD12	22:SV:101:TRP:HB2	1.85	0.58
22:SV:76:LYS:CE	32:Sf:108:VAL:HB	2.33	0.58
80:14:855:G:O2'	80:14:856:A:N7	2.36	0.58
4:SD:252:GLU:HG2	4:SD:253:TYR:CE1	2.39	0.57
38:LF:95:MET:HE2	38:LF:182:ILE:HG22	1.84	0.57
49:LQ:8:ARG:HD2	49:LQ:27:LYS:HB3	1.85	0.57
76:10:140:U:H2'	76:10:141:A:C8	2.38	0.57
18:SR:17:GLU:OE1	18:SR:17:GLU:N	2.37	0.57
18:SR:51:LYS:HG2	18:SR:53:MET:HE3	1.85	0.57
30:Sd:32:ASP:OD1	30:Sd:33:ASP:N	2.37	0.57
24:SX:15:PHE:HZ	24:SX:132:LEU:HD23	1.70	0.57
34:LB:104:LEU:HA	34:LB:107:ILE:HD12	1.86	0.57
21:SU:42:LEU:HD13	21:SU:73:MET:HE1	1.86	0.57
35:LC:177:LYS:NZ	80:14:3307:A:OP1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:11:276:G:H2'	77:11:277:G:C8	2.39	0.57
2:SB:120:ARG:HG3	2:SB:120:ARG:HH11	1.70	0.57
4:SD:52:ARG:HB2	4:SD:52:ARG:NH1	2.20	0.57
22:SV:39:LYS:HE2	22:SV:44:LEU:HD21	1.87	0.57
17:SQ:67:GLN:NE2	26:SZ:87:TYR:OH	2.25	0.56
36:LD:16:GLU:H	36:LD:176:GLN:HE22	1.50	0.56
41:LI:35:ALA:HB1	80:14:38:A:H5''	1.86	0.56
77:11:1227:G:H2'	77:11:1228:U:H6	1.70	0.56
77:11:1479:G:H2'	77:11:1480:A:C8	2.40	0.56
5:SE:47:THR:HG22	5:SE:48:ALA:N	2.21	0.56
80:14:3281:G:H2'	80:14:3282:G:C8	2.40	0.56
1:SA:93:TYR:HE2	1:SA:197:VAL:HG11	1.69	0.56
19:SS:82:ARG:HA	19:SS:85:GLU:OE2	2.05	0.56
35:LC:34:LYS:HD2	35:LC:34:LYS:N	2.17	0.56
76:10:80:C:H1'	76:10:157:A:H2	1.70	0.56
77:11:161:G:OP2	77:11:161:G:N2	2.38	0.56
80:14:2476:A:H3'	80:14:2477:A:H8	1.71	0.56
11:SK:116:LYS:O	11:SK:116:LYS:HD3	2.06	0.56
53:LU:4:TYR:OH	80:14:146:G:OP2	2.23	0.56
76:10:164:C:N4	82:10:402:HOH:O	2.38	0.56
80:14:3166:C:H2'	80:14:3167:G:C8	2.41	0.56
19:SS:12:LYS:HD2	19:SS:12:LYS:O	2.05	0.56
43:LK:83:LEU:HD13	43:LK:88:LEU:HD23	1.88	0.56
77:11:411:A:H2'	77:11:412:C:H6	1.69	0.56
11:SK:75:ARG:HG2	11:SK:75:ARG:HH11	1.71	0.56
57:LY:9:SER:O	57:LY:55:LYS:NZ	2.38	0.56
68:Lj:24:GLU:CD	68:Lj:24:GLU:H	2.12	0.56
80:14:3284:U:H2'	80:14:3285:A:C5	2.41	0.56
19:SS:155:LEU:HD11	19:SS:184:PHE:HD2	1.70	0.56
43:LK:93:THR:HG22	43:LK:157:ARG:HH12	1.70	0.56
49:LQ:41:PHE:HB3	80:14:609:G:N3	2.21	0.56
53:LU:45:PRO:O	53:LU:49:ARG:HG3	2.06	0.56
17:SQ:67:GLN:OE1	17:SQ:69:GLN:NE2	2.39	0.56
22:SV:76:LYS:NZ	32:Sf:108:VAL:HB	2.20	0.56
33:LA:4:LYS:HB2	33:LA:217:PHE:CE1	2.41	0.56
33:LA:70:ASP:OD2	33:LA:140:HIS:HE1	1.89	0.56
33:LA:204:LEU:HB2	33:LA:217:PHE:CB	2.32	0.56
36:LD:145:HIS:HD2	36:LD:182:ASP:OD2	1.89	0.56
23:SW:60:ARG:HA	23:SW:63:LYS:HG3	1.87	0.55
33:LA:213:PRO:HG3	80:14:2496:A:O3'	2.06	0.55
77:11:12:U:H2'	77:11:13:C:C6	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:14:116:U:O2	80:14:119:G:H5''	2.06	0.55
6:SF:22:LYS:NZ	29:Sc:4:SER:OG	2.25	0.55
23:SW:9:VAL:HG13	23:SW:50:ILE:HG12	1.87	0.55
36:LD:297:ILE:O	36:LD:303:GLN:NE2	2.39	0.55
37:LE:37:LYS:HB2	37:LE:37:LYS:NZ	2.20	0.55
50:LR:44:LEU:HD11	80:14:2529:A:C6	2.42	0.55
80:14:181:C:H2'	80:14:182:C:C6	2.41	0.55
20:ST:34:ALA:HB2	20:ST:57:ARG:HD2	1.89	0.55
37:LE:163:LYS:NZ	37:LE:163:LYS:HB3	2.22	0.55
77:11:789:C:H3'	77:11:790:U:H5'	1.88	0.55
21:SU:52:LYS:NZ	77:11:1440:G:N7	2.54	0.55
21:SU:101:GLU:OE1	21:SU:102:PHE:N	2.40	0.55
48:LP:67:ARG:HD3	80:14:524:A:C6	2.41	0.55
77:11:420:A:H3'	77:11:421:A:H8	1.71	0.55
80:14:1032:G:H2'	80:14:1033:G:H8	1.71	0.55
8:SH:25:ILE:HD12	8:SH:25:ILE:O	2.06	0.55
11:SK:24:GLN:HB2	11:SK:29:ALA:HB2	1.87	0.55
18:SR:185:THR:HG23	18:SR:188:THR:H	1.72	0.55
43:LK:22:ARG:HB3	43:LK:28:THR:HG22	1.89	0.55
77:11:857:U:O4	77:11:858:A:N6	2.39	0.55
80:14:625:G:O2'	80:14:3265:A:N6	2.39	0.55
17:SQ:187:ARG:NH2	77:11:756:A:OP2	2.40	0.55
26:SZ:13:PHE:HA	26:SZ:23:GLN:O	2.07	0.55
33:LA:111:LEU:HD23	33:LA:136:SER:OG	2.07	0.55
63:Le:32:TYR:CE1	63:Le:57:ARG:HG3	2.41	0.55
80:14:2507:C:H5''	80:14:2508:G:H5'	1.89	0.55
76:10:95:A:H3'	76:10:96:G:C8	2.33	0.55
24:SX:40:THR:OG1	77:11:1483:U:OP1	2.20	0.55
24:SX:134:GLN:O	24:SX:138:ARG:HG3	2.06	0.55
80:14:537:U:H3	80:14:541:U:H1'	1.71	0.55
53:LU:28:TRP:O	53:LU:32:GLN:NE2	2.40	0.54
77:11:927:A:H2'	77:11:928:G:C8	2.42	0.54
31:Se:26:LYS:NZ	77:11:591:U:OP1	2.30	0.54
36:LD:329:VAL:HA	36:LD:332:LYS:HB2	1.88	0.54
76:10:74:U:C2'	76:10:75:U:H2'	2.36	0.54
55:LW:126:LYS:HG2	55:LW:131:VAL:HG21	1.90	0.54
31:Se:29:LYS:HG3	31:Se:30:PRO:HD2	1.87	0.54
7:SG:23:ALA:HB2	7:SG:79:GLY:HA3	1.87	0.54
37:LE:51:LYS:HG2	37:LE:64:ASN:HA	1.89	0.54
55:LW:5:LYS:NZ	55:LW:5:LYS:HB3	2.23	0.54
80:14:2372:G:H2'	80:14:2373:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24: SX:75: GLY:O	24: SX:79: ILE:HG13	2.08	0.54
17: SQ:3: ARG:HB3	77: 11:94: A:H1'	1.89	0.54
48: LP:10: GLU:O	48: LP:14: LYS:HG3	2.07	0.54
67: L1:76: ARG:NH1	80: 14:1643: C:OP2	2.28	0.54
80: 14:3018: A:H2'	80: 14:3019: A:C8	2.42	0.54
5: SE:78: LEU:HD12	5: SE:157: ILE:HG23	1.90	0.54
18: SR:196: ILE:O	18: SR:200: LYS:HG2	2.08	0.54
48: LP:41: ARG:HH11	48: LP:44: ILE:HD11	1.73	0.54
49: LQ:33: ILE:HD13	80: 14:585: C:C4	2.43	0.54
76: 10:80: C:H3'	76: 10:81: U:C6	2.40	0.54
10: SJ:50: VAL:HG13	10: SJ:97: ASP:H	1.72	0.54
17: SQ:19: MET:SD	17: SQ:108: ARG:HD2	2.48	0.54
22: SV:76: LYS:HE2	32: Sf:108: VAL:HB	1.89	0.54
36: LD:87: THR:HG22	80: 14:352: A:N1	2.23	0.54
60: Lb:4: PHE:O	60: Lb:9: LYS:HD2	2.08	0.54
80: 14:3157: C:H2'	80: 14:3158: C:H6	1.73	0.54
77: 11:523: A:H2'	77: 11:524: A:C8	2.43	0.53
77: 11:1653: U:H2'	77: 11:1654: C:C6	2.42	0.53
9: SI:112: GLN:HE21	28: Sb:46: GLU:H	1.55	0.53
33: LA:30: GLU:HB2	33: LA:172: LEU:CD1	2.38	0.53
33: LA:53: VAL:O	33: LA:154: THR:HA	2.08	0.53
52: LT:117: ARG:HG2	52: LT:117: ARG:HH11	1.73	0.53
77: 11:1463: G:O2'	77: 11:1464: C:OP1	2.22	0.53
16: SP:82: ARG:NH2	16: SP:191: GLU:OE1	2.39	0.53
17: SQ:181: VAL:HG12	17: SQ:227: THR:HA	1.90	0.53
20: ST:90: GLU:OE2	80: 14:2110: A:O2'	2.27	0.53
76: 10:81: U:H2'	76: 10:82: C:O4'	2.09	0.53
77: 11:1397: C:H2'	77: 11:1398: G:H8	1.72	0.53
77: 11:1434: G:H2'	77: 11:1435: U:C6	2.43	0.53
80: 14:2774: A:O2'	80: 14:2775: C:H5''	2.09	0.53
21: SU:106: TYR:CD1	21: SU:107: LEU:HD13	2.42	0.53
35: LC:34: LYS:H	35: LC:34: LYS:CD	2.17	0.53
43: LK:122: ASN:OD1	43: LK:122: ASN:N	2.41	0.53
45: LM:147: VAL:O	45: LM:151: ILE:HG13	2.08	0.53
52: LT:71: LEU:O	52: LT:75: MET:HG3	2.07	0.53
77: 11:1223: C:H2'	77: 11:1224: A:H8	1.74	0.53
80: 14:2379: G:H2'	80: 14:2380: G:C8	2.44	0.53
70: Ll:3: LYS:HD2	70: Ll:41: TYR:CD2	2.44	0.53
70: Ll:30: ASP:OD1	70: Ll:30: ASP:N	2.40	0.53
76: 10:98: G:H2'	76: 10:99: U:O4'	2.08	0.53
77: 11:1174: A:H2'	77: 11:1175: G:H8	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:LF:143:VAL:HB	38:LF:146:GLU:HG3	1.90	0.53
17:SQ:97:GLU:C	17:SQ:98:ASN:HD22	2.16	0.53
26:SZ:99:ASP:OD1	26:SZ:100:THR:N	2.41	0.53
77:11:141:G:H2'	77:11:142:G:C8	2.44	0.53
77:11:648:U:O2	77:11:688:G:O6	2.27	0.53
77:11:1235:U:H2'	77:11:1236:G:C8	2.44	0.53
80:14:437:G:O6	80:14:633:G:H1'	2.09	0.53
80:14:3270:C:HO2'	80:14:3271:A:H8	1.55	0.53
7:SG:57:GLU:OE1	7:SG:89:ARG:NH1	2.41	0.53
21:SU:107:LEU:HB2	21:SU:109:LEU:HD21	1.90	0.53
80:14:2446:A:H3'	80:14:2447:C:C6	2.44	0.53
80:14:3018:A:H2'	80:14:3019:A:H8	1.74	0.53
5:SE:130:ASP:HB2	5:SE:147:ILE:HD11	1.91	0.53
48:LP:167:SER:O	48:LP:171:GLN:HG3	2.08	0.53
80:14:1680:A:H2	80:14:1696:G:H22	1.56	0.53
6:SF:26:MET:HE1	6:SF:60:LYS:HD3	1.91	0.53
7:SG:114:ASP:OD2	7:SG:118:ARG:NH2	2.38	0.53
18:SR:162:TYR:CE2	18:SR:178:PRO:HG3	2.44	0.53
80:14:138:U:H2'	80:14:139:C:C6	2.44	0.53
80:14:1215:A:H2'	80:14:1216:A:C8	2.44	0.53
24:SX:97:SER:OG	77:11:1511:C:OP1	2.26	0.52
43:LK:76:ALA:HB3	43:LK:109:VAL:HG22	1.91	0.52
76:10:73:U:H1'	76:10:93:G:O6	2.08	0.52
3:SC:112:GLN:NE2	3:SC:128:ARG:HB2	2.24	0.52
35:LC:139:THR:O	35:LC:143:LYS:NZ	2.42	0.52
77:11:631:G:N2	77:11:974:A:H62	2.07	0.52
77:11:1364:U:H3	77:11:1367:C:H41	1.57	0.52
15:SO:134:LYS:NZ	77:11:1185:U:OP1	2.42	0.52
56:LX:157:LYS:HG3	56:LX:159:ARG:HD3	1.91	0.52
76:10:139:A:H2'	76:10:140:U:O4'	2.10	0.52
11:SK:89:ASP:OD1	11:SK:90:TYR:N	2.41	0.52
17:SQ:129:VAL:HG12	17:SQ:139:LEU:HB3	1.92	0.52
23:SW:18:GLU:OE2	23:SW:19:ARG:HG2	2.10	0.52
34:LB:147:ARG:HG2	34:LB:157:ILE:HG12	1.91	0.52
42:LJ:184:TYR:CE1	42:LJ:219:VAL:HG11	2.45	0.52
57:LY:150:THR:HG22	57:LY:151:PRO:O	2.10	0.52
69:Lk:17:THR:HG23	69:Lk:29:ILE:HD11	1.90	0.52
77:11:117:U:H2'	77:11:118:U:C6	2.44	0.52
3:SC:69:PRO:HA	3:SC:72:ILE:HD12	1.91	0.52
11:SK:116:LYS:HD3	11:SK:116:LYS:C	2.35	0.52
18:SR:14:LYS:HA	18:SR:14:LYS:HE2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Sf:126:CYS:SG	32:Sf:144:CYS:HB3	2.50	0.52
3:SC:169:GLY:O	3:SC:170:ARG:C	2.52	0.52
42:LJ:184:TYR:HE1	42:LJ:219:VAL:HG11	1.74	0.52
37:LE:112:ILE:HG21	37:LE:118:TYR:HB2	1.91	0.52
49:LQ:36:LYS:HD2	80:14:586:G:H4'	1.91	0.52
49:LQ:106:LEU:HD13	49:LQ:149:VAL:HG11	1.91	0.52
80:14:1819:A:C2'	80:14:1822:G:H21	2.22	0.52
80:14:2508:G:H2'	80:14:2509:U:C6	2.45	0.52
1:SA:52:GLY:O	1:SA:56:GLU:HG2	2.10	0.52
12:SL:22:ARG:NH1	12:SL:36:LEU:O	2.43	0.52
18:SR:200:LYS:HA	18:SR:203:ILE:HG22	1.92	0.52
60:Lb:99:VAL:HG21	60:Lb:109:ALA:HB2	1.92	0.52
77:11:1455:U:H2'	77:11:1456:C:H6	1.74	0.52
77:11:1656:U:H2'	77:11:1657:A:C8	2.45	0.52
17:SQ:212:ASP:OD1	17:SQ:213:ALA:N	2.38	0.52
18:SR:13:GLN:O	18:SR:14:LYS:HE2	2.09	0.52
28:Sb:37:LYS:HG2	28:Sb:72:GLN:HG2	1.91	0.52
31:Se:27:LYS:HD3	31:Se:28:LYS:N	2.25	0.52
77:11:68:A:H5''	77:11:69:A:C5'	2.40	0.52
77:11:1055:U:H2'	77:11:1056:G:C8	2.45	0.52
77:11:1653:U:H2'	77:11:1654:C:H6	1.75	0.52
17:SQ:19:MET:HE3	77:11:792:U:C4	2.45	0.52
19:SS:157:PRO:O	19:SS:160:ARG:HB2	2.08	0.52
46:LN:87:GLU:H	46:LN:87:GLU:CD	2.18	0.52
59:La:5:THR:HG23	59:La:15:ILE:O	2.10	0.52
76:10:57:A:H2'	76:10:58:C:C6	2.45	0.52
80:14:1550:U:O4	80:14:1563:G:O2'	2.27	0.52
43:LK:277:LYS:O	43:LK:281:ILE:HG13	2.09	0.51
53:LU:2:GLY:O	68:Lj:39:ARG:NH2	2.43	0.51
76:10:113:G:H2'	76:10:114:C:O4'	2.09	0.51
17:SQ:115:ARG:HA	17:SQ:115:ARG:NH1	2.25	0.51
20:ST:156:ARG:NH2	77:11:192:G:N7	2.58	0.51
38:LF:93:TYR:CE2	38:LF:187:LYS:HG2	2.45	0.51
53:LU:99:ARG:HG2	53:LU:167:ALA:HB2	1.92	0.51
53:LU:121:ILE:HG21	53:LU:131:GLU:HG3	1.92	0.51
77:11:483:C:H2'	77:11:484:A:C8	2.44	0.51
8:SH:29:SER:OG	8:SH:31:ASN:OD1	2.24	0.51
43:LK:222:PHE:O	43:LK:226:ILE:HG13	2.11	0.51
69:Lk:76:THR:HG22	69:Lk:79:ARG:HB3	1.92	0.51
80:14:3270:C:O2'	80:14:3271:A:H8	1.93	0.51
16:SP:168:MET:O	16:SP:172:MET:HG3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Sf:100:LEU:HD21	32:Sf:103:LEU:HB2	1.92	0.51
61:Lc:139:LYS:HB3	61:Lc:141:ARG:HG3	1.93	0.51
10:SJ:52:GLU:OE1	10:SJ:70:ARG:NH1	2.43	0.51
77:11:1371:U:H2'	77:11:1372:C:C6	2.45	0.51
5:SE:110:THR:O	5:SE:111:ASP:OD1	2.28	0.51
35:LC:103:ASN:ND2	35:LC:149:GLN:HG2	2.23	0.51
40:LH:96:MET:HE2	59:La:22:ARG:HH11	1.76	0.51
49:LQ:21:ARG:NH1	80:14:581:C:OP2	2.43	0.51
61:Lc:62:GLU:HG3	61:Lc:63:GLY:H	1.75	0.51
76:10:70:G:H1'	76:10:88:A:H62	1.75	0.51
77:11:1612:C:H2'	77:11:1613:G:C8	2.45	0.51
80:14:3225:C:H2'	80:14:3226:A:C8	2.43	0.51
15:SO:18:THR:HB	15:SO:21:LYS:HZ3	1.76	0.51
20:ST:62:ASP:OD1	20:ST:62:ASP:N	2.44	0.51
24:SX:15:PHE:CZ	24:SX:132:LEU:HD23	2.45	0.51
50:LR:66:ARG:HG3	80:14:2519:U:H5'	1.92	0.51
4:SD:242:GLU:H	4:SD:242:GLU:CD	2.19	0.51
26:SZ:13:PHE:CB	26:SZ:24:PHE:HB3	2.40	0.51
80:14:853:A:H2'	80:14:854:G:C8	2.46	0.51
80:14:2447:C:H42	80:14:2506:A:H61	1.58	0.51
1:SA:36:ARG:O	1:SA:53:LYS:NZ	2.41	0.51
33:LA:58:ILE:HD13	33:LA:153:ALA:HB2	1.93	0.51
68:Lj:30:SER:O	68:Lj:33:LYS:HG2	2.11	0.51
7:SG:44:GLU:OE1	7:SG:44:GLU:O	2.28	0.51
80:14:569:U:O2'	80:14:570:G:H5'	2.11	0.51
7:SG:32:GLY:HA3	7:SG:71:ASP:CG	2.36	0.50
19:SS:34:ASN:OD1	19:SS:34:ASN:N	2.45	0.50
50:LR:114:GLU:OE2	50:LR:119:THR:OG1	2.25	0.50
55:LW:163:ARG:N	77:11:819:G:H22	2.09	0.50
61:Lc:76:LYS:NZ	61:Lc:77:LYS:HD2	2.25	0.50
76:10:88:A:H1'	76:10:89:A:C8	2.46	0.50
77:11:77:A:H2'	77:11:78:G:C8	2.47	0.50
77:11:1271:G:H1'	77:11:1453:G:H5'	1.94	0.50
80:14:1:G:H2'	80:14:2:C:H6	1.75	0.50
80:14:609:G:H2'	80:14:610:C:C6	2.45	0.50
4:SD:153:TYR:CD1	4:SD:157:LYS:HG2	2.46	0.50
4:SD:252:GLU:HG2	4:SD:253:TYR:CD1	2.46	0.50
5:SE:190:SER:HB2	76:10:96:G:H4'	1.93	0.50
61:Lc:77:LYS:HG3	61:Lc:80:LYS:HG3	1.94	0.50
72:Ln:97:ARG:NH1	80:14:2850:A:OP2	2.44	0.50
76:10:70:G:H21	76:10:89:A:H61	1.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:14:2268:C:C2'	80:14:2269:U:H5'	2.41	0.50
2:SB:141:VAL:HG12	2:SB:185:LEU:HD11	1.90	0.50
33:LA:33:GLU:OE2	80:14:2469:G:H1'	2.11	0.50
65:Lg:106:ARG:NH2	80:14:1423:G:OP1	2.44	0.50
77:11:16:G:H2'	77:11:17:C:C6	2.47	0.50
80:14:3072:A:H2'	80:14:3073:A:C8	2.46	0.50
14:SN:126:ILE:HG22	14:SN:140:VAL:HA	1.92	0.50
19:SS:100:ARG:HH21	77:11:859:A:P	2.35	0.50
36:LD:303:GLN:HG3	48:LP:18:ARG:HH12	1.76	0.50
43:LK:83:LEU:HB3	43:LK:88:LEU:HB3	1.93	0.50
50:LR:145:GLN:HG3	50:LR:197:THR:O	2.12	0.50
76:10:95:A:C8	76:10:95:A:H5''	2.47	0.50
77:11:193:G:O2'	77:11:194:A:H8	1.93	0.50
22:SV:64:VAL:HG13	22:SV:90:ILE:HG23	1.94	0.50
23:SW:2:GLY:N	77:11:1419:U:OP1	2.44	0.50
30:Sd:22:GLN:HG2	30:Sd:23:VAL:HG23	1.93	0.50
33:LA:18:LYS:HD2	33:LA:176:GLU:HG2	1.92	0.50
35:LC:220:ILE:HD12	35:LC:283:LYS:HG3	1.92	0.50
77:11:1227:G:H2'	77:11:1228:U:C6	2.46	0.50
1:SA:39:PHE:O	1:SA:40:LYS:HB3	2.11	0.50
1:SA:84:GLN:O	1:SA:87:VAL:HG22	2.12	0.50
21:SU:107:LEU:HB2	21:SU:109:LEU:CD2	2.41	0.50
77:11:1290:A:H4'	77:11:1291:G:H5'	1.93	0.50
79:13:86:C:H4'	79:13:88:G:N3	2.27	0.50
20:ST:161:ARG:NH2	77:11:184:C:OP1	2.38	0.50
26:SZ:12:LYS:O	26:SZ:24:PHE:HA	2.10	0.50
26:SZ:38:LYS:HG2	77:11:525:U:OP1	2.12	0.50
32:Sf:98:VAL:HG21	32:Sf:101:ALA:HB2	1.93	0.50
32:Sf:132:MET:HE3	32:Sf:139:HIS:HB2	1.94	0.50
33:LA:204:LEU:CB	33:LA:217:PHE:HB3	2.34	0.50
49:LQ:204:GLU:OE2	49:LQ:210:LYS:HD2	2.12	0.50
56:LX:9:TYR:CE1	56:LX:65:GLU:HG3	2.46	0.50
80:14:764:G:H2'	80:14:765:A:C8	2.43	0.50
80:14:3380:C:H2'	80:14:3381:U:C6	2.46	0.50
52:LT:117:ARG:HG2	52:LT:117:ARG:NH1	2.26	0.50
58:LZ:30:GLU:HA	58:LZ:30:GLU:OE1	2.12	0.50
76:10:126:G:H2'	76:10:127:U:O4'	2.12	0.50
33:LA:138:VAL:HG22	33:LA:147:LYS:HG2	1.93	0.50
53:LU:19:MET:HE2	53:LU:19:MET:HA	1.94	0.50
76:10:71:U:H1'	76:10:89:A:H62	1.77	0.50
17:SQ:3:ARG:HG2	77:11:403:A:H4'	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:LB:170:ALA:CB	75:Lq:65:VAL:HG12	2.42	0.49
42:LJ:216:LEU:HD12	43:LK:284:LEU:HD13	1.94	0.49
48:LP:17:LYS:NZ	48:LP:21:GLU:OE2	2.44	0.49
77:11:1570:U:H2'	77:11:1571:C:C6	2.47	0.49
1:SA:27:THR:HG22	1:SA:28:LYS:H	1.77	0.49
18:SR:134:MET:SD	18:SR:135:ARG:NH1	2.85	0.49
56:LX:29:MET:HG3	56:LX:43:PHE:CD1	2.46	0.49
80:14:709:G:H4'	80:14:710:U:H5'	1.94	0.49
80:14:2549:C:H2'	80:14:2550:C:C6	2.47	0.49
5:SE:34:GLN:OE1	5:SE:34:GLN:N	2.45	0.49
19:SS:101:ILE:O	19:SS:103:ARG:NH1	2.45	0.49
20:ST:74:THR:CG2	77:11:260:A:H1'	2.43	0.49
22:SV:51:GLY:HA2	22:SV:54:VAL:HG12	1.94	0.49
33:LA:70:ASP:OD2	33:LA:140:HIS:CE1	2.64	0.49
34:LB:183:GLY:HA2	80:14:906:A:H5''	1.93	0.49
36:LD:333:LEU:HD22	48:LP:181:ILE:HD12	1.94	0.49
44:LL:7:GLU:HG3	44:LL:8:PRO:HD2	1.94	0.49
61:Lc:74:LYS:O	61:Lc:78:GLN:NE2	2.45	0.49
70:LI:14:THR:O	70:LI:17:ARG:HG2	2.13	0.49
75:Lq:16:THR:HG22	80:14:1933:G:C8	2.48	0.49
31:Se:27:LYS:HD3	31:Se:28:LYS:H	1.77	0.49
37:LE:117:LYS:NZ	37:LE:117:LYS:HB3	2.27	0.49
56:LX:35:ASN:HB2	56:LX:38:ARG:HG3	1.93	0.49
80:14:246:C:H5'	80:14:247:C:H5'	1.94	0.49
20:ST:85:ASN:HD22	20:ST:88:ASN:H	1.59	0.49
21:SU:96:THR:O	21:SU:100:ILE:HG22	2.12	0.49
36:LD:368:LYS:HD3	80:14:549:U:H5''	1.94	0.49
50:LR:235:GLY:O	50:LR:239:GLN:HG3	2.13	0.49
77:11:68:A:H5''	77:11:69:A:H5''	1.94	0.49
77:11:419:C:H2'	77:11:421:A:N7	2.27	0.49
77:11:1356:U:H2'	77:11:1357:G:H8	1.77	0.49
79:13:133:G:H2'	79:13:134:G:H8	1.76	0.49
80:14:3157:C:H2'	80:14:3158:C:C6	2.48	0.49
2:SB:60:ASN:OD1	2:SB:60:ASN:N	2.43	0.49
6:SF:107:SER:HB3	77:11:806:G:H21	1.77	0.49
15:SO:103:ILE:HD13	15:SO:123:LEU:HB3	1.95	0.49
33:LA:38:LEU:HA	33:LA:200:ASN:O	2.13	0.49
36:LD:314:ASN:OD1	80:14:1357:G:N2	2.45	0.49
48:LP:11:SER:HB2	80:14:1361:A:O2'	2.13	0.49
76:10:85:C:H2'	76:10:86:U:O4'	2.13	0.49
77:11:776:G:N2	77:11:778:A:H1'	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:11:1262:C:H2'	77:11:1263:U:H6	1.76	0.49
2:SB:214:HIS:O	23:SW:20:TYR:OH	2.21	0.49
6:SF:14:MET:HE2	6:SF:27:ILE:HD11	1.95	0.49
11:SK:88:LYS:O	15:SO:25:ARG:NH1	2.46	0.49
19:SS:19:PHE:HE2	19:SS:51:GLN:HB2	1.78	0.49
41:LI:2:THR:HG22	41:LI:4:ARG:HG2	1.95	0.49
69:Lk:77:ASN:OD1	69:Lk:77:ASN:O	2.31	0.49
77:11:588:A:H2'	77:11:589:G:H8	1.78	0.49
2:SB:160:MET:HE2	2:SB:160:MET:HB2	1.71	0.49
33:LA:159:LEU:HG	33:LA:160:LYS:N	2.28	0.49
36:LD:142:ALA:HB1	61:Lc:17:ASN:HB2	1.95	0.49
58:LZ:100:ARG:HE	58:LZ:102:ILE:HD11	1.77	0.49
64:Lf:113:THR:O	80:14:3377:U:O2'	2.30	0.49
76:10:149:A:H2'	76:10:150:G:C8	2.48	0.49
77:11:610:G:H5'	77:11:616:G:N2	2.28	0.49
77:11:1225:U:H2'	77:11:1226:A:H8	1.77	0.49
11:SK:77:PHE:C	11:SK:78:LYS:HD3	2.37	0.49
43:LK:270:LYS:HG2	78:12:60:G:H5''	1.93	0.49
80:14:92:G:H2'	80:14:93:A:C8	2.48	0.49
80:14:2263:U:O2'	80:14:2264:G:H8	1.93	0.49
80:14:3006:C:H2'	80:14:3007:A:O4'	2.12	0.49
1:SA:194:LYS:HE3	1:SA:195:TRP:H	1.78	0.49
3:SC:134:ARG:NH2	77:11:535:U:OP1	2.36	0.49
11:SK:48:ALA:HB2	11:SK:70:VAL:HG21	1.95	0.49
18:SR:63:MET:SD	18:SR:108:LEU:HD11	2.53	0.49
26:SZ:82:GLU:HA	26:SZ:85:LYS:HG3	1.94	0.49
36:LD:272:ASP:OD1	36:LD:272:ASP:N	2.37	0.49
58:LZ:43:LEU:O	58:LZ:47:ILE:HG13	2.13	0.49
77:11:183:C:H2'	77:11:184:C:H6	1.76	0.49
77:11:1173:G:C2	77:11:1174:A:C8	3.01	0.49
80:14:1700:A:H2'	80:14:1701:A:C8	2.48	0.49
80:14:3169:U:H5	80:14:3172:C:OP2	1.96	0.49
33:LA:36:ILE:CD1	33:LA:190:LEU:HD22	2.42	0.48
63:Le:32:TYR:OH	63:Le:60:GLU:OE1	2.31	0.48
77:11:184:C:H2'	77:11:185:G:O4'	2.12	0.48
78:12:24:C:H2'	78:12:25:G:O4'	2.13	0.48
80:14:3158:C:H2'	80:14:3159:C:C6	2.48	0.48
1:SA:198:MET:HE3	1:SA:200:ASP:OD1	2.13	0.48
10:SJ:65:ILE:HD12	10:SJ:65:ILE:O	2.13	0.48
11:SK:12:ILE:HD11	11:SK:19:ASN:HB3	1.95	0.48
24:SX:130:ARG:O	24:SX:134:GLN:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:LP:41:ARG:HH21	80:14:579:A:H4'	1.77	0.48
59:La:48:PRO:HB2	59:La:56:MET:HE3	1.96	0.48
60:Lb:60:LYS:HE2	60:Lb:64:LYS:HE2	1.95	0.48
76:10:97:G:H3'	76:10:98:G:H8	1.79	0.48
80:14:206:A:O2'	80:14:208:A:OP2	2.30	0.48
80:14:802:C:H2'	80:14:803:C:C6	2.49	0.48
80:14:2446:A:H3'	80:14:2447:C:H6	1.77	0.48
2:SB:58:THR:H	2:SB:93:LYS:NZ	2.10	0.48
2:SB:88:GLU:OE1	2:SB:90:TYR:OH	2.25	0.48
20:ST:174:GLN:HE22	20:ST:181:LEU:HB2	1.77	0.48
33:LA:196:LYS:HB2	33:LA:200:ASN:OD1	2.12	0.48
53:LU:168:GLY:HA2	53:LU:171:TYR:CE2	2.49	0.48
55:LW:162:ARG:NH2	77:11:852:C:OP1	2.43	0.48
76:10:71:U:C2	76:10:72:G:C8	3.01	0.48
77:11:541:A:H5'	77:11:546:C:H41	1.77	0.48
77:11:594:A:H2'	77:11:595:A:C8	2.48	0.48
80:14:3224:U:H2'	80:14:3225:C:C6	2.47	0.48
11:SK:65:ASP:O	11:SK:69:VAL:HG12	2.12	0.48
18:SR:45:PHE:CE1	18:SR:123:LEU:HD11	2.48	0.48
18:SR:69:THR:O	18:SR:101:GLY:HA3	2.12	0.48
18:SR:166:PHE:CE1	18:SR:176:LYS:HG3	2.46	0.48
19:SS:17:THR:OG1	19:SS:18:GLU:N	2.46	0.48
24:SX:109:GLN:HG3	24:SX:114:VAL:HG23	1.94	0.48
76:10:84:A:H2'	76:10:85:C:C6	2.48	0.48
77:11:1204:G:N2	77:11:1606:A:H5'	2.27	0.48
15:SO:36:SER:OG	15:SO:39:GLU:OE1	2.32	0.48
19:SS:100:ARG:NH2	77:11:859:A:OP1	2.45	0.48
24:SX:127:ASN:HA	24:SX:130:ARG:HH12	1.78	0.48
25:SY:70:ARG:NH1	29:Sc:6:ASP:OD1	2.45	0.48
32:Sf:105:PHE:CD1	32:Sf:118:ARG:HG3	2.49	0.48
38:LF:61:ASP:N	38:LF:61:ASP:OD1	2.44	0.48
52:LT:45:ARG:HE	56:LX:72:THR:HG22	1.79	0.48
77:11:1253:U:H3'	77:11:1254:U:H5''	1.96	0.48
77:11:1570:U:H2'	77:11:1571:C:H6	1.78	0.48
9:SI:33:PHE:HB3	9:SI:40:PHE:HB2	1.96	0.48
9:SI:112:GLN:NE2	28:Sb:46:GLU:H	2.11	0.48
23:SW:21:TYR:CE2	23:SW:73:LEU:HD22	2.47	0.48
36:LD:335:PRO:HD3	48:LP:41:ARG:HH12	1.78	0.48
77:11:1292:U:H5	77:11:1317:U:C5	2.31	0.48
77:11:1661:A:N6	77:11:1753:G:O2'	2.46	0.48
11:SK:130:ARG:NH2	77:11:1176:C:OP1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:SW:3:ARG:HD2	77:11:1395:U:H5'	1.95	0.48
43:LK:264:LYS:HG2	43:LK:265:ARG:H	1.77	0.48
49:LQ:34:LYS:NZ	80:14:608:U:OP1	2.47	0.48
64:Lf:62:LYS:HB2	64:Lf:62:LYS:HE3	1.57	0.48
77:11:183:C:H2'	77:11:184:C:C6	2.49	0.48
80:14:2750:A:H2'	80:14:2751:A:C8	2.49	0.48
42:LJ:153:ARG:O	42:LJ:156:LYS:HB2	2.14	0.48
53:LU:176:GLY:O	53:LU:185:ARG:NH2	2.46	0.48
77:11:304:A:H2'	77:11:305:A:C8	2.49	0.48
80:14:978:G:H2'	80:14:979:C:C6	2.48	0.48
1:SA:130:ASP:O	1:SA:134:ILE:HG13	2.13	0.48
2:SB:141:VAL:HG22	2:SB:187:ILE:HG22	1.95	0.48
22:SV:45:ALA:HB1	22:SV:50:GLU:OE2	2.13	0.48
22:SV:80:ALA:O	22:SV:81:LEU:C	2.56	0.48
22:SV:98:LEU:HD21	22:SV:122:VAL:H	1.79	0.48
34:LB:42:LYS:HG3	34:LB:89:TYR:CE2	2.49	0.48
38:LF:118:ARG:HG2	38:LF:126:VAL:HG12	1.96	0.48
77:11:65:A:O2'	77:11:66:U:H5''	2.14	0.48
77:11:1311:G:H2'	77:11:1312:G:C8	2.49	0.48
80:14:1748:G:H2'	80:14:1749:G:H8	1.78	0.48
2:SB:66:GLY:O	2:SB:69:ILE:HG22	2.13	0.48
3:SC:39:ARG:HG2	3:SC:43:GLU:OE2	2.14	0.48
3:SC:149:MET:HB3	3:SC:149:MET:HE3	1.84	0.48
4:SD:164:VAL:HG11	4:SD:179:MET:HE3	1.95	0.48
5:SE:58:THR:OG1	5:SE:76:GLU:OE1	2.22	0.48
14:SN:122:ASP:HB2	14:SN:144:ILE:O	2.13	0.48
32:Sf:108:VAL:HG13	32:Sf:109:ASP:N	2.29	0.48
39:LG:17:ARG:HA	39:LG:45:GLU:HB2	1.96	0.48
43:LK:105:LEU:O	43:LK:109:VAL:HG23	2.13	0.48
48:LP:142:LYS:O	48:LP:146:GLU:HG3	2.14	0.48
48:LP:178:ILE:HG23	48:LP:183:ASP:HB3	1.96	0.48
57:LY:109:MET:HE2	80:14:1075:G:N7	2.29	0.48
76:10:71:U:H1'	76:10:89:A:N6	2.29	0.48
76:10:72:G:H21	76:10:92:C:H42	1.60	0.48
77:11:129:U:O4	77:11:179:A:N6	2.47	0.48
28:Sb:89:VAL:HG23	77:11:1634:U:OP1	2.14	0.47
36:LD:287:LYS:NZ	54:LV:23:ASP:OD2	2.44	0.47
77:11:776:G:H21	77:11:778:A:H1'	1.79	0.47
77:11:1311:G:N2	77:11:1321:G:H1'	2.29	0.47
80:14:1921:A:H2'	80:14:1922:U:C6	2.49	0.47
6:SF:32:LYS:O	6:SF:36:LYS:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:SW:11:LYS:HE3	23:SW:11:LYS:HB3	1.67	0.47
33:LA:57:HIS:O	33:LA:58:ILE:C	2.57	0.47
35:LC:92:TYR:HB2	35:LC:159:VAL:HG22	1.95	0.47
77:11:1585:U:H2'	77:11:1586:C:C6	2.49	0.47
80:14:2904:G:O2'	80:14:3026:A:N1	2.46	0.47
80:14:3072:A:H2'	80:14:3073:A:H8	1.79	0.47
19:SS:30:MET:SD	19:SS:83:GLU:HB3	2.54	0.47
19:SS:88:PHE:O	19:SS:91:LYS:HD2	2.14	0.47
23:SW:30:THR:O	23:SW:34:ILE:HD12	2.15	0.47
33:LA:68:LEU:O	33:LA:112:ALA:HA	2.14	0.47
42:LJ:162:ARG:HG3	42:LJ:162:ARG:HH11	1.79	0.47
50:LR:47:PHE:O	80:14:2528:A:H2'	2.14	0.47
59:La:9:ARG:HH22	59:La:29:GLN:HE22	1.62	0.47
79:13:135:C:H2'	79:13:136:C:C6	2.49	0.47
80:14:3271:A:H1'	80:14:3272:U:H5'	1.97	0.47
15:SO:62:ALA:HA	15:SO:65:LYS:HE3	1.96	0.47
33:LA:68:LEU:HD22	33:LA:90:LEU:HD21	1.97	0.47
33:LA:93:LEU:HD22	33:LA:99:LEU:HB3	1.97	0.47
71:Lm:36:ARG:HH22	80:14:399:G:H1'	1.80	0.47
76:10:89:A:H2'	76:10:90:A:C8	2.48	0.47
77:11:1263:U:H2'	77:11:1264:A:H8	1.79	0.47
80:14:3133:U:H2'	80:14:3134:C:C6	2.49	0.47
2:SB:178:ILE:HD13	2:SB:185:LEU:HD23	1.96	0.47
15:SO:88:ARG:HB3	15:SO:124:ALA:HB2	1.95	0.47
23:SW:28:PHE:HE1	23:SW:51:ALA:HB3	1.79	0.47
39:LG:59:TYR:OH	39:LG:78:PHE:O	2.30	0.47
42:LJ:164:LYS:HB2	42:LJ:164:LYS:HE2	1.64	0.47
74:Lp:89:LYS:O	76:10:185:U:N3	2.47	0.47
75:Lq:36:LYS:HG3	75:Lq:48:LYS:HE2	1.96	0.47
77:11:597:A:H4'	77:11:598:G:H5'	1.97	0.47
80:14:1131:A:H2'	80:14:1132:U:H6	1.79	0.47
80:14:2574:U:H4'	80:14:2575:G:N7	2.28	0.47
3:SC:159:ASP:OD1	3:SC:160:PHE:N	2.46	0.47
38:LF:142:LYS:HG3	38:LF:143:VAL:HG23	1.96	0.47
42:LJ:38:MET:HE3	42:LJ:41:LYS:HG2	1.97	0.47
55:LW:136:ARG:O	55:LW:140:GLU:HG3	2.14	0.47
76:10:83:C:H2'	76:10:84:A:C8	2.49	0.47
77:11:1597:C:H2'	77:11:1598:G:H8	1.79	0.47
80:14:3164:U:H2'	80:14:3165:C:C6	2.50	0.47
26:SZ:55:ASN:HB3	26:SZ:98:LEU:HD21	1.95	0.47
27:Sa:86:ARG:HG3	27:Sa:86:ARG:HH11	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:LD:109:LYS:HG2	36:LD:111:TRP:CZ2	2.50	0.47
36:LD:113:ARG:NH2	80:14:801:A:OP1	2.42	0.47
43:LK:81:ARG:HB2	43:LK:81:ARG:CZ	2.45	0.47
45:LM:80:THR:O	45:LM:80:THR:HG22	2.13	0.47
48:LP:145:ARG:HG2	48:LP:149:TYR:CE2	2.50	0.47
77:11:69:A:H2'	77:11:70:C:C6	2.49	0.47
77:11:323:U:H4'	77:11:327:A:C8	2.49	0.47
80:14:1045:U:H2'	80:14:1046:C:C6	2.49	0.47
80:14:1059:A:N3	80:14:2636:U:O2'	2.46	0.47
80:14:3002:G:H2'	80:14:3003:U:C6	2.50	0.47
1:SA:40:LYS:C	1:SA:40:LYS:HD2	2.40	0.47
41:LI:76:ASP:HB3	41:LI:114:GLY:HA3	1.95	0.47
65:Lg:107:LYS:O	65:Lg:111:GLU:OE1	2.32	0.47
76:10:127:U:H2'	76:10:128:A:O4'	2.15	0.47
77:11:864:U:H2'	77:11:865:A:O4'	2.15	0.47
77:11:1250:U:H2'	77:11:1251:C:H6	1.78	0.47
7:SG:57:GLU:OE2	7:SG:119:TYR:OH	2.26	0.47
77:11:71:A:H2'	77:11:72:A:C8	2.50	0.47
80:14:3015:U:H2'	80:14:3016:U:C6	2.50	0.47
49:LQ:10:PRO:HG2	49:LQ:18:LYS:HD2	1.96	0.47
77:11:1733:C:H2'	77:11:1734:C:C6	2.50	0.47
80:14:897:G:H2'	80:14:898:U:C6	2.49	0.47
80:14:955:C:H2'	80:14:956:C:H6	1.78	0.47
6:SF:26:MET:CE	6:SF:60:LYS:HD3	2.45	0.46
36:LD:309:ILE:HG22	48:LP:22:TRP:CZ3	2.49	0.46
55:LW:163:ARG:HA	77:11:819:G:N2	2.29	0.46
63:Le:104:ASP:OD1	63:Le:104:ASP:N	2.47	0.46
76:10:153:A:H2'	76:10:154:C:O4'	2.15	0.46
79:13:162:G:H2'	79:13:163:C:O4'	2.15	0.46
80:14:805:G:H2'	80:14:806:U:C6	2.49	0.46
80:14:1084:G:H2'	80:14:1085:C:C6	2.50	0.46
80:14:2476:A:H3'	80:14:2477:A:C8	2.49	0.46
1:SA:17:MET:HE1	1:SA:176:TRP:CZ3	2.51	0.46
11:SK:16:GLN:HE21	11:SK:68:MET:CE	2.27	0.46
15:SO:65:LYS:HD2	15:SO:65:LYS:C	2.41	0.46
20:ST:171:ILE:HD11	20:ST:200:GLU:HG2	1.97	0.46
43:LK:5:LYS:HG2	80:14:1050:C:H5''	1.97	0.46
58:LZ:40:GLU:HG3	58:LZ:64:ARG:HB3	1.98	0.46
77:11:1463:G:N3	77:11:1463:G:H2'	2.29	0.46
80:14:652:C:H42	80:14:656:A:H2	1.62	0.46
80:14:2845:U:OP1	80:14:2847:C:N4	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:SA:194:LYS:HE3	1:SA:195:TRP:N	2.30	0.46
16:SP:36:SER:HB3	16:SP:231:VAL:O	2.15	0.46
22:SV:94:ASN:HB3	22:SV:97:THR:HG22	1.98	0.46
24:SX:43:LEU:HA	24:SX:84:GLN:HG3	1.97	0.46
50:LR:202:GLU:OE1	50:LR:202:GLU:N	2.47	0.46
77:11:891:U:H2'	77:11:892:U:C6	2.50	0.46
77:11:1656:U:H2'	77:11:1657:A:H8	1.80	0.46
80:14:174:G:C4	80:14:175:A:C8	3.04	0.46
80:14:3170:U:H1'	80:14:3273:C:O2	2.14	0.46
2:SB:71:GLU:OE1	2:SB:71:GLU:HA	2.16	0.46
3:SC:72:ILE:HG22	3:SC:76:GLU:OE2	2.16	0.46
11:SK:91:LYS:NZ	11:SK:91:LYS:HB3	2.30	0.46
15:SO:65:LYS:NZ	15:SO:66:LYS:HG3	2.29	0.46
17:SQ:197:ASN:OD1	17:SQ:209:HIS:HB2	2.15	0.46
18:SR:147:PHE:CD1	18:SR:147:PHE:N	2.82	0.46
19:SS:81:VAL:HG23	19:SS:93:VAL:HB	1.96	0.46
32:Sf:107:LYS:HG2	32:Sf:117:LEU:HD21	1.97	0.46
34:LB:48:ILE:HG12	75:Lq:65:VAL:HG22	1.98	0.46
37:LE:51:LYS:O	37:LE:53:ARG:NH1	2.48	0.46
80:14:371:A:N3	80:14:373:G:H5'	2.30	0.46
80:14:1543:C:H2'	80:14:1544:U:C6	2.51	0.46
80:14:2697:A:H3'	80:14:2698:G:N2	2.30	0.46
38:LF:10:MET:HE3	38:LF:10:MET:HB2	1.83	0.46
38:LF:135:VAL:HG23	38:LF:157:VAL:HG22	1.96	0.46
38:LF:180:ASP:OD1	38:LF:180:ASP:N	2.49	0.46
42:LJ:162:ARG:HG3	42:LJ:162:ARG:NH1	2.30	0.46
44:LL:2:VAL:HG22	44:LL:3:LYS:H	1.80	0.46
77:11:690:C:H2'	77:11:691:C:C6	2.51	0.46
77:11:971:U:H2'	77:11:972:C:O4'	2.16	0.46
80:14:129:G:H1	80:14:135:U:H3	1.64	0.46
26:SZ:13:PHE:HB2	26:SZ:24:PHE:HB3	1.97	0.46
45:LM:120:LYS:HD3	45:LM:137:ARG:HD3	1.96	0.46
53:LU:46:ASP:OD1	53:LU:46:ASP:N	2.47	0.46
76:10:171:U:H2'	76:10:172:U:O4'	2.16	0.46
77:11:1310:U:C4	77:11:1322:U:H1'	2.50	0.46
77:11:1371:U:H2'	77:11:1372:C:H6	1.80	0.46
33:LA:207:LYS:HB3	33:LA:213:PRO:HA	1.98	0.46
39:LG:10:ARG:HB3	39:LG:10:ARG:HH11	1.80	0.46
76:10:117:G:H2'	76:10:118:G:H5'	1.98	0.46
77:11:818:A:N6	77:11:861:G:H1'	2.31	0.46
77:11:1320:C:O2'	77:11:1405:U:O2	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:14:1131:A:H2'	80:14:1132:U:C6	2.51	0.46
2:SB:49:THR:HB	2:SB:87:VAL:HG12	1.98	0.46
3:SC:53:ARG:HA	3:SC:53:ARG:HD3	1.70	0.46
24:SX:15:PHE:HA	24:SX:139:ILE:HD11	1.97	0.46
34:LB:48:ILE:HG12	75:Lq:65:VAL:CG2	2.46	0.46
50:LR:205:MET:O	50:LR:208:SER:OG	2.20	0.46
51:LS:126:PRO:HB3	51:LS:136:ASP:OD2	2.16	0.46
65:Lg:97:ILE:HG21	65:Lg:106:ARG:HG2	1.98	0.46
69:Lk:5:THR:OG1	80:14:894:A:OP1	2.31	0.46
76:10:87:U:O2	76:10:88:A:N6	2.49	0.46
77:11:192:G:H2'	77:11:193:G:C8	2.51	0.46
77:11:1203:G:H4'	77:11:1204:G:O5'	2.15	0.46
80:14:2504:U:H2'	80:14:2505:A:C8	2.51	0.46
17:SQ:37:LYS:HB2	17:SQ:40:GLU:HG3	1.98	0.46
18:SR:67:VAL:HB	18:SR:101:GLY:HA2	1.98	0.46
18:SR:164:ARG:HE	18:SR:176:LYS:HB2	1.79	0.46
33:LA:211:GLY:O	80:14:2495:C:O2'	2.32	0.46
33:LA:213:PRO:HG3	80:14:2496:A:H4'	1.97	0.46
35:LC:143:LYS:O	35:LC:147:GLN:HG2	2.16	0.46
37:LE:152:ILE:HA	37:LE:155:ARG:HG3	1.98	0.46
49:LQ:152:PHE:HE2	49:LQ:195:VAL:HG21	1.80	0.46
51:LS:26:GLN:HB3	51:LS:27:PRO:HD3	1.97	0.46
76:10:51:G:H22	76:10:68:U:H3	1.64	0.46
76:10:143:A:H5'	76:10:144:U:C5	2.50	0.46
77:11:182:C:H2'	77:11:183:C:H6	1.81	0.46
77:11:279:C:H1'	77:11:285:G:N1	2.30	0.46
80:14:2506:A:H5'	80:14:2507:C:N3	2.30	0.46
3:SC:156:LYS:NZ	3:SC:156:LYS:HB3	2.31	0.46
6:SF:90:THR:HG22	6:SF:102:ILE:HD12	1.97	0.46
17:SQ:55:ALA:HB1	17:SQ:60:GLU:HB2	1.98	0.46
25:SY:40:ASP:OD1	25:SY:44:ARG:N	2.46	0.46
27:Sa:58:LYS:HG2	27:Sa:103:ARG:HH21	1.82	0.46
31:Se:33:ARG:HE	31:Se:33:ARG:HB3	1.29	0.46
61:Lc:36:GLU:HG2	61:Lc:39:ASN:HB2	1.98	0.46
63:Le:39:LEU:HD13	63:Le:64:TYR:HB3	1.98	0.46
77:11:1160:A:H2'	77:11:1163:A:N7	2.31	0.46
77:11:1543:A:H2'	77:11:1543:A:N3	2.30	0.46
77:11:1559:G:N2	77:11:1561:A:H3'	2.31	0.46
17:SQ:141:THR:OG1	17:SQ:143:ASP:OD1	2.22	0.45
33:LA:53:VAL:O	33:LA:155:ILE:N	2.44	0.45
46:LN:47:MET:HE3	46:LN:47:MET:HB3	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:La:9:ARG:HH22	59:La:29:GLN:NE2	2.14	0.45
77:11:1234:U:H2'	77:11:1235:U:C6	2.51	0.45
80:14:856:A:P	80:14:856:A:H8	2.39	0.45
80:14:2658:U:H4'	80:14:2659:A:O4'	2.16	0.45
3:SC:96:ASP:OD1	3:SC:96:ASP:N	2.49	0.45
5:SE:172:ILE:HG13	77:11:1541:U:C5	2.51	0.45
6:SF:55:ASP:OD1	6:SF:55:ASP:N	2.48	0.45
17:SQ:220:THR:HG22	17:SQ:221:ARG:N	2.32	0.45
26:SZ:8:ILE:HG13	26:SZ:44:LYS:HD2	1.97	0.45
55:LW:146:LYS:HB3	55:LW:146:LYS:HE3	1.78	0.45
61:Lc:76:LYS:C	61:Lc:76:LYS:HZ1	2.24	0.45
67:Li:98:GLU:HA	67:Li:98:GLU:OE1	2.15	0.45
77:11:128:G:H1'	77:11:177:C:N4	2.31	0.45
77:11:782:C:H2'	77:11:783:U:C6	2.51	0.45
77:11:1257:U:H2'	77:11:1258:G:C8	2.51	0.45
77:11:1322:U:H2'	77:11:1323:U:O4'	2.16	0.45
80:14:2164:G:H2'	80:14:2165:G:H8	1.81	0.45
80:14:2700:A:H2'	80:14:2701:G:C8	2.51	0.45
80:14:2964:G:H2'	80:14:2965:U:C6	2.51	0.45
5:SE:97:ARG:HD2	27:Sa:95:HIS:CE1	2.52	0.45
8:SH:25:ILE:HD11	8:SH:92:ILE:HB	1.97	0.45
38:LF:7:SER:HB2	38:LF:61:ASP:HB3	1.98	0.45
44:LL:15:CYS:SG	44:LL:103:ALA:HB2	2.57	0.45
58:LZ:22:VAL:HB	58:LZ:110:VAL:HG12	1.98	0.45
65:Lg:3:VAL:HG12	65:Lg:91:ARG:HH21	1.81	0.45
76:10:190:C:H2'	76:10:191:C:C6	2.51	0.45
77:11:504:U:H2'	77:11:505:G:C8	2.51	0.45
77:11:1271:G:H8	77:11:1271:G:H5''	1.80	0.45
80:14:859:C:H2'	80:14:860:U:H6	1.76	0.45
4:SD:132:ALA:O	4:SD:136:ARG:HG3	2.16	0.45
7:SG:75:ARG:NH1	77:11:1353:C:H4'	2.31	0.45
12:SL:52:PHE:C	12:SL:53:ILE:HD13	2.41	0.45
50:LR:202:GLU:H	50:LR:202:GLU:CD	2.24	0.45
55:LW:162:ARG:C	77:11:819:G:H22	2.25	0.45
77:11:973:A:H3'	77:11:974:A:H8	1.82	0.45
77:11:1263:U:H2'	77:11:1264:A:C8	2.52	0.45
80:14:498:G:H2'	80:14:499:A:C8	2.52	0.45
80:14:2888:C:O2'	80:14:2889:U:H5'	2.17	0.45
15:SO:58:ARG:NH2	77:11:1246:G:H5''	2.31	0.45
26:SZ:22:LYS:HB2	26:SZ:77:ILE:HG13	1.99	0.45
26:SZ:37:SER:O	26:SZ:41:LEU:HD23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:LF:190:ILE:HG22	38:LF:191:VAL:HG23	1.99	0.45
49:LQ:153:ASP:N	49:LQ:153:ASP:OD1	2.48	0.45
55:LW:139:MET:HE3	55:LW:139:MET:HB3	1.81	0.45
70:Ll:60:LEU:HD13	70:Ll:61:PRO:HD2	1.99	0.45
79:13:7:C:H2'	79:13:8:U:C6	2.51	0.45
80:14:243:G:H2'	80:14:244:C:C6	2.50	0.45
80:14:2844:G:H3'	80:14:2847:C:H42	1.80	0.45
2:SB:79:ARG:HH21	21:SU:90:HIS:CE1	2.34	0.45
2:SB:141:VAL:HG13	2:SB:185:LEU:HD11	1.96	0.45
4:SD:189:VAL:O	4:SD:208:THR:OG1	2.26	0.45
11:SK:51:ASP:HB3	11:SK:54:LYS:HD2	1.99	0.45
11:SK:124:ARG:HB2	11:SK:131:VAL:HG12	1.98	0.45
17:SQ:220:THR:HG22	17:SQ:221:ARG:H	1.81	0.45
21:SU:109:LEU:HD22	21:SU:109:LEU:H	1.81	0.45
24:SX:61:MET:HE1	24:SX:101:ALA:HA	1.98	0.45
26:SZ:13:PHE:CZ	77:11:785:C:H1'	2.51	0.45
47:LO:119:TYR:CZ	51:LS:47:ARG:HG2	2.52	0.45
51:LS:103:ARG:NH1	80:14:72:A:H5''	2.30	0.45
58:LZ:24:ASP:OD1	58:LZ:24:ASP:C	2.59	0.45
76:10:93:G:O5'	76:10:93:G:H8	1.99	0.45
77:11:1495:U:O2'	77:11:1496:U:H5'	2.17	0.45
80:14:692:A:O2'	80:14:708:C:N4	2.49	0.45
80:14:1185:G:H2'	80:14:1186:C:C6	2.52	0.45
80:14:1679:G:H2'	80:14:1680:A:C8	2.52	0.45
18:SR:122:ASP:OD1	18:SR:122:ASP:N	2.49	0.45
22:SV:36:ARG:O	22:SV:37:LYS:C	2.58	0.45
33:LA:44:GLN:CD	33:LA:44:GLN:H	2.25	0.45
59:La:15:ILE:HG12	59:La:34:LEU:HD13	1.99	0.45
62:Ld:6:ASN:HB2	80:14:1146:A:OP1	2.16	0.45
72:Ln:89:TYR:C	72:Ln:90:ASN:HD22	2.25	0.45
76:10:73:U:H2'	76:10:74:U:C6	2.51	0.45
77:11:1203:G:H4'	77:11:1204:G:C5'	2.46	0.45
77:11:1479:G:H2'	77:11:1480:A:H8	1.78	0.45
78:12:37:A:H2'	78:12:38:U:C6	2.51	0.45
80:14:978:G:H2'	80:14:979:C:H6	1.82	0.45
80:14:2576:C:H2'	80:14:2577:A:H8	1.82	0.45
14:SN:23:GLY:HA2	14:SN:26:LYS:HG3	1.99	0.45
22:SV:35:LEU:N	22:SV:101:TRP:HB3	2.32	0.45
29:Sc:16:VAL:O	29:Sc:20:LYS:HG3	2.16	0.45
52:LT:23:LYS:HB3	52:LT:23:LYS:HE3	1.69	0.45
76:10:87:U:H1'	76:10:88:A:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:10:125:U:H1'	76:10:126:G:C8	2.51	0.45
77:11:1623:U:H2'	77:11:1624:C:C6	2.51	0.45
80:14:2257:U:H2'	80:14:2264:G:C2	2.51	0.45
16:SP:159:SER:O	16:SP:163:GLN:HG3	2.17	0.45
26:SZ:62:PHE:HB3	26:SZ:73:GLY:HA3	1.99	0.45
37:LE:139:ARG:NH1	78:12:28:C:OP1	2.50	0.45
38:LF:140:SER:HB3	38:LF:146:GLU:HB2	1.99	0.45
49:LQ:24:MET:HA	49:LQ:24:MET:CE	2.42	0.45
63:Le:34:THR:O	63:Le:38:THR:HG23	2.17	0.45
69:Lk:81:GLY:N	79:13:99:A:OP1	2.40	0.45
76:10:56:U:H2'	76:10:57:A:O4'	2.16	0.45
80:14:11:G:H5'	80:14:12:U:P	2.57	0.45
80:14:1476:A:H2'	80:14:1477:G:O4'	2.17	0.45
2:SB:126:LEU:O	2:SB:130:MET:HG2	2.16	0.45
13:SM:55:ARG:NH1	77:11:963:U:OP2	2.49	0.45
23:SW:32:LYS:O	23:SW:36:GLU:HG2	2.16	0.45
30:Sd:12:LYS:HE3	30:Sd:12:LYS:HB2	1.81	0.45
35:LC:8:HIS:ND1	35:LC:9:PRO:O	2.50	0.45
47:LO:12:LYS:NZ	47:LO:20:GLN:OE1	2.50	0.45
76:10:70:G:N2	76:10:89:A:H61	2.15	0.45
77:11:1352:G:H2'	77:11:1353:C:C6	2.52	0.45
80:14:547:C:H2'	80:14:548:G:C8	2.52	0.45
80:14:637:C:H2'	80:14:638:C:H6	1.82	0.45
80:14:801:A:H2'	80:14:802:C:C6	2.52	0.45
80:14:1449:U:H2'	80:14:1450:U:C6	2.52	0.45
1:SA:154:MET:HE3	1:SA:154:MET:HB3	1.93	0.44
7:SG:37:LYS:HG2	7:SG:42:PRO:HA	1.99	0.44
18:SR:145:LYS:HD3	18:SR:145:LYS:HA	1.79	0.44
35:LC:253:ALA:HB3	80:14:2883:U:H1'	1.99	0.44
36:LD:34:PRO:HG3	36:LD:286:PRO:HD3	1.99	0.44
46:LN:50:ARG:HG2	46:LN:51:LYS:H	1.82	0.44
79:13:136:C:H2'	79:13:137:G:C8	2.52	0.44
80:14:641:A:H2'	80:14:642:U:C6	2.52	0.44
80:14:1958:G:H2'	80:14:2096:A:H61	1.81	0.44
80:14:2638:A:H4'	80:14:2639:A:O5'	2.17	0.44
80:14:3162:C:C4	80:14:3279:G:C6	3.06	0.44
80:14:3195:G:H2'	80:14:3196:C:C6	2.51	0.44
2:SB:35:ASP:OD2	2:SB:68:ARG:NH1	2.51	0.44
24:SX:111:MET:HE3	24:SX:111:MET:HB3	1.79	0.44
33:LA:18:LYS:HD2	33:LA:176:GLU:CG	2.47	0.44
56:LX:14:ARG:HG3	56:LX:15:ALA:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:LZ:67:THR:HG23	58:LZ:68:LYS:HG3	1.99	0.44
59:La:40:ARG:HD3	80:14:3086:C:H5'	1.98	0.44
62:Ld:5:LYS:HD2	62:Ld:5:LYS:HA	1.71	0.44
73:Lo:20:MET:HE3	73:Lo:20:MET:HB3	1.77	0.44
80:14:301:G:N3	80:14:301:G:H5'	2.31	0.44
7:SG:102:LYS:HD3	7:SG:103:TYR:CZ	2.53	0.44
21:SU:28:MET:HE1	21:SU:67:LEU:HG	2.00	0.44
42:LJ:40:LYS:HB2	42:LJ:40:LYS:HE2	1.73	0.44
45:LM:77:TYR:CD1	47:LO:36:VAL:HG21	2.52	0.44
77:11:811:A:H2'	77:11:812:C:H6	1.80	0.44
1:SA:29:ASN:OD1	1:SA:29:ASN:N	2.48	0.44
10:SJ:87:ASP:HA	77:11:571:G:O5'	2.17	0.44
18:SR:27:PHE:CE1	18:SR:36:VAL:HG11	2.51	0.44
21:SU:110:PRO:HD2	21:SU:113:ILE:HD12	2.00	0.44
32:Sf:83:LYS:NZ	32:Sf:85:TYR:OH	2.38	0.44
33:LA:55:LEU:HD12	33:LA:59:PRO:HD3	1.98	0.44
40:LH:30:ASP:OD2	40:LH:32:THR:HG23	2.17	0.44
49:LQ:35:LYS:HE3	49:LQ:35:LYS:HB3	1.83	0.44
55:LW:95:TRP:CH2	55:LW:99:MET:HE3	2.52	0.44
77:11:172:U:H3	77:11:269:A:H62	1.65	0.44
77:11:483:C:H2'	77:11:484:A:H8	1.81	0.44
80:14:2990:A:H2'	80:14:2991:C:C6	2.53	0.44
80:14:3273:C:H2'	80:14:3274:G:C8	2.53	0.44
5:SE:108:LEU:HD11	27:Sa:102:THR:HG21	2.00	0.44
7:SG:31:ARG:HE	7:SG:31:ARG:HB2	1.66	0.44
9:SI:95:LYS:HG2	9:SI:131:VAL:HG21	1.98	0.44
15:SO:95:GLU:C	15:SO:95:GLU:OE1	2.61	0.44
16:SP:56:ILE:HG22	16:SP:58:SER:H	1.82	0.44
26:SZ:90:LYS:HE2	26:SZ:94:ILE:HD11	2.00	0.44
77:11:819:G:O4'	77:11:819:G:N3	2.50	0.44
77:11:974:A:H2	80:14:856:A:H61	1.62	0.44
78:12:33:U:H2'	78:12:34:C:O4'	2.18	0.44
28:Sb:64:LEU:HA	28:Sb:65:PRO:HD3	1.89	0.44
49:LQ:20:SER:O	49:LQ:24:MET:HB2	2.18	0.44
51:LS:101:ARG:HH11	51:LS:103:ARG:HE	1.64	0.44
60:Lb:53:VAL:HG13	60:Lb:62:GLN:HG2	1.99	0.44
77:11:490:G:H1	77:11:504:U:H3	1.64	0.44
80:14:771:A:N6	80:14:780:G:H1'	2.32	0.44
80:14:1821:U:H4'	80:14:1822:G:O4'	2.18	0.44
80:14:2216:A:H2'	80:14:2217:A:H8	1.79	0.44
1:SA:72:LYS:HA	1:SA:72:LYS:HD3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SM:110:ASP:O	13:SM:114:ARG:HG2	2.16	0.44
41:LI:104:GLN:HB3	51:LS:160:PRO:HB3	1.98	0.44
45:LM:143:ASP:C	45:LM:143:ASP:OD1	2.60	0.44
48:LP:86:ILE:O	48:LP:114:GLY:HA2	2.18	0.44
70:LI:24:LYS:HB2	70:LI:24:LYS:HE2	1.71	0.44
77:11:1030:A:OP1	77:11:1797:G:O2'	2.32	0.44
77:11:1225:U:H2'	77:11:1226:A:C8	2.52	0.44
77:11:1530:A:H2'	77:11:1531:A:C8	2.52	0.44
79:13:126:G:H2'	79:13:127:C:C6	2.52	0.44
80:14:2726:U:H2'	80:14:2727:U:C6	2.53	0.44
80:14:3172:C:H5''	80:14:3268:U:C5	2.52	0.44
2:SB:195:TRP:HD1	2:SB:203:PRO:O	2.01	0.44
13:SM:83:GLU:HG2	13:SM:84:ILE:HG23	1.99	0.44
33:LA:10:LEU:HD23	33:LA:180:PHE:CE2	2.53	0.44
33:LA:159:LEU:HG	33:LA:160:LYS:H	1.82	0.44
58:LZ:80:ARG:HG3	58:LZ:80:ARG:HH11	1.82	0.44
76:10:69:A:H2	76:10:88:A:H61	1.66	0.44
76:10:73:U:H2'	76:10:74:U:H6	1.83	0.44
77:11:468:A:C2	77:11:469:G:C8	3.05	0.44
77:11:811:A:H2'	77:11:812:C:C6	2.53	0.44
80:14:1120:C:H2'	80:14:1121:C:C6	2.52	0.44
80:14:2210:A:O2'	80:14:2211:A:O4'	2.36	0.44
80:14:3307:A:O2'	80:14:3308:A:OP1	2.26	0.44
15:SO:21:LYS:HE2	15:SO:21:LYS:N	2.33	0.44
21:SU:59:HIS:CG	21:SU:60:PRO:HD2	2.53	0.44
24:SX:25:ARG:HB2	24:SX:25:ARG:HH11	1.81	0.44
57:LY:13:ASP:OD2	80:14:1006:G:H3'	2.17	0.44
72:Ln:83:MET:HE2	72:Ln:83:MET:HB3	1.87	0.44
76:10:188:C:H2'	76:10:189:C:C6	2.52	0.44
77:11:1110:G:O2'	77:11:1111:G:H5'	2.18	0.44
80:14:2402:A:H2'	80:14:2403:G:O4'	2.18	0.44
80:14:3025:U:H2'	80:14:3026:A:H8	1.83	0.44
2:SB:81:LYS:HE3	2:SB:81:LYS:HA	1.98	0.43
3:SC:104:GLU:O	3:SC:108:GLU:HG2	2.18	0.43
22:SV:81:LEU:O	22:SV:85:HIS:ND1	2.46	0.43
80:14:107:A:H4'	80:14:108:G:OP1	2.17	0.43
80:14:2122:C:H2'	80:14:2123:A:O4'	2.18	0.43
7:SG:46:VAL:HG12	7:SG:52:ARG:HG3	1.99	0.43
11:SK:137:LYS:HG3	77:11:1464:C:N4	2.33	0.43
18:SR:19:ASP:OD1	18:SR:19:ASP:N	2.50	0.43
20:ST:17:LYS:HE2	20:ST:17:LYS:HB2	1.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:SU:34:ASN:OD1	21:SU:64:VAL:HG22	2.17	0.43
32:Sf:107:LYS:HE2	32:Sf:107:LYS:HB2	1.38	0.43
32:Sf:119:LYS:HG2	32:Sf:132:MET:HB2	2.00	0.43
41:LI:4:ARG:NH2	80:14:1438:C:OP2	2.33	0.43
66:Lh:14:VAL:HG23	66:Lh:105:VAL:HB	2.00	0.43
67:Li:60:THR:HG21	80:14:1598:A:H5'	2.01	0.43
80:14:666:C:H2'	80:14:667:A:C8	2.52	0.43
80:14:2272:U:O2'	80:14:2274:A:N7	2.47	0.43
80:14:2711:U:H2'	80:14:2712:C:C6	2.53	0.43
3:SC:50:ALA:O	3:SC:54:ILE:HD12	2.17	0.43
14:SN:117:ARG:HH11	14:SN:117:ARG:HG2	1.83	0.43
21:SU:53:ASP:OD1	21:SU:53:ASP:C	2.60	0.43
76:10:80:C:H1'	76:10:157:A:C2	2.52	0.43
80:14:537:U:N3	80:14:541:U:H1'	2.33	0.43
80:14:3284:U:H2'	80:14:3285:A:C4	2.53	0.43
5:SE:192:ASN:ND2	76:10:96:G:OP1	2.51	0.43
7:SG:20:LYS:HG2	7:SG:83:SER:HA	2.00	0.43
26:SZ:28:VAL:HG22	26:SZ:30:HIS:HD2	1.83	0.43
34:LB:181:LYS:NZ	80:14:870:G:OP2	2.52	0.43
46:LN:51:LYS:O	46:LN:69:VAL:HB	2.19	0.43
48:LP:52:ALA:O	48:LP:56:GLU:HG2	2.18	0.43
53:LU:47:LYS:HE2	80:14:266:G:OP1	2.18	0.43
63:Le:17:ASN:H	63:Le:17:ASN:ND2	2.17	0.43
76:10:69:A:H3'	76:10:70:G:H8	1.82	0.43
76:10:130:A:H3'	76:10:131:U:C6	2.52	0.43
77:11:417:U:H2'	77:11:418:C:C6	2.54	0.43
79:13:129:A:C8	79:13:133:G:N1	2.86	0.43
80:14:1770:G:N2	80:14:1772:G:HO2'	2.16	0.43
80:14:2210:A:H2'	80:14:2211:A:C5	2.54	0.43
2:SB:201:GLN:OE1	2:SB:201:GLN:HA	2.17	0.43
5:SE:47:THR:CG2	5:SE:48:ALA:N	2.82	0.43
9:SI:34:ALA:CB	9:SI:111:ALA:HB2	2.48	0.43
20:ST:65:ASN:C	20:ST:65:ASN:HD22	2.26	0.43
51:LS:171:MET:H	51:LS:171:MET:HG3	1.64	0.43
52:LT:61:ASP:OD1	52:LT:61:ASP:C	2.62	0.43
60:Lb:31:GLU:CD	60:Lb:31:GLU:H	2.26	0.43
73:Lo:10:MET:HE2	73:Lo:10:MET:HB3	1.85	0.43
77:11:628:C:H2'	77:11:629:U:C6	2.53	0.43
80:14:245:A:H2'	80:14:246:C:O4'	2.18	0.43
80:14:2470:G:H21	80:14:2493:A:H62	1.66	0.43
80:14:2576:C:H2'	80:14:2577:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:SH:41:ASP:OD1	8:SH:41:ASP:C	2.61	0.43
13:SM:55:ARG:HD3	77:11:963:U:H5'	2.00	0.43
15:SO:59:LYS:N	15:SO:60:PRO:HD2	2.34	0.43
18:SR:191:ARG:NH2	77:11:272:G:OP2	2.46	0.43
22:SV:76:LYS:HD3	32:Sf:108:VAL:HG11	2.00	0.43
26:SZ:21:ARG:HD2	26:SZ:76:LEU:HD22	2.00	0.43
36:LD:79:ILE:HG13	36:LD:80:PRO:HD2	2.01	0.43
36:LD:368:LYS:HE2	36:LD:368:LYS:HB3	1.82	0.43
63:Le:27:LYS:HE3	63:Le:99:ASP:HB3	2.00	0.43
77:11:588:A:H2'	77:11:589:G:C8	2.54	0.43
77:11:1354:U:H2'	77:11:1355:A:C8	2.54	0.43
80:14:957:U:H2'	80:14:958:C:C6	2.54	0.43
80:14:2594:A:C6	80:14:2595:G:C4	3.06	0.43
80:14:3159:C:H2'	80:14:3160:G:H8	1.80	0.43
18:SR:144:ARG:HE	18:SR:144:ARG:HB2	1.65	0.43
18:SR:222:LYS:O	18:SR:222:LYS:HD3	2.19	0.43
23:SW:27:ASP:O	23:SW:31:ASN:ND2	2.35	0.43
27:Sa:37:ASN:O	27:Sa:70:ARG:NH2	2.46	0.43
32:Sf:119:LYS:HG3	32:Sf:120:GLU:N	2.32	0.43
33:LA:42:ASP:O	33:LA:43:PRO:C	2.62	0.43
33:LA:58:ILE:H	33:LA:58:ILE:HG12	1.65	0.43
49:LQ:144:VAL:HG12	49:LQ:144:VAL:O	2.18	0.43
52:LT:102:LEU:HD22	52:LT:106:ASP:HB2	2.00	0.43
53:LU:85:THR:HG21	80:14:43:A:P	2.59	0.43
76:10:96:G:H3'	76:10:97:G:C8	2.47	0.43
77:11:420:A:H5''	77:11:421:A:N7	2.33	0.43
77:11:1403:U:H2'	77:11:1405:U:C4	2.54	0.43
80:14:786:U:H5	80:14:2740:C:N3	2.16	0.43
12:SL:26:ASN:O	12:SL:30:ILE:HD11	2.18	0.43
20:ST:47:ILE:CD1	20:ST:57:ARG:HB2	2.49	0.43
21:SU:60:PRO:HG2	21:SU:61:LEU:HD22	2.01	0.43
33:LA:56:PRO:HD3	33:LA:185:MET:SD	2.58	0.43
46:LN:83:ARG:HG3	46:LN:83:ARG:HH11	1.84	0.43
49:LQ:210:LYS:O	49:LQ:214:SER:OG	2.30	0.43
51:LS:101:ARG:NH1	51:LS:103:ARG:HH21	2.17	0.43
53:LU:84:PRO:HA	53:LU:87:GLN:HG3	2.00	0.43
60:Lb:90:ASP:O	60:Lb:116:ARG:NH1	2.52	0.43
67:Li:68:SER:OG	67:Li:70:ASN:OD1	2.35	0.43
69:Lk:87:ARG:HD2	79:13:71:G:OP2	2.19	0.43
76:10:118:G:H3'	76:10:119:G:H4'	2.01	0.43
77:11:334:G:H2'	77:11:335:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:11:1686:G:H1'	77:11:1729:A:H61	1.84	0.43
80:14:855:G:N2	80:14:857:A:H3'	2.34	0.43
80:14:1119:U:H2'	80:14:1120:C:C6	2.53	0.43
6:SF:14:MET:HE3	6:SF:14:MET:HB2	1.83	0.43
17:SQ:115:ARG:HA	17:SQ:115:ARG:CZ	2.49	0.43
18:SR:5:ILE:HD11	18:SR:16:LEU:HD22	2.01	0.43
18:SR:144:ARG:HG2	18:SR:145:LYS:HE2	2.00	0.43
22:SV:78:VAL:O	22:SV:79:LYS:C	2.62	0.43
26:SZ:11:ARG:HA	77:11:784:A:H61	1.83	0.43
32:Sf:143:LYS:NZ	77:11:1256:U:O3'	2.52	0.43
53:LU:85:THR:HG23	80:14:42:U:H5''	2.01	0.43
61:Lc:87:LYS:H	61:Lc:87:LYS:HG2	1.41	0.43
69:Lk:45:ARG:C	69:Lk:46:LYS:HG2	2.44	0.43
76:10:154:C:N4	76:10:155:G:O6	2.52	0.43
77:11:1225:U:C2	77:11:1226:A:C8	3.07	0.43
77:11:1353:C:H2'	77:11:1354:U:C6	2.54	0.43
80:14:1823:C:H2'	80:14:1824:C:C6	2.53	0.43
80:14:2571:G:H5''	80:14:2572:C:C5	2.53	0.43
19:SS:100:ARG:NH2	77:11:859:A:P	2.92	0.43
23:SW:47:ARG:HE	23:SW:47:ARG:HB3	1.46	0.43
51:LS:157:ARG:HG2	51:LS:158:GLU:N	2.34	0.43
63:Le:35:VAL:HG22	63:Le:96:SER:HB2	2.01	0.43
68:Lj:36:THR:OG1	68:Lj:37:SER:N	2.50	0.43
70:Ll:16:ARG:HG3	70:Ll:16:ARG:NH1	2.34	0.43
70:Ll:60:LEU:CD1	70:Ll:61:PRO:HD2	2.49	0.43
74:Lp:29:LYS:HA	74:Lp:29:LYS:HD3	1.39	0.43
80:14:311:U:H2'	80:14:312:C:C6	2.53	0.43
80:14:883:C:H5''	80:14:884:U:O5'	2.19	0.43
80:14:2614:U:H2'	80:14:2615:U:C6	2.53	0.43
4:SD:179:MET:HG2	4:SD:208:THR:HG22	2.00	0.42
35:LC:209:ASP:OD1	35:LC:209:ASP:N	2.49	0.42
41:LI:135:LYS:HB2	41:LI:135:LYS:HE3	1.65	0.42
45:LM:50:LEU:CD2	79:13:152:U:H4'	2.49	0.42
77:11:1362:G:OP2	77:11:1365:A:N6	2.51	0.42
80:14:743:C:O2'	80:14:745:G:O6	2.31	0.42
3:SC:31:LYS:HA	3:SC:31:LYS:HD3	1.72	0.42
15:SO:61:MET:HE3	15:SO:61:MET:HB3	1.80	0.42
16:SP:111:ARG:NH2	77:11:933:A:N3	2.67	0.42
18:SR:147:PHE:N	18:SR:147:PHE:HD1	2.17	0.42
19:SS:53:ASP:OD1	19:SS:53:ASP:N	2.35	0.42
35:LC:82:PRO:HA	35:LC:323:ASP:OD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:LC:312:MET:HE2	80:14:3321:U:H5''	2.00	0.42
37:LE:38:VAL:HG23	37:LE:122:THR:HG21	2.01	0.42
48:LP:95:MET:HE3	48:LP:100:LYS:HB2	2.00	0.42
54:LV:2:GLY:N	80:14:1171:A:OP1	2.52	0.42
76:10:70:G:H1	76:10:85:C:H42	1.67	0.42
76:10:71:U:H2'	76:10:72:G:O4'	2.19	0.42
76:10:125:U:H1'	76:10:126:G:H8	1.83	0.42
77:11:1149:G:H2'	77:11:1150:A:C8	2.54	0.42
80:14:3223:G:H2'	80:14:3224:U:C6	2.54	0.42
16:SP:195:ARG:HG3	77:11:1059:G:H1	1.84	0.42
18:SR:22:GLN:N	18:SR:22:GLN:CD	2.77	0.42
35:LC:61:GLU:OE2	35:LC:68:HIS:HE1	2.02	0.42
37:LE:97:ASN:N	37:LE:97:ASN:HD22	2.17	0.42
46:LN:112:LYS:NZ	79:13:88:G:OP2	2.53	0.42
56:LX:157:LYS:HE2	56:LX:157:LYS:HB2	1.66	0.42
56:LX:161:PRO:HD2	56:LX:165:LEU:HD12	2.00	0.42
69:Lk:39:TYR:CD1	69:Lk:40:PRO:HA	2.55	0.42
76:10:190:C:C2	76:10:199:G:C2	3.08	0.42
77:11:1524:U:H5'	77:11:1525:C:H5	1.84	0.42
77:11:1578:G:HO2'	77:11:1579:A:P	2.37	0.42
80:14:195:A:N3	80:14:215:G:O2'	2.49	0.42
80:14:2410:C:H2'	80:14:2411:U:C6	2.54	0.42
1:SA:149:ASP:HB2	1:SA:165:ASN:OD1	2.19	0.42
17:SQ:57:THR:OG1	17:SQ:60:GLU:HG3	2.20	0.42
24:SX:67:LEU:HD23	24:SX:67:LEU:HA	1.82	0.42
26:SZ:90:LYS:O	26:SZ:94:ILE:HG13	2.20	0.42
38:LF:57:LYS:HB3	38:LF:57:LYS:HE3	1.65	0.42
39:LG:117:TYR:HA	39:LG:120:ILE:HD12	2.00	0.42
76:10:54:C:H42	76:10:65:G:H1	1.67	0.42
76:10:58:C:H2'	76:10:59:G:O4'	2.19	0.42
77:11:849:G:O6	77:11:850:A:N6	2.52	0.42
80:14:2152:A:H2'	80:14:2153:A:C5	2.54	0.42
80:14:2409:C:H2'	80:14:2410:C:C6	2.54	0.42
3:SC:180:LYS:HE2	3:SC:180:LYS:HB2	1.58	0.42
4:SD:152:GLY:HA2	25:SY:1:MET:HE1	2.01	0.42
8:SH:96:SER:HB3	8:SH:100:VAL:HG21	2.00	0.42
9:SI:123:MET:HE2	9:SI:123:MET:HB3	1.98	0.42
19:SS:51:GLN:NE2	19:SS:59:LYS:HE2	2.34	0.42
26:SZ:13:PHE:HZ	77:11:785:C:H1'	1.85	0.42
33:LA:67:MET:HE2	33:LA:73:HIS:HB3	2.02	0.42
35:LC:20:LYS:HB2	35:LC:20:LYS:HE2	1.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:LD:384:THR:HG22	36:LD:385:MET:N	2.34	0.42
40:LH:17:SER:OG	80:14:3096:G:OP1	2.35	0.42
52:LT:9:ILE:HD13	52:LT:64:ARG:HB3	2.00	0.42
66:Lh:63:LYS:HG3	66:Lh:68:HIS:CE1	2.54	0.42
66:Lh:64:LYS:HG3	80:14:632:G:OP1	2.20	0.42
77:11:57:G:H2'	77:11:58:U:O4'	2.19	0.42
77:11:1433:G:H5'	77:11:1434:G:OP2	2.19	0.42
80:14:3253:C:H2'	80:14:3254:C:O4'	2.19	0.42
4:SD:81:LEU:HD23	4:SD:81:LEU:HA	1.88	0.42
25:SY:44:ARG:HD2	25:SY:44:ARG:HA	1.85	0.42
33:LA:189:PHE:CE2	33:LA:193:LEU:HD11	2.54	0.42
42:LJ:48:PHE:O	42:LJ:139:ARG:HA	2.20	0.42
50:LR:24:LEU:HD12	50:LR:24:LEU:HA	1.82	0.42
76:10:118:G:H2'	76:10:119:G:H4'	2.00	0.42
76:10:161:A:H4'	76:10:162:A:OP1	2.19	0.42
77:11:182:C:H2'	77:11:183:C:C6	2.54	0.42
80:14:419:A:C2	80:14:2366:A:H4'	2.55	0.42
80:14:2680:G:N3	80:14:2680:G:H2'	2.34	0.42
80:14:2963:C:H2'	80:14:2964:G:C8	2.55	0.42
17:SQ:240:LYS:NZ	77:11:789:C:C2	2.86	0.42
33:LA:47:LYS:H	33:LA:195:LYS:NZ	2.18	0.42
33:LA:47:LYS:HE2	33:LA:47:LYS:HB3	1.62	0.42
34:LB:116:VAL:HB	34:LB:126:PHE:HB2	2.02	0.42
36:LD:361:LYS:HA	36:LD:361:LYS:HD3	1.54	0.42
54:LV:23:ASP:O	54:LV:27:LYS:HG2	2.20	0.42
61:Lc:58:THR:HB	61:Lc:71:ALA:HB3	2.00	0.42
64:Lf:70:ARG:HH11	80:14:3060:C:N4	2.18	0.42
70:Ll:35:LYS:HA	70:Ll:43:TYR:O	2.19	0.42
77:11:397:C:H2'	77:11:398:C:C6	2.55	0.42
80:14:1128:G:H2'	80:14:1129:C:C6	2.55	0.42
80:14:2843:C:H2'	80:14:2844:G:O4'	2.19	0.42
80:14:2890:A:N3	80:14:2890:A:H2'	2.33	0.42
2:SB:140:ILE:HG12	2:SB:154:LYS:HG3	2.02	0.42
5:SE:204:ARG:O	5:SE:205:VAL:C	2.63	0.42
16:SP:184:LEU:HD12	16:SP:184:LEU:HA	1.90	0.42
20:ST:193:ARG:NH1	77:11:204:U:O2	2.52	0.42
21:SU:97:ASN:HA	21:SU:100:ILE:CG2	2.50	0.42
27:Sa:103:ARG:H	27:Sa:103:ARG:HG2	1.49	0.42
37:LE:165:PHE:CE2	37:LE:171:GLY:HA3	2.55	0.42
49:LQ:120:PHE:CZ	80:14:3258:A:H2'	2.55	0.42
61:Lc:66:LYS:H	61:Lc:66:LYS:HE2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Lj:48:ARG:O	68:Lj:48:ARG:HD3	2.20	0.42
76:10:130:A:H3'	76:10:131:U:H6	1.85	0.42
77:11:80:C:H2'	77:11:81:U:C6	2.55	0.42
77:11:510:U:H2'	77:11:511:U:C6	2.55	0.42
77:11:1493:G:H3'	77:11:1522:A:H61	1.85	0.42
77:11:1724:G:H2'	77:11:1725:C:C6	2.55	0.42
80:14:660:A:H2'	80:14:661:C:C6	2.55	0.42
8:SH:37:LYS:HB3	8:SH:37:LYS:HE2	1.66	0.42
14:SN:54:TYR:CD1	14:SN:114:PRO:HG2	2.55	0.42
14:SN:80:LYS:HG3	77:11:350:G:H5'	2.01	0.42
20:ST:114:TYR:CD2	20:ST:122:ILE:HD11	2.55	0.42
30:Sd:28:VAL:HG22	30:Sd:38:ILE:HG22	2.01	0.42
32:Sf:102:VAL:HA	32:Sf:105:PHE:CE2	2.55	0.42
37:LE:21:LEU:HD11	37:LE:81:LEU:HD13	2.02	0.42
65:Lg:10:VAL:HG22	65:Lg:64:THR:HB	2.02	0.42
77:11:516:U:H2'	77:11:517:G:C8	2.53	0.42
77:11:1127:A:H2'	77:11:1128:A:C8	2.54	0.42
77:11:1235:U:H2'	77:11:1236:G:H8	1.84	0.42
77:11:1366:U:H5''	77:11:1368:C:N4	2.35	0.42
80:14:275:U:H2'	80:14:276:U:C6	2.55	0.42
2:SB:165:GLN:N	2:SB:166:PRO:HD2	2.35	0.42
3:SC:150:VAL:HG12	3:SC:151:ARG:O	2.20	0.42
10:SJ:129:LEU:HD23	10:SJ:129:LEU:HA	1.83	0.42
15:SO:90:MET:HB2	15:SO:90:MET:HE2	1.82	0.42
26:SZ:107:LYS:HE2	77:11:463:G:O6	2.19	0.42
32:Sf:101:ALA:O	32:Sf:104:GLN:HB2	2.19	0.42
32:Sf:132:MET:HG2	32:Sf:141:CYS:HB2	2.01	0.42
54:LV:123:ASP:OD1	54:LV:124:GLN:N	2.53	0.42
76:10:82:C:H1'	76:10:95:A:N1	2.34	0.42
76:10:146:C:H2'	76:10:147:G:O4'	2.20	0.42
77:11:507:U:H2'	77:11:508:A:C8	2.54	0.42
77:11:1580:G:H5''	77:11:1581:G:OP1	2.20	0.42
80:14:1733:G:N3	80:14:1733:G:H5'	2.35	0.42
80:14:1748:G:H2'	80:14:1749:G:C8	2.55	0.42
80:14:2542:C:H2'	80:14:2543:A:O4'	2.20	0.42
3:SC:112:GLN:HE21	3:SC:128:ARG:HB2	1.84	0.41
13:SM:87:ASP:OD1	13:SM:87:ASP:N	2.52	0.41
18:SR:189:LEU:HD23	18:SR:189:LEU:HA	1.94	0.41
23:SW:23:LYS:H	23:SW:23:LYS:HG3	1.70	0.41
44:LL:61:THR:HG23	79:13:7:C:H5'	2.02	0.41
61:Lc:141:ARG:CD	80:14:438:A:H5''	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:L1:55:LYS:NZ	70:L1:55:LYS:HB2	2.35	0.41
76:10:51:G:H1	76:10:68:U:H3	1.68	0.41
77:11:1318:U:H2'	77:11:1319:C:O4'	2.19	0.41
80:14:856:A:H8	80:14:856:A:OP1	2.02	0.41
80:14:1545:A:H2'	80:14:1546:A:C8	2.55	0.41
80:14:2509:U:H2'	80:14:2510:U:O4'	2.20	0.41
80:14:2692:G:H2'	80:14:2692:G:N3	2.34	0.41
1:SA:57:LYS:HD2	1:SA:57:LYS:HA	1.81	0.41
3:SC:125:HIS:CD2	31:Se:37:ARG:HH11	2.38	0.41
4:SD:118:ASN:O	4:SD:118:ASN:ND2	2.53	0.41
18:SR:44:GLU:O	18:SR:46:LYS:HD2	2.20	0.41
18:SR:222:LYS:HE2	18:SR:222:LYS:HA	2.01	0.41
21:SU:102:PHE:CD1	21:SU:102:PHE:C	2.97	0.41
43:LK:187:LYS:HD2	43:LK:187:LYS:HA	1.83	0.41
44:LL:32:THR:HG21	44:LL:88:SER:HB3	2.02	0.41
51:LS:101:ARG:HH11	51:LS:103:ARG:HH21	1.68	0.41
51:LS:168:THR:O	51:LS:172:LYS:HG3	2.20	0.41
55:LW:114:LYS:HE3	55:LW:114:LYS:HB2	1.71	0.41
72:Ln:90:ASN:HD22	72:Ln:90:ASN:N	2.17	0.41
77:11:816:A:H4'	77:11:818:A:H5''	2.02	0.41
77:11:886:U:H3	77:11:948:U:H3	1.68	0.41
80:14:1145:G:O2'	80:14:2645:A:N3	2.45	0.41
80:14:1818:G:H2'	80:14:1819:A:C1'	2.51	0.41
80:14:2461:U:H6	80:14:2461:U:H2'	1.69	0.41
2:SB:51:ILE:HB	2:SB:89:LEU:HD13	2.01	0.41
9:SI:60:LYS:NZ	9:SI:79:ASP:OD2	2.50	0.41
17:SQ:254:LYS:NZ	17:SQ:254:LYS:HB3	2.35	0.41
20:ST:25:ARG:HA	77:11:404:A:H5''	2.01	0.41
20:ST:118:TYR:CD2	20:ST:165:ARG:HG3	2.56	0.41
24:SX:127:ASN:HA	24:SX:130:ARG:NH1	2.35	0.41
26:SZ:85:LYS:NZ	26:SZ:98:LEU:HB3	2.36	0.41
68:Lj:36:THR:HG23	68:Lj:41:HIS:CE1	2.55	0.41
69:Lk:60:GLY:HA2	69:Lk:64:MET:SD	2.60	0.41
80:14:666:C:H2'	80:14:667:A:H8	1.83	0.41
80:14:936:A:H2'	80:14:937:C:C6	2.55	0.41
80:14:2560:A:H2'	80:14:2561:C:O4'	2.21	0.41
3:SC:60:MET:HE3	3:SC:60:MET:HB3	1.88	0.41
49:LQ:64:ASP:CG	65:Lg:5:LEU:HD11	2.45	0.41
49:LQ:68:LYS:HD2	49:LQ:68:LYS:N	2.32	0.41
63:Le:18:ARG:HB3	63:Le:105:ILE:HG23	2.02	0.41
76:10:57:A:H1'	76:10:63:A:C2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:10:118:G:C3'	76:10:119:G:H4'	2.50	0.41
76:10:196:A:C6	76:10:197:G:H1'	2.55	0.41
77:11:186:A:H3'	77:11:187:C:H6	1.84	0.41
80:14:1653:U:H2'	80:14:1654:C:O4'	2.21	0.41
2:SB:21:PHE:CD1	2:SB:21:PHE:C	2.97	0.41
3:SC:30:LEU:HD23	31:Se:44:PHE:HE2	1.85	0.41
7:SG:17:PHE:O	7:SG:94:LYS:HE2	2.20	0.41
18:SR:33:SER:O	18:SR:33:SER:OG	2.37	0.41
21:SU:84:GLU:HG3	21:SU:93:TRP:NE1	2.35	0.41
28:Sb:32:LYS:O	28:Sb:37:LYS:NZ	2.52	0.41
33:LA:49:PHE:CE2	33:LA:159:LEU:HB2	2.55	0.41
38:LF:1:MET:HE3	38:LF:1:MET:HB3	1.83	0.41
43:LK:81:ARG:H	43:LK:81:ARG:HG3	1.69	0.41
47:LO:105:GLU:HA	47:LO:108:LYS:HD3	2.01	0.41
48:LP:56:GLU:HG2	48:LP:56:GLU:H	1.69	0.41
76:10:156:U:H2'	76:10:158:A:OP2	2.20	0.41
77:11:822:U:H2'	77:11:823:U:C6	2.55	0.41
77:11:967:U:H4'	77:11:968:U:O4'	2.20	0.41
77:11:1522:A:H1'	77:11:1525:C:N4	2.35	0.41
77:11:1778:U:H2'	77:11:1779:U:C6	2.56	0.41
80:14:667:A:H2'	80:14:668:A:C8	2.56	0.41
80:14:2427:A:H2'	80:14:2428:G:O4'	2.20	0.41
1:SA:109:THR:OG1	77:11:1324:A:N6	2.53	0.41
9:SI:116:ARG:NH1	28:Sb:52:ASP:OD2	2.53	0.41
11:SK:100:SER:HB3	11:SK:101:ASN:H	1.76	0.41
38:LF:112:ASN:HB3	38:LF:137:VAL:O	2.20	0.41
56:LX:29:MET:HG3	56:LX:43:PHE:HD1	1.84	0.41
68:Lj:38:LYS:HE2	68:Lj:38:LYS:HB2	1.77	0.41
76:10:123:A:H2'	76:10:124:A:O4'	2.20	0.41
1:SA:187:GLY:HA2	25:SY:44:ARG:NH2	2.34	0.41
7:SG:50:ILE:HD13	7:SG:50:ILE:HA	1.94	0.41
11:SK:94:LYS:HG3	11:SK:95:PHE:H	1.85	0.41
18:SR:1:MET:HE2	18:SR:1:MET:HB3	1.91	0.41
19:SS:40:GLU:OE1	19:SS:40:GLU:N	2.49	0.41
19:SS:106:LYS:HE2	19:SS:106:LYS:HA	2.02	0.41
20:ST:195:ASP:OD1	20:ST:195:ASP:N	2.54	0.41
21:SU:98:ASP:OD1	21:SU:98:ASP:N	2.53	0.41
50:LR:235:GLY:HA3	80:14:2589:G:C6	2.56	0.41
77:11:1497:A:H5'	77:11:1498:U:H5''	2.03	0.41
80:14:1508:C:H2'	80:14:1509:A:C8	2.55	0.41
80:14:2270:C:H2'	80:14:2271:U:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:14:2488:G:N2	80:14:2490:A:H3'	2.35	0.41
14:SN:48:GLU:OE1	14:SN:48:GLU:O	2.39	0.41
18:SR:43:ASP:OD1	18:SR:43:ASP:C	2.64	0.41
18:SR:196:ILE:HG23	18:SR:200:LYS:NZ	2.36	0.41
23:SW:63:LYS:HB2	23:SW:63:LYS:HE2	1.80	0.41
26:SZ:40:GLU:OE2	26:SZ:44:LYS:NZ	2.51	0.41
33:LA:3:SER:HA	33:LA:198:TRP:CZ2	2.56	0.41
33:LA:33:GLU:O	33:LA:206:LEU:HA	2.21	0.41
37:LE:34:ARG:NE	37:LE:122:THR:O	2.46	0.41
38:LF:121:LEU:HD23	38:LF:121:LEU:O	2.21	0.41
40:LH:109:LYS:HB2	40:LH:109:LYS:NZ	2.36	0.41
43:LK:11:ALA:O	43:LK:15:ARG:HG2	2.21	0.41
43:LK:184:LYS:HB3	43:LK:184:LYS:HE2	1.81	0.41
50:LR:30:LYS:NZ	80:14:2563:C:OP1	2.52	0.41
50:LR:47:PHE:HB3	80:14:2529:A:H5''	2.03	0.41
53:LU:136:ASP:OD2	53:LU:139:HIS:HB2	2.21	0.41
77:11:141:G:H2'	77:11:142:G:H8	1.86	0.41
77:11:591:U:H2'	77:11:592:C:O4'	2.20	0.41
77:11:1163:A:H2'	77:11:1164:C:C6	2.56	0.41
77:11:1455:U:H2'	77:11:1456:C:C6	2.55	0.41
80:14:2226:A:H2'	80:14:2227:A:C8	2.56	0.41
80:14:2551:U:H2'	80:14:2552:C:C6	2.55	0.41
80:14:3189:C:H2'	80:14:3190:C:O4'	2.21	0.41
5:SE:188:LYS:HB2	5:SE:188:LYS:HE2	1.67	0.41
9:SI:137:ASP:CG	77:11:931:G:H4'	2.46	0.41
11:SK:43:ILE:HA	11:SK:43:ILE:HD12	1.79	0.41
16:SP:42:ASN:OD1	16:SP:42:ASN:N	2.37	0.41
16:SP:173:ARG:O	16:SP:177:SER:HB2	2.21	0.41
17:SQ:108:ARG:NH1	77:11:793:A:OP1	2.54	0.41
18:SR:20:ASP:OD1	18:SR:22:GLN:NE2	2.51	0.41
18:SR:58:LYS:HE3	18:SR:58:LYS:HB2	1.89	0.41
21:SU:97:ASN:O	21:SU:101:GLU:HG3	2.20	0.41
23:SW:46:LEU:HD12	23:SW:46:LEU:HA	1.88	0.41
24:SX:113:ILE:HG22	24:SX:114:VAL:HG13	2.02	0.41
26:SZ:12:LYS:H	26:SZ:25:ILE:CG2	2.34	0.41
37:LE:15:LYS:NZ	37:LE:15:LYS:HB2	2.36	0.41
39:LG:10:ARG:HB3	39:LG:10:ARG:NH1	2.35	0.41
45:LM:53:ASP:OD1	45:LM:53:ASP:N	2.52	0.41
48:LP:54:GLU:O	48:LP:58:GLN:HG3	2.20	0.41
49:LQ:201:LYS:HE3	49:LQ:201:LYS:HA	2.01	0.41
52:LT:7:VAL:HG12	52:LT:55:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:LT:29:ASP:OD2	56:LX:74:ILE:HD12	2.21	0.41
58:LZ:66:LYS:HE3	58:LZ:66:LYS:HA	2.01	0.41
61:Lc:95:ARG:O	61:Lc:99:LYS:HD3	2.21	0.41
76:10:50:G:O2'	76:10:51:G:H3'	2.21	0.41
76:10:85:C:C4	76:10:86:U:C4	3.08	0.41
77:11:515:A:H2'	77:11:516:U:C6	2.56	0.41
77:11:644:G:H8	77:11:644:G:O5'	2.04	0.41
77:11:1202:G:H5'	77:11:1203:G:OP1	2.20	0.41
77:11:1250:U:H2'	77:11:1251:C:C6	2.56	0.41
3:SC:135:HIS:HE2	77:11:515:A:H4'	1.85	0.41
8:SH:81:ASP:OD1	12:SL:54:LYS:HD2	2.21	0.41
11:SK:118:ARG:HG3	11:SK:118:ARG:HH11	1.86	0.41
16:SP:74:GLN:O	16:SP:75:LYS:C	2.64	0.41
22:SV:90:ILE:HG12	22:SV:91:THR:N	2.35	0.41
26:SZ:121:GLY:O	26:SZ:124:LYS:HB2	2.21	0.41
52:LT:83:LYS:O	52:LT:87:SER:OG	2.39	0.41
52:LT:124:GLU:OE1	52:LT:124:GLU:HA	2.19	0.41
77:11:129:U:H3'	77:11:130:A:H5'	2.03	0.41
77:11:206:U:H2'	77:11:207:A:H8	1.86	0.41
77:11:1647:C:H2'	77:11:1648:G:C8	2.56	0.41
80:14:2765:A:H2'	80:14:2766:U:H6	1.86	0.41
21:SU:64:VAL:HG12	21:SU:65:PRO:O	2.21	0.40
76:10:74:U:O2	76:10:94:A:H3'	2.21	0.40
76:10:115:G:H2'	76:10:116:C:O4'	2.20	0.40
76:10:119:G:H2'	76:10:120:U:O4'	2.21	0.40
77:11:563:U:H2'	77:11:564:G:H8	1.86	0.40
80:14:36:U:H2'	80:14:37:A:O4'	2.22	0.40
80:14:3307:A:HO2'	80:14:3308:A:P	2.42	0.40
1:SA:84:GLN:O	1:SA:85:ARG:C	2.64	0.40
2:SB:137:CYS:SG	2:SB:138:GLU:N	2.95	0.40
4:SD:211:ARG:HD2	77:11:1100:U:O4	2.21	0.40
17:SQ:71:MET:HE3	17:SQ:74:SER:HA	2.04	0.40
22:SV:54:VAL:HG21	22:SV:125:LYS:HG2	2.03	0.40
33:LA:129:ASN:OD1	33:LA:134:PHE:CD1	2.74	0.40
76:10:47:C:H42	76:10:59:G:H1	1.69	0.40
77:11:909:A:H2'	77:11:910:A:C8	2.56	0.40
2:SB:28:LEU:C	2:SB:37:TYR:HE2	2.30	0.40
2:SB:193:LEU:H	2:SB:193:LEU:HG	1.70	0.40
11:SK:14:ARG:NH2	11:SK:17:ASN:HA	2.36	0.40
15:SO:97:ILE:CD1	15:SO:116:PRO:HA	2.51	0.40
15:SO:134:LYS:HD3	15:SO:134:LYS:H	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:SP:62:LYS:NZ	16:SP:89:GLU:O	2.55	0.40
32:Sf:95:LYS:HE2	32:Sf:95:LYS:HB3	1.81	0.40
44:LL:42:ASP:OD1	44:LL:42:ASP:N	2.45	0.40
50:LR:243:LYS:C	50:LR:243:LYS:HD2	2.46	0.40
59:La:50:LYS:HD3	80:14:2115:G:C5'	2.51	0.40
69:Lk:13:ASN:O	80:14:827:A:C4	2.74	0.40
69:Lk:76:THR:CG2	69:Lk:79:ARG:HB3	2.51	0.40
76:10:100:U:H1'	76:10:159:U:C6	2.56	0.40
77:11:1262:C:H2'	77:11:1263:U:C6	2.56	0.40
77:11:1321:G:H2'	77:11:1322:U:C6	2.56	0.40
80:14:1792:G:H2'	80:14:1793:G:C8	2.57	0.40
80:14:2164:G:H2'	80:14:2165:G:C8	2.56	0.40
5:SE:24:LEU:HD23	5:SE:115:ILE:HD11	2.03	0.40
5:SE:55:MET:HG3	5:SE:57:HIS:H	1.87	0.40
14:SN:104:ARG:NH1	77:11:311:G:OP1	2.54	0.40
33:LA:53:VAL:CG1	33:LA:155:ILE:HG13	2.51	0.40
33:LA:160:LYS:HB3	33:LA:161:LYS:H	1.70	0.40
38:LF:10:MET:HE1	38:LF:81:GLU:HG3	2.04	0.40
38:LF:95:MET:HG2	38:LF:184:VAL:HG22	2.03	0.40
40:LH:96:MET:HG2	40:LH:97:TYR:N	2.36	0.40
42:LJ:212:GLY:H	43:LK:288:ASN:ND2	2.19	0.40
48:LP:145:ARG:HG2	48:LP:149:TYR:HE2	1.87	0.40
56:LX:29:MET:HE3	57:LY:149:VAL:O	2.21	0.40
57:LY:126:ILE:O	80:14:1106:C:O2'	2.38	0.40
77:11:1397:C:H2'	77:11:1398:G:C8	2.54	0.40
79:13:134:G:C6	79:13:135:C:C4	3.10	0.40
79:13:162:G:C6	80:14:1:G:C6	3.09	0.40
80:14:1340:C:H2'	80:14:1341:U:O4'	2.22	0.40
4:SD:56:ASP:HB3	4:SD:58:LYS:HE2	2.03	0.40
5:SE:23:MET:HE3	5:SE:23:MET:HB3	1.94	0.40
24:SX:109:GLN:HE21	24:SX:115:ASP:HA	1.87	0.40
26:SZ:13:PHE:HB3	26:SZ:24:PHE:HB3	2.03	0.40
36:LD:399:LYS:HB3	36:LD:399:LYS:HE3	1.59	0.40
42:LJ:101:LYS:HZ2	42:LJ:101:LYS:HG3	1.68	0.40
45:LM:103:ASP:OD1	45:LM:103:ASP:N	2.46	0.40
49:LQ:25:TYR:HE2	80:14:608:U:H5'	1.86	0.40
51:LS:66:MET:H	51:LS:66:MET:HE3	1.85	0.40
55:LW:169:SER:HA	55:LW:172:ARG:HH11	1.86	0.40
77:11:420:A:H3'	77:11:421:A:C8	2.54	0.40
80:14:1027:A:H61	80:14:1047:G:H1	1.70	0.40
80:14:2725:U:H2'	80:14:2726:U:H6	1.85	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	SA	200/257 (78%)	196 (98%)	4 (2%)	0	100	100
2	SB	209/248 (84%)	201 (96%)	8 (4%)	0	100	100
3	SC	181/187 (97%)	175 (97%)	6 (3%)	0	100	100
4	SD	215/280 (77%)	211 (98%)	4 (2%)	0	100	100
5	SE	192/210 (91%)	176 (92%)	16 (8%)	0	100	100
6	SF	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
7	SG	139/147 (95%)	137 (99%)	2 (1%)	0	100	100
8	SH	100/122 (82%)	97 (97%)	3 (3%)	0	100	100
9	SI	130/150 (87%)	125 (96%)	5 (4%)	0	100	100
10	SJ	139/142 (98%)	135 (97%)	4 (3%)	0	100	100
11	SK	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
12	SL	53/56 (95%)	53 (100%)	0	0	100	100
13	SM	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
14	SN	143/159 (90%)	141 (99%)	2 (1%)	0	100	100
15	SO	129/152 (85%)	127 (98%)	2 (2%)	0	100	100
16	SP	214/261 (82%)	211 (99%)	3 (1%)	0	100	100
17	SQ	257/264 (97%)	254 (99%)	3 (1%)	0	100	100
18	SR	228/249 (92%)	222 (97%)	6 (3%)	0	100	100
19	SS	186/191 (97%)	180 (97%)	6 (3%)	0	100	100
20	ST	181/212 (85%)	178 (98%)	3 (2%)	0	100	100
21	SU	89/118 (75%)	85 (96%)	4 (4%)	0	100	100
22	SV	81/143 (57%)	66 (82%)	14 (17%)	1 (1%)	10	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	SW	80/131 (61%)	76 (95%)	4 (5%)	0	100	100
24	SX	134/143 (94%)	133 (99%)	1 (1%)	0	100	100
25	SY	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
26	SZ	125/133 (94%)	124 (99%)	1 (1%)	0	100	100
27	Sa	71/74 (96%)	70 (99%)	1 (1%)	0	100	100
28	Sb	96/113 (85%)	95 (99%)	1 (1%)	0	100	100
29	Sc	82/85 (96%)	80 (98%)	2 (2%)	0	100	100
30	Sd	59/65 (91%)	59 (100%)	0	0	100	100
31	Se	41/62 (66%)	41 (100%)	0	0	100	100
32	Sf	67/156 (43%)	63 (94%)	4 (6%)	0	100	100
33	LA	213/217 (98%)	196 (92%)	15 (7%)	2 (1%)	14	34
34	LB	243/260 (94%)	231 (95%)	12 (5%)	0	100	100
35	LC	384/389 (99%)	372 (97%)	12 (3%)	0	100	100
36	LD	396/405 (98%)	382 (96%)	14 (4%)	0	100	100
37	LE	167/181 (92%)	164 (98%)	3 (2%)	0	100	100
38	LF	189/194 (97%)	183 (97%)	6 (3%)	0	100	100
39	LG	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
40	LH	129/140 (92%)	127 (98%)	2 (2%)	0	100	100
41	LI	145/148 (98%)	140 (97%)	4 (3%)	1 (1%)	18	40
42	LJ	205/219 (94%)	201 (98%)	4 (2%)	0	100	100
43	LK	286/293 (98%)	278 (97%)	8 (3%)	0	100	100
44	LL	152/175 (87%)	150 (99%)	2 (1%)	0	100	100
45	LM	115/154 (75%)	114 (99%)	1 (1%)	0	100	100
46	LN	124/146 (85%)	122 (98%)	2 (2%)	0	100	100
47	LO	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
48	LP	236/242 (98%)	229 (97%)	7 (3%)	0	100	100
49	LQ	203/230 (88%)	198 (98%)	5 (2%)	0	100	100
50	LR	231/237 (98%)	228 (99%)	3 (1%)	0	100	100
51	LS	198/200 (99%)	192 (97%)	6 (3%)	0	100	100
52	LT	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
53	LU	201/204 (98%)	195 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	LV	184/187 (98%)	180 (98%)	4 (2%)	0	100	100
55	LW	180/211 (85%)	179 (99%)	1 (1%)	0	100	100
56	LX	175/178 (98%)	174 (99%)	1 (1%)	0	100	100
57	LY	161/164 (98%)	157 (98%)	4 (2%)	0	100	100
58	LZ	96/108 (89%)	94 (98%)	2 (2%)	0	100	100
59	La	60/164 (37%)	59 (98%)	1 (2%)	0	100	100
60	Lb	132/135 (98%)	130 (98%)	2 (2%)	0	100	100
61	Lc	140/143 (98%)	137 (98%)	3 (2%)	0	100	100
62	Ld	47/50 (94%)	47 (100%)	0	0	100	100
63	Le	95/113 (84%)	93 (98%)	2 (2%)	0	100	100
64	Lf	106/120 (88%)	105 (99%)	1 (1%)	0	100	100
65	Lg	124/133 (93%)	123 (99%)	1 (1%)	0	100	100
66	Lh	101/112 (90%)	100 (99%)	1 (1%)	0	100	100
67	Li	112/120 (93%)	111 (99%)	1 (1%)	0	100	100
68	Lj	96/110 (87%)	94 (98%)	2 (2%)	0	100	100
69	Lk	84/95 (88%)	83 (99%)	1 (1%)	0	100	100
70	Ll	66/69 (96%)	65 (98%)	1 (2%)	0	100	100
71	Lm	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
72	Ln	49/128 (38%)	49 (100%)	0	0	100	100
73	Lo	23/25 (92%)	23 (100%)	0	0	100	100
74	Lp	96/105 (91%)	93 (97%)	3 (3%)	0	100	100
75	Lq	74/77 (96%)	70 (95%)	4 (5%)	0	100	100
All	All	10830/12105 (90%)	10541 (97%)	285 (3%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	LA	59	PRO
22	SV	93	PRO
33	LA	61	PRO
41	LI	15	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	SA	170/209 (81%)	168 (99%)	2 (1%)	63	79
2	SB	176/215 (82%)	173 (98%)	3 (2%)	53	73
3	SC	157/164 (96%)	150 (96%)	7 (4%)	24	50
4	SD	184/225 (82%)	183 (100%)	1 (0%)	81	90
5	SE	163/175 (93%)	152 (93%)	11 (7%)	15	36
6	SF	111/112 (99%)	110 (99%)	1 (1%)	70	83
7	SG	116/120 (97%)	107 (92%)	9 (8%)	11	30
8	SH	93/108 (86%)	89 (96%)	4 (4%)	26	52
9	SI	103/120 (86%)	99 (96%)	4 (4%)	28	54
10	SJ	113/114 (99%)	109 (96%)	4 (4%)	32	57
11	SK	121/122 (99%)	117 (97%)	4 (3%)	33	58
12	SL	46/47 (98%)	46 (100%)	0	100	100
13	SM	130/131 (99%)	129 (99%)	1 (1%)	73	85
14	SN	124/131 (95%)	121 (98%)	3 (2%)	43	67
15	SO	114/130 (88%)	114 (100%)	0	100	100
16	SP	195/228 (86%)	190 (97%)	5 (3%)	40	65
17	SQ	224/228 (98%)	218 (97%)	6 (3%)	39	64
18	SR	193/213 (91%)	186 (96%)	7 (4%)	31	56
19	SS	167/170 (98%)	164 (98%)	3 (2%)	51	72
20	ST	159/176 (90%)	152 (96%)	7 (4%)	25	51
21	SU	84/109 (77%)	78 (93%)	6 (7%)	13	33
22	SV	60/112 (54%)	41 (68%)	19 (32%)	0	0
23	SW	74/119 (62%)	70 (95%)	4 (5%)	20	44
24	SX	111/114 (97%)	107 (96%)	4 (4%)	31	56
25	SY	69/69 (100%)	66 (96%)	3 (4%)	26	52
26	SZ	101/113 (89%)	92 (91%)	9 (9%)	9	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	Sa	63/64 (98%)	60 (95%)	3 (5%)	23	48
28	Sb	86/100 (86%)	85 (99%)	1 (1%)	63	79
29	Sc	75/76 (99%)	73 (97%)	2 (3%)	39	64
30	Sd	54/57 (95%)	50 (93%)	4 (7%)	13	32
31	Se	36/49 (74%)	35 (97%)	1 (3%)	38	62
32	Sf	60/134 (45%)	50 (83%)	10 (17%)	2	6
33	LA	190/196 (97%)	170 (90%)	20 (10%)	6	19
34	LB	190/197 (96%)	188 (99%)	2 (1%)	65	80
35	LC	331/333 (99%)	327 (99%)	4 (1%)	63	79
36	LD	325/331 (98%)	301 (93%)	24 (7%)	13	32
37	LE	145/157 (92%)	143 (99%)	2 (1%)	59	77
38	LF	167/170 (98%)	161 (96%)	6 (4%)	31	56
39	LG	174/175 (99%)	170 (98%)	4 (2%)	44	67
40	LH	103/109 (94%)	101 (98%)	2 (2%)	50	71
41	LI	119/120 (99%)	117 (98%)	2 (2%)	53	73
42	LJ	173/180 (96%)	167 (96%)	6 (4%)	32	57
43	LK	243/246 (99%)	233 (96%)	10 (4%)	27	53
44	LL	133/151 (88%)	131 (98%)	2 (2%)	57	76
45	LM	106/134 (79%)	104 (98%)	2 (2%)	50	71
46	LN	115/132 (87%)	114 (99%)	1 (1%)	70	83
47	LO	108/109 (99%)	106 (98%)	2 (2%)	50	71
48	LP	207/209 (99%)	202 (98%)	5 (2%)	43	67
49	LQ	174/194 (90%)	172 (99%)	2 (1%)	65	80
50	LR	201/205 (98%)	193 (96%)	8 (4%)	28	53
51	LS	166/166 (100%)	166 (100%)	0	100	100
52	LT	112/113 (99%)	109 (97%)	3 (3%)	39	64
53	LU	176/177 (99%)	173 (98%)	3 (2%)	53	73
54	LV	154/155 (99%)	151 (98%)	3 (2%)	50	71
55	LW	158/180 (88%)	152 (96%)	6 (4%)	29	55
56	LX	163/164 (99%)	160 (98%)	3 (2%)	51	72
57	LY	140/141 (99%)	137 (98%)	3 (2%)	47	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	LZ	89/97 (92%)	85 (96%)	4 (4%)	24	50
59	La	57/133 (43%)	56 (98%)	1 (2%)	51	72
60	Lb	116/117 (99%)	112 (97%)	4 (3%)	32	58
61	Lc	122/123 (99%)	118 (97%)	4 (3%)	33	58
62	Ld	42/43 (98%)	41 (98%)	1 (2%)	43	67
63	Le	85/98 (87%)	83 (98%)	2 (2%)	43	67
64	Lf	95/106 (90%)	93 (98%)	2 (2%)	47	69
65	Lg	114/121 (94%)	114 (100%)	0	100	100
66	Lh	92/99 (93%)	92 (100%)	0	100	100
67	Li	100/104 (96%)	99 (99%)	1 (1%)	68	82
68	Lj	84/91 (92%)	83 (99%)	1 (1%)	63	79
69	Lk	72/77 (94%)	72 (100%)	0	100	100
70	Ll	64/65 (98%)	63 (98%)	1 (2%)	55	75
71	Lm	47/48 (98%)	46 (98%)	1 (2%)	47	69
72	Ln	46/114 (40%)	46 (100%)	0	100	100
73	Lo	22/23 (96%)	17 (77%)	5 (23%)	1	2
74	Lp	85/91 (93%)	83 (98%)	2 (2%)	43	67
75	Lq	60/62 (97%)	58 (97%)	2 (3%)	33	58
All	All	9397/10310 (91%)	9093 (97%)	304 (3%)	35	59

All (304) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	SA	66	VAL
1	SA	186	ARG
2	SB	8	ILE
2	SB	97	ARG
2	SB	180	MET
3	SC	63	THR
3	SC	65	ASP
3	SC	96	ASP
3	SC	170	ARG
3	SC	174	VAL
3	SC	175	LYS
3	SC	180	LYS
4	SD	168	VAL

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Mol	Chain	Res	Type
5	SE	29	THR
5	SE	84	MET
5	SE	165	ARG
5	SE	172	ILE
5	SE	173	LYS
5	SE	188	LYS
5	SE	192	ASN
5	SE	193	SER
5	SE	198	LYS
5	SE	199	LYS
5	SE	207	LYS
6	SF	74	VAL
7	SG	26	VAL
7	SG	33	ARG
7	SG	35	LEU
7	SG	36	ILE
7	SG	46	VAL
7	SG	49	GLU
7	SG	50	ILE
7	SG	91	SER
7	SG	117	VAL
8	SH	27	LEU
8	SH	28	SER
8	SH	31	ASN
8	SH	42	LEU
9	SI	46	LEU
9	SI	129	GLU
9	SI	132	THR
9	SI	137	ASP
10	SJ	50	VAL
10	SJ	98	GLU
10	SJ	104	PHE
10	SJ	118	ARG
11	SK	67	LEU
11	SK	101	ASN
11	SK	112	GLU
11	SK	114	LEU
13	SM	143	SER
14	SN	45	THR
14	SN	81	MET
14	SN	118	VAL
16	SP	42	ASN

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Mol	Chain	Res	Type
16	SP	74	GLN
16	SP	75	LYS
16	SP	108	ASP
16	SP	135	LEU
17	SQ	32	SER
17	SQ	110	ARG
17	SQ	153	LEU
17	SQ	162	LEU
17	SQ	173	ILE
17	SQ	205	PHE
18	SR	35	GLU
18	SR	149	LEU
18	SR	155	VAL
18	SR	160	ASN
18	SR	164	ARG
18	SR	180	ILE
18	SR	226	GLU
19	SS	43	ASP
19	SS	65	VAL
19	SS	85	GLU
20	ST	7	SER
20	ST	71	GLU
20	ST	87	SER
20	ST	122	ILE
20	ST	162	GLN
20	ST	166	LYS
20	ST	172	GLU
21	SU	40	LYS
21	SU	45	GLU
21	SU	62	ILE
21	SU	89	MET
21	SU	100	ILE
21	SU	109	LEU
22	SV	35	LEU
22	SV	36	ARG
22	SV	61	GLN
22	SV	63	CYS
22	SV	64	VAL
22	SV	65	LEU
22	SV	75	VAL
22	SV	76	LYS
22	SV	78	VAL

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Mol	Chain	Res	Type
22	SV	86	ASN
22	SV	90	ILE
22	SV	92	VAL
22	SV	104	LEU
22	SV	114	ARG
22	SV	115	LYS
22	SV	117	VAL
22	SV	123	VAL
22	SV	125	LYS
22	SV	126	ASP
23	SW	43	SER
23	SW	47	ARG
23	SW	63	LYS
23	SW	81	ARG
24	SX	14	GLU
24	SX	35	THR
24	SX	107	GLN
24	SX	126	SER
25	SY	11	LEU
25	SY	50	THR
25	SY	73	LEU
26	SZ	8	ILE
26	SZ	13	PHE
26	SZ	15	THR
26	SZ	22	LYS
26	SZ	23	GLN
26	SZ	25	ILE
26	SZ	37	SER
26	SZ	48	MET
26	SZ	102	VAL
27	Sa	68	ARG
27	Sa	92	VAL
27	Sa	102	THR
28	Sb	44	ILE
29	Sc	45	ILE
29	Sc	67	GLN
30	Sd	5	THR
30	Sd	6	LYS
30	Sd	9	ILE
30	Sd	56	GLU
31	Se	38	MET
32	Sf	103	LEU

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Mol	Chain	Res	Type
32	Sf	104	GLN
32	Sf	105	PHE
32	Sf	107	LYS
32	Sf	108	VAL
32	Sf	118	ARG
32	Sf	119	LYS
32	Sf	134	ASN
32	Sf	137	ASP
32	Sf	139	HIS
33	LA	4	LYS
33	LA	5	LEU
33	LA	6	GLN
33	LA	24	LYS
33	LA	29	THR
33	LA	32	ILE
33	LA	41	TYR
33	LA	44	GLN
33	LA	45	LYS
33	LA	46	ASP
33	LA	47	LYS
33	LA	58	ILE
33	LA	60	ARG
33	LA	61	PRO
33	LA	63	MET
33	LA	65	ILE
33	LA	152	LYS
33	LA	160	LYS
33	LA	162	VAL
33	LA	165	MET
34	LB	181	LYS
34	LB	208	GLU
35	LC	60	VAL
35	LC	159	VAL
35	LC	295	SER
35	LC	353	VAL
36	LD	12	VAL
36	LD	205	ILE
36	LD	257	THR
36	LD	259	SER
36	LD	265	ASP
36	LD	318	THR
36	LD	343	MET

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Mol	Chain	Res	Type
36	LD	350	GLN
36	LD	353	LYS
36	LD	356	LYS
36	LD	357	GLU
36	LD	359	LEU
36	LD	361	LYS
36	LD	362	LYS
36	LD	365	GLN
36	LD	367	THR
36	LD	368	LYS
36	LD	380	SER
36	LD	384	THR
36	LD	385	MET
36	LD	388	ASP
36	LD	389	SER
36	LD	395	GLU
36	LD	396	ASN
37	LE	25	VAL
37	LE	48	VAL
38	LF	14	ASP
38	LF	33	LYS
38	LF	73	ILE
38	LF	74	ARG
38	LF	87	VAL
38	LF	136	THR
39	LG	3	SER
39	LG	25	SER
39	LG	66	ARG
39	LG	194	LEU
40	LH	77	MET
40	LH	84	GLN
41	LI	16	SER
41	LI	75	ILE
42	LJ	44	ASP
42	LJ	50	VAL
42	LJ	91	VAL
42	LJ	113	THR
42	LJ	179	THR
42	LJ	186	SER
43	LK	65	VAL
43	LK	81	ARG
43	LK	122	ASN

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Mol	Chain	Res	Type
43	LK	124	GLU
43	LK	126	THR
43	LK	128	GLU
43	LK	184	LYS
43	LK	188	GLN
43	LK	251	SER
43	LK	269	LYS
44	LL	61	THR
44	LL	91	ILE
45	LM	69	LEU
45	LM	71	GLN
46	LN	55	VAL
47	LO	18	LEU
47	LO	36	VAL
48	LP	18	ARG
48	LP	42	LYS
48	LP	62	LEU
48	LP	175	LYS
48	LP	236	GLU
49	LQ	135	VAL
49	LQ	149	VAL
50	LR	45	THR
50	LR	84	LEU
50	LR	91	MET
50	LR	105	GLU
50	LR	127	ILE
50	LR	190	THR
50	LR	197	THR
50	LR	236	SER
52	LT	7	VAL
52	LT	87	SER
52	LT	88	SER
53	LU	85	THR
53	LU	99	ARG
53	LU	169	LYS
54	LV	40	THR
54	LV	79	VAL
54	LV	162	THR
55	LW	59	SER
55	LW	106	LEU
55	LW	111	GLU
55	LW	133	LYS

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Mol	Chain	Res	Type
55	LW	157	ASP
55	LW	179	GLU
56	LX	41	SER
56	LX	106	GLU
56	LX	168	THR
57	LY	14	SER
57	LY	72	VAL
57	LY	127	SER
58	LZ	40	GLU
58	LZ	69	ILE
58	LZ	82	LEU
58	LZ	94	ASN
59	La	26	SER
60	Lb	88	ASP
60	Lb	92	LYS
60	Lb	97	VAL
60	Lb	99	VAL
61	Lc	18	SER
61	Lc	55	LYS
61	Lc	72	THR
61	Lc	87	LYS
62	Ld	22	HIS
63	Le	27	LYS
63	Le	43	LYS
64	Lf	33	LYS
64	Lf	43	LYS
67	Li	75	ASN
68	Lj	71	ARG
70	Ll	13	LEU
71	Lm	45	ARG
73	Lo	8	LYS
73	Lo	10	MET
73	Lo	13	LEU
73	Lo	14	ARG
73	Lo	15	ARG
74	Lp	24	LYS
74	Lp	29	LYS
75	Lq	6	LYS
75	Lq	29	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (150) such sidechains are listed below:

Mol	Chain	Res	Type
1	SA	16	GLN
1	SA	97	ASN
1	SA	132	GLN
1	SA	191	GLN
2	SB	7	GLN
2	SB	95	ASN
3	SC	9	ASN
4	SD	64	GLN
5	SE	26	ASN
5	SE	88	ASN
5	SE	155	GLN
5	SE	192	ASN
7	SG	15	GLN
7	SG	39	ASN
7	SG	65	HIS
9	SI	82	GLN
9	SI	112	GLN
11	SK	42	ASN
12	SL	5	ASN
12	SL	8	ASN
13	SM	49	GLN
14	SN	33	ASN
14	SN	82	ASN
14	SN	128	GLN
15	SO	110	ASN
15	SO	121	HIS
16	SP	52	GLN
16	SP	92	GLN
16	SP	150	GLN
17	SQ	8	HIS
17	SQ	50	ASN
18	SR	13	GLN
18	SR	148	ASN
19	SS	144	HIS
19	SS	162	ASN
20	ST	9	HIS
20	ST	65	ASN
20	ST	85	ASN
20	ST	95	GLN
20	ST	174	GLN
21	SU	66	ASN
22	SV	58	HIS
22	SV	61	GLN

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Mol	Chain	Res	Type
23	SW	15	GLN
23	SW	74	GLN
24	SX	107	GLN
24	SX	109	GLN
24	SX	112	ASN
25	SY	46	ASN
26	SZ	114	ASN
28	Sb	13	HIS
29	Sc	60	ASN
30	Sd	35	ASN
31	Se	39	GLN
32	Sf	104	GLN
32	Sf	123	ASN
33	LA	140	HIS
33	LA	197	ASN
33	LA	199	GLN
34	LB	115	ASN
35	LC	68	HIS
35	LC	121	ASN
35	LC	167	GLN
35	LC	273	ASN
36	LD	145	HIS
36	LD	176	GLN
36	LD	303	GLN
36	LD	334	ASN
36	LD	350	GLN
37	LE	97	ASN
37	LE	109	GLN
38	LF	101	HIS
38	LF	165	ASN
39	LG	18	HIS
39	LG	36	GLN
39	LG	73	HIS
39	LG	163	ASN
39	LG	170	GLN
41	LI	66	ASN
41	LI	84	GLN
41	LI	132	ASN
42	LJ	112	GLN
42	LJ	144	ASN
43	LK	63	GLN
43	LK	120	GLN

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Mol	Chain	Res	Type
43	LK	188	GLN
43	LK	228	GLN
43	LK	243	HIS
43	LK	288	ASN
44	LL	34	HIS
44	LL	56	GLN
44	LL	79	ASN
46	LN	18	HIS
46	LN	43	ASN
46	LN	56	GLN
46	LN	95	ASN
48	LP	46	ASN
48	LP	110	GLN
48	LP	113	ASN
48	LP	128	HIS
48	LP	171	GLN
48	LP	186	HIS
48	LP	206	GLN
49	LQ	37	ASN
50	LR	31	GLN
50	LR	57	GLN
50	LR	74	ASN
50	LR	142	ASN
50	LR	239	GLN
51	LS	60	GLN
51	LS	149	GLN
53	LU	86	ASN
53	LU	87	GLN
53	LU	144	ASN
53	LU	196	GLN
54	LV	143	ASN
54	LV	150	HIS
55	LW	141	ASN
56	LX	8	GLN
56	LX	107	GLN
56	LX	175	ASN
57	LY	54	HIS
57	LY	66	ASN
57	LY	112	ASN
57	LY	114	GLN
59	La	29	GLN
60	Lb	62	GLN

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Mol	Chain	Res	Type
60	Lb	96	ASN
61	Lc	79	ASN
62	Ld	50	ASN
63	Le	17	ASN
63	Le	52	ASN
64	Lf	46	GLN
64	Lf	85	ASN
66	Lh	27	ASN
66	Lh	41	ASN
66	Lh	68	HIS
66	Lh	111	ASN
67	Li	33	GLN
67	Li	75	ASN
68	Lj	41	HIS
68	Lj	95	ASN
69	Lk	48	ASN
69	Lk	77	ASN
70	Ll	67	GLN
71	Lm	38	ASN
72	Ln	90	ASN
74	Lp	27	GLN
74	Lp	83	HIS
74	Lp	90	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
76	10	158/204 (77%)	96 (60%)	16 (10%)
77	11	1618/1808 (89%)	300 (18%)	21 (1%)
78	12	118/119 (99%)	12 (10%)	0
79	13	162/163 (99%)	34 (20%)	0
80	14	3138/3390 (92%)	587 (18%)	28 (0%)
All	All	5194/5684 (91%)	1029 (19%)	65 (1%)

All (1029) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
76	10	48	G
76	10	49	U
76	10	50	G
76	10	53	G

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Mol	Chain	Res	Type
76	10	54	C
76	10	60	A
76	10	62	A
76	10	63	A
76	10	65	G
76	10	67	A
76	10	68	U
76	10	70	G
76	10	71	U
76	10	72	G
76	10	73	U
76	10	75	U
76	10	76	U
76	10	77	U
76	10	79	C
76	10	80	C
76	10	81	U
76	10	84	A
76	10	87	U
76	10	88	A
76	10	89	A
76	10	90	A
76	10	91	U
76	10	92	C
76	10	94	A
76	10	95	A
76	10	96	G
76	10	97	G
76	10	98	G
76	10	105	C
76	10	106	U
76	10	107	U
76	10	108	G
76	10	109	G
76	10	111	U
76	10	113	G
76	10	117	G
76	10	118	G
76	10	119	G
76	10	120	U
76	10	121	C
76	10	122	A

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Mol	Chain	Res	Type
76	10	123	A
76	10	125	U
76	10	126	G
76	10	129	U
76	10	130	A
76	10	132	G
76	10	133	G
76	10	134	U
76	10	135	U
76	10	136	C
76	10	139	A
76	10	140	U
76	10	141	A
76	10	143	A
76	10	144	U
76	10	145	C
76	10	146	C
76	10	150	G
76	10	151	G
76	10	153	A
76	10	154	C
76	10	155	G
76	10	157	A
76	10	158	A
76	10	159	U
76	10	160	A
76	10	161	A
76	10	162	A
76	10	164	C
76	10	165	G
76	10	166	A
76	10	167	G
76	10	169	G
76	10	176	A
76	10	177	U
76	10	178	C
76	10	180	C
76	10	181	C
76	10	184	G
76	10	185	U
76	10	186	U
76	10	190	C

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Mol	Chain	Res	Type
76	10	193	G
76	10	194	G
76	10	195	U
76	10	196	A
76	10	197	G
76	10	200	G
76	10	201	C
76	10	204	A
77	11	2	A
77	11	17	C
77	11	25	C
77	11	26	A
77	11	34	G
77	11	42	G
77	11	47	A
77	11	56	U
77	11	63	G
77	11	65	A
77	11	67	G
77	11	70	C
77	11	73	A
77	11	74	U
77	11	75	U
77	11	76	C
77	11	77	A
77	11	81	U
77	11	82	G
77	11	84	G
77	11	104	A
77	11	105	A
77	11	115	A
77	11	116	G
77	11	127	G
77	11	128	G
77	11	129	U
77	11	130	A
77	11	132	C
77	11	133	U
77	11	135	C
77	11	136	U
77	11	139	U
77	11	143	A

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Mol	Chain	Res	Type
77	11	151	A
77	11	158	C
77	11	178	A
77	11	186	A
77	11	189	U
77	11	190	C
77	11	191	U
77	11	192	G
77	11	193	G
77	11	194	A
77	11	201	G
77	11	207	A
77	11	214	A
77	11	246	G
77	11	252	U
77	11	253	C
77	11	274	A
77	11	277	G
77	11	278	C
77	11	286	C
77	11	289	G
77	11	291	G
77	11	318	C
77	11	320	A
77	11	323	U
77	11	326	G
77	11	341	G
77	11	342	C
77	11	363	G
77	11	365	C
77	11	373	U
77	11	374	A
77	11	384	U
77	11	385	C
77	11	397	C
77	11	404	A
77	11	405	A
77	11	406	C
77	11	420	A
77	11	421	A
77	11	426	G
77	11	427	G

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Mol	Chain	Res	Type
77	11	428	C
77	11	429	A
77	11	430	G
77	11	438	G
77	11	443	U
77	11	448	C
77	11	452	C
77	11	468	A
77	11	472	A
77	11	481	A
77	11	484	A
77	11	488	C
77	11	489	C
77	11	490	G
77	11	491	G
77	11	504	U
77	11	505	G
77	11	509	A
77	11	510	U
77	11	514	A
77	11	515	A
77	11	517	G
77	11	522	C
77	11	541	A
77	11	544	A
77	11	545	U
77	11	546	C
77	11	558	A
77	11	559	A
77	11	560	G
77	11	562	C
77	11	568	C
77	11	571	G
77	11	577	G
77	11	581	U
77	11	582	A
77	11	583	A
77	11	586	C
77	11	597	A
77	11	598	G
77	11	606	U
77	11	609	A

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Mol	Chain	Res	Type
77	11	614	U
77	11	620	U
77	11	622	A
77	11	623	A
77	11	625	A
77	11	626	A
77	11	637	G
77	11	642	U
77	11	647	A
77	11	756	A
77	11	759	A
77	11	769	G
77	11	770	C
77	11	779	A
77	11	782	C
77	11	784	A
77	11	785	C
77	11	786	G
77	11	790	U
77	11	793	A
77	11	816	A
77	11	818	A
77	11	819	G
77	11	820	G
77	11	824	U
77	11	832	A
77	11	834	U
77	11	865	A
77	11	866	A
77	11	884	A
77	11	889	U
77	11	901	A
77	11	924	G
77	11	936	A
77	11	938	U
77	11	945	G
77	11	954	A
77	11	963	U
77	11	969	A
77	11	976	A
77	11	1007	U
77	11	1008	A

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Mol	Chain	Res	Type
77	11	1029	A
77	11	1031	C
77	11	1035	G
77	11	1042	A
77	11	1059	G
77	11	1060	C
77	11	1090	A
77	11	1095	A
77	11	1100	U
77	11	1141	A
77	11	1142	A
77	11	1149	G
77	11	1153	G
77	11	1157	G
77	11	1158	G
77	11	1161	C
77	11	1170	G
77	11	1188	U
77	11	1194	U
77	11	1197	A
77	11	1199	A
77	11	1202	G
77	11	1203	G
77	11	1204	G
77	11	1205	A
77	11	1221	G
77	11	1230	A
77	11	1233	A
77	11	1235	U
77	11	1246	G
77	11	1247	A
77	11	1248	G
77	11	1249	C
77	11	1268	G
77	11	1271	G
77	11	1272	U
77	11	1294	G
77	11	1307	G
77	11	1308	U
77	11	1309	C
77	11	1310	U
77	11	1313	U

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Mol	Chain	Res	Type
77	11	1317	U
77	11	1322	U
77	11	1324	A
77	11	1325	A
77	11	1330	C
77	11	1348	A
77	11	1349	C
77	11	1350	U
77	11	1354	U
77	11	1359	G
77	11	1364	U
77	11	1365	A
77	11	1366	U
77	11	1368	C
77	11	1372	C
77	11	1375	G
77	11	1378	C
77	11	1379	A
77	11	1381	C
77	11	1392	G
77	11	1393	A
77	11	1395	U
77	11	1396	A
77	11	1403	U
77	11	1404	U
77	11	1418	U
77	11	1420	U
77	11	1432	A
77	11	1433	G
77	11	1434	G
77	11	1437	U
77	11	1438	G
77	11	1440	G
77	11	1450	G
77	11	1451	A
77	11	1464	C
77	11	1465	A
77	11	1476	A
77	11	1494	U
77	11	1495	U
77	11	1496	U
77	11	1497	A

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Mol	Chain	Res	Type
77	11	1499	A
77	11	1500	G
77	11	1518	G
77	11	1522	A
77	11	1523	A
77	11	1524	U
77	11	1528	U
77	11	1529	G
77	11	1530	A
77	11	1543	A
77	11	1563	U
77	11	1565	G
77	11	1579	A
77	11	1580	G
77	11	1581	G
77	11	1596	G
77	11	1607	G
77	11	1613	G
77	11	1617	A
77	11	1625	C
77	11	1637	A
77	11	1640	C
77	11	1644	G
77	11	1663	U
77	11	1664	G
77	11	1669	A
77	11	1670	U
77	11	1671	C
77	11	1684	C
77	11	1686	G
77	11	1687	A
77	11	1690	G
77	11	1725	C
77	11	1733	C
77	11	1736	U
77	11	1739	A
77	11	1743	U
77	11	1747	C
77	11	1750	U
77	11	1755	G
77	11	1768	G
77	11	1770	A

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Mol	Chain	Res	Type
77	11	1774	A
77	11	1775	G
77	11	1777	U
77	11	1788	G
77	11	1789	A
77	11	1790	A
77	11	1791	C
77	11	1800	G
77	11	1801	G
77	11	1802	A
77	11	1803	U
77	11	1804	C
77	11	1807	U
77	11	1808	G
78	12	2	G
78	12	10	C
78	12	13	A
78	12	25	G
78	12	33	U
78	12	38	U
78	12	53	U
78	12	54	A
78	12	64	G
78	12	89	G
78	12	110	G
78	12	117	C
79	13	2	A
79	13	5	G
79	13	26	C
79	13	27	G
79	13	37	U
79	13	38	C
79	13	41	U
79	13	62	A
79	13	65	C
79	13	66	U
79	13	77	U
79	13	78	G
79	13	83	A
79	13	84	U
79	13	85	C
79	13	87	C

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Mol	Chain	Res	Type
79	13	89	U
79	13	90	G
79	13	94	C
79	13	98	G
79	13	100	G
79	13	107	A
79	13	108	A
79	13	109	C
79	13	119	G
79	13	128	C
79	13	129	A
79	13	131	U
79	13	133	G
79	13	134	G
79	13	146	U
79	13	149	G
79	13	153	G
79	13	156	C
80	14	12	U
80	14	24	A
80	14	29	C
80	14	38	A
80	14	41	A
80	14	47	A
80	14	57	G
80	14	58	A
80	14	63	A
80	14	64	A
80	14	67	U
80	14	71	A
80	14	90	G
80	14	97	A
80	14	107	A
80	14	108	G
80	14	109	C
80	14	113	G
80	14	114	C
80	14	118	A
80	14	120	A
80	14	131	U
80	14	132	C
80	14	133	C

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Mol	Chain	Res	Type
80	14	134	G
80	14	140	C
80	14	144	U
80	14	154	G
80	14	155	A
80	14	163	C
80	14	164	C
80	14	167	A
80	14	168	G
80	14	184	A
80	14	187	U
80	14	188	C
80	14	194	G
80	14	207	G
80	14	211	G
80	14	215	G
80	14	216	A
80	14	228	U
80	14	245	A
80	14	248	A
80	14	258	G
80	14	262	A
80	14	266	G
80	14	283	U
80	14	292	A
80	14	294	U
80	14	295	C
80	14	302	U
80	14	320	A
80	14	326	G
80	14	334	G
80	14	335	A
80	14	346	A
80	14	347	C
80	14	373	G
80	14	392	A
80	14	395	G
80	14	396	A
80	14	398	U
80	14	399	G
80	14	400	C
80	14	417	G

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Mol	Chain	Res	Type
80	14	418	G
80	14	419	A
80	14	430	G
80	14	434	G
80	14	435	G
80	14	436	C
80	14	437	G
80	14	522	C
80	14	523	C
80	14	524	A
80	14	525	A
80	14	527	G
80	14	531	G
80	14	537	U
80	14	538	U
80	14	539	G
80	14	540	A
80	14	542	A
80	14	543	C
80	14	544	G
80	14	545	C
80	14	546	U
80	14	547	C
80	14	548	G
80	14	549	U
80	14	550	G
80	14	556	U
80	14	571	U
80	14	574	U
80	14	575	A
80	14	576	G
80	14	581	C
80	14	585	C
80	14	586	G
80	14	590	C
80	14	591	U
80	14	595	G
80	14	598	C
80	14	600	U
80	14	601	C
80	14	602	G
80	14	606	U

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Mol	Chain	Res	Type
80	14	607	C
80	14	608	U
80	14	610	C
80	14	617	C
80	14	618	G
80	14	619	G
80	14	620	A
80	14	621	C
80	14	631	U
80	14	636	U
80	14	637	C
80	14	657	A
80	14	660	A
80	14	671	A
80	14	688	A
80	14	692	A
80	14	693	A
80	14	694	C
80	14	695	G
80	14	698	C
80	14	701	G
80	14	710	U
80	14	711	A
80	14	718	A
80	14	725	C
80	14	727	G
80	14	728	A
80	14	729	U
80	14	730	U
80	14	731	G
80	14	746	A
80	14	747	G
80	14	752	G
80	14	770	G
80	14	775	U
80	14	777	U
80	14	786	U
80	14	787	U
80	14	791	G
80	14	795	G
80	14	816	A
80	14	827	A

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Mol	Chain	Res	Type
80	14	840	G
80	14	857	A
80	14	859	C
80	14	867	G
80	14	871	C
80	14	874	G
80	14	879	G
80	14	884	U
80	14	889	U
80	14	917	G
80	14	918	G
80	14	920	G
80	14	924	A
80	14	926	G
80	14	927	A
80	14	931	A
80	14	933	C
80	14	934	G
80	14	935	A
80	14	947	G
80	14	951	G
80	14	954	C
80	14	963	G
80	14	969	C
80	14	970	U
80	14	991	U
80	14	992	G
80	14	993	C
80	14	1006	G
80	14	1013	C
80	14	1014	A
80	14	1022	G
80	14	1028	U
80	14	1029	C
80	14	1030	G
80	14	1036	G
80	14	1037	C
80	14	1041	G
80	14	1048	A
80	14	1059	A
80	14	1064	U
80	14	1069	A

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Mol	Chain	Res	Type
80	14	1075	G
80	14	1076	A
80	14	1077	C
80	14	1087	G
80	14	1093	U
80	14	1094	U
80	14	1106	C
80	14	1107	G
80	14	1108	G
80	14	1109	A
80	14	1114	A
80	14	1115	G
80	14	1128	G
80	14	1133	U
80	14	1140	A
80	14	1142	G
80	14	1155	U
80	14	1164	A
80	14	1165	A
80	14	1166	C
80	14	1170	A
80	14	1185	G
80	14	1189	A
80	14	1191	C
80	14	1192	U
80	14	1193	G
80	14	1200	A
80	14	1201	A
80	14	1205	A
80	14	1213	C
80	14	1218	G
80	14	1221	G
80	14	1224	G
80	14	1234	G
80	14	1235	A
80	14	1236	C
80	14	1238	G
80	14	1297	G
80	14	1299	A
80	14	1321	U
80	14	1328	U
80	14	1329	A

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Mol	Chain	Res	Type
80	14	1335	G
80	14	1343	C
80	14	1344	A
80	14	1360	A
80	14	1361	A
80	14	1362	G
80	14	1363	U
80	14	1364	G
80	14	1365	C
80	14	1366	C
80	14	1367	A
80	14	1374	G
80	14	1403	A
80	14	1410	U
80	14	1413	G
80	14	1430	G
80	14	1442	G
80	14	1445	G
80	14	1448	C
80	14	1457	A
80	14	1462	C
80	14	1463	A
80	14	1466	U
80	14	1480	C
80	14	1481	U
80	14	1486	A
80	14	1491	G
80	14	1492	A
80	14	1494	G
80	14	1501	A
80	14	1513	G
80	14	1534	U
80	14	1538	C
80	14	1547	G
80	14	1566	A
80	14	1571	G
80	14	1577	U
80	14	1578	U
80	14	1585	U
80	14	1587	C
80	14	1588	U
80	14	1589	C

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Mol	Chain	Res	Type
80	14	1592	A
80	14	1593	A
80	14	1594	A
80	14	1598	A
80	14	1602	G
80	14	1609	A
80	14	1625	C
80	14	1633	U
80	14	1643	C
80	14	1646	U
80	14	1649	G
80	14	1652	G
80	14	1661	C
80	14	1698	U
80	14	1708	G
80	14	1729	G
80	14	1748	G
80	14	1755	A
80	14	1756	G
80	14	1770	G
80	14	1771	C
80	14	1772	G
80	14	1774	G
80	14	1784	G
80	14	1803	A
80	14	1816	C
80	14	1819	A
80	14	1820	G
80	14	1821	U
80	14	1823	C
80	14	1827	C
80	14	1828	C
80	14	1848	A
80	14	1852	C
80	14	1853	A
80	14	1855	C
80	14	1861	U
80	14	1872	C
80	14	1873	A
80	14	1884	G
80	14	1885	A
80	14	1886	U

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Mol	Chain	Res	Type
80	14	1912	G
80	14	1914	A
80	14	1949	C
80	14	2111	A
80	14	2115	G
80	14	2116	U
80	14	2118	C
80	14	2126	G
80	14	2135	A
80	14	2144	U
80	14	2162	A
80	14	2201	A
80	14	2208	U
80	14	2209	G
80	14	2211	A
80	14	2212	U
80	14	2213	G
80	14	2228	U
80	14	2231	A
80	14	2245	A
80	14	2252	G
80	14	2259	A
80	14	2261	U
80	14	2263	U
80	14	2264	G
80	14	2265	A
80	14	2269	U
80	14	2270	C
80	14	2275	G
80	14	2276	G
80	14	2283	A
80	14	2285	U
80	14	2286	G
80	14	2290	C
80	14	2291	G
80	14	2309	C
80	14	2310	G
80	14	2313	U
80	14	2316	A
80	14	2318	G
80	14	2321	U
80	14	2337	U

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Mol	Chain	Res	Type
80	14	2338	G
80	14	2339	U
80	14	2367	G
80	14	2368	C
80	14	2375	A
80	14	2376	A
80	14	2377	C
80	14	2378	G
80	14	2388	G
80	14	2396	G
80	14	2400	A
80	14	2404	A
80	14	2405	A
80	14	2406	G
80	14	2407	A
80	14	2414	U
80	14	2425	C
80	14	2438	G
80	14	2440	G
80	14	2442	A
80	14	2443	A
80	14	2445	G
80	14	2449	U
80	14	2450	G
80	14	2451	A
80	14	2453	A
80	14	2456	U
80	14	2457	G
80	14	2461	U
80	14	2462	A
80	14	2463	U
80	14	2464	A
80	14	2465	A
80	14	2466	G
80	14	2467	U
80	14	2469	G
80	14	2470	G
80	14	2471	A
80	14	2473	C
80	14	2475	G
80	14	2478	A
80	14	2479	G

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Mol	Chain	Res	Type
80	14	2492	U
80	14	2496	A
80	14	2502	U
80	14	2503	U
80	14	2506	A
80	14	2507	C
80	14	2508	G
80	14	2509	U
80	14	2511	A
80	14	2512	U
80	14	2513	U
80	14	2519	U
80	14	2520	A
80	14	2529	A
80	14	2534	A
80	14	2537	C
80	14	2538	G
80	14	2539	G
80	14	2540	G
80	14	2543	A
80	14	2544	C
80	14	2545	U
80	14	2546	G
80	14	2547	C
80	14	2551	U
80	14	2552	C
80	14	2553	U
80	14	2555	U
80	14	2556	U
80	14	2557	U
80	14	2558	G
80	14	2559	G
80	14	2563	C
80	14	2570	U
80	14	2571	G
80	14	2572	C
80	14	2573	U
80	14	2574	U
80	14	2575	G
80	14	2576	C
80	14	2578	G
80	14	2579	G

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Mol	Chain	Res	Type
80	14	2580	C
80	14	2588	G
80	14	2589	G
80	14	2590	C
80	14	2596	A
80	14	2598	A
80	14	2606	G
80	14	2609	G
80	14	2610	G
80	14	2617	G
80	14	2622	G
80	14	2629	A
80	14	2640	A
80	14	2655	U
80	14	2659	A
80	14	2677	A
80	14	2680	G
80	14	2692	G
80	14	2694	A
80	14	2699	A
80	14	2706	A
80	14	2707	A
80	14	2717	G
80	14	2722	U
80	14	2731	G
80	14	2732	U
80	14	2752	G
80	14	2756	G
80	14	2758	C
80	14	2762	A
80	14	2765	A
80	14	2776	C
80	14	2780	G
80	14	2781	G
80	14	2794	G
80	14	2799	G
80	14	2802	A
80	14	2803	G
80	14	2804	A
80	14	2805	A
80	14	2813	C
80	14	2820	A

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Mol	Chain	Res	Type
80	14	2832	U
80	14	2845	U
80	14	2848	A
80	14	2853	G
80	14	2870	C
80	14	2874	G
80	14	2875	A
80	14	2890	A
80	14	2892	C
80	14	2897	U
80	14	2902	C
80	14	2912	C
80	14	2914	A
80	14	2917	G
80	14	2926	U
80	14	2928	C
80	14	2933	A
80	14	2938	U
80	14	2939	A
80	14	2945	C
80	14	2948	G
80	14	2950	G
80	14	2951	C
80	14	2954	G
80	14	2974	A
80	14	2975	G
80	14	2983	U
80	14	2986	C
80	14	3000	G
80	14	3014	A
80	14	3030	G
80	14	3032	G
80	14	3059	U
80	14	3060	C
80	14	3061	G
80	14	3073	A
80	14	3080	G
80	14	3094	C
80	14	3103	G
80	14	3118	G
80	14	3132	A
80	14	3133	U

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Mol	Chain	Res	Type
80	14	3136	G
80	14	3144	A
80	14	3146	C
80	14	3154	G
80	14	3156	G
80	14	3160	G
80	14	3161	C
80	14	3166	C
80	14	3168	C
80	14	3169	U
80	14	3172	C
80	14	3173	C
80	14	3174	G
80	14	3179	G
80	14	3181	A
80	14	3185	G
80	14	3191	U
80	14	3194	G
80	14	3201	A
80	14	3203	G
80	14	3208	C
80	14	3209	G
80	14	3211	G
80	14	3212	U
80	14	3213	C
80	14	3214	G
80	14	3216	U
80	14	3219	C
80	14	3235	G
80	14	3236	A
80	14	3240	G
80	14	3254	C
80	14	3257	G
80	14	3260	G
80	14	3264	A
80	14	3266	U
80	14	3267	U
80	14	3268	U
80	14	3269	C
80	14	3271	A
80	14	3272	U
80	14	3273	C

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Mol	Chain	Res	Type
80	14	3274	G
80	14	3275	A
80	14	3284	U
80	14	3296	C
80	14	3299	A
80	14	3308	A
80	14	3311	C
80	14	3334	A
80	14	3337	G
80	14	3343	U
80	14	3344	U
80	14	3348	G
80	14	3361	G
80	14	3370	C
80	14	3374	U
80	14	3383	C
80	14	3390	U

All (65) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
76	10	47	C
76	10	74	U
76	10	76	U
76	10	87	U
76	10	88	A
76	10	95	A
76	10	106	U
76	10	124	A
76	10	134	U
76	10	135	U
76	10	144	U
76	10	157	A
76	10	159	U
76	10	161	A
76	10	177	U
76	10	186	U
77	11	81	U
77	11	127	G
77	11	191	U
77	11	373	U
77	11	503	C

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Mol	Chain	Res	Type
77	11	544	A
77	11	545	U
77	11	581	U
77	11	819	G
77	11	1059	G
77	11	1203	G
77	11	1220	A
77	11	1234	U
77	11	1324	A
77	11	1378	C
77	11	1433	G
77	11	1463	G
77	11	1578	G
77	11	1663	U
77	11	1668	G
77	11	1686	G
80	14	113	G
80	14	294	U
80	14	590	C
80	14	601	C
80	14	617	C
80	14	692	A
80	14	693	A
80	14	785	G
80	14	883	C
80	14	917	G
80	14	926	G
80	14	990	G
80	14	1027	A
80	14	1234	G
80	14	1847	A
80	14	1852	C
80	14	2264	G
80	14	2290	C
80	14	2367	G
80	14	2375	A
80	14	2376	A
80	14	2518	U
80	14	2552	C
80	14	2573	U
80	14	2589	G
80	14	2731	G

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Mol	Chain	Res	Type
80	14	2793	A
80	14	3168	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

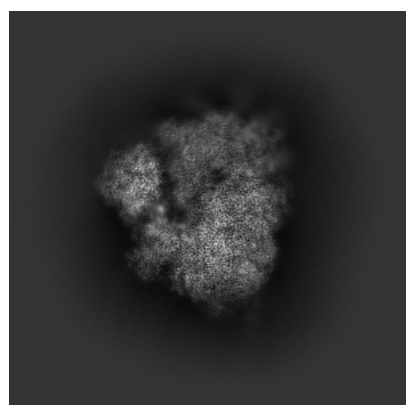
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65329. These allow visual inspection of the internal detail of the map and identification of artifacts.

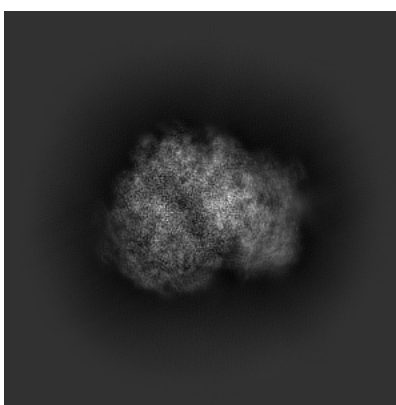
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

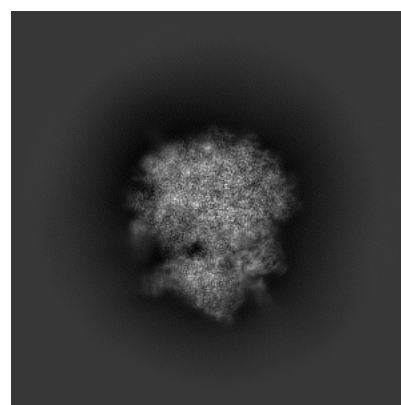
6.1.1 Primary map



X



Y

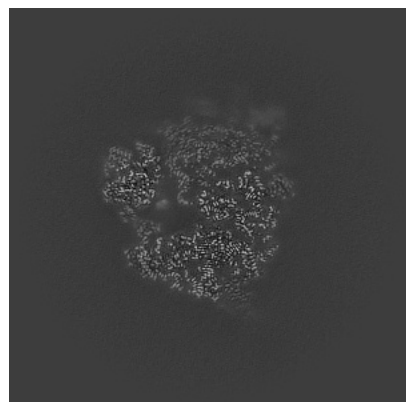


Z

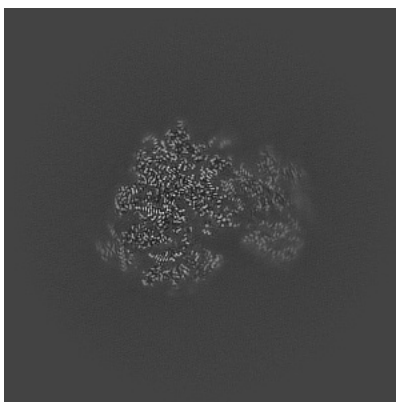
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 280



Y Index: 280

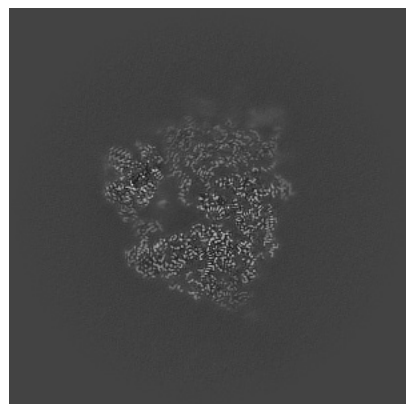


Z Index: 280

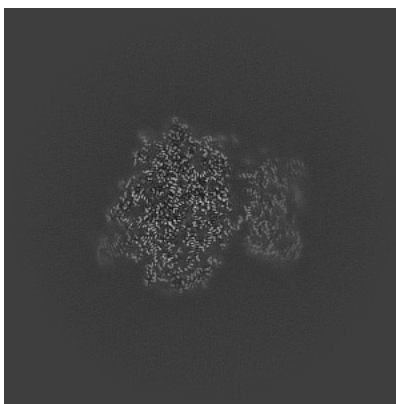
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

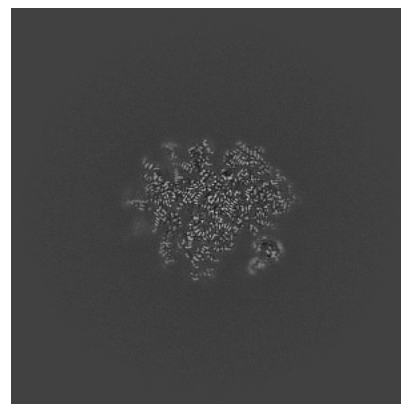
6.3.1 Primary map



X Index: 277



Y Index: 291

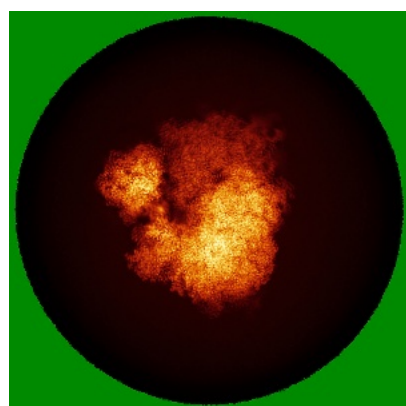


Z Index: 233

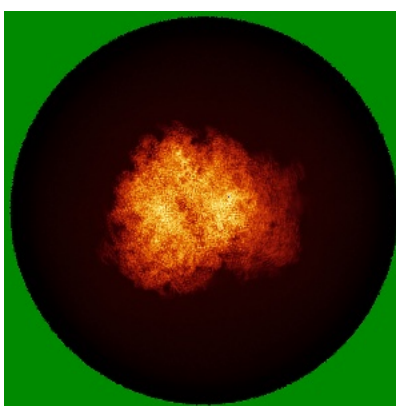
The images above show the largest variance slices of the map in three orthogonal directions.

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

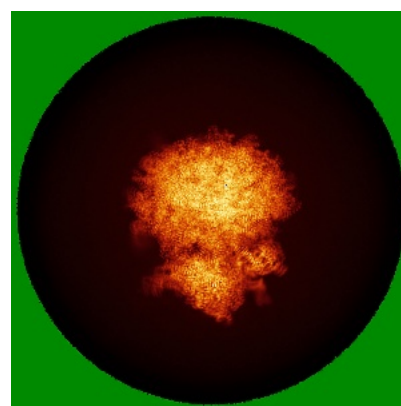
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

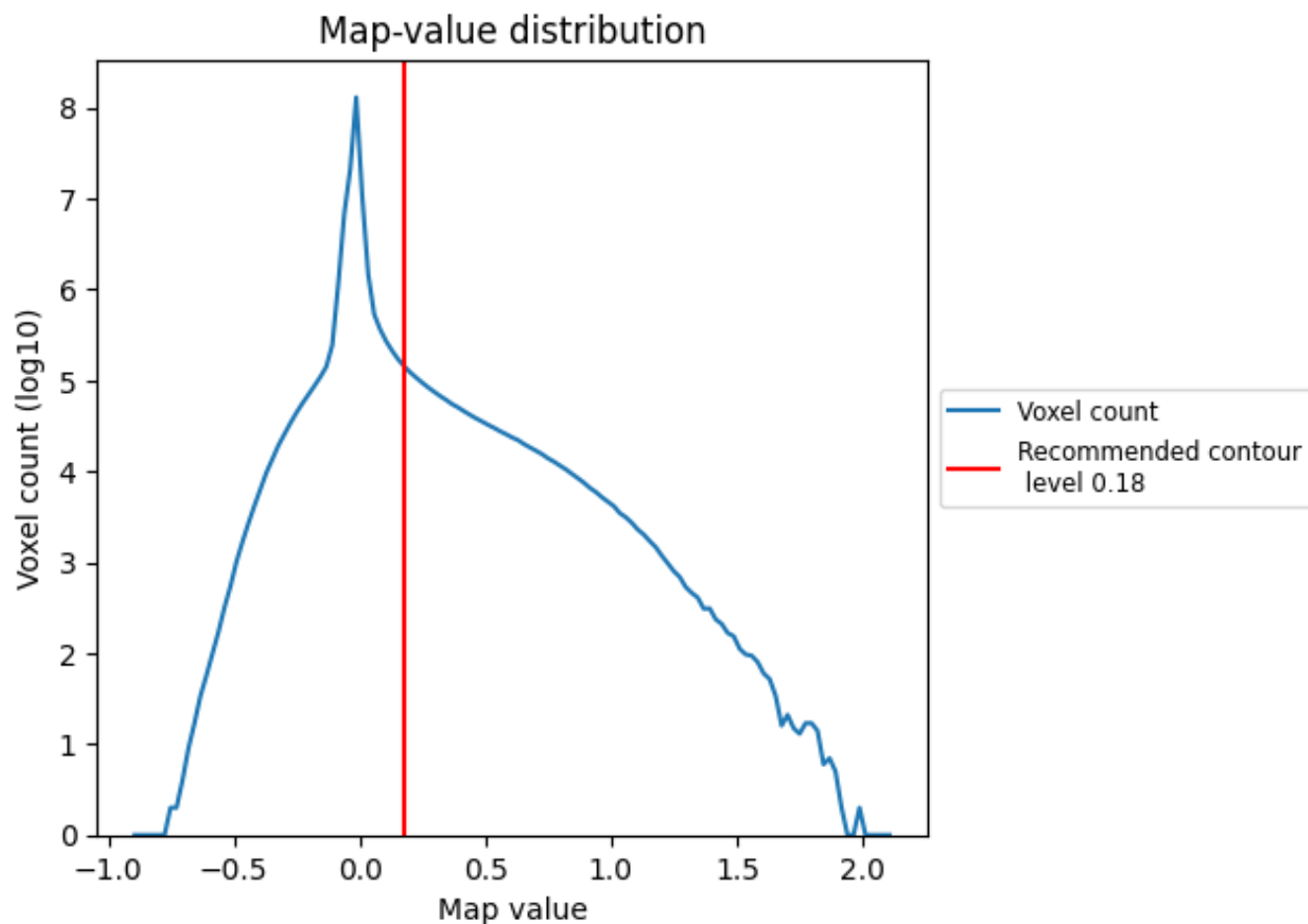
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

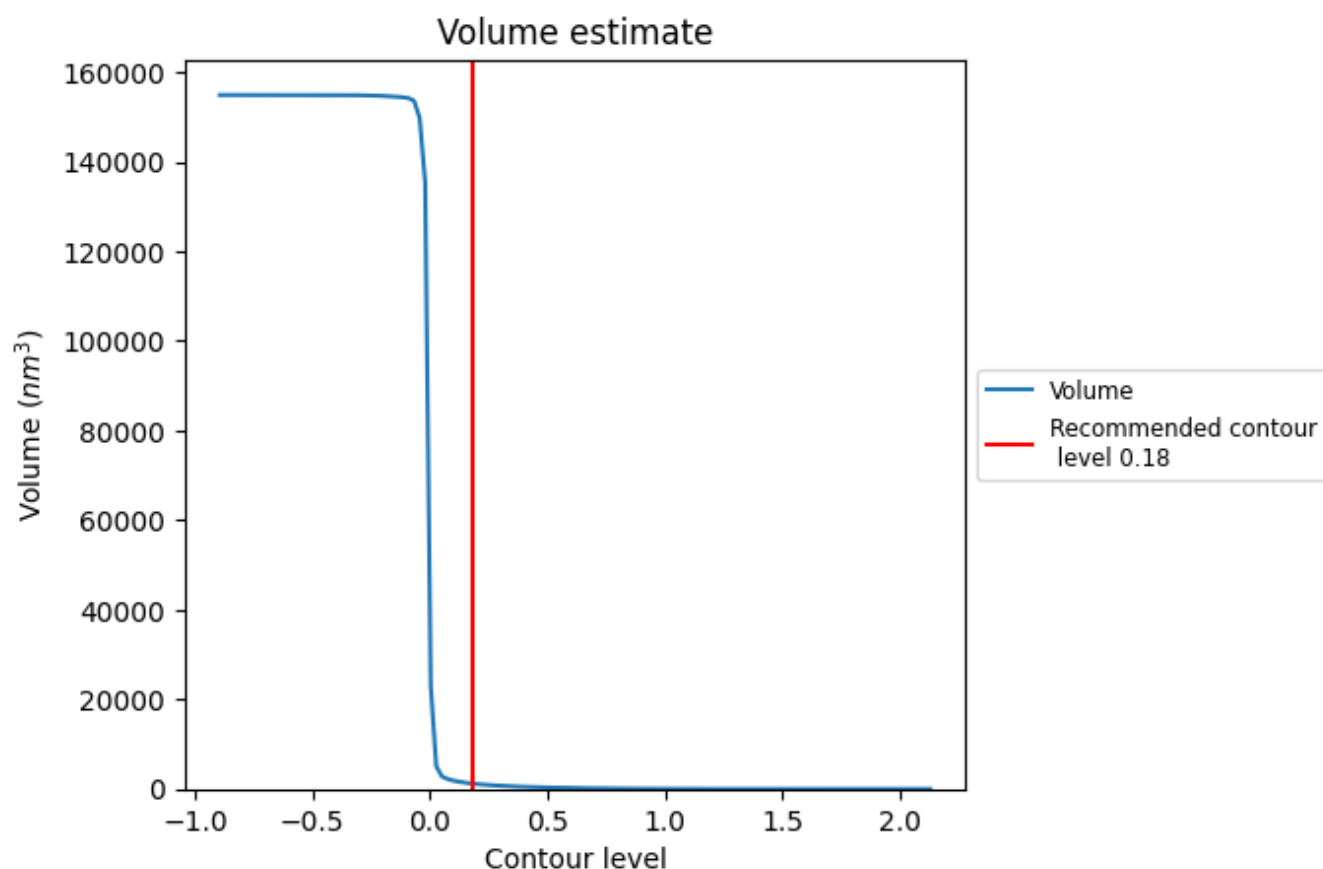
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

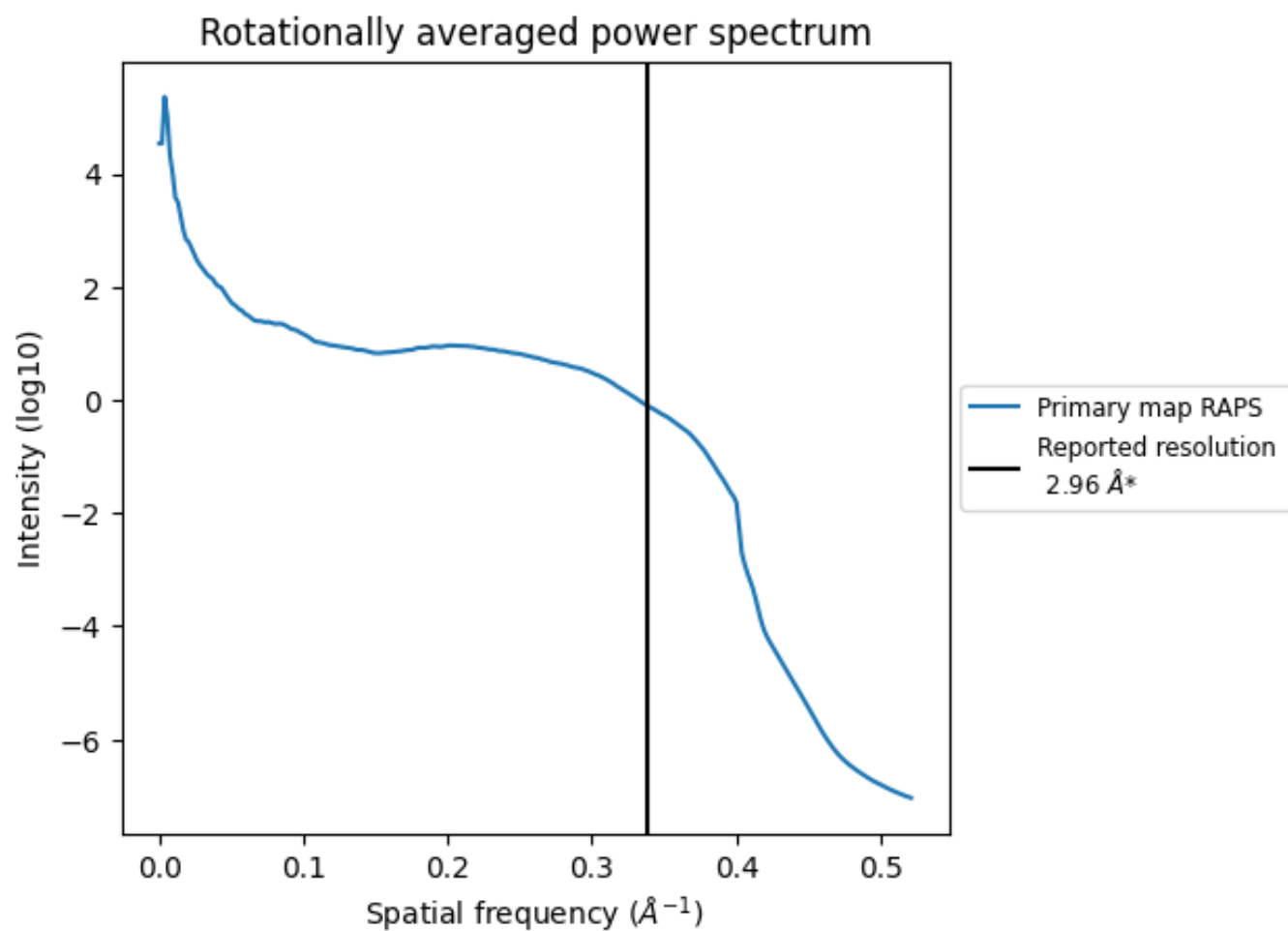
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1206 nm^3 ; this corresponds to an approximate mass of 1089 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 0.338 Å⁻¹

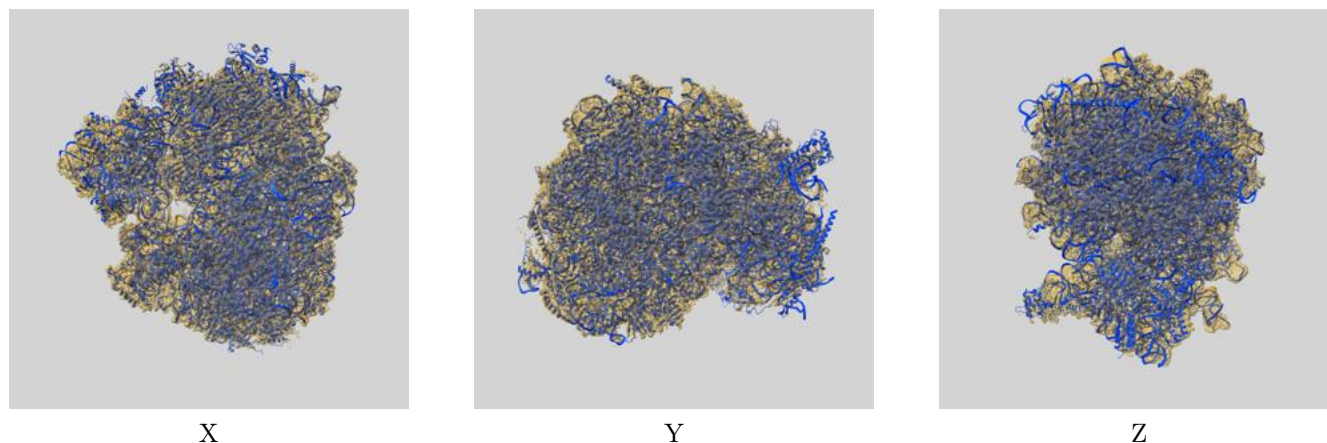
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

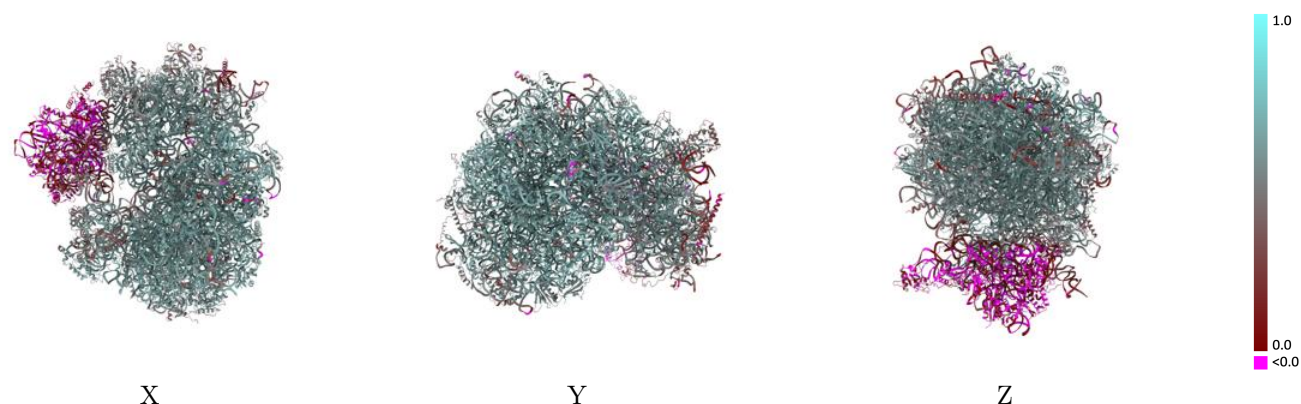
This section contains information regarding the fit between EMDB map EMD-65329 and PDB model 9VTI. Per-residue inclusion information can be found in section 3 on page 24.

9.1 Map-model overlay [i](#)



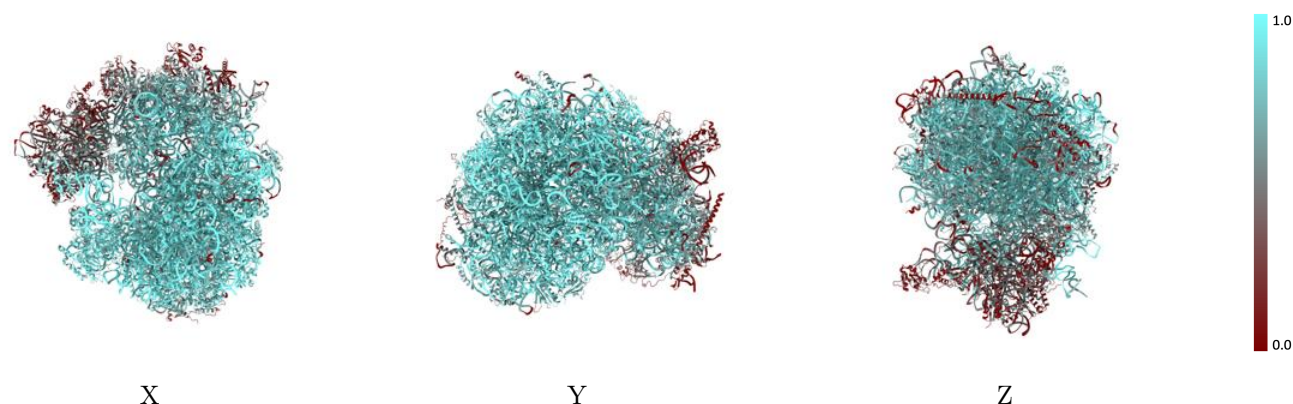
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



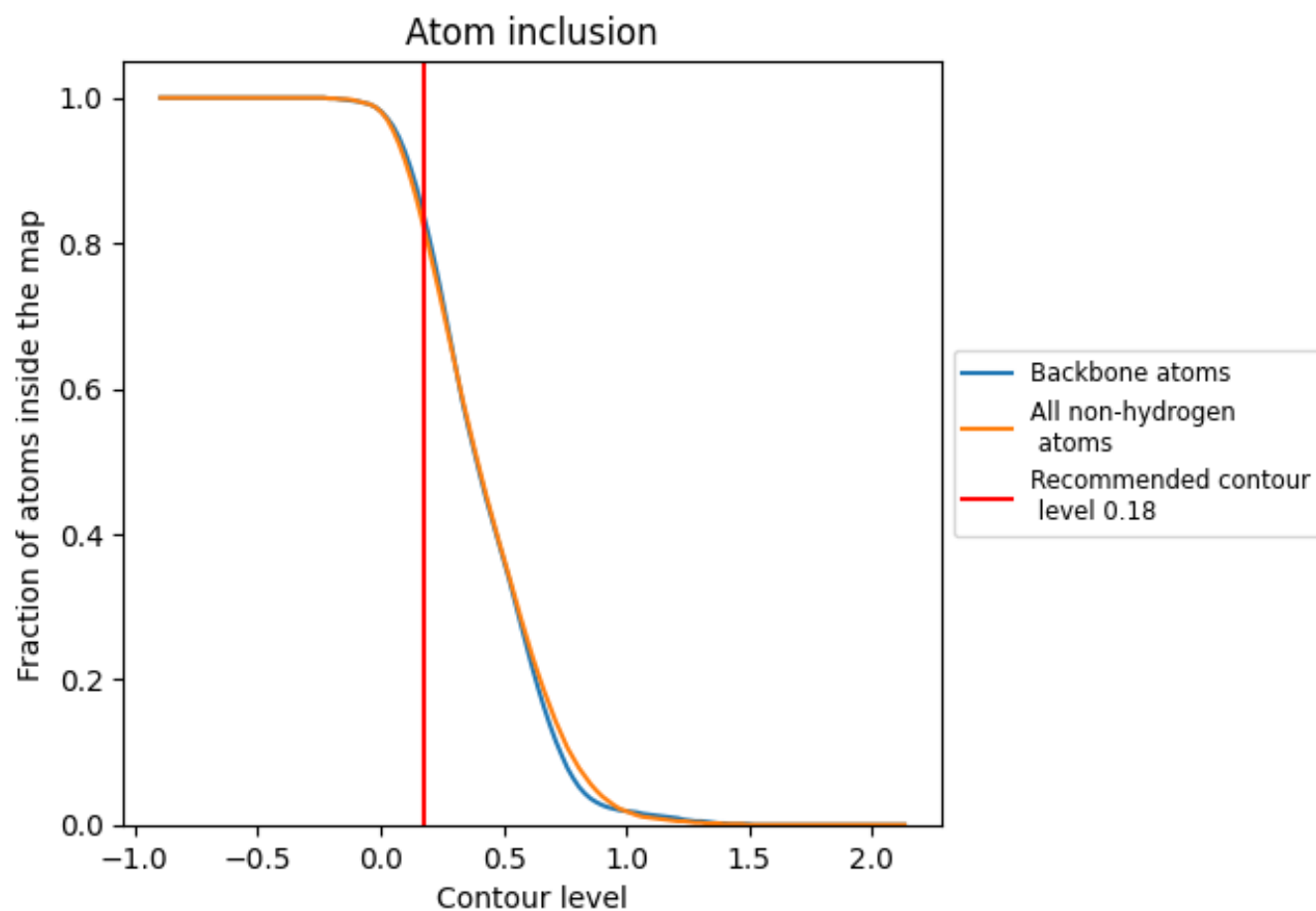
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).

9.4 Atom inclusion ⓘ



At the recommended contour level, 83% of all backbone atoms, 82% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8160	 0.5260
10	 0.9260	 0.3450
11	 0.7410	 0.4230
12	 0.9930	 0.6340
13	 0.9320	 0.5970
14	 0.9510	 0.6120
LA	 0.7940	 0.3630
LB	 0.9760	 0.6520
LC	 0.9510	 0.6460
LD	 0.8620	 0.5990
LE	 0.7320	 0.5150
LF	 0.8340	 0.5770
LG	 0.9310	 0.6250
LH	 0.9540	 0.6430
LI	 0.9540	 0.6380
LJ	 0.9220	 0.6190
LK	 0.8750	 0.5870
LL	 0.9470	 0.6350
LM	 0.9030	 0.6140
LN	 0.9310	 0.6140
LO	 0.8680	 0.5860
LP	 0.8820	 0.6060
LQ	 0.6510	 0.5090
LR	 0.8170	 0.5610
LS	 0.9110	 0.6100
LT	 0.8780	 0.5950
LU	 0.9750	 0.6520
LV	 0.9640	 0.6400
LW	 0.8020	 0.5870
LX	 0.9400	 0.6300
LY	 0.9270	 0.6270
LZ	 0.6920	 0.5300
La	 0.9350	 0.6410
Lb	 0.9060	 0.6130
Lc	 0.5790	 0.5590



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Chain	Atom inclusion	Q-score
Ld	 0.9140	 0.5950
Le	 0.9080	 0.6110
Lf	 0.8880	 0.5980
Lg	 0.9400	 0.6300
Lh	 0.9530	 0.6490
Li	 0.9020	 0.6060
Lj	 0.8770	 0.5950
Lk	 0.9740	 0.6510
Ll	 0.8360	 0.5710
Lm	 0.9720	 0.6410
Ln	 0.7730	 0.6120
Lo	 0.7710	 0.6060
Lp	 0.9400	 0.6400
Lq	 0.9250	 0.6420
SA	 0.3960	 0.4570
SB	 0.2770	 0.0150
SC	 0.5900	 0.5070
SD	 0.5950	 0.5230
SE	 0.3510	 0.0350
SF	 0.7300	 0.5790
SG	 0.3360	 0.0070
SH	 0.2780	 0.0360
SI	 0.7220	 0.5780
SJ	 0.7260	 0.5700
SK	 0.3100	 0.0360
SL	 0.5200	 0.1340
SM	 0.7610	 0.5930
SN	 0.7830	 0.6000
SO	 0.6210	 0.3080
SP	 0.7090	 0.5700
SQ	 0.6070	 0.5390
SR	 0.3440	 0.3850
SS	 0.3020	 0.4460
ST	 0.7480	 0.5720
SU	 0.2730	 -0.0330
SV	 0.1240	 0.0590
SW	 0.2210	 0.0130
SX	 0.3340	 -0.0030
SY	 0.4540	 0.4800
SZ	 0.4380	 0.4270
Sa	 0.2510	 0.0830
Sb	 0.7540	 0.5800

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Chain	Atom inclusion	Q-score
Sc	 0.5600	 0.5300
Sd	 0.3260	 0.0710
Se	 0.3680	 0.3920
Sf	 0.1250	 0.0210