



Full wwPDB EM Validation Report ⓘ

Sep 6, 2026 – 06:35 PM EDT

PDB ID : 11HV / pdb_000011hv
EMDB ID : EMD-75704
Title : Rabbit 60S ribosomal subunit with eEF2 domain IV open
Authors : Seraj, Z.; Zottig, X.; Huang, C.H.; Loveland, A.B.; Diggs, S.; Sholi, E.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2026-02-25
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

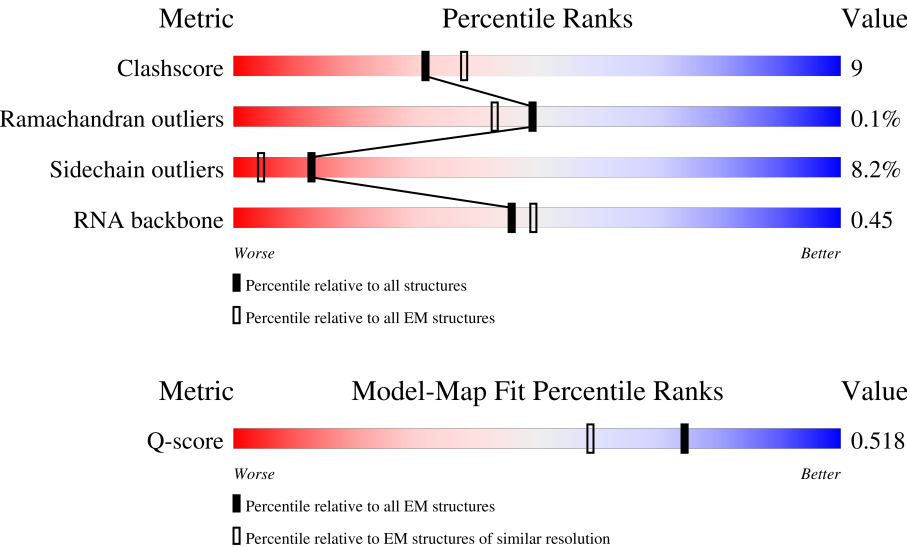
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 2.90 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.



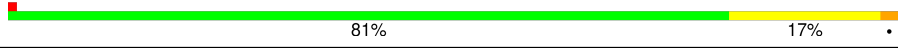
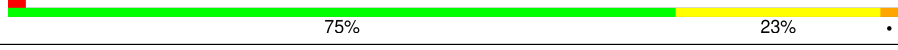
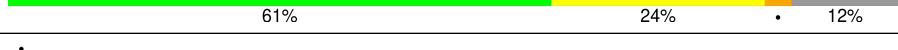
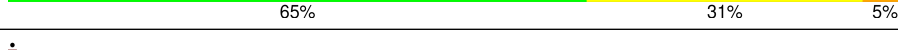
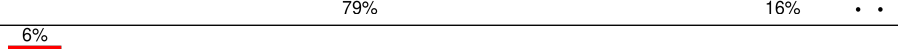
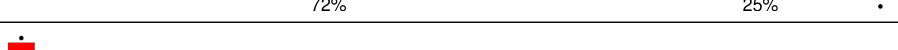
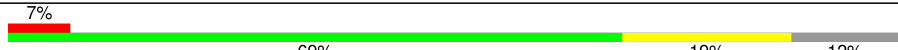
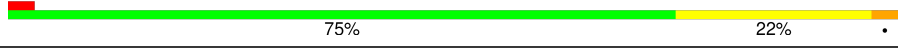
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	v	858	
2	58	156	
3	5	120	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	L8	248	
5	L3	394	
6	L4	362	
7	L5	293	
8	L6	251	
9	L7	225	
10	aa	266	
11	L9	190	
12	10	213	
13	11	170	
14	13	261	
15	14	138	
16	15	203	
17	bb	199	
18	17	153	
19	19	180	
20	20	176	
21	21	159	
22	22	99	
23	24	63	
24	cc	118	
25	26	134	
26	27	135	
27	dd	147	
28	29	245	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	30	98	
30	31	107	
31	32	128	
32	ee	109	
33	34	114	
34	35	122	
35	36	102	
36	37	86	
37	38	69	
38	39	50	
39	40	52	
40	42	104	
41	ff	91	
42	gg	124	
43	s	196	
44	t	153	
45	EB	375	
46	u	206	
47	Q	187	
48	ES	5070	
49	28	4807	
50	25	139	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 147582 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 Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	v	810	Total	C	N	O	S	0	0
			6323	4027	1082	1171	43		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L8	248	Total	C	N	O	S	0	0
			1899	1189	389	315	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L3	394	Total	C	N	O	S	0	0
			3173	2020	597	543	13		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L4	362	Total	C	N	O	S	0	0
			2884	1812	577	481	14		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L5	293	Total	C	N	O	S	0	0
			2392	1512	438	428	14		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L6	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L7	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 10 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L9	190	Total	C	N	O	S	0	0
			1517	954	284	273	6		

- Molecule 12 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	10	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	11	170	Total	C	N	O	S	0	0
			1363	861	254	242	6		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	13	210	Total	C	N	O	S	0	0
			1701	1065	354	278	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	14	138	Total	C	N	O	S	0	0
			1138	727	221	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	bb	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	17	153	Total	C	N	O	S	0	0
			1243	777	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	19	159	Total	C	N	O	S	0	0
			1325	825	283	208	9		

- Molecule 20 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	20	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 21 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 22 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	22	99	Total	C	N	O	S	0	0
			810	519	141	148	2		

- Molecule 23 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	24	63	Total	C	N	O	S	0	0
			529	337	103	86	3		

- Molecule 24 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	26	134	Total	C	N	O	S	0	0
			1116	700	226	187	3		

- Molecule 26 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 27 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	dd	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 28 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	30	98	Total	C	N	O	S	0	0
			762	481	134	141	6		

- Molecule 30 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	31	107	Total	C	N	O	S	0	0
			889	560	171	156	2		

- Molecule 31 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	32	128	Total	C	N	O	S	0	0
			1054	667	216	166	5		

- Molecule 32 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	ee	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 33 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	34	114	Total	C	N	O	S	0	0
			907	566	187	148	6		

- Molecule 34 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 35 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	36	102	Total	C	N	O	S	0	0
			831	520	176	130	5		

- Molecule 36 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	37	86	Total	C	N	O	S	0	0
			706	434	155	112	5		

- Molecule 37 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 39 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	42	104	Total	C	N	O	S	0	0
			852	533	174	139	6		

- Molecule 41 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	ff	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	gg	124	Total	C	N	O	S	0	0
			991	615	202	168	6		

- Molecule 43 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1508	959	263	277	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1161	722	218	218	3		

- Molecule 45 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	EB	375	Total	C	N	O	S	0	0
			2932	1844	509	562	17		

- Molecule 46 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	206	Total	C	N	O	S	0	0
			1655	1058	297	292	8		

- Molecule 47 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 48 is a RNA chain called ES27L.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	ES	67	Total	C	N	O	P	0	0
			1444	639	266	472	67		

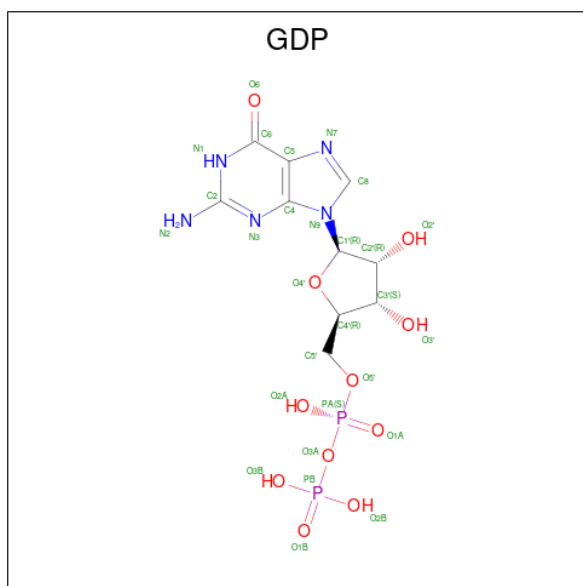
- Molecule 49 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	28	3486	Total	C	N	O	P	0	0
			74767	33297	13700	24284	3486		

- Molecule 50 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	25	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

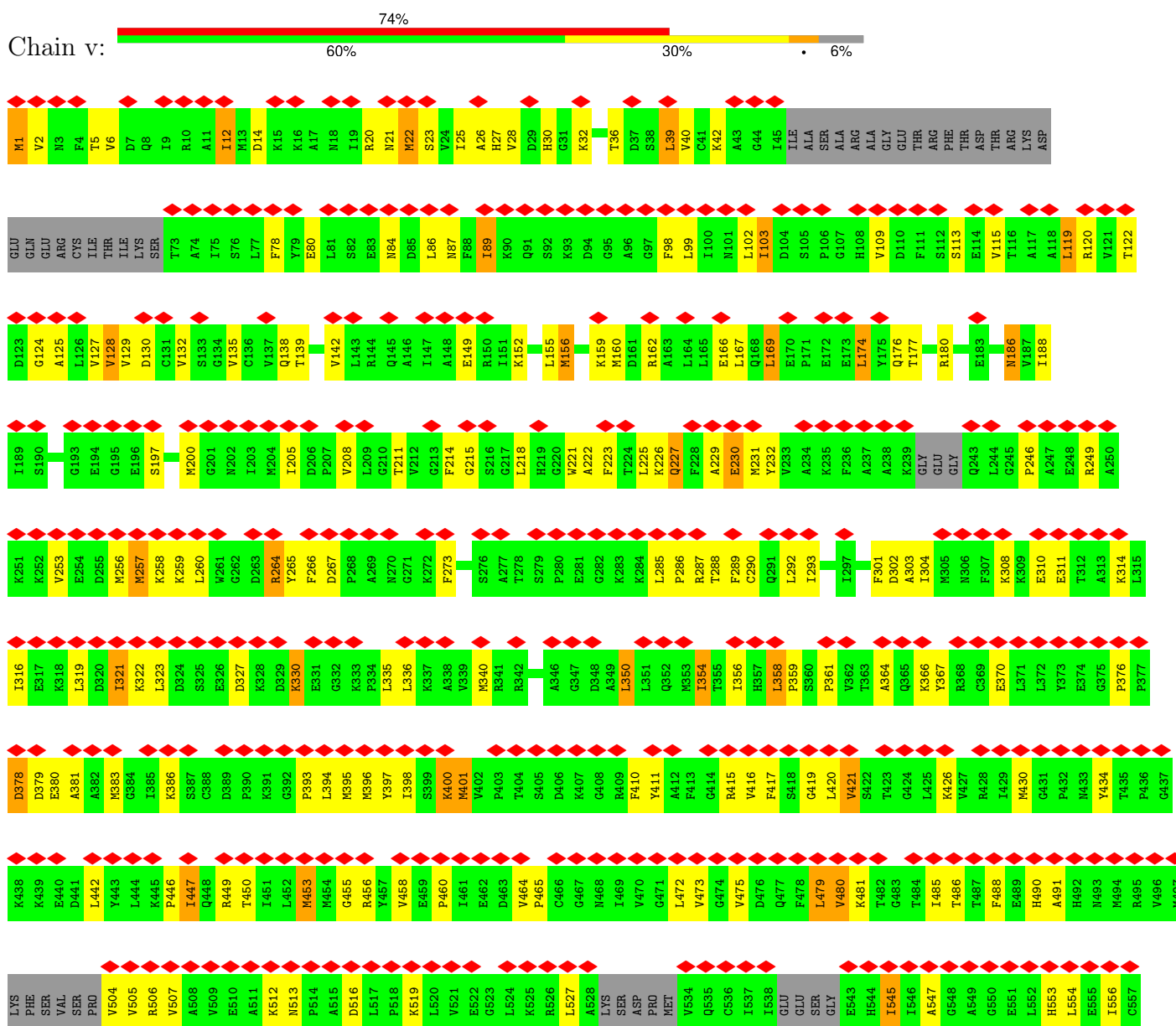
- Molecule 51 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

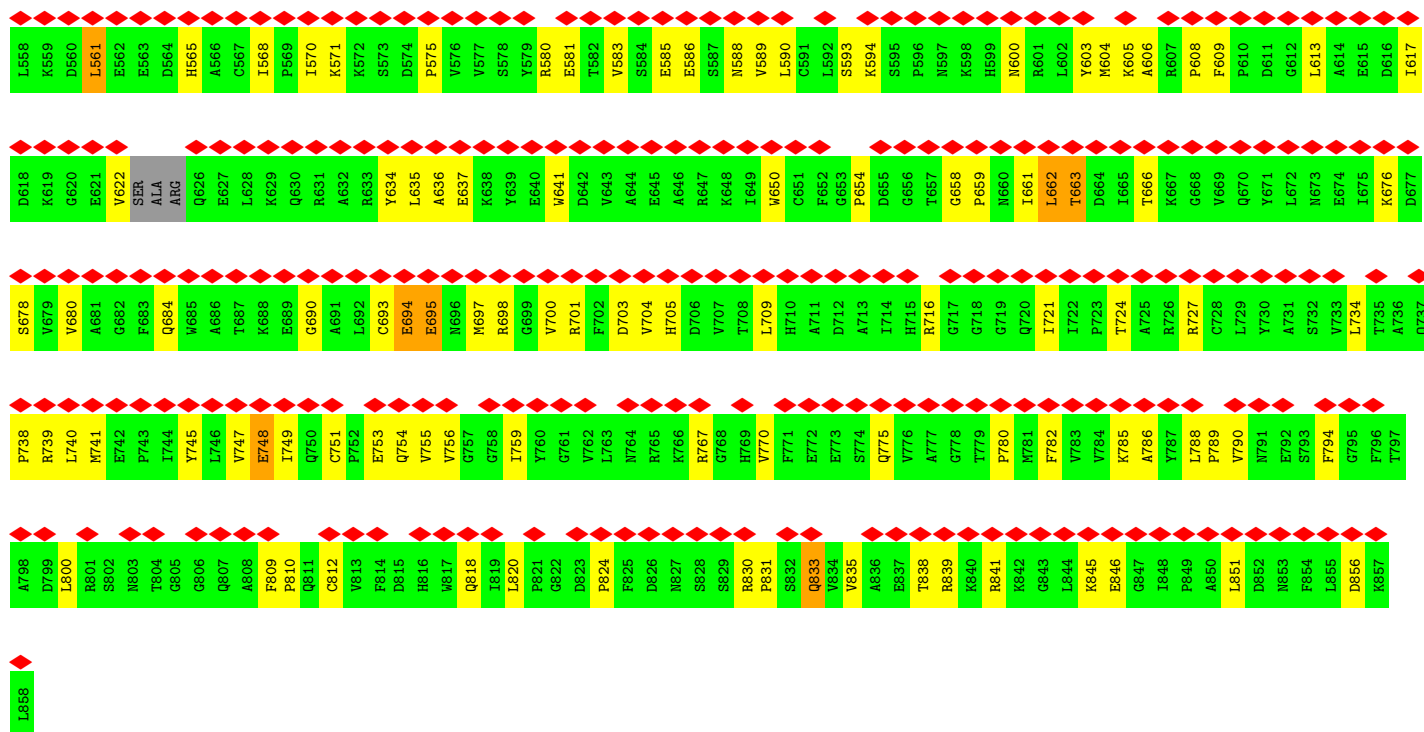


3 Residue-property plots

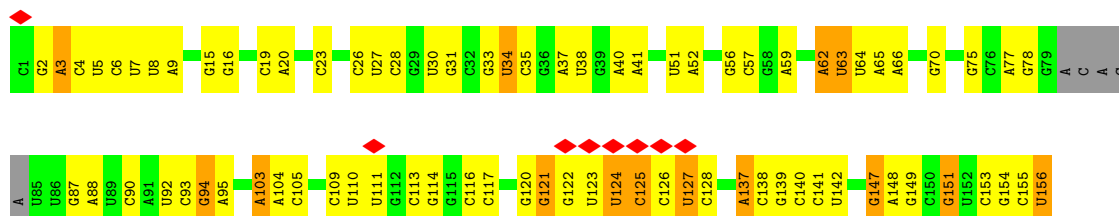
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Elongation factor 2





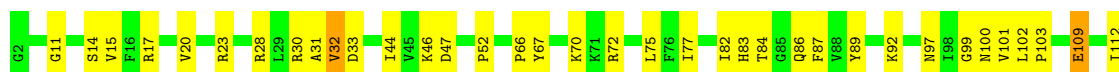
• Molecule 2: 5.8S rRNA

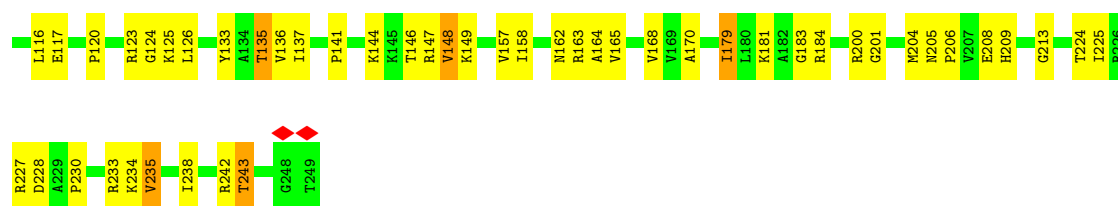


• Molecule 3: 5S rRNA

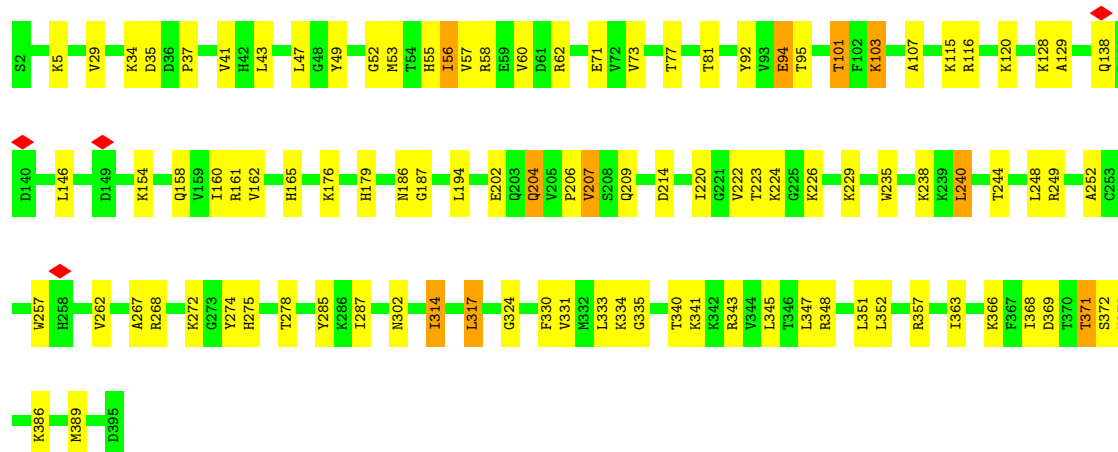
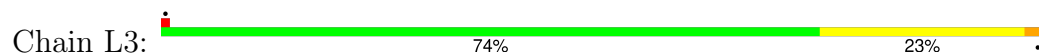


• Molecule 4: 60S ribosomal protein L8

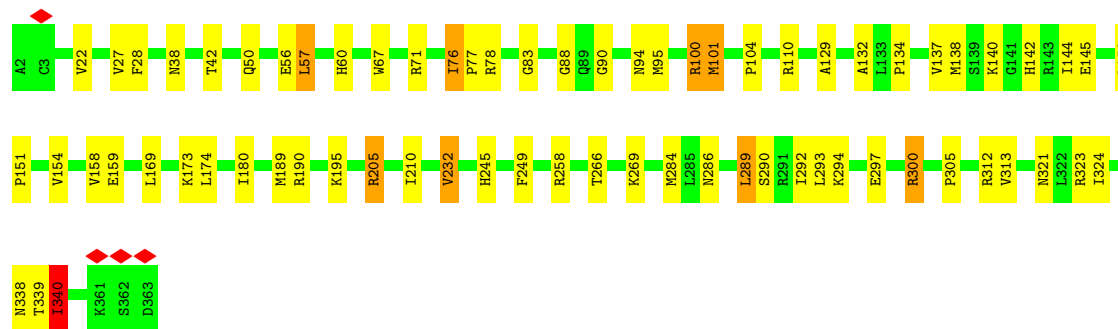
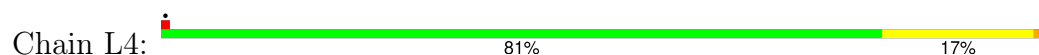




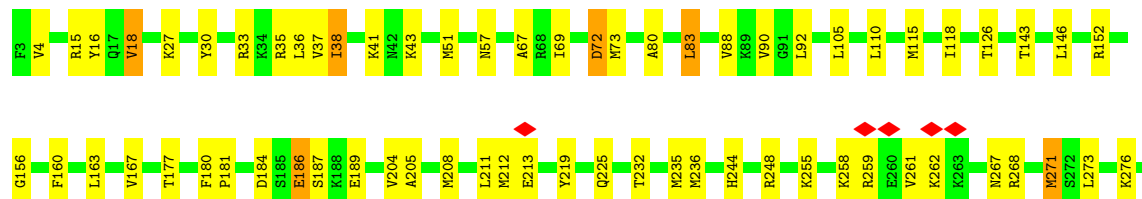
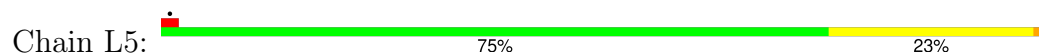
• Molecule 5: 60S ribosomal protein L3



• Molecule 6: 60S ribosomal protein L4

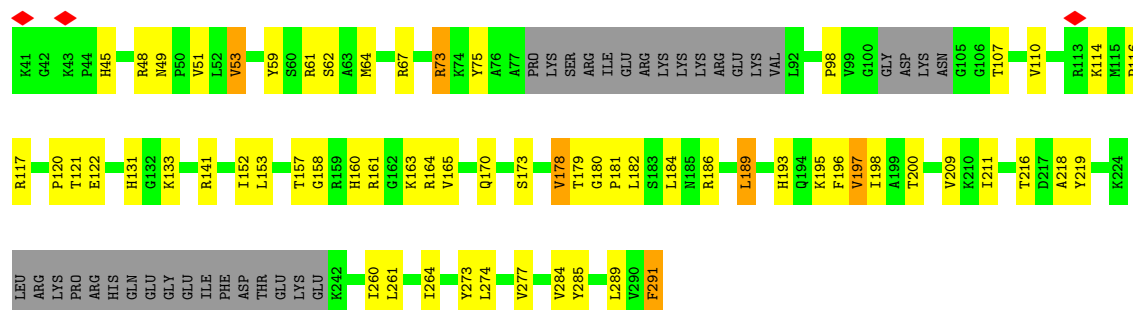


• Molecule 7: 60S ribosomal protein L5

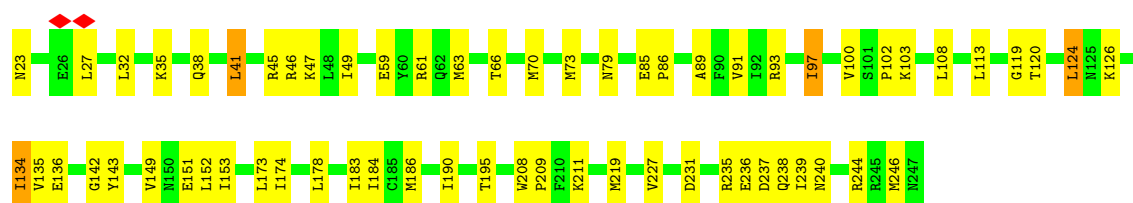




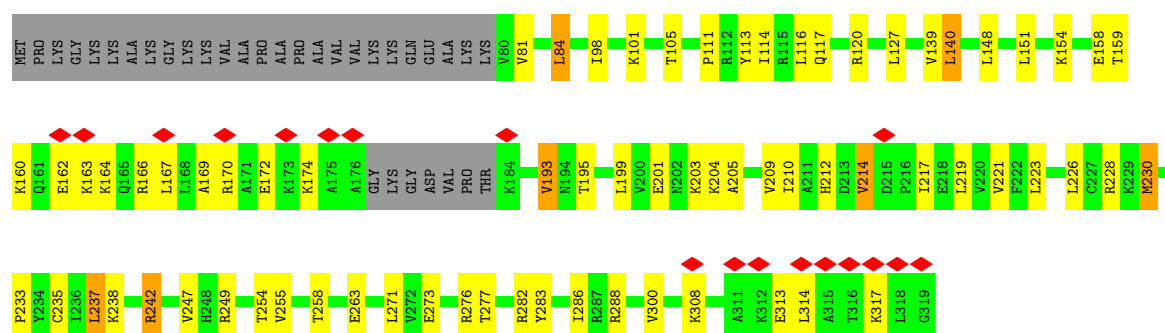
• Molecule 8: Large ribosomal subunit protein eL6



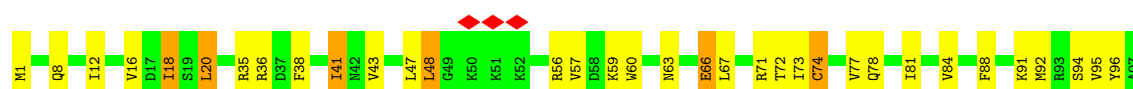
• Molecule 9: 60S ribosomal protein L7

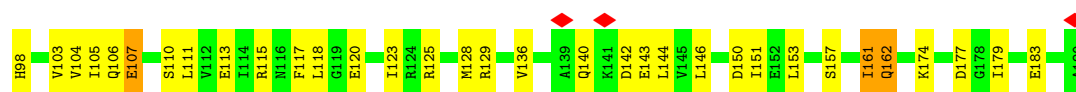


• Molecule 10: Large ribosomal subunit protein eL8

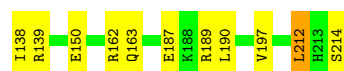
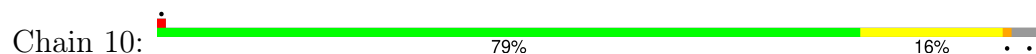


• Molecule 11: 60S ribosomal protein L9

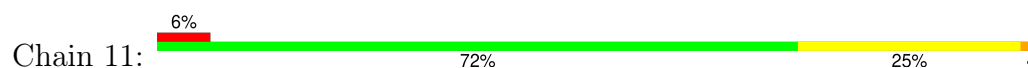




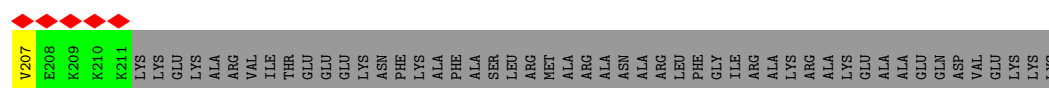
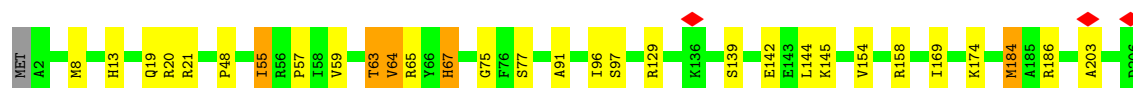
• Molecule 12: Ribosomal protein L10



• Molecule 13: 60S ribosomal protein L11



• Molecule 14: Large ribosomal subunit protein eL13

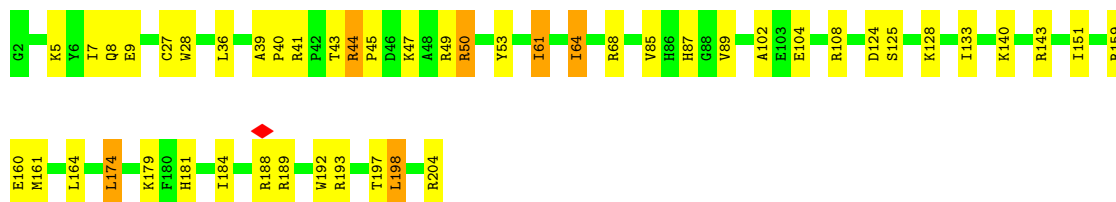


• Molecule 15: 60S ribosomal protein L14



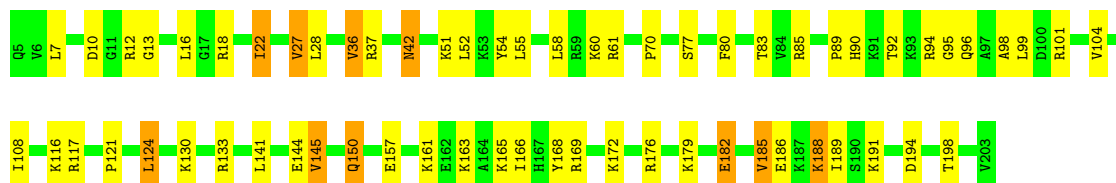
• Molecule 16: 60S ribosomal protein L15

Chain 15:  76% 21% .



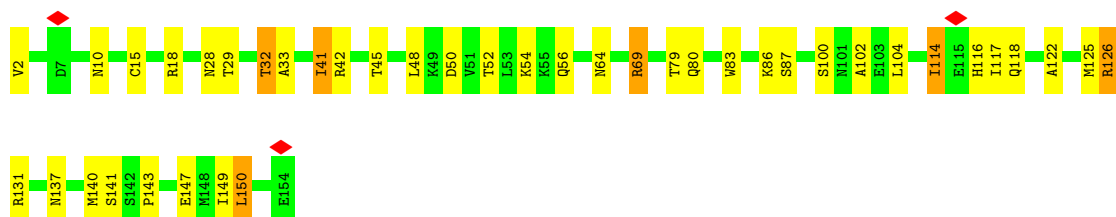
- Molecule 17: Large ribosomal subunit protein uL13

Chain bb:  68% 27% 5%



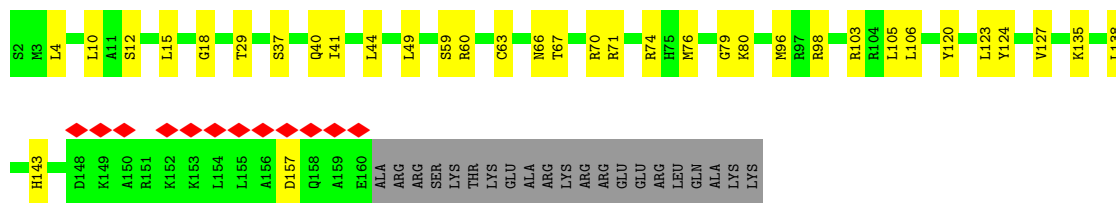
- Molecule 18: 60S ribosomal protein L17

Chain 17:  73% 23% .



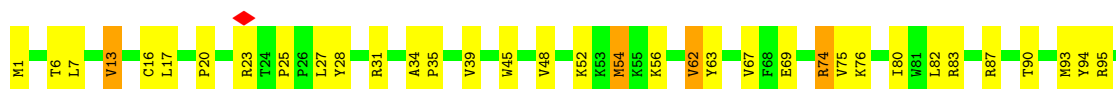
- Molecule 19: 60S ribosomal protein L19

Chain 19:  7% 69% 19% 12%



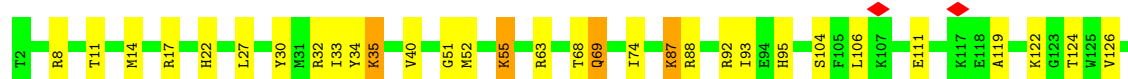
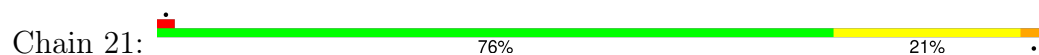
- Molecule 20: Large ribosomal subunit protein eL20

Chain 20:  67% 30% .

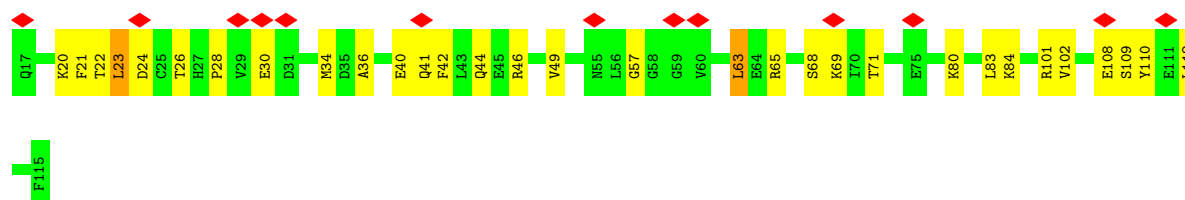




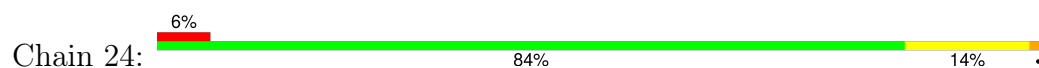
- Molecule 21: 60S ribosomal protein L21



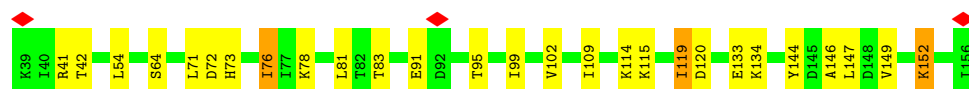
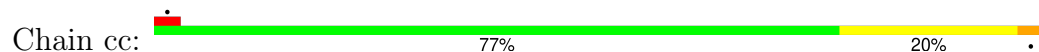
- Molecule 22: Large ribosomal subunit protein eL22



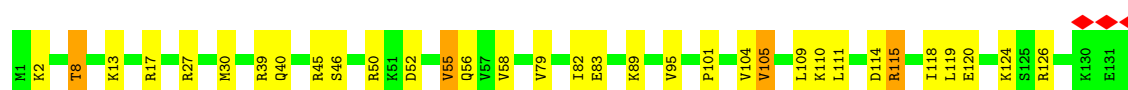
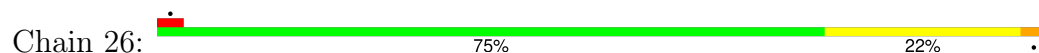
- Molecule 23: Ribosomal protein L24



- Molecule 24: Large ribosomal subunit protein uL23



- Molecule 25: 60S ribosomal protein L26



Chain 31:  72% 26%



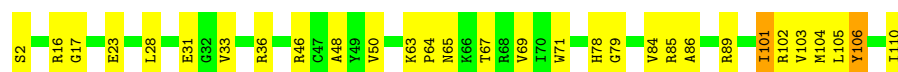
- Molecule 31: Large ribosomal subunit protein eL32

Chain 32:  70% 30%



- Molecule 32: Large ribosomal subunit protein eL33

Chain ee:  72% 26%



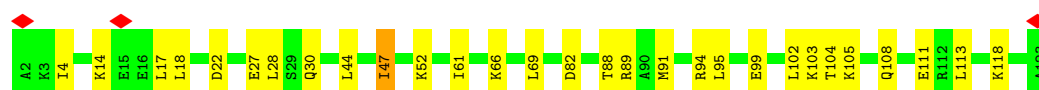
- Molecule 33: 60S ribosomal protein L34

Chain 34:  6% 76% 22%



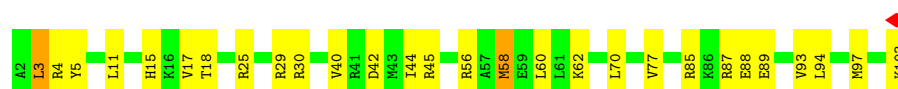
- Molecule 34: 60S ribosomal protein L35

Chain 35:  76% 23%



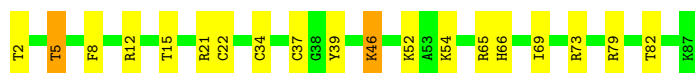
- Molecule 35: 60S ribosomal protein L36

Chain 36:  73% 25%



- Molecule 36: 60S ribosomal protein L37

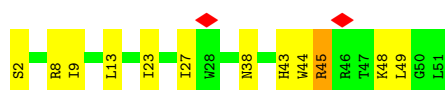
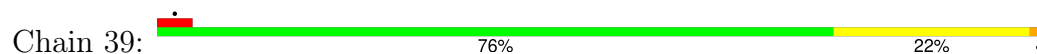
Chain 37:  78% 20%



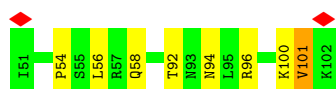
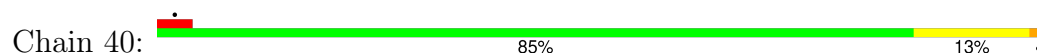
- Molecule 37: Large ribosomal subunit protein eL38



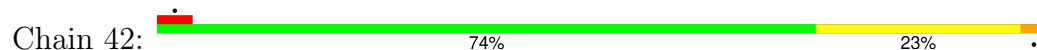
- Molecule 38: 60S ribosomal protein L39



- Molecule 39: Large ribosomal subunit protein eL40



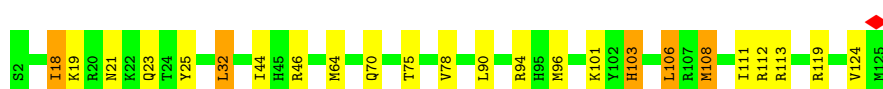
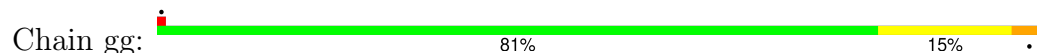
- Molecule 40: eL42



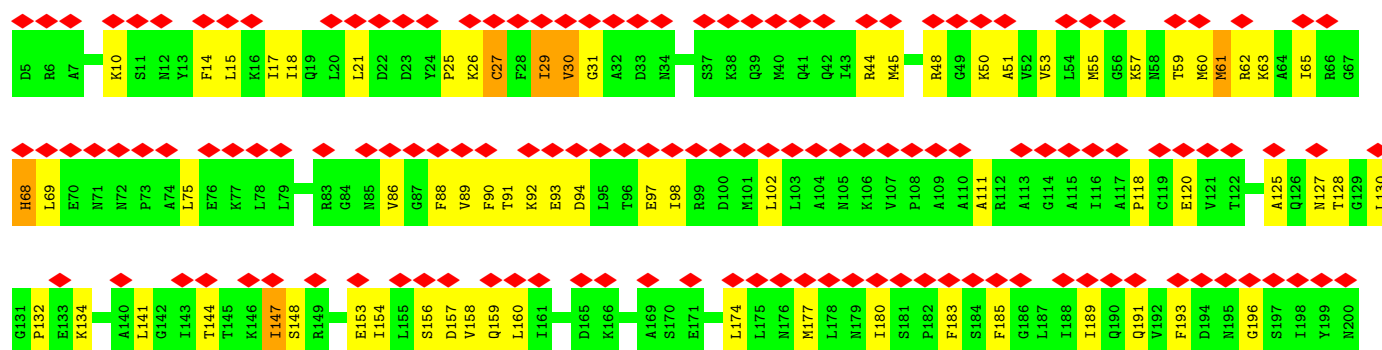
- Molecule 41: 60S ribosomal protein L37a



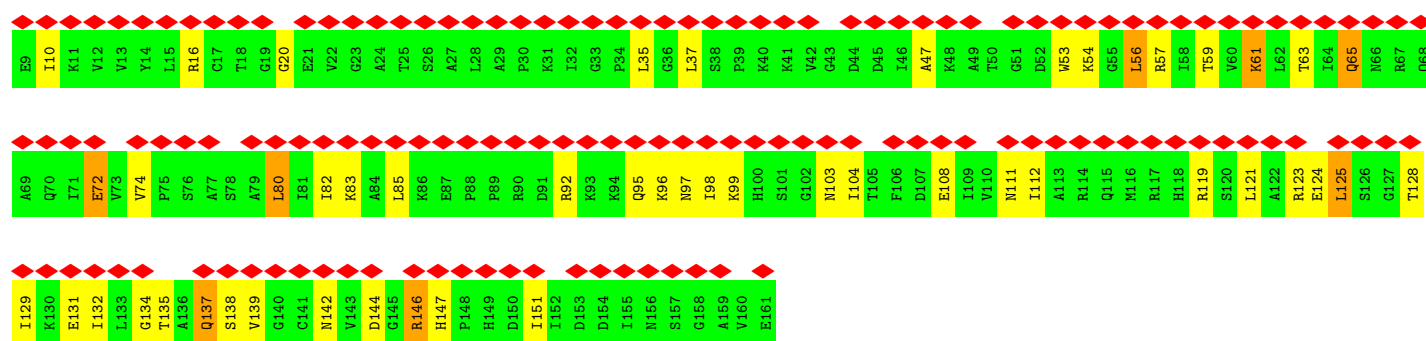
- Molecule 42: 60S ribosomal protein L28



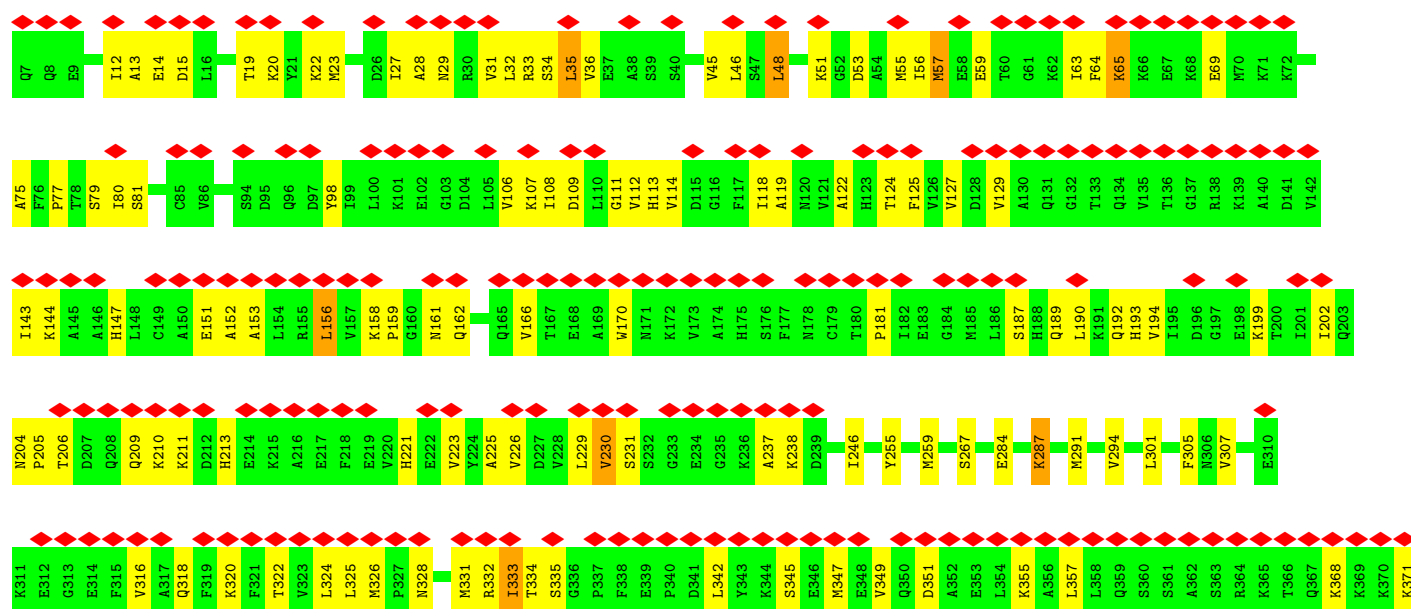
- Molecule 43: 60S acidic ribosomal protein P0



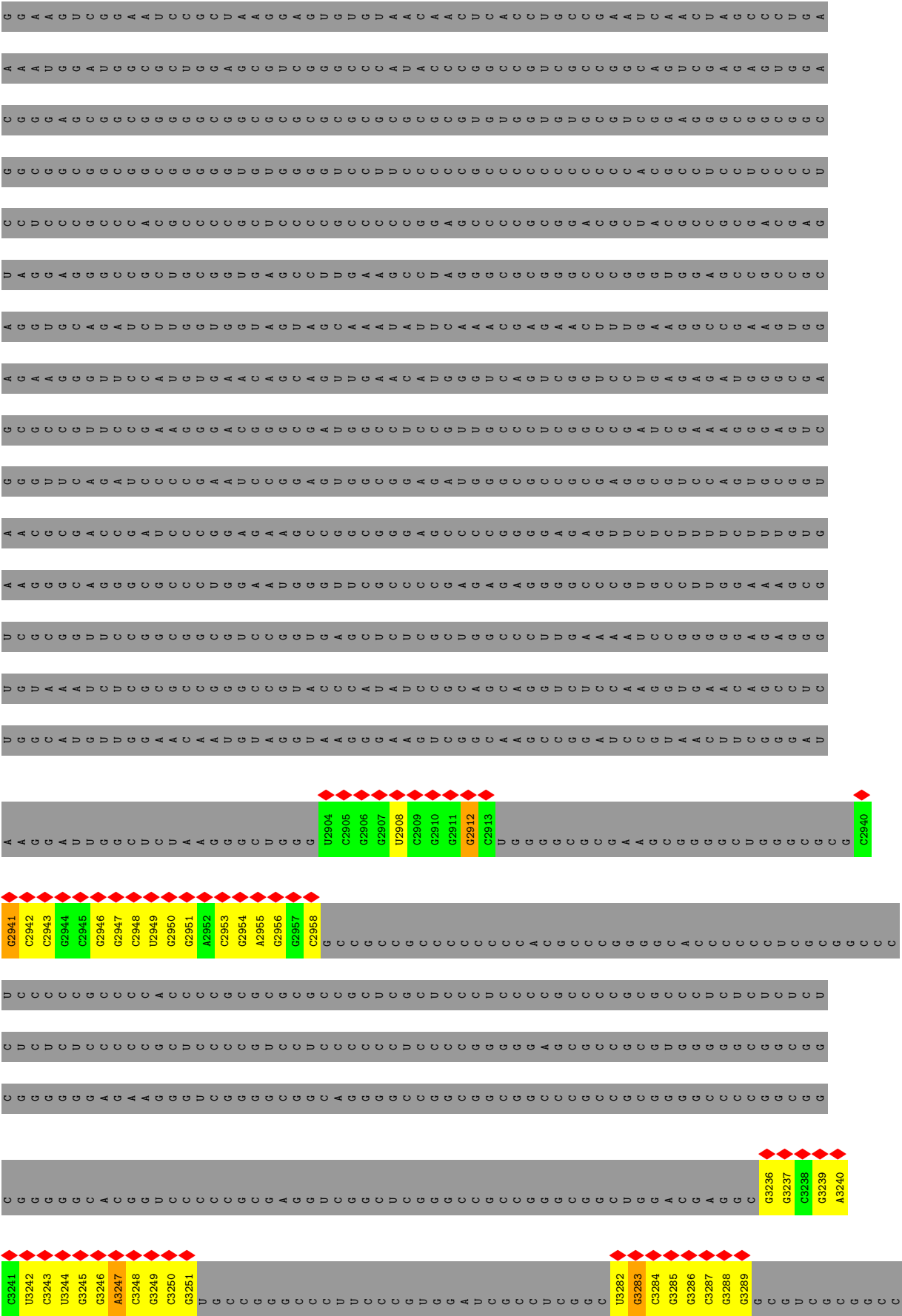
• Molecule 44: uL11



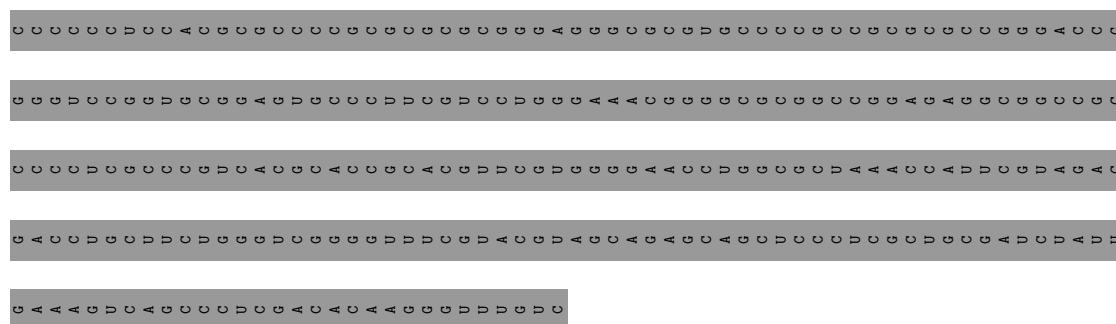
• Molecule 45: Proliferation-associated protein 2G4





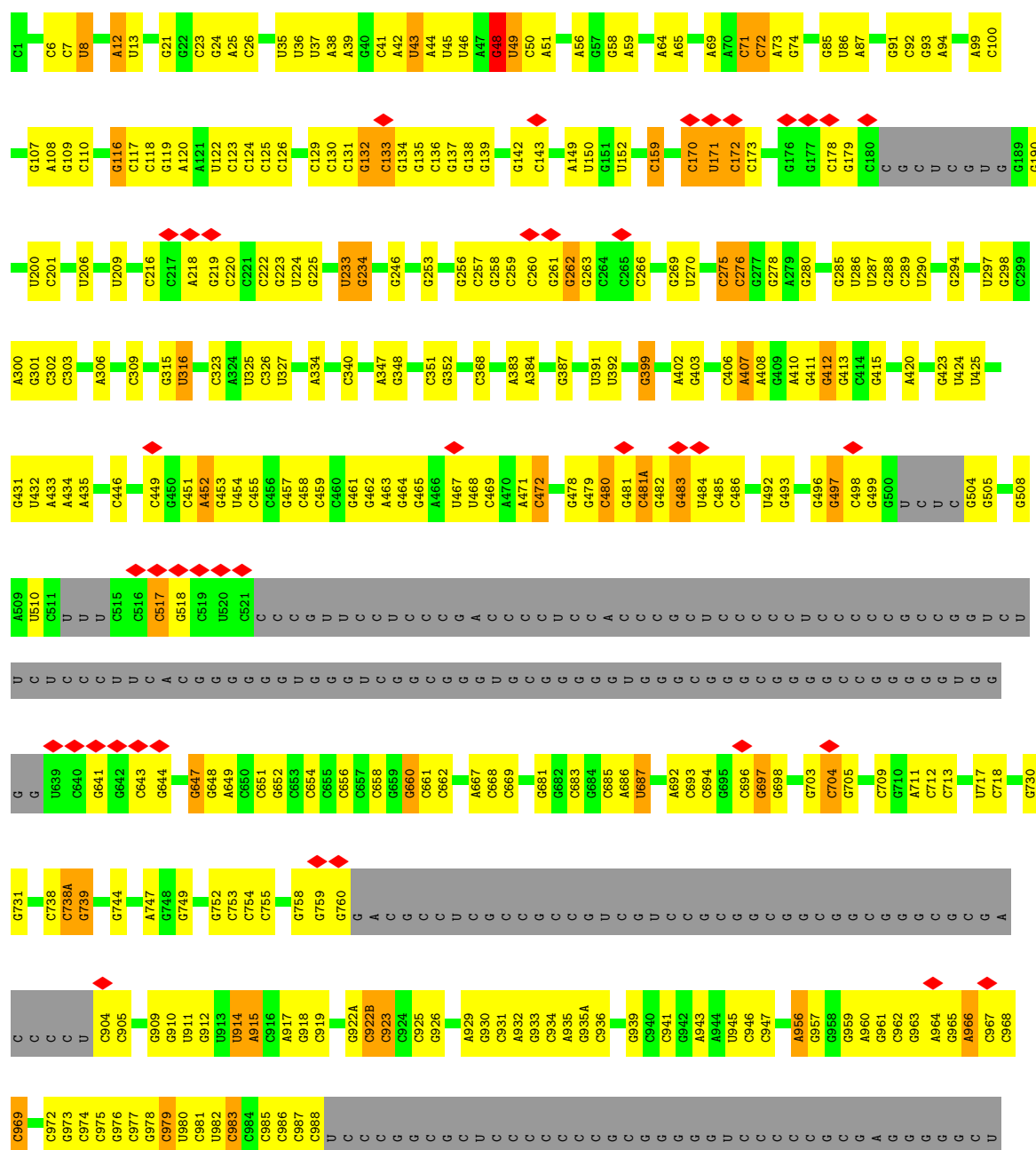


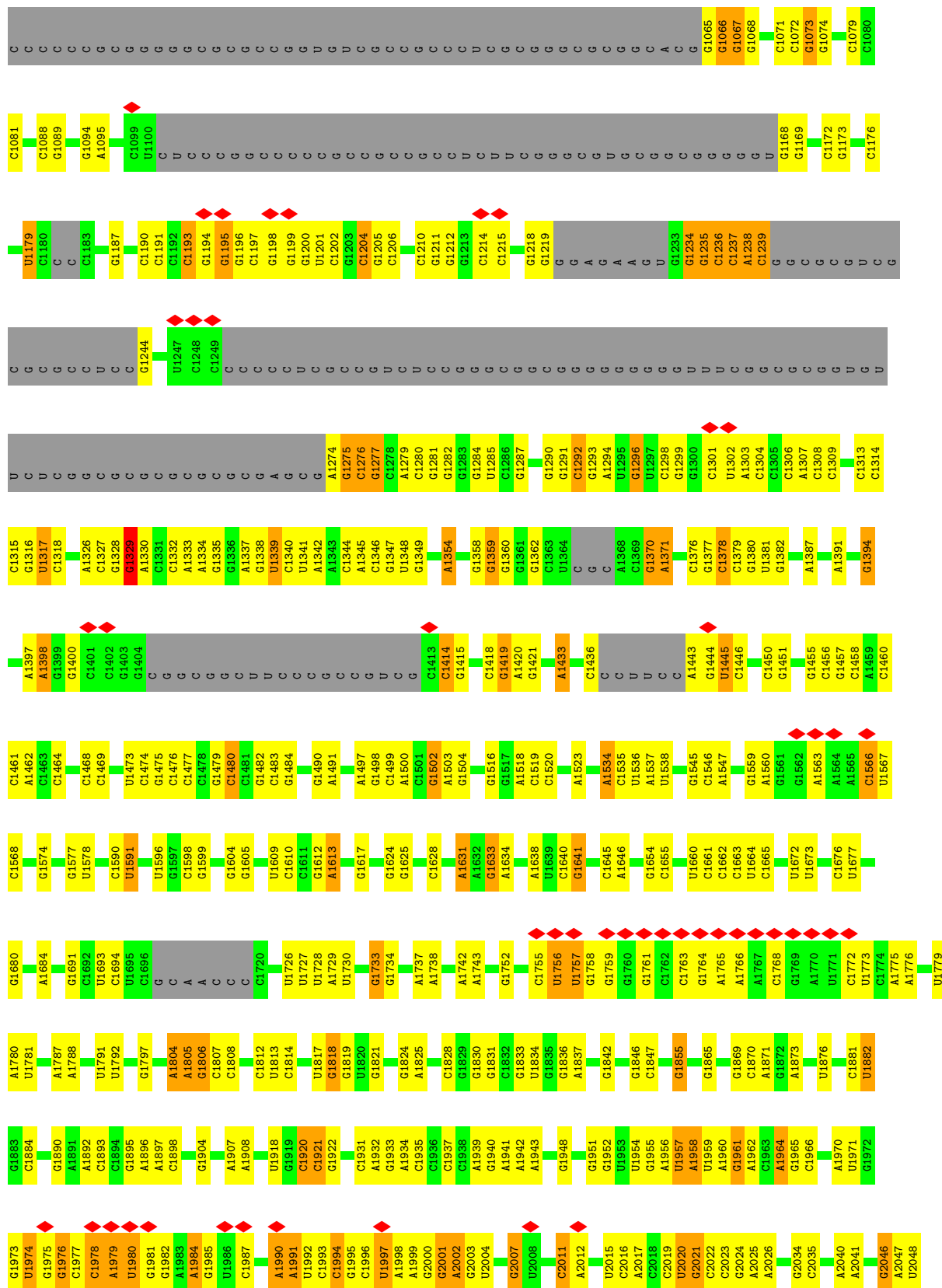




• Molecule 49: 28S rRNA

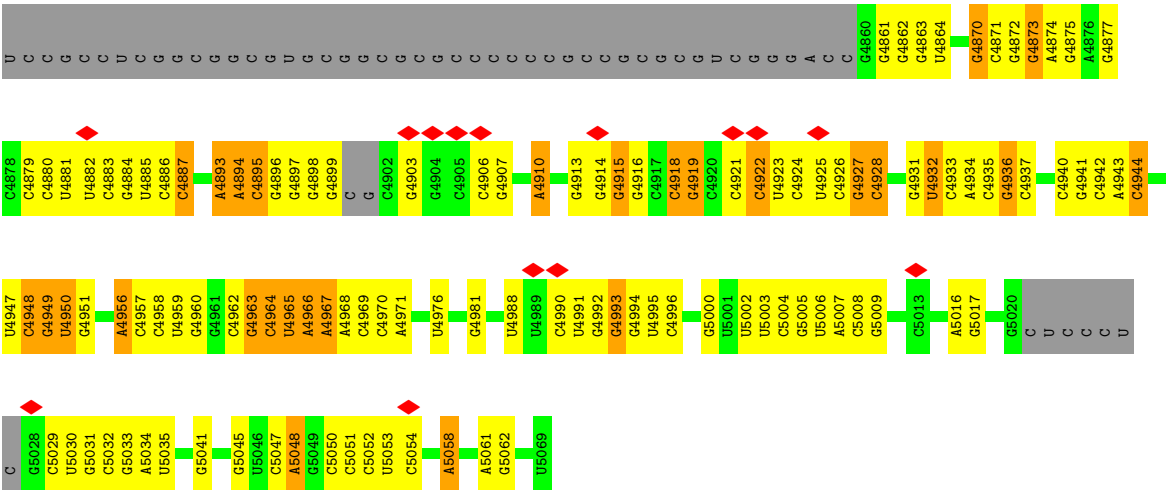
Chain 28: 40% 27% 6% 27%



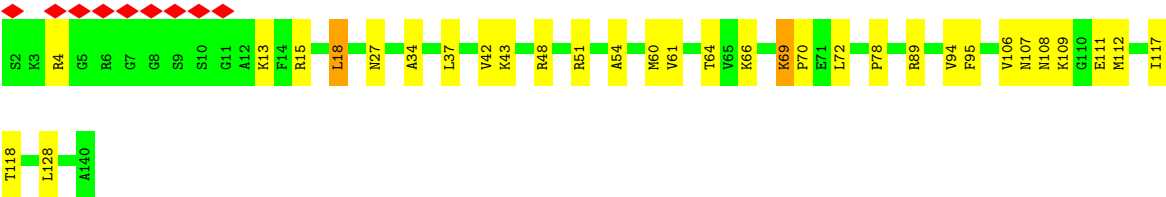
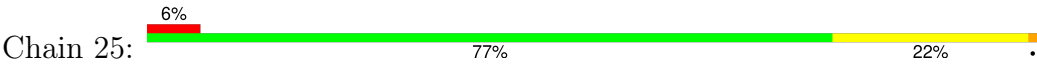








● Molecule 50: Large ribosomal subunit protein uL14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15960	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	OTHER	Depositor
Maximum map value	29.413	Depositor
Minimum map value	-17.059	Depositor
Average map value	0.003	Depositor
Map value standard deviation	1.135	Depositor
Recommended contour level	4	Depositor
Map size ($\text{\AA}$)	664.0, 664.0, 664.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	v	0.25	0/6444	0.48	0/8699
2	58	0.53	0/3581	0.41	0/5577
3	5	0.50	0/2858	0.38	0/4455
4	L8	0.51	0/1937	0.53	0/2596
5	L3	0.49	0/3241	0.52	0/4339
6	L4	0.51	0/2938	0.54	1/3946 (0.0%)
7	L5	0.41	0/2438	0.46	0/3264
8	L6	0.43	0/1762	0.51	0/2362
9	L7	0.49	0/1911	0.50	0/2549
10	aa	0.43	0/1910	0.50	0/2569
11	L9	0.44	0/1536	0.50	0/2063
12	10	0.45	0/1702	0.50	0/2272
13	11	0.37	0/1386	0.51	0/1852
14	13	0.44	0/1732	0.47	0/2316
15	14	0.45	0/1159	0.50	0/1547
16	15	0.55	0/1746	0.55	0/2338
17	bb	0.50	0/1662	0.50	0/2222
18	17	0.51	0/1269	0.53	0/1700
19	19	0.43	0/1341	0.47	0/1776
20	20	0.50	0/1501	0.51	0/2012
21	21	0.48	0/1326	0.50	0/1770
22	22	0.33	0/824	0.52	0/1104
23	24	0.45	0/542	0.45	0/720
24	cc	0.46	0/984	0.48	0/1323
25	26	0.46	0/1133	0.49	0/1504
26	27	0.44	0/1130	0.50	1/1507 (0.1%)
27	dd	0.51	0/1191	0.52	0/1590
28	29	0.38	0/861	0.46	0/1138
29	30	0.39	0/772	0.41	0/1034
30	31	0.48	0/904	0.51	0/1216
31	32	0.53	0/1072	0.52	0/1429
32	ee	0.54	0/895	0.56	2/1198 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	34	0.45	0/917	0.49	0/1220
34	35	0.44	0/1021	0.51	0/1348
35	36	0.42	0/842	0.47	0/1112
36	37	0.50	0/721	0.50	0/952
37	38	0.36	0/575	0.47	0/761
38	39	0.48	0/459	0.49	0/608
39	40	0.40	0/435	0.48	0/575
40	42	0.46	0/865	0.49	0/1140
41	ff	0.47	0/718	0.54	0/953
42	gg	0.46	0/1007	0.47	0/1349
43	s	0.24	0/1531	0.47	0/2064
44	t	0.21	0/1175	0.48	0/1582
45	EB	0.26	0/2979	0.41	0/4000
46	u	0.21	0/1681	0.47	0/2255
47	Q	0.53	0/1539	0.59	0/2054
48	ES	0.19	0/1609	0.39	0/2502
49	28	0.53	5/83635 (0.0%)	0.44	5/130433 (0.0%)
50	25	0.51	0/1048	0.51	0/1402
All	All	0.49	5/158445 (0.0%)	0.46	9/232297 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
49	28	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	28	3945	A	O3'-P	22.43	1.94	1.61
49	28	3940	U	O3'-P	-20.84	1.29	1.61
49	28	2024	G	O3'-P	8.16	1.73	1.61
49	28	3715	U	C5-C6	6.08	1.46	1.34
49	28	2026	A	O3'-P	-5.14	1.53	1.61

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L4	340	ILE	N-CA-C	-9.03	104.48	111.62
49	28	2024	G	P-O3'-C3'	-6.91	109.84	120.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	27	26	VAL	N-CA-C	-6.71	106.96	113.53
49	28	2024	G	OP2-P-O3'	5.95	125.85	108.00
32	ee	106	TYR	CA-C-N	-5.52	111.39	120.88
32	ee	106	TYR	C-N-CA	-5.52	111.39	120.88
49	28	2024	G	O3'-P-O5'	-5.36	95.96	104.00
49	28	48	G	P-O3'-C3'	5.15	127.93	120.20
49	28	1329	G	C4'-C3'-O3'	5.09	120.63	113.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
49	28	3941	G	Sidechain
49	28	3944	G	Sidechain
49	28	3945	A	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	v	6323	0	6409	184	0
2	58	3208	0	1629	52	0
3	5	2558	0	1296	28	0
4	L8	1899	0	1993	55	0
5	L3	3173	0	3310	70	0
6	L4	2884	0	3053	56	0
7	L5	2392	0	2424	50	0
8	L6	1729	0	1887	50	0
9	L7	1875	0	1995	38	0
10	aa	1879	0	2027	45	0
11	L9	1517	0	1597	44	0
12	10	1664	0	1712	24	0
13	11	1363	0	1399	30	0
14	13	1701	0	1820	25	0
15	14	1138	0	1211	33	0
16	15	1701	0	1749	39	0
17	bb	1630	0	1778	48	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	17	1243	0	1274	25	0
19	19	1325	0	1457	18	0
20	20	1462	0	1508	39	0
21	21	1298	0	1366	30	0
22	22	810	0	833	18	0
23	24	529	0	541	7	0
24	cc	967	0	1040	15	0
25	26	1116	0	1205	13	0
26	27	1107	0	1182	23	0
27	dd	1162	0	1209	33	0
28	29	848	0	920	11	0
29	30	762	0	794	13	0
30	31	889	0	930	18	0
31	32	1054	0	1147	27	0
32	ee	876	0	912	20	0
33	34	907	0	998	16	0
34	35	1013	0	1147	18	0
35	36	831	0	916	19	0
36	37	706	0	737	13	0
37	38	569	0	637	28	0
38	39	447	0	480	7	0
39	40	429	0	469	5	0
40	42	852	0	924	20	0
41	ff	708	0	756	17	0
42	gg	991	0	1044	14	0
43	s	1508	0	1564	44	0
44	t	1161	0	1218	36	0
45	EB	2932	0	2967	71	0
46	u	1655	0	1760	62	0
47	Q	1515	0	1634	42	0
48	ES	1444	0	735	45	0
49	28	74767	0	37769	906	0
50	25	1034	0	1097	17	0
51	v	28	0	12	4	0
52	34	1	0	0	0	0
52	37	1	0	0	0	0
52	ff	1	0	0	0	0
All	All	147582	0	110471	2255	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 9.

All (2255) 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)
41:ff:42:CYS:HB3	41:ff:60:CYS:SG	1.82	1.19
49:28:2638:G:H1	49:28:2697:A:N6	1.48	1.11
49:28:2007:G:N2	49:28:2012:A:H62	1.53	1.04
49:28:2007:G:H21	49:28:2012:A:N6	1.54	1.03
49:28:1398:A:H62	49:28:1419:G:N2	1.58	0.99
49:28:2638:G:N2	49:28:2697:A:N1	2.12	0.96
11:L9:41:ILE:HG21	11:L9:73:ILE:HD11	1.51	0.93
49:28:2647:A:H62	49:28:2686:G:H8	1.14	0.93
49:28:1398:A:N6	49:28:1419:G:N2	2.17	0.91
49:28:3715:U:O4	49:28:3738:G:O6	1.87	0.91
1:v:676:LYS:HZ3	1:v:680:VAL:HG21	1.35	0.91
49:28:3715:U:H5	49:28:3738:G:H1	1.12	0.90
49:28:1398:A:N6	49:28:1419:G:H21	1.69	0.90
19:19:60:ARG:HH12	49:28:2615:C:H5'	1.34	0.89
49:28:4887:C:H42	49:28:4932:U:H3	1.19	0.88
1:v:84:ASN:HB3	1:v:249:ARG:HH12	1.37	0.88
48:ES:3239:G:H2'	48:ES:3240:A:H8	1.39	0.86
49:28:2627:C:H41	49:28:4649:G:H1	1.25	0.85
30:31:57:MET:HG3	30:31:90:ARG:HE	1.41	0.85
49:28:2638:G:H1	49:28:2697:A:H61	0.85	0.85
48:ES:2947:G:H1	48:ES:3247:A:H2	1.22	0.85
39:40:92:THR:HG22	39:40:94:ASN:H	1.42	0.84
10:aa:111:PRO:HD2	10:aa:114:ILE:HD12	1.59	0.83
1:v:120:ARG:HH22	1:v:149:GLU:HG2	1.44	0.83
40:42:61:LYS:HD3	40:42:87:ARG:HH12	1.43	0.83
48:ES:2908:U:O2	48:ES:3586:G:N2	2.12	0.83
1:v:229:ALA:HB2	1:v:257:MET:HE1	1.59	0.82
1:v:486:THR:HG22	1:v:488:PHE:H	1.44	0.82
46:u:59:PRO:HB2	46:u:170:GLY:H	1.42	0.82
46:u:39:LYS:HE2	46:u:200:ASN:HA	1.62	0.81
48:ES:2947:G:O6	48:ES:3247:A:N1	2.14	0.80
42:gg:32:LEU:HD23	42:gg:32:LEU:H	1.45	0.80
49:28:3715:U:H5	49:28:3738:G:N1	1.80	0.79
8:L6:62:SER:HB2	49:28:1236:C:O2'	1.83	0.79
6:L4:323:ARG:HG3	49:28:1280:C:H2'	1.64	0.79
29:30:38:ILE:HG21	29:30:63:TYR:HB3	1.64	0.78
45:EB:181:PRO:HA	45:EB:230:VAL:HA	1.66	0.78
9:L7:97:ILE:HD11	47:Q:4:ASP:HB2	1.66	0.78
49:28:2557:G:H1	49:28:2570:U:H3	1.33	0.77
49:28:4095:G:H1	49:28:4113:U:H3	1.32	0.77
49:28:2845:A:H61	49:28:3843:C:H42	1.30	0.77
17:bb:60:LYS:HE2	49:28:2046:G:H5'	1.68	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:21:87:LYS:HZ2	49:28:4305:G:H1	1.31	0.76
49:28:4413:C:H5	49:28:4429:C:H42	1.33	0.76
4:L8:82:ILE:HD11	4:L8:99:GLY:HA3	1.67	0.76
37:38:33:LYS:HG2	37:38:46:VAL:HG22	1.67	0.76
1:v:583:VAL:HG23	1:v:608:PRO:HG3	1.66	0.76
20:20:34:ALA:HB1	20:20:39:VAL:HG23	1.69	0.75
49:28:983:C:H42	49:28:1071:C:H42	1.33	0.75
5:L3:220:ILE:HG12	5:L3:278:THR:HG23	1.68	0.75
49:28:4897:G:H2'	49:28:4898:G:H8	1.51	0.75
26:27:46:ILE:HD11	26:27:49:TYR:HA	1.68	0.75
23:24:9:SER:HB3	23:24:11:TYR:HD1	1.53	0.74
15:14:89:THR:HG22	15:14:91:TRP:H	1.52	0.74
49:28:3599:A:H2'	49:28:3600:G:H8	1.53	0.74
16:15:125:SER:HB3	49:28:3937:C:H1'	1.70	0.74
48:ES:2949:U:H3	48:ES:3245:G:H1	1.33	0.74
3:5:59:G:H4'	7:L5:267:ASN:HD21	1.53	0.73
16:15:44:ARG:HH11	16:15:47:LYS:HB2	1.51	0.73
36:37:21:ARG:HH21	36:37:39:TYR:HA	1.52	0.73
49:28:4967:A:H2'	49:28:4968:A:H8	1.53	0.73
49:28:3910:C:H2'	49:28:3911:C:C6	2.24	0.73
5:L3:94:GLU:HB2	5:L3:158:GLN:HG3	1.71	0.73
49:28:4967:A:H2'	49:28:4968:A:C8	2.23	0.73
47:Q:108:ARG:HH21	49:28:1354:A:H5'	1.53	0.73
45:EB:12:ILE:HD11	45:EB:221:HIS:HA	1.70	0.73
49:28:2786:C:H5''	49:28:2787:A:H5'	1.69	0.73
43:s:120:GLU:HG3	43:s:159:GLN:HE22	1.53	0.73
49:28:3736:A:H2'	49:28:3737:A:C8	2.24	0.73
30:31:23:ARG:HH22	49:28:5058:A:H5'	1.54	0.72
1:v:516:ASP:HB3	1:v:519:LYS:HD3	1.70	0.72
49:28:4092:G:H2'	49:28:4093:G:H8	1.54	0.72
7:L5:287:PHE:HZ	12:10:214:SER:HB3	1.53	0.72
7:L5:90:VAL:HG11	7:L5:225:GLN:HB3	1.69	0.71
42:gg:103:HIS:HD2	42:gg:106:LEU:HD22	1.54	0.71
27:dd:77:LYS:HE2	49:28:1502:G:H22	1.54	0.71
49:28:4635:A:H8	49:28:5048:A:H61	1.34	0.71
21:21:69:GLN:H	21:21:69:GLN:HE21	1.37	0.71
1:v:394:LEU:HA	1:v:419:GLY:HA3	1.70	0.71
46:u:68:LEU:HB2	46:u:85:MET:HB3	1.73	0.71
47:Q:82:VAL:HG12	47:Q:84:GLY:H	1.56	0.71
46:u:69:GLY:HA2	46:u:113:SER:HB3	1.72	0.71
31:32:22:ARG:HH11	31:32:31:ILE:HG23	1.56	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:2553:A:H2	49:28:2765:A:H62	1.38	0.70
49:28:4067:U:H2'	49:28:4068:U:C6	2.26	0.70
47:Q:67:ILE:HD12	47:Q:96:PRO:HD2	1.74	0.70
31:32:22:ARG:HE	31:32:36:ARG:HG3	1.57	0.70
6:L4:67:TRP:HB3	6:L4:71:ARG:HD3	1.73	0.70
44:t:97:ASN:HB3	44:t:99:LYS:HE2	1.73	0.70
30:31:64:ILE:HD11	49:28:2373:C:H4'	1.72	0.70
1:v:103:ILE:HD11	1:v:122:THR:HB	1.74	0.70
11:L9:174:LYS:HG3	49:28:4477:A:H4'	1.73	0.70
49:28:2639:U:H2'	49:28:2694:G:H1	1.56	0.70
49:28:4127:A:HO2'	49:28:4128:A:H8	1.36	0.70
1:v:218:LEU:HD13	51:v:900:GDP:H2'	1.74	0.69
49:28:1073:G:H1	49:28:1238:A:H2	1.39	0.69
49:28:2007:G:H21	49:28:2012:A:H62	0.76	0.69
1:v:152:LYS:HD3	1:v:359:PRO:HD3	1.74	0.69
1:v:267:ASP:HA	1:v:285:LEU:HD11	1.74	0.69
45:EB:159:PRO:HD3	45:EB:325:LEU:HD11	1.74	0.69
27:dd:85:GLN:HE22	49:28:508:G:H21	1.40	0.69
49:28:1198:G:H2'	49:28:1199:G:C8	2.28	0.69
45:EB:158:LYS:HG2	45:EB:161:ASN:HB2	1.74	0.69
49:28:4886:C:H42	49:28:4933:C:H42	1.39	0.69
8:L6:216:THR:H	8:L6:219:TYR:HB3	1.58	0.69
16:15:44:ARG:NH1	16:15:47:LYS:HB2	2.07	0.69
49:28:2627:C:H5	49:28:4649:G:H22	1.36	0.69
1:v:504:VAL:HG12	1:v:505:VAL:HG23	1.75	0.69
14:13:55:ILE:HD11	14:13:96:ILE:HG12	1.75	0.69
48:ES:2950:G:O6	48:ES:3244:U:O4	2.10	0.69
8:L6:181:PRO:HB2	8:L6:184:LEU:HG	1.75	0.68
48:ES:2949:U:O4	48:ES:3245:G:O6	2.10	0.68
16:15:159:ARG:HB3	16:15:164:LEU:HB2	1.74	0.68
20:20:35:PRO:HD2	20:20:39:VAL:HG21	1.74	0.68
49:28:1461:C:H2'	49:28:1462:A:H8	1.58	0.68
1:v:480:VAL:HG22	1:v:481:LYS:HG3	1.75	0.68
5:L3:223:THR:HB	5:L3:275:HIS:H	1.59	0.68
6:L4:323:ARG:HH12	49:28:977:C:H1'	1.58	0.68
5:L3:128:LYS:HG3	49:28:4966:A:H5'	1.75	0.68
48:ES:2908:U:H3	48:ES:3586:G:H1	1.42	0.68
1:v:594:LYS:HE2	1:v:856:ASP:HB3	1.76	0.68
46:u:52:THR:HG22	46:u:156:LYS:HB3	1.75	0.68
49:28:3848:U:H2'	49:28:3849:A:H8	1.58	0.68
4:L8:117:GLU:HB2	4:L8:162:ASN:HB2	1.75	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L4:140:LYS:HE2	6:L4:245:HIS:HB2	1.75	0.68
11:L9:48:LEU:HD21	11:L9:56:ARG:HD2	1.76	0.68
49:28:3934:G:H2'	49:28:3935:C:C6	2.29	0.68
1:v:400:LYS:HD3	1:v:401:MET:H	1.59	0.68
11:L9:120:GLU:HG2	49:28:4611:A:H2	1.59	0.68
37:38:26:LYS:HE2	49:28:2696:A:H5'	1.74	0.68
49:28:3598:C:H2'	49:28:3599:A:C8	2.29	0.68
49:28:3910:C:H2'	49:28:3911:C:H6	1.58	0.67
11:L9:59:LYS:HE3	11:L9:66:GLU:HB3	1.76	0.67
8:L6:165:VAL:HG11	8:L6:178:VAL:HG13	1.75	0.67
46:u:67:VAL:HG12	46:u:111:LEU:HB3	1.75	0.67
46:u:99:LEU:HA	46:u:102:LYS:HE2	1.75	0.67
49:28:1818:G:O2'	49:28:1819:G:H5'	1.93	0.67
49:28:138:G:H2'	49:28:139:G:C8	2.28	0.67
46:u:196:LYS:HG3	46:u:200:ASN:HB2	1.77	0.67
48:ES:2912:G:N1	48:ES:3282:U:N3	2.38	0.67
14:13:142:GLU:HA	14:13:145:LYS:HE2	1.75	0.67
37:38:12:LEU:HB3	37:38:16:ARG:HH12	1.59	0.67
49:28:3734:U:H2'	49:28:3735:G:O4'	1.95	0.67
1:v:663:THR:HG23	1:v:703:ASP:HA	1.76	0.67
49:28:2587:A:H5'	49:28:2770:C:H5'	1.77	0.67
49:28:4949:G:H4'	49:28:4950:U:H5'	1.75	0.67
25:26:8:THR:HG21	25:26:13:LYS:HD2	1.77	0.67
17:bb:27:VAL:HG13	17:bb:98:ALA:HB1	1.75	0.67
49:28:129:C:H2'	49:28:130:C:C6	2.30	0.67
8:L6:152:ILE:HD13	8:L6:274:LEU:HD21	1.76	0.66
45:EB:32:LEU:HA	45:EB:35:LEU:HD23	1.76	0.66
1:v:754:GLN:HG2	1:v:755:VAL:HG13	1.75	0.66
5:L3:240:LEU:HB3	5:L3:244:THR:HG21	1.77	0.66
8:L6:277:VAL:HG11	32:ee:2:SER:HB3	1.75	0.66
31:32:126:ASN:HB2	31:32:129:LEU:HD11	1.76	0.66
48:ES:3244:U:H2'	48:ES:3245:G:H8	1.59	0.66
49:28:1332:C:H2'	49:28:1333:A:H8	1.59	0.66
49:28:4915:G:H2'	49:28:4916:G:H8	1.60	0.66
46:u:171:HIS:CD2	46:u:173:LYS:HG2	2.30	0.66
6:L4:60:HIS:HE1	6:L4:100:ARG:HD3	1.61	0.66
49:28:4594:U:H2'	49:28:4595:G:H8	1.60	0.66
49:28:4887:C:N4	49:28:4932:U:H3	1.91	0.66
13:11:15:LEU:HD21	13:11:134:LEU:HD13	1.77	0.66
49:28:2016:C:H2'	49:28:2017:A:H8	1.61	0.66
49:28:3934:G:H2'	49:28:3935:C:H6	1.59	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L8:181:LYS:HB2	49:28:1577:G:C5	2.31	0.66
44:t:10:ILE:HG23	44:t:65:GLN:HG3	1.78	0.66
1:v:839:ARG:CZ	1:v:846:GLU:HA	2.27	0.66
42:gg:90:LEU:HG	42:gg:111:ILE:HG23	1.77	0.66
10:aa:170:ARG:HH12	10:aa:174:LYS:HB2	1.60	0.65
11:L9:106:GLN:HB2	11:L9:111:LEU:HB3	1.79	0.65
12:10:95:HIS:HD2	12:10:128:ARG:HD3	1.61	0.65
48:ES:2950:G:H1	48:ES:3244:U:H3	1.43	0.65
49:28:25:A:H2'	49:28:26:C:H6	1.61	0.65
49:28:3641:U:H5	49:28:3646:A:N7	1.93	0.65
44:t:59:THR:HG23	44:t:74:VAL:HB	1.78	0.65
15:14:57:LEU:HD23	15:14:57:LEU:H	1.62	0.65
7:L5:211:LEU:HB3	7:L5:219:TYR:HB2	1.78	0.65
14:13:21:ARG:HB3	16:15:197:THR:HG22	1.77	0.65
49:28:2457:G:H21	49:28:3672:G:N2	1.95	0.65
50:25:43:LYS:HD3	50:25:60:MET:HE3	1.78	0.65
49:28:1806:G:H2'	49:28:1807:C:H6	1.61	0.65
49:28:2448:G:H2'	49:28:2449:A:C8	2.32	0.65
4:L8:83:HIS:HB3	41:ff:64:VAL:HG22	1.79	0.65
49:28:4994:G:H2'	49:28:4995:U:H6	1.61	0.65
26:27:53:VAL:HG21	26:27:62:ILE:HG23	1.78	0.65
49:28:1461:C:H2'	49:28:1462:A:C8	2.32	0.65
4:L8:137:ILE:HD11	4:L8:149:LYS:HB3	1.77	0.64
48:ES:3248:C:H2'	48:ES:3249:G:H8	1.62	0.64
49:28:4915:G:H2'	49:28:4916:G:C8	2.32	0.64
35:36:25:ARG:NH1	49:28:159:C:H5'	2.12	0.64
46:u:171:HIS:H	46:u:174:MET:HE3	1.62	0.64
12:10:87:ILE:HG12	12:10:138:ILE:HG12	1.79	0.64
32:ee:78:HIS:HB2	32:ee:85:ARG:HG3	1.79	0.64
46:u:100:VAL:HG11	46:u:128:LEU:HD13	1.80	0.64
49:28:2486:G:H2'	49:28:2487:G:C8	2.31	0.64
6:L4:266:THR:HG22	6:L4:269:LYS:HB3	1.79	0.64
49:28:752:G:H1	49:28:911:U:H3	1.45	0.64
49:28:3861:A:H2'	49:28:3862:A:C8	2.33	0.64
16:15:50:ARG:HH11	49:28:278:G:H4'	1.63	0.64
18:17:69:ARG:HH22	49:28:4568:A:H2	1.46	0.64
44:t:137:GLN:HE21	49:28:1993:C:H1'	1.63	0.64
49:28:709:C:H1'	49:28:4942:C:H5	1.62	0.64
1:v:1:MET:HE1	1:v:5:THR:HG22	1.80	0.64
6:L4:22:VAL:HG22	6:L4:258:ARG:HE	1.62	0.64
34:35:91:MET:HA	34:35:94:ARG:HG3	1.79	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L5:67:ALA:HA	7:L5:72:ASP:HB3	1.79	0.64
8:L6:165:VAL:HG13	8:L6:180:GLY:N	2.13	0.64
49:28:2492:C:H2'	49:28:2493:G:H8	1.61	0.64
1:v:396:MET:HE1	1:v:472:LEU:HD11	1.79	0.63
12:10:38:ARG:HD3	12:10:83:ASP:HB2	1.79	0.63
37:38:35:LYS:HB3	37:38:42:LEU:HD11	1.79	0.63
49:28:4618:G:H5''	50:25:15:ARG:HB3	1.78	0.63
45:EB:75:ALA:HB2	45:EB:113:HIS:HB3	1.78	0.63
49:28:914:U:H2'	49:28:915:A:H5''	1.79	0.63
49:28:2557:G:O6	49:28:2570:U:O4	2.15	0.63
49:28:4385:A:H4'	49:28:4386:C:H5''	1.81	0.63
49:28:5034:A:H2'	49:28:5035:U:O4'	1.98	0.63
2:58:141:C:H2'	2:58:142:U:C6	2.34	0.63
10:aa:139:VAL:HG11	10:aa:238:LYS:HD2	1.81	0.63
17:bb:10:ASP:HB2	17:bb:117:ARG:HB3	1.79	0.63
16:15:184:ILE:HD12	49:28:99:A:H5''	1.79	0.63
44:t:53:TRP:HE3	44:t:56:LEU:HD12	1.64	0.63
49:28:4378:A:O2'	49:28:4379:A:H2'	1.98	0.63
7:L5:51:MET:HE3	7:L5:105:LEU:HD23	1.81	0.62
45:EB:349:VAL:HG11	45:EB:355:LYS:HD3	1.81	0.62
49:28:711:A:H2'	49:28:712:C:C6	2.34	0.62
1:v:507:VAL:HG21	1:v:554:LEU:HD21	1.81	0.62
49:28:1984:A:H2'	49:28:2011:C:H5'	1.82	0.62
6:L4:169:LEU:HD11	6:L4:173:LYS:HE2	1.80	0.62
13:11:10:ASN:HB3	13:11:13:ARG:HG3	1.80	0.62
49:28:2844:A:O2'	49:28:4631:G:H4'	1.99	0.62
49:28:4260:U:H2'	49:28:4261:C:C6	2.35	0.62
49:28:4994:G:H2'	49:28:4995:U:C6	2.35	0.62
1:v:119:LEU:HB3	1:v:120:ARG:HH21	1.64	0.62
12:10:95:HIS:CD2	12:10:128:ARG:HD3	2.35	0.62
49:28:2480:G:H2'	49:28:2481:G:H8	1.63	0.62
14:13:8:MET:HG3	47:Q:166:TYR:HB3	1.82	0.62
46:u:86:ASP:HB3	46:u:88:GLU:HG3	1.82	0.62
12:10:36:LEU:HD11	12:10:87:ILE:HD12	1.81	0.62
27:dd:87:ARG:HH21	47:Q:93:GLN:HG2	1.65	0.62
35:36:62:LYS:HE3	35:36:94:LEU:HD11	1.82	0.62
49:28:978:G:N2	49:28:1277:G:H22	1.98	0.62
1:v:449:ARG:HB3	1:v:473:VAL:HB	1.80	0.61
49:28:2845:A:H61	49:28:3843:C:N4	1.97	0.61
32:ee:46:ARG:HH21	32:ee:89:ARG:HH22	1.46	0.61
49:28:1195:G:H2'	49:28:1196:G:H8	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:738:PRO:HG2	1:v:824:PRO:HD2	1.81	0.61
4:L8:23:ARG:HA	4:L8:52:PRO:HD2	1.81	0.61
17:bb:36:VAL:HG21	17:bb:108:ILE:HG23	1.82	0.61
44:t:80:LEU:HD12	44:t:112:ILE:HG12	1.81	0.61
49:28:137:G:H2'	49:28:138:G:C8	2.35	0.61
49:28:3848:U:H2'	49:28:3849:A:C8	2.34	0.61
44:t:128:THR:HA	44:t:131:GLU:HG2	1.83	0.61
49:28:4927:G:H3'	49:28:4928:C:O2	2.01	0.61
49:28:5016:A:N1	49:28:5033:G:N2	2.38	0.61
12:10:190:LEU:HB3	12:10:197:VAL:HG21	1.83	0.61
43:s:57:LYS:HB3	43:s:60:MET:HB3	1.82	0.61
43:s:134:LYS:HE3	43:s:177:MET:HE3	1.82	0.61
5:L3:41:VAL:HA	5:L3:187:GLY:HA3	1.82	0.61
49:28:4729:A:H5'	49:28:4965:U:H1'	1.82	0.61
11:L9:94:SER:HB3	11:L9:142:ASP:HB3	1.83	0.61
25:26:30:MET:HB3	25:26:101:PRO:HG2	1.82	0.61
37:38:8:ILE:HD11	37:38:56:LEU:HD13	1.82	0.61
1:v:350:LEU:HD13	1:v:354:ILE:HD13	1.82	0.61
6:L4:138:MET:HE1	6:L4:145:GLU:HG3	1.83	0.61
48:ES:2953:C:H2'	48:ES:2954:G:C8	2.36	0.61
49:28:2465:C:H1'	49:28:3672:G:H22	1.65	0.61
49:28:4940:C:H5''	49:28:4941:G:H5''	1.82	0.61
49:28:1196:G:H2'	49:28:1197:C:C6	2.35	0.60
49:28:3717:A:H2'	49:28:3718:A:C8	2.35	0.60
1:v:678:SER:HB3	1:v:721:ILE:HG21	1.83	0.60
3:5:52:C:H1'	13:11:12:MET:HE2	1.82	0.60
48:ES:2955:A:H2	48:ES:3239:G:H1	1.49	0.60
49:28:1978:C:H3'	49:28:1979:A:H8	1.66	0.60
11:L9:111:LEU:HD11	11:L9:125:ARG:HG2	1.82	0.60
45:EB:287:LYS:HZ2	45:EB:287:LYS:H	1.48	0.60
46:u:10:LEU:HD13	46:u:183:ILE:HD11	1.83	0.60
49:28:2669:C:H2'	49:28:2670:C:O4'	2.02	0.60
6:L4:142:HIS:CD2	6:L4:249:PHE:H	2.19	0.60
35:36:3:LEU:HD12	35:36:4:ARG:H	1.65	0.60
49:28:1195:G:H2'	49:28:1196:G:C8	2.36	0.60
5:L3:371:THR:HG21	23:24:17:HIS:CE1	2.36	0.60
20:20:127:MET:HE1	21:21:155:PRO:HA	1.83	0.60
37:38:69:LEU:HD21	49:28:2696:A:C5	2.37	0.60
49:28:4448:G:H5''	49:28:4449:A:H5'	1.83	0.60
49:28:4751:G:H1	49:28:4948:C:H5	1.49	0.60
5:L3:317:LEU:HB2	5:L3:372:SER:HB2	1.84	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:ES:2912:G:H1	48:ES:3282:U:H3	1.34	0.60
49:28:1298:C:H2'	49:28:1299:G:C8	2.36	0.60
8:L6:291:PHE:HE1	32:ee:110:ILE:HG21	1.66	0.60
19:19:105:LEU:HD22	19:19:135:LYS:HG3	1.82	0.60
49:28:4897:G:H2'	49:28:4898:G:C8	2.33	0.60
3:5:120:U:H3'	7:L5:259:ARG:HE	1.66	0.60
19:19:4:LEU:HD11	19:19:29:THR:HG23	1.83	0.60
49:28:1339:U:H2'	49:28:1340:C:C6	2.37	0.60
49:28:3711:A:H2'	49:28:3712:A:O4'	2.02	0.60
49:28:4635:A:H8	49:28:5048:A:N6	2.00	0.60
6:L4:321:ASN:OD1	6:L4:324:ILE:HG12	2.02	0.60
9:L7:126:LYS:HB2	21:21:133:ALA:HB3	1.84	0.60
50:25:13:LYS:HB2	50:25:128:LEU:HD21	1.84	0.60
7:L5:33:ARG:HH11	21:21:27:LEU:HD12	1.67	0.60
49:28:4537:C:H2'	49:28:4538:G:C8	2.36	0.60
4:L8:183:GLY:HA2	49:28:1613:A:H5''	1.83	0.59
40:42:69:ARG:HG2	40:42:82:MET:HE1	1.84	0.59
42:gg:108:MET:O	42:gg:112:ARG:HG2	2.01	0.59
5:L3:229:LYS:HG3	5:L3:272:LYS:HD3	1.83	0.59
6:L4:77:PRO:O	6:L4:90:GLY:HA2	2.02	0.59
8:L6:48:ARG:HB3	8:L6:67:ARG:HD3	1.83	0.59
8:L6:158:GLY:HA2	49:28:4942:C:H5''	1.83	0.59
27:dd:32:ARG:HD2	49:28:37:U:H4'	1.85	0.59
43:s:25:PRO:HD2	43:s:92:LYS:HD2	1.82	0.59
44:t:134:GLY:HA2	44:t:137:GLN:NE2	2.17	0.59
1:v:830:ARG:NH1	1:v:833:GLN:HG2	2.17	0.59
44:t:20:GLY:HA2	44:t:47:ALA:O	2.02	0.59
44:t:119:ARG:NH1	44:t:121:LEU:H	2.00	0.59
49:28:1824:G:H2'	49:28:1825:A:C8	2.38	0.59
1:v:767:ARG:HH12	1:v:820:LEU:HD13	1.67	0.59
15:14:129:LYS:O	15:14:132:ARG:HG3	2.02	0.59
20:20:83:ARG:HB2	20:20:127:MET:HE3	1.84	0.59
49:28:2639:U:H2'	49:28:2694:G:N1	2.17	0.59
7:L5:146:LEU:HD22	49:28:4323:A:C2	2.37	0.59
8:L6:53:VAL:HG11	49:28:947:C:H5''	1.84	0.59
17:bb:121:PRO:HD3	20:20:168:THR:HG22	1.85	0.59
9:L7:46:ARG:HH11	9:L7:46:ARG:HG3	1.67	0.59
10:aa:203:LYS:HE2	10:aa:230:MET:HE2	1.85	0.59
37:38:49:ASP:HB3	37:38:52:LYS:HB2	1.83	0.59
47:Q:63:LEU:O	47:Q:67:ILE:HG12	2.03	0.59
49:28:2409:U:H4'	49:28:2428:A:H4'	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L5:291:GLN:HE22	12:10:214:SER:HA	1.67	0.59
49:28:1348:U:H2'	49:28:1349:G:H8	1.68	0.59
5:L3:52:GLY:HA2	5:L3:341:LYS:HE3	1.85	0.59
46:u:195:LYS:HG3	46:u:196:LYS:HE3	1.84	0.59
15:14:39:ASP:HB2	15:14:47:ARG:HE	1.67	0.59
10:aa:139:VAL:HG21	10:aa:238:LYS:HG3	1.85	0.59
49:28:969:C:N4	49:28:2095:A:H61	2.00	0.59
49:28:1199:G:H2'	49:28:1200:G:H8	1.67	0.59
49:28:3652:A:H2'	49:28:3653:A:C8	2.38	0.59
49:28:4508:C:N3	49:28:4512:U:H5	2.01	0.59
49:28:325:U:H2'	49:28:326:C:C6	2.38	0.58
49:28:2495:U:H2'	49:28:2496:G:H8	1.67	0.58
1:v:830:ARG:HH11	1:v:833:GLN:HG2	1.67	0.58
8:L6:49:ASN:N	8:L6:64:MET:HE1	2.18	0.58
47:Q:181:ARG:HH22	49:28:1391:A:H5'	1.68	0.58
49:28:1598:C:H2'	49:28:1599:G:H8	1.67	0.58
49:28:2497:C:H2'	49:28:2498:C:H6	1.68	0.58
5:L3:57:VAL:HG22	5:L3:73:VAL:HG12	1.84	0.58
12:10:61:SER:HA	12:10:126:VAL:HG23	1.85	0.58
20:20:69:GLU:OE1	20:20:102:THR:HG23	2.03	0.58
25:26:52:ASP:O	25:26:110:LYS:HB2	2.03	0.58
30:31:22:THR:HG22	30:31:89:SER:HB2	1.85	0.58
44:t:108:GLU:HA	44:t:111:ASN:ND2	2.18	0.58
49:28:1970:A:H5''	49:28:1971:U:H5'	1.84	0.58
49:28:3715:U:C4	49:28:3738:G:O6	2.55	0.58
4:L8:20:VAL:HA	4:L8:23:ARG:HG3	1.85	0.58
16:15:143:ARG:HG3	34:35:99:GLU:OE1	2.04	0.58
31:32:22:ARG:NH1	31:32:31:ILE:HD12	2.19	0.58
49:28:1218:G:H2'	49:28:1219:G:C8	2.38	0.58
5:L3:56:ILE:HD11	5:L3:368:ILE:HG12	1.84	0.58
38:39:8:ARG:H	38:39:8:ARG:HD2	1.68	0.58
1:v:304:ILE:HD11	1:v:335:LEU:HG	1.84	0.58
6:L4:297:GLU:HA	6:L4:300:ARG:HH21	1.68	0.58
17:bb:185:VAL:HG22	17:bb:188:LYS:HG3	1.85	0.58
49:28:1308:C:H2'	49:28:1309:C:C6	2.38	0.58
49:28:1756:U:H2'	49:28:1757:U:C6	2.39	0.58
6:L4:78:ARG:HB3	6:L4:88:GLY:HA2	1.86	0.58
49:28:4739:C:H2'	49:28:4740:G:C8	2.39	0.58
11:L9:105:ILE:HD11	11:L9:136:VAL:HG23	1.84	0.58
20:20:80:ILE:HG23	20:20:126:ILE:HD13	1.86	0.58
45:EB:223:VAL:HG22	45:EB:324:LEU:HG	1.84	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1490:G:H2'	49:28:1491:A:H8	1.69	0.58
49:28:3648:A:H1'	49:28:3785:A:N6	2.19	0.58
40:42:6:LYS:HG2	40:42:93:LEU:HB3	1.86	0.58
48:ES:2955:A:N1	48:ES:3239:G:O6	2.37	0.58
49:28:4274:A:H2'	49:28:4275:G:H8	1.69	0.58
49:28:4537:C:H2'	49:28:4538:G:H8	1.67	0.58
16:15:49:ARG:HH12	49:28:152:U:P	2.27	0.58
37:38:34:PHE:CE1	37:38:47:ILE:HD11	2.39	0.58
49:28:257:C:H2'	49:28:258:G:C8	2.39	0.58
49:28:3611:A:H2	49:28:5016:A:H8	1.52	0.58
49:28:4935:C:H2'	49:28:4936:G:H8	1.69	0.58
2:58:5:U:H2'	2:58:6:C:H6	1.68	0.57
37:38:35:LYS:HE2	49:28:2696:A:H62	1.69	0.57
45:EB:56:ILE:HD11	45:EB:112:VAL:HB	1.86	0.57
19:19:79:GLY:O	49:28:3619:G:H4'	2.03	0.57
49:28:1298:C:H2'	49:28:1299:G:H8	1.68	0.57
49:28:2093:G:H22	49:28:2262:G:H1	1.51	0.57
5:L3:56:ILE:O	5:L3:73:VAL:HA	2.04	0.57
48:ES:3239:G:H2'	48:ES:3240:A:C8	2.30	0.57
49:28:1490:G:H2'	49:28:1491:A:C8	2.39	0.57
49:28:3861:A:H2'	49:28:3862:A:H8	1.69	0.57
1:v:488:PHE:HB3	1:v:491:ALA:HB2	1.87	0.57
4:L8:133:TYR:HB3	4:L8:168:VAL:HG12	1.86	0.57
49:28:2544:G:H5''	49:28:2545:U:H5	1.69	0.57
8:L6:61:ARG:HD3	49:28:1237:C:C2	2.39	0.57
10:aa:101:LYS:HB3	24:cc:42:THR:HG23	1.86	0.57
37:38:5:ILE:HD11	37:38:10:ASP:HB3	1.87	0.57
45:EB:22:LYS:HA	45:EB:333:ILE:HD11	1.86	0.57
36:37:46:LYS:HE2	36:37:54:LYS:HE2	1.86	0.57
49:28:2845:A:N6	49:28:3843:C:H42	2.00	0.57
49:28:3880:G:H2'	49:28:3881:G:C8	2.39	0.57
1:v:129:VAL:HG21	1:v:135:VAL:HG22	1.86	0.57
5:L3:95:THR:HG22	49:28:4910:A:H4'	1.86	0.57
6:L4:100:ARG:HG3	6:L4:101:MET:O	2.03	0.57
11:L9:41:ILE:HG23	11:L9:43:VAL:HG13	1.85	0.57
20:20:118:ARG:HE	49:28:2035:C:H5'	1.68	0.57
29:30:57:LYS:HD3	29:30:73:HIS:HE1	1.70	0.57
32:ee:50:VAL:HG22	32:ee:69:VAL:HG12	1.87	0.57
37:38:69:LEU:HD21	49:28:2696:A:C6	2.40	0.57
44:t:53:TRP:H	44:t:53:TRP:CD1	2.22	0.57
49:28:233:U:H2'	49:28:234:G:H8	1.68	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:2482:C:H2'	49:28:2483:G:H8	1.69	0.57
49:28:4274:A:H2'	49:28:4275:G:C8	2.39	0.57
40:42:61:LYS:HD3	40:42:87:ARG:NH1	2.18	0.57
46:u:148:VAL:HA	46:u:151:VAL:HG12	1.87	0.57
48:ES:2947:G:N1	48:ES:3247:A:C2	2.67	0.57
49:28:643:C:H2'	49:28:644:G:H8	1.69	0.57
49:28:1779:U:H2'	49:28:1780:A:C8	2.40	0.57
49:28:1806:G:H2'	49:28:1807:C:C6	2.40	0.57
12:10:118:ALA:O	49:28:1865:G:H5'	2.05	0.57
25:26:50:ARG:HB2	25:26:115:ARG:HH21	1.69	0.57
40:42:61:LYS:CD	40:42:87:ARG:HH12	2.15	0.57
49:28:4956:A:H8	49:28:4956:A:OP2	1.88	0.57
21:21:55:LYS:HE2	49:28:4217:G:OP1	2.05	0.56
33:34:74:VAL:HG21	49:28:2583:C:H5''	1.87	0.56
49:28:3599:A:H2'	49:28:3600:G:C8	2.38	0.56
2:58:78:G:O5'	2:58:78:G:H8	1.88	0.56
6:L4:292:ILE:HG23	47:Q:128:LEU:HD21	1.87	0.56
17:bb:194:ASP:O	17:bb:198:THR:HG23	2.05	0.56
45:EB:107:LYS:HD2	45:EB:318:GLN:HB2	1.87	0.56
45:EB:333:ILE:HG23	45:EB:334:THR:HG23	1.88	0.56
46:u:113:SER:HA	46:u:138:LEU:HD11	1.88	0.56
46:u:184:HIS:CE1	46:u:188:ASN:HD22	2.23	0.56
49:28:137:G:H2'	49:28:138:G:H8	1.70	0.56
49:28:2539:C:H2'	49:28:2540:C:C6	2.40	0.56
49:28:3662:A:H4'	49:28:3663:A:H5''	1.86	0.56
49:28:4493:U:H5	49:28:4512:U:HO2'	1.54	0.56
4:L8:209:HIS:CE1	4:L8:235:VAL:HG11	2.41	0.56
6:L4:76:ILE:HG13	6:L4:77:PRO:HD2	1.85	0.56
9:L7:153:ILE:HG13	9:L7:190:ILE:HG12	1.87	0.56
16:15:85:VAL:HG23	49:28:43:U:OP1	2.04	0.56
49:28:1292:C:H3'	49:28:1293:G:H21	1.70	0.56
49:28:2480:G:H2'	49:28:2481:G:C8	2.41	0.56
1:v:208:VAL:HG21	1:v:258:LYS:HD3	1.87	0.56
11:L9:63:ASN:H	11:L9:66:GLU:HG3	1.70	0.56
43:s:30:VAL:HB	43:s:189:ILE:HG22	1.88	0.56
49:28:2411:C:H2'	49:28:2412:A:C8	2.40	0.56
1:v:447:ILE:HD13	1:v:472:LEU:HB3	1.87	0.56
12:10:116:ARG:HG3	49:28:4195:G:OP1	2.06	0.56
18:17:116:HIS:HB3	18:17:149:ILE:HB	1.88	0.56
49:28:2497:C:H2'	49:28:2498:C:C6	2.40	0.56
49:28:3732:A:H2'	49:28:3733:A:C8	2.40	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:4273:A:H2'	49:28:4274:A:C8	2.41	0.56
9:L7:49:ILE:HD11	9:L7:184:ILE:HG13	1.87	0.56
10:aa:313:GLU:O	10:aa:317:LYS:HG2	2.04	0.56
21:21:51:GLY:HA3	21:21:92:ARG:HG3	1.87	0.56
22:22:84:LYS:HE3	22:22:102:VAL:HB	1.87	0.56
49:28:2482:C:H2'	49:28:2483:G:C8	2.40	0.56
49:28:2539:C:H2'	49:28:2540:C:H6	1.71	0.56
49:28:4260:U:H2'	49:28:4261:C:H6	1.70	0.56
1:v:167:LEU:HB3	1:v:169:LEU:HD22	1.87	0.56
5:L3:287:ILE:HG12	5:L3:331:VAL:HG12	1.88	0.56
40:42:43:ARG:HH12	49:28:294:G:P	2.29	0.56
48:ES:3244:U:H2'	48:ES:3245:G:C8	2.41	0.56
49:28:3775:A:H2'	49:28:3776:G:O4'	2.06	0.56
6:L4:290:SER:O	6:L4:294:LYS:HG2	2.06	0.56
41:ff:9:GLY:H	41:ff:27:LYS:HE2	1.71	0.56
49:28:1617:G:H1'	49:28:2513:A:N6	2.21	0.56
7:L5:15:ARG:CZ	49:28:1743:A:H1'	2.36	0.56
27:dd:26:ARG:HD2	49:28:1655:C:C5	2.41	0.56
36:37:2:THR:N	49:28:3642:A:HO2'	2.03	0.56
45:EB:202:ILE:HG12	45:EB:205:PRO:HB3	1.86	0.56
49:28:275:C:H2'	49:28:276:C:C6	2.40	0.56
49:28:1995:G:H2'	49:28:1996:C:C6	2.41	0.56
49:28:4584:A:H2'	49:28:4585:U:O4'	2.06	0.56
41:ff:74:THR:O	41:ff:78:THR:HG23	2.06	0.55
45:EB:29:ASN:HD21	45:EB:334:THR:HA	1.71	0.55
49:28:1198:G:H2'	49:28:1199:G:H8	1.71	0.55
49:28:1662:C:H2'	49:28:1663:C:C6	2.40	0.55
49:28:3920:U:H2'	49:28:3921:U:C6	2.41	0.55
50:25:18:LEU:HD13	50:25:54:ALA:HB3	1.88	0.55
5:L3:107:ALA:HB1	5:L3:202:GLU:HG3	1.89	0.55
9:L7:149:VAL:O	9:L7:153:ILE:HG12	2.06	0.55
10:aa:163:LYS:HD2	10:aa:166:ARG:HH12	1.72	0.55
13:11:95:ARG:H	13:11:98:ASN:HD22	1.54	0.55
45:EB:229:LEU:HG	45:EB:318:GLN:HG2	1.89	0.55
49:28:2601:A:C5	49:28:2743:A:H5''	2.41	0.55
3:5:117:G:OP2	7:L5:255:LYS:HE3	2.06	0.55
26:27:28:ASN:HB2	26:27:77:TYR:OH	2.06	0.55
6:L4:56:GLU:HG3	6:L4:57:LEU:HD22	1.88	0.55
9:L7:93:ARG:HE	9:L7:108:LEU:HD13	1.71	0.55
19:19:103:ARG:HD3	19:19:124:TYR:CE2	2.42	0.55
49:28:1333:A:H2'	49:28:1334:A:C8	2.41	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L6:122:GLU:HG3	31:32:7:LEU:HD22	1.89	0.55
14:13:158:ARG:HB3	49:28:1378:C:N3	2.22	0.55
16:15:8:GLN:OE1	49:28:278:G:H5''	2.05	0.55
17:bb:12:ARG:HH12	49:28:4761:G:H3'	1.71	0.55
17:bb:176:ARG:HD3	49:28:4769:G:H5'	1.88	0.55
49:28:1468:C:H2'	49:28:1469:C:H6	1.72	0.55
49:28:2503:G:H2'	49:28:2504:C:N1	2.22	0.55
49:28:3911:C:H2'	49:28:3912:U:H6	1.71	0.55
32:ee:65:ASN:HB2	32:ee:67:THR:HG22	1.89	0.55
36:37:22:CYS:HB3	36:37:37:CYS:SG	2.47	0.55
49:28:1893:C:H1'	49:28:1937:C:O2	2.06	0.55
7:L5:259:ARG:HH22	7:L5:262:LYS:HE2	1.72	0.55
14:13:64:VAL:HG23	14:13:67:HIS:NE2	2.21	0.55
17:bb:13:GLY:HA2	17:bb:42:ASN:HD21	1.70	0.55
40:42:4:VAL:HG23	40:42:93:LEU:HD13	1.89	0.55
48:ES:3247:A:H2'	48:ES:3248:C:H6	1.71	0.55
49:28:2624:G:H2'	49:28:2625:U:H6	1.71	0.55
2:58:4:C:H2'	2:58:5:U:C6	2.42	0.55
17:bb:37:ARG:HH22	49:28:4761:G:P	2.30	0.55
33:34:69:LYS:HG3	33:34:73:HIS:CD2	2.42	0.55
1:v:364:ALA:HA	1:v:367:TYR:CE2	2.41	0.55
18:17:118:GLN:HE22	49:28:423:G:H21	1.53	0.55
49:28:2503:G:H2'	49:28:2504:C:C6	2.42	0.55
5:L3:37:PRO:HA	5:L3:187:GLY:O	2.07	0.55
49:28:1566:C:H2'	49:28:1567:U:H6	1.72	0.55
49:28:4637:G:H2'	49:28:4638:U:C6	2.42	0.55
1:v:327:ASP:HA	1:v:330:LYS:HE2	1.89	0.54
17:bb:54:TYR:CD2	17:bb:145:VAL:HG21	2.41	0.54
49:28:2521:G:H2'	49:28:2522:G:C8	2.42	0.54
1:v:176:GLN:O	1:v:180:ARG:HG2	2.08	0.54
23:24:56:ARG:HG3	23:24:61:LYS:HB2	1.89	0.54
43:s:48:ARG:HH11	44:t:123:ARG:HD3	1.72	0.54
44:t:82:ILE:HD12	44:t:85:LEU:HB2	1.89	0.54
46:u:26:ARG:HH22	46:u:208:SER:HB2	1.72	0.54
49:28:1332:C:H2'	49:28:1333:A:C8	2.40	0.54
49:28:2654:C:H2'	49:28:2655:C:C6	2.42	0.54
49:28:3656:A:H2'	49:28:3657:U:H6	1.72	0.54
49:28:4395:U:H6	49:28:4395:U:H5'	1.72	0.54
9:L7:70:MET:O	9:L7:73:MET:HG2	2.08	0.54
9:L7:89:ALA:HB2	9:L7:124:LEU:HD21	1.90	0.54
30:31:23:ARG:NH2	49:28:5058:A:H5'	2.20	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:2632:U:H2'	49:28:2633:U:C6	2.42	0.54
49:28:4192:A:H2'	49:28:4193:C:H6	1.71	0.54
49:28:1218:G:H2'	49:28:1219:G:H8	1.71	0.54
7:L5:43:LYS:HE2	49:28:1817:U:H4'	1.88	0.54
18:17:125:MET:HB2	18:17:141:SER:HB3	1.89	0.54
27:dd:71:PRO:HG2	27:dd:108:TYR:HA	1.88	0.54
41:ff:38:THR:HA	41:ff:45:THR:HA	1.88	0.54
45:EB:192:GLN:HE21	45:EB:193:HIS:CD2	2.25	0.54
49:28:4092:G:H2'	49:28:4093:G:C8	2.38	0.54
49:28:4459:U:H2'	49:28:4460:U:C6	2.42	0.54
1:v:159:LYS:HD3	51:v:900:GDP:C2	2.42	0.54
2:58:123:U:H5'	2:58:124:U:C5	2.43	0.54
5:L3:224:LYS:HE3	5:L3:226:LYS:HZ1	1.72	0.54
43:s:14:PHE:HE2	43:s:60:MET:HG3	1.73	0.54
49:28:1239:C:O2'	49:28:1244:G:H5'	2.08	0.54
1:v:724:THR:HA	1:v:727:ARG:HG2	1.89	0.54
1:v:753:GLU:HB3	1:v:780:PRO:HB2	1.90	0.54
5:L3:53:MET:HG2	5:L3:77:THR:HG22	1.88	0.54
46:u:104:ALA:HB2	46:u:133:LYS:HE2	1.90	0.54
11:L9:12:ILE:HD12	11:L9:18:ILE:HG23	1.90	0.54
44:t:134:GLY:O	44:t:137:GLN:HG2	2.08	0.54
5:L3:77:THR:HG23	5:L3:335:GLY:O	2.08	0.54
8:L6:182:LEU:HD12	8:L6:186:ARG:HA	1.90	0.54
11:L9:16:VAL:HG21	11:L9:81:ILE:HG23	1.90	0.54
20:20:126:ILE:HD11	20:20:129:VAL:HG23	1.90	0.54
46:u:171:HIS:HD2	46:u:173:LYS:HG2	1.71	0.54
49:28:93:G:H2'	49:28:94:A:C8	2.43	0.54
49:28:2411:C:H2'	49:28:2412:A:H8	1.71	0.54
49:28:2492:C:H2'	49:28:2493:G:C8	2.41	0.54
4:L8:243:THR:O	49:28:3746:A:H5'	2.08	0.54
18:17:29:THR:HA	18:17:87:SER:OG	2.08	0.54
21:21:52:MET:HG2	21:21:95:HIS:CE1	2.42	0.54
46:u:55:LEU:HD21	46:u:59:PRO:HD3	1.90	0.54
49:28:1294:A:H5'	49:28:1296:G:N2	2.23	0.54
49:28:4188:U:H2'	49:28:4189:U:C6	2.43	0.54
2:58:4:C:H2'	2:58:5:U:H6	1.73	0.53
6:L4:137:VAL:HG21	6:L4:150:LEU:HD21	1.89	0.53
15:14:40:GLY:HA3	15:14:45:VAL:HB	1.90	0.53
40:42:98:LYS:HE3	49:28:4233:A:H4'	1.90	0.53
44:t:137:GLN:HB3	44:t:146:ARG:HE	1.72	0.53
46:u:5:VAL:HG22	46:u:9:THR:HG21	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:132:G:N3	49:28:133:C:H1'	2.23	0.53
49:28:2376:A:H2'	49:28:2377:C:C6	2.44	0.53
49:28:4523:A:H5''	49:28:4524:G:H5'	1.90	0.53
1:v:14:ASP:HA	1:v:465:PRO:HG2	1.90	0.53
1:v:527:LEU:HD11	1:v:561:LEU:HB3	1.89	0.53
7:L5:291:GLN:NE2	12:10:214:SER:HA	2.23	0.53
7:L5:184:ASP:OD2	7:L5:186:GLU:HG2	2.08	0.53
31:32:22:ARG:HE	31:32:36:ARG:CG	2.21	0.53
37:38:17:ARG:HH21	49:28:2773:G:H5'	1.73	0.53
45:EB:65:LYS:HB2	48:ES:3247:A:OP1	2.09	0.53
49:28:4897:G:N1	49:28:4923:U:O2	2.41	0.53
1:v:634:TYR:HA	1:v:637:GLU:HG2	1.90	0.53
9:L7:79:ASN:HA	21:21:143:THR:HG22	1.89	0.53
17:bb:166:ILE:HD13	17:bb:169:ARG:HH12	1.73	0.53
25:26:39:ARG:HD2	25:26:45:ARG:HD3	1.89	0.53
49:28:4548:A:H4'	49:28:4549:G:O5'	2.08	0.53
1:v:583:VAL:HG12	1:v:738:PRO:HA	1.91	0.53
6:L4:340:ILE:HD11	49:28:947:C:H5'	1.89	0.53
8:L6:157:THR:HG23	49:28:4942:C:H4'	1.90	0.53
11:L9:36:ARG:HD3	11:L9:38:PHE:CZ	2.44	0.53
14:13:169:ILE:HB	14:13:174:LYS:HE2	1.89	0.53
42:gg:46:ARG:HA	42:gg:70:GLN:HE22	1.72	0.53
43:s:18:ILE:HD12	43:s:68:HIS:CD2	2.43	0.53
45:EB:192:GLN:HG3	45:EB:193:HIS:HD2	1.72	0.53
48:ES:3248:C:H2'	48:ES:3249:G:C8	2.43	0.53
49:28:132:G:C2	49:28:133:C:H1'	2.43	0.53
49:28:1942:A:H2'	49:28:1943:A:C8	2.44	0.53
46:u:107:TYR:HB2	46:u:110:PHE:HE1	1.73	0.53
47:Q:75:ARG:HA	47:Q:78:LYS:HE3	1.91	0.53
49:28:25:A:H2'	49:28:26:C:C6	2.43	0.53
49:28:1727:U:H2'	49:28:1728:U:C6	2.44	0.53
50:25:78:PRO:HG2	50:25:106:VAL:O	2.09	0.53
1:v:379:ASP:O	1:v:383:MET:HG2	2.08	0.53
11:L9:60:TRP:CE3	20:20:153:PRO:HD2	2.44	0.53
13:11:152:GLY:O	13:11:156:ARG:HG3	2.07	0.53
49:28:1932:A:H2'	49:28:1933:G:C8	2.44	0.53
49:28:2015:U:H2'	49:28:2016:C:C6	2.44	0.53
1:v:561:LEU:HA	1:v:565:HIS:HB2	1.91	0.53
1:v:608:PRO:HB3	1:v:700:VAL:HG23	1.90	0.53
10:aa:105:THR:HG22	24:cc:41:ARG:HG3	1.91	0.53
28:29:114:ARG:HA	28:29:117:ARG:HB2	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:31:37:GLY:O	30:31:41:ARG:HG3	2.09	0.53
36:37:65:ARG:HG3	36:37:66:HIS:CD2	2.44	0.53
48:ES:3245:G:H2'	48:ES:3246:G:H8	1.72	0.53
10:aa:199:LEU:HD13	10:aa:205:ALA:HB2	1.90	0.53
16:15:85:VAL:HA	40:42:49:GLY:HA2	1.90	0.53
26:27:50:PRO:HD3	26:27:68:ILE:HG12	1.90	0.53
49:28:1168:G:H2'	49:28:1169:G:H8	1.74	0.53
49:28:1662:C:H2'	49:28:1663:C:H6	1.74	0.53
49:28:2757:A:H2'	49:28:2758:G:C8	2.44	0.53
49:28:4339:A:H2'	49:28:4340:U:H6	1.73	0.53
4:L8:147:ARG:HG2	4:L8:157:VAL:HG22	1.90	0.53
7:L5:83:LEU:HB3	7:L5:88:VAL:HB	1.91	0.53
20:20:45:TRP:CD1	20:20:56:LYS:HD3	2.44	0.53
21:21:17:ARG:HB2	21:21:22:HIS:ND1	2.24	0.53
30:31:53:ALA:HA	30:31:88:LEU:HD21	1.91	0.53
35:36:62:LYS:HG3	35:36:94:LEU:HD21	1.91	0.53
45:EB:64:PHE:H	48:ES:3246:G:H5''	1.74	0.53
48:ES:2950:G:O6	48:ES:3244:U:C4	2.62	0.53
49:28:2859:G:H2'	49:28:2860:C:H6	1.73	0.53
49:28:3736:A:H2'	49:28:3737:A:H8	1.73	0.53
49:28:3928:A:H2'	49:28:3929:G:O4'	2.08	0.53
49:28:4303:C:H2'	49:28:4305:G:C8	2.43	0.53
2:58:124:U:H4'	2:58:125:C:O5'	2.08	0.52
12:10:187:GLU:HG3	12:10:189:ARG:HG2	1.91	0.52
22:22:84:LYS:HB2	22:22:110:TYR:CE2	2.44	0.52
49:28:738(A):C:H3'	49:28:739:G:H5''	1.90	0.52
49:28:1954:U:H2'	49:28:1955:G:C8	2.44	0.52
49:28:4941:G:O2'	49:28:4942:C:H5'	2.10	0.52
1:v:600:ASN:HD21	1:v:716:ARG:HA	1.74	0.52
7:L5:268:ARG:NH2	49:28:1176:C:H5''	2.24	0.52
49:28:4158:C:H2'	49:28:4159:C:H6	1.73	0.52
50:25:48:ARG:HD2	50:25:51:ARG:HH21	1.74	0.52
13:11:56:THR:HG23	13:11:63:ARG:HA	1.90	0.52
20:20:139:ARG:HH21	49:28:1952:G:H5'	1.74	0.52
46:u:16:GLU:HA	46:u:19:HIS:CD2	2.44	0.52
46:u:195:LYS:HE2	46:u:196:LYS:NZ	2.25	0.52
49:28:233:U:H2'	49:28:234:G:C8	2.45	0.52
49:28:1980:U:H2'	49:28:1982:G:OP2	2.09	0.52
49:28:4479:A:H2'	49:28:4480:A:O4'	2.09	0.52
1:v:159:LYS:HD2	1:v:162:ARG:HD2	1.90	0.52
18:17:69:ARG:NH2	49:28:4568:A:H2	2.07	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:u:180:VAL:HA	46:u:183:ILE:HG12	1.92	0.52
49:28:1094:G:H2'	49:28:1095:A:H8	1.74	0.52
49:28:5003:U:H2'	49:28:5004:C:C6	2.44	0.52
1:v:586:GLU:HA	1:v:606:ALA:O	2.09	0.52
4:L8:116:LEU:HB3	4:L8:126:LEU:HB2	1.91	0.52
8:L6:193:HIS:HB3	8:L6:196:PHE:HD2	1.75	0.52
29:30:17:ARG:HH11	29:30:104:ILE:HA	1.74	0.52
42:gg:103:HIS:CD2	42:gg:106:LEU:HD22	2.41	0.52
43:s:118:PRO:HD2	43:s:183:PHE:CE1	2.44	0.52
47:Q:69:LYS:HE2	49:28:1458:C:H5''	1.90	0.52
49:28:1965:G:H2'	49:28:1966:C:C6	2.44	0.52
1:v:378:ASP:HA	1:v:383:MET:HE2	1.91	0.52
1:v:659:PRO:HG2	1:v:698:ARG:HA	1.92	0.52
22:22:36:ALA:HB3	22:22:65:ARG:HE	1.72	0.52
29:30:91:VAL:HG12	49:28:2673:G:O2'	2.10	0.52
43:s:44:ARG:HH11	49:28:1997:U:H4'	1.74	0.52
44:t:119:ARG:HH11	44:t:121:LEU:H	1.58	0.52
49:28:651:C:H2'	49:28:652:G:H8	1.74	0.52
49:28:1645:C:H2'	49:28:1646:A:C8	2.45	0.52
49:28:4174:U:H2'	49:28:4175:G:H8	1.75	0.52
49:28:4466:C:H2'	49:28:4467:A:H8	1.73	0.52
1:v:770:VAL:HG22	1:v:786:ALA:HB2	1.91	0.52
17:bb:121:PRO:HD2	20:20:166:ARG:O	2.10	0.52
21:21:69:GLN:HE21	21:21:69:GLN:N	2.07	0.52
45:EB:29:ASN:O	45:EB:33:ARG:HG2	2.10	0.52
49:28:4915:G:C2	49:28:4916:G:C4	2.97	0.52
1:v:124:GLY:HA3	1:v:358:LEU:HD21	1.92	0.52
13:11:95:ARG:H	13:11:98:ASN:ND2	2.08	0.52
22:22:49:VAL:HB	22:22:57:GLY:HA3	1.92	0.52
31:32:7:LEU:HB2	31:32:93:LYS:HB3	1.91	0.52
45:EB:147:HIS:O	45:EB:151:GLU:HG2	2.10	0.52
46:u:36:ILE:HG21	46:u:190:LEU:HD21	1.92	0.52
5:L3:249:ARG:HG3	49:28:2838:G:OP1	2.09	0.52
27:dd:66:ASN:H	27:dd:66:ASN:HD22	1.57	0.52
28:29:30:GLU:CD	28:29:30:GLU:H	2.17	0.52
1:v:26:ALA:HB3	1:v:32:LYS:HG3	1.91	0.52
1:v:308:LYS:HB2	1:v:311:GLU:HB2	1.92	0.52
2:58:141:C:H2'	2:58:142:U:H6	1.73	0.52
5:L3:222:VAL:HB	5:L3:343:ARG:HH11	1.73	0.52
8:L6:133:LYS:HE3	49:28:713:C:O2	2.10	0.52
14:13:19:GLN:HE22	49:28:1518:A:H61	1.57	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:ff:52:VAL:HG21	49:28:2739:C:H4'	1.91	0.52
45:EB:77:PRO:HG2	45:EB:246:ILE:HD12	1.92	0.52
49:28:1239:C:H4'	49:28:1244:G:P	2.50	0.52
49:28:2537:A:H2'	49:28:2538:U:O4'	2.10	0.52
5:L3:49:TYR:OH	5:L3:179:HIS:HD2	1.93	0.51
6:L4:305:PRO:HD3	47:Q:38:ARG:NH2	2.25	0.51
8:L6:196:PHE:HD1	32:ee:106:TYR:HB2	1.75	0.51
9:L7:59:GLU:O	9:L7:63:MET:HG2	2.10	0.51
11:L9:146:LEU:HD11	11:L9:161:ILE:HD11	1.92	0.51
13:11:18:ARG:HG3	13:11:135:GLY:HA3	1.91	0.51
31:32:66:THR:HA	31:32:69:MET:HE3	1.92	0.51
45:EB:156:LEU:HB3	45:EB:166:VAL:HG22	1.92	0.51
49:28:461:G:H2'	49:28:462:G:C8	2.45	0.51
49:28:648:G:H2'	49:28:649:A:H8	1.75	0.51
49:28:1468:C:H2'	49:28:1469:C:C6	2.45	0.51
1:v:358:LEU:HD22	1:v:359:PRO:HD2	1.93	0.51
8:L6:216:THR:HG23	8:L6:218:ALA:H	1.76	0.51
35:36:15:HIS:HB3	49:28:72:C:O4'	2.11	0.51
49:28:1398:A:N6	49:28:1419:G:C2	2.68	0.51
1:v:831:PRO:O	1:v:835:VAL:HG23	2.11	0.51
7:L5:208:MET:O	7:L5:212:MET:HG2	2.11	0.51
26:27:122:TYR:HB2	26:27:131:PHE:CE1	2.46	0.51
45:EB:332:ARG:HH21	45:EB:335:SER:HA	1.75	0.51
49:28:433:A:C2	49:28:3867:A:H4'	2.45	0.51
49:28:1317:U:H2'	49:28:1318:C:C6	2.46	0.51
49:28:1779:U:H2'	49:28:1780:A:H8	1.76	0.51
49:28:1890:G:N2	49:28:1939:A:H61	2.08	0.51
49:28:2542:G:H2'	49:28:2543:A:C8	2.45	0.51
2:58:5:U:H2'	2:58:6:C:C6	2.45	0.51
4:L8:66:PRO:HG2	4:L8:67:TYR:CE2	2.46	0.51
5:L3:92:TYR:HE1	5:L3:161:ARG:HG3	1.75	0.51
9:L7:227:VAL:HA	20:20:39:VAL:HG12	1.93	0.51
11:L9:92:MET:HE1	11:L9:161:ILE:HG13	1.90	0.51
11:L9:157:SER:O	11:L9:161:ILE:HG12	2.11	0.51
18:17:41:ILE:O	18:17:45:THR:HG23	2.10	0.51
21:21:87:LYS:NZ	49:28:4305:G:H22	2.08	0.51
49:28:1757:U:H2'	49:28:1758:G:H8	1.75	0.51
49:28:4193:C:H3'	49:28:4194:U:O2	2.10	0.51
11:L9:120:GLU:HG2	49:28:4611:A:C2	2.42	0.51
15:14:57:LEU:H	15:14:57:LEU:CD2	2.23	0.51
21:21:8:ARG:HD2	21:21:52:MET:HE1	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:22:26:THR:HA	22:22:68:SER:HB3	1.92	0.51
45:EB:192:GLN:HG3	45:EB:193:HIS:CD2	2.44	0.51
45:EB:255:TYR:HB3	45:EB:301:LEU:HD21	1.93	0.51
49:28:911:U:H2'	49:28:912:G:O4'	2.10	0.51
49:28:2098:G:H2'	49:28:2099:C:C6	2.46	0.51
1:v:703:ASP:HB2	1:v:705:HIS:HE1	1.74	0.51
26:27:3:LYS:O	26:27:6:LYS:HE3	2.11	0.51
26:27:11:VAL:HG11	26:27:80:LEU:HD13	1.93	0.51
43:s:193:PHE:CE1	43:s:196:GLY:HA2	2.46	0.51
49:28:4188:U:H2'	49:28:4189:U:H6	1.75	0.51
49:28:4219:A:H2'	49:28:4220:A:C8	2.46	0.51
49:28:4462:C:O2'	49:28:4463:U:H5'	2.10	0.51
1:v:617:ILE:HG21	1:v:659:PRO:HA	1.93	0.51
1:v:748:GLU:HB3	1:v:785:LYS:HD2	1.93	0.51
5:L3:58:ARG:HA	5:L3:366:LYS:HG3	1.93	0.51
9:L7:134:ILE:HG22	9:L7:135:VAL:HG13	1.93	0.51
19:19:44:LEU:HD22	19:19:49:LEU:HD12	1.93	0.51
24:cc:102:VAL:HA	24:cc:134:LYS:HE3	1.91	0.51
37:38:35:LYS:HE3	49:28:2693:G:OP1	2.11	0.51
49:28:1990:A:H3'	49:28:1991:A:H5''	1.92	0.51
49:28:2726:G:H2'	49:28:2727:C:C6	2.46	0.51
49:28:4665:A:H2'	49:28:4666:G:O4'	2.11	0.51
49:28:4723:A:H2'	49:28:4724:A:C8	2.46	0.51
49:28:5004:C:H2'	49:28:5005:G:O4'	2.11	0.51
7:L5:259:ARG:HH12	7:L5:262:LYS:NZ	2.08	0.51
11:L9:95:VAL:HG22	39:40:56:LEU:HB3	1.91	0.51
17:bb:18:ARG:O	17:bb:22:ILE:HG13	2.10	0.51
17:bb:92:THR:O	17:bb:96:GLN:HG3	2.11	0.51
32:ee:46:ARG:HH21	32:ee:89:ARG:NH2	2.09	0.51
45:EB:152:ALA:O	45:EB:156:LEU:HB2	2.10	0.51
48:ES:3284:C:H2'	48:ES:3285:G:H8	1.74	0.51
49:28:257:C:H2'	49:28:258:G:H8	1.74	0.51
49:28:1503:A:H4'	49:28:1504:G:H5'	1.93	0.51
49:28:1757:U:H2'	49:28:1758:G:C8	2.46	0.51
49:28:1884:C:H4'	49:28:2070:U:C4	2.45	0.51
4:L8:44:ILE:HG12	4:L8:87:PHE:HE1	1.74	0.51
22:22:40:GLU:O	22:22:44:GLN:HG3	2.11	0.51
31:32:91:CYS:HB3	31:32:95:TYR:HD2	1.76	0.51
45:EB:80:ILE:HG12	45:EB:108:ILE:HG12	1.93	0.51
45:EB:122:ALA:HB3	45:EB:320:LYS:N	2.25	0.51
4:L8:32:VAL:HG13	4:L8:163:ARG:CZ	2.41	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L7:240:ASN:O	9:L7:244:ARG:HG2	2.11	0.51
43:s:45:MET:HG2	44:t:123:ARG:NH1	2.26	0.51
49:28:1804:A:H5''	49:28:1806:G:C8	2.45	0.51
49:28:2602:G:H2'	49:28:2603:C:C6	2.46	0.51
1:v:119:LEU:HA	1:v:122:THR:HG22	1.92	0.50
5:L3:224:LYS:HG3	5:L3:340:THR:HB	1.92	0.50
15:14:123:ILE:HD11	17:bb:189:ILE:HD13	1.93	0.50
20:20:16:CYS:O	20:20:25:PRO:HG2	2.11	0.50
43:s:10:LYS:HE2	43:s:60:MET:HE1	1.92	0.50
48:ES:2949:U:H2'	48:ES:2950:G:H8	1.75	0.50
49:28:981:C:H42	49:28:1274:A:H61	1.59	0.50
49:28:1341:U:H2'	49:28:1342:A:C8	2.46	0.50
49:28:3652:A:H2'	49:28:3653:A:N7	2.26	0.50
49:28:4538:G:H2'	49:28:4539:U:C6	2.45	0.50
17:bb:12:ARG:HE	20:20:171:ARG:HH22	1.60	0.50
18:17:50:ASP:HB3	18:17:56:GLN:HG3	1.93	0.50
20:20:93:MET:HE1	20:20:117:HIS:NE2	2.27	0.50
35:36:85:ARG:O	35:36:88:GLU:HG2	2.11	0.50
40:42:51:GLN:HG2	40:42:55:ILE:HD11	1.92	0.50
46:u:124:LEU:HD23	46:u:124:LEU:H	1.75	0.50
49:28:262:G:H2'	49:28:263:G:H8	1.76	0.50
49:28:717:U:H2'	49:28:718:C:C6	2.46	0.50
2:58:7:U:H2'	2:58:8:U:C6	2.45	0.50
17:bb:85:ARG:HD3	17:bb:90:HIS:ND1	2.27	0.50
24:cc:73:HIS:CD2	24:cc:115:LYS:HD3	2.46	0.50
42:gg:19:LYS:HB3	49:28:2289:C:N4	2.26	0.50
43:s:14:PHE:O	43:s:17:ILE:HG22	2.11	0.50
43:s:183:PHE:HB3	43:s:185:PHE:CE2	2.46	0.50
49:28:259:C:H2'	49:28:260:C:C6	2.47	0.50
49:28:1933:G:H2'	49:28:1934:A:C8	2.46	0.50
49:28:2504:C:H2'	49:28:2505:C:O2	2.11	0.50
49:28:3911:C:H2'	49:28:3912:U:C6	2.46	0.50
1:v:553:HIS:O	1:v:556:ILE:HG22	2.10	0.50
2:58:127:U:O2	49:28:2543:A:H4'	2.11	0.50
4:L8:15:VAL:HG21	49:28:1628:C:H5''	1.93	0.50
4:L8:230:PRO:HB3	49:28:3928:A:N1	2.27	0.50
16:15:108:ARG:HB2	16:15:161:MET:HE1	1.93	0.50
18:17:122:ALA:HB3	18:17:143:PRO:HG2	1.92	0.50
45:EB:368:LYS:O	45:EB:371:LYS:HG2	2.11	0.50
49:28:178:C:H2'	49:28:179:G:C8	2.46	0.50
49:28:643:C:H2'	49:28:644:G:C8	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:2521:G:H2'	49:28:2522:G:H8	1.75	0.50
49:28:4158:C:H2'	49:28:4159:C:C6	2.47	0.50
49:28:4518:A:H8	49:28:4518:A:OP2	1.94	0.50
49:28:5002:U:H2'	49:28:5003:U:C6	2.46	0.50
5:L3:285:TYR:CD1	5:L3:363:ILE:HD13	2.47	0.50
25:26:55:VAL:HG11	25:26:82:ILE:HD13	1.94	0.50
29:30:81:LEU:HG	29:30:91:VAL:HG23	1.92	0.50
43:s:14:PHE:CE2	43:s:60:MET:HG3	2.46	0.50
48:ES:2947:G:C6	48:ES:3247:A:N1	2.78	0.50
49:28:1590:C:H5''	49:28:1591:U:O5'	2.12	0.50
49:28:4894:A:H5''	49:28:4895:C:C6	2.47	0.50
1:v:109:VAL:HG23	1:v:809:PHE:CZ	2.46	0.50
2:58:19:C:H2'	2:58:20:A:C8	2.46	0.50
3:5:111:C:H2'	3:5:112:U:O4'	2.12	0.50
5:L3:92:TYR:CE1	5:L3:161:ARG:HG3	2.46	0.50
5:L3:302:ASN:HD22	5:L3:330:PHE:HE1	1.58	0.50
7:L5:205:ALA:HB2	7:L5:236:MET:HE2	1.93	0.50
15:14:11:ARG:HD2	15:14:57:LEU:HD12	1.93	0.50
31:32:50:LYS:HB2	49:28:1884:C:OP1	2.12	0.50
36:37:15:THR:HG23	49:28:1534:A:C8	2.46	0.50
43:s:65:ILE:HG23	43:s:75:LEU:HB3	1.94	0.50
49:28:1870:C:H2'	49:28:1871:A:H8	1.77	0.50
49:28:3637:U:O4	49:28:3651:A:H2	1.95	0.50
1:v:128:VAL:HA	1:v:156:MET:O	2.11	0.50
2:58:40:A:H2'	2:58:41:A:C8	2.47	0.50
5:L3:224:LYS:HE3	5:L3:226:LYS:NZ	2.26	0.50
7:L5:280:VAL:O	7:L5:284:LYS:HG3	2.11	0.50
17:bb:12:ARG:HH21	20:20:171:ARG:NH2	2.09	0.50
43:s:61:MET:O	43:s:65:ILE:HG12	2.11	0.50
45:EB:13:ALA:HB2	45:EB:221:HIS:CD2	2.46	0.50
46:u:160:LYS:HB2	46:u:162:VAL:HG22	1.94	0.50
49:28:1294:A:H5'	49:28:1296:G:H21	1.77	0.50
49:28:4964:C:H2'	49:28:4965:U:C6	2.46	0.50
1:v:264:ARG:HH12	1:v:273:PHE:HB3	1.76	0.50
1:v:265:TYR:HA	1:v:287:ARG:HA	1.94	0.50
1:v:380:GLU:OE1	1:v:393:PRO:HG2	2.12	0.50
3:5:59:G:H4'	7:L5:267:ASN:ND2	2.23	0.50
4:L8:183:GLY:CA	49:28:1613:A:H5''	2.42	0.50
10:aa:214:VAL:HG13	10:aa:217:ILE:HD12	1.93	0.50
13:11:109:ILE:HD12	13:11:115:LEU:HD21	1.94	0.50
14:13:186:ARG:HH11	49:28:1394:G:H5'	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:19:105:LEU:HD23	19:19:138:LEU:HD22	1.94	0.50
21:21:17:ARG:HB2	21:21:22:HIS:CE1	2.47	0.50
31:32:8:VAL:HG23	31:32:10:PRO:HD3	1.93	0.50
42:gg:46:ARG:HA	42:gg:70:GLN:NE2	2.25	0.50
45:EB:57:MET:HE2	45:EB:57:MET:HA	1.94	0.50
48:ES:2946:G:H2'	48:ES:2947:G:C8	2.46	0.50
49:28:2865:U:H2'	49:28:2866:C:C6	2.47	0.50
1:v:20:ARG:NH2	1:v:98:PHE:HE2	2.09	0.50
12:10:55:ASP:HB2	12:10:162:ARG:O	2.12	0.50
16:15:181:HIS:CD2	49:28:99:A:H4'	2.46	0.50
43:s:93:GLU:HB3	43:s:97:GLU:OE2	2.12	0.50
45:EB:45:VAL:HG21	45:EB:98:TYR:HD2	1.76	0.50
49:28:1341:U:H2'	49:28:1342:A:H8	1.77	0.50
49:28:1473:U:H2'	49:28:1474:C:C6	2.47	0.50
49:28:4109:G:H2'	49:28:4110:C:C6	2.47	0.50
1:v:775:GLN:HA	1:v:782:PHE:HD1	1.77	0.49
2:58:37:A:OP2	34:35:89:ARG:HD2	2.11	0.49
2:58:70:G:H5''	25:26:27:ARG:CZ	2.42	0.49
8:L6:98:PRO:HA	8:L6:107:THR:HG22	1.93	0.49
13:11:16:ARG:HE	13:11:137:PRO:HG3	1.76	0.49
13:11:167:GLN:HE21	13:11:174:ILE:HD12	1.77	0.49
16:15:53:TYR:HB2	16:15:133:ILE:HD13	1.94	0.49
19:19:63:CYS:O	19:19:67:THR:HG23	2.11	0.49
26:27:38:TYR:HB3	49:28:2656:U:H5''	1.94	0.49
27:dd:134:GLU:O	27:dd:138:LYS:HG2	2.12	0.49
26:27:51:ARG:HB2	26:27:65:ARG:HG3	1.94	0.49
37:38:12:LEU:HB3	37:38:16:ARG:NH1	2.26	0.49
43:s:132:PRO:HB3	43:s:147:ILE:HD11	1.93	0.49
48:ES:2949:U:H2'	48:ES:2950:G:C8	2.47	0.49
49:28:1066:G:H2'	49:28:1067:G:C8	2.47	0.49
49:28:2409:U:H5	49:28:2783:A:N1	2.09	0.49
49:28:2862:G:N3	49:28:3624:A:H2'	2.26	0.49
49:28:4232:U:H4'	49:28:4233:A:O5'	2.12	0.49
49:28:4966:A:H2'	49:28:4967:A:O4'	2.12	0.49
14:13:186:ARG:NH1	49:28:1394:G:H5'	2.27	0.49
17:bb:54:TYR:HD2	17:bb:145:VAL:HG21	1.76	0.49
17:bb:80:PHE:HA	17:bb:83:THR:HG22	1.94	0.49
49:28:2264:C:H2'	49:28:2265:G:O4'	2.13	0.49
1:v:265:TYR:HB2	1:v:285:LEU:HD23	1.94	0.49
2:58:153:C:OP1	10:aa:238:LYS:HE2	2.11	0.49
14:13:91:ALA:HB1	14:13:96:ILE:HB	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:15:5:LYS:HG2	35:36:40:VAL:HG11	1.94	0.49
24:cc:72:ASP:O	24:cc:76:ILE:HG22	2.12	0.49
49:28:451:C:O2'	49:28:1293:G:H2'	2.11	0.49
49:28:1333:A:H2'	49:28:1334:A:H8	1.76	0.49
49:28:4915:G:C2	49:28:4916:G:C5	3.00	0.49
1:v:256:MET:HG3	1:v:260:LEU:HD13	1.94	0.49
1:v:613:LEU:HD23	1:v:701:ARG:HH21	1.77	0.49
4:L8:31:ALA:HB2	4:L8:123:ARG:HH21	1.77	0.49
7:L5:80:ALA:HA	7:L5:83:LEU:HD23	1.94	0.49
10:aa:247:VAL:HB	10:aa:249:ARG:HH11	1.78	0.49
20:20:31:ARG:HH21	20:20:129:VAL:HB	1.77	0.49
21:21:126:VAL:O	49:28:1834:U:H5	1.94	0.49
22:22:42:PHE:CZ	22:22:46:ARG:HG3	2.48	0.49
49:28:1314:C:C2	49:28:1315:C:C5	3.00	0.49
49:28:1348:U:H2'	49:28:1349:G:C8	2.46	0.49
49:28:2893:U:H2'	49:28:2894:A:C8	2.47	0.49
49:28:4872:G:H4'	49:28:4873:G:H5'	1.94	0.49
1:v:289:PHE:HD1	1:v:293:ILE:HD13	1.76	0.49
1:v:581:GLU:HG3	1:v:697:MET:HG3	1.95	0.49
2:58:151:G:O4'	10:aa:117:GLN:HG2	2.13	0.49
5:L3:116:ARG:HH22	5:L3:176:LYS:HD2	1.78	0.49
29:30:52:CYS:SG	29:30:57:LYS:HB2	2.53	0.49
31:32:22:ARG:NH1	31:32:31:ILE:HG23	2.26	0.49
44:t:135:THR:O	44:t:139:VAL:HG23	2.13	0.49
46:u:92:LYS:HG2	46:u:93:LEU:HD22	1.93	0.49
49:28:383:A:H2'	49:28:384:A:C8	2.48	0.49
49:28:471:A:H2'	49:28:472:C:H6	1.77	0.49
49:28:969:C:H42	49:28:2095:A:H61	1.60	0.49
49:28:1275:G:N2	49:28:1276:C:H1'	2.28	0.49
18:17:28:ASN:O	18:17:32:THR:HG22	2.12	0.49
45:EB:28:ALA:HB2	45:EB:112:VAL:HG12	1.95	0.49
49:28:2022:C:H2'	49:28:2023:C:C6	2.48	0.49
49:28:2425:U:H5'	49:28:2426:U:H5	1.77	0.49
49:28:2858:A:H2'	49:28:2859:G:C8	2.48	0.49
1:v:39:LEU:O	1:v:42:LYS:HG3	2.12	0.49
2:58:3:A:H2'	2:58:4:C:H6	1.78	0.49
5:L3:324:GLY:HA2	49:28:5051:C:O3'	2.12	0.49
8:L6:165:VAL:HG12	8:L6:178:VAL:HG22	1.95	0.49
27:dd:57:GLY:HA3	47:Q:172:ARG:HD2	1.94	0.49
28:29:4:SER:HB2	49:28:1855:G:OP1	2.11	0.49
31:32:70:LEU:HD11	31:32:76:LYS:HG2	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:ES:3248:C:C2	48:ES:3249:G:C8	3.00	0.49
49:28:956:A:H8	49:28:957:G:C8	2.29	0.49
49:28:4958:C:H2'	49:28:4959:U:C6	2.47	0.49
1:v:575:PRO:HG2	1:v:794:PHE:CZ	2.47	0.49
17:bb:27:VAL:HG22	17:bb:101:ARG:HB2	1.94	0.49
27:dd:132:ARG:O	27:dd:136:LYS:HG2	2.12	0.49
49:28:517:C:H2'	49:28:518:G:C8	2.48	0.49
49:28:4174:U:H2'	49:28:4175:G:C8	2.47	0.49
1:v:25:ILE:HB	1:v:142:VAL:HG21	1.95	0.49
3:5:66:G:H2'	3:5:67:C:H6	1.78	0.49
13:11:50:PHE:CD2	13:11:67:LYS:HD3	2.48	0.49
42:gg:94:ARG:HB2	42:gg:111:ILE:HD11	1.93	0.49
49:28:116:G:H2'	49:28:117:C:C6	2.48	0.49
49:28:651:C:H2'	49:28:652:G:C8	2.48	0.49
49:28:1994:C:H2'	49:28:1995:G:C8	2.47	0.49
2:58:92:U:H2'	2:58:93:C:O4'	2.12	0.48
5:L3:252:ALA:HB1	49:28:4524:G:C2	2.48	0.48
11:L9:104:VAL:HG13	11:L9:113:GLU:HB2	1.95	0.48
20:20:20:PRO:HA	20:20:23:ARG:HH22	1.78	0.48
26:27:97:ASN:HB3	26:27:99:ASP:OD1	2.12	0.48
30:31:23:ARG:HA	30:31:122:VAL:HG22	1.94	0.48
48:ES:3286:G:H2'	48:ES:3287:C:H6	1.78	0.48
49:28:496:G:O2'	49:28:497:G:H5'	2.12	0.48
49:28:1954:U:H2'	49:28:1955:G:H8	1.78	0.48
49:28:3873:G:H2'	49:28:3874:G:C8	2.48	0.48
49:28:5030:U:H2'	49:28:5031:G:H8	1.77	0.48
5:L3:252:ALA:HB1	49:28:4524:G:N3	2.28	0.48
6:L4:42:THR:HG21	49:28:2340:C:H5'	1.94	0.48
6:L4:76:ILE:HG13	6:L4:77:PRO:CD	2.43	0.48
17:bb:157:GLU:HG3	17:bb:161:LYS:HE2	1.94	0.48
27:dd:75:LEU:HD11	27:dd:133:ALA:HA	1.94	0.48
49:28:451:C:H2'	49:28:1294:A:N7	2.28	0.48
49:28:2661:U:O2'	49:28:2662:G:H4'	2.14	0.48
49:28:4263:C:H2'	49:28:4264:G:O4'	2.12	0.48
1:v:753:GLU:HA	1:v:782:PHE:CE2	2.49	0.48
5:L3:55:HIS:HB2	5:L3:369:ASP:HB2	1.94	0.48
7:L5:286:SER:OG	49:28:1179:U:H5''	2.13	0.48
8:L6:198:ILE:HD11	32:ee:105:LEU:HD23	1.95	0.48
17:bb:61:ARG:HA	17:bb:70:PRO:HD2	1.95	0.48
18:17:118:GLN:NE2	49:28:423:G:H21	2.11	0.48
19:19:10:LEU:HB3	19:19:41:ILE:HG13	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:20:27:LEU:HB3	21:21:148:PRO:HB3	1.95	0.48
25:26:114:ASP:O	25:26:118:ILE:HG12	2.13	0.48
49:28:35:U:H5'	49:28:36:U:OP2	2.13	0.48
49:28:302:C:H2'	49:28:303:C:C6	2.49	0.48
49:28:1345:A:H2'	49:28:1346:C:C6	2.48	0.48
49:28:3843:C:P	50:25:51:ARG:HG3	2.54	0.48
10:aa:247:VAL:HB	10:aa:249:ARG:NH1	2.29	0.48
12:10:75:TYR:CZ	12:10:150:GLU:HG2	2.48	0.48
13:11:50:PHE:CG	13:11:67:LYS:HD3	2.49	0.48
14:13:75:GLY:HA2	14:13:97:SER:HB3	1.95	0.48
17:bb:166:ILE:HD13	17:bb:169:ARG:NH1	2.28	0.48
22:22:22:THR:O	22:22:109:SER:HA	2.14	0.48
24:cc:119:ILE:HA	24:cc:144:TYR:CZ	2.47	0.48
26:27:10:VAL:O	26:27:83:THR:HG22	2.13	0.48
45:EB:144:LYS:HD2	45:EB:345:SER:HB3	1.95	0.48
49:28:754:C:H2'	49:28:755:C:H6	1.78	0.48
49:28:1444:G:H2'	49:28:1445:U:C5	2.48	0.48
49:28:1727:U:H2'	49:28:1728:U:H6	1.77	0.48
49:28:3923:A:H2'	49:28:3924:C:C6	2.48	0.48
49:28:4564:A:H2'	49:28:4565:C:O4'	2.13	0.48
49:28:4600:G:O6	50:25:4:ARG:HB3	2.13	0.48
4:L8:47:ASP:HA	4:L8:84:THR:HG22	1.95	0.48
4:L8:70:LYS:HD3	4:L8:72:ARG:NH1	2.28	0.48
4:L8:224:THR:HG21	4:L8:243:THR:HG21	1.95	0.48
5:L3:160:ILE:HD13	5:L3:194:LEU:HD13	1.94	0.48
7:L5:146:LEU:HD12	7:L5:163:LEU:HB2	1.95	0.48
10:aa:170:ARG:NH1	10:aa:174:LYS:HB2	2.28	0.48
13:11:83:LEU:O	13:11:87:LEU:HG	2.13	0.48
14:13:203:ALA:O	14:13:207:VAL:HG23	2.13	0.48
25:26:13:LYS:O	25:26:17:ARG:HG2	2.13	0.48
38:39:44:TRP:CZ3	38:39:45:ARG:HG2	2.48	0.48
45:EB:32:LEU:O	45:EB:36:VAL:HG23	2.13	0.48
46:u:26:ARG:HE	46:u:210:MET:HB3	1.78	0.48
47:Q:159:PRO:HB2	47:Q:160:HIS:HD2	1.78	0.48
49:28:48:G:O6	49:28:290:U:H5'	2.12	0.48
49:28:2467:U:H4'	49:28:2468:U:H5'	1.96	0.48
49:28:2521:G:H5'	49:28:2640:G:H1'	1.94	0.48
1:v:167:LEU:HD13	1:v:169:LEU:HD21	1.95	0.48
1:v:366:LYS:HA	1:v:386:LYS:HA	1.94	0.48
5:L3:206:PRO:HG2	5:L3:209:GLN:HG2	1.96	0.48
9:L7:113:LEU:HD21	9:L7:120:THR:HG22	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:21:74:ILE:O	21:21:88:ARG:HA	2.13	0.48
49:28:411:G:H4'	49:28:412:G:H5''	1.96	0.48
49:28:1942:A:H2'	49:28:1943:A:H8	1.78	0.48
1:v:227:GLN:HA	1:v:230:GLU:OE1	2.14	0.48
1:v:421:VAL:HG13	1:v:464:VAL:HG13	1.94	0.48
1:v:488:PHE:CE2	1:v:490:HIS:HB3	2.49	0.48
2:58:8:U:H2'	2:58:9:A:C8	2.49	0.48
2:58:65:A:C4	2:58:66:A:C8	3.02	0.48
29:30:20:LEU:HD23	29:30:102:SER:HB2	1.96	0.48
46:u:194:LEU:HB3	46:u:200:ASN:HD22	1.78	0.48
49:28:1476:C:H2'	49:28:1477:C:O4'	2.13	0.48
49:28:4130:C:H2'	49:28:4131:G:C8	2.48	0.48
49:28:4591:U:H2'	49:28:4592:C:C6	2.49	0.48
49:28:4674:C:H2'	49:28:4675:U:C6	2.47	0.48
14:13:129:ARG:HH12	49:28:173:C:H5''	1.79	0.48
15:14:9:VAL:HG11	15:14:66:HIS:HA	1.95	0.48
18:17:83:TRP:O	49:28:3856:A:H5''	2.14	0.48
22:22:80:LYS:HZ1	22:22:109:SER:C	2.21	0.48
43:s:128:THR:HG23	43:s:130:LEU:H	1.79	0.48
45:EB:75:ALA:HB1	45:EB:118:ILE:HG23	1.96	0.48
49:28:517:C:H2'	49:28:518:G:H8	1.79	0.48
49:28:1196:G:H2'	49:28:1197:C:H6	1.77	0.48
49:28:2654:C:H2'	49:28:2655:C:H6	1.77	0.48
49:28:2893:U:H2'	49:28:2894:A:H8	1.78	0.48
49:28:3868:G:H22	49:28:3900:G:H1'	1.79	0.48
49:28:5002:U:H2'	49:28:5003:U:H6	1.78	0.48
1:v:676:LYS:NZ	1:v:680:VAL:HG21	2.19	0.48
5:L3:154:LYS:HG2	5:L3:194:LEU:HD23	1.95	0.48
5:L3:204:GLN:HE21	5:L3:204:GLN:HB3	1.46	0.48
8:L6:49:ASN:HB2	8:L6:59:TYR:HD2	1.79	0.48
24:cc:78:LYS:HD2	24:cc:99:ILE:HG22	1.95	0.48
36:37:12:ARG:HH11	49:28:2404:A:H1'	1.79	0.48
45:EB:55:MET:O	45:EB:59:GLU:HG2	2.14	0.48
1:v:453:MET:HG2	1:v:455:GLY:H	1.79	0.48
1:v:650:TRP:HB3	1:v:676:LYS:HE2	1.94	0.48
6:L4:289:LEU:O	6:L4:293:LEU:HG	2.14	0.48
7:L5:69:ILE:HD11	21:21:32:ARG:NH2	2.29	0.48
9:L7:219:MET:HB3	9:L7:231:ASP:OD2	2.13	0.48
10:aa:212:HIS:ND1	10:aa:238:LYS:HA	2.28	0.48
17:bb:51:LYS:O	17:bb:55:LEU:HG	2.13	0.48
17:bb:83:THR:OG1	49:28:2052:G:H5'	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:27:23:ALA:HA	26:27:45:GLY:HA2	1.95	0.48
27:dd:77:LYS:HE3	27:dd:77:LYS:HB3	1.60	0.48
32:ee:63:LYS:HG2	32:ee:64:PRO:HD2	1.96	0.48
32:ee:79:GLY:HA2	49:28:2066:C:O2'	2.14	0.48
38:39:2:SER:N	49:28:2406:G:N7	2.61	0.48
45:EB:287:LYS:H	45:EB:287:LYS:HD3	1.78	0.48
47:Q:121:LEU:HB2	47:Q:125:GLN:HB2	1.94	0.48
49:28:347:A:H2'	49:28:348:G:C8	2.49	0.48
49:28:2412:A:H2'	49:28:2413:U:C6	2.49	0.48
32:ee:16:ARG:HG3	32:ee:17:GLY:O	2.14	0.47
45:EB:51:LYS:HB3	45:EB:51:LYS:HE3	1.70	0.47
47:Q:14:ARG:NH1	47:Q:16:LYS:HE2	2.29	0.47
49:28:2007:G:N2	49:28:2012:A:N7	2.62	0.47
49:28:3664:G:H2'	49:28:3665:G:H8	1.78	0.47
1:v:287:ARG:HG2	1:v:290:CYS:SG	2.53	0.47
1:v:590:LEU:HA	1:v:605:LYS:HD3	1.96	0.47
5:L3:165:HIS:HA	5:L3:179:HIS:O	2.13	0.47
38:39:23:ILE:HG23	38:39:38:ASN:HB2	1.95	0.47
49:28:222:C:H2'	49:28:223:G:O4'	2.14	0.47
49:28:1381:U:H5'	49:28:1382:G:OP2	2.14	0.47
49:28:2602:G:H2'	49:28:2603:C:H6	1.76	0.47
1:v:580:ARG:C	1:v:741:MET:HB2	2.40	0.47
4:L8:204:MET:HG2	49:28:1631:A:C2	2.49	0.47
32:ee:48:ALA:HB2	32:ee:71:TRP:CZ3	2.49	0.47
44:t:61:LYS:HG2	44:t:72:GLU:HG2	1.96	0.47
45:EB:206:THR:O	45:EB:210:LYS:HG3	2.15	0.47
47:Q:46:VAL:HG11	47:Q:138:LEU:HD21	1.95	0.47
49:28:45:U:H2'	49:28:46:U:O4'	2.15	0.47
49:28:1693:U:H2'	49:28:1694:C:O4'	2.13	0.47
8:L6:120:PRO:O	42:gg:112:ARG:HD2	2.14	0.47
9:L7:66:THR:O	9:L7:70:MET:HG2	2.14	0.47
14:13:8:MET:HE3	47:Q:168:ARG:HB3	1.97	0.47
17:bb:77:SER:HB2	17:bb:104:VAL:HG23	1.96	0.47
18:17:131:ARG:HG3	18:17:137:ASN:ND2	2.29	0.47
49:28:86:U:H2'	49:28:87:A:C8	2.50	0.47
49:28:1418:C:C2	49:28:1419:G:H1'	2.48	0.47
49:28:1545:G:H2'	49:28:1546:C:C6	2.49	0.47
49:28:4594:U:H2'	49:28:4595:G:C8	2.46	0.47
10:aa:249:ARG:NH2	49:28:149:A:C5	2.82	0.47
26:27:30:ASP:O	26:27:39:SER:HB3	2.14	0.47
49:28:1733:G:N3	49:28:4214:A:H2'	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:2306:G:H1'	49:28:2332:A:N6	2.29	0.47
49:28:4344:U:H2'	49:28:4345:C:C6	2.49	0.47
1:v:588:ASN:OD1	1:v:589:VAL:HG13	2.15	0.47
1:v:650:TRP:HB2	1:v:662:LEU:HB3	1.96	0.47
31:32:23:HIS:HA	31:32:53:ILE:HD12	1.95	0.47
45:EB:15:ASP:O	45:EB:19:THR:HG23	2.14	0.47
49:28:1199:G:H2'	49:28:1200:G:C8	2.47	0.47
49:28:1205:G:H2'	49:28:1206:C:C6	2.49	0.47
49:28:1346:C:H2'	49:28:1347:G:H8	1.78	0.47
49:28:1920:C:H3'	49:28:1921:C:H5''	1.97	0.47
49:28:2019:C:H2'	49:28:2020:U:C6	2.50	0.47
49:28:2730:U:H2'	49:28:2731:C:C6	2.50	0.47
49:28:4110:C:H2'	49:28:4111:U:C6	2.50	0.47
49:28:4300:U:H2'	49:28:4301:U:C6	2.49	0.47
49:28:4699:U:H1'	49:28:4700:A:H5''	1.97	0.47
2:58:30:U:H2'	2:58:31:G:H8	1.79	0.47
2:58:148:A:H2'	2:58:149:G:C8	2.50	0.47
3:5:107:G:H5''	7:L5:273:LEU:HD21	1.97	0.47
4:L8:149:LYS:HE3	4:L8:149:LYS:HB2	1.76	0.47
7:L5:38:ILE:HD12	21:21:30:TYR:HB3	1.95	0.47
9:L7:142:GLY:HA3	9:L7:239:ILE:HB	1.97	0.47
11:L9:96:TYR:HA	11:L9:177:ASP:OD1	2.15	0.47
15:14:25:VAL:HG11	15:14:50:MET:HE1	1.96	0.47
15:14:117:LYS:O	15:14:121:ARG:HG2	2.15	0.47
18:17:54:LYS:HA	18:17:83:TRP:CD1	2.49	0.47
20:20:13:VAL:HA	20:20:28:TYR:O	2.15	0.47
22:22:28:PRO:HB2	22:22:34:MET:HG2	1.97	0.47
29:30:57:LYS:HD3	29:30:73:HIS:CE1	2.50	0.47
30:31:31:LYS:HE2	49:28:4996:C:OP2	2.15	0.47
33:34:26:PRO:HB3	49:28:2639:U:O2	2.14	0.47
33:34:43:LYS:HE2	33:34:43:LYS:HB2	1.45	0.47
45:EB:246:ILE:HB	45:EB:305:PHE:HB2	1.97	0.47
49:28:1190:C:H2'	49:28:1191:C:C6	2.49	0.47
49:28:1306:C:H2'	49:28:1307:A:H8	1.80	0.47
49:28:3690:U:H2'	49:28:3691:G:O4'	2.15	0.47
49:28:4507:A:H2'	49:28:4508:C:C6	2.49	0.47
1:v:745:TYR:HD2	1:v:812:CYS:HB2	1.80	0.47
2:58:33:G:H5''	2:58:34:U:OP1	2.14	0.47
15:14:91:TRP:CZ2	49:28:4870:G:H2'	2.49	0.47
18:17:48:LEU:O	18:17:52:THR:HG23	2.15	0.47
45:EB:231:SER:HB3	45:EB:316:VAL:HG22	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:660:G:H2'	49:28:661:C:H6	1.80	0.47
49:28:1964:A:H3'	49:28:1965:G:H8	1.79	0.47
49:28:2640:G:H2'	49:28:2641:A:C8	2.49	0.47
1:v:654:PRO:HD2	1:v:658:GLY:HA3	1.97	0.47
2:58:94:G:H21	36:37:82:THR:HB	1.79	0.47
10:aa:210:ILE:HD11	10:aa:223:LEU:HD22	1.96	0.47
33:34:11:LEU:HG	49:28:2513:A:OP1	2.15	0.47
40:42:74:GLU:HG2	40:42:76:ASN:H	1.79	0.47
43:s:48:ARG:NH1	44:t:123:ARG:HD3	2.30	0.47
46:u:175:THR:OG1	46:u:178:GLU:HB2	2.15	0.47
48:ES:3246:G:H2'	48:ES:3247:A:C8	2.49	0.47
49:28:4336:A:H5''	49:28:4337:C:H5'	1.97	0.47
1:v:21:ASN:OD1	1:v:361:PRO:HG3	2.15	0.47
1:v:430:MET:HG2	1:v:434:TYR:CD1	2.50	0.47
5:L3:314:ILE:HG21	5:L3:330:PHE:CZ	2.50	0.47
14:13:67:HIS:HD2	49:28:71:C:H4'	1.79	0.47
15:14:98:ARG:HE	15:14:98:ARG:HB2	1.39	0.47
26:27:73:LYS:HG2	26:27:75:TYR:CE2	2.50	0.47
27:dd:13:GLY:HA2	49:28:1660:U:H3'	1.95	0.47
41:ff:7:LYS:HE3	49:28:2875:C:H5''	1.97	0.47
43:s:55:MET:HB2	49:28:1998:A:C8	2.50	0.47
46:u:152:LYS:HB3	46:u:152:LYS:HE2	1.78	0.47
49:28:2686:G:H5'	49:28:2687:U:OP1	2.15	0.47
49:28:4127:A:O2'	49:28:4128:A:H8	1.95	0.47
49:28:4863:G:H2'	49:28:4864:U:H6	1.79	0.47
49:28:5031:G:H2'	49:28:5032:C:H6	1.80	0.47
1:v:188:ILE:HD12	1:v:188:ILE:HA	1.78	0.46
1:v:513:ASN:OD1	1:v:568:ILE:HD11	2.14	0.46
4:L8:31:ALA:HB2	4:L8:123:ARG:NH2	2.30	0.46
6:L4:101:MET:SD	6:L4:104:PRO:HA	2.55	0.46
10:aa:113:TYR:O	10:aa:117:GLN:HB2	2.15	0.46
20:20:94:TYR:CE2	20:20:138:ARG:HD3	2.50	0.46
20:20:112:ASP:OD1	20:20:116:ARG:HG3	2.15	0.46
27:dd:77:LYS:H	27:dd:77:LYS:HG2	1.53	0.46
31:32:43:ASN:HB3	31:32:46:ARG:HB2	1.96	0.46
37:38:61:PRO:HG2	37:38:64:LEU:HB2	1.97	0.46
41:ff:10:ILE:HG21	41:ff:30:GLU:HB3	1.97	0.46
45:EB:153:ALA:HB2	45:EB:170:TRP:HZ2	1.80	0.46
49:28:99:A:H2'	49:28:100:C:O2	2.15	0.46
49:28:479:G:H2'	49:28:480:C:C6	2.50	0.46
49:28:1194:G:C6	49:28:1195:G:C8	3.03	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1998:A:C6	49:28:1999:A:N1	2.83	0.46
49:28:4992:G:H2'	49:28:4993:G:C8	2.50	0.46
1:v:650:TRP:CE3	1:v:662:LEU:HD22	2.50	0.46
11:L9:150:ASP:OD2	11:L9:153:LEU:HG	2.15	0.46
12:10:86:HIS:HB3	12:10:139:ARG:HG2	1.96	0.46
13:11:42:GLN:HE22	13:11:117:ILE:HG21	1.80	0.46
29:30:20:LEU:HA	29:30:23:LYS:HG2	1.97	0.46
29:30:45:LEU:HD23	29:30:96:ILE:HD13	1.97	0.46
35:36:56:ARG:O	35:36:60:LEU:HD23	2.15	0.46
35:36:89:GLU:O	35:36:93:VAL:HG13	2.14	0.46
37:38:23:VAL:HA	37:38:35:LYS:O	2.14	0.46
44:t:137:GLN:NE2	49:28:1993:C:H1'	2.27	0.46
49:28:1172:C:H2'	49:28:1173:G:C8	2.50	0.46
49:28:1359:G:H3'	49:28:1360:G:H8	1.80	0.46
49:28:2488:C:H3'	49:28:2490:U:C4	2.50	0.46
2:58:26:C:H2'	2:58:27:U:C6	2.50	0.46
3:5:108:G:OP1	7:L5:273:LEU:HB2	2.15	0.46
6:L4:312:ARG:HB3	49:28:2274:C:H5'	1.98	0.46
18:17:15:CYS:SG	18:17:102:ALA:HB2	2.54	0.46
22:22:101:ARG:O	22:22:112:LEU:HA	2.16	0.46
27:dd:51:GLY:HA2	47:Q:178:ARG:N	2.30	0.46
31:32:57:ASN:O	49:28:2319:C:H1'	2.14	0.46
49:28:1590:C:H3'	49:28:1591:U:H4'	1.96	0.46
49:28:2815:A:H2'	49:28:2816:G:C8	2.51	0.46
49:28:4385:A:N6	49:28:4531:U:H5'	2.31	0.46
49:28:4601:U:H2'	49:28:4602:A:H8	1.81	0.46
50:25:89:ARG:HB2	50:25:95:PHE:CE2	2.50	0.46
1:v:604:MET:HG2	1:v:703:ASP:O	2.15	0.46
1:v:749:ILE:HG12	1:v:810:PRO:HB3	1.96	0.46
6:L4:38:ASN:O	6:L4:42:THR:HG23	2.15	0.46
7:L5:204:VAL:O	7:L5:208:MET:HG3	2.15	0.46
9:L7:63:MET:HE1	9:L7:195:THR:HG22	1.97	0.46
21:21:119:ALA:HA	21:21:122:LYS:HB2	1.97	0.46
24:cc:114:LYS:HG3	24:cc:119:ILE:O	2.16	0.46
28:29:32:LEU:HD23	28:29:43:MET:HE1	1.96	0.46
30:31:68:LEU:HA	30:31:108:TYR:HB2	1.97	0.46
30:31:85:ARG:NH1	30:31:117:LEU:HB3	2.30	0.46
37:38:4:LYS:HD3	49:28:2692:U:H5'	1.97	0.46
49:28:50:C:C2	49:28:51:A:C8	3.04	0.46
49:28:302:C:H2'	49:28:303:C:H6	1.81	0.46
49:28:1327:C:H2'	49:28:1328:G:C8	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1479:G:O2'	49:28:1480:C:H5'	2.15	0.46
49:28:2065:G:H2'	49:28:2066:C:O4'	2.15	0.46
49:28:2102:G:O2'	49:28:2103:A:H5'	2.15	0.46
49:28:3651:A:H2'	49:28:3652:A:C8	2.50	0.46
1:v:115:VAL:O	1:v:119:LEU:HD22	2.16	0.46
1:v:401:MET:HB2	1:v:410:PHE:HD2	1.81	0.46
2:58:27:U:H2'	2:58:28:C:C6	2.50	0.46
2:58:116:C:H2'	2:58:117:C:H6	1.80	0.46
6:L4:138:MET:HE2	6:L4:144:ILE:HG13	1.97	0.46
16:15:45:PRO:O	16:15:49:ARG:HG3	2.16	0.46
17:bb:124:LEU:HD12	17:bb:124:LEU:HA	1.75	0.46
26:27:89:ILE:HD12	26:27:90:PRO:HD2	1.97	0.46
27:dd:51:GLY:H	47:Q:179:GLY:H	1.62	0.46
35:36:70:LEU:HB2	35:36:87:ARG:NH1	2.30	0.46
49:28:693:C:H2'	49:28:694:C:H6	1.81	0.46
49:28:697:G:H2'	49:28:698:G:H8	1.81	0.46
49:28:985:C:H2'	49:28:986:C:C6	2.50	0.46
49:28:3860:A:H61	49:28:4560:C:H5	1.62	0.46
49:28:3920:U:H2'	49:28:3921:U:H6	1.79	0.46
49:28:4635:A:H2	49:28:4663:G:H21	1.64	0.46
1:v:310:GLU:O	1:v:314:LYS:HG2	2.16	0.46
4:L8:234:LYS:HG2	4:L8:238:ILE:HD12	1.97	0.46
42:gg:18:ILE:HG13	42:gg:25:TYR:HB2	1.98	0.46
43:s:125:ALA:HB1	43:s:154:ILE:O	2.16	0.46
48:ES:2949:U:C4	48:ES:3245:G:O6	2.68	0.46
49:28:922(B):C:H3'	49:28:923:C:H5''	1.98	0.46
49:28:3711:A:C8	49:28:3712:A:H1'	2.51	0.46
1:v:788:LEU:HD12	1:v:789:PRO:HD2	1.98	0.46
3:5:18:C:H2'	3:5:19:C:H6	1.81	0.46
5:L3:5:LYS:HD2	49:28:4455:G:OP1	2.15	0.46
5:L3:373:LYS:HE2	49:28:4627:U:H4'	1.97	0.46
10:aa:237:LEU:HD23	10:aa:237:LEU:HA	1.76	0.46
20:20:62:VAL:HG22	21:21:141:VAL:HG21	1.97	0.46
35:36:94:LEU:HD12	35:36:94:LEU:HA	1.79	0.46
49:28:37:U:H2'	49:28:38:A:O4'	2.15	0.46
49:28:1907:A:H2'	49:28:1908:A:C8	2.51	0.46
49:28:3774:A:H2'	49:28:3775:A:N3	2.30	0.46
1:v:264:ARG:NH1	1:v:273:PHE:HB3	2.30	0.46
1:v:617:ILE:HA	1:v:622:VAL:O	2.16	0.46
4:L8:89:TYR:HB2	4:L8:100:ASN:HD21	1.81	0.46
14:13:13:HIS:CD2	49:28:85:G:C6	3.04	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:20:80:ILE:HG12	20:20:129:VAL:HG22	1.98	0.46
30:31:28:ASN:HD22	30:31:31:LYS:HD3	1.81	0.46
45:EB:181:PRO:HG2	45:EB:204:ASN:CG	2.40	0.46
46:u:133:LYS:HE3	46:u:133:LYS:HB3	1.66	0.46
47:Q:148:VAL:HG12	49:28:1346:C:OP1	2.16	0.46
49:28:985:C:H2'	49:28:986:C:H6	1.80	0.46
49:28:4339:A:H2'	49:28:4340:U:C6	2.50	0.46
50:25:108:ASN:OD1	50:25:109:LYS:HG2	2.15	0.46
1:v:21:ASN:HD21	1:v:415:ARG:NH1	2.14	0.46
2:58:30:U:H2'	2:58:31:G:C8	2.50	0.46
5:L3:103:LYS:HB2	5:L3:103:LYS:HE3	1.60	0.46
6:L4:94:ASN:HA	6:L4:100:ARG:O	2.15	0.46
6:L4:305:PRO:HD3	47:Q:38:ARG:HH22	1.80	0.46
16:15:143:ARG:HA	16:15:143:ARG:HD3	1.69	0.46
16:15:192:TRP:NE1	49:28:48:G:H5'	2.31	0.46
17:bb:85:ARG:HD3	17:bb:90:HIS:CE1	2.51	0.46
49:28:922(A):G:H2'	49:28:922(B):C:H6	1.81	0.46
49:28:2034:G:H2'	49:28:2035:C:C6	2.51	0.46
49:28:3698:G:C8	49:28:3698:G:OP2	2.69	0.46
7:L5:177:THR:HG22	7:L5:180:PHE:CE2	2.51	0.46
8:L6:45:HIS:O	49:28:980:U:H4'	2.16	0.46
11:L9:106:GLN:C	11:L9:107:GLU:HG2	2.40	0.46
11:L9:162:GLN:HG2	11:L9:179:ILE:O	2.16	0.46
13:11:52:LYS:HD3	13:11:65:ASN:OD1	2.16	0.46
15:14:104:MET:HE3	15:14:109:ARG:HG3	1.97	0.46
25:26:56:GLN:HB2	25:26:105:VAL:HG13	1.97	0.46
28:29:32:LEU:HD22	49:28:1464:C:H5''	1.98	0.46
34:35:103:LYS:HD3	34:35:103:LYS:HA	1.61	0.46
46:u:39:LYS:HG2	46:u:200:ASN:O	2.15	0.46
49:28:478:G:H2'	49:28:479:G:H8	1.81	0.46
49:28:922(A):G:H2'	49:28:922(B):C:C6	2.51	0.46
49:28:1204:C:H2'	49:28:1205:G:C8	2.51	0.46
49:28:1344:C:H2'	49:28:1345:A:C8	2.50	0.46
49:28:2519:U:H1'	49:28:2520:C:C6	2.51	0.46
49:28:4236:G:H4'	49:28:4328:G:O2'	2.16	0.46
6:L4:284:MET:HE2	6:L4:286:ASN:O	2.16	0.45
9:L7:73:MET:HE1	49:28:1088:C:O2	2.16	0.45
14:13:169:ILE:HG12	27:dd:123:ILE:HD11	1.98	0.45
25:26:82:ILE:HG22	25:26:83:GLU:H	1.80	0.45
33:34:45:ALA:HB3	33:34:82:MET:HG3	1.98	0.45
45:EB:209:GLN:O	45:EB:213:HIS:HB2	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:471:A:H2'	49:28:472:C:C6	2.51	0.45
49:28:1193:C:H2'	49:28:1194:G:C8	2.51	0.45
49:28:2376:A:H2'	49:28:2377:C:H6	1.80	0.45
1:v:506:ARG:HG2	1:v:547:ALA:HB2	1.99	0.45
1:v:695:GLU:H	1:v:695:GLU:HG2	1.51	0.45
12:10:190:LEU:HB3	12:10:197:VAL:CG2	2.46	0.45
17:bb:150:GLN:HE21	17:bb:150:GLN:HB3	1.50	0.45
29:30:90:ARG:NH1	41:ff:44:LYS:HG2	2.31	0.45
34:35:66:LYS:NZ	34:35:82:ASP:HB3	2.32	0.45
44:t:147:HIS:O	44:t:151:ILE:HG13	2.16	0.45
46:u:7:ARG:O	46:u:10:LEU:HG	2.15	0.45
47:Q:15:ARG:HG3	49:28:1691:G:H5'	1.98	0.45
49:28:976:G:H22	49:28:1279:A:H2	1.63	0.45
49:28:2870:A:H2'	49:28:2871:A:H8	1.81	0.45
49:28:3715:U:C5	49:28:3738:G:O6	2.69	0.45
50:25:34:ALA:HB2	50:25:72:LEU:HD13	1.98	0.45
1:v:738:PRO:O	1:v:739:ARG:HD3	2.16	0.45
4:L8:89:TYR:H	4:L8:100:ASN:ND2	2.14	0.45
6:L4:60:HIS:CE1	6:L4:100:ARG:HD3	2.46	0.45
8:L6:179:THR:OG1	8:L6:189:LEU:HD23	2.17	0.45
17:bb:163:LYS:HE3	17:bb:163:LYS:HB2	1.74	0.45
19:19:106:LEU:HB3	19:19:120:TYR:CE1	2.52	0.45
20:20:31:ARG:NH2	20:20:129:VAL:HB	2.31	0.45
33:34:54:ARG:HB2	49:28:2583:C:OP1	2.17	0.45
40:42:37:GLY:HA3	49:28:4342:C:O3'	2.16	0.45
45:EB:79:SER:OG	45:EB:109:ASP:HB2	2.15	0.45
45:EB:326:MET:HE3	45:EB:328:ASN:HD21	1.80	0.45
46:u:112:ALA:HB1	46:u:116:LEU:HD21	1.98	0.45
46:u:113:SER:HA	46:u:138:LEU:HD21	1.97	0.45
49:28:4762:A:H2'	49:28:4763:U:O4'	2.17	0.45
49:28:4895:C:H3'	49:28:4896:G:H8	1.82	0.45
49:28:4935:C:H2'	49:28:4936:G:C8	2.50	0.45
5:L3:252:ALA:HB3	49:28:4457:U:H1'	1.98	0.45
5:L3:252:ALA:HB3	49:28:4457:U:O2	2.16	0.45
5:L3:285:TYR:CE1	5:L3:334:LYS:HB2	2.51	0.45
7:L5:35:ARG:HB2	49:28:4325:A:C2	2.52	0.45
7:L5:73:MET:HE2	7:L5:73:MET:HB3	1.86	0.45
9:L7:91:VAL:O	9:L7:119:GLY:HA2	2.15	0.45
13:11:32:ARG:HD2	13:11:35:ARG:HH21	1.82	0.45
22:22:40:GLU:HG3	22:22:63:LEU:HD21	1.97	0.45
30:31:113:THR:OG1	30:31:115:LYS:HG2	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:s:26:LYS:HE3	43:s:92:LYS:HE3	1.98	0.45
44:t:108:GLU:HA	44:t:111:ASN:HD21	1.80	0.45
47:Q:95:VAL:HG21	47:Q:112:ARG:HG2	1.98	0.45
48:ES:3245:G:H2'	48:ES:3246:G:C8	2.50	0.45
49:28:6:C:H2'	49:28:7:C:C6	2.51	0.45
49:28:262:G:H2'	49:28:263:G:C8	2.51	0.45
49:28:923:C:H4'	49:28:923:C:OP1	2.15	0.45
49:28:973:G:N2	49:28:1282:G:N7	2.65	0.45
49:28:1329:G:C8	49:28:1329:G:H3'	2.52	0.45
49:28:1450:C:H2'	49:28:1451:G:C8	2.51	0.45
49:28:1633:G:H2'	49:28:1641:G:N7	2.32	0.45
49:28:2710:C:H2'	49:28:2712:G:H5''	1.97	0.45
1:v:285:LEU:HD12	1:v:286:PRO:HD2	1.98	0.45
2:58:15:G:H1'	49:28:420:A:H61	1.82	0.45
8:L6:160:HIS:HB3	8:L6:163:LYS:HD2	1.99	0.45
8:L6:285:TYR:HE1	32:ee:31:GLU:HG2	1.80	0.45
15:14:10:GLY:HA2	15:14:64:PHE:CE1	2.51	0.45
34:35:95:LEU:HB3	34:35:99:GLU:HB2	1.98	0.45
38:39:48:LYS:HD3	38:39:48:LYS:HA	1.63	0.45
44:t:16:ARG:CZ	44:t:57:ARG:HE	2.29	0.45
44:t:63:THR:HG22	44:t:65:GLN:OE1	2.17	0.45
45:EB:53:ASP:O	45:EB:56:ILE:HG22	2.17	0.45
48:ES:2950:G:H2'	48:ES:2951:G:C8	2.51	0.45
49:28:4619:U:H2'	49:28:4620:U:C6	2.51	0.45
50:25:107:ASN:HD21	50:25:111:GLU:HB2	1.81	0.45
2:58:8:U:H2'	2:58:9:A:H8	1.80	0.45
3:5:11:A:H4'	3:5:13:A:C8	2.52	0.45
5:L3:120:LYS:HD3	5:L3:120:LYS:HA	1.79	0.45
19:19:106:LEU:HB3	19:19:120:TYR:HE1	1.82	0.45
24:cc:91:GLU:HG3	24:cc:147:LEU:HD21	1.98	0.45
27:dd:145:VAL:HG13	35:36:5:TYR:CZ	2.52	0.45
31:32:35:TRP:CZ2	31:32:56:PRO:HD2	2.51	0.45
41:ff:39:CYS:HB3	41:ff:42:CYS:SG	2.56	0.45
44:t:61:LYS:HD2	44:t:74:VAL:HG22	1.97	0.45
48:ES:3247:A:H2'	48:ES:3248:C:C6	2.49	0.45
49:28:1338:G:H4'	49:28:1339:U:C6	2.51	0.45
49:28:1535:C:H2'	49:28:1536:U:O4'	2.17	0.45
49:28:3802:U:O2'	49:28:3803:A:H5'	2.16	0.45
49:28:4475:G:OP2	49:28:4476:C:H5''	2.17	0.45
49:28:4564:A:H2'	49:28:4565:C:C6	2.52	0.45
1:v:398:ILE:HG21	1:v:479:LEU:HD23	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:716:ARG:O	1:v:716:ARG:HG2	2.17	0.45
2:58:151:G:H8	2:58:151:G:OP1	1.99	0.45
3:5:89:G:OP2	3:5:89:G:H8	1.99	0.45
4:L8:44:ILE:HG12	4:L8:87:PHE:CE1	2.52	0.45
10:aa:148:LEU:HD21	10:aa:209:VAL:HG21	1.97	0.45
14:13:57:PRO:HG3	14:13:75:GLY:O	2.17	0.45
29:30:35:LEU:HD12	29:30:35:LEU:HA	1.83	0.45
30:31:62:VAL:HG22	30:31:104:THR:HB	1.98	0.45
37:38:42:LEU:HD22	49:28:2536:A:H5'	1.99	0.45
40:42:61:LYS:H	40:42:61:LYS:HG2	1.65	0.45
45:EB:322:THR:O	45:EB:333:ILE:HG22	2.17	0.45
46:u:191:VAL:HG21	46:u:198:TRP:CD1	2.52	0.45
48:ES:3580:G:H3'	48:ES:3581:C:H5''	1.98	0.45
49:28:407:A:O2'	49:28:408:A:H5'	2.17	0.45
49:28:914:U:C2'	49:28:915:A:H5''	2.47	0.45
49:28:3933:G:H2'	49:28:3934:G:H8	1.82	0.45
49:28:4130:C:H2'	49:28:4131:G:H8	1.82	0.45
49:28:4163:U:H5'	49:28:4164:C:H5''	1.99	0.45
49:28:4653:C:H2'	49:28:4654:C:C6	2.52	0.45
49:28:4761:G:H2'	49:28:4762:A:H8	1.82	0.45
49:28:4886:C:H2'	49:28:4887:C:H5''	1.97	0.45
1:v:590:LEU:HD11	1:v:603:TYR:HB3	1.99	0.45
2:58:70:G:H1'	2:58:88:A:N6	2.31	0.45
3:5:87:G:C5'	20:20:87:ARG:HD3	2.47	0.45
4:L8:116:LEU:HA	4:L8:164:ALA:HB2	1.99	0.45
5:L3:302:ASN:ND2	5:L3:330:PHE:HE1	2.14	0.45
8:L6:48:ARG:HD3	49:28:980:U:OP1	2.17	0.45
9:L7:85:GLU:HB3	21:21:135:PRO:HB3	1.98	0.45
10:aa:195:THR:O	10:aa:199:LEU:HG	2.16	0.45
11:L9:140:GLN:HB3	11:L9:143:GLU:HG3	1.98	0.45
13:11:78:LYS:O	13:11:82:ILE:HG13	2.16	0.45
17:bb:51:LYS:HA	17:bb:141:LEU:HD11	1.98	0.45
33:34:2:VAL:HG21	49:28:2807:A:H4'	1.98	0.45
35:36:58:MET:HG2	35:36:94:LEU:HD13	1.99	0.45
46:u:179:LEU:O	46:u:183:ILE:HG23	2.17	0.45
49:28:979:C:H42	49:28:1276:C:H42	1.65	0.45
49:28:1737:A:H2'	49:28:1738:A:O4'	2.17	0.45
49:28:2268:A:H4'	49:28:2269:C:H5''	1.98	0.45
49:28:2484:A:H2	49:28:2494:U:H3	1.65	0.45
49:28:3737:A:H2'	49:28:3738:G:O4'	2.17	0.45
1:v:12:ILE:HD13	1:v:99:LEU:HD21	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:aa:219:LEU:HA	16:15:7:ILE:HD11	1.99	0.45
15:14:77:TRP:NE1	15:14:82:ILE:HB	2.32	0.45
19:19:18:GLY:HA3	49:28:2822:G:H5''	1.99	0.45
40:42:68:LEU:HD11	40:42:85:ILE:HD11	1.98	0.45
43:s:29:ILE:HG23	43:s:191:GLN:H	1.81	0.45
49:28:1359:G:H3'	49:28:1360:G:C8	2.52	0.45
49:28:1414:C:H2'	49:28:1415:G:H8	1.81	0.45
49:28:2453:A:C5	49:28:2454:U:C5	3.05	0.45
49:28:2520:C:H2'	49:28:2521:G:H8	1.81	0.45
49:28:2633:U:H2'	49:28:2634:C:H6	1.81	0.45
49:28:3722:G:H2'	49:28:3723:A:H8	1.82	0.45
49:28:4948:C:H2'	49:28:4949:G:N2	2.32	0.45
4:L8:206:PRO:HD3	4:L8:213:GLY:CA	2.47	0.45
6:L4:150:LEU:HD12	6:L4:150:LEU:HA	1.69	0.45
8:L6:216:THR:HG23	8:L6:218:ALA:N	2.31	0.45
9:L7:46:ARG:NH1	49:28:976:G:H5''	2.32	0.45
10:aa:140:LEU:HD12	10:aa:140:LEU:HA	1.77	0.45
17:bb:165:LYS:HB2	17:bb:165:LYS:HE2	1.80	0.45
19:19:66:ASN:O	19:19:70:ARG:HG2	2.17	0.45
24:cc:64:SER:HB2	34:35:69:LEU:HD13	1.99	0.45
32:ee:28:LEU:HD22	32:ee:86:ALA:HB2	1.97	0.45
49:28:1398:A:C6	49:28:1419:G:N2	2.84	0.45
49:28:1559:G:H2'	49:28:1560:A:C8	2.52	0.45
49:28:1976:G:H1	49:28:1990:A:H61	1.65	0.45
49:28:3889:G:N7	49:28:4720:C:H2'	2.32	0.45
49:28:4518:A:O5'	49:28:4520:G:H4'	2.17	0.45
1:v:42:LYS:NZ	1:v:78:PHE:H	2.15	0.44
1:v:156:MET:HE2	1:v:156:MET:HB2	1.89	0.44
1:v:257:MET:HA	1:v:257:MET:HE3	1.99	0.44
1:v:456:ARG:HA	1:v:456:ARG:HD2	1.87	0.44
20:20:13:VAL:HG22	20:20:63:TYR:HB3	2.00	0.44
21:21:35:LYS:HE2	49:28:1824:G:H5''	1.99	0.44
43:s:31:GLY:HA2	43:s:86:VAL:HA	1.98	0.44
45:EB:192:GLN:O	45:EB:194:VAL:HG23	2.17	0.44
46:u:94:ASN:OD1	46:u:124:LEU:HD22	2.17	0.44
49:28:260:C:H2'	49:28:261:G:H8	1.81	0.44
49:28:647:G:H3'	49:28:648:G:H8	1.81	0.44
49:28:1234:G:C4	49:28:1235:G:N7	2.85	0.44
49:28:3664:G:H2'	49:28:3665:G:C8	2.52	0.44
1:v:89:ILE:HG22	1:v:356:ILE:HA	1.99	0.44
1:v:130:ASP:OD2	1:v:159:LYS:HE2	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:751:CYS:SG	1:v:755:VAL:HG23	2.56	0.44
3:5:3:C:H2'	3:5:4:U:H6	1.82	0.44
9:L7:32:LEU:O	9:L7:35:LYS:HG3	2.18	0.44
10:aa:273:GLU:O	10:aa:277:THR:HG23	2.17	0.44
18:17:42:ARG:HD3	18:17:42:ARG:HA	1.76	0.44
23:24:1:MET:HE3	23:24:1:MET:HB3	1.90	0.44
24:cc:152:LYS:HE2	24:cc:152:LYS:HB2	1.66	0.44
30:31:33:ILE:HA	30:31:33:ILE:HD13	1.63	0.44
31:32:90:MET:HE3	42:gg:113:ARG:HA	1.99	0.44
32:ee:46:ARG:O	32:ee:104:MET:HE2	2.17	0.44
45:EB:190:LEU:HD21	45:EB:225:ALA:HB2	1.98	0.44
49:28:1094:G:H2'	49:28:1095:A:C8	2.51	0.44
49:28:4684:A:H2'	49:28:4685:U:O4'	2.17	0.44
1:v:411:TYR:CD1	1:v:473:VAL:HG22	2.52	0.44
4:L8:141:PRO:O	4:L8:144:LYS:HD3	2.17	0.44
9:L7:97:ILE:HD12	9:L7:97:ILE:HA	1.75	0.44
10:aa:308:LYS:HB3	10:aa:308:LYS:HE3	1.79	0.44
11:L9:107:GLU:HG3	11:L9:110:SER:HB2	2.00	0.44
13:11:151:ILE:HD11	13:11:156:ARG:HG2	1.98	0.44
49:28:316:U:H3'	49:28:316:U:OP1	2.17	0.44
49:28:754:C:C2	49:28:755:C:C5	3.05	0.44
49:28:1846:G:H2'	49:28:1847:C:H6	1.83	0.44
49:28:1895:G:H2'	49:28:1896:A:O4'	2.17	0.44
49:28:1979:A:H4'	49:28:1980:U:OP1	2.18	0.44
1:v:215:GLY:HA3	1:v:222:ALA:HA	1.99	0.44
1:v:449:ARG:CZ	1:v:460:PRO:HB3	2.47	0.44
1:v:709:LEU:HD13	1:v:716:ARG:HD2	1.99	0.44
1:v:734:LEU:HD13	1:v:851:LEU:HD13	2.00	0.44
3:5:35:U:H2'	3:5:36:C:O4'	2.18	0.44
4:L8:117:GLU:HG2	4:L8:124:GLY:H	1.83	0.44
4:L8:181:LYS:HB2	49:28:1577:G:N7	2.32	0.44
5:L3:257:TRP:C	5:L3:257:TRP:CD1	2.95	0.44
5:L3:267:ALA:O	5:L3:268:ARG:HD2	2.16	0.44
8:L6:131:HIS:HB2	49:28:1281:G:C6	2.52	0.44
8:L6:193:HIS:HD2	8:L6:195:LYS:H	1.65	0.44
13:11:31:ASP:HA	13:11:34:THR:HG22	1.98	0.44
18:17:69:ARG:HD3	49:28:4981:G:H1'	1.99	0.44
27:dd:87:ARG:HE	47:Q:93:GLN:HG2	1.83	0.44
38:39:43:HIS:CE1	38:39:45:ARG:HB2	2.53	0.44
43:s:27:CYS:HB2	43:s:90:PHE:HD1	1.82	0.44
47:Q:11:ARG:HG3	49:28:2081:C:H5''	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:172:C:OP2	49:28:172:C:H6	2.01	0.44
49:28:481(A):C:H4'	49:28:484:U:P	2.58	0.44
49:28:1473:U:H2'	49:28:1474:C:H6	1.81	0.44
49:28:2683:C:H2'	49:28:2684:C:H6	1.83	0.44
49:28:2873:U:H2'	49:28:2875:C:C5	2.52	0.44
49:28:4093:G:H2'	49:28:4094:G:C8	2.53	0.44
1:v:636:ALA:HA	1:v:641:TRP:HB2	2.00	0.44
3:5:16:A:H2'	3:5:17:C:C6	2.51	0.44
8:L6:161:ARG:H	8:L6:161:ARG:HG3	1.43	0.44
12:10:22:PHE:CZ	49:28:1788:A:H2'	2.52	0.44
12:10:59:GLN:HB3	12:10:126:VAL:HG21	1.99	0.44
15:14:123:ILE:HD12	17:bb:182:GLU:HG3	1.97	0.44
34:35:52:LYS:HD3	34:35:52:LYS:HA	1.65	0.44
40:42:9:ARG:HA	40:42:20:PRO:HA	1.99	0.44
43:s:60:MET:HB2	43:s:60:MET:HE3	1.55	0.44
49:28:1882:U:C4	49:28:2279:A:C2	3.05	0.44
49:28:2546:G:H4'	49:28:2547:G:OP1	2.17	0.44
49:28:4670:C:O3'	49:28:4671:C:H3'	2.17	0.44
1:v:316:ILE:HG12	1:v:321:ILE:HD11	2.00	0.44
4:L8:14:SER:H	4:L8:17:ARG:HG3	1.82	0.44
4:L8:201:GLY:HA2	4:L8:204:MET:SD	2.58	0.44
5:L3:386:LYS:HE2	5:L3:386:LYS:HB3	1.75	0.44
9:L7:174:ILE:HD11	9:L7:186:MET:SD	2.57	0.44
44:t:54:LYS:HB3	44:t:54:LYS:HE3	1.75	0.44
45:EB:20:LYS:HA	45:EB:23:MET:HG2	1.99	0.44
49:28:1604:G:H2'	49:28:1605:G:C8	2.53	0.44
49:28:2715:G:H2'	49:28:2716:C:H6	1.83	0.44
49:28:4192:A:H2'	49:28:4193:C:C6	2.51	0.44
49:28:4602:A:H3'	49:28:4603:C:H6	1.83	0.44
49:28:5031:G:H2'	49:28:5032:C:C6	2.53	0.44
1:v:186:ASN:HD21	43:s:147:ILE:HD12	1.83	0.44
1:v:400:LYS:NZ	1:v:481:LYS:HA	2.33	0.44
2:58:116:C:H2'	2:58:117:C:C6	2.53	0.44
8:L6:49:ASN:H	8:L6:64:MET:HE1	1.80	0.44
8:L6:114:LYS:HG2	49:28:459:C:OP1	2.18	0.44
11:L9:174:LYS:HG2	39:40:101:VAL:HG21	1.99	0.44
15:14:119:ARG:O	15:14:123:ILE:HG12	2.17	0.44
43:s:30:VAL:HA	43:s:189:ILE:HA	1.99	0.44
43:s:59:THR:O	43:s:62:ARG:HG2	2.18	0.44
49:28:1338:G:H4'	49:28:1339:U:H6	1.82	0.44
49:28:2391:G:H2'	49:28:2392:C:C6	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:2624:G:H2'	49:28:2625:U:C6	2.50	0.44
49:28:2671:C:H2'	49:28:2672:C:C6	2.53	0.44
49:28:4345:C:H2'	49:28:4346:U:C6	2.53	0.44
1:v:690:GLY:H	1:v:694:GLU:C	2.26	0.44
4:L8:75:LEU:HD23	4:L8:75:LEU:HA	1.79	0.44
5:L3:223:THR:O	5:L3:274:TYR:HA	2.17	0.44
7:L5:187:SER:HB2	7:L5:189:GLU:OE1	2.17	0.44
10:aa:199:LEU:HB2	10:aa:204:LYS:HB2	2.00	0.44
35:36:30:ARG:HD2	49:28:327:U:O2'	2.18	0.44
47:Q:144:LYS:HG2	49:28:1460:C:H5''	1.98	0.44
49:28:391:U:H2'	49:28:392:U:C6	2.52	0.44
49:28:434:A:H2'	49:28:435:A:O4'	2.18	0.44
49:28:483:G:H5'	49:28:484:U:H2'	1.98	0.44
49:28:976:G:O5'	49:28:976:G:H8	2.00	0.44
49:28:1999:A:H2'	49:28:2000:G:C4	2.53	0.44
49:28:3727:A:H2'	49:28:3728:A:C8	2.52	0.44
49:28:4491:G:N3	49:28:4511:A:H2	2.15	0.44
1:v:200:MET:HE3	1:v:200:MET:HB3	1.80	0.44
1:v:214:PHE:HB2	1:v:223:PHE:CE1	2.53	0.44
1:v:396:MET:HG3	1:v:415:ARG:C	2.43	0.44
4:L8:225:ILE:HD13	4:L8:234:LYS:HA	1.99	0.44
8:L6:116:PRO:HA	49:28:458:C:OP1	2.18	0.44
9:L7:93:ARG:HB2	9:L7:113:LEU:HB3	2.00	0.44
11:L9:117:PHE:CE1	11:L9:118:LEU:HD23	2.53	0.44
15:14:53:LYS:HE2	15:14:53:LYS:HB2	1.54	0.44
26:27:51:ARG:HB2	26:27:65:ARG:CG	2.48	0.44
49:28:2465:C:H2'	49:28:2466:G:O4'	2.18	0.44
49:28:4503:A:H2'	49:28:4504:C:C6	2.52	0.44
49:28:4968:A:H2'	49:28:4969:C:H6	1.83	0.44
1:v:376:PRO:HG2	1:v:379:ASP:OD1	2.18	0.43
3:5:27:G:H5''	7:L5:57:ASN:ND2	2.32	0.43
5:L3:34:LYS:HE2	5:L3:34:LYS:HB2	1.83	0.43
5:L3:285:TYR:OH	5:L3:334:LYS:HD2	2.18	0.43
10:aa:158:GLU:HB2	10:aa:162:GLU:HB2	2.00	0.43
11:L9:43:VAL:HG12	11:L9:59:LYS:HD3	2.00	0.43
13:11:20:LEU:HG	13:11:22:LEU:HD21	2.00	0.43
15:14:15:VAL:HG23	15:14:23:LYS:O	2.18	0.43
17:bb:28:LEU:HD22	17:bb:94:ARG:NH2	2.33	0.43
19:19:71:ARG:HH12	49:28:3604:A:H5''	1.83	0.43
37:38:7:GLU:CG	37:38:10:ASP:HB2	2.48	0.43
49:28:286:U:H2'	49:28:287:U:C6	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1205:G:H2'	49:28:1206:C:H6	1.82	0.43
49:28:1941:A:C2	49:28:4434:C:H5'	2.53	0.43
49:28:3933:G:H2'	49:28:3934:G:C8	2.54	0.43
49:28:4607:A:O5'	49:28:4607:A:H8	2.01	0.43
49:28:4770:U:H2'	49:28:4771:C:O4'	2.18	0.43
49:28:4879:C:H2'	49:28:4880:C:O2	2.18	0.43
1:v:231:MET:HE2	1:v:231:MET:HB2	1.84	0.43
13:11:136:ARG:HB2	13:11:139:PHE:CE1	2.52	0.43
20:20:115:ALA:HB2	49:28:2060:G:N2	2.32	0.43
25:26:109:LEU:HA	25:26:109:LEU:HD23	1.76	0.43
34:35:4:ILE:HD13	34:35:4:ILE:HA	1.83	0.43
44:t:53:TRP:CZ3	44:t:83:LYS:HD2	2.53	0.43
45:EB:80:ILE:HG23	45:EB:106:VAL:HG13	2.01	0.43
49:28:2001:G:OP2	49:28:2001:G:H8	2.01	0.43
49:28:2020:U:H2'	49:28:2021:G:H8	1.83	0.43
49:28:2040:A:H4'	49:28:2041:A:H5''	2.00	0.43
49:28:2715:G:H2'	49:28:2716:C:C6	2.52	0.43
49:28:3684:G:H2'	49:28:3685:C:C6	2.52	0.43
49:28:4390:A:H2'	49:28:4391:G:O4'	2.18	0.43
1:v:174:LEU:O	1:v:177:THR:HG22	2.18	0.43
6:L4:305:PRO:HB3	47:Q:38:ARG:HH12	1.83	0.43
7:L5:41:LYS:HB2	21:21:68:THR:O	2.19	0.43
7:L5:244:HIS:O	7:L5:248:ARG:HG3	2.19	0.43
14:13:129:ARG:HH22	49:28:173:C:H5''	1.82	0.43
16:15:64:ILE:HD11	16:15:102:ALA:HA	2.00	0.43
18:17:69:ARG:H	18:17:69:ARG:HG3	1.52	0.43
39:40:54:PRO:O	39:40:58:GLN:HG2	2.18	0.43
46:u:156:LYS:HE2	46:u:158:GLN:HB2	2.00	0.43
46:u:207:LYS:HD3	46:u:207:LYS:HA	1.72	0.43
49:28:966:A:N6	49:28:2096:G:H2'	2.34	0.43
49:28:1973:G:H2'	49:28:1974:U:H5	1.83	0.43
49:28:4459:U:H2'	49:28:4460:U:H6	1.83	0.43
49:28:4543:G:H2'	49:28:4544:A:C8	2.52	0.43
49:28:4907:G:C2	49:28:4915:G:C2	3.07	0.43
2:58:19:C:H2'	2:58:20:A:H8	1.83	0.43
13:11:60:PHE:HB3	49:28:4257:A:C2	2.54	0.43
45:EB:36:VAL:HG13	45:EB:125:PHE:CE1	2.53	0.43
46:u:91:LYS:HD3	46:u:91:LYS:HA	1.63	0.43
48:ES:2941:G:H2'	48:ES:2941:G:N3	2.33	0.43
48:ES:3242:U:H2'	48:ES:3243:C:C6	2.53	0.43
49:28:402:A:H2'	49:28:403:G:H8	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:983:C:N4	49:28:1071:C:H42	2.09	0.43
49:28:2784:C:H2'	49:28:2785:C:H6	1.83	0.43
49:28:3697:U:H5''	49:28:3698:G:H5'	2.01	0.43
49:28:3911:C:C2	49:28:3912:U:C5	3.07	0.43
49:28:4933:C:H2'	49:28:4934:A:C8	2.53	0.43
6:L4:305:PRO:HB3	47:Q:38:ARG:NH1	2.34	0.43
11:L9:115:ARG:HG2	11:L9:123:ILE:HG22	2.00	0.43
14:13:63:THR:O	14:13:65:ARG:N	2.52	0.43
15:14:12:VAL:HG11	15:14:24:LEU:HD13	1.99	0.43
18:17:131:ARG:HH11	18:17:137:ASN:HD22	1.66	0.43
28:29:105:GLY:O	28:29:109:ARG:HG2	2.18	0.43
43:s:50:LYS:NZ	43:s:98:ILE:HG13	2.33	0.43
49:28:137:G:C2	49:28:138:G:C5	3.06	0.43
49:28:1065:G:H2'	49:28:1066:G:C8	2.54	0.43
49:28:1959:U:O4'	49:28:1961:G:H1'	2.18	0.43
49:28:2870:A:H2'	49:28:2871:A:C8	2.54	0.43
49:28:4088:C:H2'	49:28:4089:G:C8	2.54	0.43
49:28:4421:C:H42	49:28:4475:G:H22	1.66	0.43
49:28:4477:A:H2'	49:28:4478:G:C8	2.54	0.43
49:28:4962:C:H2'	49:28:4963:G:O4'	2.18	0.43
1:v:266:PHE:HB2	1:v:288:THR:HG22	2.01	0.43
1:v:303:ALA:HA	1:v:308:LYS:HG3	2.00	0.43
3:5:3:C:H2'	3:5:4:U:C6	2.54	0.43
5:L3:29:VAL:HG13	5:L3:348:ARG:HD3	2.01	0.43
5:L3:357:ARG:CZ	49:28:4615:C:H5''	2.49	0.43
18:17:33:ALA:HB1	18:17:117:ILE:HG12	2.01	0.43
23:24:44:ARG:HA	23:24:44:ARG:HD3	1.71	0.43
27:dd:38:MET:HE1	49:28:4340:U:H1'	2.00	0.43
27:dd:100:ILE:HG13	27:dd:123:ILE:HB	1.99	0.43
31:32:12:ILE:HD13	31:32:66:THR:HB	2.00	0.43
34:35:104:THR:O	34:35:108:GLN:HG3	2.18	0.43
49:28:987:C:H2'	49:28:988:C:C6	2.54	0.43
49:28:1672:U:H2'	49:28:1673:U:C6	2.52	0.43
49:28:1830:G:O2'	49:28:1831:G:H5'	2.19	0.43
49:28:2015:U:H2'	49:28:2016:C:H6	1.84	0.43
49:28:2515:G:H1'	49:28:2745:A:N1	2.33	0.43
49:28:2683:C:H2'	49:28:2684:C:C6	2.54	0.43
49:28:3715:U:H5	49:28:3738:G:C6	2.37	0.43
49:28:4970:C:C2	49:28:4971:A:C8	3.06	0.43
3:5:52:C:H1'	13:11:12:MET:CE	2.49	0.43
7:L5:258:LYS:HB2	7:L5:258:LYS:HE2	1.91	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L6:193:HIS:CD2	8:L6:195:LYS:H	2.37	0.43
8:L6:285:TYR:CE1	32:ee:31:GLU:HG2	2.53	0.43
12:10:28:ASP:OD2	12:10:32:ARG:HD3	2.19	0.43
13:11:109:ILE:HD11	13:11:128:LEU:HD21	2.00	0.43
16:15:179:LYS:O	49:28:298:G:H5'	2.19	0.43
16:15:198:LEU:HA	16:15:198:LEU:HD23	1.76	0.43
24:cc:146:ALA:HA	24:cc:149:VAL:HG22	1.99	0.43
28:29:36:ASP:HB2	49:28:4314:C:O2'	2.19	0.43
47:Q:14:ARG:HH12	47:Q:16:LYS:HE2	1.84	0.43
49:28:300:A:H2'	49:28:301:G:H8	1.84	0.43
49:28:1433:A:N7	49:28:1451:G:N2	2.66	0.43
49:28:2268:A:H5''	49:28:2270:G:O4'	2.19	0.43
49:28:2439:G:H5'	49:28:2778:G:OP2	2.18	0.43
49:28:4344:U:H2'	49:28:4345:C:H6	1.84	0.43
49:28:4761:G:H2'	49:28:4762:A:C8	2.53	0.43
49:28:5008:C:H2'	49:28:5009:G:O4'	2.18	0.43
1:v:839:ARG:HD2	1:v:845:LYS:O	2.18	0.43
2:58:27:U:H2'	2:58:28:C:H6	1.82	0.43
5:L3:71:GLU:OE1	23:24:1:MET:HB2	2.18	0.43
6:L4:42:THR:HB	49:28:2340:C:H4'	2.00	0.43
11:L9:98:HIS:CD2	49:28:4602:A:H5''	2.53	0.43
12:10:36:LEU:CD2	12:10:69:ARG:HH11	2.31	0.43
18:17:64:ASN:HD22	18:17:80:GLN:HE22	1.66	0.43
20:20:28:TYR:CE1	20:20:52:LYS:HE3	2.54	0.43
21:21:34:TYR:HE2	21:21:93:ILE:HG23	1.83	0.43
46:u:24:LYS:HA	46:u:24:LYS:HD2	1.74	0.43
49:28:2381:A:H1'	49:28:2383:C:OP2	2.18	0.43
49:28:2784:C:H2'	49:28:2785:C:C6	2.54	0.43
49:28:3722:G:H2'	49:28:3723:A:C8	2.54	0.43
49:28:4361:U:H2'	49:28:4362:A:O4'	2.18	0.43
49:28:4756:C:H5'	49:28:4757:C:OP1	2.19	0.43
1:v:32:LYS:HB2	51:v:900:GDP:O1B	2.19	0.43
2:58:103:A:N3	49:28:21:G:H1'	2.34	0.43
2:58:120:G:H2'	2:58:121:G:C8	2.53	0.43
4:L8:11:GLY:HA3	49:28:3667:C:O2'	2.19	0.43
5:L3:101:THR:HG21	49:28:4723:A:N3	2.34	0.43
9:L7:27:LEU:HD12	9:L7:27:LEU:HA	1.81	0.43
9:L7:235:ARG:HB2	9:L7:238:GLN:HB2	2.00	0.43
18:17:114:ILE:HB	18:17:150:LEU:HD22	2.00	0.43
20:20:48:VAL:HG12	20:20:54:MET:HB2	2.01	0.43
26:27:12:LEU:HB2	26:27:81:MET:HB3	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:dd:74:ASN:HA	27:dd:112:LEU:O	2.19	0.43
33:34:26:PRO:HA	49:28:2639:U:H1'	2.00	0.43
43:s:120:GLU:HG3	43:s:159:GLN:NE2	2.26	0.43
45:EB:259:MET:HE3	45:EB:259:MET:HB2	1.75	0.43
47:Q:49:LYS:HB3	47:Q:49:LYS:HE2	1.76	0.43
49:28:2391:G:H2'	49:28:2392:C:H6	1.84	0.43
49:28:4345:C:H2'	49:28:4346:U:H6	1.82	0.43
49:28:4893:A:H2'	49:28:4894:A:C4	2.54	0.43
49:28:4944:C:H4'	49:28:4944:C:OP1	2.19	0.43
1:v:226:LYS:NZ	1:v:226:LYS:HB3	2.34	0.43
4:L8:109:GLU:H	4:L8:109:GLU:HG2	1.61	0.43
4:L8:112:ILE:HD13	4:L8:135:THR:HB	2.01	0.43
5:L3:115:LYS:HE3	5:L3:129:ALA:O	2.19	0.43
8:L6:164:ARG:HD3	8:L6:273:TYR:CZ	2.54	0.43
17:bb:16:LEU:HD11	17:bb:83:THR:HG21	1.99	0.43
20:20:102:THR:O	20:20:106:VAL:HG23	2.19	0.43
37:38:12:LEU:HD21	37:38:56:LEU:HD11	2.01	0.43
49:28:269:G:H2'	49:28:270:U:H6	1.84	0.43
49:28:351:C:H2'	49:28:352:G:O4'	2.19	0.43
49:28:964:A:C2	49:28:968:C:H1'	2.54	0.43
49:28:1218:G:C2	49:28:1219:G:C5	3.07	0.43
49:28:2095:A:H2'	49:28:2096:G:C8	2.54	0.43
49:28:2409:U:C5	49:28:2783:A:N1	2.87	0.43
49:28:2491:C:H2'	49:28:2492:C:C6	2.53	0.43
49:28:3652:A:H2'	49:28:3653:A:C5	2.53	0.43
49:28:3821:A:H2'	49:28:3822:U:O4'	2.18	0.43
49:28:4311:A:O2'	49:28:4312:U:H5'	2.19	0.43
49:28:4520:G:H2'	49:28:4521:U:O4'	2.18	0.43
1:v:218:LEU:HB2	51:v:900:GDP:C5	2.54	0.42
1:v:430:MET:HE1	1:v:486:THR:H	1.83	0.42
3:5:18:C:H2'	3:5:19:C:C6	2.53	0.42
3:5:66:G:H2'	3:5:67:C:C6	2.54	0.42
4:L8:46:LYS:HD3	4:L8:46:LYS:HA	1.88	0.42
6:L4:338:ASN:C	6:L4:340:ILE:H	2.27	0.42
8:L6:59:TYR:CZ	8:L6:67:ARG:NH2	2.87	0.42
11:L9:91:LYS:HB2	11:L9:183:GLU:HB3	2.01	0.42
15:14:13:ALA:HA	15:14:57:LEU:HA	2.01	0.42
31:32:11:LYS:HB2	31:32:11:LYS:HE2	1.69	0.42
33:34:44:SER:HA	33:34:53:LEU:HD11	2.00	0.42
46:u:90:LEU:HA	46:u:90:LEU:HD13	1.66	0.42
46:u:93:LEU:HD13	46:u:93:LEU:HA	1.66	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:424:U:H2'	49:28:425:U:C6	2.54	0.42
49:28:1370:G:H4'	49:28:1371:A:O5'	2.18	0.42
49:28:1813:U:H2'	49:28:1814:C:C6	2.53	0.42
1:v:767:ARG:HD2	1:v:789:PRO:HG2	2.00	0.42
1:v:838:THR:O	1:v:841:ARG:HG2	2.18	0.42
2:58:3:A:H2'	2:58:4:C:C6	2.53	0.42
7:L5:30:TYR:HA	7:L5:33:ARG:HB3	2.01	0.42
7:L5:156:GLY:HA2	7:L5:181:PRO:HD3	2.00	0.42
16:15:68:ARG:HD2	16:15:124:ASP:O	2.19	0.42
20:20:161:ARG:HD2	49:28:1921:C:C2	2.54	0.42
27:dd:62:HIS:NE2	27:dd:64:LYS:HE2	2.34	0.42
33:34:82:MET:HE2	33:34:82:MET:HB3	1.88	0.42
37:38:9:LYS:HG3	37:38:10:ASP:N	2.35	0.42
37:38:41:TYR:HE2	49:28:2772:C:OP1	2.01	0.42
38:39:9:ILE:O	38:39:13:LEU:HG	2.19	0.42
41:ff:46:LYS:HE3	41:ff:46:LYS:HB3	1.83	0.42
45:EB:35:LEU:HD21	45:EB:108:ILE:HG21	2.00	0.42
45:EB:63:ILE:HB	45:EB:64:PHE:HD2	1.84	0.42
46:u:22:GLN:NE2	46:u:22:GLN:H	2.17	0.42
47:Q:18:PRO:HD3	47:Q:52:PHE:CD1	2.53	0.42
48:ES:3587:C:H2'	48:ES:3588:C:C6	2.54	0.42
49:28:38:A:H61	49:28:41:C:H3'	1.83	0.42
49:28:1200:G:H2'	49:28:1201:U:C6	2.54	0.42
49:28:1201:U:H2'	49:28:1202:C:C6	2.53	0.42
49:28:1443:A:H3'	49:28:1444:G:H8	1.83	0.42
49:28:2002:A:H2'	49:28:2002:A:N3	2.33	0.42
49:28:4233:A:C5	49:28:4235:G:C8	3.08	0.42
49:28:4652:G:H2'	49:28:4653:C:C6	2.54	0.42
1:v:39:LEU:HA	1:v:39:LEU:HD13	1.82	0.42
1:v:128:VAL:HB	1:v:156:MET:HG3	2.01	0.42
1:v:180:ARG:HH22	43:s:144:THR:HG22	1.84	0.42
1:v:259:LYS:HA	1:v:264:ARG:HD2	2.01	0.42
2:58:147:G:H2'	2:58:148:A:H8	1.85	0.42
6:L4:101:MET:HE2	6:L4:101:MET:HB2	1.80	0.42
11:L9:20:LEU:HD21	11:L9:47:LEU:HB2	2.01	0.42
14:13:48:PRO:HG3	34:35:118:LYS:HE3	2.01	0.42
17:bb:182:GLU:O	17:bb:186:GLU:HG3	2.19	0.42
19:19:59:SER:HA	49:28:2634:C:H5'	2.00	0.42
21:21:87:LYS:HE3	49:28:4305:G:H22	1.84	0.42
24:cc:76:ILE:HD11	24:cc:109:ILE:HA	2.02	0.42
31:32:38:PRO:O	31:32:46:ARG:HG3	2.18	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:34:60:ARG:HG3	33:34:61:PRO:HD2	2.01	0.42
48:ES:2950:G:H2'	48:ES:2951:G:H8	1.83	0.42
49:28:323:C:H1'	49:28:4355:G:N2	2.35	0.42
49:28:760:G:H3'	49:28:760:G:N3	2.34	0.42
49:28:1081:C:H42	49:28:1218:G:H1	1.66	0.42
49:28:1956:A:O2'	49:28:1957:U:H5'	2.20	0.42
49:28:3665:G:H2'	49:28:3666:C:C6	2.53	0.42
49:28:4499:G:C2	49:28:4529:G:H1'	2.54	0.42
1:v:426:LYS:HE2	1:v:446:PRO:HD3	2.02	0.42
2:58:154:G:H4'	10:aa:242:ARG:NH2	2.34	0.42
3:5:55:A:H4'	13:11:155:HIS:HB2	2.02	0.42
5:L3:331:VAL:HG21	5:L3:347:LEU:HD21	2.02	0.42
6:L4:110:ARG:HD2	16:15:204:ARG:HG3	2.02	0.42
6:L4:150:LEU:HB3	6:L4:151:PRO:HD3	2.01	0.42
11:L9:88:PHE:CZ	11:L9:151:ILE:HB	2.54	0.42
28:29:3:LYS:HD3	49:28:4194:U:H3'	2.00	0.42
47:Q:168:ARG:HG2	47:Q:169:SER:OG	2.18	0.42
48:ES:2947:G:N1	48:ES:3247:A:H2	2.03	0.42
49:28:171:U:H4'	49:28:172:C:OP1	2.19	0.42
49:28:754:C:H2'	49:28:755:C:C6	2.54	0.42
49:28:760:G:O2'	49:28:904:C:H1'	2.19	0.42
49:28:2019:C:H2'	49:28:2020:U:H6	1.84	0.42
49:28:3652:A:C2'	49:28:3653:A:C8	3.02	0.42
49:28:4582:C:O2'	49:28:4583:C:H5'	2.18	0.42
49:28:4638:U:H2'	49:28:4639:G:N3	2.34	0.42
1:v:301:PHE:CE2	1:v:336:LEU:HD21	2.54	0.42
1:v:650:TRP:CZ3	1:v:704:VAL:HG21	2.55	0.42
3:5:82:G:H2'	3:5:83:A:C8	2.54	0.42
4:L8:242:ARG:HG2	49:28:3745:U:H4'	2.00	0.42
6:L4:28:PHE:HA	6:L4:129:ALA:HA	2.00	0.42
10:aa:160:LYS:HD3	10:aa:160:LYS:HA	1.80	0.42
15:14:3:PHE:HE1	20:20:155:PRO:HA	1.84	0.42
16:15:41:ARG:CZ	16:15:41:ARG:HB3	2.49	0.42
19:19:96:MET:HG2	49:28:2667:C:O4'	2.20	0.42
27:dd:87:ARG:NH2	47:Q:93:GLN:HG2	2.32	0.42
34:35:113:LEU:HD23	34:35:113:LEU:HA	1.86	0.42
44:t:142:ASN:HA	44:t:146:ARG:NH1	2.34	0.42
46:u:191:VAL:HG11	46:u:198:TRP:CD1	2.55	0.42
49:28:1307:A:H2'	49:28:1308:C:C6	2.54	0.42
49:28:1804:A:H4'	49:28:1805:A:O5'	2.19	0.42
49:28:2485:U:H2'	49:28:2486:G:C8	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:2633:U:H2'	49:28:2634:C:C6	2.54	0.42
49:28:4419:U:OP1	49:28:4421:C:N4	2.52	0.42
49:28:4458:C:H2'	49:28:4459:U:C6	2.54	0.42
6:L4:110:ARG:CD	16:15:204:ARG:HG3	2.49	0.42
7:L5:279:ARG:HD3	7:L5:283:LYS:HE3	2.02	0.42
10:aa:282:ARG:O	10:aa:286:ILE:HG13	2.19	0.42
11:L9:8:GLN:HE21	11:L9:8:GLN:HB2	1.59	0.42
11:L9:74:CYS:O	11:L9:78:GLN:HG3	2.20	0.42
16:15:192:TRP:CD1	49:28:48:G:H5'	2.55	0.42
37:38:7:GLU:HG3	37:38:10:ASP:H	1.84	0.42
44:t:138:SER:HA	49:28:1976:G:H21	1.85	0.42
45:EB:23:MET:O	45:EB:27:ILE:HG13	2.19	0.42
46:u:157:PHE:HB2	46:u:193:LEU:HD23	2.02	0.42
49:28:170:C:H2'	49:28:171:U:H4'	2.01	0.42
49:28:1609:U:H2'	49:28:1610:C:O4'	2.20	0.42
49:28:2488:C:H3'	49:28:2490:U:O4	2.20	0.42
49:28:2632:U:H2'	49:28:2633:U:H6	1.84	0.42
1:v:232:TYR:HE2	1:v:292:LEU:HB3	1.84	0.42
5:L3:235:TRP:CD1	5:L3:267:ALA:HB1	2.54	0.42
8:L6:121:THR:HG22	31:32:90:MET:HE2	2.02	0.42
9:L7:86:PRO:HG3	9:L7:143:TYR:CE2	2.54	0.42
9:L7:143:TYR:CE2	9:L7:236:GLU:HB3	2.55	0.42
13:11:13:ARG:HE	13:11:13:ARG:HB3	1.42	0.42
20:20:87:ARG:HG3	49:28:2034:G:OP1	2.19	0.42
28:29:36:ASP:OD1	28:29:39:PHE:HB3	2.20	0.42
37:38:5:ILE:HD12	37:38:6:GLU:H	1.85	0.42
46:u:190:LEU:O	46:u:194:LEU:HG	2.18	0.42
47:Q:78:LYS:HG3	47:Q:135:GLY:O	2.20	0.42
49:28:1479:G:H2'	49:28:1480:C:C6	2.55	0.42
49:28:2865:U:H2'	49:28:2866:C:H6	1.83	0.42
49:28:4350:C:C2	49:28:4351:U:C5	3.08	0.42
49:28:5006:U:H4'	49:28:5007:A:H5'	2.02	0.42
1:v:27:HIS:HB3	1:v:30:HIS:CD2	2.55	0.42
1:v:221:TRP:CG	1:v:340:MET:HB3	2.54	0.42
2:58:62:A:H4'	2:58:63:U:O5'	2.20	0.42
4:L8:179:ILE:HG23	4:L8:184:ARG:HB2	2.01	0.42
5:L3:60:VAL:HG12	5:L3:62:ARG:HG2	2.00	0.42
7:L5:259:ARG:NH2	7:L5:262:LYS:HE2	2.34	0.42
10:aa:193:VAL:HG22	49:28:150:U:OP2	2.20	0.42
10:aa:228:ARG:HG3	10:aa:283:TYR:CG	2.54	0.42
15:14:69:ARG:HG2	49:28:919:C:OP1	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:bb:89:PRO:O	17:bb:95:GLY:HA3	2.20	0.42
18:17:18:ARG:O	49:28:399:G:H4'	2.19	0.42
22:22:21:PHE:CE1	22:22:80:LYS:HB2	2.55	0.42
26:27:98:LYS:HE2	26:27:98:LYS:HB3	1.82	0.42
46:u:68:LEU:HG	46:u:116:LEU:HD22	2.02	0.42
48:ES:3250:C:H2'	48:ES:3251:G:C8	2.54	0.42
49:28:1957:U:O2'	49:28:1958:A:H8	2.03	0.42
49:28:4899:G:H1	49:28:4922:C:H42	1.67	0.42
10:aa:169:ALA:O	10:aa:172:GLU:HG3	2.20	0.42
11:L9:35:ARG:HB2	11:L9:35:ARG:NH1	2.35	0.42
11:L9:63:ASN:O	11:L9:67:LEU:HG	2.20	0.42
15:14:93:LYS:O	15:14:96:GLU:HG3	2.20	0.42
22:22:40:GLU:HG2	22:22:44:GLN:HE21	1.85	0.42
30:31:91:LYS:HB2	30:31:103:TYR:CZ	2.55	0.42
41:ff:36:LYS:NZ	41:ff:36:LYS:HB2	2.34	0.42
43:s:94:ASP:HB3	43:s:97:GLU:OE1	2.20	0.42
43:s:125:ALA:HB2	43:s:156:SER:C	2.45	0.42
49:28:717:U:O2'	49:28:1904:G:H4'	2.20	0.42
49:28:963:G:O2'	49:28:964:A:H5''	2.20	0.42
49:28:1235:G:O2'	49:28:1236:C:H2'	2.20	0.42
49:28:1559:G:H2'	49:28:1560:A:H8	1.84	0.42
49:28:2745:A:H2'	49:28:2746:A:C8	2.55	0.42
49:28:3900:G:OP1	49:28:3901:A:H4'	2.20	0.42
49:28:3916:G:H2'	49:28:3917:A:C8	2.55	0.42
49:28:4093:G:C2	49:28:4094:G:C5	3.08	0.42
3:5:22:A:H2'	3:5:23:A:C8	2.55	0.42
4:L8:30:ARG:HH12	4:L8:33:ASP:CG	2.28	0.42
5:L3:81:THR:OG1	5:L3:207:VAL:HG21	2.20	0.42
9:L7:178:LEU:HB3	9:L7:183:ILE:HB	2.02	0.42
12:10:189:ARG:HD2	12:10:189:ARG:HA	1.67	0.42
21:21:11:THR:HG22	21:21:14:MET:HE2	2.01	0.42
28:29:7:HIS:O	49:28:1873:A:H5'	2.19	0.42
30:31:64:ILE:HB	30:31:68:LEU:HD23	2.01	0.42
31:32:58:ILE:HA	31:32:58:ILE:HD12	1.84	0.42
33:34:9:ARG:HD3	49:28:2441:C:H4'	2.02	0.42
33:34:97:ILE:HD13	49:28:4120:U:C4	2.55	0.42
34:35:102:LEU:HD23	34:35:102:LEU:HA	1.82	0.42
40:42:55:ILE:HB	40:42:57:ARG:NH1	2.34	0.42
45:EB:181:PRO:HG2	45:EB:204:ASN:ND2	2.35	0.42
46:u:195:LYS:HG3	46:u:196:LYS:HG2	2.01	0.42
47:Q:13:VAL:O	49:28:1691:G:H5''	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:23:C:H2'	49:28:24:G:O4'	2.20	0.42
49:28:423:G:H2'	49:28:424:U:O4'	2.20	0.42
49:28:478:G:H2'	49:28:479:G:C8	2.55	0.42
4:L8:225:ILE:HD11	4:L8:233:ARG:HG3	2.02	0.41
6:L4:134:PRO:HA	6:L4:150:LEU:HD22	2.01	0.41
11:L9:128:MET:SD	11:L9:157:SER:HB2	2.59	0.41
12:10:212:LEU:HA	12:10:212:LEU:HD13	1.82	0.41
22:22:23:LEU:HD21	22:22:83:LEU:HD11	2.02	0.41
24:cc:83:THR:HG21	49:28:2434:G:O3'	2.20	0.41
25:26:89:LYS:HE2	25:26:95:VAL:HG21	2.02	0.41
28:29:113:ALA:O	28:29:117:ARG:HG3	2.20	0.41
39:40:100:LYS:HE3	39:40:100:LYS:HB3	1.81	0.41
40:42:61:LYS:HE2	40:42:61:LYS:HB3	1.46	0.41
45:EB:355:LYS:HA	45:EB:355:LYS:HD2	1.68	0.41
49:28:1499:C:H2'	49:28:1500:A:O4'	2.20	0.41
49:28:1519:C:H2'	49:28:1520:C:H6	1.85	0.41
49:28:1973:G:OP2	49:28:1974:U:H3'	2.19	0.41
49:28:2705:G:C6	49:28:2706:G:C6	3.07	0.41
49:28:4266:G:N3	49:28:4266:G:H2'	2.35	0.41
49:28:4861:G:H2'	49:28:4862:G:H8	1.84	0.41
49:28:4948:C:H2'	49:28:4949:G:H21	1.85	0.41
1:v:232:TYR:OH	1:v:292:LEU:HD12	2.20	0.41
1:v:415:ARG:HD2	1:v:417:PHE:CD1	2.55	0.41
2:58:56:G:H2'	2:58:57:C:O4'	2.20	0.41
2:58:94:G:H1'	36:37:82:THR:O	2.19	0.41
6:L4:76:ILE:HG13	6:L4:77:PRO:N	2.35	0.41
14:13:184:MET:HE2	14:13:184:MET:HB2	1.61	0.41
17:bb:99:LEU:HD23	17:bb:99:LEU:HA	1.93	0.41
27:dd:59:ARG:HE	27:dd:59:ARG:HB2	1.69	0.41
34:35:17:LEU:HB3	34:35:61:ILE:HD11	2.01	0.41
35:36:97:MET:HE3	35:36:97:MET:HB2	1.84	0.41
37:38:33:LYS:HE2	49:28:2693:G:OP2	2.19	0.41
40:42:26:TYR:HB3	40:42:67:VAL:HB	2.02	0.41
43:s:51:ALA:HB2	43:s:91:THR:HB	2.02	0.41
45:EB:347:MET:HE3	45:EB:347:MET:HB3	1.88	0.41
49:28:123:C:H2'	49:28:124:C:C6	2.56	0.41
49:28:2704:C:H2'	49:28:2705:G:O4'	2.19	0.41
49:28:4068:U:H2'	49:28:4069:U:O4'	2.19	0.41
49:28:4071:U:H2'	49:28:4072:C:C6	2.55	0.41
49:28:4625:C:O2'	49:28:4626:A:H5'	2.20	0.41
1:v:364:ALA:HA	1:v:367:TYR:CZ	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:58:139:G:H2'	2:58:140:C:O4'	2.20	0.41
2:58:151:G:OP1	2:58:151:G:C8	2.73	0.41
3:5:94:C:H2'	3:5:95:C:H6	1.84	0.41
4:L8:92:LYS:HA	4:L8:103:PRO:HD2	2.03	0.41
4:L8:136:VAL:HA	4:L8:148:VAL:HG22	2.01	0.41
4:L8:201:GLY:HA3	4:L8:209:HIS:CE1	2.55	0.41
6:L4:174:LEU:HD23	6:L4:174:LEU:HA	1.84	0.41
7:L5:160:PHE:HA	7:L5:163:LEU:HB3	2.02	0.41
8:L6:49:ASN:HB3	8:L6:64:MET:SD	2.61	0.41
11:L9:129:ARG:HD3	11:L9:129:ARG:HA	1.90	0.41
14:13:65:ARG:HA	27:dd:69:PHE:CD2	2.56	0.41
19:19:103:ARG:HD3	19:19:124:TYR:CZ	2.56	0.41
22:22:21:PHE:HD1	22:22:108:GLU:HA	1.84	0.41
29:30:79:ILE:HD13	29:30:90:ARG:HB3	2.01	0.41
42:gg:21:ASN:HB2	42:gg:23:GLN:HE21	1.85	0.41
46:u:81:ASP:O	46:u:82:ILE:HD13	2.20	0.41
49:28:1200:G:H2'	49:28:1201:U:H6	1.84	0.41
49:28:2864:A:H2'	49:28:2865:U:C6	2.56	0.41
49:28:3793:U:H2'	49:28:3794:C:C6	2.56	0.41
49:28:3923:A:H2'	49:28:3924:C:H6	1.84	0.41
1:v:22:MET:O	1:v:102:LEU:HA	2.20	0.41
1:v:246:PRO:HA	1:v:249:ARG:HG2	2.01	0.41
2:58:7:U:H2'	2:58:8:U:H6	1.86	0.41
4:L8:205:ASN:O	4:L8:208:GLU:HG2	2.21	0.41
5:L3:238:LYS:HD2	5:L3:238:LYS:HA	1.80	0.41
6:L4:132:ALA:C	6:L4:150:LEU:HD23	2.45	0.41
7:L5:271:MET:HE2	7:L5:276:LYS:HG2	2.02	0.41
9:L7:41:LEU:HD21	9:L7:45:ARG:NH1	2.35	0.41
10:aa:210:ILE:HG12	10:aa:254:THR:HG22	2.03	0.41
44:t:16:ARG:HD3	44:t:57:ARG:HG3	2.02	0.41
49:28:48:G:H1'	49:28:49:U:OP2	2.20	0.41
49:28:3930:U:H2'	49:28:3931:C:C6	2.55	0.41
49:28:4605:A:H8	49:28:4605:A:OP1	2.03	0.41
50:25:69:LYS:HD2	50:25:70:PRO:HD2	2.03	0.41
1:v:27:HIS:ND1	1:v:138:GLN:HB2	2.35	0.41
1:v:322:LYS:HD2	1:v:322:LYS:HA	1.94	0.41
1:v:507:VAL:O	1:v:545:ILE:HA	2.20	0.41
2:58:120:G:H2'	2:58:121:G:H8	1.85	0.41
3:5:4:U:H2'	3:5:5:A:C8	2.56	0.41
6:L4:190:ARG:O	6:L4:195:LYS:HD3	2.20	0.41
14:13:19:GLN:NE2	49:28:1518:A:H61	2.18	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:15:174:LEU:H	16:15:174:LEU:HG	1.70	0.41
26:27:39:SER:HB2	26:27:77:TYR:CD2	2.55	0.41
43:s:45:MET:HE3	43:s:45:MET:HB3	1.86	0.41
43:s:127:ASN:HB2	43:s:153:GLU:OE1	2.20	0.41
44:t:80:LEU:HB3	44:t:112:ILE:HD13	2.03	0.41
46:u:120:ILE:HD13	46:u:120:ILE:HA	1.85	0.41
49:28:703:G:H2'	49:28:704:C:H4'	2.02	0.41
49:28:909:G:C2	49:28:910:G:C8	3.09	0.41
49:28:1824:G:H2'	49:28:1825:A:H8	1.84	0.41
49:28:2369:U:O2'	49:28:2370:A:H8	2.03	0.41
49:28:2520:C:H2'	49:28:2521:G:C8	2.56	0.41
50:25:66:LYS:HD3	50:25:66:LYS:HA	1.89	0.41
50:25:112:MET:SD	50:25:117:ILE:HD11	2.60	0.41
1:v:232:TYR:CE2	1:v:292:LEU:HB3	2.56	0.41
1:v:394:LEU:HD13	1:v:420:LEU:N	2.35	0.41
2:58:5:U:C2	2:58:6:C:C5	3.09	0.41
4:L8:120:PRO:HA	4:L8:162:ASN:HB3	2.02	0.41
6:L4:101:MET:H	6:L4:101:MET:HG3	1.45	0.41
15:14:25:VAL:HG21	15:14:38:VAL:HG13	2.01	0.41
16:15:50:ARG:NH1	49:28:278:G:H4'	2.31	0.41
16:15:140:LYS:HD3	16:15:140:LYS:HA	1.88	0.41
27:dd:64:LYS:HD3	49:28:69:A:H5'	2.03	0.41
31:32:43:ASN:O	31:32:47:ARG:HG3	2.20	0.41
36:37:52:LYS:HB2	36:37:52:LYS:HE2	1.84	0.41
44:t:103:ASN:HD22	44:t:144:ASP:H	1.68	0.41
49:28:285:G:H2'	49:28:286:U:O4'	2.21	0.41
49:28:3784:A:O2'	49:28:3785:A:H3'	2.20	0.41
49:28:4477:A:H2'	49:28:4478:G:H8	1.85	0.41
1:v:36:THR:O	1:v:40:VAL:HG23	2.21	0.41
1:v:132:VAL:HG12	1:v:167:LEU:HD12	2.03	0.41
1:v:512:LYS:HG2	1:v:571:LYS:HB2	2.03	0.41
1:v:605:LYS:HB2	1:v:705:HIS:CE1	2.56	0.41
5:L3:254:ILE:HD12	49:28:3897:G:H4'	2.03	0.41
6:L4:83:GLY:H	49:28:368:C:H1'	1.86	0.41
6:L4:289:LEU:HA	6:L4:292:ILE:HD12	2.03	0.41
7:L5:16:TYR:HE1	7:L5:18:VAL:HG12	1.86	0.41
7:L5:177:THR:HG22	7:L5:180:PHE:HE2	1.85	0.41
7:L5:255:LYS:HB3	7:L5:255:LYS:HE2	1.64	0.41
10:aa:160:LYS:O	10:aa:164:LYS:HG3	2.21	0.41
13:11:95:ARG:HB3	13:11:177:GLY:O	2.19	0.41
16:15:193:ARG:O	16:15:197:THR:HG23	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:dd:51:GLY:N	47:Q:179:GLY:H	2.18	0.41
30:31:50:ARG:HE	30:31:50:ARG:HB2	1.50	0.41
32:ee:28:LEU:HD21	32:ee:101:ILE:HD11	2.02	0.41
33:34:41:ALA:O	33:34:52:ARG:HD3	2.20	0.41
34:35:44:LEU:O	34:35:47:ILE:HG23	2.19	0.41
36:37:34:CYS:HB3	36:37:39:TYR:H	1.85	0.41
43:s:18:ILE:HD13	43:s:18:ILE:HA	1.86	0.41
43:s:63:LYS:HE3	49:28:1960:A:C8	2.55	0.41
46:u:14:VAL:HA	46:u:17:VAL:HG12	2.02	0.41
49:28:269:G:H2'	49:28:270:U:C6	2.55	0.41
49:28:1519:C:H2'	49:28:1520:C:C6	2.56	0.41
49:28:2461:G:H2'	49:28:2462:C:C6	2.55	0.41
49:28:4464:A:H2'	49:28:4464:A:N3	2.36	0.41
2:58:155:C:H2'	2:58:156:U:O4'	2.20	0.41
6:L4:95:MET:HB2	49:28:1335:G:N2	2.35	0.41
9:L7:47:LYS:HE3	49:28:1237:C:O2'	2.21	0.41
9:L7:103:LYS:HE3	9:L7:103:LYS:HB2	1.76	0.41
9:L7:152:LEU:HD23	9:L7:152:LEU:HA	1.87	0.41
9:L7:208:TRP:CD1	9:L7:209:PRO:HD2	2.56	0.41
10:aa:120:ARG:HB3	16:15:28:TRP:HZ3	1.86	0.41
10:aa:201:GLU:HA	10:aa:230:MET:SD	2.60	0.41
10:aa:217:ILE:O	10:aa:221:VAL:HG13	2.20	0.41
10:aa:223:LEU:HD13	10:aa:254:THR:HG21	2.01	0.41
19:19:37:SER:OG	19:19:40:GLN:HG3	2.21	0.41
21:21:8:ARG:HH11	21:21:52:MET:HE1	1.84	0.41
22:22:24:ASP:HA	22:22:69:LYS:HA	2.03	0.41
31:32:19:LYS:HB3	31:32:19:LYS:HE2	1.70	0.41
35:36:3:LEU:HD12	35:36:4:ARG:N	2.31	0.41
43:s:111:ALA:HA	43:s:183:PHE:HD2	1.85	0.41
45:EB:109:ASP:OD1	45:EB:122:ALA:HB2	2.20	0.41
45:EB:189:GLN:HB3	45:EB:199:LYS:HB2	2.03	0.41
46:u:45:LYS:HD3	46:u:45:LYS:HA	1.73	0.41
47:Q:82:VAL:O	47:Q:102:ALA:HA	2.20	0.41
49:28:2504:C:H2'	49:28:2505:C:C2	2.56	0.41
49:28:4637:G:H4'	49:28:5045:G:O2'	2.20	0.41
49:28:4918:C:H2'	49:28:4919:G:C8	2.55	0.41
50:25:42:VAL:HG21	50:25:54:ALA:C	2.46	0.41
2:58:64:U:C2	2:58:65:A:C8	3.08	0.41
3:5:43:U:C4	3:5:44:C:C4	3.09	0.41
4:L8:124:GLY:O	4:L8:125:LYS:HD3	2.21	0.41
5:L3:222:VAL:HB	5:L3:343:ARG:NH1	2.35	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L6:73:ARG:HD3	49:28:983:C:C6	2.56	0.41
8:L6:75:TYR:CE1	49:28:982:U:H2'	2.56	0.41
8:L6:98:PRO:HG2	49:28:687:U:C4	2.55	0.41
9:L7:102:PRO:HD3	49:28:1876:U:O3'	2.20	0.41
10:aa:140:LEU:HD22	10:aa:235:CYS:HB2	2.03	0.41
11:L9:8:GLN:HE22	11:L9:71:ARG:HG3	1.84	0.41
15:14:62:LEU:HD12	15:14:64:PHE:CD1	2.55	0.41
15:14:71:LYS:NZ	49:28:738(A):C:H5''	2.36	0.41
15:14:123:ILE:O	15:14:127:VAL:HG23	2.21	0.41
15:14:137:LYS:HD3	15:14:137:LYS:HA	1.80	0.41
16:15:43:THR:O	16:15:45:PRO:HD3	2.21	0.41
17:bb:58:LEU:HD23	17:bb:58:LEU:HA	1.91	0.41
17:bb:116:LYS:HD3	20:20:169:THR:HG21	2.02	0.41
21:21:17:ARG:HD2	21:21:17:ARG:HA	1.86	0.41
21:21:87:LYS:CE	49:28:4305:G:H22	2.34	0.41
23:24:41:LEU:HD13	23:24:41:LEU:HA	1.80	0.41
26:27:41:ALA:HB2	26:27:77:TYR:HE1	1.86	0.41
26:27:77:TYR:HD1	26:27:77:TYR:HA	1.76	0.41
27:dd:53:PHE:O	47:Q:178:ARG:HB2	2.21	0.41
31:32:109:LYS:HB3	31:32:109:LYS:HE3	1.87	0.41
32:ee:101:ILE:HG13	32:ee:102:ARG:N	2.31	0.41
33:34:37:LYS:HE2	49:28:2516:G:OP2	2.20	0.41
35:36:103:LYS:HD3	35:36:103:LYS:HA	1.84	0.41
37:38:67:LYS:NZ	37:38:69:LEU:HD13	2.36	0.41
41:ff:8:VAL:HG13	49:28:2875:C:H5'	2.03	0.41
41:ff:52:VAL:CG2	49:28:2739:C:H4'	2.51	0.41
41:ff:59:SER:HA	49:28:2652:G:O6	2.21	0.41
46:u:66:CYS:HB3	46:u:110:PHE:CD1	2.56	0.41
47:Q:66:MET:HE3	47:Q:66:MET:HB2	1.73	0.41
49:28:752:G:H2'	49:28:753:C:H6	1.86	0.41
49:28:1088:C:H2'	49:28:1089:G:C8	2.55	0.41
49:28:1306:C:H2'	49:28:1307:A:C8	2.55	0.41
49:28:1443:A:H3'	49:28:1444:G:C8	2.56	0.41
49:28:2306:G:H1'	49:28:2332:A:H61	1.85	0.41
49:28:3600:G:H2'	49:28:3601:C:C6	2.56	0.41
49:28:3671:G:H2'	49:28:3672:G:C8	2.56	0.41
49:28:4122:G:H2'	49:28:4123:C:C6	2.55	0.41
1:v:397:TYR:HB3	1:v:417:PHE:HZ	1.86	0.41
1:v:738:PRO:HG2	1:v:824:PRO:CD	2.50	0.41
3:5:27:G:H2'	3:5:28:C:O4'	2.20	0.41
4:L8:83:HIS:CD2	4:L8:86:GLN:HB2	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L8:170:ALA:CB	41:ff:65:ALA:HB1	2.51	0.41
10:aa:233:PRO:HG3	10:aa:276:ARG:NH2	2.36	0.41
12:10:36:LEU:O	12:10:86:HIS:HD2	2.04	0.41
15:14:37:LEU:HD12	15:14:48:GLN:O	2.20	0.41
16:15:104:GLU:HA	16:15:160:GLU:HG3	2.01	0.41
18:17:126:ARG:CD	18:17:140:MET:HE1	2.51	0.41
20:20:164:LYS:HD3	20:20:164:LYS:HA	1.55	0.41
27:dd:92:LYS:HE3	27:dd:92:LYS:HB2	1.79	0.41
27:dd:100:ILE:HG21	27:dd:125:LYS:HE2	2.01	0.41
34:35:14:LYS:O	34:35:18:LEU:HG	2.21	0.41
34:35:27:GLU:O	34:35:30:GLN:HG2	2.21	0.41
35:36:25:ARG:HH11	49:28:159:C:H5'	1.86	0.41
35:36:70:LEU:HB2	35:36:87:ARG:HH11	1.86	0.41
44:t:92:ARG:HE	44:t:92:ARG:HB3	1.78	0.41
48:ES:3283:G:HO2'	48:ES:3284:C:H6	1.67	0.41
49:28:12:A:H5''	49:28:12:A:H8	1.85	0.41
49:28:123:C:H2'	49:28:124:C:H6	1.85	0.41
49:28:452:A:H62	49:28:1293:G:H3'	1.86	0.41
49:28:2336:G:H2'	49:28:2337:C:C6	2.56	0.41
49:28:2705:G:H2'	49:28:2706:G:C8	2.56	0.41
49:28:3837:C:H2'	49:28:3838:U:O4'	2.21	0.41
49:28:4538:G:H2'	49:28:4539:U:H6	1.85	0.41
49:28:4642:U:H2'	49:28:4643:G:C8	2.56	0.41
49:28:4863:G:H2'	49:28:4864:U:C6	2.56	0.41
1:v:749:ILE:HG21	1:v:759:ILE:HG21	2.03	0.40
6:L4:269:LYS:HD3	49:28:654:C:O2'	2.21	0.40
7:L5:27:LYS:HG2	13:11:147:ARG:HD3	2.02	0.40
15:14:9:VAL:HG22	15:14:28:VAL:O	2.22	0.40
15:14:100:ARG:HD3	17:bb:198:THR:O	2.21	0.40
16:15:27:CYS:SG	16:15:124:ASP:HB2	2.61	0.40
17:bb:179:LYS:HA	17:bb:179:LYS:HD3	1.89	0.40
20:20:74:ARG:O	20:20:76:LYS:HG3	2.21	0.40
22:22:20:LYS:HE3	22:22:71:THR:HG21	2.03	0.40
34:35:105:LYS:HB2	34:35:105:LYS:HE2	1.69	0.40
37:38:7:GLU:HG2	37:38:10:ASP:HB2	2.02	0.40
37:38:60:LEU:HD13	37:38:60:LEU:HA	1.86	0.40
46:u:184:HIS:HA	46:u:187:VAL:HG12	2.03	0.40
49:28:288:G:H2'	49:28:289:C:C6	2.56	0.40
49:28:974:C:H2'	49:28:975:C:C6	2.56	0.40
49:28:1204:C:H2'	49:28:1205:G:H8	1.86	0.40
49:28:1292:C:H2'	49:28:1293:G:O4'	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:28:1537:A:H2'	49:28:1538:U:C6	2.57	0.40
49:28:2859:G:H2'	49:28:2860:C:C6	2.54	0.40
49:28:3842:C:H3'	49:28:3843:C:H2'	2.02	0.40
49:28:4349:C:H3'	49:28:4350:C:H5'	2.03	0.40
49:28:4964:C:H2'	49:28:4965:U:N1	2.36	0.40
1:v:23:SER:O	1:v:125:ALA:HA	2.22	0.40
1:v:680:VAL:O	1:v:684:GLN:HG2	2.21	0.40
2:58:137:A:H2'	2:58:138:C:H6	1.85	0.40
5:L3:35:ASP:HB3	5:L3:186:ASN:CG	2.46	0.40
6:L4:27:VAL:H	6:L4:27:VAL:HG23	1.70	0.40
7:L5:4:VAL:HG11	49:28:4247:G:C5'	2.52	0.40
8:L6:117:ARG:HG2	49:28:458:C:OP1	2.21	0.40
8:L6:153:LEU:HB3	8:L6:197:VAL:HG13	2.04	0.40
8:L6:195:LYS:HE2	49:28:711:A:OP1	2.21	0.40
11:L9:77:VAL:O	11:L9:81:ILE:HG13	2.21	0.40
16:15:40:PRO:HG3	49:28:8:U:C5'	2.51	0.40
17:bb:130:LYS:HB2	17:bb:133:ARG:HG2	2.03	0.40
26:27:12:LEU:HD23	26:27:12:LEU:HA	1.87	0.40
27:dd:51:GLY:HA2	47:Q:178:ARG:H	1.86	0.40
36:37:69:ILE:O	36:37:73:ARG:HG3	2.21	0.40
45:EB:237:ALA:O	45:EB:238:LYS:HD3	2.21	0.40
47:Q:45:GLN:O	47:Q:49:LYS:HG3	2.21	0.40
49:28:261:G:H2'	49:28:262:G:O4'	2.21	0.40
49:28:1074:G:O5'	49:28:1074:G:H8	2.04	0.40
49:28:1201:U:H2'	49:28:1202:C:H6	1.86	0.40
49:28:1292:C:H3'	49:28:1293:G:N2	2.36	0.40
49:28:2338:C:H2'	49:28:2339:G:O4'	2.21	0.40
49:28:2601:A:N6	49:28:2743:A:H3'	2.37	0.40
49:28:3715:U:C5	49:28:3738:G:N1	2.72	0.40
49:28:4433:G:H2'	49:28:4434:C:C6	2.57	0.40
1:v:225:LEU:HB3	1:v:257:MET:HE2	2.03	0.40
1:v:506:ARG:HA	1:v:547:ALA:HA	2.04	0.40
5:L3:5:LYS:HE3	5:L3:5:LYS:HB3	1.90	0.40
10:aa:84:LEU:HD13	10:aa:84:LEU:HA	1.80	0.40
11:L9:1:MET:HE3	11:L9:1:MET:HB2	1.89	0.40
16:15:68:ARG:HG2	16:15:128:LYS:HG3	2.04	0.40
31:32:35:TRP:CE2	31:32:56:PRO:HD2	2.57	0.40
36:37:5:THR:HA	36:37:8:PHE:HD2	1.87	0.40
40:42:17:LYS:HA	49:28:4318:C:H4'	2.04	0.40
45:EB:27:ILE:O	45:EB:31:VAL:HG22	2.21	0.40
45:EB:111:GLY:HA2	45:EB:119:ALA:O	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:u:46:ASP:C	46:u:47:LYS:HG3	2.46	0.40
49:28:1664:U:H2'	49:28:1665:C:C6	2.57	0.40
49:28:1981:G:H2'	49:28:1982:G:C8	2.56	0.40
49:28:2417:A:C4	49:28:2418:A:C8	3.10	0.40
49:28:3799:A:H5'	50:25:64:THR:HG21	2.04	0.40
49:28:4756:C:H5''	49:28:4756:C:H6	1.87	0.40
1:v:666:THR:HG22	1:v:705:HIS:O	2.21	0.40
8:L6:291:PHE:CE1	32:ee:110:ILE:HG21	2.52	0.40
13:11:42:GLN:HE22	13:11:117:ILE:CG2	2.34	0.40
16:15:39:ALA:O	16:15:61:ILE:HD12	2.21	0.40
17:bb:168:TYR:CZ	17:bb:172:LYS:HD2	2.56	0.40
17:bb:191:LYS:HE2	17:bb:191:LYS:HB2	1.80	0.40
24:cc:71:LEU:HA	24:cc:71:LEU:HD12	1.85	0.40
27:dd:28:HIS:CD2	27:dd:32:ARG:HG2	2.56	0.40
41:ff:69:TRP:CH2	49:28:2739:C:H5'	2.56	0.40
44:t:125:LEU:HA	44:t:128:THR:OG1	2.21	0.40
46:u:107:TYR:HB2	46:u:110:PHE:CE1	2.55	0.40
49:28:910:G:H2'	49:28:911:U:H6	1.86	0.40
49:28:1973:G:H2'	49:28:1974:U:C5	2.56	0.40
49:28:2297:G:H2'	49:28:2298:U:O4'	2.21	0.40
49:28:2380:G:C5	49:28:2425:U:C4	3.09	0.40
49:28:2544:G:N3	49:28:2544:G:H2'	2.36	0.40
49:28:4874:A:C5	49:28:4877:G:H4'	2.56	0.40
1:v:249:ARG:O	1:v:253:VAL:HG23	2.22	0.40
1:v:381:ALA:HB1	1:v:395:MET:HE1	2.03	0.40
5:L3:340:THR:HG23	5:L3:341:LYS:O	2.22	0.40
6:L4:205:ARG:HD2	49:28:2297:G:OP1	2.22	0.40
6:L4:210:ILE:CG2	6:L4:232:VAL:HG13	2.51	0.40
10:aa:317:LYS:HA	10:aa:317:LYS:HD3	1.84	0.40
26:27:45:GLY:HA3	26:27:71:PHE:CZ	2.56	0.40
40:42:85:ILE:HG22	40:42:86:LYS:N	2.36	0.40
42:gg:101:LYS:HZ1	49:28:2093:G:P	2.45	0.40
43:s:61:MET:HE3	43:s:88:PHE:CE2	2.57	0.40
45:EB:35:LEU:HD12	45:EB:48:LEU:HD22	2.04	0.40
45:EB:291:MET:O	45:EB:294:VAL:HG12	2.22	0.40
49:28:1197:C:H3'	49:28:1198:G:C8	2.56	0.40
49:28:1340:C:H6	49:28:1340:C:O5'	2.05	0.40
49:28:1414:C:H2'	49:28:1415:G:C8	2.57	0.40
49:28:3865:A:H2'	49:28:3866:C:C6	2.56	0.40
49:28:4488:A:H4'	49:28:4489:G:C8	2.56	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	v	796/858 (93%)	771 (97%)	25 (3%)	0	100	100
4	L8	246/248 (99%)	232 (94%)	14 (6%)	0	100	100
5	L3	392/394 (100%)	379 (97%)	13 (3%)	0	100	100
6	L4	360/362 (99%)	348 (97%)	12 (3%)	0	100	100
7	L5	291/293 (99%)	273 (94%)	16 (6%)	2 (1%)	18	48
8	L6	208/251 (83%)	198 (95%)	10 (5%)	0	100	100
9	L7	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
10	aa	229/266 (86%)	221 (96%)	8 (4%)	0	100	100
11	L9	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
12	10	201/213 (94%)	193 (96%)	8 (4%)	0	100	100
13	11	168/170 (99%)	163 (97%)	5 (3%)	0	100	100
14	13	208/261 (80%)	199 (96%)	7 (3%)	2 (1%)	12	39
15	14	136/138 (99%)	130 (96%)	6 (4%)	0	100	100
16	15	201/203 (99%)	194 (96%)	7 (4%)	0	100	100
17	bb	197/199 (99%)	192 (98%)	5 (2%)	0	100	100
18	17	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
19	19	157/180 (87%)	153 (98%)	4 (2%)	0	100	100
20	20	174/176 (99%)	167 (96%)	6 (3%)	1 (1%)	21	51
21	21	157/159 (99%)	151 (96%)	6 (4%)	0	100	100
22	22	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
23	24	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
24	cc	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
25	26	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
26	27	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
27	dd	145/147 (99%)	134 (92%)	11 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	29	100/245 (41%)	96 (96%)	4 (4%)	0	100	100
29	30	96/98 (98%)	96 (100%)	0	0	100	100
30	31	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
31	32	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
32	ee	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
33	34	112/114 (98%)	112 (100%)	0	0	100	100
34	35	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
35	36	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
36	37	84/86 (98%)	80 (95%)	4 (5%)	0	100	100
37	38	67/69 (97%)	64 (96%)	3 (4%)	0	100	100
38	39	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
39	40	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
40	42	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
41	ff	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
42	gg	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
43	s	194/196 (99%)	181 (93%)	13 (7%)	0	100	100
44	t	151/153 (99%)	135 (89%)	16 (11%)	0	100	100
45	EB	373/375 (100%)	358 (96%)	15 (4%)	0	100	100
46	u	204/206 (99%)	183 (90%)	21 (10%)	0	100	100
47	Q	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
50	25	137/139 (99%)	135 (98%)	2 (2%)	0	100	100
All	All	8039/8492 (95%)	7712 (96%)	322 (4%)	5 (0%)	49	77

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	13	64	VAL
7	L5	36	LEU
14	13	63	THR
20	20	165	PRO
7	L5	37	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	v	690/730 (94%)	615 (89%)	75 (11%)	6	20
4	L8	190/190 (100%)	172 (90%)	18 (10%)	8	26
5	L3	342/342 (100%)	318 (93%)	24 (7%)	14	40
6	L4	302/302 (100%)	285 (94%)	17 (6%)	19	50
7	L5	247/247 (100%)	229 (93%)	18 (7%)	13	38
8	L6	190/223 (85%)	171 (90%)	19 (10%)	7	24
9	L7	196/196 (100%)	182 (93%)	14 (7%)	13	40
10	aa	200/224 (89%)	177 (88%)	23 (12%)	5	18
11	L9	169/169 (100%)	155 (92%)	14 (8%)	10	32
12	10	175/180 (97%)	165 (94%)	10 (6%)	18	49
13	11	143/143 (100%)	135 (94%)	8 (6%)	19	50
14	13	175/215 (81%)	166 (95%)	9 (5%)	21	53
15	14	117/117 (100%)	104 (89%)	13 (11%)	6	20
16	15	171/171 (100%)	158 (92%)	13 (8%)	12	36
17	bb	171/171 (100%)	158 (92%)	13 (8%)	12	36
18	17	134/134 (100%)	121 (90%)	13 (10%)	8	25
19	19	141/159 (89%)	131 (93%)	10 (7%)	13	40
20	20	157/157 (100%)	140 (89%)	17 (11%)	6	21
21	21	139/139 (100%)	127 (91%)	12 (9%)	10	30
22	22	89/89 (100%)	85 (96%)	4 (4%)	24	58
23	24	55/55 (100%)	52 (94%)	3 (6%)	19	50
24	cc	106/106 (100%)	98 (92%)	8 (8%)	12	37
25	26	124/124 (100%)	109 (88%)	15 (12%)	5	16
26	27	117/117 (100%)	108 (92%)	9 (8%)	12	35
27	dd	119/119 (100%)	114 (96%)	5 (4%)	26	60
28	29	84/184 (46%)	78 (93%)	6 (7%)	13	40

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	30	84/84 (100%)	80 (95%)	4 (5%)	23	55
30	31	98/98 (100%)	91 (93%)	7 (7%)	13	40
31	32	114/114 (100%)	107 (94%)	7 (6%)	17	46
32	ee	88/88 (100%)	82 (93%)	6 (7%)	14	42
33	34	98/98 (100%)	88 (90%)	10 (10%)	7	23
34	35	109/109 (100%)	104 (95%)	5 (5%)	24	57
35	36	86/86 (100%)	76 (88%)	10 (12%)	5	18
36	37	73/73 (100%)	70 (96%)	3 (4%)	27	61
37	38	64/64 (100%)	62 (97%)	2 (3%)	35	69
38	39	47/47 (100%)	44 (94%)	3 (6%)	16	44
39	40	48/48 (100%)	46 (96%)	2 (4%)	26	60
40	42	92/92 (100%)	86 (94%)	6 (6%)	15	44
41	ff	74/74 (100%)	71 (96%)	3 (4%)	27	61
42	gg	107/108 (99%)	95 (89%)	12 (11%)	6	19
43	s	164/164 (100%)	145 (88%)	19 (12%)	5	18
44	t	126/126 (100%)	109 (86%)	17 (14%)	4	12
45	EB	321/321 (100%)	290 (90%)	31 (10%)	8	25
46	u	186/186 (100%)	173 (93%)	13 (7%)	14	40
47	Q	164/164 (100%)	146 (89%)	18 (11%)	6	20
50	25	106/106 (100%)	99 (93%)	7 (7%)	15	43
All	All	6992/7253 (96%)	6417 (92%)	575 (8%)	13	32

All (575) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	v	1	MET
1	v	2	VAL
1	v	6	VAL
1	v	12	ILE
1	v	22	MET
1	v	28	VAL
1	v	39	LEU
1	v	80	GLU
1	v	86	LEU
1	v	87	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	v	89	ILE
1	v	103	ILE
1	v	113	SER
1	v	119	LEU
1	v	127	VAL
1	v	128	VAL
1	v	139	THR
1	v	155	LEU
1	v	156	MET
1	v	160	MET
1	v	166	GLU
1	v	169	LEU
1	v	174	LEU
1	v	186	ASN
1	v	197	SER
1	v	205	ILE
1	v	211	THR
1	v	227	GLN
1	v	230	GLU
1	v	257	MET
1	v	264	ARG
1	v	302	ASP
1	v	319	LEU
1	v	321	ILE
1	v	323	LEU
1	v	330	LYS
1	v	350	LEU
1	v	354	ILE
1	v	358	LEU
1	v	370	GLU
1	v	378	ASP
1	v	400	LYS
1	v	401	MET
1	v	416	VAL
1	v	421	VAL
1	v	442	LEU
1	v	447	ILE
1	v	450	THR
1	v	453	MET
1	v	458	VAL
1	v	475	VAL
1	v	479	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	v	480	VAL
1	v	485	ILE
1	v	545	ILE
1	v	561	LEU
1	v	570	ILE
1	v	585	GLU
1	v	593	SER
1	v	609	PHE
1	v	635	LEU
1	v	661	ILE
1	v	662	LEU
1	v	663	THR
1	v	693	CYS
1	v	694	GLU
1	v	695	GLU
1	v	740	LEU
1	v	747	VAL
1	v	748	GLU
1	v	756	VAL
1	v	790	VAL
1	v	800	LEU
1	v	818	GLN
1	v	833	GLN
4	L8	28	ARG
4	L8	32	VAL
4	L8	77	ILE
4	L8	97	ASN
4	L8	101	VAL
4	L8	102	LEU
4	L8	109	GLU
4	L8	135	THR
4	L8	146	THR
4	L8	148	VAL
4	L8	158	ILE
4	L8	165	VAL
4	L8	179	ILE
4	L8	200	ARG
4	L8	227	ARG
4	L8	228	ASP
4	L8	235	VAL
4	L8	243	THR
5	L3	43	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	L3	47	LEU
5	L3	56	ILE
5	L3	94	GLU
5	L3	101	THR
5	L3	103	LYS
5	L3	138	GLN
5	L3	146	LEU
5	L3	162	VAL
5	L3	204	GLN
5	L3	207	VAL
5	L3	214	ASP
5	L3	240	LEU
5	L3	248	LEU
5	L3	254	ILE
5	L3	262	VAL
5	L3	314	ILE
5	L3	317	LEU
5	L3	333	LEU
5	L3	345	LEU
5	L3	351	LEU
5	L3	352	LEU
5	L3	371	THR
5	L3	389	MET
6	L4	50	GLN
6	L4	57	LEU
6	L4	76	ILE
6	L4	100	ARG
6	L4	101	MET
6	L4	154	VAL
6	L4	158	VAL
6	L4	159	GLU
6	L4	180	ILE
6	L4	189	MET
6	L4	205	ARG
6	L4	232	VAL
6	L4	289	LEU
6	L4	300	ARG
6	L4	313	VAL
6	L4	339	THR
6	L4	340	ILE
7	L5	18	VAL
7	L5	38	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	L5	72	ASP
7	L5	83	LEU
7	L5	92	LEU
7	L5	110	LEU
7	L5	115	MET
7	L5	118	ILE
7	L5	126	THR
7	L5	143	THR
7	L5	152	ARG
7	L5	167	VAL
7	L5	186	GLU
7	L5	213	GLU
7	L5	232	THR
7	L5	235	MET
7	L5	261	VAL
7	L5	271	MET
8	L6	51	VAL
8	L6	53	VAL
8	L6	73	ARG
8	L6	110	VAL
8	L6	141	ARG
8	L6	170	GLN
8	L6	173	SER
8	L6	178	VAL
8	L6	189	LEU
8	L6	197	VAL
8	L6	200	THR
8	L6	209	VAL
8	L6	211	ILE
8	L6	260	ILE
8	L6	261	LEU
8	L6	264	ILE
8	L6	284	VAL
8	L6	289	LEU
8	L6	291	PHE
9	L7	23	ASN
9	L7	38	GLN
9	L7	41	LEU
9	L7	61	ARG
9	L7	97	ILE
9	L7	100	VAL
9	L7	124	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	L7	134	ILE
9	L7	136	GLU
9	L7	151	GLU
9	L7	173	LEU
9	L7	211	LYS
9	L7	237	ASP
9	L7	246	MET
10	aa	81	VAL
10	aa	84	LEU
10	aa	98	ILE
10	aa	116	LEU
10	aa	127	LEU
10	aa	140	LEU
10	aa	151	LEU
10	aa	154	LYS
10	aa	159	THR
10	aa	167	LEU
10	aa	193	VAL
10	aa	214	VAL
10	aa	226	LEU
10	aa	230	MET
10	aa	237	LEU
10	aa	242	ARG
10	aa	255	VAL
10	aa	258	THR
10	aa	263	GLU
10	aa	271	LEU
10	aa	288	ARG
10	aa	300	VAL
10	aa	314	LEU
11	L9	18	ILE
11	L9	20	LEU
11	L9	41	ILE
11	L9	48	LEU
11	L9	57	VAL
11	L9	66	GLU
11	L9	72	THR
11	L9	74	CYS
11	L9	84	VAL
11	L9	103	VAL
11	L9	107	GLU
11	L9	144	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	L9	161	ILE
11	L9	162	GLN
12	10	7	ARG
12	10	36	LEU
12	10	58	GLU
12	10	63	GLU
12	10	71	CYS
12	10	76	MET
12	10	97	ILE
12	10	99	ILE
12	10	163	GLN
12	10	212	LEU
13	11	29	SER
13	11	49	VAL
13	11	52	LYS
13	11	65	ASN
13	11	70	VAL
13	11	109	ILE
13	11	128	LEU
13	11	175	LEU
14	13	20	ARG
14	13	55	ILE
14	13	59	VAL
14	13	67	HIS
14	13	77	SER
14	13	139	SER
14	13	144	LEU
14	13	154	VAL
14	13	184	MET
15	14	7	VAL
15	14	8	GLU
15	14	32	ASP
15	14	38	VAL
15	14	46	ARG
15	14	55	MET
15	14	57	LEU
15	14	58	THR
15	14	61	ILE
15	14	62	LEU
15	14	105	THR
15	14	112	VAL
15	14	130	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
16	15	9	GLU
16	15	36	LEU
16	15	44	ARG
16	15	50	ARG
16	15	61	ILE
16	15	64	ILE
16	15	87	HIS
16	15	89	VAL
16	15	151	ILE
16	15	174	LEU
16	15	188	ARG
16	15	189	ARG
16	15	198	LEU
17	bb	7	LEU
17	bb	22	ILE
17	bb	27	VAL
17	bb	36	VAL
17	bb	42	ASN
17	bb	52	LEU
17	bb	124	LEU
17	bb	144	GLU
17	bb	145	VAL
17	bb	150	GLN
17	bb	182	GLU
17	bb	185	VAL
17	bb	188	LYS
18	17	2	VAL
18	17	10	ASN
18	17	32	THR
18	17	41	ILE
18	17	69	ARG
18	17	79	THR
18	17	86	LYS
18	17	100	SER
18	17	104	LEU
18	17	114	ILE
18	17	126	ARG
18	17	147	GLU
18	17	150	LEU
19	19	12	SER
19	19	15	LEU
19	19	74	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
19	19	76	MET
19	19	80	LYS
19	19	98	ARG
19	19	123	LEU
19	19	127	VAL
19	19	143	HIS
19	19	157	ASP
20	20	1	MET
20	20	6	THR
20	20	7	LEU
20	20	13	VAL
20	20	17	LEU
20	20	54	MET
20	20	62	VAL
20	20	67	VAL
20	20	74	ARG
20	20	75	VAL
20	20	82	LEU
20	20	90	THR
20	20	95	ARG
20	20	98	ARG
20	20	102	THR
20	20	126	ILE
20	20	159	LEU
21	21	33	ILE
21	21	35	LYS
21	21	40	VAL
21	21	55	LYS
21	21	63	ARG
21	21	69	GLN
21	21	87	LYS
21	21	104	SER
21	21	106	LEU
21	21	111	GLU
21	21	124	THR
21	21	146	LYS
22	22	23	LEU
22	22	30	GLU
22	22	41	GLN
22	22	63	LEU
23	24	12	LYS
23	24	30	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
23	24	41	LEU
24	cc	54	LEU
24	cc	76	ILE
24	cc	81	LEU
24	cc	95	THR
24	cc	119	ILE
24	cc	120	ASP
24	cc	133	GLU
24	cc	152	LYS
25	26	2	LYS
25	26	8	THR
25	26	40	GLN
25	26	46	SER
25	26	55	VAL
25	26	58	VAL
25	26	79	VAL
25	26	104	VAL
25	26	105	VAL
25	26	111	LEU
25	26	115	ARG
25	26	119	LEU
25	26	120	GLU
25	26	124	LYS
25	26	126	ARG
26	27	11	VAL
26	27	26	VAL
26	27	46	ILE
26	27	53	VAL
26	27	65	ARG
26	27	72	VAL
26	27	77	TYR
26	27	91	LEU
26	27	120	GLU
27	dd	66	ASN
27	dd	68	SER
27	dd	77	LYS
27	dd	106	SER
27	dd	140	VAL
28	29	9	THR
28	29	14	ARG
28	29	32	LEU
28	29	35	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
28	29	96	LEU
28	29	104	LEU
29	30	11	LEU
29	30	28	VAL
29	30	52	CYS
29	30	92	CYS
30	31	26	THR
30	31	29	ILE
30	31	33	ILE
30	31	46	LEU
30	31	56	GLU
30	31	57	MET
30	31	86	VAL
31	32	4	LEU
31	32	13	VAL
31	32	44	ARG
31	32	48	ARG
31	32	87	VAL
31	32	89	LEU
31	32	94	SER
32	ee	23	GLU
32	ee	33	VAL
32	ee	36	ARG
32	ee	84	VAL
32	ee	101	ILE
32	ee	103	VAL
33	34	5	LEU
33	34	6	THR
33	34	59	VAL
33	34	60	ARG
33	34	65	MET
33	34	66	ARG
33	34	74	VAL
33	34	88	ARG
33	34	105	LYS
33	34	110	GLN
34	35	22	ASP
34	35	28	LEU
34	35	47	ILE
34	35	88	THR
34	35	111	GLU
35	36	3	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
35	36	11	LEU
35	36	17	VAL
35	36	18	THR
35	36	29	ARG
35	36	42	ASP
35	36	44	ILE
35	36	45	ARG
35	36	58	MET
35	36	77	VAL
36	37	5	THR
36	37	46	LYS
36	37	79	ARG
37	38	23	VAL
37	38	47	ILE
38	39	27	ILE
38	39	45	ARG
38	39	49	LEU
39	40	96	ARG
39	40	101	VAL
40	42	61	LYS
40	42	66	ILE
40	42	69	ARG
40	42	71	GLU
40	42	93	LEU
40	42	103	VAL
41	ff	30	GLU
41	ff	52	VAL
41	ff	73	THR
42	gg	18	ILE
42	gg	32	LEU
42	gg	44	ILE
42	gg	64	MET
42	gg	75	THR
42	gg	78	VAL
42	gg	96	MET
42	gg	103	HIS
42	gg	106	LEU
42	gg	108	MET
42	gg	119	ARG
42	gg	124	VAL
43	s	15	LEU
43	s	21	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
43	s	27	CYS
43	s	29	ILE
43	s	30	VAL
43	s	53	VAL
43	s	61	MET
43	s	68	HIS
43	s	69	LEU
43	s	89	VAL
43	s	102	LEU
43	s	141	LEU
43	s	147	ILE
43	s	148	SER
43	s	157	ASP
43	s	158	VAL
43	s	160	LEU
43	s	174	LEU
43	s	180	ILE
44	t	35	LEU
44	t	37	LEU
44	t	56	LEU
44	t	61	LYS
44	t	65	GLN
44	t	72	GLU
44	t	80	LEU
44	t	95	GLN
44	t	96	LYS
44	t	98	ILE
44	t	104	ILE
44	t	124	GLU
44	t	125	LEU
44	t	129	ILE
44	t	132	ILE
44	t	137	GLN
44	t	146	ARG
45	EB	14	GLU
45	EB	34	SER
45	EB	35	LEU
45	EB	46	LEU
45	EB	48	LEU
45	EB	57	MET
45	EB	65	LYS
45	EB	69	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
45	EB	81	SER
45	EB	114	VAL
45	EB	124	THR
45	EB	127	VAL
45	EB	129	VAL
45	EB	143	ILE
45	EB	156	LEU
45	EB	162	GLN
45	EB	187	SER
45	EB	211	LYS
45	EB	226	VAL
45	EB	230	VAL
45	EB	267	SER
45	EB	284	GLU
45	EB	287	LYS
45	EB	307	VAL
45	EB	331	MET
45	EB	333	ILE
45	EB	342	LEU
45	EB	351	ASP
45	EB	357	LEU
45	EB	373	LYS
45	EB	379	GLU
46	u	21	ASN
46	u	38	LEU
46	u	53	VAL
46	u	80	VAL
46	u	88	GLU
46	u	90	LEU
46	u	93	LEU
46	u	116	LEU
46	u	117	ILE
46	u	138	LEU
46	u	156	LYS
46	u	173	LYS
46	u	201	VAL
47	Q	13	VAL
47	Q	16	LYS
47	Q	37	ARG
47	Q	38	ARG
47	Q	42	THR
47	Q	49	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
47	Q	63	LEU
47	Q	66	MET
47	Q	77	ASN
47	Q	78	LYS
47	Q	91	ARG
47	Q	93	GLN
47	Q	121	LEU
47	Q	126	LEU
47	Q	154	LYS
47	Q	168	ARG
47	Q	169	SER
47	Q	173	LYS
50	25	18	LEU
50	25	27	ASN
50	25	37	LEU
50	25	61	VAL
50	25	69	LYS
50	25	94	VAL
50	25	118	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (148) such sidechains are listed below:

Mol	Chain	Res	Type
1	v	30	HIS
1	v	184	ASN
1	v	186	ASN
1	v	202	ASN
1	v	490	HIS
1	v	492	HIS
1	v	493	ASN
1	v	535	GLN
1	v	597	ASN
1	v	684	GLN
1	v	710	HIS
1	v	764	ASN
1	v	833	GLN
4	L8	22	HIS
4	L8	38	HIS
4	L8	83	HIS
4	L8	100	ASN
4	L8	215	ASN
4	L8	216	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	L3	42	HIS
5	L3	179	HIS
5	L3	203	GLN
5	L3	204	GLN
5	L3	209	GLN
6	L4	21	ASN
6	L4	41	HIS
6	L4	60	HIS
6	L4	119	GLN
6	L4	198	ASN
6	L4	212	ASN
6	L4	338	ASN
6	L4	346	ASN
7	L5	45	ASN
7	L5	111	ASN
7	L5	131	ASN
7	L5	175	HIS
7	L5	191	ASN
7	L5	202	GLN
7	L5	291	GLN
8	L6	193	HIS
9	L7	62	GLN
10	aa	119	GLN
10	aa	161	GLN
10	aa	248	HIS
11	L9	8	GLN
11	L9	79	ASN
11	L9	98	HIS
11	L9	106	GLN
11	L9	189	GLN
12	10	92	HIS
12	10	95	HIS
12	10	166	HIS
13	11	42	GLN
13	11	46	GLN
13	11	71	HIS
14	13	19	GLN
14	13	149	GLN
14	13	205	GLN
15	14	20	HIS
15	14	70	GLN
15	14	131	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
16	15	15	GLN
16	15	29	GLN
17	bb	42	ASN
17	bb	72	HIS
17	bb	150	GLN
17	bb	167	HIS
17	bb	184	ASN
18	17	75	GLN
18	17	80	GLN
18	17	133	HIS
18	17	137	ASN
20	20	91	HIS
20	20	122	HIS
21	21	3	ASN
21	21	69	GLN
21	21	112	ASN
21	21	131	GLN
22	22	38	ASN
22	22	44	GLN
22	22	95	ASN
23	24	30	GLN
24	cc	57	GLN
24	cc	107	HIS
24	cc	125	ASN
24	cc	151	ASN
25	26	72	GLN
26	27	127	ASN
27	dd	19	HIS
27	dd	39	HIS
27	dd	66	ASN
27	dd	85	GLN
27	dd	93	ASN
30	31	28	ASN
30	31	34	HIS
30	31	79	ASN
30	31	116	ASN
31	32	34	ASN
31	32	107	ASN
32	ee	56	ASN
33	34	112	GLN
34	35	68	ASN
36	37	13	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	37	28	HIS
36	37	48	ASN
36	37	57	ASN
36	37	66	HIS
38	39	19	GLN
38	39	33	ASN
39	40	64	ASN
39	40	94	ASN
40	42	51	GLN
41	ff	92	GLN
42	gg	21	ASN
42	gg	30	ASN
42	gg	70	GLN
42	gg	95	HIS
42	gg	103	HIS
43	s	39	GLN
43	s	159	GLN
44	t	65	GLN
44	t	103	ASN
44	t	147	HIS
44	t	156	ASN
45	EB	113	HIS
45	EB	134	GLN
45	EB	147	HIS
45	EB	161	ASN
45	EB	165	GLN
45	EB	192	GLN
45	EB	193	HIS
45	EB	221	HIS
45	EB	299	HIS
45	EB	306	ASN
46	u	19	HIS
46	u	22	GLN
46	u	84	HIS
46	u	94	ASN
46	u	158	GLN
46	u	171	HIS
46	u	184	HIS
46	u	199	GLN
47	Q	57	ASN
47	Q	93	GLN
47	Q	125	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
47	Q	160	HIS
47	Q	162	HIS
50	25	50	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	58	149/156 (95%)	36 (24%)	1 (0%)
3	5	119/120 (99%)	12 (10%)	0
48	ES	63/5070 (1%)	16 (25%)	1 (1%)
49	28	3461/4807 (71%)	778 (22%)	49 (1%)
All	All	3792/10153 (37%)	842 (22%)	51 (1%)

All (842) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	58	2	G
2	58	3	A
2	58	16	G
2	58	23	C
2	58	34	U
2	58	35	C
2	58	38	U
2	58	51	U
2	58	52	A
2	58	59	A
2	58	62	A
2	58	63	U
2	58	75	G
2	58	77	A
2	58	87	G
2	58	90	C
2	58	94	G
2	58	95	A
2	58	103	A
2	58	104	A
2	58	105	C
2	58	109	C
2	58	110	U
2	58	111	U
2	58	113	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	58	114	G
2	58	121	G
2	58	122	G
2	58	125	C
2	58	126	C
2	58	127	U
2	58	128	C
2	58	137	A
2	58	147	G
2	58	151	G
2	58	156	U
3	5	7	G
3	5	21	G
3	5	22	A
3	5	33	U
3	5	53	U
3	5	54	A
3	5	64	G
3	5	89	G
3	5	100	A
3	5	110	G
3	5	111	C
3	5	120	U
48	ES	2912	G
48	ES	2941	G
48	ES	2942	C
48	ES	2943	C
48	ES	2948	C
48	ES	2956	G
48	ES	2958	C
48	ES	3237	G
48	ES	3247	A
48	ES	3283	G
48	ES	3288	G
48	ES	3289	G
48	ES	3581	C
48	ES	3582	C
48	ES	3583	U
48	ES	3591	C
49	28	8	U
49	28	12	A
49	28	13	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	39	A
49	28	42	A
49	28	43	U
49	28	44	A
49	28	48	G
49	28	49	U
49	28	56	A
49	28	58	G
49	28	59	A
49	28	64	A
49	28	65	A
49	28	71	C
49	28	72	C
49	28	73	A
49	28	74	G
49	28	91	G
49	28	92	C
49	28	107	G
49	28	108	A
49	28	109	G
49	28	110	C
49	28	116	G
49	28	118	C
49	28	119	G
49	28	120	A
49	28	122	U
49	28	126	C
49	28	131	C
49	28	132	G
49	28	133	C
49	28	134	G
49	28	135	G
49	28	136	C
49	28	142	G
49	28	143	C
49	28	159	C
49	28	170	C
49	28	171	U
49	28	172	C
49	28	190	G
49	28	200	U
49	28	201	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	206	U
49	28	209	U
49	28	216	C
49	28	218	A
49	28	219	G
49	28	220	C
49	28	224	U
49	28	225	G
49	28	233	U
49	28	234	G
49	28	246	G
49	28	253	G
49	28	256	G
49	28	262	G
49	28	266	C
49	28	275	C
49	28	276	C
49	28	280	G
49	28	297	U
49	28	306	A
49	28	309	C
49	28	315	G
49	28	316	U
49	28	334	A
49	28	340	C
49	28	387	G
49	28	399	G
49	28	406	C
49	28	407	A
49	28	410	A
49	28	412	G
49	28	413	G
49	28	415	G
49	28	431	G
49	28	432	U
49	28	446	C
49	28	449	C
49	28	452	A
49	28	453	G
49	28	454	U
49	28	455	C
49	28	457	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	463	A
49	28	464	G
49	28	465	G
49	28	467	U
49	28	468	U
49	28	469	C
49	28	472	C
49	28	481	G
49	28	481(A)	C
49	28	482	G
49	28	483	G
49	28	485	C
49	28	486	C
49	28	492	U
49	28	493	G
49	28	497	G
49	28	498	C
49	28	499	G
49	28	505	G
49	28	510	U
49	28	517	C
49	28	641	G
49	28	647	G
49	28	656	C
49	28	658	C
49	28	660	G
49	28	662	C
49	28	667	A
49	28	668	C
49	28	669	C
49	28	681	G
49	28	683	C
49	28	685	C
49	28	686	A
49	28	687	U
49	28	692	A
49	28	696	C
49	28	697	G
49	28	704	C
49	28	705	G
49	28	730	G
49	28	731	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	738	C
49	28	738(A)	C
49	28	739	G
49	28	744	G
49	28	747	A
49	28	749	G
49	28	758	G
49	28	759	G
49	28	905	C
49	28	914	U
49	28	915	A
49	28	917	A
49	28	918	G
49	28	922(B)	C
49	28	923	C
49	28	925	C
49	28	926	G
49	28	929	A
49	28	931	C
49	28	932	A
49	28	933	G
49	28	934	C
49	28	935	A
49	28	935(A)	G
49	28	936	C
49	28	939	G
49	28	941	C
49	28	943	A
49	28	945	U
49	28	946	C
49	28	956	A
49	28	959	G
49	28	960	A
49	28	961	G
49	28	962	C
49	28	965	G
49	28	966	A
49	28	967	C
49	28	969	C
49	28	972	C
49	28	979	C
49	28	983	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	1066	G
49	28	1067	G
49	28	1068	G
49	28	1072	C
49	28	1073	G
49	28	1079	C
49	28	1179	U
49	28	1187	G
49	28	1193	C
49	28	1195	G
49	28	1204	C
49	28	1210	C
49	28	1211	G
49	28	1212	G
49	28	1214	C
49	28	1215	C
49	28	1234	G
49	28	1235	G
49	28	1236	C
49	28	1237	C
49	28	1238	A
49	28	1239	C
49	28	1275	G
49	28	1276	C
49	28	1277	G
49	28	1284	G
49	28	1285	U
49	28	1287	G
49	28	1290	G
49	28	1292	C
49	28	1296	G
49	28	1301	C
49	28	1302	U
49	28	1303	A
49	28	1304	C
49	28	1313	C
49	28	1316	G
49	28	1317	U
49	28	1326	A
49	28	1330	A
49	28	1337	A
49	28	1339	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	1354	A
49	28	1358	G
49	28	1359	G
49	28	1362	G
49	28	1371	A
49	28	1376	C
49	28	1377	G
49	28	1378	C
49	28	1379	C
49	28	1380	G
49	28	1387	A
49	28	1394	G
49	28	1397	A
49	28	1398	A
49	28	1400	G
49	28	1414	C
49	28	1419	G
49	28	1420	A
49	28	1421	G
49	28	1433	A
49	28	1436	C
49	28	1445	U
49	28	1446	C
49	28	1456	C
49	28	1457	G
49	28	1475	G
49	28	1480	C
49	28	1482	G
49	28	1483	C
49	28	1484	G
49	28	1497	A
49	28	1498	G
49	28	1502	G
49	28	1516	G
49	28	1523	A
49	28	1534	A
49	28	1547	A
49	28	1563	A
49	28	1566	C
49	28	1568	C
49	28	1574	G
49	28	1578	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	1591	U
49	28	1596	U
49	28	1612	G
49	28	1613	A
49	28	1624	G
49	28	1625	G
49	28	1631	A
49	28	1633	G
49	28	1634	A
49	28	1638	A
49	28	1640	C
49	28	1641	G
49	28	1654	G
49	28	1661	C
49	28	1676	C
49	28	1677	U
49	28	1680	G
49	28	1684	A
49	28	1726	U
49	28	1729	A
49	28	1730	U
49	28	1733	G
49	28	1734	G
49	28	1742	A
49	28	1752	G
49	28	1755	C
49	28	1756	U
49	28	1757	U
49	28	1759	G
49	28	1761	G
49	28	1763	C
49	28	1764	G
49	28	1765	A
49	28	1766	A
49	28	1768	C
49	28	1772	C
49	28	1773	U
49	28	1775	A
49	28	1776	A
49	28	1781	U
49	28	1787	A
49	28	1791	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	1792	U
49	28	1797	G
49	28	1804	A
49	28	1805	A
49	28	1806	G
49	28	1808	C
49	28	1812	C
49	28	1818	G
49	28	1821	G
49	28	1828	C
49	28	1833	G
49	28	1836	G
49	28	1837	A
49	28	1842	G
49	28	1855	G
49	28	1869	G
49	28	1881	C
49	28	1882	U
49	28	1892	A
49	28	1897	A
49	28	1898	C
49	28	1918	U
49	28	1920	C
49	28	1921	C
49	28	1922	G
49	28	1931	C
49	28	1935	C
49	28	1940	G
49	28	1948	G
49	28	1951	G
49	28	1957	U
49	28	1958	A
49	28	1961	G
49	28	1962	A
49	28	1964	A
49	28	1974	U
49	28	1975	G
49	28	1976	G
49	28	1977	C
49	28	1978	C
49	28	1979	A
49	28	1980	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	1984	A
49	28	1985	G
49	28	1987	C
49	28	1990	A
49	28	1991	A
49	28	1992	U
49	28	1994	C
49	28	1997	U
49	28	2001	G
49	28	2002	A
49	28	2003	G
49	28	2004	U
49	28	2007	G
49	28	2011	C
49	28	2020	U
49	28	2021	G
49	28	2025	A
49	28	2046	G
49	28	2047	A
49	28	2048	U
49	28	2052	G
49	28	2055	G
49	28	2056	G
49	28	2062	C
49	28	2064	G
49	28	2069	A
49	28	2072	C
49	28	2084	U
49	28	2089	G
49	28	2090	U
49	28	2092	G
49	28	2093	G
49	28	2094	C
49	28	2095	A
49	28	2097	A
49	28	2098	G
49	28	2100	G
49	28	2102	G
49	28	2104	A
49	28	2105	A
49	28	2107	A
49	28	2108	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	2110	G
49	28	2267	U
49	28	2268	A
49	28	2273	G
49	28	2274	C
49	28	2275	G
49	28	2279	A
49	28	2280	G
49	28	2289	C
49	28	2300	A
49	28	2301	G
49	28	2306	G
49	28	2313	A
49	28	2314	G
49	28	2316	G
49	28	2322	G
49	28	2326	G
49	28	2333	G
49	28	2345	G
49	28	2348	G
49	28	2351	C
49	28	2360	A
49	28	2395	A
49	28	2402	G
49	28	2417	A
49	28	2422	C
49	28	2425	U
49	28	2433	G
49	28	2434	G
49	28	2441	C
49	28	2447	U
49	28	2450	G
49	28	2475	G
49	28	2488	C
49	28	2489	C
49	28	2490	U
49	28	2491	C
49	28	2503	G
49	28	2505	C
49	28	2506	G
49	28	2513	A
49	28	2529	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	2530	U
49	28	2536	A
49	28	2537	A
49	28	2544	G
49	28	2545	U
49	28	2546	G
49	28	2547	G
49	28	2549	G
49	28	2553	A
49	28	2554	U
49	28	2571	C
49	28	2575	U
49	28	2583	C
49	28	2586	G
49	28	2587	A
49	28	2588	C
49	28	2589	C
49	28	2601	A
49	28	2602	G
49	28	2612	G
49	28	2618	G
49	28	2627	C
49	28	2638	G
49	28	2639	U
49	28	2640	G
49	28	2647	A
49	28	2649	G
49	28	2653	C
49	28	2658	G
49	28	2661	U
49	28	2662	G
49	28	2669	C
49	28	2673	G
49	28	2675	G
49	28	2679	G
49	28	2680	G
49	28	2686	G
49	28	2687	U
49	28	2695	A
49	28	2696	A
49	28	2704	C
49	28	2705	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	2707	U
49	28	2708	U
49	28	2709	C
49	28	2710	C
49	28	2711	G
49	28	2712	G
49	28	2714	G
49	28	2719	C
49	28	2721	G
49	28	2725	A
49	28	2726	G
49	28	2735	G
49	28	2740	U
49	28	2742	G
49	28	2743	A
49	28	2744	A
49	28	2753	G
49	28	2754	G
49	28	2758	G
49	28	2760	G
49	28	2761	U
49	28	2763	U
49	28	2764	A
49	28	2768	C
49	28	2769	U
49	28	2787	A
49	28	2788	U
49	28	2790	U
49	28	2794	C
49	28	2798	A
49	28	2806	A
49	28	2826	U
49	28	2827	G
49	28	2829	U
49	28	2837	U
49	28	2838	G
49	28	2842	G
49	28	2848	G
49	28	2855	G
49	28	2856	C
49	28	2875	C
49	28	2897	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	2898	G
49	28	3602	C
49	28	3604	A
49	28	3605	C
49	28	3615	G
49	28	3616	U
49	28	3617	G
49	28	3625	G
49	28	3626	G
49	28	3635	A
49	28	3644	U
49	28	3662	A
49	28	3663	A
49	28	3664	G
49	28	3673	C
49	28	3674	G
49	28	3698	G
49	28	3709	U
49	28	3710	G
49	28	3713	U
49	28	3714	G
49	28	3753	G
49	28	3754	G
49	28	3755	G
49	28	3757	G
49	28	3765	G
49	28	3773	U
49	28	3776	G
49	28	3777	G
49	28	3778	U
49	28	3784	A
49	28	3786	U
49	28	3811	G
49	28	3814	U
49	28	3817	A
49	28	3819	G
49	28	3822	U
49	28	3824	A
49	28	3830	A
49	28	3831	U
49	28	3838	U
49	28	3839	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	3840	U
49	28	3859	G
49	28	3869	C
49	28	3876	A
49	28	3877	A
49	28	3878	C
49	28	3879	G
49	28	3889	G
49	28	3892	U
49	28	3897	G
49	28	3901	A
49	28	3905	A
49	28	3906	A
49	28	3907	G
49	28	3908	A
49	28	3915	U
49	28	3916	G
49	28	3917	A
49	28	3918	G
49	28	3926	C
49	28	3927	U
49	28	3938	G
49	28	3939	G
49	28	4069	U
49	28	4076	G
49	28	4084	G
49	28	4085	A
49	28	4086	G
49	28	4088	C
49	28	4097	G
49	28	4099	G
49	28	4116	C
49	28	4119	C
49	28	4120	U
49	28	4121	G
49	28	4122	G
49	28	4125	C
49	28	4127	A
49	28	4137	C
49	28	4158	C
49	28	4162	C
49	28	4163	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	4166	G
49	28	4167	G
49	28	4170	A
49	28	4183	G
49	28	4184	G
49	28	4191	G
49	28	4201	G
49	28	4203	A
49	28	4225	G
49	28	4229	U
49	28	4233	A
49	28	4243	C
49	28	4249	G
49	28	4251	A
49	28	4252	C
49	28	4253	A
49	28	4254	G
49	28	4257	A
49	28	4266	G
49	28	4268	A
49	28	4271	A
49	28	4273	A
49	28	4281	A
49	28	4291	G
49	28	4297	G
49	28	4304	A
49	28	4305	G
49	28	4306	U
49	28	4314	C
49	28	4317	A
49	28	4318	C
49	28	4319	C
49	28	4326	G
49	28	4329	G
49	28	4330	G
49	28	4332	C
49	28	4336	A
49	28	4349	C
49	28	4350	C
49	28	4354	U
49	28	4355	G
49	28	4373	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	4376	A
49	28	4377	G
49	28	4378	A
49	28	4379	A
49	28	4380	A
49	28	4386	C
49	28	4387	C
49	28	4391	G
49	28	4394	A
49	28	4395	U
49	28	4401	G
49	28	4415	A
49	28	4419	U
49	28	4421	C
49	28	4422	A
49	28	4430	G
49	28	4436	U
49	28	4444	C
49	28	4448	G
49	28	4449	A
49	28	4450	U
49	28	4453	C
49	28	4463	U
49	28	4464	A
49	28	4466	C
49	28	4471	U
49	28	4475	G
49	28	4488	A
49	28	4500	U
49	28	4512	U
49	28	4513	A
49	28	4519	C
49	28	4520	G
49	28	4524	G
49	28	4525	C
49	28	4532	U
49	28	4548	A
49	28	4549	G
49	28	4557	U
49	28	4560	C
49	28	4567	G
49	28	4569	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	4573	G
49	28	4574	U
49	28	4575	G
49	28	4577	U
49	28	4584	A
49	28	4586	G
49	28	4587	G
49	28	4590	A
49	28	4599	A
49	28	4606	G
49	28	4627	U
49	28	4636	U
49	28	4637	G
49	28	4639	G
49	28	4656	A
49	28	4657	U
49	28	4667	C
49	28	4670	C
49	28	4672	A
49	28	4677	U
49	28	4687	A
49	28	4694	G
49	28	4700	A
49	28	4709	U
49	28	4719	G
49	28	4720	C
49	28	4729	A
49	28	4747	C
49	28	4751	G
49	28	4752	U
49	28	4754	G
49	28	4755	G
49	28	4756	C
49	28	4757	C
49	28	4759	C
49	28	4761	G
49	28	4764	A
49	28	4765	G
49	28	4769	G
49	28	4771	C
49	28	4772	C
49	28	4870	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	4871	C
49	28	4873	G
49	28	4875	G
49	28	4881	U
49	28	4882	U
49	28	4883	C
49	28	4885	U
49	28	4887	C
49	28	4893	A
49	28	4894	A
49	28	4895	C
49	28	4903	G
49	28	4906	C
49	28	4910	A
49	28	4913	G
49	28	4914	G
49	28	4915	G
49	28	4918	C
49	28	4919	G
49	28	4921	C
49	28	4922	C
49	28	4924	C
49	28	4925	U
49	28	4926	C
49	28	4927	G
49	28	4928	C
49	28	4931	G
49	28	4932	U
49	28	4937	C
49	28	4943	A
49	28	4944	C
49	28	4948	C
49	28	4949	G
49	28	4950	U
49	28	4951	G
49	28	4956	A
49	28	4957	C
49	28	4960	G
49	28	4963	G
49	28	4964	C
49	28	4965	U
49	28	4966	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	4967	A
49	28	4976	U
49	28	4988	U
49	28	4990	C
49	28	4991	U
49	28	4993	G
49	28	5000	G
49	28	5017	G
49	28	5029	C
49	28	5041	G
49	28	5047	C
49	28	5048	A
49	28	5050	C
49	28	5052	C
49	28	5053	U
49	28	5054	C
49	28	5058	A
49	28	5061	A
49	28	5062	G

All (51) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	58	124	U
48	ES	3236	G
49	28	12	A
49	28	48	G
49	28	125	C
49	28	142	G
49	28	275	C
49	28	406	C
49	28	480	C
49	28	485	C
49	28	492	U
49	28	504	G
49	28	696	C
49	28	930	G
49	28	1072	C
49	28	1211	G
49	28	1238	A
49	28	1291	G
49	28	1329	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	28	1370	G
49	28	1445	U
49	28	1455	G
49	28	1633	G
49	28	1804	A
49	28	1979	A
49	28	2046	G
49	28	2089	G
49	28	2266	C
49	28	2502	A
49	28	2513	A
49	28	2546	G
49	28	2587	A
49	28	2639	U
49	28	2661	U
49	28	2695	A
49	28	3625	G
49	28	3697	U
49	28	3876	A
49	28	3888	G
49	28	3945	A
49	28	4119	C
49	28	4232	U
49	28	4378	A
49	28	4395	U
49	28	4448	G
49	28	4699	U
49	28	4719	G
49	28	4884	G
49	28	4925	U
49	28	4936	G
49	28	4947	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

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
51	GDP	v	900	-	29,30,30	3.51	13 (44%)	45,47,47	1.83	11 (24%)

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
51	GDP	v	900	-	-	3/16/32/32	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	v	900	GDP	O6-C6	9.38	1.41	1.23
51	v	900	GDP	C2'-C3'	-8.43	1.30	1.53
51	v	900	GDP	O4'-C4'	-7.01	1.29	1.45
51	v	900	GDP	O4'-C1'	5.34	1.54	1.42
51	v	900	GDP	C2-N2	4.74	1.45	1.34
51	v	900	GDP	C1'-N9	-4.72	1.34	1.47
51	v	900	GDP	C6-N1	-3.72	1.31	1.38
51	v	900	GDP	C3'-C4'	3.70	1.62	1.53
51	v	900	GDP	O2'-C2'	3.09	1.50	1.43
51	v	900	GDP	PA-O3A	2.68	1.62	1.59
51	v	900	GDP	C2-N1	-2.65	1.31	1.37
51	v	900	GDP	C8-N9	-2.40	1.32	1.37
51	v	900	GDP	C5-N7	-2.32	1.34	1.39

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	v	900	GDP	C5-C4-N3	-5.65	119.39	128.39
51	v	900	GDP	C2-N3-C4	4.86	120.67	112.30
51	v	900	GDP	N9-C4-N3	3.88	133.71	125.95
51	v	900	GDP	C3'-C2'-C1'	3.05	107.23	101.46
51	v	900	GDP	C6-C5-N7	2.83	135.44	130.29
51	v	900	GDP	N9-C8-N7	-2.79	108.23	113.40
51	v	900	GDP	C2'-C3'-C4'	2.67	107.77	102.61
51	v	900	GDP	C8-N7-C5	2.62	108.92	104.26
51	v	900	GDP	C4-C5-N7	-2.59	106.56	110.67
51	v	900	GDP	C5-C6-N1	2.20	118.86	113.25
51	v	900	GDP	C2-N1-C6	-2.00	121.48	125.11

There are no chirality outliers.

All (3) torsion outliers are listed below:

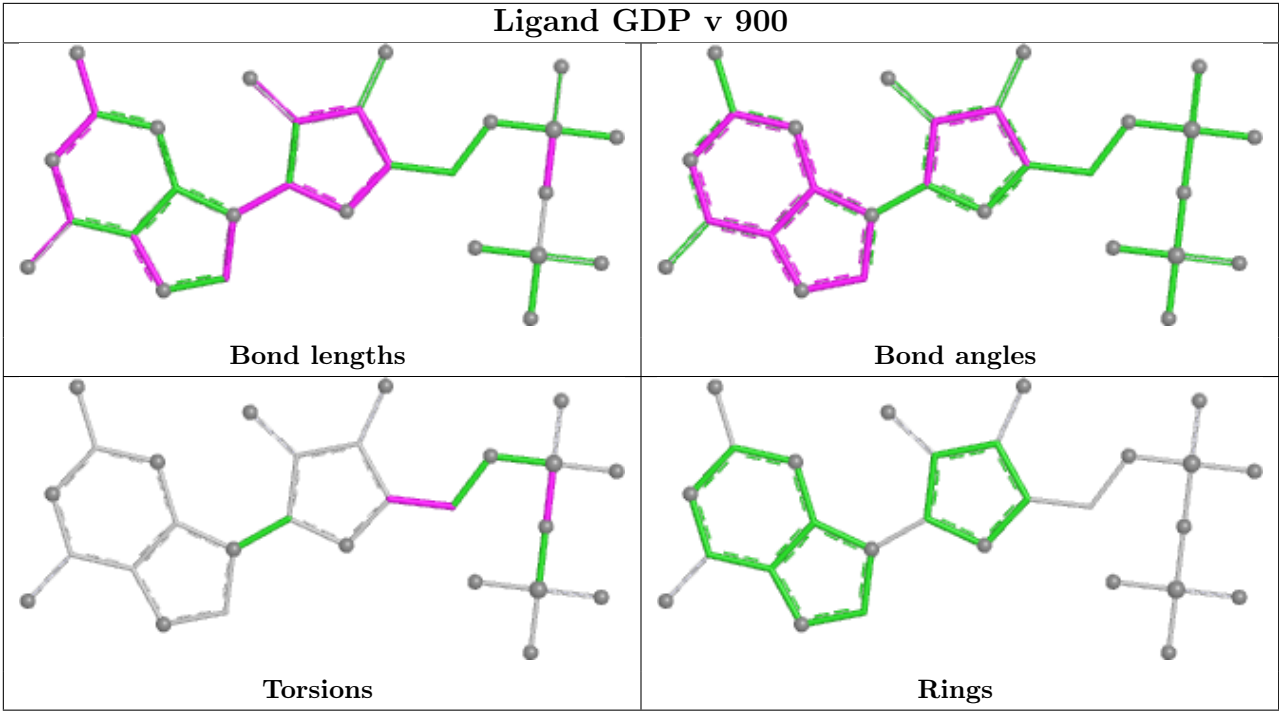
Mol	Chain	Res	Type	Atoms
51	v	900	GDP	C3'-C4'-C5'-O5'
51	v	900	GDP	O4'-C4'-C5'-O5'
51	v	900	GDP	PB-O3A-PA-O2A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
51	v	900	GDP	4	0

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
49	28	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	28	3945:A	O3'	3946:G	P	1.94
1	28	3940:U	O3'	3941:G	P	1.29

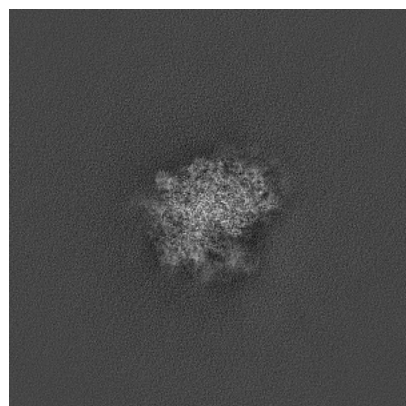
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75704. These allow visual inspection of the internal detail of the map and identification of artifacts.

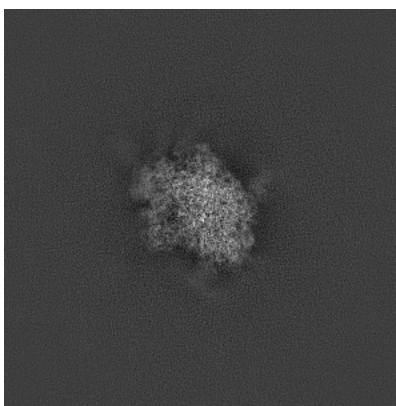
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

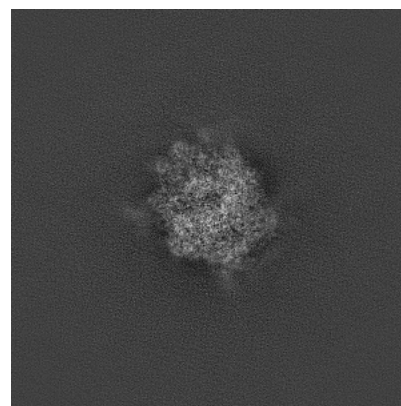
6.1.1 Primary map



X

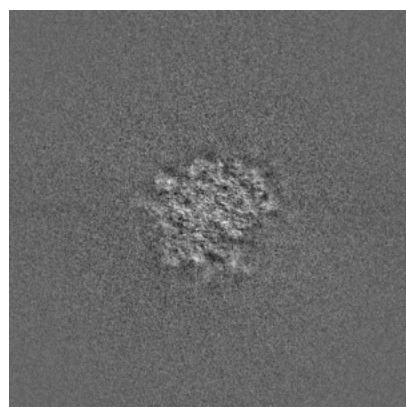


Y

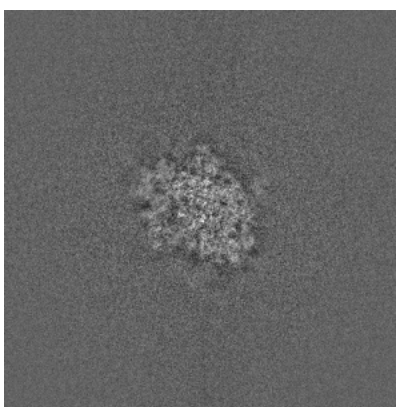


Z

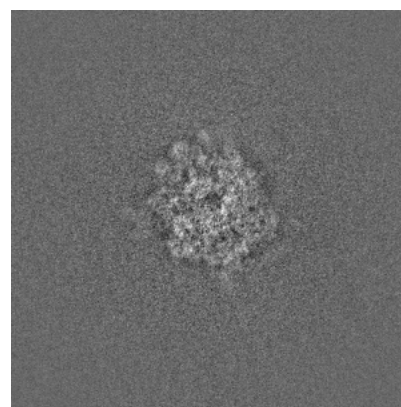
6.1.2 Raw map



X



Y

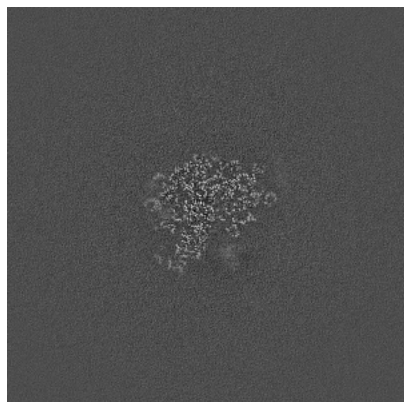


Z

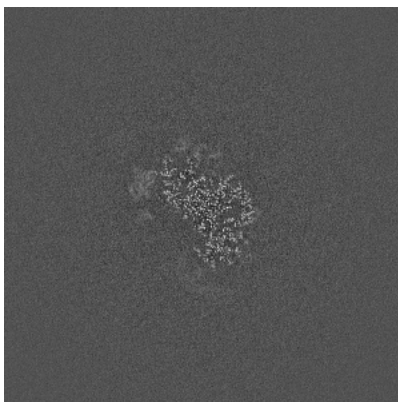
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

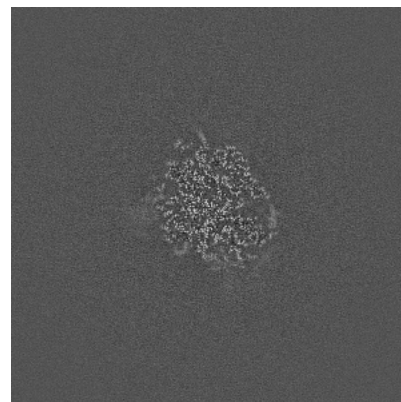
6.2.1 Primary map



X Index: 400

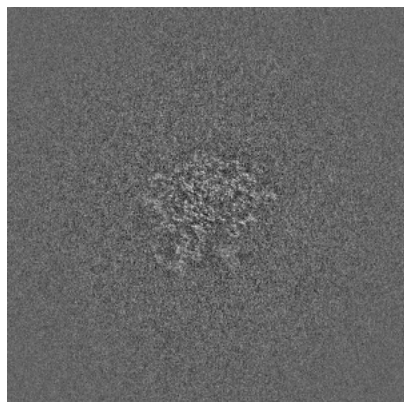


Y Index: 400

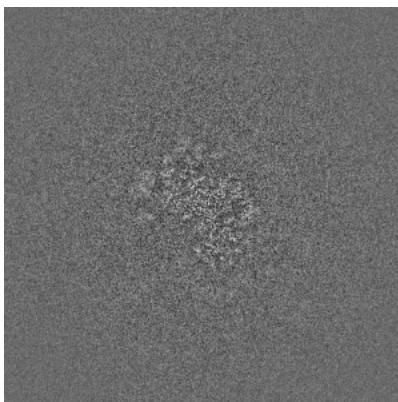


Z Index: 400

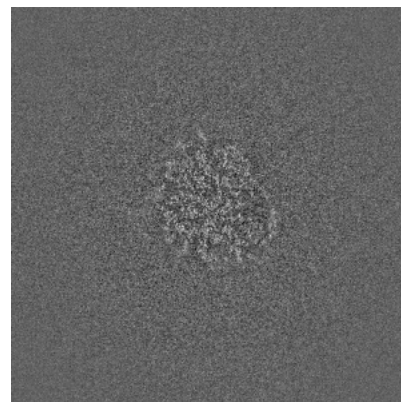
6.2.2 Raw map



X Index: 400



Y Index: 400

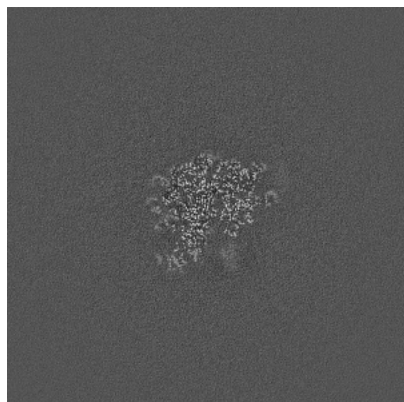


Z Index: 400

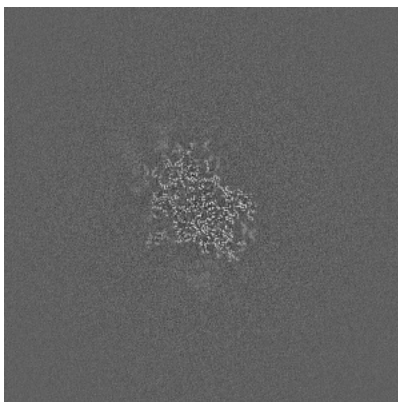
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

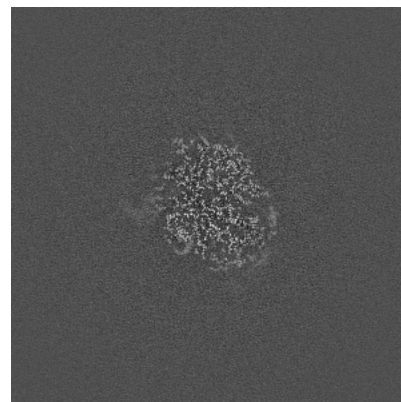
6.3.1 Primary map



X Index: 396

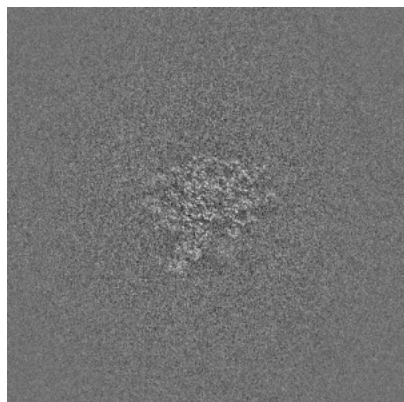


Y Index: 380

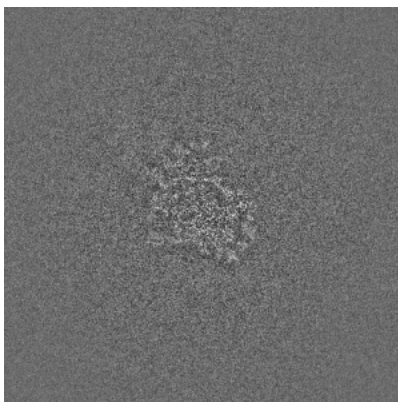


Z Index: 403

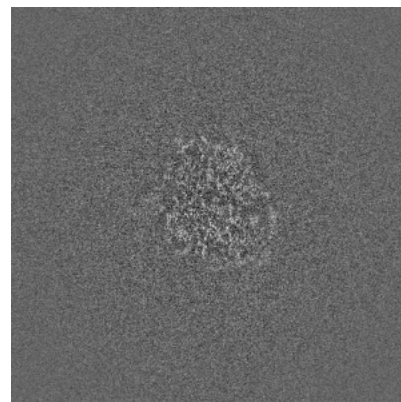
6.3.2 Raw map



X Index: 398



Y Index: 380

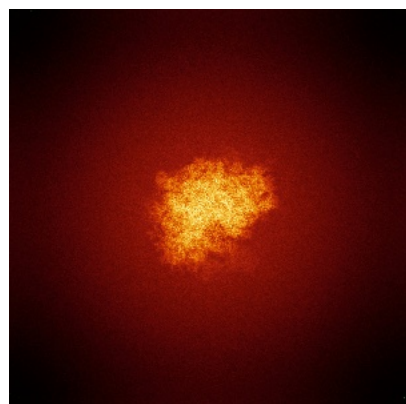


Z Index: 403

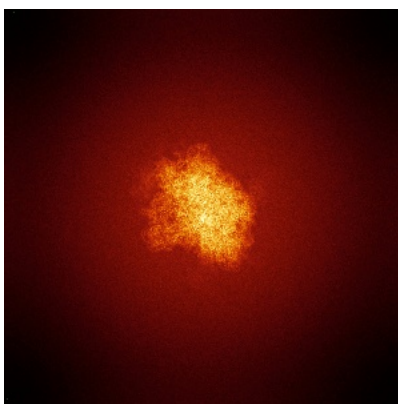
The images above show the largest variance slices of the map in three orthogonal directions.

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

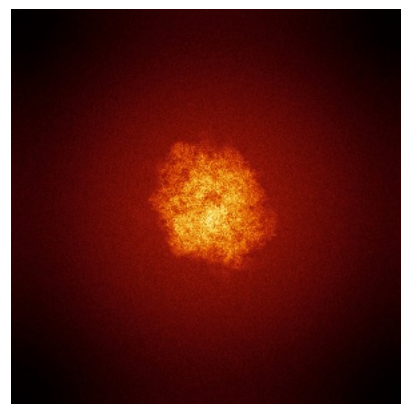
6.4.1 Primary map



X

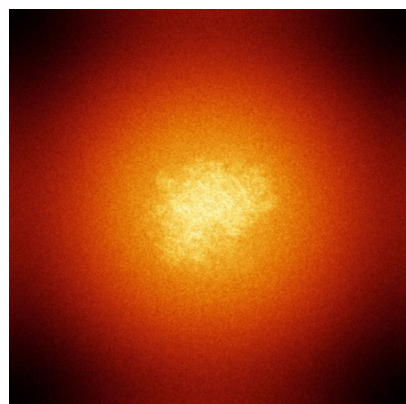


Y

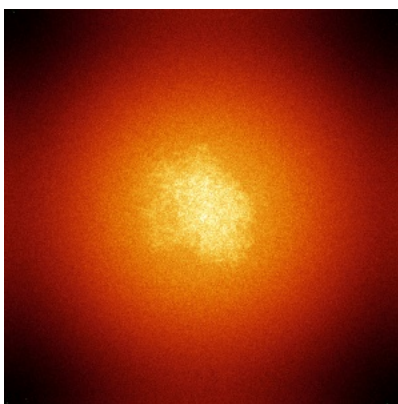


Z

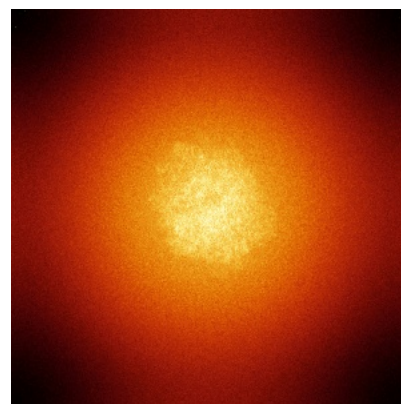
6.4.2 Raw map



X



Y

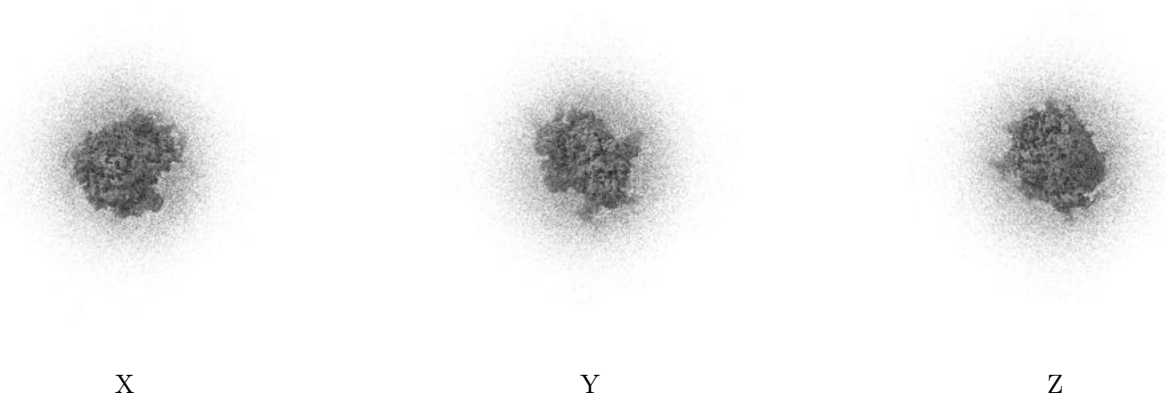


Z

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

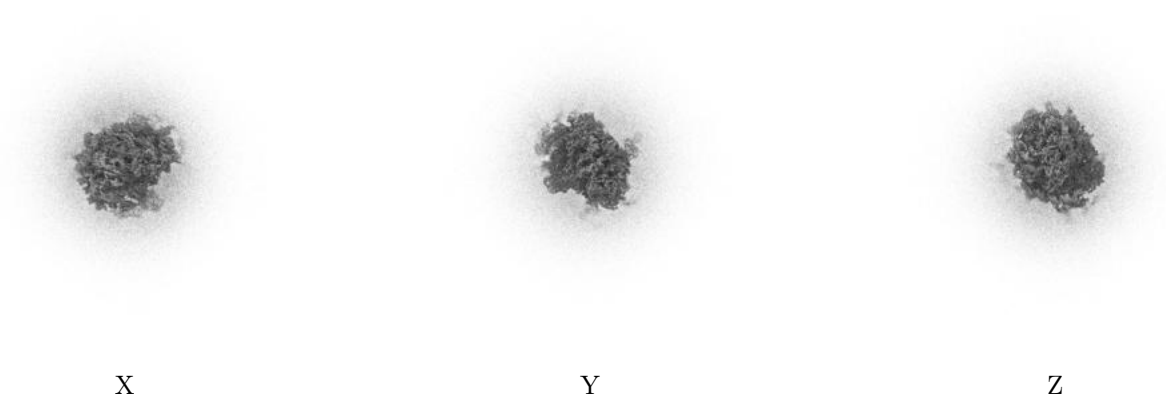
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. 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



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.

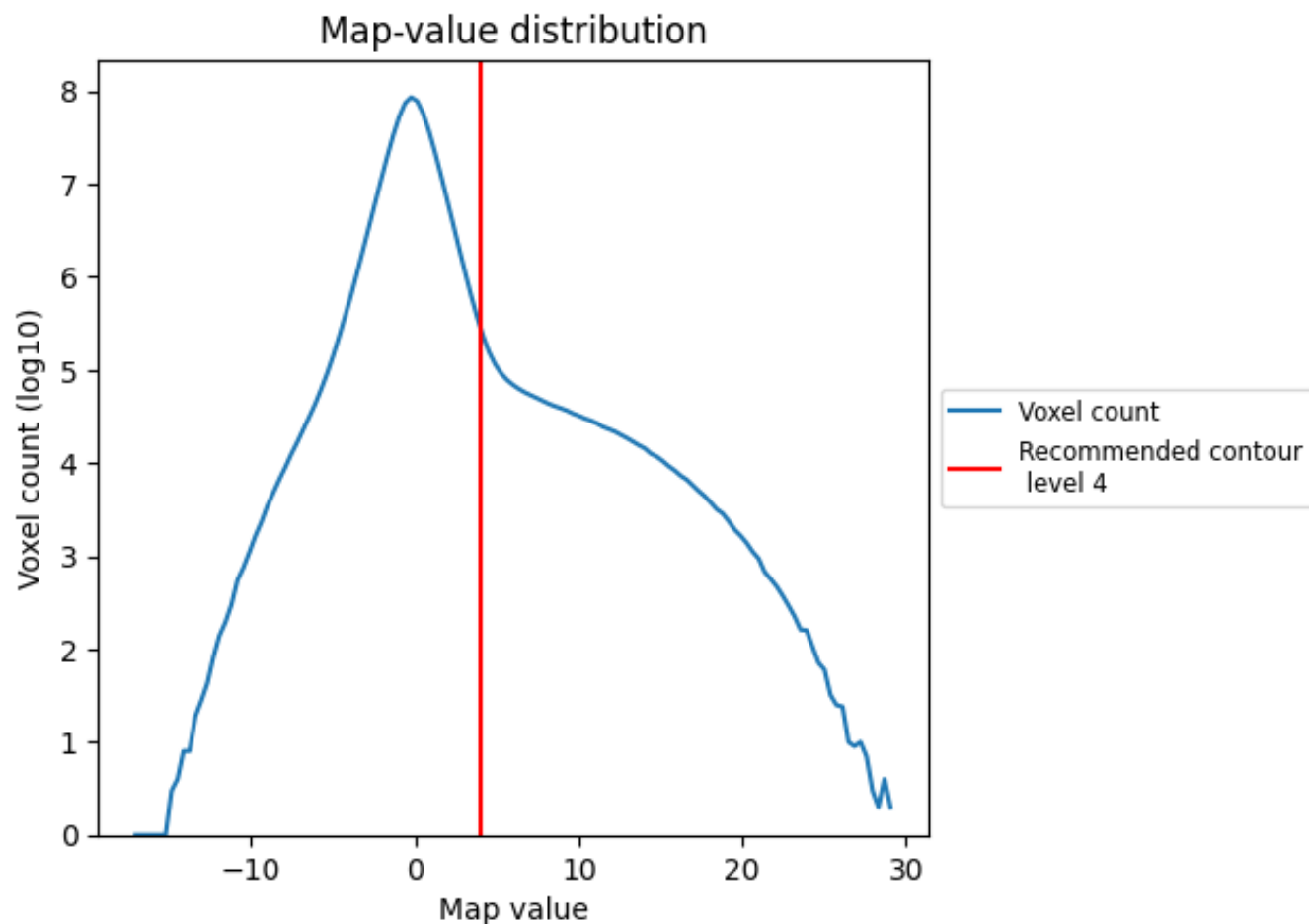
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

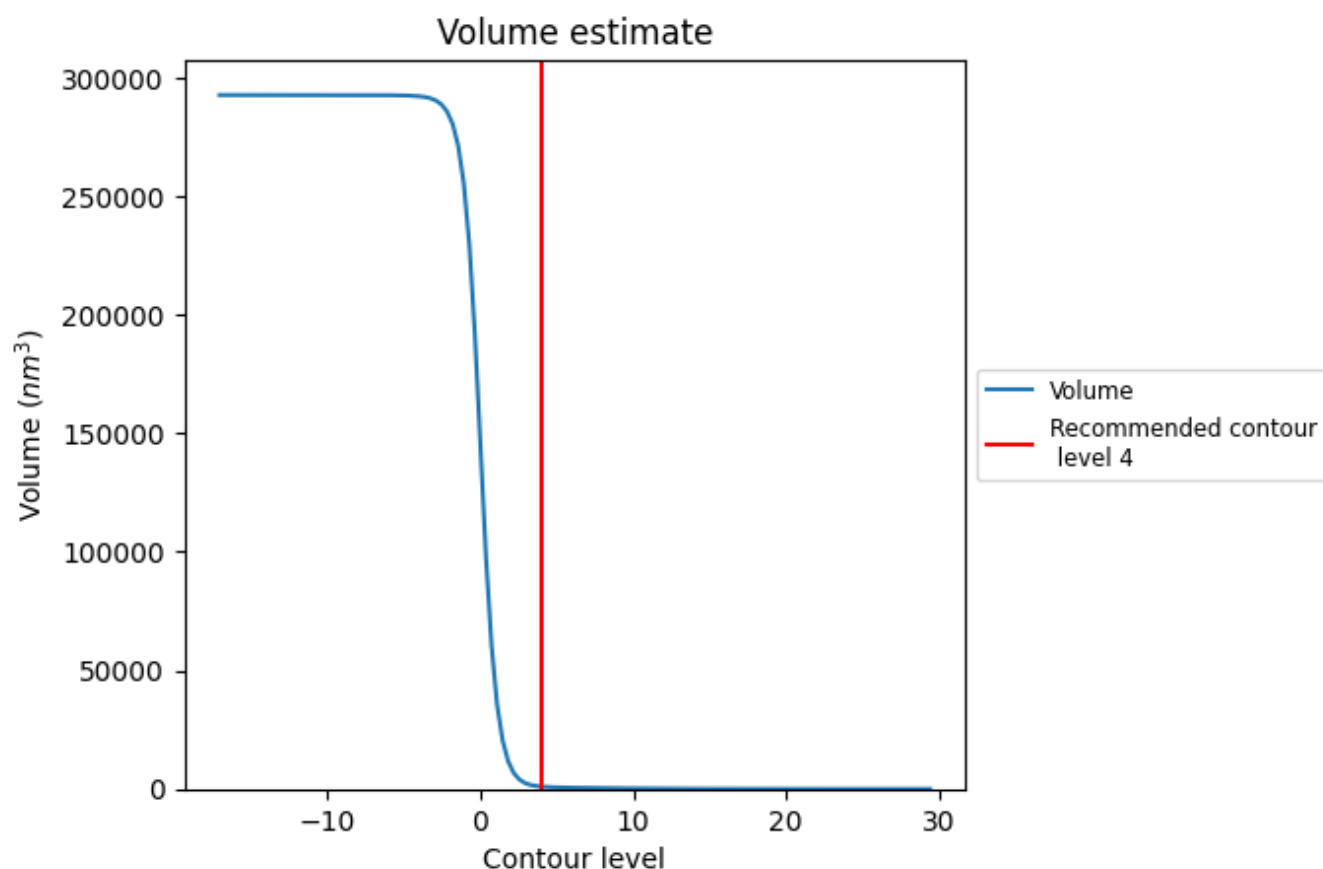
This section contains the results of statistical analysis of the map.

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.

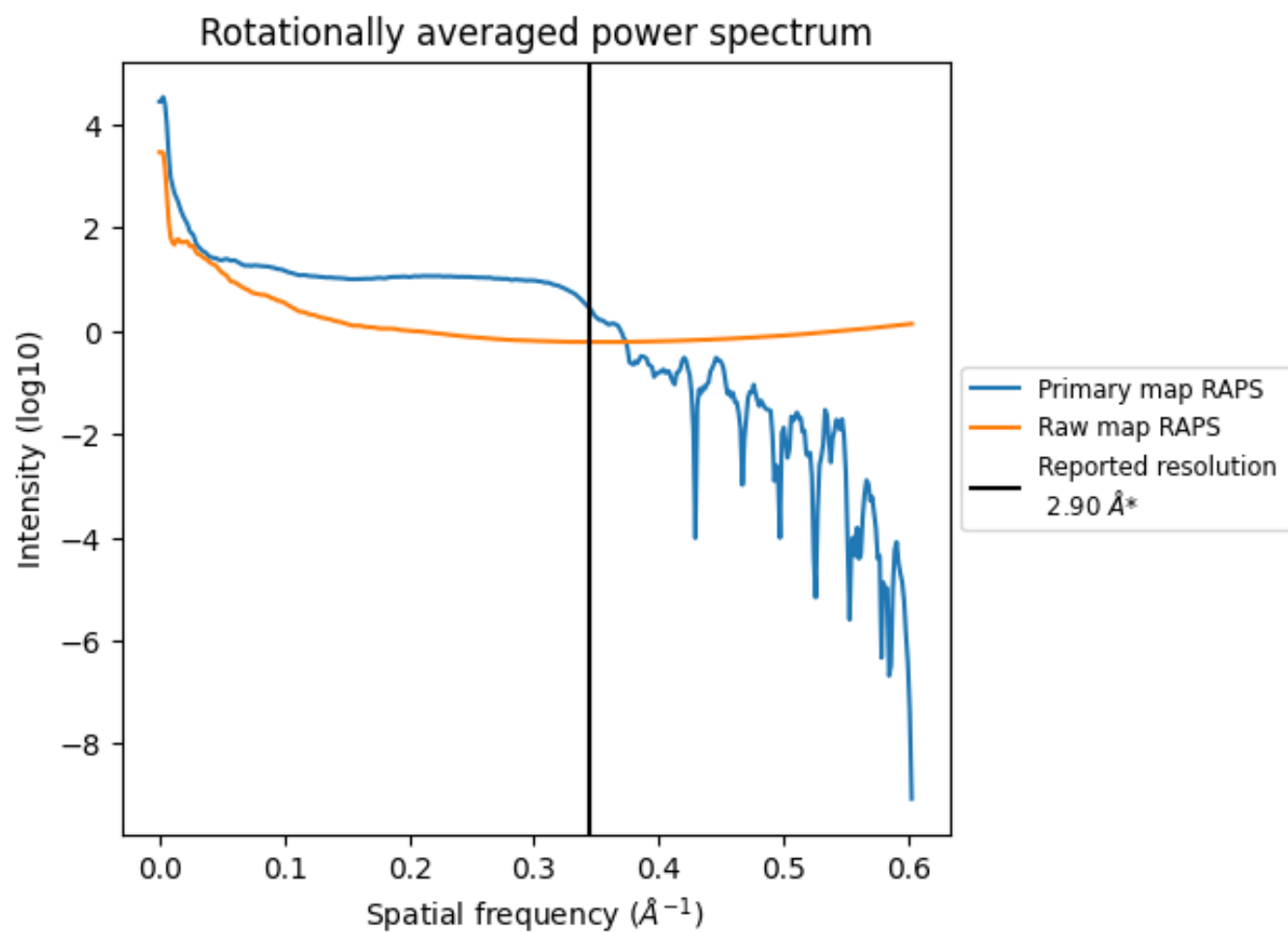
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 986 nm^3 ; this corresponds to an approximate mass of 891 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 ⓘ

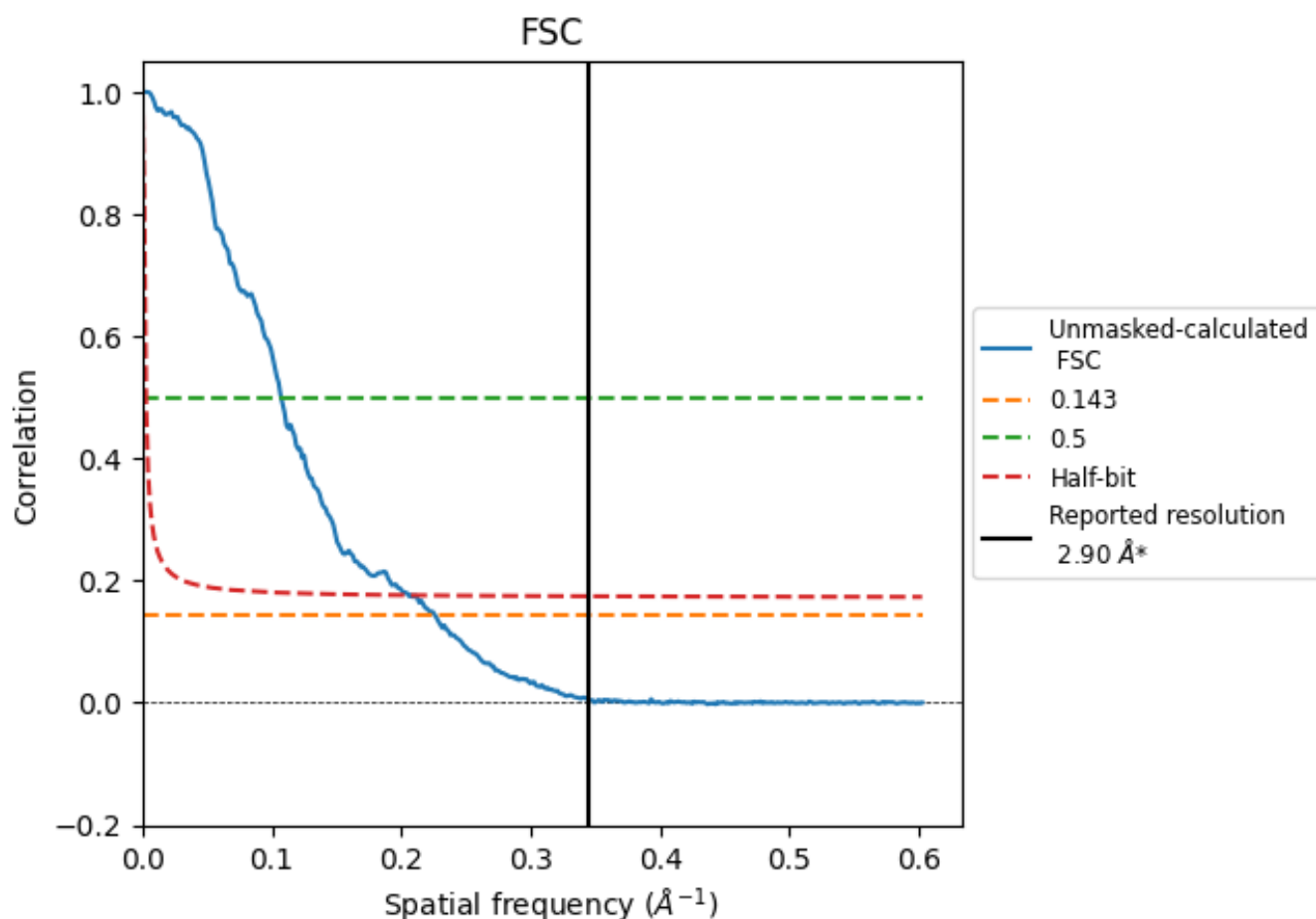


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

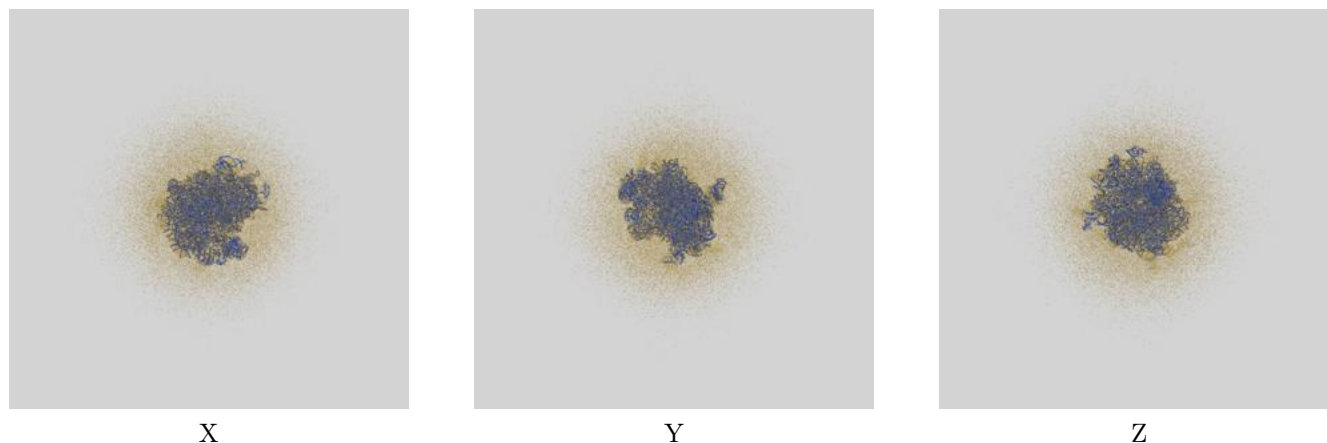
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.42	9.33	4.86

*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 4.42 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

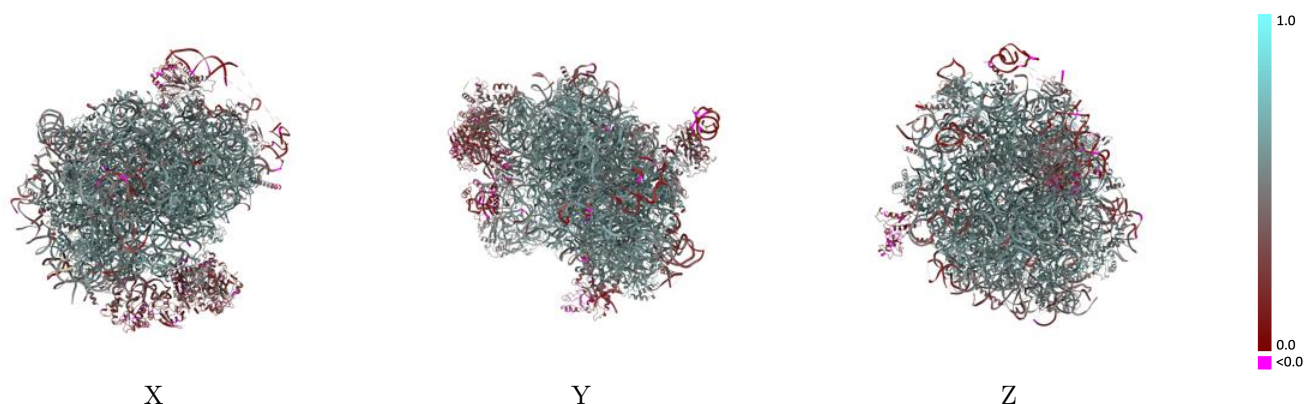
This section contains information regarding the fit between EMDB map EMD-75704 and PDB model 11HV. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



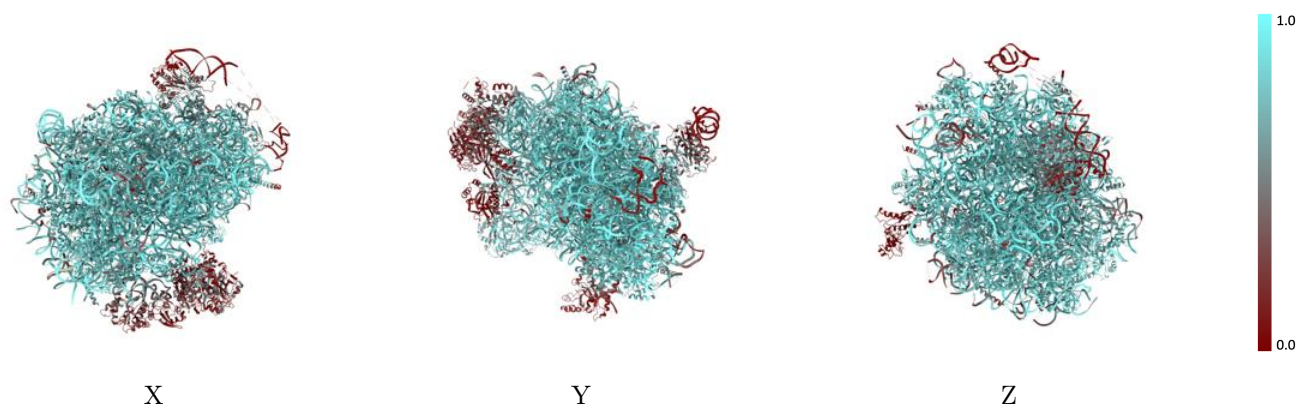
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



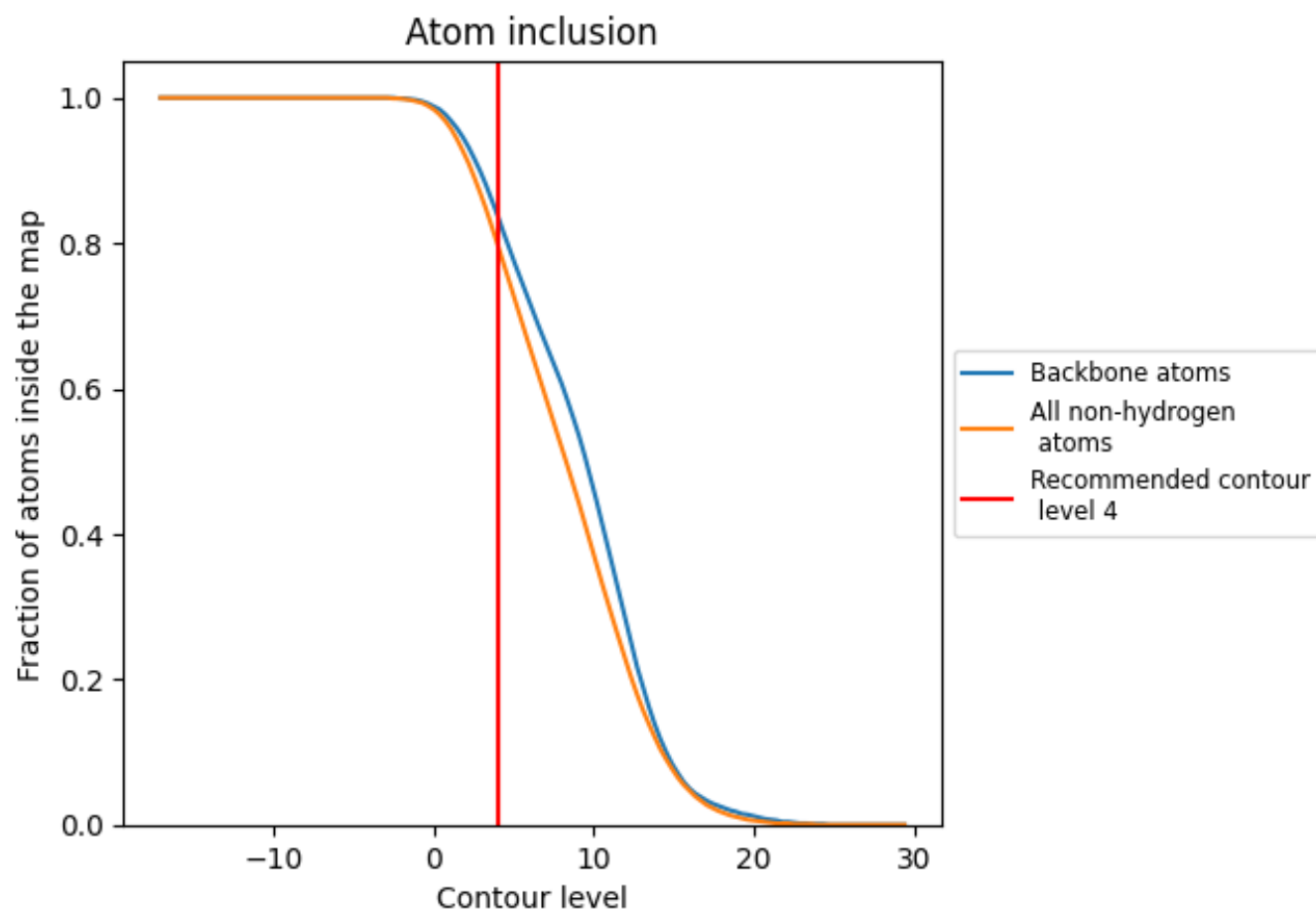
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7980	 0.5180
10	 0.8430	 0.5600
11	 0.7050	 0.4760
13	 0.8180	 0.5450
14	 0.8250	 0.5480
15	 0.8940	 0.6010
17	 0.8600	 0.5870
19	 0.7910	 0.5260
20	 0.8710	 0.5780
21	 0.8330	 0.5590
22	 0.6540	 0.4420
24	 0.7920	 0.5530
25	 0.8060	 0.5640
26	 0.8280	 0.5570
27	 0.8130	 0.5490
28	 0.8810	 0.5400
29	 0.7070	 0.4810
30	 0.7450	 0.5030
31	 0.7970	 0.5430
32	 0.8840	 0.5910
34	 0.7980	 0.5530
35	 0.8010	 0.5500
36	 0.8160	 0.5400
37	 0.8950	 0.5990
38	 0.7070	 0.4920
39	 0.8450	 0.5680
40	 0.8170	 0.5580
42	 0.8230	 0.5610
5	 0.9480	 0.5830
58	 0.8990	 0.5580
EB	 0.3880	 0.3420
ES	 0.0670	 0.1190
L3	 0.8530	 0.5770
L4	 0.8580	 0.5780
L5	 0.8010	 0.5350



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
L6	 0.8340	 0.5450
L7	 0.8630	 0.5840
L8	 0.8740	 0.5900
L9	 0.7860	 0.5500
Q	 0.8790	 0.5870
aa	 0.7650	 0.5190
bb	 0.8690	 0.5730
cc	 0.8070	 0.5610
dd	 0.8860	 0.5970
ee	 0.8990	 0.6050
ff	 0.8160	 0.5590
gg	 0.8720	 0.5820
s	 0.3190	 0.2860
t	 0.1320	 0.1730
u	 0.0450	 0.1410
v	 0.2400	 0.2810