



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 05:18 AM UTC

PDB ID : 6WDF / pdb_00006wdf
EMDB ID : EMD-21634
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure VI-A)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.30 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
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

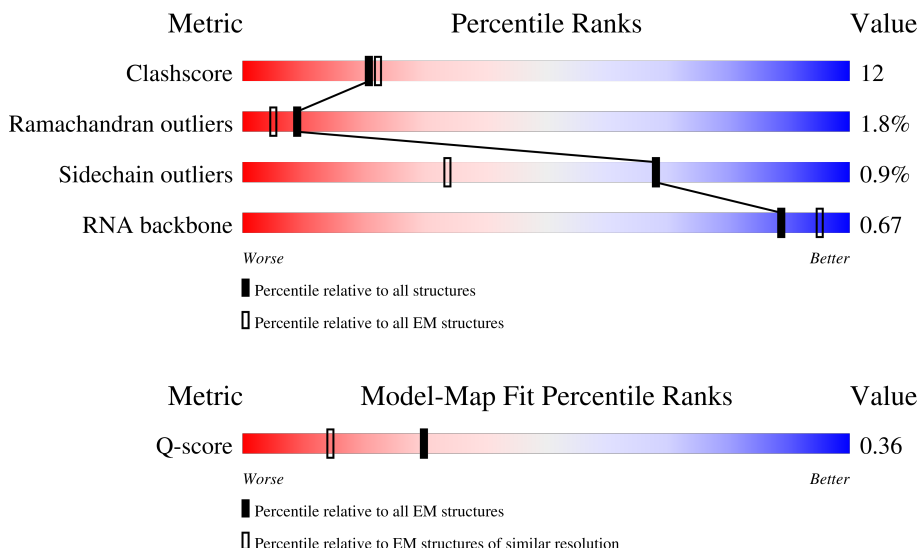
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



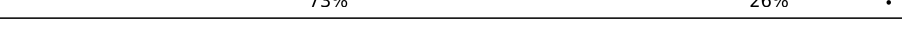
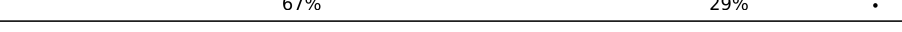
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	b	271	
2	c	209	
3	d	201	

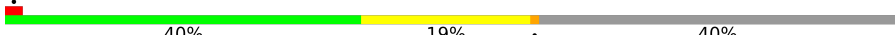
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	223	
52	3	1539	
53	1	2903	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	2	120	56%38%6%
55	5	77	32%47%19%
56	4	18	11%50%44%6%
57	7	76	39%51%9%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 148582 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	E	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 33 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 37 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	M	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 38 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 41 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 43 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 44 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 45 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 47 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 49 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 50 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 55 is a RNA chain called tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

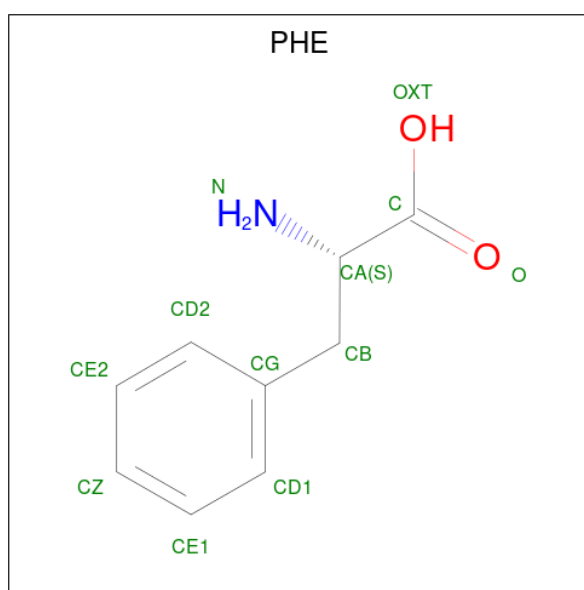
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 57 is a RNA chain called tRNA^PPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 58 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).



Mol	Chain	Residues	Atoms				AltConf
58	7	1	Total	C	N	O	0
			11	9	1	1	

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

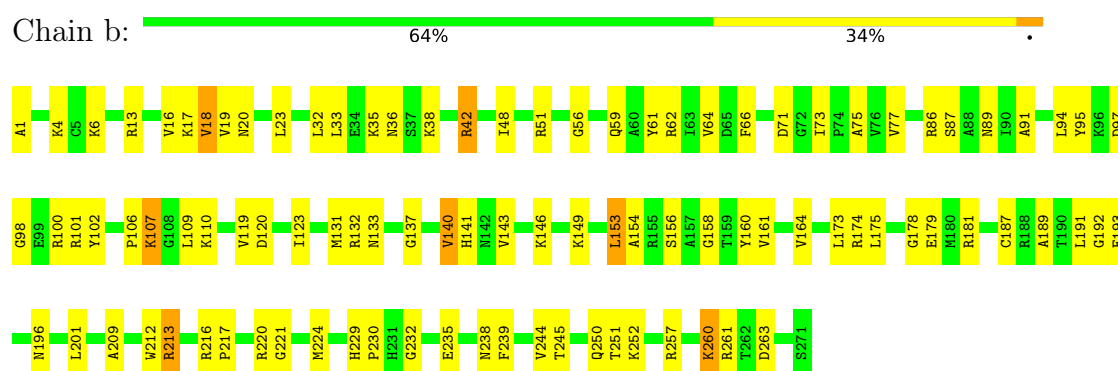


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	7	1	10	6	1	2	1	0

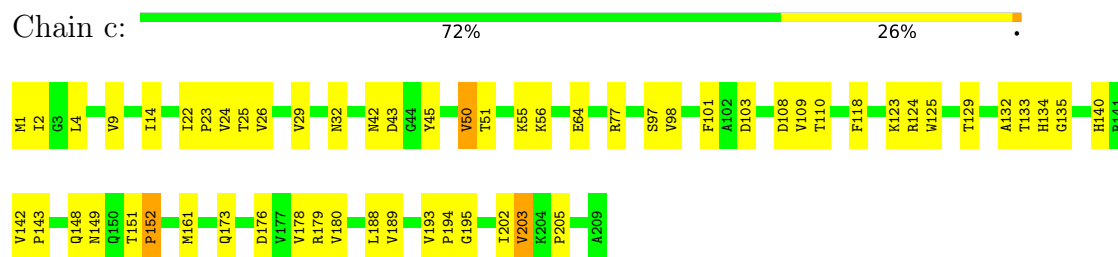
3 Residue-property plots

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

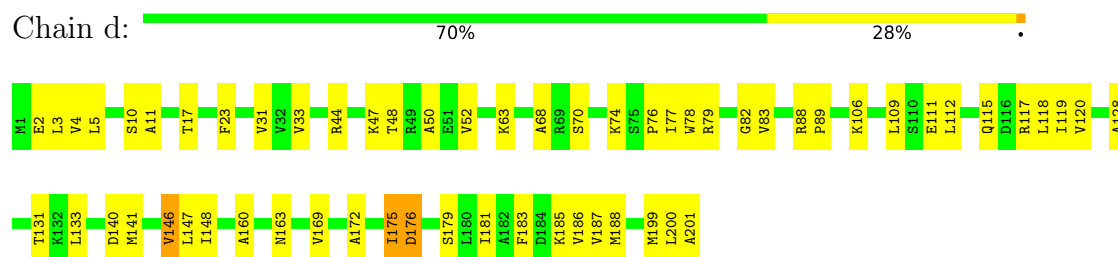
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3



• Molecule 3: 50S ribosomal protein L4



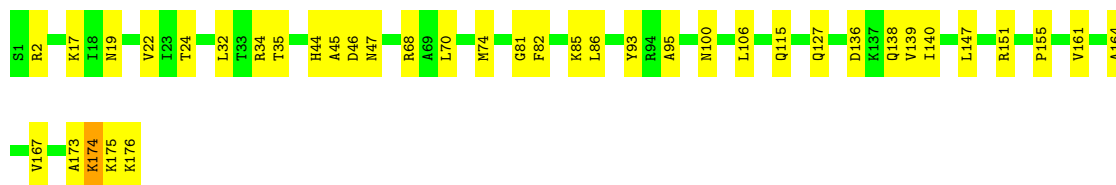
• Molecule 4: 50S ribosomal protein L5





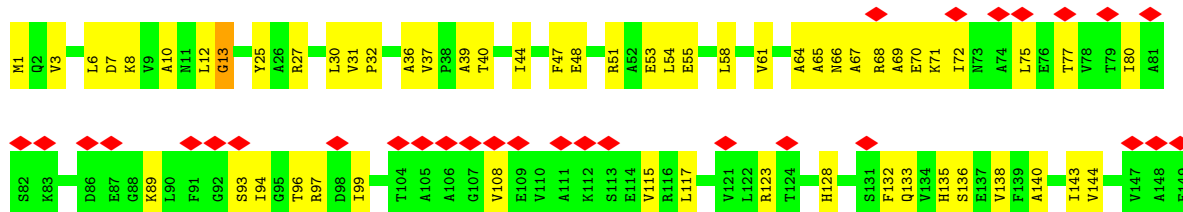
- Molecule 5: 50S ribosomal protein L6

Chain f: 78% 22% .



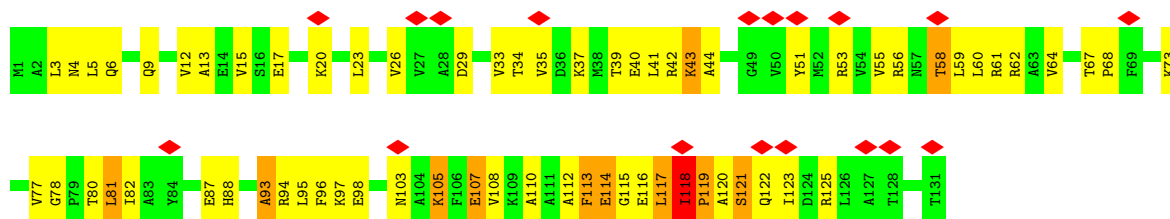
- Molecule 6: 50S ribosomal protein L9

Chain g: 20% 62% 38% .



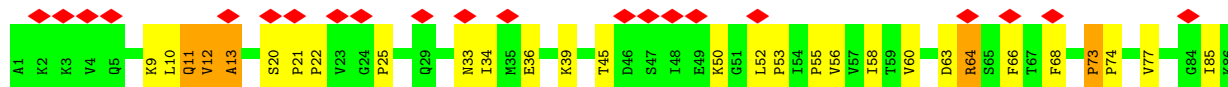
- Molecule 7: 50S ribosomal protein L10

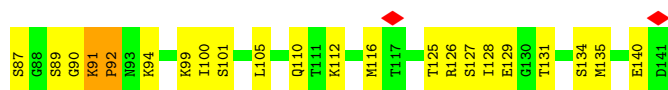
Chain h: 14% 49% 42% 8% .



- Molecule 8: 50S ribosomal protein L11

Chain i: 16% 64% 31% 5% .





- Molecule 9: 50S ribosomal protein L13

Chain j: 77% 22%



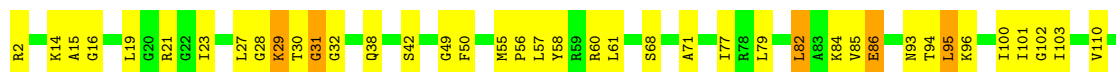
- Molecule 10: 50S ribosomal protein L14

Chain k: 67% 30%



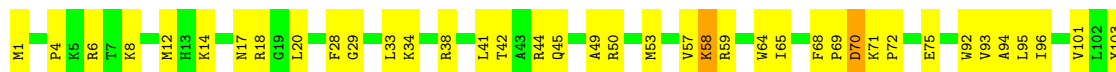
- Molecule 11: 50S ribosomal protein L15

Chain l: 64% 31% 5%



- Molecule 12: 50S ribosomal protein L16

Chain m: 67% 32%



- Molecule 13: 50S ribosomal protein L17

Chain n: 75% 23%



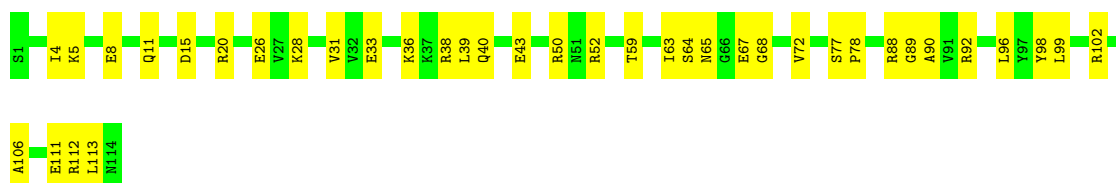
- Molecule 14: 50S ribosomal protein L18

Chain o:  72% 28%



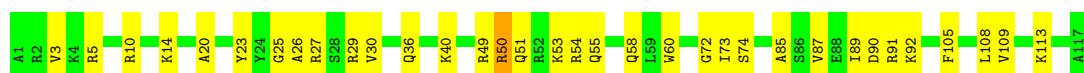
- Molecule 15: 50S ribosomal protein L19

Chain p:  67% 33%



- Molecule 16: 50S ribosomal protein L20

Chain q:  71% 28%



- Molecule 17: 50S ribosomal protein L21

Chain r:  70% 27%



- Molecule 18: 50S ribosomal protein L22

Chain s:  78% 19%



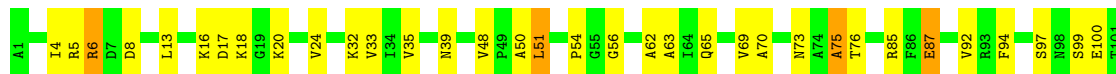
- Molecule 19: 50S ribosomal protein L23

Chain t:  73% 26%



- Molecule 20: 50S ribosomal protein L24

Chain u:  67% 29%



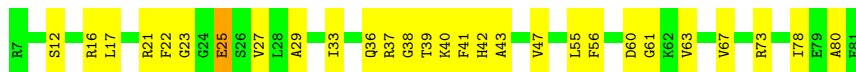
I102

- Molecule 21: 50S ribosomal protein L25

Chain v:  61% 37%


A94

- Molecule 22: 50S ribosomal protein L27

Chain w:  63% 36%


- Molecule 23: 50S ribosomal protein L28

Chain x:  79% 21%


- Molecule 24: 50S ribosomal protein L29

Chain y:  68% 32%


- Molecule 25: 50S ribosomal protein L30

Chain z:  66% 34%


- Molecule 26: 50S ribosomal protein L32

Chain B:  62% 38%

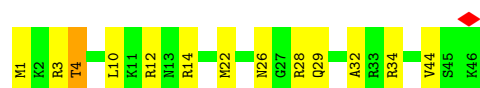

- Molecule 27: 50S ribosomal protein L33

Chain C:  70% 28% .



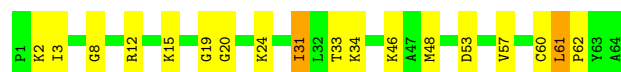
- Molecule 28: 50S ribosomal protein L34

Chain D:  72% 26% .



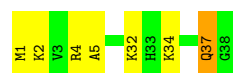
- Molecule 29: 50S ribosomal protein L35

Chain E:  72% 25% .



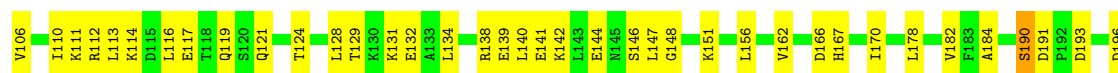
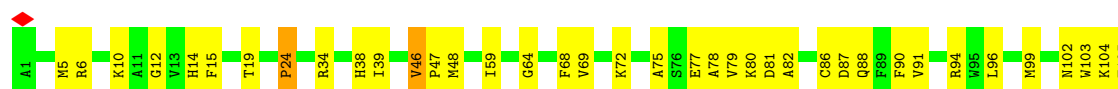
- Molecule 30: 50S ribosomal protein L36

Chain F:  82% 16% .



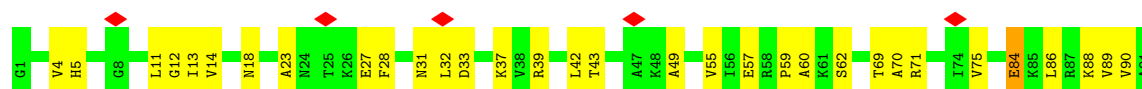
- Molecule 31: 30S ribosomal protein S2

Chain G:  62% 36% .



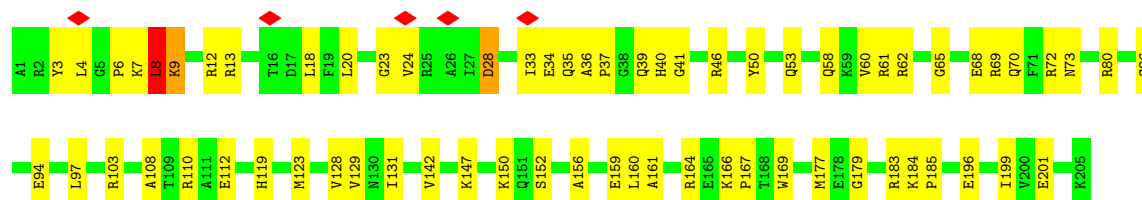
- Molecule 32: 30S ribosomal protein S3

Chain H:  73% 25% .

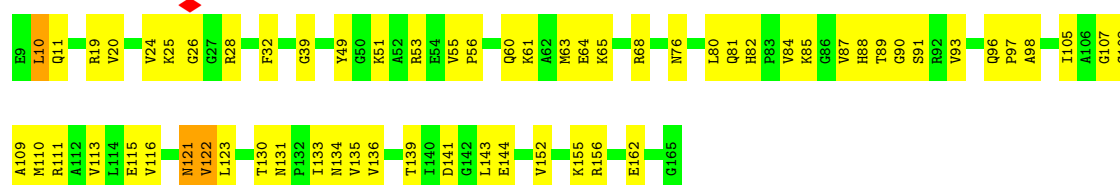




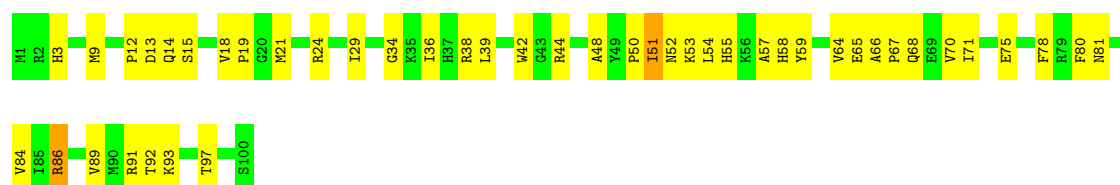
- Molecule 33: 30S ribosomal protein S4



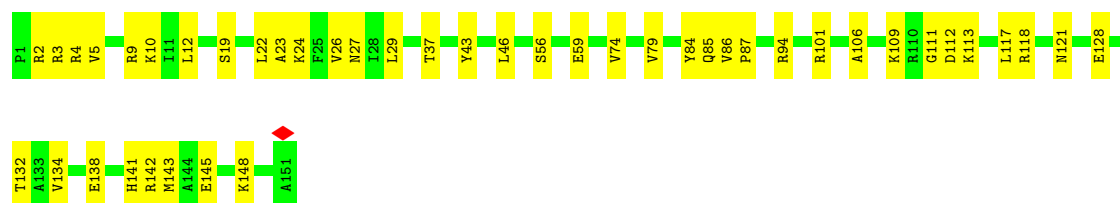
- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6

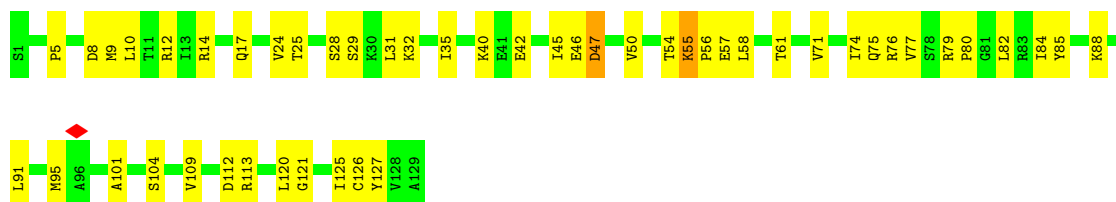


- Molecule 36: 30S ribosomal protein S7

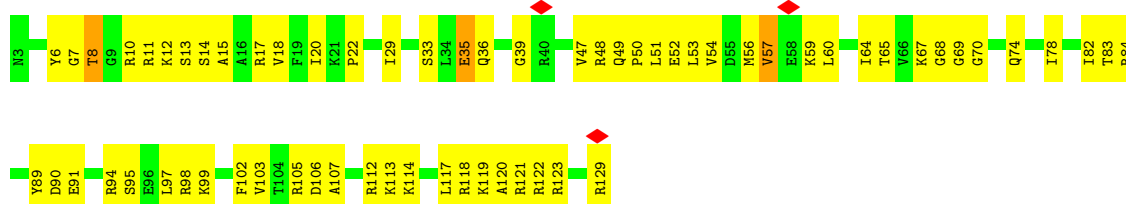


- Molecule 37: 30S ribosomal protein S8





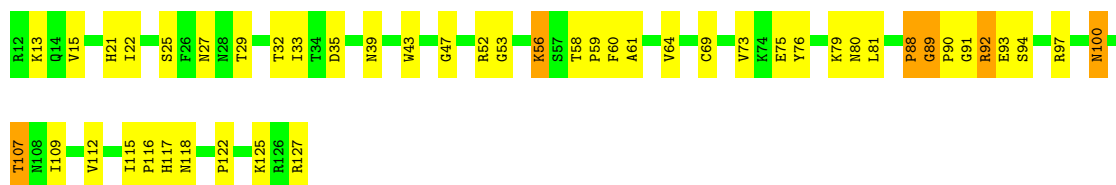
- Molecule 38: 30S ribosomal protein S9



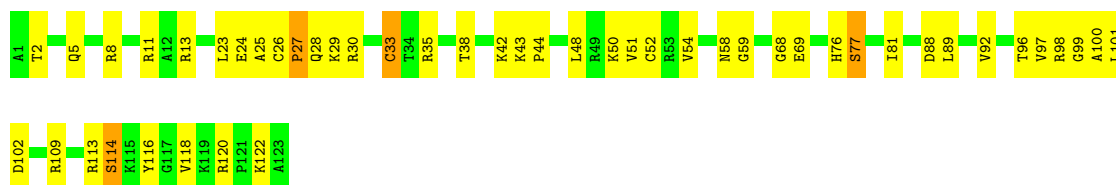
- Molecule 39: 30S ribosomal protein S10



- Molecule 40: 30S ribosomal protein S11

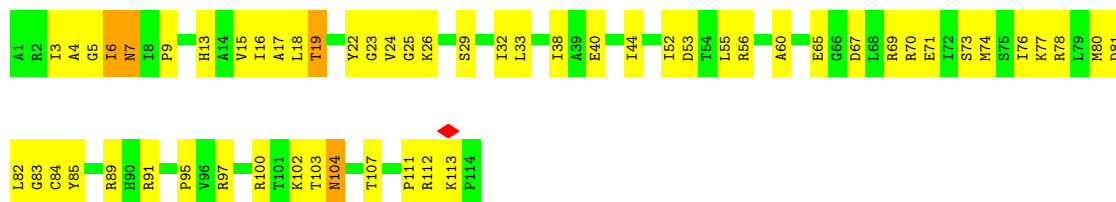


- Molecule 41: 30S ribosomal protein S12



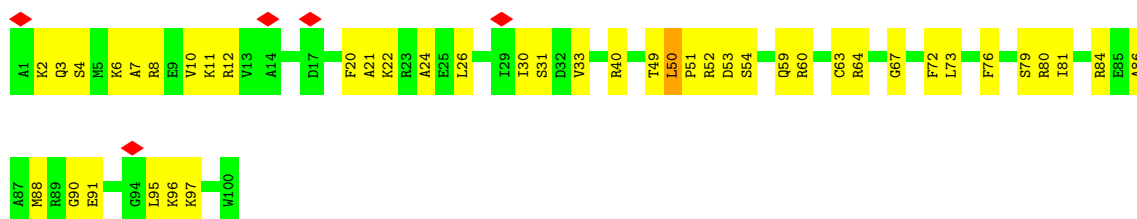
- Molecule 42: 30S ribosomal protein S13

Chain R:  51% 46%



- Molecule 43: 30S ribosomal protein S14

Chain S:  5% 57% 42%



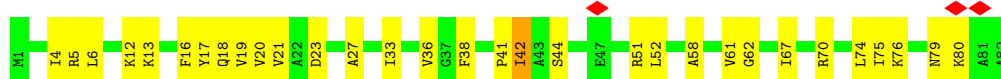
- Molecule 44: 30S ribosomal protein S15

Chain T:  77% 20%



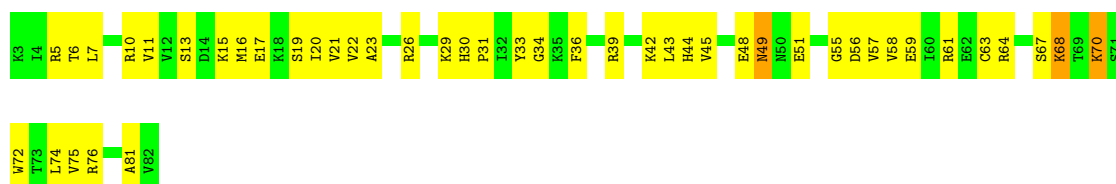
- Molecule 45: 30S ribosomal protein S16

Chain U:  62% 37%



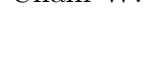
- Molecule 46: 30S ribosomal protein S17

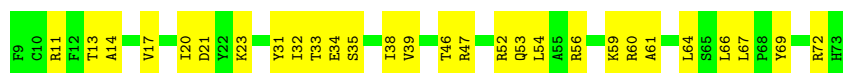
Chain V:  44% 52%



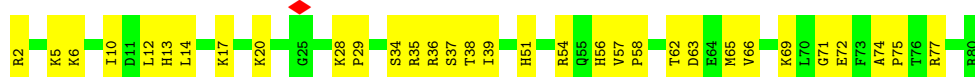
- Molecule 47: 30S ribosomal protein S18

Chain W:  57% 43%





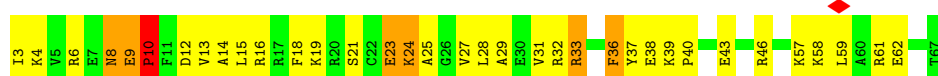
- Molecule 48: 30S ribosomal protein S19



- Molecule 49: 30S ribosomal protein S20



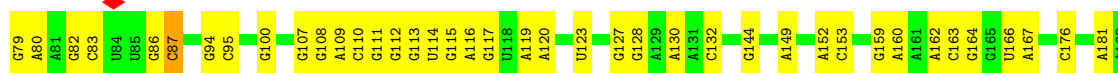
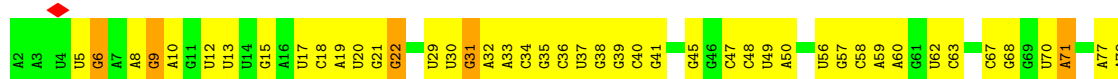
- Molecule 50: 30S ribosomal protein S21



- Molecule 51: 50S ribosomal protein L1



- Molecule 52: 16S ribosomal RNA

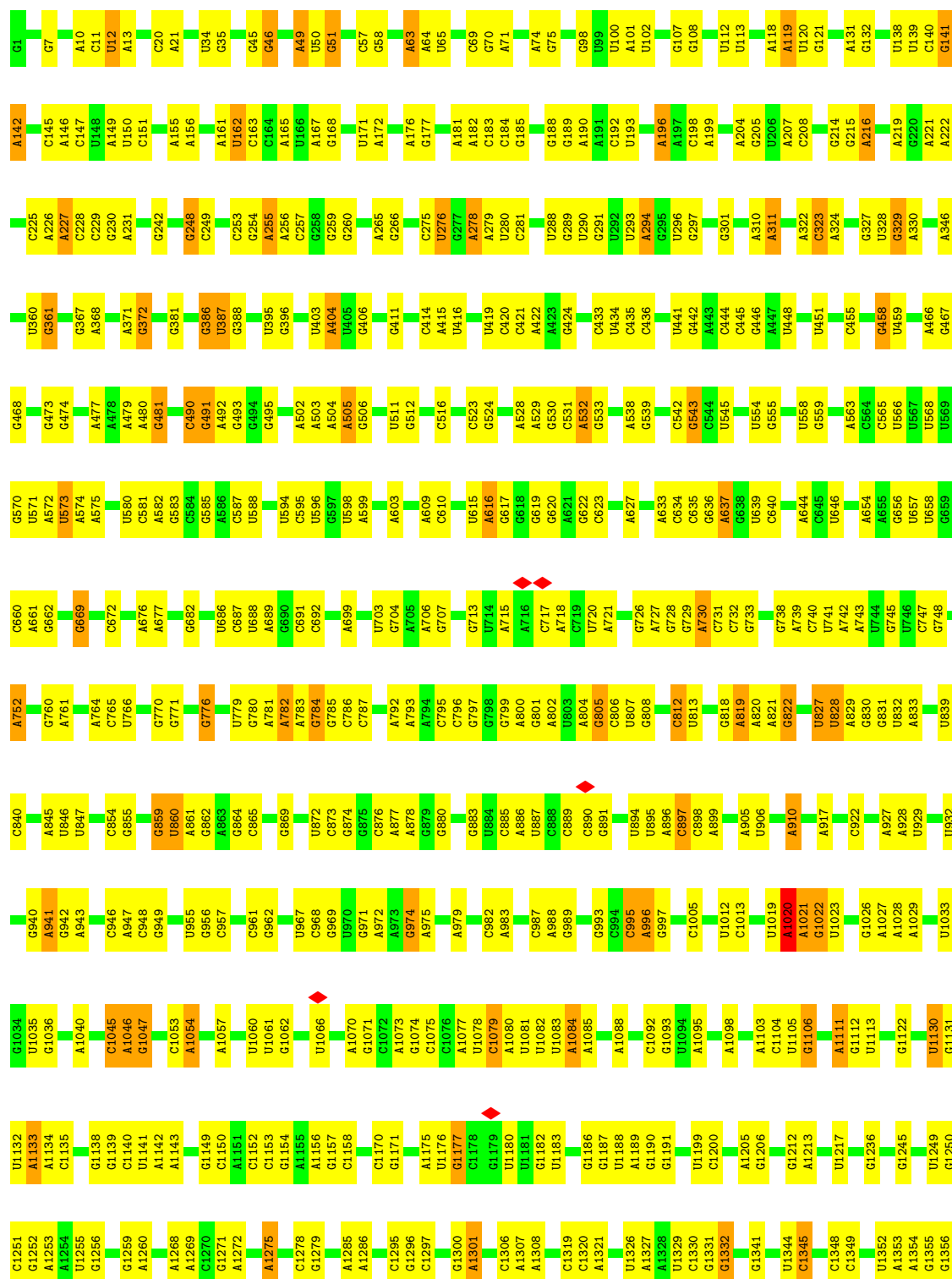


U1450	U1451	G1452	G1453	A1456	G1457	G1458	G1459	C1460	G1461	U1464	A1465	C1466	U1467	U1468	U1469	U1470	U1471	U1472	G1473	C1484	U1485	G1486	G1487	G1488	G1489	A1492	A1493	G1494	U1495	C1496	G1497	U1498	A1499	A1500	C1501	A1502	A1503	G1504	G1505	U1506	A1507	U1512	A1513	G1514	G1515	G1516	G1517	A1518	C1519	C1520	C1521	U1522	G1523	C1524	G1525	G1526
G1373	A1374	A1375	U1376	A1377	C1378	G1379	U1380	U1381	G1385	G1386	G1387	C1388	U1391	G1392	U1393	A1394	C1395	A1396	C1397	G1400	G1401	C1402	C1403	C1404	G1405	C1409	A1410	G1411	C1412	A1413	U1414	G1415	G1416	U1419	G1422	G1423	U1424	U1425	G1432	A1433	G1434	G1435	U1436	A1437	G1438	A1441	A1446	A1447	C1448	C1449						
C1303	G1304	G1305	A1306	U1307	U1308	G1309	G1310	A1311	G1312	U1313	C1314	U1315	G1316	A1317	A1318	A1319	C1320	U1321	C1322	U1326	C1327	C1328	A1329	U1330	G1331	A1332	A1333	G1338	A1339	C1342	G1343	C1344	U1345	A1346	G1347	U1348	A1349	C1352	G1353	U1354	G1355	G1356	A1357	A1362	A1363	U1364	C1365	G1366	C1367	A1368	C1369	U1370	G1371	U1372		
G1220	G1221	G1222	C1223	U1224	A1225	C1226	A1227	C1228	A1229	U1230	G1233	C1234	U1235	A1236	C1237	C1238	A1239	U1240	G1241	G1242	C1245	A1246	A1250	A1251	A1252	G1253	A1254	G1255	A1256	A1257	G1258	C1259	G1260	A1261	G1270	A1271	G1272	C1273	A1274	A1275	G1276	C1277	G1278	G1279	A1280	C1281	C1282	U1286	A1287	A1289	G1300	U1301	C1302			
G1138	G1139	C1140	G1144	A1145	A1146	A1147	U1148	A1149	A1150	A1157	C1158	U1159	A1160	C1161	A1162	A1163	A1167	U1168	A1169	A1170	A1171	A1176	G1177	G1178	G1182	U1183	G1184	G1185	G1186	G1187	G1190	A1191	C1192	G1193	U1194	A1196	A1197	U1198	U1199	A1201	U1202	C1203	A1204	U1205	A1213	A1216	C1217	U1218	A1219							
U1030	C1031	G1032	G1033	U1034	G1047	U1048	U1049	G1053	C1054	U1055	C1059	U1060	G1061	C1066	U1067	U1070	C1071	G1072	U1073	G1074	U1075	G1079	A1080	G1088	A1092	A1093	G1094	U1095	C1096	C1097	C1098	C1099	C1100	A1101	A1111	C1112	C1119	U1123	G1124	U1125	U1126	G1127	C1128	C1129	A1130	G1131	C1136	C1137								
G939	U843	G844	G845	C846	C856	G857	U858	G859	A865	C866	G867	C868	G869	U870	U871	C876	G877	G878	C882	C883	U884	G885	C889	A894	G895	A897	G898	A899	C900	A901	C902	G903	A908	A909	C912	A913	G917	A918	A919	U920	U921	G922	A923	G926	G927	G928	G929	A1016	U1023	G1024	U1025	C1028	U1029			
U1030	C1031	G1032	G1033	U1034	G1047	U1048	U1049	G1053	C1054	U1055	C1059	U1060	G1061	C1066	U1067	U1070	C1071	G1072	U1073	G1074	U1075	G1079	A1080	G1088	A1092	A1093	G1094	U1095	C1096	C1097	C1098	C1099	C1100	A1101	A1111	C1112	C1119	U1123	G1124	U1125	U1126	G1127	C1128	C1129	A1130	G1131	C1136	C1137								
G1138	G1139	C1140	G1144	A1145	A1146	A1147	U1148	A1149	A1150	A1157	C1158	U1159	A1160	C1161	A1162	A1163	A1167	U1168	A1169	A1170	A1171	A1176	G1177	G1178	G1182	U1183	G1184	G1185	G1186	G1187	G1190	A1191	C1192	G1193	U1194	A1196	A1197	U1198	U1199	A1201	U1202	C1203	A1204	U1205	A1213	A1216	C1217	U1218	A1219							
G1220	G1221	G1222	C1223	U1224	A1225	C1226	A1227	C1228	A1229	U1230	G1233	C1234	U1235	A1236	C1237	C1238	A1239	U1240	G1241	G1242	C1245	A1246	A1250	A1251	A1252	G1253	A1254	G1255	A1256	A1257	G1258	C1259	G1260	A1261	G1270	A1271	G1272	C1273	A1274	A1275	G1276	C1277	G1278	G1279	A1280	C1281	C1282	U1286	A1287	A1289	G1300	U1301	C1302			
C1303	G1304	G1305	A1306	U1307	U1308	G1309	G1310	A1311	G1312	U1313	C1314	U1315	G1316	A1317	A1318	A1319	C1320	U1321	C1322	U1326	C1327	C1328	A1329	U1330	G1331	A1332	A1333	G1338	A1339	C1342	G1343	C1344	U1345	A1346	G1347	U1348	A1349	C1352	G1353	U1354	G1355	G1356	A1357	A1362	A1363	U1364	C1365	G1366	C1367	A1368	C1369	U1370	G1371	U1372		
G1373	A1374	A1375	U1376	A1377	C1378	G1379	U1380	U1381	G1385	G1386	G1387	C1388	U1391	G1392	U1393	A1394	C1395	A1396	C1397	G1400	G1401	C1402	C1403	C1404	G1405	C1409	A1410	G1411	C1412	A1413	U1414	G1415	G1416	U1419	G1422	G1423	U1424	U1425	G1432	A1433	G1434	G1435	U1436	A1437	G1438	A1441	A1446	A1447	C1448	C1449						
U1450	U1451	G1452	G1453	A1456	G1457	G1458	G1459	C1460	G1461	U1464	A1465	C1466	U1467	U1468	U1469	U1470	U1471	U1472	G1473	C1484	U1485	G1486	G1487	G1488	G1489	A1492	A1493	G1494	U1495	C1496	G1497	U1498	A1499	A1500	C1501	A1502	A1503	G1504	G1505	U1506	A1507	U1512	A1513	G1514	G1515	G1516	G1517	A1518	C1519	C1520	C1521	U1522	G1523	C1524	G1525	G1526

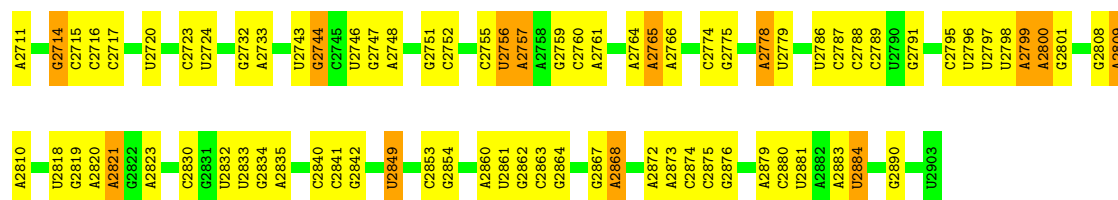


• Molecule 53: 23S ribosomal RNA

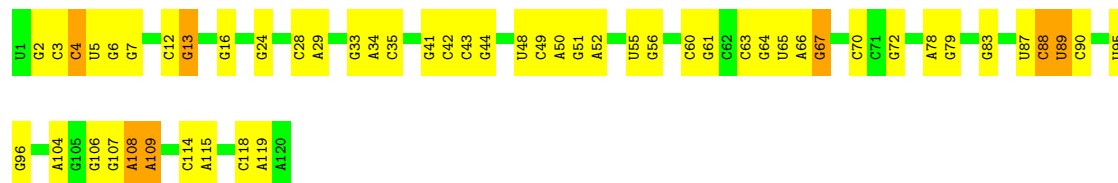
Chain 1: 58% 37% 5%



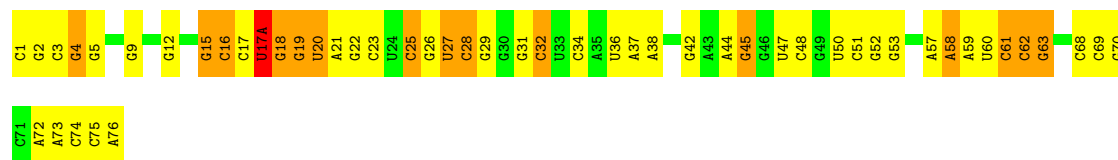




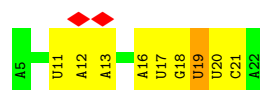
• Molecule 54: 5S ribosomal RNA



• Molecule 55: tRNA^{fMet}



• Molecule 56: mRNA



• Molecule 57: tRNA^{Phe}



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18925	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	23.785	Depositor
Minimum map value	-12.967	Depositor
Average map value	0.117	Depositor
Map value standard deviation	0.971	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FME

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	b	0.29	0/2122	0.96	8/2852 (0.3%)
2	c	0.30	0/1586	0.87	4/2134 (0.2%)
3	d	0.28	0/1571	0.88	5/2113 (0.2%)
4	e	0.31	0/1435	0.92	7/1926 (0.4%)
5	f	0.30	0/1343	0.87	3/1816 (0.2%)
6	g	0.32	0/1122	1.01	10/1515 (0.7%)
7	h	0.35	0/1002	1.11	12/1350 (0.9%)
8	i	0.38	0/1046	0.98	6/1410 (0.4%)
9	j	0.29	0/1152	0.89	2/1551 (0.1%)
10	k	0.29	0/948	0.94	2/1268 (0.2%)
11	l	0.30	0/1054	0.98	6/1403 (0.4%)
12	m	0.29	0/1093	0.88	2/1460 (0.1%)
13	n	0.29	0/974	0.90	3/1301 (0.2%)
14	o	0.29	0/902	0.90	1/1209 (0.1%)
15	p	0.29	0/929	0.82	0/1242
16	q	0.28	0/960	0.95	4/1278 (0.3%)
17	r	0.29	0/829	0.90	2/1107 (0.2%)
18	s	0.28	0/864	0.86	2/1156 (0.2%)
19	t	0.28	0/745	0.81	0/994
20	u	0.30	0/788	0.94	3/1051 (0.3%)
21	v	0.29	0/766	0.99	5/1025 (0.5%)
22	w	0.28	0/582	0.81	0/769
23	x	0.28	0/635	0.93	1/848 (0.1%)
24	y	0.27	0/510	0.92	2/677 (0.3%)
25	z	0.28	0/453	0.88	2/605 (0.3%)
26	B	0.30	0/450	0.84	0/599
27	C	0.32	0/417	0.84	3/554 (0.5%)
28	D	0.32	0/380	0.86	1/498 (0.2%)
29	E	0.28	0/513	0.86	2/676 (0.3%)
30	F	0.30	0/303	0.87	0/397
31	G	0.30	0/1788	0.92	6/2408 (0.2%)
32	H	0.33	0/1652	0.93	6/2225 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.32	0/1665	0.96	9/2227 (0.4%)
34	J	0.33	0/1170	0.90	1/1573 (0.1%)
35	K	0.31	0/836	0.96	4/1128 (0.4%)
36	L	0.31	0/1196	0.93	4/1602 (0.2%)
37	M	0.31	0/989	0.96	2/1326 (0.2%)
38	N	0.33	0/1034	0.95	3/1375 (0.2%)
39	O	0.34	0/797	0.94	6/1077 (0.6%)
40	P	0.33	0/886	0.97	8/1195 (0.7%)
41	Q	0.33	0/969	0.97	3/1300 (0.2%)
42	R	0.32	0/893	0.94	4/1193 (0.3%)
43	S	0.32	0/817	0.94	5/1088 (0.5%)
44	T	0.29	0/722	0.97	3/964 (0.3%)
45	U	0.32	0/659	0.95	2/884 (0.2%)
46	V	0.31	0/658	0.89	1/881 (0.1%)
47	W	0.31	0/545	0.81	1/731 (0.1%)
48	X	0.34	0/653	0.86	0/877
49	Y	0.29	0/671	0.92	1/888 (0.1%)
50	Z	0.34	0/551	1.08	3/728 (0.4%)
51	a	0.32	0/1034	0.86	3/1387 (0.2%)
52	3	0.42	0/36963	0.47	2/57662 (0.0%)
53	1	0.40	0/69796	0.47	4/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.65	0/1832	0.57	1/2855 (0.0%)
56	4	0.49	0/436	0.48	0/679
57	7	0.64	0/1809	0.59	0/2819
All	All	0.39	0/161367	0.63	180/241223 (0.1%)

There are no bond length outliers.

All (180) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	Z	59	LEU	N-CA-C	-10.43	99.42	112.88
44	T	49	HIS	N-CA-C	9.38	121.11	111.07
1	b	87	SER	N-CA-C	-8.21	103.78	113.88
1	b	213	ARG	N-CA-C	-8.08	101.54	111.40
43	S	49	THR	N-CA-C	-7.91	102.65	111.82
37	M	55	LYS	CA-C-N	7.49	129.20	119.84
37	M	55	LYS	C-N-CA	7.49	129.20	119.84
11	l	114	GLY	N-CA-C	7.47	119.66	112.04
33	I	166	LYS	CA-C-N	7.44	127.49	119.90
33	I	166	LYS	C-N-CA	7.44	127.49	119.90
4	e	137	PHE	CA-C-N	7.36	129.03	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	e	137	PHE	C-N-CA	7.36	129.03	119.84
16	q	72	GLY	N-CA-C	7.36	121.45	113.58
41	Q	25	ALA	N-CA-C	7.28	121.50	111.90
7	h	51	TYR	N-CA-C	7.19	119.98	111.71
7	h	114	GLU	N-CA-C	7.19	120.03	111.33
11	l	115	GLU	N-CA-C	7.17	119.99	111.02
8	i	91	LYS	CA-C-N	7.11	128.73	119.84
8	i	91	LYS	C-N-CA	7.11	128.73	119.84
47	W	69	TYR	N-CA-C	-7.09	103.89	112.54
32	H	89	VAL	N-CA-C	7.09	117.85	110.62
11	l	113	ALA	N-CA-C	-7.08	105.25	114.04
2	c	195	GLY	N-CA-C	7.00	118.60	111.95
44	T	62	ARG	N-CA-C	-6.91	103.83	111.36
6	g	30	LEU	N-CA-C	6.86	118.55	111.14
41	Q	114	SER	N-CA-C	-6.84	103.88	111.82
7	h	117	LEU	N-CA-C	6.80	119.77	109.23
1	b	132	ARG	N-CA-C	-6.59	105.81	114.31
16	q	85	ALA	N-CA-C	-6.58	104.88	113.17
40	P	100	ASN	N-CA-C	-6.57	104.20	111.82
25	z	42	ALA	N-CA-C	-6.54	103.43	111.40
33	I	169	TRP	N-CA-C	-6.53	104.45	112.88
21	v	59	GLU	N-CA-C	6.52	118.94	110.53
29	E	61	LEU	CA-C-N	6.52	127.98	119.84
29	E	61	LEU	C-N-CA	6.52	127.98	119.84
39	O	77	VAL	N-CA-C	6.49	118.07	111.00
4	e	97	GLU	N-CA-C	-6.47	104.65	112.54
5	f	139	VAL	N-CA-C	6.47	117.25	110.72
45	U	36	VAL	N-CA-C	6.41	117.61	111.91
32	H	39	ARG	N-CA-C	-6.40	104.39	111.82
7	h	44	ALA	N-CA-C	-6.40	104.40	111.82
21	v	52	ALA	N-CA-C	-6.38	104.41	111.82
35	K	80	PHE	N-CA-C	6.35	120.13	112.38
3	d	115	GLN	N-CA-C	-6.32	105.20	113.17
16	q	50	ARG	N-CA-C	-6.31	105.60	113.55
5	f	47	ASN	N-CA-C	-6.28	105.57	112.72
53	l	1130	U	C2'-C3'-O3'	6.28	118.91	109.50
13	n	78	LYS	N-CA-C	-6.26	104.55	111.82
40	P	56	LYS	N-CA-C	-6.24	105.67	113.28
33	I	46	ARG	N-CA-C	-6.23	105.16	112.89
33	I	97	LEU	N-CA-C	6.21	118.57	111.11
2	c	152	PRO	N-CA-C	-6.20	105.10	113.40
21	v	80	HIS	CA-C-N	6.18	127.57	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	v	80	HIS	C-N-CA	6.18	127.57	119.84
21	v	44	HIS	N-CA-C	6.18	117.89	111.03
23	x	67	LEU	N-CA-C	-6.17	104.66	111.82
10	k	111	LYS	N-CA-C	-6.15	105.78	113.28
31	G	139	GLU	N-CA-C	-6.13	104.50	112.23
6	g	117	LEU	CA-C-N	6.13	125.85	119.05
6	g	117	LEU	C-N-CA	6.13	125.85	119.05
7	h	121	SER	N-CA-C	6.11	116.34	108.34
41	Q	99	GLY	N-CA-C	-6.10	106.51	115.72
43	S	50	LEU	N-CA-C	-6.08	101.99	109.65
7	h	80	THR	N-CA-C	6.03	117.97	110.91
49	Y	79	THR	N-CA-C	-6.02	104.83	111.82
4	e	39	VAL	N-CA-C	5.99	116.17	110.42
31	G	191	ASP	CA-C-N	5.96	125.50	119.19
31	G	191	ASP	C-N-CA	5.96	125.50	119.19
18	s	35	ILE	N-CA-C	-5.88	105.34	111.58
32	H	124	GLU	N-CA-C	-5.88	106.14	113.38
46	V	68	LYS	N-CA-C	-5.86	105.03	111.82
36	L	79	VAL	N-CA-C	-5.85	104.79	113.39
24	y	50	VAL	N-CA-C	-5.84	105.04	110.53
40	P	125	LYS	N-CA-C	5.83	118.39	110.35
7	h	105	LYS	N-CA-C	5.82	116.95	107.23
7	h	58	THR	N-CA-C	5.79	120.12	112.25
6	g	67	ALA	N-CA-C	-5.79	104.94	112.23
20	u	76	THR	N-CA-C	-5.74	106.93	114.04
10	k	32	TYR	N-CA-C	5.73	118.56	110.14
35	K	66	ALA	N-CA-C	5.72	113.37	108.22
40	P	97	ARG	N-CA-C	-5.71	105.04	112.23
8	i	127	SER	N-CA-C	-5.69	105.16	111.36
1	b	178	GLY	N-CA-C	-5.68	107.26	115.27
40	P	69	CYS	N-CA-C	-5.67	106.49	113.41
45	U	62	GLY	N-CA-C	-5.67	107.64	114.66
17	r	14	VAL	N-CA-C	5.66	116.03	108.11
35	K	39	LEU	N-CA-C	-5.65	105.30	113.21
55	5	17(A)	U	C2'-C3'-O3'	5.63	117.95	109.50
52	3	1190	G	C2'-C3'-O3'	5.63	117.94	109.50
9	j	7	LYS	CA-C-N	5.62	125.99	119.47
9	j	7	LYS	C-N-CA	5.62	125.99	119.47
39	O	95	GLY	N-CA-C	-5.60	107.29	114.85
39	O	42	LEU	CA-C-N	5.60	126.84	119.84
39	O	42	LEU	C-N-CA	5.60	126.84	119.84
7	h	43	LYS	N-CA-C	-5.59	105.33	111.82

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	n	53	THR	N-CA-C	-5.59	105.19	112.23
20	u	75	ALA	N-CA-C	-5.57	107.13	114.04
27	C	42	VAL	N-CA-C	-5.56	104.88	113.16
42	R	17	ALA	N-CA-C	-5.51	106.56	113.28
18	s	61	ASN	N-CA-C	5.48	119.97	112.68
2	c	132	ALA	N-CA-C	-5.45	106.21	112.92
17	r	50	GLY	N-CA-C	-5.45	100.25	113.18
52	3	1201	A	C2'-C3'-O3'	5.45	117.68	109.50
42	R	19	THR	N-CA-C	-5.44	106.14	112.89
36	L	128	GLU	N-CA-C	-5.43	106.43	112.57
13	n	10	LEU	N-CA-C	5.43	118.92	111.54
42	R	104	ASN	N-CA-C	5.42	117.90	109.60
7	h	93	ALA	N-CA-C	5.42	117.89	109.60
33	I	9	LYS	N-CA-C	-5.42	105.54	111.82
38	N	56	MET	N-CA-C	5.41	119.38	112.12
33	I	8	LEU	N-CA-C	-5.41	107.23	113.88
7	h	4	ASN	N-CA-C	5.38	117.15	111.28
6	g	64	ALA	N-CA-C	-5.37	105.59	111.82
34	J	10	LEU	N-CA-C	-5.37	106.67	113.43
32	H	107	LYS	CA-C-N	5.37	124.98	119.56
32	H	107	LYS	C-N-CA	5.37	124.98	119.56
20	u	6	ARG	N-CA-C	5.35	117.54	111.02
51	a	21	TYR	N-CA-C	5.35	116.82	110.19
1	b	245	THR	N-CA-C	-5.34	103.90	110.31
25	z	24	LEU	N-CA-C	-5.34	105.63	111.82
7	h	103	ASN	N-CA-C	-5.33	106.28	112.89
53	1	372	G	N9-C1'-C2'	5.32	119.99	112.00
38	N	57	VAL	N-CA-C	5.32	120.41	109.34
44	T	59	VAL	N-CA-C	-5.32	105.34	110.72
8	i	110	GLN	N-CA-C	-5.31	105.57	111.36
11	l	95	LEU	N-CA-C	-5.31	105.54	112.23
28	D	4	THR	N-CA-C	5.31	118.06	110.68
51	a	175	ILE	N-CA-C	5.31	116.20	111.90
50	Z	10	PRO	N-CA-C	5.31	119.90	112.26
11	l	96	LYS	N-CA-C	-5.29	105.56	112.23
31	G	144	GLU	N-CA-C	-5.29	105.97	112.90
53	1	2287	A	N9-C1'-C2'	5.29	119.93	112.00
40	P	75	GLU	N-CA-C	-5.28	106.79	113.18
36	L	94	ARG	N-CA-C	-5.27	106.98	113.41
1	b	6	LYS	CA-C-N	5.25	126.40	119.84
1	b	6	LYS	C-N-CA	5.25	126.40	119.84
33	I	60	VAL	N-CA-C	-5.24	105.61	110.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	S	22	LYS	N-CA-C	-5.24	106.22	113.18
3	d	176	ASP	CA-C-N	5.23	124.68	119.24
3	d	176	ASP	C-N-CA	5.23	124.68	119.24
5	f	81	GLY	N-CA-C	-5.23	104.58	112.84
38	N	35	GLU	N-CA-C	5.22	117.05	111.36
4	e	5	ASP	N-CA-C	-5.21	105.77	111.82
32	H	177	LEU	N-CA-C	5.21	118.42	111.75
31	G	193	ASP	N-CA-C	5.20	116.95	111.28
50	Z	8	ASN	N-CA-C	5.20	121.87	110.80
53	l	1020	A	C2'-C3'-O3'	5.20	117.29	109.50
36	L	143	MET	N-CA-C	-5.18	107.13	113.50
3	d	31	VAL	N-CA-C	5.15	115.81	110.82
12	m	118	LYS	N-CA-C	-5.15	106.69	113.12
6	g	40	THR	N-CA-C	-5.14	102.17	110.14
3	d	146	VAL	N-CA-C	5.14	116.26	108.96
43	S	31	SER	N-CA-C	-5.14	105.73	112.41
39	O	40	ILE	CA-C-N	5.13	126.26	119.84
39	O	40	ILE	C-N-CA	5.13	126.26	119.84
33	I	94	GLU	N-CA-C	-5.13	106.70	113.17
12	m	18	ARG	N-CA-C	5.13	116.95	110.33
35	K	48	ALA	N-CA-C	-5.12	107.16	113.41
14	o	84	GLU	N-CA-C	-5.12	106.54	112.89
6	g	13	GLY	N-CA-C	5.11	119.08	112.54
6	g	39	ALA	N-CA-C	5.10	117.60	108.17
51	a	7	ARG	N-CA-C	5.10	116.53	111.07
40	P	94	SER	N-CA-C	-5.10	107.45	113.97
31	G	190	SER	N-CA-C	5.09	116.68	110.41
6	g	99	ILE	N-CA-C	-5.09	105.58	110.72
4	e	6	TYR	N-CA-C	-5.08	105.92	111.82
6	g	55	GLU	N-CA-C	5.07	116.81	111.28
2	c	203	VAL	N-CA-C	5.07	115.15	107.80
27	C	39	ASP	CA-C-N	5.07	126.17	119.84
27	C	39	ASP	C-N-CA	5.07	126.17	119.84
42	R	60	ALA	N-CA-C	-5.06	106.61	112.89
16	q	40	LYS	N-CA-C	-5.04	106.30	112.90
24	y	17	GLU	N-CA-C	-5.04	105.97	111.82
1	b	66	PHE	N-CA-C	-5.04	106.83	113.12
40	P	107	THR	N-CA-C	-5.02	105.27	111.40
43	S	24	ALA	N-CA-C	-5.02	106.94	113.16
8	i	73	PRO	CA-C-N	5.01	125.00	119.89
8	i	73	PRO	C-N-CA	5.01	125.00	119.89
4	e	52	ALA	N-CA-C	-5.00	106.02	111.82

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	l	103	ILE	N-CA-C	5.00	115.77	110.72

There are no chirality outliers.

There are no planarity outliers.

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	b	2083	0	2157	81	0
2	c	1565	0	1616	45	0
3	d	1552	0	1619	48	0
4	e	1411	0	1447	71	0
5	f	1323	0	1374	27	0
6	g	1111	0	1148	39	0
7	h	989	0	1025	61	0
8	i	1032	0	1088	39	0
9	j	1129	0	1162	32	0
10	k	939	0	1012	33	0
11	l	1045	0	1117	42	0
12	m	1074	0	1157	35	0
13	n	961	0	1000	23	0
14	o	892	0	923	24	0
15	p	917	0	965	35	0
16	q	947	0	1022	35	0
17	r	816	0	839	31	0
18	s	857	0	922	16	0
19	t	739	0	807	19	0
20	u	780	0	834	20	0
21	v	753	0	780	23	0
22	w	575	0	592	20	0
23	x	625	0	655	12	0
24	y	509	0	543	12	0
25	z	449	0	491	13	0
26	B	444	0	461	20	0
27	C	410	0	440	8	0
28	D	377	0	418	9	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	E	504	0	574	17	0
30	F	302	0	343	11	0
31	G	1757	0	1787	59	0
32	H	1625	0	1699	40	0
33	I	1643	0	1710	56	0
34	J	1157	0	1199	55	0
35	K	818	0	808	30	0
36	L	1182	0	1240	40	0
37	M	979	0	1034	45	0
38	N	1022	0	1070	59	0
39	O	787	0	828	32	0
40	P	870	0	878	35	0
41	Q	955	0	1019	42	0
42	R	884	0	944	47	0
43	S	805	0	847	45	0
44	T	714	0	737	19	0
45	U	649	0	666	22	0
46	V	649	0	691	33	0
47	W	536	0	552	23	0
48	X	638	0	665	29	0
49	Y	665	0	714	38	0
50	Z	545	0	579	32	0
51	a	1027	0	1092	33	0
52	3	33012	0	16618	701	0
53	1	62317	0	31346	918	0
54	2	2568	0	1303	44	0
55	5	1640	0	837	54	0
56	4	388	0	196	10	0
57	7	1619	0	821	33	0
58	7	11	0	8	0	0
59	7	10	0	10	0	0
All	All	148582	0	100429	2979	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 12.

All (2979) 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)
53:1:45:G:H5''	53:1:46:G:H5'	1.27	1.17
43:S:3:GLN:HA	43:S:6:LYS:HE2	1.39	1.00

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:111:PRO:HB2	42:R:113:LYS:HE2	1.45	0.99
53:1:2048:G:H2'	53:1:2049:G:H5''	1.45	0.96
53:1:2277:G:H2'	53:1:2278:A:H5''	1.50	0.93
54:2:3:C:H2'	54:2:4:C:H5''	1.50	0.92
53:1:1801:A:H5''	53:1:2203:U:H2'	1.53	0.91
33:I:9:LYS:HD2	52:3:428:G:H5''	1.51	0.91
51:a:37:LYS:HB2	53:1:2127:G:H5'	1.52	0.89
55:5:62:C:H2'	55:5:63:G:H5''	1.53	0.89
31:G:104:LYS:HD2	52:3:1073:U:H4'	1.55	0.88
12:m:12:MET:HA	53:1:910:A:H62	1.38	0.87
52:3:1259:C:H3'	52:3:1260:G:H5''	1.55	0.87
52:3:405:U:H3'	52:3:406:G:H5'	1.56	0.87
32:H:113:LYS:HE2	32:H:184:ASN:HD22	1.39	0.86
34:J:39:GLY:HA3	34:J:116:VAL:HB	1.56	0.86
55:5:61:C:H3'	55:5:62:C:H5''	1.57	0.86
34:J:64:GLU:HG3	34:J:68:ARG:HH12	1.41	0.85
31:G:105:THR:HG21	52:3:1072:G:H21	1.39	0.85
52:3:516:U:H3	52:3:533:A:H62	1.23	0.85
48:X:14:LEU:HD11	48:X:34:SER:HB3	1.56	0.85
12:m:64:TRP:HE1	53:1:873:C:H4'	1.42	0.84
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.58	0.84
42:R:52:ILE:HG23	42:R:56:ARG:HH12	1.42	0.84
42:R:100:ARG:HH12	52:3:950:U:H3'	1.44	0.83
24:y:1:MET:HA	24:y:4:LYS:HD2	1.58	0.83
52:3:327:A:O2'	52:3:328:C:H4'	1.79	0.83
53:1:2421:G:H2'	55:5:76:A:N6	1.95	0.82
37:M:10:LEU:HD22	37:M:74:ILE:HD11	1.61	0.82
44:T:42:PHE:HB3	53:1:715:A:N3	1.94	0.82
43:S:50:LEU:HD12	43:S:51:PRO:HD2	1.62	0.82
35:K:50:PRO:HG3	35:K:55:HIS:HE1	1.43	0.82
40:P:109:ILE:HG21	50:Z:16:ARG:HH22	1.42	0.82
45:U:41:PRO:HG2	45:U:42:ILE:HD12	1.61	0.82
49:Y:28:ARG:HH12	52:3:1437:A:H5''	1.45	0.82
52:3:1130:A:H61	52:3:1144:G:H1'	1.45	0.81
53:1:1053:C:H2'	53:1:1054:A:H5''	1.62	0.81
12:m:75:GLU:OE2	53:1:957:C:H5'	1.80	0.81
52:3:1534:A:H61	56:4:11:U:H3	1.27	0.81
38:N:98:ARG:HG3	38:N:103:VAL:HG21	1.62	0.81
53:1:2114:A:H61	53:1:2117:A:H62	1.28	0.81
53:1:1020:A:H1'	53:1:1021:A:OP2	1.81	0.81
4:e:63:LYS:O	54:2:42:C:H1'	1.80	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:O:40:ILE:HB	39:O:73:LEU:HB3	1.63	0.80
53:1:2048:G:C2'	53:1:2049:G:H5''	2.10	0.80
55:5:15:G:H3'	55:5:16:C:H5'	1.62	0.80
44:T:39:GLN:HE22	53:1:715:A:H4'	1.47	0.79
43:S:3:GLN:OE1	52:3:1047:G:H5''	1.83	0.79
53:1:2800:A:H3'	53:1:2801:G:H5'	1.64	0.79
53:1:962:G:H21	53:1:2250:G:H1	1.27	0.79
49:Y:11:ILE:H	49:Y:11:ILE:HD12	1.47	0.79
51:a:11:ILE:HG23	51:a:33:LEU:HD21	1.65	0.79
53:1:2112:G:H2'	53:1:2113:U:H5'	1.63	0.79
41:Q:51:VAL:HG22	41:Q:52:CYS:H	1.48	0.79
36:L:24:LYS:HA	36:L:27:ASN:HD21	1.47	0.78
34:J:80:LEU:HG	34:J:122:VAL:HG11	1.64	0.78
53:1:1141:U:H4'	53:1:1142:A:O4'	1.84	0.78
33:I:37:PRO:HD2	33:I:41:GLY:HA3	1.65	0.78
57:7:23:A:H2'	57:7:24:G:C8	2.19	0.78
1:b:221:GLY:HA2	1:b:224:MET:HE3	1.63	0.78
53:1:713:G:H21	53:1:718:A:H62	1.31	0.77
4:e:84:ILE:CD1	53:1:2312:U:H5'	2.14	0.77
53:1:2277:G:C2'	53:1:2278:A:H5''	2.14	0.77
39:O:53:ILE:HD12	43:S:84:ARG:HD2	1.66	0.77
10:k:76:VAL:HG22	15:p:72:VAL:HG22	1.66	0.77
43:S:81:ILE:HG21	52:3:1202:U:N3	2.00	0.77
55:5:15:G:H3'	55:5:16:C:C5'	2.14	0.77
38:N:17:ARG:HH22	52:3:1129:C:H5''	1.48	0.77
1:b:235:GLU:HG2	53:1:2600:A:H62	1.49	0.77
49:Y:66:ILE:HG22	49:Y:68:LYS:H	1.48	0.77
4:e:34:THR:HG21	53:1:2314:A:H5'	1.67	0.76
31:G:46:VAL:HG23	31:G:47:PRO:HD3	1.67	0.76
53:1:275:C:H2'	53:1:276:U:H4'	1.66	0.76
16:q:108:LEU:HD21	17:r:40:MET:HE1	1.67	0.76
13:n:22:ARG:HG3	13:n:70:THR:HA	1.67	0.76
52:3:1502:A:H8	52:3:1505:G:H22	1.32	0.76
1:b:137:GLY:HA3	52:3:712:A:H5'	1.69	0.75
38:N:123:ARG:HB2	52:3:1343:G:H4'	1.66	0.75
1:b:153:LEU:HD22	1:b:175:LEU:HD21	1.69	0.75
33:I:160:LEU:HD22	33:I:164:ARG:HE	1.50	0.75
39:O:59:LYS:HE2	39:O:62:ARG:HE	1.51	0.75
53:1:1900:A:H1'	53:1:1970:A:H2'	1.69	0.75
35:K:50:PRO:HG3	35:K:55:HIS:CE1	2.22	0.75
53:1:1077:A:H2'	53:1:1078:U:H5'	1.68	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:113:ARG:HE	41:Q:120:ARG:HA	1.51	0.75
2:c:109:VAL:HG12	2:c:203:VAL:HG22	1.68	0.75
42:R:6:ILE:HG13	42:R:7:ASN:H	1.50	0.75
7:h:87:GLU:HB3	7:h:95:LEU:HD12	1.69	0.74
7:h:33:VAL:HG13	7:h:35:VAL:H	1.52	0.74
55:5:3:C:H3'	55:5:4:G:H5''	1.69	0.74
29:E:31:ILE:HD11	53:1:2391:G:H5'	1.69	0.74
54:2:3:C:C2'	54:2:4:C:H5''	2.17	0.74
7:h:64:VAL:O	7:h:67:THR:HG22	1.88	0.74
1:b:64:VAL:HG21	1:b:86:ARG:HH12	1.53	0.74
53:1:329:G:O4'	53:1:477:A:H1'	1.88	0.74
53:1:1476:U:H3	53:1:1515:A:H62	1.36	0.74
16:q:3:VAL:HG21	53:1:1249:U:H4'	1.70	0.73
12:m:4:PRO:HG3	12:m:68:PHE:HE2	1.53	0.73
53:1:742:A:H2'	53:1:743:A:H8	1.52	0.73
7:h:59:LEU:HB3	7:h:62:ARG:HB2	1.69	0.73
48:X:12:LEU:HD12	48:X:13:HIS:N	2.03	0.73
53:1:215:G:H4'	53:1:216:A:H4'	1.70	0.73
53:1:1306:C:H41	53:1:1606:C:H2'	1.52	0.73
31:G:94:ARG:HD3	52:3:1100:C:OP2	1.88	0.73
35:K:42:TRP:HB2	35:K:59:TYR:HB2	1.69	0.73
9:j:123:LYS:HZ2	53:1:7:G:H5''	1.54	0.73
36:L:4:ARG:HH21	52:3:1377:A:H2'	1.54	0.73
53:1:2296:U:H5''	53:1:2297:A:OP1	1.87	0.73
38:N:33:SER:OG	38:N:36:GLN:HG2	1.89	0.73
53:1:1394:U:H4'	53:1:1603:A:H4'	1.68	0.73
5:f:34:ARG:HE	5:f:70:LEU:HD21	1.54	0.73
48:X:10:ILE:HD12	48:X:37:SER:HB3	1.68	0.73
6:g:72:ILE:HB	6:g:108:VAL:HG12	1.72	0.72
12:m:42:THR:OG1	12:m:45:GLN:HG3	1.89	0.72
53:1:1807:G:H2'	53:1:1808:A:H5'	1.71	0.72
55:5:3:C:C3'	55:5:4:G:H5''	2.19	0.72
38:N:17:ARG:NH2	52:3:1129:C:H5''	2.04	0.72
34:J:141:ASP:HA	34:J:144:GLU:HG2	1.71	0.72
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.70	0.72
1:b:201:LEU:HD13	52:3:773:G:H5''	1.69	0.72
45:U:5:ARG:HB2	52:3:376:G:H5''	1.72	0.72
42:R:22:TYR:CE1	52:3:1330:U:H4'	2.25	0.72
5:f:138:GLN:HE22	53:1:2759:G:H21	1.38	0.72
52:3:944:G:H21	52:3:1339:A:H62	1.35	0.72
18:s:59:GLU:HB2	18:s:66:ILE:HD11	1.72	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2286:G:H5''	53:1:2287:A:OP1	1.90	0.72
53:1:49:A:H5'	53:1:51:G:O4'	1.90	0.71
6:g:128:HIS:HB2	6:g:144:VAL:HB	1.72	0.71
8:i:20:SER:OG	8:i:21:PRO:HD3	1.89	0.71
34:J:24:VAL:HG22	34:J:25:LYS:H	1.54	0.71
43:S:81:ILE:HG21	52:3:1202:U:H3	1.55	0.71
53:1:1278:C:H2'	53:1:1279:G:H8	1.56	0.71
39:O:53:ILE:HG22	39:O:61:ALA:O	1.89	0.71
1:b:146:LYS:HB2	1:b:149:LYS:HB2	1.71	0.71
37:M:31:LEU:HD11	52:3:643:C:H5'	1.72	0.71
52:3:1201:A:H1'	52:3:1202:U:OP2	1.90	0.71
13:n:53:THR:HG21	53:1:2840:C:H5''	1.71	0.71
36:L:3:ARG:HH21	52:3:932:C:H5''	1.56	0.71
53:1:1909:C:H2'	53:1:1910:G:H8	1.55	0.71
55:5:3:C:H2'	55:5:4:G:H5''	1.72	0.71
37:M:54:THR:O	37:M:56:PRO:HD3	1.90	0.71
41:Q:109:ARG:NH1	52:3:537:G:H5''	2.05	0.71
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.72	0.71
4:e:132:ARG:CZ	53:1:2305:U:H4'	2.21	0.71
52:3:1033:G:H2'	52:3:1034:G:H5''	1.73	0.71
7:h:33:VAL:HG22	7:h:34:THR:H	1.56	0.70
55:5:59:A:H2'	55:5:60:U:H5'	1.73	0.70
37:M:31:LEU:HD21	52:3:643:C:H5''	1.72	0.70
53:1:1645:G:H5''	53:1:1646:C:H5'	1.71	0.70
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.74	0.70
3:d:52:VAL:HG23	3:d:74:LYS:HG2	1.73	0.70
29:E:61:LEU:HD12	29:E:61:LEU:O	1.91	0.70
38:N:17:ARG:HH12	52:3:1129:C:H4'	1.56	0.70
53:1:511:U:H2'	53:1:512:G:H5'	1.72	0.70
55:5:61:C:C3'	55:5:62:C:H5''	2.20	0.70
8:i:89:SER:HB2	8:i:92:PRO:HG3	1.71	0.70
10:k:7:MET:HE1	10:k:44:LYS:HG3	1.73	0.70
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.73	0.70
53:1:473:G:O2'	53:1:474:G:H5'	1.91	0.70
54:2:66:A:H5''	54:2:67:G:OP1	1.92	0.70
55:5:25:C:H6	55:5:25:C:H5'	1.56	0.70
31:G:116:LEU:HB3	31:G:140:LEU:HD13	1.72	0.70
33:I:50:TYR:CD2	52:3:509:A:H5'	2.27	0.70
41:Q:69:GLU:HG2	52:3:521:G:H4'	1.73	0.70
46:V:16:MET:HG3	46:V:19:SER:HB2	1.73	0.69
53:1:2553:G:H3'	53:1:2554:U:H5''	1.74	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:528:A:N1	53:1:2042:A:H2'	2.07	0.69
2:c:151:THR:HB	2:c:152:PRO:HD3	1.74	0.69
8:i:13:ALA:HA	8:i:53:PRO:HA	1.73	0.69
10:k:35:VAL:HG23	10:k:36:GLY:H	1.57	0.69
32:H:57:GLU:HG3	32:H:59:PRO:HD3	1.75	0.69
52:3:1088:G:H21	52:3:1167:A:H61	1.39	0.69
35:K:3:HIS:HB2	35:K:92:THR:HA	1.73	0.69
15:p:90:ALA:HB2	15:p:112:ARG:HG2	1.73	0.69
22:w:38:GLY:HA2	53:1:2330:G:H21	1.55	0.69
54:2:72:G:H21	54:2:104:A:H62	1.39	0.69
10:k:109:SER:O	10:k:110:GLU:HG3	1.93	0.69
42:R:73:SER:O	42:R:77:LYS:HD3	1.92	0.69
46:V:26:ARG:HH22	52:3:237:G:H5'	1.56	0.69
48:X:5:LYS:HG3	48:X:6:LYS:HD3	1.75	0.69
53:1:310:A:H2'	53:1:311:A:H5''	1.73	0.69
53:1:310:A:C2'	53:1:311:A:H5''	2.22	0.69
53:1:1796:U:H2'	53:1:1797:G:H8	1.57	0.69
53:1:2391:G:H4'	53:1:2392:A:OP1	1.92	0.69
4:e:107:VAL:HB	4:e:108:PRO:HD3	1.75	0.68
21:v:75:GLN:HB2	21:v:92:VAL:HG13	1.75	0.68
4:e:84:ILE:HD11	53:1:2312:U:H5'	1.75	0.68
20:u:16:LYS:HB3	53:1:329:G:H1	1.58	0.68
45:U:58:ALA:O	45:U:61:VAL:HG22	1.93	0.68
7:h:55:VAL:HA	53:1:1084:A:H4'	1.75	0.68
1:b:260:LYS:HA	1:b:263:ASP:OD2	1.93	0.68
46:V:30:HIS:HD2	46:V:33:TYR:H	1.41	0.68
1:b:153:LEU:HD21	1:b:181:ARG:HH22	1.58	0.68
39:O:57:VAL:HG12	39:O:58:ASN:H	1.59	0.68
43:S:63:CYS:HB2	43:S:67:GLY:H	1.59	0.68
53:1:2698:U:H2'	53:1:2699:C:C6	2.29	0.68
21:v:9:ARG:HG2	21:v:41:GLU:HB2	1.73	0.68
41:Q:113:ARG:HH21	41:Q:120:ARG:HG3	1.59	0.68
44:T:39:GLN:NE2	53:1:715:A:H4'	2.07	0.68
17:r:49:ILE:HG22	17:r:54:VAL:HG13	1.75	0.68
51:a:221:GLY:N	53:1:2176:A:H5''	2.07	0.68
53:1:45:G:H5''	53:1:46:G:C5'	2.16	0.68
53:1:2055:C:H2'	53:1:2504:U:H5'	1.75	0.68
6:g:12:LEU:HD12	6:g:13:GLY:N	2.09	0.68
21:v:64:VAL:HG12	21:v:69:GLU:HG2	1.76	0.68
2:c:123:LYS:HE2	13:n:1:MET:HE1	1.76	0.68
39:O:41:PRO:HG2	52:3:1150:A:H2	1.59	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1414:U:H2'	52:3:1415:G:H8	1.58	0.68
53:1:441:U:O2'	53:1:442:G:H5'	1.94	0.68
16:q:50:ARG:HH11	16:q:50:ARG:HG3	1.59	0.67
52:3:1497:G:O2'	52:3:1498:U:H5'	1.93	0.67
15:p:89:GLY:HA2	15:p:111:GLU:HA	1.76	0.67
43:S:4:SER:OG	52:3:1216:A:H5''	1.95	0.67
9:j:123:LYS:NZ	53:1:7:G:H5''	2.10	0.67
30:F:32:LYS:CE	53:1:2478:A:H5'	2.24	0.67
37:M:80:PRO:HG2	52:3:878:A:H5'	1.77	0.67
38:N:113:LYS:HD2	52:3:1369:C:H5	1.58	0.67
11:l:49:GLY:HA3	11:l:58:TYR:HE1	1.59	0.67
52:3:354:G:H2'	52:3:355:C:H5'	1.76	0.67
53:1:1133:A:H4'	53:1:1134:A:H5''	1.77	0.67
11:l:95:LEU:HD22	11:l:100:ILE:HD11	1.74	0.67
3:d:146:VAL:HG12	3:d:185:LYS:HB2	1.76	0.67
5:f:174:LYS:HE3	53:1:2529:G:H4'	1.76	0.67
9:j:30:THR:HG21	53:1:1005:C:O2'	1.95	0.67
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.76	0.67
32:H:69:THR:HG21	32:H:75:VAL:HG21	1.76	0.67
52:3:1379:G:O2'	52:3:1380:U:H5'	1.95	0.66
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.58	0.66
19:t:15:HIS:H	19:t:32:LEU:HA	1.59	0.66
17:r:78:ARG:HB3	17:r:83:TYR:HB3	1.76	0.66
33:I:3:TYR:C	33:I:4:LEU:HD23	2.20	0.66
53:1:742:A:H2'	53:1:743:A:C8	2.29	0.66
15:p:33:GLU:HB3	15:p:36:LYS:HB2	1.78	0.66
53:1:1909:C:H2'	53:1:1910:G:C8	2.30	0.66
38:N:49:GLN:O	38:N:52:GLU:HG3	1.95	0.66
39:O:41:PRO:HG2	52:3:1150:A:C2	2.30	0.66
40:P:43:TRP:HZ2	52:3:686:U:H1'	1.61	0.66
52:3:1306:A:H61	52:3:1331:G:H1'	1.60	0.66
53:1:1373:A:C5'	53:1:2212:A:H1'	2.25	0.66
53:1:2710:C:H2'	53:1:2711:A:C8	2.31	0.66
55:5:3:C:C2'	55:5:4:G:H5''	2.25	0.66
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.75	0.66
4:e:84:ILE:HG13	53:1:2312:U:H5'	1.78	0.66
6:g:58:LEU:O	6:g:61:VAL:HG22	1.95	0.66
9:j:17:VAL:HG23	9:j:137:PRO:HB2	1.77	0.66
11:l:110:VAL:HB	11:l:127:VAL:HG13	1.78	0.66
12:m:57:VAL:HG12	12:m:112:LEU:HG	1.77	0.66
17:r:54:VAL:HG23	17:r:55:ASP:H	1.61	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:28:LEU:HA	50:Z:31:VAL:HG12	1.78	0.66
34:J:28:ARG:HH12	52:3:15:G:H4'	1.60	0.66
15:p:28:LYS:HB3	15:p:39:LEU:HD11	1.77	0.65
13:n:49:GLU:HB2	13:n:50:PRO:HD3	1.78	0.65
34:J:98:ALA:HB1	52:3:6:G:C6	2.31	0.65
52:3:1218:C:H2'	52:3:1219:A:C8	2.31	0.65
53:1:1053:C:C2'	53:1:1054:A:H5''	2.26	0.65
48:X:28:LYS:HE3	48:X:29:PRO:HD2	1.78	0.65
52:3:1071:C:H2'	52:3:1072:G:H8	1.61	0.65
53:1:676:A:H62	53:1:802:A:H61	1.44	0.65
55:5:62:C:C2'	55:5:63:G:H5''	2.25	0.65
4:e:120:SER:HB3	4:e:127:TYR:CE1	2.32	0.65
15:p:88:ARG:HE	15:p:112:ARG:HD2	1.61	0.65
33:I:33:ILE:HG13	33:I:34:GLU:N	2.11	0.65
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.78	0.65
33:I:9:LYS:HD2	52:3:428:G:C5'	2.24	0.65
53:1:2799:A:H2'	53:1:2800:A:H5'	1.79	0.65
3:d:148:ILE:HB	3:d:169:VAL:HG22	1.79	0.65
38:N:114:LYS:HG2	38:N:120:ALA:HA	1.79	0.65
49:Y:58:ASP:CG	52:3:194:C:H1'	2.21	0.65
50:Z:18:PHE:HA	50:Z:21:SER:HB2	1.79	0.65
31:G:210:THR:HG23	31:G:211:LEU:HD12	1.79	0.65
52:3:17:U:H2'	52:3:18:C:C6	2.32	0.65
16:q:51:GLN:HE22	16:q:55:GLN:HG3	1.62	0.64
45:U:76:LYS:HE2	52:3:474:G:OP1	1.97	0.64
4:e:71:LYS:HG3	4:e:72:SER:H	1.62	0.64
37:M:29:SER:OG	37:M:32:LYS:HG2	1.96	0.64
53:1:745:G:O2'	53:1:748:G:H1'	1.97	0.64
53:1:2423:U:O2'	53:1:2425:A:H2'	1.97	0.64
4:e:142:TYR:HA	4:e:145:VAL:HG12	1.78	0.64
19:t:75:GLY:C	19:t:76:ARG:HD3	2.22	0.64
42:R:107:THR:OG1	52:3:947:G:H5''	1.97	0.64
52:3:1497:G:C2'	52:3:1498:U:H5'	2.28	0.64
40:P:115:ILE:HD12	40:P:116:PRO:HD2	1.80	0.64
52:3:297:G:H4'	52:3:557:G:H4'	1.80	0.64
52:3:939:G:H21	52:3:1375:A:H2	1.43	0.64
53:1:1539:U:H2'	53:1:1540:G:H8	1.62	0.64
7:h:77:VAL:HG22	7:h:82:ILE:HG21	1.80	0.64
19:t:61:LEU:HD22	53:1:1341:G:H5'	1.79	0.64
26:B:24:VAL:HG13	26:B:25:THR:H	1.61	0.64
47:W:59:LYS:HD3	52:3:734:G:O2'	1.98	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:112:G:H21	52:3:354:G:H5'	1.61	0.64
53:1:1872:A:H2'	53:1:1873:G:O4'	1.98	0.64
6:g:31:VAL:HG23	6:g:32:PRO:HD3	1.80	0.64
16:q:51:GLN:HA	16:q:54:ARG:HE	1.63	0.64
23:x:13:THR:HG21	53:1:188:G:H5'	1.80	0.64
31:G:112:ARG:O	31:G:112:ARG:HD3	1.98	0.64
53:1:1319:C:O2'	53:1:1320:C:H5'	1.98	0.64
53:1:2452:C:H42	53:1:2504:U:H3	1.47	0.63
36:L:19:SER:OG	36:L:22:LEU:HB2	1.99	0.63
52:3:714:G:H2'	52:3:715:A:C8	2.33	0.63
6:g:6:LEU:HD22	6:g:51:ARG:HD2	1.81	0.63
12:m:50:ARG:HH12	57:7:54:U:H4'	1.63	0.63
30:F:2:LYS:NZ	53:1:2477:U:H2'	2.12	0.63
43:S:3:GLN:CA	43:S:6:LYS:HE2	2.22	0.63
47:W:11:ARG:NE	52:3:845:A:H4'	2.14	0.63
2:c:129:THR:OG1	2:c:140:HIS:O	2.16	0.63
42:R:77:LYS:HA	42:R:80:MET:HE3	1.79	0.63
46:V:11:VAL:HG22	46:V:22:VAL:HG22	1.79	0.63
50:Z:23:GLU:O	50:Z:24:LYS:HG3	1.99	0.63
51:a:209:ILE:H	51:a:209:ILE:HD12	1.64	0.63
7:h:55:VAL:HA	53:1:1084:A:C5'	2.28	0.63
37:M:54:THR:C	37:M:56:PRO:HD3	2.23	0.63
38:N:112:ARG:HG2	52:3:1369:C:P	2.39	0.63
53:1:948:C:H2'	53:1:949:G:H8	1.64	0.63
3:d:68:ALA:HA	53:1:1255:U:C5	2.33	0.63
52:3:1356:G:H2'	52:3:1357:A:C8	2.33	0.63
6:g:44:ILE:O	6:g:48:GLU:HG2	1.98	0.63
52:3:484:G:H4'	52:3:485:U:H5''	1.81	0.63
53:1:161:A:H3'	53:1:162:U:H5''	1.81	0.63
53:1:2834:G:O2'	53:1:2835:A:H5'	1.99	0.63
5:f:85:LYS:HB3	5:f:164:ALA:HB2	1.80	0.63
3:d:148:ILE:HD13	3:d:187:VAL:HG21	1.81	0.63
53:1:1926:U:O2	53:1:1926:U:H2'	1.98	0.63
39:O:57:VAL:HG12	39:O:58:ASN:N	2.14	0.62
53:1:1078:U:H5''	53:1:1079:C:H5''	1.81	0.62
53:1:2600:A:O2'	53:1:2601:C:H5'	1.98	0.62
7:h:87:GLU:OE1	7:h:93:ALA:HB3	1.99	0.62
8:i:74:PRO:HG3	53:1:1060:U:OP2	1.98	0.62
34:J:53:ARG:HH21	52:3:1071:C:C5'	2.12	0.62
52:3:202:G:H21	52:3:466:A:H61	1.47	0.62
3:d:106:LYS:HG3	3:d:200:LEU:HD23	1.81	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:63:LYS:HB2	54:2:42:C:H4'	1.79	0.62
15:p:113:LEU:O	15:p:113:LEU:HD12	1.98	0.62
34:J:133:ILE:O	34:J:136:VAL:HG12	1.98	0.62
47:W:11:ARG:HG3	47:W:14:ALA:HB3	1.80	0.62
53:1:807:U:H2'	53:1:808:G:H8	1.62	0.62
53:1:1956:U:H2'	53:1:1957:C:H5'	1.81	0.62
4:e:48:LEU:HG	4:e:149:ARG:HH12	1.64	0.62
52:3:1280:A:O2'	52:3:1281:C:H5'	1.99	0.62
52:3:1346:A:H2'	52:3:1347:G:H4'	1.81	0.62
9:j:31:GLU:HG2	9:j:142:ILE:HG12	1.81	0.62
38:N:112:ARG:HD2	38:N:113:LYS:O	2.00	0.62
53:1:2267:A:H5''	53:1:2268:A:H5'	1.82	0.62
8:i:25:PRO:HB2	53:1:1095:A:N6	2.15	0.62
14:o:24:THR:HG23	14:o:90:VAL:HG23	1.80	0.62
35:K:36:ILE:HA	35:K:64:VAL:HG23	1.80	0.62
52:3:1158:C:H2'	52:3:1159:U:H4'	1.81	0.62
40:P:43:TRP:CZ2	52:3:686:U:H1'	2.34	0.62
44:T:53:ARG:HH21	52:3:579:A:H4'	1.65	0.62
53:1:581:C:H2'	53:1:582:A:C8	2.35	0.62
49:Y:28:ARG:HH12	52:3:1437:A:C5'	2.13	0.62
51:a:4:LEU:HG	51:a:8:MET:HB2	1.82	0.62
52:3:265:G:H2'	52:3:267:C:H5	1.64	0.62
1:b:48:ILE:HG22	53:1:779:U:OP1	2.00	0.62
29:E:57:VAL:HA	29:E:60:CYS:SG	2.40	0.62
41:Q:26:CYS:SG	41:Q:29:LYS:HD3	2.39	0.62
52:3:1139:G:H5''	52:3:1140:C:H5	1.65	0.62
53:1:2156:G:H2'	53:1:2157:G:H5'	1.81	0.62
53:1:2277:G:C3'	53:1:2278:A:H5''	2.30	0.62
2:c:32:ASN:HB3	2:c:50:VAL:HG11	1.81	0.61
3:d:119:ILE:HB	3:d:187:VAL:HG12	1.82	0.61
4:e:84:ILE:CG1	53:1:2312:U:H5'	2.29	0.61
4:e:161:SER:OG	4:e:164:GLU:HG2	2.00	0.61
34:J:20:VAL:HG11	52:3:1080:A:H5''	1.81	0.61
48:X:62:THR:HG22	48:X:63:ASP:H	1.64	0.61
53:1:2514:U:H2'	53:1:2515:C:C6	2.34	0.61
25:z:23:LEU:HD22	25:z:28:LEU:HD12	1.81	0.61
41:Q:88:ASP:HB2	52:3:523:A:N1	2.14	0.61
52:3:235:C:H2'	52:3:236:A:H8	1.64	0.61
52:3:1137:C:H5'	52:3:1138:G:H5'	1.82	0.61
52:3:1506:U:O2'	52:3:1507:A:H5'	2.01	0.61
2:c:142:VAL:HG13	2:c:143:PRO:HD2	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:87:LYS:HD3	53:1:2313:C:H4'	1.83	0.61
21:v:73:LYS:HG3	21:v:94:ALA:HB2	1.82	0.61
22:w:21:ARG:HH11	22:w:27:VAL:HG12	1.65	0.61
29:E:33:THR:HG23	53:1:2420:C:OP1	2.00	0.61
32:H:59:PRO:HG2	32:H:62:SER:OG	2.00	0.61
53:1:554:U:H2'	53:1:555:G:O4'	2.00	0.61
5:f:68:ARG:HD3	5:f:68:ARG:C	2.26	0.61
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.82	0.61
49:Y:48:LYS:O	49:Y:52:GLU:HG3	2.00	0.61
22:w:23:GLY:HA2	22:w:63:VAL:HG13	1.83	0.61
45:U:41:PRO:HG2	45:U:42:ILE:CD1	2.30	0.61
52:3:396:C:H2'	52:3:397:A:H5''	1.81	0.61
53:1:2512:C:H2'	53:1:2513:A:O4'	2.00	0.61
54:2:106:G:H2'	54:2:107:G:O4'	2.00	0.61
4:e:75:GLY:HA3	53:1:2310:C:O2	1.99	0.61
42:R:25:GLY:H	52:3:1329:A:H5''	1.65	0.61
53:1:542:C:H2'	53:1:543:G:H5''	1.83	0.61
53:1:729:G:H2'	53:1:1775:U:H1'	1.83	0.61
53:1:2297:A:N6	53:1:2319:G:H1'	2.14	0.61
7:h:114:GLU:HA	7:h:123:ILE:HG12	1.83	0.61
32:H:12:GLY:H	43:S:96:LYS:HZ1	1.48	0.61
38:N:119:LYS:HG3	52:3:1349:A:OP1	2.00	0.61
52:3:1422:G:O2'	52:3:1423:G:H5'	2.01	0.61
52:3:1513:A:H2'	52:3:1514:G:C8	2.35	0.61
37:M:80:PRO:HG2	52:3:878:A:C5'	2.30	0.61
40:P:88:PRO:HG2	40:P:89:GLY:H	1.66	0.61
52:3:502:A:H2'	52:3:503:C:C6	2.36	0.61
3:d:118:LEU:HD11	3:d:188:MET:SD	2.40	0.61
27:C:20:TYR:OH	53:1:2348:U:H5'	2.01	0.61
7:h:116:GLU:HG3	7:h:117:LEU:HG	1.83	0.61
30:F:5:ALA:HB3	53:1:2466:C:H5'	1.81	0.61
53:1:1278:C:H2'	53:1:1279:G:C8	2.35	0.61
53:1:2849:U:H4'	53:1:2868:A:C2	2.36	0.61
9:j:81:ILE:HD11	53:1:2514:U:H5''	1.82	0.60
31:G:102:ASN:O	31:G:106:VAL:HG23	2.01	0.60
34:J:97:PRO:HA	34:J:122:VAL:HG12	1.83	0.60
50:Z:57:LYS:HE2	50:Z:57:LYS:HA	1.82	0.60
52:3:235:C:H2'	52:3:236:A:C8	2.35	0.60
53:1:435:C:H2'	53:1:436:C:H5'	1.83	0.60
31:G:156:LEU:HD13	31:G:178:LEU:HD11	1.81	0.60
40:P:53:GLY:O	40:P:56:LYS:HG2	2.01	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:67:ASP:O	42:R:71:GLU:HG3	2.02	0.60
53:1:2533:U:H2'	53:1:2534:A:O4'	2.00	0.60
34:J:96:GLN:NE2	34:J:97:PRO:HG2	2.17	0.60
52:3:78:A:H2'	52:3:79:G:O4'	2.02	0.60
52:3:784:A:H2'	52:3:785:G:C8	2.36	0.60
53:1:1507:C:H2'	53:1:1508:A:O4'	2.01	0.60
5:f:86:LEU:HD22	5:f:147:LEU:HD12	1.83	0.60
3:d:3:LEU:HB3	3:d:120:VAL:HG21	1.83	0.60
37:M:91:LEU:HD21	37:M:112:ASP:HB2	1.83	0.60
38:N:17:ARG:HB2	38:N:65:THR:HG23	1.82	0.60
20:u:17:ASP:HB3	20:u:20:LYS:HD2	1.83	0.60
33:I:69:ARG:O	33:I:72:ARG:HG2	2.00	0.60
52:3:350:G:H2'	52:3:351:G:C8	2.37	0.60
53:1:1415:U:H2'	53:1:1416:G:H4'	1.84	0.60
32:H:119:ILE:HG21	32:H:197:VAL:HG21	1.84	0.60
53:1:1758:U:C5	53:1:2696:U:H5'	2.37	0.60
53:1:2364:C:H2'	53:1:2365:G:O4'	2.02	0.60
5:f:2:ARG:NH1	53:1:1113:U:H5'	2.17	0.60
52:3:1370:G:H2'	52:3:1371:G:H8	1.66	0.60
4:e:132:ARG:NH2	53:1:2305:U:OP1	2.27	0.60
6:g:97:ARG:HH22	53:1:2220:U:H4'	1.67	0.60
11:l:101:ILE:HG13	11:l:102:GLY:H	1.67	0.60
22:w:39:THR:H	53:1:2331:G:H4'	1.66	0.60
33:I:80:ARG:HE	52:3:613:C:P	2.24	0.60
39:O:55:PRO:HA	43:S:81:ILE:HD11	1.82	0.60
46:V:13:SER:HB3	46:V:21:VAL:CG1	2.32	0.60
28:D:14:ARG:HD2	53:1:771:G:OP1	2.02	0.60
38:N:121:ARG:HG3	52:3:1348:U:H4'	1.84	0.60
47:W:11:ARG:CD	52:3:845:A:H4'	2.32	0.60
52:3:110:C:H2'	52:3:111:G:O4'	2.02	0.60
52:3:1170:A:H2'	52:3:1171:A:O4'	2.02	0.60
52:3:1236:A:H2'	52:3:1237:C:O4'	2.01	0.60
34:J:107:GLY:HA3	52:3:9:G:H5'	1.83	0.59
41:Q:27:PRO:HG3	52:3:553:A:H1'	1.83	0.59
52:3:578:C:H2'	52:3:579:A:H8	1.67	0.59
6:g:69:ALA:O	6:g:72:ILE:HD12	2.01	0.59
40:P:91:GLY:C	40:P:93:GLU:H	2.11	0.59
42:R:102:LYS:HG3	52:3:1226:C:N4	2.17	0.59
53:1:481:G:H1'	53:1:506:G:N2	2.17	0.59
47:W:53:GLN:NE2	47:W:56:ARG:HH21	2.01	0.59
52:3:107:G:H2'	52:3:108:G:H5'	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:225:C:H2'	52:3:226:G:H5''	1.84	0.59
53:1:215:G:C4'	53:1:216:A:H4'	2.32	0.59
53:1:2360:G:H2'	53:1:2361:G:H5'	1.85	0.59
55:5:1:C:H2'	55:5:2:G:C8	2.37	0.59
4:e:62:GLN:HG2	4:e:90:LEU:HD12	1.85	0.59
26:B:8:THR:HG21	53:1:2020:A:H5'	1.83	0.59
52:3:1413:A:H2	52:3:1487:G:H22	1.50	0.59
53:1:615:U:H5''	53:1:616:A:OP2	2.02	0.59
53:1:799:G:H5''	53:1:800:A:H2'	1.83	0.59
53:1:1509:A:H2'	53:1:1510:G:C8	2.37	0.59
53:1:2114:A:N6	53:1:2117:A:H62	2.00	0.59
53:1:2345:G:N3	53:1:2381:A:H2'	2.17	0.59
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.84	0.59
31:G:86:CYS:HB2	31:G:220:VAL:HG11	1.84	0.59
38:N:11:ARG:HH11	38:N:12:LYS:HB2	1.68	0.59
53:1:1045:C:H5'	53:1:1046:A:H5''	1.85	0.59
20:u:48:VAL:HG22	20:u:50:ALA:H	1.67	0.59
32:H:49:ALA:HB1	32:H:75:VAL:HG22	1.84	0.59
53:1:2286:G:H4'	53:1:2287:A:O5'	2.03	0.59
53:1:2446:G:H2'	53:1:2447:G:H5''	1.85	0.59
53:1:69:C:O2'	53:1:70:G:H5'	2.03	0.59
53:1:2508:G:H1	53:1:2580:U:H3	1.49	0.59
36:L:24:LYS:HA	36:L:27:ASN:ND2	2.17	0.59
52:3:692:U:H2'	52:3:694:A:OP2	2.03	0.59
52:3:1200:C:H5''	52:3:1201:A:H3'	1.85	0.59
53:1:1077:A:C2'	53:1:1078:U:H5'	2.32	0.59
53:1:2443:C:H2'	53:1:2444:G:H8	1.68	0.59
32:H:185:THR:HG22	32:H:198:LYS:HG2	1.83	0.59
53:1:118:A:OP2	53:1:119:A:H5''	2.03	0.59
1:b:201:LEU:HD11	52:3:773:G:O3'	2.03	0.59
3:d:148:ILE:HD13	3:d:187:VAL:CG2	2.32	0.59
5:f:82:PHE:HB2	5:f:140:ILE:CD1	2.33	0.59
7:h:34:THR:HG21	53:1:1057:A:H1'	1.85	0.59
41:Q:42:LYS:HE2	41:Q:44:PRO:HD2	1.83	0.59
52:3:495:A:H4'	52:3:496:A:O5'	2.03	0.59
53:1:704:G:H1'	53:1:727:A:H61	1.67	0.59
9:j:47:HIS:ND1	9:j:48:VAL:HG23	2.18	0.58
10:k:76:VAL:HG22	15:p:72:VAL:CG2	2.32	0.58
41:Q:23:LEU:HD12	41:Q:58:ASN:HB3	1.85	0.58
49:Y:28:ARG:HH22	52:3:1437:A:H5''	1.68	0.58
50:Z:3:ILE:N	50:Z:3:ILE:HD12	2.17	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:7:30:G:H2'	57:7:31:A:C8	2.38	0.58
1:b:59:GLN:HA	53:1:1568:G:H5'	1.84	0.58
33:I:23:GLY:HA3	52:3:409:U:OP1	2.02	0.58
46:V:59:GLU:HG3	46:V:76:ARG:NH1	2.18	0.58
53:1:433:C:O2'	53:1:434:U:H5'	2.03	0.58
53:1:1614:A:H2'	53:1:1615:C:H5'	1.85	0.58
11:l:55:MET:HE3	53:1:2392:A:C2	2.39	0.58
36:L:3:ARG:NH1	52:3:1092:A:H5'	2.19	0.58
52:3:29:U:O2'	52:3:30:U:H5'	2.03	0.58
55:5:59:A:C2'	55:5:60:U:H5'	2.34	0.58
1:b:160:TYR:HB3	1:b:193:GLU:HG2	1.85	0.58
4:e:65:LEU:HD22	54:2:42:C:C5	2.38	0.58
7:h:107:GLU:HG2	7:h:110:ALA:HB2	1.85	0.58
8:i:9:LYS:O	8:i:10:LEU:HD22	2.03	0.58
10:k:108:ARG:NH2	52:3:346:G:OP1	2.35	0.58
17:r:25:LEU:HD23	17:r:25:LEU:H	1.68	0.58
21:v:49:ASN:OD1	53:1:1040:A:H5'	2.04	0.58
25:z:30:ARG:HD3	53:1:1158:C:H5''	1.85	0.58
31:G:96:LEU:HB2	31:G:99:MET:HG3	1.85	0.58
34:J:26:GLY:O	52:3:1194:U:H4'	2.03	0.58
36:L:148:LYS:HE3	40:P:60:PHE:CZ	2.39	0.58
37:M:76:ARG:NH1	37:M:125:ILE:HG23	2.18	0.58
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.86	0.58
53:1:2710:C:H2'	53:1:2711:A:H8	1.68	0.58
20:u:32:LYS:HB3	20:u:63:ALA:HB1	1.86	0.58
23:x:2:ARG:O	23:x:11:PRO:HD3	2.04	0.58
53:1:948:C:H2'	53:1:949:G:C8	2.39	0.58
2:c:56:LYS:NZ	53:1:2830:C:H5''	2.19	0.58
5:f:82:PHE:HB2	5:f:140:ILE:HD12	1.86	0.58
52:3:876:C:H2'	52:3:877:G:C8	2.38	0.58
52:3:1237:C:OP1	52:3:1238:A:H1'	2.03	0.58
53:1:310:A:O2'	53:1:311:A:H5''	2.04	0.58
57:7:68:C:H2'	57:7:69:G:C8	2.39	0.58
15:p:52:ARG:NH2	53:1:2720:U:H5''	2.19	0.58
16:q:5:ARG:NH1	53:1:585:G:N7	2.52	0.58
30:F:2:LYS:HZ3	53:1:2477:U:H2'	1.69	0.58
33:I:13:ARG:NH2	52:3:510:A:H4'	2.19	0.58
52:3:211:G:H2'	52:3:212:G:H5'	1.85	0.58
52:3:1513:A:H2'	52:3:1514:G:H8	1.69	0.58
42:R:103:THR:HG21	52:3:1230:C:H41	1.68	0.58
52:3:34:C:H2'	52:3:35:G:C8	2.39	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:304:U:H2'	52:3:305:G:C8	2.39	0.58
11:l:38:GLN:HE21	53:1:805:G:H5''	1.69	0.58
48:X:71:GLY:HA3	52:3:1320:C:O2	2.04	0.58
53:1:1912:A:H62	53:1:1917:U:H3	1.52	0.58
55:5:51:C:H2'	55:5:52:G:C8	2.38	0.58
7:h:55:VAL:HA	53:1:1084:A:C4'	2.34	0.57
20:u:94:PHE:HB2	20:u:100:GLU:O	2.04	0.57
53:1:1373:A:H5'	53:1:2212:A:H1'	1.86	0.57
53:1:2190:G:H2'	53:1:2191:A:O4'	2.04	0.57
54:2:3:C:C3'	54:2:4:C:H5''	2.34	0.57
55:5:25:C:H2'	55:5:26:G:O4'	2.04	0.57
9:j:88:THR:OG1	9:j:91:GLU:HG3	2.04	0.57
25:z:23:LEU:HD11	25:z:53:MET:HE3	1.86	0.57
33:I:39:GLN:HE21	33:I:40:HIS:HE1	1.53	0.57
35:K:81:ASN:HB3	35:K:84:VAL:HG12	1.86	0.57
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.86	0.57
52:3:1271:A:H5'	52:3:1314:C:H5''	1.86	0.57
53:1:717:C:H2'	53:1:718:A:H5'	1.86	0.57
53:1:821:A:H5''	53:1:822:G:C5'	2.34	0.57
53:1:2238:G:H2'	53:1:2238:G:N3	2.18	0.57
52:3:181:A:N6	52:3:194:C:H2'	2.19	0.57
52:3:331:G:OP1	52:3:332:G:H5''	2.04	0.57
52:3:1287:A:C2	52:3:1353:G:H1'	2.39	0.57
53:1:146:A:H2'	53:1:147:C:C6	2.40	0.57
53:1:2391:G:H2'	53:1:2424:C:H41	1.69	0.57
53:1:2834:G:H2'	53:1:2879:A:H61	1.69	0.57
57:7:39:U:H2'	57:7:40:C:C6	2.40	0.57
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.86	0.57
45:U:33:ILE:H	45:U:33:ILE:HD12	1.69	0.57
46:V:10:ARG:NH1	46:V:55:GLY:HA2	2.19	0.57
49:Y:67:HIS:CE1	52:3:132:C:H4'	2.39	0.57
53:1:2287:A:O2'	53:1:2288:A:H2'	2.04	0.57
13:n:96:ARG:HD3	13:n:98:LEU:HD21	1.86	0.57
17:r:14:VAL:CG1	17:r:98:ILE:HG13	2.34	0.57
51:a:208:TYR:HB3	51:a:209:ILE:HD12	1.87	0.57
52:3:1402:C:H2'	52:3:1403:C:O4'	2.03	0.57
53:1:1035:U:H2'	53:1:1036:G:H8	1.70	0.57
53:1:1139:G:O2'	53:1:1140:C:H5'	2.04	0.57
53:1:2104:C:H2'	53:1:2105:U:C6	2.40	0.57
16:q:23:TYR:CD1	53:1:533:G:H5'	2.40	0.57
52:3:405:U:O2	52:3:498:A:H2'	2.03	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1005:A:H2'	52:3:1006:G:O4'	2.05	0.57
36:L:113:LYS:HB3	36:L:117:LEU:HD23	1.86	0.57
50:Z:13:VAL:HG23	50:Z:15:LEU:HG	1.85	0.57
53:1:2628:C:H3'	53:1:2629:U:H5'	1.85	0.57
55:5:47:U:H2'	55:5:50:U:OP1	2.05	0.57
57:7:16:U:H5''	57:7:17:C:OP2	2.04	0.57
2:c:202:ILE:HD12	2:c:202:ILE:N	2.19	0.57
3:d:23:PHE:HB2	3:d:111:GLU:OE1	2.04	0.57
7:h:117:LEU:HD23	7:h:120:ALA:HA	1.87	0.57
15:p:63:ILE:HA	15:p:68:GLY:HA2	1.87	0.57
40:P:25:SER:O	40:P:89:GLY:HA2	2.05	0.57
47:W:11:ARG:H	47:W:11:ARG:HD3	1.69	0.57
49:Y:28:ARG:NH1	52:3:1437:A:H5''	2.15	0.57
52:3:503:C:H2'	52:3:504:C:C6	2.39	0.57
53:1:1348:C:H2'	53:1:1349:C:H5'	1.87	0.57
53:1:2183:A:H2'	53:1:2184:A:C8	2.40	0.57
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.86	0.57
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.85	0.57
31:G:146:SER:C	31:G:147:LEU:HD12	2.29	0.57
32:H:141:MET:HA	32:H:145:ALA:HB3	1.86	0.57
43:S:20:PHE:O	43:S:21:ALA:HB3	2.04	0.57
52:3:371:A:H2'	52:3:372:C:O4'	2.05	0.57
52:3:917:G:H2'	52:3:918:A:C8	2.40	0.57
53:1:112:U:H2'	53:1:113:U:H5'	1.86	0.57
53:1:598:U:H2'	53:1:599:A:C8	2.40	0.57
53:1:1053:C:C3'	53:1:1054:A:H5''	2.34	0.57
53:1:1417:C:H4'	53:1:1587:G:H21	1.70	0.57
53:1:2498:C:O2'	53:1:2499:C:H5'	2.05	0.57
13:n:6:SER:OG	13:n:46:ARG:NH2	2.38	0.57
22:w:12:SER:OG	53:1:2262:U:H5	1.87	0.57
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.87	0.57
53:1:1837:C:H2'	53:1:1899:A:N6	2.20	0.57
2:c:133:THR:HG23	2:c:134:HIS:CD2	2.39	0.56
12:m:45:GLN:NE2	53:1:2485:G:H5''	2.19	0.56
35:K:91:ARG:HG3	35:K:92:THR:H	1.69	0.56
49:Y:25:SER:OG	52:3:1458:G:H5''	2.05	0.56
52:3:1128:C:O2'	52:3:1129:C:H5'	2.04	0.56
12:m:4:PRO:HG3	12:m:68:PHE:CE2	2.39	0.56
18:s:4:ILE:HG22	18:s:106:VAL:HG22	1.86	0.56
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.21	0.56
31:G:72:LYS:HE2	31:G:167:HIS:CG	2.39	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:23:ALA:O	36:L:26:VAL:HG12	2.05	0.56
37:M:82:LEU:O	37:M:82:LEU:HD23	2.05	0.56
52:3:70:U:H4'	52:3:71:A:H8	1.70	0.56
53:1:1979:U:O2'	53:1:1980:G:H5'	2.04	0.56
8:i:12:VAL:O	8:i:13:ALA:C	2.48	0.56
31:G:106:VAL:O	31:G:110:ILE:HG13	2.04	0.56
37:M:12:ARG:NH2	52:3:826:C:H5'	2.19	0.56
40:P:107:THR:O	50:Z:6:ARG:HG3	2.05	0.56
43:S:2:LYS:NZ	52:3:1049:U:H2'	2.21	0.56
45:U:42:ILE:HD11	52:3:450:G:H4'	1.87	0.56
47:W:61:ALA:HB1	47:W:67:LEU:HD23	1.86	0.56
49:Y:18:LYS:NZ	52:3:1459:G:H4'	2.19	0.56
49:Y:30:PHE:HA	49:Y:33:LYS:HD3	1.86	0.56
52:3:1256:A:O2'	52:3:1257:A:H5''	2.05	0.56
53:1:189:G:H2'	53:1:205:G:N2	2.20	0.56
53:1:639:U:H2'	53:1:640:C:C6	2.40	0.56
53:1:1367:A:H2'	53:1:1368:G:H5'	1.86	0.56
53:1:1810:A:H2'	53:1:1811:G:O4'	2.04	0.56
53:1:2220:U:H2'	53:1:2221:G:H8	1.69	0.56
53:1:2313:C:H2'	53:1:2314:A:C8	2.40	0.56
4:e:21:TYR:HB3	4:e:26:GLN:HB3	1.86	0.56
22:w:41:PHE:O	22:w:55:LEU:HD11	2.05	0.56
39:O:10:LEU:HD23	39:O:10:LEU:H	1.70	0.56
39:O:11:LYS:HE3	39:O:69:THR:OG1	2.05	0.56
52:3:1137:C:H4'	52:3:1138:G:N2	2.21	0.56
53:1:828:U:H2'	53:1:829:A:C8	2.40	0.56
10:k:108:ARG:NH1	15:p:33:GLU:OE1	2.38	0.56
11:l:79:LEU:HD12	11:l:114:GLY:H	1.70	0.56
12:m:45:GLN:HE21	53:1:2485:G:H5''	1.70	0.56
39:O:59:LYS:HE2	39:O:62:ARG:NE	2.20	0.56
44:T:31:LEU:HD22	44:T:58:MET:HB2	1.86	0.56
51:a:209:ILE:HD12	51:a:209:ILE:N	2.21	0.56
52:3:876:C:H2'	52:3:877:G:H8	1.70	0.56
52:3:1342:C:H2'	52:3:1343:G:C8	2.41	0.56
52:3:1414:U:H2'	52:3:1415:G:C8	2.40	0.56
53:1:996:A:H2'	53:1:997:G:H8	1.69	0.56
6:g:97:ARG:NH2	53:1:2220:U:H4'	2.20	0.56
19:t:8:LEU:HD13	24:y:21:LEU:HB3	1.87	0.56
36:L:56:SER:OG	36:L:59:GLU:HG2	2.06	0.56
43:S:40:ARG:HE	48:X:6:LYS:HG2	1.70	0.56
52:3:40:C:H2'	52:3:41:G:H8	1.71	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1395:C:O2'	52:3:1396:A:H5'	2.05	0.56
53:1:940:G:H3'	53:1:941:A:H5''	1.87	0.56
53:1:1779:U:OP2	53:1:1784:A:N6	2.39	0.56
3:d:5:LEU:HB2	3:d:10:SER:H	1.69	0.56
4:e:151:LEU:HA	53:1:2305:U:C4	2.41	0.56
14:o:7:ARG:NH1	14:o:95:SER:O	2.39	0.56
36:L:101:ARG:NH2	52:3:1375:A:O2'	2.38	0.56
52:3:352:C:H4'	52:3:354:G:OP1	2.06	0.56
53:1:2048:G:C3'	53:1:2049:G:H5''	2.35	0.56
2:c:194:PRO:HA	53:1:2680:U:H5'	1.87	0.56
22:w:17:LEU:HD21	22:w:37:ARG:NH2	2.20	0.56
39:O:65:TYR:HB3	43:S:95:LEU:HD11	1.86	0.56
52:3:1259:C:H3'	52:3:1260:G:C5'	2.30	0.56
52:3:1405:G:H21	52:3:1518:A:H1'	1.70	0.56
53:1:821:A:H5''	53:1:822:G:H5'	1.87	0.56
57:7:28:G:H1	57:7:42:C:H42	1.52	0.56
57:7:30:G:H2'	57:7:31:A:H8	1.69	0.56
6:g:47:PHE:HA	6:g:51:ARG:HB3	1.87	0.56
37:M:55:LYS:HE3	52:3:653:U:O4'	2.06	0.56
46:V:45:VAL:HG12	46:V:72:TRP:HB2	1.87	0.56
52:3:606:G:H5''	52:3:607:A:H5'	1.88	0.56
52:3:902:G:H2'	52:3:903:G:H8	1.71	0.56
6:g:7:ASP:CG	6:g:8:LYS:H	2.12	0.56
7:h:6:GLN:O	7:h:9:GLN:HG2	2.06	0.56
30:F:32:LYS:NZ	53:1:2478:A:H5'	2.21	0.56
34:J:133:ILE:HD11	52:3:1079:G:H5'	1.88	0.56
36:L:4:ARG:NH2	52:3:1377:A:H2'	2.21	0.56
37:M:101:ALA:HB3	37:M:112:ASP:HB3	1.88	0.56
53:1:278:A:H2'	53:1:278:A:N3	2.21	0.56
53:1:367:G:H2'	53:1:368:A:O4'	2.06	0.56
7:h:105:LYS:O	7:h:105:LYS:HD3	2.06	0.55
53:1:2001:C:H4'	53:1:2689:U:O2'	2.06	0.55
3:d:117:ARG:HH12	11:l:2:ARG:HG2	1.70	0.55
14:o:73:ALA:O	14:o:76:LYS:HB3	2.06	0.55
26:B:2:VAL:HG22	26:B:3:GLN:H	1.71	0.55
26:B:9:ARG:H	26:B:9:ARG:HD2	1.70	0.55
52:3:31:G:N2	52:3:47:C:H5''	2.20	0.55
52:3:77:A:H2'	52:3:78:A:C8	2.41	0.55
52:3:211:G:C2'	52:3:212:G:H5'	2.36	0.55
53:1:807:U:H2'	53:1:808:G:C8	2.39	0.55
53:1:2747:G:O6	53:1:2755:C:H5''	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:216:ARG:CG	1:b:217:PRO:HD2	2.37	0.55
31:G:46:VAL:HG23	31:G:47:PRO:CD	2.35	0.55
31:G:138:ARG:O	31:G:141:GLU:HG2	2.07	0.55
52:3:107:G:C2'	52:3:108:G:H5'	2.37	0.55
53:1:669:G:H2'	53:1:669:G:N3	2.20	0.55
53:1:2196:C:O2'	53:1:2197:U:H5'	2.05	0.55
53:1:2467:C:H2'	53:1:2468:A:O4'	2.06	0.55
29:E:20:GLY:HA3	29:E:48:MET:HE1	1.89	0.55
34:J:133:ILE:CD1	52:3:1079:G:H5'	2.36	0.55
46:V:10:ARG:HH11	46:V:55:GLY:HA2	1.71	0.55
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.87	0.55
53:1:502:A:H2'	53:1:503:A:H5'	1.88	0.55
1:b:216:ARG:HG3	1:b:217:PRO:HD2	1.89	0.55
1:b:250:GLN:NE2	1:b:251:THR:O	2.38	0.55
52:3:193:C:H2'	52:3:194:C:C6	2.40	0.55
53:1:2071:A:H2'	53:1:2072:C:C6	2.41	0.55
1:b:140:VAL:HG12	1:b:141:HIS:H	1.71	0.55
4:e:130:GLY:HA3	53:1:2305:U:H5''	1.88	0.55
7:h:118:ILE:HG22	7:h:119:PRO:CD	2.36	0.55
10:k:87:LEU:HA	10:k:94:PRO:HA	1.87	0.55
31:G:142:LYS:HE2	52:3:1098:C:OP1	2.07	0.55
42:R:3:ILE:HD12	42:R:3:ILE:H	1.71	0.55
52:3:86:G:H4'	52:3:87:C:C5	2.42	0.55
52:3:390:U:H2'	52:3:391:G:H8	1.71	0.55
5:f:151:ARG:HB3	5:f:161:VAL:HG23	1.88	0.55
11:l:95:LEU:HD22	11:l:100:ILE:CD1	2.36	0.55
17:r:55:ASP:CG	17:r:56:GLY:H	2.15	0.55
48:X:28:LYS:CE	48:X:29:PRO:HD2	2.36	0.55
52:3:31:G:H21	52:3:47:C:H5''	1.71	0.55
53:1:2086:U:H2'	53:1:2087:G:C8	2.41	0.55
1:b:42:ARG:N	1:b:42:ARG:HD2	2.22	0.55
11:l:118:THR:HG23	11:l:120:VAL:HG13	1.89	0.55
17:r:76:LYS:HB2	17:r:85:LYS:HB3	1.87	0.55
32:H:181:ILE:HD12	32:H:181:ILE:N	2.22	0.55
52:3:1540:U:O2	52:3:1540:U:H3'	2.07	0.55
53:1:1344:U:H3'	53:1:1345:C:H5'	1.88	0.55
53:1:2156:G:C2'	53:1:2157:G:H5'	2.37	0.55
52:3:20:U:H2'	52:3:21:G:O4'	2.06	0.55
53:1:279:A:H2'	53:1:280:U:H5'	1.88	0.55
53:1:979:A:H2'	53:1:982:C:N4	2.22	0.55
53:1:1936:A:H2	53:1:1943:U:H3	1.54	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:154:ALA:HB2	1:b:161:VAL:HG23	1.86	0.55
52:3:1524:C:H2'	52:3:1525:G:C8	2.41	0.55
53:1:738:G:O2'	53:1:739:A:H5'	2.06	0.55
53:1:1827:U:O2'	53:1:1828:G:H5'	2.07	0.55
53:1:1874:C:H2'	53:1:1875:G:O4'	2.07	0.55
10:k:70:ARG:HG2	10:k:76:VAL:HG12	1.90	0.54
28:D:26:ASN:CG	53:1:682:G:H5'	2.32	0.54
29:E:31:ILE:O	29:E:31:ILE:HG13	2.07	0.54
33:I:12:ARG:HG2	33:I:33:ILE:HD12	1.89	0.54
33:I:69:ARG:NH2	52:3:547:A:OP1	2.40	0.54
39:O:5:ARG:HB3	39:O:6:ILE:HD12	1.88	0.54
42:R:53:ASP:HA	42:R:56:ARG:HH11	1.70	0.54
52:3:865:A:H2'	52:3:866:C:C6	2.42	0.54
53:1:1078:U:C5'	53:1:1079:C:H5''	2.38	0.54
4:e:116:LEU:H	4:e:175:PRO:HB2	1.72	0.54
5:f:174:LYS:CE	53:1:2529:G:H4'	2.37	0.54
40:P:122:PRO:HB2	50:Z:33:ARG:HA	1.89	0.54
45:U:6:LEU:HD22	45:U:17:TYR:HB3	1.89	0.54
52:3:715:A:H2'	52:3:716:A:C8	2.43	0.54
53:1:290:U:H2'	53:1:291:G:H8	1.73	0.54
53:1:1571:A:H2'	53:1:1572:A:C8	2.43	0.54
19:t:8:LEU:HD13	24:y:21:LEU:C	2.32	0.54
36:L:43:TYR:HA	36:L:46:LEU:HD12	1.88	0.54
51:a:67:HIS:HB2	51:a:188:ASN:HD21	1.73	0.54
52:3:245:U:O2'	52:3:246:A:H5'	2.06	0.54
52:3:1391:U:H2'	52:3:1392:G:C8	2.42	0.54
52:3:1527:U:H2'	52:3:1528:U:C6	2.42	0.54
53:1:1854:A:N6	53:1:1888:G:H1'	2.22	0.54
53:1:2163:A:H2'	53:1:2164:C:H5'	1.89	0.54
1:b:62:ARG:HG3	1:b:62:ARG:HH11	1.72	0.54
15:p:96:LEU:HB3	15:p:99:LEU:HD13	1.88	0.54
35:K:38:ARG:HD3	35:K:97:THR:HA	1.89	0.54
36:L:19:SER:HG	36:L:22:LEU:HB2	1.70	0.54
38:N:59:LYS:HD2	38:N:60:LEU:HG	1.89	0.54
51:a:173:THR:HG22	51:a:174:THR:H	1.72	0.54
52:3:1512:U:H2'	52:3:1513:A:C8	2.43	0.54
53:1:818:G:C2'	53:1:819:A:H5''	2.37	0.54
53:1:876:C:H2'	53:1:877:A:O4'	2.08	0.54
53:1:2485:G:O2'	53:1:2486:C:H5'	2.08	0.54
48:X:38:THR:HA	48:X:69:LYS:HA	1.90	0.54
52:3:21:G:H2'	52:3:22:G:C8	2.42	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:578:C:H2'	52:3:579:A:C8	2.43	0.54
53:1:293:U:H2'	53:1:294:A:H5''	1.89	0.54
53:1:619:G:H3'	53:1:620:G:H21	1.73	0.54
53:1:2066:C:O2'	53:1:2067:G:H5'	2.08	0.54
57:7:40:C:H2'	57:7:41:C:C6	2.43	0.54
5:f:22:VAL:HG12	5:f:35:THR:HB	1.88	0.54
5:f:173:ALA:O	5:f:174:LYS:HG2	2.08	0.54
19:t:6:ARG:NH2	19:t:37:ASP:O	2.41	0.54
31:G:12:GLY:HA2	31:G:14:HIS:CE1	2.42	0.54
31:G:77:GLU:HA	31:G:80:LYS:HZ1	1.72	0.54
40:P:58:THR:HG22	40:P:60:PHE:H	1.73	0.54
48:X:5:LYS:HB3	52:3:1313:U:OP2	2.08	0.54
50:Z:16:ARG:HB2	50:Z:19:LYS:HG2	1.89	0.54
52:3:236:A:H2'	52:3:237:G:C8	2.43	0.54
52:3:1060:U:H2'	52:3:1061:G:H8	1.72	0.54
54:2:66:A:H4'	54:2:67:G:C8	2.43	0.54
57:7:47:U:C4	57:7:49:C:H4'	2.43	0.54
5:f:32:LEU:HD23	5:f:74:MET:HG2	1.90	0.54
40:P:47:GLY:HA3	40:P:52:ARG:HH11	1.72	0.54
57:7:14:A:H2'	57:7:15:G:O4'	2.07	0.54
4:e:31:GLU:OE2	4:e:91:ARG:NH2	2.40	0.54
7:h:37:LYS:HG3	7:h:41:LEU:HD12	1.90	0.54
9:j:101:ILE:H	9:j:101:ILE:HD12	1.72	0.54
24:y:3:ALA:O	24:y:7:ARG:NH1	2.41	0.54
36:L:109:LYS:HD2	36:L:132:THR:HG21	1.89	0.54
38:N:15:ALA:HB1	52:3:1148:U:O3'	2.08	0.54
42:R:6:ILE:HG13	42:R:7:ASN:N	2.22	0.54
52:3:77:A:H2'	52:3:78:A:H8	1.73	0.54
52:3:530:G:H22	52:3:1492:A:H61	1.54	0.54
53:1:2155:U:H2'	53:1:2156:G:H5'	1.90	0.54
53:1:2774:C:H2'	53:1:2775:G:O4'	2.08	0.54
55:5:68:C:C2'	55:5:69:C:H5'	2.38	0.54
9:j:84:ILE:HG23	9:j:84:ILE:O	2.08	0.54
19:t:47:VAL:HG13	19:t:51:PHE:HD2	1.73	0.54
31:G:117:GLU:O	31:G:121:GLN:HG2	2.07	0.54
51:a:9:ARG:O	51:a:13:GLU:HG3	2.07	0.54
52:3:423:G:H2'	52:3:424:G:H5'	1.90	0.54
53:1:752:A:O2'	53:1:1781:U:H5'	2.07	0.54
53:1:760:G:H2'	53:1:761:A:O4'	2.08	0.54
53:1:1437:C:H2'	53:1:1438:U:C6	2.43	0.54
53:1:1936:A:H3'	53:1:1937:A:H5'	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2655:G:O2'	53:1:2656:U:H5	1.91	0.54
53:1:2808:G:H2'	53:1:2890:G:O6	2.08	0.54
54:2:13:G:H21	54:2:16:G:H1'	1.73	0.54
17:r:49:ILE:HD12	17:r:52:PRO:HA	1.90	0.54
32:H:11:LEU:HB3	43:S:96:LYS:NZ	2.23	0.54
33:I:147:LYS:O	33:I:147:LYS:HD3	2.08	0.54
37:M:46:GLU:O	37:M:61:THR:HB	2.08	0.54
41:Q:51:VAL:HG22	41:Q:52:CYS:N	2.20	0.54
45:U:4:ILE:HB	45:U:67:ILE:HA	1.90	0.54
52:3:502:A:H2'	52:3:503:C:H6	1.72	0.54
53:1:184:C:H2'	53:1:185:G:H8	1.73	0.54
53:1:594:U:H2'	53:1:595:C:C6	2.43	0.54
53:1:2799:A:C2'	53:1:2800:A:H5'	2.38	0.54
32:H:122:GLN:HB3	32:H:127:VAL:HG21	1.89	0.53
39:O:29:ALA:O	39:O:33:GLY:N	2.41	0.53
42:R:89:ARG:HH21	42:R:95:PRO:HG2	1.73	0.53
52:3:505:G:H5'	52:3:534:U:H2'	1.89	0.53
53:1:1550:C:H2'	53:1:1551:A:H8	1.73	0.53
53:1:2029:G:O6	53:1:2032:G:H5''	2.08	0.53
41:Q:68:GLY:O	52:3:521:G:H5'	2.08	0.53
49:Y:23:ARG:HH12	52:3:176:C:H5''	1.73	0.53
53:1:481:G:H1'	53:1:506:G:H21	1.73	0.53
54:2:51:G:H2'	54:2:52:A:O4'	2.08	0.53
1:b:89:ASN:CG	1:b:196:ASN:HD22	2.16	0.53
9:j:81:ILE:HD11	53:1:2514:U:C5'	2.38	0.53
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.89	0.53
25:z:8:GLN:HB2	25:z:28:LEU:HD13	1.90	0.53
32:H:86:LEU:O	32:H:90:VAL:HG22	2.08	0.53
33:I:18:LEU:HB2	33:I:20:LEU:HD23	1.90	0.53
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.44	0.53
45:U:16:PHE:HZ	45:U:38:PHE:HB2	1.73	0.53
53:1:1176:U:H2'	53:1:1177:G:C8	2.43	0.53
53:1:1736:U:H2'	53:1:1737:G:O4'	2.08	0.53
53:1:2019:A:H2	53:1:2035:G:H22	1.55	0.53
53:1:2266:A:H4'	53:1:2267:A:N3	2.24	0.53
1:b:1:ALA:N	1:b:19:VAL:O	2.42	0.53
12:m:50:ARG:HD3	12:m:65:ILE:HD11	1.90	0.53
15:p:31:VAL:HG11	15:p:40:GLN:HE21	1.73	0.53
49:Y:53:MET:HA	49:Y:56:ILE:HD11	1.90	0.53
55:5:61:C:H3'	55:5:62:C:C5'	2.34	0.53
13:n:29:VAL:HB	13:n:75:ILE:HD12	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:1:MET:HB3	6:g:3:VAL:HG23	1.89	0.53
25:z:41:PRO:HA	25:z:44:ARG:HB2	1.90	0.53
32:H:5:HIS:CD2	43:S:88:MET:HG3	2.44	0.53
32:H:119:ILE:HG13	32:H:132:ALA:HB1	1.89	0.53
44:T:49:HIS:CE1	52:3:764:C:H5''	2.42	0.53
47:W:31:TYR:CG	47:W:54:LEU:HD21	2.43	0.53
52:3:313:A:H2'	52:3:314:C:C6	2.44	0.53
52:3:945:G:H2'	52:3:945:G:N3	2.23	0.53
53:1:226:A:H2'	53:1:227:A:O4'	2.08	0.53
53:1:974:G:H1'	53:1:975:A:C8	2.44	0.53
53:1:974:G:N3	53:1:974:G:H2'	2.24	0.53
53:1:1830:C:H2'	53:1:1831:G:H8	1.73	0.53
53:1:2788:C:H2'	53:1:2789:C:C6	2.43	0.53
2:c:101:PHE:HE1	2:c:205:PRO:HG3	1.73	0.53
48:X:17:LYS:HA	48:X:20:LYS:HE3	1.90	0.53
52:3:763:G:H2'	52:3:764:C:C6	2.44	0.53
52:3:1287:A:H2	52:3:1353:G:H1'	1.73	0.53
53:1:2286:G:H4'	53:1:2287:A:O4'	2.08	0.53
53:1:2743:U:C3'	53:1:2744:G:H5''	2.39	0.53
55:5:36:U:H3	56:4:16:A:H61	1.57	0.53
18:s:77:ASP:OD2	18:s:102:HIS:HB2	2.09	0.53
20:u:85:ARG:HD3	20:u:87:GLU:HG2	1.90	0.53
31:G:134:LEU:HG	31:G:138:ARG:HE	1.74	0.53
33:I:201:GLU:HB3	52:3:8:A:N6	2.24	0.53
52:3:33:A:H2'	52:3:34:C:C6	2.43	0.53
52:3:881:G:O2'	52:3:882:C:H5'	2.08	0.53
52:3:1412:C:H2'	52:3:1413:A:C8	2.43	0.53
1:b:209:ALA:O	1:b:213:ARG:HG2	2.08	0.53
2:c:133:THR:OG1	2:c:134:HIS:N	2.40	0.53
12:m:17:ASN:ND2	12:m:95:LEU:HD22	2.24	0.53
28:D:22:MET:O	28:D:28:ARG:NH1	2.42	0.53
32:H:177:LEU:HG	52:3:1112:C:N3	2.24	0.53
41:Q:33:CYS:HA	41:Q:54:VAL:HA	1.90	0.53
52:3:503:C:H2'	52:3:504:C:H6	1.73	0.53
52:3:673:A:H2'	52:3:674:G:C8	2.44	0.53
52:3:966:G:H1'	55:5:34:C:H4'	1.91	0.53
52:3:1352:C:H2'	52:3:1353:G:H8	1.74	0.53
52:3:1484:C:H2'	52:3:1485:U:C6	2.43	0.53
4:e:92:GLY:O	4:e:95:MET:HG2	2.09	0.53
4:e:132:ARG:NE	53:1:2305:U:H4'	2.24	0.53
7:h:118:ILE:CG2	7:h:119:PRO:HD3	2.39	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:41:ILE:HD11	10:k:86:LEU:HD21	1.91	0.53
10:k:68:GLY:HA3	10:k:78:ARG:HG2	1.90	0.53
35:K:75:GLU:HA	35:K:78:PHE:HD2	1.73	0.53
52:3:225:C:C3'	52:3:226:G:H5''	2.39	0.53
52:3:411:A:H1'	52:3:413:G:H1'	1.91	0.53
52:3:663:A:H5'	52:3:836:G:OP1	2.09	0.53
52:3:1033:G:C2'	52:3:1034:G:H5''	2.39	0.53
52:3:1060:U:H2'	52:3:1061:G:C8	2.43	0.53
52:3:1404:C:H2'	52:3:1405:G:C8	2.44	0.53
21:v:48:MET:SD	21:v:51:GLN:NE2	2.82	0.52
41:Q:11:ARG:NH1	52:3:563:A:H2	2.07	0.52
41:Q:13:ARG:HH22	52:3:302:G:H4'	1.74	0.52
50:Z:39:LYS:HB3	50:Z:43:GLU:HG2	1.90	0.52
52:3:346:G:H2'	52:3:347:G:H5'	1.90	0.52
52:3:1368:A:O2'	52:3:1369:C:H5'	2.09	0.52
53:1:414:C:H2'	53:1:415:A:C8	2.44	0.52
53:1:1421:G:H1'	53:1:1494:A:H61	1.73	0.52
53:1:2185:U:H2'	53:1:2186:G:C8	2.44	0.52
4:e:142:TYR:HB2	42:R:70:ARG:HH21	1.74	0.52
19:t:57:VAL:HG12	19:t:58:VAL:H	1.72	0.52
38:N:105:ARG:O	38:N:105:ARG:HD3	2.09	0.52
43:S:40:ARG:HH21	48:X:6:LYS:HG2	1.74	0.52
52:3:372:C:N4	52:3:387:U:H2'	2.23	0.52
52:3:1193:G:O2'	52:3:1194:U:H5'	2.09	0.52
53:1:968:C:H2'	53:1:969:G:C8	2.44	0.52
53:1:2832:U:H1'	53:1:2834:G:C2	2.44	0.52
54:2:49:C:H2'	54:2:50:A:C8	2.44	0.52
1:b:86:ARG:HE	53:1:1817:G:H5''	1.74	0.52
1:b:131:MET:HE2	1:b:187:CYS:HB2	1.91	0.52
8:i:45:THR:HG22	8:i:50:LYS:HG2	1.90	0.52
10:k:13:ASN:HD22	52:3:339:C:P	2.31	0.52
33:I:33:ILE:HG13	33:I:34:GLU:H	1.74	0.52
38:N:78:ILE:O	38:N:82:ILE:HG12	2.10	0.52
42:R:33:LEU:HD21	42:R:40:GLU:HG2	1.92	0.52
52:3:784:A:H2'	52:3:785:G:H8	1.74	0.52
52:3:1306:A:N6	52:3:1331:G:H1'	2.24	0.52
53:1:818:G:O2'	53:1:819:A:H5''	2.09	0.52
53:1:2372:U:H2'	53:1:2373:G:H8	1.73	0.52
1:b:251:THR:HG23	1:b:252:LYS:HG2	1.92	0.52
18:s:93:ALA:HB2	53:1:1614:A:N1	2.24	0.52
31:G:6:ARG:HH21	31:G:10:LYS:HG3	1.74	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:2:ARG:HB3	52:3:933:G:OP2	2.09	0.52
38:N:29:ILE:N	38:N:29:ILE:HD12	2.23	0.52
53:1:466:A:H2'	53:1:467:G:H5'	1.91	0.52
3:d:109:LEU:HD13	3:d:112:LEU:HD12	1.91	0.52
4:e:70:ARG:HD2	53:1:2298:A:OP1	2.09	0.52
8:i:53:PRO:HD2	8:i:77:VAL:HG21	1.91	0.52
41:Q:101:LEU:HD12	41:Q:101:LEU:H	1.74	0.52
42:R:52:ILE:HG23	42:R:56:ARG:NH1	2.20	0.52
49:Y:70:LYS:HE2	49:Y:74:HIS:NE2	2.24	0.52
52:3:948:C:H2'	52:3:949:A:H8	1.74	0.52
53:1:1547:C:H2'	53:1:1548:A:H8	1.75	0.52
53:1:2480:C:H2'	53:1:2481:G:O4'	2.08	0.52
53:1:2489:U:O2'	53:1:2490:G:H5'	2.09	0.52
1:b:38:LYS:HE2	1:b:59:GLN:HE21	1.75	0.52
14:o:98:GLN:HE22	53:1:2293:G:H4'	1.75	0.52
16:q:108:LEU:HD23	17:r:48:LYS:NZ	2.25	0.52
20:u:50:ALA:O	20:u:51:LEU:HG	2.10	0.52
41:Q:30:ARG:HH22	52:3:362:G:P	2.32	0.52
48:X:39:ILE:HB	48:X:66:VAL:HA	1.91	0.52
52:3:37:U:H2'	52:3:38:G:H8	1.74	0.52
52:3:361:G:H2'	52:3:362:G:O4'	2.10	0.52
52:3:946:A:H2'	52:3:947:G:C8	2.44	0.52
53:1:1026:G:H2'	53:1:1027:A:H8	1.74	0.52
53:1:1378:A:H1'	53:1:1379:U:C5	2.43	0.52
53:1:1796:U:H2'	53:1:1797:G:C8	2.42	0.52
15:p:59:THR:HG22	15:p:72:VAL:HG12	1.91	0.52
33:I:50:TYR:HD2	52:3:509:A:H5'	1.73	0.52
49:Y:67:HIS:CB	52:3:262:A:H5'	2.40	0.52
50:Z:9:GLU:CB	50:Z:10:PRO:HD3	2.40	0.52
52:3:70:U:H4'	52:3:71:A:C8	2.45	0.52
52:3:920:U:H2'	52:3:921:U:C6	2.45	0.52
24:y:43:LEU:O	24:y:46:VAL:HG12	2.10	0.52
26:B:9:ARG:HD2	26:B:9:ARG:N	2.24	0.52
32:H:32:LEU:HD11	43:S:64:ARG:HH22	1.75	0.52
45:U:33:ILE:HD12	45:U:33:ILE:N	2.24	0.52
48:X:2:ARG:HD2	52:3:1312:G:N7	2.24	0.52
48:X:54:ARG:HB3	52:3:958:A:C2	2.44	0.52
48:X:62:THR:H	48:X:65:MET:HE3	1.74	0.52
52:3:243:A:H4'	52:3:244:U:H3'	1.91	0.52
52:3:285:C:H2'	52:3:286:C:C6	2.45	0.52
52:3:1096:C:H2'	52:3:1097:C:C6	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:167:A:H2'	53:1:168:G:O4'	2.09	0.52
53:1:290:U:H2'	53:1:291:G:C8	2.45	0.52
53:1:2818:U:H2'	53:1:2819:G:H8	1.75	0.52
4:e:62:GLN:OE1	54:2:43:C:H4'	2.10	0.52
11:l:23:ILE:HG23	17:r:82:HIS:CD2	2.44	0.52
16:q:105:PHE:HA	16:q:108:LEU:HD12	1.92	0.52
18:s:57:ASN:OD1	18:s:61:ASN:ND2	2.43	0.52
19:t:8:LEU:CD1	24:y:21:LEU:HB3	2.40	0.52
26:B:8:THR:CG2	53:1:2020:A:H5'	2.40	0.52
47:W:21:ASP:OD2	47:W:23:LYS:HB2	2.08	0.52
52:3:766:A:H2'	52:3:767:A:O4'	2.09	0.52
52:3:1404:C:H2'	52:3:1405:G:H8	1.74	0.52
52:3:1434:A:H2'	52:3:1435:G:O4'	2.10	0.52
53:1:112:U:C2'	53:1:113:U:H5'	2.40	0.52
53:1:1935:G:H1'	53:1:1964:G:N2	2.24	0.52
53:1:2073:C:O2'	53:1:2074:U:H5'	2.10	0.52
53:1:2756:U:H4'	53:1:2757:A:OP1	2.10	0.52
57:7:57:G:H2'	57:7:58:A:H5'	1.92	0.52
2:c:55:LYS:HD2	2:c:77:ARG:HA	1.92	0.52
3:d:48:THR:HG23	3:d:88:ARG:HH12	1.76	0.52
8:i:12:VAL:HG12	53:1:1061:U:O2	2.09	0.52
11:l:16:GLY:HA2	53:1:662:G:O3'	2.09	0.52
14:o:51:ALA:HB3	14:o:78:VAL:HG22	1.92	0.52
18:s:57:ASN:OD1	53:1:495:G:H1'	2.10	0.52
27:C:7:LYS:HA	27:C:23:THR:HA	1.92	0.52
40:P:35:ASP:OD1	40:P:39:ASN:N	2.41	0.52
41:Q:77:SER:OG	41:Q:102:ASP:HB3	2.10	0.52
53:1:346:A:H2'	53:1:346:A:N3	2.25	0.52
53:1:479:A:H4'	53:1:480:A:H5'	1.92	0.52
53:1:819:A:C4	53:1:1189:A:C2	2.98	0.52
53:1:1213:A:N6	53:1:1236:G:H1'	2.25	0.52
53:1:1300:G:H4'	53:1:1301:A:H5''	1.92	0.52
53:1:1664:A:H2'	53:1:1664:A:N3	2.25	0.52
53:1:2329:U:H2'	53:1:2330:G:C8	2.44	0.52
55:5:27:U:H2'	55:5:28:C:H5'	1.92	0.52
1:b:73:ILE:HG23	53:1:1490:A:H62	1.74	0.51
11:l:77:ILE:HB	11:l:110:VAL:HA	1.92	0.51
16:q:20:ALA:HA	16:q:23:TYR:CE2	2.45	0.51
26:B:24:VAL:HG13	26:B:25:THR:N	2.24	0.51
37:M:25:THR:HG23	37:M:57:GLU:HG3	1.92	0.51
38:N:7:GLY:O	38:N:18:VAL:HG22	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:15:VAL:O	42:R:19:THR:HG23	2.09	0.51
48:X:54:ARG:HA	52:3:986:U:H1'	1.92	0.51
52:3:34:C:H2'	52:3:35:G:H8	1.73	0.51
52:3:1070:U:H2'	52:3:1071:C:C6	2.45	0.51
53:1:11:C:H2'	53:1:12:U:H5''	1.92	0.51
53:1:703:U:H2'	53:1:704:G:O4'	2.09	0.51
53:1:2469:A:H2'	53:1:2470:G:O4'	2.10	0.51
1:b:156:SER:OG	53:1:1818:U:H5'	2.10	0.51
23:x:18:SER:OG	23:x:19:HIS:N	2.43	0.51
35:K:75:GLU:HA	35:K:78:PHE:CD2	2.46	0.51
37:M:14:ARG:HE	37:M:74:ILE:HG23	1.75	0.51
42:R:25:GLY:N	52:3:1329:A:H5''	2.25	0.51
49:Y:11:ILE:HD12	49:Y:11:ILE:N	2.21	0.51
53:1:2281:A:O2'	53:1:2282:G:H5'	2.09	0.51
53:1:2391:G:H2'	53:1:2424:C:N4	2.26	0.51
54:2:65:U:H3'	54:2:108:A:H61	1.75	0.51
8:i:25:PRO:HB2	53:1:1095:A:H61	1.75	0.51
10:k:71:ARG:HE	10:k:72:PRO:HD2	1.75	0.51
12:m:34:LYS:HA	12:m:101:VAL:HA	1.93	0.51
14:o:5:SER:O	14:o:8:ILE:HG22	2.10	0.51
28:D:12:ARG:NE	28:D:44:VAL:HG21	2.25	0.51
36:L:141:HIS:O	36:L:145:GLU:HG2	2.10	0.51
42:R:85:TYR:CZ	42:R:89:ARG:HD3	2.46	0.51
52:3:236:A:H2'	52:3:237:G:H8	1.75	0.51
52:3:952:U:H2'	52:3:953:G:H8	1.74	0.51
52:3:1436:U:H2'	52:3:1437:A:H8	1.75	0.51
53:1:565:C:H2'	53:1:566:U:C6	2.45	0.51
53:1:765:C:H2'	53:1:766:U:C6	2.45	0.51
53:1:1103:A:H2'	53:1:1103:A:N3	2.26	0.51
53:1:1528:A:H2'	53:1:1529:G:O4'	2.10	0.51
56:4:20:U:C2'	56:4:21:C:H5'	2.40	0.51
4:e:35:LEU:HD22	4:e:153:ILE:HG12	1.91	0.51
6:g:66:ASN:HB3	6:g:135:HIS:HB2	1.92	0.51
10:k:23:LYS:NZ	53:1:2548:U:H1'	2.25	0.51
21:v:26:PHE:HE2	21:v:89:ILE:HG13	1.75	0.51
37:M:9:MET:SD	37:M:32:LYS:HD2	2.50	0.51
37:M:77:VAL:HG12	37:M:84:ILE:HD12	1.92	0.51
50:Z:23:GLU:HB3	50:Z:27:VAL:HG22	1.93	0.51
52:3:560:A:H4'	52:3:561:U:H5'	1.91	0.51
52:3:1157:A:N6	52:3:1178:G:H1'	2.25	0.51
52:3:1352:C:H2'	52:3:1353:G:C8	2.45	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1401:G:H2'	52:3:1402:C:O4'	2.11	0.51
53:1:873:C:H2'	53:1:874:G:C8	2.46	0.51
53:1:1083:U:H2'	53:1:1085:A:OP2	2.11	0.51
53:1:1300:G:H4'	53:1:1301:A:C5'	2.39	0.51
53:1:2047:C:H2'	53:1:2048:G:H8	1.75	0.51
53:1:2443:C:H2'	53:1:2444:G:C8	2.44	0.51
53:1:2665:A:O2'	53:1:2666:C:H5'	2.09	0.51
55:5:68:C:H2'	55:5:69:C:H5'	1.91	0.51
6:g:93:SER:HB3	6:g:123:ARG:HG2	1.93	0.51
10:k:41:ILE:HD11	10:k:86:LEU:CD2	2.41	0.51
35:K:9:MET:HE2	35:K:86:ARG:HD2	1.93	0.51
49:Y:67:HIS:HE1	52:3:132:C:H4'	1.73	0.51
51:a:215:SER:CB	53:1:2176:A:H4'	2.39	0.51
53:1:2358:A:H2'	53:1:2359:C:O4'	2.10	0.51
1:b:235:GLU:HG3	1:b:238:ASN:HD21	1.75	0.51
4:e:140:ILE:N	4:e:140:ILE:HD12	2.26	0.51
17:r:49:ILE:O	17:r:49:ILE:HG13	2.10	0.51
23:x:2:ARG:HD2	53:1:1365:A:OP1	2.10	0.51
31:G:162:VAL:HB	31:G:184:ALA:HB2	1.92	0.51
33:I:119:HIS:HD1	52:3:437:U:HO2'	1.59	0.51
34:J:76:ASN:N	34:J:81:GLN:HE22	2.08	0.51
36:L:106:ALA:HA	36:L:109:LYS:HE3	1.93	0.51
42:R:18:LEU:HD23	42:R:29:SER:HB2	1.92	0.51
52:3:731:G:O2'	52:3:732:C:H5'	2.10	0.51
52:3:1372:U:H2'	52:3:1373:G:O4'	2.11	0.51
53:1:962:G:N2	53:1:2250:G:H1	2.03	0.51
53:1:2291:U:H2'	53:1:2292:U:C6	2.46	0.51
55:5:44:A:H2'	55:5:45:G:C8	2.46	0.51
16:q:50:ARG:HG3	16:q:50:ARG:NH1	2.21	0.51
19:t:61:LEU:CD2	53:1:1341:G:H5'	2.41	0.51
28:D:34:ARG:NH1	53:1:467:G:OP2	2.40	0.51
35:K:21:MET:HA	35:K:24:ARG:HD3	1.93	0.51
38:N:112:ARG:HH22	52:3:1187:G:H4'	1.75	0.51
41:Q:109:ARG:HH12	52:3:537:G:H5''	1.73	0.51
52:3:600:A:H2'	52:3:601:G:C8	2.46	0.51
52:3:1369:C:H2'	52:3:1370:G:C8	2.45	0.51
52:3:1374:A:H2'	52:3:1375:A:O4'	2.11	0.51
53:1:1420:A:H5'	53:1:1421:G:OP2	2.11	0.51
53:1:2297:A:H62	53:1:2319:G:H1'	1.76	0.51
2:c:148:GLN:N	2:c:148:GLN:OE1	2.43	0.51
4:e:76:PHE:HE2	53:1:2310:C:H2'	1.76	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:170:ILE:H	31:G:170:ILE:HD12	1.76	0.51
32:H:13:ILE:HG22	32:H:14:VAL:HG13	1.92	0.51
33:I:196:GLU:HA	33:I:199:ILE:HD12	1.93	0.51
34:J:24:VAL:HG22	34:J:25:LYS:N	2.26	0.51
36:L:134:VAL:O	36:L:138:GLU:HG2	2.11	0.51
43:S:2:LYS:HD3	52:3:1049:U:C6	2.46	0.51
52:3:744:C:H2'	52:3:745:G:H8	1.75	0.51
52:3:981:U:H2'	52:3:982:U:C5	2.46	0.51
53:1:2475:C:C2'	53:1:2476:A:H5'	2.40	0.51
3:d:4:VAL:HA	3:d:11:ALA:HA	1.91	0.51
7:h:67:THR:CG2	7:h:68:PRO:HD3	2.41	0.51
38:N:70:GLY:O	38:N:74:GLN:HG3	2.11	0.51
52:3:309:A:H2'	52:3:310:G:H8	1.76	0.51
52:3:536:C:H2'	52:3:537:G:C8	2.45	0.51
52:3:1066:C:C2'	52:3:1067:A:H5'	2.40	0.51
53:1:532:A:H2'	53:1:532:A:N3	2.24	0.51
53:1:2605:U:H2'	53:1:2606:C:C6	2.45	0.51
53:1:2808:G:H2'	53:1:2890:G:C6	2.46	0.51
4:e:90:LEU:HD21	4:e:94:ARG:HB2	1.92	0.51
7:h:95:LEU:HD23	7:h:98:GLU:HG3	1.93	0.51
10:k:108:ARG:NH2	52:3:345:C:H3'	2.25	0.51
33:I:13:ARG:HD3	33:I:37:PRO:HB3	1.92	0.51
33:I:73:ASN:ND2	52:3:401:C:OP1	2.44	0.51
51:a:218:MET:HE1	53:1:2128:G:H4'	1.93	0.51
52:3:355:C:H2'	52:3:356:A:O4'	2.11	0.51
53:1:288:U:H2'	53:1:289:G:C8	2.46	0.51
53:1:1772:A:H2'	53:1:1773:A:H5'	1.93	0.51
53:1:2030:A:N3	53:1:2499:C:H5''	2.26	0.51
4:e:98:PHE:O	4:e:102:LEU:HG	2.10	0.50
11:l:135:ILE:HD12	11:l:142:ILE:HD11	1.94	0.50
14:o:80:GLU:O	14:o:84:GLU:HG2	2.10	0.50
33:I:103:ARG:HD2	33:I:167:PRO:HG2	1.92	0.50
36:L:3:ARG:HH12	52:3:1092:A:H4'	1.76	0.50
38:N:118:ARG:HB3	38:N:122:ARG:HB3	1.93	0.50
44:T:46:LYS:HA	53:1:715:A:H2	1.76	0.50
52:3:680:C:H2'	52:3:681:A:C8	2.45	0.50
53:1:395:U:H2'	53:1:396:G:C8	2.46	0.50
53:1:1023:U:O2'	53:1:1122:G:H5'	2.11	0.50
53:1:2743:U:H2'	53:1:2744:G:H5''	1.93	0.50
57:7:53:G:H2'	57:7:54:U:C6	2.46	0.50
18:s:74:ILE:HG23	18:s:74:ILE:O	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:2:VAL:HG22	26:B:3:GLN:N	2.25	0.50
34:J:55:VAL:N	34:J:56:PRO:HD2	2.26	0.50
37:M:31:LEU:HD11	52:3:643:C:C5'	2.40	0.50
50:Z:61:ARG:NH1	50:Z:62:GLU:OE2	2.44	0.50
51:a:6:LYS:HA	51:a:9:ARG:HH21	1.76	0.50
52:3:336:A:H2'	52:3:337:G:H8	1.75	0.50
52:3:423:G:C2'	52:3:424:G:H5'	2.42	0.50
52:3:971:G:H1'	52:3:1365:G:O2'	2.10	0.50
52:3:1014:A:H2'	52:3:1015:G:O4'	2.11	0.50
53:1:873:C:H2'	53:1:874:G:H8	1.75	0.50
53:1:2323:G:H2'	53:1:2324:U:O4'	2.11	0.50
57:7:57:G:C2'	57:7:58:A:H5'	2.41	0.50
3:d:44:ARG:HD3	53:1:444:C:OP2	2.12	0.50
9:j:77:HIS:HE1	9:j:80:HIS:O	1.95	0.50
9:j:117:ALA:HA	9:j:120:ARG:HH21	1.76	0.50
22:w:56:PHE:CE1	53:1:2365:G:H4'	2.46	0.50
37:M:28:SER:HB2	37:M:56:PRO:HB2	1.91	0.50
51:a:38:PHE:CD1	53:1:2127:G:H4'	2.46	0.50
52:3:422:C:H5'	52:3:423:G:N3	2.27	0.50
53:1:572:A:H5''	53:1:573:U:OP2	2.11	0.50
53:1:1475:G:O2'	53:1:1476:U:H6	1.95	0.50
55:5:51:C:H2'	55:5:52:G:H8	1.75	0.50
16:q:108:LEU:HA	17:r:48:LYS:HZ1	1.77	0.50
36:L:74:VAL:HB	36:L:85:GLN:HB3	1.94	0.50
39:O:8:ILE:HD12	39:O:8:ILE:N	2.27	0.50
46:V:48:GLU:O	46:V:49:ASN:C	2.55	0.50
52:3:225:C:H2'	52:3:226:G:O4'	2.11	0.50
52:3:437:U:H2'	52:3:438:U:O4'	2.10	0.50
53:1:386:G:H3'	53:1:387:U:H5''	1.94	0.50
53:1:445:C:O2'	53:1:446:G:H5'	2.11	0.50
53:1:783:A:H2'	53:1:784:G:H5'	1.93	0.50
53:1:2121:G:H2'	53:1:2122:U:O4'	2.11	0.50
2:c:1:MET:HE3	2:c:2:ILE:HG12	1.92	0.50
3:d:68:ALA:HA	53:1:1255:U:C6	2.46	0.50
4:e:139:GLU:HG2	4:e:140:ILE:HD12	1.92	0.50
7:h:118:ILE:CB	7:h:119:PRO:HD3	2.41	0.50
8:i:85:ILE:HG13	8:i:87:SER:H	1.76	0.50
17:r:7:SER:OG	17:r:8:GLY:N	2.45	0.50
53:1:543:G:H8	53:1:543:G:H5'	1.77	0.50
53:1:634:C:H2'	53:1:635:C:C6	2.46	0.50
53:1:1111:A:H2'	53:1:1111:A:N3	2.25	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1450:G:O2'	53:1:1451:C:H5'	2.12	0.50
53:1:1856:U:H2'	53:1:1857:G:O4'	2.11	0.50
53:1:2024:G:OP2	53:1:2034:U:H4'	2.11	0.50
53:1:2671:G:H2'	53:1:2672:U:C6	2.47	0.50
54:2:5:U:H2'	54:2:6:G:H8	1.76	0.50
54:2:5:U:H2'	54:2:6:G:C8	2.47	0.50
5:f:34:ARG:NE	5:f:70:LEU:HD21	2.22	0.50
7:h:26:VAL:HB	7:h:82:ILE:HG23	1.92	0.50
11:l:93:ASN:O	11:l:94:THR:OG1	2.24	0.50
41:Q:43:LYS:HB3	41:Q:44:PRO:HD3	1.93	0.50
51:a:60:ARG:HG2	51:a:164:ARG:HG3	1.94	0.50
52:3:1488:G:H2'	52:3:1489:G:H8	1.77	0.50
53:1:467:G:O2'	53:1:468:G:H5'	2.11	0.50
54:2:49:C:H2'	54:2:50:A:H8	1.77	0.50
7:h:33:VAL:HG22	7:h:34:THR:N	2.26	0.50
12:m:57:VAL:O	12:m:59:ARG:N	2.45	0.50
22:w:16:ARG:HG3	53:1:2271:G:H5'	1.94	0.50
31:G:5:MET:SD	31:G:5:MET:N	2.82	0.50
38:N:112:ARG:HG2	52:3:1369:C:OP2	2.11	0.50
40:P:91:GLY:O	40:P:92:ARG:HG2	2.12	0.50
49:Y:58:ASP:OD2	52:3:194:C:H1'	2.12	0.50
52:3:304:U:O2'	52:3:305:G:H5'	2.12	0.50
52:3:946:A:H2'	52:3:947:G:H8	1.76	0.50
53:1:184:C:H2'	53:1:185:G:C8	2.47	0.50
53:1:699:A:H4'	53:1:1634:A:N7	2.27	0.50
8:i:126:ARG:HA	8:i:129:GLU:HB2	1.93	0.50
12:m:108:VAL:CG1	12:m:112:LEU:HB3	2.41	0.50
14:o:32:PRO:HD2	54:2:29:A:OP2	2.12	0.50
19:t:29:THR:HG23	19:t:85:VAL:C	2.37	0.50
31:G:110:ILE:O	31:G:114:LYS:HG2	2.12	0.50
34:J:162:GLU:OE2	37:M:113:ARG:NH2	2.44	0.50
45:U:16:PHE:CZ	45:U:38:PHE:HB2	2.47	0.50
52:3:552:U:H2'	52:3:553:A:H8	1.77	0.50
52:3:765:G:H2'	52:3:812:G:N2	2.26	0.50
53:1:2180:U:H2'	53:1:2181:U:O4'	2.12	0.50
53:1:2678:C:H2'	53:1:2679:A:H8	1.76	0.50
2:c:14:ILE:HA	15:p:11:GLN:HE22	1.75	0.50
4:e:76:PHE:CE2	53:1:2311:A:H5''	2.46	0.50
34:J:96:GLN:HB3	34:J:123:LEU:HD11	1.94	0.50
44:T:46:LYS:HA	53:1:715:A:C2	2.47	0.50
52:3:67:C:H2'	52:3:68:G:C8	2.47	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:396:C:C3'	52:3:397:A:H5''	2.42	0.50
52:3:1004:A:H2'	52:3:1005:A:O4'	2.12	0.50
53:1:1190:G:H2'	53:1:1191:G:H8	1.77	0.50
53:1:1550:C:H2'	53:1:1551:A:C8	2.47	0.50
53:1:1571:A:H2'	53:1:1572:A:H8	1.77	0.50
53:1:1857:G:H1'	53:1:1885:A:N6	2.27	0.50
53:1:1926:U:O2	53:1:1926:U:C2'	2.60	0.50
53:1:2183:A:H2'	53:1:2184:A:H8	1.76	0.50
53:1:2389:G:H5''	53:1:2390:U:O4'	2.12	0.50
1:b:73:ILE:HG12	53:1:1490:A:C5	2.47	0.49
4:e:39:VAL:HG22	4:e:41:GLU:H	1.76	0.49
9:j:81:ILE:HG23	9:j:82:GLY:N	2.27	0.49
35:K:13:ASP:OD2	35:K:14:GLN:NE2	2.45	0.49
38:N:113:LYS:HD2	52:3:1369:C:C5	2.44	0.49
49:Y:28:ARG:HD3	52:3:1438:G:OP1	2.12	0.49
49:Y:53:MET:SD	49:Y:78:LEU:HD13	2.52	0.49
52:3:79:G:O2'	52:3:80:A:H5'	2.11	0.49
52:3:258:G:H2'	52:3:259:G:O4'	2.12	0.49
52:3:396:C:C2'	52:3:397:A:H5''	2.42	0.49
52:3:680:C:H2'	52:3:681:A:H8	1.77	0.49
52:3:1301:U:O2	52:3:1301:U:H2'	2.11	0.49
52:3:1415:G:H2'	52:3:1416:G:H8	1.77	0.49
53:1:942:G:H2'	53:1:943:A:O4'	2.12	0.49
53:1:967:U:H2'	53:1:968:C:C6	2.47	0.49
53:1:1275:A:N6	53:1:1296:G:H4'	2.26	0.49
53:1:1919:A:H2'	53:1:1919:A:N3	2.27	0.49
53:1:2297:A:N1	53:1:2321:U:H5	2.10	0.49
53:1:2343:U:O2'	53:1:2344:U:H5'	2.12	0.49
55:5:3:C:H3'	55:5:4:G:C5'	2.39	0.49
2:c:77:ARG:HH21	2:c:77:ARG:HG3	1.76	0.49
6:g:96:THR:HG23	6:g:115:VAL:HB	1.94	0.49
31:G:162:VAL:HB	31:G:184:ALA:CB	2.41	0.49
34:J:105:ILE:HD11	34:J:123:LEU:HB3	1.93	0.49
52:3:1316:G:H2'	52:3:1317:C:H5''	1.93	0.49
53:1:189:G:H2'	53:1:205:G:H22	1.77	0.49
53:1:1092:C:H2'	53:1:1093:G:O4'	2.12	0.49
53:1:1326:U:H2'	53:1:1327:A:H8	1.77	0.49
54:2:2:G:H2'	54:2:3:C:C6	2.47	0.49
1:b:220:ARG:NH2	53:1:1788:C:OP1	2.45	0.49
16:q:10:ARG:O	16:q:14:LYS:HG3	2.12	0.49
26:B:30:ASP:HB3	26:B:34:GLY:H	1.76	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:121:ARG:HB2	52:3:1348:U:O3'	2.12	0.49
40:P:112:VAL:HG22	40:P:112:VAL:O	2.12	0.49
52:3:422:C:H4'	52:3:423:G:H5''	1.93	0.49
52:3:428:G:H4'	52:3:429:U:O5'	2.11	0.49
52:3:696:A:H2'	52:3:697:U:H6	1.77	0.49
53:1:1539:U:H2'	53:1:1540:G:C8	2.46	0.49
53:1:2011:U:H2'	53:1:2012:G:O4'	2.12	0.49
53:1:2149:U:H2'	53:1:2150:C:O4'	2.12	0.49
1:b:133:ASN:HD22	6:g:89:LYS:HE3	1.77	0.49
3:d:33:VAL:HG21	53:1:1245:G:H4'	1.94	0.49
3:d:119:ILE:HD12	3:d:119:ILE:N	2.28	0.49
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.93	0.49
17:r:46:GLU:OE1	17:r:46:GLU:N	2.45	0.49
19:t:53:VAL:HG11	19:t:87:LEU:HD13	1.95	0.49
22:w:36:GLN:OE1	22:w:40:LYS:N	2.44	0.49
52:3:1330:U:H2'	52:3:1331:G:O4'	2.12	0.49
52:3:1342:C:H2'	52:3:1343:G:H8	1.75	0.49
53:1:296:U:H2'	53:1:297:G:C8	2.48	0.49
53:1:582:A:H2'	53:1:583:G:H8	1.76	0.49
53:1:2060:A:O4'	53:1:2502:G:H1'	2.12	0.49
53:1:2257:U:O2'	53:1:2258:C:H5'	2.13	0.49
53:1:2360:G:C2'	53:1:2361:G:H5'	2.43	0.49
53:1:2553:G:C3'	53:1:2554:U:H5''	2.41	0.49
56:4:17:U:O2'	56:4:18:G:H5'	2.12	0.49
1:b:137:GLY:HA3	52:3:712:A:C5'	2.38	0.49
6:g:80:ILE:HG21	6:g:94:ILE:HD13	1.95	0.49
7:h:73:LYS:HB2	7:h:117:LEU:HD11	1.95	0.49
23:x:15:ASN:HD22	53:1:381:G:H5''	1.76	0.49
31:G:182:VAL:HB	31:G:196:ASP:H	1.78	0.49
37:M:75:GLN:NE2	37:M:77:VAL:HA	2.27	0.49
51:a:173:THR:HG21	51:a:192:LEU:HD11	1.95	0.49
52:3:252:U:O2	52:3:252:U:H2'	2.12	0.49
52:3:665:A:O4'	52:3:733:G:H1'	2.13	0.49
52:3:721:G:H4'	52:3:722:G:O4'	2.12	0.49
52:3:948:C:H2'	52:3:949:A:C8	2.47	0.49
53:1:414:C:H2'	53:1:415:A:H8	1.77	0.49
53:1:503:A:H4'	53:1:505:A:H5''	1.93	0.49
53:1:2270:A:H2'	53:1:2271:G:O4'	2.12	0.49
55:5:19:G:H5'	55:5:20:U:C5	2.48	0.49
6:g:31:VAL:CG2	6:g:32:PRO:HD3	2.41	0.49
19:t:48:GLN:HE22	19:t:54:GLU:HA	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:w:61:GLY:HA3	22:w:80:ALA:HA	1.94	0.49
23:x:70:LEU:HD23	23:x:73:ARG:HH21	1.76	0.49
31:G:166:ASP:HB3	31:G:190:SER:HA	1.95	0.49
39:O:6:ILE:HD12	39:O:6:ILE:N	2.28	0.49
41:Q:89:LEU:HD22	41:Q:92:VAL:HG13	1.94	0.49
50:Z:23:GLU:O	50:Z:25:ALA:N	2.43	0.49
51:a:184:LYS:O	51:a:188:ASN:ND2	2.45	0.49
52:3:537:G:H2'	52:3:538:G:H8	1.76	0.49
52:3:1299:A:H2'	52:3:1300:G:H4'	1.95	0.49
53:1:598:U:H2'	53:1:599:A:H8	1.75	0.49
53:1:1432:G:H2'	53:1:1433:A:C8	2.48	0.49
53:1:1447:C:H2'	53:1:1448:G:H8	1.78	0.49
53:1:2134:A:N6	53:1:2157:G:H4'	2.28	0.49
53:1:2266:A:H4'	53:1:2267:A:C2	2.47	0.49
1:b:229:HIS:ND1	1:b:230:PRO:HD2	2.27	0.49
8:i:125:THR:O	8:i:129:GLU:HG3	2.12	0.49
16:q:109:VAL:HG12	16:q:113:LYS:HE2	1.94	0.49
20:u:33:VAL:HG11	20:u:69:VAL:HG11	1.95	0.49
31:G:59:ILE:HG22	31:G:64:GLY:HA3	1.93	0.49
52:3:977:A:H3'	52:3:977:A:N3	2.27	0.49
52:3:1168:U:H5''	52:3:1169:A:OP2	2.13	0.49
53:1:395:U:H2'	53:1:396:G:H8	1.78	0.49
53:1:1213:A:H62	53:1:1236:G:H1'	1.78	0.49
53:1:2520:C:O2'	53:1:2521:C:H5'	2.12	0.49
5:f:175:LYS:HG3	5:f:176:LYS:HG3	1.95	0.49
25:z:11:SER:OG	53:1:989:G:OP2	2.27	0.49
27:C:6:GLU:HG2	27:C:7:LYS:N	2.28	0.49
31:G:75:ALA:O	31:G:79:VAL:HG23	2.12	0.49
43:S:96:LYS:HD3	43:S:97:LYS:H	1.77	0.49
52:3:70:U:H2'	52:3:94:G:O6	2.12	0.49
53:1:971:G:H2'	53:1:972:A:O4'	2.12	0.49
53:1:2093:G:O2'	53:1:2094:A:H5'	2.12	0.49
53:1:2372:U:H2'	53:1:2373:G:C8	2.47	0.49
4:e:125:GLY:HA2	4:e:162:ASP:HA	1.94	0.49
5:f:136:ASP:OD2	5:f:138:GLN:HB3	2.12	0.49
15:p:20:ARG:HD3	15:p:112:ARG:NH2	2.28	0.49
34:J:141:ASP:CA	34:J:144:GLU:HG2	2.41	0.49
38:N:18:VAL:HG12	38:N:64:ILE:HG23	1.93	0.49
45:U:51:ARG:C	45:U:52:LEU:HD12	2.37	0.49
52:3:112:G:N2	52:3:354:G:H5'	2.27	0.49
52:3:764:C:H2'	52:3:765:G:O4'	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:769:G:H4'	52:3:1513:A:H4'	1.93	0.49
53:1:1547:C:H2'	53:1:1548:A:C8	2.48	0.49
54:2:118:C:H2'	54:2:119:A:C8	2.48	0.49
9:j:25:LEU:HB3	53:1:1140:C:OP1	2.11	0.49
10:k:64:ARG:NE	15:p:67:GLU:OE1	2.46	0.49
22:w:43:ALA:HB1	22:w:47:VAL:HG23	1.95	0.49
32:H:115:VAL:HG21	32:H:201:ILE:HD11	1.95	0.49
36:L:138:GLU:O	36:L:142:ARG:HG2	2.12	0.49
52:3:1270:G:H2'	52:3:1271:A:C8	2.47	0.49
53:1:192:C:H2'	53:1:193:U:H5'	1.94	0.49
53:1:688:U:H2'	53:1:689:A:H8	1.78	0.49
53:1:2329:U:H2'	53:1:2330:G:H8	1.75	0.49
53:1:2619:C:O2'	53:1:2620:C:H5'	2.12	0.49
53:1:2636:C:H2'	53:1:2637:U:C6	2.47	0.49
57:7:8:U:H5'	57:7:8:U:H6	1.78	0.49
1:b:251:THR:OG1	1:b:252:LYS:N	2.45	0.48
3:d:2:GLU:HB3	3:d:11:ALA:HB1	1.95	0.48
3:d:199:MET:HE2	3:d:200:LEU:HD12	1.94	0.48
3:d:200:LEU:O	3:d:201:ALA:HB3	2.12	0.48
10:k:109:SER:C	10:k:110:GLU:HG3	2.37	0.48
18:s:98:LYS:HD2	53:1:2012:G:OP1	2.13	0.48
33:I:33:ILE:HG13	33:I:34:GLU:HG2	1.95	0.48
35:K:92:THR:OG1	35:K:93:LYS:N	2.40	0.48
50:Z:58:LYS:O	50:Z:61:ARG:CD	2.60	0.48
52:3:902:G:H2'	52:3:903:G:C8	2.48	0.48
53:1:279:A:C2'	53:1:280:U:H5'	2.42	0.48
53:1:511:U:C2'	53:1:512:G:H5'	2.40	0.48
53:1:2111:U:H3	53:1:2147:A:H1'	1.77	0.48
53:1:2112:G:C2'	53:1:2113:U:H5'	2.39	0.48
53:1:2514:U:H2'	53:1:2515:C:H6	1.76	0.48
2:c:97:SER:OG	2:c:98:VAL:N	2.46	0.48
11:l:23:ILE:HD12	11:l:23:ILE:N	2.28	0.48
16:q:27:ARG:HH12	53:1:532:A:H5''	1.78	0.48
37:M:120:LEU:HA	52:3:600:A:H5'	1.95	0.48
40:P:79:LYS:HG3	40:P:80:ASN:H	1.77	0.48
42:R:103:THR:OG1	52:3:1229:A:N6	2.45	0.48
43:S:52:ARG:NH2	52:3:1219:A:H5''	2.28	0.48
52:3:744:C:H2'	52:3:745:G:C8	2.48	0.48
52:3:1251:A:H2'	52:3:1252:A:C8	2.48	0.48
52:3:1436:U:H2'	52:3:1437:A:C8	2.48	0.48
57:7:70:G:H2'	57:7:71:G:O4'	2.12	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:2:ARG:HH11	53:1:1113:U:H5'	1.78	0.48
7:h:55:VAL:HA	53:1:1084:A:H5''	1.94	0.48
50:Z:6:ARG:C	50:Z:8:ASN:H	2.21	0.48
52:3:208:U:H2'	52:3:210:C:H1'	1.95	0.48
53:1:1285:A:H2'	53:1:1286:A:H5'	1.95	0.48
53:1:1594:U:H2'	53:1:1595:C:C6	2.47	0.48
53:1:2224:G:H4'	53:1:2226:C:C2	2.48	0.48
53:1:2636:C:H2'	53:1:2637:U:H6	1.77	0.48
9:j:124:VAL:HG22	9:j:125:TYR:N	2.28	0.48
10:k:76:VAL:H	15:p:72:VAL:HG22	1.79	0.48
19:t:6:ARG:O	19:t:10:VAL:HG23	2.14	0.48
25:z:36:GLU:O	25:z:37:ARG:NH1	2.46	0.48
33:l:142:VAL:HG22	33:l:179:GLY:O	2.14	0.48
34:J:51:LYS:HE3	52:3:1080:A:OP1	2.14	0.48
34:J:64:GLU:HG3	34:J:68:ARG:NH1	2.19	0.48
35:K:68:GLN:O	35:K:71:ILE:HG22	2.13	0.48
40:P:117:HIS:HA	52:3:718:A:O4'	2.13	0.48
41:Q:28:GLN:O	41:Q:29:LYS:HD2	2.13	0.48
42:R:74:MET:SD	42:R:74:MET:C	2.96	0.48
52:3:1131:G:H22	52:3:1144:G:H4'	1.79	0.48
53:1:898:C:H2'	53:1:899:A:O4'	2.12	0.48
53:1:2623:G:H2'	53:1:2624:G:H8	1.78	0.48
2:c:135:GLY:HA2	53:1:743:A:OP1	2.13	0.48
11:l:79:LEU:H	11:l:113:ALA:HB3	1.78	0.48
11:l:101:ILE:HG13	11:l:102:GLY:N	2.28	0.48
52:3:376:G:H2'	52:3:377:G:H8	1.78	0.48
53:1:176:A:O2'	53:1:177:G:H5'	2.13	0.48
53:1:582:A:H2'	53:1:583:G:C8	2.49	0.48
53:1:704:G:H1'	53:1:727:A:N6	2.29	0.48
53:1:890:C:H2'	53:1:891:G:H5'	1.95	0.48
53:1:1360:G:H2'	53:1:1361:G:H5'	1.94	0.48
53:1:2853:C:H2'	53:1:2854:G:H8	1.78	0.48
2:c:9:VAL:HG23	2:c:26:VAL:HG13	1.95	0.48
2:c:142:VAL:CG1	2:c:143:PRO:HD2	2.43	0.48
18:s:29:VAL:HG23	18:s:69:LEU:O	2.14	0.48
26:B:4:GLN:O	53:1:2017:U:H4'	2.13	0.48
29:E:2:LYS:HG3	53:1:242:G:C8	2.47	0.48
31:G:105:THR:HG21	52:3:1072:G:N2	2.17	0.48
35:K:89:VAL:HG23	52:3:737:C:H5'	1.94	0.48
40:P:61:ALA:O	40:P:64:VAL:HG12	2.13	0.48
52:3:664:G:H22	52:3:741:G:H1	1.60	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1366:C:H2'	52:3:1367:C:C6	2.49	0.48
53:1:741:U:H2'	53:1:742:A:C8	2.49	0.48
53:1:765:C:H2'	53:1:766:U:H6	1.78	0.48
53:1:1105:U:C2'	53:1:1106:G:H5''	2.43	0.48
53:1:2714:G:O2'	53:1:2715:C:H5'	2.14	0.48
53:1:2743:U:H3'	53:1:2744:G:H5''	1.94	0.48
53:1:2818:U:H2'	53:1:2819:G:C8	2.49	0.48
54:2:78:A:H2'	54:2:79:G:O4'	2.14	0.48
7:h:17:GLU:HG3	7:h:53:ARG:HD3	1.95	0.48
15:p:88:ARG:NH1	15:p:112:ARG:HH11	2.10	0.48
33:l:68:GLU:HB3	52:3:546:A:P	2.54	0.48
41:Q:23:LEU:HD13	41:Q:29:LYS:HE2	1.95	0.48
42:R:19:THR:HG21	42:R:26:LYS:HD3	1.96	0.48
52:3:159:G:H1'	52:3:162:A:N6	2.29	0.48
53:1:1300:G:C4'	53:1:1301:A:H5''	2.43	0.48
53:1:2646:C:H2'	53:1:2647:U:O4'	2.14	0.48
57:7:10:G:N2	57:7:26:A:H1'	2.29	0.48
6:g:75:LEU:HD23	6:g:75:LEU:H	1.79	0.48
8:i:100:ILE:N	8:i:100:ILE:HD12	2.28	0.48
11:l:27:LEU:O	11:l:31:GLY:HA2	2.13	0.48
21:v:35:GLU:OE1	21:v:35:GLU:N	2.47	0.48
27:C:21:THR:OG1	29:E:33:THR:HG22	2.13	0.48
47:W:72:ARG:HH22	50:Z:4:LYS:HD3	1.79	0.48
50:Z:39:LYS:O	50:Z:43:GLU:N	2.33	0.48
52:3:1228:C:H2'	52:3:1229:A:H8	1.79	0.48
53:1:1268:A:H2'	53:1:1269:A:O4'	2.13	0.48
53:1:2126:A:H2'	53:1:2162:G:C2	2.48	0.48
1:b:36:ASN:HB2	1:b:61:TYR:HB2	1.96	0.48
7:h:3:LEU:HD23	7:h:3:LEU:H	1.78	0.48
34:J:121:ASN:OD1	34:J:122:VAL:HG13	2.14	0.48
36:L:9:ARG:NH2	52:3:1345:U:O2'	2.46	0.48
45:U:12:LYS:O	45:U:13:LYS:HB2	2.13	0.48
47:W:66:LEU:C	47:W:67:LEU:HD22	2.39	0.48
52:3:955:U:H3	52:3:1225:A:H61	1.61	0.48
52:3:1160:G:H1	52:3:1176:A:H61	1.62	0.48
52:3:1353:G:O2'	52:3:1354:U:H5'	2.14	0.48
53:1:827:U:H4'	53:1:828:U:C5	2.49	0.48
53:1:1186:G:H2'	53:1:1187:G:O4'	2.13	0.48
53:1:2105:U:H2'	53:1:2106:U:O4'	2.14	0.48
1:b:257:ARG:NH1	53:1:1799:G:OP1	2.46	0.48
16:q:10:ARG:O	16:q:10:ARG:NH1	2.47	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:w:22:PHE:HD2	53:1:922:C:H1'	1.79	0.48
23:x:16:ASN:HB2	23:x:26:ARG:HB3	1.95	0.48
31:G:178:LEU:HD23	31:G:178:LEU:O	2.13	0.48
33:I:131:ILE:HD12	33:I:131:ILE:N	2.28	0.48
34:J:156:ARG:HE	37:M:42:GLU:HG3	1.79	0.48
36:L:87:PRO:HG3	36:L:148:LYS:HA	1.96	0.48
36:L:145:GLU:O	36:L:148:LYS:HG2	2.14	0.48
38:N:11:ARG:HE	38:N:106:ASP:HB2	1.78	0.48
47:W:46:THR:HG22	47:W:47:ARG:N	2.28	0.48
50:Z:28:LEU:O	50:Z:32:ARG:HB3	2.14	0.48
52:3:556:C:O2'	52:3:557:G:H5'	2.14	0.48
52:3:1504:G:OP1	52:3:1507:A:H4'	2.14	0.48
53:1:1138:G:H2'	53:1:1139:G:O4'	2.14	0.48
53:1:1355:G:H2'	53:1:1356:G:H8	1.79	0.48
53:1:1360:G:H22	53:1:2214:C:H42	1.62	0.48
53:1:2751:G:O2'	53:1:2752:C:H5'	2.14	0.48
6:g:3:VAL:HG12	6:g:36:ALA:HB1	1.96	0.47
6:g:3:VAL:HG13	6:g:37:VAL:C	2.39	0.47
11:l:57:LEU:HD22	29:E:53:ASP:HB3	1.96	0.47
12:m:72:PRO:HD3	12:m:92:TRP:CZ3	2.48	0.47
17:r:40:MET:HE2	17:r:48:LYS:HG2	1.95	0.47
24:y:22:LEU:HG	24:y:23:ARG:HD2	1.95	0.47
34:J:131:ASN:ND2	52:3:19:A:OP2	2.47	0.47
36:L:3:ARG:NH1	52:3:1092:A:C5'	2.77	0.47
40:P:21:HIS:C	40:P:22:ILE:HD12	2.39	0.47
44:T:88:ARG:HD3	53:1:713:G:OP2	2.14	0.47
53:1:713:G:N2	53:1:718:A:H62	2.06	0.47
53:1:1590:A:H2'	53:1:1591:A:C8	2.49	0.47
54:2:65:U:H3'	54:2:108:A:N6	2.28	0.47
1:b:119:VAL:HG23	1:b:133:ASN:OD1	2.15	0.47
1:b:213:ARG:CZ	53:1:1566:A:H5'	2.44	0.47
2:c:25:THR:HG21	2:c:193:VAL:HG22	1.95	0.47
2:c:109:VAL:HG21	2:c:193:VAL:HG12	1.96	0.47
8:i:52:LEU:HD12	8:i:53:PRO:HD2	1.94	0.47
19:t:39:THR:O	19:t:43:ILE:HG13	2.14	0.47
42:R:76:ILE:HG13	42:R:77:LYS:HD2	1.95	0.47
52:3:56:U:H2'	52:3:57:G:C8	2.49	0.47
52:3:163:C:H2'	52:3:164:G:O4'	2.14	0.47
52:3:337:G:H2'	52:3:338:A:H8	1.78	0.47
52:3:666:G:H5'	52:3:726:C:H1'	1.96	0.47
53:1:542:C:C2'	53:1:543:G:H5''	2.43	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:968:C:H2'	53:1:969:G:H8	1.78	0.47
53:1:2114:A:H61	53:1:2117:A:N6	2.06	0.47
53:1:2328:A:H2'	53:1:2329:U:C6	2.49	0.47
53:1:2371:G:O2'	53:1:2372:U:H5'	2.15	0.47
6:g:70:GLU:HB3	6:g:71:LYS:HD2	1.96	0.47
7:h:60:LEU:O	7:h:64:VAL:HB	2.14	0.47
8:i:99:LYS:O	8:i:99:LYS:HD2	2.14	0.47
14:o:51:ALA:HB3	14:o:78:VAL:CG2	2.44	0.47
38:N:94:ARG:HA	38:N:97:LEU:HB3	1.95	0.47
47:W:64:LEU:HB2	47:W:66:LEU:HG	1.96	0.47
52:3:922:G:H2'	52:3:923:A:C8	2.49	0.47
53:1:1801:A:H5''	53:1:2203:U:C2'	2.37	0.47
1:b:62:ARG:HG3	1:b:62:ARG:NH1	2.30	0.47
13:n:94:TYR:O	13:n:116:VAL:HG22	2.14	0.47
23:x:13:THR:CG2	53:1:188:G:H5'	2.44	0.47
28:D:12:ARG:CZ	28:D:44:VAL:HG21	2.44	0.47
40:P:91:GLY:O	40:P:93:GLU:N	2.47	0.47
42:R:78:ARG:O	42:R:82:LEU:HG	2.15	0.47
52:3:422:C:H5'	52:3:423:G:C4	2.49	0.47
52:3:950:U:H2'	52:3:951:G:H8	1.79	0.47
53:1:2333:A:H5'	53:1:2335:A:H1'	1.96	0.47
3:d:70:SER:HG	3:d:78:TRP:HZ2	1.62	0.47
7:h:20:LYS:NZ	7:h:88:HIS:O	2.48	0.47
9:j:58:ASN:HD21	9:j:128:ASN:HB2	1.78	0.47
12:m:53:MET:HE1	12:m:103:TYR:CD1	2.50	0.47
20:u:85:ARG:HB2	20:u:87:GLU:HG2	1.96	0.47
27:C:37:LYS:HB2	27:C:48:TYR:CD2	2.49	0.47
34:J:97:PRO:O	34:J:122:VAL:HA	2.15	0.47
38:N:95:SER:O	38:N:99:LYS:HG2	2.14	0.47
39:O:48:ARG:NH2	52:3:1252:A:O2'	2.47	0.47
46:V:30:HIS:HB3	46:V:34:GLY:H	1.79	0.47
46:V:61:ARG:NH1	46:V:63:CYS:SG	2.87	0.47
52:3:336:A:H2'	52:3:337:G:C8	2.49	0.47
52:3:543:U:H2'	52:3:544:G:C8	2.49	0.47
52:3:1499:A:O2'	52:3:1500:A:H5'	2.13	0.47
53:1:1326:U:H2'	53:1:1327:A:C8	2.50	0.47
53:1:2190:G:N3	53:1:2191:A:H1'	2.29	0.47
7:h:39:THR:HG23	7:h:40:GLU:OE1	2.13	0.47
33:I:160:LEU:O	33:I:160:LEU:HD23	2.15	0.47
39:O:52:LEU:HD13	39:O:59:LYS:HD2	1.97	0.47
39:O:53:ILE:HD13	39:O:63:ASP:HB2	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:112:ARG:HD3	52:3:1229:A:OP1	2.15	0.47
52:3:1391:U:H2'	52:3:1392:G:H8	1.78	0.47
52:3:1435:G:H2'	52:3:1436:U:C6	2.49	0.47
53:1:2421:G:H2'	55:5:76:A:H62	1.77	0.47
55:5:18:G:H22	55:5:57:A:H2'	1.78	0.47
1:b:4:LYS:HD2	1:b:16:VAL:HG22	1.96	0.47
1:b:216:ARG:NH2	53:1:781:A:OP1	2.47	0.47
2:c:50:VAL:HG12	2:c:51:THR:N	2.30	0.47
11:l:49:GLY:HA3	11:l:58:TYR:CE1	2.45	0.47
15:p:112:ARG:O	15:p:113:LEU:HG	2.15	0.47
29:E:15:LYS:HD2	29:E:19:GLY:HA2	1.95	0.47
30:F:2:LYS:HD3	30:F:4:ARG:NH1	2.30	0.47
35:K:15:SER:HA	35:K:18:VAL:HG23	1.97	0.47
37:M:79:ARG:HH11	37:M:79:ARG:HG3	1.79	0.47
42:R:83:GLY:HA2	42:R:91:ARG:HH22	1.80	0.47
44:T:42:PHE:CE2	44:T:55:LEU:HD22	2.50	0.47
52:3:35:G:H2'	52:3:36:C:C6	2.49	0.47
52:3:127:G:O2'	52:3:128:G:H5'	2.14	0.47
52:3:225:C:C2'	52:3:226:G:H5''	2.44	0.47
52:3:346:G:C2'	52:3:347:G:H5'	2.44	0.47
52:3:390:U:H2'	52:3:391:G:C8	2.50	0.47
52:3:696:A:H2'	52:3:697:U:C6	2.50	0.47
52:3:715:A:H5''	52:3:805:C:H1'	1.95	0.47
52:3:785:G:O2'	52:3:786:G:H5'	2.14	0.47
52:3:1074:G:H2'	52:3:1075:U:C6	2.50	0.47
52:3:1201:A:C1'	52:3:1202:U:OP2	2.59	0.47
53:1:1370:C:H2'	53:1:1371:G:O4'	2.14	0.47
53:1:1965:C:H5''	53:1:1966:A:H2'	1.97	0.47
53:1:2131:U:O5'	53:1:2133:G:H4'	2.15	0.47
53:1:2572:A:OP1	53:1:2574:G:H4'	2.14	0.47
53:1:2853:C:H2'	53:1:2854:G:C8	2.49	0.47
54:2:88:C:H5''	54:2:89:U:OP1	2.15	0.47
55:5:44:A:H3'	55:5:45:G:H5''	1.96	0.47
7:h:23:LEU:HD21	7:h:96:PHE:HB2	1.97	0.47
9:j:2:LYS:HA	53:1:995:C:N3	2.29	0.47
15:p:26:GLU:HA	15:p:43:GLU:HA	1.95	0.47
16:q:23:TYR:HD1	53:1:533:G:H5'	1.79	0.47
21:v:30:ILE:HG22	21:v:91:PHE:HB2	1.96	0.47
22:w:17:LEU:HD21	22:w:37:ARG:HH22	1.77	0.47
32:H:156:LEU:HD12	32:H:156:LEU:O	2.15	0.47
33:I:39:GLN:NE2	52:3:540:G:H21	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:161:ALA:HA	33:I:164:ARG:HD2	1.97	0.47
34:J:20:VAL:HB	52:3:1080:A:O3'	2.14	0.47
39:O:8:ILE:HB	39:O:74:VAL:HB	1.95	0.47
45:U:18:GLN:O	45:U:20:VAL:HG13	2.14	0.47
49:Y:2:ASN:HB3	52:3:332:G:OP2	2.13	0.47
49:Y:28:ARG:NH1	52:3:1437:A:O3'	2.48	0.47
51:a:221:GLY:H	53:1:2176:A:H5''	1.78	0.47
52:3:927:G:H21	52:3:1532:U:H5''	1.79	0.47
52:3:1354:U:H2'	52:3:1355:G:C8	2.50	0.47
53:1:12:U:O2'	53:1:13:A:H5'	2.15	0.47
53:1:776:G:H1	53:1:2072:C:H5'	1.80	0.47
53:1:1060:U:H4'	53:1:1061:U:H5'	1.97	0.47
53:1:1479:G:O2'	53:1:1480:C:H5'	2.15	0.47
53:1:2655:G:O2'	53:1:2656:U:C5	2.67	0.47
7:h:121:SER:OG	7:h:122:GLN:N	2.44	0.47
16:q:108:LEU:HD23	17:r:48:LYS:HZ2	1.80	0.47
32:H:33:ASP:O	32:H:37:LYS:HG2	2.14	0.47
33:I:24:VAL:HG22	52:3:409:U:H5''	1.97	0.47
33:I:183:ARG:HG2	33:I:183:ARG:HH11	1.80	0.47
46:V:64:ARG:HG3	52:3:130:A:C8	2.50	0.47
48:X:36:ARG:NH2	52:3:1318:A:O4'	2.48	0.47
52:3:505:G:H4'	52:3:534:U:C4	2.49	0.47
52:3:1376:U:H2'	52:3:1377:A:C8	2.50	0.47
52:3:1409:C:H2'	52:3:1410:A:H8	1.80	0.47
56:4:19:U:H2'	56:4:20:U:C6	2.50	0.47
1:b:201:LEU:HD22	52:3:773:G:H5''	1.97	0.47
5:f:100:ASN:ND2	5:f:115:GLN:OE1	2.47	0.47
5:f:155:PRO:HG3	53:1:2530:A:N6	2.30	0.47
9:j:47:HIS:CE1	9:j:48:VAL:HG23	2.50	0.47
10:k:40:LYS:HD2	10:k:57:VAL:HG12	1.97	0.47
31:G:216:VAL:HA	31:G:219:THR:HG22	1.96	0.47
32:H:4:VAL:HG22	32:H:5:HIS:N	2.30	0.47
32:H:176:THR:HG22	52:3:1111:A:N1	2.30	0.47
35:K:3:HIS:HA	35:K:65:GLU:HA	1.96	0.47
37:M:35:ILE:HG22	37:M:109:VAL:HG11	1.97	0.47
43:S:7:ALA:O	43:S:10:VAL:HG22	2.15	0.47
51:a:174:THR:CG2	53:1:2124:G:H5''	2.45	0.47
52:3:715:A:H2'	52:3:716:A:H8	1.80	0.47
52:3:1125:U:H2'	52:3:1126:U:H2'	1.97	0.47
52:3:1287:A:H61	52:3:1371:G:H1'	1.80	0.47
53:1:1153:C:H2'	53:1:1154:G:O4'	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1170:C:H2'	53:1:1171:G:C8	2.50	0.47
53:1:2176:A:H2'	53:1:2177:C:C6	2.50	0.47
53:1:2182:U:H2'	53:1:2183:A:C8	2.50	0.47
57:7:29:G:O2'	57:7:30:G:H5'	2.15	0.47
1:b:18:VAL:O	1:b:18:VAL:HG13	2.16	0.46
4:e:39:VAL:O	53:1:2307:G:O6	2.32	0.46
16:q:30:VAL:HG13	53:1:580:U:O3'	2.16	0.46
16:q:51:GLN:NE2	16:q:55:GLN:HG3	2.29	0.46
17:r:14:VAL:HG11	17:r:98:ILE:HG13	1.97	0.46
37:M:121:GLY:O	52:3:599:C:H4'	2.15	0.46
46:V:48:GLU:HB2	46:V:51:GLU:OE1	2.15	0.46
47:W:13:THR:HG21	47:W:20:ILE:HD11	1.97	0.46
48:X:51:HIS:HB2	48:X:56:HIS:CD2	2.50	0.46
52:3:273:U:H2'	52:3:274:A:H5'	1.98	0.46
52:3:543:U:H2'	52:3:544:G:H8	1.80	0.46
52:3:702:A:H61	53:1:1846:G:H4'	1.80	0.46
54:2:64:G:H2'	54:2:65:U:C6	2.51	0.46
2:c:1:MET:SD	2:c:205:PRO:HG2	2.55	0.46
15:p:38:ARG:NH2	15:p:38:ARG:HG3	2.31	0.46
26:B:30:ASP:HB3	26:B:34:GLY:N	2.30	0.46
31:G:48:MET:HG3	31:G:199:ILE:HD13	1.97	0.46
33:I:53:GLN:HE22	33:I:201:GLU:HB2	1.80	0.46
37:M:17:GLN:HE21	37:M:71:VAL:HG22	1.79	0.46
52:3:1245:C:H2'	52:3:1246:A:C8	2.50	0.46
53:1:786:C:O2'	53:1:787:C:H5'	2.14	0.46
53:1:1570:A:H2'	53:1:1571:A:C8	2.50	0.46
53:1:2376:A:H2'	53:1:2377:A:O4'	2.14	0.46
53:1:2688:G:N1	53:1:2720:U:OP2	2.47	0.46
53:1:2860:A:H2'	53:1:2861:U:H5'	1.98	0.46
53:1:2863:C:H2'	53:1:2864:G:C8	2.50	0.46
55:5:28:C:H2'	55:5:29:G:O4'	2.15	0.46
56:4:20:U:H2'	56:4:21:C:H5'	1.96	0.46
15:p:102:ARG:NH1	15:p:106:ALA:O	2.48	0.46
23:x:54:GLY:O	23:x:58:ILE:HG12	2.15	0.46
32:H:69:THR:OG1	32:H:70:ALA:N	2.45	0.46
38:N:20:ILE:HD11	38:N:60:LEU:HD13	1.96	0.46
39:O:50:THR:HG21	52:3:1367:C:O2'	2.15	0.46
46:V:10:ARG:C	46:V:22:VAL:HG13	2.40	0.46
49:Y:70:LYS:HE2	49:Y:74:HIS:CD2	2.50	0.46
52:3:437:U:HO2'	52:3:438:U:H5'	1.80	0.46
52:3:467:U:H5'	52:3:468:A:OP2	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:663:A:H61	52:3:742:G:H1	1.62	0.46
53:1:1680:U:H2'	53:1:1681:G:H5'	1.97	0.46
53:1:1790:C:H2'	53:1:1791:A:C5	2.50	0.46
53:1:2361:G:O2'	53:1:2362:C:H5'	2.15	0.46
53:1:2641:G:H2'	53:1:2642:G:H8	1.80	0.46
3:d:148:ILE:O	3:d:169:VAL:HA	2.15	0.46
3:d:181:ILE:HG23	11:l:2:ARG:CG	2.46	0.46
4:e:113:PHE:C	4:e:114:ARG:HD2	2.41	0.46
7:h:112:ALA:O	7:h:114:GLU:N	2.49	0.46
13:n:64:ARG:NH1	53:1:2705:A:H2	2.14	0.46
20:u:6:ARG:O	20:u:24:VAL:HB	2.15	0.46
29:E:53:ASP:OD2	53:1:2359:C:H4'	2.14	0.46
33:I:108:ALA:HB3	33:I:112:GLU:OE1	2.15	0.46
41:Q:89:LEU:C	41:Q:89:LEU:HD23	2.41	0.46
46:V:56:ASP:HB3	46:V:81:ALA:HB2	1.98	0.46
50:Z:32:ARG:HG3	50:Z:33:ARG:HG2	1.96	0.46
51:a:49:GLY:HA3	51:a:210:LYS:HE3	1.98	0.46
52:3:982:U:H4'	52:3:983:A:O5'	2.15	0.46
52:3:1485:U:H5'	53:1:1961:C:H5''	1.97	0.46
53:1:255:A:H2'	53:1:256:A:O4'	2.15	0.46
53:1:1020:A:C1'	53:1:1021:A:OP2	2.59	0.46
53:1:1695:G:H2'	53:1:1696:G:O4'	2.16	0.46
53:1:2070:A:H2'	53:1:2071:A:O4'	2.14	0.46
53:1:2590:A:H2'	53:1:2591:C:C6	2.50	0.46
1:b:123:ILE:HG23	1:b:191:LEU:HD13	1.98	0.46
4:e:91:ARG:HA	4:e:95:MET:HB3	1.98	0.46
9:j:68:LYS:HD3	53:1:1022:G:N7	2.30	0.46
11:l:50:PHE:HZ	53:1:196:A:C2	2.33	0.46
14:o:74:VAL:HG23	14:o:106:LEU:HD13	1.98	0.46
16:q:73:ILE:HG23	16:q:74:SER:O	2.15	0.46
16:q:92:LYS:HE2	53:1:995:C:O2'	2.15	0.46
42:R:112:ARG:HD3	52:3:1229:A:P	2.55	0.46
47:W:20:ILE:HG21	47:W:54:LEU:HA	1.96	0.46
52:3:5:U:H4'	52:3:6:G:C5	2.50	0.46
52:3:418:C:H2'	52:3:419:C:C6	2.51	0.46
53:1:795:C:H2'	53:1:796:C:C6	2.50	0.46
53:1:1105:U:H2'	53:1:1106:G:H5''	1.97	0.46
53:1:2443:C:O2'	53:1:2444:G:H5'	2.16	0.46
11:l:29:LYS:HE3	53:1:566:U:H5''	1.98	0.46
31:G:15:PHE:O	31:G:202:ASN:HB2	2.15	0.46
31:G:129:THR:HG23	31:G:131:LYS:HG2	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:23:GLU:C	50:Z:25:ALA:H	2.24	0.46
52:3:206:C:H2'	52:3:207:C:O4'	2.16	0.46
52:3:284:C:H2'	52:3:285:C:C6	2.49	0.46
52:3:1202:U:H2'	52:3:1203:C:H5'	1.98	0.46
52:3:1306:A:H2'	52:3:1307:U:O4'	2.16	0.46
53:1:1045:C:P	53:1:1047:G:H5'	2.56	0.46
53:1:1188:U:O2'	53:1:1189:A:H5'	2.15	0.46
53:1:2569:G:O2'	53:1:2570:G:H5'	2.16	0.46
3:d:50:ALA:HB2	53:1:801:G:C8	2.51	0.46
6:g:68:ARG:HH12	6:g:72:ILE:HD11	1.81	0.46
10:k:13:ASN:ND2	52:3:339:C:OP2	2.45	0.46
10:k:109:SER:C	10:k:111:LYS:H	2.24	0.46
42:R:24:VAL:HA	52:3:1329:A:H5''	1.97	0.46
42:R:104:ASN:ND2	52:3:950:U:O4	2.49	0.46
52:3:82:G:H2'	52:3:83:C:O4'	2.16	0.46
53:1:1637:A:H5'	53:1:1760:C:O2'	2.16	0.46
53:1:1686:C:H2'	53:1:1687:G:O4'	2.16	0.46
53:1:2463:C:H2'	53:1:2464:G:H8	1.81	0.46
1:b:17:LYS:HD2	53:1:1565:C:H5''	1.97	0.46
3:d:186:VAL:HG23	3:d:186:VAL:O	2.16	0.46
4:e:73:VAL:H	4:e:78:ILE:HG13	1.81	0.46
7:h:67:THR:N	7:h:68:PRO:CD	2.79	0.46
14:o:29:HIS:CD2	54:2:7:G:H4'	2.51	0.46
17:r:35:PHE:HB2	17:r:59:ILE:HB	1.98	0.46
17:r:80:ARG:NH1	53:1:571:U:OP1	2.49	0.46
18:s:2:GLU:O	18:s:3:THR:C	2.58	0.46
34:J:139:THR:O	34:J:143:LEU:HD13	2.16	0.46
38:N:14:SER:HB3	38:N:69:GLY:HA3	1.98	0.46
38:N:68:GLY:HA2	52:3:1250:A:H5'	1.97	0.46
43:S:20:PHE:O	43:S:21:ALA:CB	2.63	0.46
43:S:63:CYS:HB2	43:S:67:GLY:N	2.29	0.46
46:V:23:ALA:HA	46:V:42:LYS:HA	1.97	0.46
52:3:990:C:H2'	52:3:991:U:O4'	2.16	0.46
52:3:1251:A:O2'	52:3:1370:G:H5'	2.15	0.46
52:3:1527:U:O2'	52:3:1528:U:H5'	2.16	0.46
53:1:259:G:H2'	53:1:260:G:H8	1.81	0.46
53:1:2407:A:H2'	53:1:2408:U:C6	2.50	0.46
7:h:56:ARG:HH12	7:h:81:LEU:HG	1.80	0.46
12:m:33:LEU:HD13	12:m:103:TYR:HD2	1.81	0.46
20:u:65:GLN:HE21	53:1:328:U:H4'	1.80	0.46
35:K:12:PRO:O	35:K:15:SER:OG	2.26	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:77:VAL:HG23	37:M:126:CYS:HA	1.97	0.46
40:P:33:ILE:HD11	40:P:73:VAL:HG11	1.96	0.46
52:3:113:G:H2'	52:3:114:U:C6	2.51	0.46
52:3:974:A:H5'	52:3:976:G:OP1	2.16	0.46
52:3:1302:C:O2'	52:3:1303:C:H5'	2.15	0.46
53:1:296:U:H2'	53:1:297:G:H8	1.81	0.46
53:1:741:U:H2'	53:1:742:A:H8	1.81	0.46
53:1:1475:G:HO2'	53:1:1476:U:H6	1.64	0.46
53:1:1772:A:C2'	53:1:1773:A:H5'	2.46	0.46
53:1:1775:U:H2'	53:1:1776:G:O4'	2.16	0.46
53:1:2604:U:H2'	53:1:2605:U:C6	2.51	0.46
7:h:60:LEU:O	7:h:61:ARG:NH1	2.47	0.46
12:m:64:TRP:NE1	53:1:873:C:H4'	2.22	0.46
16:q:3:VAL:CG2	53:1:1249:U:H4'	2.42	0.46
24:y:2:LYS:O	24:y:6:LEU:HB2	2.15	0.46
33:I:110:ARG:N	33:I:110:ARG:HD2	2.31	0.46
34:J:53:ARG:HH21	52:3:1071:C:H5'	1.79	0.46
42:R:13:HIS:O	42:R:16:ILE:HG22	2.15	0.46
46:V:5:ARG:NH1	52:3:127:G:O2'	2.48	0.46
52:3:130:A:O2'	52:3:264:C:H5'	2.15	0.46
52:3:390:U:O2'	52:3:391:G:H5'	2.16	0.46
52:3:702:A:N6	53:1:1846:G:H4'	2.30	0.46
52:3:1144:G:H21	52:3:1146:A:H62	1.63	0.46
53:1:1516:G:O2'	53:1:1517:G:H5'	2.16	0.46
53:1:2106:U:H2'	53:1:2107:G:C8	2.51	0.46
54:2:108:A:H5'	54:2:109:A:O5'	2.16	0.46
6:g:47:PHE:HD1	6:g:51:ARG:HE	1.64	0.45
8:i:105:LEU:HD21	8:i:128:ILE:HB	1.98	0.45
10:k:40:LYS:HE3	53:1:2561:U:O3'	2.15	0.45
12:m:1:MET:SD	12:m:44:ARG:HG2	2.56	0.45
14:o:53:THR:HG22	14:o:74:VAL:HG11	1.97	0.45
35:K:29:ILE:HG12	35:K:64:VAL:HG21	1.96	0.45
52:3:256:U:H2'	52:3:257:G:C8	2.51	0.45
52:3:337:G:H2'	52:3:338:A:C8	2.52	0.45
52:3:1033:G:H2'	52:3:1034:G:C5'	2.43	0.45
52:3:1273:C:H2'	52:3:1274:A:O4'	2.16	0.45
53:1:20:C:H2'	53:1:21:A:C8	2.51	0.45
53:1:542:C:H2'	53:1:543:G:C5'	2.46	0.45
53:1:580:U:H2'	53:1:581:C:C6	2.51	0.45
53:1:580:U:H2'	53:1:581:C:H6	1.81	0.45
53:1:940:G:C3'	53:1:941:A:H5''	2.45	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1609:A:H1'	53:1:1616:A:C1'	2.45	0.45
53:1:2055:C:H5'	53:1:2056:G:O5'	2.16	0.45
53:1:2350:C:H2'	53:1:2351:G:O4'	2.16	0.45
53:1:2819:G:H2'	53:1:2821:A:N7	2.31	0.45
53:1:2841:C:H2'	53:1:2842:G:C8	2.50	0.45
53:1:2861:U:H2'	53:1:2862:G:H8	1.80	0.45
55:5:62:C:C3'	55:5:63:G:H5''	2.45	0.45
10:k:86:LEU:HB3	10:k:95:ILE:HD12	1.98	0.45
37:M:88:LYS:HB3	52:3:600:A:OP1	2.16	0.45
39:O:88:MET:C	39:O:89:ARG:HD3	2.41	0.45
43:S:12:ARG:HB3	43:S:59:GLN:HE21	1.81	0.45
49:Y:23:ARG:O	49:Y:26:MET:HG3	2.16	0.45
51:a:4:LEU:CG	51:a:8:MET:HB2	2.47	0.45
52:3:1354:U:H2'	52:3:1355:G:H8	1.80	0.45
53:1:523:C:H2'	53:1:524:G:H8	1.80	0.45
53:1:779:U:H2'	53:1:780:G:C8	2.51	0.45
53:1:2128:G:H21	53:1:2173:A:H1'	1.80	0.45
54:2:28:C:H2'	54:2:29:A:C8	2.52	0.45
54:2:48:U:H2'	54:2:49:C:C6	2.51	0.45
55:5:37:A:H2'	55:5:38:A:O4'	2.15	0.45
3:d:163:ASN:HB2	53:1:322:A:OP2	2.15	0.45
4:e:7:TYR:HA	4:e:11:VAL:CG2	2.45	0.45
7:h:87:GLU:CB	7:h:95:LEU:HD12	2.45	0.45
12:m:12:MET:HA	53:1:910:A:N6	2.19	0.45
13:n:69:ARG:O	13:n:70:THR:OG1	2.27	0.45
14:o:90:VAL:HG22	14:o:91:SER:N	2.31	0.45
15:p:31:VAL:HG23	15:p:38:ARG:HB3	1.99	0.45
25:z:52:PHE:CD2	54:2:83:G:H4'	2.51	0.45
32:H:23:ALA:HB3	32:H:28:PHE:HD1	1.82	0.45
42:R:26:LYS:O	42:R:29:SER:OG	2.30	0.45
52:3:1494:G:O2'	52:3:1495:U:H5'	2.17	0.45
53:1:161:A:H62	53:1:165:A:H61	1.62	0.45
53:1:360:U:H2'	53:1:361:G:O4'	2.17	0.45
53:1:661:A:O2'	53:1:662:G:H5'	2.16	0.45
3:d:147:LEU:HD23	3:d:147:LEU:C	2.42	0.45
8:i:73:PRO:HA	8:i:74:PRO:HD3	1.89	0.45
10:k:71:ARG:HB2	10:k:75:SER:HB2	1.99	0.45
24:y:9:LYS:HB2	24:y:12:GLU:HG3	1.99	0.45
34:J:133:ILE:HG23	34:J:134:ASN:N	2.31	0.45
35:K:29:ILE:HD11	35:K:34:GLY:HA3	1.97	0.45
41:Q:2:THR:HG22	41:Q:5:GLN:HG3	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:2:ASN:OD1	49:Y:3:ILE:N	2.45	0.45
52:3:594:U:O2'	52:3:595:A:H5'	2.16	0.45
52:3:929:G:H2'	52:3:930:C:C6	2.51	0.45
52:3:1319:A:H4'	52:3:1320:C:H5	1.81	0.45
52:3:1464:U:H2'	52:3:1465:A:C8	2.52	0.45
53:1:435:C:C2'	53:1:436:C:H5'	2.45	0.45
53:1:1869:G:H2'	53:1:1871:A:OP1	2.16	0.45
53:1:1991:U:H2'	53:1:1992:G:H5''	1.99	0.45
53:1:2139:U:H2'	53:1:2140:G:C8	2.52	0.45
53:1:2233:U:H2'	53:1:2234:G:H8	1.81	0.45
55:5:36:U:H2'	55:5:37:A:H8	1.81	0.45
1:b:20:ASN:ND2	1:b:23:LEU:HG	2.32	0.45
8:i:63:ASP:C	8:i:64:ARG:HD3	2.42	0.45
21:v:44:HIS:NE2	21:v:85:LYS:HB2	2.32	0.45
32:H:122:GLN:O	32:H:127:VAL:HG22	2.16	0.45
34:J:39:GLY:CA	34:J:116:VAL:HB	2.38	0.45
34:J:84:VAL:HG22	34:J:85:LYS:N	2.31	0.45
37:M:12:ARG:NH1	37:M:25:THR:O	2.49	0.45
38:N:10:ARG:NH2	52:3:1149:C:OP2	2.49	0.45
38:N:60:LEU:HD11	38:N:89:TYR:HE2	1.80	0.45
40:P:81:LEU:HD12	40:P:81:LEU:O	2.16	0.45
51:a:201:PRO:HB2	51:a:204:ALA:HB2	1.98	0.45
52:3:58:C:O2'	52:3:59:A:H5'	2.16	0.45
53:1:171:U:H2'	53:1:172:A:H8	1.82	0.45
53:1:492:A:H2'	53:1:493:G:O4'	2.17	0.45
53:1:660:C:H2'	53:1:661:A:C8	2.52	0.45
53:1:804:A:H2'	53:1:806:C:C4	2.51	0.45
53:1:1590:A:H2'	53:1:1591:A:H8	1.80	0.45
53:1:2423:U:H5'	53:1:2424:C:C5'	2.46	0.45
1:b:35:LYS:HZ3	53:1:1353:A:H5''	1.81	0.45
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.17	0.45
4:e:45:ASP:HB3	4:e:48:LEU:HB2	1.98	0.45
12:m:58:LYS:HG3	12:m:59:ARG:N	2.32	0.45
14:o:101:GLY:HA3	54:2:49:C:OP1	2.16	0.45
25:z:50:VAL:O	25:z:54:VAL:HG22	2.16	0.45
31:G:90:PHE:O	31:G:91:VAL:HG13	2.17	0.45
32:H:151:GLU:HG2	32:H:198:LYS:HB2	1.99	0.45
34:J:61:LYS:NZ	52:3:1073:U:OP2	2.50	0.45
49:Y:73:ARG:CZ	52:3:261:U:H5	2.29	0.45
52:3:49:U:O2'	52:3:50:A:H2'	2.16	0.45
52:3:1015:G:O2'	52:3:1016:A:H5'	2.15	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1305:G:H22	52:3:1331:G:H2'	1.82	0.45
52:3:1520:C:H2'	52:3:1521:C:C6	2.51	0.45
53:1:225:C:H2'	53:1:226:A:O4'	2.16	0.45
53:1:1609:A:H1'	53:1:1616:A:O4'	2.16	0.45
53:1:1827:U:C2'	53:1:1828:G:H5'	2.47	0.45
1:b:97:ASP:OD1	1:b:98:GLY:N	2.48	0.45
15:p:92:ARG:HD3	53:1:1753:G:OP1	2.17	0.45
19:t:75:GLY:HA2	19:t:76:ARG:NH1	2.31	0.45
20:u:85:ARG:HG3	20:u:92:VAL:HG23	1.98	0.45
31:G:86:CYS:O	31:G:87:ASP:OD2	2.35	0.45
31:G:103:TRP:HA	31:G:106:VAL:HB	1.99	0.45
31:G:104:LYS:CD	52:3:1073:U:H4'	2.38	0.45
34:J:65:LYS:HA	34:J:68:ARG:HH11	1.80	0.45
34:J:141:ASP:O	34:J:144:GLU:HG2	2.17	0.45
43:S:84:ARG:NH2	52:3:1059:C:H4'	2.32	0.45
52:3:552:U:H2'	52:3:553:A:C8	2.52	0.45
52:3:1071:C:H2'	52:3:1072:G:C8	2.46	0.45
52:3:1270:G:H2'	52:3:1271:A:H8	1.80	0.45
52:3:1460:C:H2'	52:3:1461:G:C8	2.51	0.45
53:1:819:A:C2	53:1:820:A:C4	3.05	0.45
53:1:861:A:H2'	53:1:862:G:O4'	2.16	0.45
53:1:1536:C:H4'	53:1:1537:G:C2	2.52	0.45
53:1:1758:U:H5	53:1:2696:U:H5'	1.79	0.45
53:1:1948:G:O2'	53:1:1949:G:H5'	2.17	0.45
53:1:2760:C:O2'	53:1:2761:A:H5'	2.17	0.45
53:1:2875:C:H2'	53:1:2876:G:C8	2.52	0.45
54:2:87:U:H5''	54:2:88:C:OP2	2.16	0.45
55:5:59:A:H2'	55:5:60:U:C5'	2.45	0.45
57:7:28:G:H1	57:7:42:C:N4	2.15	0.45
57:7:75:C:C4	57:7:76:A:N6	2.85	0.45
3:d:128:ALA:HB3	3:d:133:LEU:HD12	1.99	0.45
7:h:112:ALA:O	7:h:113:PHE:C	2.58	0.45
14:o:108:ASP:HA	14:o:111:ARG:HB2	1.99	0.45
17:r:83:TYR:CZ	53:1:1187:G:H5''	2.51	0.45
31:G:19:THR:HG22	31:G:38:HIS:CD2	2.52	0.45
32:H:113:LYS:HB2	32:H:184:ASN:ND2	2.31	0.45
37:M:28:SER:OG	37:M:58:LEU:HB2	2.17	0.45
43:S:8:ARG:NH1	52:3:981:U:OP1	2.49	0.45
48:X:36:ARG:CZ	52:3:1318:A:H1'	2.47	0.45
52:3:428:G:O4'	52:3:430:A:C8	2.70	0.45
52:3:629:A:H2'	52:3:630:A:O4'	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:632:U:H3'	52:3:633:G:H5'	1.98	0.45
52:3:1162:C:H2'	52:3:1163:A:H8	1.82	0.45
52:3:1204:A:H2'	52:3:1205:U:O4'	2.17	0.45
53:1:248:G:N3	53:1:2431:U:H4'	2.32	0.45
53:1:720:U:H2'	53:1:721:A:H8	1.80	0.45
53:1:1680:U:C2'	53:1:1681:G:H5'	2.47	0.45
53:1:2047:C:H2'	53:1:2048:G:C8	2.52	0.45
53:1:2323:G:O2'	53:1:2324:U:H5'	2.16	0.45
53:1:2339:C:H2'	53:1:2340:A:H8	1.82	0.45
53:1:2699:C:H2'	53:1:2700:A:H8	1.82	0.45
53:1:2798:U:H4'	53:1:2799:A:C4	2.51	0.45
54:2:55:U:O2'	54:2:56:G:H5'	2.16	0.45
54:2:95:U:H2'	54:2:96:G:H8	1.81	0.45
4:e:132:ARG:HG3	53:1:2305:U:O2'	2.16	0.45
29:E:8:GLY:O	29:E:12:ARG:NH2	2.50	0.45
31:G:34:ARG:HG2	31:G:39:ILE:HG13	1.97	0.45
40:P:15:VAL:HG22	40:P:76:TYR:HB3	1.98	0.45
52:3:123:U:H5''	52:3:311:C:O2'	2.17	0.45
52:3:1096:C:H2'	52:3:1097:C:H6	1.81	0.45
53:1:987:C:H2'	53:1:988:A:O4'	2.16	0.45
53:1:1434:A:H2'	53:1:1435:G:H8	1.82	0.45
53:1:2678:C:H2'	53:1:2679:A:C8	2.51	0.45
55:5:4:G:H2'	55:5:5:G:O4'	2.17	0.45
55:5:12:G:H1	55:5:23:C:H42	1.63	0.45
55:5:26:G:H2'	55:5:27:U:OP1	2.17	0.45
1:b:32:LEU:HD21	1:b:101:ARG:HA	1.99	0.45
1:b:140:VAL:HG11	1:b:189:ALA:HB1	1.99	0.45
7:h:13:ALA:HB1	7:h:53:ARG:HH12	1.81	0.45
7:h:118:ILE:HD13	7:h:118:ILE:HA	1.85	0.45
21:v:56:PHE:CE1	21:v:61:LEU:HD21	2.52	0.45
22:w:33:ILE:HD11	22:w:78:ILE:HD11	1.99	0.45
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.85	0.45
42:R:9:PRO:HG2	42:R:44:ILE:HG21	1.99	0.45
52:3:12:U:H2'	52:3:13:U:H5''	1.99	0.45
52:3:70:U:H5''	52:3:71:A:OP1	2.16	0.45
52:3:422:C:H5''	52:3:423:G:O5'	2.17	0.45
52:3:426:U:H2'	52:3:427:U:C6	2.52	0.45
52:3:817:C:H4'	52:3:818:G:H5''	1.99	0.45
52:3:1400:C:H5'	56:4:18:G:C5	2.52	0.45
53:1:182:A:O2'	53:1:183:C:H5'	2.17	0.45
53:1:780:G:H2'	53:1:782:A:N7	2.32	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1078:U:H4'	53:1:1079:C:H5''	1.98	0.45
53:1:1837:C:H2'	53:1:1899:A:H61	1.80	0.45
4:e:66:ILE:HD13	4:e:86:CYS:SG	2.57	0.44
17:r:80:ARG:NH2	53:1:572:A:OP2	2.50	0.44
25:z:37:ARG:NH2	53:1:929:U:H4'	2.32	0.44
33:I:8:LEU:HD22	52:3:429:U:H5'	1.99	0.44
34:J:108:GLY:O	34:J:109:ALA:HB3	2.17	0.44
38:N:65:THR:OG1	38:N:67:LYS:NZ	2.46	0.44
38:N:112:ARG:NH2	52:3:1187:G:H4'	2.32	0.44
42:R:18:LEU:HD21	42:R:32:ILE:HG13	1.99	0.44
46:V:30:HIS:CD2	46:V:33:TYR:H	2.29	0.44
52:3:291:U:H2'	52:3:292:G:H8	1.82	0.44
52:3:822:U:O2'	52:3:823:C:H5'	2.18	0.44
52:3:952:U:H2'	52:3:953:G:C8	2.52	0.44
53:1:796:C:H2'	53:1:797:G:C8	2.51	0.44
53:1:905:A:O2'	53:1:906:U:H5'	2.16	0.44
53:1:1877:A:H2'	53:1:1878:G:O4'	2.16	0.44
53:1:2126:A:H2'	53:1:2162:G:N2	2.32	0.44
53:1:2432:A:H1'	55:5:75:C:O4'	2.16	0.44
57:7:68:C:H2'	57:7:69:G:H8	1.81	0.44
1:b:235:GLU:HG2	53:1:2600:A:N6	2.26	0.44
2:c:22:ILE:HA	2:c:23:PRO:HD3	1.83	0.44
2:c:77:ARG:HG3	2:c:77:ARG:NH2	2.32	0.44
6:g:115:VAL:HG22	6:g:132:PHE:HE1	1.82	0.44
14:o:29:HIS:HB3	14:o:36:TYR:HD2	1.82	0.44
21:v:20:LEU:HD21	21:v:41:GLU:HG3	1.99	0.44
40:P:115:ILE:HG23	40:P:115:ILE:O	2.18	0.44
41:Q:5:GLN:HA	41:Q:8:ARG:HH12	1.81	0.44
42:R:78:ARG:HA	42:R:81:ASP:OD2	2.17	0.44
49:Y:4:LYS:HG2	49:Y:6:ALA:H	1.83	0.44
52:3:285:C:H2'	52:3:286:C:H6	1.81	0.44
52:3:730:G:H2'	52:3:731:G:H5'	1.98	0.44
52:3:770:C:H2'	52:3:771:G:H8	1.82	0.44
52:3:801:U:H2'	52:3:802:A:C8	2.53	0.44
52:3:1370:G:H2'	52:3:1371:G:C8	2.50	0.44
52:3:1497:G:H2'	52:3:1498:U:H5'	1.98	0.44
52:3:1515:G:O2'	52:3:1516:G:H5'	2.17	0.44
53:1:828:U:H4'	53:1:831:G:N1	2.32	0.44
53:1:1199:U:H2'	53:1:1200:C:C6	2.52	0.44
53:1:1357:C:H2'	53:1:1358:G:O4'	2.16	0.44
53:1:1435:G:O2'	53:1:1436:G:H5'	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1720:U:H2'	53:1:1721:G:O4'	2.17	0.44
55:5:26:G:C2'	55:5:27:U:OP1	2.66	0.44
18:s:77:ASP:OD2	18:s:77:ASP:N	2.50	0.44
27:C:38:PHE:O	27:C:40:PRO:HD3	2.17	0.44
33:I:201:GLU:HB3	52:3:8:A:H61	1.81	0.44
34:J:141:ASP:HA	34:J:144:GLU:CG	2.44	0.44
38:N:18:VAL:HG12	38:N:64:ILE:HD12	2.00	0.44
40:P:100:ASN:ND2	50:Z:12:ASP:O	2.50	0.44
52:3:539:A:H2'	52:3:540:G:H8	1.81	0.44
52:3:922:G:H2'	52:3:923:A:H8	1.82	0.44
52:3:1415:G:H2'	52:3:1416:G:C8	2.52	0.44
53:1:198:C:O2'	53:1:199:A:H5'	2.17	0.44
53:1:996:A:H2'	53:1:997:G:C8	2.49	0.44
53:1:1019:U:H3	53:1:1142:A:N6	2.14	0.44
53:1:1572:A:O2'	53:1:1573:G:H5'	2.17	0.44
53:1:2266:A:H4'	53:1:2267:A:C4	2.53	0.44
2:c:4:LEU:HD23	2:c:29:VAL:HG11	1.99	0.44
3:d:118:LEU:HD23	3:d:119:ILE:N	2.33	0.44
5:f:17:LYS:HB2	5:f:24:THR:HB	1.99	0.44
10:k:109:SER:O	10:k:111:LYS:N	2.51	0.44
11:l:128:THR:HG22	53:1:636:G:OP2	2.18	0.44
13:n:38:LEU:N	13:n:39:PRO:CD	2.81	0.44
19:t:15:HIS:HD2	19:t:33:LYS:NZ	2.16	0.44
40:P:21:HIS:N	40:P:32:THR:O	2.46	0.44
52:3:1123:U:O2'	52:3:1124:G:H5'	2.18	0.44
52:3:1258:G:H2'	52:3:1259:C:C6	2.53	0.44
53:1:473:G:C2'	53:1:474:G:H5'	2.48	0.44
53:1:940:G:H2'	53:1:941:A:C4'	2.48	0.44
53:1:947:A:H2'	53:1:948:C:C6	2.53	0.44
53:1:1331:G:O2'	53:1:1332:G:H5''	2.17	0.44
6:g:53:GLU:N	6:g:53:GLU:OE1	2.51	0.44
7:h:59:LEU:HD21	53:1:1047:G:C8	2.51	0.44
9:j:113:PRO:HD2	53:1:558:U:P	2.58	0.44
11:l:85:VAL:O	11:l:86:GLU:HB2	2.17	0.44
17:r:14:VAL:HG13	17:r:98:ILE:HG13	1.98	0.44
37:M:57:GLU:O	37:M:57:GLU:HG2	2.17	0.44
38:N:129:ARG:C	52:3:970:C:H42	2.25	0.44
45:U:70:ARG:NH2	52:3:451:A:H5''	2.32	0.44
50:Z:58:LYS:HA	50:Z:58:LYS:HD3	1.72	0.44
52:3:181:A:H62	52:3:194:C:H2'	1.82	0.44
52:3:434:U:H2'	52:3:435:A:C8	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:634:C:H2'	52:3:635:A:C8	2.52	0.44
52:3:1319:A:H4'	52:3:1320:C:C5	2.52	0.44
53:1:253:C:H2'	53:1:254:G:O4'	2.18	0.44
53:1:288:U:H2'	53:1:289:G:H8	1.81	0.44
53:1:490:C:O2'	53:1:491:G:P	2.76	0.44
53:1:2066:C:C2'	53:1:2067:G:H5'	2.47	0.44
53:1:2412:A:H2'	53:1:2413:G:O4'	2.17	0.44
53:1:2453:A:H2'	53:1:2454:G:H8	1.83	0.44
53:1:2699:C:H2'	53:1:2700:A:C8	2.53	0.44
2:c:118:PHE:HB2	53:1:2823:A:OP1	2.17	0.44
15:p:38:ARG:HG3	15:p:38:ARG:HH21	1.82	0.44
16:q:87:VAL:HG12	16:q:89:ILE:HG13	2.00	0.44
31:G:119:GLN:O	31:G:124:THR:HG22	2.18	0.44
40:P:91:GLY:C	40:P:93:GLU:N	2.75	0.44
43:S:8:ARG:HA	43:S:11:LYS:HD3	2.00	0.44
49:Y:11:ILE:H	49:Y:11:ILE:CD1	2.23	0.44
52:3:742:G:H2'	52:3:743:A:H8	1.82	0.44
52:3:1098:C:H2'	52:3:1099:G:H8	1.82	0.44
52:3:1245:C:H2'	52:3:1246:A:H8	1.82	0.44
53:1:657:U:H2'	53:1:658:U:C6	2.52	0.44
53:1:1434:A:H2'	53:1:1435:G:C8	2.52	0.44
53:1:1535:A:H3'	53:1:1536:C:H5'	2.00	0.44
53:1:2417:C:H2'	53:1:2418:A:H8	1.82	0.44
53:1:2884:U:O2	53:1:2884:U:H3'	2.18	0.44
6:g:6:LEU:HD11	6:g:37:VAL:HG23	1.99	0.44
7:h:118:ILE:N	7:h:119:PRO:CD	2.81	0.44
11:l:19:LEU:O	11:l:21:ARG:NH2	2.51	0.44
14:o:68:LYS:HG3	54:2:50:A:OP1	2.17	0.44
15:p:15:ASP:OD1	15:p:15:ASP:N	2.48	0.44
18:s:11:ARG:HH21	53:1:1321:A:HO2'	1.66	0.44
42:R:33:LEU:CD2	42:R:40:GLU:HG2	2.48	0.44
43:S:3:GLN:HG2	43:S:6:LYS:HE2	1.99	0.44
43:S:72:PHE:C	43:S:73:LEU:HD22	2.43	0.44
52:3:114:U:O2'	52:3:115:G:H5'	2.18	0.44
52:3:116:A:C2'	52:3:117:G:H5'	2.47	0.44
52:3:770:C:H2'	52:3:771:G:C8	2.53	0.44
52:3:868:C:H2'	52:3:869:G:O4'	2.18	0.44
52:3:1328:C:H2'	52:3:1329:A:C8	2.53	0.44
53:1:64:A:H2'	53:1:65:U:C6	2.52	0.44
53:1:214:G:H2'	53:1:215:G:C8	2.53	0.44
53:1:854:C:H2'	53:1:855:G:H8	1.83	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:955:U:H3	53:1:962:G:H1	1.64	0.44
53:1:1259:G:O2'	53:1:1260:A:H5'	2.18	0.44
53:1:2153:C:H2'	53:1:2154:A:C8	2.52	0.44
53:1:2723:C:H2'	53:1:2724:U:O4'	2.18	0.44
54:2:51:G:O2'	54:2:52:A:H5'	2.18	0.44
54:2:60:C:H2'	54:2:61:G:H8	1.83	0.44
10:k:13:ASN:CG	10:k:98:ARG:HB3	2.43	0.44
21:v:9:ARG:HD3	21:v:39:ALA:HB1	1.98	0.44
21:v:32:GLY:O	21:v:93:ARG:NH1	2.51	0.44
22:w:29:ALA:N	22:w:60:ASP:OD1	2.51	0.44
26:B:10:SER:OG	26:B:11:LYS:N	2.50	0.44
26:B:52:LYS:HE2	26:B:56:LYS:H	1.82	0.44
30:F:1:MET:HE2	30:F:34:LYS:HD2	1.99	0.44
31:G:69:VAL:HG12	31:G:91:VAL:HG23	1.99	0.44
37:M:77:VAL:HG21	37:M:127:TYR:CD1	2.52	0.44
38:N:11:ARG:NH1	38:N:12:LYS:HB2	2.31	0.44
39:O:6:ILE:HD12	39:O:6:ILE:H	1.82	0.44
41:Q:50:LYS:HD2	41:Q:50:LYS:N	2.33	0.44
42:R:53:ASP:OD1	42:R:53:ASP:N	2.51	0.44
49:Y:70:LYS:HA	49:Y:73:ARG:NH1	2.33	0.44
50:Z:29:ALA:HA	50:Z:32:ARG:NE	2.33	0.44
51:a:212:VAL:HG13	51:a:212:VAL:O	2.18	0.44
52:3:225:C:H2'	52:3:226:G:C5'	2.47	0.44
52:3:881:G:C2'	52:3:882:C:H5'	2.48	0.44
52:3:1375:A:H2'	52:3:1376:U:C6	2.53	0.44
53:1:656:G:O2'	53:1:657:U:H5'	2.18	0.44
53:1:677:A:O2'	53:1:2071:A:H5'	2.18	0.44
53:1:2716:C:O2'	53:1:2717:C:H5'	2.18	0.44
54:2:3:C:H3'	54:2:4:C:H5''	2.00	0.44
6:g:54:LEU:HD23	6:g:54:LEU:C	2.42	0.44
8:i:36:GLU:O	8:i:39:LYS:HG3	2.17	0.44
12:m:20:LEU:HD23	21:v:81:PRO:HG2	2.00	0.44
16:q:90:ASP:OD2	16:q:92:LYS:HB3	2.18	0.44
33:I:150:LYS:HD2	33:I:177:MET:HE1	2.00	0.44
34:J:111:ARG:O	34:J:115:GLU:HB2	2.17	0.44
34:J:121:ASN:O	34:J:122:VAL:O	2.36	0.44
36:L:3:ARG:HH21	52:3:932:C:C5'	2.28	0.44
36:L:37:THR:HG21	52:3:1240:U:H4'	2.00	0.44
43:S:30:ILE:O	43:S:30:ILE:HG13	2.18	0.44
46:V:29:LYS:HB2	46:V:36:PHE:CE1	2.53	0.44
47:W:32:ILE:HD13	47:W:67:LEU:HD12	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:X:77:ARG:HG2	52:3:959:A:N6	2.33	0.44
52:3:1488:G:H2'	52:3:1489:G:C8	2.53	0.44
52:3:1496:C:H2'	52:3:1497:G:O4'	2.18	0.44
53:1:190:A:C5	53:1:207:A:C2	3.06	0.44
53:1:622:G:H2'	53:1:623:C:C6	2.52	0.44
53:1:1079:C:H2'	53:1:1080:A:C8	2.52	0.44
53:1:2088:A:H2'	53:1:2089:C:C6	2.53	0.44
55:5:69:C:O2'	55:5:70:G:H5''	2.18	0.44
1:b:149:LYS:HD3	53:1:2204:G:H4'	2.00	0.43
2:c:56:LYS:HZ1	53:1:2830:C:H5''	1.83	0.43
3:d:176:ASP:OD2	3:d:179:SER:HB2	2.18	0.43
4:e:76:PHE:CE2	53:1:2310:C:H2'	2.53	0.43
12:m:41:LEU:HD22	12:m:124:LEU:HD22	2.00	0.43
12:m:41:LEU:HG	12:m:96:ILE:HG13	1.99	0.43
16:q:10:ARG:HA	16:q:10:ARG:HH11	1.82	0.43
20:u:16:LYS:HD2	53:1:329:G:H1	1.83	0.43
21:v:26:PHE:HE1	21:v:44:HIS:HA	1.83	0.43
31:G:78:ALA:HB1	31:G:213:LEU:HD21	1.99	0.43
33:I:13:ARG:HH22	52:3:510:A:H4'	1.82	0.43
34:J:10:LEU:HD13	34:J:10:LEU:HA	1.91	0.43
34:J:156:ARG:NE	37:M:42:GLU:HG3	2.33	0.43
35:K:15:SER:OG	35:K:44:ARG:NH1	2.51	0.43
46:V:61:ARG:HD3	46:V:75:VAL:HG22	1.99	0.43
48:X:57:VAL:HG21	48:X:75:PRO:HD2	2.00	0.43
52:3:212:G:O2'	52:3:213:G:H5'	2.17	0.43
52:3:604:G:H2'	52:3:605:U:O4'	2.18	0.43
53:1:146:A:H2'	53:1:147:C:H6	1.82	0.43
53:1:633:A:H2'	53:1:634:C:O4'	2.18	0.43
53:1:1444:G:H2'	53:1:1445:G:H8	1.83	0.43
53:1:1697:G:H4'	53:1:1978:A:H5''	2.00	0.43
53:1:2639:A:H1'	53:1:2778:A:C2	2.53	0.43
55:5:27:U:H2'	55:5:28:C:C5'	2.47	0.43
1:b:141:HIS:ND1	1:b:192:GLY:O	2.50	0.43
1:b:175:LEU:HB2	1:b:179:GLU:HB3	2.00	0.43
1:b:216:ARG:HG3	1:b:216:ARG:HH11	1.83	0.43
3:d:63:LYS:HD2	53:1:2444:G:OP2	2.19	0.43
11:l:93:ASN:OD1	11:l:94:THR:HG23	2.17	0.43
17:r:45:GLU:H	17:r:45:GLU:CD	2.25	0.43
17:r:91:GLN:HE21	53:1:993:G:H1'	1.83	0.43
20:u:13:LEU:O	20:u:18:LYS:HG3	2.18	0.43
26:B:49:ARG:HG2	53:1:2884:U:C6	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:D:3:ARG:HH21	28:D:4:THR:H	1.66	0.43
30:F:5:ALA:HB3	53:1:2466:C:C5'	2.48	0.43
32:H:71:ARG:O	32:H:75:VAL:HG23	2.18	0.43
32:H:112:ALA:HB3	32:H:184:ASN:OD1	2.17	0.43
34:J:68:ARG:CZ	52:3:1074:G:OP1	2.66	0.43
43:S:86:ALA:HB1	43:S:91:GLU:HB2	2.00	0.43
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.80	0.43
52:3:600:A:H2'	52:3:601:G:H8	1.82	0.43
52:3:729:A:H2'	52:3:730:G:C8	2.54	0.43
52:3:884:U:H4'	52:3:885:G:H5''	1.99	0.43
52:3:938:A:C2	52:3:1376:U:H1'	2.53	0.43
52:3:955:U:H2'	52:3:956:U:O4'	2.19	0.43
53:1:145:C:H2'	53:1:146:A:C8	2.54	0.43
53:1:633:A:H2'	53:1:634:C:H5'	2.00	0.43
53:1:1447:C:H2'	53:1:1448:G:C8	2.53	0.43
53:1:2118:U:H5	53:1:2149:U:H1'	1.82	0.43
53:1:2705:A:H2'	53:1:2706:A:O4'	2.17	0.43
53:1:2765:A:H5'	53:1:2766:A:OP2	2.18	0.43
7:h:94:ARG:HB2	7:h:97:LYS:HE2	2.01	0.43
8:i:91:LYS:HD2	8:i:94:LYS:HE2	2.00	0.43
14:o:49:VAL:HG11	14:o:81:ARG:HG3	2.00	0.43
14:o:90:VAL:HG22	14:o:91:SER:H	1.82	0.43
15:p:77:SER:HA	15:p:78:PRO:HD3	1.86	0.43
17:r:26:ASP:O	17:r:27:ILE:HD13	2.17	0.43
20:u:4:ILE:HD12	20:u:4:ILE:N	2.32	0.43
25:z:7:THR:OG1	25:z:55:LYS:HB3	2.18	0.43
32:H:27:GLU:O	32:H:31:ASN:ND2	2.51	0.43
32:H:42:LEU:HD12	32:H:43:THR:N	2.33	0.43
36:L:148:LYS:HE3	40:P:60:PHE:HZ	1.78	0.43
37:M:104:SER:HB2	37:M:109:VAL:HG22	1.99	0.43
39:O:10:LEU:HA	39:O:98:VAL:HA	2.00	0.43
39:O:76:ILE:O	39:O:76:ILE:HG13	2.17	0.43
43:S:33:VAL:O	43:S:33:VAL:HG22	2.18	0.43
44:T:71:ARG:NH2	52:3:754:C:OP1	2.52	0.43
46:V:57:VAL:HG12	46:V:58:VAL:N	2.34	0.43
52:3:59:A:H5''	52:3:387:U:H5''	1.99	0.43
52:3:537:G:H2'	52:3:538:G:C8	2.52	0.43
52:3:545:C:H2'	52:3:546:A:C8	2.54	0.43
52:3:960:U:O2'	52:3:1223:C:H4'	2.18	0.43
52:3:1329:A:O2'	52:3:1330:U:H5'	2.19	0.43
52:3:1516:G:H2'	52:3:1518:A:OP2	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:616:A:H2'	53:1:617:G:O4'	2.19	0.43
53:1:821:A:H5''	53:1:822:G:H5''	1.99	0.43
53:1:2339:C:H2'	53:1:2340:A:C8	2.54	0.43
53:1:2556:C:H2'	53:1:2557:G:O4'	2.19	0.43
53:1:2670:A:H2'	53:1:2671:G:C8	2.53	0.43
1:b:120:ASP:OD1	1:b:120:ASP:N	2.51	0.43
4:e:102:LEU:HA	4:e:106:ALA:HB3	1.99	0.43
4:e:110:ILE:HB	4:e:113:PHE:HB2	2.00	0.43
6:g:25:TYR:CZ	53:1:2094:A:H4'	2.53	0.43
6:g:133:GLN:HE21	6:g:136:SER:HA	1.84	0.43
8:i:10:LEU:HB3	8:i:11:GLN:H	1.45	0.43
10:k:1:MET:HA	10:k:32:TYR:HB3	2.01	0.43
11:l:60:ARG:O	53:1:2393:U:H5'	2.19	0.43
11:l:130:GLY:HA3	53:1:637:A:OP1	2.18	0.43
13:n:49:GLU:O	13:n:53:THR:HG23	2.19	0.43
17:r:78:ARG:CG	17:r:81:LYS:HB2	2.48	0.43
23:x:6:VAL:HG21	23:x:58:ILE:HD11	2.01	0.43
29:E:31:ILE:HD11	53:1:2391:G:C5'	2.45	0.43
34:J:88:HIS:O	34:J:90:GLY:N	2.52	0.43
48:X:39:ILE:HD12	48:X:39:ILE:N	2.32	0.43
52:3:166:U:H2'	52:3:167:A:C8	2.53	0.43
52:3:225:C:H3'	52:3:226:G:H5''	1.99	0.43
52:3:583:A:H2'	52:3:584:G:O4'	2.19	0.43
52:3:1033:G:C3'	52:3:1034:G:H5''	2.48	0.43
52:3:1413:A:O2'	52:3:1414:U:H5'	2.18	0.43
52:3:1449:C:H2'	52:3:1450:U:O4'	2.18	0.43
53:1:1028:A:H2'	53:1:1029:A:C8	2.53	0.43
53:1:1275:A:C6	53:1:1296:G:H4'	2.52	0.43
53:1:1507:C:H2'	53:1:1508:A:C4'	2.49	0.43
53:1:2248:C:C2'	53:1:2249:U:H5'	2.48	0.43
53:1:2327:A:H2'	53:1:2328:A:C8	2.53	0.43
53:1:2714:G:H2'	53:1:2715:C:C6	2.53	0.43
53:1:2861:U:H2'	53:1:2862:G:C8	2.52	0.43
54:2:13:G:N7	54:2:70:C:H4'	2.33	0.43
4:e:21:TYR:CD1	4:e:26:GLN:HG2	2.52	0.43
4:e:69:ALA:HB3	4:e:82:TYR:H	1.83	0.43
4:e:128:SER:HA	4:e:154:THR:HA	2.00	0.43
6:g:69:ALA:HA	6:g:72:ILE:HD11	2.01	0.43
16:q:10:ARG:NH2	53:1:1217:U:OP1	2.51	0.43
16:q:36:GLN:OE1	53:1:1252:G:N1	2.52	0.43
40:P:79:LYS:HG3	40:P:80:ASN:OD1	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:13:LYS:HE3	52:3:392:C:H5'	2.00	0.43
49:Y:28:ARG:NH2	52:3:1437:A:H5''	2.32	0.43
52:3:464:U:H2'	52:3:466:A:OP2	2.18	0.43
52:3:920:U:H2'	52:3:921:U:H6	1.84	0.43
52:3:1162:C:H2'	52:3:1163:A:C8	2.53	0.43
52:3:1167:A:H2'	52:3:1167:A:N3	2.33	0.43
52:3:1502:A:H5'	52:3:1504:G:N7	2.33	0.43
53:1:204:A:O3'	53:1:205:G:H4'	2.18	0.43
53:1:581:C:H2'	53:1:582:A:H8	1.80	0.43
53:1:1105:U:H2'	53:1:1106:G:C5'	2.49	0.43
53:1:1295:C:H2'	53:1:1296:G:C8	2.53	0.43
53:1:1969:A:H2'	53:1:1972:G:H21	1.84	0.43
2:c:43:ASP:HB3	2:c:45:TYR:CE1	2.53	0.43
2:c:50:VAL:HG12	2:c:51:THR:H	1.84	0.43
6:g:132:PHE:HB2	6:g:140:ALA:HB3	2.00	0.43
8:i:55:PRO:HD3	8:i:74:PRO:HD3	2.01	0.43
9:j:113:PRO:HD2	53:1:558:U:OP1	2.17	0.43
11:l:68:SER:HB3	11:l:71:ALA:HB2	2.01	0.43
11:l:79:LEU:O	11:l:82:LEU:HB3	2.17	0.43
12:m:14:LYS:NZ	53:1:956:G:O6	2.52	0.43
33:I:160:LEU:HD13	33:I:164:ARG:HH21	1.83	0.43
35:K:9:MET:HB3	35:K:57:ALA:HB1	1.99	0.43
38:N:10:ARG:O	38:N:105:ARG:NH2	2.51	0.43
41:Q:38:THR:HG22	41:Q:50:LYS:HA	2.01	0.43
41:Q:81:ILE:HD13	41:Q:96:THR:HA	2.01	0.43
43:S:8:ARG:HA	43:S:11:LYS:CD	2.49	0.43
43:S:64:ARG:NH2	43:S:76:PHE:O	2.51	0.43
52:3:62:U:H2'	52:3:63:C:C6	2.53	0.43
52:3:321:A:H2	52:3:332:G:H22	1.65	0.43
53:1:883:G:N2	53:1:894:U:H1'	2.32	0.43
53:1:917:A:H5''	53:1:2268:A:H61	1.83	0.43
53:1:1354:A:H2'	53:1:1355:G:O4'	2.19	0.43
53:1:1794:A:O2'	53:1:1795:C:H5'	2.18	0.43
53:1:2189:U:H2'	53:1:2190:G:H8	1.82	0.43
53:1:2800:A:H3'	53:1:2801:G:C5'	2.43	0.43
55:5:17(A):U:H1'	55:5:18:G:O5'	2.18	0.43
1:b:77:VAL:HG13	1:b:91:ALA:HB1	2.01	0.43
1:b:201:LEU:HD22	52:3:773:G:OP1	2.18	0.43
7:h:67:THR:HG22	7:h:68:PRO:HD3	2.00	0.43
10:k:30:ARG:HD2	53:1:2674:G:H4'	2.00	0.43
16:q:50:ARG:HD3	53:1:1156:A:C5	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:v:77:VAL:HG23	21:v:89:ILE:HG12	2.00	0.43
32:H:18:ASN:O	32:H:55:VAL:HA	2.19	0.43
34:J:19:ARG:HB3	34:J:32:PHE:CE1	2.54	0.43
35:K:18:VAL:HB	35:K:19:PRO:HD3	2.00	0.43
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.18	0.43
44:T:42:PHE:HE1	44:T:48:ASP:HB3	1.83	0.43
44:T:51:SER:HB3	52:3:666:G:H22	1.84	0.43
47:W:35:SER:HB3	50:Z:3:ILE:HG12	2.00	0.43
53:1:1077:A:C3'	53:1:1078:U:H5'	2.48	0.43
53:1:1149:G:H2'	53:1:1150:C:C6	2.53	0.43
53:1:2208:C:H2'	53:1:2209:G:C8	2.54	0.43
53:1:2440:C:H5''	53:1:2587:A:H4'	2.01	0.43
57:7:59:U:H2'	57:7:60:U:O4'	2.18	0.43
3:d:4:VAL:HG22	3:d:5:LEU:N	2.33	0.43
3:d:176:ASP:OD2	3:d:176:ASP:N	2.51	0.43
5:f:44:HIS:O	5:f:46:ASP:N	2.52	0.43
9:j:58:ASN:ND2	9:j:128:ASN:HB2	2.34	0.43
14:o:49:VAL:HG13	14:o:81:ARG:HD2	2.00	0.43
32:H:177:LEU:HG	52:3:1112:C:C4	2.54	0.43
33:I:7:LYS:HD2	33:I:20:LEU:HD12	2.00	0.43
35:K:18:VAL:HG21	35:K:58:HIS:CD2	2.54	0.43
35:K:51:ILE:O	35:K:52:ASN:CG	2.61	0.43
41:Q:5:GLN:HA	41:Q:8:ARG:NH1	2.34	0.43
46:V:20:ILE:O	46:V:45:VAL:HG22	2.19	0.43
50:Z:39:LYS:O	50:Z:40:PRO:C	2.60	0.43
51:a:163:TYR:HB2	51:a:171:ILE:HD11	2.00	0.43
52:3:119:A:H4'	52:3:120:A:C8	2.54	0.43
52:3:594:U:H2'	52:3:595:A:O4'	2.19	0.43
52:3:1241:G:H2'	52:3:1242:G:H8	1.84	0.43
52:3:1338:G:H1'	55:5:42:G:H5'	2.00	0.43
52:3:1394:A:H3'	52:3:1395:C:H5'	1.99	0.43
53:1:100:U:H4'	53:1:101:A:C4	2.54	0.43
53:1:155:A:H2'	53:1:156:A:C8	2.54	0.43
53:1:415:A:H2'	53:1:416:U:C6	2.53	0.43
53:1:704:G:H2'	53:1:726:G:N2	2.33	0.43
53:1:812:C:O2'	53:1:813:U:H5'	2.18	0.43
53:1:832:U:H2'	53:1:833:A:C8	2.54	0.43
53:1:1111:A:O2'	53:1:1112:G:H4'	2.19	0.43
53:1:1561:C:H2'	53:1:1562:U:C6	2.53	0.43
53:1:2013:A:H61	53:1:2613:U:H3	1.65	0.43
55:5:1:C:H1'	55:5:73:A:C2	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:147:LEU:HD12	3:d:183:PHE:HD2	1.83	0.43
4:e:105:ILE:HD12	4:e:138:PRO:HG2	2.01	0.43
7:h:3:LEU:HG	7:h:5:LEU:HG	2.01	0.43
11:l:14:LYS:O	11:l:15:ALA:HB3	2.18	0.43
14:o:3:LYS:C	14:o:3:LYS:HD3	2.44	0.43
16:q:49:ARG:O	16:q:53:LYS:NZ	2.47	0.43
18:s:72:THR:OG1	18:s:73:LYS:N	2.51	0.43
34:J:152:VAL:HA	34:J:155:LYS:HG2	2.00	0.43
35:K:3:HIS:HB2	35:K:92:THR:CA	2.45	0.43
38:N:47:VAL:O	38:N:51:LEU:HD13	2.19	0.43
52:3:729:A:H2'	52:3:730:G:H8	1.84	0.43
52:3:978:A:H4'	52:3:1322:C:N3	2.34	0.43
52:3:1309:G:H2'	52:3:1310:G:C8	2.54	0.43
52:3:1472:U:H2'	52:3:1473:G:C8	2.54	0.43
53:1:568:U:H2'	53:1:570:G:OP2	2.18	0.43
53:1:1182:G:H2'	53:1:1183:U:O4'	2.19	0.43
53:1:1412:U:H2'	53:1:1413:A:C8	2.53	0.43
53:1:2298:A:H2'	53:1:2299:U:O4'	2.19	0.43
53:1:2537:U:H2'	53:1:2538:C:C6	2.54	0.43
2:c:101:PHE:O	2:c:180:VAL:HG21	2.19	0.43
10:k:107:LEU:HD23	10:k:107:LEU:O	2.19	0.43
18:s:88:ARG:HA	18:s:88:ARG:HD2	1.86	0.43
20:u:5:ARG:N	20:u:8:ASP:OD2	2.40	0.43
31:G:24:PRO:HB3	52:3:828:U:H2'	2.01	0.43
37:M:5:PRO:O	37:M:8:ASP:HB3	2.19	0.43
46:V:56:ASP:N	46:V:56:ASP:OD1	2.51	0.43
52:3:152:A:H2'	52:3:153:C:H5'	2.00	0.43
52:3:160:A:N1	52:3:343:U:H1'	2.34	0.43
52:3:406:G:H2'	52:3:407:U:C6	2.54	0.43
52:3:538:G:H2'	52:3:539:A:C8	2.54	0.43
52:3:1253:G:H2'	52:3:1254:A:C8	2.54	0.43
53:1:706:A:H2'	53:1:707:G:O4'	2.19	0.43
53:1:927:A:H2'	53:1:928:A:C8	2.54	0.43
53:1:2163:A:H2'	53:1:2163:A:N3	2.34	0.43
53:1:2841:C:H2'	53:1:2842:G:H8	1.83	0.43
55:5:19:G:H5'	55:5:20:U:H5	1.83	0.43
4:e:71:LYS:HG3	4:e:72:SER:N	2.29	0.42
4:e:113:PHE:HZ	4:e:175:PRO:HG2	1.84	0.42
4:e:121:PHE:CE1	4:e:127:TYR:HB2	2.54	0.42
7:h:77:VAL:HG22	7:h:77:VAL:O	2.19	0.42
12:m:49:ALA:O	12:m:53:MET:HB2	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:106:ASP:OD2	13:n:106:ASP:N	2.49	0.42
17:r:16:GLU:OE1	17:r:100:GLY:HA2	2.18	0.42
33:I:58:GLN:O	33:I:62:ARG:HG2	2.19	0.42
37:M:12:ARG:CZ	52:3:826:C:H5'	2.49	0.42
43:S:3:GLN:CD	52:3:1047:G:H5''	2.43	0.42
49:Y:27:MET:HE1	49:Y:66:ILE:HG13	2.01	0.42
50:Z:9:GLU:CB	50:Z:10:PRO:CD	2.97	0.42
52:3:257:G:H2'	52:3:258:G:H8	1.84	0.42
52:3:266:G:H1'	52:3:268:U:OP2	2.19	0.42
52:3:295:C:H2'	52:3:296:U:O4'	2.19	0.42
52:3:893:C:H2'	52:3:894:G:C8	2.54	0.42
52:3:1456:A:H2'	52:3:1457:G:O4'	2.19	0.42
53:1:479:A:H1'	53:1:481:G:H5''	2.00	0.42
53:1:1367:A:C2'	53:1:1368:G:H5'	2.47	0.42
53:1:1772:A:H2'	53:1:1773:A:C5'	2.48	0.42
53:1:2584:U:H2'	53:1:2585:U:H2'	2.00	0.42
53:1:2632:A:O2'	53:1:2633:G:H5'	2.19	0.42
4:e:12:VAL:O	4:e:16:MET:HG2	2.18	0.42
6:g:77:THR:HG22	6:g:143:ILE:HB	2.01	0.42
8:i:36:GLU:HG3	8:i:66:PHE:HZ	1.84	0.42
11:l:19:LEU:HB2	53:1:587:C:O2'	2.19	0.42
11:l:93:ASN:C	11:l:95:LEU:H	2.27	0.42
11:l:116:VAL:O	11:l:116:VAL:HG13	2.19	0.42
13:n:60:VAL:HG22	53:1:1454:C:O2'	2.19	0.42
13:n:90:ARG:HH21	53:1:2881:U:H5'	1.84	0.42
14:o:31:THR:OG1	14:o:33:ARG:O	2.33	0.42
24:y:10:SER:O	24:y:14:LEU:HB2	2.18	0.42
26:B:30:ASP:OD2	26:B:33:SER:N	2.51	0.42
31:G:170:ILE:HD12	31:G:170:ILE:N	2.33	0.42
38:N:48:ARG:HA	38:N:51:LEU:HB2	2.01	0.42
40:P:118:ASN:CG	52:3:718:A:H5'	2.43	0.42
43:S:63:CYS:SG	43:S:79:SER:HB3	2.59	0.42
46:V:44:HIS:C	46:V:70:LYS:HG3	2.44	0.42
52:3:67:C:H2'	52:3:68:G:H8	1.83	0.42
52:3:250:A:H4'	52:3:251:G:O5'	2.19	0.42
52:3:483:C:H2'	52:3:484:G:C8	2.54	0.42
52:3:539:A:H2'	52:3:540:G:C8	2.55	0.42
53:1:171:U:H2'	53:1:172:A:C8	2.53	0.42
53:1:403:U:O3'	53:1:404:A:H4'	2.19	0.42
53:1:1444:G:H2'	53:1:1445:G:C8	2.53	0.42
53:1:1779:U:H5	53:1:1784:A:N7	2.17	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1934:C:O2'	53:1:1935:G:H5'	2.19	0.42
53:1:2623:G:H2'	53:1:2624:G:C8	2.53	0.42
57:7:37:A:H2'	57:7:38:A:O4'	2.19	0.42
1:b:64:VAL:HA	1:b:102:TYR:HB2	2.01	0.42
1:b:89:ASN:ND2	1:b:196:ASN:HD22	2.17	0.42
1:b:239:PHE:HB3	53:1:1903:G:OP1	2.20	0.42
2:c:108:ASP:OD2	2:c:173:GLN:HG2	2.19	0.42
2:c:110:THR:OG1	2:c:202:ILE:HB	2.19	0.42
3:d:181:ILE:HG23	11:l:2:ARG:HG3	2.01	0.42
7:h:96:PHE:HD2	7:h:125:ARG:NH2	2.18	0.42
13:n:100:CYS:SG	26:B:42:ILE:HD11	2.59	0.42
31:G:78:ALA:HA	31:G:81:ASP:HB2	2.01	0.42
31:G:151:LYS:HE2	31:G:151:LYS:HB3	1.94	0.42
34:J:110:MET:O	34:J:113:VAL:HG12	2.19	0.42
35:K:67:PRO:HG2	35:K:70:VAL:HG12	2.02	0.42
41:Q:98:ARG:CB	41:Q:116:TYR:HA	2.48	0.42
44:T:87:ARG:O	44:T:88:ARG:C	2.62	0.42
48:X:35:ARG:NH1	52:3:1221:G:OP1	2.52	0.42
52:3:969:A:H2'	52:3:970:C:O4'	2.19	0.42
53:1:275:C:H3'	53:1:276:U:H5''	2.01	0.42
53:1:1112:G:O2'	53:1:1113:U:H5'	2.19	0.42
53:1:1683:U:H2'	53:1:1684:G:H8	1.83	0.42
55:5:52:G:O2'	55:5:53:G:H5'	2.19	0.42
4:e:24:VAL:O	4:e:27:VAL:HG22	2.19	0.42
7:h:42:ARG:HH12	53:1:1082:U:H4'	1.84	0.42
7:h:122:GLN:CG	7:h:123:ILE:H	2.31	0.42
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.48	0.42
8:i:101:SER:HA	8:i:140:GLU:O	2.19	0.42
11:l:61:LEU:O	29:E:12:ARG:HD3	2.20	0.42
12:m:17:ASN:O	12:m:38:ARG:NH1	2.53	0.42
17:r:55:ASP:OD1	17:r:55:ASP:N	2.53	0.42
20:u:13:LEU:HD11	20:u:70:ALA:CB	2.49	0.42
27:C:12:SER:OG	27:C:13:SER:N	2.52	0.42
31:G:104:LYS:HD2	52:3:1073:U:C4'	2.39	0.42
32:H:148:ILE:HD12	32:H:201:ILE:HG12	2.01	0.42
34:J:87:VAL:HA	34:J:91:SER:O	2.19	0.42
35:K:64:VAL:HG22	35:K:65:GLU:N	2.34	0.42
38:N:114:LYS:HB2	38:N:117:LEU:HD13	2.01	0.42
46:V:42:LYS:C	46:V:43:LEU:HD22	2.45	0.42
46:V:67:SER:OG	46:V:68:LYS:N	2.53	0.42
52:3:406:G:O2'	52:3:407:U:H5'	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:494:G:O2'	52:3:496:A:H1'	2.19	0.42
52:3:654:G:H2'	52:3:655:A:O4'	2.20	0.42
52:3:1217:C:O2'	52:3:1218:C:H5'	2.18	0.42
53:1:558:U:H2'	53:1:559:G:C8	2.53	0.42
53:1:1297:C:OP1	53:1:2710:C:H4'	2.19	0.42
53:1:1854:A:H61	53:1:1888:G:H1'	1.84	0.42
53:1:2070:A:O2'	53:1:2071:A:H5'	2.19	0.42
53:1:2786:U:O2'	53:1:2787:C:H5'	2.20	0.42
53:1:2795:C:H2'	53:1:2796:U:O4'	2.19	0.42
55:5:32:C:O5'	55:5:32:C:H6	2.03	0.42
56:4:20:U:O2'	56:4:21:C:H5'	2.19	0.42
1:b:75:ALA:HB2	1:b:95:TYR:CD1	2.55	0.42
4:e:73:VAL:HG12	4:e:78:ILE:HD11	2.00	0.42
4:e:84:ILE:HD11	53:1:2312:U:C5'	2.45	0.42
8:i:112:LYS:O	8:i:116:MET:N	2.46	0.42
8:i:134:SER:HB3	53:1:1077:A:N3	2.35	0.42
10:k:37:ASP:OD1	10:k:37:ASP:N	2.52	0.42
19:t:76:ARG:NH2	53:1:65:U:OP1	2.53	0.42
20:u:39:ASN:HB3	20:u:62:ALA:HB3	2.02	0.42
24:y:23:ARG:NE	24:y:27:ASN:HD21	2.18	0.42
31:G:111:LYS:HA	31:G:114:LYS:HG2	2.00	0.42
33:I:123:MET:HB2	33:I:128:VAL:HG22	2.00	0.42
34:J:60:GLN:HA	34:J:63:MET:HG2	2.00	0.42
36:L:10:LYS:HZ2	36:L:12:LEU:HD13	1.85	0.42
38:N:50:PRO:HG2	38:N:51:LEU:HD12	2.00	0.42
42:R:52:ILE:O	42:R:56:ARG:HG3	2.19	0.42
43:S:2:LYS:HZ3	52:3:1049:U:P	2.43	0.42
49:Y:4:LYS:HE2	52:3:60:A:O2'	2.19	0.42
50:Z:36:PHE:C	50:Z:38:GLU:H	2.27	0.42
52:3:45:G:H5''	52:3:307:C:O2'	2.19	0.42
52:3:571:U:H2'	52:3:572:A:H5''	2.01	0.42
52:3:810:C:O2'	52:3:811:C:H5'	2.19	0.42
52:3:832:G:O2'	52:3:833:G:H5'	2.19	0.42
52:3:908:A:O2'	52:3:909:A:H5'	2.19	0.42
52:3:1066:C:H2'	52:3:1067:A:H5'	2.02	0.42
52:3:1487:G:O2'	52:3:1488:G:H5'	2.19	0.42
53:1:207:A:H2'	53:1:208:C:O4'	2.20	0.42
53:1:839:U:H2'	53:1:840:C:C6	2.55	0.42
53:1:2743:U:H2'	53:1:2744:G:C4'	2.50	0.42
1:b:56:GLY:HA2	1:b:212:TRP:HA	2.01	0.42
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:122:ASP:OD1	4:e:126:ASN:N	2.49	0.42
6:g:135:HIS:HB3	6:g:138:VAL:HB	2.02	0.42
9:j:36:LEU:HD22	9:j:121:LYS:HB2	2.02	0.42
21:v:80:HIS:HA	21:v:81:PRO:HD3	1.90	0.42
22:w:22:PHE:O	22:w:25:GLU:HB2	2.20	0.42
33:I:61:ARG:O	33:I:65:GLY:N	2.50	0.42
38:N:105:ARG:HH11	38:N:107:ALA:HA	1.85	0.42
40:P:27:ASN:ND2	52:3:691:G:OP2	2.50	0.42
41:Q:48:LEU:HB2	52:3:520:A:OP1	2.19	0.42
43:S:80:ARG:NE	52:3:974:A:OP2	2.46	0.42
47:W:31:TYR:O	47:W:39:VAL:HG12	2.19	0.42
47:W:52:ARG:HE	52:3:664:G:H5''	1.84	0.42
52:3:1387:G:H2'	52:3:1388:C:C6	2.55	0.42
52:3:1467:C:H2'	52:3:1468:A:C8	2.55	0.42
53:1:1498:C:H2'	53:1:1499:C:H6	1.85	0.42
53:1:1542:U:H2'	53:1:1543:G:O4'	2.20	0.42
53:1:2285:C:O2'	53:1:2287:A:H1'	2.19	0.42
53:1:2399:G:H2'	53:1:2400:G:H8	1.85	0.42
53:1:2591:C:H2'	53:1:2592:G:C8	2.55	0.42
57:7:15:G:C2'	57:7:16:U:H5'	2.50	0.42
1:b:143:VAL:HG11	1:b:173:LEU:HD11	2.01	0.42
5:f:19:ASN:O	5:f:22:VAL:HG22	2.20	0.42
7:h:53:ARG:H	7:h:53:ARG:HG2	1.74	0.42
8:i:131:THR:HG23	53:1:1060:U:O4	2.19	0.42
13:n:29:VAL:HG11	13:n:75:ILE:HG23	2.00	0.42
14:o:12:THR:OG1	53:1:2334:U:H4'	2.20	0.42
33:I:123:MET:HA	33:I:128:VAL:HA	2.02	0.42
39:O:57:VAL:CG1	39:O:58:ASN:H	2.29	0.42
40:P:59:PRO:HB3	40:P:90:PRO:O	2.20	0.42
40:P:127:ARG:NH2	52:3:1523:G:OP2	2.53	0.42
45:U:75:ILE:HG22	45:U:80:LYS:NZ	2.34	0.42
52:3:514:C:H2'	52:3:515:G:C8	2.54	0.42
52:3:801:U:H2'	52:3:802:A:H8	1.84	0.42
52:3:1138:G:H3'	52:3:1138:G:N3	2.35	0.42
52:3:1139:G:H5''	52:3:1140:C:C5	2.50	0.42
52:3:1195:C:H5''	52:3:1196:A:OP2	2.20	0.42
53:1:1935:G:O2'	53:1:1936:A:H5'	2.19	0.42
53:1:2102:G:H2'	53:1:2103:C:O4'	2.20	0.42
57:7:19:G:H4'	57:7:20:U:O2	2.19	0.42
2:c:9:VAL:HG23	2:c:26:VAL:CG1	2.50	0.42
11:l:117:THR:OG1	11:l:118:THR:N	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:108:LEU:HA	17:r:48:LYS:NZ	2.34	0.42
25:z:5:LYS:O	25:z:56:VAL:HG23	2.20	0.42
30:F:2:LYS:HZ1	53:1:2477:U:H2'	1.84	0.42
32:H:18:ASN:HB2	43:S:90:GLY:O	2.19	0.42
38:N:8:THR:HG23	52:3:1148:U:H5''	2.02	0.42
42:R:76:ILE:HG22	52:3:1309:G:H5'	2.02	0.42
43:S:53:ASP:CG	43:S:54:SER:H	2.28	0.42
44:T:52:ARG:NH2	53:1:715:A:N1	2.68	0.42
52:3:322:C:H2'	52:3:323:U:C6	2.55	0.42
52:3:668:G:H2'	52:3:669:G:H8	1.85	0.42
52:3:1524:C:H2'	52:3:1525:G:H8	1.83	0.42
53:1:20:C:H2'	53:1:21:A:H8	1.84	0.42
53:1:327:G:H2'	53:1:328:U:O4'	2.20	0.42
53:1:727:A:O2'	53:1:728:G:H5'	2.20	0.42
53:1:1989:G:H2'	53:1:1990:C:O4'	2.20	0.42
53:1:2039:U:H2'	53:1:2040:G:C8	2.55	0.42
53:1:2053:G:O2'	53:1:2054:A:H5'	2.19	0.42
54:2:114:C:H2'	54:2:115:A:C8	2.55	0.42
57:7:44:G:H5''	57:7:45:U:H5	1.84	0.42
1:b:13:ARG:NH2	53:1:1693:U:H1'	2.35	0.42
1:b:94:LEU:HD13	1:b:100:ARG:HG2	2.01	0.42
4:e:133:GLU:OE2	4:e:148:VAL:HG12	2.20	0.42
5:f:93:TYR:CD1	5:f:106:LEU:HD23	2.54	0.42
7:h:95:LEU:HD23	7:h:95:LEU:HA	1.91	0.42
7:h:122:GLN:HE21	7:h:123:ILE:HG13	1.84	0.42
8:i:33:ASN:ND2	8:i:34:ILE:H	2.16	0.42
21:v:9:ARG:CG	21:v:41:GLU:HB2	2.47	0.42
21:v:28:ALA:N	21:v:40:ILE:O	2.49	0.42
31:G:113:LEU:O	31:G:117:GLU:HG3	2.19	0.42
32:H:5:HIS:HD2	43:S:88:MET:HG3	1.83	0.42
33:I:35:GLN:NE2	33:I:36:ALA:HB2	2.35	0.42
39:O:8:ILE:O	39:O:73:LEU:HD12	2.19	0.42
47:W:38:ILE:O	52:3:720:C:H5'	2.20	0.42
47:W:60:ARG:NH2	52:3:736:C:OP1	2.52	0.42
52:3:162:A:H2'	52:3:163:C:O4'	2.20	0.42
52:3:856:C:O2'	52:3:857:C:H5'	2.20	0.42
52:3:858:G:O6	52:3:869:G:H3'	2.20	0.42
52:3:967:C:H2'	52:3:968:A:C8	2.55	0.42
53:1:230:G:O2'	53:1:231:A:H5'	2.20	0.42
53:1:760:G:C2'	53:1:761:A:H5'	2.50	0.42
53:1:1430:G:H2'	53:1:1431:A:O4'	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2318:G:H2'	53:1:2319:G:O4'	2.18	0.42
53:1:2704:C:H2'	53:1:2705:A:O4'	2.20	0.42
1:b:164:VAL:CG2	1:b:174:ARG:HB2	2.50	0.42
15:p:4:ILE:O	15:p:8:GLU:HG2	2.19	0.42
29:E:34:LYS:HE2	29:E:34:LYS:HB3	1.88	0.42
31:G:128:LEU:HB3	31:G:132:GLU:HG3	2.02	0.42
36:L:84:TYR:CD2	36:L:86:VAL:HG22	2.55	0.42
38:N:22:PRO:HA	38:N:60:LEU:HD23	2.01	0.42
38:N:84:ARG:HH22	52:3:1119:C:C5'	2.33	0.42
42:R:38:ILE:HG13	42:R:55:LEU:HD21	2.02	0.42
45:U:19:VAL:O	45:U:19:VAL:HG13	2.20	0.42
48:X:13:HIS:CE1	48:X:14:LEU:HG	2.55	0.42
49:Y:63:LYS:HB3	49:Y:63:LYS:HE3	1.89	0.42
52:3:37:U:H2'	52:3:38:G:C8	2.53	0.42
52:3:303:A:H2'	52:3:304:U:O4'	2.20	0.42
52:3:518:C:H5'	52:3:530:G:O4'	2.20	0.42
52:3:1520:C:H2'	52:3:1521:C:H6	1.84	0.42
53:1:644:A:H61	53:1:2349:G:H21	1.67	0.42
53:1:752:A:H62	53:1:2609:U:H3	1.67	0.42
53:1:1956:U:C2'	53:1:1957:C:H5'	2.47	0.42
53:1:2243:U:H2'	53:1:2244:U:C6	2.54	0.42
53:1:2404:U:H2'	53:1:2405:G:O4'	2.19	0.42
56:4:19:U:H2'	56:4:20:U:H6	1.85	0.42
1:b:107:LYS:N	1:b:193:GLU:O	2.52	0.41
1:b:201:LEU:CD1	52:3:773:G:H5''	2.45	0.41
1:b:209:ALA:HA	1:b:212:TRP:CE2	2.55	0.41
2:c:161:MET:SD	53:1:2049:G:N2	2.93	0.41
33:I:50:TYR:CD2	52:3:508:U:H4'	2.55	0.41
36:L:29:LEU:HD23	36:L:29:LEU:O	2.20	0.41
39:O:29:ALA:O	39:O:33:GLY:CA	2.68	0.41
39:O:40:ILE:HD12	39:O:73:LEU:HG	2.02	0.41
46:V:13:SER:HB3	46:V:21:VAL:HG11	2.02	0.41
49:Y:78:LEU:HA	49:Y:81:GLN:HB2	2.01	0.41
52:3:918:A:H2'	52:3:919:A:O4'	2.20	0.41
53:1:150:U:H2'	53:1:151:C:C6	2.54	0.41
53:1:864:G:O2'	53:1:865:C:H5'	2.19	0.41
53:1:1873:G:O2'	53:1:1874:C:H5'	2.20	0.41
53:1:2732:G:O2'	53:1:2733:A:H5'	2.20	0.41
57:7:23:A:H2'	57:7:24:G:H8	1.73	0.41
1:b:244:VAL:HG12	1:b:250:GLN:HA	2.02	0.41
3:d:44:ARG:HD2	53:1:444:C:H4'	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:56:ARG:NH2	7:h:81:LEU:HD11	2.36	0.41
9:j:117:ALA:HA	9:j:120:ARG:NH2	2.34	0.41
13:n:10:LEU:O	13:n:12:ARG:HG3	2.19	0.41
15:p:50:ARG:NH1	53:1:2684:U:OP2	2.53	0.41
25:z:51:SER:HA	25:z:54:VAL:HG22	2.02	0.41
31:G:68:PHE:CE2	31:G:88:GLN:HB2	2.55	0.41
33:I:68:GLU:OE1	52:3:545:C:OP1	2.38	0.41
38:N:84:ARG:HH22	52:3:1119:C:H5'	1.85	0.41
38:N:98:ARG:NH2	52:3:1178:G:N7	2.68	0.41
41:Q:114:SER:HB3	52:3:35:G:H21	1.84	0.41
42:R:84:CYS:HB2	48:X:72:GLU:HG2	2.02	0.41
44:T:42:PHE:HE2	44:T:55:LEU:HD22	1.84	0.41
52:3:687:A:N3	52:3:688:G:H1'	2.35	0.41
52:3:824:G:H2'	52:3:825:A:H8	1.85	0.41
52:3:953:G:H2'	52:3:954:G:O4'	2.19	0.41
52:3:1024:G:H2'	52:3:1025:U:H5'	2.01	0.41
52:3:1186:G:H2'	52:3:1187:G:C8	2.54	0.41
52:3:1218:C:H2'	52:3:1219:A:H8	1.83	0.41
52:3:1453:G:H3'	52:3:1453:G:N3	2.34	0.41
52:3:1498:U:C4	56:4:17:U:H5'	2.55	0.41
53:1:466:A:C2'	53:1:467:G:H5'	2.50	0.41
53:1:1152:C:H2'	53:1:1153:C:C6	2.55	0.41
55:5:16:C:H5'	55:5:59:A:N1	2.35	0.41
4:e:38:GLY:O	53:1:2306:C:N4	2.53	0.41
7:h:114:GLU:HG2	7:h:115:GLY:N	2.36	0.41
8:i:9:LYS:C	8:i:10:LEU:HD22	2.45	0.41
17:r:6:GLN:HG2	17:r:11:GLN:HG3	2.01	0.41
26:B:9:ARG:NH1	53:1:516:C:OP1	2.54	0.41
30:F:4:ARG:O	30:F:37:GLN:O	2.38	0.41
31:G:82:ALA:HB2	31:G:213:LEU:HD13	2.01	0.41
33:I:6:PRO:HA	52:3:430:A:P	2.60	0.41
36:L:24:LYS:HD2	36:L:27:ASN:HD21	1.84	0.41
36:L:117:LEU:O	36:L:121:ASN:ND2	2.54	0.41
47:W:11:ARG:HD2	52:3:845:A:H4'	2.02	0.41
51:a:5:THR:OG1	51:a:6:LYS:N	2.53	0.41
51:a:44:VAL:HG21	51:a:175:ILE:HG23	2.03	0.41
52:3:149:A:H1'	52:3:1446:A:C2	2.55	0.41
52:3:237:G:H2'	52:3:238:A:C8	2.55	0.41
53:1:57:C:H2'	53:1:58:G:O4'	2.20	0.41
53:1:523:C:H2'	53:1:524:G:C8	2.55	0.41
53:1:2679:A:O2'	53:1:2680:U:H5'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2743:U:C2'	53:1:2744:G:H5''	2.50	0.41
11:l:30:THR:O	11:l:32:GLY:N	2.52	0.41
11:l:42:SER:OG	53:1:672:C:H5	2.04	0.41
36:L:101:ARG:NH1	52:3:939:G:H4'	2.36	0.41
42:R:22:TYR:HE2	42:R:69:ARG:HG3	1.86	0.41
45:U:5:ARG:NH2	45:U:23:ASP:O	2.54	0.41
51:a:51:ASP:HB3	51:a:57:GLN:NE2	2.35	0.41
52:3:273:U:C2'	52:3:274:A:H5'	2.50	0.41
52:3:309:A:H2'	52:3:310:G:C8	2.55	0.41
52:3:757:U:H2'	52:3:758:C:O4'	2.20	0.41
52:3:763:G:H2'	52:3:764:C:H6	1.85	0.41
52:3:817:C:H5'	52:3:820:U:OP2	2.20	0.41
52:3:912:C:O2'	52:3:913:A:H5'	2.21	0.41
52:3:976:G:N2	52:3:1362:A:H2'	2.36	0.41
53:1:688:U:H2'	53:1:689:A:C8	2.56	0.41
53:1:872:U:H2'	53:1:873:C:C6	2.56	0.41
53:1:2292:U:H2'	53:1:2293:G:C8	2.55	0.41
53:1:2757:A:H2'	53:1:2757:A:N3	2.35	0.41
54:2:3:C:H3'	54:2:4:C:C5'	2.50	0.41
57:7:6:G:O2'	57:7:7:A:H5'	2.20	0.41
1:b:158:GLY:HA3	53:1:1820:U:C4	2.55	0.41
2:c:64:GLU:H	2:c:64:GLU:HG2	1.58	0.41
3:d:148:ILE:HA	3:d:187:VAL:HG23	2.01	0.41
8:i:89:SER:HA	8:i:135:MET:O	2.21	0.41
12:m:1:MET:HE1	12:m:44:ARG:HA	2.03	0.41
22:w:37:ARG:HA	22:w:37:ARG:HD3	1.92	0.41
24:y:5:GLU:HA	24:y:8:GLU:OE1	2.21	0.41
33:I:70:GLN:NE2	52:3:402:G:OP1	2.47	0.41
34:J:131:ASN:O	34:J:135:VAL:HG22	2.21	0.41
36:L:117:LEU:HD12	36:L:117:LEU:HA	1.81	0.41
37:M:85:TYR:CB	52:3:598:U:H4'	2.50	0.41
49:Y:2:ASN:HB3	52:3:331:G:O3'	2.21	0.41
51:a:38:PHE:HD1	53:1:2127:G:H4'	1.84	0.41
51:a:202:THR:O	51:a:205:LYS:NZ	2.52	0.41
52:3:393:A:H5'	52:3:483:C:O2'	2.21	0.41
52:3:580:C:H2'	52:3:581:G:O4'	2.20	0.41
52:3:1409:C:H5'	53:1:1916:A:N1	2.35	0.41
53:1:538:A:H2'	53:1:539:G:O4'	2.20	0.41
53:1:609:A:H2'	53:1:610:C:O4'	2.19	0.41
53:1:730:A:O2'	53:1:731:C:H5'	2.19	0.41
53:1:740:C:H5'	53:1:1784:A:O2'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1386:C:H2'	53:1:1387:A:H8	1.85	0.41
53:1:1906:G:H2'	53:1:1907:G:O4'	2.20	0.41
53:1:2377:A:H2'	53:1:2378:A:C8	2.56	0.41
53:1:2746:U:O4	53:1:2755:C:H4'	2.20	0.41
55:5:58:A:H1'	55:5:60:U:C5	2.56	0.41
7:h:58:THR:OG1	7:h:78:GLY:O	2.37	0.41
7:h:117:LEU:CD2	7:h:120:ALA:HA	2.50	0.41
9:j:80:HIS:CD2	53:1:2642:G:H5''	2.55	0.41
9:j:124:VAL:HG22	9:j:125:TYR:H	1.86	0.41
10:k:108:ARG:HH22	52:3:345:C:H3'	1.84	0.41
14:o:92:PHE:HB2	14:o:117:PHE:CD2	2.56	0.41
15:p:31:VAL:HG11	15:p:40:GLN:NE2	2.35	0.41
23:x:2:ARG:HB2	53:1:1365:A:OP2	2.21	0.41
26:B:6:LYS:HA	26:B:7:PRO:HD3	1.89	0.41
27:C:16:THR:OG1	27:C:17:GLY:N	2.53	0.41
31:G:6:ARG:HE	31:G:10:LYS:HE2	1.86	0.41
32:H:107:LYS:HE3	32:H:143:LEU:HD23	2.03	0.41
36:L:106:ALA:O	36:L:109:LYS:HG2	2.20	0.41
38:N:53:LEU:HD12	38:N:54:VAL:HG23	2.02	0.41
39:O:50:THR:HG22	39:O:64:GLN:HG2	2.02	0.41
44:T:65:LEU:HD23	44:T:65:LEU:HA	1.93	0.41
47:W:33:THR:OG1	47:W:34:GLU:N	2.53	0.41
51:a:42:VAL:HG11	51:a:175:ILE:HD11	2.01	0.41
52:3:1186:G:H2'	52:3:1187:G:H8	1.85	0.41
52:3:1538:C:H2'	52:3:1539:C:H5'	2.01	0.41
53:1:121:G:H4'	53:1:149:A:H5'	2.03	0.41
53:1:323:C:H2'	53:1:1205:A:N6	2.36	0.41
53:1:595:C:H2'	53:1:596:U:H6	1.86	0.41
53:1:1078:U:C4'	53:1:1079:C:H5''	2.50	0.41
53:1:1080:A:H2'	53:1:1081:U:O4'	2.21	0.41
53:1:1565:C:O2'	53:1:1566:A:H2'	2.20	0.41
53:1:2049:G:O2'	53:1:2050:C:H5'	2.20	0.41
53:1:2247:A:O2'	53:1:2248:C:H5'	2.20	0.41
53:1:2557:G:H2'	53:1:2558:C:C6	2.55	0.41
53:1:2670:A:H2'	53:1:2671:G:H8	1.84	0.41
53:1:2693:G:O2'	53:1:2694:G:H5'	2.20	0.41
54:2:33:G:O2'	54:2:34:A:H5'	2.21	0.41
55:5:3:C:C3'	55:5:4:G:C5'	2.96	0.41
4:e:36:ASN:HB3	4:e:152:ASP:OD1	2.21	0.41
9:j:57:LEU:O	9:j:58:ASN:HB2	2.19	0.41
29:E:24:LYS:HD3	29:E:46:LYS:HE3	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:112:ASP:OD2	36:L:112:ASP:N	2.53	0.41
37:M:40:LYS:HA	37:M:45:ILE:O	2.20	0.41
37:M:58:LEU:HD12	37:M:58:LEU:HA	1.91	0.41
41:Q:114:SER:OG	52:3:501:C:O3'	2.32	0.41
46:V:21:VAL:O	46:V:21:VAL:HG13	2.20	0.41
52:3:47:C:H5'	52:3:365:U:C2	2.56	0.41
52:3:825:A:H2'	52:3:826:C:C6	2.55	0.41
53:1:63:A:O2'	53:1:64:A:H5'	2.20	0.41
53:1:256:A:O2'	53:1:257:C:H5'	2.21	0.41
53:1:458:G:O2'	53:1:459:U:H5	2.03	0.41
53:1:1106:G:H5'	53:1:1106:G:H8	1.86	0.41
53:1:1994:C:O2'	53:1:1995:U:H5'	2.20	0.41
53:1:2061:G:H4'	53:1:2061:G:OP1	2.21	0.41
53:1:2873:A:O2'	53:1:2874:C:H5'	2.20	0.41
2:c:124:ARG:HD3	2:c:125:TRP:NE1	2.35	0.41
3:d:47:LYS:NZ	53:1:451:U:H4'	2.35	0.41
3:d:140:ASP:OD1	3:d:141:MET:HG3	2.21	0.41
4:e:111:ARG:NH2	4:e:112:ASP:OD2	2.54	0.41
5:f:167:VAL:HG13	5:f:167:VAL:O	2.21	0.41
8:i:99:LYS:C	8:i:100:ILE:HD12	2.45	0.41
9:j:101:ILE:O	9:j:105:VAL:HG23	2.21	0.41
10:k:63:VAL:HG11	10:k:103:VAL:HG12	2.03	0.41
19:t:65:GLY:N	19:t:79:ASP:OD2	2.41	0.41
28:D:10:LEU:HD23	53:1:770:G:H5''	2.01	0.41
41:Q:58:ASN:OD1	41:Q:59:GLY:N	2.54	0.41
52:3:300:A:H1'	52:3:565:U:O2	2.20	0.41
52:3:378:G:H2'	52:3:379:C:C6	2.56	0.41
52:3:538:G:H2'	52:3:539:A:H8	1.85	0.41
52:3:613:C:H2'	52:3:614:C:C6	2.56	0.41
52:3:621:A:H2'	52:3:622:A:C8	2.55	0.41
52:3:631:C:H5''	52:3:632:U:O4'	2.21	0.41
52:3:800:G:H2'	52:3:801:U:C5	2.55	0.41
53:1:1073:A:H2'	53:1:1074:G:H5'	2.02	0.41
53:1:1093:G:H21	53:1:1098:A:H62	1.67	0.41
53:1:1307:A:H2'	53:1:1308:A:O4'	2.19	0.41
53:1:2809:A:H2'	53:1:2810:A:C8	2.56	0.41
1:b:32:LEU:O	1:b:33:LEU:HD12	2.20	0.41
3:d:17:THR:O	3:d:106:LYS:HE3	2.21	0.41
6:g:47:PHE:HB2	6:g:51:ARG:HH21	1.86	0.41
12:m:8:LYS:HD2	53:1:869:G:H1'	2.02	0.41
12:m:69:PRO:O	12:m:70:ASP:OD1	2.38	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:19:ALA:O	13:n:22:ARG:HB3	2.21	0.41
21:v:83:LYS:HA	21:v:84:PRO:HD3	1.91	0.41
23:x:42:GLU:HB2	23:x:44:ARG:HG2	2.03	0.41
28:D:29:GLN:O	28:D:32:ALA:HB3	2.20	0.41
29:E:3:ILE:HG21	29:E:62:PRO:HG2	2.02	0.41
30:F:32:LYS:NZ	53:1:2478:A:C5'	2.84	0.41
33:I:156:ALA:O	33:I:159:GLU:HG3	2.21	0.41
39:O:78:GLU:OE2	39:O:79:PRO:HD2	2.21	0.41
41:Q:69:GLU:HG2	52:3:521:G:C4'	2.47	0.41
41:Q:76:HIS:O	41:Q:77:SER:C	2.63	0.41
41:Q:109:ARG:HG3	41:Q:118:VAL:HG21	2.03	0.41
42:R:74:MET:O	42:R:78:ARG:N	2.53	0.41
44:T:3:SER:O	44:T:7:THR:HG23	2.20	0.41
45:U:70:ARG:O	45:U:74:LEU:HD23	2.21	0.41
46:V:39:ARG:HA	52:3:280:C:O2	2.21	0.41
51:a:41:SER:HB2	51:a:177:LYS:NZ	2.36	0.41
52:3:17:U:H2'	52:3:18:C:H6	1.84	0.41
52:3:109:A:C8	52:3:327:A:O4'	2.74	0.41
52:3:243:A:C2	52:3:246:A:C8	3.08	0.41
52:3:291:U:H2'	52:3:292:G:C8	2.56	0.41
52:3:415:A:H2'	52:3:416:G:O4'	2.21	0.41
52:3:1202:U:C2'	52:3:1203:C:H5'	2.50	0.41
52:3:1332:A:H2'	52:3:1333:A:C8	2.56	0.41
53:1:279:A:H2'	53:1:280:U:C5'	2.51	0.41
53:1:419:U:H2'	53:1:420:C:C6	2.55	0.41
53:1:558:U:H2'	53:1:559:G:H8	1.85	0.41
53:1:595:C:H2'	53:1:596:U:C6	2.55	0.41
53:1:783:A:H2'	53:1:784:G:C5'	2.49	0.41
53:1:792:A:C3'	53:1:793:A:H5'	2.51	0.41
53:1:796:C:H2'	53:1:797:G:H8	1.86	0.41
53:1:1373:A:H5''	53:1:2212:A:H1'	2.03	0.41
53:1:1386:C:H2'	53:1:1387:A:C8	2.55	0.41
53:1:1417:C:C4'	53:1:1587:G:H21	2.33	0.41
53:1:1418:G:H21	53:1:1580:A:H62	1.68	0.41
53:1:1473:G:O2'	53:1:1474:U:H5'	2.21	0.41
53:1:1549:A:H2'	53:1:1550:C:C6	2.56	0.41
53:1:1635:A:H2'	53:1:1636:U:O4'	2.21	0.41
53:1:2030:A:C2	53:1:2499:C:H5''	2.56	0.41
53:1:2190:G:C2	53:1:2191:A:H1'	2.56	0.41
53:1:2220:U:H2'	53:1:2221:G:C8	2.54	0.41
53:1:2282:G:H4'	53:1:2389:G:O2'	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2564:A:OP1	53:1:2648:G:H4'	2.21	0.41
53:1:2590:A:H2'	53:1:2591:C:H6	1.86	0.41
53:1:2637:U:H2'	53:1:2638:G:O4'	2.20	0.41
1:b:71:ASP:O	1:b:73:ILE:HG13	2.20	0.41
15:p:88:ARG:O	15:p:112:ARG:HG3	2.21	0.41
26:B:43:THR:OG1	26:B:47:TYR:HB2	2.20	0.41
32:H:32:LEU:CD1	43:S:64:ARG:HH22	2.34	0.41
32:H:84:GLU:O	32:H:88:LYS:HG2	2.20	0.41
41:Q:122:LYS:H	41:Q:122:LYS:HD3	1.85	0.41
52:3:606:G:C5'	52:3:607:A:H5'	2.51	0.41
52:3:634:C:H2'	52:3:635:A:H8	1.85	0.41
52:3:1277:C:H2'	52:3:1278:G:H5''	2.03	0.41
52:3:1332:A:H2'	52:3:1333:A:H8	1.86	0.41
52:3:1409:C:H2'	52:3:1410:A:C8	2.56	0.41
53:1:107:G:H2'	53:1:108:G:H8	1.86	0.41
53:1:792:A:H3'	53:1:793:A:H5'	2.03	0.41
53:1:859:G:O2'	53:1:860:U:C6	2.70	0.41
53:1:995:C:H6	53:1:995:C:H5'	1.86	0.41
53:1:1594:U:H2'	53:1:1595:C:H6	1.86	0.41
53:1:1795:C:O2'	53:1:1796:U:H5'	2.20	0.41
53:1:1967:C:H2'	53:1:1968:G:O4'	2.20	0.41
53:1:2393:U:H2'	53:1:2394:C:O4'	2.21	0.41
53:1:2437:G:O2'	53:1:2438:U:H5'	2.21	0.41
54:2:63:C:H2'	54:2:64:G:H8	1.87	0.41
57:7:14:A:C2	57:7:15:G:H1'	2.56	0.41
1:b:261:ARG:NH2	53:1:1801:A:C4	2.89	0.40
4:e:120:SER:OG	53:1:2304:G:H5'	2.21	0.40
4:e:151:LEU:HD12	4:e:151:LEU:C	2.45	0.40
5:f:86:LEU:HD12	5:f:86:LEU:N	2.36	0.40
8:i:99:LYS:HB2	8:i:140:GLU:HG2	2.03	0.40
16:q:26:ALA:HB1	16:q:30:VAL:HB	2.03	0.40
22:w:42:HIS:CD2	22:w:73:ARG:HD3	2.56	0.40
33:I:86:GLY:HA3	33:I:196:GLU:OE1	2.21	0.40
33:I:129:VAL:HA	52:3:619:U:O2	2.21	0.40
34:J:82:HIS:CE1	37:M:95:MET:HE3	2.56	0.40
36:L:10:LYS:C	36:L:10:LYS:HD3	2.46	0.40
42:R:23:GLY:O	52:3:1329:A:H4'	2.20	0.40
43:S:60:ARG:HD3	52:3:980:C:H2'	2.03	0.40
49:Y:28:ARG:NH1	52:3:1438:G:P	2.94	0.40
50:Z:46:ARG:NH2	52:3:1533:C:N3	2.70	0.40
52:3:709:U:H2'	52:3:710:G:C8	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:732:C:H2'	53:1:733:G:O4'	2.21	0.40
53:1:1838:C:H4'	53:1:1839:G:H8	1.85	0.40
53:1:2039:U:H2'	53:1:2040:G:H8	1.86	0.40
3:d:172:ALA:O	3:d:175:ILE:HD11	2.22	0.40
4:e:76:PHE:HE2	53:1:2311:A:H5''	1.86	0.40
4:e:120:SER:OG	4:e:128:SER:O	2.38	0.40
12:m:133:LYS:HD2	12:m:133:LYS:C	2.46	0.40
15:p:98:TYR:CD2	15:p:102:ARG:HD2	2.57	0.40
15:p:98:TYR:HD2	15:p:102:ARG:HD2	1.86	0.40
16:q:91:ARG:HH11	16:q:91:ARG:HG3	1.85	0.40
21:v:72:VAL:HA	21:v:94:ALA:H	1.85	0.40
22:w:21:ARG:NH1	22:w:27:VAL:HG12	2.34	0.40
31:G:207:ARG:O	31:G:210:THR:HG22	2.21	0.40
37:M:71:VAL:HG23	37:M:71:VAL:O	2.21	0.40
37:M:121:GLY:C	52:3:599:C:H4'	2.45	0.40
44:T:70:LYS:HE2	44:T:70:LYS:HB3	1.94	0.40
46:V:6:THR:C	46:V:7:LEU:HD22	2.47	0.40
46:V:30:HIS:HA	46:V:31:PRO:HD3	1.85	0.40
48:X:35:ARG:HH21	48:X:74:ALA:HB3	1.86	0.40
50:Z:19:LYS:O	50:Z:24:LYS:HG2	2.22	0.40
52:3:9:G:H2'	52:3:10:A:C8	2.56	0.40
52:3:668:G:H2'	52:3:669:G:C8	2.56	0.40
52:3:742:G:H2'	52:3:743:A:C8	2.57	0.40
52:3:1157:A:H61	52:3:1178:G:H1'	1.86	0.40
52:3:1424:U:H2'	52:3:1425:U:O4'	2.21	0.40
53:1:894:U:O2'	53:1:895:U:H5'	2.21	0.40
53:1:1355:G:O2'	53:1:1356:G:H5'	2.21	0.40
53:1:1683:U:H2'	53:1:1684:G:C8	2.55	0.40
53:1:2626:C:O2'	53:1:2627:G:H5'	2.21	0.40
1:b:35:LYS:NZ	53:1:1353:A:H5''	2.36	0.40
2:c:103:ASP:OD1	2:c:103:ASP:N	2.53	0.40
4:e:114:ARG:HD2	4:e:114:ARG:N	2.37	0.40
5:f:95:ALA:H	5:f:127:GLN:HB3	1.86	0.40
6:g:31:VAL:HG23	6:g:32:PRO:CD	2.50	0.40
6:g:68:ARG:HG2	6:g:68:ARG:HH11	1.86	0.40
7:h:43:LYS:HE3	7:h:98:GLU:HG3	2.02	0.40
11:l:30:THR:O	11:l:31:GLY:C	2.64	0.40
12:m:28:PHE:HB2	12:m:104:GLU:OE1	2.22	0.40
21:v:45:ASP:N	21:v:45:ASP:OD1	2.54	0.40
35:K:51:ILE:C	35:K:53:LYS:H	2.29	0.40
38:N:113:LYS:H	38:N:113:LYS:HG3	1.67	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:21:VAL:HG12	45:U:33:ILE:HD13	2.03	0.40
51:a:41:SER:HB3	53:1:2124:G:O2'	2.21	0.40
52:3:1177:G:H2'	52:3:1178:G:O4'	2.22	0.40
52:3:1233:G:H2'	52:3:1234:C:C6	2.57	0.40
52:3:1326:U:O2'	52:3:1327:C:H5'	2.21	0.40
52:3:1441:A:H62	52:3:1461:G:N2	2.19	0.40
53:1:691:C:O2'	53:1:692:C:H5'	2.21	0.40
53:1:1486:U:H2'	53:1:1487:U:C6	2.56	0.40
53:1:2231:U:H2'	53:1:2232:C:C6	2.56	0.40
53:1:2432:A:H5'	55:5:76:A:O3'	2.21	0.40
57:7:14:A:H61	57:7:21:A:H2	1.69	0.40
57:7:55:U:H2'	57:7:57:G:OP2	2.21	0.40
1:b:110:LYS:HD2	1:b:110:LYS:C	2.45	0.40
2:c:24:VAL:HG12	2:c:178:VAL:HG21	2.02	0.40
3:d:76:PRO:HA	3:d:82:GLY:HA2	2.03	0.40
4:e:140:ILE:HD12	4:e:140:ILE:H	1.86	0.40
6:g:65:ALA:O	6:g:68:ARG:HB3	2.21	0.40
8:i:56:VAL:CG1	8:i:68:PHE:HB2	2.52	0.40
8:i:58:ILE:H	8:i:58:ILE:HG12	1.71	0.40
8:i:60:VAL:HA	8:i:66:PHE:HB3	2.04	0.40
12:m:71:LYS:HB3	12:m:93:VAL:O	2.22	0.40
13:n:71:ARG:NH2	53:1:2707:U:O2	2.55	0.40
15:p:5:LYS:HD3	15:p:5:LYS:HA	1.93	0.40
16:q:60:TRP:CZ2	16:q:92:LYS:HG3	2.56	0.40
31:G:96:LEU:N	31:G:96:LEU:HD22	2.36	0.40
34:J:133:ILE:HG23	34:J:134:ASN:H	1.86	0.40
41:Q:69:GLU:HG2	52:3:521:G:C5'	2.52	0.40
41:Q:97:VAL:O	41:Q:100:ALA:HB2	2.22	0.40
52:3:113:G:H1'	52:3:354:G:H5'	2.03	0.40
52:3:212:G:H2'	52:3:213:G:H8	1.87	0.40
52:3:791:G:N2	52:3:1497:G:H4'	2.37	0.40
52:3:979:C:H2'	52:3:980:C:H5'	2.04	0.40
52:3:1023:U:H2'	52:3:1024:G:C8	2.56	0.40
52:3:1412:C:H2'	52:3:1413:A:H8	1.87	0.40
52:3:1432:G:H1'	52:3:1468:A:N6	2.36	0.40
53:1:141:G:H3'	53:1:142:A:O4'	2.22	0.40
53:1:889:C:H2'	53:1:890:C:O4'	2.21	0.40
53:1:1654:A:H2'	53:1:1655:A:H8	1.87	0.40
53:1:2743:U:H2'	53:1:2744:G:O4'	2.21	0.40
57:7:44:G:H2'	57:7:44:G:N3	2.37	0.40
2:c:4:LEU:HD22	2:c:101:PHE:CD2	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:79:ARG:HH21	53:1:448:U:C4'	2.34	0.40
3:d:131:THR:HG22	3:d:160:ALA:HA	2.04	0.40
7:h:12:VAL:HA	7:h:15:VAL:HG22	2.03	0.40
9:j:81:ILE:CD1	53:1:2514:U:H5''	2.51	0.40
16:q:25:GLY:O	16:q:29:ARG:NH1	2.55	0.40
18:s:89:ALA:C	18:s:91:GLY:H	2.29	0.40
20:u:85:ARG:HD3	20:u:87:GLU:CG	2.50	0.40
33:I:6:PRO:HG2	52:3:428:G:OP2	2.21	0.40
34:J:123:LEU:HD12	34:J:123:LEU:C	2.47	0.40
40:P:52:ARG:NH1	52:3:689:C:OP2	2.53	0.40
46:V:74:LEU:HD23	46:V:74:LEU:C	2.47	0.40
51:a:186:LYS:O	51:a:189:LEU:HG	2.22	0.40
52:3:40:C:H2'	52:3:41:G:C8	2.52	0.40
52:3:1238:A:H2'	52:3:1239:A:H5'	2.02	0.40
52:3:1256:A:H1'	52:3:1258:G:C5	2.56	0.40
52:3:1306:A:O2'	52:3:1307:U:H5'	2.21	0.40
52:3:1385:G:O2'	52:3:1386:G:H5'	2.21	0.40
53:1:131:A:H2'	53:1:132:G:H8	1.87	0.40
53:1:880:G:H1	53:1:897:C:H42	1.69	0.40
53:1:1295:C:H2'	53:1:1296:G:H8	1.85	0.40
53:1:2063:C:O2'	57:7:76:A:H4'	2.21	0.40
53:1:2508:G:H2'	53:1:2509:G:H8	1.86	0.40
53:1:2642:G:O2'	53:1:2643:G:H5'	2.22	0.40
54:2:63:C:H2'	54:2:64:G:C8	2.56	0.40
55:5:73:A:N3	55:5:73:A:H2'	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	b	269/271 (99%)	230 (86%)	36 (13%)	3 (1%)	11 39

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	c	207/209 (99%)	185 (89%)	22 (11%)	0	100	100
3	d	199/201 (99%)	183 (92%)	14 (7%)	2 (1%)	12	40
4	e	175/177 (99%)	156 (89%)	19 (11%)	0	100	100
5	f	174/176 (99%)	153 (88%)	19 (11%)	2 (1%)	11	39
6	g	147/149 (99%)	124 (84%)	22 (15%)	1 (1%)	18	49
7	h	129/131 (98%)	92 (71%)	31 (24%)	6 (5%)	2	12
8	i	139/141 (99%)	119 (86%)	14 (10%)	6 (4%)	2	14
9	j	140/142 (99%)	123 (88%)	17 (12%)	0	100	100
10	k	120/122 (98%)	98 (82%)	16 (13%)	6 (5%)	1	11
11	l	141/143 (99%)	116 (82%)	19 (14%)	6 (4%)	2	14
12	m	134/136 (98%)	111 (83%)	19 (14%)	4 (3%)	3	20
13	n	118/120 (98%)	99 (84%)	18 (15%)	1 (1%)	16	45
14	o	114/116 (98%)	107 (94%)	6 (5%)	1 (1%)	14	43
15	p	112/114 (98%)	94 (84%)	17 (15%)	1 (1%)	14	43
16	q	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
17	r	101/103 (98%)	86 (85%)	13 (13%)	2 (2%)	6	27
18	s	108/110 (98%)	96 (89%)	9 (8%)	3 (3%)	4	21
19	t	91/93 (98%)	83 (91%)	8 (9%)	0	100	100
20	u	100/102 (98%)	85 (85%)	9 (9%)	6 (6%)	1	9
21	v	92/94 (98%)	82 (89%)	9 (10%)	1 (1%)	11	39
22	w	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
23	x	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
24	y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
25	z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
26	B	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
27	C	48/50 (96%)	40 (83%)	7 (15%)	1 (2%)	5	26
28	D	44/46 (96%)	38 (86%)	6 (14%)	0	100	100
29	E	62/64 (97%)	52 (84%)	9 (14%)	1 (2%)	7	31
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	21
31	G	223/225 (99%)	205 (92%)	16 (7%)	2 (1%)	14	43
32	H	204/206 (99%)	186 (91%)	17 (8%)	1 (0%)	24	55

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	I	203/205 (99%)	179 (88%)	22 (11%)	2 (1%)	12	40
34	J	155/157 (99%)	128 (83%)	21 (14%)	6 (4%)	2	16
35	K	98/100 (98%)	80 (82%)	16 (16%)	2 (2%)	6	27
36	L	149/151 (99%)	134 (90%)	15 (10%)	0	100	100
37	M	127/129 (98%)	115 (91%)	11 (9%)	1 (1%)	16	45
38	N	125/127 (98%)	104 (83%)	17 (14%)	4 (3%)	3	19
39	O	96/98 (98%)	78 (81%)	13 (14%)	5 (5%)	1	11
40	P	114/116 (98%)	92 (81%)	18 (16%)	4 (4%)	3	18
41	Q	121/123 (98%)	91 (75%)	25 (21%)	5 (4%)	2	15
42	R	112/114 (98%)	96 (86%)	10 (9%)	6 (5%)	1	10
43	S	98/100 (98%)	79 (81%)	19 (19%)	0	100	100
44	T	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	37
45	U	80/82 (98%)	68 (85%)	9 (11%)	3 (4%)	2	16
46	V	78/80 (98%)	61 (78%)	13 (17%)	4 (5%)	1	11
47	W	63/65 (97%)	57 (90%)	5 (8%)	1 (2%)	7	31
48	X	77/79 (98%)	65 (84%)	12 (16%)	0	100	100
49	Y	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	3
51	a	130/223 (58%)	123 (95%)	6 (5%)	1 (1%)	16	45
All	All	5919/6112 (97%)	5125 (87%)	686 (12%)	108 (2%)	9	29

All (108) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
3	d	83	VAL
5	f	45	ALA
7	h	107	GLU
7	h	108	VAL
7	h	113	PHE
7	h	118	ILE
10	k	35	VAL
10	k	89	ASN
11	l	31	GLY
11	l	84	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	m	58	LYS
17	r	54	VAL
30	F	37	GLN
34	J	89	THR
34	J	93	VAL
34	J	122	VAL
37	M	47	ASP
38	N	90	ASP
41	Q	27	PRO
42	R	4	ALA
42	R	65	GLU
45	U	79	ASN
46	V	49	ASN
50	Z	24	LYS
10	k	110	GLU
11	l	28	GLY
12	m	6	ARG
12	m	70	ASP
14	o	34	HIS
20	u	51	LEU
20	u	56	GLY
29	E	31	ILE
38	N	13	SER
39	O	89	ARG
40	P	89	GLY
40	P	92	ARG
41	Q	33	CYS
41	Q	35	ARG
42	R	7	ASN
46	V	15	LYS
46	V	17	GLU
1	b	107	LYS
6	g	10	ALA
7	h	81	LEU
8	i	13	ALA
10	k	48	PRO
11	l	29	LYS
11	l	86	GLU
15	p	64	SER
18	s	3	THR
18	s	67	ASP
20	u	99	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	H	60	ALA
33	I	28	ASP
34	J	11	GLN
34	J	121	ASN
35	K	54	LEU
38	N	57	VAL
39	O	35	GLN
40	P	13	LYS
41	Q	24	GLU
45	U	27	ALA
50	Z	9	GLU
50	Z	23	GLU
1	b	260	LYS
5	f	174	LYS
8	i	64	ARG
10	k	101	GLY
17	r	26	ASP
18	s	11	ARG
33	I	152	SER
34	J	49	TYR
41	Q	77	SER
42	R	5	GLY
45	U	44	SER
46	V	70	LYS
50	Z	37	TYR
51	a	167	LYS
8	i	11	GLN
13	n	32	GLU
20	u	87	GLU
31	G	24	PRO
31	G	148	GLY
35	K	86	ARG
38	N	8	THR
39	O	43	PRO
42	R	97	ARG
50	Z	14	ALA
7	h	119	PRO
8	i	92	PRO
10	k	26	GLY
12	m	29	GLY
20	u	97	SER
21	v	58	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
44	T	46	LYS
47	W	17	VAL
50	Z	33	ARG
8	i	90	GLY
20	u	54	PRO
39	O	41	PRO
11	l	56	PRO
42	R	6	ILE
3	d	89	PRO
27	C	40	PRO
40	P	88	PRO
8	i	12	VAL
39	O	42	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	212 (98%)	4 (2%)	50	68
2	c	164/164 (100%)	160 (98%)	4 (2%)	43	65
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	81
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	78
7	h	100/100 (100%)	98 (98%)	2 (2%)	48	68
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	114 (98%)	2 (2%)	53	71
10	k	103/103 (100%)	99 (96%)	4 (4%)	28	56
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	76
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	86 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	76
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	76
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	78 (98%)	2 (2%)	42	64
20	u	83/83 (100%)	82 (99%)	1 (1%)	63	75
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	74
22	w	57/57 (100%)	55 (96%)	2 (4%)	32	58
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	46 (98%)	1 (2%)	47	67
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	37 (97%)	1 (3%)	40	64
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	185 (100%)	1 (0%)	81	83
32	H	170/170 (100%)	168 (99%)	2 (1%)	63	75
33	I	172/172 (100%)	170 (99%)	2 (1%)	63	75
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	79
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	76
36	L	124/124 (100%)	123 (99%)	1 (1%)	73	79
37	M	104/104 (100%)	101 (97%)	3 (3%)	37	62
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	86 (100%)	0	100	100
40	P	89/89 (100%)	88 (99%)	1 (1%)	65	76
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	75
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	72

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	53 (96%)	2 (4%)	31	58
51	a	110/174 (63%)	109 (99%)	1 (1%)	70	78
All	All	4908/4972 (99%)	4862 (99%)	46 (1%)	68	78

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	18	VAL
1	b	42	ARG
1	b	140	VAL
1	b	153	LEU
2	c	42	ASN
2	c	50	VAL
2	c	176	ASP
2	c	189	VAL
3	d	175	ILE
6	g	27	ARG
7	h	29	ASP
7	h	118	ILE
9	j	57	LEU
9	j	58	ASN
10	k	25	LEU
10	k	32	TYR
10	k	58	LEU
10	k	69	VAL
11	l	82	LEU
15	p	65	ASN
16	q	58	GLN
19	t	2	ILE
19	t	57	VAL
20	u	35	VAL
21	v	65	VAL
22	w	25	GLU
22	w	67	VAL
26	B	54	ILE
28	D	1	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
31	G	46	VAL
32	H	84	GLU
32	H	181	ILE
33	I	8	LEU
33	I	28	ASP
34	J	130	THR
35	K	51	ILE
36	L	5	VAL
37	M	24	VAL
37	M	47	ASP
37	M	50	VAL
40	P	29	THR
43	S	26	LEU
45	U	42	ILE
50	Z	10	PRO
50	Z	36	PHE
51	a	212	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (120) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	20	ASN
1	b	36	ASN
1	b	44	ASN
1	b	59	GLN
1	b	89	ASN
1	b	162	GLN
1	b	196	ASN
1	b	225	ASN
2	c	42	ASN
2	c	130	GLN
2	c	150	GLN
2	c	164	GLN
2	c	185	ASN
3	d	24	ASN
3	d	41	GLN
3	d	90	GLN
3	d	97	ASN
4	e	51	ASN
4	e	80	GLN
5	f	29	ASN
5	f	138	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	f	142	GLN
6	g	11	ASN
6	g	18	GLN
6	g	66	ASN
6	g	119	ASN
6	g	145	ASN
7	h	103	ASN
7	h	122	GLN
8	i	18	ASN
8	i	33	ASN
9	j	40	HIS
9	j	58	ASN
9	j	80	HIS
9	j	128	ASN
9	j	135	GLN
10	k	89	ASN
11	l	38	GLN
13	n	3	HIS
13	n	62	ASN
14	o	98	GLN
14	o	100	HIS
15	p	11	GLN
15	p	40	GLN
16	q	43	GLN
16	q	71	ASN
17	r	43	ASN
17	r	86	GLN
18	s	7	HIS
18	s	9	HIS
18	s	15	GLN
19	t	15	HIS
19	t	48	GLN
19	t	59	ASN
20	u	65	GLN
20	u	68	ASN
20	u	73	ASN
21	v	24	ASN
21	v	51	GLN
21	v	87	GLN
22	w	8	ASN
22	w	42	HIS
22	w	72	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
23	x	15	ASN
23	x	19	HIS
23	x	33	HIS
24	y	20	ASN
24	y	27	ASN
24	y	58	ASN
26	B	3	GLN
26	B	5	ASN
26	B	18	HIS
27	C	18	HIS
28	D	26	ASN
28	D	29	GLN
29	E	30	HIS
29	E	42	HIS
31	G	17	HIS
31	G	38	HIS
31	G	88	GLN
31	G	145	ASN
31	G	189	ASN
32	H	5	HIS
32	H	99	GLN
32	H	138	GLN
32	H	184	ASN
33	I	35	GLN
33	I	39	GLN
33	I	40	HIS
33	I	88	ASN
33	I	99	ASN
33	I	151	GLN
34	J	60	GLN
34	J	81	GLN
34	J	96	GLN
34	J	131	ASN
35	K	55	HIS
35	K	58	HIS
35	K	81	ASN
36	L	27	ASN
36	L	85	GLN
36	L	147	ASN
40	P	39	ASN
41	Q	45	ASN
43	S	59	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
44	T	27	GLN
44	T	34	GLN
44	T	37	HIS
44	T	39	GLN
46	V	30	HIS
47	W	51	GLN
47	W	53	GLN
48	X	51	HIS
48	X	55	GLN
49	Y	12	GLN
49	Y	47	GLN
50	Z	8	ASN
51	a	57	GLN
51	a	188	ASN
51	a	203	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	143 (9%)	3 (0%)
53	1	2902/2903 (99%)	330 (11%)	12 (0%)
54	2	119/120 (99%)	12 (10%)	1 (0%)
55	5	76/77 (98%)	24 (31%)	1 (1%)
56	4	17/18 (94%)	3 (17%)	0
57	7	75/76 (98%)	12 (16%)	1 (1%)
All	All	4727/4733 (99%)	524 (11%)	18 (0%)

All (524) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	71	A
52	3	87	C
52	3	95	C
52	3	100	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	3	144	G
52	3	183	C
52	3	184	G
52	3	197	A
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	253	A
52	3	266	G
52	3	267	C
52	3	281	G
52	3	289	G
52	3	345	C
52	3	346	G
52	3	352	C
52	3	355	C
52	3	367	U
52	3	372	C
52	3	411	A
52	3	412	A
52	3	413	G
52	3	429	U
52	3	467	U
52	3	484	G
52	3	485	U
52	3	486	U
52	3	496	A
52	3	497	G
52	3	518	C
52	3	531	U
52	3	533	A
52	3	547	A
52	3	561	U
52	3	564	C
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C
52	3	577	G
52	3	633	G
52	3	653	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	3	665	A
52	3	688	G
52	3	702	A
52	3	703	G
52	3	713	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	902	G
52	3	926	G
52	3	934	C
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1053	G
52	3	1054	C
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1253	G
52	3	1258	G
52	3	1260	G
52	3	1261	A
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1282	C
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1381	U
52	3	1394	A
52	3	1395	C
52	3	1397	C
52	3	1419	G
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	A
52	3	1502	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	46	G
53	1	49	A
53	1	50	U
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A
53	1	75	G
53	1	98	G
53	1	102	U
53	1	119	A
53	1	120	U
53	1	138	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	216	A
53	1	219	A
53	1	221	A
53	1	222	A
53	1	228	C
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A
53	1	265	A
53	1	266	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	276	U
53	1	278	A
53	1	281	C
53	1	294	A
53	1	301	G
53	1	311	A
53	1	323	C
53	1	324	A
53	1	329	G
53	1	330	A
53	1	361	G
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	388	G
53	1	404	A
53	1	406	G
53	1	411	G
53	1	422	A
53	1	424	G
53	1	455	C
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	530	G
53	1	531	C
53	1	532	A
53	1	543	G
53	1	545	U
53	1	563	A
53	1	573	U
53	1	574	A
53	1	575	A
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	646	U
53	1	654	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	730	A
53	1	747	C
53	1	752	A
53	1	764	A
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	822	G
53	1	827	U
53	1	828	U
53	1	830	G
53	1	845	A
53	1	846	U
53	1	847	U
53	1	860	U
53	1	878	A
53	1	885	C
53	1	886	A
53	1	887	U
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	983	A
53	1	995	C
53	1	996	A
53	1	1012	U
53	1	1013	C
53	1	1021	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	1022	G
53	1	1033	U
53	1	1045	C
53	1	1046	A
53	1	1047	G
53	1	1054	A
53	1	1062	G
53	1	1066	U
53	1	1070	A
53	1	1071	G
53	1	1075	C
53	1	1079	C
53	1	1084	A
53	1	1088	A
53	1	1104	C
53	1	1106	G
53	1	1111	A
53	1	1131	G
53	1	1132	U
53	1	1133	A
53	1	1135	C
53	1	1143	A
53	1	1157	G
53	1	1175	A
53	1	1177	G
53	1	1180	U
53	1	1206	G
53	1	1212	G
53	1	1250	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1275	A
53	1	1301	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1352	U
53	1	1365	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1395	A
53	1	1396	U
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1791	A
53	1	1800	C
53	1	1801	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1833	C
53	1	1839	G
53	1	1871	A
53	1	1901	A
53	1	1913	A
53	1	1914	C
53	1	1925	C
53	1	1926	U
53	1	1930	G
53	1	1937	A
53	1	1938	A
53	1	1944	U
53	1	1955	U
53	1	1963	U
53	1	1966	A
53	1	1967	C
53	1	1970	A
53	1	1972	G
53	1	1991	U
53	1	1993	U
53	1	1997	C
53	1	2022	U
53	1	2023	C
53	1	2030	A
53	1	2031	A
53	1	2036	C
53	1	2043	C
53	1	2049	G
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2072	C
53	1	2096	C
53	1	2110	G
53	1	2111	U
53	1	2112	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2131	U
53	1	2132	U
53	1	2133	G
53	1	2147	A
53	1	2162	G
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2213	U
53	1	2225	A
53	1	2238	G
53	1	2239	G
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2403	C
53	1	2423	U
53	1	2424	C
53	1	2427	C
53	1	2429	G
53	1	2430	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2498	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	2502	G
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2603	G
53	1	2609	U
53	1	2613	U
53	1	2646	C
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2744	G
53	1	2748	A
53	1	2757	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2797	U
53	1	2799	A
53	1	2800	A
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2849	U
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C
53	1	2883	A
53	1	2884	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
54	2	4	C
54	2	12	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	41	G
54	2	44	G
54	2	67	G
54	2	89	U
54	2	90	C
54	2	108	A
54	2	109	A
55	5	4	G
55	5	9	G
55	5	15	G
55	5	16	C
55	5	17	C
55	5	17(A)	U
55	5	18	G
55	5	19	G
55	5	20	U
55	5	21	A
55	5	22	G
55	5	25	C
55	5	27	U
55	5	28	C
55	5	31	G
55	5	32	C
55	5	45	G
55	5	48	C
55	5	58	A
55	5	61	C
55	5	62	C
55	5	63	G
55	5	72	A
55	5	74	C
56	4	12	A
56	4	13	A
56	4	19	U
57	7	8	U
57	7	9	A
57	7	17	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
57	7	18	G
57	7	20	U
57	7	21	A
57	7	22	G
57	7	45	U
57	7	46	G
57	7	47	U
57	7	48	C
57	7	59	U

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	495	A
52	3	1190	G
52	3	1201	A
53	1	227	A
53	1	421	C
53	1	490	C
53	1	859	G
53	1	1020	A
53	1	1130	U
53	1	1475	G
53	1	2286	G
53	1	2296	U
53	1	2326	C
53	1	2391	G
53	1	2756	U
54	2	88	C
55	5	17(A)	U
57	7	45	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	PHE	7	101	59,57	10,11,12	0.73	0	8,13,15	0.36	0
59	FME	7	102	58	8,9,10	0.47	0	8,9,11	1.47	3 (37%)

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
58	PHE	7	101	59,57	-	1/5/6/8	0/1/1/1
59	FME	7	102	58	-	4/7/9/11	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	7	102	FME	CG-CB-CA	-2.37	105.62	112.87
59	7	102	FME	O-C-CA	-2.25	118.98	124.77
59	7	102	FME	C-CA-N	2.21	113.77	109.50

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	7	102	FME	O1-CN-N-CA
59	7	102	FME	O-C-CA-CB
59	7	102	FME	N-CA-CB-CG
58	7	101	PHE	N-CA-CB-CG
59	7	102	FME	CB-CG-SD-CE

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

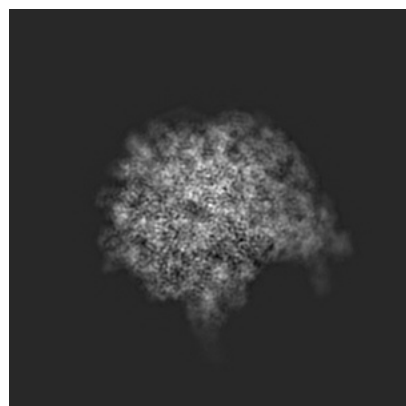
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21634. These allow visual inspection of the internal detail of the map and identification of artifacts.

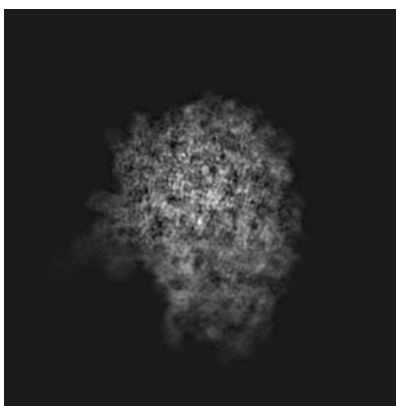
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

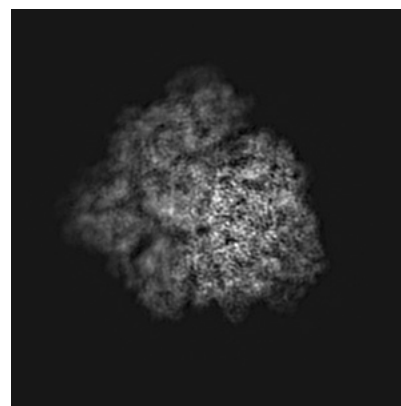
6.1.1 Primary map



X

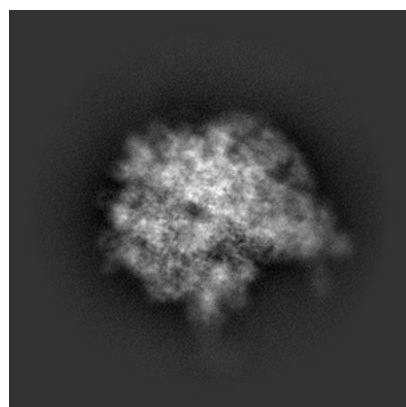


Y

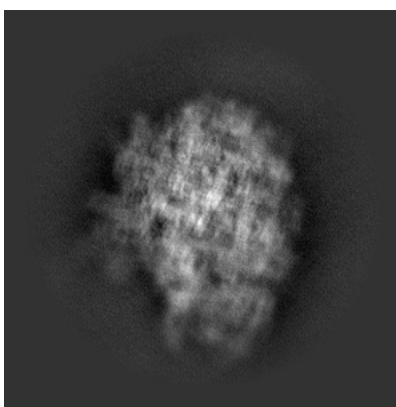


Z

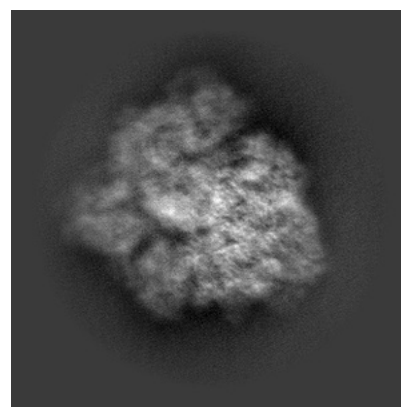
6.1.2 Raw map



X



Y

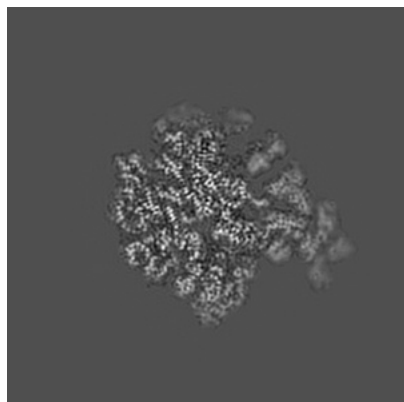


Z

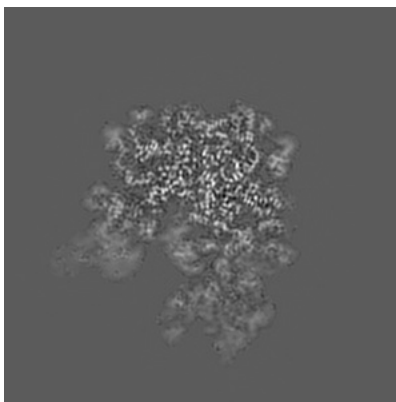
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

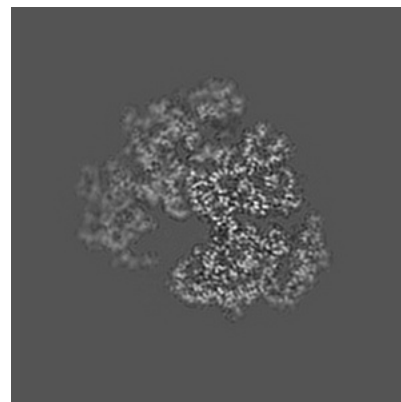
6.2.1 Primary map



X Index: 144

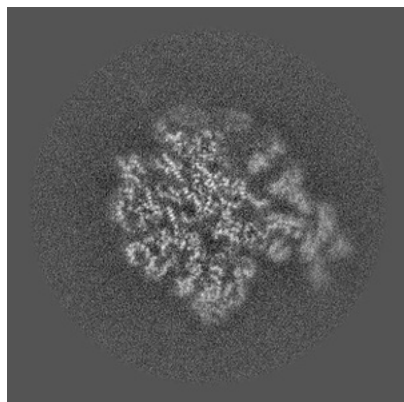


Y Index: 144

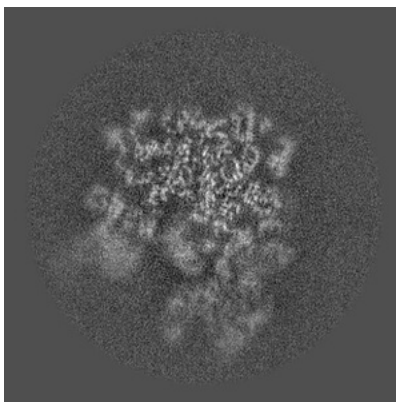


Z Index: 144

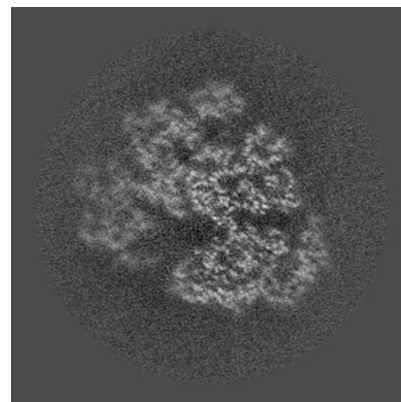
6.2.2 Raw map



X Index: 144



Y Index: 144

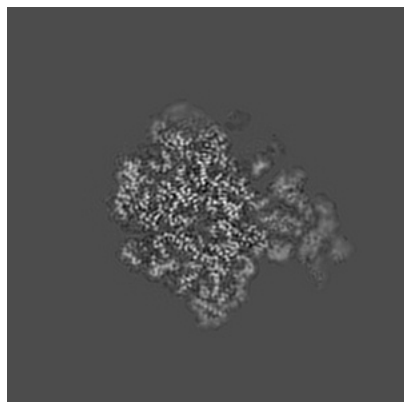


Z Index: 144

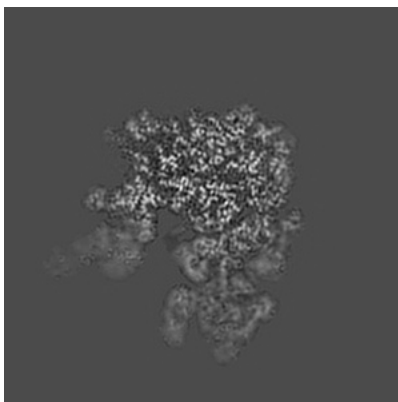
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

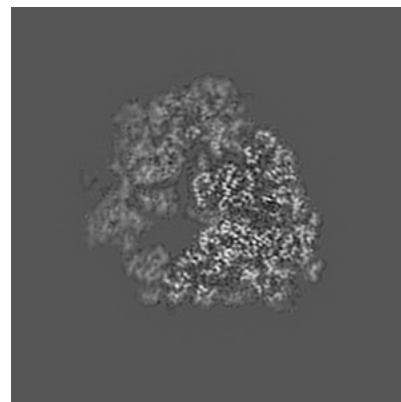
6.3.1 Primary map



X Index: 147

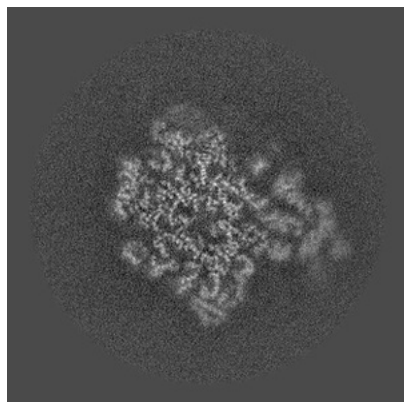


Y Index: 150

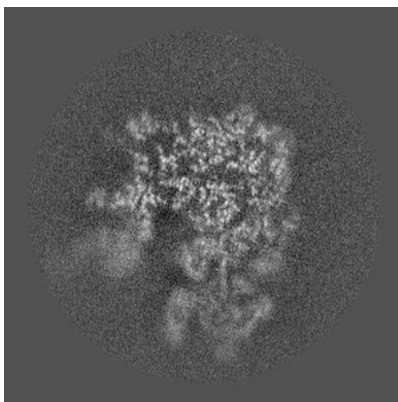


Z Index: 135

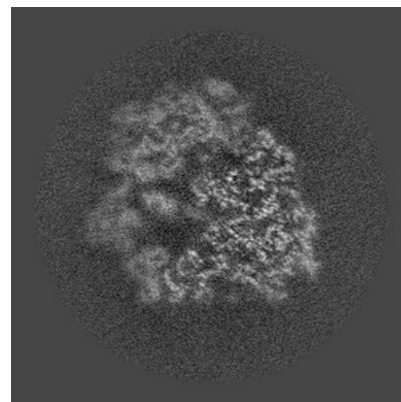
6.3.2 Raw map



X Index: 147



Y Index: 150

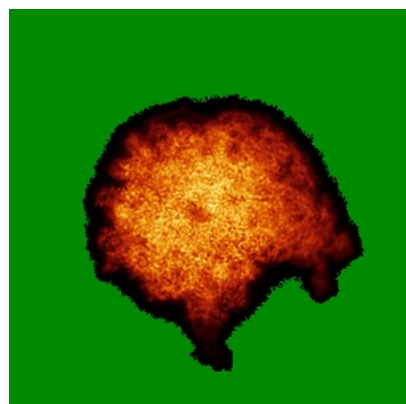


Z Index: 133

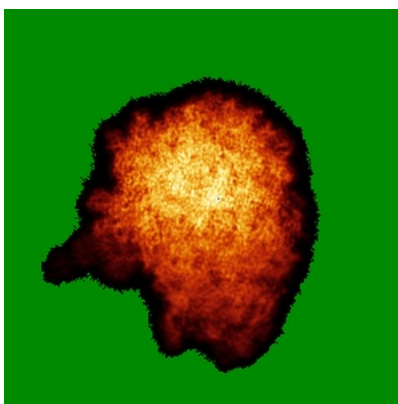
The images above show the largest variance slices of the map in three orthogonal directions.

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

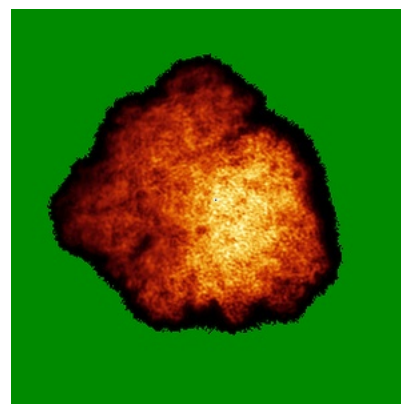
6.4.1 Primary map



X

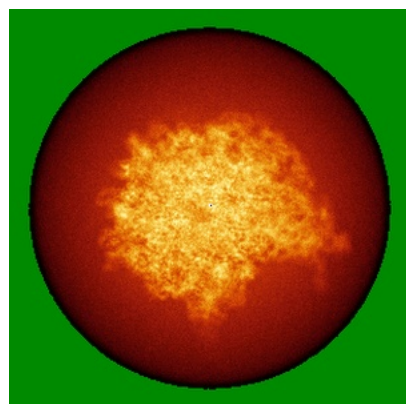


Y

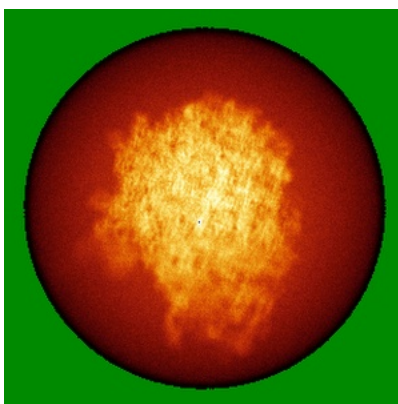


Z

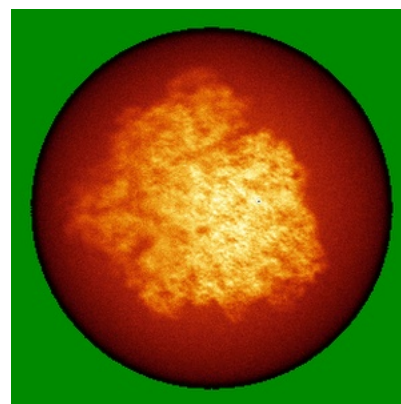
6.4.2 Raw map



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



X



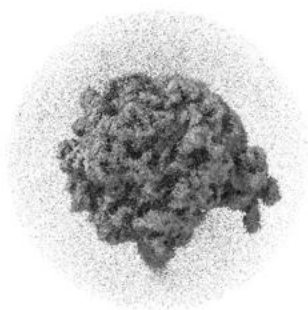
Y



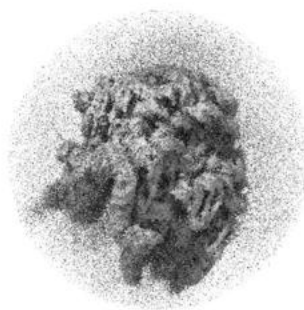
Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

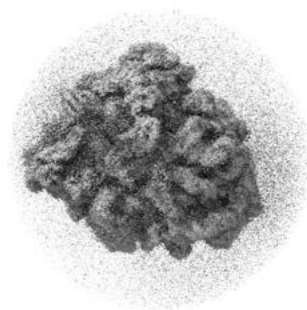
6.5.2 Raw map



X



Y



Z

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.

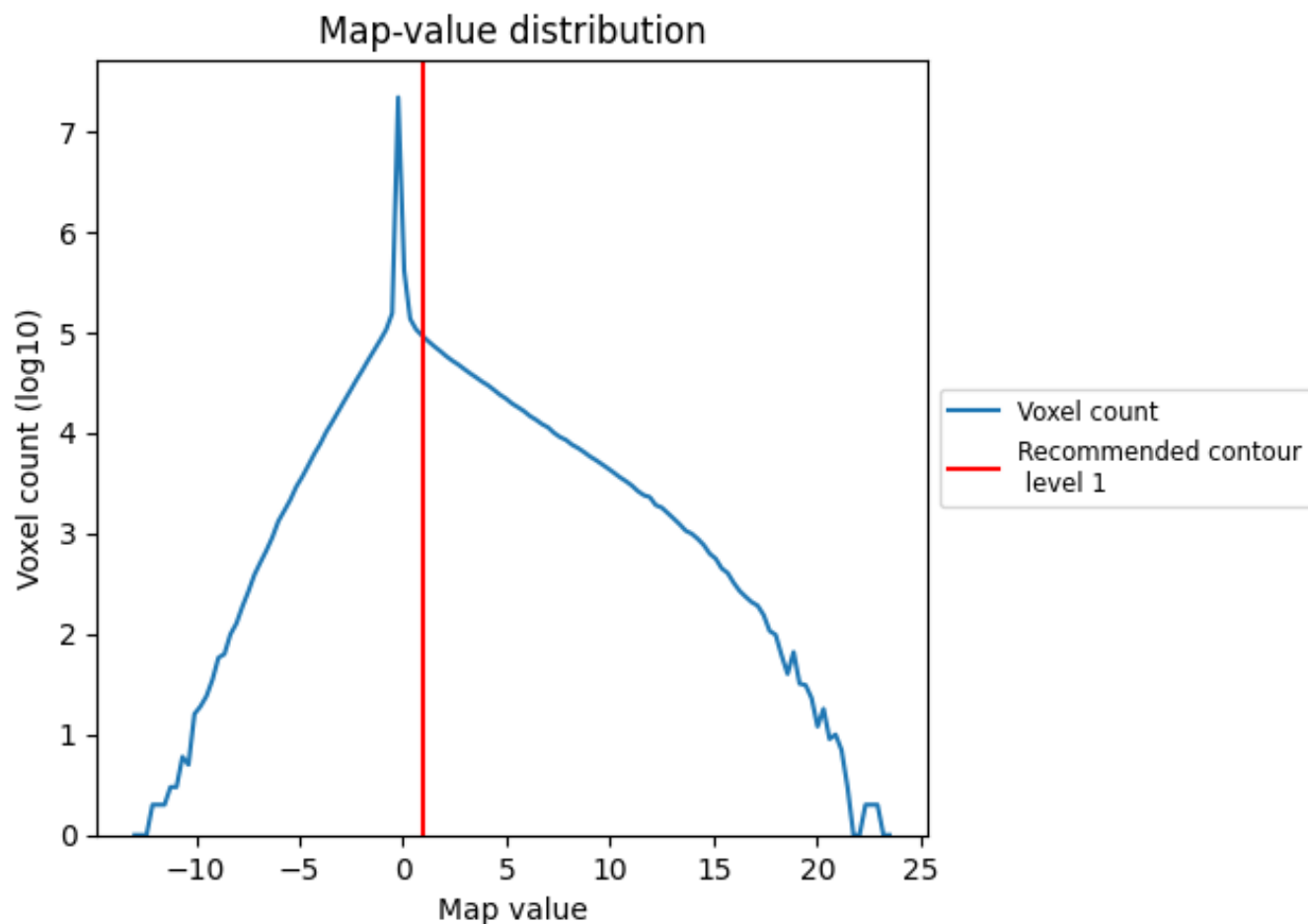
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

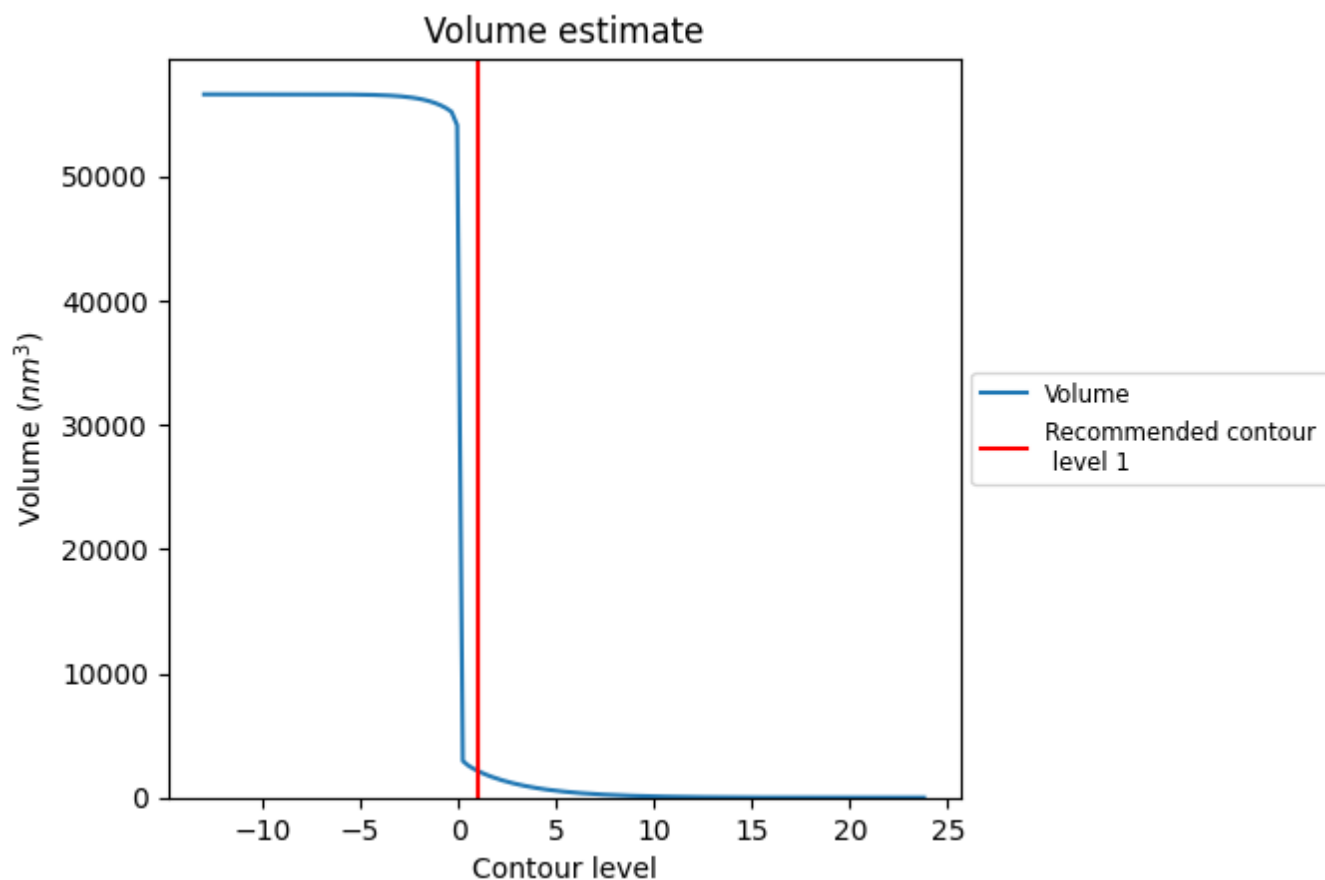
This section contains the results of statistical analysis of the map.

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.

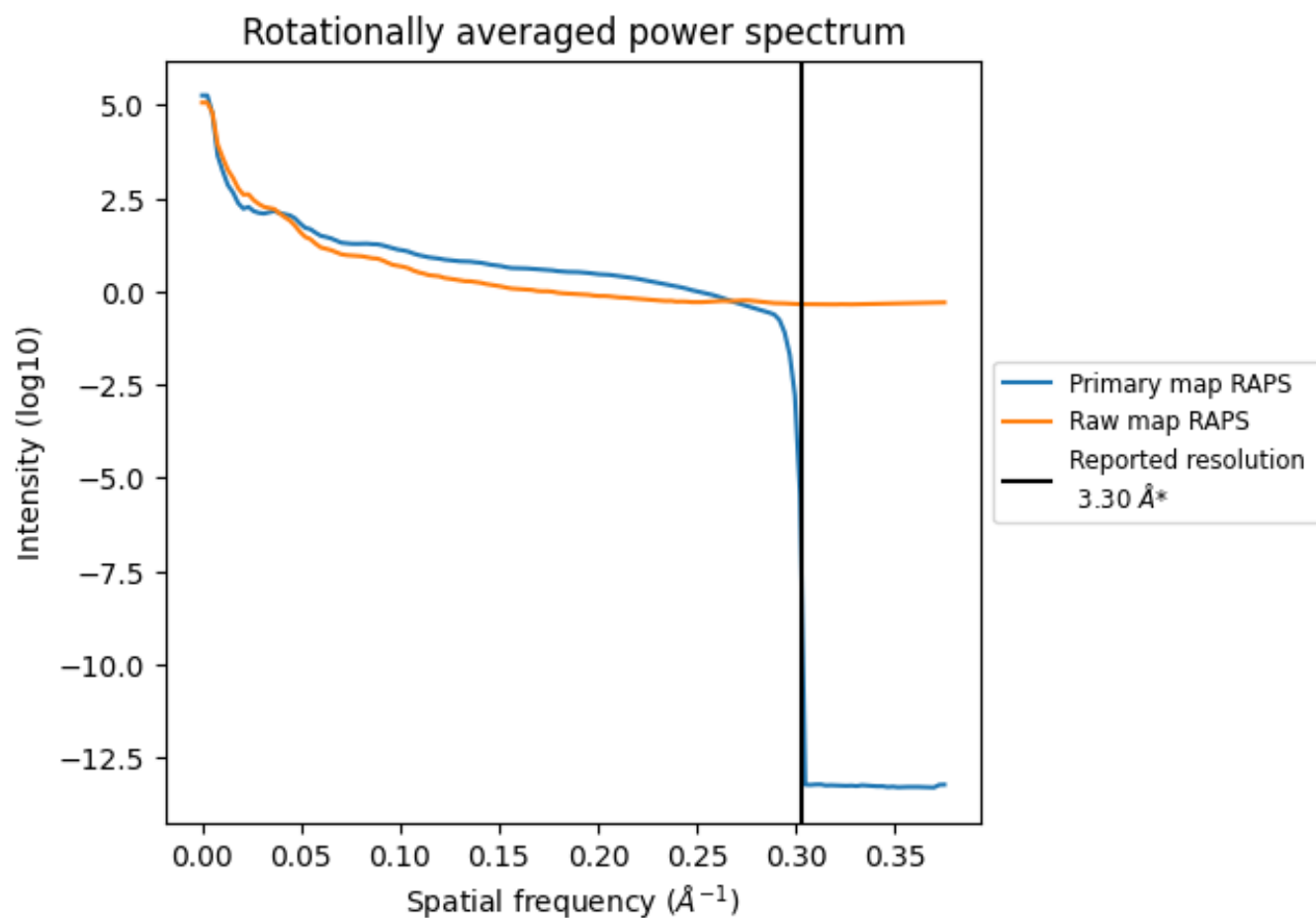
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2152 nm^3 ; this corresponds to an approximate mass of 1944 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 ⓘ

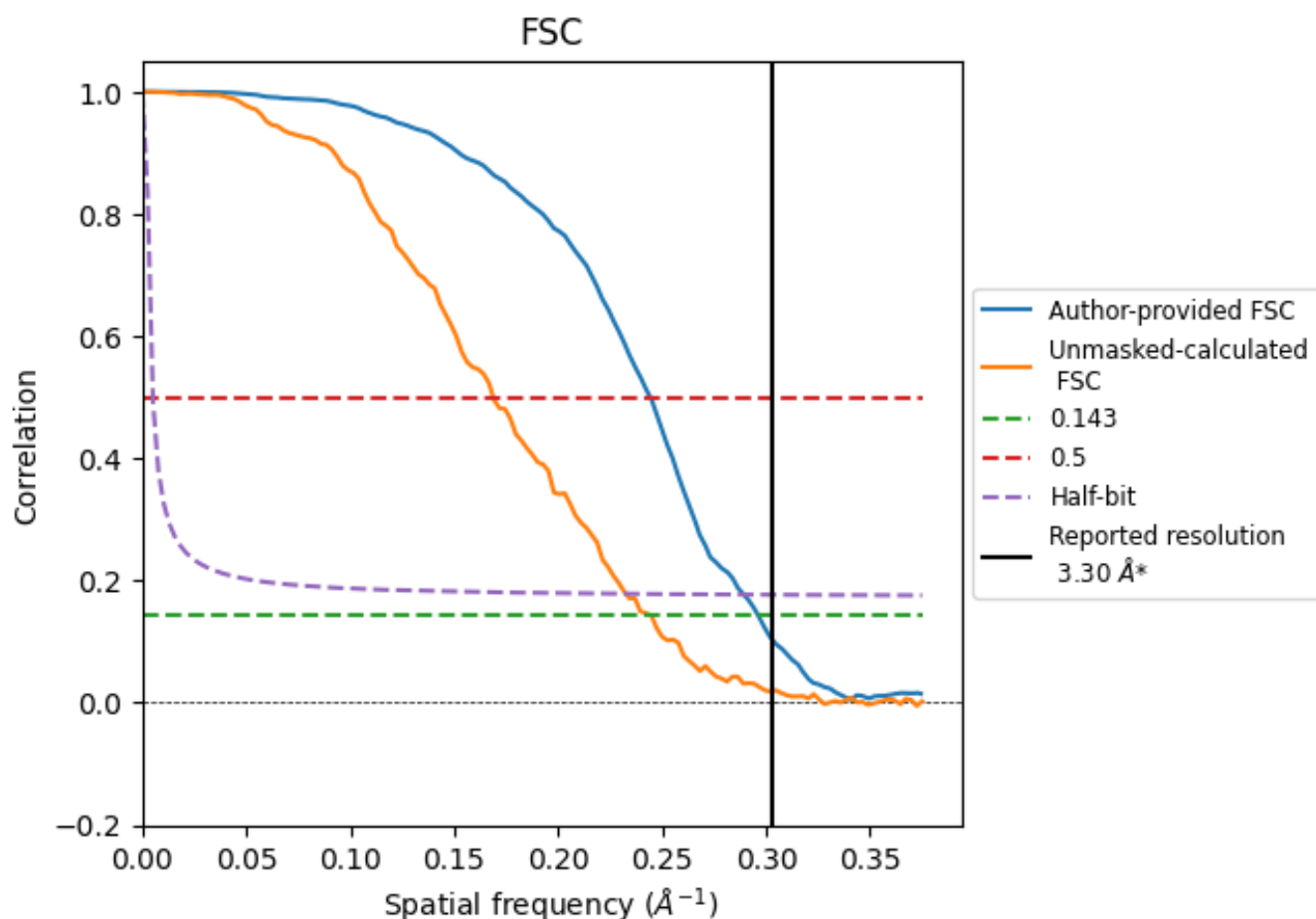


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

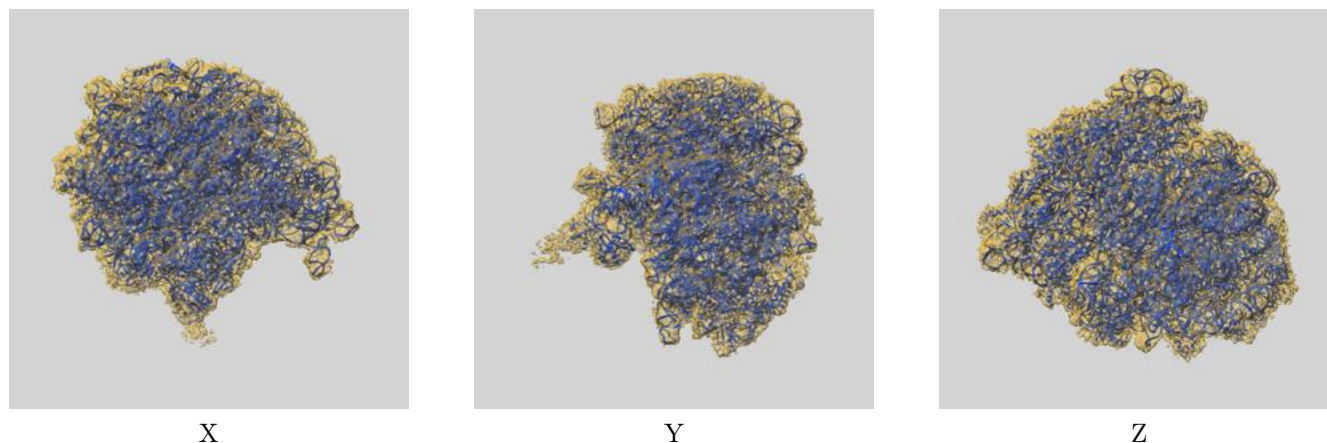
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.38	4.09	3.46
Unmasked-calculated*	4.09	5.92	4.30

*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 4.09 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

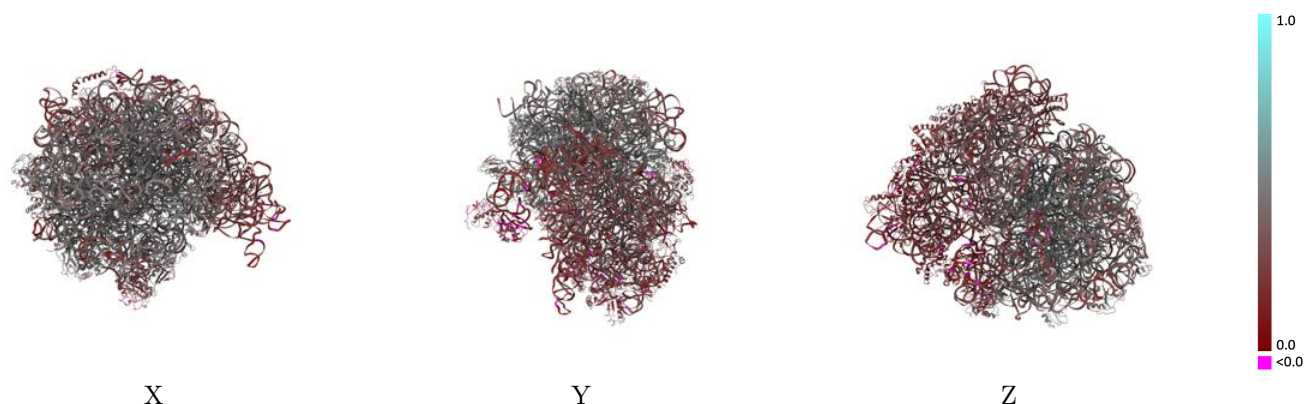
This section contains information regarding the fit between EMDB map EMD-21634 and PDB model 6WDF. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



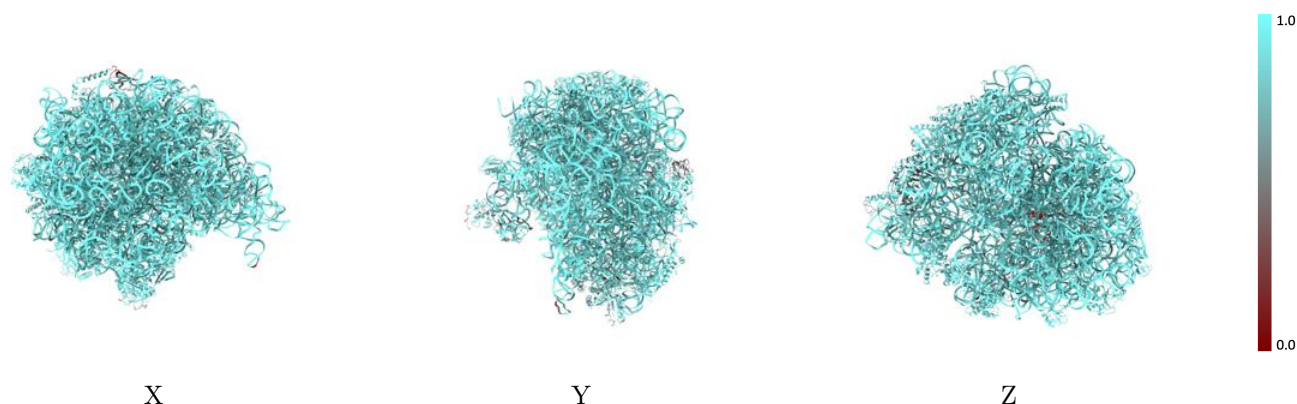
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



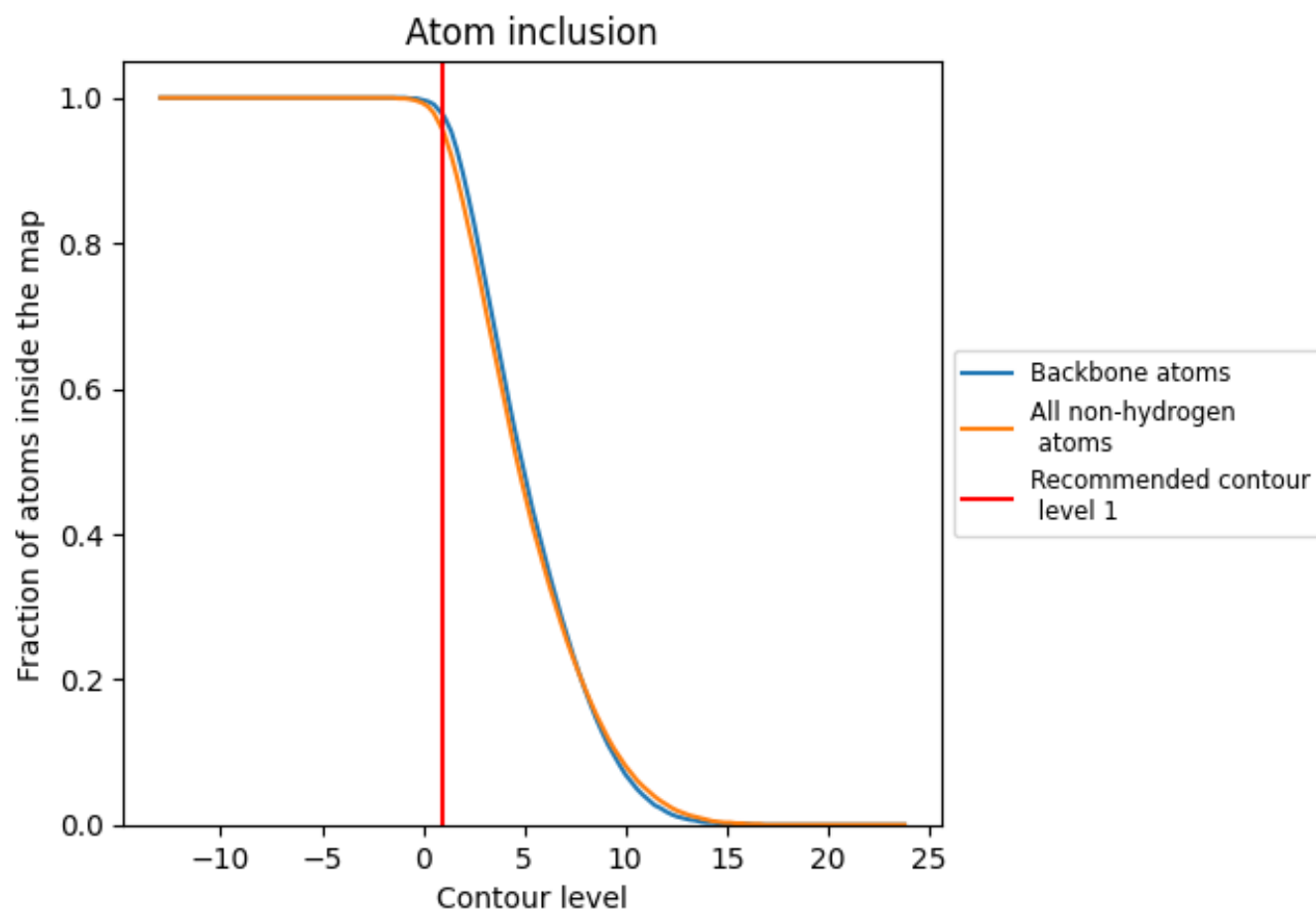
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9540	 0.3600
1	 0.9810	 0.4080
2	 0.9790	 0.3470
3	 0.9670	 0.2920
4	 0.8270	 0.1820
5	 0.9670	 0.2430
7	 0.9390	 0.2460
B	 0.9580	 0.4730
C	 0.8210	 0.4180
D	 0.9320	 0.4840
E	 0.9490	 0.5000
F	 0.8840	 0.4350
G	 0.8750	 0.2610
H	 0.8110	 0.2460
I	 0.8530	 0.2430
J	 0.9040	 0.3250
K	 0.9640	 0.3450
L	 0.8830	 0.2200
M	 0.9050	 0.3560
N	 0.8600	 0.2160
O	 0.7210	 0.2120
P	 0.9490	 0.3590
Q	 0.9330	 0.3770
R	 0.9010	 0.2200
S	 0.7800	 0.2150
T	 0.9360	 0.3700
U	 0.9010	 0.3160
V	 0.9340	 0.3480
W	 0.9260	 0.3430
X	 0.9390	 0.2330
Y	 0.8980	 0.2840
Z	 0.8690	 0.3090
a	 0.8770	 0.1790
b	 0.9650	 0.4860
c	 0.9480	 0.4780



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
d	 0.9460	 0.4330
e	 0.9370	 0.2620
f	 0.9700	 0.3940
g	 0.7090	 0.2330
h	 0.7330	 0.1710
i	 0.7610	 0.1180
j	 0.9660	 0.4770
k	 0.9440	 0.4670
l	 0.9460	 0.4580
m	 0.9430	 0.4600
n	 0.9640	 0.4720
o	 0.9410	 0.3880
p	 0.9600	 0.4550
q	 0.9470	 0.4670
r	 0.9620	 0.4560
s	 0.9380	 0.4660
t	 0.9500	 0.4400
u	 0.9520	 0.4060
v	 0.9570	 0.4430
w	 0.9500	 0.4740
x	 0.9650	 0.4740
y	 0.9620	 0.3730
z	 0.9520	 0.4510