



Full wwPDB EM Validation Report ⓘ

Jul 6, 2026 – 06:53 PM JST

PDB ID : 9VTH / pdb_00009vth
EMDB ID : EMD-65328
Title : cryoEM structure of tobacco mosaic virus tRNA-like structure complexed with tobacco 80S and initiator tRNA
Authors : Lu, G.; Lin, J.
Deposited on : 2025-07-10
Resolution : 4.70 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

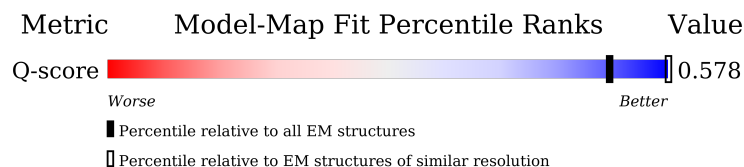
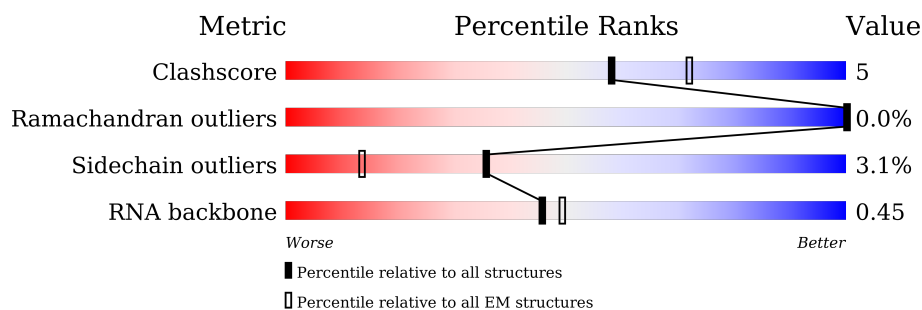
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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.



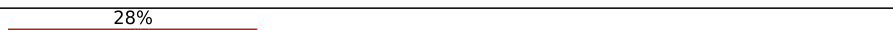
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1989 (4.20 - 5.20)

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	

Continued on next page...

Continued from previous page...

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	
22	SV	143	
23	SW	131	
24	SX	143	
25	SY	82	
26	SZ	133	
27	Sa	74	
28	Sb	113	

Continued on next page...

Continued from previous page...

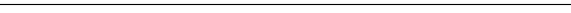
Mol	Chain	Length	Quality of chain
29	Sc	85	
30	Sd	65	
31	Se	62	
32	Sf	156	
33	LA	217	
34	LB	260	
35	LC	389	
36	LD	405	
37	LE	181	
38	LF	194	
39	LG	206	
40	LH	140	
41	LI	148	
42	LJ	219	
43	LK	293	
44	LL	175	
45	LM	154	
46	LN	146	
47	LO	123	
48	LP	242	
49	LQ	230	
50	LR	237	
51	LS	200	
52	LT	130	
53	LU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

Continued on next page...

Continued from previous page...

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	

Continued on next page...

Mol	Chain	Length	Quality of chain
79	13	163	 70%27%
80	14	3390	 67%22%7%
81	15	6	 83%17%
82	16	75	 45%37%16%

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 201638 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
			1609	1022	289	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
			1661	1052	306	295	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
			1519	961	300	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
			1532	954	290	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	140	Total	C	N	O	S	0	0
			1130	719	220	187	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
			995	610	197	183	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SJ	139	Total	C	N	O	S	0	0
			1082	686	210	183	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
			1147	715	225	201	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SL	54	Total	C	N	O	S	0	0
			437	272	89	70	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	125	Total	C	N	O	S	0	0
			1005	644	187	169	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SP	215	Total	C	N	O	S	0	0
			1751	1112	312	319	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
			2074	1323	387	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
			1840	1150	356	326	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
			1537	978	280	276	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	83	Total	C	N	O	S	0	0
			716	471	117	124	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	117	Total	C	N	O	S	0	0
			880	553	155	165	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SW	119	Total	C	N	O	S	0	0
			960	603	178	174	5		

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
			1034	657	200	174	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Sa	70	Total	C	N	O	S	0	0
			549	343	103	100	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
			793	493	161	131	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	47	Total	C	N	O	S	0	0
			375	228	86	60	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
			1712	1095	299	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

Continued on next page...

Continued from previous page...

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
			1107	700	206	199	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

Continued on next page...

Continued from previous page...

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	24	Total	C	N	O	S	0	0
			227	136	63	25	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 RNA (204-MER).

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 a RNA chain called RNA (5'-R(P*AP*CP*AP*AP*UP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
81	15	6	Total	C	N	O	P	0	0
			129	58	25	40	6		

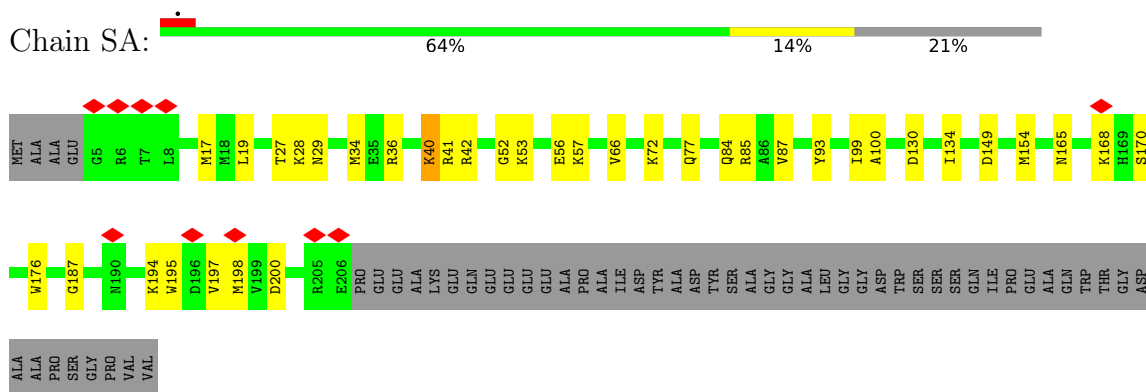
- Molecule 82 is a RNA chain called tRNA(iMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
82	16	75	Total	C	N	O	P	0	0
			1625	729	298	523	75		

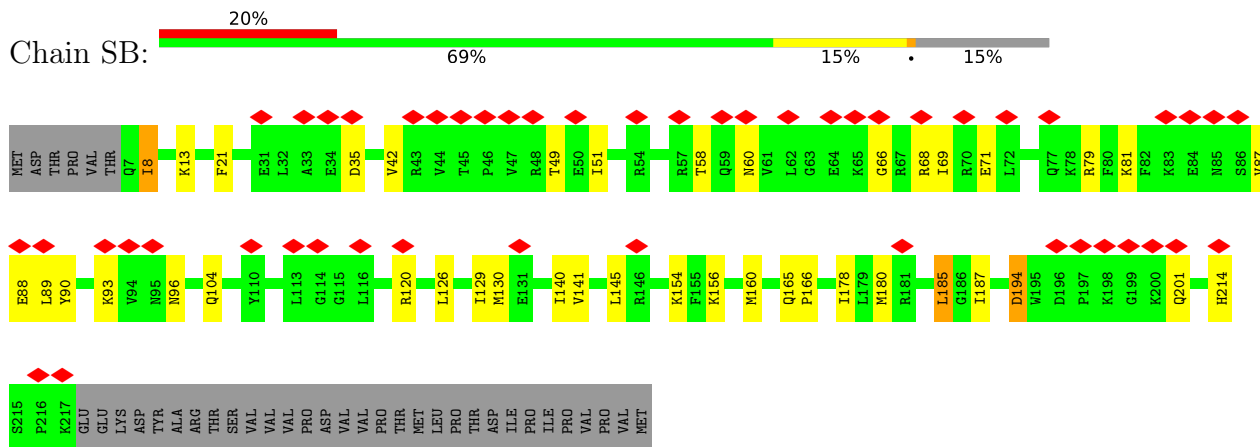
3 Residue-property plots

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.

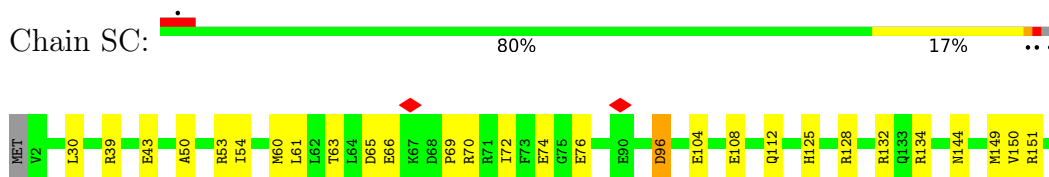
- Molecule 1: Small ribosomal subunit protein uS2

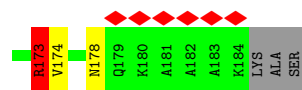


- Molecule 2: 30S ribosomal protein S3, chloroplastic



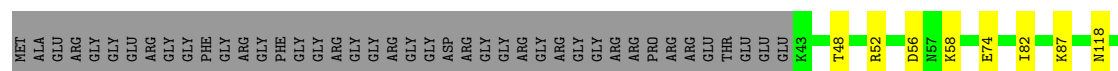
- Molecule 3: 40S ribosomal protein S9-2-like





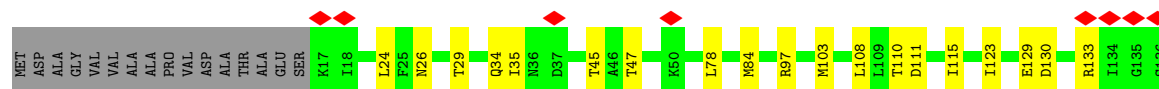
- Molecule 4: Small ribosomal subunit protein uS5

Chain SD: 69% 8% 22%



- Molecule 5: 40S ribosomal protein S5

Chain SE: 6% 78% 14% 8%



- Molecule 6: Small ribosomal subunit protein uS8c

Chain SF: 89% 10%



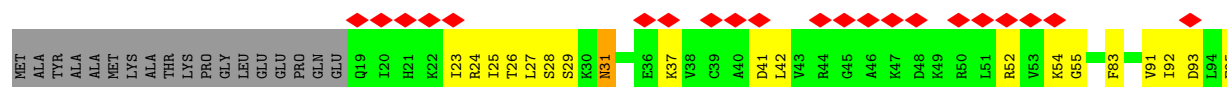
- Molecule 7: 40S ribosomal protein S16

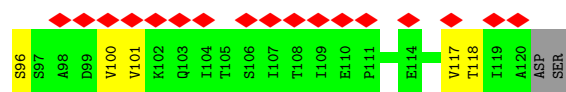
Chain SG: 78% 17% 5%



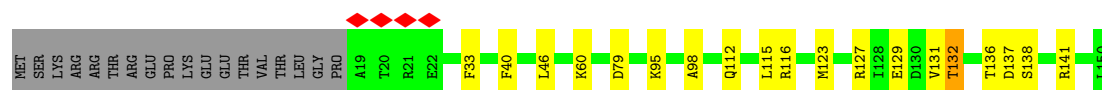
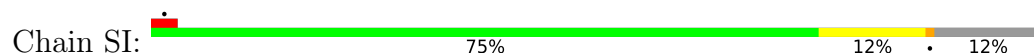
- Molecule 8: 40S ribosomal protein S20-2

Chain SH: 31% 64% 19% 16%





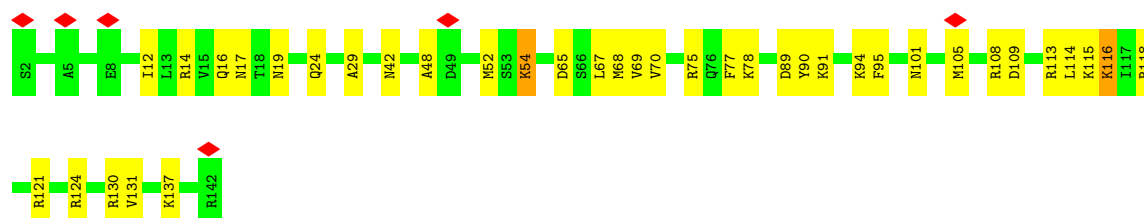
- Molecule 9: 40S ribosomal protein S14-2



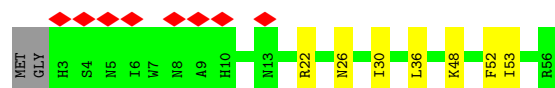
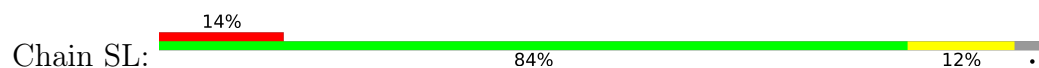
- Molecule 10: 40S ribosomal protein S23



- Molecule 11: 40S ribosomal protein S18



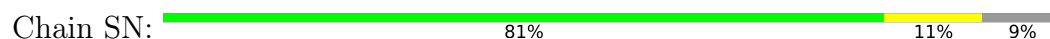
- Molecule 12: 40S ribosomal protein S29



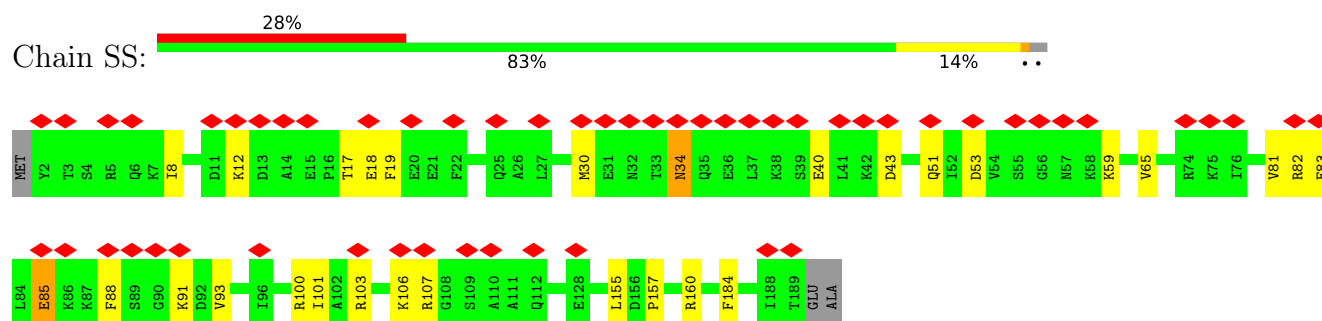
- Molecule 13: 40S ribosomal protein S13



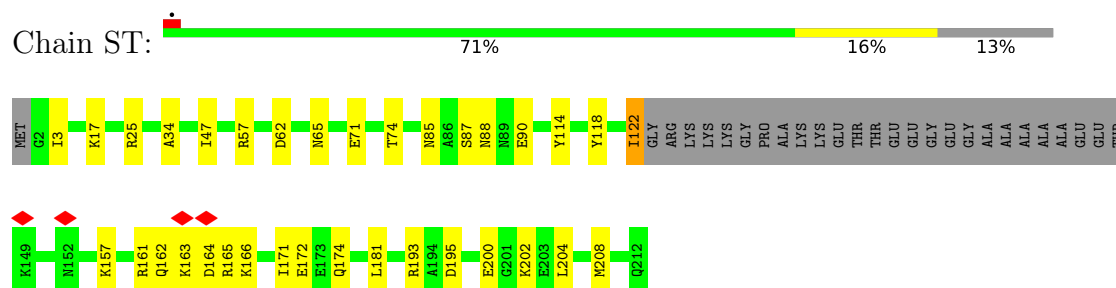
- Molecule 14: 40S ribosomal protein S11



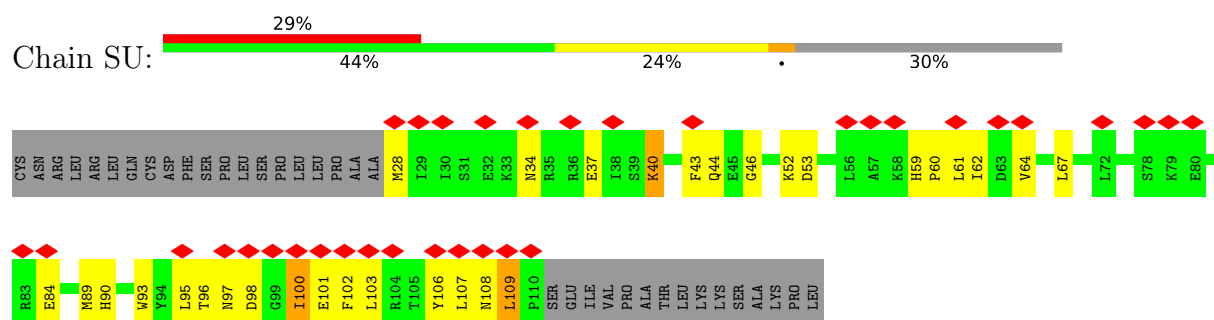
- Molecule 19: 40S ribosomal protein S7



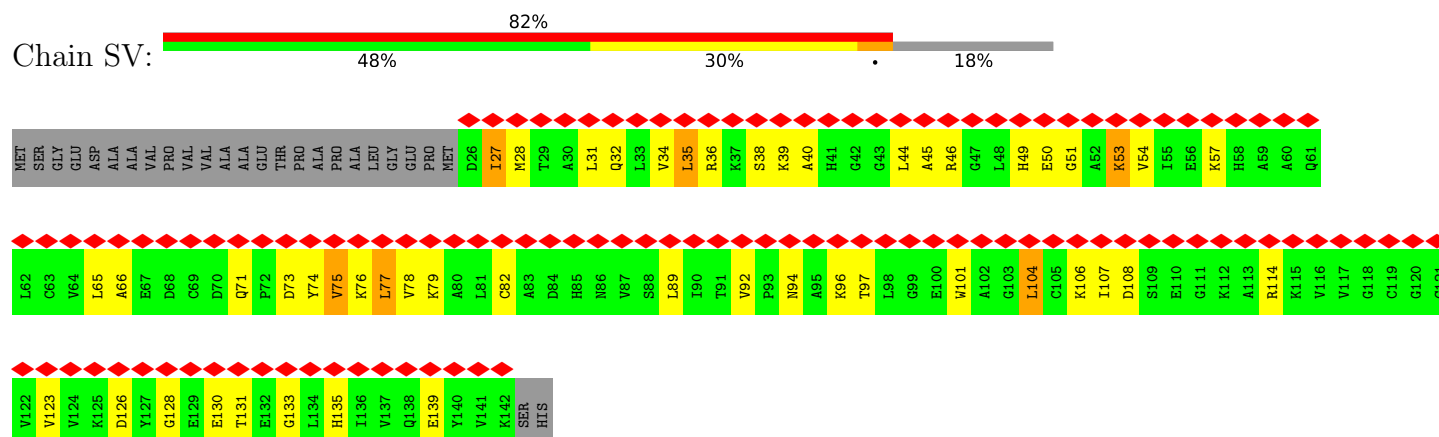
- Molecule 20: 40S ribosomal protein S8



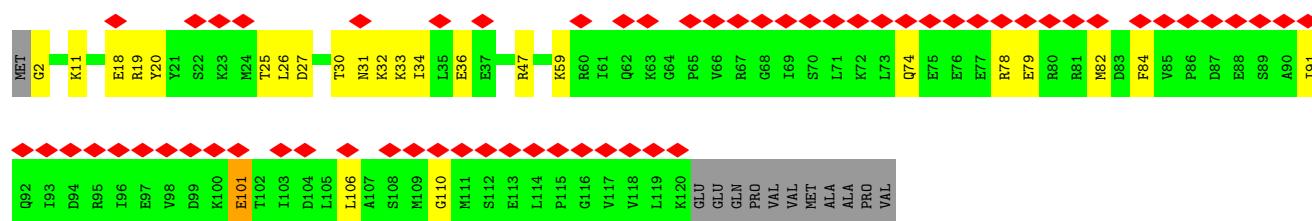
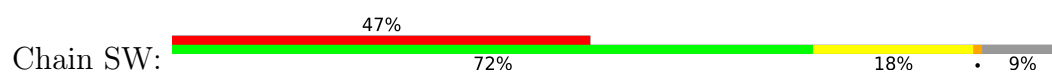
- Molecule 21: 40S ribosomal protein S10-1



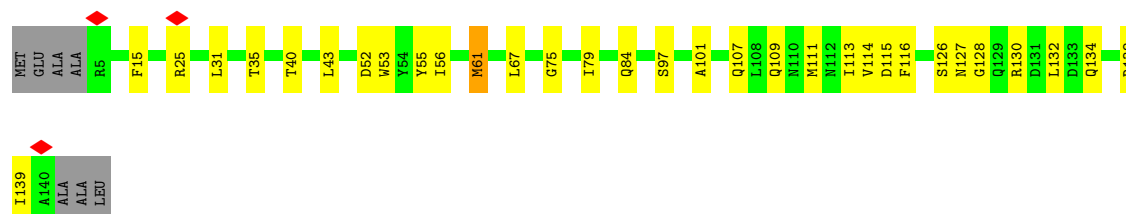
- Molecule 22: 40S ribosomal protein S12



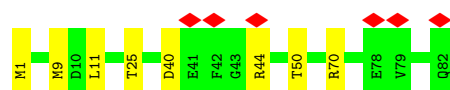
- Molecule 23: 40S ribosomal protein S17-like



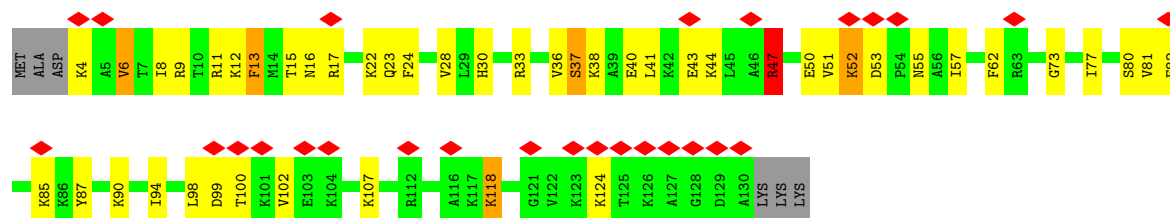
- Molecule 24: 40S ribosomal protein S19-3-like



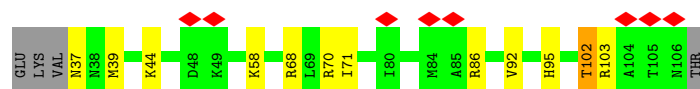
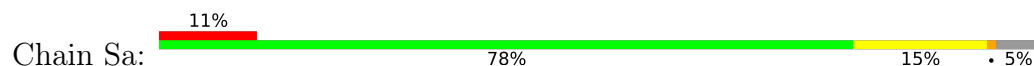
- Molecule 25: 40S ribosomal protein S21



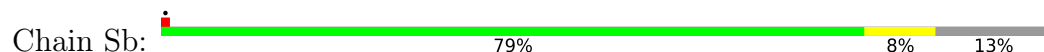
- Molecule 26: 40S ribosomal protein S24

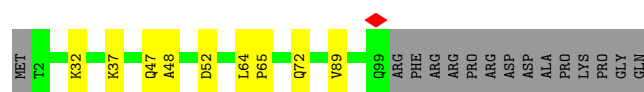


- Molecule 27: 40S ribosomal protein S25

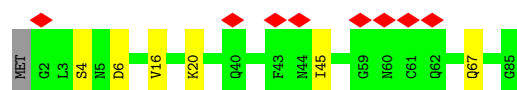
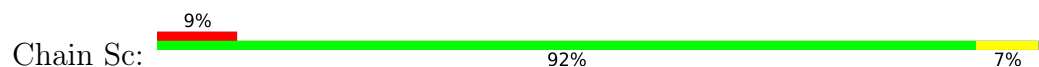


- Molecule 28: 40S ribosomal protein S26

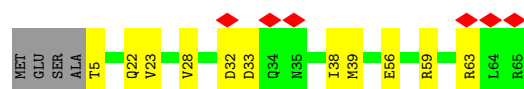
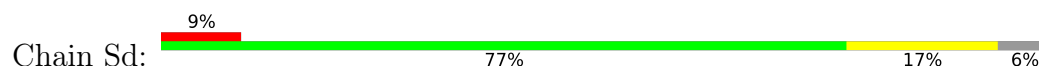




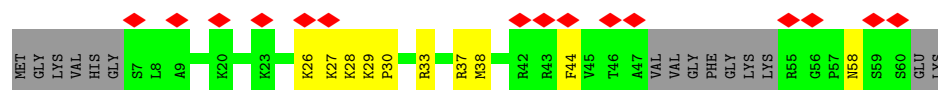
- Molecule 29: 40S ribosomal protein S27



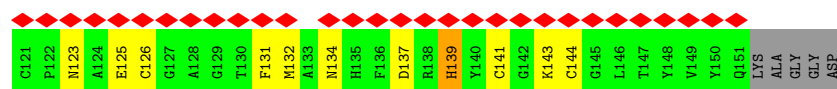
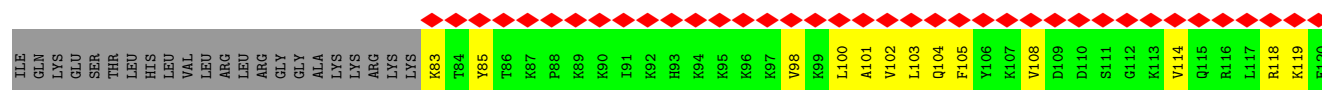
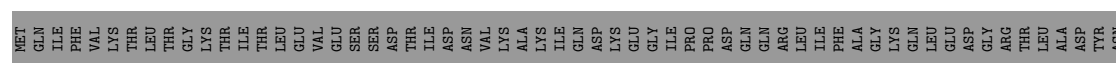
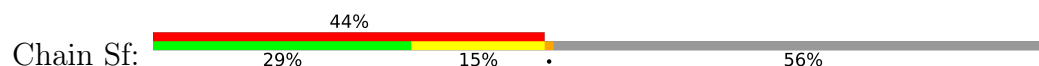
- Molecule 30: 40S ribosomal protein S28



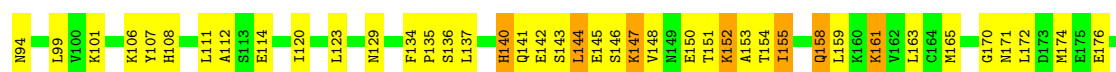
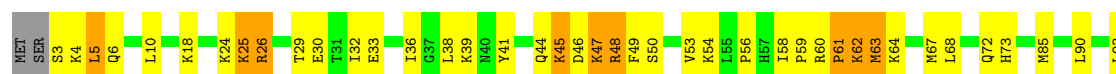
- Molecule 31: 40S ribosomal protein S30

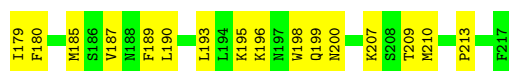


- Molecule 32: Ubiquitin-40S ribosomal protein S27a-like



- Molecule 33: Ribosomal protein





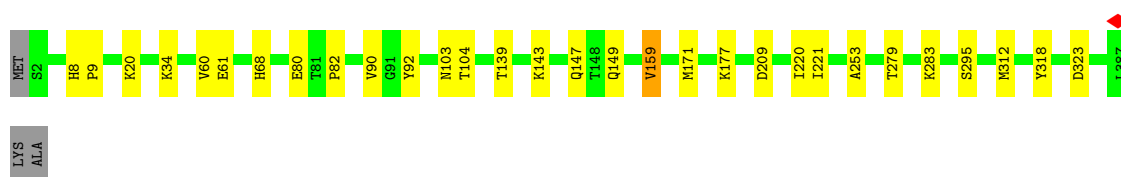
- Molecule 34: 60S ribosomal protein L8-like

Chain LB: 89% 5% 6%



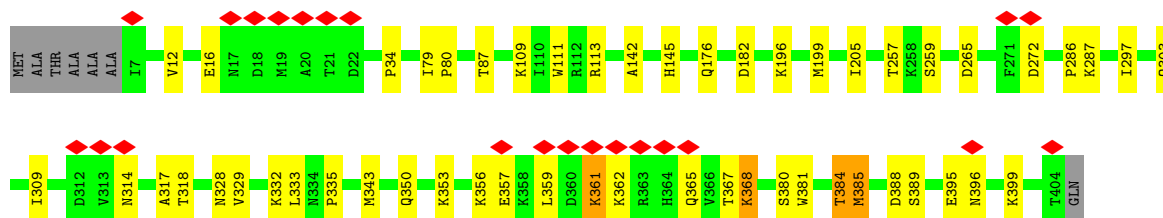
- Molecule 35: 60S ribosomal protein L3

Chain LC: 92% 7%



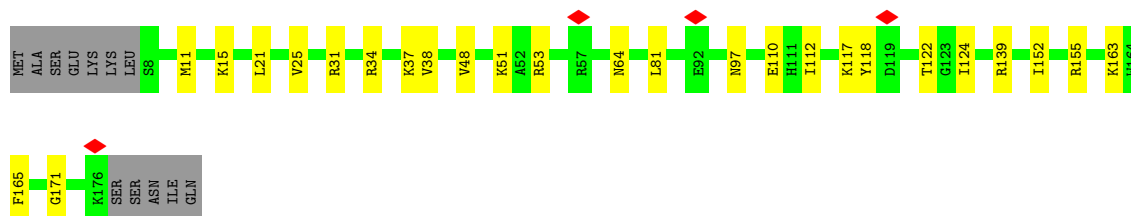
- Molecule 36: 60S ribosomal protein L4-like

Chain LD: 5% 85% 12%



- Molecule 37: 60S ribosomal protein L11-1

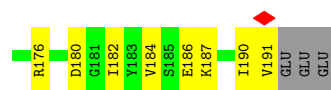
Chain LE: 79% 14% 7%



- Molecule 38: 60S ribosomal protein L9-1

Chain LF: 78% 20%

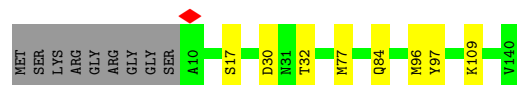




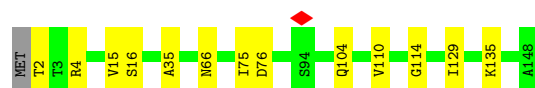
- Molecule 39: 60S ribosomal protein L13a-4



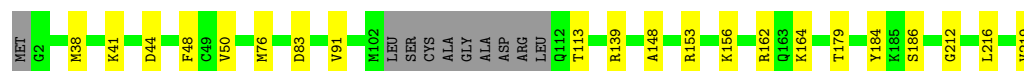
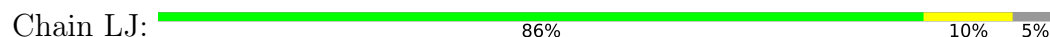
- Molecule 40: 60S ribosomal protein L23



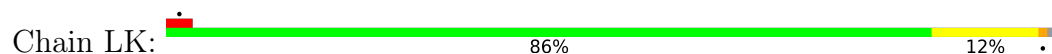
- Molecule 41: 60s ribosomal protein l27a-3



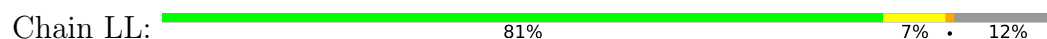
- Molecule 42: 60S ribosomal protein L10



- Molecule 43: 60S ribosomal protein L5-like

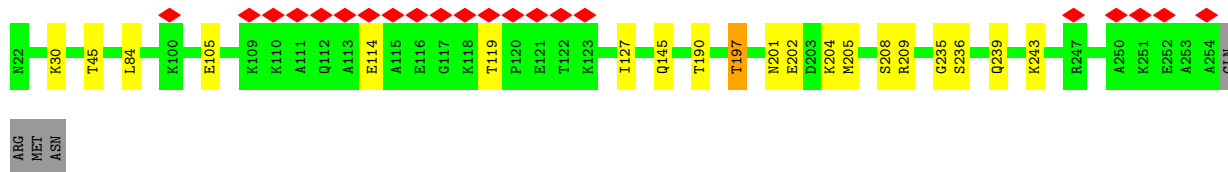


- Molecule 44: 60S ribosomal protein L17-1 isoform X2





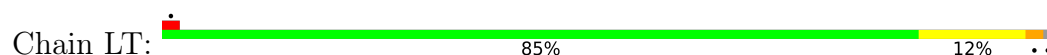
- Molecule 50: 60S ribosomal protein L7a



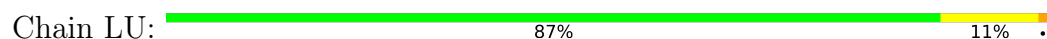
- Molecule 51: 60S ribosomal protein L13



- Molecule 52: 60S ribosomal protein L14-1



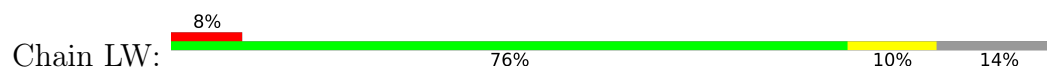
- Molecule 53: Ribosomal protein L15

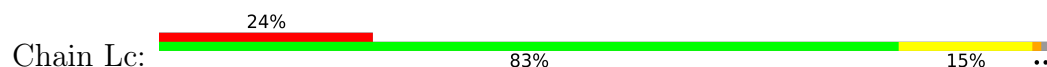


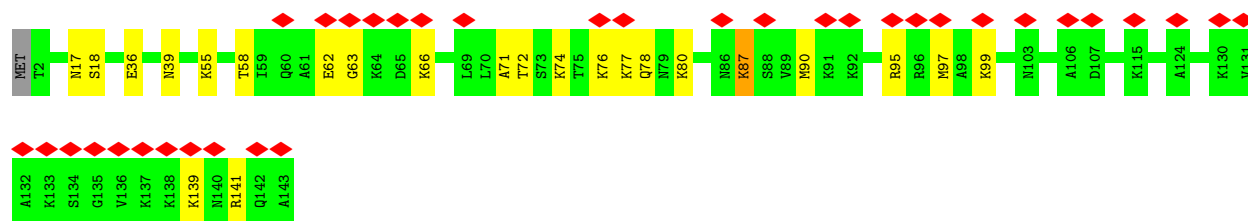
- Molecule 54: 60S ribosomal protein L18-2



- Molecule 55: Ribosomal protein L19

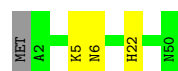






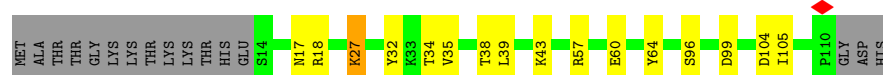
- Molecule 62: 60S ribosomal protein L29

Chain Ld: 92% 6% .



- Molecule 63: 60S ribosomal protein L30

Chain Le: 72% 13% . 14%



- Molecule 64: 60S ribosomal protein L31

Chain Lf: 5% 85% 5% 10%



- Molecule 65: 60S ribosomal protein L32-1

Chain Lg: 86% 8% 5%



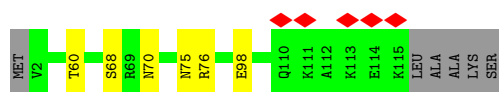
- Molecule 66: 60S ribosomal protein L35a-3-like

Chain Lh: 87% 5% 8%

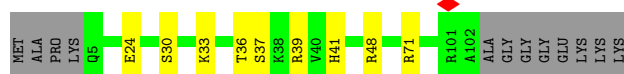
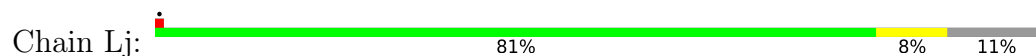


- Molecule 67: Large ribosomal subunit protein eL34

Chain Li: 90% 5% 5%



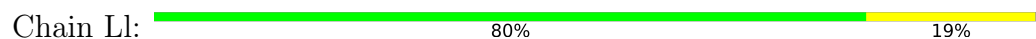
- Molecule 68: 60S ribosomal protein L36



- Molecule 69: Ribosomal protein L37



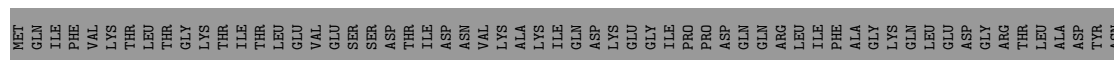
- Molecule 70: 60S ribosomal protein L38



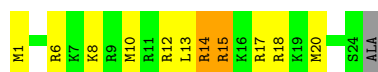
- Molecule 71: 60S ribosomal protein L39-3



- Molecule 72: Ubiquitin-60S ribosomal protein L40



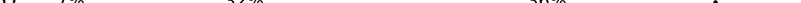
- Molecule 73: 60s ribosomal protein l41-like



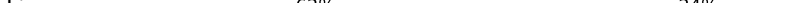
- Molecule 74: 60S ribosomal protein L44

MET
V2
K6
K24
V25
T26
K29
L72
G94
G99
LYS
GLY
THR
SER
LEU
PHE

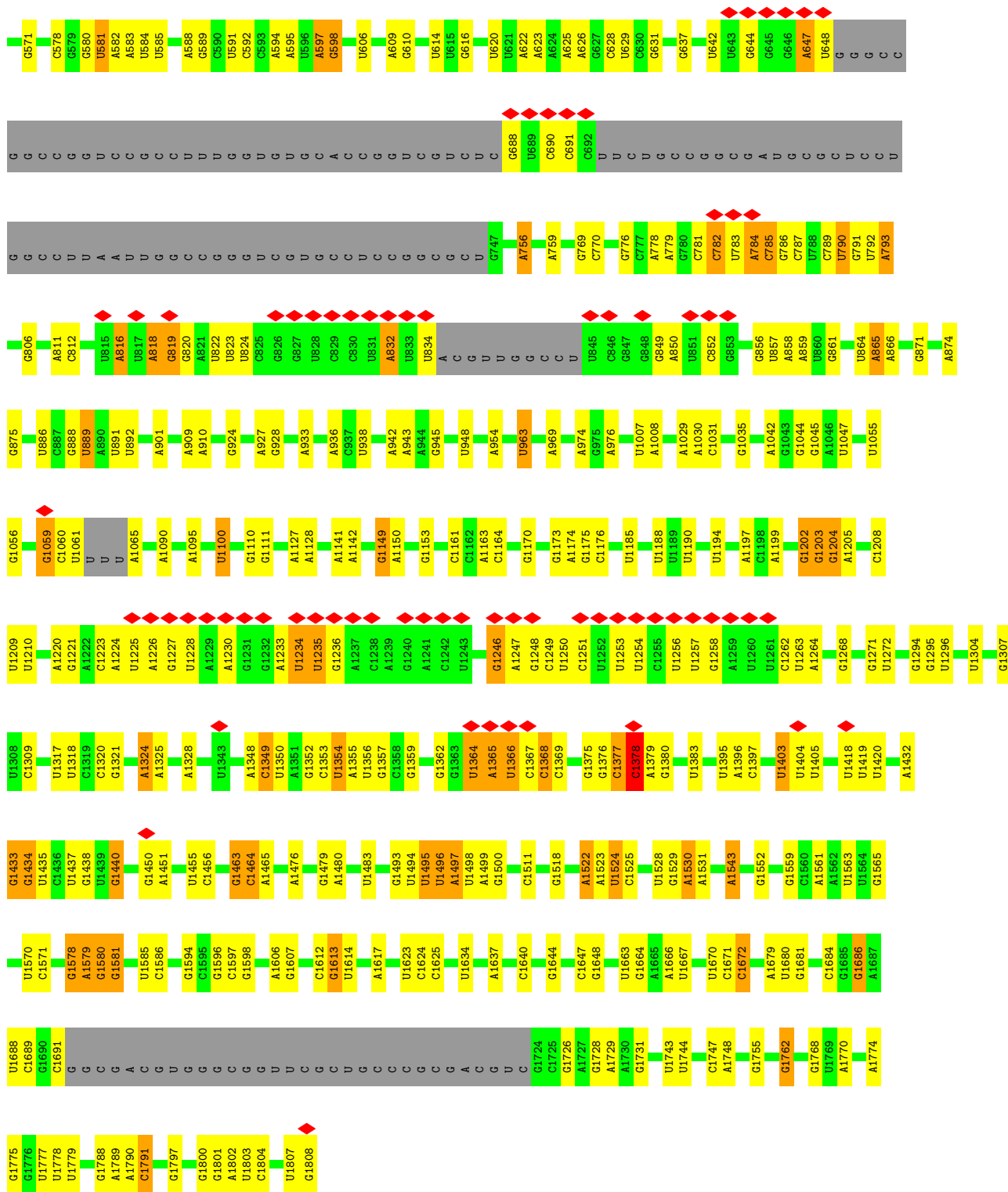
- Chain Lq: 92% 6%

- Chain 10:  7% 32% 36% • 23%

[illegible]

- Chain 11:  6% 62% 24% 5% 10%

Category	Item	Value	Color
A	A468	10	Red
	A469	10	Green
	A470	10	Green
	A471	10	Green
	A472	10	Green
	A473	10	Green
	A474	10	Green
	A475	10	Green
	A476	10	Green
	A477	10	Green
B	B468	10	Red
	B469	10	Green
	B470	10	Green
	B471	10	Green
	B472	10	Green
	B473	10	Green
	B474	10	Green
	B475	10	Green
	B476	10	Green
	B477	10	Green
C	C468	10	Red
	C469	10	Green
	C470	10	Green
	C471	10	Green
	C472	10	Green
	C473	10	Green
	C474	10	Green
	C475	10	Green
	C476	10	Green
	C477	10	Green
D	D468	10	Red
	D469	10	Green
	D470	10	Green
	D471	10	Green
	D472	10	Green
	D473	10	Green
	D474	10	Green
	D475	10	Green
	D476	10	Green
	D477	10	Green
E	E468	10	Red
	E469	10	Green
	E470	10	Green
	E471	10	Green
	E472	10	Green
	E473	10	Green
	E474	10	Green
	E475	10	Green
	E476	10	Green
	E477	10	Green
F	F468	10	Red
	F469	10	Green
	F470	10	Green
	F471	10	Green
	F472	10	Green
	F473	10	Green
	F474	10	Green
	F475	10	Green
	F476	10	Green
	F477	10	Green
G	G468	10	Red
	G469	10	Green
	G470	10	Green
	G471	10	Green
	G472	10	Green
	G473	10	Green
	G474	10	Green
	G475	10	Green
	G476	10	Green
	G477	10	Green
H	H468	10	Red
	H469	10	Green
	H470	10	Green
	H471	10	Green
	H472	10	Green
	H473	10	Green
	H474	10	Green
	H475	10	Green
	H476	10	Green
	H477	10	Green
I	I468	10	Red
	I469	10	Green
	I470	10	Green
	I471	10	Green
	I472	10	Green
	I473	10	Green
	I474	10	Green
	I475	10	Green
	I476	10	Green
	I477	10	Green
J	J468	10	Red
	J469	10	Green
	J470	10	Green
	J471	10	Green
	J472	10	Green
	J473	10	Green
	J474	10	Green
	J475	10	Green
	J476	10	Green
	J477	10	Green
K	K468	10	Red
	K469	10	Green
	K470	10	Green
	K471	10	Green
	K472	10	Green
	K473	10	Green
	K474	10	Green
	K475	10	Green
	K476	10	Green
	K477	10	Green
L	L468	10	Red
	L469	10	Green
	L470	10	Green
	L471	10	Green
	L472	10	Green
	L473	10	Green
	L474	10	Green
	L475	10	Green
	L476	10	Green
	L477	10	Green
M	M468	10	Red
	M469	10	Green
	M470	10	Green
	M471	10	Green
	M472	10	Green
	M473	10	Green
	M474	10	Green
	M475	10	Green
	M476	10	Green
	M477	10	Green
N	N468	10	Red
	N469	10	Green
	N470	10	Green
	N471	10	Green
	N472	10	Green
	N473	10	Green
	N474	10	Green
	N475	10	Green
	N476	10	Green
	N477	10	Green
O	O468	10	Red
	O469	10	Green
	O470	10	Green
	O471	10	Green
	O472	10	Green
	O473	10	Green
	O474	10	Green
	O475	10	Green
	O476	10	Green
	O477	10	Green</



• Molecule 78: 5S rRNA

Chain 12:

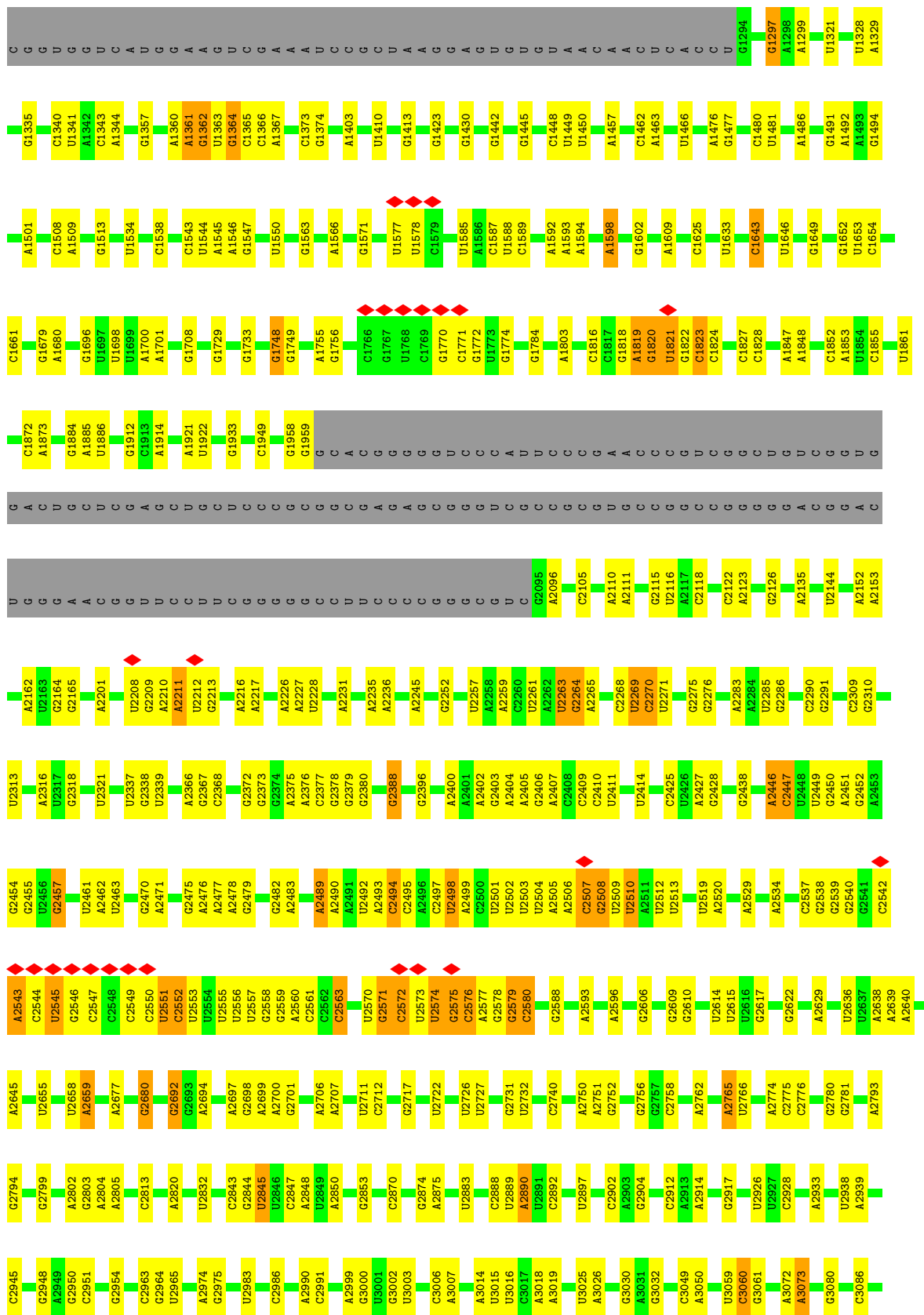


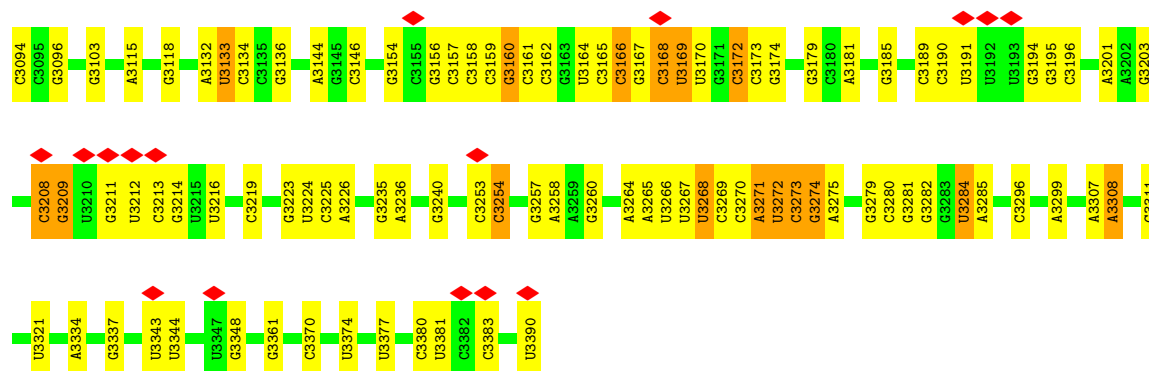
Chain 13:



Chain 14:







- Molecule 81: RNA (5'-R(P*AP*CP*AP*AP*UP*G)-3')

Chain 15: 83% 17%



- Molecule 82: tRNA(iMet)

Chain 16: 45% 37% 16%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32882	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	2.236	Depositor
Minimum map value	-0.784	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.061	Depositor
Recommended contour level	0.19	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: T6A, 7MG, 1MG, 2MG, H2U, M2G, 1MA, 5MC

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	0.26	0/1643	0.41	0/2221
2	SB	0.23	0/1684	0.43	0/2257
3	SC	0.22	0/1546	0.39	0/2069
4	SD	0.23	0/1721	0.41	0/2320
5	SE	0.20	0/1554	0.35	0/2096
6	SF	0.25	0/1050	0.41	0/1405
7	SG	0.21	0/1149	0.38	0/1535
8	SH	0.20	0/813	0.46	0/1095
9	SI	0.42	0/1007	0.68	2/1348 (0.1%)
10	SJ	0.23	0/1101	0.40	0/1465
11	SK	0.35	0/1164	0.55	0/1554
12	SL	0.18	0/449	0.31	0/600
13	SM	0.24	0/1214	0.34	0/1632
14	SN	0.27	0/1180	0.45	0/1579
15	SO	0.31	0/1027	0.58	0/1377
16	SP	0.30	0/1781	0.44	0/2391
17	SQ	0.26	0/2114	0.43	0/2837
18	SR	0.32	0/1864	0.56	0/2482
19	SS	0.19	0/1565	0.44	0/2103
20	ST	0.27	0/1528	0.43	0/2041
21	SU	0.40	0/736	0.72	0/993
22	SV	0.27	0/891	0.66	2/1201 (0.2%)
23	SW	0.27	0/970	0.53	0/1294
24	SX	0.22	0/1103	0.39	0/1480
25	SY	0.21	0/661	0.39	0/888
26	SZ	0.46	0/1049	0.68	0/1391
27	Sa	0.21	0/555	0.47	0/745
28	Sb	0.34	0/806	0.46	0/1077
29	Sc	0.18	0/661	0.30	0/888
30	Sd	0.18	0/496	0.36	0/661
31	Se	0.24	0/379	0.53	0/498
32	Sf	0.15	0/574	0.40	0/763

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LA	0.76	0/1737	1.12	3/2319 (0.1%)
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	0.39	0/1183	0.61	2/1581 (0.1%)
42	LJ	0.25	0/1707	0.39	0/2283
43	LK	0.35	0/2384	0.49	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	0.30	0/1993	0.49	0/2672
49	LQ	0.20	0/1634	0.38	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	0.33	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	0.34	0/810	0.56	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	0/1122	0.53	0/1503
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	0.28	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	0.73	0/228	1.18	0/292
74	Lp	0.47	0/799	0.61	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	0.68	0/3752	1.09	9/5844 (0.2%)
77	11	0.32	0/38798	0.44	4/60451 (0.0%)
78	12	0.31	0/2837	0.35	0/4420
79	13	0.37	0/3889	0.44	0/6060
80	14	0.42	0/75291	0.53	2/117423 (0.0%)
81	15	0.25	0/144	0.24	0/222
82	16	0.38	0/1555	0.54	0/2423
All	All	0.36	0/216371	0.51	24/317467 (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
1	SA	0	2
3	SC	0	1
9	SI	0	1
11	SK	0	2
17	SQ	0	1
18	SR	0	1
26	SZ	0	2
33	LA	0	2
37	LE	0	1
38	LF	0	1
73	Lo	0	6
All	All	0	20

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	LI	15	VAL	N-CA-C	7.65	118.39	110.36
76	10	68	U	C4'-C3'-C2'	-7.54	95.06	102.60
76	10	134	U	O3'-P-O5'	-6.50	94.26	104.00
9	SI	136	THR	N-CA-C	-6.32	105.52	112.72
9	SI	138	SER	N-CA-C	6.29	118.74	109.69
33	LA	61	PRO	N-CA-C	-6.15	104.58	113.75
80	14	1093	U	C2'-C3'-O3'	-6.07	104.60	113.70
33	LA	155	ILE	CA-C-N	-6.03	111.40	121.89
33	LA	155	ILE	C-N-CA	-6.03	111.40	121.89
76	10	86	U	C1'-C2'-O2'	-5.97	102.85	111.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	11	581	U	C2'-C3'-O3'	5.85	118.27	109.50
76	10	120	U	C2'-C3'-O3'	5.81	118.22	109.50
77	11	1762	G	O3'-P-O5'	-5.76	95.36	104.00
77	11	1378	C	C3'-C2'-C1'	-5.64	95.86	101.50
76	10	70	G	C4'-C3'-C2'	-5.48	97.12	102.60
80	14	2498	U	OP1-P-O3'	5.41	124.24	108.00
76	10	134	U	OP1-P-O3'	5.36	124.07	108.00
22	SV	53	LYS	CA-CB-CG	5.30	124.71	114.10
76	10	68	U	O4'-C4'-C3'	-5.25	98.75	104.00
77	11	581	U	O3'-P-O5'	-5.23	96.16	104.00
76	10	52	U	C4'-C3'-C2'	-5.18	97.42	102.60
22	SV	77	LEU	CA-CB-CG	5.14	134.30	116.30
76	10	93	G	C3'-C2'-C1'	-5.07	96.43	101.50
41	LI	15	VAL	N-CA-CB	-5.03	104.93	110.51

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	LA	26	ARG	Sidechain
33	LA	48	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
1	SA	41	ARG	Sidechain
1	SA	42	ARG	Sidechain
3	SC	173	ARG	Sidechain
9	SI	141	ARG	Sidechain
11	SK	108	ARG	Sidechain
11	SK	113	ARG	Sidechain
17	SQ	221	ARG	Sidechain
18	SR	133	ARG	Sidechain
26	SZ	17	ARG	Sidechain
26	SZ	47	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	SA	1609	0	1622	24	0
2	SB	1661	0	1754	32	0
3	SC	1519	0	1584	25	0
4	SD	1686	0	1789	16	0
5	SE	1532	0	1575	18	0
6	SF	1032	0	1068	11	0
7	SG	1130	0	1193	14	0
8	SH	804	0	865	15	0
9	SI	995	0	1026	8	0
10	SJ	1082	0	1147	6	0
11	SK	1147	0	1180	22	0
12	SL	437	0	431	5	0
13	SM	1189	0	1278	5	0
14	SN	1155	0	1210	10	0
15	SO	1005	0	1063	20	0
16	SP	1751	0	1804	14	0
17	SQ	2074	0	2181	29	0
18	SR	1840	0	1948	49	0
19	SS	1537	0	1591	23	0
20	ST	1504	0	1557	21	0
21	SU	716	0	715	25	0
22	SV	880	0	905	47	0
23	SW	960	0	1023	18	0
24	SX	1081	0	1091	24	0
25	SY	651	0	630	6	0
26	SZ	1034	0	1110	37	0
27	Sa	549	0	579	9	0
28	Sb	793	0	828	7	0
29	Sc	650	0	649	3	0
30	Sd	493	0	524	7	0
31	Se	375	0	405	8	0
32	Sf	562	0	584	18	0
33	LA	1712	0	1823	79	0
34	LB	1880	0	1915	9	0
35	LC	3107	0	3232	21	0
36	LD	3087	0	3207	27	0
37	LE	1362	0	1405	17	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	LF	1520	0	1614	24	0
39	LG	1644	0	1773	7	0
40	LH	985	0	1046	6	0
41	LI	1155	0	1197	7	0
42	LJ	1671	0	1731	12	0
43	LK	2339	0	2377	21	0
44	LL	1236	0	1262	7	0
45	LM	950	0	1029	12	0
46	LN	1023	0	1105	7	0
47	LO	997	0	1136	8	0
48	LP	1958	0	2057	20	0
49	LQ	1600	0	1731	22	0
50	LR	1874	0	2030	10	0
51	LS	1608	0	1697	13	0
52	LT	1046	0	1144	13	0
53	LU	1701	0	1771	16	0
54	LV	1462	0	1581	6	0
55	LW	1519	0	1630	15	0
56	LX	1505	0	1557	13	0
57	LY	1306	0	1367	8	0
58	LZ	799	0	836	11	0
59	La	526	0	554	9	0
60	Lb	1097	0	1182	7	0
61	Lc	1107	0	1182	14	0
62	Ld	407	0	393	2	0
63	Le	745	0	783	10	0
64	Lf	875	0	934	4	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	4	0
73	Lo	227	0	262	2	0
74	Lp	785	0	844	4	0
75	Lq	586	0	611	5	0
76	10	3359	0	1699	137	0
77	11	34688	0	17477	252	0
78	12	2538	0	1286	6	0
79	13	3478	0	1761	19	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	14	67280	0	33921	291	0
81	15	129	0	66	2	0
82	16	1625	0	843	14	0
All	All	201638	0	150093	1607	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 5.

All (1607) 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:4:LYS:HD2	33:LA:198:TRP:HB3	1.32	1.07
26:SZ:44:LYS:HG3	26:SZ:47:ARG:HH11	1.23	1.03
33:LA:48:ARG:HA	33:LA:159:LEU:HD23	1.50	0.94
21:SU:43:PHE:HB2	21:SU:103:LEU:HD21	1.49	0.93
57:LY:129:LYS:HB3	80:14:1109:A:H5'	1.51	0.91
33:LA:39:LYS:HE3	33:LA:199:GLN:O	1.70	0.90
7:SG:33:ARG:HH12	77:11:1369:C:H4'	1.36	0.89
77:11:1594:G:H1	77:11:1614:U:H3	1.13	0.88
77:11:631:G:H21	77:11:974:A:H62	1.19	0.87
33:LA:171:ASN:OD1	33:LA:174:MET:HG3	1.74	0.86
33:LA:36:ILE:HG21	33:LA:190:LEU:HD21	1.57	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	0.83
26:SZ:12:LYS:HD3	77:11:787:C:H41	1.44	0.82
33:LA:4:LYS:CD	33:LA:198:TRP:HB3	2.09	0.81
77:11:631:G:N2	77:11:974:A:H62	1.79	0.81
77:11:276:G:H2'	77:11:277:G:H8	1.47	0.80
79:13:85:C:H2'	79:13:88:G:H4'	1.63	0.80
15:SO:60:PRO:HA	15:SO:90:MET:HE1	1.63	0.79
33:LA:4:LYS:HD2	33:LA:198:TRP:CB	2.13	0.79
26:SZ:6:VAL:HG21	26:SZ:33:ARG:HH21	1.48	0.78
23:SW:33:LYS:HE2	23:SW:33:LYS:HA	1.64	0.78
26:SZ:13:PHE:HA	26:SZ:23:GLN:O	1.82	0.78
76:10:56:U:H3	76:10:63:A:H2	1.32	0.78
21:SU:62:ILE:HG12	21:SU:64:VAL:HG23	1.66	0.77
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
49:LQ:24:MET:HE2	49:LQ:24:MET:HA	1.66	0.77
80:14:424:G:H22	80:14:643:U:H3	1.31	0.77
76:10:98:G:H3'	76:10:99:U:C6	2.21	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:SA:84:GLN:HG2	1:SA:100:ALA:HB1	1.66	0.75
36:LD:317:ALA:HB2	80:14:1373:C:H5''	1.69	0.75
76:10:112:C:H2'	76:10:113:G:C8	2.20	0.75
80:14:3208:C:H4'	80:14:3209:G:H5'	1.68	0.75
5:SE:130:ASP:HB2	5:SE:147:ILE:HD11	1.67	0.74
76:10:118:G:C4	76:10:119:G:H1'	2.22	0.74
22:SV:57:LYS:HE3	22:SV:57:LYS:HA	1.68	0.74
1:SA:40:LYS:HB3	23:SW:101:GLU:OE2	1.88	0.74
76:10:72:G:H2'	76:10:73:U:C6	2.23	0.73
8:SH:54:LYS:HA	8:SH:54:LYS:HE3	1.70	0.73
18:SR:156:ARG:HH22	77:11:80:C:H41	1.34	0.73
77:11:1:U:H2'	77:11:374:A:H5'	1.69	0.73
26:SZ:44:LYS:CG	26:SZ:47:ARG:HH11	1.99	0.73
61:Lc:90:MET:HE2	61:Lc:97:MET:HG2	1.71	0.73
76:10:84:A:H1'	76:10:92:C:H1'	1.72	0.72
80:14:746:A:H5'	80:14:991:U:C4	2.24	0.72
8:SH:26:THR:HG22	8:SH:91:VAL:HG23	1.71	0.72
15:SO:117:GLU:OE1	15:SO:117:GLU:N	2.22	0.72
18:SR:69:THR:HG22	18:SR:71:GLY:H	1.52	0.72
38:LF:74:ARG:HG2	80:14:3115:A:H4'	1.72	0.72
2:SB:96:ASN:HD22	2:SB:201:GLN:HE21	1.35	0.71
80:14:2507:C:H5''	80:14:2508:G:H5'	1.72	0.71
80:14:434:G:H4'	80:14:435:G:H5''	1.73	0.71
33:LA:39:LYS:CE	33:LA:199:GLN:O	2.39	0.70
66:Lh:61:LYS:HB2	80:14:3168:C:H42	1.56	0.70
80:14:859:C:H2'	80:14:860:U:C6	2.26	0.70
8:SH:55:GLY:HA3	8:SH:92:ILE:HG23	1.72	0.70
80:14:2263:U:HO2'	80:14:2264:G:H8	1.36	0.70
77:11:783:U:O2	77:11:784:A:N6	2.25	0.70
18:SR:23:LYS:HD2	18:SR:42:GLY:H	1.57	0.70
55:LW:67:LYS:NZ	80:14:2105:C:OP1	2.24	0.70
65:Lg:103:THR:HG22	65:Lg:126:ARG:HB3	1.74	0.70
73:Lo:1:MET:HG3	77:11:1791:C:OP2	1.92	0.69
36:LD:381:TRP:O	36:LD:385:MET:HG3	1.92	0.69
33:LA:114:GLU:HG2	33:LA:137:LEU:HD11	1.75	0.69
9:SI:127:ARG:NH2	16:SP:72:ASP:OD1	2.22	0.69
22:SV:114:ARG:HD3	22:SV:114:ARG:H	1.57	0.69
49:LQ:68:LYS:H	49:LQ:68:LYS:HD2	1.57	0.69
76:10:200:G:OP1	76:10:200:G:C5	2.46	0.69
76:10:72:G:H2'	76:10:73:U:H6	1.56	0.69
77:11:276:G:H2'	77:11:277:G:C8	2.28	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:SR:160:ASN:HA	18:SR:163:ARG:HD2	1.75	0.69
33:LA:36:ILE:HD13	33:LA:190:LEU:HD22	1.75	0.69
26:SZ:44:LYS:HG3	26:SZ:47:ARG:NH1	2.04	0.69
35:LC:103:ASN:HD21	35:LC:149:GLN:HG2	1.58	0.69
77:11:76:C:H2'	77:11:77:A:C8	2.28	0.69
33:LA:120:ILE:HD13	33:LA:135:PRO:HG2	1.75	0.68
55:LW:123:MET:HE2	55:LW:123:MET:HA	1.75	0.68
43:LK:93:THR:HG22	43:LK:157:ARG:NH1	2.08	0.68
51:LS:37:ARG:NH2	80:14:696:G:OP1	2.26	0.68
80:14:3225:C:H2'	80:14:3226:A:H8	1.57	0.68
19:SS:17:THR:OG1	19:SS:18:GLU:OE1	2.10	0.67
25:SY:9:MET:HE3	25:SY:9:MET:HA	1.76	0.67
26:SZ:12:LYS:HD3	77:11:787:C:N4	2.09	0.67
76:10:89:A:H2'	76:10:90:A:C4	2.29	0.67
80:14:764:G:H2'	80:14:765:A:H8	1.60	0.67
40:LH:96:MET:HE2	59:La:22:ARG:HD2	1.77	0.67
56:LX:28:ARG:NH1	57:LY:148:THR:OG1	2.27	0.67
44:LL:57:ALA:HB3	44:LL:73:VAL:HG13	1.76	0.67
59:La:5:THR:HG21	59:La:14:LYS:HG3	1.76	0.67
15:SO:63:LEU:HD23	15:SO:90:MET:HE3	1.77	0.67
21:SU:108:ASN:ND2	22:SV:40:ALA:O	2.27	0.67
8:SH:83:PHE:HB3	12:SL:52:PHE:HB3	1.76	0.67
77:11:647:A:N1	77:11:690:C:N4	2.43	0.66
18:SR:53:MET:HB3	77:11:161:G:H4'	1.76	0.66
77:11:871:G:H1	77:11:963:U:H3	1.43	0.66
5:SE:35:ILE:HG23	5:SE:123:ILE:HD11	1.78	0.66
17:SQ:54:TYR:O	26:SZ:16:ASN:ND2	2.28	0.66
2:SB:58:THR:H	2:SB:93:LYS:HZ1	1.41	0.66
2:SB:145:LEU:HD21	2:SB:185:LEU:HD11	1.77	0.66
76:10:91:U:H6	76:10:91:U:H5'	1.61	0.66
80:14:3159:C:H2'	80:14:3160:G:C8	2.31	0.66
22:SV:73:ASP:OD1	22:SV:73:ASP:N	2.28	0.66
77:11:104:A:H2	77:11:362:U:H3	1.43	0.66
11:SK:121:ARG:NH1	77:11:1552:G:OP1	2.28	0.65
55:LW:7:GLN:NE2	55:LW:35:ALA:O	2.27	0.65
38:LF:94:LYS:NZ	38:LF:186:GLU:OE2	2.24	0.65
45:LM:93:THR:HG22	45:LM:137:ARG:HG3	1.77	0.65
69:Lk:46:LYS:NZ	80:14:22:C:OP1	2.26	0.65
76:10:88:A:H1'	76:10:89:A:C5	2.32	0.65
77:11:109:A:H2'	77:11:110:G:C8	2.32	0.65
80:14:3280:C:H2'	80:14:3281:G:C8	2.32	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:LW:162:ARG:HG2	77:11:819:G:N2	2.11	0.65
76:10:140:U:H2'	76:10:141:A:H8	1.60	0.65
38:LF:176:ARG:NH1	72:Ln:125:LYS:O	2.29	0.65
74:Lp:6:LYS:HD3	74:Lp:94:GLY:HA3	1.79	0.65
15:SO:65:LYS:HD2	15:SO:66:LYS:N	2.12	0.64
79:13:1:A:O2'	80:14:2999:A:N7	2.29	0.64
76:10:94:A:H2'	76:10:95:A:O4'	1.97	0.64
8:SH:54:LYS:HB2	8:SH:93:ASP:HB2	1.79	0.64
77:11:1377:C:H4'	77:11:1378:C:H6	1.62	0.64
22:SV:131:THR:O	22:SV:135:HIS:NE2	2.31	0.64
38:LF:141:GLU:N	38:LF:141:GLU:OE1	2.30	0.64
76:10:76:U:H2'	76:10:77:U:H3'	1.79	0.64
2:SB:104:GLN:HG3	2:SB:129:ILE:HD11	1.80	0.64
38:LF:131:MET:HB3	38:LF:135:VAL:HG13	1.78	0.64
43:LK:89:LYS:HG2	43:LK:90:VAL:HG13	1.79	0.64
1:SA:77:GLN:HB3	1:SA:99:ILE:HB	1.79	0.64
31:Se:26:LYS:NZ	77:11:591:U:OP1	2.30	0.64
33:LA:64:LYS:HB3	33:LA:107:TYR:HA	1.78	0.64
69:Lk:65:ARG:NH2	79:13:103:U:O4	2.23	0.64
6:SF:55:ASP:OD2	6:SF:60:LYS:NZ	2.31	0.64
45:LM:145:LEU:O	45:LM:149:ASN:ND2	2.31	0.64
50:LR:201:ASN:HA	50:LR:204:LYS:HG3	1.80	0.64
77:11:1044:G:H2'	77:11:1045:G:C8	2.32	0.64
80:14:2216:A:H2'	80:14:2217:A:C8	2.33	0.64
50:LR:205:MET:HE1	50:LR:209:ARG:HE	1.63	0.63
20:ST:163:LYS:HE3	20:ST:164:ASP:HB3	1.80	0.63
16:SP:91:VAL:HG22	16:SP:96:VAL:HG12	1.79	0.63
33:LA:54:LYS:HA	33:LA:154:THR:HA	1.79	0.63
80:14:2543:A:H2	80:14:2545:U:H3	1.44	0.63
20:ST:204:LEU:O	20:ST:208:MET:HG3	1.98	0.63
22:SV:50:GLU:HA	22:SV:53:LYS:NZ	2.13	0.63
47:LO:55:ALA:O	47:LO:59:THR:HG23	1.99	0.63
77:11:1174:A:H2'	77:11:1175:G:C8	2.34	0.63
17:SQ:146:THR:HG21	77:11:124:G:H21	1.63	0.63
27:Sa:39:MET:HE2	27:Sa:71:ILE:HG22	1.79	0.63
38:LF:12:ILE:HD13	38:LF:18:ILE:HG21	1.81	0.63
77:11:942:A:H2'	77:11:943:A:C8	2.34	0.63
35:LC:82:PRO:HG2	35:LC:171:MET:HE2	1.80	0.63
38:LF:97:PHE:HB2	38:LF:145:ASP:HB3	1.81	0.63
77:11:1356:U:H3	77:11:1375:G:H1	1.46	0.63
79:13:133:G:H2'	79:13:134:G:C8	2.34	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:10:92:C:H2'	76:10:93:G:C8	2.34	0.62
80:14:417:G:N2	80:14:2388:G:OP2	2.30	0.62
45:LM:71:GLN:NE2	45:LM:114:MET:SD	2.73	0.62
58:LZ:100:ARG:HD3	58:LZ:116:PHE:HB3	1.80	0.62
80:14:692:A:N6	80:14:708:C:H2'	2.14	0.62
5:SE:137:ALA:HB1	81:15:31:A:H62	1.64	0.62
33:LA:59:PRO:O	33:LA:60:ARG:C	2.41	0.62
76:10:78:C:H2'	76:10:79:C:H6	1.63	0.62
8:SH:23:ILE:HG21	8:SH:101:VAL:HG21	1.81	0.62
76:10:195:U:H2'	76:10:196:A:H4'	1.81	0.62
2:SB:68:ARG:O	2:SB:71:GLU:HB2	2.00	0.62
76:10:74:U:C6	76:10:74:U:H5'	2.35	0.62
33:LA:161:LYS:NZ	76:10:171:U:H4'	2.14	0.62
4:SD:244:ARG:CZ	4:SD:244:ARG:HA	2.30	0.62
47:LO:3:ARG:NH2	79:13:90:G:OP2	2.32	0.62
48:LP:217:LYS:NZ	80:14:1169:G:OP1	2.31	0.62
16:SP:152:ARG:NH2	77:11:1047:U:OP1	2.28	0.62
18:SR:138:LYS:NZ	18:SR:179:LYS:O	2.25	0.62
32:Sf:104:GLN:N	32:Sf:104:GLN:OE1	2.32	0.62
80:14:858:A:H3'	80:14:859:C:O4'	2.00	0.62
17:SQ:110:ARG:NH1	77:11:789:C:O2	2.33	0.61
76:10:126:G:H2'	76:10:127:U:O4'	2.00	0.61
80:14:1819:A:H2'	80:14:1820:G:C8	2.35	0.61
11:SK:105:MET:HE3	11:SK:105:MET:HA	1.82	0.61
31:Se:58:ASN:ND2	77:11:591:U:O2	2.32	0.61
41:LI:110:VAL:HB	41:LI:129:ILE:HD12	1.82	0.61
22:SV:27:ILE:HG23	22:SV:28:MET:SD	2.39	0.61
76:10:78:C:H2'	76:10:79:C:C6	2.34	0.61
76:10:112:C:H2'	76:10:113:G:H8	1.65	0.61
3:SC:132:ARG:NH1	3:SC:144:ASN:O	2.33	0.61
56:LX:84:GLN:HG3	56:LX:89:TYR:CE1	2.35	0.61
80:14:2235:A:H2'	80:14:2236:A:C8	2.36	0.61
77:11:631:G:H21	77:11:974:A:N6	1.96	0.61
80:14:3270:C:HO2'	80:14:3271:A:H8	1.47	0.61
76:10:56:U:N3	76:10:63:A:H2	1.96	0.61
19:SS:18:GLU:OE1	19:SS:18:GLU:N	2.34	0.61
76:10:81:U:H3'	76:10:82:C:H6	1.65	0.61
15:SO:110:ASN:ND2	15:SO:127:SER:OG	2.34	0.60
13:SM:46:THR:H	13:SM:49:GLN:HE21	1.49	0.60
24:SX:25:ARG:HB2	24:SX:25:ARG:NH1	2.16	0.60
26:SZ:28:VAL:HG21	26:SZ:36:VAL:HG21	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:SB:79:ARG:NH1	2:SB:79:ARG:O	2.34	0.60
77:11:874:A:H2'	77:11:875:G:C8	2.37	0.60
80:14:1236:C:H41	80:14:1297:G:H21	1.49	0.60
17:SQ:151:ASP:HB3	17:SQ:154:ILE:HG13	1.83	0.60
80:14:1959:G:O4'	80:14:2096:A:N6	2.35	0.60
17:SQ:67:GLN:NE2	26:SZ:87:TYR:OH	2.25	0.60
32:Sf:119:LYS:HZ2	32:Sf:132:MET:HE2	1.66	0.60
42:LJ:76:MET:HE2	42:LJ:148:ALA:HA	1.84	0.60
77:11:888:G:H2'	77:11:889:U:C6	2.35	0.60
14:SN:34:ARG:NH1	14:SN:49:ALA:O	2.34	0.60
18:SR:32:ILE:HG12	18:SR:102:CYS:HB2	1.82	0.60
18:SR:150:SER:OG	18:SR:151:LYS:N	2.31	0.60
36:LD:16:GLU:H	36:LD:176:GLN:NE2	1.99	0.60
2:SB:96:ASN:HD22	2:SB:201:GLN:NE2	2.00	0.60
4:SD:82:ILE:O	4:SD:82:ILE:HG13	2.00	0.60
80:14:1206:G:H2'	80:14:1207:A:C8	2.36	0.60
8:SH:25:ILE:HG22	8:SH:117:VAL:HG12	1.83	0.60
33:LA:85:MET:HE1	33:LA:93:LEU:HD11	1.83	0.60
21:SU:106:TYR:HD1	21:SU:107:LEU:HD13	1.67	0.59
39:LG:179:LEU:HD11	52:LT:129:LYS:HE2	1.84	0.59
18:SR:46:LYS:H	18:SR:46:LYS:HD2	1.67	0.59
33:LA:5:LEU:HB3	33:LA:198:TRP:CH2	2.37	0.59
43:LK:265:ARG:NH1	43:LK:267:ASN:O	2.36	0.59
6:SF:20:ARG:HG2	6:SF:22:LYS:HE2	1.85	0.59
77:11:818:A:H1'	77:11:819:G:H3'	1.83	0.59
17:SQ:196:LYS:NZ	17:SQ:211:GLN:OE1	2.34	0.59
77:11:411:A:H2'	77:11:412:C:C6	2.36	0.59
5:SE:133:ARG:NH2	5:SE:139:VAL:O	2.36	0.59
80:14:692:A:H62	80:14:708:C:H2'	1.66	0.59
19:SS:53:ASP:HA	19:SS:59:LYS:HG2	1.84	0.59
24:SX:109:GLN:HE22	24:SX:116:PHE:HD1	1.50	0.59
2:SB:178:ILE:HD11	2:SB:187:ILE:HD13	1.84	0.59
24:SX:128:GLY:O	24:SX:132:LEU:HD12	2.03	0.59
26:SZ:52:LYS:HZ3	26:SZ:53:ASP:H	1.49	0.59
33:LA:48:ARG:HH12	33:LA:161:LYS:HE2	1.68	0.59
33:LA:161:LYS:HZ1	76:10:171:U:H4'	1.66	0.59
35:LC:90:VAL:HG22	35:LC:104:THR:HG23	1.85	0.59
76:10:93:G:H4'	76:10:94:A:H5'	1.84	0.59
7:SG:12:GLU:OE1	7:SG:31:ARG:NH2	2.35	0.59
33:LA:53:VAL:O	33:LA:154:THR:HA	2.03	0.59
82:16:37:T6A:ODA	82:16:38:A:N6	2.36	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:SF:22:LYS:NZ	29:Sc:4:SER:OG	2.25	0.59
47:LO:107:GLU:O	47:LO:111:GLU:HG2	2.03	0.59
76:10:140:U:H2'	76:10:141:A:C8	2.38	0.59
80:14:162:U:H3	80:14:253:G:H1	1.51	0.59
80:14:673:U:H2'	80:14:674:C:C6	2.37	0.59
5:SE:108:LEU:HD21	27:Sa:102:THR:HG22	1.85	0.58
19:SS:106:LYS:HD3	19:SS:107:ARG:N	2.18	0.58
76:10:132:G:H1'	76:10:137:A:H2	1.68	0.58
2:SB:42:VAL:HG22	2:SB:51:ILE:HG12	1.84	0.58
33:LA:4:LYS:HE3	33:LA:198:TRP:HB2	1.85	0.58
80:14:955:C:H2'	80:14:956:C:C6	2.37	0.58
80:14:3049:C:O2'	80:14:3050:A:H5'	2.03	0.58
17:SQ:187:ARG:HH21	77:11:756:A:P	2.26	0.58
80:14:1818:G:H2'	80:14:1819:A:O4'	2.04	0.58
76:10:76:U:C5	76:10:78:C:H3'	2.37	0.58
4:SD:252:GLU:HG2	4:SD:253:TYR:CE1	2.39	0.58
19:SS:30:MET:HE3	19:SS:30:MET:HA	1.86	0.58
38:LF:95:MET:HE2	38:LF:182:ILE:HG22	1.84	0.58
77:11:789:C:N4	77:11:791:G:OP1	2.37	0.58
80:14:1:G:H2'	80:14:2:C:C6	2.39	0.58
80:14:394:A:H4'	80:14:395:G:H3'	1.85	0.58
82:16:37:T6A:N7	82:16:37:T6A:N11	2.48	0.58
77:11:1061:U:H3	77:11:1065:A:H62	1.50	0.58
7:SG:116:LEU:HD22	7:SG:123:LEU:HD13	1.84	0.58
32:Sf:105:PHE:HD1	32:Sf:118:ARG:HD2	1.68	0.58
49:LQ:8:ARG:HD2	49:LQ:27:LYS:HB3	1.85	0.58
76:10:74:U:H3'	76:10:75:U:H2'	1.86	0.58
19:SS:53:ASP:OD1	19:SS:53:ASP:N	2.35	0.58
18:SR:156:ARG:NH1	77:11:79:A:O5'	2.37	0.57
42:LJ:83:ASP:OD1	42:LJ:83:ASP:N	2.36	0.57
76:10:70:G:C2'	76:10:88:A:H61	2.16	0.57
8:SH:52:ARG:O	8:SH:95:PHE:HB2	2.03	0.57
33:LA:63:MET:HB2	33:LA:152:LYS:HE2	1.86	0.57
5:SE:24:LEU:HD23	5:SE:115:ILE:HD11	1.85	0.57
22:SV:50:GLU:HA	22:SV:53:LYS:HD2	1.85	0.57
30:Sd:32:ASP:OD1	30:Sd:33:ASP:N	2.37	0.57
68:Lj:24:GLU:CD	68:Lj:24:GLU:H	2.12	0.57
34:LB:104:LEU:HA	34:LB:107:ILE:HD12	1.86	0.57
76:10:77:U:H1'	76:10:160:A:C6	2.40	0.57
76:10:98:G:H3'	76:10:99:U:H6	1.65	0.57
18:SR:17:GLU:OE1	18:SR:17:GLU:N	2.38	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LA:94:ASN:HA	33:LA:123:LEU:O	2.04	0.57
35:LC:34:LYS:HD2	35:LC:34:LYS:N	2.17	0.57
18:SR:51:LYS:HG2	18:SR:53:MET:HE3	1.85	0.57
32:Sf:123:ASN:HD21	32:Sf:125:GLU:HB3	1.68	0.57
1:SA:93:TYR:HE2	1:SA:197:VAL:HG11	1.69	0.57
4:SD:52:ARG:HB2	4:SD:52:ARG:NH1	2.20	0.57
53:LU:4:TYR:OH	80:14:146:G:OP2	2.23	0.57
77:11:161:G:OP2	77:11:161:G:N2	2.38	0.57
19:SS:12:LYS:HD2	19:SS:12:LYS:O	2.05	0.57
24:SX:40:THR:OG1	77:11:1483:U:OP1	2.20	0.57
35:LC:177:LYS:NZ	80:14:3307:A:OP1	2.34	0.57
77:11:1227:G:H2'	77:11:1228:U:H6	1.70	0.57
15:SO:93:VAL:H	15:SO:96:MET:HG3	1.69	0.57
76:10:74:U:H4'	76:10:91:U:N3	2.20	0.57
19:SS:82:ARG:HA	19:SS:85:GLU:OE2	2.05	0.56
22:SV:39:LYS:HE2	22:SV:44:LEU:HD21	1.87	0.56
22:SV:71:GLN:NE2	22:SV:73:ASP:OD2	2.38	0.56
36:LD:16:GLU:H	36:LD:176:GLN:HE22	1.50	0.56
4:SD:48:THR:OG1	4:SD:74:GLU:OE1	2.21	0.56
41:LI:35:ALA:HB1	80:14:38:A:H5''	1.87	0.56
77:11:12:U:H2'	77:11:13:C:C6	2.41	0.56
7:SG:23:ALA:HB2	7:SG:79:GLY:HA3	1.88	0.56
11:SK:24:GLN:HB2	11:SK:29:ALA:HB2	1.87	0.56
21:SU:37:GLU:HA	21:SU:40:LYS:HD3	1.87	0.56
33:LA:209:THR:HG21	80:14:2470:G:H4'	1.86	0.56
76:10:101:G:C2	76:10:155:G:H1'	2.39	0.56
77:11:1479:G:H2'	77:11:1480:A:C8	2.40	0.56
80:14:3281:G:H2'	80:14:3282:G:C8	2.40	0.56
24:SX:15:PHE:HZ	24:SX:132:LEU:HD23	1.70	0.56
43:LK:93:THR:HG22	43:LK:157:ARG:HH12	1.70	0.56
22:SV:75:VAL:O	22:SV:79:LYS:HG2	2.06	0.56
33:LA:145:GLU:CD	33:LA:145:GLU:H	2.13	0.56
76:10:81:U:H3'	76:10:82:C:C6	2.40	0.56
77:11:857:U:O4	77:11:858:A:N6	2.39	0.56
78:12:29:C:O2'	78:12:50:A:N1	2.35	0.56
2:SB:120:ARG:HG3	2:SB:120:ARG:HH11	1.70	0.56
76:10:98:G:C2	76:10:99:U:H1'	2.40	0.56
77:11:79:A:H2'	77:11:80:C:C6	2.41	0.56
22:SV:75:VAL:HG22	22:SV:79:LYS:HE3	1.87	0.56
33:LA:209:THR:HG21	80:14:2470:G:C4'	2.36	0.56
19:SS:155:LEU:HD11	19:SS:184:PHE:HD2	1.70	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:LE:37:LYS:HB2	37:LE:37:LYS:NZ	2.20	0.56
80:14:625:G:O2'	80:14:3265:A:N6	2.38	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
80:14:116:U:O2	80:14:119:G:H5''	2.06	0.56
80:14:1032:G:H2'	80:14:1033:G:H8	1.71	0.56
11:SK:75:ARG:HG2	11:SK:75:ARG:HH11	1.71	0.55
18:SR:118:LYS:HD2	18:SR:127:THR:HG21	1.88	0.55
43:LK:83:LEU:HD13	43:LK:88:LEU:HD23	1.88	0.55
80:14:537:U:H3	80:14:541:U:H1'	1.71	0.55
18:SR:185:THR:HG23	18:SR:188:THR:H	1.72	0.55
20:ST:34:ALA:HB2	20:ST:57:ARG:HD2	1.89	0.55
76:10:119:G:N3	76:10:119:G:H2'	2.20	0.55
77:11:411:A:H2'	77:11:412:C:H6	1.69	0.55
80:14:181:C:H2'	80:14:182:C:C6	2.41	0.55
80:14:3284:U:H2'	80:14:3285:A:C5	2.41	0.55
21:SU:52:LYS:NZ	77:11:1440:G:N7	2.54	0.55
17:SQ:67:GLN:OE1	17:SQ:69:GLN:NE2	2.39	0.55
26:SZ:6:VAL:CG2	26:SZ:33:ARG:HH21	2.18	0.55
33:LA:64:LYS:CB	33:LA:107:TYR:HA	2.36	0.55
36:LD:297:ILE:O	36:LD:303:GLN:NE2	2.39	0.55
63:Le:32:TYR:CE1	63:Le:57:ARG:HG3	2.41	0.55
76:10:150:G:O2'	80:14:2457:G:H5''	2.06	0.55
2:SB:96:ASN:HB2	2:SB:201:GLN:HE22	1.72	0.55
7:SG:114:ASP:OD2	7:SG:118:ARG:NH2	2.38	0.55
8:SH:25:ILE:HD12	8:SH:25:ILE:O	2.06	0.55
33:LA:72:GLN:HB3	33:LA:140:HIS:CE1	2.42	0.55
76:10:200:G:OP1	76:10:200:G:C4	2.59	0.55
21:SU:101:GLU:OE1	21:SU:102:PHE:N	2.40	0.55
24:SX:134:GLN:O	24:SX:138:ARG:HG3	2.06	0.55
48:LP:67:ARG:HD3	80:14:524:A:C6	2.41	0.55
77:11:781:C:OP2	77:11:782:C:N4	2.40	0.55
77:11:927:A:H2'	77:11:928:G:C8	2.42	0.55
17:SQ:187:ARG:NH2	77:11:756:A:OP2	2.40	0.55
31:Se:29:LYS:HG3	31:Se:30:PRO:HD2	1.87	0.55
36:LD:145:HIS:HD2	36:LD:182:ASP:OD2	1.89	0.55
76:10:189:C:H2'	76:10:190:C:C6	2.42	0.55
80:14:3166:C:H2'	80:14:3167:G:C8	2.41	0.55
5:SE:129:GLU:OE1	5:SE:210:ARG:NH1	2.40	0.55
16:SP:82:ARG:NH2	16:SP:191:GLU:OE1	2.39	0.55
76:10:185:U:H4'	76:10:186:U:H5	1.72	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:11:789:C:H3'	77:11:790:U:H5'	1.88	0.55
10:SJ:50:VAL:HG13	10:SJ:97:ASP:H	1.72	0.54
43:LK:22:ARG:HB3	43:LK:28:THR:HG22	1.89	0.54
53:LU:28:TRP:O	53:LU:32:GLN:NE2	2.40	0.54
76:10:82:C:H2'	76:10:83:C:C6	2.41	0.54
17:SQ:212:ASP:OD1	17:SQ:213:ALA:N	2.38	0.54
21:SU:106:TYR:CD1	21:SU:107:LEU:HD13	2.42	0.54
21:SU:107:LEU:HB2	21:SU:109:LEU:HD21	1.90	0.54
37:LE:51:LYS:HG2	37:LE:64:ASN:HA	1.89	0.54
55:LW:126:LYS:HG2	55:LW:131:VAL:HG21	1.90	0.54
17:SQ:3:ARG:HB3	77:11:94:A:H1'	1.89	0.54
36:LD:329:VAL:HA	36:LD:332:LYS:HB2	1.88	0.54
80:14:764:G:H2'	80:14:765:A:C8	2.43	0.54
24:SX:53:TRP:HA	24:SX:56:ILE:HD12	1.90	0.54
55:LW:5:LYS:NZ	55:LW:5:LYS:HB3	2.23	0.54
77:11:974:A:H2	80:14:856:A:N1	2.06	0.54
77:11:1174:A:H2'	77:11:1175:G:H8	1.72	0.54
80:14:2372:G:H2'	80:14:2373:G:C8	2.42	0.54
80:14:3018:A:H2'	80:14:3019:A:C8	2.42	0.54
36:LD:87:THR:HG22	80:14:352:A:N1	2.23	0.54
45:LM:147:VAL:O	45:LM:151:ILE:HG13	2.08	0.54
22:SV:28:MET:SD	22:SV:28:MET:N	2.81	0.54
76:10:69:A:H3'	76:10:70:G:H8	1.72	0.54
33:LA:111:LEU:HD23	33:LA:136:SER:OG	2.07	0.54
37:LE:163:LYS:NZ	37:LE:163:LYS:HB3	2.22	0.54
52:LT:71:LEU:O	52:LT:75:MET:HG3	2.07	0.54
60:Lb:4:PHE:O	60:Lb:9:LYS:HD2	2.08	0.54
24:SX:75:GLY:O	24:SX:79:ILE:HG13	2.08	0.54
48:LP:10:GLU:O	48:LP:14:LYS:HG3	2.07	0.54
77:11:782:C:O2'	77:11:783:U:O4'	2.23	0.54
18:SR:196:ILE:O	18:SR:200:LYS:HG2	2.08	0.54
22:SV:50:GLU:HA	22:SV:53:LYS:HZ2	1.72	0.54
23:SW:32:LYS:HG3	23:SW:47:ARG:HD3	1.89	0.54
33:LA:30:GLU:HB2	33:LA:172:LEU:CD1	2.38	0.54
48:LP:41:ARG:HH11	48:LP:44:ILE:HD11	1.73	0.54
70:Ll:30:ASP:OD1	70:Ll:30:ASP:N	2.40	0.54
77:11:523:A:H2'	77:11:524:A:C8	2.43	0.54
20:ST:90:GLU:OE2	80:14:2110:A:O2'	2.26	0.53
22:SV:49:HIS:C	22:SV:53:LYS:HZ2	2.16	0.53
23:SW:78:ARG:O	23:SW:82:MET:HB2	2.07	0.53
26:SZ:99:ASP:OD1	26:SZ:100:THR:N	2.41	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:11:1671:C:H2'	77:11:1672:C:C6	2.43	0.53
3:SC:60:MET:HE1	3:SC:70:ARG:HH22	1.71	0.53
11:SK:89:ASP:OD1	11:SK:90:TYR:N	2.41	0.53
32:Sf:105:PHE:HA	32:Sf:118:ARG:NH1	2.23	0.53
77:11:128:G:H1'	77:11:177:C:H42	1.73	0.53
77:11:1235:U:H2'	77:11:1236:G:C8	2.44	0.53
80:14:2774:A:O2'	80:14:2775:C:H5''	2.09	0.53
17:SQ:19:MET:SD	17:SQ:108:ARG:HD2	2.48	0.53
33:LA:4:LYS:CE	33:LA:198:TRP:CB	2.87	0.53
50:LR:205:MET:O	50:LR:208:SER:OG	2.20	0.53
70:Ll:3:LYS:HD2	70:Ll:41:TYR:CD2	2.44	0.53
77:11:193:G:O2'	77:11:194:A:H8	1.91	0.53
80:14:1680:A:H2	80:14:1696:G:H22	1.56	0.53
56:LX:157:LYS:HG3	56:LX:159:ARG:HD3	1.91	0.53
77:11:1434:G:H2'	77:11:1435:U:C6	2.44	0.53
7:SG:57:GLU:OE1	7:SG:89:ARG:NH1	2.41	0.53
17:SQ:181:VAL:HG12	17:SQ:227:THR:HA	1.90	0.53
18:SR:169:LYS:NZ	77:11:70:C:OP1	2.30	0.53
80:14:2476:A:H3'	80:14:2477:A:H8	1.73	0.53
80:14:3018:A:H2'	80:14:3019:A:H8	1.74	0.53
6:SF:26:MET:HE1	6:SF:60:LYS:HD3	1.91	0.53
43:LK:122:ASN:OD1	43:LK:122:ASN:N	2.41	0.53
77:11:1223:C:H2'	77:11:1224:A:H8	1.74	0.53
80:14:437:G:O6	80:14:633:G:H1'	2.09	0.53
80:14:1215:A:H2'	80:14:1216:A:C8	2.44	0.53
80:14:1819:A:C2'	80:14:1822:G:H21	2.22	0.53
80:14:3307:A:O2'	80:14:3308:A:OP1	2.26	0.53
82:16:17:H2U:H5'	82:16:60:A:H2	1.73	0.53
23:SW:79:GLU:O	23:SW:82:MET:N	2.41	0.53
49:LQ:34:LYS:O	49:LQ:39:GLY:N	2.30	0.53
80:14:3157:C:H2'	80:14:3158:C:H6	1.73	0.53
2:SB:214:HIS:O	23:SW:20:TYR:OH	2.21	0.53
17:SQ:97:GLU:C	17:SQ:98:ASN:HD22	2.16	0.53
49:LQ:33:ILE:HD13	80:14:585:C:C4	2.43	0.53
77:11:141:G:H2'	77:11:142:G:C8	2.44	0.53
15:SO:134:LYS:NZ	77:11:1185:U:OP1	2.42	0.53
19:SS:157:PRO:O	19:SS:160:ARG:HB2	2.08	0.53
67:Li:76:ARG:NH1	80:14:1643:C:OP2	2.28	0.53
69:Lk:17:THR:HG23	69:Lk:29:ILE:HD11	1.90	0.53
80:14:2379:G:H2'	80:14:2380:G:C8	2.44	0.53
18:SR:166:PHE:CE2	77:11:68:A:H5'	2.44	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:SR:200:LYS:HA	18:SR:203:ILE:HG22	1.91	0.52
18:SR:13:GLN:O	18:SR:14:LYS:HE2	2.10	0.52
18:SR:14:LYS:HE2	18:SR:14:LYS:HA	1.91	0.52
35:LC:139:THR:O	35:LC:143:LYS:NZ	2.42	0.52
38:LF:143:VAL:HB	38:LF:146:GLU:HG3	1.89	0.52
43:LK:76:ALA:HB3	43:LK:109:VAL:HG22	1.91	0.52
77:11:648:U:O2	77:11:688:G:O6	2.27	0.52
80:14:138:U:H2'	80:14:139:C:C6	2.44	0.52
23:SW:18:GLU:OE2	23:SW:19:ARG:HG2	2.10	0.52
37:LE:112:ILE:HG21	37:LE:118:TYR:HB2	1.91	0.52
24:SX:97:SER:OG	77:11:1511:C:OP1	2.26	0.52
42:LJ:184:TYR:HE1	42:LJ:219:VAL:HG11	1.74	0.52
49:LQ:106:LEU:HD13	49:LQ:149:VAL:HG11	1.91	0.52
52:LT:117:ARG:HG2	52:LT:117:ARG:HH11	1.73	0.52
76:10:113:G:H2'	76:10:114:C:O4'	2.09	0.52
11:SK:12:ILE:HG21	37:LE:118:TYR:HB3	1.92	0.52
12:SL:22:ARG:NH1	12:SL:36:LEU:O	2.43	0.52
17:SQ:129:VAL:HG12	17:SQ:139:LEU:HB3	1.92	0.52
42:LJ:184:TYR:CE1	42:LJ:219:VAL:HG11	2.45	0.52
48:LP:167:SER:O	48:LP:171:GLN:HG3	2.08	0.52
80:14:3225:C:H2'	80:14:3226:A:C8	2.43	0.52
17:SQ:115:ARG:HA	17:SQ:115:ARG:NH1	2.25	0.52
46:LN:87:GLU:H	46:LN:87:GLU:CD	2.18	0.52
57:LY:150:THR:HG22	57:LY:151:PRO:O	2.10	0.52
76:10:188:C:H3'	76:10:189:C:C6	2.44	0.52
77:11:193:G:O2'	77:11:194:A:O5'	2.27	0.52
80:14:2263:U:O2'	80:14:2264:G:H8	1.93	0.52
28:Sb:37:LYS:HG2	28:Sb:72:GLN:HG2	1.91	0.52
34:LB:147:ARG:HG2	34:LB:157:ILE:HG12	1.92	0.52
69:Lk:76:THR:HG22	69:Lk:79:ARG:HB3	1.92	0.52
76:10:74:U:H5''	76:10:93:G:O2'	2.09	0.52
77:11:1364:U:H3	77:11:1367:C:H41	1.57	0.52
80:14:1550:U:O4	80:14:1563:G:O2'	2.27	0.52
3:SC:69:PRO:HA	3:SC:72:ILE:HD12	1.92	0.52
3:SC:112:GLN:NE2	3:SC:128:ARG:HB2	2.24	0.52
5:SE:78:LEU:HD12	5:SE:157:ILE:HG23	1.91	0.52
7:SG:44:GLU:OE1	7:SG:44:GLU:O	2.28	0.52
10:SJ:52:GLU:OE1	10:SJ:70:ARG:NH1	2.43	0.52
60:Lb:99:VAL:HG21	60:Lb:109:ALA:HB2	1.92	0.52
76:10:139:A:H2'	76:10:140:U:O4'	2.10	0.52
33:LA:4:LYS:CE	33:LA:198:TRP:HB3	2.38	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:LQ:36:LYS:HD2	80:14:586:G:H4'	1.91	0.52
61:Lc:76:LYS:NZ	61:Lc:77:LYS:HD2	2.25	0.52
80:14:609:G:H2'	80:14:610:C:C6	2.45	0.52
82:16:20:A:N6	82:16:57:G:N3	2.57	0.52
17:SQ:19:MET:HE3	77:11:792:U:C4	2.45	0.52
31:Se:27:LYS:HD3	31:Se:28:LYS:N	2.25	0.52
33:LA:32:ILE:CD1	33:LA:179:ILE:HD13	2.40	0.52
43:LK:277:LYS:O	43:LK:281:ILE:HG13	2.09	0.52
49:LQ:21:ARG:NH1	80:14:581:C:OP2	2.43	0.52
77:11:1055:U:H2'	77:11:1056:G:C8	2.45	0.52
4:SD:242:GLU:CD	4:SD:242:GLU:H	2.18	0.51
1:SA:36:ARG:O	1:SA:53:LYS:NZ	2.41	0.51
9:SI:98:ALA:H	9:SI:132:THR:HB	1.75	0.51
33:LA:49:PHE:CD2	33:LA:159:LEU:HB2	2.45	0.51
77:11:117:U:H2'	77:11:118:U:C6	2.44	0.51
77:11:1455:U:H2'	77:11:1456:C:H6	1.74	0.51
53:LU:2:GLY:O	68:Lj:39:ARG:NH2	2.43	0.51
77:11:68:A:H5''	77:11:69:A:C5'	2.40	0.51
43:LK:222:PHE:O	43:LK:226:ILE:HG13	2.11	0.51
50:LR:114:GLU:OE2	50:LR:119:THR:OG1	2.25	0.51
59:La:5:THR:HG23	59:La:15:ILE:O	2.10	0.51
76:10:83:C:H2'	76:10:84:A:O4'	2.11	0.51
1:SA:52:GLY:O	1:SA:56:GLU:HG2	2.10	0.51
5:SE:137:ALA:O	81:15:31:A:N6	2.44	0.51
18:SR:10:THR:HG21	18:SR:127:THR:HA	1.92	0.51
30:Sd:22:GLN:HG2	30:Sd:23:VAL:HG23	1.93	0.51
40:LH:96:MET:HE2	59:La:22:ARG:HH11	1.76	0.51
56:LX:9:TYR:CE1	56:LX:65:GLU:HG3	2.46	0.51
5:SE:110:THR:O	5:SE:111:ASP:OD1	2.29	0.51
16:SP:168:MET:O	16:SP:172:MET:HG3	2.10	0.51
36:LD:272:ASP:OD1	36:LD:272:ASP:N	2.36	0.51
53:LU:99:ARG:HG2	53:LU:167:ALA:HB2	1.91	0.51
53:LU:121:ILE:HG21	53:LU:131:GLU:HG3	1.92	0.51
80:14:3270:C:O2'	80:14:3271:A:H8	1.93	0.51
61:Lc:62:GLU:HG3	61:Lc:63:GLY:H	1.75	0.51
76:10:191:C:H2'	76:10:192:C:O4'	2.11	0.51
80:14:853:A:H2'	80:14:854:G:C8	2.46	0.51
24:SX:15:PHE:CZ	24:SX:132:LEU:HD23	2.45	0.51
33:LA:18:LYS:HD2	33:LA:176:GLU:HG2	1.92	0.51
36:LD:303:GLN:HG3	48:LP:18:ARG:HH12	1.76	0.51
68:Lj:30:SER:O	68:Lj:33:LYS:HG2	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:SU:107:LEU:HB2	21:SU:109:LEU:CD2	2.41	0.51
38:LF:93:TYR:CE2	38:LF:187:LYS:HG2	2.45	0.51
76:10:76:U:C4	76:10:78:C:H3'	2.46	0.51
76:10:148:C:H4'	76:10:162:A:N7	2.25	0.51
76:10:184:G:H1'	76:10:196:A:H5'	1.92	0.51
76:10:200:G:H1'	76:10:201:C:H42	1.75	0.51
77:11:1225:U:H2'	77:11:1226:A:H8	1.76	0.51
77:11:1612:C:H2'	77:11:1613:G:C8	2.45	0.51
80:14:2268:C:C2'	80:14:2269:U:H5'	2.41	0.51
19:SS:100:ARG:HH21	77:11:859:A:P	2.34	0.50
32:Sf:126:CYS:SG	32:Sf:144:CYS:HB3	2.50	0.50
52:LT:117:ARG:HG2	52:LT:117:ARG:NH1	2.26	0.50
61:Lc:139:LYS:HB3	61:Lc:141:ARG:HG3	1.93	0.50
80:14:3072:A:H2'	80:14:3073:A:C8	2.46	0.50
56:LX:29:MET:HG3	56:LX:43:PHE:CD1	2.46	0.50
65:Lg:106:ARG:NH2	80:14:1423:G:OP1	2.44	0.50
35:LC:220:ILE:HD12	35:LC:283:LYS:HG3	1.92	0.50
43:LK:83:LEU:HB3	43:LK:88:LEU:HB3	1.93	0.50
61:Lc:77:LYS:HG3	61:Lc:80:LYS:HG3	1.94	0.50
76:10:69:A:H2'	76:10:70:G:O4'	2.12	0.50
14:SN:126:ILE:HG22	14:SN:140:VAL:HA	1.92	0.50
26:SZ:57:ILE:HD12	26:SZ:77:ILE:HG22	1.92	0.50
33:LA:101:LYS:HZ1	80:14:2490:A:P	2.34	0.50
76:10:79:C:H2'	76:10:80:C:C6	2.46	0.50
80:14:569:U:O2'	80:14:570:G:H5'	2.11	0.50
4:SD:252:GLU:HG2	4:SD:253:TYR:CD1	2.46	0.50
5:SE:34:GLN:OE1	5:SE:34:GLN:N	2.45	0.50
23:SW:2:GLY:N	77:11:1419:U:OP1	2.44	0.50
76:10:67:A:C2'	76:10:68:U:H5'	2.41	0.50
77:11:16:G:H2'	77:11:17:C:C6	2.47	0.50
1:SA:85:ARG:HD2	23:SW:82:MET:HE1	1.94	0.50
9:SI:116:ARG:NH2	28:Sb:48:ALA:O	2.45	0.50
33:LA:4:LYS:CD	33:LA:198:TRP:CB	2.81	0.50
50:LR:145:GLN:HG3	50:LR:197:THR:O	2.12	0.50
53:LU:19:MET:HE2	53:LU:19:MET:HA	1.94	0.50
80:14:3380:C:H2'	80:14:3381:U:C6	2.46	0.50
6:SF:107:SER:HB3	77:11:806:G:H21	1.77	0.50
8:SH:29:SER:OG	8:SH:31:ASN:OD1	2.24	0.50
16:SP:72:ASP:O	16:SP:75:LYS:NZ	2.45	0.50
20:ST:161:ARG:NH2	77:11:184:C:OP1	2.38	0.50
21:SU:96:THR:O	21:SU:100:ILE:HG22	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:11:1349:C:H41	77:11:1378:C:H5	1.60	0.50
35:LC:103:ASN:ND2	35:LC:149:GLN:HG2	2.23	0.50
36:LD:368:LYS:HD3	80:14:549:U:H5''	1.94	0.50
49:LQ:204:GLU:OE2	49:LQ:210:LYS:HD2	2.12	0.50
79:13:133:G:H2'	79:13:134:G:H8	1.76	0.50
80:14:709:G:H4'	80:14:710:U:H5'	1.94	0.50
72:Ln:97:ARG:NH1	80:14:2850:A:OP2	2.44	0.50
77:11:68:A:H5''	77:11:69:A:H5''	1.94	0.50
77:11:1356:U:H2'	77:11:1357:G:H8	1.77	0.50
80:14:855:G:N2	80:14:858:A:OP2	2.25	0.50
23:SW:74:GLN:HE21	23:SW:78:ARG:HG3	1.77	0.49
24:SX:109:GLN:HG3	24:SX:114:VAL:HG23	1.95	0.49
33:LA:5:LEU:HB3	33:LA:198:TRP:HH2	1.76	0.49
33:LA:196:LYS:HB2	33:LA:200:ASN:OD1	2.12	0.49
34:LB:183:GLY:HA2	80:14:906:A:H5''	1.93	0.49
55:LW:163:ARG:N	77:11:819:G:H22	2.10	0.49
80:14:1:G:H2'	80:14:2:C:H6	1.75	0.49
82:16:26:M2G:HM22	82:16:44:A:H2	1.77	0.49
11:SK:65:ASP:O	11:SK:69:VAL:HG12	2.12	0.49
17:SQ:3:ARG:HG2	77:11:403:A:H4'	1.93	0.49
26:SZ:38:LYS:HG2	77:11:525:U:OP1	2.12	0.49
34:LB:170:ALA:CB	75:Lq:65:VAL:HG12	2.42	0.49
36:LD:287:LYS:NZ	54:LV:23:ASP:OD2	2.44	0.49
56:LX:35:ASN:HB2	56:LX:38:ARG:HG3	1.93	0.49
58:LZ:100:ARG:HE	58:LZ:102:ILE:HD11	1.77	0.49
1:SA:84:GLN:O	1:SA:87:VAL:HG22	2.12	0.49
6:SF:14:MET:HE2	6:SF:27:ILE:HD11	1.95	0.49
19:SS:101:ILE:O	19:SS:103:ARG:NH1	2.45	0.49
20:ST:174:GLN:HE22	20:ST:181:LEU:HB2	1.77	0.49
32:Sf:98:VAL:HG21	32:Sf:101:ALA:HB2	1.93	0.49
36:LD:314:ASN:OD1	80:14:1357:G:N2	2.45	0.49
44:LL:7:GLU:HG3	44:LL:8:PRO:HD2	1.93	0.49
48:LP:11:SER:HB2	80:14:1361:A:O2'	2.13	0.49
75:Lq:16:THR:HG22	80:14:1933:G:C8	2.48	0.49
76:10:146:C:C4	76:10:147:G:C8	3.00	0.49
80:14:3157:C:H2'	80:14:3158:C:C6	2.48	0.49
1:SA:27:THR:HG22	1:SA:28:LYS:H	1.77	0.49
10:SJ:65:ILE:HD12	10:SJ:65:ILE:O	2.13	0.49
20:ST:74:THR:CG2	77:11:260:A:H1'	2.43	0.49
23:SW:27:ASP:O	23:SW:31:ASN:ND2	2.35	0.49
48:LP:17:LYS:NZ	48:LP:21:GLU:OE2	2.44	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:LW:162:ARG:NH2	77:11:852:C:OP1	2.42	0.49
58:LZ:30:GLU:HA	58:LZ:30:GLU:OE1	2.12	0.49
70:Ll:14:THR:O	70:Ll:17:ARG:HG2	2.13	0.49
76:10:61:U:OP2	76:10:62:A:N6	2.46	0.49
76:10:74:U:H4'	76:10:91:U:C4	2.46	0.49
77:11:1227:G:H2'	77:11:1228:U:C6	2.46	0.49
77:11:1578:G:O2'	77:11:1579:A:OP2	2.26	0.49
11:SK:77:PHE:C	11:SK:78:LYS:HD3	2.37	0.49
20:ST:85:ASN:HD22	20:ST:88:ASN:H	1.59	0.49
25:SY:70:ARG:NH1	29:Sc:6:ASP:OD1	2.45	0.49
31:Se:27:LYS:HD3	31:Se:28:LYS:H	1.77	0.49
77:11:1204:G:N2	77:11:1606:A:H5'	2.27	0.49
77:11:1570:U:H2'	77:11:1571:C:C6	2.48	0.49
80:14:2549:C:H2'	80:14:2550:C:C6	2.47	0.49
22:SV:74:TYR:O	22:SV:77:LEU:HD12	2.12	0.49
33:LA:147:LYS:O	33:LA:150:GLU:HB3	2.12	0.49
36:LD:333:LEU:HD22	48:LP:181:ILE:HD12	1.94	0.49
37:LE:117:LYS:NZ	37:LE:117:LYS:HB3	2.27	0.49
50:LR:235:GLY:O	50:LR:239:GLN:HG3	2.13	0.49
80:14:246:C:H5'	80:14:247:C:H5'	1.94	0.49
2:SB:66:GLY:O	2:SB:69:ILE:HG22	2.13	0.49
24:SX:127:ASN:HA	24:SX:130:ARG:HH12	1.78	0.49
77:11:1262:C:H2'	77:11:1263:U:H6	1.76	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
2:SB:141:VAL:HG22	2:SB:187:ILE:HG22	1.95	0.49
15:SO:88:ARG:HB3	15:SO:124:ALA:HB2	1.95	0.49
22:SV:131:THR:HG23	22:SV:133:GLY:H	1.78	0.49
33:LA:53:VAL:O	33:LA:155:ILE:N	2.41	0.49
36:LD:142:ALA:HB1	61:Lc:17:ASN:HB2	1.95	0.49
45:LM:69:LEU:HD23	45:LM:69:LEU:HA	1.72	0.49
69:Lk:77:ASN:OD1	69:Lk:77:ASN:O	2.31	0.49
77:11:594:A:H2'	77:11:595:A:C8	2.48	0.49
77:11:1680:U:H2'	77:11:1681:G:C8	2.48	0.49
1:SA:130:ASP:O	1:SA:134:ILE:HG13	2.13	0.49
18:SR:63:MET:SD	18:SR:108:LEU:HD11	2.53	0.49
19:SS:17:THR:OG1	19:SS:18:GLU:N	2.46	0.49
33:LA:54:LYS:HG3	33:LA:153:ALA:HB3	1.95	0.49
41:LI:2:THR:HG22	41:LI:4:ARG:HG2	1.95	0.49
42:LJ:216:LEU:HD12	43:LK:284:LEU:HD13	1.94	0.49
58:LZ:43:LEU:O	58:LZ:47:ILE:HG13	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:Lc:74:LYS:O	61:Lc:78:GLN:NE2	2.45	0.49
77:11:184:C:H2'	77:11:185:G:O4'	2.12	0.49
77:11:1250:U:H2'	77:11:1251:C:H6	1.78	0.49
80:14:3224:U:H2'	80:14:3225:C:C6	2.47	0.49
11:SK:12:ILE:HD11	11:SK:19:ASN:HB3	1.95	0.49
15:SO:62:ALA:HA	15:SO:65:LYS:HE3	1.95	0.49
76:10:129:U:H2'	76:10:130:A:C1'	2.42	0.49
77:11:183:C:H2'	77:11:184:C:H6	1.76	0.49
77:11:610:G:H5'	77:11:616:G:N2	2.28	0.49
77:11:776:G:N2	77:11:778:A:H1'	2.28	0.49
77:11:1570:U:H2'	77:11:1571:C:H6	1.78	0.49
80:14:92:G:H2'	80:14:93:A:C8	2.48	0.49
80:14:3158:C:H2'	80:14:3159:C:C6	2.48	0.49
18:SR:69:THR:O	18:SR:101:GLY:HA3	2.12	0.48
20:ST:62:ASP:OD1	20:ST:62:ASP:N	2.44	0.48
33:LA:38:LEU:HA	33:LA:200:ASN:O	2.13	0.48
76:10:74:U:O4'	76:10:93:G:H1'	2.13	0.48
80:14:3169:U:H5	80:14:3172:C:OP2	1.96	0.48
2:SB:60:ASN:OD1	2:SB:60:ASN:N	2.43	0.48
19:SS:19:PHE:HE2	19:SS:51:GLN:HB2	1.78	0.48
43:LK:264:LYS:HG2	43:LK:265:ARG:H	1.77	0.48
53:LU:168:GLY:HA2	53:LU:171:TYR:CE2	2.49	0.48
59:La:48:PRO:HB2	59:La:56:MET:HE3	1.95	0.48
63:Le:32:TYR:OH	63:Le:60:GLU:OE1	2.31	0.48
76:10:132:G:H3'	76:10:133:G:N2	2.28	0.48
77:11:1597:C:H2'	77:11:1598:G:H8	1.78	0.48
80:14:1748:G:H2'	80:14:1749:G:H8	1.78	0.48
15:SO:103:ILE:HD13	15:SO:123:LEU:HB3	1.94	0.48
18:SR:164:ARG:NH2	77:11:68:A:OP1	2.46	0.48
80:14:978:G:H2'	80:14:979:C:C6	2.48	0.48
80:14:1700:A:H2'	80:14:1701:A:C8	2.48	0.48
22:SV:51:GLY:HA2	22:SV:54:VAL:HG12	1.94	0.48
43:LK:105:LEU:O	43:LK:109:VAL:HG23	2.13	0.48
43:LK:270:LYS:HG2	78:12:60:G:H5''	1.93	0.48
53:LU:176:GLY:O	53:LU:185:ARG:NH2	2.46	0.48
64:Lf:113:THR:O	80:14:3377:U:O2'	2.30	0.48
76:10:132:G:O5'	76:10:133:G:N2	2.45	0.48
77:11:588:A:H2'	77:11:589:G:H8	1.78	0.48
78:12:24:C:H2'	78:12:25:G:O4'	2.13	0.48
80:14:802:C:H2'	80:14:803:C:C6	2.48	0.48
27:Sa:86:ARG:HG3	27:Sa:86:ARG:HH11	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:LJ:153:ARG:O	42:LJ:156:LYS:HB2	2.13	0.48
60:Lb:60:LYS:HE2	60:Lb:64:LYS:HE2	1.95	0.48
76:10:56:U:C2	76:10:63:A:H2	2.30	0.48
76:10:179:C:H2'	76:10:180:C:C6	2.49	0.48
77:11:1173:G:C2	77:11:1174:A:C8	3.01	0.48
4:SD:164:VAL:HG11	4:SD:179:MET:HE3	1.95	0.48
5:SE:173:LYS:NZ	5:SE:181:ASP:OD2	2.40	0.48
7:SG:57:GLU:OE2	7:SG:119:TYR:OH	2.26	0.48
19:SS:30:MET:SD	19:SS:83:GLU:HB3	2.54	0.48
22:SV:45:ALA:HB1	22:SV:50:GLU:OE2	2.13	0.48
22:SV:46:ARG:HE	22:SV:104:LEU:HD21	1.78	0.48
38:LF:118:ARG:HG2	38:LF:126:VAL:HG12	1.96	0.48
76:10:66:C:H2'	76:10:67:A:O4'	2.12	0.48
76:10:72:G:O3'	76:10:90:A:N6	2.46	0.48
76:10:123:A:H2'	76:10:124:A:O4'	2.14	0.48
76:10:184:G:H1'	76:10:196:A:C5'	2.44	0.48
80:14:2512:U:H2'	80:14:2513:U:C6	2.48	0.48
80:14:2750:A:H2'	80:14:2751:A:C8	2.49	0.48
19:SS:34:ASN:OD1	19:SS:34:ASN:N	2.45	0.48
33:LA:5:LEU:HD22	33:LA:187:VAL:HG11	1.95	0.48
33:LA:68:LEU:O	33:LA:112:ALA:HA	2.14	0.48
45:LM:103:ASP:OD1	45:LM:103:ASP:N	2.46	0.48
48:LP:142:LYS:O	48:LP:146:GLU:HG3	2.14	0.48
80:14:1145:G:O2'	80:14:2645:A:N3	2.45	0.48
80:14:2446:A:H3'	80:14:2447:C:H6	1.79	0.48
6:SF:32:LYS:O	6:SF:36:LYS:HG2	2.14	0.48
32:Sf:132:MET:HE3	32:Sf:139:HIS:HB2	1.94	0.48
36:LD:309:ILE:HG22	48:LP:22:TRP:CZ3	2.49	0.48
39:LG:17:ARG:HA	39:LG:45:GLU:HB2	1.96	0.48
48:LP:41:ARG:HH21	80:14:579:A:H4'	1.77	0.48
49:LQ:34:LYS:NZ	80:14:608:U:OP1	2.47	0.48
76:10:86:U:O3'	76:10:87:U:H4'	2.13	0.48
76:10:161:A:H4'	76:10:162:A:OP1	2.14	0.48
77:11:65:A:O2'	77:11:66:U:H5''	2.14	0.48
77:11:504:U:H2'	77:11:505:G:C8	2.49	0.48
80:14:955:C:H2'	80:14:956:C:H6	1.78	0.48
1:SA:198:MET:HE3	1:SA:200:ASP:OD1	2.13	0.48
9:SI:33:PHE:HB3	9:SI:40:PHE:HB2	1.96	0.48
11:SK:16:GLN:HE21	11:SK:68:MET:CE	2.27	0.48
32:Sf:83:LYS:NZ	32:Sf:85:TYR:OH	2.38	0.48
38:LF:61:ASP:N	38:LF:61:ASP:OD1	2.44	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:LT:45:ARG:HE	56:LX:72:THR:HG22	1.79	0.48
76:10:124:A:H2'	76:10:125:U:C2	2.48	0.48
77:11:1463:G:O2'	77:11:1464:C:OP1	2.22	0.48
80:14:2574:U:H4'	80:14:2575:G:N7	2.28	0.48
11:SK:130:ARG:NH2	77:11:1176:C:OP1	2.47	0.48
31:Se:33:ARG:HE	31:Se:33:ARG:HB3	1.29	0.48
33:LA:56:PRO:HD3	33:LA:185:MET:SD	2.54	0.48
36:LD:335:PRO:HD3	48:LP:41:ARG:HH12	1.78	0.48
39:LG:59:TYR:OH	39:LG:78:PHE:O	2.30	0.48
77:11:1479:G:H2'	77:11:1480:A:H8	1.78	0.48
80:14:2508:G:H2'	80:14:2509:U:C6	2.49	0.48
28:Sb:89:VAL:HG23	77:11:1634:U:OP1	2.14	0.47
33:LA:45:LYS:HE3	33:LA:45:LYS:HB2	1.51	0.47
34:LB:42:LYS:HG3	34:LB:89:TYR:CE2	2.49	0.47
77:11:304:A:H2'	77:11:305:A:C8	2.49	0.47
77:11:776:G:H21	77:11:778:A:H1'	1.79	0.47
77:11:1686:G:H1'	77:11:1729:A:N6	2.29	0.47
80:14:897:G:H2'	80:14:898:U:C6	2.49	0.47
82:16:18:G:N2	82:16:57:G:H2'	2.29	0.47
3:SC:65:ASP:OD1	3:SC:66:GLU:N	2.45	0.47
26:SZ:55:ASN:HB3	26:SZ:98:LEU:HD21	1.95	0.47
71:Lm:36:ARG:HH22	80:14:399:G:H1'	1.80	0.47
77:11:323:U:H4'	77:11:327:A:C8	2.49	0.47
77:11:510:U:H2'	77:11:511:U:C6	2.49	0.47
2:SB:8:ILE:HD13	2:SB:13:LYS:HB2	1.96	0.47
3:SC:39:ARG:HG2	3:SC:43:GLU:OE2	2.14	0.47
5:SE:45:THR:O	5:SE:45:THR:OG1	2.30	0.47
19:SS:100:ARG:NH2	77:11:859:A:OP1	2.45	0.47
35:LC:92:TYR:HB2	35:LC:159:VAL:HG22	1.95	0.47
55:LW:136:ARG:O	55:LW:140:GLU:HG3	2.14	0.47
76:10:57:A:H1'	76:10:63:A:H1'	1.95	0.47
80:14:1059:A:N3	80:14:2636:U:O2'	2.46	0.47
80:14:3133:U:H2'	80:14:3134:C:C6	2.49	0.47
80:14:3170:U:H1'	80:14:3273:C:O2	2.14	0.47
82:16:23:C:O2'	82:16:24:G:H8	1.97	0.47
1:SA:40:LYS:HA	1:SA:40:LYS:HD2	1.70	0.47
57:LY:109:MET:HE2	80:14:1075:G:N7	2.29	0.47
59:La:9:ARG:HH22	59:La:29:GLN:HE22	1.62	0.47
80:14:1045:U:H2'	80:14:1046:C:C6	2.49	0.47
80:14:1921:A:H2'	80:14:1922:U:C6	2.49	0.47
80:14:3271:A:H1'	80:14:3272:U:H5'	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:SB:58:THR:H	2:SB:93:LYS:NZ	2.10	0.47
22:SV:126:ASP:OD1	22:SV:128:GLY:N	2.42	0.47
76:10:99:U:H2'	76:10:100:U:C5	2.49	0.47
76:10:193:G:N2	76:10:196:A:OP2	2.45	0.47
77:11:1463:G:N3	77:11:1463:G:H2'	2.29	0.47
80:14:3164:U:H2'	80:14:3165:C:C6	2.49	0.47
26:SZ:22:LYS:HB2	26:SZ:77:ILE:CG1	2.44	0.47
36:LD:109:LYS:HG2	36:LD:111:TRP:CZ2	2.50	0.47
1:SA:19:LEU:HD11	23:SW:106:LEU:HD21	1.97	0.47
11:SK:48:ALA:HB2	11:SK:70:VAL:HG21	1.95	0.47
11:SK:91:LYS:NZ	11:SK:91:LYS:HB3	2.30	0.47
20:ST:171:ILE:HD11	20:ST:200:GLU:HG2	1.97	0.47
22:SV:71:GLN:NE2	22:SV:73:ASP:CG	2.73	0.47
22:SV:94:ASN:OD1	22:SV:97:THR:N	2.35	0.47
24:SX:15:PHE:HA	24:SX:139:ILE:HD11	1.97	0.47
24:SX:130:ARG:O	24:SX:134:GLN:HG3	2.14	0.47
36:LD:361:LYS:HA	36:LD:361:LYS:HD3	1.54	0.47
42:LJ:38:MET:HE3	42:LJ:41:LYS:HG2	1.97	0.47
42:LJ:162:ARG:HG3	42:LJ:162:ARG:HH11	1.79	0.47
48:LP:178:ILE:HG23	48:LP:183:ASP:HB3	1.96	0.47
65:Lg:107:LYS:O	65:Lg:111:GLU:OE1	2.32	0.47
75:Lq:36:LYS:HG3	75:Lq:48:LYS:HE2	1.96	0.47
76:10:61:U:H4'	76:10:62:A:OP1	2.14	0.47
77:11:69:A:H2'	77:11:70:C:C6	2.48	0.47
77:11:597:A:H4'	77:11:598:G:H5'	1.97	0.47
77:11:1263:U:H2'	77:11:1264:A:H8	1.79	0.47
77:11:1585:U:H2'	77:11:1586:C:C6	2.49	0.47
79:13:135:C:H2'	79:13:136:C:C6	2.49	0.47
80:14:1084:G:H2'	80:14:1085:C:C6	2.50	0.47
80:14:1131:A:H2'	80:14:1132:U:H6	1.79	0.47
80:14:2904:G:O2'	80:14:3026:A:N1	2.46	0.47
80:14:3272:U:HO2'	80:14:3273:C:H6	1.61	0.47
3:SC:159:ASP:OD1	3:SC:160:PHE:N	2.47	0.47
22:SV:73:ASP:O	22:SV:77:LEU:HG	2.15	0.47
24:SX:43:LEU:HA	24:SX:84:GLN:HG3	1.97	0.47
55:LW:163:ARG:HA	77:11:819:G:N2	2.29	0.47
76:10:161:A:H1'	76:10:162:A:H5'	1.96	0.47
77:11:864:U:H2'	77:11:865:A:O4'	2.15	0.47
77:11:1030:A:OP1	77:11:1797:G:O2'	2.33	0.47
80:14:855:G:O2'	80:14:856:A:N7	2.36	0.47
80:14:859:C:H2'	80:14:860:U:H6	1.76	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:SB:178:ILE:HG22	2:SB:180:MET:HG2	1.97	0.47
6:SF:26:MET:CE	6:SF:60:LYS:HD3	2.45	0.47
22:SV:73:ASP:O	22:SV:76:LYS:HG3	2.14	0.47
41:LI:76:ASP:HB3	41:LI:114:GLY:HA3	1.96	0.47
49:LQ:153:ASP:N	49:LQ:153:ASP:OD1	2.48	0.47
77:11:183:C:H2'	77:11:184:C:C6	2.49	0.47
80:14:805:G:H2'	80:14:806:U:C6	2.49	0.47
11:SK:116:LYS:HD3	11:SK:116:LYS:HA	1.35	0.47
15:SO:36:SER:OG	15:SO:39:GLU:OE1	2.32	0.47
16:SP:75:LYS:HA	16:SP:75:LYS:HD3	1.64	0.47
19:SS:88:PHE:O	19:SS:91:LYS:HD2	2.14	0.47
21:SU:46:GLY:HA2	21:SU:95:LEU:HD12	1.96	0.47
38:LF:142:LYS:HG3	38:LF:143:VAL:HG23	1.96	0.47
49:LQ:10:PRO:HG2	49:LQ:18:LYS:HD2	1.96	0.47
76:10:70:G:O2'	76:10:88:A:N6	2.48	0.47
80:14:3072:A:H2'	80:14:3073:A:H8	1.79	0.47
33:LA:47:LYS:HB3	33:LA:47:LYS:HE2	1.62	0.46
43:LK:81:ARG:CZ	43:LK:81:ARG:HB2	2.45	0.46
48:LP:145:ARG:HG2	48:LP:149:TYR:CE2	2.50	0.46
54:LV:98:LYS:HE3	54:LV:98:LYS:HB2	1.63	0.46
69:Lk:5:THR:OG1	80:14:894:A:OP1	2.31	0.46
76:10:152:C:H2'	76:10:153:A:C8	2.50	0.46
76:10:168:G:C2	76:10:181:C:C2	3.03	0.46
80:14:2493:A:H3'	80:14:2494:C:H6	1.79	0.46
80:14:3002:G:H2'	80:14:3003:U:C6	2.50	0.46
3:SC:174:VAL:HG13	77:11:514:A:H5''	1.96	0.46
19:SS:81:VAL:HG23	19:SS:93:VAL:HB	1.96	0.46
23:SW:30:THR:O	23:SW:34:ILE:HD12	2.15	0.46
38:LF:135:VAL:HG23	38:LF:157:VAL:HG22	1.96	0.46
44:LL:2:VAL:HG22	44:LL:3:LYS:H	1.80	0.46
76:10:98:G:H3'	76:10:99:U:C5	2.50	0.46
76:10:194:G:H5''	76:10:195:U:C5	2.51	0.46
77:11:891:U:H2'	77:11:892:U:C6	2.50	0.46
79:13:86:C:H4'	79:13:88:G:N3	2.30	0.46
80:14:371:A:N3	80:14:373:G:H5''	2.30	0.46
80:14:2476:A:H3'	80:14:2477:A:C8	2.50	0.46
27:Sa:103:ARG:H	27:Sa:103:ARG:HG2	1.49	0.46
42:LJ:162:ARG:HG3	42:LJ:162:ARG:NH1	2.30	0.46
45:LM:80:THR:O	45:LM:80:THR:HG22	2.13	0.46
53:LU:46:ASP:OD1	53:LU:46:ASP:N	2.47	0.46
58:LZ:40:GLU:HG3	58:LZ:64:ARG:HB3	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:11:1253:U:H3'	77:11:1254:U:H5''	1.96	0.46
79:13:162:G:H2'	79:13:163:C:O4'	2.15	0.46
15:SO:65:LYS:HD2	15:SO:65:LYS:C	2.41	0.46
22:SV:35:LEU:HD13	22:SV:101:TRP:O	2.15	0.46
34:LB:48:ILE:HG12	75:Lq:65:VAL:HG22	1.98	0.46
35:LC:80:GLU:OE1	35:LC:318:TYR:OH	2.26	0.46
45:LM:120:LYS:HD3	45:LM:137:ARG:HD3	1.96	0.46
80:14:2845:U:OP1	80:14:2847:C:N4	2.49	0.46
82:16:62:C:H2'	82:16:63:G:C8	2.51	0.46
1:SA:29:ASN:OD1	1:SA:29:ASN:N	2.48	0.46
15:SO:65:LYS:NZ	15:SO:66:LYS:HG3	2.29	0.46
18:SR:156:ARG:HH22	77:11:80:C:N4	2.07	0.46
33:LA:93:LEU:HD22	33:LA:99:LEU:HB3	1.97	0.46
33:LA:143:SER:O	33:LA:146:SER:N	2.49	0.46
43:LK:5:LYS:HG2	80:14:1050:C:H5''	1.97	0.46
76:10:193:G:H1'	76:10:196:A:C6	2.50	0.46
77:11:818:A:N6	77:11:861:G:H1'	2.31	0.46
80:14:129:G:H1	80:14:135:U:H3	1.64	0.46
80:14:174:G:C4	80:14:175:A:C8	3.04	0.46
16:SP:36:SER:HB3	16:SP:231:VAL:O	2.15	0.46
21:SU:109:LEU:HD22	21:SU:109:LEU:H	1.81	0.46
23:SW:32:LYS:O	23:SW:36:GLU:HG2	2.16	0.46
24:SX:25:ARG:HB2	24:SX:25:ARG:HH11	1.81	0.46
35:LC:34:LYS:H	35:LC:34:LYS:CD	2.17	0.46
37:LE:34:ARG:NE	37:LE:122:THR:O	2.46	0.46
51:LS:26:GLN:HB3	51:LS:27:PRO:HD3	1.97	0.46
76:10:74:U:H2'	76:10:75:U:C6	2.51	0.46
76:10:82:C:O2'	76:10:94:A:N6	2.49	0.46
76:10:125:U:H1'	76:10:126:G:H8	1.81	0.46
77:11:182:C:H2'	77:11:183:C:H6	1.81	0.46
77:11:1543:A:H2'	77:11:1543:A:N3	2.30	0.46
80:14:652:C:H42	80:14:656:A:H2	1.62	0.46
80:14:1131:A:H2'	80:14:1132:U:C6	2.51	0.46
80:14:1543:C:H2'	80:14:1544:U:C6	2.51	0.46
82:16:63:G:H2'	82:16:64:A:C8	2.51	0.46
8:SH:25:ILE:HD11	8:SH:92:ILE:HB	1.97	0.46
17:SQ:37:LYS:HB2	17:SQ:40:GLU:HG3	1.98	0.46
18:SR:147:PHE:CD1	18:SR:147:PHE:N	2.82	0.46
37:LE:152:ILE:HA	37:LE:155:ARG:HG3	1.98	0.46
38:LF:57:LYS:HB3	38:LF:57:LYS:HE3	1.65	0.46
39:LG:10:ARG:HB3	39:LG:10:ARG:HH11	1.80	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:11:279:C:H1'	77:11:285:G:N1	2.30	0.46
80:14:243:G:H2'	80:14:244:C:C6	2.50	0.46
80:14:856:A:P	80:14:856:A:H8	2.39	0.46
18:SR:27:PHE:CE1	18:SR:36:VAL:HG11	2.51	0.46
26:SZ:8:ILE:HG13	26:SZ:44:LYS:HD2	1.97	0.46
30:Sd:39:MET:HE2	30:Sd:39:MET:HB2	1.76	0.46
33:LA:143:SER:C	33:LA:145:GLU:N	2.74	0.46
37:LE:51:LYS:O	37:LE:53:ARG:NH1	2.48	0.46
61:Lc:87:LYS:H	61:Lc:87:LYS:HG2	1.41	0.46
76:10:99:U:H2'	76:10:100:U:C6	2.51	0.46
77:11:1234:U:H2'	77:11:1235:U:C6	2.51	0.46
77:11:1257:U:H2'	77:11:1258:G:C8	2.51	0.46
80:14:2509:U:H2'	80:14:2510:U:C6	2.51	0.46
3:SC:72:ILE:HG22	3:SC:76:GLU:OE2	2.16	0.46
17:SQ:220:THR:HG22	17:SQ:221:ARG:H	1.81	0.46
18:SR:133:ARG:HD2	77:11:164:C:H4'	1.98	0.46
59:La:9:ARG:HH22	59:La:29:GLN:NE2	2.14	0.46
77:11:1623:U:H2'	77:11:1624:C:C6	2.51	0.46
21:SU:43:PHE:CZ	21:SU:109:LEU:HG	2.51	0.46
24:SX:61:MET:HE1	24:SX:101:ALA:HA	1.98	0.46
38:LF:180:ASP:N	38:LF:180:ASP:OD1	2.49	0.46
47:LO:18:LEU:HD12	47:LO:18:LEU:HA	1.82	0.46
49:LQ:152:PHE:HE2	49:LQ:195:VAL:HG21	1.80	0.46
58:LZ:22:VAL:HB	58:LZ:110:VAL:HG12	1.98	0.46
63:Le:39:LEU:HD13	63:Le:64:TYR:HB3	1.98	0.46
63:Le:104:ASP:OD1	63:Le:104:ASP:N	2.47	0.46
76:10:100:U:H5''	76:10:155:G:H22	1.81	0.46
76:10:115:G:H2'	76:10:116:C:C6	2.51	0.46
77:11:1377:C:H4'	77:11:1378:C:C6	2.47	0.46
80:14:301:G:N3	80:14:301:G:H5'	2.31	0.46
2:SB:126:LEU:O	2:SB:130:MET:HG2	2.16	0.45
17:SQ:220:THR:HG22	17:SQ:221:ARG:N	2.31	0.45
22:SV:31:LEU:O	22:SV:35:LEU:HG	2.16	0.45
57:LY:9:SER:O	57:LY:55:LYS:NZ	2.38	0.45
64:Lf:83:LYS:HB2	64:Lf:83:LYS:HE3	1.73	0.45
65:Lg:97:ILE:HG21	65:Lg:106:ARG:HG2	1.98	0.45
67:Li:98:GLU:HA	67:Li:98:GLU:OE1	2.15	0.45
76:10:132:G:H1'	76:10:137:A:C2	2.49	0.45
77:11:974:A:C2	80:14:856:A:N6	2.85	0.45
78:12:37:A:H2'	78:12:38:U:C6	2.51	0.45
80:14:2697:A:H3'	80:14:2698:G:N2	2.31	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:14:3015:U:H2'	80:14:3016:U:C6	2.50	0.45
82:16:75:C:H2'	82:16:76:A:O4'	2.16	0.45
1:SA:194:LYS:HE3	1:SA:195:TRP:N	2.30	0.45
2:SB:49:THR:HB	2:SB:87:VAL:HG12	1.97	0.45
11:SK:124:ARG:HB2	11:SK:131:VAL:HG12	1.98	0.45
12:SL:52:PHE:C	12:SL:53:ILE:HD13	2.41	0.45
33:LA:68:LEU:HD22	33:LA:90:LEU:HD21	1.97	0.45
35:LC:143:LYS:O	35:LC:147:GLN:HG2	2.16	0.45
61:Lc:36:GLU:HG2	61:Lc:39:ASN:HB2	1.98	0.45
76:10:101:G:N2	76:10:155:G:H1'	2.31	0.45
76:10:130:A:H2'	76:10:131:U:O4'	2.16	0.45
77:11:77:A:H2'	77:11:78:G:O4'	2.17	0.45
77:11:1203:G:H4'	77:11:1204:G:O5'	2.16	0.45
80:14:1362:G:H2'	80:14:1364:G:C8	2.52	0.45
80:14:2700:A:H2'	80:14:2701:G:C8	2.51	0.45
80:14:2888:C:O2'	80:14:2889:U:H5'	2.17	0.45
82:16:66:C:H2'	82:16:67:G:H8	1.81	0.45
1:SA:17:MET:HE1	1:SA:176:TRP:CZ3	2.51	0.45
3:SC:61:LEU:HD11	3:SC:74:GLU:HB3	1.98	0.45
17:SQ:55:ALA:HB1	17:SQ:60:GLU:HB2	1.98	0.45
33:LA:36:ILE:CD1	33:LA:190:LEU:HD22	2.42	0.45
33:LA:61:PRO:HG2	33:LA:62:LYS:HD2	1.98	0.45
48:LP:42:LYS:HE3	48:LP:42:LYS:HB3	1.55	0.45
79:13:7:C:H2'	79:13:8:U:C6	2.51	0.45
80:14:498:G:H2'	80:14:499:A:C8	2.52	0.45
80:14:1958:G:H2'	80:14:2096:A:H61	1.81	0.45
2:SB:79:ARG:HH21	21:SU:90:HIS:CE1	2.34	0.45
4:SD:132:ALA:O	4:SD:136:ARG:HG3	2.16	0.45
6:SF:90:THR:HG22	6:SF:102:ILE:HD12	1.97	0.45
13:SM:55:ARG:NH1	77:11:963:U:OP2	2.49	0.45
18:SR:179:LYS:HA	77:11:79:A:H1'	1.98	0.45
32:Sf:118:ARG:HG3	32:Sf:131:PHE:HB3	1.99	0.45
34:LB:48:ILE:HG12	75:Lq:65:VAL:CG2	2.46	0.45
58:LZ:80:ARG:HG3	58:LZ:80:ARG:HH11	1.82	0.45
77:11:974:A:H2	80:14:856:A:H61	1.65	0.45
77:11:1203:G:H4'	77:11:1204:G:C5'	2.46	0.45
80:14:2964:G:H2'	80:14:2965:U:C6	2.51	0.45
3:SC:96:ASP:OD1	3:SC:96:ASP:N	2.49	0.45
29:Sc:16:VAL:O	29:Sc:20:LYS:HG3	2.16	0.45
59:La:15:ILE:HG12	59:La:34:LEU:HD13	1.99	0.45
77:11:690:C:H2'	77:11:691:C:C6	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:14:2257:U:H2'	80:14:2264:G:C2	2.51	0.45
7:SG:46:VAL:HG12	7:SG:52:ARG:HG3	1.99	0.45
13:SM:110:ASP:O	13:SM:114:ARG:HG2	2.16	0.45
22:SV:75:VAL:HA	22:SV:78:VAL:HG12	1.98	0.45
26:SZ:11:ARG:O	77:11:784:A:N6	2.49	0.45
33:LA:47:LYS:H	33:LA:195:LYS:NZ	2.14	0.45
38:LF:7:SER:HB2	38:LF:61:ASP:HB3	1.98	0.45
38:LF:190:ILE:HG22	38:LF:191:VAL:HG23	1.99	0.45
59:La:40:ARG:HD3	80:14:3086:C:H5''	1.98	0.45
60:Lb:6:LYS:HB2	60:Lb:6:LYS:HE3	1.48	0.45
80:14:1120:C:H2'	80:14:1121:C:C6	2.52	0.45
2:SB:71:GLU:OE1	2:SB:71:GLU:HA	2.16	0.45
2:SB:81:LYS:HE3	2:SB:81:LYS:HA	1.98	0.45
3:SC:156:LYS:NZ	3:SC:156:LYS:HB3	2.31	0.45
11:SK:14:ARG:NH2	37:LE:110:GLU:OE2	2.49	0.45
14:SN:23:GLY:HA2	14:SN:26:LYS:HG3	1.99	0.45
17:SQ:197:ASN:OD1	17:SQ:209:HIS:HB2	2.15	0.45
18:SR:67:VAL:HB	18:SR:101:GLY:HA2	1.98	0.45
51:LS:126:PRO:HB3	51:LS:136:ASP:OD2	2.16	0.45
55:LW:95:TRP:CH2	55:LW:99:MET:HE3	2.52	0.45
58:LZ:24:ASP:OD1	58:LZ:24:ASP:C	2.59	0.45
65:Lg:3:VAL:HG12	65:Lg:91:ARG:HH21	1.81	0.45
72:Ln:89:TYR:C	72:Ln:90:ASN:HD22	2.25	0.45
77:11:541:A:H5'	77:11:546:C:H41	1.81	0.45
77:11:811:A:H2'	77:11:812:C:H6	1.80	0.45
77:11:1263:U:H2'	77:11:1264:A:C8	2.51	0.45
80:14:2498:U:H2'	80:14:2499:A:H8	1.82	0.45
80:14:2844:G:H3'	80:14:2847:C:H42	1.80	0.45
80:14:3172:C:H5''	80:14:3268:U:C5	2.52	0.45
4:SD:189:VAL:O	4:SD:208:THR:OG1	2.26	0.45
5:SE:210:ARG:HD3	30:Sd:59:ARG:HH21	1.81	0.45
18:SR:32:ILE:HD13	18:SR:32:ILE:HA	1.74	0.45
51:LS:103:ARG:NH1	80:14:72:A:H5''	2.31	0.45
62:Ld:6:ASN:HB2	80:14:1146:A:OP1	2.16	0.45
76:10:80:C:C2	76:10:97:G:C2	3.04	0.45
77:11:886:U:H3	77:11:948:U:H3	1.63	0.45
79:13:126:G:H2'	79:13:127:C:C6	2.52	0.45
80:14:978:G:H2'	80:14:979:C:H6	1.82	0.45
80:14:1679:G:H2'	80:14:1680:A:C8	2.52	0.45
40:LH:30:ASP:OD2	40:LH:32:THR:HG23	2.17	0.45
41:LI:104:GLN:HB3	51:LS:160:PRO:HB3	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Lj:36:THR:OG1	68:Lj:37:SER:N	2.50	0.45
70:Ll:60:LEU:HD13	70:Ll:61:PRO:HD2	1.99	0.45
80:14:2576:C:H2'	80:14:2577:A:H8	1.82	0.45
16:SP:159:SER:O	16:SP:163:GLN:HG3	2.17	0.45
36:LD:34:PRO:HG3	36:LD:286:PRO:HD3	1.99	0.45
38:LF:140:SER:HB3	38:LF:146:GLU:HB2	1.99	0.45
44:LL:15:CYS:SG	44:LL:103:ALA:HB2	2.57	0.45
46:LN:50:ARG:HG2	46:LN:51:LYS:H	1.82	0.45
76:10:51:G:O4'	76:10:86:U:O2'	2.31	0.45
77:11:1225:U:H2'	77:11:1226:A:C8	2.52	0.45
79:13:136:C:H2'	79:13:137:G:C8	2.52	0.45
80:14:206:A:O2'	80:14:208:A:OP2	2.30	0.45
80:14:2658:U:H4'	80:14:2659:A:O4'	2.16	0.45
80:14:3162:C:C4	80:14:3279:G:C6	3.05	0.45
26:SZ:37:SER:O	26:SZ:41:LEU:HD23	2.17	0.44
33:LA:143:SER:O	33:LA:144:LEU:C	2.59	0.44
33:LA:207:LYS:HB3	33:LA:213:PRO:HA	1.98	0.44
36:LD:328:ASN:ND2	80:14:617:C:O4'	2.44	0.44
45:LM:77:TYR:CD1	47:LO:36:VAL:HG21	2.52	0.44
47:LO:119:TYR:CZ	51:LS:47:ARG:HG2	2.52	0.44
70:Ll:24:LYS:HE2	70:Ll:24:LYS:HB2	1.71	0.44
77:11:71:A:H2'	77:11:72:A:C8	2.52	0.44
77:11:1362:G:OP2	77:11:1365:A:N6	2.51	0.44
77:11:1495:U:O2'	77:11:1496:U:H5'	2.17	0.44
80:14:1185:G:H2'	80:14:1186:C:C6	2.52	0.44
80:14:2726:U:H2'	80:14:2727:U:C6	2.53	0.44
7:SG:102:LYS:HD3	7:SG:103:TYR:CZ	2.53	0.44
15:SO:58:ARG:NH2	77:11:1246:G:H5''	2.31	0.44
18:SR:20:ASP:OD1	18:SR:22:GLN:NE2	2.51	0.44
37:LE:139:ARG:NH1	78:12:28:C:OP1	2.50	0.44
58:LZ:67:THR:HG23	58:LZ:68:LYS:HG3	1.99	0.44
76:10:108:G:N2	76:10:175:A:O5'	2.50	0.44
80:14:801:A:H2'	80:14:802:C:C6	2.52	0.44
80:14:1476:A:H2'	80:14:1477:G:O4'	2.17	0.44
7:SG:75:ARG:NH1	77:11:1353:C:H4'	2.31	0.44
14:SN:44:LYS:HB3	14:SN:44:LYS:HE3	1.70	0.44
27:Sa:37:ASN:O	27:Sa:70:ARG:NH2	2.46	0.44
33:LA:18:LYS:HD2	33:LA:176:GLU:CG	2.47	0.44
44:LL:42:ASP:OD1	44:LL:42:ASP:N	2.45	0.44
45:LM:143:ASP:C	45:LM:143:ASP:OD1	2.60	0.44
50:LR:202:GLU:OE1	50:LR:202:GLU:N	2.47	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Le:27:LYS:HE3	63:Le:27:LYS:HB2	1.75	0.44
76:10:136:C:H2'	76:10:137:A:O4'	2.17	0.44
76:10:146:C:H2'	76:10:147:G:O4'	2.17	0.44
77:11:172:U:H3	77:11:269:A:H62	1.65	0.44
77:11:1352:G:H2'	77:11:1353:C:C6	2.52	0.44
77:11:1559:G:N2	77:11:1561:A:H3'	2.31	0.44
80:14:637:C:H2'	80:14:638:C:H6	1.82	0.44
21:SU:34:ASN:OD1	21:SU:64:VAL:HG22	2.17	0.44
22:SV:96:LYS:HA	22:SV:96:LYS:HD3	1.66	0.44
26:SZ:90:LYS:HE2	26:SZ:94:ILE:HD11	2.00	0.44
57:LY:13:ASP:OD2	80:14:1006:G:H3'	2.17	0.44
63:Le:34:THR:O	63:Le:38:THR:HG23	2.17	0.44
76:10:70:G:N2	76:10:89:A:H2	2.15	0.44
77:11:811:A:H2'	77:11:812:C:C6	2.53	0.44
80:14:2164:G:H2'	80:14:2165:G:H8	1.81	0.44
80:14:2216:A:H2'	80:14:2217:A:H8	1.79	0.44
2:SB:88:GLU:OE1	2:SB:90:TYR:OH	2.25	0.44
5:SE:97:ARG:HD2	27:Sa:95:HIS:CE1	2.52	0.44
13:SM:83:GLU:HG2	13:SM:84:ILE:HG23	1.98	0.44
21:SU:59:HIS:CG	21:SU:60:PRO:HD2	2.53	0.44
26:SZ:12:LYS:HD2	26:SZ:12:LYS:HA	1.71	0.44
27:Sa:58:LYS:HG2	27:Sa:103:ARG:HH21	1.82	0.44
76:10:135:U:H4'	76:10:136:C:C6	2.52	0.44
76:10:194:G:H5''	76:10:195:U:H5	1.82	0.44
80:14:107:A:H4'	80:14:108:G:OP1	2.17	0.44
6:SF:55:ASP:OD1	6:SF:55:ASP:N	2.48	0.44
22:SV:106:LYS:O	22:SV:106:LYS:HD3	2.18	0.44
28:Sb:64:LEU:HA	28:Sb:65:PRO:HD3	1.89	0.44
32:Sf:105:PHE:CD1	32:Sf:118:ARG:HD2	2.51	0.44
56:LX:157:LYS:HB2	56:LX:157:LYS:HE2	1.66	0.44
76:10:118:G:N3	76:10:119:G:H1'	2.32	0.44
80:14:641:A:H2'	80:14:642:U:C6	2.53	0.44
80:14:771:A:N6	80:14:780:G:H1'	2.33	0.44
80:14:1449:U:H2'	80:14:1450:U:C6	2.52	0.44
80:14:2990:A:H2'	80:14:2991:C:C6	2.53	0.44
80:14:3159:C:H2'	80:14:3160:G:H8	1.80	0.44
1:SA:72:LYS:HD3	1:SA:72:LYS:HA	1.82	0.44
2:SB:201:GLN:OE1	2:SB:201:GLN:HA	2.17	0.44
3:SC:173:ARG:NH1	77:11:540:G:N7	2.65	0.44
9:SI:95:LYS:HG2	9:SI:131:VAL:HG21	1.98	0.44
11:SK:137:LYS:HG3	77:11:1464:C:N4	2.33	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:SP:42:ASN:OD1	16:SP:42:ASN:N	2.37	0.44
18:SR:19:ASP:OD1	18:SR:19:ASP:N	2.50	0.44
33:LA:145:GLU:O	33:LA:148:VAL:HB	2.18	0.44
35:LC:8:HIS:ND1	35:LC:9:PRO:O	2.50	0.44
77:11:1110:G:O2'	77:11:1111:G:H5'	2.18	0.44
77:11:1530:A:H2'	77:11:1531:A:C8	2.52	0.44
80:14:1821:U:H4'	80:14:1822:G:O4'	2.18	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	2.50	0.44
3:SC:50:ALA:O	3:SC:54:ILE:HD12	2.17	0.44
3:SC:60:MET:HE1	3:SC:70:ARG:NH2	2.33	0.44
16:SP:56:ILE:HG22	16:SP:58:SER:H	1.82	0.44
21:SU:53:ASP:OD1	21:SU:53:ASP:C	2.60	0.44
22:SV:107:ILE:HD12	22:SV:107:ILE:C	2.43	0.44
26:SZ:28:VAL:HG22	26:SZ:30:HIS:HD2	1.83	0.44
35:LC:253:ALA:HB3	80:14:2883:U:H1'	1.98	0.44
66:Lh:14:VAL:HG23	66:Lh:105:VAL:HB	2.00	0.44
76:10:88:A:H1'	76:10:89:A:N7	2.32	0.44
76:10:188:C:H3'	76:10:189:C:H6	1.82	0.44
77:11:486:U:H2'	77:11:487:A:C8	2.53	0.44
79:13:129:A:C8	79:13:133:G:N1	2.86	0.44
1:SA:34:MET:HE3	1:SA:34:MET:HB3	1.88	0.44
8:SH:96:SER:HB3	8:SH:100:VAL:HG21	2.00	0.44
26:SZ:62:PHE:HB3	26:SZ:73:GLY:HA3	1.99	0.44
48:LP:86:ILE:O	48:LP:114:GLY:HA2	2.18	0.44
51:LS:101:ARG:HH11	51:LS:103:ARG:HE	1.64	0.44
52:LT:23:LYS:HB3	52:LT:23:LYS:HE3	1.69	0.44
76:10:182:C:H2'	76:10:183:C:C6	2.53	0.44
80:14:3273:C:H2'	80:14:3274:G:C8	2.53	0.44
3:SC:53:ARG:HA	3:SC:53:ARG:HD3	1.70	0.43
3:SC:134:ARG:NH2	77:11:535:U:OP1	2.36	0.43
22:SV:31:LEU:HA	22:SV:34:VAL:HG12	1.99	0.43
22:SV:71:GLN:CG	22:SV:74:TYR:HB2	2.48	0.43
55:LW:114:LYS:HE3	55:LW:114:LYS:HB2	1.71	0.43
56:LX:14:ARG:HG3	56:LX:15:ALA:O	2.17	0.43
67:Li:68:SER:OG	67:Li:70:ASN:OD1	2.35	0.43
76:10:74:U:H5'	76:10:74:U:H6	1.83	0.43
76:10:127:U:H2'	76:10:128:A:O4'	2.18	0.43
76:10:180:C:H2'	76:10:181:C:H6	1.82	0.43
80:14:11:G:H5'	80:14:12:U:P	2.57	0.43
80:14:666:C:H2'	80:14:667:A:C8	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:14:2498:U:H2'	80:14:2499:A:C8	2.53	0.43
80:14:3025:U:H2'	80:14:3026:A:H8	1.83	0.43
80:14:3284:U:H2'	80:14:3285:A:C4	2.53	0.43
1:SA:154:MET:HE3	1:SA:154:MET:HB3	1.93	0.43
18:SR:33:SER:O	18:SR:33:SER:OG	2.36	0.43
18:SR:166:PHE:CE1	18:SR:174:ALA:HB3	2.53	0.43
22:SV:50:GLU:HA	22:SV:53:LYS:CD	2.48	0.43
26:SZ:40:GLU:OE2	26:SZ:44:LYS:NZ	2.51	0.43
32:Sf:102:VAL:HA	32:Sf:105:PHE:CE2	2.54	0.43
32:Sf:143:LYS:NZ	77:11:1256:U:O3'	2.52	0.43
33:LA:10:LEU:HD23	33:LA:180:PHE:CE2	2.53	0.43
35:LC:312:MET:HE2	80:14:3321:U:H5''	1.99	0.43
42:LJ:164:LYS:HB2	42:LJ:164:LYS:HE2	1.64	0.43
48:LP:52:ALA:O	48:LP:56:GLU:HG2	2.18	0.43
53:LU:84:PRO:HA	53:LU:87:GLN:HG3	2.00	0.43
60:Lb:53:VAL:HG13	60:Lb:62:GLN:HG2	1.99	0.43
77:11:129:U:H3'	77:11:130:A:H5'	2.00	0.43
77:11:974:A:H2	80:14:856:A:N6	2.16	0.43
77:11:1320:C:H2'	77:11:1321:G:O4'	2.18	0.43
80:14:537:U:N3	80:14:541:U:H1'	2.33	0.43
80:14:786:U:H5	80:14:2740:C:N3	2.16	0.43
80:14:2638:A:H4'	80:14:2639:A:O5'	2.17	0.43
3:SC:104:GLU:O	3:SC:108:GLU:HG2	2.18	0.43
12:SL:26:ASN:O	12:SL:30:ILE:HD11	2.18	0.43
13:SM:55:ARG:HD3	77:11:963:U:H5'	2.00	0.43
15:SO:95:GLU:C	15:SO:95:GLU:OE1	2.61	0.43
18:SR:147:PHE:N	18:SR:147:PHE:HD1	2.17	0.43
32:Sf:100:LEU:HD22	32:Sf:104:GLN:HE22	1.83	0.43
32:Sf:108:VAL:HG23	32:Sf:114:VAL:HG12	2.00	0.43
55:LW:162:ARG:C	77:11:819:G:H22	2.26	0.43
56:LX:161:PRO:HD2	56:LX:165:LEU:HD12	2.00	0.43
67:Li:60:THR:HG21	80:14:1598:A:H5'	2.01	0.43
77:11:628:C:H2'	77:11:629:U:C6	2.53	0.43
80:14:2614:U:H2'	80:14:2615:U:C6	2.53	0.43
15:SO:59:LYS:N	15:SO:60:PRO:HD2	2.34	0.43
18:SR:133:ARG:HA	18:SR:133:ARG:HD3	1.39	0.43
20:ST:17:LYS:HB2	20:ST:17:LYS:HE2	1.71	0.43
22:SV:35:LEU:HD11	22:SV:101:TRP:HB3	2.00	0.43
32:Sf:102:VAL:HG13	32:Sf:103:LEU:HD12	2.01	0.43
34:LB:181:LYS:NZ	80:14:870:G:OP2	2.52	0.43
49:LQ:20:SER:O	49:LQ:24:MET:HB2	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:LS:101:ARG:NH1	51:LS:103:ARG:HH21	2.17	0.43
73:Lo:20:MET:HE3	73:Lo:20:MET:HB3	1.77	0.43
77:11:468:A:C2	77:11:469:G:C8	3.05	0.43
77:11:819:G:O4'	77:11:819:G:N3	2.50	0.43
78:12:33:U:H2'	78:12:34:C:O4'	2.18	0.43
80:14:2402:A:H2'	80:14:2403:G:O4'	2.18	0.43
80:14:2503:U:H2'	80:14:2504:U:C6	2.54	0.43
80:14:3253:C:H2'	80:14:3254:C:O4'	2.19	0.43
82:16:66:C:H2'	82:16:67:G:C8	2.53	0.43
3:SC:112:GLN:HE21	3:SC:128:ARG:HB2	1.84	0.43
17:SQ:240:LYS:NZ	77:11:789:C:C2	2.86	0.43
63:Le:35:VAL:HG22	63:Le:96:SER:HB2	2.01	0.43
76:10:183:C:H2'	76:10:184:G:O4'	2.19	0.43
80:14:547:C:H2'	80:14:548:G:C8	2.52	0.43
80:14:1823:C:H2'	80:14:1824:C:C6	2.53	0.43
80:14:2210:A:H2'	80:14:2211:A:C5	2.54	0.43
18:SR:22:GLN:N	18:SR:22:GLN:CD	2.77	0.43
22:SV:71:GLN:NE2	22:SV:73:ASP:OD1	2.51	0.43
26:SZ:9:ARG:HD2	77:11:783:U:C6	2.53	0.43
33:LA:25:LYS:HB2	33:LA:25:LYS:HE2	1.56	0.43
33:LA:210:MET:O	80:14:2495:C:H4'	2.19	0.43
55:LW:146:LYS:HB3	55:LW:146:LYS:HE3	1.78	0.43
80:14:2571:G:H5''	80:14:2572:C:C5	2.53	0.43
8:SH:41:ASP:C	8:SH:41:ASP:OD1	2.61	0.43
17:SQ:115:ARG:HA	17:SQ:115:ARG:CZ	2.49	0.43
18:SR:163:ARG:HH22	77:11:78:G:H2'	1.84	0.43
19:SS:100:ARG:NH2	77:11:859:A:P	2.92	0.43
21:SU:28:MET:HE1	21:SU:67:LEU:HG	2.00	0.43
33:LA:64:LYS:NZ	33:LA:106:LYS:HG2	2.33	0.43
35:LC:61:GLU:OE2	35:LC:68:HIS:HE1	2.02	0.43
47:LO:12:LYS:NZ	47:LO:20:GLN:OE1	2.50	0.43
52:LT:9:ILE:HD13	52:LT:64:ARG:HB3	2.00	0.43
53:LU:47:LYS:HE2	80:14:266:G:OP1	2.18	0.43
53:LU:85:THR:HG23	80:14:42:U:H5''	2.01	0.43
63:Le:27:LYS:HE3	63:Le:99:ASP:HB3	2.00	0.43
70:Ll:60:LEU:CD1	70:Ll:61:PRO:HD2	2.49	0.43
76:10:68:U:H2'	76:10:69:A:O4'	2.18	0.43
77:11:974:A:H2	80:14:856:A:C6	2.36	0.43
77:11:1403:U:H2'	77:11:1405:U:C4	2.54	0.43
5:SE:108:LEU:HD11	27:Sa:102:THR:HG21	2.00	0.43
18:SR:5:ILE:HD11	18:SR:16:LEU:HD22	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:LD:79:ILE:HG13	36:LD:80:PRO:HD2	2.01	0.43
37:LE:38:VAL:HG23	37:LE:122:THR:HG21	2.01	0.43
46:LN:83:ARG:HG3	46:LN:83:ARG:HH11	1.83	0.43
69:Lk:45:ARG:C	69:Lk:46:LYS:HG2	2.44	0.43
74:Lp:29:LYS:HA	74:Lp:29:LYS:HD3	1.38	0.43
76:10:70:G:C2	76:10:71:U:H1'	2.54	0.43
77:11:1666:A:H2'	77:11:1667:U:C6	2.53	0.43
80:14:855:G:N2	80:14:857:A:H3'	2.34	0.43
80:14:883:C:H5''	80:14:884:U:O5'	2.19	0.43
80:14:2576:C:H2'	80:14:2577:A:C8	2.53	0.43
2:SB:160:MET:HE2	2:SB:160:MET:HB2	1.72	0.43
15:SO:61:MET:HE3	15:SO:61:MET:HB3	1.80	0.43
16:SP:111:ARG:NH2	77:11:933:A:N3	2.67	0.43
19:SS:51:GLN:NE2	19:SS:59:LYS:HE2	2.34	0.43
20:ST:47:ILE:CD1	20:ST:57:ARG:HB2	2.49	0.43
20:ST:65:ASN:C	20:ST:65:ASN:HD22	2.26	0.43
33:LA:4:LYS:CE	33:LA:198:TRP:HB2	2.48	0.43
46:LN:51:LYS:O	46:LN:69:VAL:HB	2.19	0.43
49:LQ:144:VAL:HG12	49:LQ:144:VAL:O	2.18	0.43
49:LQ:210:LYS:O	49:LQ:214:SER:OG	2.30	0.43
53:LU:85:THR:HG21	80:14:43:A:P	2.59	0.43
60:Lb:31:GLU:CD	60:Lb:31:GLU:H	2.27	0.43
70:Ll:16:ARG:HG3	70:Ll:16:ARG:NH1	2.34	0.43
77:11:588:A:H2'	77:11:589:G:C8	2.54	0.43
77:11:1433:G:H5'	77:11:1434:G:OP2	2.19	0.43
80:14:2446:A:H3'	80:14:2447:C:C6	2.53	0.43
1:SA:168:LYS:H	1:SA:168:LYS:HG2	1.64	0.43
2:SB:194:ASP:OD1	2:SB:194:ASP:N	2.52	0.43
15:SO:90:MET:HE2	15:SO:90:MET:HB2	1.82	0.43
22:SV:114:ARG:HD3	22:SV:114:ARG:N	2.26	0.43
25:SY:40:ASP:OD1	25:SY:44:ARG:N	2.46	0.43
52:LT:61:ASP:OD1	52:LT:61:ASP:C	2.62	0.43
63:Le:17:ASN:H	63:Le:17:ASN:ND2	2.17	0.43
76:10:80:C:P	76:10:157:A:H1'	2.58	0.43
77:11:334:G:H2'	77:11:335:A:C8	2.54	0.43
77:11:397:C:H2'	77:11:398:C:C6	2.54	0.43
77:11:1149:G:H2'	77:11:1150:A:C8	2.54	0.43
80:14:245:A:H2'	80:14:246:C:O4'	2.18	0.43
80:14:1119:U:H2'	80:14:1120:C:C6	2.53	0.43
18:SR:145:LYS:HD3	18:SR:145:LYS:HA	1.79	0.42
22:SV:82:CYS:SG	22:SV:89:LEU:HD12	2.60	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:SW:11:LYS:HB3	23:SW:11:LYS:HE3	1.67	0.42
23:SW:59:LYS:HE3	77:11:1397:C:OP1	2.18	0.42
30:Sd:63:ARG:HA	30:Sd:63:ARG:HD3	1.88	0.42
33:LA:209:THR:O	80:14:2495:C:H1'	2.19	0.42
77:11:1324:A:H4'	77:11:1325:A:O5'	2.19	0.42
80:14:195:A:N3	80:14:215:G:O2'	2.49	0.42
80:14:957:U:H2'	80:14:958:C:C6	2.54	0.42
80:14:2410:C:H2'	80:14:2411:U:C6	2.54	0.42
80:14:2711:U:H2'	80:14:2712:C:C6	2.53	0.42
80:14:2843:C:H2'	80:14:2844:G:O4'	2.19	0.42
3:SC:149:MET:HB3	3:SC:149:MET:HE3	1.84	0.42
5:SE:24:LEU:HD21	5:SE:103:MET:HE1	2.00	0.42
10:SJ:67:LYS:HE2	77:11:571:G:OP2	2.19	0.42
14:SN:54:TYR:CD1	14:SN:114:PRO:HG2	2.54	0.42
16:SP:195:ARG:HG3	77:11:1059:G:H1	1.84	0.42
21:SU:60:PRO:HG2	21:SU:61:LEU:HD22	2.00	0.42
26:SZ:9:ARG:HD2	77:11:783:U:H6	1.83	0.42
33:LA:50:SER:HB2	33:LA:158:GLN:NE2	2.34	0.42
45:LM:50:LEU:CD2	79:13:152:U:H4'	2.49	0.42
46:LN:112:LYS:NZ	79:13:88:G:OP2	2.53	0.42
51:LS:168:THR:O	51:LS:172:LYS:HG3	2.20	0.42
52:LT:102:LEU:HD22	52:LT:106:ASP:HB2	2.00	0.42
77:11:57:G:H2'	77:11:58:U:O4'	2.19	0.42
77:11:1353:C:H2'	77:11:1354:U:C6	2.54	0.42
80:14:2409:C:H2'	80:14:2410:C:C6	2.54	0.42
4:SD:152:GLY:HA2	25:SY:1:MET:HE1	2.02	0.42
14:SN:117:ARG:HH11	14:SN:117:ARG:HG2	1.83	0.42
20:ST:193:ARG:NH1	77:11:204:U:O2	2.52	0.42
33:LA:147:LYS:HE2	33:LA:147:LYS:HB2	1.83	0.42
41:LI:66:ASN:HD22	41:LI:66:ASN:HA	1.65	0.42
68:Lj:48:ARG:O	68:Lj:48:ARG:HD3	2.20	0.42
76:10:58:C:H2'	76:10:59:G:C8	2.53	0.42
76:10:70:G:HO2'	76:10:88:A:N6	2.16	0.42
76:10:130:A:H2'	76:10:131:U:C6	2.54	0.42
80:14:2122:C:H2'	80:14:2123:A:O4'	2.18	0.42
1:SA:187:GLY:HA2	25:SY:44:ARG:NH2	2.35	0.42
23:SW:106:LEU:O	23:SW:110:GLY:N	2.51	0.42
32:Sf:132:MET:HG2	32:Sf:141:CYS:HB2	2.01	0.42
46:LN:47:MET:HB3	46:LN:47:MET:HE3	1.83	0.42
54:LV:2:GLY:N	80:14:1171:A:OP1	2.52	0.42
58:LZ:46:ARG:HA	58:LZ:46:ARG:HD2	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:Lb:90:ASP:O	60:Lb:116:ARG:NH1	2.52	0.42
62:Ld:5:LYS:HA	62:Ld:5:LYS:HD2	1.71	0.42
69:Lk:39:TYR:CD1	69:Lk:40:PRO:HA	2.55	0.42
77:11:1354:U:H2'	77:11:1355:A:C8	2.54	0.42
80:14:2680:G:N3	80:14:2680:G:H2'	2.34	0.42
1:SA:57:LYS:HD2	1:SA:57:LYS:HA	1.81	0.42
2:SB:51:ILE:HB	2:SB:89:LEU:HD13	2.01	0.42
6:SF:14:MET:HE3	6:SF:14:MET:HB2	1.83	0.42
19:SS:40:GLU:OE1	19:SS:40:GLU:N	2.49	0.42
20:ST:157:LYS:HE2	20:ST:157:LYS:HB3	1.61	0.42
22:SV:32:GLN:OE1	22:SV:36:ARG:HD3	2.20	0.42
22:SV:46:ARG:NH2	22:SV:104:LEU:HD11	2.35	0.42
27:Sa:44:LYS:HD2	27:Sa:44:LYS:HA	1.94	0.42
30:Sd:28:VAL:HG22	30:Sd:38:ILE:HG22	2.01	0.42
33:LA:60:ARG:O	33:LA:61:PRO:C	2.62	0.42
41:LI:135:LYS:HE3	41:LI:135:LYS:HB2	1.65	0.42
76:10:85:C:O2'	76:10:89:A:N3	2.45	0.42
77:11:182:C:H2'	77:11:183:C:C6	2.54	0.42
77:11:276:G:H8	77:11:276:G:P	2.42	0.42
80:14:1545:A:H2'	80:14:1546:A:C8	2.54	0.42
80:14:2152:A:H2'	80:14:2153:A:C5	2.54	0.42
80:14:2454:G:H2'	80:14:2455:G:C8	2.54	0.42
1:SA:149:ASP:HB2	1:SA:165:ASN:OD1	2.19	0.42
2:SB:21:PHE:CD1	2:SB:21:PHE:C	2.97	0.42
3:SC:30:LEU:HD23	31:Se:44:PHE:HE2	1.84	0.42
17:SQ:57:THR:OG1	17:SQ:60:GLU:HG3	2.20	0.42
18:SR:222:LYS:HE2	18:SR:222:LYS:HA	2.01	0.42
21:SU:102:PHE:CD1	21:SU:102:PHE:C	2.97	0.42
24:SX:67:LEU:HD23	24:SX:67:LEU:HA	1.82	0.42
26:SZ:12:LYS:O	26:SZ:24:PHE:HA	2.20	0.42
26:SZ:90:LYS:O	26:SZ:94:ILE:HG13	2.20	0.42
45:LM:53:ASP:N	45:LM:53:ASP:OD1	2.52	0.42
48:LP:95:MET:HE3	48:LP:100:LYS:HB2	2.00	0.42
54:LV:23:ASP:O	54:LV:27:LYS:HG2	2.20	0.42
54:LV:123:ASP:OD1	54:LV:124:GLN:N	2.53	0.42
76:10:136:C:H2'	76:10:137:A:C8	2.55	0.42
80:14:2963:C:H2'	80:14:2964:G:C8	2.55	0.42
10:SJ:7:MET:HE2	10:SJ:7:MET:HB2	1.88	0.42
24:SX:113:ILE:HG22	24:SX:114:VAL:HG13	2.02	0.42
36:LD:113:ARG:NH2	80:14:801:A:OP1	2.42	0.42
77:11:424:A:H2'	77:11:425:A:O4'	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:11:849:G:O6	77:11:850:A:N6	2.52	0.42
80:14:666:C:H2'	80:14:667:A:H8	1.83	0.42
4:SD:179:MET:HG2	4:SD:208:THR:HG22	2.00	0.42
18:SR:144:ARG:HG2	18:SR:145:LYS:HE2	2.01	0.42
20:ST:202:LYS:HB3	20:ST:202:LYS:HE3	1.77	0.42
37:LE:165:PHE:CE2	37:LE:171:GLY:HA3	2.55	0.42
40:LH:17:SER:OG	80:14:3096:G:OP1	2.35	0.42
61:Lc:58:THR:HB	61:Lc:71:ALA:HB3	2.00	0.42
61:Lc:141:ARG:CD	80:14:438:A:H5''	2.50	0.42
66:Lh:63:LYS:HG3	66:Lh:68:HIS:CE1	2.54	0.42
72:Ln:83:MET:HE2	72:Ln:83:MET:HB3	1.87	0.42
76:10:114:C:H2'	76:10:115:G:C8	2.55	0.42
76:10:186:U:H4'	76:10:188:C:H5	1.84	0.42
77:11:1225:U:C2	77:11:1226:A:C8	3.07	0.42
80:14:1733:G:N3	80:14:1733:G:H5'	2.35	0.42
80:14:2210:A:O2'	80:14:2211:A:O4'	2.36	0.42
80:14:2890:A:N3	80:14:2890:A:H2'	2.33	0.42
11:SK:94:LYS:HG3	11:SK:95:PHE:H	1.85	0.42
21:SU:98:ASP:OD1	21:SU:98:ASP:N	2.52	0.42
26:SZ:13:PHE:CE1	77:11:785:C:H4'	2.54	0.42
33:LA:59:PRO:HB3	33:LA:170:GLY:HA2	2.01	0.42
37:LE:21:LEU:HD11	37:LE:81:LEU:HD13	2.02	0.42
39:LG:10:ARG:HB3	39:LG:10:ARG:NH1	2.35	0.42
39:LG:104:LEU:HD23	39:LG:104:LEU:HA	1.84	0.42
42:LJ:48:PHE:O	42:LJ:139:ARG:HA	2.20	0.42
47:LO:105:GLU:HA	47:LO:108:LYS:HD3	2.01	0.42
61:Lc:66:LYS:H	61:Lc:66:LYS:HE2	1.85	0.42
74:Lp:6:LYS:HE2	74:Lp:6:LYS:HB2	1.85	0.42
76:10:60:A:O4'	76:10:62:A:N6	2.52	0.42
76:10:78:C:H6	76:10:78:C:OP2	2.02	0.42
77:11:513:G:H2'	77:11:514:A:H8	1.85	0.42
77:11:1493:G:H3'	77:11:1522:A:H61	1.85	0.42
77:11:1522:A:H1'	77:11:1525:C:N4	2.35	0.42
80:14:275:U:H2'	80:14:276:U:C6	2.55	0.42
80:14:311:U:H2'	80:14:312:C:C6	2.54	0.42
80:14:2542:C:H2'	80:14:2543:A:O4'	2.20	0.42
16:SP:184:LEU:HD12	16:SP:184:LEU:HA	1.90	0.42
18:SR:144:ARG:HE	18:SR:144:ARG:HB2	1.65	0.42
26:SZ:107:LYS:HE2	77:11:463:G:O6	2.19	0.42
34:LB:116:VAL:HB	34:LB:126:PHE:HB2	2.02	0.42
35:LC:82:PRO:HA	35:LC:323:ASP:OD2	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:LF:1:MET:HE3	38:LF:1:MET:HB3	1.83	0.42
64:Lf:70:ARG:HH11	80:14:3060:C:N4	2.18	0.42
65:Lg:10:VAL:HG22	65:Lg:64:THR:HB	2.02	0.42
68:Lj:33:LYS:HD2	68:Lj:33:LYS:HA	1.80	0.42
69:Lk:87:ARG:HD2	79:13:71:G:OP2	2.19	0.42
76:10:51:G:N3	76:10:87:U:H5	2.17	0.42
77:11:816:A:H4'	77:11:818:A:H5''	2.02	0.42
80:14:936:A:H2'	80:14:937:C:C6	2.55	0.42
80:14:1128:G:H2'	80:14:1129:C:C6	2.55	0.42
80:14:2692:G:H2'	80:14:2692:G:N3	2.34	0.42
80:14:3223:G:H2'	80:14:3224:U:C6	2.54	0.42
4:SD:118:ASN:O	4:SD:118:ASN:ND2	2.53	0.41
11:SK:54:LYS:HB2	11:SK:54:LYS:HE3	1.75	0.41
18:SR:222:LYS:O	18:SR:222:LYS:HD3	2.19	0.41
21:SU:97:ASN:HA	21:SU:100:ILE:CG2	2.50	0.41
32:Sf:118:ARG:HG2	32:Sf:118:ARG:HH11	1.84	0.41
51:LS:101:ARG:HH11	51:LS:103:ARG:HH21	1.68	0.41
58:LZ:66:LYS:HE3	58:LZ:66:LYS:HA	2.01	0.41
63:Le:18:ARG:HB3	63:Le:105:ILE:HG23	2.02	0.41
74:Lp:25:VAL:HG22	74:Lp:72:LEU:HD22	2.01	0.41
77:11:822:U:H2'	77:11:823:U:C6	2.55	0.41
77:11:1366:U:H5''	77:11:1368:C:N4	2.35	0.41
80:14:1653:U:H2'	80:14:1654:C:O4'	2.20	0.41
82:16:2:A:H2'	82:16:3:G:C8	2.55	0.41
3:SC:125:HIS:CD2	31:Se:37:ARG:HH11	2.39	0.41
7:SG:20:LYS:HG2	7:SG:83:SER:HA	2.00	0.41
20:ST:25:ARG:HA	77:11:404:A:H5''	2.01	0.41
26:SZ:85:LYS:NZ	26:SZ:98:LEU:HB3	2.36	0.41
33:LA:189:PHE:CE2	33:LA:193:LEU:HD11	2.54	0.41
39:LG:117:TYR:HA	39:LG:120:ILE:HD12	2.01	0.41
48:LP:54:GLU:O	48:LP:58:GLN:HG3	2.20	0.41
68:Lj:36:THR:HG23	68:Lj:41:HIS:CE1	2.56	0.41
77:11:1127:A:H2'	77:11:1128:A:C8	2.55	0.41
80:14:419:A:C2	80:14:2366:A:H4'	2.55	0.41
80:14:2427:A:H2'	80:14:2428:G:O4'	2.20	0.41
3:SC:150:VAL:HG12	3:SC:151:ARG:O	2.20	0.41
7:SG:17:PHE:O	7:SG:94:LYS:HE2	2.20	0.41
14:SN:24:LYS:HD2	14:SN:24:LYS:HA	1.79	0.41
14:SN:80:LYS:HG3	77:11:350:G:H5'	2.01	0.41
22:SV:135:HIS:O	22:SV:139:GLU:HG2	2.20	0.41
24:SX:111:MET:HE3	24:SX:111:MET:HB3	1.79	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LA:101:LYS:NZ	80:14:2490:A:OP2	2.52	0.41
35:LC:20:LYS:HB2	35:LC:20:LYS:HE2	1.78	0.41
36:LD:399:LYS:HE3	36:LD:399:LYS:HB3	1.59	0.41
44:LL:61:THR:HG23	79:13:7:C:H5'	2.03	0.41
49:LQ:120:PHE:CZ	80:14:3258:A:H2'	2.55	0.41
76:10:132:G:H3'	76:10:133:G:H21	1.84	0.41
80:14:1818:G:H2'	80:14:1819:A:C1'	2.50	0.41
80:14:2560:A:H2'	80:14:2561:C:O4'	2.21	0.41
11:SK:14:ARG:NH2	11:SK:17:ASN:HA	2.36	0.41
17:SQ:254:LYS:NZ	17:SQ:254:LYS:HB3	2.35	0.41
18:SR:156:ARG:NH2	77:11:80:C:H41	2.08	0.41
20:ST:114:TYR:CD2	20:ST:122:ILE:HD11	2.55	0.41
20:ST:118:TYR:CD2	20:ST:165:ARG:HG3	2.56	0.41
24:SX:31:LEU:HD21	24:SX:55:TYR:CE1	2.56	0.41
33:LA:4:LYS:HE3	33:LA:198:TRP:CB	2.48	0.41
46:LN:83:ARG:HG3	46:LN:83:ARG:NH1	2.35	0.41
51:LS:105:LEU:O	51:LS:109:GLN:HG3	2.21	0.41
52:LT:124:GLU:OE1	52:LT:124:GLU:HA	2.19	0.41
77:11:1202:G:H5'	77:11:1203:G:OP1	2.20	0.41
77:11:1524:U:H5'	77:11:1525:C:H5	1.84	0.41
77:11:1580:G:H5''	77:11:1581:G:OP1	2.20	0.41
77:11:1778:U:H2'	77:11:1779:U:C6	2.55	0.41
2:SB:140:ILE:HG12	2:SB:154:LYS:HG3	2.02	0.41
9:SI:116:ARG:NH1	28:Sb:52:ASP:OD2	2.53	0.41
33:LA:30:GLU:HB2	33:LA:172:LEU:HD12	2.02	0.41
37:LE:51:LYS:HE2	37:LE:51:LYS:HB2	1.91	0.41
44:LL:32:THR:HG21	44:LL:88:SER:HB3	2.02	0.41
49:LQ:201:LYS:HE3	49:LQ:201:LYS:HA	2.01	0.41
57:LY:126:ILE:O	80:14:1106:C:O2'	2.38	0.41
66:Lh:64:LYS:HG3	80:14:632:G:OP1	2.19	0.41
70:Ll:35:LYS:HA	70:Ll:43:TYR:O	2.19	0.41
70:Ll:55:LYS:NZ	70:Ll:55:LYS:HB2	2.35	0.41
76:10:68:U:H2'	76:10:69:A:C1'	2.50	0.41
76:10:195:U:H2'	76:10:196:A:C4'	2.49	0.41
15:SO:134:LYS:H	15:SO:134:LYS:HD3	1.86	0.41
22:SV:97:THR:O	22:SV:101:TRP:CD1	2.74	0.41
26:SZ:22:LYS:HB2	26:SZ:77:ILE:HG12	2.03	0.41
55:LW:180:ARG:HH12	77:11:856:G:H5''	1.86	0.41
69:Lk:60:GLY:HA2	69:Lk:64:MET:SD	2.60	0.41
76:10:63:A:H2'	76:10:64:C:C6	2.55	0.41
22:SV:106:LYS:HE2	22:SV:114:ARG:NH2	2.36	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:LF:121:LEU:O	38:LF:121:LEU:HD23	2.21	0.41
43:LK:11:ALA:O	43:LK:15:ARG:HG2	2.21	0.41
50:LR:202:GLU:CD	50:LR:202:GLU:H	2.23	0.41
51:LS:157:ARG:HG2	51:LS:158:GLU:N	2.34	0.41
77:11:1163:A:H2'	77:11:1164:C:C6	2.56	0.41
80:14:660:A:H2'	80:14:661:C:C6	2.55	0.41
80:14:2482:G:H3'	80:14:2483:A:H8	1.86	0.41
80:14:2551:U:H2'	80:14:2552:C:C6	2.55	0.41
5:SE:185:ASN:O	5:SE:190:SER:HB3	2.20	0.41
19:SS:106:LYS:HE2	19:SS:106:LYS:HA	2.02	0.41
22:SV:75:VAL:HA	22:SV:78:VAL:CG1	2.50	0.41
24:SX:127:ASN:HA	24:SX:130:ARG:NH1	2.35	0.41
33:LA:26:ARG:HD3	33:LA:26:ARG:HA	1.83	0.41
36:LD:368:LYS:HE2	36:LD:368:LYS:HB3	1.82	0.41
51:LS:66:MET:HE3	51:LS:66:MET:H	1.84	0.41
56:LX:29:MET:HG3	56:LX:43:PHE:HD1	1.84	0.41
77:11:510:U:H2'	77:11:511:U:H6	1.85	0.41
77:11:1208:C:H2'	77:11:1209:U:O4'	2.20	0.41
80:14:667:A:H2'	80:14:668:A:C8	2.56	0.41
80:14:2470:G:H21	80:14:2493:A:H62	1.67	0.41
80:14:2765:A:H2'	80:14:2766:U:H6	1.86	0.41
80:14:3189:C:H2'	80:14:3190:C:O4'	2.21	0.41
2:SB:165:GLN:N	2:SB:166:PRO:HD2	2.35	0.41
3:SC:178:ASN:ND2	77:11:514:A:OP2	2.54	0.41
7:SG:50:ILE:HD13	7:SG:50:ILE:HA	1.94	0.41
9:SI:123:MET:HE2	9:SI:123:MET:HB3	1.98	0.41
12:SL:48:LYS:HE3	12:SL:48:LYS:HB3	1.70	0.41
18:SR:44:GLU:O	18:SR:46:LYS:HD2	2.21	0.41
20:ST:195:ASP:N	20:ST:195:ASP:OD1	2.54	0.41
21:SU:84:GLU:HG3	21:SU:93:TRP:NE1	2.35	0.41
21:SU:97:ASN:O	21:SU:101:GLU:HG3	2.20	0.41
23:SW:25:THR:OG1	23:SW:26:LEU:N	2.52	0.41
24:SX:52:ASP:O	24:SX:56:ILE:HD12	2.21	0.41
26:SZ:118:LYS:HB2	26:SZ:118:LYS:HE2	1.80	0.41
28:Sb:32:LYS:O	28:Sb:37:LYS:NZ	2.53	0.41
36:LD:384:THR:HG22	36:LD:385:MET:N	2.34	0.41
38:LF:112:ASN:HB3	38:LF:137:VAL:O	2.20	0.41
49:LQ:64:ASP:CG	65:Lg:5:LEU:HD11	2.45	0.41
50:LR:243:LYS:C	50:LR:243:LYS:HD2	2.46	0.41
52:LT:83:LYS:O	52:LT:87:SER:OG	2.39	0.41
56:LX:29:MET:HE3	57:LY:149:VAL:O	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:Lk:13:ASN:O	80:14:827:A:C4	2.74	0.41
69:Lk:81:GLY:N	79:13:99:A:OP1	2.40	0.41
76:10:161:A:HO2'	76:10:162:A:H8	1.64	0.41
76:10:173:C:H2'	76:10:174:G:O4'	2.21	0.41
76:10:189:C:H1'	76:10:200:G:H1	1.86	0.41
76:10:198:G:H2'	76:10:199:G:C8	2.56	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
77:11:644:G:H8	77:11:644:G:O5'	2.04	0.41
77:11:1262:C:H2'	77:11:1263:U:C6	2.56	0.41
77:11:1295:G:H2'	77:11:1296:U:C6	2.56	0.41
80:14:826:A:H1'	80:14:829:U:O4	2.21	0.41
80:14:856:A:H8	80:14:856:A:OP1	2.02	0.41
80:14:2226:A:H2'	80:14:2227:A:C8	2.56	0.41
80:14:2489:A:H2'	80:14:2490:A:C8	2.56	0.41
3:SC:96:ASP:OD2	4:SD:156:ASN:ND2	2.42	0.41
9:SI:60:LYS:NZ	9:SI:79:ASP:OD2	2.50	0.41
14:SN:48:GLU:O	14:SN:48:GLU:OE1	2.39	0.41
17:SQ:141:THR:OG1	17:SQ:143:ASP:OD1	2.22	0.41
26:SZ:13:PHE:CB	26:SZ:24:PHE:HB3	2.50	0.41
33:LA:67:MET:HE2	33:LA:73:HIS:HB3	2.02	0.41
33:LA:129:ASN:OD1	33:LA:134:PHE:CD1	2.74	0.41
37:LE:15:LYS:NZ	37:LE:15:LYS:HB2	2.36	0.41
37:LE:97:ASN:N	37:LE:97:ASN:HD22	2.17	0.41
40:LH:96:MET:HG2	40:LH:97:TYR:N	2.36	0.41
52:LT:7:VAL:HG12	52:LT:55:LEU:HD11	2.03	0.41
53:LU:201:ARG:O	53:LU:204:ARG:HD3	2.22	0.41
69:Lk:76:THR:CG2	69:Lk:79:ARG:HB3	2.51	0.41
77:11:513:G:H2'	77:11:514:A:C8	2.55	0.41
77:11:523:A:H2'	77:11:524:A:H8	1.86	0.41
77:11:1455:U:H2'	77:11:1456:C:C6	2.55	0.41
77:11:1647:C:H2'	77:11:1648:G:C8	2.56	0.41
80:14:692:A:O2'	80:14:708:C:N4	2.54	0.41
80:14:1748:G:H2'	80:14:1749:G:C8	2.55	0.41
80:14:2270:C:H2'	80:14:2271:U:O4'	2.20	0.41
80:14:2579:G:H3'	80:14:2580:C:H6	1.85	0.41
82:16:17:H2U:H2'	82:16:17:H2U:H62	1.86	0.41
11:SK:118:ARG:HG3	11:SK:118:ARG:HH11	1.86	0.40
14:SN:104:ARG:NH1	77:11:311:G:OP1	2.54	0.40
18:SR:196:ILE:HG23	18:SR:200:LYS:NZ	2.36	0.40
22:SV:65:LEU:HD22	22:SV:66:ALA:H	1.86	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:SY:44:ARG:HA	25:SY:44:ARG:HD2	1.86	0.40
33:LA:62:LYS:HE2	33:LA:62:LYS:HB3	1.27	0.40
33:LA:64:LYS:HB2	33:LA:108:HIS:ND1	2.36	0.40
33:LA:148:VAL:O	33:LA:152:LYS:N	2.50	0.40
76:10:156:U:C2	76:10:158:A:H5''	2.55	0.40
76:10:189:C:H1'	76:10:200:G:H22	1.86	0.40
77:11:81:U:H4'	77:11:82:G:OP2	2.21	0.40
77:11:1356:U:H2'	77:11:1357:G:C8	2.56	0.40
77:11:1679:A:H2'	77:11:1680:U:C6	2.56	0.40
80:14:545:C:H2'	80:14:546:U:C6	2.57	0.40
11:SK:42:ASN:ND2	11:SK:52:MET:SD	2.95	0.40
17:SQ:108:ARG:NH1	77:11:793:A:OP1	2.54	0.40
20:ST:85:ASN:ND2	20:ST:88:ASN:H	2.19	0.40
22:SV:35:LEU:HA	22:SV:38:SER:OG	2.22	0.40
38:LF:10:MET:HE1	38:LF:81:GLU:HG3	2.04	0.40
40:LH:109:LYS:HB2	40:LH:109:LYS:NZ	2.36	0.40
49:LQ:25:TYR:HE2	80:14:608:U:H5'	1.86	0.40
49:LQ:75:LYS:NZ	80:14:615:U:OP2	2.54	0.40
77:11:909:A:H2'	77:11:910:A:C8	2.56	0.40
77:11:1235:U:H2'	77:11:1236:G:H8	1.84	0.40
77:11:1250:U:H2'	77:11:1251:C:C6	2.56	0.40
77:11:1497:A:H5'	77:11:1498:U:H5''	2.03	0.40
80:14:1508:C:H2'	80:14:1509:A:C8	2.55	0.40
8:SH:37:LYS:HE2	8:SH:37:LYS:HB3	1.66	0.40
10:SJ:129:LEU:HD23	10:SJ:129:LEU:HA	1.83	0.40
24:SX:109:GLN:HE21	24:SX:115:ASP:HA	1.86	0.40
26:SZ:13:PHE:HB3	26:SZ:24:PHE:HB3	2.02	0.40
35:LC:209:ASP:OD1	35:LC:209:ASP:N	2.49	0.40
43:LK:196:LYS:HG2	43:LK:201:GLY:HA3	2.03	0.40
50:LR:30:LYS:NZ	80:14:2563:C:OP1	2.52	0.40
52:LT:29:ASP:OD2	56:LX:74:ILE:HD12	2.21	0.40
77:11:782:C:O2'	77:11:783:U:O5'	2.39	0.40
4:SD:56:ASP:HB3	4:SD:58:LYS:HE2	2.03	0.40
4:SD:211:ARG:HD2	77:11:1100:U:O4	2.21	0.40
8:SH:24:ARG:HB3	8:SH:118:THR:HG23	2.04	0.40
28:Sb:48:ALA:HB2	30:Sd:63:ARG:HH22	1.86	0.40
38:LF:95:MET:HG2	38:LF:184:VAL:HG22	2.03	0.40
61:Lc:76:LYS:HZ1	61:Lc:76:LYS:C	2.30	0.40
64:Lf:62:LYS:HB2	64:Lf:62:LYS:HE3	1.57	0.40
76:10:58:C:H1'	76:10:62:A:O2'	2.21	0.40
76:10:77:U:O2'	76:10:159:U:O2	2.38	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:10:149:A:H2'	76:10:150:G:H8	1.87	0.40
77:11:206:U:H2'	77:11:207:A:H8	1.87	0.40
77:11:214:A:H62	77:11:832:A:H1'	1.87	0.40
77:11:490:G:H1	77:11:504:U:H3	1.69	0.40
79:13:162:G:C6	80:14:1:G:C6	3.09	0.40
80:14:882:A:H2'	80:14:883:C:C6	2.56	0.40
80:14:1340:C:H2'	80:14:1341:U:O4'	2.22	0.40
15:SO:97:ILE:CD1	15:SO:116:PRO:HA	2.51	0.40
22:SV:108:ASP:HB3	22:SV:114:ARG:NH1	2.36	0.40
26:SZ:43:GLU:OE1	26:SZ:43:GLU:C	2.65	0.40
35:LC:221:ILE:HG12	35:LC:279:THR:HG23	2.03	0.40
36:LD:196:LYS:O	36:LD:199:MET:HG2	2.22	0.40
42:LJ:212:GLY:H	43:LK:288:ASN:ND2	2.19	0.40
43:LK:238:MET:HE2	43:LK:238:MET:HB3	1.90	0.40
53:LU:136:ASP:OD2	53:LU:139:HIS:HB2	2.21	0.40
61:Lc:95:ARG:O	61:Lc:99:LYS:HD3	2.21	0.40
76:10:149:A:H2'	76:10:150:G:C8	2.57	0.40
76:10:193:G:N3	76:10:193:G:H2'	2.36	0.40
80:14:1076:A:N6	80:14:1105:A:H2'	2.36	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%)	197 (98%)	3 (2%)	0	100	100
2	SB	209/248 (84%)	200 (96%)	9 (4%)	0	100	100
3	SC	181/187 (97%)	180 (99%)	1 (1%)	0	100	100
4	SD	215/280 (77%)	211 (98%)	4 (2%)	0	100	100
5	SE	192/210 (91%)	184 (96%)	8 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	SF	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
7	SG	138/147 (94%)	135 (98%)	3 (2%)	0	100	100
8	SH	100/122 (82%)	97 (97%)	3 (3%)	0	100	100
9	SI	130/150 (87%)	125 (96%)	4 (3%)	1 (1%)	16	53
10	SJ	137/142 (96%)	133 (97%)	4 (3%)	0	100	100
11	SK	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
12	SL	52/56 (93%)	52 (100%)	0	0	100	100
13	SM	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
14	SN	143/159 (90%)	140 (98%)	3 (2%)	0	100	100
15	SO	123/152 (81%)	120 (98%)	3 (2%)	0	100	100
16	SP	213/261 (82%)	210 (99%)	3 (1%)	0	100	100
17	SQ	257/264 (97%)	254 (99%)	3 (1%)	0	100	100
18	SR	228/249 (92%)	219 (96%)	9 (4%)	0	100	100
19	SS	186/191 (97%)	180 (97%)	6 (3%)	0	100	100
20	ST	181/212 (85%)	179 (99%)	2 (1%)	0	100	100
21	SU	81/118 (69%)	79 (98%)	2 (2%)	0	100	100
22	SV	115/143 (80%)	107 (93%)	8 (7%)	0	100	100
23	SW	117/131 (89%)	116 (99%)	1 (1%)	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%)	122 (98%)	3 (2%)	0	100	100
27	Sa	68/74 (92%)	68 (100%)	0	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	43/62 (69%)	42 (98%)	1 (2%)	0	100	100
32	Sf	67/156 (43%)	67 (100%)	0	0	100	100
33	LA	213/217 (98%)	195 (92%)	18 (8%)	0	100	100
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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	139 (96%)	6 (4%)	0	100	100
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
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%)	138 (99%)	2 (1%)	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%)	110 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	22/25 (88%)	22 (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	10880/12105 (90%)	10611 (98%)	268 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	SI	137	ASP

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	171/209 (82%)	168 (98%)	3 (2%)	51	67
2	SB	179/215 (83%)	175 (98%)	4 (2%)	45	64
3	SC	160/164 (98%)	157 (98%)	3 (2%)	50	66
4	SD	184/225 (82%)	181 (98%)	3 (2%)	55	69
5	SE	165/175 (94%)	159 (96%)	6 (4%)	31	52
6	SF	111/112 (99%)	110 (99%)	1 (1%)	70	77
7	SG	116/120 (97%)	112 (97%)	4 (3%)	32	55
8	SH	93/108 (86%)	89 (96%)	4 (4%)	26	48
9	SI	102/120 (85%)	97 (95%)	5 (5%)	22	44
10	SJ	111/114 (97%)	107 (96%)	4 (4%)	31	52

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	SK	122/122 (100%)	115 (94%)	7 (6%)	18	41
12	SL	46/47 (98%)	46 (100%)	0	100	100
13	SM	130/131 (99%)	129 (99%)	1 (1%)	73	78
14	SN	124/131 (95%)	121 (98%)	3 (2%)	43	63
15	SO	109/130 (84%)	108 (99%)	1 (1%)	70	77
16	SP	194/228 (85%)	190 (98%)	4 (2%)	47	65
17	SQ	225/228 (99%)	219 (97%)	6 (3%)	39	60
18	SR	197/213 (92%)	188 (95%)	9 (5%)	24	46
19	SS	168/170 (99%)	163 (97%)	5 (3%)	36	57
20	ST	159/176 (90%)	152 (96%)	7 (4%)	25	47
21	SU	78/109 (72%)	73 (94%)	5 (6%)	16	38
22	SV	94/112 (84%)	87 (93%)	7 (7%)	13	34
23	SW	108/119 (91%)	105 (97%)	3 (3%)	38	59
24	SX	111/114 (97%)	107 (96%)	4 (4%)	31	52
25	SY	69/69 (100%)	66 (96%)	3 (4%)	26	48
26	SZ	108/113 (96%)	93 (86%)	15 (14%)	3	15
27	Sa	60/64 (94%)	57 (95%)	3 (5%)	22	43
28	Sb	87/100 (87%)	86 (99%)	1 (1%)	65	74
29	Sc	75/76 (99%)	73 (97%)	2 (3%)	39	60
30	Sd	54/57 (95%)	52 (96%)	2 (4%)	30	51
31	Se	38/49 (78%)	37 (97%)	1 (3%)	40	61
32	Sf	60/134 (45%)	57 (95%)	3 (5%)	22	43
33	LA	193/196 (98%)	167 (86%)	26 (14%)	4	16
34	LB	190/197 (96%)	187 (98%)	3 (2%)	55	69
35	LC	331/333 (99%)	328 (99%)	3 (1%)	70	77
36	LD	325/331 (98%)	301 (93%)	24 (7%)	13	34
37	LE	145/157 (92%)	141 (97%)	4 (3%)	38	59
38	LF	167/170 (98%)	161 (96%)	6 (4%)	31	52
39	LG	174/175 (99%)	170 (98%)	4 (2%)	44	64
40	LH	103/109 (94%)	101 (98%)	2 (2%)	50	66
41	LI	119/120 (99%)	117 (98%)	2 (2%)	53	68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	LJ	173/180 (96%)	167 (96%)	6 (4%)	32	54
43	LK	243/246 (99%)	233 (96%)	10 (4%)	27	49
44	LL	133/151 (88%)	131 (98%)	2 (2%)	57	71
45	LM	106/134 (79%)	104 (98%)	2 (2%)	50	66
46	LN	115/132 (87%)	114 (99%)	1 (1%)	70	77
47	LO	108/109 (99%)	106 (98%)	2 (2%)	50	66
48	LP	207/209 (99%)	202 (98%)	5 (2%)	43	63
49	LQ	174/194 (90%)	171 (98%)	3 (2%)	53	68
50	LR	201/205 (98%)	194 (96%)	7 (4%)	32	54
51	LS	166/166 (100%)	166 (100%)	0	100	100
52	LT	112/113 (99%)	109 (97%)	3 (3%)	39	60
53	LU	176/177 (99%)	173 (98%)	3 (2%)	53	68
54	LV	154/155 (99%)	150 (97%)	4 (3%)	40	61
55	LW	158/180 (88%)	152 (96%)	6 (4%)	29	51
56	LX	163/164 (99%)	160 (98%)	3 (2%)	51	67
57	LY	140/141 (99%)	138 (99%)	2 (1%)	59	72
58	LZ	89/97 (92%)	84 (94%)	5 (6%)	19	41
59	La	57/133 (43%)	56 (98%)	1 (2%)	51	67
60	Lb	116/117 (99%)	112 (97%)	4 (3%)	32	55
61	Lc	121/123 (98%)	117 (97%)	4 (3%)	33	55
62	Ld	42/43 (98%)	41 (98%)	1 (2%)	43	63
63	Le	85/98 (87%)	83 (98%)	2 (2%)	43	63
64	Lf	95/106 (90%)	93 (98%)	2 (2%)	47	65
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	76
68	Lj	84/91 (92%)	83 (99%)	1 (1%)	63	74
69	Lk	72/77 (94%)	72 (100%)	0	100	100
70	Ll	64/65 (98%)	63 (98%)	1 (2%)	55	69
71	Lm	47/48 (98%)	46 (98%)	1 (2%)	47	65
72	Ln	46/114 (40%)	46 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	Lo	21/23 (91%)	16 (76%)	5 (24%)	1	5
74	Lp	85/91 (93%)	82 (96%)	3 (4%)	32	54
75	Lq	60/62 (97%)	59 (98%)	1 (2%)	53	68
All	All	9474/10310 (92%)	9180 (97%)	294 (3%)	36	56

All (294) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	SA	40	LYS
1	SA	66	VAL
1	SA	170	SER
2	SB	8	ILE
2	SB	156	LYS
2	SB	185	LEU
2	SB	194	ASP
3	SC	63	THR
3	SC	96	ASP
3	SC	173	ARG
4	SD	87	LYS
4	SD	157	LYS
4	SD	168	VAL
5	SE	26	ASN
5	SE	29	THR
5	SE	47	THR
5	SE	84	MET
5	SE	161	THR
5	SE	188	LYS
6	SF	74	VAL
7	SG	26	VAL
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	112	GLN
9	SI	115	LEU
9	SI	129	GLU
9	SI	132	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	SJ	50	VAL
10	SJ	98	GLU
10	SJ	104	PHE
10	SJ	118	ARG
11	SK	54	LYS
11	SK	67	LEU
11	SK	101	ASN
11	SK	109	ASP
11	SK	114	LEU
11	SK	115	LYS
11	SK	116	LYS
13	SM	143	SER
14	SN	45	THR
14	SN	81	MET
14	SN	118	VAL
15	SO	21	LYS
16	SP	22	ASP
16	SP	42	ASN
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	123	LEU
18	SR	126	LEU
18	SR	127	THR
18	SR	128	ASP
18	SR	129	THR
18	SR	133	ARG
18	SR	180	ILE
18	SR	226	GLU
19	SS	8	ILE
19	SS	34	ASN
19	SS	43	ASP
19	SS	65	VAL
19	SS	85	GLU
20	ST	3	ILE
20	ST	71	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	44	GLN
21	SU	89	MET
21	SU	100	ILE
21	SU	109	LEU
22	SV	27	ILE
22	SV	35	LEU
22	SV	75	VAL
22	SV	92	VAL
22	SV	104	LEU
22	SV	123	VAL
22	SV	130	GLU
23	SW	84	PHE
23	SW	91	ILE
23	SW	101	GLU
24	SX	35	THR
24	SX	61	MET
24	SX	107	GLN
24	SX	126	SER
25	SY	11	LEU
25	SY	25	THR
25	SY	50	THR
26	SZ	4	LYS
26	SZ	6	VAL
26	SZ	13	PHE
26	SZ	15	THR
26	SZ	37	SER
26	SZ	47	ARG
26	SZ	50	GLU
26	SZ	51	VAL
26	SZ	52	LYS
26	SZ	80	SER
26	SZ	81	VAL
26	SZ	82	GLU
26	SZ	102	VAL
26	SZ	118	LYS
26	SZ	124	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	Sa	68	ARG
27	Sa	92	VAL
27	Sa	102	THR
28	Sb	47	GLN
29	Sc	45	ILE
29	Sc	67	GLN
30	Sd	5	THR
30	Sd	56	GLU
31	Se	38	MET
32	Sf	134	ASN
32	Sf	137	ASP
32	Sf	139	HIS
33	LA	3	SER
33	LA	5	LEU
33	LA	6	GLN
33	LA	24	LYS
33	LA	25	LYS
33	LA	29	THR
33	LA	33	GLU
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	62	LYS
33	LA	63	MET
33	LA	140	HIS
33	LA	141	GLN
33	LA	142	GLU
33	LA	144	LEU
33	LA	147	LYS
33	LA	151	THR
33	LA	152	LYS
33	LA	158	GLN
33	LA	161	LYS
33	LA	163	LEU
33	LA	165	MET
34	LB	176	GLU
34	LB	181	LYS
34	LB	208	GLU
35	LC	60	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
35	LC	159	VAL
35	LC	295	SER
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
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	11	MET
37	LE	25	VAL
37	LE	48	VAL
37	LE	124	ILE
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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
49	LQ	190	ASP
50	LR	45	THR
50	LR	84	LEU
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
54	LV	166	VAL
55	LW	59	SER
55	LW	106	LEU
55	LW	111	GLU
55	LW	133	LYS
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
58	LZ	40	GLU
58	LZ	59	SER
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	26	THR
74	Lp	29	LYS
75	Lq	6	LYS

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	169	HIS
1	SA	191	GLN
2	SB	148	GLN
2	SB	201	GLN
3	SC	9	ASN
4	SD	64	GLN
5	SE	26	ASN
5	SE	88	ASN
6	SF	98	GLN
7	SG	15	GLN
7	SG	39	ASN
7	SG	65	HIS
9	SI	82	GLN
11	SK	42	ASN
12	SL	5	ASN
12	SL	8	ASN
12	SL	46	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
15	SO	144	HIS
16	SP	52	GLN
16	SP	92	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
16	SP	150	GLN
17	SQ	8	HIS
17	SQ	50	ASN
17	SQ	67	GLN
17	SQ	69	GLN
17	SQ	133	GLN
18	SR	13	GLN
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	44	GLN
21	SU	66	ASN
22	SV	61	GLN
23	SW	15	GLN
23	SW	74	GLN
24	SX	109	GLN
24	SX	112	ASN
25	SY	46	ASN
26	SZ	83	ASN
26	SZ	114	ASN
28	Sb	13	HIS
29	Sc	60	ASN
30	Sd	35	ASN
31	Se	39	GLN
32	Sf	123	ASN
32	Sf	134	ASN
33	LA	6	GLN
33	LA	44	GLN
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	19	HIS
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
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
48	LP	46	ASN
48	LP	110	GLN
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
60	Lb	96	ASN
61	Lc	78	GLN
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	41	ASN
66	Lh	111	ASN
67	Li	75	ASN
68	Lj	41	HIS
68	Lj	95	ASN
69	Lk	48	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 ⓘ

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
76	10	157/204 (76%)	105 (66%)	17 (10%)
77	11	1618/1808 (89%)	292 (18%)	15 (0%)
78	12	118/119 (99%)	12 (10%)	0
79	13	162/163 (99%)	33 (20%)	0
80	14	3138/3390 (92%)	574 (18%)	26 (0%)
81	15	5/6 (83%)	0	0
82	16	74/75 (98%)	26 (35%)	3 (4%)
All	All	5272/5765 (91%)	1042 (19%)	61 (1%)

All (1042) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
76	10	49	U
76	10	50	G
76	10	53	G
76	10	54	C
76	10	59	G
76	10	60	A
76	10	61	U
76	10	62	A
76	10	64	C
76	10	65	G
76	10	67	A
76	10	68	U
76	10	69	A
76	10	70	G
76	10	71	U
76	10	72	G
76	10	73	U
76	10	74	U
76	10	75	U
76	10	76	U
76	10	77	U
76	10	78	C
76	10	80	C
76	10	82	C
76	10	86	U
76	10	87	U
76	10	88	A
76	10	89	A
76	10	90	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
76	10	91	U
76	10	92	C
76	10	93	G
76	10	94	A
76	10	95	A
76	10	100	U
76	10	105	C
76	10	106	U
76	10	107	U
76	10	108	G
76	10	109	G
76	10	112	C
76	10	113	G
76	10	118	G
76	10	119	G
76	10	120	U
76	10	121	C
76	10	122	A
76	10	123	A
76	10	125	U
76	10	126	G
76	10	129	U
76	10	130	A
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	147	G
76	10	148	C
76	10	152	C
76	10	154	C
76	10	155	G
76	10	156	U
76	10	157	A
76	10	158	A
76	10	159	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
76	10	160	A
76	10	161	A
76	10	162	A
76	10	163	G
76	10	165	G
76	10	166	A
76	10	167	G
76	10	169	G
76	10	172	U
76	10	173	C
76	10	176	A
76	10	177	U
76	10	178	C
76	10	181	C
76	10	183	C
76	10	184	G
76	10	185	U
76	10	186	U
76	10	187	A
76	10	188	C
76	10	190	C
76	10	191	C
76	10	193	G
76	10	194	G
76	10	195	U
76	10	196	A
76	10	197	G
76	10	198	G
76	10	199	G
76	10	200	G
76	10	201	C
76	10	202	C
76	10	203	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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	77	A
77	11	80	C
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
77	11	151	A
77	11	158	C
77	11	178	A
77	11	186	A
77	11	188	U
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	427	G
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
77	11	509	A
77	11	510	U
77	11	513	G
77	11	517	G
77	11	522	C
77	11	539	C
77	11	541	A
77	11	545	U
77	11	558	A
77	11	560	G
77	11	568	C
77	11	578	C
77	11	580	G
77	11	581	U
77	11	582	A
77	11	583	A
77	11	584	U
77	11	585	U
77	11	597	A
77	11	598	G
77	11	606	U
77	11	609	A
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	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
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	1161	C
77	11	1170	G
77	11	1188	U
77	11	1190	U
77	11	1194	U
77	11	1197	A
77	11	1199	A
77	11	1202	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
77	11	1203	G
77	11	1204	G
77	11	1205	A
77	11	1210	U
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	1304	U
77	11	1307	G
77	11	1309	C
77	11	1317	U
77	11	1318	U
77	11	1324	A
77	11	1328	A
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	1376	G
77	11	1377	C
77	11	1378	C
77	11	1379	A
77	11	1380	G
77	11	1383	U
77	11	1395	U
77	11	1396	A
77	11	1403	U
77	11	1404	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
77	11	1670	U
77	11	1672	C
77	11	1684	C
77	11	1686	G
77	11	1688	U
77	11	1689	C
77	11	1691	C
77	11	1726	G
77	11	1728	G
77	11	1731	G
77	11	1743	U
77	11	1744	U
77	11	1747	C
77	11	1748	A
77	11	1755	G
77	11	1762	G
77	11	1768	G
77	11	1770	A
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	84	U
79	13	85	C
79	13	87	C
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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	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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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	2446	A
80	14	2447	C
80	14	2449	U
80	14	2450	G
80	14	2451	A
80	14	2452	G
80	14	2457	G
80	14	2461	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
80	14	2462	A
80	14	2463	U
80	14	2471	A
80	14	2475	G
80	14	2478	A
80	14	2479	G
80	14	2489	A
80	14	2492	U
80	14	2494	C
80	14	2497	C
80	14	2501	U
80	14	2502	U
80	14	2505	A
80	14	2506	A
80	14	2507	C
80	14	2508	G
80	14	2510	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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
80	14	2573	U
80	14	2574	U
80	14	2575	G
80	14	2576	C
80	14	2578	G
80	14	2579	G
80	14	2580	C
80	14	2588	G
80	14	2593	A
80	14	2596	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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
80	14	2804	A
80	14	2805	A
80	14	2813	C
80	14	2820	A
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
80	14	3103	G
80	14	3118	G
80	14	3132	A
80	14	3133	U
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
80	14	3269	C
80	14	3271	A
80	14	3272	U
80	14	3273	C
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
82	16	8	G
82	16	9	U
82	16	12	C
82	16	13	G
82	16	14	C
82	16	15	A
82	16	16	G
82	16	17	H2U
82	16	18	G
82	16	19	G
82	16	20	A
82	16	21	A
82	16	22	G
82	16	23	C
82	16	24	G
82	16	44	A
82	16	45	U
82	16	46	7MG
82	16	47	H2U
82	16	48	5MC
82	16	51	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
82	16	58	1MA
82	16	62	C
82	16	68	G
82	16	72	U
82	16	76	A

All (61) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
76	10	60	A
76	10	68	U
76	10	74	U
76	10	88	A
76	10	93	G
76	10	106	U
76	10	120	U
76	10	124	A
76	10	133	G
76	10	134	U
76	10	144	U
76	10	157	A
76	10	160	A
76	10	161	A
76	10	177	U
76	10	185	U
76	10	194	G
77	11	127	G
77	11	128	G
77	11	373	U
77	11	503	C
77	11	544	A
77	11	819	G
77	11	1059	G
77	11	1203	G
77	11	1220	A
77	11	1234	U
77	11	1433	G
77	11	1463	G
77	11	1578	G
77	11	1663	U
77	11	1686	G
80	14	113	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
80	14	294	U
80	14	590	C
80	14	601	C
80	14	617	C
80	14	692	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	2529	A
80	14	2552	C
80	14	2573	U
80	14	2731	G
80	14	2793	A
80	14	3168	C
82	16	17	H2U
82	16	18	G
82	16	46	7MG

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

10 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
82	1MG	16	10	82	22,26,27	1.09	2 (9%)	33,39,42	1.76	5 (15%)
82	7MG	16	46	82	22,26,27	0.93	1 (4%)	29,39,42	0.78	1 (3%)
82	H2U	16	17	82	18,21,22	0.73	0	21,30,33	1.09	2 (9%)
82	2MG	16	11	82	23,26,27	1.29	3 (13%)	32,38,41	2.23	8 (25%)
82	1MA	16	58	82	21,25,26	0.38	0	31,37,40	0.75	0
82	H2U	16	47	82	18,21,22	0.69	1 (5%)	21,30,33	1.55	3 (14%)
82	5MC	16	48	82	18,22,23	0.35	0	26,32,35	0.58	1 (3%)
82	T6A	16	37	82	31,34,35	0.53	0	44,49,52	0.86	1 (2%)
82	5MC	16	49	82	18,22,23	1.00	2 (11%)	26,32,35	1.20	3 (11%)
82	M2G	16	26	82	24,27,28	1.31	4 (16%)	35,40,43	1.85	6 (17%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	1MG	16	10	82	-	0/7/25/26	0/3/3/3
82	7MG	16	46	82	-	5/7/37/38	0/3/3/3
82	H2U	16	17	82	-	7/7/38/39	0/2/2/2
82	2MG	16	11	82	-	0/9/27/28	0/3/3/3
82	1MA	16	58	82	-	0/7/25/26	0/3/3/3
82	H2U	16	47	82	-	5/7/38/39	0/2/2/2
82	5MC	16	48	82	-	3/7/25/26	0/2/2/2
82	T6A	16	37	82	-	1/23/41/42	0/3/3/3
82	5MC	16	49	82	-	2/7/25/26	0/2/2/2
82	M2G	16	26	82	-	1/11/29/30	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	16	46	7MG	C5-N7	3.63	1.39	1.35
82	16	26	M2G	C5-C4	3.08	1.47	1.38
82	16	10	1MG	C5-C4	3.03	1.47	1.38
82	16	11	2MG	C5-C4	3.02	1.47	1.38
82	16	26	M2G	C6-N1	-2.84	1.33	1.38
82	16	11	2MG	C6-N1	-2.72	1.33	1.38
82	16	49	5MC	C6-C5	2.72	1.39	1.34
82	16	26	M2G	C2-N2	2.52	1.39	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	16	49	5MC	C6-N1	-2.48	1.33	1.38
82	16	11	2MG	C5-N7	-2.40	1.34	1.39
82	16	26	M2G	C5-N7	-2.38	1.34	1.39
82	16	10	1MG	C5-N7	-2.35	1.34	1.39
82	16	47	H2U	C2-N3	-2.19	1.34	1.38

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	16	11	2MG	C2-N3-C4	7.05	120.78	112.04
82	16	11	2MG	C5-C4-N3	-6.47	117.96	128.46
82	16	26	M2G	C5-C4-N3	-6.40	118.08	128.46
82	16	47	H2U	C4-N3-C2	-6.19	120.66	125.79
82	16	10	1MG	C5-C4-N3	-5.35	119.78	128.46
82	16	26	M2G	N9-C4-N3	4.85	135.69	125.94
82	16	11	2MG	N9-C4-N3	4.82	135.63	125.94
82	16	26	M2G	C2-N3-C4	4.47	120.77	112.51
82	16	10	1MG	C2-N3-C4	4.36	121.78	111.98
82	16	10	1MG	N9-C4-N3	4.02	134.02	125.94
82	16	37	T6A	C5-C6-N6	3.56	128.13	118.71
82	16	17	H2U	C4-N3-C2	-3.38	122.98	125.79
82	16	49	5MC	C5-C6-N1	-3.14	120.11	123.34
82	16	11	2MG	C6-C5-N7	2.80	135.45	130.25
82	16	26	M2G	C6-C5-N7	2.80	135.45	130.25
82	16	10	1MG	C4-C5-N7	-2.77	106.34	110.72
82	16	49	5MC	O2-C2-N3	-2.74	117.88	122.33
82	16	49	5MC	C5-C4-N3	-2.66	118.81	121.67
82	16	10	1MG	C6-C5-N7	2.65	135.34	129.35
82	16	26	M2G	C4-C5-N7	-2.58	106.64	110.72
82	16	11	2MG	C4-C5-N7	-2.57	106.66	110.72
82	16	11	2MG	CM2-N2-C2	-2.55	118.22	123.86
82	16	11	2MG	C2-N1-C6	-2.44	121.67	124.48
82	16	47	H2U	N3-C2-N1	-2.40	114.11	116.65
82	16	26	M2G	O6-C6-C5	-2.22	120.70	126.60
82	16	11	2MG	O6-C6-C5	-2.22	120.72	126.60
82	16	48	5MC	C5-C6-N1	-2.15	121.13	123.34
82	16	47	H2U	C3'-C2'-C1'	2.10	105.41	101.43
82	16	46	7MG	N9-C8-N7	-2.05	100.44	103.38
82	16	17	H2U	C3'-C2'-C1'	2.04	105.29	101.43

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
82	16	17	H2U	O4'-C4'-C5'-O5'
82	16	17	H2U	C3'-C4'-C5'-O5'
82	16	17	H2U	O4'-C1'-N1-C6
82	16	17	H2U	C2'-C1'-N1-C2
82	16	17	H2U	C2'-C1'-N1-C6
82	16	47	H2U	C2'-C1'-N1-C2
82	16	47	H2U	O4'-C4'-C5'-O5'
82	16	48	5MC	O4'-C4'-C5'-O5'
82	16	48	5MC	C3'-C4'-C5'-O5'
82	16	47	H2U	C3'-C4'-C5'-O5'
82	16	47	H2U	C2'-C1'-N1-C6
82	16	46	7MG	O4'-C4'-C5'-O5'
82	16	46	7MG	C4'-C5'-O5'-P
82	16	46	7MG	C2'-C1'-N9-C8
82	16	17	H2U	C4'-C5'-O5'-P
82	16	46	7MG	C3'-C4'-C5'-O5'
82	16	49	5MC	C3'-C4'-C5'-O5'
82	16	48	5MC	C4'-C5'-O5'-P
82	16	49	5MC	O4'-C4'-C5'-O5'
82	16	37	T6A	N1-C6-N6-C10
82	16	26	M2G	C3'-C4'-C5'-O5'
82	16	46	7MG	O4'-C1'-N9-C8
82	16	47	H2U	O4'-C1'-N1-C2
82	16	17	H2U	O4'-C1'-N1-C2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	16	17	H2U	2	0
82	16	37	T6A	2	0
82	16	26	M2G	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

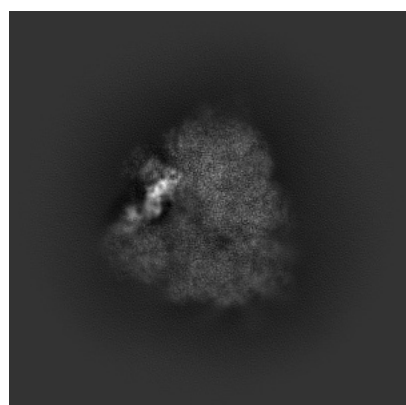
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65328. These allow visual inspection of the internal detail of the map and identification of artifacts.

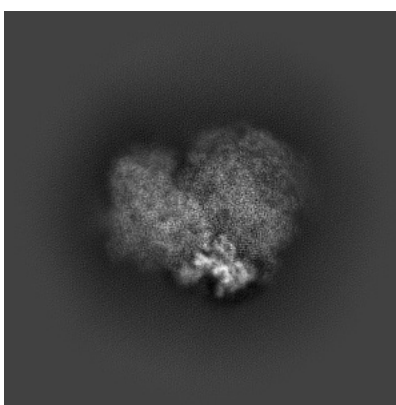
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

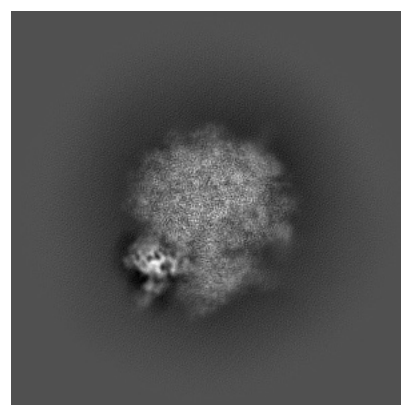
6.1.1 Primary map



X



Y

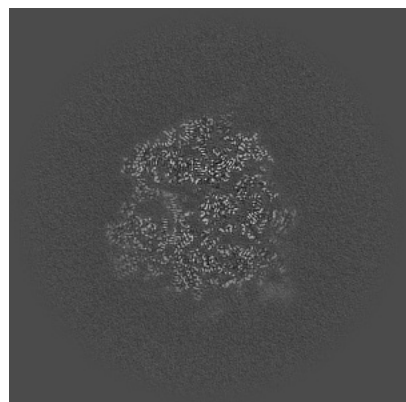


Z

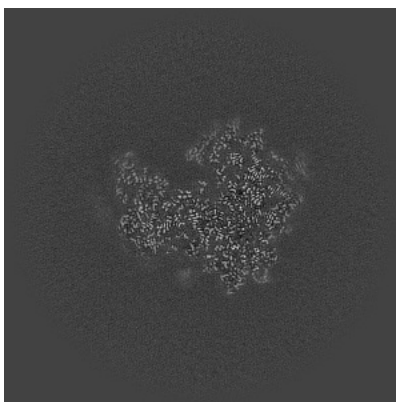
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

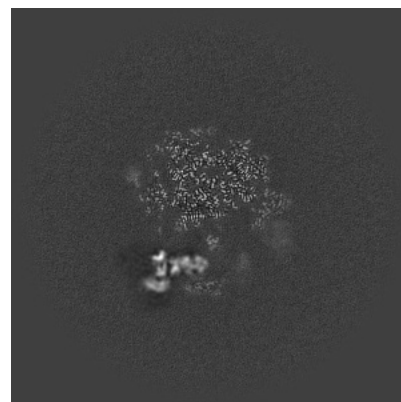
6.2.1 Primary map



X Index: 280



Y Index: 280

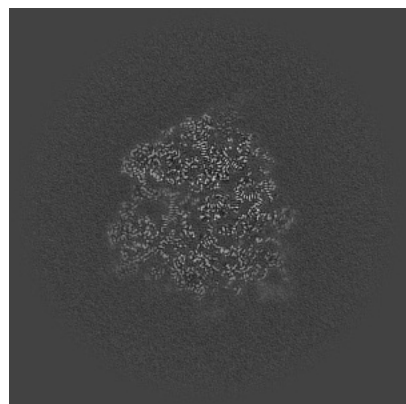


Z Index: 280

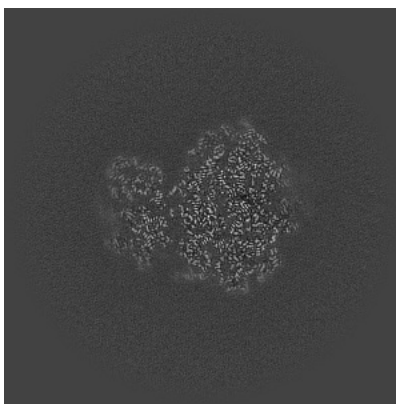
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

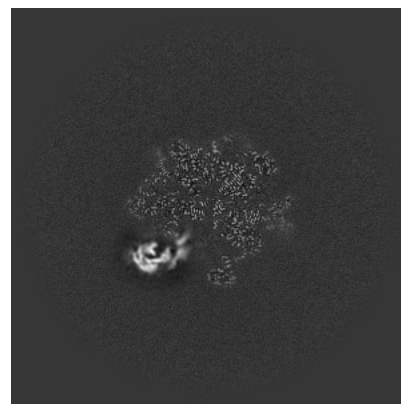
6.3.1 Primary map



X Index: 283



Y Index: 294

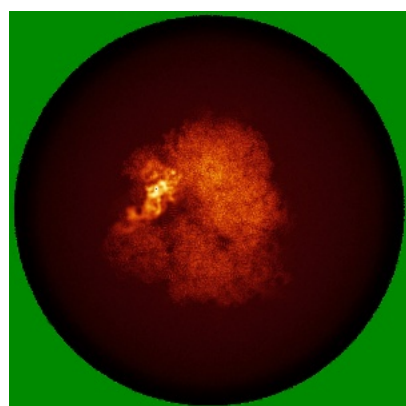


Z Index: 310

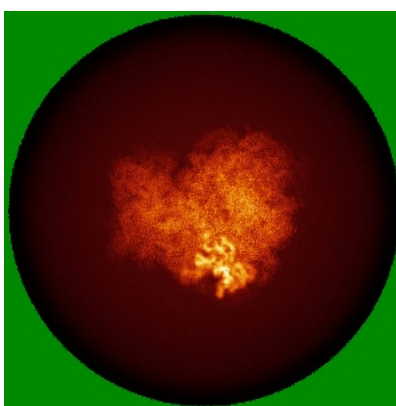
The images above show the largest variance slices of the map in three orthogonal directions.

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

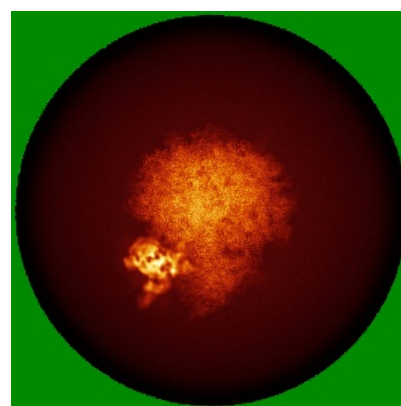
6.4.1 Primary map



X



Y

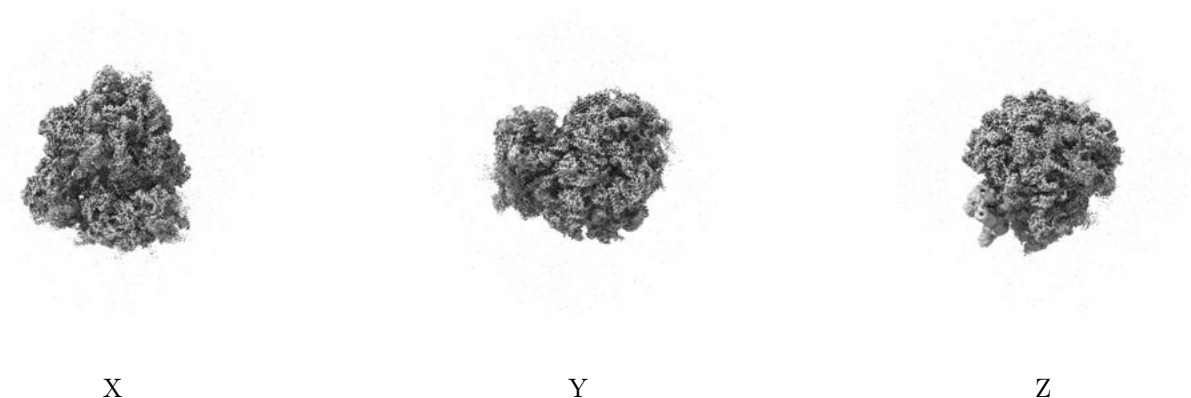


Z

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

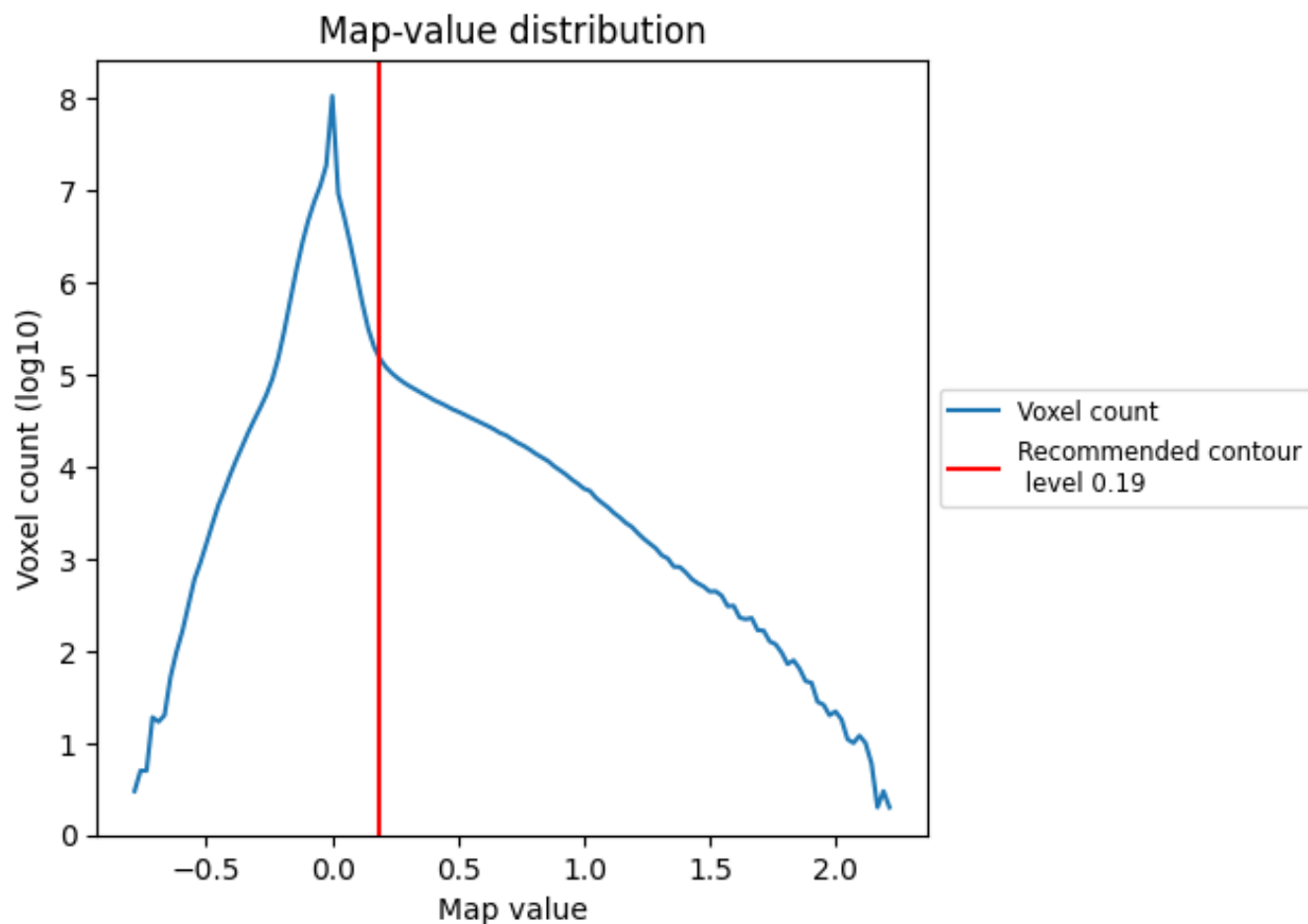
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

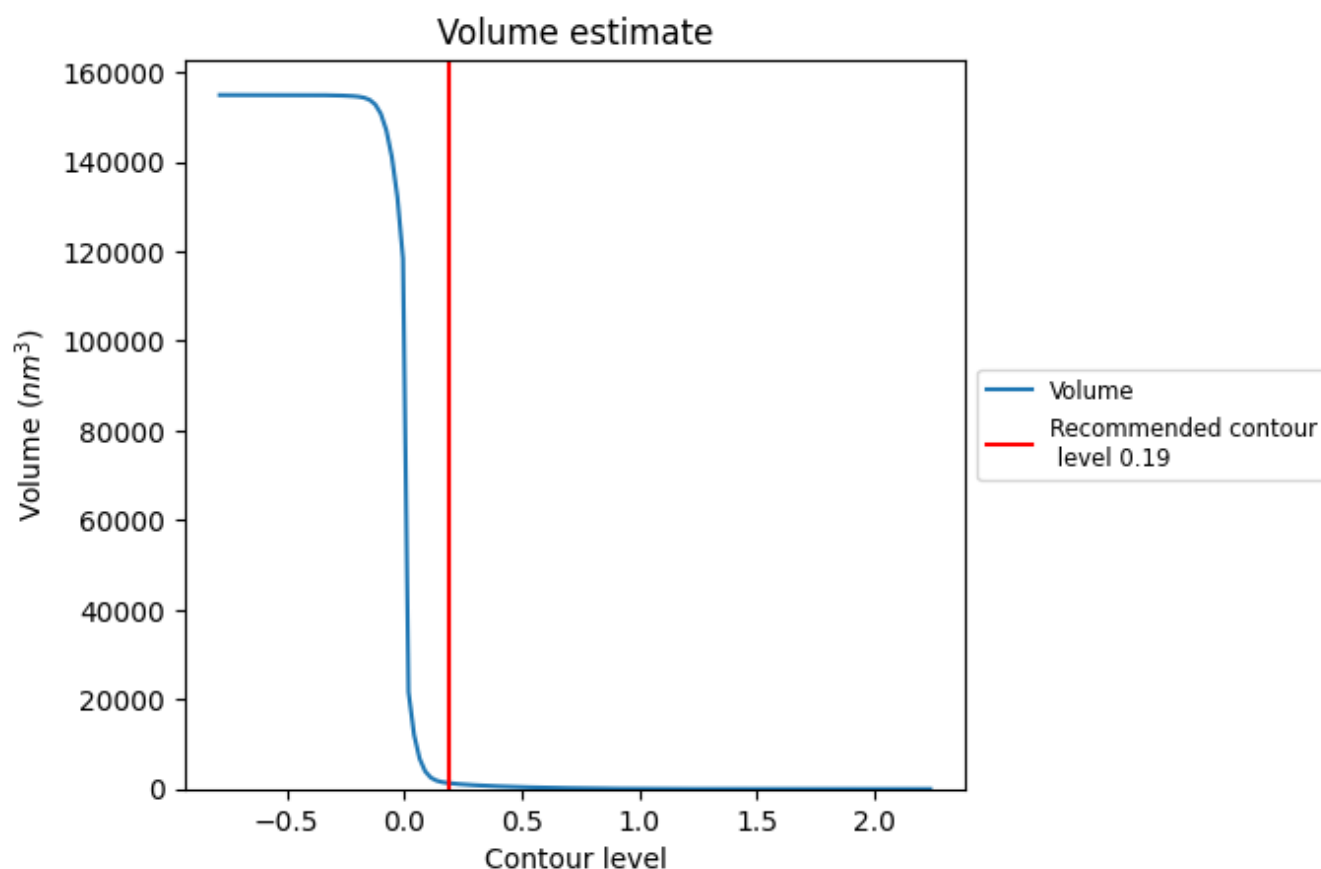
This section contains the results of statistical analysis of the map.

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.

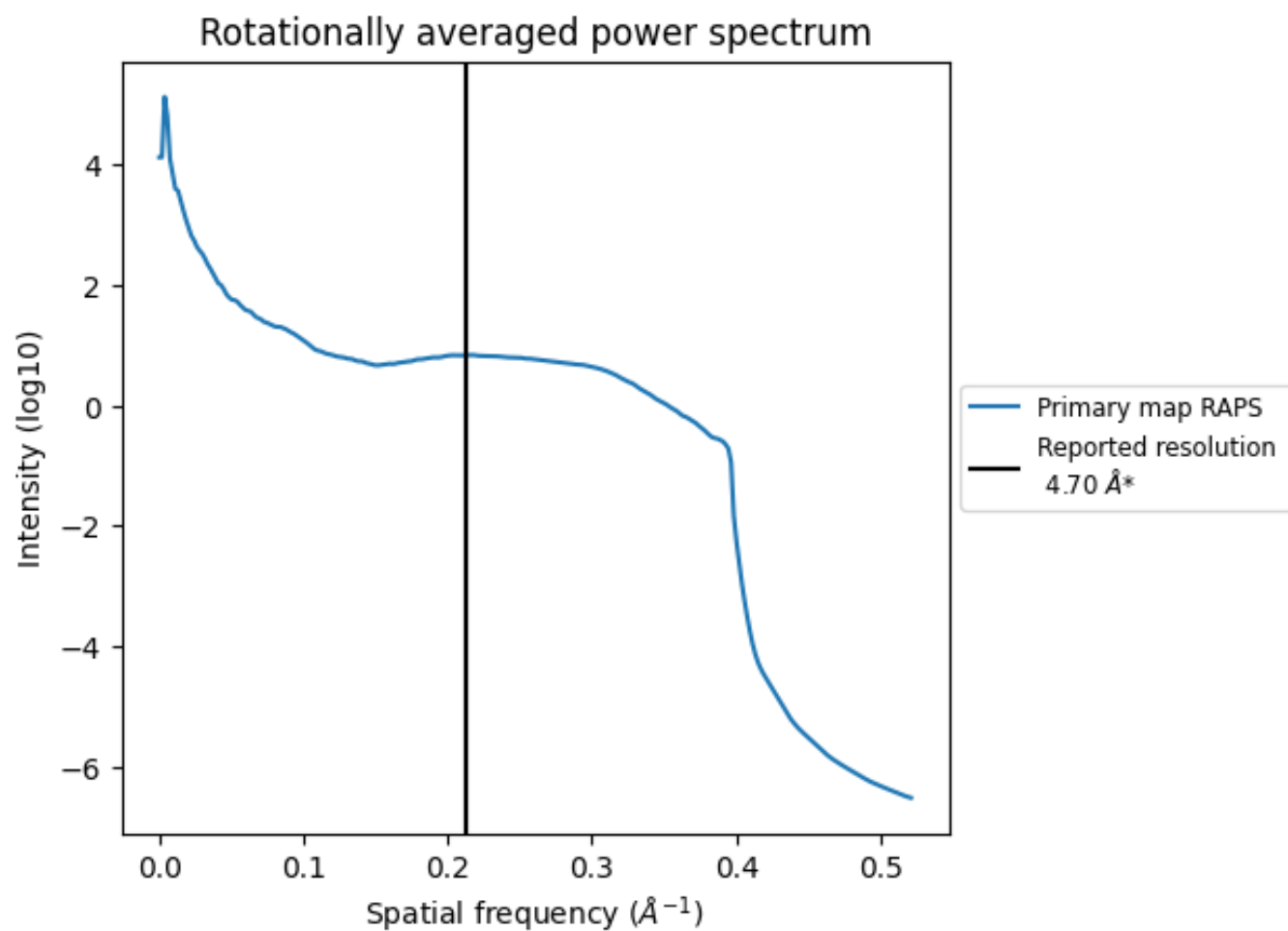
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1306 nm³; this corresponds to an approximate mass of 1179 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 0.213 Å⁻¹

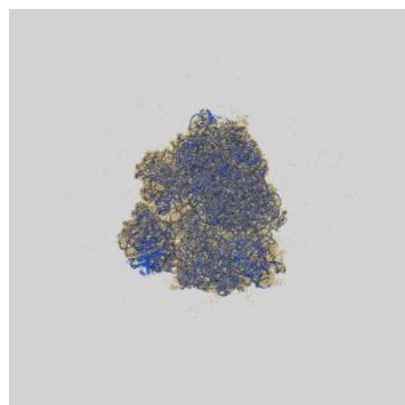
8 Fourier-Shell correlation

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

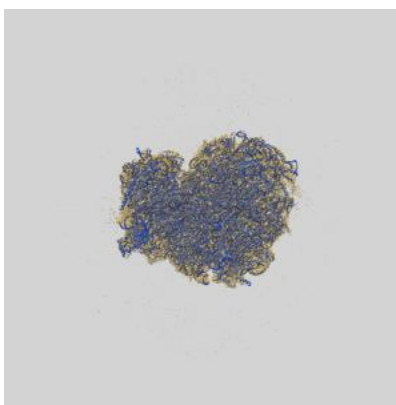
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65328 and PDB model 9VTH. Per-residue inclusion information can be found in [section 3](#) on [page 24](#).

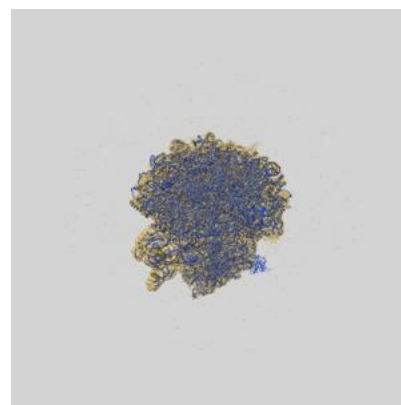
9.1 Map-model overlay [i](#)



X



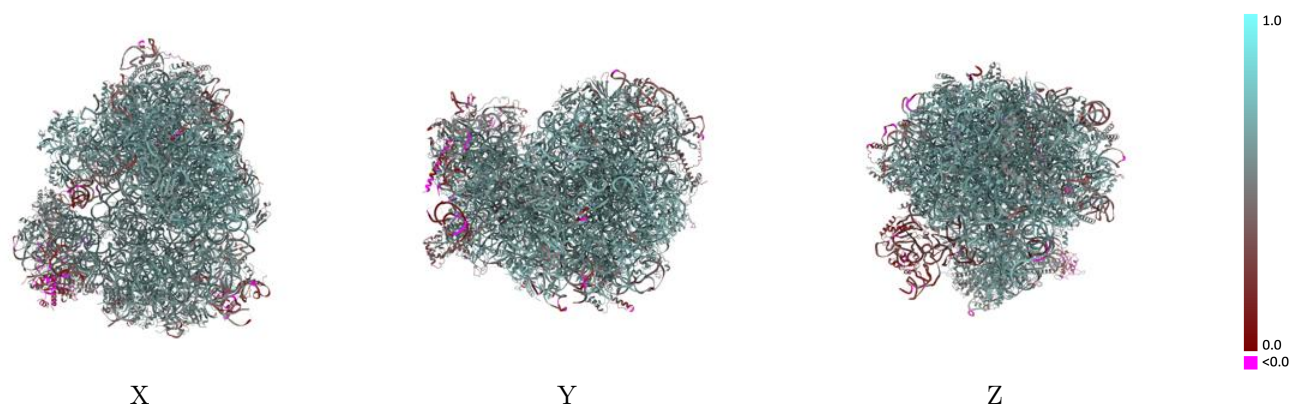
Y



Z

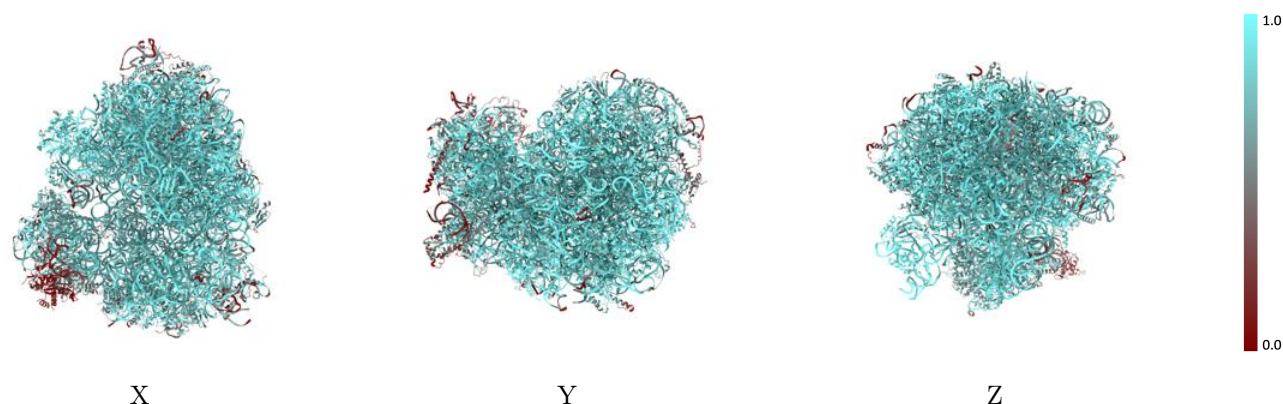
The images above show the 3D surface view of the map at the recommended contour level 0.19 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



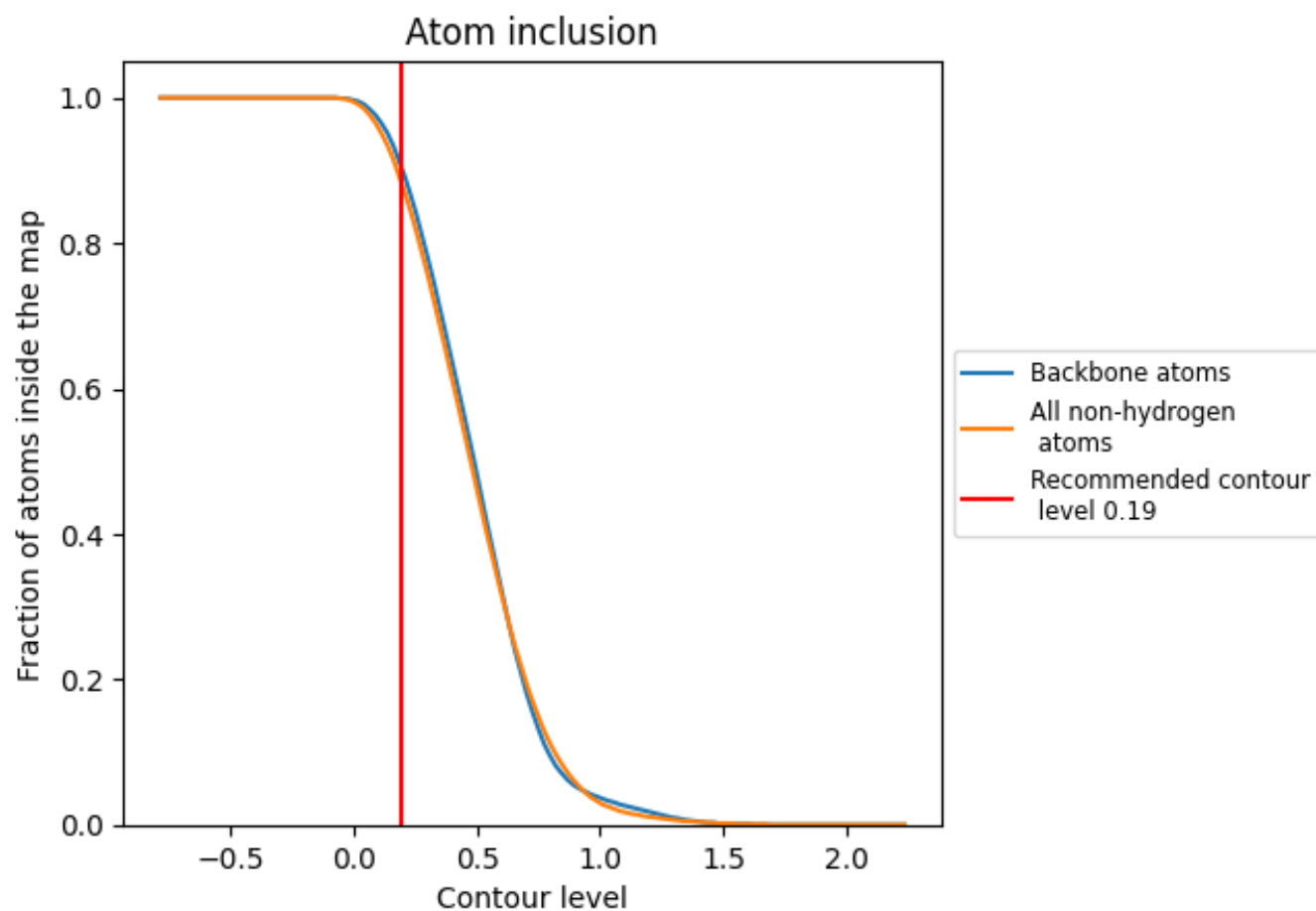
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.19).

9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 89% 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 (0.19) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8870	 0.5780
10	 0.9790	 0.2270
11	 0.8960	 0.5710
12	 0.9960	 0.6410
13	 0.9280	 0.6000
14	 0.9460	 0.6090
15	 0.9300	 0.6190
16	 0.8760	 0.5440
LA	 0.9230	 0.2010
LB	 0.9790	 0.6650
LC	 0.9530	 0.6490
LD	 0.8610	 0.6010
LE	 0.8480	 0.5770
LF	 0.8280	 0.5600
LG	 0.9300	 0.6300
LH	 0.9510	 0.6480
LI	 0.9580	 0.6480
LJ	 0.9280	 0.6270
LK	 0.8880	 0.5960
LL	 0.9530	 0.6500
LM	 0.9030	 0.6230
LN	 0.9460	 0.6320
LO	 0.8670	 0.5930
LP	 0.8850	 0.6130
LQ	 0.6500	 0.4780
LR	 0.8220	 0.5580
LS	 0.9230	 0.6240
LT	 0.8780	 0.5930
LU	 0.9870	 0.6650
LV	 0.9730	 0.6540
LW	 0.8390	 0.5940
LX	 0.9340	 0.6350
LY	 0.9210	 0.6320
LZ	 0.6950	 0.5060
La	 0.9210	 0.6420



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Lb	 0.9220	 0.6160
Lc	 0.5840	 0.5350
Ld	 0.9220	 0.6110
Le	 0.9290	 0.6200
Lf	 0.8900	 0.6100
Lg	 0.9610	 0.6490
Lh	 0.9670	 0.6540
Li	 0.9080	 0.6140
Lj	 0.9060	 0.6070
Lk	 0.9790	 0.6630
Ll	 0.8300	 0.5710
Lm	 0.9720	 0.6550
Ln	 0.7680	 0.6020
Lo	 0.8770	 0.6070
Lp	 0.9570	 0.6490
Lq	 0.9490	 0.6530
SA	 0.8030	 0.5650
SB	 0.5890	 0.4730
SC	 0.8160	 0.5600
SD	 0.8860	 0.6080
SE	 0.7970	 0.5520
SF	 0.9350	 0.6380
SG	 0.7900	 0.5480
SH	 0.5480	 0.4640
SI	 0.9120	 0.6200
SJ	 0.8880	 0.6140
SK	 0.7630	 0.5470
SL	 0.7600	 0.5540
SM	 0.9020	 0.6200
SN	 0.9170	 0.6290
SO	 0.6150	 0.4720
SP	 0.8840	 0.6050
SQ	 0.8540	 0.5850
SR	 0.5100	 0.3770
SS	 0.5680	 0.4580
ST	 0.8610	 0.5980
SU	 0.4510	 0.3870
SV	 0.0110	 0.0690
SW	 0.4370	 0.4190
SX	 0.8160	 0.5560
SY	 0.7930	 0.5530
SZ	 0.6440	 0.4740

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Sa	 0.6790	 0.5070
Sb	 0.9080	 0.6240
Sc	 0.7770	 0.5470
Sd	 0.7650	 0.5490
Se	 0.5920	 0.4170
Sf	 0.0240	 0.0810