



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 02:20 AM UTC

PDB ID : 5OT7 / pdb_00005ot7
EMDB ID : EMD-3852
Title : Elongation factor G-ribosome complex captures in the absence of inhibitors.
Authors : Mace, K.; Giudice, E.; Chat, S.; Gillet, R.
Deposited on : 2017-08-21
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

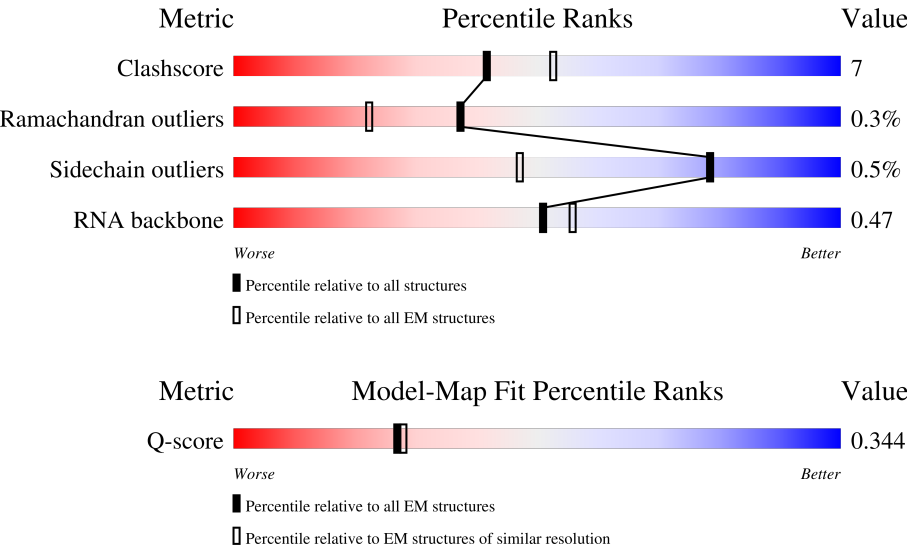
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 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.



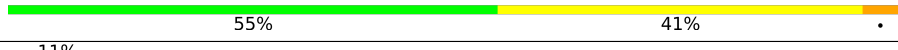
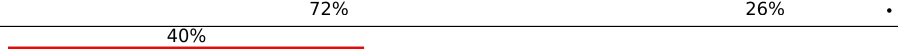
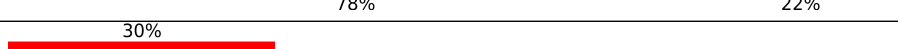
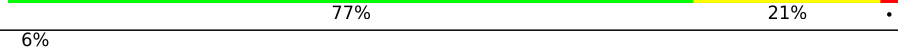
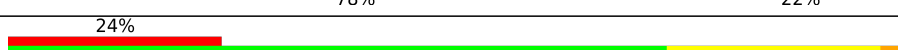
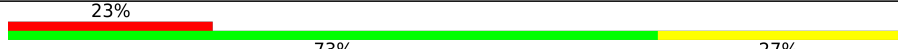
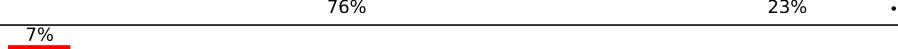
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	1	1507	22% 55% 37% 8%
2	2	76	57% 38% 5%
3	3	15	13% 47% 7% 33%

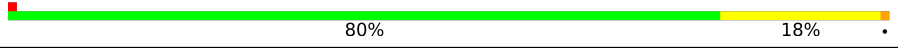
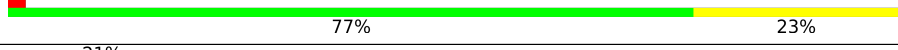
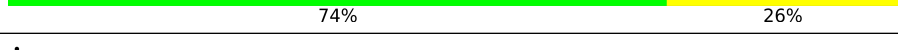
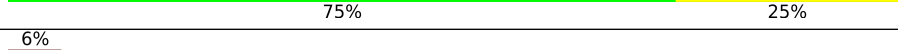
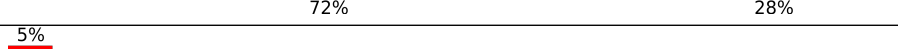
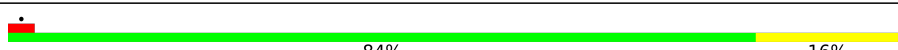
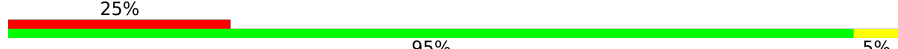
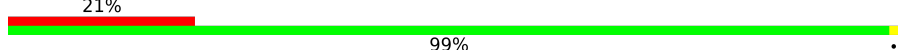
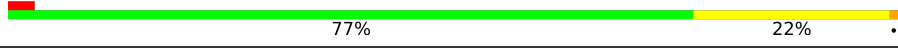
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	4	2901	
5	5	119	
6	6	178	
7	7	146	
8	A	235	
9	B	207	
10	C	208	
11	D	151	
12	E	101	
13	F	155	
14	G	138	
15	H	127	
16	I	99	
17	J	119	
18	K	125	
19	L	119	
20	M	60	
21	N	88	
22	O	84	
23	P	100	
24	Q	70	
25	R	88	
26	S	99	
27	T	25	
28	U	687	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	V	78	
30	W	94	
31	X	71	
32	Y	60	
33	Z	71	
34	a	59	
35	b	50	
36	c	48	
37	d	64	
38	e	37	
39	f	227	
40	g	275	
41	h	205	
42	i	208	
43	j	179	
44	k	176	
45	l	130	
46	m	140	
47	n	71	
48	o	139	
49	p	122	
50	q	150	
51	r	141	
52	s	118	
53	t	99	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	u	138	7% 69% 31%
55	v	117	83% 17%
56	w	101	82% 18%
57	x	113	86% 12%
58	y	93	81% 18%
59	z	101	66% 27% 7%

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 154665 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 RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1507	Total	C	N	O	P	0	0
			32391	14418	6002	10465	1506		

- Molecule 2 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	10	Total	C	N	O	P	0	0
			214	95	35	74	10		

- Molecule 4 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	2901	Total	C	N	O	P	0	0
			62476	27807	11683	20086	2900		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	1041	G	C	conflict	GB 55771382
4	2133	A	G	conflict	GB 55771382

- Molecule 5 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	119	Total	C	N	O	P	0	0
			2551	1136	471	826	118		

- Molecule 6 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	178	Total	C	N	O	S	0	0
			1418	906	254	256	2		

- Molecule 7 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	146	Total	C	N	O	S	0	0
			1136	726	201	208	1		

- Molecule 8 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	235	Total	C	N	O	S	0	1
			1901	1213	342	341	5		

- Molecule 9 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	207	Total	C	N	O	S	0	1
			1613	1016	315	281	1		

- Molecule 10 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 11 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	151	Total	C	N	O	S	0	1
			1147	724	218	201	4		

- Molecule 12 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 13 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 14 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 15 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	127	Total	C	N	O	S	0	0
			1010	639	197	174			

- Molecule 16 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	99	Total	C	N	O	S	0	1
			795	499	157	138	1		

- Molecule 17 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 18 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	125	Total	C	N	O	S	0	1
			971	611	196	163	1		

- Molecule 19 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	119	Total	C	N	O	S	0	1
			938	579	194	163	2		

- Molecule 20 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 21 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 22 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	84	Total	C	N	O	S	0	1
			701	443	140	117	1		

- Molecule 23 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	100	Total	C	N	O	S	0	1
			824	528	152	142	2		

- Molecule 24 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Q	70	Total	C	N	O	0	0
			574	367	112	95		

- Molecule 25 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R	88	Total	C	N	O	S	0	1
			692	440	128	122	2		

- Molecule 26 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 27 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	T	25	Total	C	N	O	0	1
			209	128	51	30		

- Molecule 28 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	661	Total	C	N	O	S	0	0
			5173	3288	884	983	18		

- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	78	Total	C	N	O	S	0	0
			617	381	130	105	1		

- Molecule 30 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	94	Total	C	N	O	S	0	1
			732	460	146	125	1		

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	71	Total	C	N	O	S	0	0
			598	370	121	106	1		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	60	Total	C	N	O	S	0	1
			468	298	91	78	1		

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	71	Total	C	N	O	S	0	0
			581	364	108	104	5		

- Molecule 34 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	59	Total	C	N	O	S	0	0
			459	288	90	76	5		

- Molecule 35 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	50	Total	C	N	O	S	0	0
			433	270	88	71	4		

- Molecule 36 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	48	Total	C	N	O	S	0	0
			419	257	104	56	2		

- Molecule 37 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	64	Total	C	N	O	S	0	1
			508	326	102	78	2		

- Molecule 38 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 39 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	227	Total	C	N	O	S	0	0
			1735	1096	318	318	3		

- Molecule 40 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	275	Total	C	N	O	S	0	0
			2145	1353	428	361	3		

- Molecule 41 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h	205	Total	C	N	O	S	0	1
			1564	988	300	270	6		

- Molecule 42 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i	208	Total	C	N	O	S	0	1
			1624	1035	304	282	3		

- Molecule 43 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	179	Total	C	N	O	S	0	0
			1459	931	266	258	4		

- Molecule 44 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	176	Total	C	N	O	S	0	1
			1345	853	253	237	2		

- Molecule 45 is a protein called Ribosomal protein uL10.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	l	130	Total	C	N	O	0	0
			654	393	130	131		

- Molecule 46 is a protein called Ribosomal protein uL11.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	m	140	Total	C	N	O	0	0
			701	420	140	141		

- Molecule 47 is a protein called Ribosomal protein bL12.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	n	71	Total	C	N	O	0	0
			356	213	71	72		

- Molecule 48 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	139	Total	C	N	O	S	0	1
			1105	712	207	182	4		

- Molecule 49 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

- Molecule 50 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	150	Total	C	N	O	S	0	0
			1145	712	232	198	3		

- Molecule 51 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

- Molecule 52 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	118	Total	C	N	O	S	0	0
			968	604	203	160	1		

- Molecule 53 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	t	99	Total	C	N	O	0	1
			771	486	155	130		

- Molecule 54 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	138	Total	C	N	O	S	0	1
			1142	710	235	196	1		

- Molecule 55 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	117	Total	C	N	O	S	0	0
			958	604	202	151	1		

- Molecule 56 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	w	101	Total	C	N	O	S	0	0
			779	501	142	135	1		

- Molecule 57 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	113	Total	C	N	O	S	0	0
			896	563	176	155	2		

- Molecule 58 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	93	Total	C	N	O		0	1
			726	471	132	123			

- Molecule 59 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	z	101	Total	C	N	O	S	0	1
			776	500	149	123	4		

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	1	125	Total	Mg	0
			125	125	
60	4	320	Total	Mg	0
			320	320	
60	D	1	Total	Mg	0
			1	1	
60	K	1	Total	Mg	0
			1	1	
60	O	2	Total	Mg	0
			2	2	
60	S	1	Total	Mg	0
			1	1	

Continued on next page...

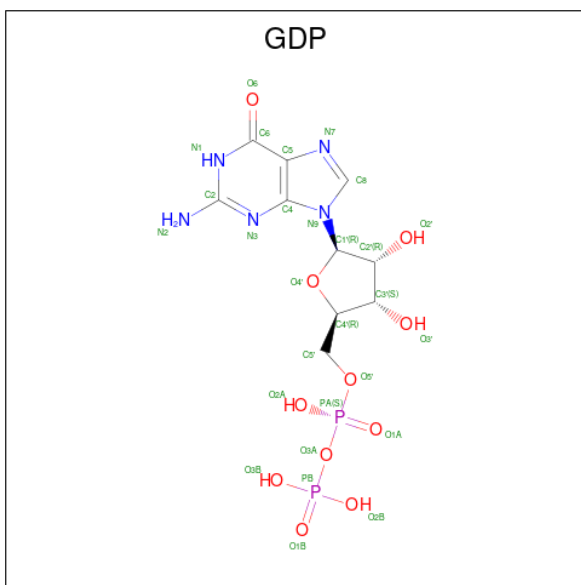
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
60	U	1	Total	Mg	0
			1	1	
60	a	1	Total	Mg	0
			1	1	
60	c	1	Total	Mg	0
			1	1	
60	e	1	Total	Mg	0
			1	1	
60	h	1	Total	Mg	0
			1	1	
60	i	1	Total	Mg	0
			1	1	
60	q	1	Total	Mg	0
			1	1	
60	t	3	Total	Mg	0
			3	3	
60	u	1	Total	Mg	0
			1	1	
60	x	1	Total	Mg	0
			1	1	

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	C	1	Total	Zn	0
			1	1	
61	M	1	Total	Zn	0
			1	1	
61	e	1	Total	Zn	0
			1	1	

- Molecule 62 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

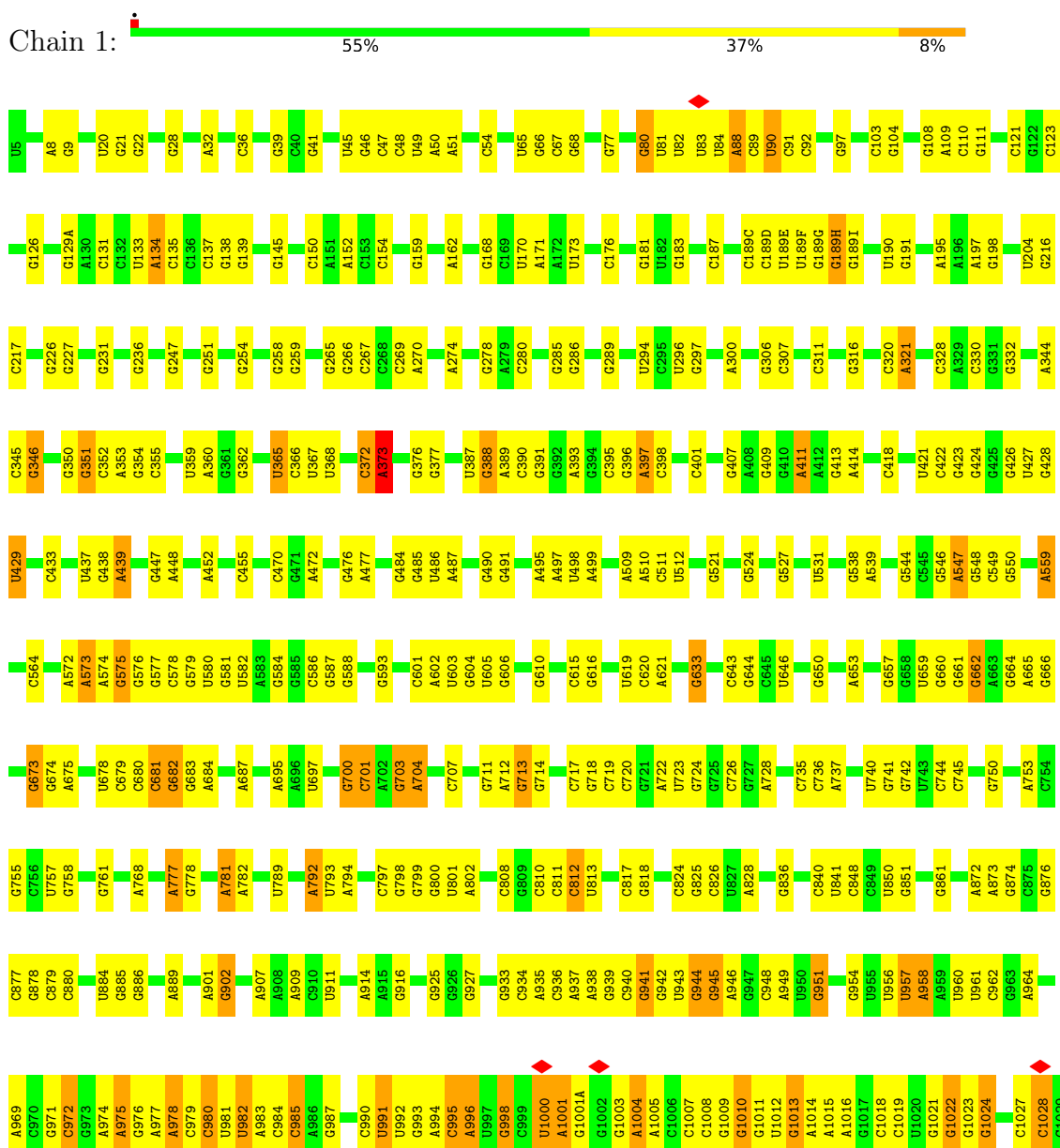


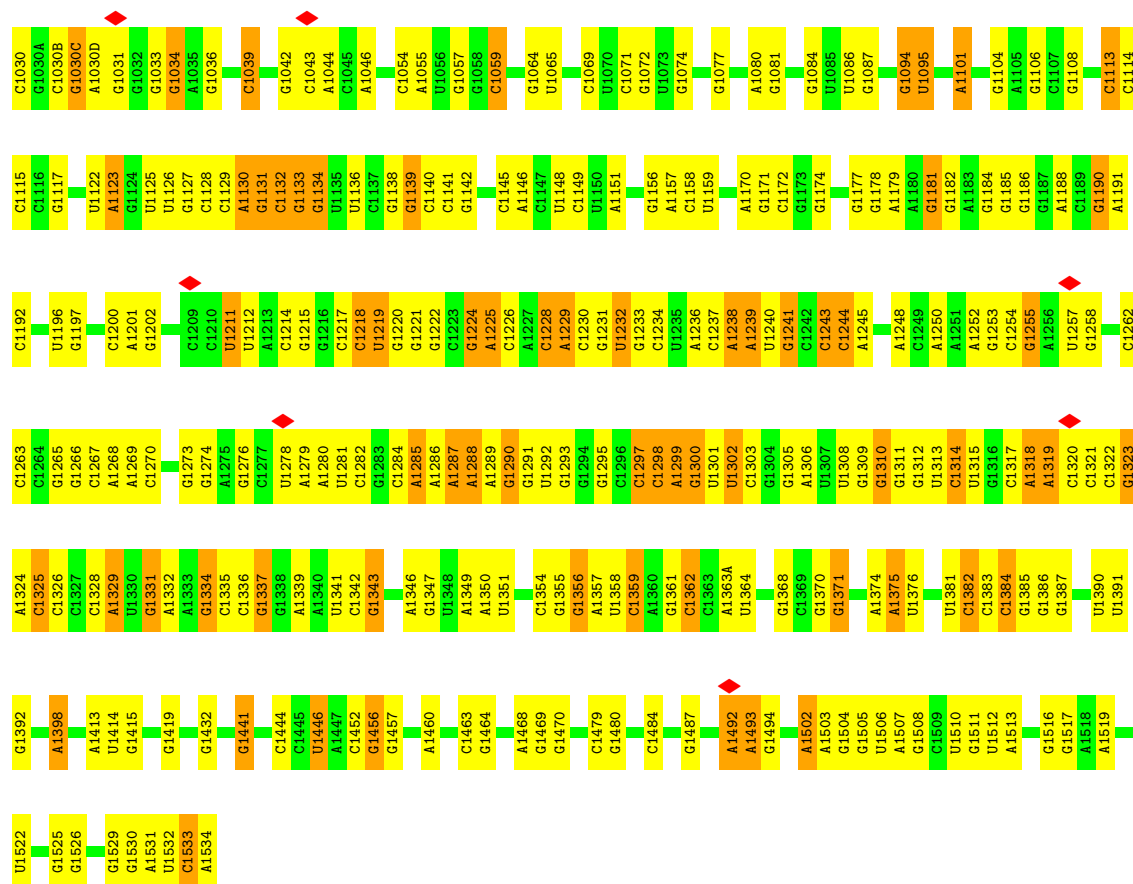
Mol	Chain	Residues	Atoms					AltConf
62	U	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots

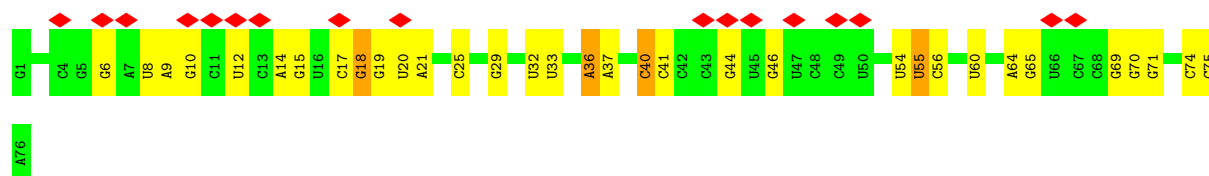
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S Ribosomal RNA





• Molecule 2: tRNA-Phe



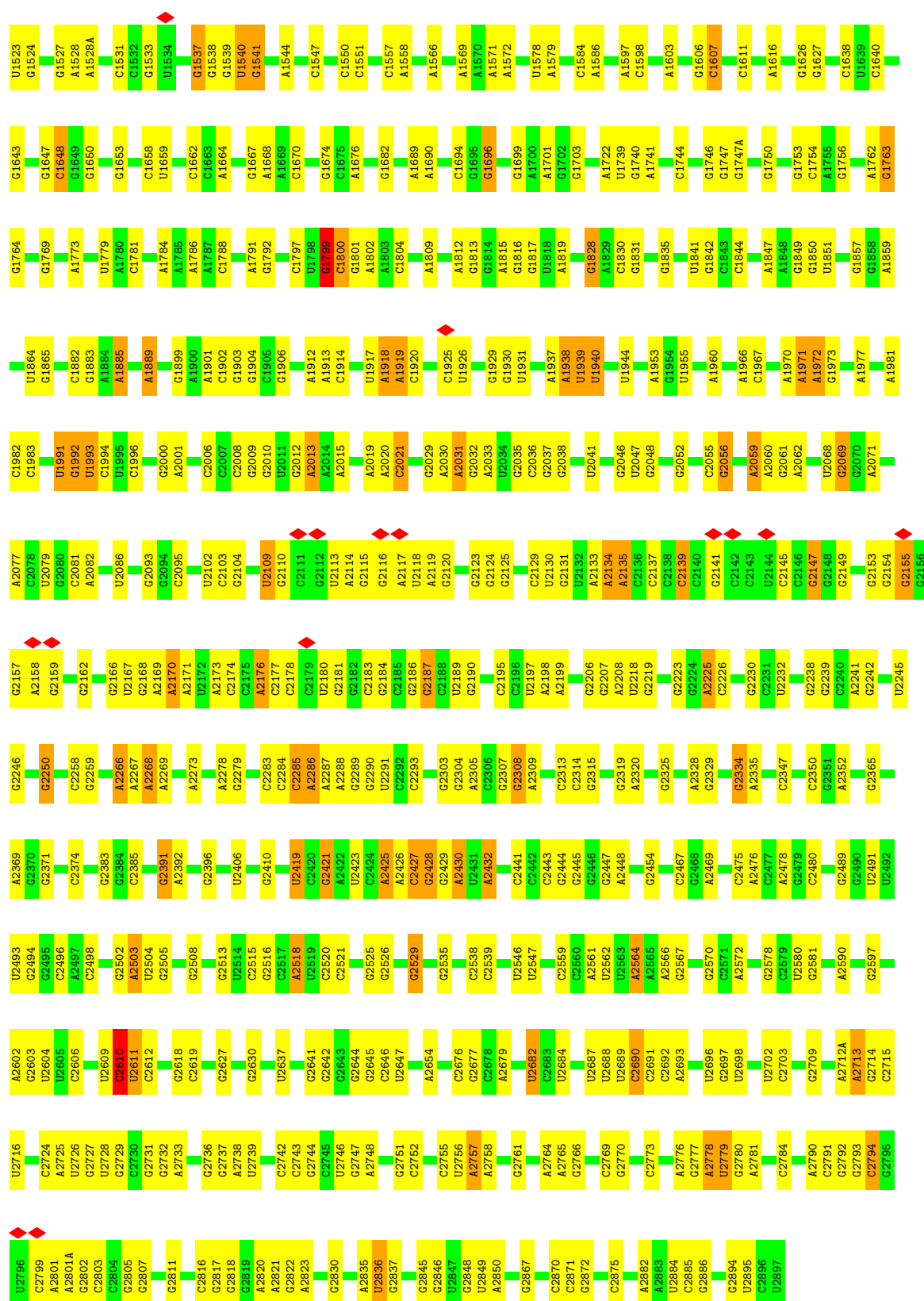
• Molecule 3: mRNA



• Molecule 4: 23S Ribosomal RNA



C1411	G1296	G1186	C1092	C395	A887	C790	A670	A609	A526	G438	G327	C264	G125
A1412	U1300	A1189	G1093	A996	C888	C791	A675	U614	C527	G442	U328	A265	C128
G1416	A1301	G1190	U1094	A1009	C889	A792	A676	U614A	A528	G443	C267	C266	G131
C1417	C1306	G1193	U1097	A1010	C892	A800	C679	G614B	G530	G446	A330	C268	A330
U1420	G1309	C1196	C1102	U1012	C893	G805	G680	A614C	A532	A449	A331	U269	G139A
G1423	G1310	G1197	A1103	U1014	C894	C806	G681	G620	G533	G450	A270	G140	G140
G1424	G1311	G1203	G1106	G1015	A896	U807	G686	A621	U534	C271B	C271C	A141	A141
A1427	C1314	G1204	C1116	G1022	C897	U811	G690	G622	A536	A340	G143	G177	G177
C1428	G1325	U1205	C1116	G1025	G906	C812	G690	A627	G552	A457	C271G	U156	U156
U1431	A1210	A1206	G1122	U1026	A909	U613	G690	G628	G553	C271H	U157	U157	U157
G1435	U1211	A1212	C1123	A1027	A910	C814	C698	G629	U554	A459	U271L	U159	U159
U1438	G1212	G1212	G1124	A1028	C915	G818	A699	G630	U555	A460	U271M	G352	G352
A1439	U1329	A1220	G1125	U1033	G919	G819	G704	A631	G556	G463	U271N	G353	G353
G1445	C1330	A1227	A1126	U1038	G922	U826	G726	G636	U557	A466	G271R	U358	U358
U1452	A1331	A1235	A1127	C1038	A941	U827	A727	A637	G558	C467	U359	A384	A384
A1453	G1332	U1231	U1141	A1045	A945	U828	G728	G638	G559	G468	G271U	U185	U185
G1455	G1334	G1222	U1130	A1046	G946	A829	G729	U639	C560	G469	G362	A196	A196
C1458	U1341	G1225	C1135	G1051	G947	U830	G730	G642	U568	A471	U363	A197	A197
U1459	C1346	A1235	U1142	A1055	G948	C831	G733	A643	A572	A472	G366	C198	C198
A1460	G1236	U1236	A1142A	G1055	G948	U832	A734	G645	A573	U475	C370	A199	A199
C1467	U1352	G1247	G1144	G1059	A953	U833	U740	G651	C574	A476	A371	U200	U200
A1477	A1353	G1252	A1148	U1060	G954	C840	G743	A654	C575	A477	G372	G205	G205
G1478	C1359	A1253	C1152	U1061	A957	A841	G744	G654A	A578	A482	A374	C210	C210
U1482	U1255	A1254	C1153	U1065	U958	U851	G748	C654B	G579	G494	A276	C211	C211
G1484	G1256	U1255	G1154	U1066	A959	G852	C766	G654C	C581	G495	C277	A278	A278
A1486	U1263	G1263	A1155	A1067	C961	G855	A752	G654D	G582	G496	U380	G212	G212
G1487	U1264	G1265	U1156	G1068	C962	C856	C753	G654E	G585	A501	G381	A283	A283
A1490	G1377	A1265	G1157	A1069	C963	U857	G765	C654F	U588	A505	G386	G215	G215
C1493	A1378	G1266	C1161	A1070	C964	G859	G766	G654G	C589	A509	U387	A216	A216
A1494	G1384	U1267	G1162	G1071	U969	U860	G767	G654H	A590	C302	A289	G217	G217
C1499	U1388	A1271	U1165	C1075	G972	C864	A774	G654I	C591	A300	A294	A222	A222
G1500	G1389	U1272	G1173	A1077	A973	C865	G775	G654J	G592	G396	G295	A223	A223
C1504	U1392	U1273	U1175	C1078	C975	A866	G776	G654K	G593	G397	A294	A227	A227
C1505	A1393	A1274	G1176	C1079	G975A	G873	A777	G654L	U594	A304	A300	A228	A228
U1509	U1394	C1177	C1178	A1084	A980	G874	G778	G654M	C598	U404	G398	A229	A229
A1509A	A1395	A1278	A1179	A1085	A983	C875	A781	G654N	U597	G411	U305	C237	C237
U1516	U1396	G1279	C1181	A1086	A984	G875	A782	A654O	C601	A412	G309	A244	A244
G1517	U1397	U1289	A1182	A1087	C985	G881	A783	A655	G602	C413	A310	G245	G245
C1516	C1398	C1184	G1183	A1088	C986	G882	A784	G656	A603	C414	A311	C246	C246
G1517	U1399	C1184	C1185	A1089	G989	G883	G785	U657	G604	A415	G312	G247	G247
C1517	G1400	C1295	C1185	U1090	C994	C884	A788	G658	C605	A422	G313	C249	C249
C1517	C1400	C1295	C1185	G1091	C994	C885	A789	U659	U606	A428	G317	G250	G250
C1517	C1400	C1295	C1185	G1091	C994	C886	A789	U660	A608	A429	C318	A251	A251
C1517	C1400	C1295	C1185	G1091	C994	C886	A789	U660	A608	A429	G321	G252	G252
C1517	C1400	C1295	C1185	G1091	C994	C886	A789	U660	A608	A429	A322	G254	G254
C1517	C1400	C1295	C1185	G1091	C994	C886	A789	U660	A608	A429	G323	C263	C263

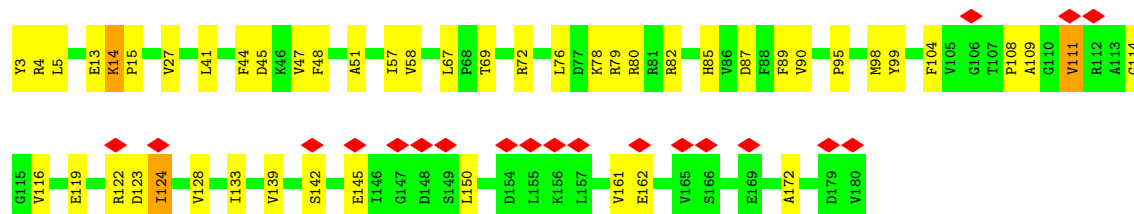


• Molecule 5: 5S Ribosomal RNA

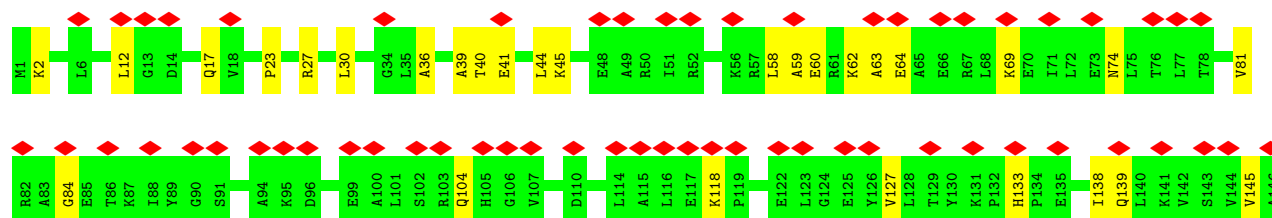
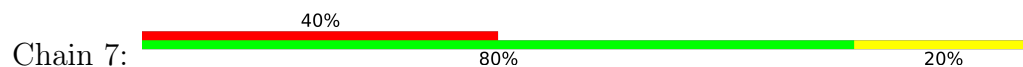
Chain 5: 55% 41%



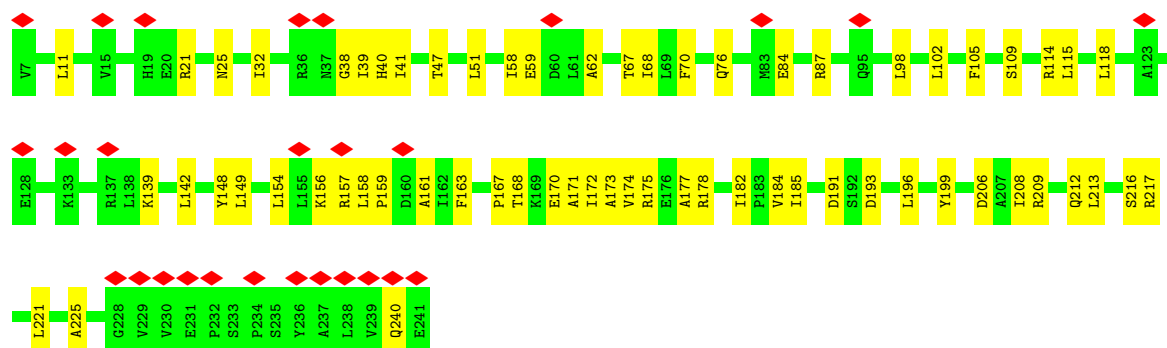
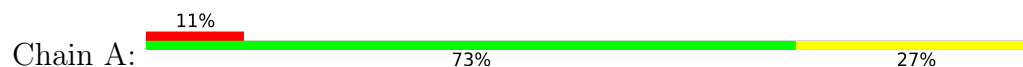
• Molecule 6: 50S ribosomal protein L25



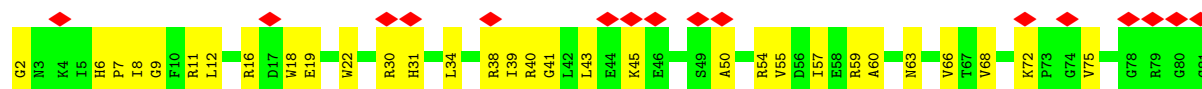
• Molecule 7: 50S ribosomal protein L9

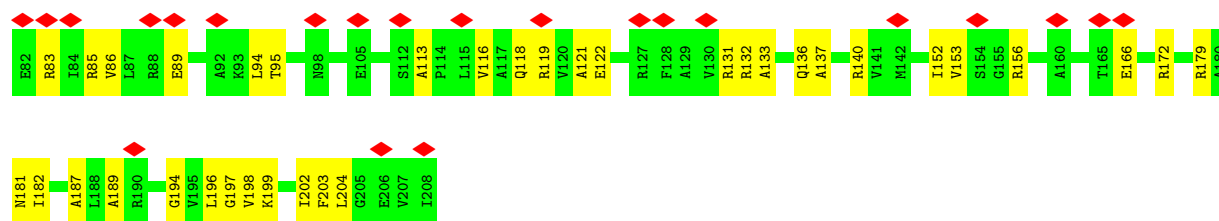


• Molecule 8: 30S ribosomal protein S2

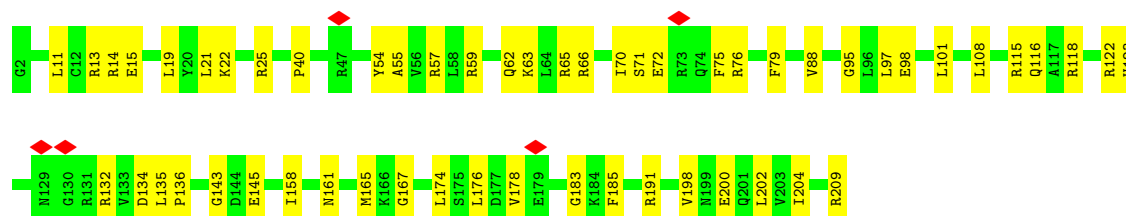


• Molecule 9: 30S ribosomal protein S3

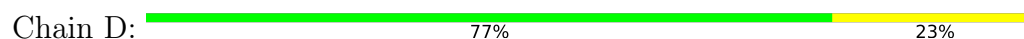




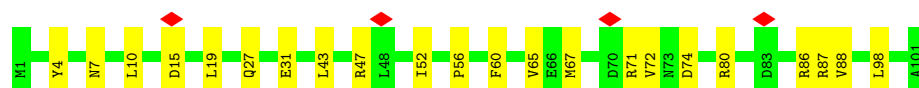
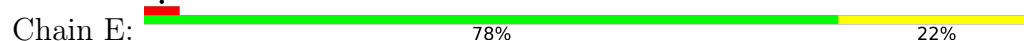
- Molecule 10: 30S ribosomal protein S4



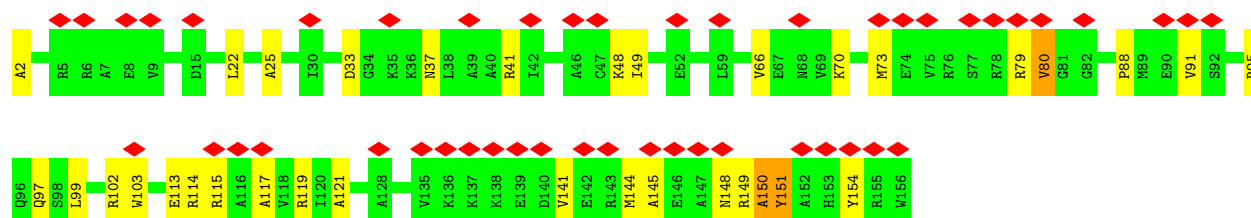
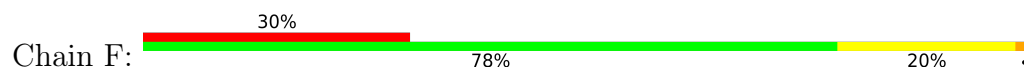
- Molecule 11: 30S ribosomal protein S5



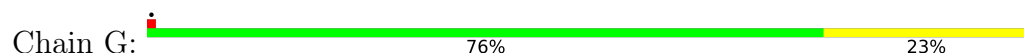
- Molecule 12: 30S ribosomal protein S6

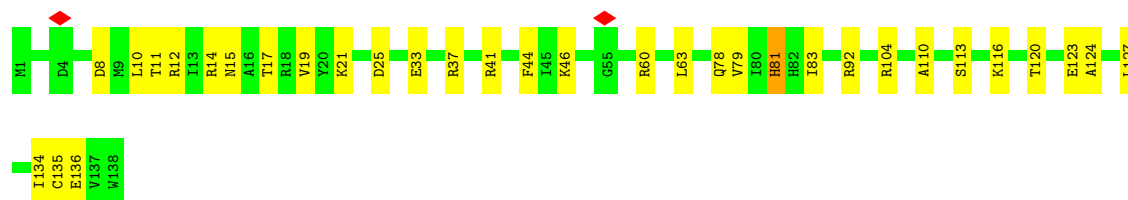


- Molecule 13: 30S ribosomal protein S7

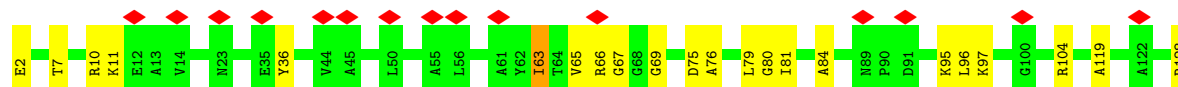
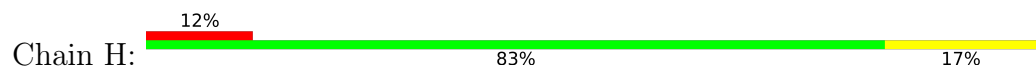


- Molecule 14: 30S ribosomal protein S8

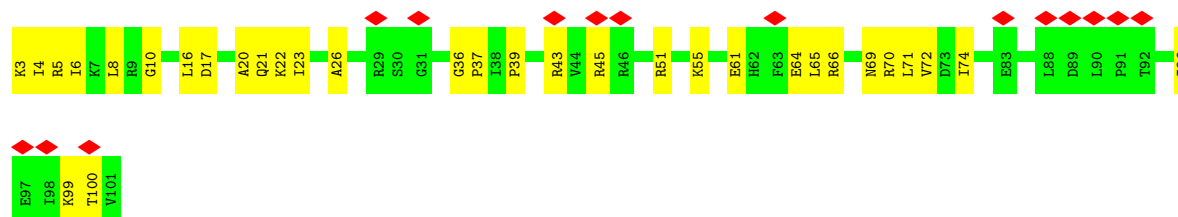




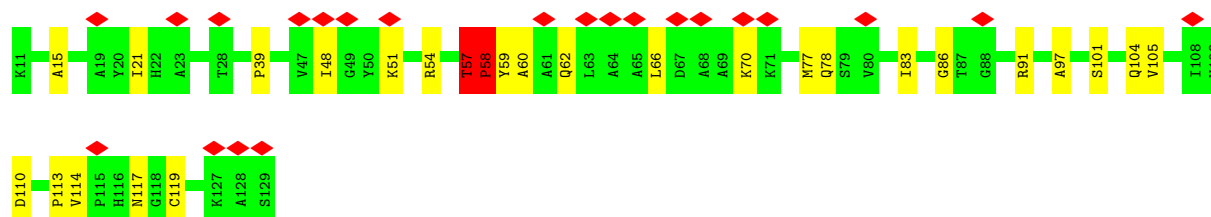
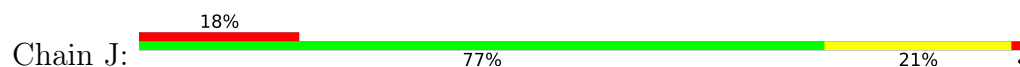
- Molecule 15: 30S ribosomal protein S9



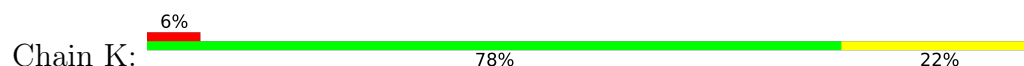
- Molecule 16: 30S ribosomal protein S10



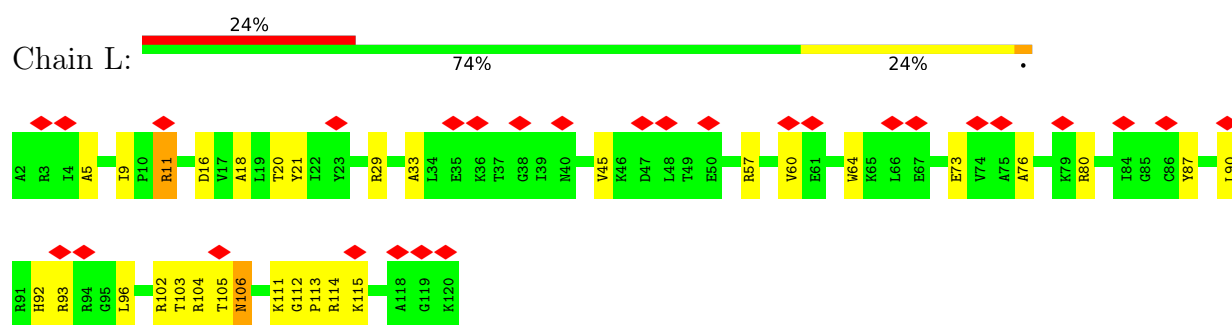
- Molecule 17: 30S ribosomal protein S11



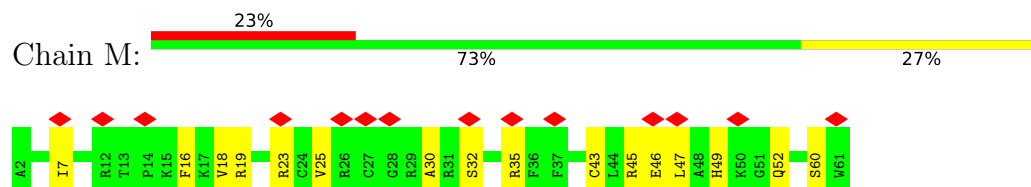
- Molecule 18: 30S ribosomal protein S12



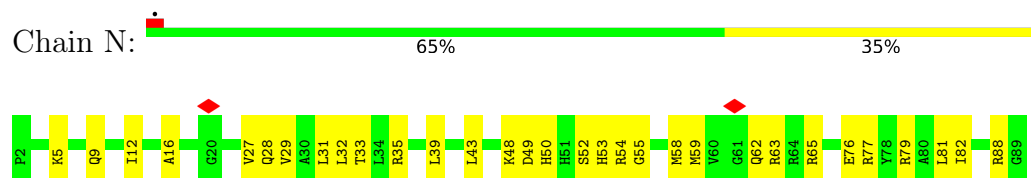
- Molecule 19: 30S ribosomal protein S13



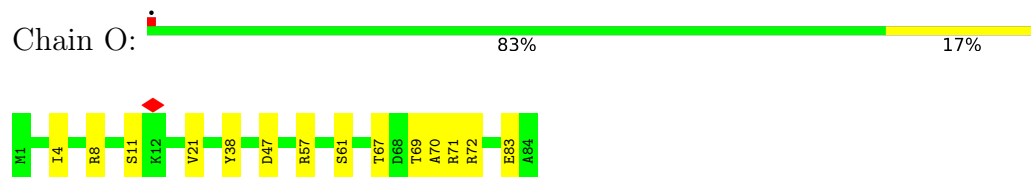
- Molecule 20: 30S ribosomal protein S14 type Z



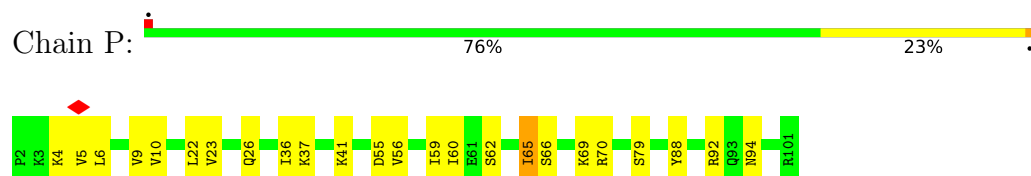
- Molecule 21: 30S ribosomal protein S15



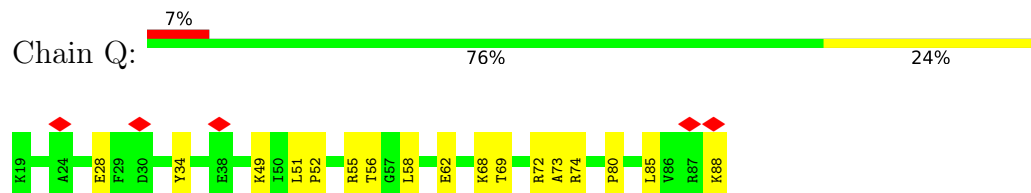
- Molecule 22: 30S ribosomal protein S16



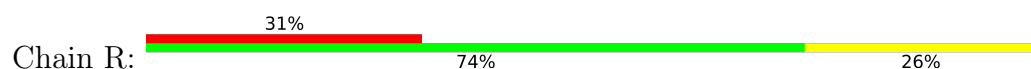
- Molecule 23: 30S ribosomal protein S17

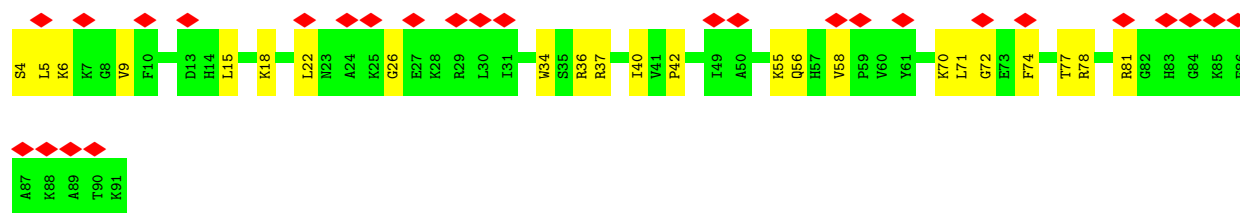


- Molecule 24: 30S ribosomal protein S18

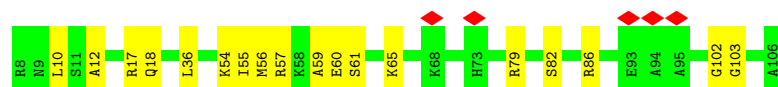
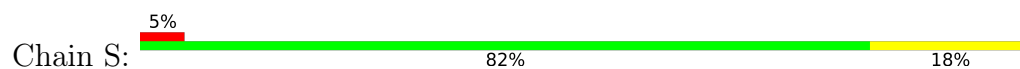


- Molecule 25: 30S ribosomal protein S19

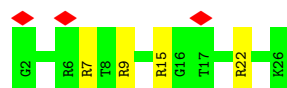
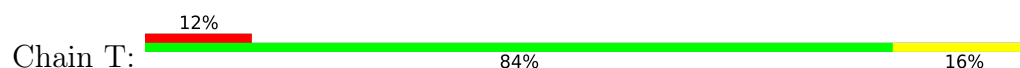




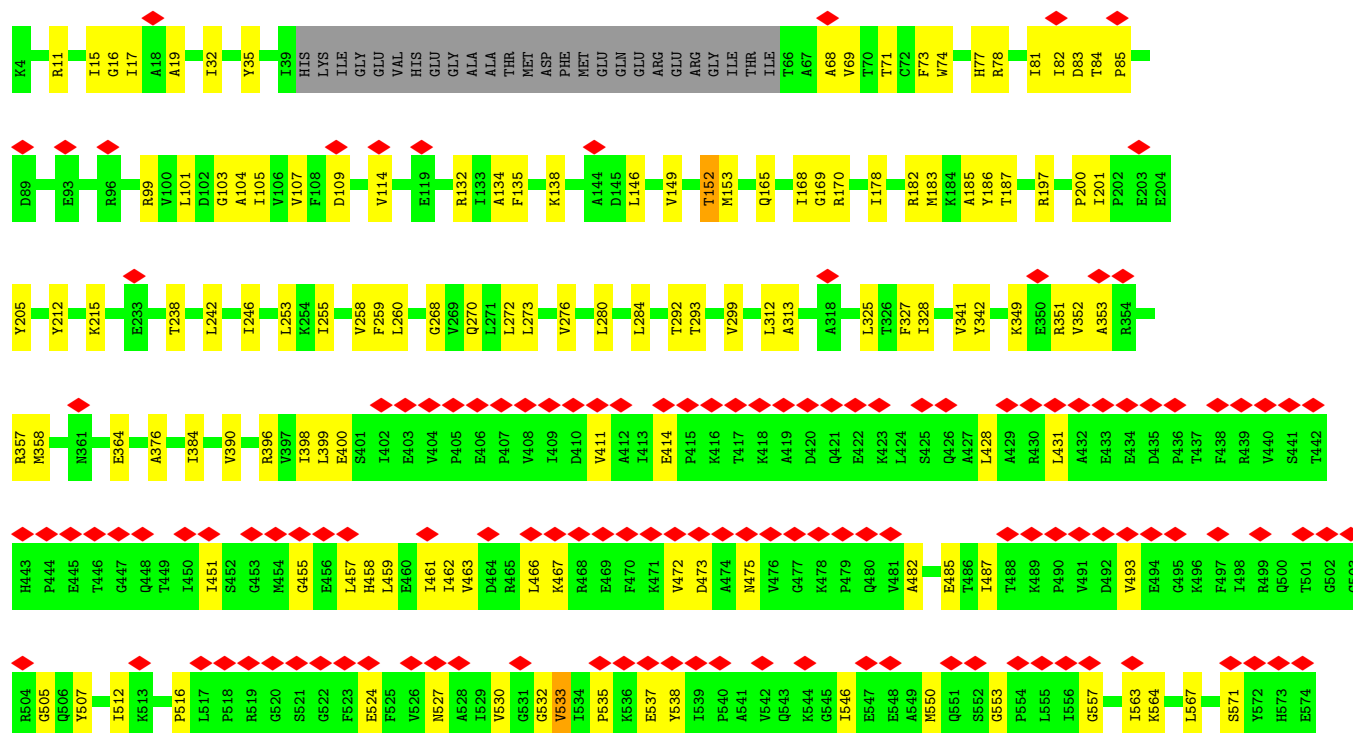
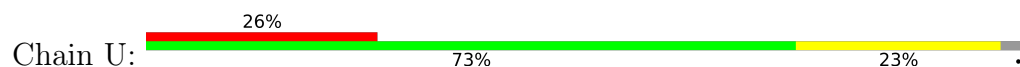
- Molecule 26: 30S ribosomal protein S20

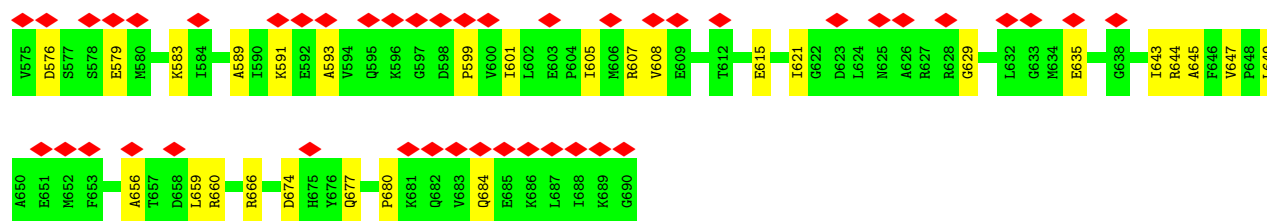


- Molecule 27: 30S ribosomal protein Thx

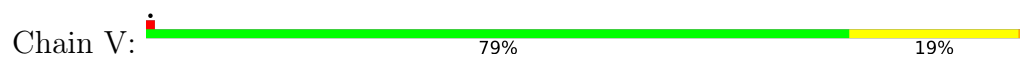


- Molecule 28: Elongation factor G





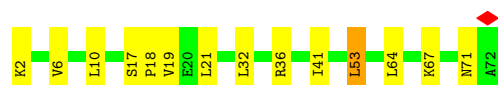
- Molecule 29: 50S ribosomal protein L27



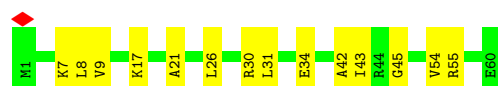
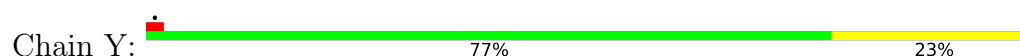
- Molecule 30: 50S ribosomal protein L28



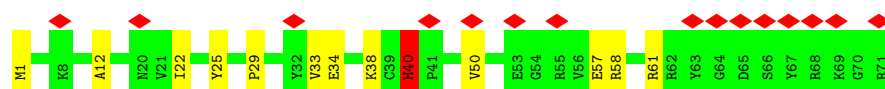
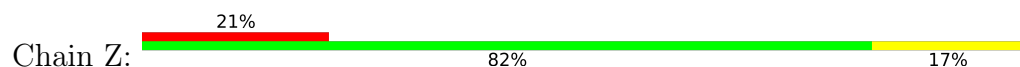
- Molecule 31: 50S ribosomal protein L29



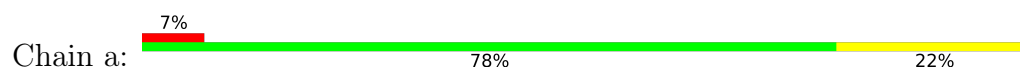
- Molecule 32: 50S ribosomal protein L30



- Molecule 33: 50S ribosomal protein L31

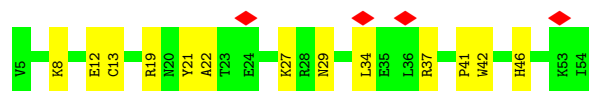
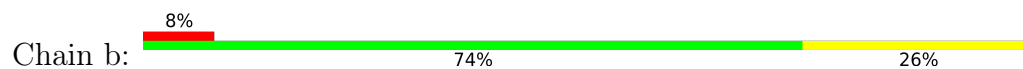


- Molecule 34: 50S ribosomal protein L32

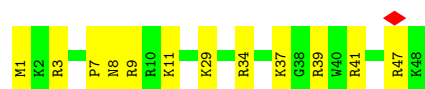
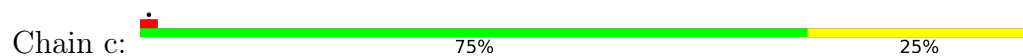




- Molecule 35: 50S ribosomal protein L33



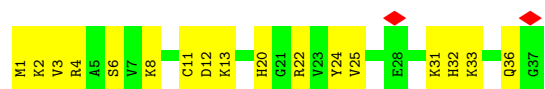
- Molecule 36: 50S ribosomal protein L34



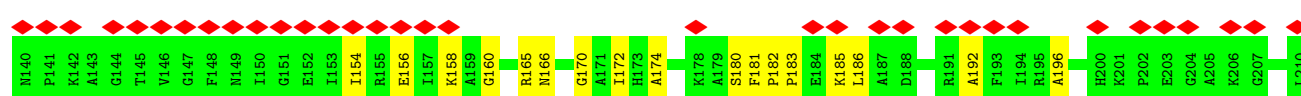
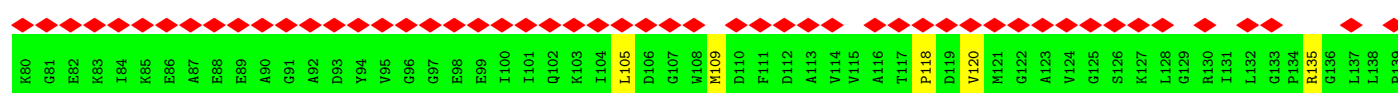
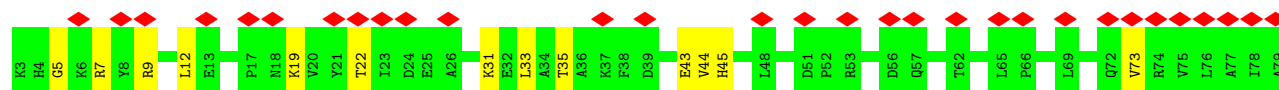
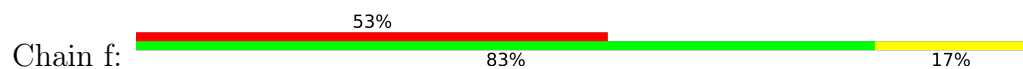
- Molecule 37: 50S ribosomal protein L35

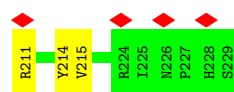


- Molecule 38: 50S ribosomal protein L36



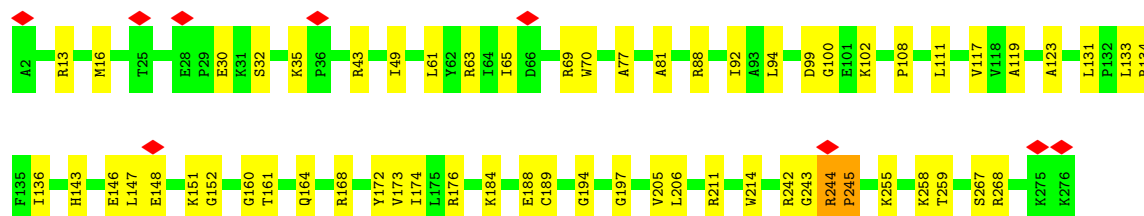
- Molecule 39: 50S ribosomal protein L1





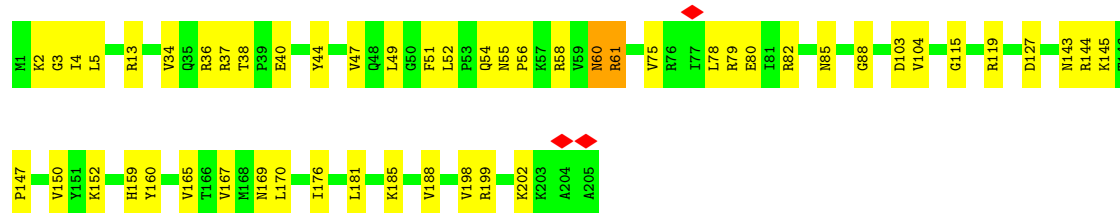
- Molecule 40: 50S ribosomal protein L2

Chain g: 78% 21%



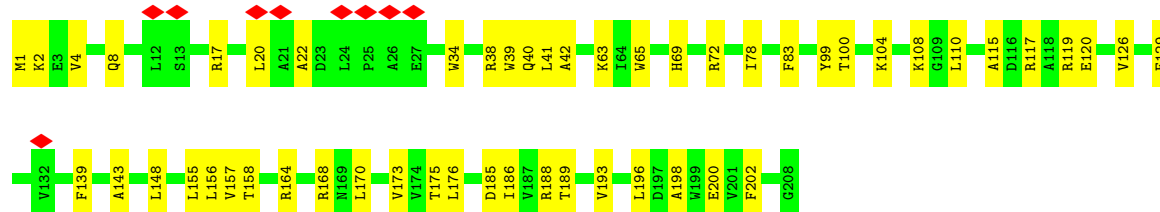
- Molecule 41: 50S ribosomal protein L3

Chain h: 75% 24%



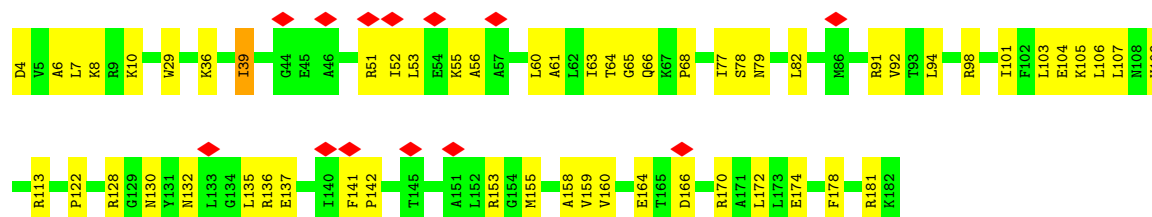
- Molecule 42: 50S ribosomal protein L4

Chain i: 75% 25%



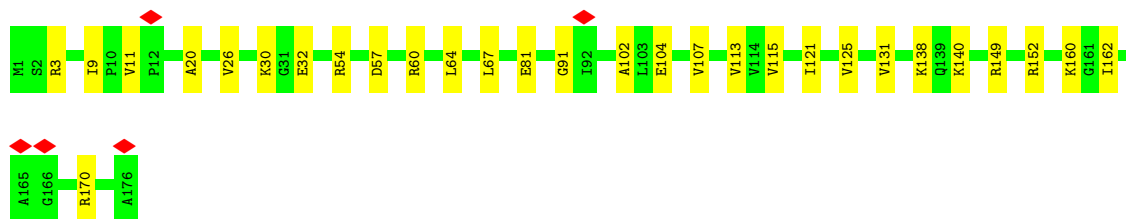
- Molecule 43: 50S ribosomal protein L5

Chain j: 7% 68% 31%

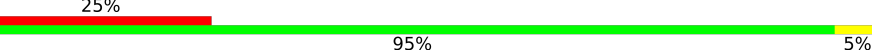


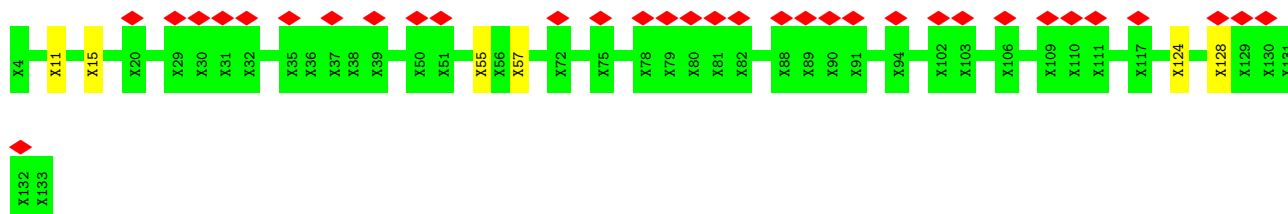
- Molecule 44: 50S ribosomal protein L6

Chain k:  84% 16%

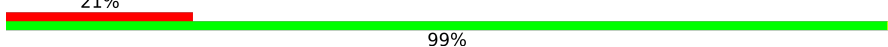


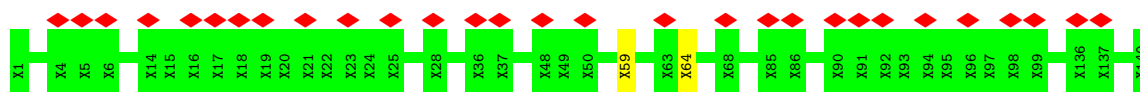
- Molecule 45: Ribosomal protein uL10

Chain l:  25% 95% 5%



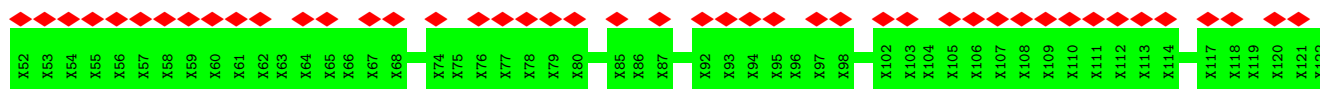
- Molecule 46: Ribosomal protein uL11

Chain m:  21% 99%



- Molecule 47: Ribosomal protein bL12

Chain n:  63% 100%



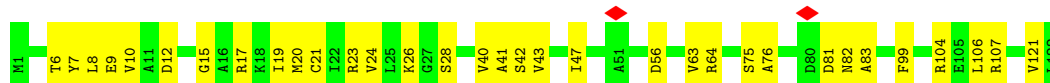
- Molecule 48: 50S ribosomal protein L13

Chain o:  86% 14%

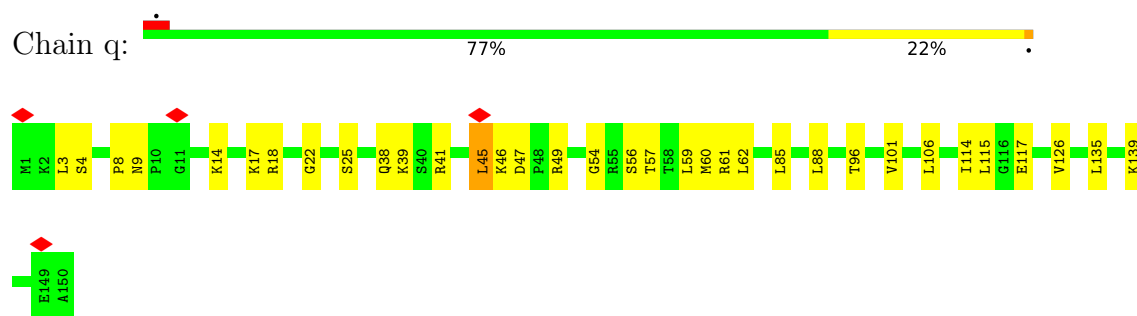


- Molecule 49: 50S ribosomal protein L14

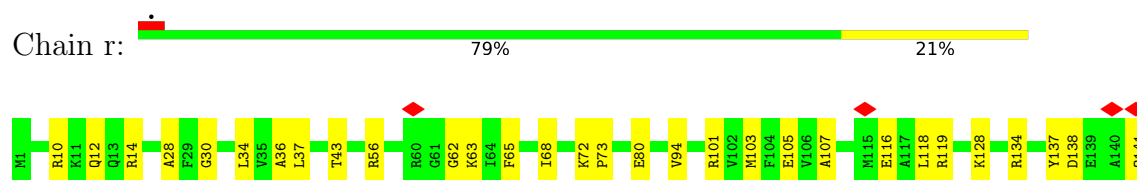
Chain p:  73% 27%



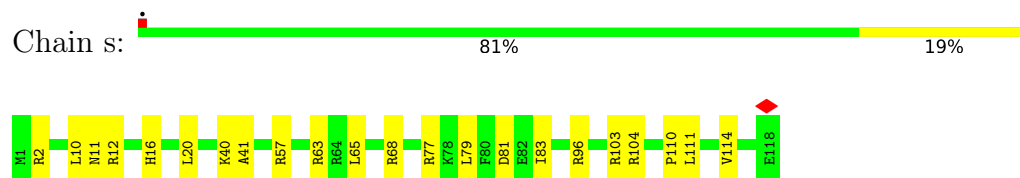
- Molecule 50: 50S ribosomal protein L15



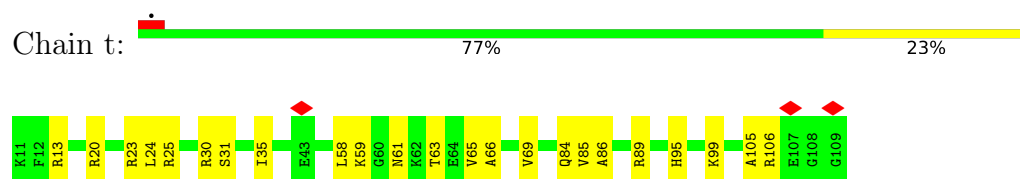
- Molecule 51: 50S ribosomal protein L16



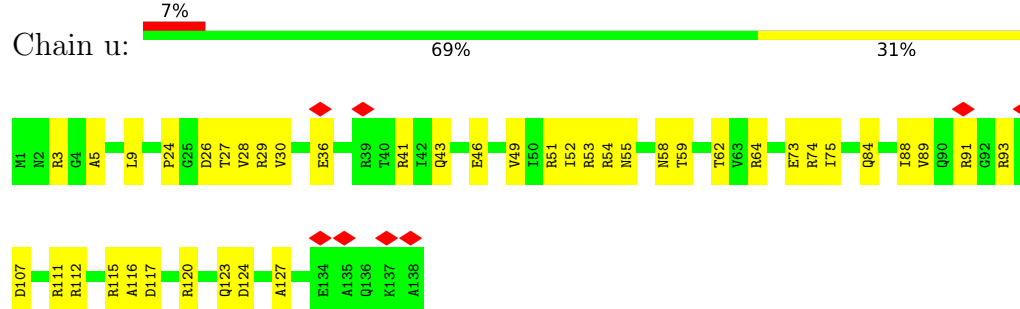
- Molecule 52: 50S ribosomal protein L17



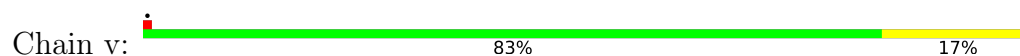
- Molecule 53: 50S ribosomal protein L18



- Molecule 54: 50S ribosomal protein L19

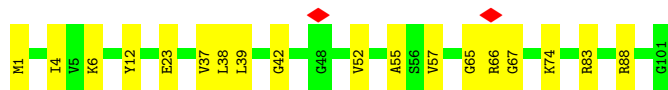
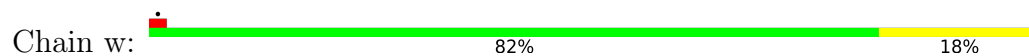


- Molecule 55: 50S ribosomal protein L20

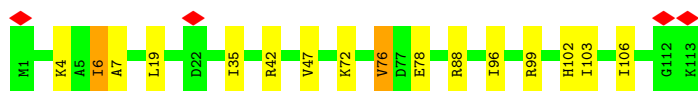
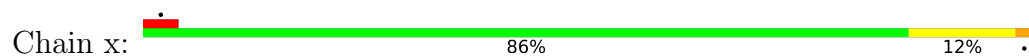




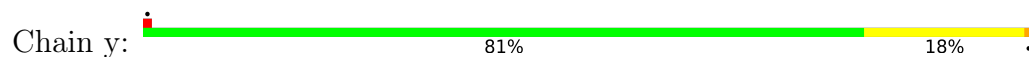
- Molecule 56: 50S ribosomal protein L21



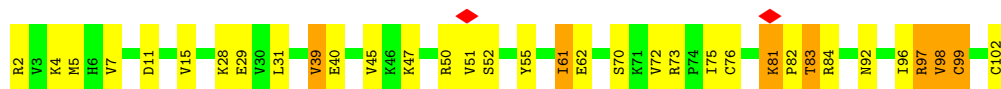
- Molecule 57: 50S ribosomal protein L22



- Molecule 58: 50S ribosomal protein L23



- Molecule 59: 50S ribosomal protein L24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32383	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	120443	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.453	Depositor
Minimum map value	-0.272	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	463.05, 463.05, 463.05	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1025, 1.1025, 1.1025	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.14	0/36259	0.33	5/56593 (0.0%)
2	2	0.13	0/1809	0.30	0/2819
3	3	0.22	0/238	0.54	0/369
4	4	0.15	0/69975	0.32	3/109242 (0.0%)
5	5	0.17	0/2853	0.38	0/4451
6	6	0.27	0/1450	0.77	7/1970 (0.4%)
7	7	0.25	0/1151	0.69	4/1558 (0.3%)
8	A	0.21	0/1936	0.59	0/2611
9	B	0.24	0/1637	0.66	0/2207
10	C	0.20	0/1733	0.55	0/2318
11	D	0.20	0/1163	0.53	0/1566
12	E	0.21	0/856	0.56	0/1154
13	F	0.28	0/1276	0.72	1/1709 (0.1%)
14	G	0.21	0/1136	0.55	0/1527
15	H	0.27	0/1029	0.72	2/1379 (0.1%)
16	I	0.21	0/808	0.55	0/1087
17	J	0.29	0/900	0.75	3/1213 (0.2%)
18	K	0.23	0/987	0.52	0/1322
19	L	0.24	0/948	0.73	1/1272 (0.1%)
20	M	0.22	0/501	0.60	0/664
21	N	0.20	0/745	0.57	0/992
22	O	0.18	0/717	0.53	0/965
23	P	0.19	0/837	0.57	0/1119
24	Q	0.19	0/579	0.51	0/768
25	R	0.19	0/706	0.56	0/950
26	S	0.17	0/765	0.51	0/1007
27	T	0.19	0/213	0.59	0/279
28	U	0.22	0/5270	0.61	3/7135 (0.0%)
29	V	0.24	0/625	0.63	0/832
30	W	0.23	0/739	0.57	0/983
31	X	0.20	0/600	0.54	0/793
32	Y	0.16	0/473	0.52	0/636

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Z	0.28	0/594	0.93	2/795 (0.3%)
34	a	0.24	0/473	0.62	0/639
35	b	0.29	0/440	0.89	1/586 (0.2%)
36	c	0.16	0/427	0.48	0/561
37	d	0.31	0/516	0.65	0/681
38	e	0.26	0/310	0.78	0/407
39	f	0.24	0/1766	0.66	2/2380 (0.1%)
40	g	0.23	0/2195	0.65	3/2955 (0.1%)
41	h	0.24	0/1597	0.75	6/2155 (0.3%)
42	i	0.20	0/1659	0.55	0/2246
43	j	0.28	0/1483	0.84	0/1994
44	k	0.23	0/1371	0.66	0/1853
45	l	0.05	0/7	0.09	0/8
48	o	0.21	0/1132	0.58	0/1527
49	p	0.19	0/943	0.50	0/1269
50	q	0.28	0/1162	0.83	4/1544 (0.3%)
51	r	0.18	0/1143	0.48	0/1527
52	s	0.25	0/982	0.62	0/1312
53	t	0.25	0/779	0.77	0/1038
54	u	0.25	0/1156	0.63	0/1544
55	v	0.17	0/975	0.52	0/1297
56	w	0.19	0/790	0.53	0/1057
57	x	0.22	0/907	0.64	0/1216
58	y	0.24	0/740	0.68	0/995
59	z	0.43	1/789 (0.1%)	1.09	10/1053 (0.9%)
All	All	0.18	1/165250 (0.0%)	0.44	57/246129 (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
6	6	0	3
7	7	0	1
8	A	0	2
9	B	0	1
13	F	0	2
14	G	0	1
23	P	0	1
28	U	0	3
29	V	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
33	Z	0	1
40	g	0	2
41	h	0	3
43	j	0	2
44	k	0	2
45	l	0	1
50	q	0	1
57	x	0	1
58	y	0	2
59	z	0	5
All	All	0	35

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	z	98	VAL	CA-C	5.11	1.59	1.52

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	373	A	OP1-P-O3'	-9.35	79.96	108.00
1	1	231	G	OP1-P-O3'	-9.25	80.24	108.00
41	h	61	ARG	CA-C-N	-8.44	109.29	119.84
41	h	61	ARG	C-N-CA	-8.44	109.29	119.84
6	6	78	LYS	CA-C-N	7.74	136.33	121.54
6	6	78	LYS	C-N-CA	7.74	136.33	121.54
17	J	57	THR	N-CA-C	7.17	125.65	109.81
7	7	84	GLY	CA-C-N	7.14	134.56	121.70
7	7	84	GLY	C-N-CA	7.14	134.56	121.70
17	J	58	PRO	N-CA-C	7.00	126.90	112.47
17	J	48	ILE	N-CA-C	-6.94	105.84	111.81
1	1	231	G	OP2-P-O3'	-6.88	87.35	108.00
1	1	373	A	OP2-P-O3'	-6.80	87.59	108.00
40	g	244	ARG	CA-C-N	-6.57	113.62	120.38
40	g	244	ARG	C-N-CA	-6.57	113.62	120.38
4	4	1799	G	C2'-C3'-O3'	6.55	119.32	109.50
28	U	152	THR	N-CA-C	-6.47	106.34	114.56
41	h	202	LYS	CA-C-N	6.22	132.90	121.70
41	h	202	LYS	C-N-CA	6.22	132.90	121.70
33	Z	40	HIS	CA-C-N	-6.20	112.10	119.84
33	Z	40	HIS	C-N-CA	-6.20	112.10	119.84
6	6	14	LYS	CA-C-N	6.14	127.51	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	6	14	LYS	C-N-CA	6.14	127.51	119.84
13	F	150	ALA	N-CA-C	6.13	123.86	110.80
59	z	52	SER	C-N-CD	-6.07	107.25	120.60
59	z	98	VAL	N-CA-C	6.01	121.83	109.34
50	q	45	LEU	CA-C-N	5.77	129.47	120.82
50	q	45	LEU	C-N-CA	5.77	129.47	120.82
6	6	124	ILE	N-CA-C	5.66	121.11	109.34
15	H	119	ALA	CA-C-N	5.66	130.68	122.36
15	H	119	ALA	C-N-CA	5.66	130.68	122.36
35	b	19	ARG	N-CA-C	5.60	120.63	113.18
40	g	244	ARG	CA-CB-CG	5.58	125.27	114.10
28	U	455	GLY	CA-C-N	5.55	132.15	121.54
28	U	455	GLY	C-N-CA	5.55	132.15	121.54
50	q	17	LYS	CA-C-N	5.31	130.36	122.82
50	q	17	LYS	C-N-CA	5.31	130.36	122.82
39	f	105	LEU	CA-C-N	5.27	131.60	121.54
39	f	105	LEU	C-N-CA	5.27	131.60	121.54
59	z	50	ARG	CA-C-N	5.24	127.91	120.53
59	z	50	ARG	C-N-CA	5.24	127.91	120.53
41	h	60	ASN	CA-C-N	5.19	134.47	121.80
41	h	60	ASN	C-N-CA	5.19	134.47	121.80
59	z	51	VAL	N-CA-C	5.18	116.53	110.62
19	L	11	ARG	CA-CB-CG	5.17	124.44	114.10
59	z	99	CYS	CA-CB-SG	5.16	126.27	114.40
4	4	1077	A	P-O3'-C3'	5.16	127.94	120.20
6	6	13	GLU	CA-C-N	5.13	134.32	121.80
6	6	13	GLU	C-N-CA	5.13	134.32	121.80
59	z	52	SER	CA-C-N	5.10	139.25	127.00
59	z	52	SER	C-N-CA	5.10	139.25	127.00
4	4	2610	C	P-O3'-C3'	5.07	127.81	120.20
7	7	104	GLN	CA-C-N	5.07	131.22	121.54
7	7	104	GLN	C-N-CA	5.07	131.22	121.54
59	z	81	LYS	CA-C-N	5.07	126.17	119.84
59	z	81	LYS	C-N-CA	5.07	126.17	119.84
1	1	982	U	P-O3'-C3'	5.05	127.78	120.20

There are no chirality outliers.

All (35) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	6	123	ASP	Peptide
6	6	14	LYS	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
6	6	142	SER	Peptide
7	7	133	HIS	Peptide
8	A	156	LYS	Peptide
8	A	157	ARG	Peptide
9	B	18	TRP	Peptide
13	F	121	ALA	Peptide
13	F	80	VAL	Peptide
14	G	81	HIS	Peptide
23	P	65	ILE	Peptide
28	U	183	MET	Peptide
28	U	352	VAL	Peptide
28	U	533	VAL	Peptide
29	V	71	ASP	Peptide
33	Z	40	HIS	Peptide
40	g	244	ARG	Peptide
40	g	245	PRO	Peptide
41	h	144	ARG	Peptide
41	h	51	PHE	Peptide
41	h	61	ARG	Peptide
43	j	141	PHE	Peptide
43	j	172	LEU	Peptide
44	k	20	ALA	Peptide
44	k	9	ILE	Peptide
45	l	55	UNK	Peptide
50	q	18	ARG	Peptide
57	x	6	ILE	Peptide
58	y	6	ASP	Peptide
58	y	7	VAL	Peptide
59	z	55	TYR	Peptide
59	z	62	GLU	Peptide
59	z	81	LYS	Peptide
59	z	83	THR	Peptide
59	z	97	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	32391	0	16347	342	0
2	2	1619	0	822	6	0
3	3	214	0	106	3	0
4	4	62476	0	31492	503	0
5	5	2551	0	1295	15	0
6	6	1418	0	1445	28	0
7	7	1136	0	1223	17	0
8	A	1901	0	1951	40	0
9	B	1613	0	1677	47	0
10	C	1703	0	1765	38	0
11	D	1147	0	1207	23	0
12	E	843	0	857	13	0
13	F	1257	0	1296	27	0
14	G	1116	0	1177	21	0
15	H	1010	0	1037	17	0
16	I	795	0	840	24	0
17	J	885	0	904	25	0
18	K	971	0	1057	15	0
19	L	938	0	995	22	0
20	M	492	0	529	15	0
21	N	734	0	771	22	0
22	O	701	0	720	8	0
23	P	824	0	891	15	0
24	Q	574	0	644	14	0
25	R	692	0	714	20	0
26	S	763	0	861	15	0
27	T	209	0	221	9	0
28	U	5173	0	5238	95	0
29	V	617	0	636	10	0
30	W	732	0	808	17	0
31	X	598	0	653	10	0
32	Y	468	0	523	9	0
33	Z	581	0	577	13	0
34	a	459	0	476	12	0
35	b	433	0	461	10	0
36	c	419	0	467	9	0
37	d	508	0	576	17	0
38	e	307	0	337	11	0
39	f	1735	0	1790	26	0
40	g	2145	0	2234	45	0
41	h	1564	0	1629	35	0
42	i	1624	0	1677	37	0
43	j	1459	0	1516	37	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	k	1345	0	1430	14	0
45	l	654	0	160	3	0
46	m	701	0	168	1	0
47	n	356	0	89	0	0
48	o	1105	0	1180	13	0
49	p	933	0	996	22	0
50	q	1145	0	1228	26	0
51	r	1122	0	1179	24	0
52	s	968	0	1033	16	0
53	t	771	0	832	18	0
54	u	1142	0	1202	32	0
55	v	958	0	1015	15	0
56	w	779	0	852	13	0
57	x	896	0	953	11	0
58	y	726	0	778	11	0
59	z	776	0	867	16	0
60	1	125	0	0	0	0
60	4	320	0	0	0	0
60	D	1	0	0	0	0
60	K	1	0	0	0	0
60	O	2	0	0	0	0
60	S	1	0	0	0	0
60	U	1	0	0	0	0
60	a	1	0	0	0	0
60	c	1	0	0	0	0
60	e	1	0	0	0	0
60	h	1	0	0	0	0
60	i	1	0	0	0	0
60	q	1	0	0	0	0
60	t	3	0	0	0	0
60	u	1	0	0	0	0
60	x	1	0	0	0	0
61	C	1	0	0	0	0
61	M	1	0	0	0	0
61	e	1	0	0	0	0
62	U	28	0	12	0	0
All	All	154665	0	106416	1684	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 7.

All (1684) 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)
1:1:1243:C:O2'	27:T:7:ARG:NH2	1.73	1.19
4:4:827:U:O2	4:4:2426:A:C2	2.02	1.12
1:1:1238:A:N6	1:1:1299:A:N6	2.00	1.10
1:1:941:G:O2'	1:1:942:G:C5'	2.01	1.07
4:4:827:U:C2	4:4:2426:A:H2	1.70	1.07
4:4:2428:G:C2	50:q:61:ARG:NH1	2.22	1.07
4:4:827:U:O2	4:4:2426:A:H2	1.39	1.02
4:4:1800:C:H42	4:4:1817:G:H22	1.07	1.02
4:4:827:U:C2	4:4:2426:A:C2	2.47	1.01
4:4:2428:G:N2	50:q:61:ARG:HH11	1.59	0.99
1:1:941:G:H2'	1:1:942:G:H8	1.27	0.99
1:1:372:C:N4	1:1:389:A:H62	1.58	0.99
1:1:447:G:H21	1:1:487:A:N6	1.60	0.99
1:1:447:G:N2	1:1:487:A:H62	1.61	0.99
1:1:372:C:H42	1:1:389:A:N6	1.61	0.98
1:1:941:G:O2'	1:1:942:G:H5'	1.63	0.98
1:1:1238:A:N6	1:1:1299:A:C6	2.32	0.97
4:4:954:G:H1	4:4:963:U:H3	1.10	0.97
4:4:1800:C:H42	4:4:1817:G:N2	1.61	0.96
4:4:2475:C:H42	4:4:2529:G:N2	1.62	0.96
4:4:2259:G:O4'	4:4:2427:C:C5	2.19	0.95
1:1:941:G:O2'	1:1:942:G:O4'	1.86	0.94
4:4:2259:G:C8	4:4:2427:C:N4	2.35	0.94
4:4:2475:C:H42	4:4:2529:G:H22	1.02	0.94
28:U:69:VAL:HA	28:U:81:ILE:O	1.68	0.93
4:4:1800:C:N4	4:4:1817:G:H22	1.66	0.93
1:1:782:A:H62	1:1:800:G:H21	1.16	0.92
1:1:150:C:H42	1:1:171:A:H62	1.04	0.91
1:1:939:G:H2'	1:1:940:C:C6	2.06	0.91
4:4:2475:C:N4	4:4:2529:G:H22	1.69	0.89
10:C:71:SER:O	10:C:75:PHE:HB2	1.71	0.89
41:h:3:GLY:HA2	41:h:198:VAL:O	1.72	0.89
1:1:925:G:H1	1:1:1391:U:H3	1.22	0.88
39:f:45:HIS:HB2	39:f:214:TYR:O	1.76	0.86
1:1:1238:A:H61	1:1:1299:A:N6	1.72	0.85
17:J:21:ILE:HB	17:J:83:ILE:O	1.76	0.84
35:b:13:CYS:O	35:b:21:TYR:HA	1.77	0.83
14:G:37:ARG:O	14:G:41:ARG:HB2	1.76	0.83
4:4:2392:A:C8	4:4:2429:G:C6	2.66	0.83
1:1:372:C:H42	1:1:389:A:H62	0.84	0.81
13:F:151:TYR:H	17:J:59:TYR:H	1.26	0.81
44:k:104:GLU:HA	44:k:113:VAL:O	1.80	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:7:59:ALA:O	7:7:63:ALA:HB3	1.82	0.80
1:1:941:G:O6	1:1:1343:G:O6	1.99	0.80
1:1:150:C:N4	1:1:171:A:H62	1.79	0.79
4:4:2425:A:O4'	4:4:2427:C:C2	2.34	0.79
4:4:2428:G:N2	50:q:61:ARG:NH1	2.28	0.79
4:4:2391:G:C2	4:4:2427:C:O2'	2.35	0.78
30:W:15:ALA:O	30:W:40:ARG:HB3	1.84	0.78
32:Y:17:LYS:O	32:Y:21:ALA:HB3	1.83	0.77
4:4:948:G:H1	4:4:969:U:H3	1.31	0.77
21:N:55:GLY:O	21:N:59:MET:HB2	1.85	0.77
4:4:1664:A:H61	4:4:1996:C:H42	1.33	0.76
6:6:44:PHE:O	6:6:48:PHE:HB2	1.85	0.76
15:H:76:ALA:O	15:H:80:GLY:HA3	1.85	0.76
4:4:2259:G:C1'	4:4:2427:C:C5	2.69	0.76
1:1:941:G:H2'	1:1:942:G:C8	2.18	0.75
1:1:941:G:O2'	1:1:942:G:C4'	2.34	0.75
12:E:27:GLN:O	12:E:31:GLU:HB3	1.87	0.75
1:1:782:A:H62	1:1:800:G:N2	1.86	0.73
1:1:1238:A:N6	1:1:1299:A:H61	1.83	0.73
4:4:2392:A:C8	4:4:2429:G:O6	2.42	0.73
17:J:62:GLN:O	17:J:66:LEU:HB3	1.87	0.72
4:4:827:U:O2	4:4:2426:A:N1	2.21	0.72
1:1:150:C:H42	1:1:171:A:N6	1.86	0.72
4:4:2258:C:O2'	4:4:2427:C:OP2	2.08	0.72
26:S:61:SER:O	26:S:65:LYS:HB3	1.90	0.72
41:h:47:VAL:O	41:h:80:GLU:HA	1.89	0.72
51:r:63:LYS:O	51:r:107:ALA:HB3	1.89	0.71
14:G:123:GLU:O	14:G:127:LEU:HB2	1.91	0.71
48:o:15:LEU:HA	48:o:53:VAL:O	1.90	0.71
1:1:1001:A:H2'	1:1:1001:A:N3	2.05	0.71
28:U:135:PHE:HA	28:U:259:PHE:O	1.91	0.71
4:4:196:A:H61	4:4:831:G:H21	1.39	0.71
4:4:2425:A:O4'	4:4:2427:C:O2	2.08	0.70
13:F:113:GLU:H	13:F:119:ARG:HE	1.39	0.70
50:q:135:LEU:O	50:q:139:LYS:HB2	1.92	0.70
6:6:104:PHE:HA	6:6:139:VAL:O	1.92	0.69
13:F:115:ARG:HG3	13:F:117:ALA:H	1.57	0.69
4:4:1093:G:H21	4:4:1098:A:H62	1.38	0.69
43:j:61:ALA:O	43:j:65:GLY:HA2	1.92	0.69
36:c:34:ARG:HE	36:c:39:ARG:HG3	1.59	0.68
4:4:818:G:H21	4:4:1189:A:H62	1.41	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:x:76:VAL:HA	57:x:102:HIS:O	1.94	0.68
34:a:36:CYS:N	34:a:49:CYS:SG	2.62	0.68
4:4:2259:G:O4'	4:4:2427:C:H5	1.77	0.67
28:U:313:ALA:HA	28:U:327:PHE:O	1.95	0.67
8:A:70:PHE:HA	8:A:163:PHE:O	1.94	0.67
1:1:1237:C:H5'	1:1:1238:A:H4'	1.75	0.67
4:4:2120:G:H1	4:4:2178:C:H42	1.42	0.67
1:1:1413:A:H2	1:1:1487:G:H1	1.43	0.67
54:u:5:ALA:O	54:u:9:LEU:HB2	1.95	0.67
28:U:15:ILE:HA	28:U:103:GLY:O	1.95	0.67
1:1:939:G:H2'	1:1:940:C:C5	2.30	0.67
4:4:534:U:H3	4:4:559:G:H1	1.43	0.67
1:1:447:G:H21	1:1:487:A:H62	0.80	0.67
15:H:11:LYS:HD2	15:H:69:GLY:H	1.58	0.66
54:u:62:THR:HA	54:u:74:ARG:O	1.95	0.66
1:1:940:C:O5'	1:1:940:C:H6	1.78	0.66
16:I:17:ASP:O	16:I:21:GLN:HB2	1.95	0.66
25:R:70:LYS:HG3	25:R:72:GLY:H	1.59	0.66
1:1:1046:A:N7	1:1:1211:U:O2	2.28	0.66
4:4:2259:G:C5	4:4:2427:C:N4	2.64	0.66
20:M:43:CYS:O	20:M:47:LEU:HB2	1.95	0.66
51:r:62:GLY:HA2	51:r:107:ALA:O	1.95	0.66
4:4:2259:G:C8	4:4:2427:C:C5	2.84	0.66
7:7:60:GLU:O	7:7:64:GLU:HB3	1.96	0.66
8:A:58:ILE:O	8:A:62:ALA:HB3	1.96	0.66
1:1:782:A:N6	1:1:800:G:H21	1.90	0.65
33:Z:38:LYS:HG2	33:Z:40:HIS:H	1.59	0.65
14:G:33:GLU:O	14:G:37:ARG:NH1	2.28	0.65
33:Z:25:TYR:HH	43:j:4:ASP:N	1.94	0.65
18:K:17:LYS:HD3	18:K:19:ARG:H	1.61	0.65
4:4:614:U:H6	4:4:614:U:O5'	1.80	0.64
20:M:7:ILE:HG13	20:M:23:ARG:HH12	1.61	0.64
43:j:39:ILE:HG23	43:j:92:VAL:HG13	1.79	0.64
54:u:120:ARG:O	54:u:124:ASP:HB2	1.97	0.64
4:4:2392:A:N7	4:4:2429:G:C5	2.65	0.64
9:B:132:ARG:O	9:B:136:GLN:HB2	1.97	0.64
51:r:65:PHE:HB2	51:r:105:GLU:O	1.98	0.64
1:1:1270:C:HO2'	1:1:1313:U:HO2'	1.46	0.64
10:C:118:ARG:O	10:C:122:ARG:HB2	1.97	0.64
1:1:1324:A:H4'	1:1:1362:C:H4'	1.80	0.63
4:4:1800:C:N3	4:4:1817:G:N1	2.45	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:g:32:SER:HA	40:g:35:LYS:HE3	1.79	0.63
1:1:1297:C:H1'	13:F:114:ARG:HB2	1.80	0.63
31:X:32:LEU:HB2	31:X:53:LEU:HD12	1.80	0.63
1:1:664:G:H22	1:1:741:G:H1	1.44	0.63
4:4:2012:G:H4'	57:x:96:ILE:HD11	1.80	0.63
37:d:53:PRO:HA	37:d:56:GLU:HB3	1.81	0.63
1:1:1177:G:N7	15:H:97:LYS:NZ	2.46	0.63
23:P:6:LEU:O	23:P:59:ILE:HB	1.99	0.63
1:1:674:G:H2'	1:1:675:A:H8	1.63	0.63
16:I:8:LEU:O	16:I:69:ASN:HA	1.98	0.63
1:1:437:U:H3	1:1:495:A:H62	1.47	0.62
1:1:1179:A:H4'	15:H:104:ARG:HD2	1.80	0.62
16:I:5:ARG:O	16:I:99:LYS:HB2	2.00	0.62
4:4:2015:A:N3	34:a:2:ALA:N	2.47	0.62
4:4:1668:A:N3	4:4:1670:C:N4	2.47	0.62
40:g:81:ALA:HB3	40:g:94:LEU:HB3	1.80	0.62
8:A:177:ALA:HB1	8:A:182:ILE:HB	1.81	0.62
21:N:49:ASP:HB3	21:N:52:SER:HB2	1.82	0.62
1:1:1244:C:H5	27:T:9:ARG:HH21	1.48	0.62
21:N:5:LYS:O	21:N:9:GLN:HB2	1.99	0.62
28:U:457:LEU:HB2	28:U:660:ARG:HE	1.64	0.62
4:4:196:A:H61	4:4:831:G:N2	1.97	0.61
9:B:118:GLN:O	9:B:121:ALA:N	2.29	0.61
1:1:778:G:N2	17:J:119:CYS:SG	2.73	0.61
6:6:95:PRO:HA	6:6:128:VAL:O	2.00	0.61
56:w:38:LEU:HD11	56:w:57:VAL:HG12	1.82	0.61
1:1:1510:U:H3	1:1:1525:G:H1	1.48	0.61
4:4:1263:U:H5''	34:a:16:ARG:HD3	1.82	0.61
1:1:1312:G:OP1	33:Z:58:ARG:NH2	2.32	0.61
4:4:2392:A:C5	4:4:2429:G:C5	2.89	0.61
8:A:163:PHE:HA	8:A:185:ILE:O	2.01	0.61
11:D:103:GLY:O	11:D:107:ARG:HB2	2.01	0.61
27:T:7:ARG:HH11	27:T:22:ARG:HB2	1.66	0.61
43:j:136:ARG:HG3	43:j:137:GLU:HG3	1.82	0.61
1:1:367:U:H4'	28:U:351:ARG:HD2	1.82	0.61
4:4:2392:A:N7	4:4:2429:G:C6	2.69	0.61
56:w:74:LYS:HB2	56:w:83:ARG:HB2	1.82	0.61
14:G:83:ILE:HD11	14:G:135:CYS:HB2	1.83	0.61
10:C:118:ARG:HD2	10:C:136:PRO:HG2	1.82	0.60
28:U:238:THR:O	28:U:242:LEU:HB2	2.01	0.60
1:1:1306:A:N6	1:1:1331:G:O2'	2.32	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:2197:U:O2	4:4:2225:A:N7	2.34	0.60
34:a:30:LEU:HB3	34:a:39:MET:HB3	1.82	0.60
1:1:836:G:H1	1:1:850:U:H3	1.49	0.60
26:S:82:SER:O	26:S:86:ARG:HB2	2.02	0.60
28:U:507:TYR:HH	28:U:571:SER:HG	1.49	0.60
1:1:941:G:C6	1:1:1343:G:O6	2.55	0.60
4:4:2010:G:H5''	57:x:42:ARG:HB2	1.82	0.60
28:U:17:ILE:HA	28:U:105:ILE:O	2.01	0.60
9:B:113:ALA:HA	9:B:116:VAL:HG12	1.82	0.60
1:1:949:A:N7	19:L:106:ASN:ND2	2.49	0.60
49:p:75:SER:HB2	54:u:74:ARG:HH12	1.66	0.60
49:p:76:ALA:O	54:u:74:ARG:NH1	2.35	0.60
1:1:111:G:H1	1:1:330:C:H41	1.49	0.60
1:1:1244:C:OP2	27:T:9:ARG:HG2	2.02	0.60
42:i:1:MET:HG2	42:i:115:ALA:HB1	1.82	0.60
1:1:998:G:H1	1:1:1044:A:H1'	1.67	0.59
9:B:39:ILE:O	9:B:43:LEU:HB2	2.01	0.59
1:1:1533:C:C4	3:3:7:U:O4	2.56	0.59
4:4:2259:G:C4	4:4:2427:C:N4	2.70	0.59
9:B:187:ALA:HB2	9:B:198:VAL:HG12	1.82	0.59
4:4:366:C:H5'	4:4:370:G:H5'	1.84	0.59
4:4:1791:A:N6	4:4:1828:G:O2'	2.35	0.59
56:w:4:ILE:HB	56:w:39:LEU:HB2	1.83	0.59
4:4:676:A:H8	4:4:2069:G:H21	1.50	0.59
4:4:2743:C:OP1	38:e:33:LYS:NZ	2.36	0.59
11:D:103:GLY:O	11:D:107:ARG:CB	2.49	0.59
43:j:103:LEU:O	43:j:107:LEU:HB2	2.02	0.59
1:1:958:A:N3	1:1:985:C:O2'	2.35	0.59
11:D:11:ILE:HG21	11:D:108:ALA:HB1	1.84	0.59
1:1:1243:C:HO2'	27:T:7:ARG:HH21	1.50	0.59
11:D:134:ALA:O	11:D:138:ALA:HB2	2.02	0.59
28:U:16:GLY:HA3	28:U:101:LEU:HD22	1.84	0.59
34:a:25:LEU:HD23	57:x:19:LEU:HB3	1.83	0.59
4:4:2885:C:H42	34:a:42:PRO:HB3	1.67	0.59
4:4:2008:C:H2'	4:4:2009:G:H8	1.68	0.59
18:K:76:ASN:HD21	18:K:108:ALA:HB3	1.68	0.59
54:u:27:THR:OG1	54:u:29:ARG:NH1	2.36	0.59
17:J:62:GLN:HG3	17:J:66:LEU:HB2	1.85	0.59
42:i:196:LEU:O	42:i:200:GLU:HB2	2.02	0.59
4:4:466:A:OP1	36:c:34:ARG:NH1	2.35	0.59
8:A:25:ASN:H	8:A:191:ASP:HA	1.68	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:60:ALA:HB3	9:B:63:ASN:HB2	1.83	0.59
1:1:942:G:N2	1:1:1232:U:OP1	2.36	0.58
4:4:1065:U:O2	4:4:1074:G:N2	2.35	0.58
4:4:2396:G:N2	4:4:2421:G:N7	2.51	0.58
19:L:9:ILE:HG22	19:L:11:ARG:H	1.66	0.58
1:1:1237:C:H5'	1:1:1238:A:C4'	2.33	0.58
4:4:1664:A:H61	4:4:1996:C:N4	2.01	0.58
57:x:78:GLU:OE2	57:x:99:ARG:NH1	2.37	0.58
28:U:680:PRO:O	28:U:684:GLN:HB2	2.03	0.58
41:h:104:VAL:HG11	41:h:188:VAL:HG23	1.85	0.58
43:j:56:ALA:O	43:j:60:LEU:HB2	2.03	0.58
1:1:1297:C:OP1	1:1:1299:A:N6	2.35	0.58
28:U:312:LEU:O	28:U:328:ILE:HA	2.04	0.58
1:1:943:U:OP1	1:1:946:A:N6	2.35	0.58
4:4:529:A:H62	4:4:2041:U:H3	1.52	0.58
4:4:1819:A:H5''	40:g:161:THR:HG21	1.86	0.58
23:P:62:SER:O	23:P:70:ARG:NH2	2.36	0.58
1:1:1305:G:O2'	1:1:1332:A:N6	2.36	0.58
36:c:34:ARG:NH2	36:c:41:ARG:O	2.36	0.58
4:4:1363:C:OP1	30:W:61:ARG:NH2	2.37	0.58
4:4:1365:A:O2'	30:W:11:ARG:NH2	2.36	0.58
17:J:66:LEU:O	17:J:70:LYS:HB2	2.04	0.58
25:R:40:ILE:HB	25:R:71:LEU:HD13	1.85	0.58
55:v:10:ARG:O	55:v:14:HIS:ND1	2.31	0.58
4:4:752:A:H61	4:4:2609:U:H3	1.52	0.58
31:X:67:LYS:O	31:X:71:ASN:HB2	2.03	0.58
42:i:39:TRP:NE1	42:i:99:TYR:O	2.36	0.58
42:i:155:LEU:HD11	42:i:176:LEU:HD13	1.85	0.58
56:w:67:GLY:H	56:w:88:ARG:HE	1.51	0.58
9:B:94:LEU:HD12	9:B:95:THR:HG22	1.86	0.57
40:g:147:LEU:HD23	40:g:148:GLU:HG3	1.85	0.57
51:r:34:LEU:HB2	51:r:118:LEU:HD22	1.84	0.57
1:1:1432:G:O2'	1:1:1468:A:N6	2.37	0.57
4:4:2425:A:H5''	4:4:2427:C:H1'	1.85	0.57
7:7:58:LEU:O	7:7:62:LYS:HB2	2.03	0.57
39:f:7:ARG:HH21	39:f:35:THR:H	1.51	0.57
1:1:768:A:N3	1:1:1512:U:O2'	2.37	0.57
1:1:1134:G:H22	1:1:1141:C:H1'	1.69	0.57
1:1:1308:U:N3	1:1:1329:A:C6	2.72	0.57
4:4:910:A:H62	51:r:12:GLN:HA	1.67	0.57
6:6:44:PHE:O	6:6:48:PHE:CB	2.53	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:W:24:ALA:HB2	30:W:32:LYS:HE3	1.86	0.57
4:4:2392:A:C5	4:4:2429:G:C6	2.92	0.57
1:1:21:G:H21	1:1:914:A:H62	1.53	0.57
1:1:1039:C:H42	1:1:1042:G:H8	1.52	0.57
1:1:1319:A:H2'	1:1:1323:G:H5''	1.86	0.57
4:4:1499:C:H2'	4:4:1500:G:H8	1.69	0.57
5:5:24:G:N3	5:5:27:C:N4	2.53	0.57
4:4:1664:A:N6	4:4:1996:C:H42	2.02	0.57
4:4:2259:G:N9	4:4:2427:C:N4	2.52	0.57
44:k:54:ARG:NH1	44:k:57:ASP:OD1	2.37	0.57
9:B:136:GLN:O	9:B:140:ARG:NH1	2.33	0.57
16:I:8:LEU:HA	16:I:96:ILE:HG22	1.87	0.57
28:U:11:ARG:HG3	28:U:77:HIS:HA	1.87	0.57
31:X:18:PRO:HA	31:X:21:LEU:HD13	1.87	0.57
33:Z:22:ILE:HG12	43:j:104:GLU:HB3	1.87	0.57
55:v:97:ASP:O	55:v:101:ARG:HB3	2.05	0.57
4:4:827:U:H5'	4:4:828:U:OP1	2.03	0.57
4:4:2115:G:N2	4:4:2166:G:N3	2.53	0.57
19:L:5:ALA:HA	19:L:57:ARG:HG3	1.87	0.57
1:1:20:U:O2'	1:1:573:A:N6	2.38	0.56
4:4:2845:G:H2'	4:4:2846:G:H8	1.70	0.56
4:4:589:C:H2'	4:4:590:A:H8	1.70	0.56
28:U:605:ILE:HG13	28:U:677:GLN:HG2	1.87	0.56
58:y:54:VAL:HG22	58:y:81:VAL:HG12	1.86	0.56
1:1:1298:C:H5'	13:F:114:ARG:HB3	1.87	0.56
1:1:1343:G:N2	1:1:1349:A:O2'	2.38	0.56
4:4:321:G:O2'	4:4:340:A:N3	2.38	0.56
4:4:334:C:O2'	59:z:84:ARG:NH2	2.38	0.56
4:4:1165:U:H3	4:4:1184:G:H1	1.53	0.56
6:6:76:LEU:HD21	51:r:137:TYR:HB3	1.86	0.56
15:H:63:ILE:HD13	15:H:65:VAL:HG12	1.88	0.56
17:J:51:LYS:H	17:J:54:ARG:HH21	1.51	0.56
17:J:91:ARG:NH1	24:Q:88:LYS:O	2.38	0.56
28:U:104:ALA:O	28:U:132:ARG:HA	2.06	0.56
41:h:54:GLN:NE2	41:h:55:ASN:OD1	2.38	0.56
44:k:91:GLY:HA2	44:k:160:LYS:HG2	1.86	0.56
50:q:39:LYS:HG2	50:q:45:LEU:HB3	1.87	0.56
1:1:736:C:H2'	1:1:737:A:H8	1.71	0.56
4:4:2508:G:H1	4:4:2580:U:H3	1.52	0.56
1:1:397:A:N7	1:1:547:A:O2'	2.39	0.56
4:4:2293:C:OP1	53:t:89:ARG:NH1	2.39	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:U:461:ILE:HG13	28:U:462:ILE:HG12	1.87	0.56
1:1:159:G:N2	1:1:162:A:OP2	2.38	0.56
12:E:10:LEU:O	12:E:86:ARG:NH2	2.39	0.56
4:4:642:G:N2	4:4:645:C:OP2	2.36	0.56
4:4:996:A:OP2	55:v:94:ASN:ND2	2.38	0.56
26:S:56:MET:HE3	26:S:103:GLY:HA3	1.88	0.56
40:g:134:ARG:HH12	40:g:188:GLU:HB3	1.71	0.56
1:1:1221:G:OP1	1:1:1320:C:N4	2.39	0.56
4:4:1779:U:OP2	4:4:1784:A:N6	2.39	0.56
4:4:2546:U:H5''	4:4:2547:U:H5'	1.87	0.56
18:K:73:GLU:HB2	18:K:110:VAL:HG11	1.87	0.56
24:Q:74:ARG:NH1	24:Q:80:PRO:O	2.39	0.56
28:U:629:GLY:HA3	28:U:647:VAL:HG12	1.87	0.56
39:f:73:VAL:HG21	39:f:154:ILE:HG23	1.88	0.56
4:4:1435:G:N2	4:4:1477:A:O2'	2.39	0.56
13:F:99:LEU:O	13:F:103:TRP:HB2	2.06	0.56
16:I:8:LEU:HD11	16:I:72:VAL:HG23	1.87	0.56
19:L:104:ARG:HD3	19:L:105:THR:HG23	1.88	0.56
29:V:27:GLU:HA	29:V:67:VAL:HG23	1.88	0.56
37:d:10:ALA:HB2	50:q:59:LEU:HD11	1.88	0.56
1:1:1533:C:N3	3:3:7:U:O4	2.39	0.56
4:4:826:U:O2'	50:q:54:GLY:C	2.48	0.56
4:4:994:C:OP1	55:v:53:ARG:NH2	2.39	0.56
4:4:2199:A:N1	4:4:2226:C:N4	2.51	0.56
8:A:59:GLU:HB2	8:A:221:LEU:HD21	1.87	0.56
12:E:80:ARG:NH2	12:E:88:VAL:O	2.39	0.56
41:h:34:VAL:HG21	41:h:78:LEU:HD23	1.87	0.56
57:x:47:VAL:HG22	57:x:103:ILE:HG21	1.87	0.56
1:1:603:U:H2'	1:1:604:G:H8	1.71	0.55
1:1:1318:A:N3	25:R:37:ARG:NH2	2.53	0.55
6:6:109:ALA:HB3	6:6:114:GLY:HA2	1.86	0.55
10:C:63:LYS:HE2	10:C:198:VAL:HA	1.88	0.55
39:f:44:VAL:HB	39:f:174:ALA:HB3	1.87	0.55
1:1:137:C:H2'	1:1:138:G:H8	1.69	0.55
1:1:359:U:H2'	1:1:360:A:H8	1.71	0.55
1:1:909:A:N3	1:1:1413:A:O2'	2.38	0.55
1:1:1262:C:N3	1:1:1274:G:N2	2.54	0.55
1:1:1516:G:N2	1:1:1519:A:OP2	2.39	0.55
4:4:309:G:N3	4:4:329:G:O2'	2.37	0.55
4:4:443:A:N6	42:i:41:LEU:O	2.40	0.55
1:1:401:C:O2'	1:1:621:A:N3	2.39	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:572:A:H61	4:4:2029:G:H21	1.55	0.55
4:4:629:G:N3	4:4:639:U:O2'	2.39	0.55
23:P:10:VAL:HB	23:P:55:ASP:H	1.71	0.55
35:b:41:PRO:HD2	35:b:46:HIS:H	1.71	0.55
39:f:183:PRO:HA	39:f:186:LEU:HB2	1.87	0.55
1:1:744:C:O2'	1:1:851:G:N2	2.39	0.55
20:M:45:ARG:HD3	20:M:46:GLU:HG3	1.87	0.55
1:1:941:G:O2'	1:1:942:G:O5'	2.25	0.55
4:4:397:G:O2'	4:4:2230:G:N2	2.38	0.55
4:4:788:A:OP1	4:4:791:C:N4	2.39	0.55
13:F:22:LEU:HD22	13:F:97:GLN:HE22	1.72	0.55
1:1:958:A:N6	25:R:55:LYS:O	2.40	0.55
4:4:477:A:OP1	4:4:501:A:N6	2.39	0.55
4:4:636:G:H2'	50:q:115:LEU:HD21	1.89	0.55
16:I:39:PRO:HA	16:I:70:ARG:HG3	1.88	0.55
28:U:487:ILE:HG22	28:U:599:PRO:HG3	1.89	0.55
9:B:85:ARG:O	9:B:89:GLU:HB3	2.06	0.55
14:G:46:LYS:NZ	14:G:63:LEU:O	2.39	0.55
28:U:68:ALA:O	28:U:82:ILE:HA	2.07	0.55
37:d:40:GLU:O	37:d:44:LYS:NZ	2.38	0.55
4:4:827:U:C5	4:4:2430:A:C2	2.95	0.55
4:4:2682:U:O2'	54:u:58:ASN:ND2	2.40	0.55
5:5:76:G:H22	5:5:102:A:H61	1.55	0.55
7:7:127:VAL:HG12	7:7:139:GLN:HG3	1.89	0.55
28:U:579:GLU:O	28:U:583:LYS:HB2	2.07	0.55
1:1:448:A:OP2	1:1:485:G:N2	2.40	0.55
1:1:877:C:H2'	1:1:878:G:H8	1.72	0.55
4:4:527:C:H41	4:4:2779:U:H5''	1.72	0.55
4:4:1193:G:OP1	50:q:14:LYS:NZ	2.39	0.55
1:1:941:G:C2	1:1:942:G:C5	2.94	0.54
4:4:271(G):C:H2'	4:4:271(H):G:H8	1.72	0.54
4:4:922:U:O2'	29:V:29:GLN:NE2	2.41	0.54
4:4:1653:G:H5''	52:s:2:ARG:HD2	1.88	0.54
26:S:61:SER:O	26:S:65:LYS:CB	2.55	0.54
1:1:103:C:OP1	26:S:17:ARG:NH1	2.40	0.54
4:4:2419:U:OP2	37:d:33:ASN:ND2	2.41	0.54
38:e:20:HIS:O	38:e:22:ARG:NH1	2.40	0.54
43:j:170:ARG:NH1	43:j:174:GLU:OE2	2.40	0.54
4:4:83:G:OP2	59:z:92:ASN:ND2	2.40	0.54
4:4:2467:C:OP1	38:e:8:LYS:NZ	2.41	0.54
4:4:2747:G:H21	4:4:2757:A:H62	1.54	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C:191:ARG:HE	10:C:200:GLU:HB2	1.71	0.54
15:H:11:LYS:NZ	15:H:67:GLY:O	2.35	0.54
28:U:467:LYS:NZ	28:U:473:ASP:OD1	2.41	0.54
28:U:533:VAL:HG23	28:U:538:TYR:HB3	1.90	0.54
35:b:27:LYS:HG2	35:b:29:ASN:H	1.72	0.54
39:f:7:ARG:NH2	39:f:33:LEU:O	2.40	0.54
1:1:544:G:OP1	10:C:59:ARG:NH2	2.41	0.54
1:1:1308:U:C2	1:1:1329:A:C6	2.96	0.54
4:4:196:A:N6	4:4:831:G:H21	2.03	0.54
4:4:2502:G:H5''	4:4:2503:A:H5'	1.89	0.54
8:A:208:ILE:O	8:A:212:GLN:HB2	2.08	0.54
10:C:165:MET:N	10:C:165:MET:SD	2.80	0.54
43:j:174:GLU:HA	43:j:178:PHE:H	1.73	0.54
52:s:16:HIS:O	52:s:20:LEU:HB2	2.07	0.54
4:4:631:A:OP2	37:d:46:ARG:NH2	2.41	0.54
4:4:1076:C:OP2	4:4:1077:A:N6	2.40	0.54
4:4:1311:G:H21	4:4:1603:A:H62	1.53	0.54
4:4:2081:C:H2'	4:4:2082:A:H8	1.73	0.54
5:5:30:C:O2'	5:5:57:A:N6	2.41	0.54
6:6:119:GLU:HB3	6:6:172:ALA:HA	1.89	0.54
8:A:98:LEU:HD21	8:A:148:TYR:HB3	1.89	0.54
8:A:174:VAL:HG13	8:A:184:VAL:HG11	1.88	0.54
52:s:65:LEU:HG	52:s:68:ARG:HE	1.72	0.54
59:z:73:ARG:NH1	59:z:83:THR:OG1	2.40	0.54
4:4:2259:G:N7	4:4:2427:C:N4	2.47	0.54
12:E:67:MET:HE1	12:E:72:VAL:HG22	1.90	0.54
19:L:60:VAL:O	19:L:64:TRP:NE1	2.41	0.54
56:w:65:GLY:O	56:w:88:ARG:NH2	2.40	0.54
1:1:826:C:O2	14:G:15:ASN:ND2	2.40	0.54
1:1:1323:G:H4'	1:1:1361:G:H21	1.73	0.54
4:4:2259:G:C8	4:4:2427:C:C4	2.95	0.54
4:4:2428:G:N1	50:q:61:ARG:NH1	2.51	0.54
28:U:99:ARG:NH1	28:U:400:GLU:O	2.40	0.54
28:U:109:ASP:OD1	28:U:138:LYS:NZ	2.41	0.54
42:i:117:ARG:NH2	42:i:189:THR:O	2.41	0.54
55:v:24:TYR:HB2	55:v:29:SER:HB3	1.90	0.54
1:1:1248:A:N6	1:1:1288:A:OP2	2.41	0.54
4:4:1844:C:H5''	40:g:258:LYS:HG2	1.90	0.54
4:4:2515:C:H2'	4:4:2516:G:H8	1.72	0.54
6:6:161:VAL:HG13	6:6:162:GLU:HG2	1.90	0.54
11:D:28:PHE:HB2	11:D:48:ALA:O	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1414:U:H2'	1:1:1415:G:H8	1.73	0.54
4:4:659:C:H2'	4:4:660:G:H8	1.71	0.54
4:4:2056:G:N2	34:a:4:HIS:O	2.41	0.54
9:B:40:ARG:NH1	20:M:52:GLN:OE1	2.41	0.54
10:C:62:GLN:HE22	10:C:65:ARG:HH21	1.55	0.54
23:P:88:TYR:OH	23:P:92:ARG:NH2	2.40	0.54
4:4:1786:A:O2'	4:4:1938:A:N6	2.40	0.54
4:4:2250:G:O2'	4:4:2496:C:OP1	2.26	0.54
1:1:745:C:H5''	1:1:851:G:H1'	1.89	0.53
1:1:781:A:N7	1:1:801:U:O2	2.41	0.53
9:B:131:ARG:NH1	9:B:166:GLU:OE2	2.40	0.53
22:O:57:ARG:O	22:O:61:SER:HB3	2.08	0.53
22:O:69:THR:HA	22:O:72:ARG:HG2	1.90	0.53
51:r:12:GLN:HE21	51:r:72:LYS:HA	1.72	0.53
56:w:1:MET:HA	56:w:42:GLY:HA3	1.90	0.53
4:4:827:U:C6	4:4:2430:A:C2	2.95	0.53
5:5:78:A:H62	5:5:99:G:H21	1.56	0.53
14:G:44:PHE:HA	14:G:79:VAL:HG11	1.90	0.53
1:1:927:G:H1	1:1:1390:U:H3	1.56	0.53
4:4:1333:C:H2'	4:4:1334:G:H8	1.73	0.53
4:4:1484:G:H22	4:4:1505:C:H42	1.56	0.53
4:4:1626:G:H5''	4:4:1627:G:H5'	1.90	0.53
4:4:2259:G:C8	4:4:2427:C:H5	2.25	0.53
4:4:2291:U:O2'	4:4:2374:C:O2	2.26	0.53
4:4:2637:U:H3	4:4:2776:A:H62	1.54	0.53
8:A:178:ARG:NH2	8:A:196:LEU:O	2.42	0.53
28:U:212:TYR:HA	28:U:215:LYS:HB2	1.89	0.53
42:i:2:LYS:HG3	42:i:4:VAL:H	1.72	0.53
6:6:72:ARG:HB2	6:6:87:ASP:HB3	1.91	0.53
13:F:151:TYR:HB2	17:J:58:PRO:HG2	1.90	0.53
28:U:553:GLY:O	28:U:591:LYS:NZ	2.39	0.53
1:1:126:G:OP1	1:1:605:U:O2'	2.25	0.53
1:1:1130:A:H4'	15:H:2:GLU:HG2	1.90	0.53
4:4:2286:A:N7	35:b:37:ARG:NH2	2.56	0.53
9:B:19:GLU:OE1	9:B:54:ARG:NH2	2.41	0.53
16:I:3:LYS:N	16:I:74:ILE:O	2.41	0.53
30:W:5:CYS:HB2	30:W:9:GLY:H	1.74	0.53
40:g:172:TYR:HB3	40:g:184:LYS:HB3	1.91	0.53
52:s:41:ALA:HB1	52:s:114:VAL:HG21	1.91	0.53
1:1:187:C:OP1	26:S:86:ARG:NH2	2.41	0.53
1:1:1224:G:OP2	19:L:102:ARG:NH2	2.41	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:2822:G:OP1	41:h:159:HIS:NE2	2.40	0.53
11:D:43:LEU:HB2	11:D:136:MET:HE3	1.89	0.53
13:F:141:VAL:HA	13:F:144:MET:HE2	1.91	0.53
35:b:13:CYS:HB2	35:b:22:ALA:HB3	1.91	0.53
43:j:135:LEU:HD21	43:j:155:MET:HG2	1.90	0.53
54:u:26:ASP:HB2	54:u:91:ARG:HH21	1.74	0.53
4:4:1696:G:N2	4:4:1977:A:O2'	2.41	0.53
4:4:2425:A:C8	4:4:2427:C:O2	2.61	0.53
39:f:166:ASN:HD22	39:f:170:GLY:HA2	1.74	0.53
1:1:376:G:H1	1:1:387:U:H3	1.57	0.53
4:4:271(R):G:OP1	30:W:76:ARG:NH1	2.42	0.53
4:4:2392:A:C6	4:4:2429:G:C4	2.97	0.53
14:G:17:THR:HB	14:G:78:GLN:HG2	1.91	0.53
1:1:582:U:O2'	23:P:94:ASN:ND2	2.40	0.53
1:1:1239:A:O5'	13:F:119:ARG:NH1	2.41	0.53
42:i:156:LEU:O	42:i:175:THR:HA	2.09	0.53
1:1:258:G:H2'	1:1:259:G:H8	1.74	0.53
1:1:587:G:OP1	14:G:92:ARG:NH2	2.42	0.53
16:I:5:ARG:HG3	16:I:71:LEU:HD13	1.90	0.53
19:L:80:ARG:HH22	33:Z:50:VAL:HG11	1.74	0.53
21:N:27:VAL:HG12	21:N:31:LEU:HD23	1.91	0.53
49:p:9:GLU:O	49:p:83:ALA:HA	2.09	0.53
1:1:559:A:OP2	11:D:126:ARG:NH2	2.41	0.52
1:1:1010:G:O6	1:1:1019:C:N4	2.42	0.52
1:1:1178:G:N2	1:1:1181:G:OP2	2.40	0.52
4:4:442:G:H5''	4:4:614(B):G:H22	1.73	0.52
4:4:1124:C:O2	38:e:36:GLN:NE2	2.42	0.52
4:4:1993:U:H5''	41:h:127:ASP:HB2	1.90	0.52
16:I:5:ARG:HE	16:I:99:LYS:HG3	1.74	0.52
43:j:166:ASP:O	43:j:170:ARG:CB	2.57	0.52
43:j:166:ASP:O	43:j:170:ARG:HB2	2.09	0.52
58:y:52:VAL:N	58:y:82:GLN:O	2.41	0.52
2:2:18:G:N2	2:2:55:U:O2'	2.42	0.52
4:4:184:C:O2'	4:4:217:G:N3	2.41	0.52
4:4:468:G:OP2	36:c:37:LYS:NZ	2.40	0.52
4:4:814:C:OP2	50:q:25:SER:OG	2.27	0.52
8:A:25:ASN:ND2	8:A:193:ASP:OD1	2.42	0.52
28:U:73:PHE:HD1	28:U:78:ARG:HE	1.58	0.52
1:1:719:C:H1'	24:Q:49:LYS:HD2	1.92	0.52
1:1:1238:A:H2'	1:1:1238:A:N3	2.23	0.52
4:4:340:A:O2'	42:i:168:ARG:NH2	2.41	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:7:PRO:O	9:B:16:ARG:NH1	2.42	0.52
10:C:143:GLY:N	10:C:185:PHE:O	2.40	0.52
12:E:47:ARG:HH22	12:E:56:PRO:HB2	1.73	0.52
15:H:95:LYS:HG3	15:H:96:LEU:HG	1.92	0.52
28:U:459:LEU:HG	28:U:463:VAL:HB	1.90	0.52
1:1:581:G:OP1	21:N:65:ARG:NH1	2.43	0.52
1:1:1255:G:OP1	1:1:1359:C:N4	2.43	0.52
1:1:1464:G:OP1	54:u:112:ARG:NH2	2.40	0.52
4:4:2308:G:H22	43:j:79:ASN:HB3	1.74	0.52
4:4:2746:U:H5''	44:k:138:LYS:HE2	1.91	0.52
6:6:122:ARG:NE	51:r:138:ASP:OD2	2.43	0.52
13:F:150:ALA:H	17:J:59:TYR:N	2.06	0.52
23:P:6:LEU:HD12	23:P:23:VAL:HG11	1.92	0.52
28:U:276:VAL:HA	28:U:280:LEU:HD23	1.90	0.52
28:U:635:GLU:OE1	28:U:644:ARG:NH2	2.43	0.52
49:p:10:VAL:HG12	49:p:12:ASP:H	1.74	0.52
1:1:757:U:O2'	1:1:879:C:O2	2.28	0.52
4:4:601:C:O2'	42:i:104:LYS:NZ	2.43	0.52
4:4:654(D):G:O2'	4:4:654(Q):C:N4	2.39	0.52
4:4:2168:G:N1	39:f:109:MET:SD	2.83	0.52
10:C:11:LEU:O	10:C:15:GLU:HB2	2.10	0.52
19:L:112:GLY:HA3	19:L:115:LYS:HD3	1.90	0.52
26:S:10:LEU:HG	26:S:12:ALA:H	1.74	0.52
26:S:57:ARG:HD3	26:S:102:GLY:HA3	1.91	0.52
1:1:509:A:H5'	10:C:54:TYR:HD2	1.73	0.52
4:4:2278:A:OP1	51:r:10:ARG:NH2	2.42	0.52
40:g:13:ARG:NH1	40:g:16:MET:SD	2.83	0.52
41:h:36:ARG:NH1	41:h:85:ASN:OD1	2.43	0.52
54:u:123:GLN:O	54:u:127:ALA:HB3	2.09	0.52
1:1:1254:C:OP2	16:l:43:ARG:NH2	2.42	0.52
4:4:744:G:H4'	4:4:1658:C:H4'	1.92	0.52
4:4:1161:C:O2'	56:w:23:GLU:OE1	2.25	0.52
39:f:181:PHE:HB2	39:f:185:LYS:HD2	1.92	0.52
1:1:886:G:H1	1:1:911:U:H3	1.57	0.52
4:4:251:A:OP1	37:d:7:HIS:NE2	2.40	0.52
4:4:654(A):G:N2	4:4:654(V):A:N3	2.58	0.52
4:4:704:G:H21	4:4:727:A:H62	1.58	0.52
4:4:2811:G:H5''	41:h:60:ASN:HB2	1.92	0.52
8:A:168:THR:HA	8:A:171:ALA:HB2	1.92	0.52
9:B:119:ARG:HA	9:B:122:GLU:HB2	1.90	0.52
9:B:181:ASN:O	9:B:203:PHE:HA	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Z:22:ILE:O	43:j:105:LYS:NZ	2.41	0.52
44:k:30:LYS:HG3	44:k:81:GLU:HG2	1.92	0.52
59:z:96:ILE:HD12	59:z:97:ARG:HH21	1.75	0.52
1:1:365:U:H5''	1:1:366:C:H5'	1.92	0.52
1:1:861:G:HO2'	1:1:874:G:HO2'	1.56	0.52
4:4:223:A:O2'	4:4:420:C:O2	2.28	0.52
4:4:475:U:H4'	4:4:510:C:H5'	1.92	0.52
4:4:2848:G:O2'	4:4:2867:G:N2	2.39	0.52
28:U:459:LEU:HB3	28:U:660:ARG:HH12	1.74	0.52
28:U:524:GLU:HB3	28:U:564:LYS:HD3	1.91	0.52
48:o:15:LEU:HD22	48:o:134:ARG:HB3	1.92	0.52
56:w:4:ILE:HA	56:w:12:TYR:O	2.10	0.52
1:1:1030(C):G:O2'	1:1:1031:G:N7	2.40	0.52
4:4:2139:C:O2'	4:4:2154:G:N1	2.42	0.52
23:P:26:GLN:HE21	23:P:37:LYS:HE3	1.74	0.52
31:X:21:LEU:HB3	31:X:64:LEU:HD12	1.91	0.52
1:1:1226:C:H5'	19:L:96:LEU:HD13	1.92	0.51
1:1:1253:G:H1	1:1:1285:A:H61	1.57	0.51
4:4:463:G:N2	4:4:466:A:OP2	2.36	0.51
4:4:2777:G:H5''	4:4:2778:A:H5'	1.92	0.51
10:C:88:VAL:HG13	11:D:97:GLY:HA3	1.91	0.51
28:U:390:VAL:HG21	28:U:396:ARG:HA	1.91	0.51
42:i:20:LEU:HD23	42:i:22:ALA:H	1.74	0.51
4:4:1799:G:N2	4:4:1819:A:OP2	2.41	0.51
8:A:58:ILE:O	8:A:62:ALA:CB	2.58	0.51
11:D:102:ALA:HB1	11:D:106:PRO:HB2	1.92	0.51
11:D:140:ARG:O	11:D:143:ARG:NH1	2.43	0.51
28:U:482:ALA:H	28:U:649:LEU:HD22	1.75	0.51
28:U:493:VAL:HG11	28:U:593:ALA:HA	1.92	0.51
40:g:143:HIS:ND1	40:g:194:GLY:O	2.41	0.51
1:1:1071:C:H2'	1:1:1072:G:H8	1.75	0.51
4:4:9:U:OP1	48:o:115:ARG:NH2	2.43	0.51
4:4:1177:A:H5''	4:4:1178:C:H5	1.75	0.51
4:4:1830:C:H2'	4:4:1831:G:H8	1.75	0.51
4:4:2521:C:O2'	4:4:2564:A:N3	2.40	0.51
31:X:32:LEU:O	31:X:36:ARG:HB2	2.09	0.51
40:g:88:ARG:HH21	40:g:92:ILE:HG21	1.75	0.51
42:i:117:ARG:NH2	42:i:186:ILE:O	2.43	0.51
1:1:21:G:H5'	1:1:573:A:H61	1.76	0.51
4:4:2688:U:OP1	4:4:2713:A:N6	2.44	0.51
28:U:414:GLU:HB3	28:U:475:ASN:HB2	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:i:185:ASP:OD1	42:i:188:ARG:NH2	2.43	0.51
54:u:93:ARG:HG3	54:u:115:ARG:HB3	1.93	0.51
59:z:15:VAL:HG12	59:z:72:VAL:HG12	1.91	0.51
1:1:411:A:O2'	1:1:413:G:N7	2.42	0.51
1:1:697:U:H3	1:1:798:G:H1'	1.76	0.51
4:4:247:G:OP2	4:4:249:C:N4	2.43	0.51
4:4:1363:C:O2'	4:4:1809:A:N3	2.43	0.51
4:4:2135:A:OP1	4:4:2159:G:N2	2.44	0.51
41:h:38:THR:HG22	41:h:40:GLU:H	1.76	0.51
49:p:6:THR:O	49:p:20:MET:HA	2.11	0.51
1:1:1101:A:N7	8:A:175:ARG:NH2	2.56	0.51
4:4:1682:G:OP2	4:4:1699:G:N2	2.43	0.51
6:6:41:LEU:O	6:6:45:ASP:HB2	2.10	0.51
18:K:49:ASN:ND2	18:K:92:ASP:OD2	2.42	0.51
54:u:55:ASN:H	54:u:59:THR:HG22	1.75	0.51
55:v:90:VAL:HG13	56:w:39:LEU:HG	1.91	0.51
1:1:991:U:O2	1:1:1215:G:O6	2.29	0.51
4:4:482:A:H4'	59:z:47:LYS:HG3	1.93	0.51
4:4:2743:C:OP2	4:4:2755:C:N4	2.43	0.51
15:H:10:ARG:NH1	15:H:75:ASP:OD2	2.41	0.51
1:1:104:G:OP2	26:S:18:GLN:NE2	2.42	0.51
4:4:2259:G:O4'	4:4:2427:C:C6	2.61	0.51
4:4:2870:C:OP1	52:s:57:ARG:NH1	2.39	0.51
29:V:52:GLY:O	29:V:59:LEU:HA	2.09	0.51
40:g:211:ARG:HA	40:g:214:TRP:HB2	1.92	0.51
43:j:51:ARG:NH1	43:j:52:ILE:O	2.44	0.51
1:1:941:G:C6	1:1:1343:G:C6	2.98	0.51
4:4:13:A:O2'	4:4:15:G:N7	2.41	0.51
4:4:249:C:O2	37:d:12:LYS:NZ	2.44	0.51
4:4:851:U:H2'	4:4:852:G:H8	1.76	0.51
4:4:1953:A:O2'	4:4:2559:C:O2	2.29	0.51
4:4:2284:C:H5''	35:b:8:LYS:HE3	1.93	0.51
6:6:72:ARG:NH2	51:r:141:GLN:O	2.44	0.51
9:B:30:ARG:HE	20:M:35:ARG:HD2	1.76	0.51
9:B:152:ILE:HB	9:B:199:LYS:HD2	1.93	0.51
38:e:4:ARG:NH1	38:e:6:SER:O	2.44	0.51
40:g:108:PRO:HD2	40:g:111:LEU:HD11	1.93	0.51
1:1:735:C:OP1	24:Q:68:LYS:NZ	2.40	0.51
1:1:757:U:H1'	1:1:879:C:H1'	1.92	0.51
1:1:951:G:O2'	1:1:972:C:N4	2.43	0.51
1:1:1308:U:C2	1:1:1329:A:N6	2.79	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:105:PHE:O	8:A:109:SER:OG	2.27	0.51
10:C:209:ARG:NH1	11:D:102:ALA:O	2.44	0.51
21:N:82:ILE:HD12	21:N:88:ARG:HH21	1.76	0.51
25:R:4:SER:O	25:R:6:LYS:NZ	2.41	0.51
1:1:538:G:H2'	1:1:539:A:H8	1.76	0.50
1:1:995:C:O2'	1:1:996:A:N7	2.43	0.50
4:4:2489:G:N2	4:4:2491:U:O4	2.42	0.50
10:C:72:GLU:OE2	10:C:76:ARG:NE	2.40	0.50
18:K:69:TYR:HB2	18:K:96:VAL:HG11	1.93	0.50
50:q:57:THR:HG23	50:q:60:MET:H	1.76	0.50
1:1:546:G:H4'	1:1:548:G:H4'	1.92	0.50
1:1:687:A:O2'	1:1:701:C:N4	2.44	0.50
1:1:1000:U:C1'	1:1:1001:A:OP1	2.59	0.50
1:1:1254:C:OP1	16:I:45:ARG:NE	2.44	0.50
4:4:1196:C:H2'	4:4:1197:G:H8	1.76	0.50
4:4:1399:C:H2'	4:4:1400:G:H8	1.76	0.50
4:4:1500:G:H21	40:g:100:GLY:HA3	1.76	0.50
7:7:60:GLU:O	7:7:64:GLU:CB	2.59	0.50
8:A:167:PRO:O	8:A:171:ALA:HA	2.11	0.50
11:D:11:ILE:HD11	11:D:31:LEU:HD12	1.92	0.50
28:U:487:ILE:HG13	28:U:516:PRO:HD3	1.94	0.50
49:p:104:ARG:NH2	49:p:121:VAL:O	2.43	0.50
52:s:104:ARG:HG3	52:s:111:LEU:HD21	1.92	0.50
4:4:288:C:H2'	4:4:289:A:H8	1.76	0.50
4:4:560:C:O2	55:v:49:HIS:NE2	2.37	0.50
4:4:581:C:H2'	4:4:582:G:H8	1.77	0.50
4:4:1902:C:OP1	40:g:242:ARG:NH1	2.44	0.50
21:N:12:ILE:O	21:N:16:ALA:HB2	2.11	0.50
1:1:1484:C:HO2'	4:4:1960:A:HO2'	1.59	0.50
4:4:98:G:OP1	31:X:2:LYS:N	2.44	0.50
4:4:875:G:H5''	6:6:150:LEU:HD13	1.92	0.50
9:B:22:TRP:HB3	9:B:59:ARG:HD2	1.94	0.50
14:G:11:THR:O	14:G:15:ASN:HB2	2.12	0.50
42:i:156:LEU:HA	42:i:193:VAL:O	2.10	0.50
1:1:362:G:N2	1:1:365:U:OP2	2.41	0.50
4:4:698:C:H5''	4:4:699:A:H5'	1.94	0.50
20:M:23:ARG:HA	20:M:30:ALA:HA	1.92	0.50
4:4:65:C:H5'	58:y:71:GLY:HA3	1.94	0.50
4:4:263:C:O2'	4:4:429:A:N3	2.40	0.50
4:4:514:A:N3	4:4:581:C:O2'	2.38	0.50
4:4:517:C:OP1	34:a:16:ARG:NH2	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:1864:U:OP1	4:4:2410:G:O2'	2.30	0.50
4:4:2690:C:N4	4:4:2713:A:O3'	2.44	0.50
14:G:25:ASP:OD1	14:G:60:ARG:NH1	2.44	0.50
40:g:136:ILE:O	40:g:168:ARG:NH2	2.45	0.50
49:p:8:LEU:HD13	49:p:82:ASN:HB3	1.92	0.50
4:4:1606:G:H5''	4:4:1607:C:H5'	1.93	0.50
10:C:95:GLY:HA2	10:C:98:GLU:HB2	1.94	0.50
28:U:107:VAL:HA	28:U:135:PHE:HB3	1.94	0.50
30:W:69:LYS:O	30:W:73:LEU:HB2	2.11	0.50
41:h:103:ASP:O	41:h:198:VAL:HA	2.11	0.50
51:r:30:GLY:O	51:r:134:ARG:NH2	2.45	0.50
1:1:154:C:N4	1:1:168:G:O6	2.45	0.50
1:1:1325:C:H5'	27:T:15:ARG:HH11	1.76	0.50
4:4:106:C:O2	4:4:294:A:O2'	2.29	0.50
4:4:1093:G:N2	4:4:1098:A:H62	2.07	0.50
4:4:1254:A:H5''	4:4:1255:U:H5''	1.94	0.50
4:4:1537:G:H2'	4:4:1538:G:H8	1.76	0.50
9:B:40:ARG:HH21	9:B:57:ILE:H	1.60	0.50
25:R:77:THR:HG23	25:R:78:ARG:HD2	1.93	0.50
26:S:36:LEU:HD12	26:S:55:ILE:HG23	1.92	0.50
1:1:45:U:OP1	1:1:307:C:O2'	2.29	0.50
1:1:294:U:OP1	1:1:610:G:O2'	2.28	0.50
1:1:427:U:OP1	10:C:13:ARG:NH2	2.45	0.50
15:H:65:VAL:O	15:H:66:ARG:NE	2.44	0.50
49:p:23:ARG:NH2	49:p:28:SER:O	2.45	0.50
4:4:244:A:H62	4:4:254:G:H21	1.59	0.49
28:U:553:GLY:H	28:U:557:GLY:HA2	1.76	0.49
40:g:61:LEU:O	40:g:63:ARG:NH1	2.43	0.49
1:1:36:C:O2'	18:K:117:ARG:NH2	2.45	0.49
1:1:808:C:OP1	21:N:48:LYS:NZ	2.40	0.49
4:4:1329:U:H5''	4:4:1330:C:H5	1.77	0.49
4:4:1689:A:H2'	4:4:1690:A:H8	1.76	0.49
4:4:2103:C:O2'	4:4:2187:G:N1	2.44	0.49
4:4:2597:G:H4'	40:g:243:GLY:HA2	1.94	0.49
5:5:40:U:O4	33:Z:1:MET:N	2.44	0.49
5:5:50:G:OP1	53:t:63:THR:OG1	2.29	0.49
29:V:37:LEU:HD11	29:V:67:VAL:HG11	1.95	0.49
40:g:173:VAL:O	40:g:184:LYS:HA	2.12	0.49
59:z:75:ILE:HA	59:z:82:PRO:HB3	1.94	0.49
1:1:936:C:H1'	1:1:1382:C:H42	1.77	0.49
1:1:1113:C:O2'	9:B:11:ARG:NH1	2.35	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:793:A:OP2	4:4:2071:A:O2'	2.30	0.49
4:4:941:A:N3	4:4:1190:G:O2'	2.46	0.49
4:4:2036:C:H2'	4:4:2037:G:H8	1.78	0.49
4:4:2419:U:O4	37:d:30:ARG:NH2	2.45	0.49
30:W:44:PRO:HG2	30:W:46:LEU:HG	1.94	0.49
43:j:77:ILE:HB	43:j:82:LEU:HD12	1.94	0.49
1:1:28:G:O2'	1:1:296:U:OP1	2.31	0.49
1:1:486:U:H2'	1:1:487:A:H8	1.77	0.49
1:1:593:G:H1	1:1:646:U:H3	1.61	0.49
1:1:789:U:N3	1:1:792:A:OP2	2.45	0.49
1:1:1463:C:OP1	54:u:111:ARG:NE	2.43	0.49
18:K:113:ARG:HH21	18:K:115:LYS:HB2	1.77	0.49
1:1:80:G:H1	1:1:90:U:H3	1.60	0.49
1:1:1244:C:OP2	27:T:9:ARG:CG	2.60	0.49
4:4:271(C):C:O2	4:4:271(U):G:N2	2.38	0.49
4:4:681:G:O2'	36:c:29:LYS:NZ	2.44	0.49
4:4:1482:G:H2'	4:4:1484:G:H8	1.78	0.49
4:4:1797:C:OP1	40:g:258:LYS:NZ	2.45	0.49
4:4:1912:A:N1	4:4:1919:A:N6	2.61	0.49
37:d:36:LYS:HB3	37:d:40:GLU:HB3	1.95	0.49
39:f:44:VAL:HG13	39:f:215:VAL:HG22	1.95	0.49
43:j:56:ALA:O	43:j:60:LEU:CB	2.60	0.49
44:k:107:VAL:O	44:k:152:ARG:NH2	2.40	0.49
54:u:24:PRO:HA	54:u:49:VAL:HG13	1.94	0.49
1:1:133:U:O2'	1:1:134:A:N7	2.42	0.49
1:1:680:C:N4	1:1:711:G:O6	2.46	0.49
1:1:1004:A:H5''	1:1:1024:G:H22	1.76	0.49
1:1:1059:C:H4'	20:M:45:ARG:HH22	1.78	0.49
1:1:1248:A:N6	1:1:1289:A:OP2	2.41	0.49
4:4:953:A:H61	4:4:964:C:H42	1.58	0.49
43:j:132:ASN:HA	43:j:158:ALA:HA	1.95	0.49
1:1:1000:U:H1'	1:1:1001:A:OP1	2.11	0.49
1:1:1331:G:N7	19:L:21:TYR:OH	2.44	0.49
4:4:654(T):C:O2	4:4:654(U):A:N6	2.45	0.49
4:4:840:C:OP2	4:4:932:G:N2	2.44	0.49
4:4:1792:G:H5'	40:g:205:VAL:HG13	1.95	0.49
4:4:2006:C:O2'	4:4:2823:A:N3	2.46	0.49
4:4:2619:C:H5''	41:h:152:LYS:HG2	1.94	0.49
8:A:105:PHE:O	8:A:109:SER:CB	2.60	0.49
9:B:9:GLY:HA2	9:B:12:LEU:HD23	1.95	0.49
13:F:150:ALA:HB3	17:J:60:ALA:HB3	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:U:132:ARG:HH12	28:U:253:LEU:HB2	1.78	0.49
28:U:246:ILE:HG23	28:U:255:ILE:HD13	1.95	0.49
40:g:164:GLN:OE1	40:g:176:ARG:NH2	2.45	0.49
42:i:4:VAL:HA	42:i:17:ARG:HD2	1.94	0.49
1:1:297:G:N2	1:1:300:A:OP2	2.45	0.49
1:1:580:U:O4	1:1:761:G:O6	2.31	0.49
1:1:666:G:N2	21:N:52:SER:OG	2.46	0.49
1:1:1074:G:O2'	1:1:1101:A:N1	2.37	0.49
4:4:1453:U:OP1	52:s:63:ARG:NH2	2.45	0.49
6:6:116:VAL:HG11	51:r:107:ALA:HB1	1.95	0.49
10:C:15:GLU:HG2	10:C:19:LEU:HD11	1.94	0.49
12:E:98:LEU:HD13	24:Q:28:GLU:HG2	1.95	0.49
18:K:59:ARG:HA	18:K:65:GLU:HA	1.95	0.49
25:R:36:ARG:NH1	25:R:74:PHE:O	2.46	0.49
41:h:4:ILE:HG22	41:h:198:VAL:HB	1.95	0.49
55:v:24:TYR:HB3	55:v:28:ARG:HG3	1.94	0.49
1:1:189(D):C:H42	1:1:189(H):G:H22	1.61	0.49
1:1:615:C:H2'	1:1:616:G:H8	1.77	0.49
4:4:679:C:H2'	4:4:680:G:H8	1.77	0.49
8:A:47:THR:O	8:A:51:LEU:CB	2.60	0.49
14:G:120:THR:O	14:G:124:ALA:HB2	2.12	0.49
53:t:23:ARG:NH1	53:t:84:GLN:OE1	2.45	0.49
1:1:714:G:H21	1:1:777:A:H1'	1.77	0.49
4:4:271(X):G:H4'	4:4:272(D):G:H4'	1.94	0.49
4:4:2031:A:O2'	4:4:2454:G:N2	2.46	0.49
4:4:2564:A:N6	4:4:2647:U:O2'	2.46	0.49
7:7:41:GLU:O	7:7:45:LYS:HB2	2.13	0.49
10:C:108:LEU:HD22	10:C:174:LEU:HD22	1.95	0.49
21:N:32:LEU:HD12	21:N:35:ARG:HD3	1.93	0.49
4:4:615:G:OP1	42:i:40:GLN:NE2	2.39	0.48
4:4:690:G:H21	40:g:43:ARG:HH22	1.60	0.48
19:L:90:LEU:HA	19:L:93:ARG:HG2	1.93	0.48
42:i:119:ARG:NH1	42:i:120:GLU:OE2	2.46	0.48
43:j:60:LEU:HA	43:j:63:ILE:HG12	1.95	0.48
1:1:619:U:N3	10:C:134:ASP:OD1	2.45	0.48
1:1:1287:A:H61	1:1:1371:G:H1'	1.77	0.48
1:1:1392:G:O2'	1:1:1502:A:OP1	2.31	0.48
4:4:605:C:O2	4:4:657:U:O2'	2.31	0.48
11:D:82:VAL:HG21	11:D:138:ALA:HA	1.95	0.48
40:g:30:GLU:OE2	40:g:63:ARG:NE	2.45	0.48
40:g:77:ALA:HB3	40:g:117:VAL:HG13	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:316:G:O3'	1:1:353:A:N6	2.46	0.48
4:4:1653:G:O6	52:s:11:ASN:N	2.46	0.48
4:4:2731:G:OP1	41:h:169:ASN:ND2	2.39	0.48
23:P:9:VAL:HG12	23:P:56:VAL:HG22	1.95	0.48
26:S:82:SER:O	26:S:86:ARG:CB	2.61	0.48
28:U:341:VAL:O	28:U:349:LYS:HA	2.12	0.48
34:a:16:ARG:HH11	34:a:20:ARG:HH22	1.59	0.48
35:b:12:GLU:HB2	35:b:21:TYR:HB3	1.94	0.48
40:g:70:TRP:HH2	40:g:152:GLY:H	1.61	0.48
54:u:88:ILE:HG22	54:u:89:VAL:HG23	1.96	0.48
1:1:407:G:OP1	10:C:115:ARG:NH2	2.46	0.48
1:1:797:C:H2'	1:1:798:G:H8	1.78	0.48
4:4:826:U:O5'	4:4:2428:G:O2'	2.31	0.48
4:4:2245:U:H5''	4:4:2246:G:H5'	1.94	0.48
8:A:76:GLN:NE2	8:A:206:ASP:O	2.47	0.48
19:L:73:GLU:HA	19:L:76:ALA:HB3	1.95	0.48
28:U:182:ARG:NH2	28:U:186:TYR:OH	2.47	0.48
36:c:9:ARG:HH12	36:c:47:ARG:HB3	1.77	0.48
37:d:26:LYS:HD3	37:d:44:LYS:HA	1.94	0.48
43:j:78:SER:H	43:j:82:LEU:HB2	1.78	0.48
49:p:7:TYR:HA	49:p:19:ILE:O	2.13	0.48
1:1:580:U:H3	1:1:761:G:H1	1.60	0.48
4:4:1500:G:N2	40:g:99:ASP:O	2.46	0.48
4:4:1918:A:H4'	4:4:1919:A:H5'	1.94	0.48
8:A:213:LEU:HD21	8:A:217:ARG:HE	1.78	0.48
9:B:132:ARG:O	9:B:136:GLN:CB	2.61	0.48
28:U:74:TRP:HB3	28:U:77:HIS:HB2	1.95	0.48
37:d:13:ARG:NH1	50:q:62:LEU:O	2.41	0.48
40:g:133:LEU:HB3	40:g:173:VAL:HG11	1.95	0.48
40:g:148:GLU:OE1	40:g:151:LYS:NZ	2.40	0.48
41:h:49:LEU:O	41:h:78:LEU:HA	2.12	0.48
1:1:1310:G:H2'	1:1:1311:G:H8	1.78	0.48
4:4:373:U:H2'	4:4:374:A:H8	1.78	0.48
4:4:1859:A:N6	4:4:1883:G:O2'	2.46	0.48
4:4:2109:U:OP2	4:4:2149:G:N2	2.45	0.48
4:4:2168:G:H21	4:4:2170:A:H5''	1.78	0.48
16:I:45:ARG:HB2	16:I:65:LEU:HB3	1.93	0.48
17:J:104:GLN:NE2	17:J:105:VAL:O	2.46	0.48
28:U:178:ILE:HA	28:U:185:ALA:HA	1.95	0.48
33:Z:33:VAL:O	43:j:113:ARG:NH1	2.47	0.48
40:g:43:ARG:HH21	40:g:49:ILE:HD11	1.77	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:824:C:H2'	1:1:825:G:H8	1.78	0.48
1:1:944:G:O2'	1:1:1231:G:OP1	2.29	0.48
4:4:2561:A:H4'	49:p:40:VAL:HG11	1.96	0.48
7:7:12:LEU:O	7:7:17:GLN:NE2	2.46	0.48
22:O:4:ILE:HG12	22:O:21:VAL:HB	1.96	0.48
1:1:373:A:H61	1:1:391:G:H1'	1.79	0.48
1:1:643:C:H2'	1:1:644:G:H8	1.78	0.48
4:4:1638:C:O2	4:4:2698:U:O2'	2.32	0.48
4:4:2875:C:O2'	54:u:3:ARG:O	2.32	0.48
13:F:66:VAL:HA	13:F:70:LYS:HE2	1.95	0.48
26:S:56:MET:O	26:S:60:GLU:HB2	2.13	0.48
26:S:79:ARG:HA	26:S:82:SER:HB3	1.96	0.48
28:U:607:ARG:NE	28:U:674:ASP:OD1	2.37	0.48
48:o:70:LYS:HE3	48:o:72:TYR:HE1	1.79	0.48
50:q:101:VAL:HG12	50:q:106:LEU:HB3	1.96	0.48
53:t:58:LEU:HD11	53:t:65:VAL:HA	1.96	0.48
4:4:1940:U:OP2	4:4:2603:G:N2	2.43	0.48
4:4:2021:C:OP1	34:a:12:SER:OG	2.29	0.48
10:C:176:LEU:HA	10:C:183:GLY:HA2	1.95	0.48
13:F:88:PRO:HG3	13:F:145:ALA:HB1	1.94	0.48
28:U:457:LEU:O	28:U:660:ARG:NH1	2.45	0.48
31:X:36:ARG:NH2	58:y:7:VAL:O	2.46	0.48
39:f:9:ARG:HA	39:f:12:LEU:HD23	1.96	0.48
48:o:34:LEU:HD21	48:o:120:LEU:HD23	1.96	0.48
1:1:964:A:O2'	16:I:55:LYS:NZ	2.47	0.47
4:4:442:G:H5''	4:4:614(B):G:N2	2.29	0.47
4:4:1309:G:HO2'	4:4:1611:C:HO2'	1.57	0.47
4:4:1849:G:H2'	4:4:1850:G:H8	1.79	0.47
4:4:2334:G:OP2	53:t:13:ARG:NH2	2.47	0.47
9:B:182:ILE:HA	9:B:202:ILE:O	2.14	0.47
19:L:103:THR:O	19:L:111:LYS:NZ	2.43	0.47
29:V:71:ASP:HB3	29:V:78:TYR:HD2	1.79	0.47
30:W:18:ILE:HG12	30:W:37:ILE:HG22	1.96	0.47
37:d:29:LYS:HG3	37:d:44:LYS:HG3	1.96	0.47
39:f:73:VAL:HB	39:f:158:LYS:HB2	1.95	0.47
1:1:346:G:H4'	54:u:41:ARG:HH21	1.80	0.47
1:1:605:U:O2	1:1:633:G:O6	2.31	0.47
1:1:941:G:C2'	1:1:942:G:H8	2.11	0.47
4:4:1571:A:H2'	4:4:1572:A:H8	1.80	0.47
4:4:2313:C:H5''	43:j:91:ARG:HD3	1.95	0.47
7:7:69:LYS:O	7:7:74:ASN:ND2	2.47	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:102:LEU:HD11	8:A:159:PRO:HD3	1.96	0.47
22:O:8:ARG:NH2	22:O:11:SER:O	2.44	0.47
37:d:38:GLY:O	37:d:42:ARG:HB2	2.13	0.47
42:i:198:ALA:O	42:i:202:PHE:HB2	2.13	0.47
53:t:99:LYS:O	53:t:106:ARG:NH2	2.47	0.47
1:1:700:G:H4'	1:1:704:A:H1'	1.95	0.47
1:1:1386:G:H2'	1:1:1387:G:H8	1.78	0.47
2:2:71:G:H21	4:4:1851:U:H4'	1.79	0.47
4:4:822:U:H2'	4:4:823:G:H8	1.79	0.47
9:B:85:ARG:O	9:B:89:GLU:CB	2.62	0.47
12:E:7:ASN:ND2	24:Q:34:TYR:OH	2.47	0.47
1:1:21:G:H2'	1:1:22:G:H8	1.79	0.47
1:1:1254:C:H4'	1:1:1356:G:H4'	1.97	0.47
4:4:269:U:H2'	4:4:270:A:H8	1.80	0.47
4:4:1270:C:O2'	4:4:1648:C:OP2	2.29	0.47
4:4:1315:C:O2'	4:4:1392:A:N3	2.45	0.47
4:4:1411:C:H2'	4:4:1412:A:H8	1.78	0.47
4:4:2059:A:H4'	42:i:69:HIS:HA	1.95	0.47
8:A:39:ILE:HD12	8:A:41:ILE:HD11	1.96	0.47
8:A:170:GLU:HB3	8:A:173:ALA:HB3	1.97	0.47
9:B:41:GLY:O	9:B:45:LYS:CB	2.63	0.47
9:B:83:ARG:NH1	9:B:86:VAL:O	2.47	0.47
21:N:58:MET:O	21:N:62:GLN:HB2	2.14	0.47
36:c:1:MET:HG3	36:c:3:ARG:HH21	1.80	0.47
1:1:1113:C:HO2'	9:B:11:ARG:HH12	1.58	0.47
1:1:1132:C:O2	1:1:1133:G:O2'	2.32	0.47
4:4:1288:U:H3	4:4:1326:U:H3	1.62	0.47
4:4:1701:A:OP1	4:4:1763:G:N1	2.37	0.47
7:7:23:PRO:O	7:7:27:ARG:CB	2.62	0.47
40:g:206:LEU:HA	40:g:211:ARG:HD3	1.96	0.47
42:i:1:MET:HB2	42:i:119:ARG:HB2	1.96	0.47
43:j:64:THR:HG23	43:j:66:GLN:HG3	1.97	0.47
54:u:91:ARG:HA	54:u:116:ALA:HA	1.97	0.47
1:1:1185:G:H2'	1:1:1186:G:C8	2.49	0.47
1:1:1191:A:OP2	9:B:2:GLY:N	2.47	0.47
1:1:1228:C:H5''	19:L:114:ARG:HD2	1.97	0.47
4:4:512:G:OP1	4:4:1234:U:O2'	2.29	0.47
4:4:1060:U:H4'	4:4:1061:U:H5'	1.95	0.47
9:B:72:LYS:HE3	9:B:75:VAL:HG23	1.97	0.47
20:M:43:CYS:HB3	20:M:47:LEU:HD12	1.97	0.47
37:d:38:GLY:O	37:d:42:ARG:CB	2.62	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:t:35:ILE:HD11	53:t:69:VAL:HG11	1.96	0.47
1:1:584:G:H1	1:1:757:U:H3	1.61	0.47
1:1:941:G:HO2'	1:1:942:G:C4'	2.08	0.47
1:1:1375:A:H5'	13:F:25:ALA:HB1	1.97	0.47
4:4:536:A:H4'	55:v:57:PHE:HZ	1.80	0.47
4:4:629:G:O2'	4:4:639:U:O2	2.33	0.47
4:4:733:G:N2	4:4:734:A:N7	2.63	0.47
4:4:860:U:H2'	4:4:861:A:H8	1.79	0.47
4:4:1142(A):A:H4'	48:o:25:ARG:HH22	1.80	0.47
4:4:1341:U:OP2	4:4:1394:U:O2'	2.33	0.47
4:4:2154:G:N1	4:4:2155:G:O6	2.48	0.47
4:4:2525:G:H2'	4:4:2526:G:H8	1.80	0.47
7:7:30:LEU:HB3	7:7:36:ALA:HB3	1.97	0.47
14:G:10:LEU:HD22	14:G:83:ILE:HG12	1.96	0.47
19:L:87:TYR:OH	25:R:78:ARG:O	2.30	0.47
21:N:32:LEU:HD23	21:N:63:ARG:HB3	1.96	0.47
28:U:78:ARG:HH12	28:U:357:ARG:HH12	1.63	0.47
28:U:169:GLY:O	28:U:170:ARG:NE	2.45	0.47
32:Y:8:LEU:HA	32:Y:54:VAL:HG12	1.96	0.47
53:t:25:ARG:HA	53:t:86:ALA:HB3	1.95	0.47
53:t:59:LYS:HD3	53:t:61:ASN:H	1.79	0.47
53:t:84:GLN:HA	53:t:105:ALA:HB3	1.97	0.47
4:4:2698:U:H3	4:4:2709:G:H1	1.62	0.47
13:F:95:ARG:HH22	13:F:102:ARG:HE	1.63	0.47
24:Q:69:THR:O	24:Q:73:ALA:HB2	2.14	0.47
29:V:19:LYS:HB2	29:V:41:ARG:HH22	1.80	0.47
38:e:11:CYS:HG	38:e:32:HIS:HD1	1.58	0.47
40:g:168:ARG:HG2	40:g:173:VAL:HG23	1.95	0.47
1:1:1492:A:O2'	1:1:1493:A:O4'	2.31	0.47
3:3:8:G:O5'	13:F:154:TYR:OH	2.33	0.47
4:4:185:U:O2	4:4:212:G:N2	2.46	0.47
4:4:555:U:O2'	4:4:556:G:N7	2.47	0.47
4:4:1028:A:OP2	4:4:1126:A:N6	2.47	0.47
4:4:1222:C:OP1	56:w:66:ARG:NH1	2.47	0.47
14:G:81:HIS:CE1	14:G:104:ARG:HH12	2.33	0.47
20:M:45:ARG:HA	20:M:49:HIS:HD2	1.80	0.47
28:U:516:PRO:HA	28:U:563:ILE:HA	1.95	0.47
51:r:36:ALA:HB2	51:r:103:MET:HE2	1.96	0.47
54:u:51:ARG:HE	54:u:53:ARG:HB2	1.80	0.47
1:1:1013:G:H5''	25:R:18:LYS:HD2	1.96	0.47
4:4:449:A:O2'	55:v:3:ARG:NH1	2.47	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:585:G:H21	4:4:1254:A:N6	2.13	0.47
4:4:2079:U:H5''	30:W:21:ARG:HH12	1.80	0.47
4:4:2729:G:H5''	41:h:185:LYS:HE2	1.97	0.47
5:5:87:G:N2	5:5:90:A:OP2	2.38	0.47
11:D:9:LYS:HE2	11:D:112:LEU:HD21	1.97	0.47
1:1:580:U:H5'	21:N:58:MET:HE3	1.96	0.46
1:1:1094:G:O2'	1:1:1108:G:N2	2.46	0.46
5:5:106:G:H2'	5:5:107:G:H8	1.79	0.46
24:Q:52:PRO:HD2	24:Q:55:ARG:HD3	1.97	0.46
28:U:615:GLU:OE2	28:U:666:ARG:NH1	2.47	0.46
41:h:115:GLY:O	41:h:119:ARG:HB2	2.14	0.46
43:j:130:ASN:HA	43:j:160:VAL:HA	1.97	0.46
1:1:77:G:N2	1:1:92:C:O2	2.46	0.46
4:4:26:G:H1'	4:4:515:A:H61	1.80	0.46
6:6:47:VAL:O	6:6:51:ALA:HB3	2.15	0.46
49:p:64:ARG:NH1	49:p:81:ASP:OD1	2.41	0.46
54:u:30:VAL:HG22	54:u:84:GLN:H	1.80	0.46
1:1:812:C:OP1	1:1:902:G:N2	2.42	0.46
4:4:295:G:OP1	59:z:2:ARG:NH2	2.47	0.46
4:4:2195:C:O2'	7:7:118:LYS:NZ	2.48	0.46
10:C:14:ARG:HB2	10:C:40:PRO:HD2	1.96	0.46
13:F:73:MET:HA	13:F:91:VAL:HG11	1.96	0.46
4:4:272(B):G:H2'	4:4:272(C):G:H8	1.81	0.46
4:4:637:A:H5''	50:q:117:GLU:HB2	1.96	0.46
4:4:919:G:N2	4:4:2269:A:OP2	2.48	0.46
4:4:975(A):G:N2	4:4:1156:A:O2'	2.49	0.46
4:4:2047:U:H2'	4:4:2048:G:H8	1.80	0.46
4:4:2742:C:OP2	38:e:24:TYR:OH	2.31	0.46
17:J:15:ALA:HB1	17:J:78:GLN:HG2	1.96	0.46
17:J:86:GLY:H	17:J:113:PRO:HG3	1.80	0.46
40:g:211:ARG:H	40:g:214:TRP:HD1	1.63	0.46
1:1:181:G:O2'	1:1:183:G:O6	2.32	0.46
1:1:1281:U:OP1	1:1:1282:C:N4	2.49	0.46
4:4:2116:G:N1	4:4:2162:G:OP1	2.48	0.46
13:F:79:ARG:HG3	13:F:80:VAL:H	1.81	0.46
22:O:67:THR:H	22:O:70:ALA:HB3	1.80	0.46
25:R:15:LEU:HD11	25:R:34:TRP:HB2	1.97	0.46
1:1:1001:A:N3	1:1:1001:A:C2'	2.77	0.46
4:4:265:A:N6	4:4:283:A:O4'	2.48	0.46
4:4:884:C:N4	4:4:894:C:N3	2.59	0.46
4:4:2259:G:N9	4:4:2427:C:C5	2.83	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:7:81:VAL:HG21	7:7:145:VAL:HA	1.96	0.46
9:B:12:LEU:HA	9:B:16:ARG:HB2	1.97	0.46
28:U:99:ARG:HH22	28:U:399:LEU:HB3	1.80	0.46
40:g:30:GLU:OE1	40:g:63:ARG:NH2	2.49	0.46
43:j:53:LEU:HD12	43:j:55:LYS:H	1.80	0.46
50:q:96:THR:HG22	50:q:126:VAL:HB	1.98	0.46
52:s:12:ARG:HG2	52:s:16:HIS:ND1	2.31	0.46
52:s:103:ARG:HA	52:s:111:LEU:HD23	1.97	0.46
1:1:123:C:OP1	1:1:311:C:O2'	2.33	0.46
1:1:957:U:OP1	25:R:81:ARG:NH2	2.48	0.46
4:4:210:C:H2'	4:4:211:A:C8	2.51	0.46
4:4:437:G:H2'	4:4:438:G:C8	2.51	0.46
4:4:472:A:O2'	4:4:508:G:N1	2.43	0.46
4:4:748:G:OP1	57:x:88:ARG:NH2	2.49	0.46
4:4:1939:U:OP1	4:4:2604:U:O2'	2.32	0.46
4:4:2610:C:H4'	4:4:2611:U:H5'	1.97	0.46
5:5:16:G:H22	5:5:69:G:H1'	1.80	0.46
14:G:8:ASP:OD1	14:G:12:ARG:NH1	2.48	0.46
23:P:4:LYS:HE2	23:P:6:LEU:HD22	1.98	0.46
36:c:8:ASN:HB3	36:c:11:LYS:HB3	1.98	0.46
52:s:103:ARG:HG2	52:s:110:PRO:HA	1.97	0.46
1:1:680:C:H2'	1:1:681:C:H4'	1.98	0.46
1:1:1314:C:H42	1:1:1319:A:H8	1.64	0.46
2:2:74:C:H4'	30:W:23:LYS:HE2	1.98	0.46
44:k:60:ARG:O	44:k:64:LEU:HB2	2.15	0.46
1:1:741:G:H4'	21:N:55:GLY:HA3	1.97	0.46
1:1:1318:A:H61	20:M:18:VAL:HG13	1.81	0.46
4:4:300:A:O2'	4:4:318:C:O2	2.33	0.46
4:4:675:A:OP1	42:i:63:LYS:NZ	2.48	0.46
12:E:71:ARG:HB2	12:E:74:ASP:HB2	1.98	0.46
14:G:11:THR:O	14:G:15:ASN:CB	2.64	0.46
18:K:86:ARG:HB2	18:K:101:VAL:HG23	1.98	0.46
1:1:687:A:H62	1:1:703:G:H21	1.64	0.46
1:1:1000:U:C4'	1:1:1001:A:OP1	2.64	0.46
1:1:1139:G:N3	1:1:1141:C:N4	2.64	0.46
1:1:1335:C:OP1	1:1:1337:G:N2	2.48	0.46
1:1:1413:A:N1	1:1:1487:G:O6	2.49	0.46
4:4:77:C:H2'	4:4:78:A:H8	1.81	0.46
4:4:2176:A:H1'	4:4:2177:C:H5	1.81	0.46
10:C:118:ARG:O	10:C:122:ARG:CB	2.63	0.46
23:P:5:VAL:HG22	23:P:60:ILE:HD13	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:r:116:GLU:OE2	51:r:119:ARG:NH2	2.40	0.46
1:1:1309:G:OP1	19:L:92:HIS:NE2	2.37	0.45
1:1:1441:G:H21	1:1:1460:A:H62	1.64	0.45
4:4:571:A:H5'	4:4:2030:A:H62	1.81	0.45
4:4:581:C:H2'	4:4:582:G:C8	2.51	0.45
4:4:597:U:H3	4:4:660:G:H1	1.64	0.45
4:4:807:U:OP2	50:q:41:ARG:NH2	2.49	0.45
4:4:1275:A:N1	4:4:1295:C:O2'	2.44	0.45
4:4:1500:G:O2'	40:g:102:LYS:NZ	2.49	0.45
4:4:2334:G:H5'	53:t:13:ARG:HE	1.81	0.45
6:6:3:TYR:HD2	6:6:4:ARG:HE	1.64	0.45
6:6:80:ARG:HG2	6:6:82:ARG:HH21	1.81	0.45
17:J:62:GLN:O	17:J:66:LEU:CB	2.61	0.45
28:U:168:ILE:HD11	28:U:178:ILE:HG13	1.98	0.45
53:t:24:LEU:HD12	53:t:85:VAL:HA	1.98	0.45
1:1:726:C:O3'	1:1:742:G:N2	2.49	0.45
1:1:1181:G:O2'	1:1:1182:G:O4'	2.34	0.45
4:4:457:A:H61	4:4:470:A:H5''	1.81	0.45
4:4:2303:G:N3	43:j:132:ASN:ND2	2.64	0.45
4:4:2489:G:H1'	4:4:2518:A:H61	1.82	0.45
5:5:54:G:H21	43:j:29:TRP:HE1	1.65	0.45
13:F:95:ARG:HE	13:F:99:LEU:HG	1.80	0.45
28:U:99:ARG:HH22	28:U:400:GLU:H	1.64	0.45
28:U:134:ALA:HB3	28:U:258:VAL:HA	1.98	0.45
28:U:411:VAL:HG11	28:U:458:HIS:HE1	1.81	0.45
38:e:2:LYS:HG3	38:e:3:VAL:H	1.80	0.45
41:h:13:ARG:HH21	54:u:58:ASN:HB2	1.81	0.45
41:h:143:ASN:HB2	41:h:147:PRO:HD2	1.98	0.45
43:j:6:ALA:H	43:j:8:LYS:HG2	1.80	0.45
50:q:38:GLN:HG3	50:q:45:LEU:H	1.81	0.45
1:1:82:U:H2'	1:1:88:A:H62	1.81	0.45
6:6:5:LEU:HD22	6:6:57:ILE:HD11	1.98	0.45
6:6:161:VAL:HA	6:6:162:GLU:HA	1.76	0.45
12:E:15:ASP:O	12:E:19:LEU:CB	2.63	0.45
28:U:185:ALA:HB3	28:U:200:PRO:HA	1.99	0.45
28:U:325:LEU:HD21	28:U:376:ALA:HB1	1.98	0.45
29:V:74:ARG:HD3	29:V:75:LEU:HG	1.98	0.45
48:o:57:ALA:HB3	48:o:124:ALA:HB2	1.97	0.45
54:u:30:VAL:HA	54:u:43:GLN:O	2.15	0.45
1:1:355:C:H1'	1:1:388:G:H1'	1.99	0.45
4:4:2223:G:OP1	40:g:172:TYR:OH	2.30	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:2641:G:H2'	4:4:2642:G:C8	2.51	0.45
28:U:428:LEU:HD22	28:U:451:ILE:HD13	1.98	0.45
44:k:125:VAL:HG13	44:k:131:VAL:HG12	1.99	0.45
49:p:17:ARG:HH12	49:p:99:PHE:HE2	1.64	0.45
1:1:578:C:O2'	1:1:728:A:N3	2.38	0.45
1:1:673:G:H2'	1:1:674:G:C8	2.52	0.45
4:4:521:G:H2'	4:4:522:G:H8	1.81	0.45
4:4:1493:C:O2'	4:4:2207:G:N1	2.50	0.45
4:4:1972:A:H2'	4:4:1973:G:H8	1.81	0.45
4:4:2289:G:H2'	4:4:2290:G:H8	1.82	0.45
16:I:22:LYS:O	16:I:26:ALA:CB	2.65	0.45
28:U:165:GLN:HE21	28:U:260:LEU:H	1.63	0.45
28:U:530:VAL:HG13	28:U:532:GLY:H	1.81	0.45
42:i:104:LYS:O	42:i:108:LYS:HB2	2.17	0.45
4:4:1154:G:OP2	55:v:58:ARG:NH2	2.45	0.45
4:4:1309:G:H4'	36:c:7:PRO:HG2	1.99	0.45
4:4:1527:G:O2'	4:4:1544:A:N6	2.45	0.45
4:4:1938:A:N7	4:4:2590:A:O2'	2.46	0.45
4:4:2793:G:O2'	4:4:2794:C:O4'	2.35	0.45
8:A:11:LEU:HD12	8:A:213:LEU:HD22	1.99	0.45
28:U:466:LEU:HG	28:U:472:VAL:HB	1.98	0.45
43:j:56:ALA:HB2	43:j:153:ARG:HH21	1.81	0.45
43:j:106:LEU:HA	43:j:109:VAL:HG12	1.99	0.45
1:1:1095:U:OP2	1:1:1108:G:N1	2.42	0.45
4:4:2134:A:O2'	4:4:2159:G:N2	2.50	0.45
4:4:2644:G:H22	4:4:2770:G:H1	1.64	0.45
8:A:139:LYS:HD2	8:A:142:LEU:HD21	1.97	0.45
16:I:64:GLU:OE2	16:I:66:ARG:NH1	2.50	0.45
41:h:2:LYS:O	41:h:199:ARG:HA	2.17	0.45
56:w:6:LYS:HE2	56:w:37:VAL:HG21	1.99	0.45
1:1:1030(B):C:N4	1:1:1031:G:N3	2.64	0.45
4:4:1841:U:H2'	4:4:1842:G:H8	1.82	0.45
10:C:167:GLY:H	10:C:178:VAL:HG21	1.80	0.45
14:G:116:LYS:H	14:G:116:LYS:HD2	1.80	0.45
41:h:5:LEU:HD21	41:h:79:ARG:HB2	1.99	0.45
43:j:36:LYS:O	43:j:160:VAL:HB	2.16	0.45
44:k:121:ILE:HD11	44:k:140:LYS:HB3	1.98	0.45
49:p:21:CYS:HA	49:p:41:ALA:HA	1.98	0.45
57:x:4:LYS:HB3	57:x:106:ILE:HG22	1.97	0.45
1:1:877:C:H2'	1:1:878:G:C8	2.52	0.45
4:4:9:U:O2'	4:4:10:G:O4'	2.35	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:2134:A:O4'	4:4:2157:G:N2	2.50	0.45
4:4:2391:G:N1	4:4:2427:C:O2'	2.29	0.45
4:4:2830:G:H5'	41:h:58:ARG:HG2	1.99	0.45
8:A:47:THR:O	8:A:51:LEU:HB2	2.16	0.45
9:B:50:ALA:HB1	9:B:72:LYS:HB3	1.99	0.45
9:B:187:ALA:HB3	9:B:197:GLY:HA2	1.98	0.45
31:X:6:VAL:O	31:X:10:LEU:HB2	2.16	0.45
40:g:146:GLU:HB3	40:g:189:CYS:HB2	1.99	0.45
42:i:196:LEU:O	42:i:200:GLU:CB	2.65	0.45
52:s:77:ARG:O	52:s:81:ASP:HB2	2.17	0.45
59:z:76:CYS:HB2	59:z:99:CYS:HB3	1.46	0.45
1:1:176:C:O2'	1:1:1446:U:O4	2.33	0.45
1:1:476:G:H2'	1:1:477:A:H8	1.81	0.45
1:1:579:G:O2'	21:N:54:ARG:NH2	2.50	0.45
1:1:678:U:H3	1:1:713:G:H22	1.64	0.45
1:1:941:G:N3	1:1:942:G:C8	2.84	0.45
1:1:1243:C:H5'	27:T:9:ARG:HG3	1.98	0.45
1:1:1525:G:H2'	1:1:1526:G:H8	1.82	0.45
4:4:397:G:H2'	4:4:398:G:H8	1.83	0.45
11:D:100:VAL:HG12	11:D:118:ILE:HG22	1.98	0.45
21:N:29:VAL:O	21:N:33:THR:OG1	2.29	0.45
49:p:19:ILE:HG22	49:p:43:VAL:HA	1.99	0.45
54:u:62:THR:HG22	54:u:75:ILE:HG13	1.99	0.45
1:1:278:G:N7	23:P:92:ARG:NH1	2.63	0.44
4:4:414:C:O2	4:4:1864:U:O2'	2.30	0.44
5:5:24:G:O6	5:5:56:G:O2'	2.29	0.44
18:K:67:THR:HG22	18:K:96:VAL:HG22	1.99	0.44
28:U:512:ILE:HG12	28:U:589:ALA:HB1	1.99	0.44
28:U:546:ILE:HG22	28:U:550:MET:HE2	1.99	0.44
41:h:167:VAL:HG12	41:h:170:LEU:HD11	1.99	0.44
1:1:437:U:O4	1:1:495:A:N7	2.50	0.44
1:1:684:A:O2'	17:J:39:PRO:O	2.33	0.44
4:4:818:G:N2	4:4:1189:A:H62	2.13	0.44
4:4:2328:A:H2'	4:4:2329:G:C8	2.52	0.44
4:4:2676:C:H2'	4:4:2677:G:H8	1.82	0.44
9:B:34:LEU:HD21	20:M:25:VAL:HG21	1.98	0.44
40:g:267:SER:OG	40:g:268:ARG:N	2.49	0.44
50:q:56:SER:OG	50:q:60:MET:SD	2.73	0.44
54:u:91:ARG:O	54:u:117:ASP:N	2.50	0.44
59:z:11:ASP:OD1	59:z:102:CYS:N	2.50	0.44
1:1:170:U:H2'	1:1:171:A:H8	1.83	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:509:A:H5''	10:C:55:ALA:HB2	2.00	0.44
1:1:978:A:H5'	20:M:19:ARG:HH12	1.83	0.44
1:1:1123:A:H4'	16:I:36:GLY:HA3	1.99	0.44
1:1:1237:C:HO2'	1:1:1300:G:H22	1.60	0.44
4:4:2371:G:O2'	35:b:46:HIS:ND1	2.49	0.44
28:U:293:THR:HG23	28:U:299:VAL:HB	1.99	0.44
28:U:451:ILE:HG21	28:U:462:ILE:HG21	1.99	0.44
40:g:123:ALA:HB3	40:g:131:LEU:HD21	1.98	0.44
41:h:36:ARG:HH21	41:h:88:GLY:HA2	1.82	0.44
42:i:110:LEU:HG	42:i:202:PHE:HE1	1.83	0.44
44:k:149:ARG:HE	44:k:162:ILE:HG13	1.82	0.44
48:o:14:VAL:O	48:o:52:VAL:HA	2.18	0.44
53:t:30:ARG:HA	53:t:35:ILE:HG22	1.98	0.44
4:4:1326:U:O2'	4:4:2010:G:O2'	2.36	0.44
4:4:1857:G:H21	4:4:1885:A:H62	1.64	0.44
4:4:2266:A:N6	4:4:2273:A:OP2	2.50	0.44
4:4:2469:A:H4'	51:r:56:ARG:HB3	1.98	0.44
4:4:2679:A:OP2	41:h:160:TYR:OH	2.32	0.44
7:7:40:THR:O	7:7:44:LEU:CB	2.66	0.44
13:F:148:ASN:HB3	17:J:62:GLN:H	1.82	0.44
42:i:38:ARG:O	42:i:42:ALA:HB2	2.17	0.44
1:1:108:G:H5'	1:1:109:A:H5''	1.99	0.44
1:1:1229:A:H61	19:L:104:ARG:HH21	1.65	0.44
4:4:1438:U:H2'	4:4:1439:A:H8	1.83	0.44
4:4:2124:G:H1'	39:f:43:GLU:HG2	1.99	0.44
8:A:84:GLU:OE1	8:A:87:ARG:NH1	2.44	0.44
10:C:101:LEU:HB2	10:C:136:PRO:HA	1.99	0.44
10:C:145:GLU:HA	10:C:183:GLY:O	2.18	0.44
10:C:158:ILE:HA	10:C:161:ASN:HB2	1.98	0.44
11:D:97:GLY:N	11:D:117:ASP:OD2	2.48	0.44
15:H:81:ILE:HA	15:H:84:ALA:HB3	1.98	0.44
18:K:70:ILE:HG13	18:K:100:ILE:HD12	1.99	0.44
59:z:28:LYS:HA	59:z:29:GLU:HA	1.71	0.44
1:1:662:G:O2'	1:1:836:G:OP1	2.35	0.44
1:1:1512:U:H2'	1:1:1513:A:C8	2.52	0.44
4:4:305:U:O4	4:4:312:G:O6	2.35	0.44
4:4:826:U:H6	4:4:826:U:H5''	1.83	0.44
4:4:1158:C:H5''	32:Y:30:ARG:HD3	2.00	0.44
4:4:2259:G:N9	4:4:2427:C:C4	2.86	0.44
13:F:149:ARG:HE	17:J:58:PRO:HA	1.83	0.44
17:J:110:ASP:O	24:Q:85:LEU:N	2.51	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:U:238:THR:O	28:U:242:LEU:CB	2.65	0.44
28:U:462:ILE:O	28:U:466:LEU:HB2	2.18	0.44
42:i:78:ILE:HA	42:i:83:PHE:HD2	1.83	0.44
1:1:1021:G:H2'	1:1:1022:G:H4'	1.99	0.44
4:4:557:U:H2'	4:4:558:G:C8	2.53	0.44
4:4:2627:G:N2	4:4:2777:G:OP2	2.51	0.44
42:i:158:THR:O	42:i:164:ARG:NH2	2.50	0.44
49:p:104:ARG:HH11	49:p:107:ARG:HH22	1.64	0.44
51:r:12:GLN:HG2	51:r:73:PRO:HD2	2.00	0.44
53:t:20:ARG:NH1	53:t:25:ARG:HB3	2.32	0.44
1:1:1148:U:OP1	15:H:7:THR:OG1	2.31	0.44
4:4:576:U:H2'	4:4:577:G:C8	2.52	0.44
4:4:627:A:H4'	4:4:628:G:H5'	2.00	0.44
4:4:643:A:N1	4:4:2369:A:O2'	2.48	0.44
4:4:648:G:H2'	4:4:649:G:H8	1.83	0.44
4:4:1141:U:OP2	48:o:63:THR:OG1	2.30	0.44
4:4:2047:U:O2'	4:4:2823:A:N1	2.44	0.44
4:4:2304:G:O6	4:4:2313:C:N4	2.51	0.44
4:4:2392:A:C4	4:4:2429:G:N1	2.86	0.44
5:5:5:C:O2'	5:5:27:C:O2	2.28	0.44
11:D:103:GLY:O	11:D:107:ARG:HB3	2.16	0.44
25:R:5:LEU:HD21	25:R:9:VAL:HG22	2.00	0.44
49:p:63:VAL:HG12	49:p:106:LEU:HD11	2.00	0.44
1:1:1188:A:O2'	20:M:60:SER:O	2.31	0.44
1:1:1244:C:C5	27:T:9:ARG:NH2	2.85	0.44
4:4:727:A:OP2	4:4:1431:U:O2'	2.31	0.44
4:4:2491:U:O2'	4:4:2570:G:OP1	2.34	0.44
8:A:115:LEU:HA	8:A:118:LEU:HG	2.00	0.44
9:B:153:VAL:HG22	9:B:198:VAL:HA	1.99	0.44
9:B:189:ALA:HB3	9:B:196:LEU:O	2.18	0.44
16:I:4:ILE:HD11	16:I:100:THR:HA	1.98	0.44
19:L:16:ASP:O	19:L:20:THR:OG1	2.30	0.44
24:Q:56:THR:HB	24:Q:58:LEU:HD13	2.00	0.44
26:S:56:MET:HA	26:S:59:ALA:HB3	2.00	0.44
28:U:535:PRO:HG2	28:U:538:TYR:HB2	2.00	0.44
1:1:736:C:H2'	1:1:737:A:C8	2.52	0.43
1:1:740:U:H2'	1:1:741:G:H8	1.82	0.43
1:1:1243:C:H5''	1:1:1243:C:H6	1.82	0.43
4:4:552:G:H2'	4:4:553:G:H8	1.83	0.43
4:4:1597:A:H5''	4:4:1598:C:H5'	1.99	0.43
5:5:8:U:O3'	53:t:25:ARG:NH2	2.50	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:109:ALA:HB1	6:6:145:GLU:HA	2.00	0.43
11:D:10:MET:HB3	11:D:32:VAL:HG22	2.00	0.43
14:G:11:THR:HA	14:G:14:ARG:HG2	1.99	0.43
31:X:36:ARG:HD2	58:y:9:LEU:HD13	1.99	0.43
38:e:25:VAL:O	38:e:33:LYS:HA	2.18	0.43
39:f:5:GLY:O	39:f:9:ARG:NH1	2.51	0.43
42:i:65:TRP:HZ2	42:i:72:ARG:HH11	1.66	0.43
48:o:53:VAL:HG22	48:o:121:LYS:HB2	1.99	0.43
48:o:128:HIS:HE1	48:o:134:ARG:HG3	1.83	0.43
1:1:811:C:O2'	1:1:901:A:N1	2.48	0.43
1:1:941:G:C2'	1:1:942:G:C8	2.95	0.43
1:1:1218:C:O2'	1:1:1219:U:O5'	2.36	0.43
4:4:2692:C:H2'	4:4:2693:A:H8	1.81	0.43
4:4:2816:C:H2'	4:4:2817:G:H8	1.83	0.43
6:6:27:VAL:HG12	6:6:85:HIS:HE1	1.83	0.43
7:7:74:ASN:HB3	7:7:138:ILE:HD11	2.00	0.43
8:A:68:ILE:HD12	8:A:161:ALA:HB3	1.99	0.43
10:C:62:GLN:OE1	10:C:66:ARG:NE	2.49	0.43
12:E:4:TYR:N	12:E:65:VAL:O	2.51	0.43
12:E:15:ASP:O	12:E:19:LEU:HB3	2.17	0.43
23:P:22:LEU:HA	23:P:41:LYS:HA	2.00	0.43
41:h:115:GLY:O	41:h:119:ARG:CB	2.66	0.43
43:j:135:LEU:HD11	43:j:155:MET:HE2	2.00	0.43
1:1:945:G:N2	1:1:1334:G:O2'	2.48	0.43
1:1:1117:G:O2'	15:H:104:ARG:NH1	2.51	0.43
1:1:1398:A:H61	11:D:22:GLY:H	1.66	0.43
4:4:143:G:H4'	58:y:35:THR:HG21	2.00	0.43
4:4:177:G:H3'	4:4:178:G:H8	1.83	0.43
4:4:579:G:O2'	4:4:2019:A:OP1	2.36	0.43
4:4:1278:A:H2'	4:4:1279:G:H8	1.83	0.43
4:4:1516:C:H2'	4:4:1517:G:H8	1.84	0.43
4:4:1650:G:OP1	52:s:12:ARG:NH2	2.42	0.43
4:4:2845:G:H2'	4:4:2846:G:C8	2.51	0.43
8:A:21:ARG:NH2	8:A:38:GLY:O	2.51	0.43
9:B:182:ILE:HG13	9:B:203:PHE:HB3	1.99	0.43
18:K:24:VAL:HG22	18:K:26:ALA:H	1.82	0.43
24:Q:69:THR:O	24:Q:73:ALA:CB	2.67	0.43
28:U:168:ILE:HG23	28:U:205:TYR:HE2	1.83	0.43
39:f:135:ARG:O	39:f:165:ARG:NH2	2.34	0.43
43:j:7:LEU:HD21	43:j:10:LYS:HD2	2.01	0.43
52:s:10:LEU:HD13	52:s:40:LYS:HG2	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:y:43:VAL:HG13	58:y:47:PHE:HD2	1.83	0.43
59:z:4:LYS:HG3	59:z:5:MET:H	1.83	0.43
1:1:407:G:O2'	10:C:116:GLN:NE2	2.52	0.43
1:1:1225:A:H4'	25:R:78:ARG:HG2	1.99	0.43
1:1:1510:U:H2'	1:1:1511:G:H8	1.84	0.43
4:4:2581:G:OP2	4:4:2581:G:N2	2.38	0.43
7:7:23:PRO:O	7:7:27:ARG:HB3	2.19	0.43
21:N:76:GLU:HA	21:N:79:ARG:HG2	2.00	0.43
28:U:579:GLU:O	28:U:583:LYS:CB	2.66	0.43
42:i:155:LEU:HB2	42:i:189:THR:HG21	2.01	0.43
49:p:42:SER:HA	49:p:56:ASP:O	2.18	0.43
1:1:1064:G:N2	1:1:1190:G:N3	2.66	0.43
1:1:1290:G:N2	15:H:36:TYR:O	2.51	0.43
2:2:40:C:N3	2:2:41:C:N4	2.67	0.43
4:4:574:C:O2	41:h:145:LYS:NZ	2.44	0.43
4:4:767:U:H2'	4:4:768:G:H8	1.84	0.43
4:4:1203:G:OP2	4:4:1204:A:O2'	2.33	0.43
4:4:1230:C:H2'	4:4:1231:G:H8	1.84	0.43
4:4:2114:A:N7	4:4:2167:U:O2'	2.50	0.43
4:4:2684:U:OP2	54:u:53:ARG:NH2	2.44	0.43
8:A:114:ARG:HG3	8:A:118:LEU:HD23	2.01	0.43
11:D:80:ILE:HD11	11:D:91:LEU:HD13	1.99	0.43
17:J:57:THR:HG23	17:J:58:PRO:HD3	2.01	0.43
28:U:32:ILE:HG23	28:U:273:LEU:HD21	1.99	0.43
51:r:68:ILE:HG22	51:r:101:ARG:HH12	1.83	0.43
1:1:265:G:H4'	23:P:65:ILE:HA	2.00	0.43
1:1:1131:G:H2'	1:1:1132:C:H6	1.83	0.43
4:4:36:G:N2	4:4:450:G:O2'	2.39	0.43
4:4:2696:U:H2'	4:4:2697:G:H8	1.84	0.43
4:4:2836:U:H2'	4:4:2837:G:H8	1.84	0.43
25:R:22:LEU:HD22	25:R:26:GLY:HA2	2.00	0.43
28:U:537:GLU:HG2	28:U:538:TYR:H	1.84	0.43
29:V:63:VAL:HG21	29:V:83:PRO:HG3	2.00	0.43
30:W:10:LYS:NZ	30:W:65:SER:OG	2.45	0.43
33:Z:33:VAL:HG22	33:Z:34:GLU:HG2	2.01	0.43
41:h:55:ASN:HA	41:h:56:PRO:HD3	1.89	0.43
51:r:28:ALA:H	51:r:134:ARG:HH12	1.65	0.43
1:1:1310:G:H2'	1:1:1311:G:C8	2.54	0.43
4:4:607:U:H5'	42:i:100:THR:HG21	2.01	0.43
4:4:852:G:H5'	32:Y:45:GLY:HA3	2.00	0.43
18:K:37:CYS:HA	18:K:58:VAL:HA	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:29:ARG:O	19:L:33:ALA:CB	2.67	0.43
28:U:384:ILE:H	28:U:384:ILE:HG13	1.71	0.43
40:g:160:GLY:N	40:g:197:GLY:O	2.52	0.43
58:y:65:ARG:HH21	58:y:68:ARG:HA	1.84	0.43
1:1:675:A:H2	17:J:117:ASN:H	1.65	0.43
1:1:1347:G:N7	15:H:10:ARG:NH2	2.67	0.43
1:1:1479:C:H2'	1:1:1480:G:H8	1.84	0.43
4:4:774:A:O2'	4:4:777:A:N3	2.49	0.43
4:4:811:U:H3'	50:q:22:GLY:HA2	2.00	0.43
4:4:1754:C:N3	4:4:2716:U:O2'	2.52	0.43
4:4:2352:A:N6	4:4:2365:G:O2'	2.52	0.43
51:r:62:GLY:CA	51:r:107:ALA:O	2.64	0.43
58:y:89:ILE:HG12	58:y:91:ALA:H	1.84	0.43
4:4:1578:U:H2'	4:4:1579:A:H8	1.83	0.43
4:4:1667:G:O2'	4:4:1991:U:O4	2.32	0.43
4:4:2178:C:H5'	39:f:211:ARG:HH12	1.82	0.43
8:A:21:ARG:HD2	8:A:39:ILE:HA	2.01	0.43
12:E:52:ILE:HG12	12:E:87:ARG:HH12	1.82	0.43
13:F:37:ASN:OD1	13:F:41:ARG:NE	2.47	0.43
16:I:8:LEU:HB2	16:I:70:ARG:O	2.19	0.43
49:p:12:ASP:O	49:p:17:ARG:NH2	2.52	0.43
1:1:1069:C:O2'	1:1:1192:C:O2	2.32	0.43
1:1:1077:G:N2	1:1:1080:A:OP2	2.39	0.43
4:4:1537:G:H2'	4:4:1538:G:C8	2.54	0.43
4:4:2171:A:OP1	39:f:135:ARG:NH1	2.43	0.43
4:4:2285:C:OP2	35:b:27:LYS:NZ	2.37	0.43
4:4:2443:C:H2'	4:4:2444:G:C8	2.54	0.43
12:E:43:LEU:HD22	12:E:60:PHE:HB2	2.01	0.43
42:i:129:PHE:HE1	42:i:139:PHE:HD1	1.67	0.43
49:p:107:ARG:HD3	54:u:36:GLU:HG3	2.01	0.43
1:1:781:A:N7	1:1:801:U:C2	2.87	0.42
1:1:1323:G:O6	25:R:4:SER:OG	2.37	0.42
4:4:272(B):G:H2'	4:4:272(C):G:C8	2.54	0.42
4:4:959:A:H2'	4:4:960:A:C8	2.54	0.42
4:4:1385:G:O2'	4:4:1396:U:O2	2.30	0.42
4:4:1423:G:H2'	4:4:1424:G:C8	2.54	0.42
4:4:1662:C:O2'	4:4:2687:U:OP1	2.37	0.42
4:4:1971:A:O5'	40:g:242:ARG:NH2	2.52	0.42
4:4:2562:U:O2	49:p:23:ARG:NH1	2.51	0.42
16:I:6:ILE:HD11	16:I:72:VAL:HB	2.01	0.42
16:I:20:ALA:HB1	16:I:37:PRO:HG3	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:U:114:VAL:HA	28:U:152:THR:HG21	2.01	0.42
28:U:428:LEU:HD23	28:U:431:LEU:HD23	2.01	0.42
30:W:85:LEU:N	30:W:89:GLU:OE2	2.52	0.42
39:f:44:VAL:HG22	39:f:215:VAL:HG13	2.00	0.42
59:z:45:VAL:HA	59:z:61:ILE:HG22	2.00	0.42
1:1:418:C:N4	1:1:426:G:O6	2.52	0.42
1:1:620:C:C2	10:C:135:LEU:HD21	2.53	0.42
1:1:781:A:O2'	1:1:1522:U:O2	2.36	0.42
1:1:1243:C:O2	1:1:1302:U:N3	2.47	0.42
1:1:1335:C:H5'	1:1:1336:C:H5'	2.00	0.42
1:1:1350:A:O2'	13:F:33:ASP:OD1	2.31	0.42
1:1:1507:A:H2'	1:1:1508:G:C8	2.54	0.42
4:4:313:C:H2'	4:4:314:A:H8	1.84	0.42
4:4:857:C:OP1	29:V:77:ARG:NH2	2.45	0.42
4:4:1486:A:H2'	4:4:1487:G:H8	1.85	0.42
4:4:1540:U:H2'	4:4:1541:G:C2	2.54	0.42
4:4:1903:G:H2'	4:4:1904:G:C8	2.54	0.42
4:4:2696:U:H2'	4:4:2697:G:C8	2.53	0.42
4:4:2779:U:H1'	4:4:2781:A:C4	2.54	0.42
28:U:68:ALA:C	28:U:83:ASP:H	2.27	0.42
28:U:342:TYR:HD1	28:U:349:LYS:HB3	1.83	0.42
34:a:28:PRO:HD2	57:x:35:ILE:HG23	2.01	0.42
37:d:59:LYS:NZ	50:q:49:ARG:O	2.45	0.42
54:u:123:GLN:O	54:u:127:ALA:CB	2.68	0.42
59:z:5:MET:HG3	59:z:7:VAL:H	1.84	0.42
1:1:226:G:H2'	1:1:227:G:H8	1.85	0.42
1:1:490:G:OP2	10:C:132:ARG:NH2	2.52	0.42
4:4:585:G:N2	4:4:1254:A:H62	2.17	0.42
7:7:2:LYS:HB3	7:7:39:ALA:HB3	2.01	0.42
32:Y:8:LEU:HD23	32:Y:31:LEU:HD23	2.02	0.42
39:f:31:LYS:HG3	39:f:180:SER:HA	2.01	0.42
55:v:45:TYR:O	55:v:49:HIS:ND1	2.51	0.42
55:v:86:ALA:HB3	55:v:88:ILE:HG12	2.02	0.42
1:1:980:C:N4	20:M:16:PHE:O	2.51	0.42
1:1:1106:G:H4'	9:B:172:ARG:HB3	2.00	0.42
4:4:1161:C:H2'	4:4:1162:G:C8	2.53	0.42
4:4:2109:U:O2	4:4:2181:G:N2	2.53	0.42
4:4:2443:C:H2'	4:4:2444:G:H8	1.85	0.42
14:G:110:ALA:HA	14:G:136:GLU:HA	2.01	0.42
15:H:79:LEU:HD21	15:H:104:ARG:HG3	2.01	0.42
23:P:55:ASP:OD1	23:P:79:SER:OG	2.32	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:R:42:PRO:O	33:Z:61:ARG:NH2	2.52	0.42
41:h:52:LEU:HG	41:h:75:VAL:HB	2.00	0.42
54:u:64:ARG:HA	54:u:73:GLU:HA	2.01	0.42
54:u:107:ASP:OD1	54:u:107:ASP:N	2.51	0.42
1:1:605:U:H2'	1:1:606:G:C8	2.54	0.42
1:1:675:A:O2'	17:J:114:VAL:O	2.35	0.42
4:4:589:C:H2'	4:4:590:A:C8	2.51	0.42
4:4:594:U:OP1	37:d:64:TYR:OH	2.35	0.42
4:4:598:G:O2'	50:q:9:ASN:OD1	2.38	0.42
4:4:1668:A:N1	4:4:1676:A:N6	2.68	0.42
8:A:11:LEU:HD11	8:A:209:ARG:HG3	2.00	0.42
21:N:50:HIS:HA	21:N:53:HIS:CD2	2.55	0.42
49:p:24:VAL:HG12	49:p:26:LYS:HG2	2.02	0.42
56:w:52:VAL:HG11	56:w:55:ALA:HB3	2.00	0.42
1:1:439:A:OP1	10:C:123:HIS:ND1	2.40	0.42
1:1:575:G:H22	1:1:880:C:H42	1.67	0.42
4:4:532:A:H4'	4:4:533:G:C8	2.55	0.42
4:4:1352:U:H2'	4:4:1353:A:H8	1.85	0.42
4:4:1486:A:H2'	4:4:1487:G:C8	2.55	0.42
4:4:2432:A:N6	30:W:34:THR:O	2.47	0.42
4:4:2736:G:H2'	4:4:2737:G:H8	1.84	0.42
19:L:112:GLY:HA2	19:L:113:PRO:HD3	1.91	0.42
28:U:149:VAL:O	28:U:153:MET:HB2	2.19	0.42
46:m:59:UNK:HA	46:m:64:UNK:HA	1.73	0.42
58:y:27:THR:HB	58:y:80:ILE:HG22	2.01	0.42
1:1:975:A:O2'	20:M:32:SER:OG	2.32	0.42
10:C:57:ARG:HE	10:C:202:LEU:HD13	1.85	0.42
11:D:37:ARG:NE	11:D:111:GLU:O	2.52	0.42
21:N:77:ARG:O	21:N:81:LEU:HB2	2.20	0.42
25:R:56:GLN:HG3	25:R:58:VAL:HG13	2.02	0.42
28:U:621:ILE:HD11	28:U:643:ILE:HD13	2.01	0.42
28:U:656:ALA:HA	28:U:659:LEU:HB3	2.02	0.42
39:f:181:PHE:HA	39:f:182:PRO:HD3	1.81	0.42
40:g:174:ILE:HG12	40:g:184:LYS:HG2	2.02	0.42
53:t:66:ALA:HB1	53:t:99:LYS:H	1.84	0.42
54:u:52:ILE:HG22	54:u:54:ARG:HE	1.83	0.42
1:1:1028:C:N4	1:1:1034:G:O2'	2.42	0.42
1:1:1469:G:H2'	1:1:1470:G:H8	1.84	0.42
4:4:520:G:H2'	4:4:521:G:H8	1.84	0.42
4:4:2493:U:O2'	51:r:80:GLU:OE2	2.30	0.42
4:4:2758:A:C4	44:k:67:LEU:HD11	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:58:VAL:HA	6:6:67:LEU:O	2.20	0.42
6:6:99:TYR:OH	51:r:141:GLN:NE2	2.52	0.42
8:A:32:ILE:HD13	8:A:40:HIS:HB3	2.00	0.42
9:B:34:LEU:O	9:B:38:ARG:NE	2.52	0.42
16:I:22:LYS:O	16:I:26:ALA:HB3	2.20	0.42
24:Q:51:LEU:HD23	24:Q:55:ARG:HB3	2.01	0.42
42:i:170:LEU:HB2	42:i:173:VAL:HG12	2.01	0.42
1:1:951:G:H22	1:1:1231:G:H22	1.68	0.42
1:1:1021:G:N2	1:1:1022:G:O2'	2.53	0.42
1:1:1456:G:H1	26:S:54:LYS:HD2	1.85	0.42
2:2:33:U:N3	2:2:36:A:OP1	2.53	0.42
4:4:28:A:N6	4:4:512:G:O2'	2.53	0.42
4:4:2118:U:O5'	4:4:2147:G:N2	2.53	0.42
4:4:2882:A:OP1	52:s:96:ARG:NH1	2.53	0.42
10:C:21:LEU:HD12	10:C:22:LYS:HG2	2.02	0.42
10:C:79:PHE:HZ	10:C:204:ILE:HG23	1.85	0.42
13:F:149:ARG:HB2	17:J:62:GLN:HB2	2.02	0.42
14:G:113:SER:HB2	14:G:134:ILE:HD11	2.00	0.42
18:K:84:LEU:HB3	18:K:104:VAL:HG21	2.02	0.42
31:X:17:SER:O	31:X:19:VAL:N	2.53	0.42
40:g:69:ARG:HH21	40:g:119:ALA:HB2	1.85	0.42
42:i:8:GLN:HB2	42:i:126:VAL:HG12	2.02	0.42
57:x:7:ALA:HB3	57:x:103:ILE:H	1.85	0.42
1:1:1086:U:H2'	1:1:1087:G:H8	1.84	0.42
1:1:1222:G:H5''	25:R:78:ARG:HE	1.84	0.42
1:1:1354:C:H2'	1:1:1355:G:C8	2.55	0.42
4:4:1152:C:H2'	4:4:1153:C:H6	1.85	0.42
4:4:1388:G:H2'	4:4:1389:G:C8	2.55	0.42
4:4:1804:C:OP1	40:g:259:THR:OG1	2.36	0.42
4:4:2737:G:H2'	4:4:2738:A:C8	2.54	0.42
4:4:2805:G:H2'	4:4:2807:G:C8	2.55	0.42
4:4:2836:U:H2'	4:4:2837:G:C8	2.55	0.42
6:6:108:PRO:HD2	6:6:111:VAL:HG12	2.02	0.42
9:B:6:HIS:HE1	9:B:8:ILE:HD12	1.84	0.42
9:B:41:GLY:O	9:B:45:LYS:HB2	2.19	0.42
16:I:51:ARG:HD2	16:I:61:GLU:HB2	2.02	0.42
28:U:292:THR:N	28:U:398:ILE:O	2.49	0.42
41:h:176:ILE:HB	41:h:181:LEU:HB2	2.02	0.42
44:k:26:VAL:O	44:k:32:GLU:HA	2.20	0.42
45:l:124:UNK:O	45:l:128:UNK:CB	2.68	0.42
1:1:254:G:H5''	23:P:69:LYS:HD2	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:269:C:H2'	1:1:270:A:C8	2.55	0.41
4:4:654(A):G:N2	4:4:654(B):C:N3	2.68	0.41
4:4:984:A:OP1	4:4:985:C:N4	2.51	0.41
4:4:1528:A:H2'	4:4:1528(A):A:H8	1.85	0.41
21:N:55:GLY:O	21:N:59:MET:CB	2.62	0.41
28:U:187:THR:HG23	28:U:197:ARG:HB2	2.02	0.41
28:U:357:ARG:HE	28:U:364:GLU:HG3	1.83	0.41
54:u:120:ARG:O	54:u:124:ASP:CB	2.66	0.41
1:1:190:U:H2'	1:1:191:G:H8	1.84	0.41
1:1:682:G:H2'	1:1:683:G:C8	2.55	0.41
1:1:1238:A:C2	1:1:1241:G:C2	3.08	0.41
4:4:781:A:O2'	4:4:1788:C:O2	2.37	0.41
4:4:838:C:N3	4:4:941:A:N6	2.67	0.41
4:4:1266:G:N2	4:4:2013:A:OP2	2.43	0.41
4:4:1295:C:H2'	4:4:1296:G:H8	1.86	0.41
4:4:2513:G:N2	41:h:143:ASN:HD21	2.18	0.41
6:6:98:MET:HE2	6:6:133:ILE:HD11	2.02	0.41
7:7:40:THR:O	7:7:44:LEU:HB2	2.19	0.41
9:B:181:ASN:ND2	9:B:204:LEU:HB3	2.35	0.41
13:F:48:LYS:HG2	13:F:49:ILE:HG23	2.02	0.41
24:Q:69:THR:HA	24:Q:72:ARG:HG2	2.01	0.41
29:V:21:LEU:HD22	29:V:41:ARG:HB2	2.01	0.41
33:Z:12:ALA:HB1	33:Z:29:PRO:HG3	2.01	0.41
42:i:198:ALA:O	42:i:202:PHE:CB	2.68	0.41
50:q:46:LYS:HD2	50:q:47:ASP:HB2	2.01	0.41
1:1:376:G:N2	1:1:387:U:O2	2.44	0.41
1:1:951:G:H1	1:1:1231:G:H1	1.66	0.41
1:1:1013:G:C8	25:R:18:LYS:HE3	2.55	0.41
4:4:395:U:O2'	4:4:396:G:N7	2.51	0.41
4:4:414:C:H1'	4:4:1864:U:H1'	2.02	0.41
4:4:679:C:H2'	4:4:680:G:C8	2.53	0.41
4:4:865:C:H42	4:4:909:A:H62	1.67	0.41
8:A:185:ILE:HG12	8:A:199:TYR:HB2	2.01	0.41
24:Q:58:LEU:HD23	24:Q:62:GLU:HB3	2.02	0.41
28:U:35:TYR:OH	28:U:270:GLN:NE2	2.41	0.41
38:e:1:MET:N	38:e:31:LYS:O	2.52	0.41
39:f:172:ILE:HD12	39:f:172:ILE:HA	1.94	0.41
39:f:192:ALA:O	39:f:196:ALA:HB2	2.20	0.41
42:i:65:TRP:HZ3	42:i:83:PHE:HZ	1.69	0.41
43:j:60:LEU:HD22	43:j:68:PRO:HD3	2.02	0.41
48:o:132:ALA:H	48:o:134:ARG:HH12	1.68	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:320:C:H2'	1:1:321:A:C8	2.56	0.41
4:4:721:C:H2'	4:4:722:A:C8	2.55	0.41
4:4:1812:A:H2'	4:4:1813:G:H8	1.86	0.41
4:4:1992:G:H1'	4:4:1994:C:H5	1.85	0.41
4:4:2291:U:H1'	4:4:2374:C:H1'	2.01	0.41
4:4:2751:G:OP2	44:k:3:ARG:NH1	2.53	0.41
11:D:69:VAL:HG22	11:D:139:LEU:HD13	2.02	0.41
28:U:19:ALA:HB2	28:U:107:VAL:HB	2.02	0.41
28:U:505:GLY:HA3	28:U:576:ASP:HB3	2.02	0.41
37:d:29:LYS:HB2	37:d:44:LYS:HE2	2.03	0.41
42:i:143:ALA:HB1	42:i:148:LEU:HB2	2.02	0.41
43:j:98:ARG:HA	43:j:101:ILE:HD12	2.01	0.41
49:p:15:GLY:HA2	49:p:47:ILE:HG22	2.02	0.41
54:u:28:VAL:HA	54:u:46:GLU:HA	2.01	0.41
1:1:666:G:H1	1:1:740:U:H3	1.66	0.41
1:1:884:U:H4'	1:1:885:G:H5''	2.02	0.41
1:1:1311:G:H5''	33:Z:58:ARG:HH12	1.85	0.41
4:4:18:C:O2'	4:4:554:U:OP1	2.37	0.41
4:4:381:G:O6	4:4:394:A:N6	2.53	0.41
4:4:946:G:O6	4:4:972:G:N2	2.53	0.41
4:4:1126:A:H4'	4:4:1127:A:H5''	2.01	0.41
4:4:2267:A:H5''	4:4:2268:A:H5''	2.03	0.41
4:4:2314:C:H2'	4:4:2315:G:C8	2.55	0.41
4:4:2396:G:O2'	30:W:29:GLY:O	2.28	0.41
8:A:212:GLN:O	8:A:216:SER:OG	2.28	0.41
10:C:70:ILE:HD13	10:C:97:LEU:HD21	2.01	0.41
18:K:53:ARG:HB3	18:K:69:TYR:HE1	1.85	0.41
34:a:46:CYS:HB3	34:a:49:CYS:HB2	1.77	0.41
45:l:11:UNK:O	45:l:15:UNK:CB	2.68	0.41
51:r:37:LEU:HB2	51:r:128:LYS:O	2.21	0.41
51:r:43:THR:HG22	51:r:94:VAL:HG12	2.03	0.41
4:4:331:A:N6	4:4:1210:A:OP2	2.48	0.41
4:4:2241:A:H2'	4:4:2242:G:C8	2.56	0.41
4:4:2328:A:H2'	4:4:2329:G:H8	1.86	0.41
4:4:2724:C:H2'	4:4:2725:A:C8	2.56	0.41
28:U:185:ALA:H	28:U:200:PRO:HB3	1.86	0.41
33:Z:57:GLU:HG2	33:Z:58:ARG:HH21	1.85	0.41
55:v:3:ARG:HE	55:v:5:LYS:HB3	1.86	0.41
57:x:72:LYS:HB3	57:x:106:ILE:HG13	2.02	0.41
1:1:45:U:H2'	1:1:46:G:H8	1.86	0.41
1:1:54:C:OP1	1:1:351:G:N2	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:376:G:H2'	1:1:377:G:H8	1.85	0.41
1:1:1383:C:H2'	1:1:1384:C:H5	1.86	0.41
2:2:69:G:H2'	2:2:70:G:C8	2.56	0.41
4:4:1181:C:H2'	4:4:1182:A:H8	1.86	0.41
4:4:1550:C:H2'	4:4:1551:C:H6	1.86	0.41
4:4:2728:U:H2'	4:4:2729:G:C8	2.56	0.41
16:I:10:GLY:HA3	16:I:16:LEU:HB2	2.02	0.41
28:U:527:ASN:ND2	28:U:567:LEU:O	2.48	0.41
28:U:608:VAL:HB	28:U:645:ALA:HB3	2.03	0.41
39:f:165:ARG:H	39:f:172:ILE:HD11	1.86	0.41
41:h:44:TYR:O	41:h:82:ARG:NH2	2.52	0.41
43:j:128:ARG:NH1	43:j:164:GLU:OE1	2.42	0.41
1:1:933:G:OP2	13:F:2:ALA:N	2.54	0.41
4:4:327:G:N2	59:z:70:SER:OG	2.52	0.41
4:4:380:U:H2'	4:4:381:G:H8	1.86	0.41
4:4:1478:G:N3	4:4:1557:C:O2'	2.52	0.41
4:4:1889:A:N3	4:4:2086:U:O2'	2.50	0.41
4:4:2036:C:H2'	4:4:2037:G:C8	2.56	0.41
9:B:30:ARG:HG2	9:B:31:HIS:CD2	2.56	0.41
9:B:156:ARG:HH21	9:B:194:GLY:HA2	1.85	0.41
11:D:33:VAL:HG11	11:D:109:ILE:HA	2.03	0.41
52:s:79:LEU:HA	52:s:83:ILE:HD13	2.03	0.41
59:z:39:VAL:HG13	59:z:40:GLU:H	1.86	0.41
1:1:941:G:C2'	1:1:942:G:O5'	2.68	0.41
1:1:951:G:N2	1:1:1231:G:H22	2.18	0.41
1:1:1012:U:OP1	25:R:18:LYS:NZ	2.47	0.41
1:1:1231:G:N3	15:H:128:ARG:NH2	2.68	0.41
1:1:1297:C:H4'	1:1:1299:A:H62	1.86	0.41
4:4:237:C:O2	4:4:609:A:O2'	2.32	0.41
4:4:643:A:OP1	35:b:42:TRP:NE1	2.54	0.41
4:4:840:C:H2'	4:4:841:A:H8	1.86	0.41
4:4:1106:G:H5''	45:l:57:UNK:HA	2.03	0.41
4:4:1267:U:H2'	4:4:1268:A:H8	1.86	0.41
4:4:1523:U:H2'	4:4:1524:G:C8	2.56	0.41
4:4:1830:C:H2'	4:4:1831:G:C8	2.54	0.41
4:4:1901:A:OP2	40:g:255:LYS:NZ	2.43	0.41
4:4:2232:U:OP2	30:W:40:ARG:NH2	2.43	0.41
4:4:2538:C:H2'	4:4:2539:C:H6	1.85	0.41
4:4:2679:A:H5'	41:h:165:VAL:HG11	2.03	0.41
5:5:48:A:H4'	53:t:95:HIS:HD2	1.85	0.41
6:6:4:ARG:H	6:6:58:VAL:HG23	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:67:THR:OG1	8:A:158:LEU:O	2.38	0.41
8:A:172:ILE:H	8:A:172:ILE:HG13	1.68	0.41
16:I:45:ARG:HG3	16:I:65:LEU:HD23	2.03	0.41
17:J:97:ALA:O	17:J:101:SER:OG	2.25	0.41
32:Y:7:LYS:HG2	32:Y:34:GLU:HB3	2.02	0.41
32:Y:26:LEU:HD11	32:Y:43:ILE:HG23	2.02	0.41
39:f:19:LYS:HD2	39:f:22:THR:HG21	2.02	0.41
39:f:118:PRO:HG2	39:f:120:VAL:HG22	2.03	0.41
50:q:3:LEU:HD22	50:q:4:SER:H	1.86	0.41
55:v:14:HIS:CD2	55:v:36:ARG:HH22	2.38	0.41
1:1:49:U:H3	1:1:362:G:H1'	1.86	0.41
1:1:285:G:H2'	1:1:286:G:H8	1.86	0.41
1:1:395:C:N4	1:1:396:G:O6	2.54	0.41
1:1:1302:U:H5	19:L:20:THR:HG21	1.85	0.41
4:4:572:A:H61	4:4:2029:G:N2	2.19	0.41
4:4:1065:U:O4	4:4:1069:A:O2'	2.35	0.41
6:6:69:THR:HA	6:6:89:PHE:O	2.21	0.41
8:A:221:LEU:O	8:A:225:ALA:HB2	2.21	0.41
28:U:71:THR:OG1	28:U:358:MET:O	2.33	0.41
32:Y:9:VAL:HG11	32:Y:55:ARG:HE	1.85	0.41
38:e:11:CYS:O	38:e:13:LYS:N	2.54	0.41
58:y:43:VAL:O	58:y:47:PHE:HB2	2.21	0.41
1:1:429:U:H3'	10:C:25:ARG:HH12	1.86	0.40
4:4:823:G:H2'	4:4:824:A:H8	1.86	0.40
4:4:1038:C:H2'	4:4:1039:G:C8	2.56	0.40
4:4:1296:G:OP1	4:4:2709:G:O2'	2.32	0.40
4:4:1345:C:H2'	4:4:1346:G:H8	1.85	0.40
22:O:38:TYR:OH	22:O:47:ASP:OD2	2.37	0.40
56:w:38:LEU:HD21	56:w:57:VAL:HB	2.03	0.40
1:1:67:C:H2'	1:1:68:G:C8	2.56	0.40
1:1:549:C:H2'	1:1:550:G:C8	2.56	0.40
1:1:659:U:H2'	1:1:660:G:C8	2.56	0.40
1:1:941:G:N2	1:1:942:G:C5	2.89	0.40
4:4:459:U:H2'	4:4:460:A:H8	1.86	0.40
4:4:592:G:H2'	4:4:593:G:H8	1.86	0.40
4:4:851:U:H2'	4:4:852:G:C8	2.56	0.40
4:4:958:U:OP2	51:r:14:ARG:NE	2.51	0.40
8:A:105:PHE:O	8:A:109:SER:HB3	2.21	0.40
9:B:189:ALA:CB	9:B:196:LEU:O	2.69	0.40
14:G:19:VAL:HG23	14:G:21:LYS:HG2	2.02	0.40
28:U:15:ILE:HG22	28:U:103:GLY:HA3	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:U:485:GLU:HA	28:U:601:ILE:HG23	2.02	0.40
39:f:156:GLU:O	39:f:160:GLY:CA	2.70	0.40
1:1:21:G:H2'	1:1:22:G:C8	2.56	0.40
1:1:991:U:C2	1:1:1215:G:O6	2.74	0.40
1:1:1502:A:H62	1:1:1505:G:H22	1.68	0.40
4:4:358:U:H2'	4:4:359:A:C8	2.56	0.40
4:4:414:C:H2'	4:4:415:A:C8	2.56	0.40
4:4:743:G:O2'	4:4:1659:U:OP1	2.32	0.40
4:4:864:G:H21	4:4:866:A:H61	1.69	0.40
4:4:1161:C:H2'	4:4:1162:G:H8	1.87	0.40
4:4:2037:G:H2'	4:4:2038:G:C8	2.56	0.40
4:4:2618:G:H21	41:h:150:VAL:HG21	1.87	0.40
4:4:2736:G:H2'	4:4:2737:G:C8	2.56	0.40
9:B:133:ALA:O	9:B:137:ALA:HB2	2.22	0.40
17:J:15:ALA:HA	17:J:77:MET:HA	2.02	0.40
21:N:39:LEU:HD23	21:N:43:LEU:HD23	2.03	0.40
22:O:67:THR:O	22:O:71:ARG:CB	2.69	0.40
28:U:84:THR:HA	28:U:85:PRO:HD3	1.92	0.40
28:U:268:GLY:O	28:U:272:LEU:HB2	2.20	0.40
1:1:601:C:H2'	1:1:602:A:C8	2.56	0.40
1:1:657:G:O2'	21:N:28:GLN:NE2	2.39	0.40
4:4:851:U:O2'	32:Y:42:ALA:O	2.39	0.40
4:4:1747:G:H2'	4:4:1747(A):G:H8	1.86	0.40
4:4:1753:G:N2	4:4:1756:G:OP2	2.46	0.40
4:4:1864:U:H2'	4:4:1865:G:C8	2.56	0.40
4:4:1983:C:H4'	4:4:2606:C:H4'	2.02	0.40
4:4:2000:G:H2'	4:4:2001:A:H8	1.85	0.40
6:6:69:THR:HG22	6:6:90:VAL:HG22	2.04	0.40
9:B:55:VAL:HG22	9:B:68:VAL:HG23	2.02	0.40
19:L:18:ALA:HB3	19:L:45:VAL:HG21	2.02	0.40
42:i:34:TRP:CD2	50:q:8:PRO:HG3	2.56	0.40
48:o:39:ARG:HG2	48:o:41:ASP:H	1.86	0.40
50:q:85:LEU:HA	50:q:88:LEU:HD23	2.03	0.40
1:1:1071:C:H2'	1:1:1072:G:C8	2.56	0.40
4:4:1353:A:OP2	4:4:1377:G:N1	2.46	0.40
4:4:1844:C:H4'	40:g:258:LYS:HE2	2.03	0.40
4:4:2784:C:H1'	41:h:37:ARG:HH12	1.86	0.40
5:5:29:A:OP2	53:t:31:SER:OG	2.35	0.40
9:B:57:ILE:HA	9:B:66:VAL:HG23	2.03	0.40
22:O:67:THR:O	22:O:71:ARG:HB2	2.22	0.40
30:W:64:ALA:HA	30:W:67:ILE:HG12	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:j:122:PRO:HG3	43:j:181:ARG:H	1.86	0.40
44:k:102:ALA:HA	44:k:115:VAL:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	6	176/178 (99%)	134 (76%)	38 (22%)	4 (2%)	5	30
7	7	144/146 (99%)	124 (86%)	20 (14%)	0	100	100
8	A	233/235 (99%)	203 (87%)	29 (12%)	1 (0%)	30	62
9	B	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
10	C	206/208 (99%)	190 (92%)	16 (8%)	0	100	100
11	D	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
12	E	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
13	F	153/155 (99%)	118 (77%)	34 (22%)	1 (1%)	18	51
14	G	136/138 (99%)	122 (90%)	14 (10%)	0	100	100
15	H	125/127 (98%)	109 (87%)	16 (13%)	0	100	100
16	I	97/99 (98%)	87 (90%)	10 (10%)	0	100	100
17	J	117/119 (98%)	100 (86%)	16 (14%)	1 (1%)	14	45
18	K	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
19	L	117/119 (98%)	101 (86%)	15 (13%)	1 (1%)	14	45
20	M	58/60 (97%)	47 (81%)	11 (19%)	0	100	100
21	N	86/88 (98%)	79 (92%)	7 (8%)	0	100	100
22	O	82/84 (98%)	73 (89%)	8 (10%)	1 (1%)	10	40
23	P	98/100 (98%)	93 (95%)	4 (4%)	1 (1%)	12	43

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	Q	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
25	R	86/88 (98%)	76 (88%)	10 (12%)	0	100	100
26	S	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
27	T	23/25 (92%)	20 (87%)	3 (13%)	0	100	100
28	U	657/687 (96%)	555 (84%)	100 (15%)	2 (0%)	36	67
29	V	76/78 (97%)	68 (90%)	8 (10%)	0	100	100
30	W	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
31	X	69/71 (97%)	65 (94%)	4 (6%)	0	100	100
32	Y	58/60 (97%)	54 (93%)	4 (7%)	0	100	100
33	Z	69/71 (97%)	40 (58%)	29 (42%)	0	100	100
34	a	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
35	b	48/50 (96%)	36 (75%)	12 (25%)	0	100	100
36	c	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
37	d	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
38	e	35/37 (95%)	30 (86%)	4 (11%)	1 (3%)	3	25
39	f	225/227 (99%)	189 (84%)	36 (16%)	0	100	100
40	g	273/275 (99%)	244 (89%)	28 (10%)	1 (0%)	30	62
41	h	203/205 (99%)	172 (85%)	31 (15%)	0	100	100
42	i	206/208 (99%)	187 (91%)	19 (9%)	0	100	100
43	j	177/179 (99%)	145 (82%)	31 (18%)	1 (1%)	21	54
44	k	174/176 (99%)	148 (85%)	25 (14%)	1 (1%)	21	54
45	l	1/130 (1%)	1 (100%)	0	0	100	100
48	o	137/139 (99%)	126 (92%)	11 (8%)	0	100	100
49	p	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
50	q	148/150 (99%)	120 (81%)	28 (19%)	0	100	100
51	r	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
52	s	116/118 (98%)	104 (90%)	12 (10%)	0	100	100
53	t	97/99 (98%)	86 (89%)	11 (11%)	0	100	100
54	u	136/138 (99%)	121 (89%)	15 (11%)	0	100	100
55	v	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
56	w	99/101 (98%)	88 (89%)	11 (11%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	x	111/113 (98%)	102 (92%)	8 (7%)	1 (1%)	14	45
58	y	91/93 (98%)	83 (91%)	7 (8%)	1 (1%)	11	41
59	z	99/101 (98%)	72 (73%)	25 (25%)	2 (2%)	6	32
All	All	6614/6873 (96%)	5765 (87%)	829 (12%)	20 (0%)	37	67

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
59	z	98	VAL
19	L	106	ASN
22	O	83	GLU
28	U	146	LEU
38	e	12	ASP
40	g	245	PRO
28	U	353	ALA
6	6	79	ARG
8	A	240	GLN
13	F	151	TYR
23	P	66	SER
44	k	170	ARG
59	z	39	VAL
43	j	142	PRO
6	6	15	PRO
17	J	58	PRO
58	y	8	ILE
57	x	6	ILE
6	6	124	ILE
6	6	111	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	6	157/157 (100%)	157 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	7	122/122 (100%)	122 (100%)	0	100	100
8	A	202/203 (100%)	200 (99%)	2 (1%)	68	74
9	B	160/161 (99%)	159 (99%)	1 (1%)	78	79
10	C	180/180 (100%)	180 (100%)	0	100	100
11	D	115/116 (99%)	115 (100%)	0	100	100
12	E	90/90 (100%)	90 (100%)	0	100	100
13	F	126/126 (100%)	126 (100%)	0	100	100
14	G	119/119 (100%)	119 (100%)	0	100	100
15	H	98/98 (100%)	97 (99%)	1 (1%)	68	74
16	I	88/89 (99%)	87 (99%)	1 (1%)	65	73
17	J	90/90 (100%)	89 (99%)	1 (1%)	65	73
18	K	104/104 (100%)	103 (99%)	1 (1%)	68	74
19	L	94/95 (99%)	94 (100%)	0	100	100
20	M	49/49 (100%)	49 (100%)	0	100	100
21	N	79/79 (100%)	79 (100%)	0	100	100
22	O	72/72 (100%)	72 (100%)	0	100	100
23	P	94/95 (99%)	93 (99%)	1 (1%)	65	73
24	Q	61/61 (100%)	61 (100%)	0	100	100
25	R	74/75 (99%)	74 (100%)	0	100	100
26	S	76/76 (100%)	76 (100%)	0	100	100
27	T	19/20 (95%)	19 (100%)	0	100	100
28	U	558/579 (96%)	556 (100%)	2 (0%)	84	83
29	V	62/62 (100%)	62 (100%)	0	100	100
30	W	78/79 (99%)	77 (99%)	1 (1%)	61	71
31	X	66/66 (100%)	64 (97%)	2 (3%)	36	57
32	Y	51/52 (98%)	51 (100%)	0	100	100
33	Z	63/63 (100%)	63 (100%)	0	100	100
34	a	51/51 (100%)	51 (100%)	0	100	100
35	b	49/49 (100%)	48 (98%)	1 (2%)	48	65
36	c	41/41 (100%)	41 (100%)	0	100	100
37	d	53/54 (98%)	53 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	e	34/34 (100%)	34 (100%)	0	100	100
39	f	179/179 (100%)	179 (100%)	0	100	100
40	g	217/217 (100%)	216 (100%)	1 (0%)	81	81
41	h	165/165 (100%)	165 (100%)	0	100	100
42	i	165/165 (100%)	164 (99%)	1 (1%)	78	79
43	j	153/153 (100%)	150 (98%)	3 (2%)	48	65
44	k	146/146 (100%)	145 (99%)	1 (1%)	76	77
45	l	1/1 (100%)	1 (100%)	0	100	100
48	o	117/118 (99%)	117 (100%)	0	100	100
49	p	100/100 (100%)	100 (100%)	0	100	100
50	q	116/116 (100%)	115 (99%)	1 (1%)	70	74
51	r	111/111 (100%)	111 (100%)	0	100	100
52	s	101/101 (100%)	101 (100%)	0	100	100
53	t	77/77 (100%)	77 (100%)	0	100	100
54	u	120/120 (100%)	118 (98%)	2 (2%)	53	67
55	v	92/93 (99%)	91 (99%)	1 (1%)	65	73
56	w	82/82 (100%)	82 (100%)	0	100	100
57	x	91/92 (99%)	90 (99%)	1 (1%)	65	73
58	y	74/75 (99%)	74 (100%)	0	100	100
59	z	84/85 (99%)	82 (98%)	2 (2%)	43	62
All	All	5566/5603 (99%)	5539 (100%)	27 (0%)	78	81

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	A	149	LEU
8	A	154	LEU
9	B	179	ARG
15	H	63	ILE
16	I	23	ILE
17	J	57	THR
18	K	55	VAL
23	P	36	ILE
28	U	201	ILE
28	U	284	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	W	92	LYS
31	X	41	ILE
31	X	53	LEU
35	b	34	LEU
40	g	65	ILE
42	i	157	VAL
43	j	39	ILE
43	j	94	LEU
43	j	159	VAL
44	k	11	VAL
50	q	114	ILE
54	u	99	LEU
54	u	102	ILE
55	v	95	LEU
57	x	76	VAL
59	z	31	LEU
59	z	61	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
6	6	65	GLN
7	7	17	GLN
7	7	28	ASN
7	7	54	GLN
8	A	40	HIS
8	A	104	ASN
9	B	6	HIS
9	B	31	HIS
11	D	20	GLN
12	E	7	ASN
12	E	57	GLN
12	E	84	ASN
13	F	51	GLN
13	F	86	GLN
13	F	97	GLN
15	H	31	GLN
18	K	78	GLN
20	M	49	HIS
21	N	37	ASN
21	N	62	GLN
23	P	26	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
23	P	94	ASN
24	Q	36	ASN
25	R	23	ASN
26	S	42	GLN
26	S	45	GLN
28	U	165	GLN
28	U	443	HIS
28	U	641	GLN
29	V	29	GLN
32	Y	32	GLN
37	d	35	GLN
39	f	166	ASN
40	g	96	HIS
40	g	203	ASN
40	g	227	ASN
41	h	129	HIS
41	h	132	HIS
41	h	143	ASN
41	h	192	ASN
42	i	69	HIS
42	i	133	ASN
42	i	204	ASN
43	j	41	GLN
44	k	74	ASN
48	o	56	ASN
48	o	94	HIS
48	o	128	HIS
48	o	131	GLN
49	p	5	GLN
50	q	38	GLN
51	r	12	GLN
51	r	141	GLN
53	t	16	ASN
54	u	58	ASN
55	v	72	HIS
55	v	94	ASN
56	w	11	GLN
56	w	64	HIS
56	w	80	GLN
56	w	87	HIS
57	x	57	ASN
59	z	6	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1506/1507 (99%)	396 (26%)	11 (0%)
2	2	75/76 (98%)	27 (36%)	0
3	3	9/15 (60%)	7 (77%)	1 (11%)
4	4	2900/2901 (99%)	544 (18%)	10 (0%)
5	5	118/119 (99%)	36 (30%)	4 (3%)
All	All	4608/4618 (99%)	1010 (21%)	26 (0%)

All (1010) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	8	A
1	1	9	G
1	1	32	A
1	1	39	G
1	1	41	G
1	1	47	C
1	1	48	C
1	1	50	A
1	1	51	A
1	1	65	U
1	1	66	G
1	1	80	G
1	1	81	U
1	1	83	U
1	1	84	U
1	1	88	A
1	1	89	C
1	1	90	U
1	1	91	C
1	1	97	G
1	1	110	C
1	1	121	C
1	1	129(A)	G
1	1	131	C
1	1	134	A
1	1	135	C
1	1	139	G
1	1	145	G
1	1	152	A
1	1	173	U
1	1	189(C)	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	189(E)	U
1	1	189(F)	U
1	1	189(G)	G
1	1	189(H)	G
1	1	189(I)	G
1	1	195	A
1	1	197	A
1	1	198	G
1	1	204	U
1	1	216	G
1	1	217	C
1	1	236	G
1	1	247	G
1	1	251	G
1	1	266	G
1	1	267	C
1	1	274	A
1	1	280	C
1	1	289	G
1	1	306	G
1	1	321	A
1	1	328	C
1	1	332	G
1	1	344	A
1	1	345	C
1	1	346	G
1	1	350	G
1	1	351	G
1	1	352	C
1	1	354	G
1	1	365	U
1	1	368	U
1	1	372	C
1	1	373	A
1	1	388	G
1	1	390	C
1	1	393	A
1	1	397	A
1	1	398	C
1	1	409	G
1	1	411	A
1	1	414	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	421	U
1	1	422	C
1	1	423	G
1	1	424	G
1	1	428	G
1	1	429	U
1	1	433	C
1	1	438	G
1	1	439	A
1	1	452	A
1	1	455	C
1	1	470	C
1	1	472	A
1	1	484	G
1	1	491	G
1	1	497	A
1	1	498	U
1	1	499	A
1	1	510	A
1	1	511	C
1	1	512	U
1	1	521	G
1	1	524	G
1	1	527	G
1	1	531	U
1	1	547	A
1	1	559	A
1	1	564	C
1	1	572	A
1	1	573	A
1	1	574	A
1	1	575	G
1	1	576	G
1	1	577	G
1	1	586	C
1	1	588	G
1	1	633	G
1	1	650	G
1	1	653	A
1	1	661	G
1	1	662	G
1	1	665	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	673	G
1	1	679	C
1	1	681	C
1	1	682	G
1	1	695	A
1	1	700	G
1	1	701	C
1	1	703	G
1	1	704	A
1	1	707	C
1	1	712	A
1	1	713	G
1	1	717	C
1	1	718	G
1	1	720	C
1	1	722	A
1	1	723	U
1	1	724	G
1	1	750	G
1	1	753	A
1	1	755	G
1	1	758	G
1	1	777	A
1	1	781	A
1	1	792	A
1	1	793	U
1	1	794	A
1	1	799	G
1	1	802	A
1	1	810	C
1	1	812	C
1	1	813	U
1	1	817	C
1	1	818	G
1	1	828	A
1	1	840	C
1	1	841	U
1	1	848	C
1	1	872	A
1	1	873	A
1	1	876	G
1	1	889	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	902	G
1	1	907	A
1	1	916	G
1	1	934	C
1	1	935	A
1	1	937	A
1	1	938	A
1	1	941	G
1	1	944	G
1	1	945	G
1	1	948	C
1	1	951	G
1	1	954	G
1	1	956	U
1	1	957	U
1	1	958	A
1	1	960	U
1	1	961	U
1	1	962	C
1	1	969	A
1	1	971	G
1	1	972	C
1	1	974	A
1	1	975	A
1	1	976	G
1	1	977	A
1	1	978	A
1	1	979	C
1	1	980	C
1	1	981	U
1	1	982	U
1	1	983	A
1	1	984	C
1	1	985	C
1	1	987	G
1	1	990	C
1	1	991	U
1	1	992	U
1	1	993	G
1	1	994	A
1	1	995	C
1	1	996	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	998	G
1	1	1000	U
1	1	1001	A
1	1	1001(A)	G
1	1	1003	G
1	1	1004	A
1	1	1005	A
1	1	1007	C
1	1	1008	C
1	1	1009	G
1	1	1010	G
1	1	1011	G
1	1	1013	G
1	1	1014	A
1	1	1016	A
1	1	1018	C
1	1	1022	G
1	1	1023	G
1	1	1024	G
1	1	1027	C
1	1	1028	C
1	1	1030	C
1	1	1030(C)	G
1	1	1030(D)	A
1	1	1033	G
1	1	1034	G
1	1	1036	G
1	1	1039	C
1	1	1043	C
1	1	1054	C
1	1	1055	A
1	1	1057	G
1	1	1059	C
1	1	1065	U
1	1	1081	G
1	1	1084	G
1	1	1094	G
1	1	1095	U
1	1	1101	A
1	1	1104	G
1	1	1113	C
1	1	1114	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1115	C
1	1	1122	U
1	1	1123	A
1	1	1125	U
1	1	1126	U
1	1	1127	G
1	1	1128	C
1	1	1129	C
1	1	1130	A
1	1	1131	G
1	1	1132	C
1	1	1133	G
1	1	1134	G
1	1	1136	U
1	1	1138	G
1	1	1139	G
1	1	1140	C
1	1	1142	G
1	1	1145	C
1	1	1146	A
1	1	1149	C
1	1	1151	A
1	1	1156	G
1	1	1157	A
1	1	1158	C
1	1	1159	U
1	1	1170	A
1	1	1171	G
1	1	1172	C
1	1	1174	G
1	1	1181	G
1	1	1184	G
1	1	1190	G
1	1	1196	U
1	1	1197	G
1	1	1200	C
1	1	1201	A
1	1	1202	G
1	1	1211	U
1	1	1212	U
1	1	1214	C
1	1	1217	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1218	C
1	1	1219	U
1	1	1220	G
1	1	1224	G
1	1	1225	A
1	1	1228	C
1	1	1229	A
1	1	1230	C
1	1	1232	U
1	1	1233	G
1	1	1234	C
1	1	1236	A
1	1	1238	A
1	1	1239	A
1	1	1240	U
1	1	1241	G
1	1	1243	C
1	1	1244	C
1	1	1245	A
1	1	1250	A
1	1	1252	A
1	1	1255	G
1	1	1257	U
1	1	1258	G
1	1	1263	C
1	1	1265	G
1	1	1266	G
1	1	1267	C
1	1	1268	A
1	1	1269	A
1	1	1273	G
1	1	1276	G
1	1	1278	U
1	1	1279	A
1	1	1280	A
1	1	1284	C
1	1	1285	A
1	1	1286	A
1	1	1287	A
1	1	1288	A
1	1	1290	G
1	1	1291	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1292	U
1	1	1293	G
1	1	1295	G
1	1	1297	C
1	1	1298	C
1	1	1299	A
1	1	1300	G
1	1	1301	U
1	1	1302	U
1	1	1303	C
1	1	1310	G
1	1	1314	C
1	1	1315	U
1	1	1317	C
1	1	1318	A
1	1	1319	A
1	1	1321	C
1	1	1322	C
1	1	1323	G
1	1	1325	C
1	1	1326	C
1	1	1328	C
1	1	1329	A
1	1	1331	G
1	1	1334	G
1	1	1337	G
1	1	1339	A
1	1	1341	U
1	1	1342	C
1	1	1343	G
1	1	1346	A
1	1	1351	U
1	1	1356	G
1	1	1357	A
1	1	1358	U
1	1	1359	C
1	1	1362	C
1	1	1363(A)	A
1	1	1364	U
1	1	1368	G
1	1	1370	G
1	1	1371	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1374	A
1	1	1375	A
1	1	1376	U
1	1	1381	U
1	1	1382	C
1	1	1384	C
1	1	1385	G
1	1	1398	A
1	1	1419	G
1	1	1441	G
1	1	1444	C
1	1	1446	U
1	1	1452	C
1	1	1456	G
1	1	1457	G
1	1	1492	A
1	1	1493	A
1	1	1494	G
1	1	1502	A
1	1	1503	A
1	1	1504	G
1	1	1506	U
1	1	1517	G
1	1	1529	G
1	1	1530	G
1	1	1531	A
1	1	1532	U
1	1	1533	C
1	1	1534	A
2	2	6	G
2	2	8	U
2	2	9	A
2	2	10	G
2	2	12	U
2	2	14	A
2	2	15	G
2	2	17	C
2	2	18	G
2	2	19	G
2	2	20	U
2	2	21	A
2	2	25	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	29	G
2	2	32	U
2	2	36	A
2	2	37	A
2	2	40	C
2	2	44	G
2	2	46	G
2	2	54	U
2	2	55	U
2	2	56	C
2	2	60	U
2	2	64	A
2	2	65	G
2	2	75	C
3	3	7	U
3	3	9	A
3	3	11	G
3	3	12	U
3	3	13	U
3	3	14	U
3	3	15	U
4	4	10	G
4	4	11	G
4	4	13	A
4	4	14	A
4	4	27	G
4	4	32	C
4	4	34	C
4	4	41	C
4	4	45	C
4	4	55	G
4	4	64	A
4	4	71	A
4	4	74	A
4	4	75	G
4	4	84	A
4	4	88	G
4	4	92	A
4	4	110	G
4	4	114	U
4	4	118	A
4	4	120	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	122	G
4	4	125	G
4	4	128	C
4	4	131	G
4	4	139(A)	G
4	4	141	A
4	4	156	U
4	4	158	U
4	4	196	A
4	4	197	A
4	4	199	A
4	4	200	U
4	4	205	G
4	4	215	G
4	4	216	A
4	4	222	A
4	4	227	A
4	4	228	A
4	4	229	A
4	4	245	G
4	4	248	G
4	4	252	G
4	4	265	A
4	4	267	C
4	4	271(B)	C
4	4	271(L)	U
4	4	271(M)	G
4	4	271(N)	U
4	4	271(X)	G
4	4	271(Y)	U
4	4	276	A
4	4	277	C
4	4	278	A
4	4	283	A
4	4	295	G
4	4	302	C
4	4	311	A
4	4	317	G
4	4	323	G
4	4	329	G
4	4	330	A
4	4	339	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	345	A
4	4	346	A
4	4	352	G
4	4	353	G
4	4	362	U
4	4	363	G
4	4	371	A
4	4	372	G
4	4	380	U
4	4	386	G
4	4	387	U
4	4	396	G
4	4	404	C
4	4	405	U
4	4	411	G
4	4	412	A
4	4	422	A
4	4	428	A
4	4	437	G
4	4	446	G
4	4	451	C
4	4	457	A
4	4	458	G
4	4	467	G
4	4	479	A
4	4	481	G
4	4	494	G
4	4	496	G
4	4	505	A
4	4	508	G
4	4	509	C
4	4	512	G
4	4	518	G
4	4	525	U
4	4	531	C
4	4	532	A
4	4	533	G
4	4	556	G
4	4	563	G
4	4	568	U
4	4	571	A
4	4	573	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	575	A
4	4	588	U
4	4	603	A
4	4	614(B)	G
4	4	614(C)	A
4	4	615	G
4	4	620	G
4	4	622	G
4	4	637	A
4	4	645	C
4	4	650	C
4	4	651	G
4	4	654	A
4	4	654(A)	G
4	4	654(B)	C
4	4	654(C)	G
4	4	654(D)	G
4	4	654(E)	G
4	4	654(F)	C
4	4	654(G)	C
4	4	654(I)	C
4	4	654(J)	A
4	4	654(L)	G
4	4	654(M)	C
4	4	654(Q)	C
4	4	654(R)	C
4	4	654(T)	C
4	4	655	A
4	4	670	A
4	4	686	G
4	4	726	G
4	4	729	G
4	4	730	C
4	4	740	U
4	4	748	G
4	4	753	C
4	4	764	A
4	4	765	G
4	4	774	A
4	4	775	G
4	4	776	G
4	4	782	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	784	A
4	4	785	G
4	4	790	C
4	4	792	G
4	4	800	A
4	4	805	G
4	4	806	C
4	4	812	C
4	4	819	A
4	4	826	U
4	4	827	U
4	4	828	U
4	4	830	G
4	4	855	G
4	4	857	C
4	4	859	G
4	4	866	A
4	4	873	G
4	4	881	G
4	4	882	G
4	4	884	C
4	4	885	C
4	4	887	A
4	4	888	C
4	4	889	C
4	4	890	A
4	4	892	G
4	4	893	C
4	4	896	A
4	4	897	C
4	4	906	G
4	4	910	A
4	4	915	C
4	4	932	G
4	4	945	A
4	4	946	G
4	4	953	A
4	4	957	A
4	4	961	C
4	4	973	A
4	4	974	G
4	4	975	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	980	A
4	4	983	A
4	4	985	C
4	4	989	G
4	4	996	A
4	4	1009	A
4	4	1011	G
4	4	1013	C
4	4	1015	G
4	4	1022	G
4	4	1025	G
4	4	1026	U
4	4	1027	A
4	4	1033	U
4	4	1045	A
4	4	1046	A
4	4	1051	G
4	4	1055	G
4	4	1059	G
4	4	1060	U
4	4	1061	U
4	4	1064	C
4	4	1065	U
4	4	1066	U
4	4	1068	G
4	4	1070	A
4	4	1071	G
4	4	1077	A
4	4	1078	U
4	4	1080	C
4	4	1084	A
4	4	1085	A
4	4	1087	G
4	4	1088	A
4	4	1090	U
4	4	1092	C
4	4	1094	U
4	4	1097	U
4	4	1102	C
4	4	1103	A
4	4	1106	G
4	4	1116	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	1122	G
4	4	1127	A
4	4	1128	A
4	4	1130	U
4	4	1135	C
4	4	1136	G
4	4	1142(A)	A
4	4	1144	G
4	4	1148	A
4	4	1157	G
4	4	1173	G
4	4	1174	A
4	4	1175	U
4	4	1177	A
4	4	1186	G
4	4	1206	G
4	4	1210	A
4	4	1211	U
4	4	1212	G
4	4	1220	A
4	4	1225	G
4	4	1236	G
4	4	1247	A
4	4	1252	G
4	4	1253	A
4	4	1256	G
4	4	1265	A
4	4	1272	A
4	4	1273	U
4	4	1300	U
4	4	1301	A
4	4	1306	C
4	4	1314	C
4	4	1325	G
4	4	1329	U
4	4	1332	G
4	4	1333	C
4	4	1350	C
4	4	1359	A
4	4	1365	A
4	4	1368	G
4	4	1378	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	1384	A
4	4	1385	G
4	4	1395	A
4	4	1396	U
4	4	1398	C
4	4	1416	G
4	4	1417	C
4	4	1420	U
4	4	1427	A
4	4	1428	C
4	4	1445	A
4	4	1452	A
4	4	1455	G
4	4	1458	C
4	4	1460	A
4	4	1467	C
4	4	1478	G
4	4	1482	G
4	4	1490	A
4	4	1494	A
4	4	1504	C
4	4	1509	C
4	4	1509(A)	A
4	4	1531	C
4	4	1533	G
4	4	1537	G
4	4	1539	G
4	4	1540	U
4	4	1541	G
4	4	1547	C
4	4	1558	A
4	4	1566	A
4	4	1569	A
4	4	1584	C
4	4	1586	A
4	4	1607	C
4	4	1616	A
4	4	1640	C
4	4	1643	G
4	4	1648	C
4	4	1674	G
4	4	1694	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	1696	G
4	4	1703	G
4	4	1722	A
4	4	1739	U
4	4	1740	G
4	4	1741	A
4	4	1744	C
4	4	1746	G
4	4	1750	G
4	4	1762	A
4	4	1763	G
4	4	1764	G
4	4	1769	G
4	4	1773	A
4	4	1781	C
4	4	1799	G
4	4	1800	C
4	4	1801	G
4	4	1802	A
4	4	1815	A
4	4	1816	G
4	4	1828	G
4	4	1835	G
4	4	1847	A
4	4	1882	C
4	4	1885	A
4	4	1889	A
4	4	1899	G
4	4	1906	G
4	4	1913	A
4	4	1914	C
4	4	1917	U
4	4	1918	A
4	4	1919	A
4	4	1920	C
4	4	1925	C
4	4	1926	U
4	4	1929	G
4	4	1930	G
4	4	1931	U
4	4	1937	A
4	4	1938	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	1939	U
4	4	1940	U
4	4	1944	U
4	4	1955	U
4	4	1966	A
4	4	1967	C
4	4	1970	A
4	4	1971	A
4	4	1972	A
4	4	1981	A
4	4	1982	C
4	4	1991	U
4	4	1993	U
4	4	2013	A
4	4	2020	A
4	4	2021	C
4	4	2031	A
4	4	2032	G
4	4	2033	A
4	4	2035	G
4	4	2046	G
4	4	2052	G
4	4	2055	C
4	4	2056	G
4	4	2059	A
4	4	2060	A
4	4	2061	G
4	4	2062	A
4	4	2068	U
4	4	2069	G
4	4	2077	A
4	4	2093	G
4	4	2095	C
4	4	2102	U
4	4	2104	G
4	4	2109	U
4	4	2110	G
4	4	2113	U
4	4	2117	A
4	4	2119	A
4	4	2123	G
4	4	2125	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	2129	C
4	4	2130	U
4	4	2131	G
4	4	2133	A
4	4	2134	A
4	4	2135	A
4	4	2137	C
4	4	2139	C
4	4	2141	G
4	4	2145	C
4	4	2147	G
4	4	2153	G
4	4	2155	G
4	4	2158	A
4	4	2169	A
4	4	2170	A
4	4	2173	A
4	4	2174	C
4	4	2176	A
4	4	2180	U
4	4	2183	C
4	4	2184	G
4	4	2186	G
4	4	2187	G
4	4	2189	U
4	4	2190	G
4	4	2198	A
4	4	2206	G
4	4	2208	A
4	4	2218	U
4	4	2219	G
4	4	2225	A
4	4	2238	G
4	4	2239	G
4	4	2250	G
4	4	2266	A
4	4	2268	A
4	4	2279	G
4	4	2283	C
4	4	2285	C
4	4	2286	A
4	4	2287	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	2288	A
4	4	2305	A
4	4	2307	G
4	4	2308	G
4	4	2309	A
4	4	2319	G
4	4	2320	A
4	4	2325	G
4	4	2334	G
4	4	2335	A
4	4	2347	C
4	4	2350	C
4	4	2383	G
4	4	2385	C
4	4	2391	G
4	4	2406	U
4	4	2419	U
4	4	2421	G
4	4	2423	U
4	4	2425	A
4	4	2427	C
4	4	2428	G
4	4	2430	A
4	4	2432	A
4	4	2441	C
4	4	2445	G
4	4	2447	G
4	4	2448	A
4	4	2476	A
4	4	2478	A
4	4	2480	C
4	4	2494	G
4	4	2498	C
4	4	2503	A
4	4	2504	U
4	4	2505	G
4	4	2518	A
4	4	2520	C
4	4	2529	G
4	4	2535	G
4	4	2564	A
4	4	2566	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	2567	G
4	4	2572	A
4	4	2578	G
4	4	2602	A
4	4	2610	C
4	4	2611	U
4	4	2612	C
4	4	2630	G
4	4	2645	G
4	4	2646	C
4	4	2654	A
4	4	2682	U
4	4	2689	U
4	4	2690	C
4	4	2691	C
4	4	2702	U
4	4	2703	C
4	4	2712(A)	A
4	4	2713	A
4	4	2714	G
4	4	2715	C
4	4	2726	U
4	4	2727	G
4	4	2732	G
4	4	2733	A
4	4	2739	U
4	4	2744	G
4	4	2748	A
4	4	2752	C
4	4	2757	A
4	4	2761	G
4	4	2764	A
4	4	2765	A
4	4	2766	G
4	4	2769	C
4	4	2773	C
4	4	2778	A
4	4	2779	U
4	4	2780	G
4	4	2790	A
4	4	2791	C
4	4	2792	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	4	2794	C
4	4	2799	C
4	4	2801	A
4	4	2801(A)	A
4	4	2802	G
4	4	2803	C
4	4	2818	G
4	4	2820	A
4	4	2821	A
4	4	2835	A
4	4	2836	U
4	4	2849	U
4	4	2850	A
4	4	2871	C
4	4	2872	G
4	4	2884	U
4	4	2886	G
4	4	2894	G
4	4	2895	U
5	5	3	C
5	5	9	G
5	5	12	C
5	5	13	A
5	5	15	A
5	5	21	G
5	5	24	G
5	5	25	A
5	5	26	A
5	5	27	C
5	5	32	C
5	5	35	U
5	5	38	C
5	5	41	U
5	5	42	C
5	5	43	C
5	5	44	G
5	5	45	A
5	5	46	A
5	5	50	G
5	5	51	G
5	5	52	A
5	5	53	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	5	54	G
5	5	57	A
5	5	66	A
5	5	67	G
5	5	68	C
5	5	73	A
5	5	77	U
5	5	81	G
5	5	89	G
5	5	97	G
5	5	109	C
5	5	110	G
5	5	113	G

All (26) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	65	U
1	1	134	A
1	1	575	G
1	1	982	U
1	1	1000	U
1	1	1013	G
1	1	1015	A
1	1	1127	G
1	1	1218	C
1	1	1239	A
1	1	1291	G
3	3	14	U
4	4	752	A
4	4	1054	A
4	4	1077	A
4	4	1300	U
4	4	1647	G
4	4	1799	G
4	4	1919	A
4	4	1992	G
4	4	2610	C
4	4	2756	U
5	5	24	G
5	5	34	U
5	5	44	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	5	66	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 466 ligands modelled in this entry, 465 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
62	GDP	U	702	60	29,30,30	1.19	4 (13%)	45,47,47	1.77	7 (15%)

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
62	GDP	U	702	60	-	7/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	U	702	GDP	C5-C4	3.12	1.47	1.38
62	U	702	GDP	C6-N1	-2.45	1.34	1.38
62	U	702	GDP	C5-N7	-2.09	1.34	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	U	702	GDP	PA-O3A	2.05	1.61	1.59

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	U	702	GDP	C5-C4-N3	-6.17	118.57	128.39
62	U	702	GDP	C2-N3-C4	5.05	120.99	112.30
62	U	702	GDP	N9-C4-N3	4.60	135.14	125.95
62	U	702	GDP	C6-C5-N7	3.21	136.12	130.29
62	U	702	GDP	C4-C5-N7	-2.54	106.64	110.67
62	U	702	GDP	C3'-C2'-C1'	2.49	106.18	101.46
62	U	702	GDP	O6-C6-C5	-2.12	120.94	126.53

There are no chirality outliers.

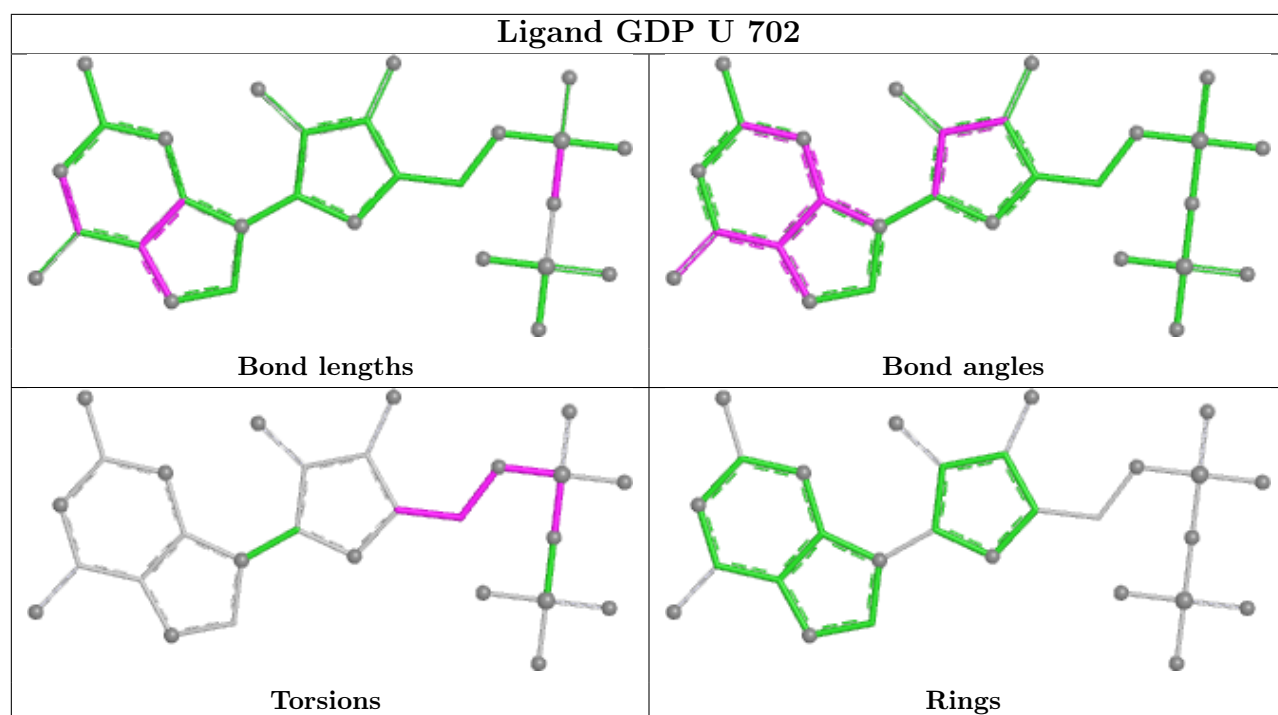
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	U	702	GDP	C5'-O5'-PA-O3A
62	U	702	GDP	C5'-O5'-PA-O2A
62	U	702	GDP	C3'-C4'-C5'-O5'
62	U	702	GDP	O4'-C4'-C5'-O5'
62	U	702	GDP	PB-O3A-PA-O5'
62	U	702	GDP	C5'-O5'-PA-O1A
62	U	702	GDP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

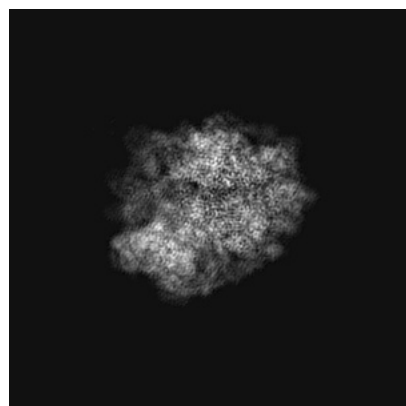
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3852. These allow visual inspection of the internal detail of the map and identification of artifacts.

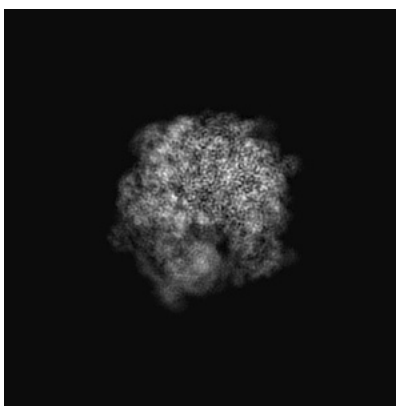
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

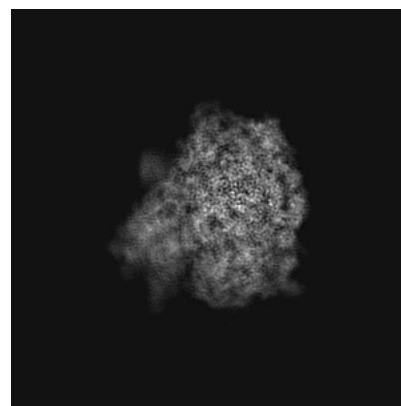
6.1.1 Primary map



X

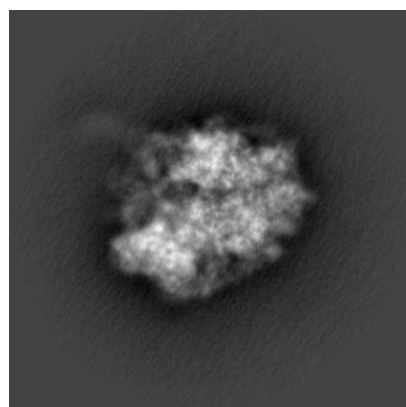


Y

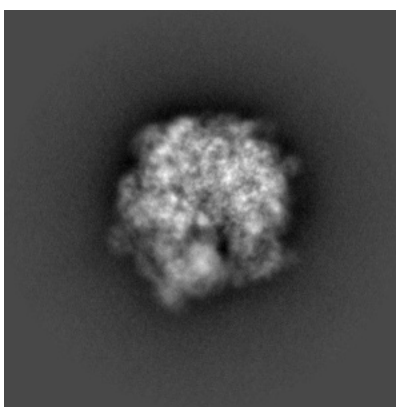


Z

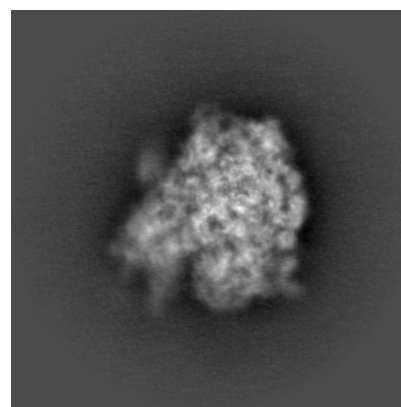
6.1.2 Raw map



X



Y

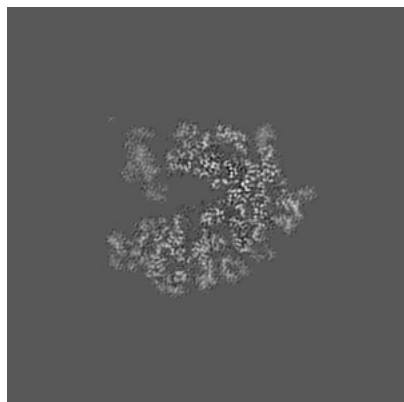


Z

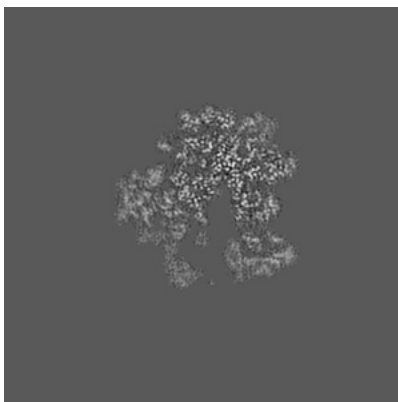
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

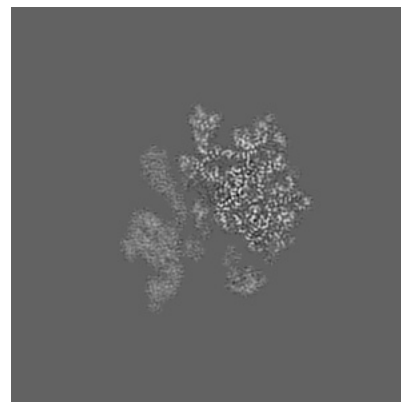
6.2.1 Primary map



X Index: 210

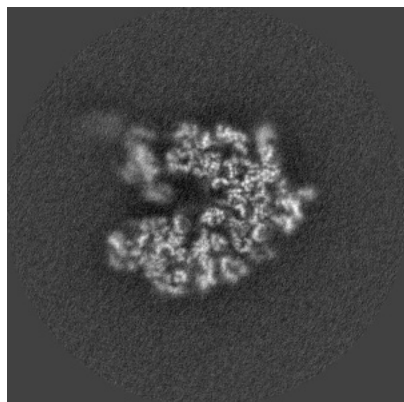


Y Index: 210

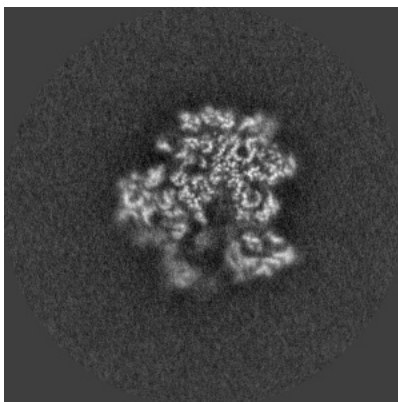


Z Index: 210

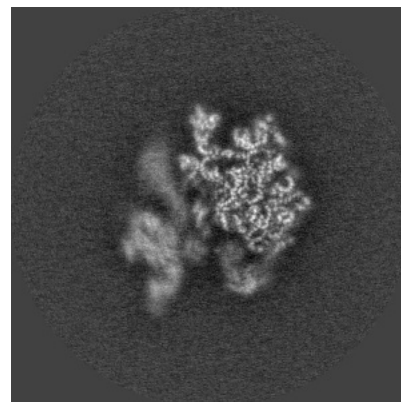
6.2.2 Raw map



X Index: 210



Y Index: 210

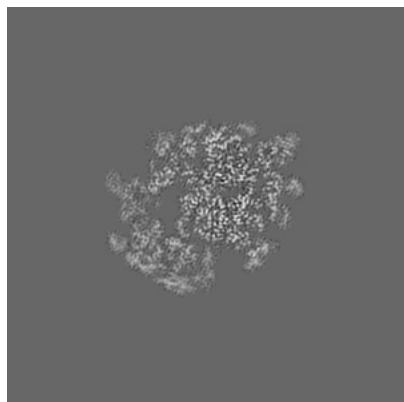


Z Index: 210

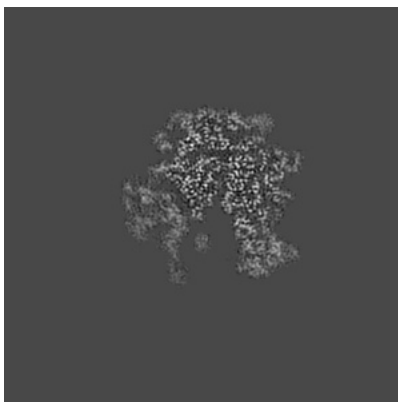
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

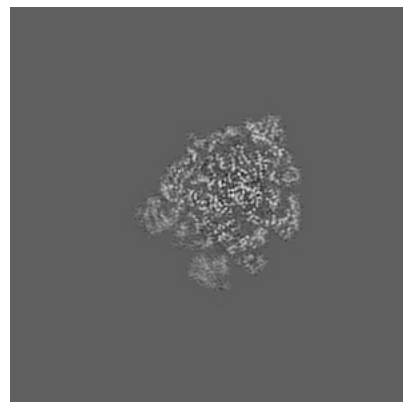
6.3.1 Primary map



X Index: 239

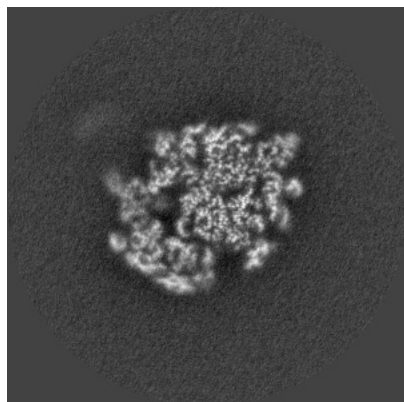


Y Index: 218

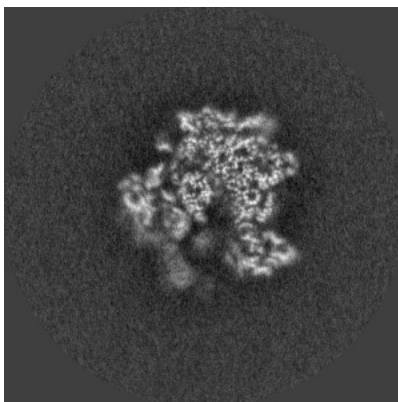


Z Index: 254

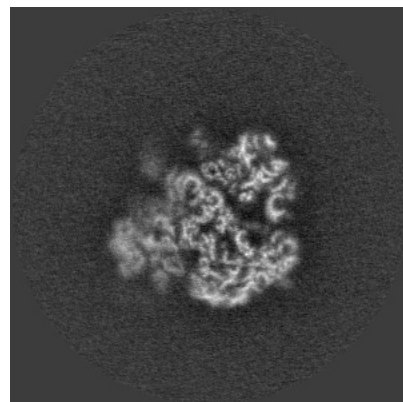
6.3.2 Raw map



X Index: 239



Y Index: 213

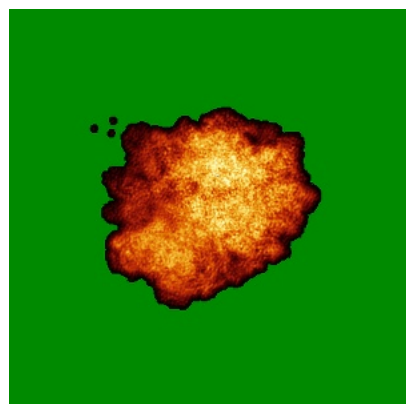


Z Index: 171

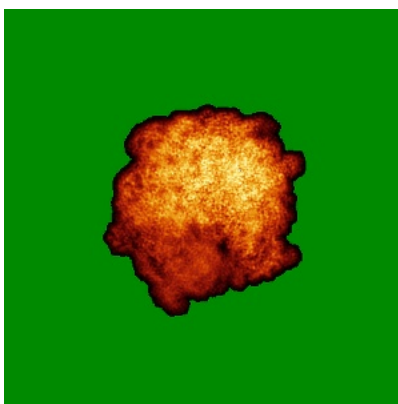
The images above show the largest variance slices of the map in three orthogonal directions.

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

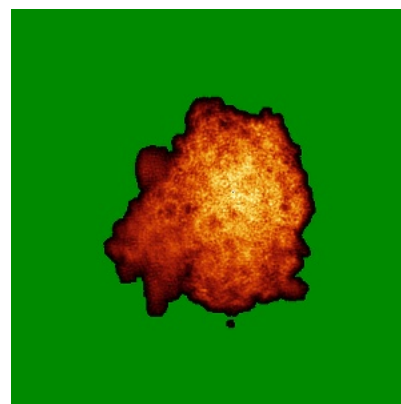
6.4.1 Primary map



X

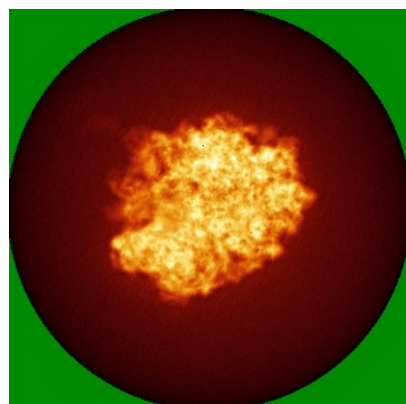


Y

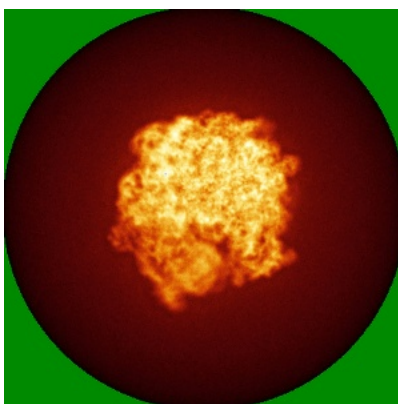


Z

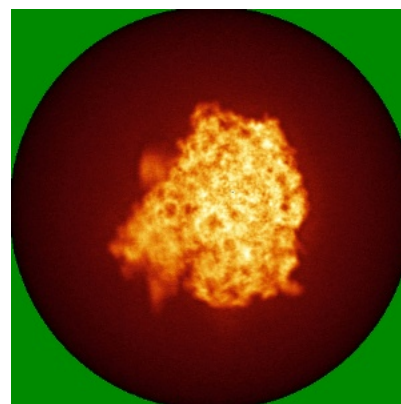
6.4.2 Raw map



X



Y

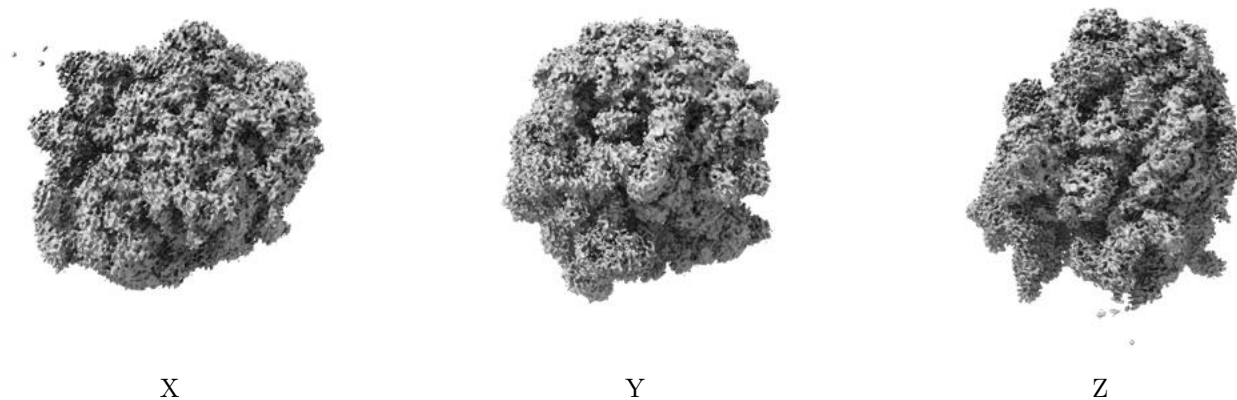


Z

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

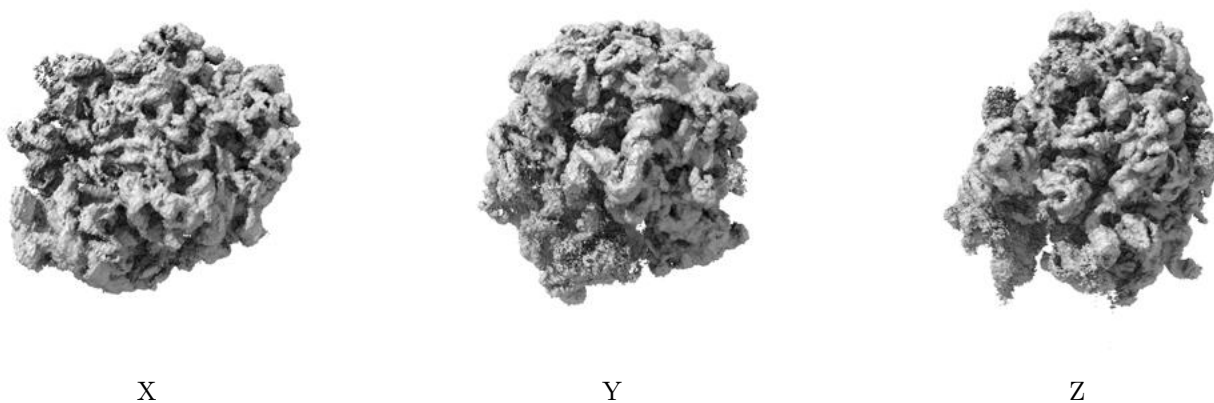
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

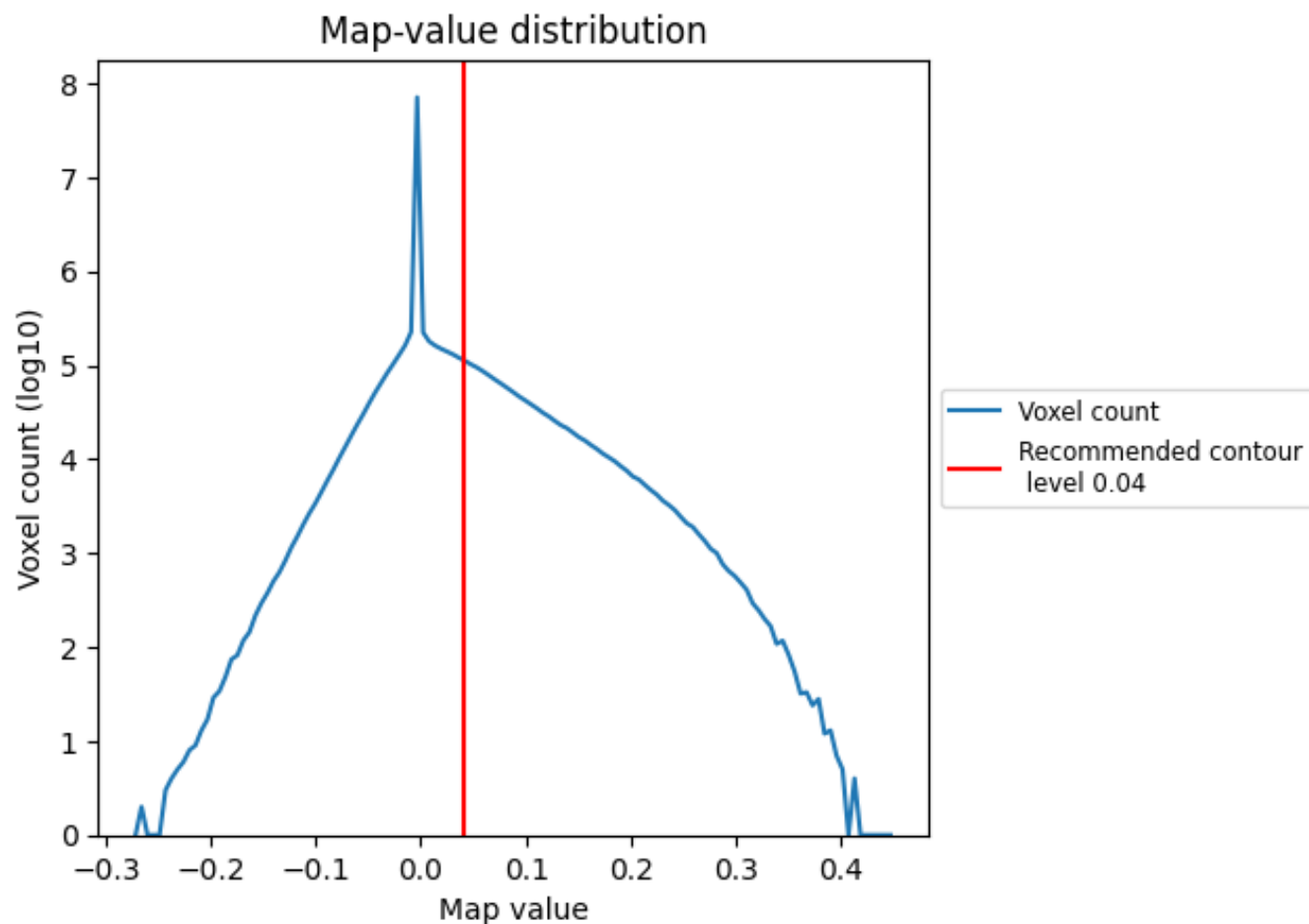
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

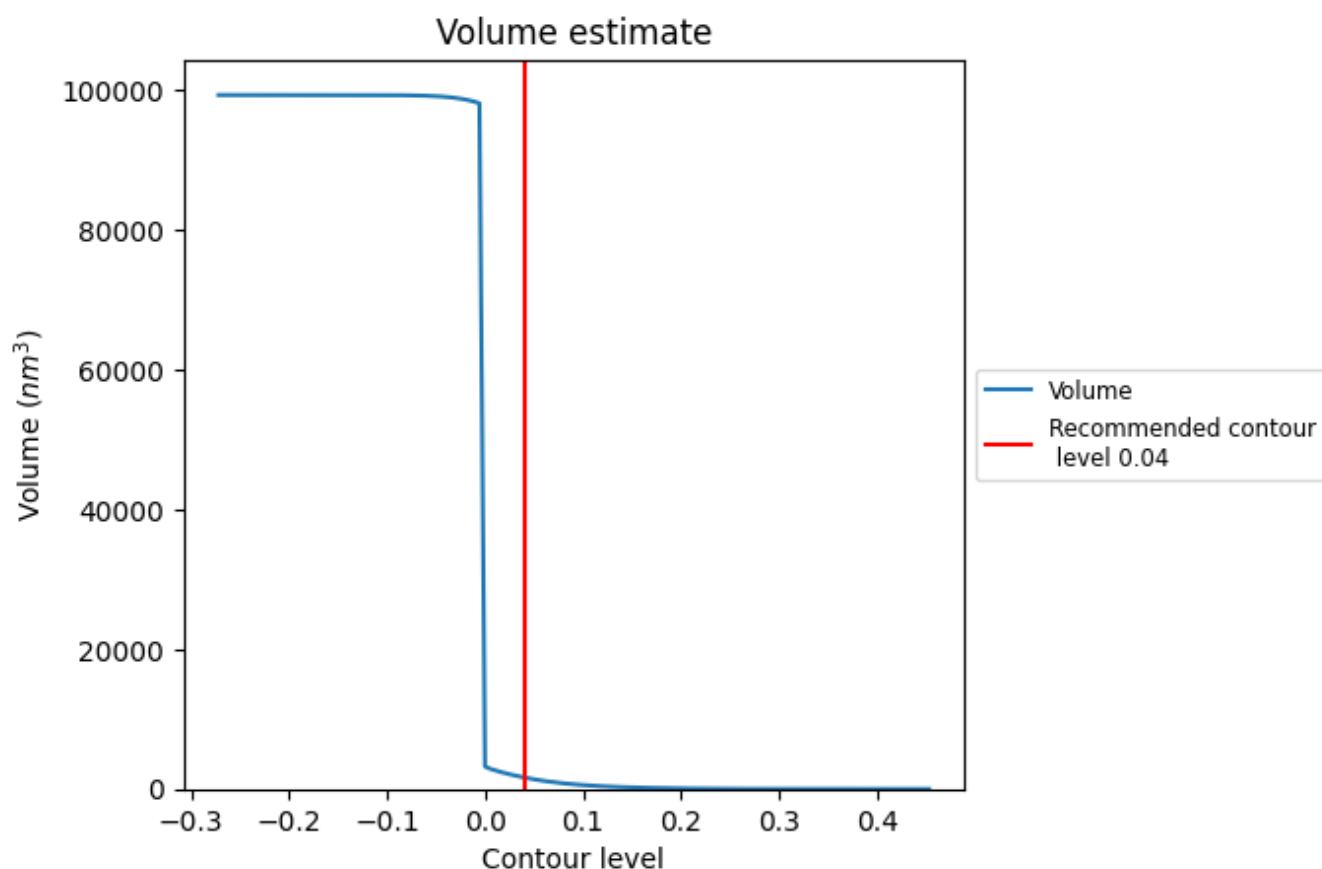
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

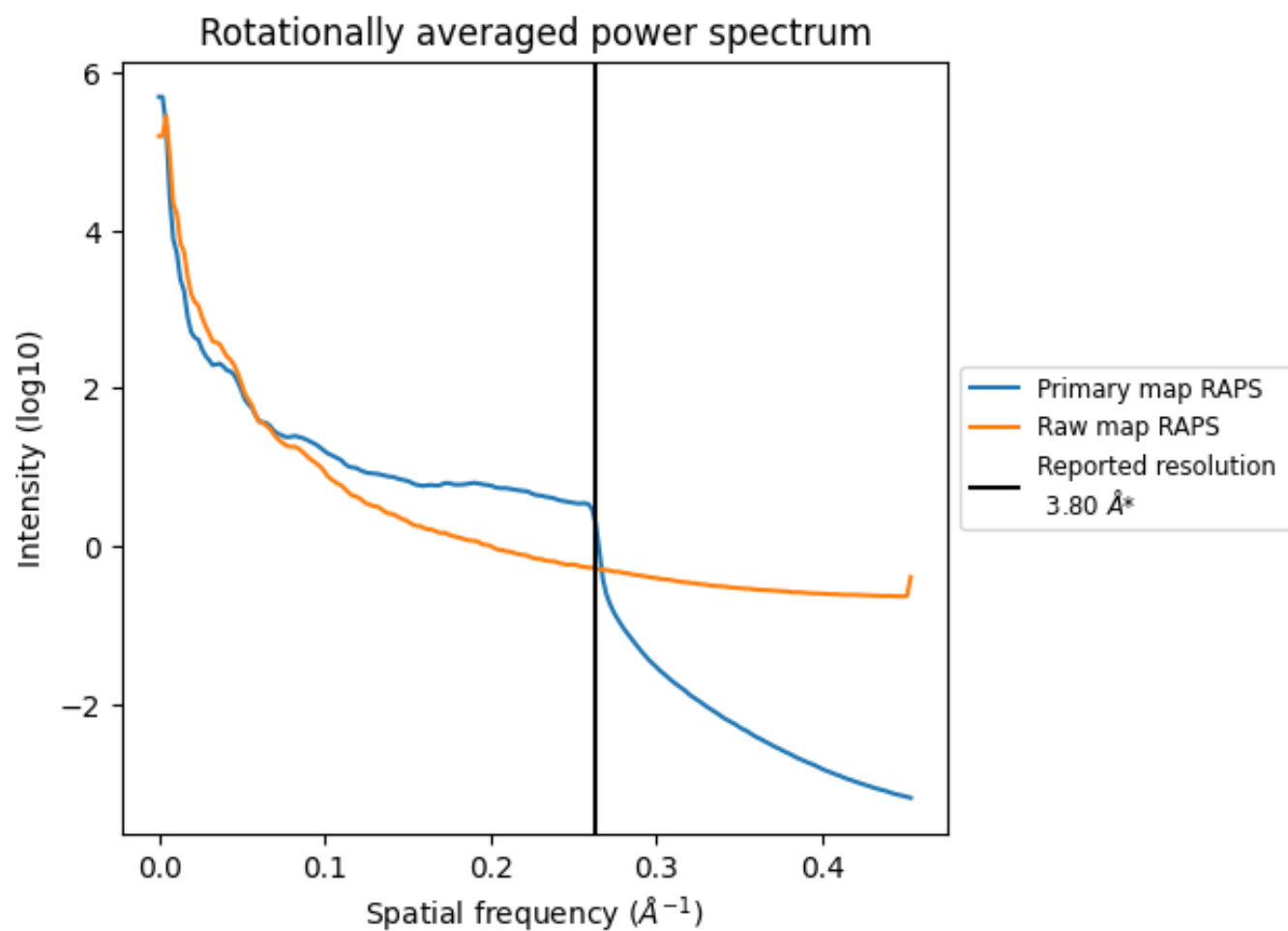
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1646 nm³; this corresponds to an approximate mass of 1487 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 ⓘ

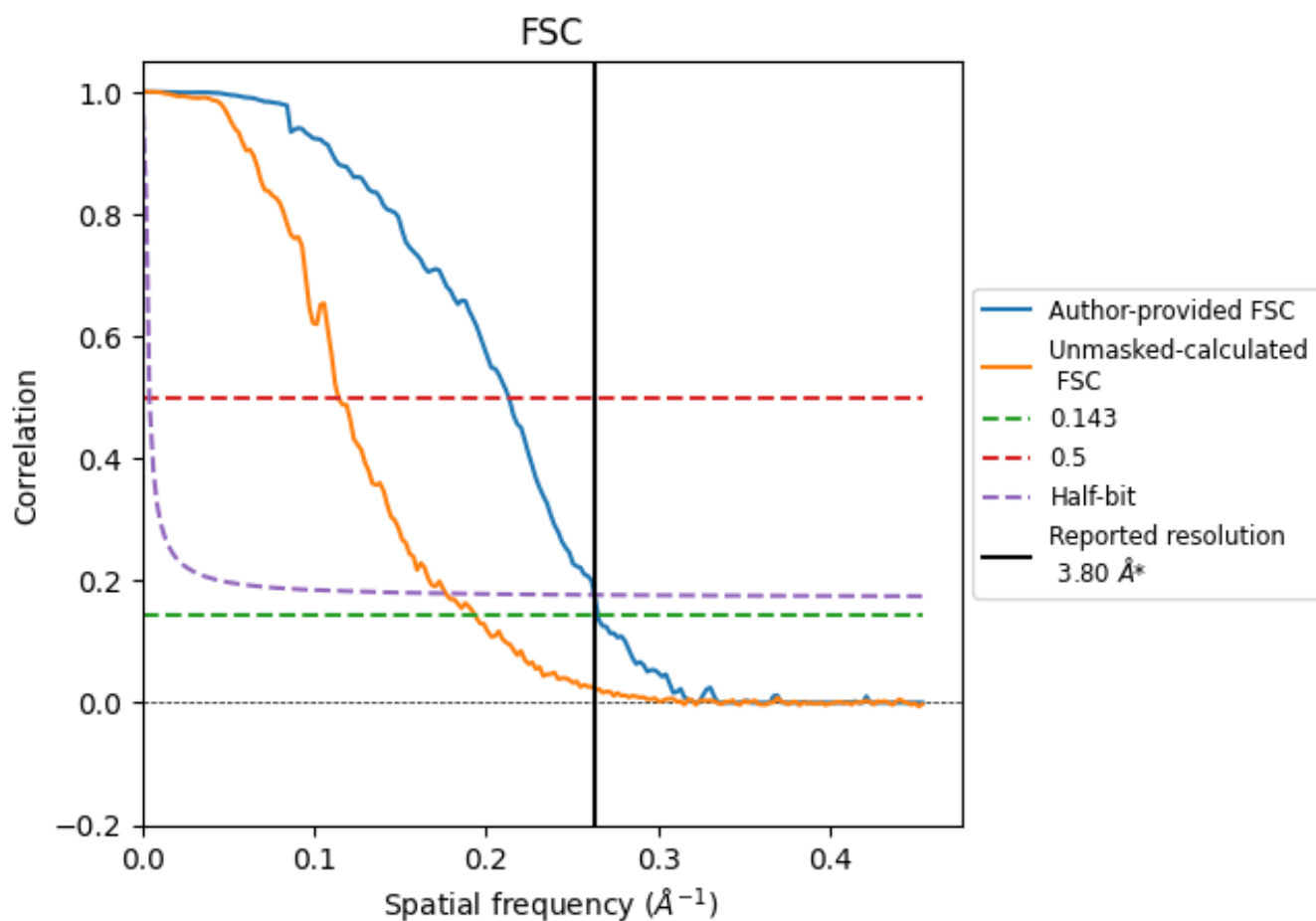


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

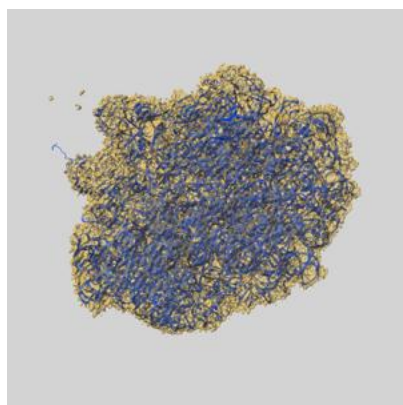
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.77	4.69	3.80
Unmasked-calculated*	5.17	8.76	5.67

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.17 differs from the reported value 3.8 by more than 10 %

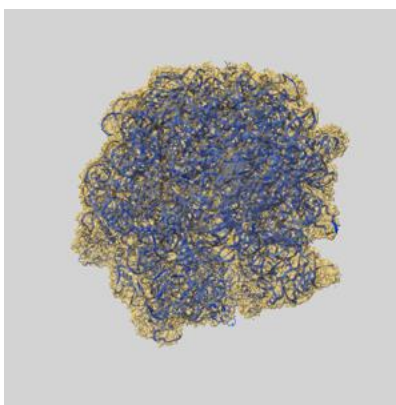
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3852 and PDB model 5OT7. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

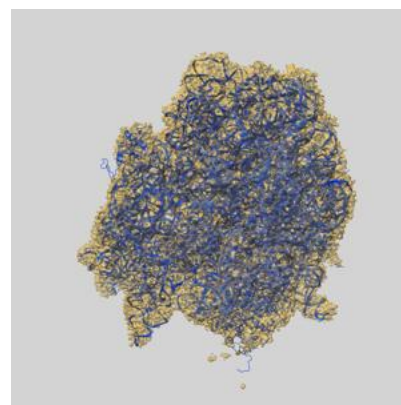
9.1 Map-model overlay [i](#)



X



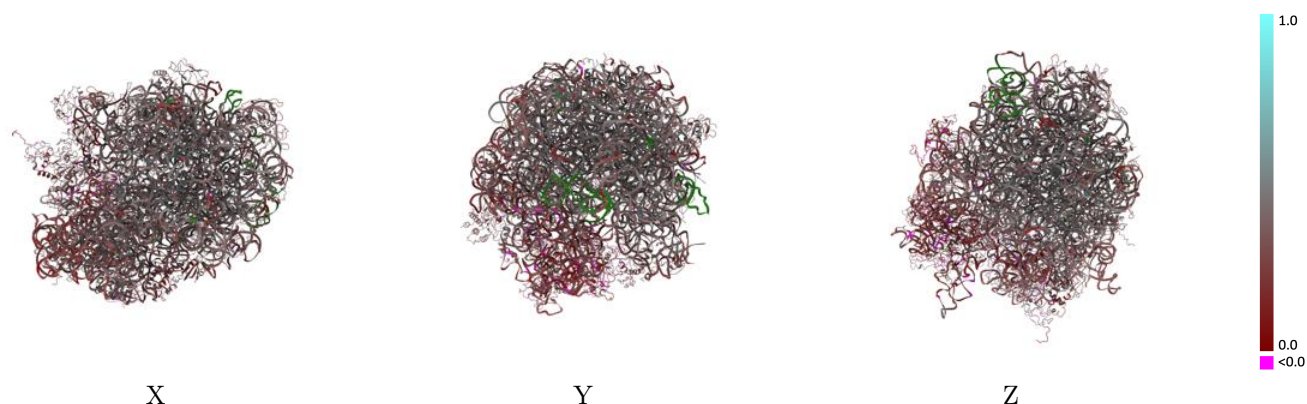
Y



Z

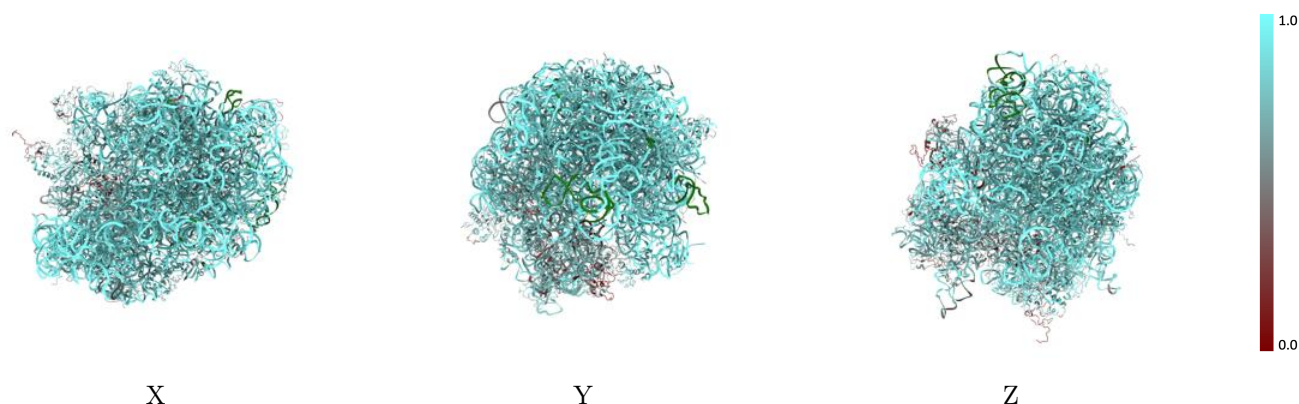
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



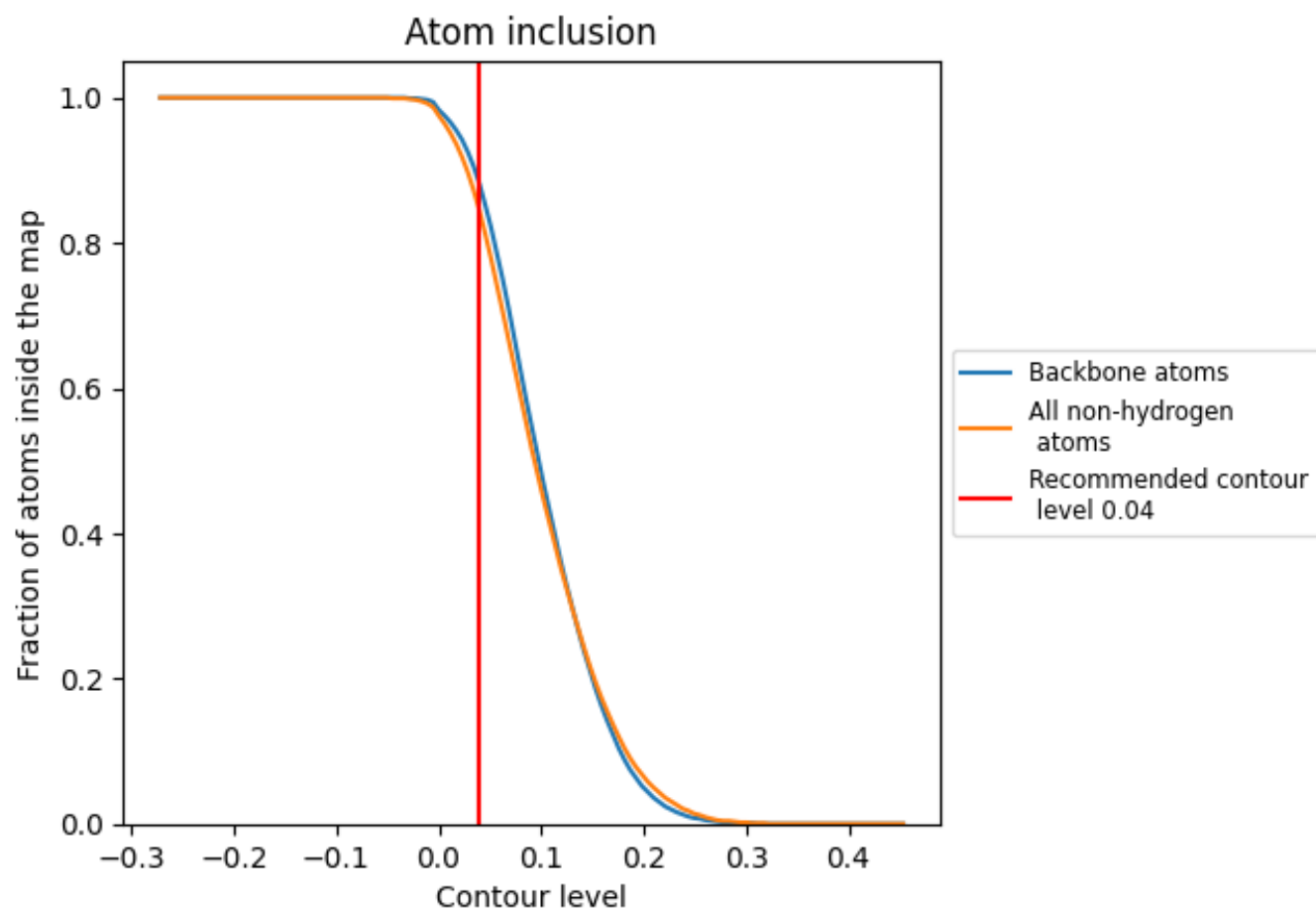
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8430	 0.3440
1	 0.8890	 0.3010
2	 0.5590	 0.2480
3	 0.6780	 0.2650
4	 0.9240	 0.3940
5	 0.9650	 0.3580
6	 0.7330	 0.3180
7	 0.4860	 0.2480
A	 0.6840	 0.2650
B	 0.6540	 0.2580
C	 0.8090	 0.3130
D	 0.8150	 0.3780
E	 0.7700	 0.2750
F	 0.5820	 0.1940
G	 0.8140	 0.3510
H	 0.7010	 0.1920
I	 0.6580	 0.2290
J	 0.6410	 0.2150
K	 0.7260	 0.3820
L	 0.5810	 0.1840
M	 0.5980	 0.2100
N	 0.7770	 0.2670
O	 0.8240	 0.3540
P	 0.7680	 0.3500
Q	 0.7220	 0.2550
R	 0.5870	 0.1950
S	 0.7810	 0.3210
T	 0.7760	 0.1910
U	 0.5980	 0.2490
V	 0.8320	 0.4170
W	 0.7910	 0.3990
X	 0.8270	 0.3490
Y	 0.8150	 0.4020
Z	 0.6210	 0.1960
a	 0.7970	 0.3880



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
b	 0.7400	 0.2870
c	 0.8360	 0.4320
d	 0.7700	 0.3950
e	 0.8110	 0.4110
f	 0.3720	 0.1640
g	 0.8040	 0.4150
h	 0.8260	 0.4170
i	 0.8170	 0.3790
j	 0.7360	 0.2460
k	 0.8160	 0.3440
l	 0.6640	 0.3220
m	 0.7230	 0.3070
n	 0.3790	 0.2920
o	 0.8370	 0.4000
p	 0.7610	 0.4150
q	 0.8120	 0.3700
r	 0.8120	 0.4220
s	 0.8320	 0.4080
t	 0.8430	 0.3330
u	 0.7780	 0.3570
v	 0.8580	 0.4180
w	 0.7910	 0.3700
x	 0.8280	 0.4310
y	 0.8470	 0.4000
z	 0.7930	 0.2990