



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 10:37 AM UTC

PDB ID : 7QWQ / pdb_00007qwq
EMDB ID : EMD-14191
Title : Ternary complex of ribosome nascent chain with SRP and NAC
Authors : Jomaa, A.; Gamerdinger, M.; Hsieh, H.; Wallisch, A.; Chandrasekaran, V.;
Ulusoy, Z.; Scaiola, A.; Hegde, R.; Shan, S.; Ban, N.; Deuerling, E.
Deposited on : 2022-01-25
Resolution : 2.83 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

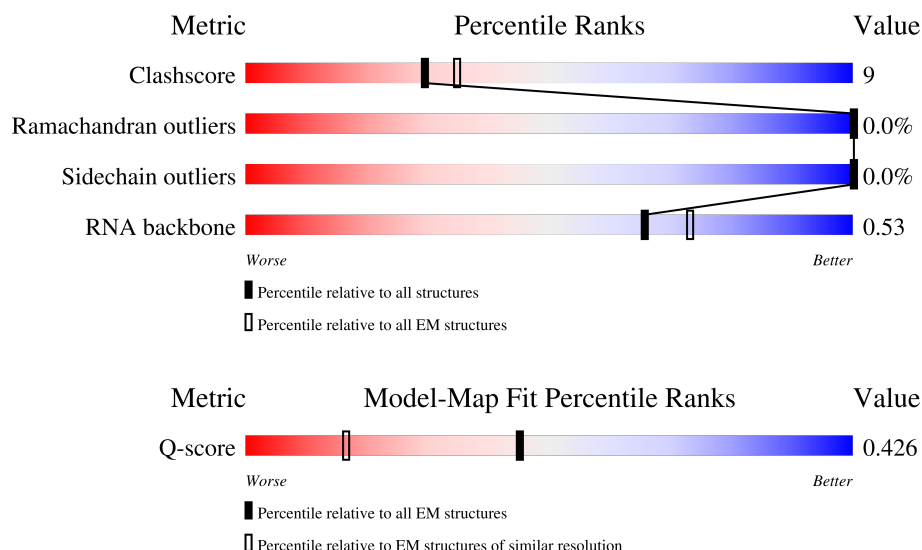
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.83 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	11847 (2.33 - 3.33)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	167	100% 47% 46% 7%
2	q	144	73% 56% 17% 27%
3	s	112	48% 47% 50%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	u	162	
5	v	627	
6	x	504	
7	A	244	
8	b	223	
9	5	4754	
10	B	403	
11	c	115	
12	C	413	
13	d	125	
14	D	297	
15	e	157	
16	E	291	
17	f	110	
18	F	225	
19	g	129	
20	G	319	
21	h	123	
22	H	192	
23	i	102	
24	I	214	
25	j	97	
26	J	178	
27	k	69	
28	L	210	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	l	51	
30	M	218	
31	m	128	
32	N	204	
33	n	25	
34	O	500	
35	o	141	
36	P	153	
37	p	92	
38	Q	187	
39	r	137	
40	R	196	
41	S	175	
42	T	160	
43	U	102	
44	V	140	
45	W	157	
46	X	156	
47	7	120	
48	Y	145	
49	8	156	
50	Z	136	
51	a	148	
52	t	215	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 143809 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called SRP RNA 7SL.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	167	Total	C	N	O	P	0	0
			3583	1596	658	1162	167		

- Molecule 2 is a protein called Signal recognition particle 19 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	q	105	Total	C	N	O	S	0	0
			844	534	152	152	6		

- Molecule 3 is a protein called Nascent chain preprolactin.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	s	56	Total	C	N	O	0	0
			283	171	56	56		

- Molecule 4 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	u	32	Total	C	N	O	S	0	0
			252	156	53	42	1		

- Molecule 5 is a protein called Signal recognition particle subunit SRP68.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	v	197	Total	C	N	O	S	0	0
			1648	1034	309	297	8		

- Molecule 6 is a protein called Signal recognition particle 54 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	x	488	Total	C	N	O	S	0	0
			3778	2380	650	715	33		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	226	GLU	GLY	engineered mutation	UNP P61011

- Molecule 7 is a protein called L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 8 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	b	75	Total	C	N	O	S	0	0
			609	378	130	98	3		

- Molecule 9 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	5	3493	Total	C	N	O	P	0	0
			74854	33335	13681	24346	3492		

- Molecule 10 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	394	Total	C	N	O	S	0	0
			3148	2007	591	537	13		

- Molecule 11 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	34	THR	SER	conflict	UNP G1TDL2

- Molecule 12 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 13 is a protein called Ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 14 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D	292	Total	C	N	O	S	0	0
			2386	1509	437	426	14		

- Molecule 15 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 16 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	E	236	Total	C	N	O	S	0	0
			1898	1215	362	318	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	126	ARG	LYS	conflict	UNP G1SKF7
E	217	GLN	LYS	conflict	UNP G1SKF7

- Molecule 17 is a protein called 60S ribosomal protein L35a.

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

- Molecule 18 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	175	ALA	THR	conflict	UNP G1SV32
F	185	GLY	ASN	conflict	UNP G1SV32
F	202	ARG	HIS	conflict	UNP G1SV32
F	233	GLU	GLY	conflict	UNP G1SV32

- Molecule 19 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 20 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	G	241	Total	C	N	O	S	0	0
			1934	1233	371	326	4		

- Molecule 21 is a protein called 60S ribosomal protein L35.

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

- Molecule 22 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 23 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 24 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	I	204	Total	C	N	O	S	0	0
			1655	1051	319	272	13		

- Molecule 25 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 26 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	J	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 27 is a protein called 60S ribosomal protein L38.

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

- Molecule 28 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L	210	Total	C	N	O	S	0	0
			1703	1065	354	280	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	SER	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0
L	55	LEU	-	insertion	UNP G1TPV0

- Molecule 29 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 30 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 31 is a protein called Ubiquitin A-52 residue ribosomal protein fusion product 1.

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

- Molecule 32 is a protein called Ribosomal protein L15.

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

- Molecule 33 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 34 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	O	199	Total	C	N	O	S	0	0
			1638	1056	321	256	5		

- Molecule 35 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 36 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 37 is a protein called eL43.

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

- Molecule 38 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	r	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 40 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 41 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 42 is a protein called 60S ribosomal protein L21.

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

- Molecule 43 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U	102	Total	C	N	O	S	0	0
			833	533	146	152	2		

- Molecule 44 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 45 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 46 is a protein called Ribosomal_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 47 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 48 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 49 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 50 is a protein called 60S ribosomal protein L27.

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

- Molecule 51 is a protein called 60S ribosomal protein L27a.

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

- Molecule 52 is a protein called Nascent polypeptide-associated complex subunit alpha.

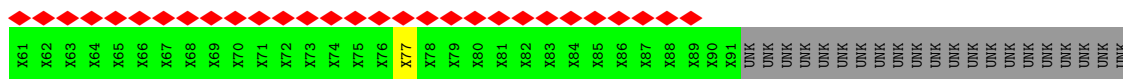
Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	47	Total	C	N	O	S	0	0
			359	217	62	77	3		

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

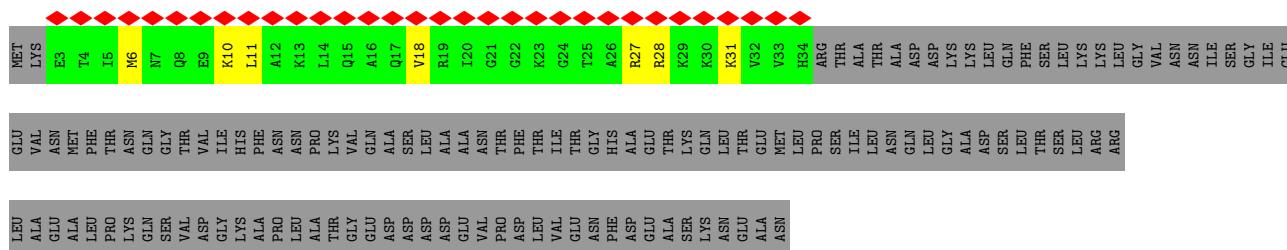
Mol	Chain	Residues	Atoms		AltConf
53	5	96	Total	Mg	0
			96	96	
53	B	1	Total	Mg	0
			1	1	

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

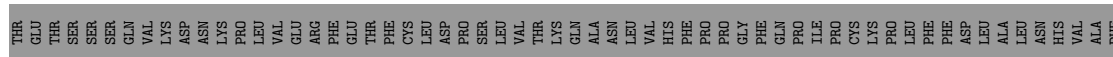
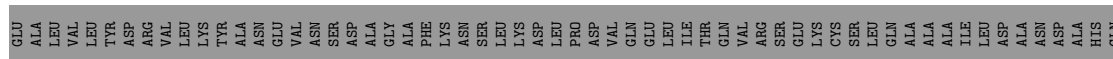
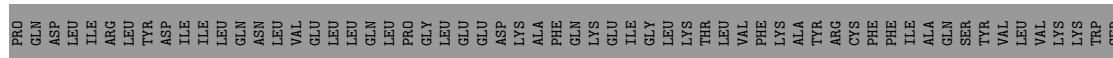
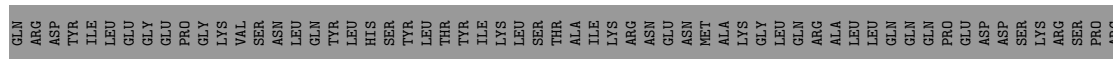
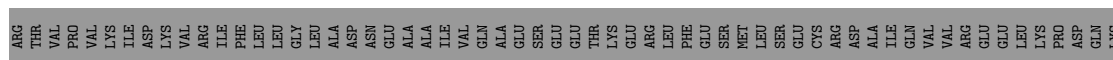
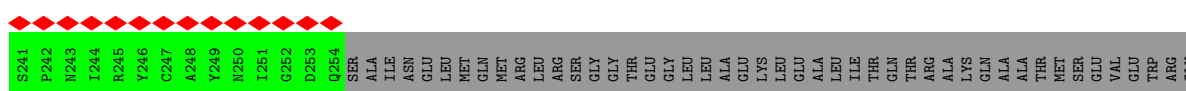
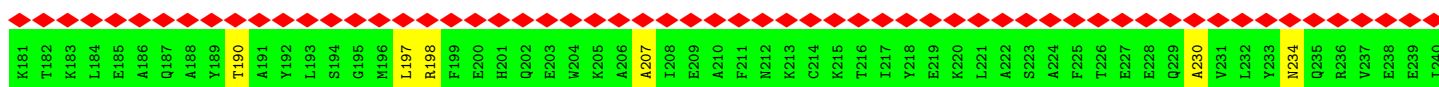
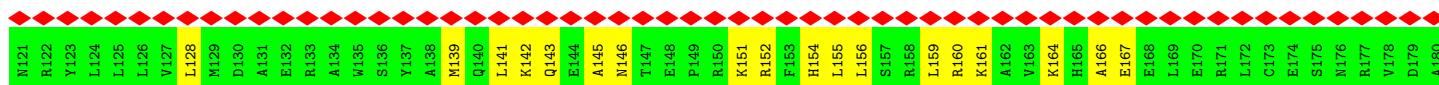
Mol	Chain	Residues	Atoms		AltConf
54	g	1	Total	Zn	0
			1	1	
54	j	1	Total	Zn	0
			1	1	
54	m	1	Total	Zn	0
			1	1	
54	o	1	Total	Zn	0
			1	1	
54	p	1	Total	Zn	0
			1	1	



• Molecule 4: Isoform 2 of Transcription factor BTF3

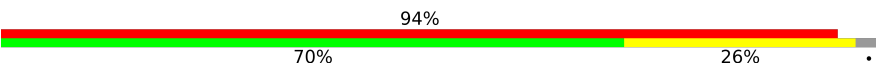


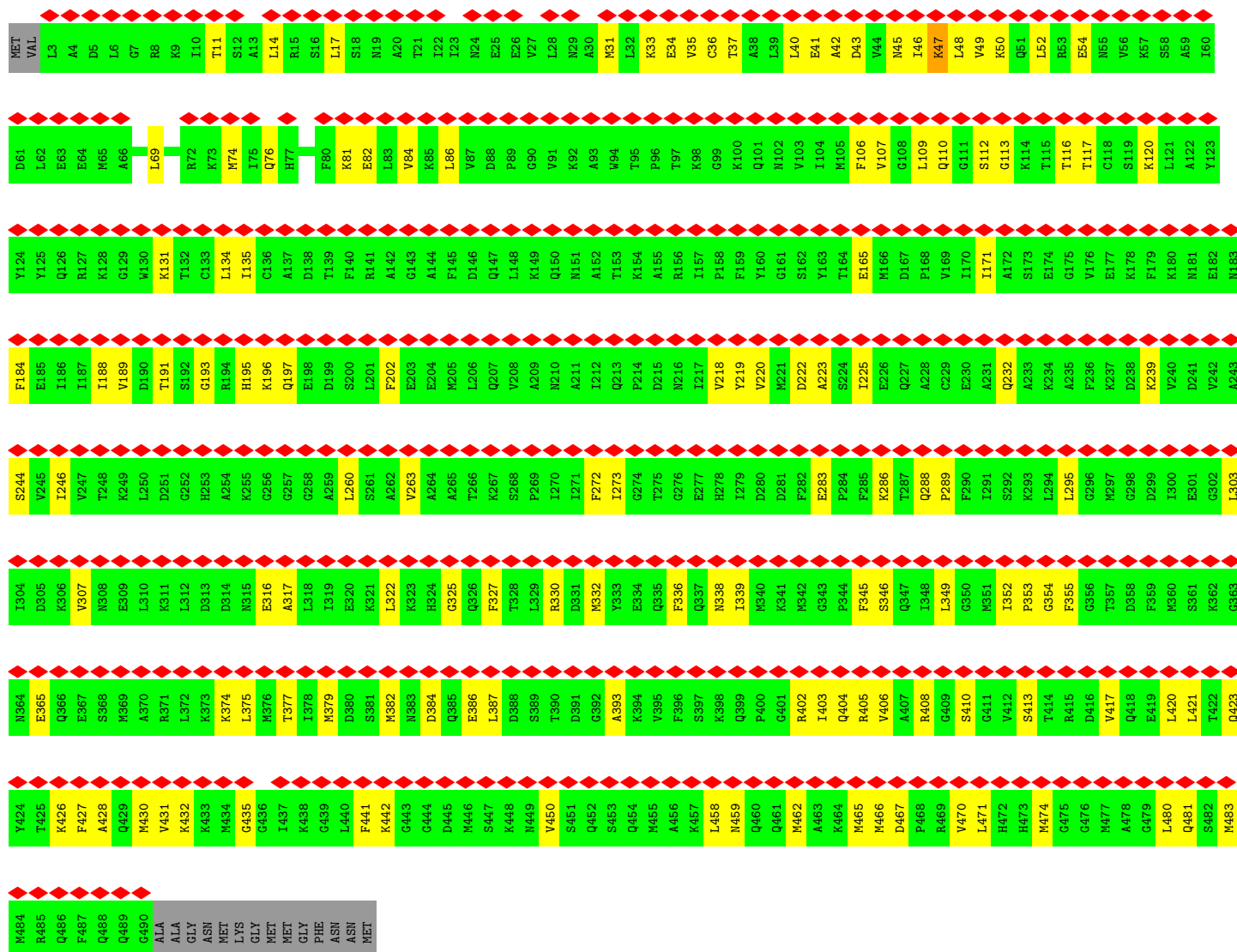
• Molecule 5: Signal recognition particle subunit SRP68



PRO PRO PRO GLU ASP LYS LEU LEU GLN THR LYS SER GLY LEU THR GLY TVR ILE LYS GLY PHE GLY PHE ARG SER

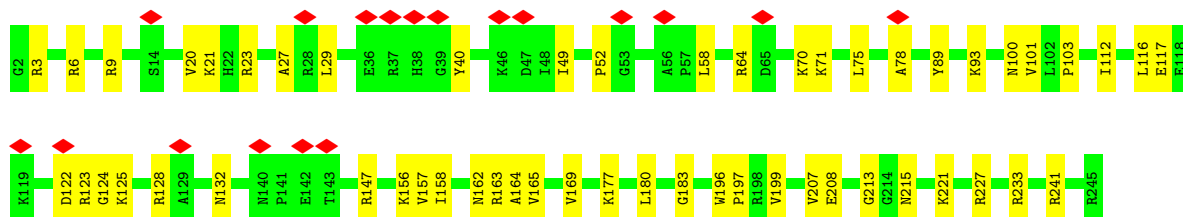
• Molecule 6: Signal recognition particle 54 kDa protein

Chain x: 

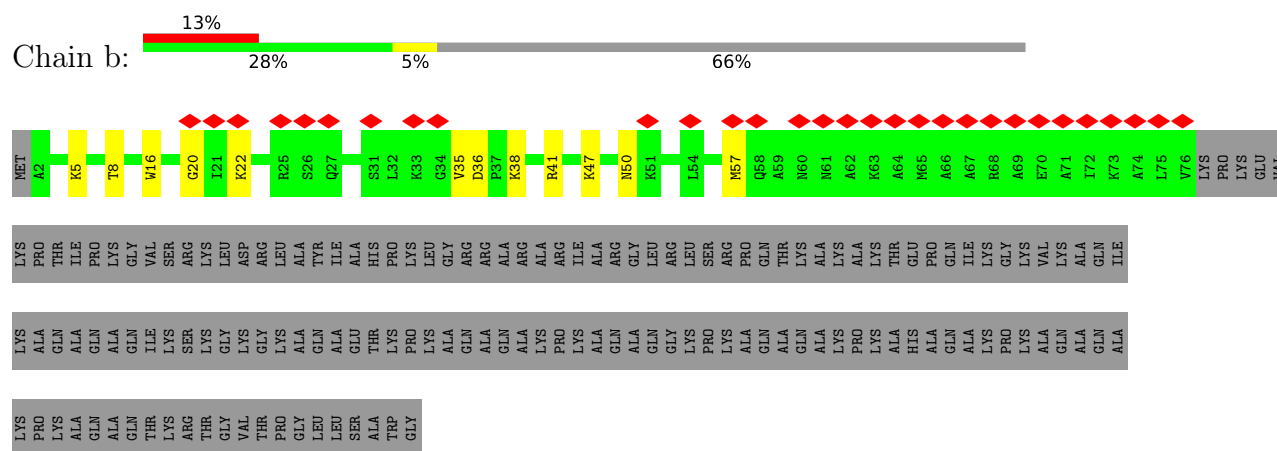


• Molecule 7: L8

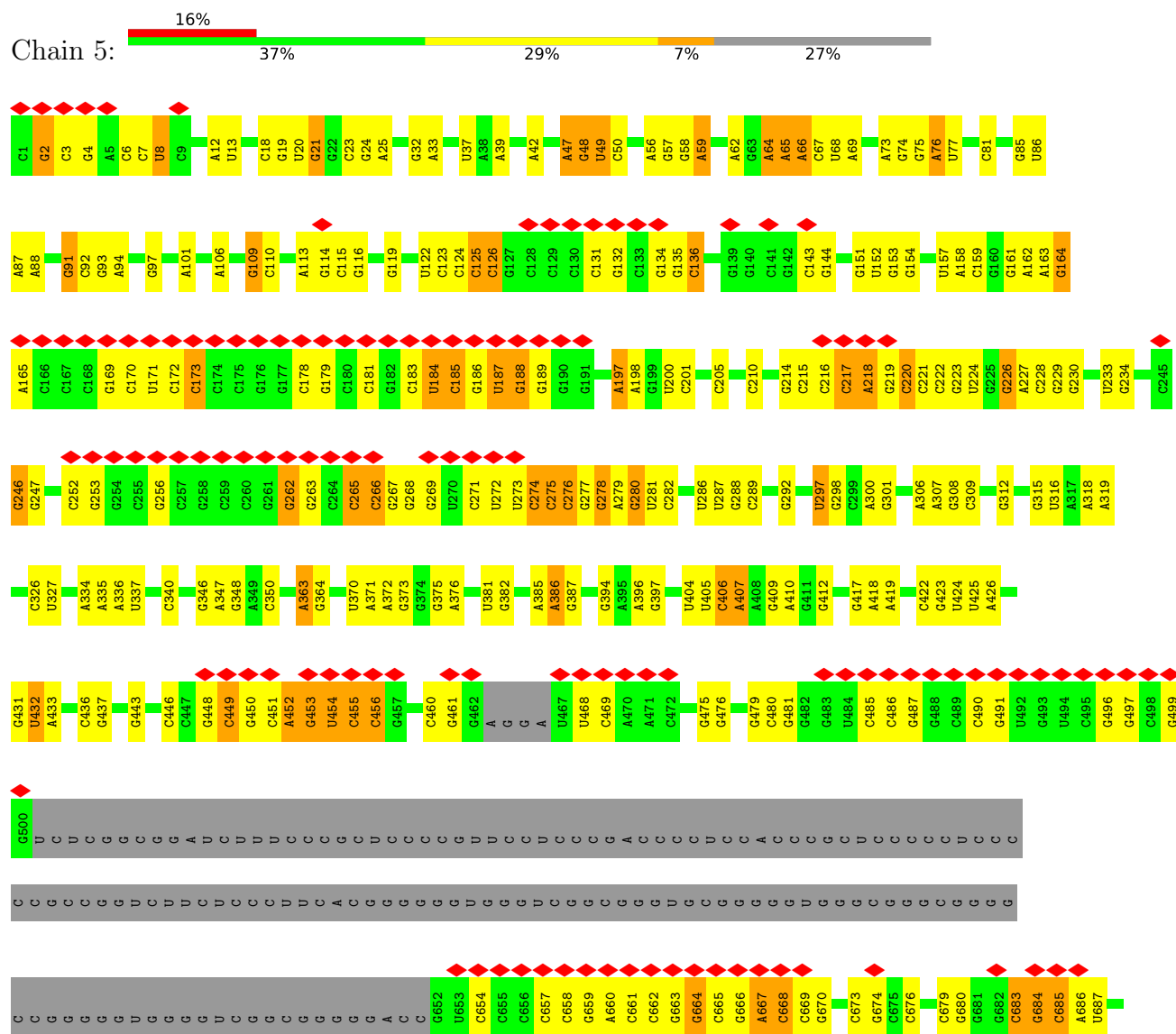
Chain A: 



• Molecule 8: 60S ribosomal protein L29

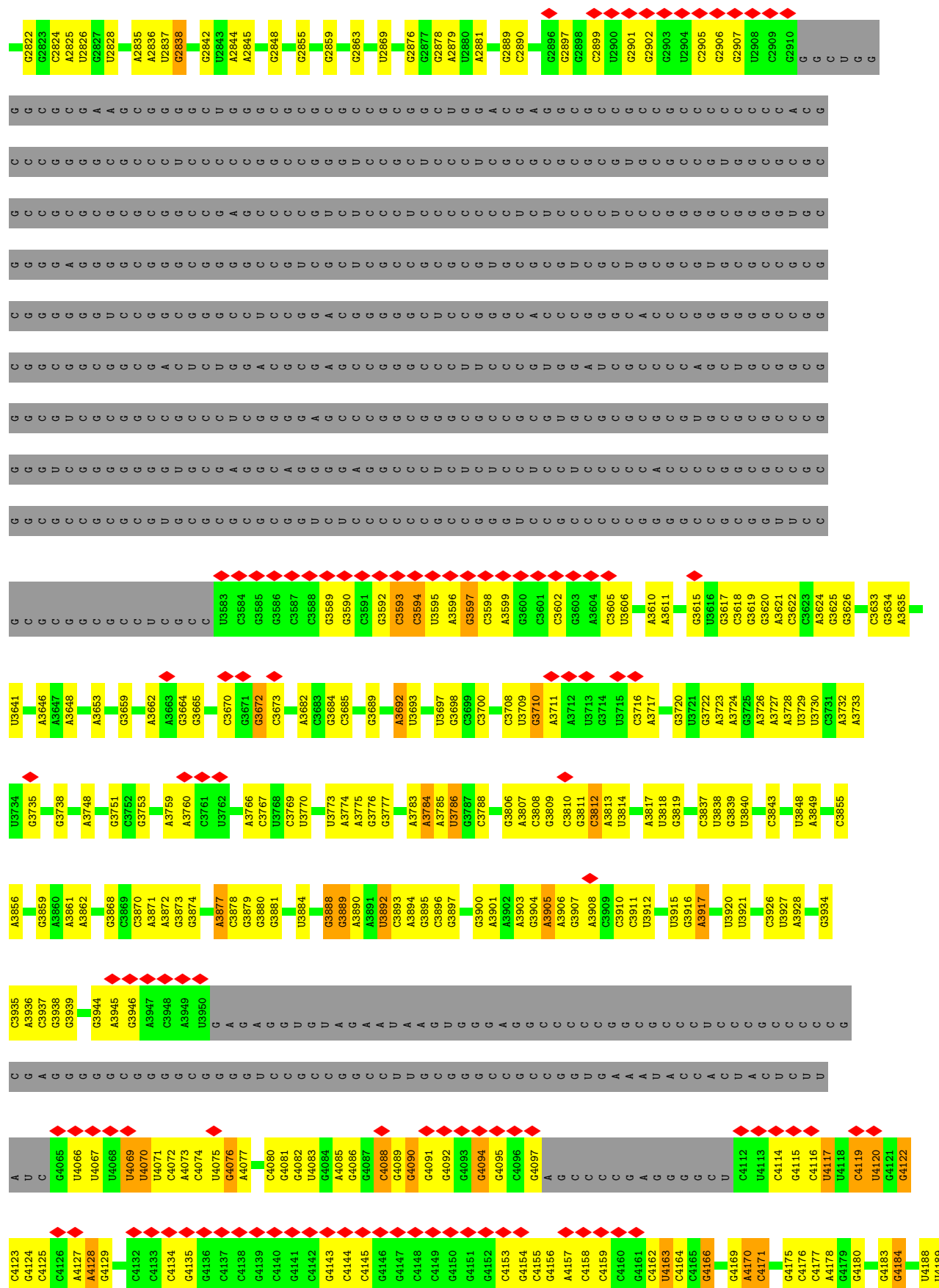


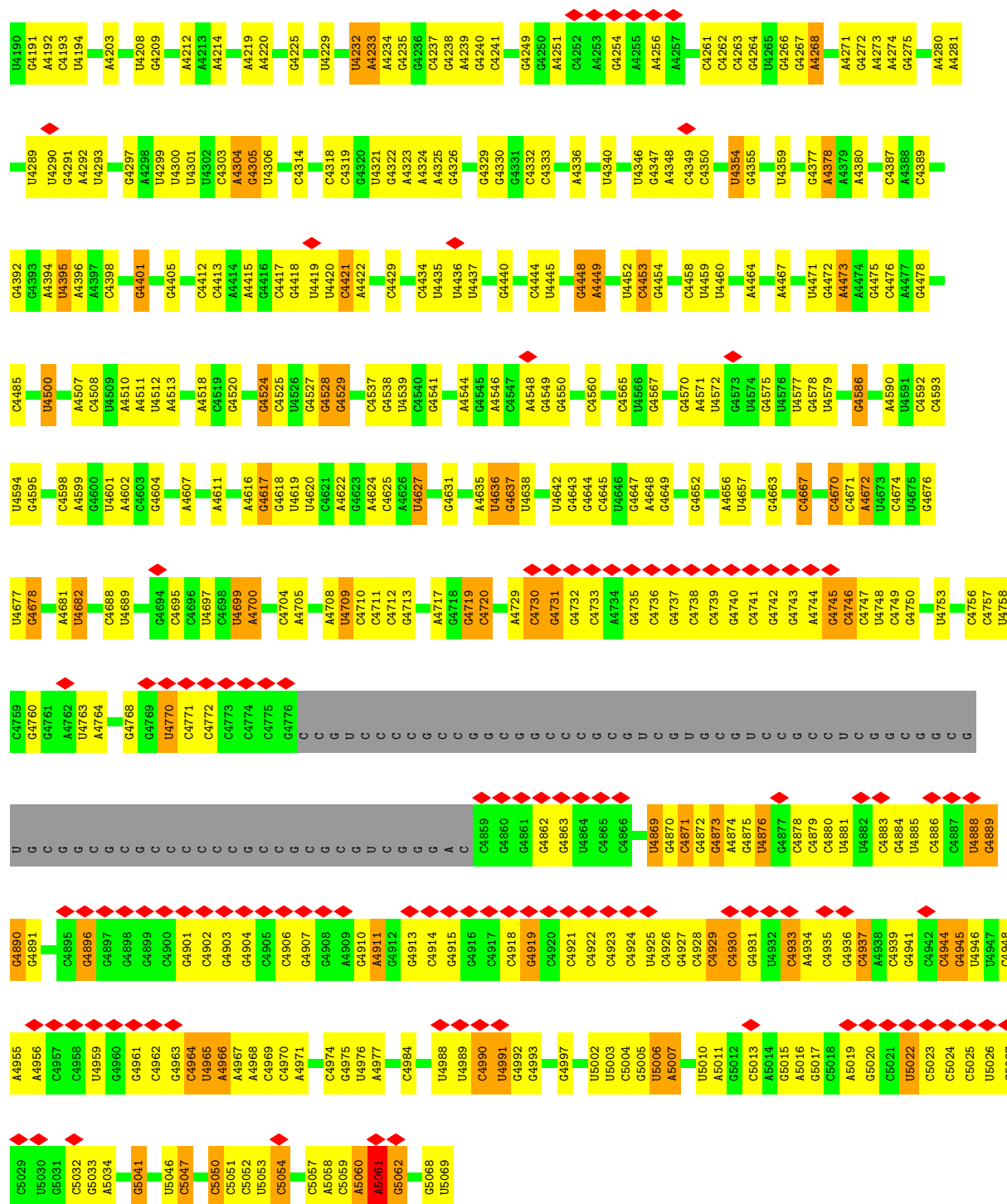
• Molecule 9: 28S rRNA



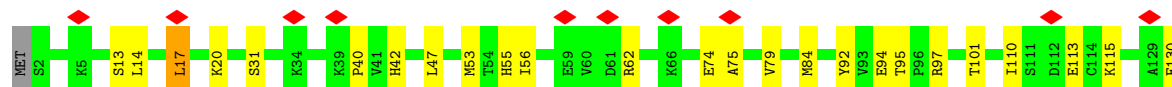
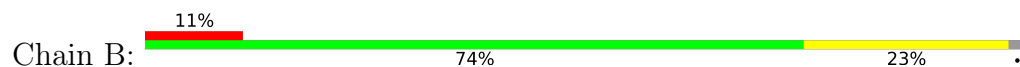


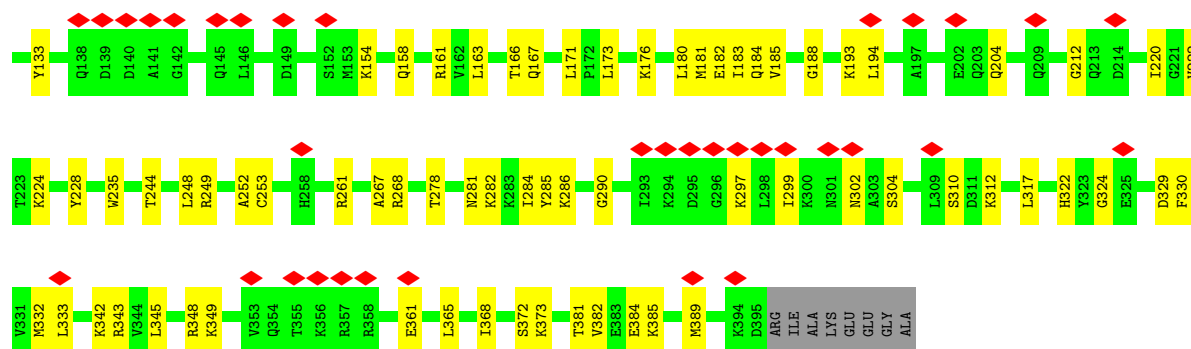




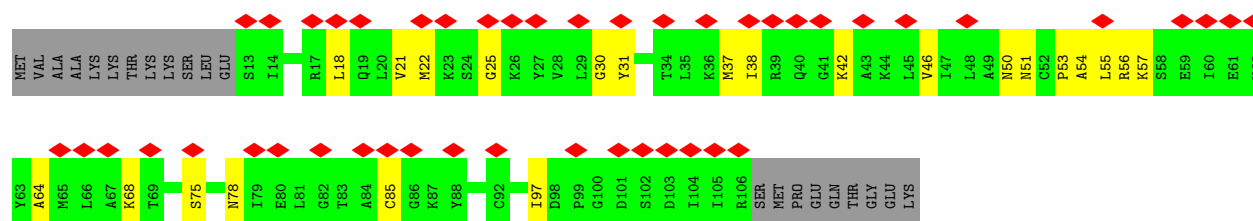


• Molecule 10: uL3

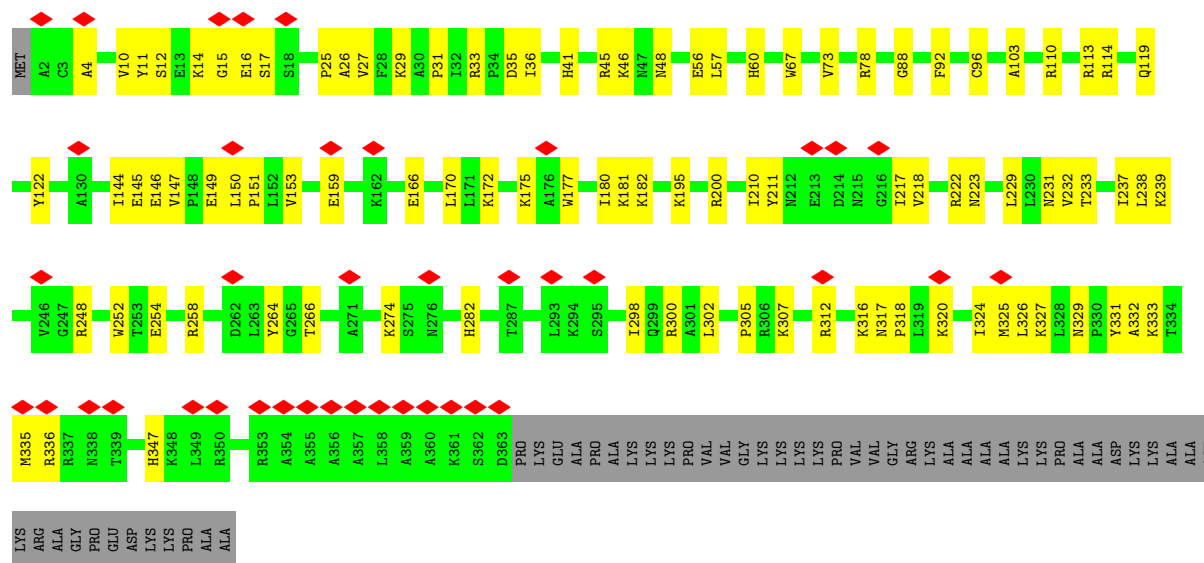




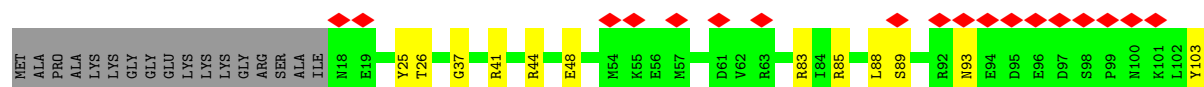
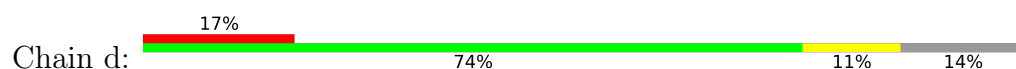
• Molecule 11: 60S ribosomal protein L30

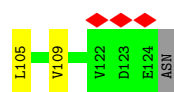


• Molecule 12: 60S ribosomal protein L4

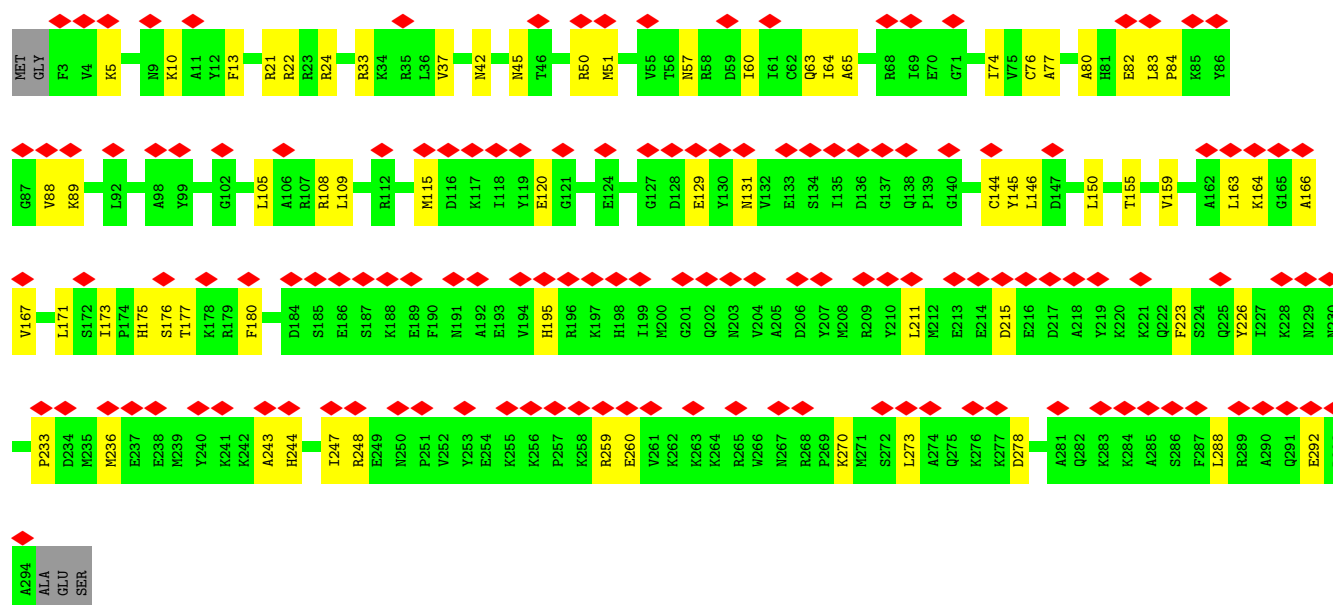
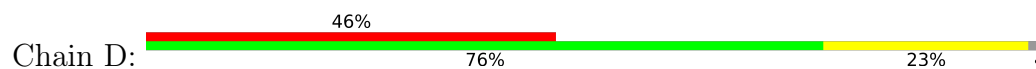


• Molecule 13: Ribosomal protein L31

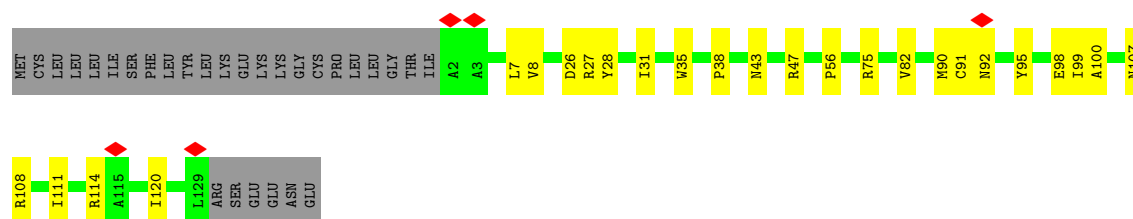




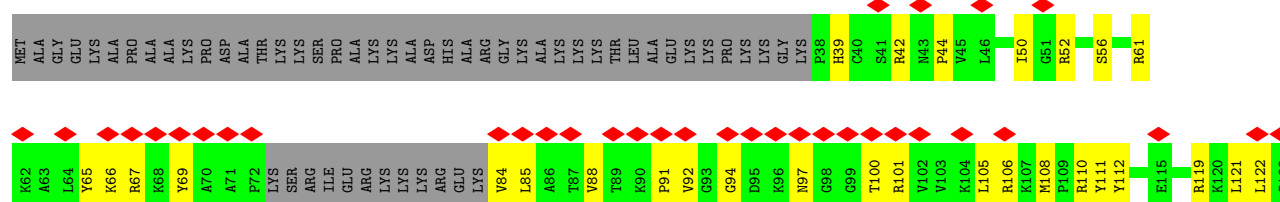
• Molecule 14: Ribosomal_L18_c domain-containing protein

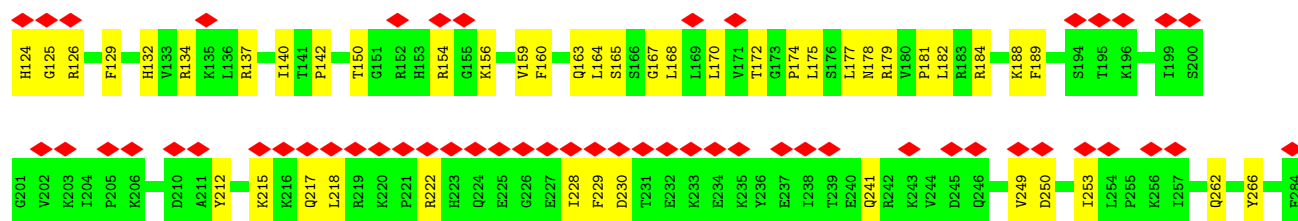


• Molecule 15: Ribosomal protein L32

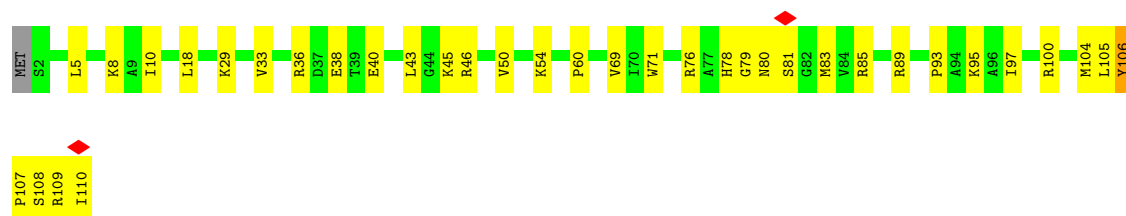


• Molecule 16: 60S ribosomal protein L6

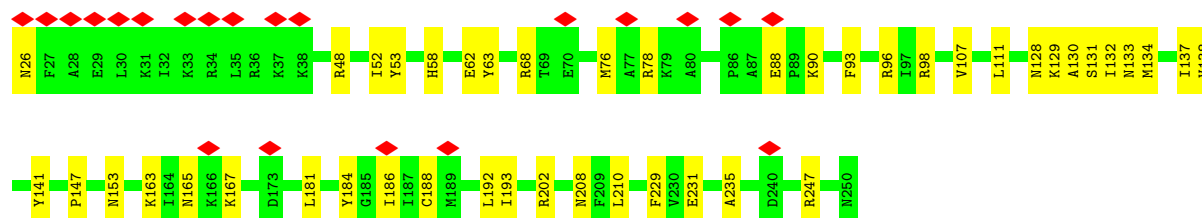
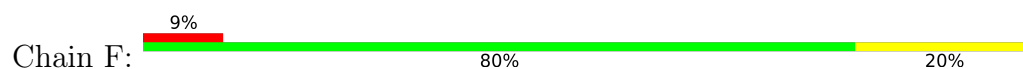




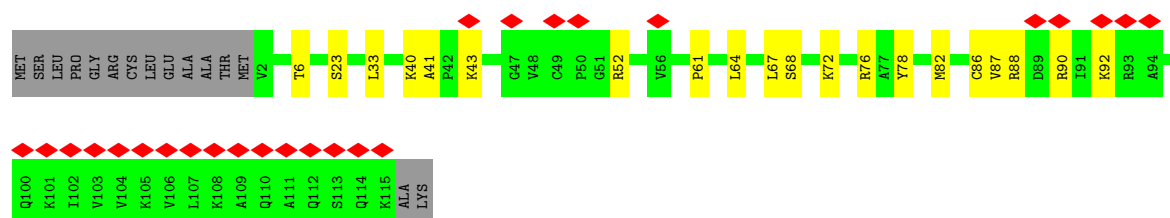
• Molecule 17: 60S ribosomal protein L35a



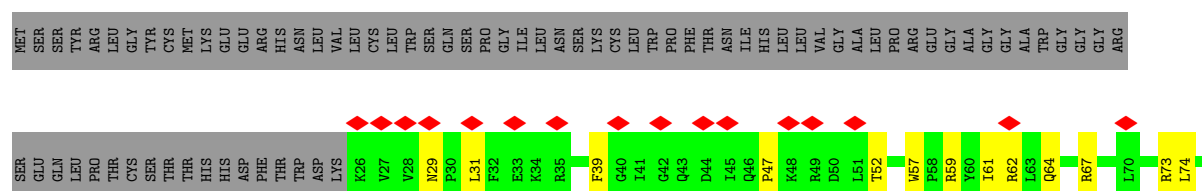
• Molecule 18: uL30

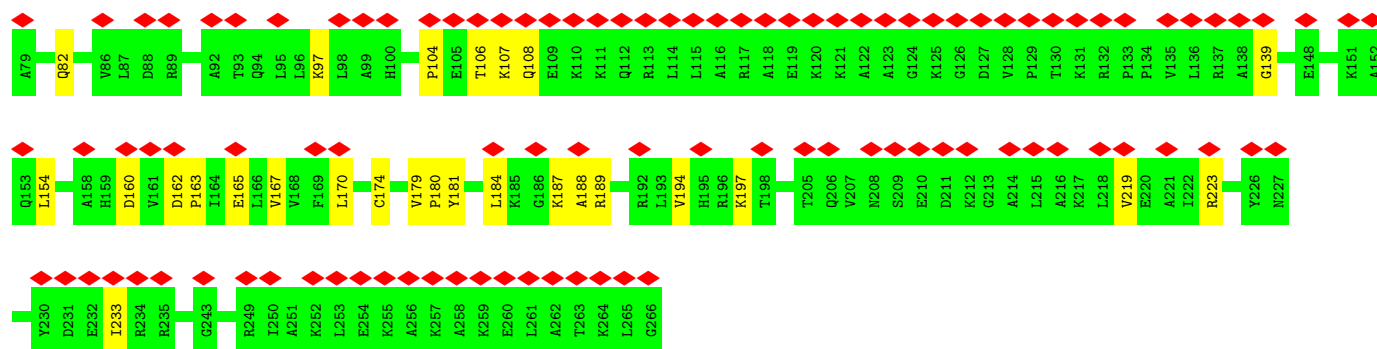


• Molecule 19: 60S ribosomal protein L34

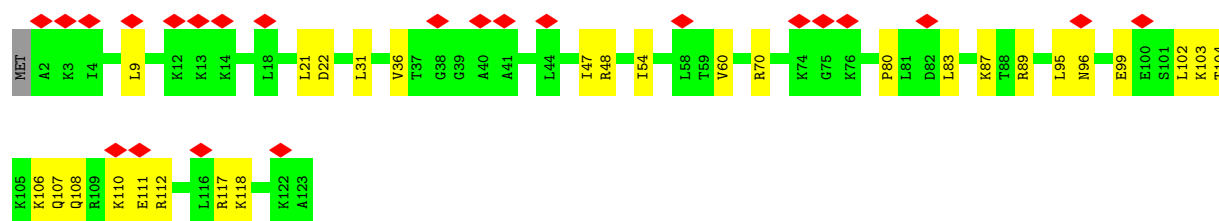
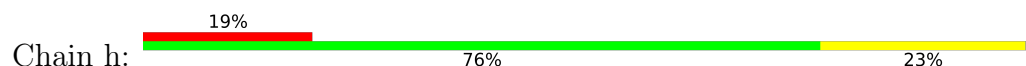


• Molecule 20: 60S ribosomal protein L7a

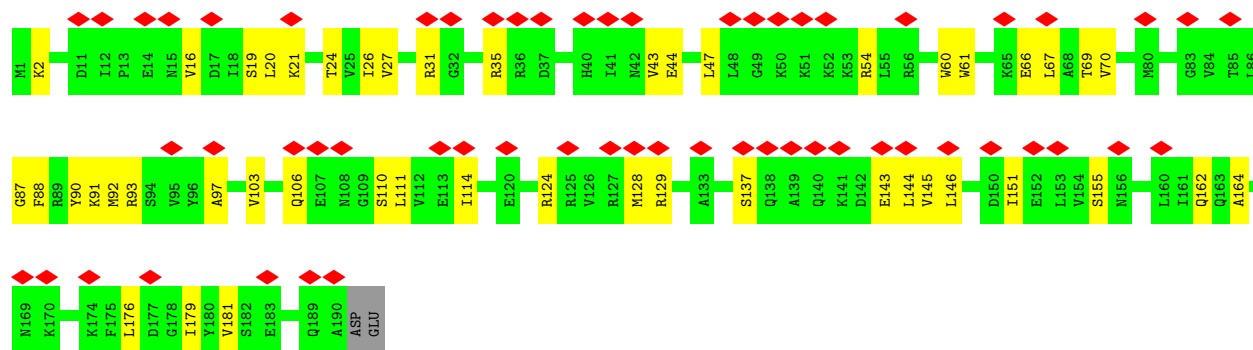
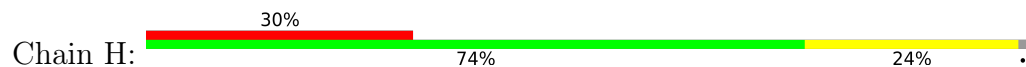




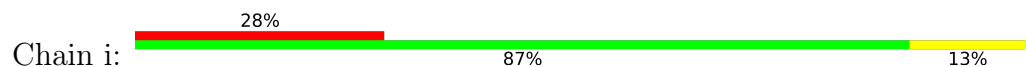
• Molecule 21: 60S ribosomal protein L35



• Molecule 22: 60S ribosomal protein L9

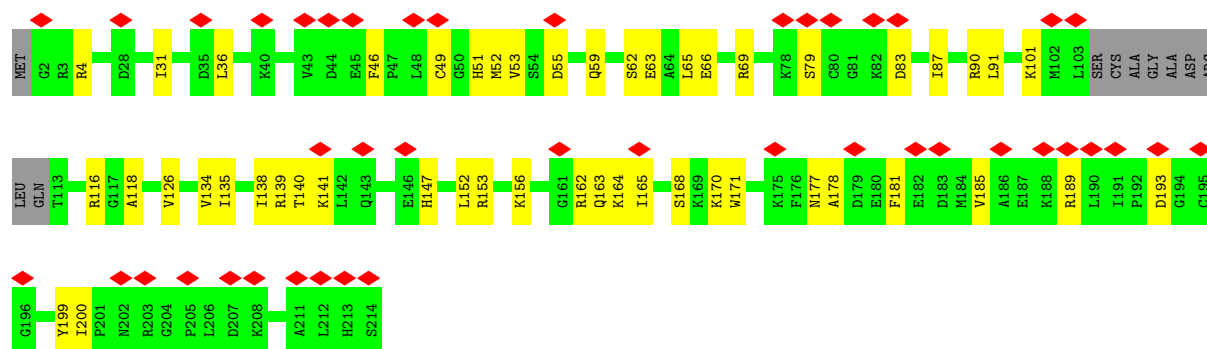


• Molecule 23: 60S ribosomal protein L36



• Molecule 24: 60S ribosomal protein L10

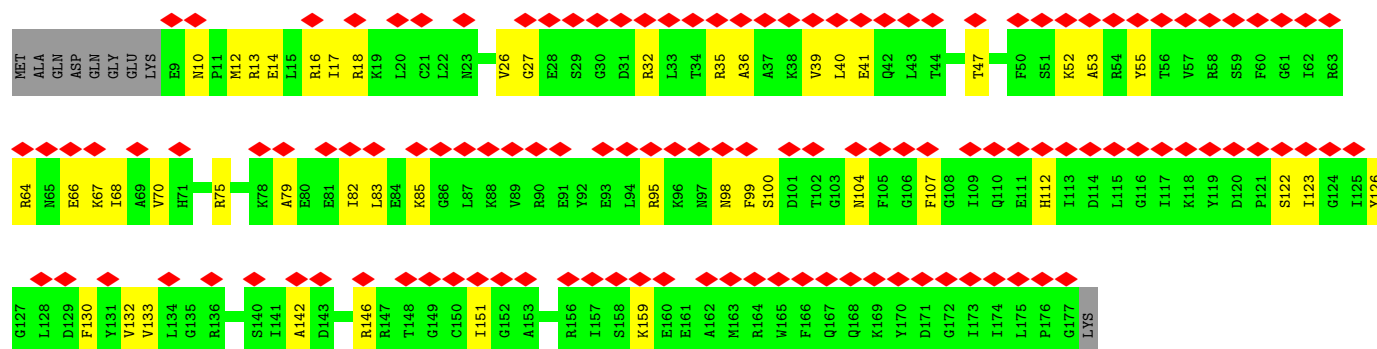




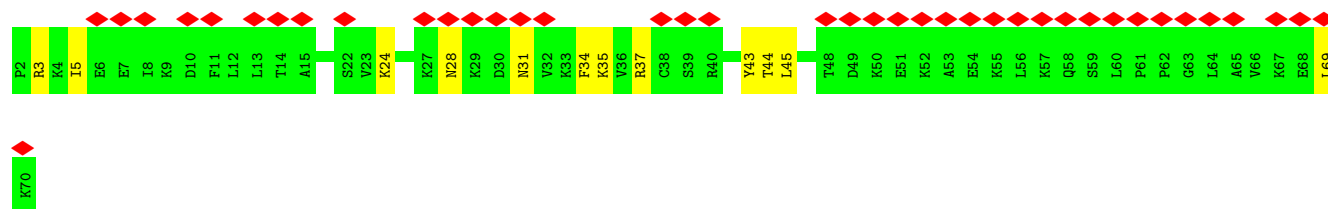
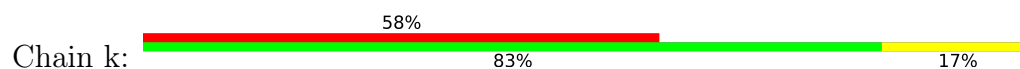
• Molecule 25: Ribosomal protein L37



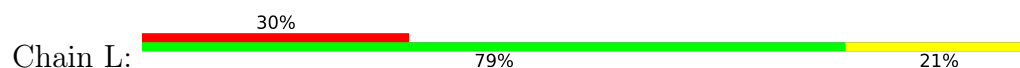
• Molecule 26: Ribosomal protein L11

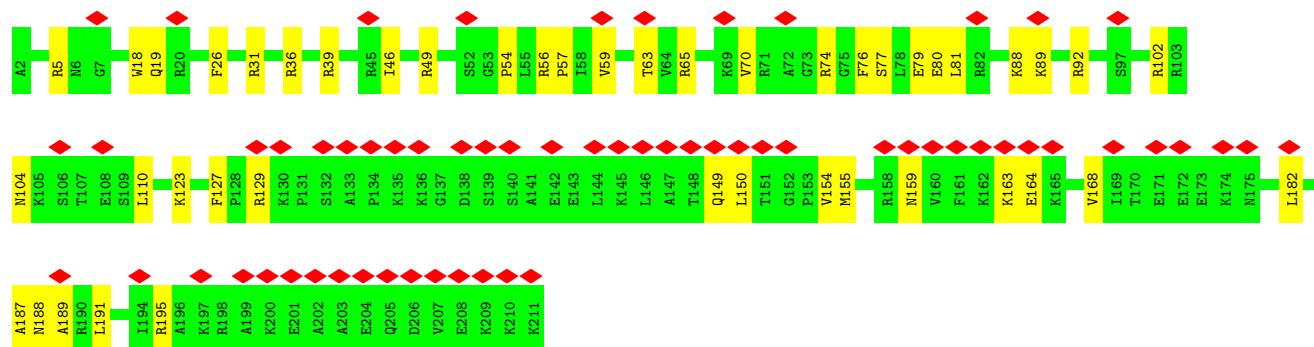


• Molecule 27: 60S ribosomal protein L38



• Molecule 28: 60S ribosomal protein L13

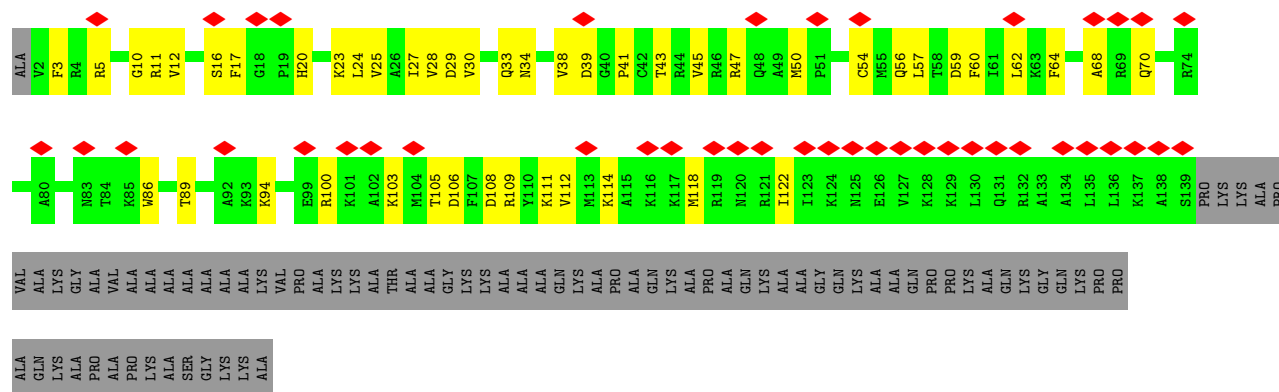




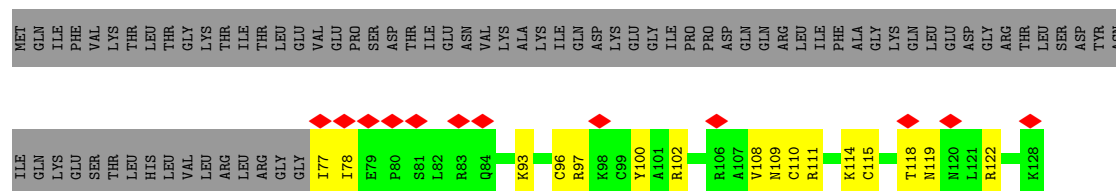
• Molecule 29: Ribosomal protein L39



• Molecule 30: 60S ribosomal protein L14



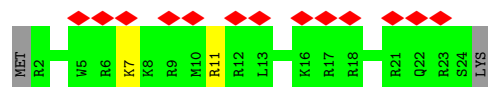
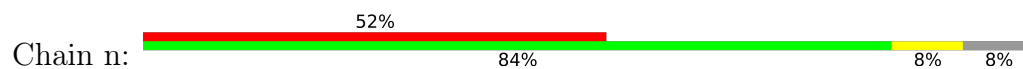
• Molecule 31: Ubiquitin A-52 residue ribosomal protein fusion product 1



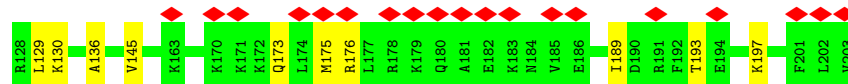
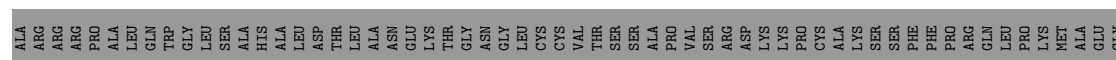
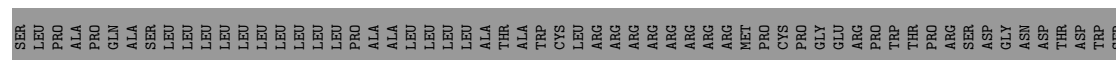
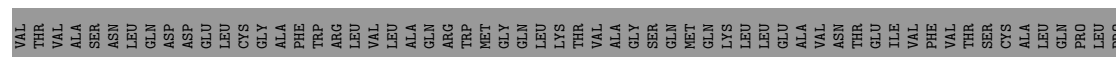
• Molecule 32: Ribosomal protein L15



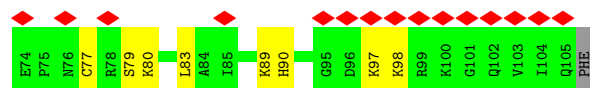
- Molecule 33: 60s ribosomal protein l41



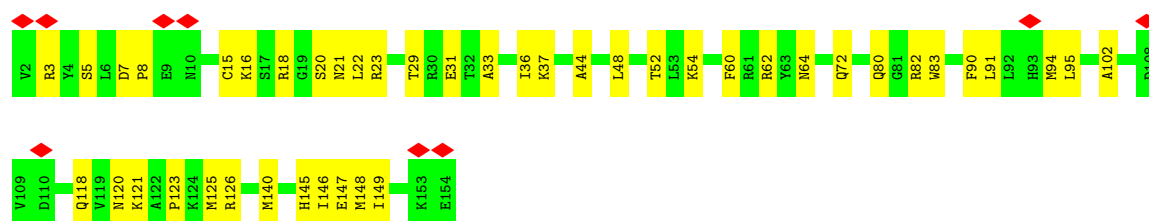
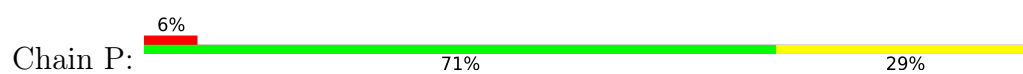
- Molecule 34: 60S ribosomal protein L13a



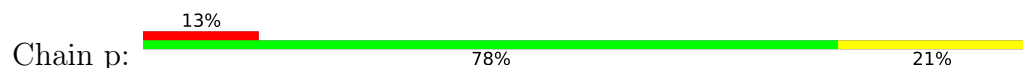
- Molecule 35: eL42



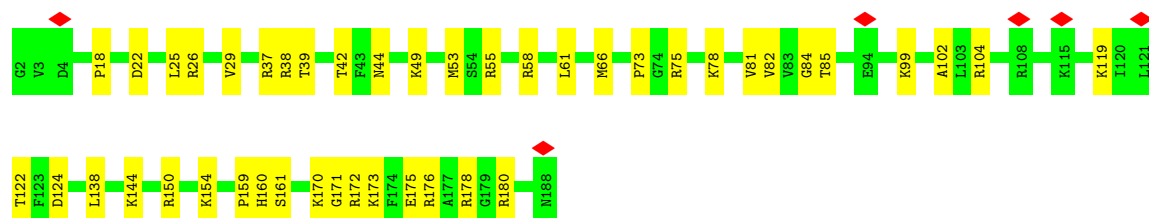
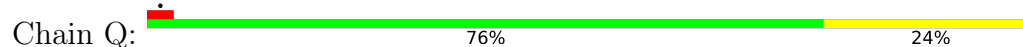
- Molecule 36: 60S ribosomal protein L17



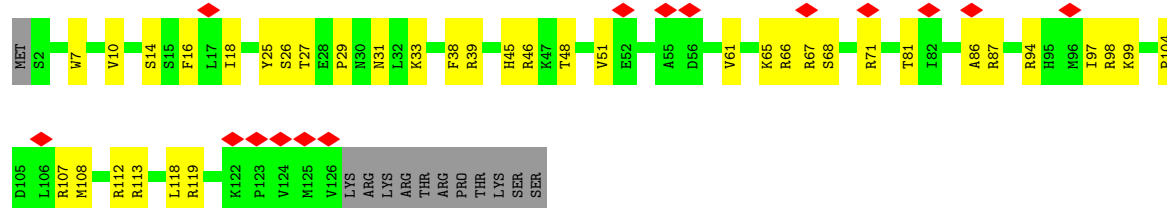
• Molecule 37: eL43



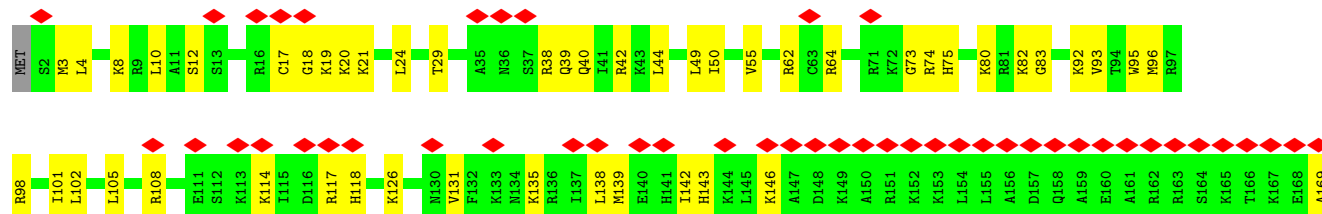
• Molecule 38: eL18

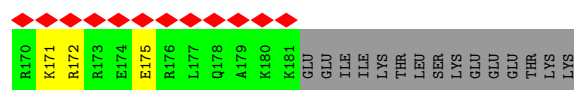


• Molecule 39: 60S ribosomal protein L28

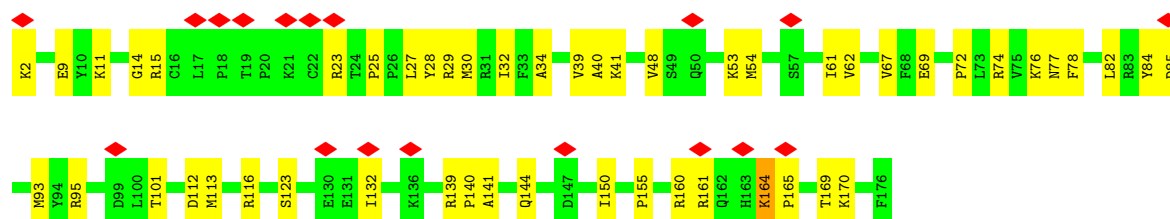


• Molecule 40: 60S ribosomal protein L19

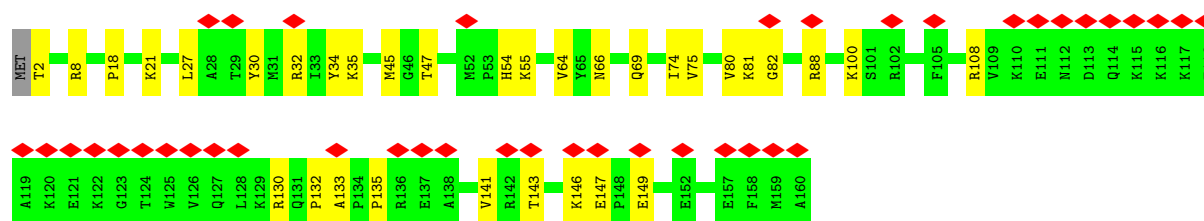
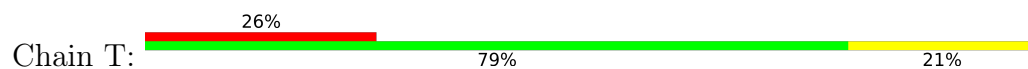




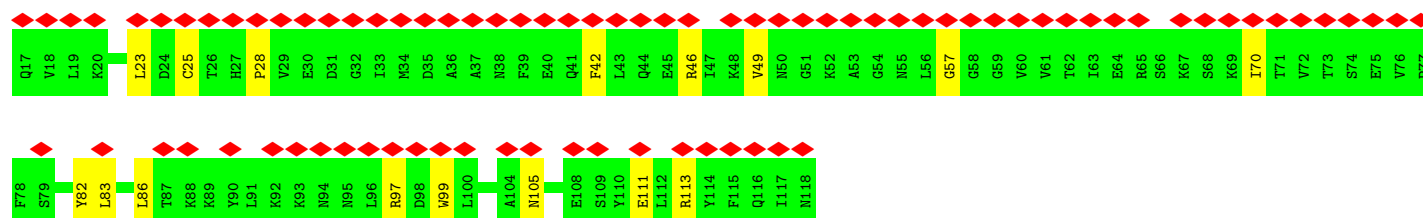
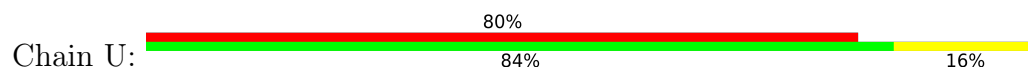
- Molecule 41: 60S ribosomal protein L18a



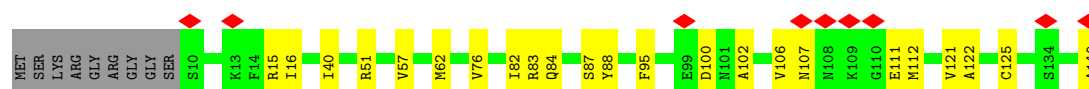
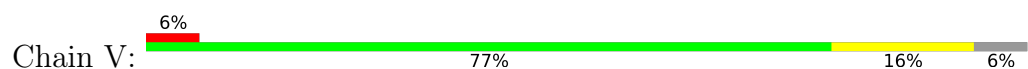
- Molecule 42: 60S ribosomal protein L21



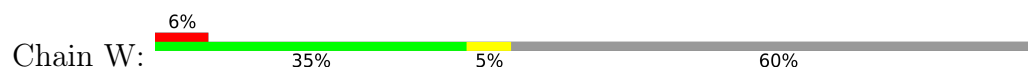
- Molecule 43: Ribosomal protein L22



- Molecule 44: Ribosomal protein L23

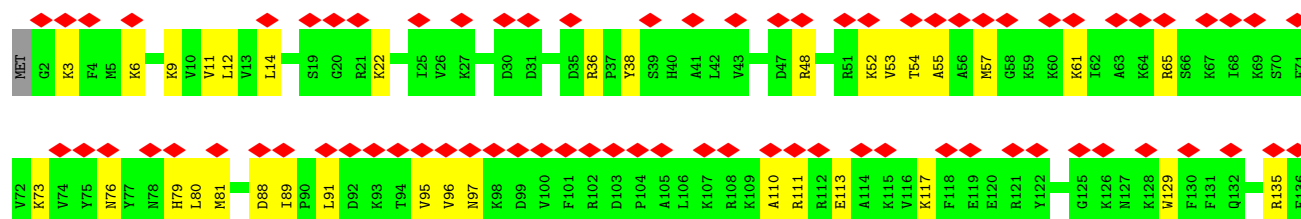


- Molecule 45: Ribosomal protein L24

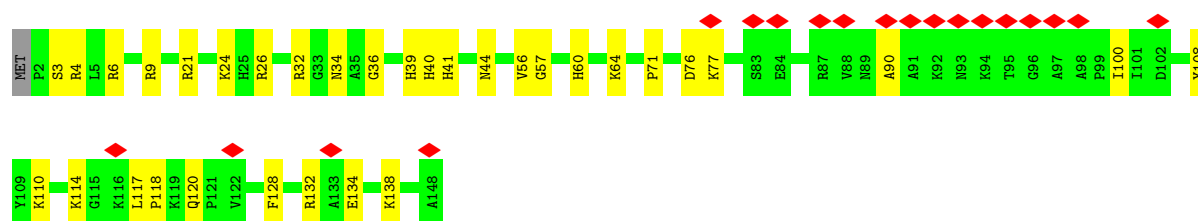
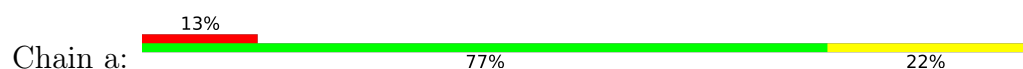




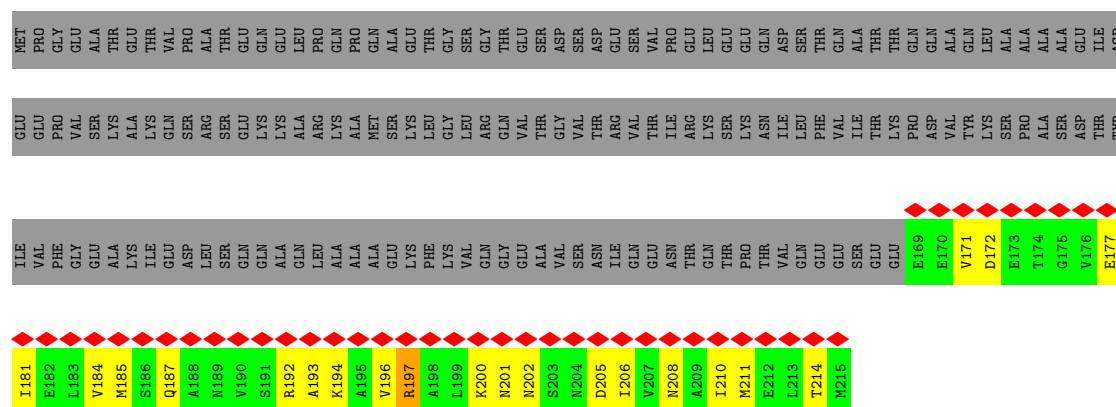
• Molecule 50: 60S ribosomal protein L27



• Molecule 51: 60S ribosomal protein L27a



• Molecule 52: Nascent polypeptide-associated complex subunit alpha



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51843	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.210	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.027	Depositor
Map size (Å)	483.84003, 483.84003, 483.84003	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.10	0/4009	0.23	0/6253
2	q	0.16	0/858	0.38	0/1156
4	u	0.06	0/252	0.19	0/331
5	v	0.11	0/1676	0.29	0/2244
6	x	0.24	0/3830	0.47	0/5131
7	A	0.13	0/1906	0.36	0/2556
8	b	0.13	0/619	0.31	0/818
9	5	0.09	0/83726	0.24	1/130593 (0.0%)
10	B	0.13	0/3216	0.34	0/4311
11	c	0.11	0/742	0.26	0/996
12	C	0.13	0/2937	0.33	0/3946
13	d	0.13	0/903	0.31	0/1216
14	D	0.15	0/2432	0.35	0/3257
15	e	0.11	0/1071	0.29	0/1429
16	E	0.16	0/1936	0.41	0/2600
17	f	0.12	0/895	0.38	0/1198
18	F	0.13	0/1905	0.31	0/2539
19	g	0.14	0/916	0.32	0/1220
20	G	0.14	0/1967	0.36	0/2647
21	h	0.12	0/1021	0.28	0/1348
22	H	0.14	0/1535	0.35	0/2063
23	i	0.12	0/841	0.35	0/1112
24	I	0.15	0/1693	0.35	0/2260
25	j	0.13	0/720	0.32	0/952
26	J	0.10	0/1376	0.31	0/1841
27	k	0.12	0/575	0.30	0/761
28	L	0.14	0/1734	0.35	0/2317
29	l	0.10	0/454	0.28	0/599
30	M	0.15	0/1158	0.34	0/1547
31	m	0.10	0/435	0.34	0/575
32	N	0.16	0/1746	0.36	0/2338
33	n	0.07	0/223	0.15	0/284

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	O	0.13	0/1671	0.31	0/2234
35	o	0.12	0/864	0.38	0/1140
36	P	0.12	0/1268	0.31	0/1700
37	p	0.10	0/718	0.28	0/953
38	Q	0.12	0/1530	0.33	0/2041
39	r	0.27	1/1017 (0.1%)	0.52	1/1364 (0.1%)
40	R	0.12	0/1524	0.35	0/2013
41	S	0.15	0/1493	0.36	1/2002 (0.0%)
42	T	0.15	0/1326	0.32	0/1770
43	U	0.10	0/847	0.29	0/1137
44	V	0.22	0/993	0.43	2/1332 (0.2%)
45	W	0.10	0/541	0.29	0/720
46	X	0.10	0/993	0.29	0/1334
47	7	0.08	0/2858	0.20	0/4455
48	Y	0.11	0/1132	0.28	0/1504
49	8	0.09	0/3701	0.21	0/5766
50	Z	0.13	0/1130	0.36	0/1507
51	a	0.08	0/1191	0.26	0/1590
52	t	0.93	0/358	1.14	0/480
All	All	0.12	1/154462 (0.0%)	0.29	5/227480 (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
10	B	0	1
17	f	0	1
41	S	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	r	29	PRO	CG-CD	-5.67	1.31	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	r	29	PRO	N-CD-CG	-9.06	89.61	103.20
41	S	140	PRO	CA-N-CD	-7.01	102.18	112.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	V	84	GLN	CA-C-N	5.39	127.45	120.44
44	V	84	GLN	C-N-CA	5.39	127.45	120.44
9	5	5061	A	P-O3'-C3'	5.14	127.92	120.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	B	17	LEU	Peptide
41	S	164	LYS	Peptide
17	f	106	TYR	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	3583	0	1809	60	0
2	q	844	0	861	21	0
3	s	283	0	64	2	0
4	u	252	0	283	4	0
5	v	1648	0	1659	22	0
6	x	3778	0	3858	90	0
7	A	1868	0	1959	44	0
8	b	609	0	650	10	0
9	5	74854	0	37827	1175	0
10	B	3148	0	3267	71	0
11	c	732	0	766	16	0
12	C	2883	0	3053	73	0
13	d	888	0	930	8	0
14	D	2386	0	2419	55	0
15	e	1053	0	1147	19	0
16	E	1898	0	2035	64	0
17	f	876	0	912	32	0
18	F	1870	0	1994	36	0
19	g	906	0	999	17	0
20	G	1934	0	2085	31	0
21	h	1013	0	1147	24	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	H	1516	0	1597	35	0
23	i	830	0	916	11	0
24	I	1655	0	1704	36	0
25	j	705	0	737	14	0
26	J	1353	0	1386	32	0
27	k	569	0	637	9	0
28	L	1703	0	1820	45	0
29	l	444	0	483	9	0
30	M	1137	0	1211	36	0
31	m	429	0	465	12	0
32	N	1701	0	1749	50	0
33	n	222	0	264	1	0
34	O	1638	0	1777	35	0
35	o	851	0	920	10	0
36	P	1242	0	1274	36	0
37	p	708	0	757	16	0
38	Q	1506	0	1623	37	0
39	r	1001	0	1060	26	0
40	R	1508	0	1664	44	0
41	S	1454	0	1496	43	0
42	T	1298	0	1366	28	0
43	U	833	0	856	10	0
44	V	979	0	1039	16	0
45	W	528	0	541	6	0
46	X	976	0	1053	20	0
47	7	2558	0	1296	34	0
48	Y	1115	0	1205	24	0
49	8	3314	0	1683	51	0
50	Z	1107	0	1182	29	0
51	a	1162	0	1209	26	0
52	t	359	0	363	34	0
53	5	96	0	0	0	0
53	B	1	0	0	0	0
54	g	1	0	0	0	0
54	j	1	0	0	0	0
54	m	1	0	0	0	0
54	o	1	0	0	0	0
54	p	1	0	0	0	0
All	All	143809	0	105057	2247	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 (2247) 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)
52:t:181:ILE:HG21	52:t:196:VAL:HG22	1.38	1.04
48:Y:74:TYR:HE2	48:Y:77:LYS:HE3	1.25	1.00
6:x:46:ILE:HG12	52:t:211:MET:HE2	1.44	1.00
9:5:2557:G:H1	9:5:2570:U:H3	1.11	0.97
9:5:2845:A:H61	9:5:3843:C:H42	0.98	0.97
9:5:2845:A:H61	9:5:3843:C:N4	1.68	0.91
6:x:50:LYS:HB2	52:t:211:MET:HE1	1.50	0.91
14:D:33:ARG:NH1	47:7:7:G:OP1	2.04	0.91
9:5:1726:U:H3	9:5:1836:G:H1	0.88	0.88
52:t:181:ILE:HD12	52:t:196:VAL:HA	1.56	0.87
7:A:233:ARG:HB2	9:5:4184:G:H5'	1.55	0.86
9:5:2845:A:N6	9:5:3843:C:H42	1.73	0.86
48:Y:74:TYR:CE2	48:Y:77:LYS:HE3	2.10	0.86
1:1:104:C:H3'	1:1:105:G:H5''	1.57	0.86
22:H:2:LYS:HE2	22:H:61:TRP:HB3	1.57	0.85
9:5:184:U:H3	9:5:253:G:H1	0.91	0.84
9:5:704:C:H2'	9:5:705:G:H8	1.39	0.84
8:b:57:MET:HE1	9:5:1811:G:H21	1.40	0.84
50:Z:57:MET:HG3	50:Z:61:LYS:HB3	1.60	0.83
9:5:1740:C:O2	9:5:1786:A:N6	2.12	0.82
32:N:155:VAL:O	32:N:162:ARG:NH2	2.13	0.82
1:1:104:C:C3'	1:1:105:G:H5''	2.09	0.81
14:D:33:ARG:HH12	47:7:7:G:H4'	1.43	0.81
9:5:4928:C:H5''	30:M:114:LYS:HD2	1.62	0.81
9:5:1444:G:N2	9:5:2100:A:H62	1.79	0.81
14:D:42:ASN:ND2	42:T:69:GLN:OE1	2.11	0.80
6:x:420:LEU:HA	6:x:423:GLN:HE21	1.44	0.80
5:v:141:LEU:O	5:v:145:ALA:HB2	1.81	0.80
9:5:1371:A:N6	49:8:28:C:O2'	2.15	0.79
9:5:2416:G:N2	9:5:2427:G:O6	2.14	0.79
9:5:2483:G:H22	9:5:2495:U:H3	1.28	0.79
9:5:4945:G:H21	17:f:71:TRP:HE1	1.28	0.79
32:N:116:LEU:O	32:N:117:ASN:ND2	2.17	0.78
24:I:87:ILE:HG12	24:I:138:ILE:HG12	1.67	0.77
9:5:1185:G:N2	14:D:278:ASP:OD2	2.17	0.77
22:H:91:LYS:HG2	22:H:145:VAL:HG22	1.67	0.77
9:5:81:C:H1'	9:5:1359:G:H21	1.50	0.76
10:B:53:MET:HE2	10:B:75:ALA:HB1	1.67	0.76
9:5:2663:G:N2	9:5:2676:A:O2'	2.17	0.76
12:C:14:LYS:NZ	12:C:16:GLU:OE1	2.19	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:74:ILE:HD11	47:7:115:A:H1'	1.68	0.76
5:v:142:LYS:HG2	5:v:155:LEU:HD11	1.68	0.75
9:5:1233:G:H2'	9:5:1234:G:H8	1.49	0.75
9:5:215:C:H2'	9:5:220:C:H5'	1.68	0.75
9:5:2777:G:H5''	9:5:2778:G:H5'	1.68	0.75
9:5:4974:C:H42	9:5:4984:C:H42	1.32	0.75
9:5:722:G:OP1	9:5:935:A:N6	2.20	0.75
52:t:171:VAL:HB	52:t:196:VAL:HG21	1.68	0.75
9:5:1353:G:N7	38:Q:104:ARG:NH1	2.35	0.75
9:5:1444:G:H21	9:5:2100:A:N6	1.84	0.74
9:5:223:G:N3	12:C:223:ASN:ND2	2.34	0.74
9:5:4272:G:OP2	9:5:4272:G:N2	2.17	0.74
9:5:1358:G:HO2'	9:5:1359:G:H8	1.36	0.74
9:5:2520:C:O2	9:5:2640:G:N2	2.20	0.74
36:P:94:MET:HG2	36:P:148:MET:HE2	1.69	0.74
9:5:4122:G:H4'	19:g:90:ARG:HD2	1.70	0.74
9:5:4747:C:H5''	17:f:54:LYS:HE3	1.70	0.74
28:L:80:GLU:HG3	28:L:110:LEU:HD12	1.70	0.74
9:5:308:G:OP2	9:5:308:G:N2	2.20	0.74
9:5:4944:C:O2	9:5:4945:G:N2	2.21	0.73
6:x:14:LEU:HD11	6:x:76:GLN:HG2	1.71	0.73
23:i:50:PHE:O	23:i:55:ARG:NH1	2.22	0.73
36:P:126:ARG:HG3	36:P:140:MET:HE1	1.70	0.73
9:5:4467:A:O2'	9:5:4510:A:N3	2.22	0.73
21:h:87:LYS:HA	25:j:73:ARG:HH22	1.52	0.73
9:5:1921:C:H5'	41:S:161:ARG:HE	1.53	0.72
9:5:2580:U:O2	50:Z:76:ASN:ND2	2.20	0.72
6:x:202:PHE:HB3	6:x:239:LYS:HE3	1.71	0.72
9:5:2255:C:O2	9:5:2258:C:N4	2.22	0.72
9:5:4421:C:H42	9:5:4475:G:N2	1.88	0.72
6:x:45:ASN:HB2	6:x:48:LEU:HG	1.70	0.72
10:B:188:GLY:O	10:B:193:LYS:NZ	2.22	0.72
25:j:59:THR:HG22	25:j:64:MET:HE1	1.71	0.72
6:x:286:LYS:HB3	6:x:289:PRO:HD2	1.72	0.72
7:A:117:GLU:HG3	7:A:162:ASN:HB2	1.72	0.72
9:5:704:C:H2'	9:5:705:G:C8	2.23	0.72
9:5:734:G:N2	9:5:930:G:O2'	2.22	0.72
44:V:106:VAL:HA	44:V:112:MET:HA	1.72	0.71
41:S:161:ARG:HD2	41:S:164:LYS:HG2	1.71	0.71
28:L:77:SER:OG	28:L:80:GLU:OE1	2.08	0.71
9:5:1912:G:H21	34:O:87:MET:HE2	1.56	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:4256:A:HO2'	26:J:55:TYR:HH	1.39	0.71
14:D:233:PRO:HA	14:D:236:MET:HE1	1.72	0.71
6:x:402:ARG:HG2	6:x:405:ARG:HH12	1.55	0.71
9:5:19:G:OP2	21:h:89:ARG:NH2	2.24	0.71
9:5:1426:G:H22	9:5:1458:C:H5''	1.56	0.70
14:D:144:CYS:H	14:D:173:ILE:HG22	1.55	0.70
9:5:2663:G:OP1	40:R:118:HIS:ND1	2.23	0.70
9:5:907:C:H2'	9:5:908:G:H8	1.56	0.70
9:5:1380:G:H21	9:5:1381:U:H3	1.39	0.70
9:5:3717:A:OP2	9:5:3735:G:N2	2.24	0.70
10:B:14:LEU:HD23	10:B:17:LEU:HD21	1.74	0.70
9:5:2:G:OP2	46:X:38:LYS:N	2.24	0.70
9:5:114:G:H1	9:5:158:A:H61	1.39	0.70
9:5:1444:G:N2	9:5:2101:C:N3	2.39	0.70
9:5:1282:G:OP1	12:C:316:LYS:NZ	2.21	0.70
39:r:16:PHE:HB3	39:r:27:THR:H	1.57	0.69
9:5:1332:C:H2'	9:5:1333:A:H8	1.55	0.69
16:E:217:GLN:HG3	16:E:218:LEU:H	1.56	0.69
47:7:63:C:H5'	47:7:64:G:H5''	1.73	0.69
9:5:4088:C:H2'	9:5:4089:G:H8	1.57	0.69
16:E:44:PRO:HG2	16:E:52:ARG:HG3	1.73	0.69
18:F:184:TYR:HB3	18:F:202:ARG:HG2	1.75	0.69
9:5:730:G:H22	9:5:939:G:H1	1.41	0.69
12:C:4:ALA:O	12:C:29:LYS:NZ	2.25	0.69
9:5:2757:A:H2'	9:5:2758:G:C4	2.28	0.69
9:5:4541:G:N2	9:5:4544:A:OP2	2.26	0.69
10:B:94:GLU:OE1	10:B:158:GLN:NE2	2.24	0.69
17:f:36:ARG:HB2	17:f:80:ASN:HA	1.75	0.69
9:5:1914:C:H4'	34:O:89:PRO:HD3	1.73	0.69
52:t:181:ILE:HG13	52:t:196:VAL:HG13	1.73	0.69
38:Q:172:ARG:HD2	51:a:57:GLY:HA3	1.75	0.68
9:5:2758:G:H21	9:5:2765:A:H2	1.41	0.68
40:R:102:LEU:HD22	40:R:138:LEU:HD13	1.76	0.68
5:v:86:TYR:OH	5:v:90:ARG:NH1	2.26	0.68
9:5:64:A:H1'	9:5:76:A:H1'	1.76	0.68
14:D:223:PHE:HB3	14:D:226:TYR:HB2	1.75	0.68
17:f:40:GLU:O	17:f:109:ARG:NH2	2.27	0.68
9:5:1208:G:N2	18:F:76:MET:SD	2.66	0.68
34:O:54:TYR:HE2	34:O:145:VAL:HG11	1.58	0.68
9:5:3868:G:H22	9:5:3900:G:H1'	1.59	0.68
9:5:1883:G:OP1	15:e:47:ARG:NH1	2.27	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:2502:G:O2'	9:5:2503:G:O5'	2.12	0.68
41:S:41:LYS:HE2	41:S:61:ILE:HG21	1.76	0.68
20:G:167:VAL:HG12	20:G:170:LEU:HD12	1.75	0.68
36:P:36:ILE:HD11	36:P:44:ALA:HB1	1.75	0.68
9:5:4072:C:H2'	9:5:4073:A:H8	1.59	0.68
6:x:69:LEU:HD22	46:X:152:LYS:HB3	1.74	0.68
9:5:3641:U:OP2	9:5:3646:A:N6	2.27	0.67
31:m:77:ILE:HG23	31:m:78:ILE:HG12	1.76	0.67
40:R:75:HIS:HB3	40:R:80:LYS:HE2	1.76	0.67
9:5:1444:G:N2	9:5:2100:A:N6	2.42	0.67
23:i:33:LEU:HD21	23:i:38:LYS:HD3	1.76	0.67
48:Y:77:LYS:HG3	48:Y:79:VAL:HG22	1.76	0.67
9:5:3809:G:N2	9:5:3809:G:OP2	2.26	0.67
46:X:89:LYS:HD3	46:X:93:ASN:HD22	1.60	0.67
28:L:49:ARG:O	28:L:149:GLN:NE2	2.27	0.67
47:7:28:C:H1'	47:7:54:A:H61	1.59	0.67
9:5:1924:C:OP1	30:M:34:ASN:ND2	2.27	0.67
9:5:475:G:H2'	9:5:476:G:H8	1.58	0.67
9:5:1378:C:H5'	9:5:1379:C:H5'	1.75	0.67
9:5:2753:G:H2'	9:5:2754:G:C4	2.30	0.67
13:d:44:ARG:NH1	13:d:48:GLU:OE2	2.26	0.67
9:5:4888:U:O2	9:5:4931:G:O6	2.12	0.67
20:G:57:TRP:O	20:G:62:ARG:NH1	2.28	0.67
9:5:1952:G:H4'	41:S:93:MET:HG3	1.76	0.67
30:M:105:THR:OG1	30:M:108:ASP:OD1	2.13	0.67
32:N:123:GLU:OE1	32:N:128:LYS:NZ	2.29	0.67
35:o:70:LEU:HD13	35:o:83:LEU:HD13	1.77	0.67
9:5:969:C:O2'	9:5:970:G:N3	2.27	0.66
9:5:971:U:O4	16:E:124:HIS:ND1	2.28	0.66
9:5:2407:G:N2	9:5:2407:G:OP2	2.28	0.66
9:5:2562:G:N2	9:5:2565:A:OP2	2.24	0.66
9:5:2663:G:H21	9:5:2676:A:HO2'	1.43	0.66
9:5:422:C:H2'	9:5:423:G:H8	1.60	0.66
41:S:95:ARG:NH2	41:S:112:ASP:OD2	2.28	0.66
7:A:29:LEU:O	7:A:123:ARG:NE	2.25	0.66
9:5:2087:C:OP2	38:Q:37:ARG:NH1	2.29	0.66
14:D:120:GLU:O	14:D:248:ARG:NH2	2.29	0.66
9:5:973:G:H21	12:C:327:LYS:HE2	1.60	0.66
52:t:185:MET:HG2	52:t:192:ARG:HE	1.59	0.66
36:P:60:PHE:HE2	36:P:82:ARG:HB2	1.61	0.66
1:1:194:G:H1	1:1:205:A:H61	1.42	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:1555:G:H1	9:5:1572:U:H3	1.44	0.66
9:5:4745:G:H21	9:5:4956:A:H61	1.42	0.66
30:M:30:VAL:HG21	41:S:150:ILE:HD13	1.78	0.66
9:5:481:G:OP1	39:r:67:ARG:NH1	2.30	0.65
9:5:1726:U:O2	9:5:1836:G:N2	2.24	0.65
9:5:3670:C:C2	32:N:74:PRO:HA	2.31	0.65
49:8:76:C:N3	49:8:77:A:N6	2.44	0.65
50:Z:36:ARG:NH1	50:Z:38:TYR:OH	2.29	0.65
11:c:78:ASN:ND2	37:p:42:CYS:O	2.29	0.65
9:5:1503:A:H4'	9:5:1504:G:H5'	1.77	0.65
31:m:93:LYS:HG3	31:m:102:ARG:HD2	1.76	0.65
9:5:1199:G:H4'	41:S:23:ARG:HG2	1.79	0.65
14:D:211:LEU:HD12	14:D:223:PHE:HE2	1.61	0.65
39:r:46:ARG:HG2	39:r:67:ARG:HG3	1.79	0.65
9:5:973:G:H22	9:5:1282:G:HO2'	1.44	0.65
9:5:1802:A:H5''	9:5:1803:G:H5'	1.78	0.65
10:B:302:ASN:HD22	10:B:330:PHE:HE1	1.43	0.65
11:c:37:MET:HE2	11:c:97:ILE:HG12	1.78	0.65
14:D:150:LEU:HD12	26:J:146:ARG:HG3	1.78	0.65
9:5:4648:A:OP1	40:R:62:ARG:NH2	2.29	0.65
36:P:5:SER:OG	36:P:118:GLN:NE2	2.30	0.65
9:5:32:G:H21	9:5:50:C:H5	1.45	0.65
9:5:3848:U:H2'	9:5:3849:A:H8	1.62	0.65
9:5:4910:G:N2	34:O:106:ASP:O	2.30	0.65
30:M:25:VAL:HG12	30:M:45:VAL:HG21	1.79	0.65
49:8:122:G:H21	49:8:128:C:H41	1.45	0.65
9:5:1389:U:OP2	38:Q:170:LYS:NZ	2.30	0.65
9:5:4704:C:O3'	22:H:129:ARG:NH2	2.30	0.65
11:c:50:ASN:ND2	11:c:75:SER:O	2.29	0.65
34:O:126:VAL:HG13	34:O:127:VAL:HG13	1.77	0.65
9:5:959:G:H21	16:E:121:LEU:H	1.45	0.65
9:5:2324:C:O2'	15:e:98:GLU:OE1	2.15	0.65
32:N:96:ARG:NH2	32:N:104:GLU:OE1	2.29	0.65
9:5:3904:G:H3'	9:5:3905:A:H5''	1.79	0.64
9:5:1743:A:N1	9:5:1789:C:O2'	2.27	0.64
9:5:2251:G:H22	39:r:98:ARG:HD3	1.60	0.64
16:E:250:ASP:HA	16:E:253:ILE:HG22	1.80	0.64
2:q:60:VAL:HG12	2:q:84:VAL:HG12	1.79	0.64
12:C:254:GLU:OE2	12:C:258:ARG:NH2	2.29	0.64
20:G:74:LEU:HD11	32:N:21:PHE:HE1	1.62	0.64
26:J:99:PHE:O	26:J:159:LYS:NZ	2.30	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:j:63:ARG:NH1	49:8:58:G:O6	2.31	0.64
48:Y:55:VAL:HG11	48:Y:82:ILE:HG12	1.79	0.64
1:1:121:U:OP2	5:v:89:ARG:NH1	2.31	0.64
2:q:107:TYR:O	2:q:110:GLU:HG2	1.97	0.64
9:5:217:C:O2	12:C:172:LYS:NZ	2.30	0.64
9:5:4527:G:OP2	9:5:4527:G:N2	2.24	0.64
10:B:56:ILE:HD11	10:B:365:LEU:HD22	1.78	0.64
26:J:35:ARG:NH1	26:J:122:SER:O	2.31	0.64
9:5:3598:C:H2'	9:5:3599:A:H8	1.63	0.64
9:5:67:C:OP2	9:5:312:G:N2	2.31	0.64
9:5:2593:C:N3	9:5:2753:G:N2	2.46	0.64
9:5:4421:C:H42	9:5:4475:G:H22	1.44	0.64
42:T:45:MET:HE3	42:T:47:THR:HB	1.80	0.64
9:5:2299:G:OP1	12:C:182:LYS:NZ	2.28	0.64
32:N:60:VAL:HG11	49:8:141:C:H5''	1.80	0.64
1:1:151:C:H2'	1:1:152:G:H8	1.63	0.63
9:5:114:G:N2	9:5:277:G:O4'	2.31	0.63
9:5:1490:G:H2'	9:5:1491:A:H8	1.63	0.63
19:g:41:ALA:HB3	19:g:52:ARG:HB3	1.80	0.63
39:r:26:SER:OG	39:r:31:ASN:ND2	2.31	0.63
9:5:4975:G:O2'	9:5:4977:A:N7	2.31	0.63
51:a:24:LYS:HD2	51:a:26:ARG:HH21	1.64	0.63
52:t:185:MET:HG2	52:t:192:ARG:NE	2.12	0.63
9:5:1233:G:H2'	9:5:1234:G:C8	2.33	0.63
9:5:1517:G:H22	12:C:103:ALA:HA	1.63	0.63
9:5:3709:U:HO2'	9:5:3710:G:H8	1.46	0.63
9:5:4075:U:H2'	9:5:4169:G:H1	1.62	0.63
9:5:4896:G:N2	9:5:4926:C:N3	2.46	0.63
17:f:97:ILE:HG21	34:O:94:ARG:HD2	1.80	0.63
32:N:116:LEU:HD22	32:N:135:ILE:HD11	1.81	0.63
1:1:173:A:OP2	5:v:161:LYS:NZ	2.31	0.63
2:q:18:ILE:HB	2:q:82:VAL:HB	1.81	0.63
9:5:3620:G:OP1	9:5:3622:C:N4	2.32	0.63
24:I:66:GLU:OE2	24:I:69:ARG:NH2	2.32	0.63
27:k:28:ASN:HB3	27:k:31:ASN:HB3	1.80	0.63
31:m:96:CYS:SG	31:m:110:CYS:HB2	2.38	0.63
48:Y:8:THR:HG23	48:Y:13:LYS:HE3	1.80	0.63
52:t:200:LYS:C	52:t:202:ASN:H	2.06	0.63
9:5:2:G:H1	49:8:156:U:H3	1.45	0.63
9:5:1850:A:OP2	28:L:5:ARG:NH2	2.31	0.63
41:S:15:ARG:HD2	41:S:25:PRO:HG2	1.81	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:1213:G:H5''	9:5:1214:C:H5''	1.80	0.63
6:x:430:MET:HE3	6:x:465:MET:HG3	1.80	0.62
12:C:149:GLU:HG2	12:C:151:PRO:HD2	1.80	0.62
9:5:4748:U:H3	9:5:4952:G:H1	1.47	0.62
10:B:110:ILE:O	10:B:115:LYS:NZ	2.33	0.62
39:r:94:ARG:HG3	39:r:107:ARG:HD2	1.81	0.62
51:a:39:HIS:O	51:a:40:HIS:ND1	2.32	0.62
5:v:80:PHE:HE1	5:v:139:MET:HE3	1.64	0.62
9:5:37:U:H4'	51:a:32:ARG:HD2	1.81	0.62
9:5:2400:G:H21	19:g:6:THR:HG22	1.63	0.62
26:J:146:ARG:NH2	47:7:27:G:OP1	2.32	0.62
52:t:197:ARG:H	52:t:197:ARG:HD3	1.64	0.62
9:5:2248:C:OP2	18:F:26:ASN:N	2.32	0.62
14:D:243:ALA:O	14:D:247:ILE:HG12	1.99	0.62
22:H:92:MET:HE2	22:H:179:ILE:HG22	1.80	0.62
9:5:959:G:O2'	16:E:119:ARG:O	2.17	0.62
9:5:2704:C:H2'	9:5:2705:G:H8	1.65	0.62
36:P:20:SER:HA	36:P:145:HIS:HD2	1.64	0.62
1:1:187:G:H2'	1:1:188:G:C8	2.34	0.62
2:q:72:TRP:HE1	6:x:408:ARG:HE	1.45	0.62
9:5:263:G:H22	21:h:112:ARG:HH22	1.48	0.62
9:5:731:G:H21	41:S:72:PRO:HG2	1.65	0.62
28:L:104:ASN:HD21	28:L:110:LEU:HB2	1.65	0.62
1:1:196:C:H2'	1:1:197:G:H8	1.63	0.62
9:5:1927:U:OP1	9:5:1949:U:O2'	2.15	0.62
24:I:162:ARG:NH1	24:I:163:GLN:O	2.33	0.62
9:5:453:G:H1	9:5:1294:A:H62	1.47	0.62
9:5:475:G:H2'	9:5:476:G:C8	2.35	0.62
9:5:2457:G:O2'	9:5:3672:G:O2'	2.18	0.62
9:5:4134:C:H2'	9:5:4135:G:H8	1.63	0.62
14:D:65:ALA:HB2	14:D:74:ILE:HG22	1.82	0.62
1:1:179:G:H1	1:1:218:U:H3	1.48	0.62
9:5:419:A:N3	9:5:1332:C:O2'	2.32	0.62
9:5:1750:G:N2	24:I:193:ASP:OD2	2.32	0.62
9:5:2520:C:H2'	9:5:2521:G:H8	1.64	0.62
9:5:4237:C:N4	9:5:4238:G:O6	2.33	0.62
9:5:1921:C:H1'	41:S:160:ARG:HB2	1.82	0.62
9:5:4520:G:N2	10:B:253:CYS:SG	2.72	0.62
16:E:188:LYS:O	17:f:108:SER:N	2.29	0.62
9:5:5047:C:O2'	9:5:5050:C:OP2	2.18	0.61
46:X:105:ASN:ND2	49:8:131:G:OP1	2.31	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:687:U:H1'	16:E:101:ARG:HG2	1.81	0.61
9:5:2411:C:O2'	9:5:2526:C:O2	2.18	0.61
30:M:38:VAL:HG21	30:M:50:MET:HE3	1.82	0.61
40:R:126:LYS:HE2	40:R:131:VAL:HG21	1.82	0.61
9:5:3928:A:OP1	32:N:90:ASN:ND2	2.33	0.61
9:5:662:C:H2'	9:5:663:G:H8	1.66	0.61
17:f:45:LYS:HD2	17:f:105:LEU:HA	1.82	0.61
9:5:2486:G:N2	49:8:126:C:OP2	2.28	0.61
9:5:2583:C:OP2	19:g:76:ARG:NH1	2.33	0.61
38:Q:172:ARG:NH1	51:a:56:VAL:O	2.32	0.61
7:A:117:GLU:HB3	7:A:124:GLY:H	1.66	0.61
9:5:973:G:N2	9:5:1282:G:O2'	2.29	0.61
9:5:4876:U:H2'	41:S:169:THR:HG22	1.82	0.61
9:5:4944:C:OP1	16:E:150:THR:OG1	2.18	0.61
17:f:46:ARG:O	17:f:104:MET:N	2.32	0.61
9:5:1727:U:OP1	18:F:133:ASN:ND2	2.33	0.61
9:5:4768:G:OP1	34:O:176:ARG:NH1	2.31	0.61
1:1:204:G:H2'	1:1:205:A:C8	2.35	0.61
6:x:330:ARG:HE	6:x:387:LEU:HD13	1.65	0.61
9:5:1352:C:N4	38:Q:55:ARG:HH22	1.99	0.61
9:5:1523:A:N3	9:5:4389:C:O2'	2.34	0.61
15:e:91:CYS:HB2	15:e:95:TYR:HD1	1.65	0.61
17:f:43:LEU:O	17:f:109:ARG:NH1	2.34	0.61
7:A:215:ASN:ND2	9:5:4546:A:N7	2.48	0.60
9:5:2595:C:H2'	9:5:2596:G:H8	1.65	0.60
9:5:4974:C:H2'	9:5:4975:G:C8	2.36	0.60
18:F:130:ALA:O	18:F:134:MET:HG3	2.01	0.60
9:5:106:A:H1'	9:5:336:A:H8	1.66	0.60
9:5:218:A:H5'	12:C:181:LYS:HE2	1.82	0.60
9:5:279:A:OP1	32:N:47:LYS:NZ	2.29	0.60
9:5:1950:U:O2'	41:S:116:ARG:NH1	2.34	0.60
50:Z:53:VAL:O	50:Z:57:MET:HE1	2.01	0.60
9:5:62:A:N3	9:5:77:U:O2'	2.32	0.60
9:5:153:G:H2'	9:5:154:G:H8	1.66	0.60
10:B:261:ARG:HB2	34:O:64:THR:HG21	1.82	0.60
18:F:58:HIS:O	18:F:62:GLU:HG3	2.02	0.60
24:I:153:ARG:HA	24:I:156:LYS:HD3	1.83	0.60
32:N:114:ARG:HD3	32:N:151:ILE:HG12	1.82	0.60
37:p:38:THR:HA	37:p:45:THR:HA	1.82	0.60
51:a:71:PRO:HG2	51:a:108:TYR:HA	1.83	0.60
9:5:2710:C:H5'	40:R:39:GLN:HE22	1.67	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:3615:G:N3	45:W:44:ARG:NH1	2.48	0.60
9:5:1376:C:OP2	9:5:1379:C:N4	2.35	0.60
9:5:4128:A:H5'	50:Z:54:THR:HB	1.82	0.60
45:W:4:GLU:OE2	45:W:20:ARG:NH2	2.35	0.60
9:5:4232:U:H4'	9:5:4233:A:O5'	2.01	0.60
42:T:27:LEU:HA	42:T:30:TYR:HD2	1.66	0.60
40:R:39:GLN:HA	40:R:42:ARG:NE	2.17	0.60
9:5:1618:G:H5''	25:j:13:ASN:HD21	1.65	0.60
9:5:4594:U:H2'	9:5:4595:G:H8	1.67	0.60
12:C:41:HIS:CE1	12:C:45:ARG:HD2	2.37	0.60
9:5:4537:C:H2'	9:5:4538:G:H8	1.67	0.60
16:E:212:TYR:OH	16:E:241:GLN:OE1	2.17	0.60
43:U:49:VAL:HB	43:U:57:GLY:HA3	1.82	0.60
43:U:105:ASN:HD21	43:U:111:GLU:HB2	1.67	0.60
17:f:45:LYS:HD3	17:f:107:PRO:HD2	1.82	0.59
2:q:66:LYS:HD3	2:q:81:ARG:HB3	1.84	0.59
9:5:4620:U:OP1	44:V:51:ARG:NH1	2.36	0.59
6:x:195:HIS:HD2	6:x:197:GLN:HG2	1.66	0.59
9:5:407:A:O2'	9:5:410:A:OP1	2.19	0.59
28:L:123:LYS:HD2	28:L:155:MET:HE2	1.84	0.59
36:P:60:PHE:CE2	36:P:82:ARG:HB2	2.37	0.59
50:Z:12:LEU:HB2	50:Z:81:MET:HB3	1.84	0.59
9:5:2647:A:H62	9:5:2686:G:H8	1.49	0.59
9:5:4604:G:N2	9:5:4607:A:OP2	2.34	0.59
12:C:10:VAL:HA	12:C:153:VAL:HG13	1.85	0.59
16:E:262:GLN:OE1	30:M:111:LYS:NZ	2.28	0.59
9:5:1758:G:H2'	9:5:1759:G:H8	1.68	0.59
9:5:3610:A:H2'	9:5:3611:A:H8	1.66	0.59
9:5:4945:G:H5'	9:5:4946:U:H5'	1.83	0.59
13:d:89:SER:O	13:d:105:LEU:N	2.30	0.59
15:e:90:MET:HG3	39:r:33:LYS:HA	1.85	0.59
22:H:20:LEU:HD23	22:H:47:LEU:HD22	1.84	0.59
9:5:1284:G:N1	9:5:2076:G:OP1	2.35	0.59
32:N:53:TYR:HB2	32:N:133:ILE:HD13	1.84	0.59
6:x:327:PHE:HB2	6:x:431:VAL:HG21	1.84	0.59
40:R:4:LEU:HD11	40:R:29:THR:HG23	1.85	0.59
42:T:64:VAL:HA	42:T:74:ILE:HG22	1.84	0.59
7:A:101:VAL:HB	7:A:165:VAL:HG22	1.85	0.59
9:5:1278:C:H3'	9:5:1279:A:H4'	1.84	0.59
9:5:1490:G:H2'	9:5:1491:A:C8	2.38	0.59
9:5:1931:C:N4	9:5:2040:A:N3	2.51	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:4235:G:N2	9:5:4292:A:OP1	2.36	0.59
16:E:94:GLY:HA2	16:E:100:THR:HG23	1.85	0.59
21:h:95:LEU:HD23	32:N:143:ARG:NH1	2.17	0.59
22:H:103:VAL:HG21	22:H:144:LEU:HD21	1.82	0.59
9:5:93:G:H2'	9:5:94:A:C8	2.38	0.59
9:5:938:C:H2'	9:5:939:G:C8	2.38	0.59
9:5:1380:G:O2'	9:5:1381:U:O5'	2.20	0.59
9:5:1937:C:OP2	9:5:1938:C:O2'	2.21	0.59
9:5:4990:C:N4	10:B:113:GLU:OE2	2.36	0.59
1:1:161:C:O2	1:1:214:A:O2'	2.20	0.59
9:5:33:A:H3'	9:5:47:A:H61	1.67	0.59
9:5:74:G:H5''	28:L:59:VAL:HG13	1.84	0.59
9:5:2459:G:N2	9:5:2462:C:OP2	2.36	0.59
9:5:1951:G:O2'	41:S:95:ARG:NH1	2.36	0.58
9:5:3945:A:H2'	9:5:3946:G:H8	1.68	0.58
9:5:4090:G:H2'	9:5:4091:G:C8	2.37	0.58
9:5:4699:U:H1'	9:5:4700:A:H5''	1.85	0.58
6:x:41:GLU:C	6:x:43:ASP:H	2.09	0.58
9:5:337:U:OP1	28:L:31:ARG:NH1	2.31	0.58
9:5:1332:C:H2'	9:5:1333:A:C8	2.37	0.58
9:5:4088:C:H2'	9:5:4089:G:C8	2.37	0.58
36:P:95:LEU:HD23	36:P:148:MET:HE1	1.84	0.58
44:V:82:ILE:HG22	44:V:83:ARG:HG3	1.84	0.58
9:5:1739:G:N3	9:5:1742:A:N6	2.51	0.58
9:5:1864:G:O2'	24:I:118:ALA:O	2.20	0.58
9:5:2624:G:O6	9:5:2632:U:O2	2.21	0.58
9:5:3873:G:H2'	9:5:3874:G:C8	2.38	0.58
14:D:22:ARG:NH2	47:7:6:C:OP2	2.37	0.58
1:1:119:A:H61	1:1:231:A:H61	1.50	0.58
1:1:198:G:N2	1:1:201:A:OP2	2.37	0.58
2:q:30:ALA:O	2:q:70:ARG:NE	2.34	0.58
9:5:3944:G:H2'	9:5:3945:A:C8	2.38	0.58
9:5:4933:C:H2'	9:5:4934:A:H8	1.67	0.58
28:L:54:PRO:HG2	28:L:56:ARG:HH22	1.68	0.58
28:L:70:VAL:H	28:L:159:ASN:HD21	1.51	0.58
41:S:15:ARG:HH21	42:T:141:VAL:HG22	1.69	0.58
1:1:167:U:OP2	5:v:152:ARG:NH1	2.37	0.58
9:5:709:C:H2'	9:5:710:G:H8	1.68	0.58
9:5:1922:G:OP1	41:S:160:ARG:NH2	2.36	0.58
9:5:3937:C:H1'	32:N:125:SER:HB3	1.85	0.58
9:5:4266:G:O2'	9:5:4268:A:N7	2.29	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:124:ARG:NH1	22:H:164:ALA:O	2.35	0.58
24:I:53:VAL:HG23	24:I:164:LYS:HB2	1.84	0.58
40:R:44:LEU:HD22	40:R:49:LEU:HD22	1.85	0.58
6:x:40:LEU:HD23	6:x:49:VAL:HG21	1.84	0.58
9:5:1352:C:H3'	38:Q:104:ARG:HH22	1.68	0.58
9:5:1795:A:N3	47:7:79:U:O2'	2.36	0.58
9:5:2489:C:O2'	9:5:2491:C:N4	2.36	0.58
9:5:3648:A:H1'	9:5:3785:A:H61	1.69	0.58
10:B:286:LYS:HE3	10:B:332:MET:HE3	1.86	0.58
14:D:84:PRO:HB3	14:D:89:LYS:HA	1.86	0.58
17:f:10:ILE:HB	17:f:29:LYS:HB3	1.84	0.58
34:O:54:TYR:CE2	34:O:145:VAL:HG11	2.39	0.58
9:5:933:G:H2'	9:5:940:C:H41	1.68	0.58
52:t:205:ASP:HB3	52:t:208:ASN:HB2	1.85	0.58
9:5:974:C:H2'	9:5:975:C:H6	1.69	0.58
9:5:2601:A:N6	9:5:2744:A:OP2	2.37	0.58
9:5:214:G:OP2	9:5:219:G:N2	2.37	0.58
9:5:371:A:H2'	9:5:372:A:C8	2.39	0.58
10:B:47:LEU:HD12	10:B:181:MET:HE2	1.84	0.58
51:a:110:LYS:HG3	51:a:128:PHE:HB2	1.84	0.58
6:x:50:LYS:HB2	52:t:211:MET:CE	2.29	0.57
9:5:2378:G:N2	9:5:2381:A:OP2	2.33	0.57
10:B:317:LEU:HB2	10:B:372:SER:HB2	1.84	0.57
24:I:170:LYS:HA	24:I:177:ASN:HA	1.85	0.57
25:j:81:GLY:N	49:8:95:A:OP1	2.22	0.57
9:5:346:G:O2'	9:5:1367:C:N4	2.37	0.57
9:5:930:G:H4'	9:5:931:C:O5'	2.04	0.57
9:5:1573:G:OP1	40:R:92:LYS:HE2	2.03	0.57
14:D:10:LYS:NZ	47:7:66:G:OP1	2.36	0.57
14:D:146:LEU:HD21	14:D:159:VAL:HG12	1.86	0.57
30:M:20:HIS:ND1	30:M:45:VAL:HG12	2.19	0.57
37:p:36:LYS:HD3	37:p:45:THR:O	2.04	0.57
6:x:382:MET:SD	6:x:386:GLU:HB2	2.43	0.57
9:5:679:C:H2'	9:5:680:G:H8	1.68	0.57
9:5:2738:C:O2'	9:5:2740:U:O2	2.21	0.57
9:5:3877:A:N3	9:5:4401:G:O2'	2.34	0.57
9:5:4485:C:O2'	31:m:114:LYS:NZ	2.37	0.57
9:5:5051:C:H4'	10:B:324:GLY:HA2	1.86	0.57
14:D:166:ALA:HB1	14:D:171:LEU:HD12	1.86	0.57
5:v:141:LEU:HD22	5:v:151:LYS:HB3	1.85	0.57
9:5:1916:G:N3	9:5:2067:C:O2'	2.37	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:2591:A:H2'	9:5:2592:U:H6	1.69	0.57
12:C:36:ILE:HD13	12:C:122:TYR:CD2	2.40	0.57
16:E:112:TYR:HB3	39:r:112:ARG:HD3	1.86	0.57
9:5:184:U:O2	9:5:253:G:N2	2.32	0.57
9:5:364:G:O6	25:j:55:ARG:NH2	2.37	0.57
9:5:2575:U:OP1	50:Z:48:ARG:NH2	2.37	0.57
9:5:2835:A:O2'	10:B:228:TYR:O	2.21	0.57
9:5:1358:G:O2'	9:5:1359:G:H8	1.88	0.57
9:5:2706:G:N2	9:5:2709:C:OP2	2.37	0.57
9:5:3892:U:O2'	36:P:80:GLN:NE2	2.38	0.57
9:5:4737:G:H5''	9:5:5069:U:H2'	1.87	0.57
35:o:33:LEU:HA	35:o:38:LYS:HG2	1.87	0.57
48:Y:114:ASP:HB2	49:8:83:C:H41	1.69	0.57
52:t:181:ILE:CG2	52:t:196:VAL:HG22	2.26	0.57
9:5:4074:C:H2'	9:5:4075:U:C6	2.40	0.57
12:C:298:ILE:O	12:C:302:LEU:HG	2.04	0.57
9:5:4768:G:H5'	34:O:176:ARG:HD3	1.87	0.57
9:5:4906:C:H2'	9:5:4907:G:H8	1.70	0.57
18:F:52:ILE:HD12	18:F:188:CYS:HB3	1.87	0.57
9:5:85:G:O2'	9:5:97:G:O6	2.19	0.57
9:5:964:A:N6	9:5:966:A:N7	2.53	0.57
9:5:4586:G:OP1	34:O:72:HIS:N	2.32	0.57
41:S:15:ARG:HB3	41:S:27:LEU:HD23	1.85	0.57
6:x:50:LYS:O	6:x:54:GLU:HG2	2.05	0.57
9:5:178:C:N4	9:5:179:G:O6	2.38	0.57
9:5:4890:G:H2'	9:5:4891:G:H8	1.70	0.57
32:N:159:ARG:HB3	32:N:164:LEU:HB2	1.86	0.57
50:Z:3:LYS:O	50:Z:6:LYS:NZ	2.38	0.57
52:t:197:ARG:HB2	52:t:197:ARG:NH1	2.19	0.57
9:5:2759:G:O2'	9:5:2763:U:O2	2.23	0.56
34:O:12:ARG:HB2	34:O:37:ARG:HD2	1.87	0.56
9:5:1217:G:N2	9:5:1218:G:O6	2.38	0.56
9:5:1370:G:OP2	12:C:48:ASN:ND2	2.37	0.56
9:5:5041:G:N1	10:B:389:MET:O	2.38	0.56
14:D:244:HIS:O	14:D:248:ARG:HG3	2.05	0.56
24:I:49:CYS:SG	24:I:168:SER:OG	2.60	0.56
43:U:25:CYS:HB2	43:U:28:PRO:HG3	1.86	0.56
1:1:175:G:O2'	1:1:177:G:OP2	2.21	0.56
9:5:124:C:OP1	32:N:144:ARG:NH1	2.34	0.56
9:5:950:G:H2'	9:5:951:G:H8	1.69	0.56
9:5:2764:A:H2'	9:5:2765:A:C8	2.40	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:2791:C:OP1	29:l:48:LYS:NZ	2.36	0.56
11:c:55:LEU:HD11	19:g:92:LYS:HG3	1.86	0.56
41:S:28:TYR:HD1	42:T:149:GLU:HB3	1.70	0.56
9:5:423:G:OP1	36:P:62:ARG:NH1	2.39	0.56
9:5:432:U:OP2	9:5:3888:G:N2	2.37	0.56
9:5:734:G:H5''	30:M:70:GLN:OE1	2.05	0.56
9:5:1240:G:OP2	9:5:1271:G:O2'	2.24	0.56
9:5:1447:C:O3'	12:C:300:ARG:NH2	2.38	0.56
9:5:2890:C:H42	9:5:3611:A:H61	1.52	0.56
9:5:4421:C:N4	9:5:4475:G:H22	2.03	0.56
12:C:305:PRO:HB3	38:Q:38:ARG:HH22	1.71	0.56
28:L:187:ALA:O	28:L:191:LEU:HG	2.05	0.56
9:5:173:C:H5'	28:L:129:ARG:HH21	1.70	0.56
9:5:710:G:H2'	9:5:711:A:C8	2.41	0.56
10:B:312:LYS:NZ	10:B:368:ILE:O	2.35	0.56
14:D:259:ARG:HE	14:D:260:GLU:H	1.53	0.56
30:M:41:PRO:HB3	30:M:70:GLN:NE2	2.21	0.56
9:5:3653:A:C2	9:5:3692:A:H4'	2.40	0.56
20:G:74:LEU:HD11	32:N:21:PHE:CE1	2.40	0.56
20:G:162:ASP:HB3	20:G:163:PRO:HD3	1.88	0.56
22:H:103:VAL:HG12	22:H:114:ILE:HG12	1.86	0.56
9:5:1326:A:OP2	9:5:4445:U:O2'	2.23	0.56
9:5:1433:A:N6	9:5:1451:G:O2'	2.38	0.56
9:5:3722:G:H2'	9:5:3723:A:H8	1.70	0.56
10:B:79:VAL:HG21	10:B:345:LEU:HD11	1.88	0.56
16:E:168:LEU:HD13	16:E:184:ARG:HB3	1.88	0.56
30:M:12:VAL:HB	30:M:60:PHE:HB2	1.88	0.56
9:5:69:A:H5'	51:a:64:LYS:HE2	1.87	0.56
9:5:287:U:H2'	9:5:288:G:H8	1.70	0.56
9:5:2638:G:H1	9:5:2697:A:H61	1.52	0.56
10:B:284:ILE:HG22	10:B:333:LEU:HD23	1.86	0.56
12:C:149:GLU:OE2	39:r:71:ARG:NH1	2.38	0.56
41:S:9:GLU:HG3	41:S:67:VAL:HB	1.88	0.56
9:5:1411:C:H2'	9:5:1412:G:H8	1.70	0.56
9:5:2568:C:H2'	9:5:2569:G:H8	1.70	0.56
9:5:2735:G:H2'	9:5:2736:G:H8	1.70	0.56
9:5:4528:G:O2'	9:5:4529:G:OP1	2.24	0.56
9:5:1241:C:H3'	9:5:1242:G:H5''	1.88	0.56
49:8:47:C:H1'	49:8:61:A:H2'	1.86	0.56
9:5:88:A:N7	38:Q:173:LYS:NZ	2.47	0.55
9:5:300:A:H2'	9:5:301:G:H8	1.71	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:452:A:H61	16:E:230:ASP:HB3	1.69	0.55
9:5:968:C:OP2	16:E:106:ARG:NH1	2.39	0.55
9:5:3617:G:O2'	9:5:3620:G:N7	2.38	0.55
9:5:4620:U:OP2	9:5:4670:C:N4	2.39	0.55
9:5:4922:C:H2'	9:5:4923:C:C6	2.42	0.55
16:E:163:GLN:HE21	16:E:167:GLY:HA2	1.71	0.55
31:m:115:CYS:O	31:m:118:THR:OG1	2.24	0.55
43:U:82:TYR:O	43:U:86:LEU:HG	2.07	0.55
6:x:471:LEU:HA	6:x:474:MET:HB3	1.88	0.55
9:5:1198:G:H2'	9:5:1199:G:C8	2.41	0.55
22:H:137:SER:HB3	22:H:143:GLU:HG3	1.88	0.55
38:Q:171:GLY:O	38:Q:176:ARG:NH1	2.39	0.55
48:Y:4:ASN:HB3	48:Y:7:VAL:HG23	1.89	0.55
8:b:41:ARG:HH12	9:5:1492:G:H4'	1.71	0.55
9:5:710:G:H21	16:E:132:HIS:CE1	2.25	0.55
9:5:1732:C:H2'	9:5:1733:G:C8	2.41	0.55
9:5:2751:G:N1	9:5:2752:G:O6	2.40	0.55
12:C:159:GLU:HA	12:C:217:ILE:HB	1.89	0.55
2:q:63:GLU:HB2	2:q:66:LYS:HD2	1.89	0.55
9:5:1918:U:OP1	17:f:81:SER:OG	2.22	0.55
17:f:29:LYS:HD3	17:f:83:MET:HE1	1.88	0.55
32:N:39:ALA:HB3	32:N:61:ILE:HG22	1.89	0.55
6:x:196:LYS:HD3	6:x:232:GLN:HG2	1.88	0.55
9:5:109:G:OP1	28:L:92:ARG:NH1	2.39	0.55
9:5:4472:G:O2'	31:m:100:TYR:O	2.25	0.55
20:G:160:ASP:OD1	20:G:187:LYS:N	2.39	0.55
27:k:34:PHE:HB2	27:k:45:LEU:HB3	1.88	0.55
39:r:10:VAL:HG22	39:r:14:SER:HB2	1.87	0.55
40:R:142:ILE:HG22	40:R:146:LYS:HE2	1.89	0.55
46:X:124:VAL:HG22	46:X:138:VAL:HG23	1.87	0.55
3:s:28:UNK:O	3:s:32:UNK:N	2.40	0.55
9:5:1214:C:C4	18:F:58:HIS:HD2	2.25	0.55
9:5:2256:C:H4'	9:5:2257:C:O5'	2.05	0.55
9:5:4537:C:H2'	9:5:4538:G:C8	2.41	0.55
26:J:26:VAL:HG13	26:J:32:ARG:HE	1.70	0.55
1:1:124:G:H1	1:1:226:U:H3	1.55	0.55
9:5:18:C:H4'	32:N:138:PHE:CE2	2.41	0.55
9:5:469:C:H3'	9:5:683:C:H42	1.72	0.55
9:5:4239:A:H2'	9:5:4240:G:C8	2.42	0.55
9:5:4688:C:O2'	22:H:155:SER:OG	2.20	0.55
10:B:290:GLY:N	10:B:329:ASP:OD1	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:G:180:PRO:HB3	20:G:223:ARG:HB3	1.89	0.55
28:L:77:SER:H	28:L:102:ARG:HH21	1.55	0.55
30:M:24:LEU:HB2	30:M:43:THR:HG21	1.88	0.55
34:O:173:GLN:OE1	34:O:176:ARG:NH2	2.36	0.55
9:5:274:C:H2'	9:5:275:C:C6	2.42	0.55
9:5:1514:U:H2'	9:5:1515:A:C8	2.42	0.55
9:5:2411:C:H2'	9:5:2412:A:H8	1.72	0.55
9:5:3598:C:H2'	9:5:3599:A:C8	2.41	0.55
9:5:3904:G:O2'	9:5:3905:A:OP1	2.20	0.55
9:5:48:G:H4'	9:5:49:U:O5'	2.05	0.54
9:5:1408:G:O2'	9:5:1411:C:N4	2.41	0.54
9:5:2869:U:O2'	9:5:2881:A:N7	2.38	0.54
9:5:4635:A:H2	9:5:4663:G:H21	1.55	0.54
20:G:174:CYS:SG	20:G:181:TYR:HB3	2.47	0.54
30:M:41:PRO:HB3	30:M:70:GLN:HE21	1.72	0.54
34:O:27:VAL:HG12	34:O:98:ALA:HB1	1.88	0.54
9:5:4156:G:OP2	9:5:4157:A:O2'	2.24	0.54
9:5:4347:G:H2'	9:5:4348:A:C8	2.42	0.54
9:5:4945:G:N2	17:f:71:TRP:HE1	2.03	0.54
18:F:153:ASN:HD22	18:F:193:ILE:HD13	1.72	0.54
32:N:10:LEU:HG	32:N:19:MET:HE3	1.88	0.54
9:5:404:U:O3'	48:Y:87:ARG:NH2	2.40	0.54
9:5:710:G:H21	16:E:132:HIS:HE1	1.54	0.54
9:5:1084:C:H42	9:5:1215:C:H42	1.55	0.54
9:5:4239:A:H2'	9:5:4240:G:H8	1.73	0.54
9:5:4967:A:H2'	9:5:4968:A:H8	1.72	0.54
20:G:154:LEU:HD13	20:G:219:VAL:HG12	1.89	0.54
36:P:121:LYS:O	49:8:13:G:O2'	2.23	0.54
7:A:122:ASP:HB2	7:A:125:LYS:HE2	1.89	0.54
9:5:2595:C:H2'	9:5:2596:G:C8	2.41	0.54
9:5:4729:A:OP2	9:5:5068:G:N1	2.29	0.54
20:G:165:GLU:OE2	32:N:26:ARG:NH1	2.38	0.54
52:t:177:GLU:HB3	52:t:180:ASP:CG	2.33	0.54
9:5:1468:C:OP1	51:a:132:ARG:NH2	2.41	0.54
9:5:4154:G:H2'	9:5:4155:C:C6	2.42	0.54
9:5:4194:U:O2'	24:I:116:ARG:NH2	2.41	0.54
9:5:280:G:C6	32:N:14:LYS:HB2	2.43	0.54
9:5:1460:C:H5''	38:Q:144:LYS:HG2	1.90	0.54
9:5:5015:G:O2'	9:5:5034:A:N6	2.40	0.54
20:G:52:THR:O	49:8:150:C:N4	2.40	0.54
51:a:90:ALA:HB1	51:a:120:GLN:HG3	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:t:210:ILE:HA	52:t:214:THR:HB	1.89	0.54
9:5:230:G:OP1	48:Y:15:ARG:NH1	2.41	0.54
9:5:1730:U:H4'	42:T:100:LYS:HB2	1.90	0.54
9:5:2607:C:H5''	40:R:96:MET:HE1	1.88	0.54
9:5:4261:C:H2'	9:5:4262:C:H6	1.73	0.54
17:f:76:ARG:HG3	17:f:85:ARG:HD2	1.90	0.54
51:a:117:LEU:HD12	51:a:118:PRO:HD2	1.89	0.54
7:A:49:ILE:HD11	7:A:75:LEU:HD11	1.90	0.54
7:A:221:LYS:HD3	7:A:233:ARG:HH22	1.73	0.54
9:5:6:C:H1'	20:G:188:ALA:HB2	1.89	0.54
9:5:2674:A:C6	11:c:53:PRO:HD3	2.43	0.54
9:5:3693:U:H5''	37:p:22:LEU:HD23	1.90	0.54
24:I:62:SER:HA	24:I:65:LEU:HD12	1.90	0.54
1:l:150:G:OP1	2:q:22:TYR:OH	2.21	0.54
7:A:132:ASN:ND2	9:5:3682:A:H5''	2.22	0.54
8:b:41:ARG:NH1	9:5:1492:G:H4'	2.23	0.54
9:5:2759:G:O2'	9:5:2762:G:N2	2.41	0.54
9:5:4507:A:H2'	9:5:4508:C:C6	2.43	0.54
9:5:4645:C:OP2	40:R:62:ARG:NH1	2.40	0.54
9:5:4992:G:H2'	9:5:4993:G:C8	2.43	0.54
12:C:78:ARG:HB3	12:C:88:GLY:HA2	1.90	0.54
52:t:197:ARG:HB2	52:t:197:ARG:HH11	1.72	0.54
9:5:278:G:OP2	32:N:12:ARG:NH2	2.39	0.54
9:5:1933:G:H2'	9:5:1934:A:C8	2.43	0.54
9:5:2467:U:H4'	9:5:2468:U:H5'	1.90	0.54
9:5:3861:A:H2'	9:5:3862:A:H8	1.72	0.54
14:D:146:LEU:HD22	14:D:163:LEU:HD13	1.88	0.54
38:Q:154:LYS:HE3	38:Q:161:SER:HB2	1.90	0.54
40:R:171:LYS:NZ	40:R:175:GLU:OE2	2.35	0.54
6:x:375:LEU:O	6:x:379:MET:HG3	2.08	0.53
9:5:979:C:H5''	16:E:39:HIS:HB3	1.89	0.53
9:5:1329:G:O2'	9:5:1330:A:OP1	2.23	0.53
9:5:2520:C:H2'	9:5:2521:G:C8	2.43	0.53
9:5:4870:G:OP2	9:5:4870:G:N2	2.39	0.53
16:E:154:ARG:HG2	17:f:5:LEU:HD22	1.91	0.53
24:I:152:LEU:HD23	24:I:165:ILE:HD12	1.90	0.53
38:Q:99:LYS:HG2	38:Q:119:LYS:HB2	1.89	0.53
9:5:1318:C:OP1	51:a:21:ARG:HB2	2.08	0.53
9:5:1484:G:H8	28:L:195:ARG:HH22	1.57	0.53
9:5:1920:C:H3'	9:5:1921:C:H5''	1.89	0.53
9:5:2745:A:H2'	9:5:2746:A:H8	1.74	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:4170:A:H4'	9:5:4171:C:O5'	2.09	0.53
9:5:4238:G:H2'	9:5:4239:A:H8	1.73	0.53
10:B:154:LYS:HG3	10:B:194:LEU:HD23	1.89	0.53
12:C:317:ASN:HD22	12:C:320:LYS:HG3	1.73	0.53
22:H:162:GLN:HE21	22:H:181:VAL:HG23	1.72	0.53
9:5:1553:A:H4'	37:p:12:GLY:HA3	1.90	0.53
9:5:2568:C:H2'	9:5:2569:G:C8	2.43	0.53
9:5:4129:G:O6	9:5:4156:G:N2	2.41	0.53
9:5:4434:C:H2'	9:5:4435:U:C6	2.43	0.53
11:c:18:LEU:HB3	11:c:22:MET:HE1	1.90	0.53
26:J:12:MET:HE2	47:7:51:G:H21	1.72	0.53
39:r:51:VAL:HB	39:r:113:ARG:HD3	1.90	0.53
47:7:58:A:H2'	47:7:59:G:C8	2.44	0.53
1:1:119:A:H61	1:1:231:A:N6	2.05	0.53
9:5:262:G:H2'	9:5:263:G:H8	1.73	0.53
9:5:2399:G:O2'	9:5:2822:G:O2'	2.24	0.53
9:5:2838:G:OP1	10:B:248:LEU:N	2.40	0.53
9:5:3621:A:C8	9:5:4642:U:H1'	2.43	0.53
9:5:3808:C:H2'	9:5:3809:G:C4	2.43	0.53
9:5:3848:U:H2'	9:5:3849:A:C8	2.42	0.53
10:B:348:ARG:HD2	10:B:349:LYS:O	2.08	0.53
22:H:44:GLU:OE1	22:H:60:TRP:NE1	2.27	0.53
40:R:73:GLY:O	40:R:74:ARG:NH1	2.36	0.53
44:V:106:VAL:HG12	44:V:112:MET:HB3	1.90	0.53
6:x:404:GLN:HE21	6:x:408:ARG:HH12	1.54	0.53
9:5:113:A:H1'	32:N:50:ARG:HA	1.91	0.53
9:5:2889:G:OP1	40:R:75:HIS:ND1	2.30	0.53
21:h:36:VAL:HG21	46:X:79:PHE:HB2	1.90	0.53
22:H:26:ILE:HD12	22:H:35:ARG:HH11	1.72	0.53
31:m:110:CYS:SG	31:m:111:ARG:N	2.82	0.53
46:X:110:LYS:HE2	46:X:121:VAL:HB	1.90	0.53
48:Y:8:THR:OG1	48:Y:17:ARG:NH1	2.41	0.53
6:x:47:LYS:H	6:x:47:LYS:CE	2.21	0.53
9:5:751:G:N2	9:5:752:G:O6	2.41	0.53
9:5:2611:A:H2'	9:5:2612:G:H8	1.74	0.53
9:5:2906:G:H2'	9:5:2907:G:C8	2.44	0.53
9:5:2906:G:H2'	9:5:2907:G:H8	1.74	0.53
9:5:4598:C:H2'	9:5:4611:A:H61	1.73	0.53
14:D:83:LEU:HG	14:D:88:VAL:HB	1.89	0.53
22:H:162:GLN:NE2	22:H:181:VAL:HG23	2.23	0.53
24:I:171:TRP:HB2	24:I:178:ALA:HA	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:158:ILE:HD12	7:A:162:ASN:HD21	1.73	0.53
7:A:180:LEU:HD21	37:p:22:LEU:HB3	1.91	0.53
7:A:183:GLY:HA2	9:5:1613:A:H5''	1.90	0.53
9:5:1484:G:O2'	9:5:1486:C:OP2	2.26	0.53
17:f:78:HIS:O	17:f:83:MET:HB2	2.09	0.53
43:U:23:LEU:HB2	43:U:70:ILE:HB	1.90	0.53
52:t:180:ASP:O	52:t:184:VAL:HG23	2.08	0.53
6:x:246:ILE:HG13	6:x:272:PHE:O	2.09	0.53
9:5:1333:A:H2'	9:5:1334:A:H8	1.74	0.53
13:d:26:THR:OG1	13:d:85:ARG:NH1	2.37	0.53
20:G:57:TRP:HB3	20:G:61:ILE:CG2	2.39	0.53
32:N:142:ILE:O	32:N:148:THR:HG23	2.09	0.53
1:1:147:G:N2	1:1:150:G:OP2	2.35	0.53
1:1:196:C:H2'	1:1:197:G:C8	2.43	0.53
9:5:2710:C:H5'	40:R:39:GLN:NE2	2.24	0.53
14:D:64:ILE:HD12	14:D:109:LEU:HD22	1.91	0.53
20:G:104:PRO:HG3	20:G:194:VAL:HG12	1.90	0.53
35:o:12:CYS:HB3	35:o:15:CYS:HB2	1.90	0.53
36:P:8:PRO:HD3	36:P:149:ILE:HD13	1.91	0.53
9:5:18:C:H2'	9:5:19:G:H8	1.74	0.53
9:5:1172:C:N4	9:5:1173:G:O6	2.42	0.53
9:5:4930:C:OP1	16:E:262:GLN:N	2.40	0.53
20:G:174:CYS:SG	20:G:179:VAL:HG13	2.49	0.53
30:M:47:ARG:NH2	30:M:68:ALA:O	2.42	0.53
7:A:213:GLY:HA3	9:5:4544:A:H5''	1.91	0.52
9:5:115:C:O2'	9:5:275:C:O2'	2.25	0.52
9:5:1482:G:N7	28:L:188:ASN:ND2	2.57	0.52
9:5:2663:G:H4'	40:R:117:ARG:HH21	1.73	0.52
9:5:3732:A:H2'	9:5:3733:A:C8	2.44	0.52
9:5:4676:G:OP1	10:B:281:ASN:ND2	2.40	0.52
9:5:4870:G:H4'	9:5:4872:G:H4'	1.90	0.52
9:5:4941:G:OP1	16:E:215:LYS:NZ	2.38	0.52
9:5:5002:U:OP2	10:B:385:LYS:NZ	2.37	0.52
10:B:381:THR:HG23	10:B:384:GLU:H	1.72	0.52
14:D:226:TYR:OH	47:7:48:G:OP1	2.20	0.52
22:H:93:ARG:HD2	22:H:143:GLU:HB3	1.91	0.52
39:r:38:PHE:O	39:r:45:HIS:HE1	1.92	0.52
47:7:64:G:H2'	47:7:65:G:H8	1.74	0.52
9:5:909:A:H2'	9:5:910:G:H8	1.75	0.52
16:E:228:ILE:HG13	16:E:229:PHE:H	1.73	0.52
20:G:82:GLN:HG3	20:G:233:ILE:HG21	1.89	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:G:107:LYS:O	20:G:108:GLN:HG2	2.08	0.52
29:l:27:ILE:O	29:l:33:ASN:ND2	2.42	0.52
34:O:61:ARG:HA	34:O:70:PRO:HD2	1.89	0.52
9:5:109:G:OP2	28:L:74:ARG:NH2	2.43	0.52
9:5:454:U:O2'	9:5:455:C:O5'	2.27	0.52
9:5:959:G:N2	16:E:121:LEU:H	2.07	0.52
9:5:3723:A:H2'	9:5:3724:A:C8	2.44	0.52
9:5:4070:U:H2'	9:5:4071:U:C6	2.44	0.52
11:c:37:MET:HE3	11:c:42:LYS:HB2	1.90	0.52
26:J:112:HIS:HD2	26:J:126:TYR:H	1.57	0.52
9:5:1211:G:O2'	9:5:1212:G:OP1	2.24	0.52
9:5:1676:C:H41	9:5:4378:A:H5''	1.74	0.52
9:5:181:C:N3	9:5:256:G:N2	2.58	0.52
9:5:700:G:H2'	9:5:701:G:C8	2.45	0.52
9:5:1794:A:H5''	9:5:4214:A:H61	1.74	0.52
9:5:2318:G:N2	9:5:2321:G:OP2	2.29	0.52
10:B:31:SER:O	10:B:348:ARG:NH1	2.42	0.52
26:J:107:PHE:O	26:J:130:PHE:N	2.42	0.52
41:S:69:GLU:HG2	41:S:101:THR:HG22	1.91	0.52
50:Z:89:ILE:HD11	50:Z:117:LYS:HB3	1.90	0.52
6:x:69:LEU:HB3	6:x:74:MET:HE1	1.92	0.52
7:A:21:LYS:HG2	9:5:1541:C:H5''	1.90	0.52
7:A:64:ARG:HB3	7:A:71:LYS:HE3	1.90	0.52
9:5:974:C:H2'	9:5:975:C:C6	2.44	0.52
9:5:1397:A:O2'	9:5:1467:C:O2'	2.27	0.52
9:5:1683:U:OP1	51:a:44:ASN:ND2	2.41	0.52
9:5:4888:U:O2'	9:5:4889:G:O5'	2.24	0.52
12:C:211:TYR:HE1	12:C:229:LEU:HB3	1.75	0.52
42:T:143:THR:OG1	42:T:146:LYS:O	2.28	0.52
9:5:1238:A:H4'	9:5:1239:C:OP1	2.08	0.52
21:h:106:LYS:HG2	21:h:110:LYS:HE2	1.90	0.52
31:m:118:THR:O	31:m:119:ASN:ND2	2.42	0.52
4:u:6:MET:HA	4:u:10:LYS:HD2	1.91	0.52
9:5:3893:C:H2'	9:5:3894:A:H8	1.75	0.52
12:C:332:ALA:HA	12:C:335:MET:HB2	1.91	0.52
9:5:701:G:O2'	15:e:7:LEU:O	2.27	0.52
9:5:4969:C:H2'	9:5:4970:C:H6	1.75	0.52
12:C:25:PRO:HB2	12:C:27:VAL:HG12	1.91	0.52
12:C:36:ILE:HD13	12:C:122:TYR:HD2	1.75	0.52
18:F:98:ARG:HD2	18:F:141:TYR:HA	1.90	0.52
40:R:139:MET:HE2	40:R:143:HIS:HE2	1.75	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:271:C:H2'	9:5:272:U:C6	2.44	0.52
9:5:2899:C:OP1	40:R:108:ARG:NH2	2.43	0.52
9:5:4763:U:O2'	22:H:43:VAL:O	2.28	0.52
11:c:38:ILE:HD11	11:c:46:VAL:HG21	1.90	0.52
21:h:104:THR:O	21:h:108:GLN:NE2	2.43	0.52
22:H:162:GLN:HE21	22:H:181:VAL:H	1.57	0.52
26:J:52:LYS:HA	26:J:67:LYS:HA	1.92	0.52
27:k:35:LYS:HG2	27:k:44:THR:HG23	1.91	0.52
40:R:3:MET:HE2	40:R:3:MET:HA	1.91	0.52
47:7:3:C:H2'	47:7:4:U:C6	2.45	0.52
1:1:195:U:O2'	2:q:74:ARG:NH2	2.33	0.51
9:5:20:U:OP2	49:8:36:G:N2	2.43	0.51
9:5:125:C:H2'	9:5:126:C:H6	1.74	0.51
9:5:1802:A:O2'	42:T:108:ARG:NH2	2.43	0.51
38:Q:85:THR:HG21	38:Q:104:ARG:HH11	1.75	0.51
9:5:2029:A:H2'	9:5:2030:A:H8	1.74	0.51
9:5:2067:C:H5''	17:f:78:HIS:CE1	2.46	0.51
9:5:4123:C:H1'	50:Z:135:ARG:HB3	1.92	0.51
12:C:239:LYS:O	12:C:248:ARG:NH1	2.44	0.51
49:8:88:A:H2'	49:8:89:U:C6	2.46	0.51
9:5:1551:C:H2'	9:5:1552:G:O4'	2.10	0.51
9:5:2555:G:H2'	9:5:2556:G:H8	1.76	0.51
9:5:3610:A:H2'	9:5:3611:A:C8	2.44	0.51
10:B:92:TYR:OH	10:B:182:GLU:OE1	2.28	0.51
42:T:18:PRO:HG2	42:T:21:LYS:HB2	1.93	0.51
42:T:54:HIS:CE1	42:T:55:LYS:HG2	2.46	0.51
1:1:204:G:H2'	1:1:205:A:H8	1.74	0.51
9:5:1457:G:O2'	38:Q:75:ARG:NH2	2.43	0.51
9:5:2028:C:H2'	9:5:2029:A:H8	1.75	0.51
9:5:2863:G:O2'	40:R:82:LYS:O	2.25	0.51
9:5:3896:C:H1'	10:B:268:ARG:NH2	2.26	0.51
9:5:4074:C:H2'	9:5:4075:U:H6	1.75	0.51
10:B:286:LYS:HD3	10:B:365:LEU:HD12	1.92	0.51
26:J:55:TYR:HA	26:J:64:ARG:HG2	1.92	0.51
9:5:1604:G:H2'	9:5:1605:G:C8	2.45	0.51
9:5:2520:C:H1'	9:5:2640:G:H21	1.74	0.51
9:5:2623:A:H2'	9:5:2624:G:C8	2.45	0.51
9:5:4862:G:H2'	9:5:4863:G:H8	1.75	0.51
21:h:99:GLU:HB3	32:N:149:GLN:OE1	2.10	0.51
44:V:16:ILE:HB	44:V:88:TYR:HB2	1.93	0.51
1:1:188:G:H2'	1:1:189:C:C6	2.46	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:3806:G:O6	9:5:3807:A:N6	2.43	0.51
1:1:170:C:H41	5:v:160:ARG:NH2	2.09	0.51
8:b:47:LYS:HA	8:b:50:ASN:ND2	2.26	0.51
9:5:91:G:H5'	9:5:92:C:H5''	1.93	0.51
9:5:664:G:N2	9:5:667:A:N1	2.59	0.51
9:5:1358:G:H4'	12:C:114:ARG:NH2	2.26	0.51
9:5:2587:A:O2'	9:5:2588:C:O4'	2.27	0.51
9:5:4704:C:H2'	9:5:4705:A:H8	1.76	0.51
9:5:5060:A:O2'	9:5:5061:A:OP1	2.26	0.51
26:J:14:GLU:OE2	26:J:16:ARG:NH2	2.44	0.51
36:P:94:MET:HE1	36:P:146:ILE:HB	1.92	0.51
43:U:105:ASN:OD1	43:U:113:ARG:NH2	2.44	0.51
1:1:129:C:C5	1:1:174:G:H2'	2.46	0.51
7:A:128:ARG:HA	7:A:169:VAL:HG21	1.92	0.51
9:5:705:G:H4'	9:5:1299:G:H5'	1.93	0.51
9:5:982:U:C4	16:E:67:ARG:HD2	2.46	0.51
9:5:1918:U:O4'	9:5:2065:G:N2	2.44	0.51
9:5:4991:U:H2'	9:5:4992:G:C8	2.46	0.51
23:i:10:GLY:HA2	28:L:189:ALA:HB2	1.92	0.51
26:J:83:LEU:HD11	26:J:132:VAL:HG22	1.92	0.51
38:Q:176:ARG:HA	38:Q:180:ARG:HD2	1.93	0.51
1:1:142:U:H3	1:1:155:G:H1	1.58	0.51
5:v:80:PHE:CE1	5:v:139:MET:HE3	2.44	0.51
7:A:40:TYR:HD2	7:A:93:LYS:HB2	1.75	0.51
9:5:3:C:H2'	9:5:4:G:H8	1.76	0.51
9:5:1177:U:H2'	9:5:1178:G:C8	2.46	0.51
9:5:4392:G:N2	9:5:4395:U:O2	2.42	0.51
9:5:4967:A:H2'	9:5:4968:A:C8	2.46	0.51
24:I:79:SER:HB2	24:I:147:HIS:HD2	1.76	0.51
5:v:198:ARG:HB3	5:v:207:ALA:HB2	1.93	0.51
6:x:322:LEU:HG	6:x:435:GLY:HA2	1.94	0.51
9:5:7:C:H42	49:8:149:G:H1	1.58	0.51
9:5:1293:G:O2'	9:5:1294:A:O4'	2.24	0.51
9:5:2029:A:H2'	9:5:2030:A:C8	2.46	0.51
9:5:2811:G:H22	9:5:2813:A:H3'	1.75	0.51
45:W:4:GLU:O	45:W:13:ILE:N	2.39	0.51
47:7:57:C:H2'	47:7:58:A:H8	1.75	0.51
49:8:77:A:H2'	49:8:78:G:O4'	2.10	0.51
9:5:1499:C:OP1	38:Q:150:ARG:NH2	2.45	0.50
9:5:2309:G:O2'	49:8:18:U:O2	2.28	0.50
12:C:60:HIS:HA	12:C:92:PHE:HE1	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:P:123:PRO:HG3	49:8:14:U:H5''	1.93	0.50
1:1:151:C:H2'	1:1:152:G:C8	2.46	0.50
9:5:370:U:O2'	25:j:16:HIS:ND1	2.34	0.50
9:5:2080:U:H2'	9:5:2081:C:C6	2.46	0.50
9:5:2576:G:P	50:Z:48:ARG:HH12	2.34	0.50
14:D:270:LYS:HD3	47:7:109:U:OP1	2.11	0.50
23:i:80:HIS:CE1	23:i:84:LYS:HD2	2.46	0.50
35:o:23:VAL:HG12	35:o:70:LEU:HG	1.91	0.50
35:o:97:LYS:O	35:o:98:LYS:HG2	2.11	0.50
6:x:459:ASN:HD22	6:x:480:LEU:HD22	1.77	0.50
9:5:281:U:H2'	9:5:282:C:H6	1.75	0.50
9:5:1518:A:H61	28:L:19:GLN:HE22	1.59	0.50
9:5:3689:G:O2'	9:5:3818:U:OP2	2.24	0.50
9:5:4717:A:H4'	10:B:20:LYS:HD3	1.94	0.50
16:E:159:VAL:HG11	16:E:253:ILE:HD11	1.93	0.50
28:L:46:ILE:O	28:L:46:ILE:HG13	2.11	0.50
46:X:129:ARG:NH2	46:X:133:GLU:OE1	2.44	0.50
5:v:69:SER:O	5:v:73:HIS:ND1	2.30	0.50
9:5:1655:C:OP2	51:a:26:ARG:NH1	2.45	0.50
9:5:2049:G:HO2'	9:5:3884:U:HO2'	1.59	0.50
9:5:2415:U:H2'	9:5:2416:G:C8	2.46	0.50
9:5:4974:C:H42	9:5:4984:C:N4	2.06	0.50
14:D:60:ILE:HB	14:D:80:ALA:HB2	1.92	0.50
44:V:107:ASN:OD1	44:V:111:GLU:N	2.45	0.50
6:x:110:GLN:HG3	6:x:193:GLY:HA3	1.94	0.50
9:5:280:G:OP2	32:N:44:ARG:NH1	2.32	0.50
9:5:448:G:H2'	9:5:449:C:O4'	2.11	0.50
9:5:957:G:H4'	9:5:958:G:O5'	2.10	0.50
9:5:1321:G:O4'	9:5:1891:A:N6	2.45	0.50
9:5:2844:A:N6	9:5:3839:G:O2'	2.44	0.50
9:5:3619:G:H22	9:5:3624:A:H1'	1.76	0.50
9:5:4704:C:H2'	9:5:4705:A:C8	2.47	0.50
9:5:4925:U:O2	9:5:4926:C:N4	2.44	0.50
9:5:4997:G:OP1	13:d:83:ARG:NE	2.32	0.50
16:E:175:LEU:HD22	16:E:179:ARG:HD3	1.94	0.50
18:F:128:ASN:H	18:F:131:SER:HB3	1.75	0.50
18:F:129:LYS:HB2	42:T:133:ALA:HB3	1.94	0.50
20:G:29:ASN:HD21	20:G:31:LEU:HD12	1.76	0.50
32:N:187:SER:H	32:N:190:ALA:HB3	1.76	0.50
41:S:84:TYR:HE1	41:S:93:MET:HE3	1.77	0.50
52:t:177:GLU:HG3	52:t:179:LYS:HG2	1.92	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:q:107:TYR:CD1	2:q:111:MET:HE1	2.46	0.50
9:5:1278:C:N4	9:5:1279:A:N3	2.59	0.50
9:5:1351:G:O6	38:Q:55:ARG:NH2	2.45	0.50
9:5:1351:G:O4'	12:C:119:GLN:NE2	2.44	0.50
9:5:1362:G:OP1	28:L:39:ARG:NH1	2.39	0.50
9:5:3944:G:H2'	9:5:3945:A:H8	1.74	0.50
9:5:4293:U:OP2	9:5:4329:G:O2'	2.28	0.50
22:H:21:LYS:HB3	22:H:24:THR:HB	1.94	0.50
28:L:182:LEU:HD21	51:a:128:PHE:HD1	1.76	0.50
52:t:184:VAL:HA	52:t:210:ILE:HD11	1.92	0.50
1:1:130:A:H2'	1:1:131:A:H8	1.76	0.50
9:5:3723:A:H2'	9:5:3724:A:H8	1.76	0.50
9:5:3870:C:H2'	9:5:3871:A:H8	1.76	0.50
20:G:39:PHE:CD1	20:G:47:PRO:HD3	2.46	0.50
24:I:189:ARG:NH2	24:I:199:TYR:OH	2.44	0.50
1:1:141:C:N3	1:1:157:A:N6	2.59	0.50
1:1:219:C:H2'	1:1:220:C:C6	2.46	0.50
2:q:14:ARG:O	2:q:85:GLN:NE2	2.45	0.50
5:v:143:GLN:O	5:v:146:ASN:ND2	2.44	0.50
9:5:2395:A:O2'	9:5:2806:A:H1'	2.11	0.50
9:5:2734:U:H2'	9:5:2735:G:C8	2.47	0.50
9:5:3726:A:N6	9:5:4359:U:O2'	2.44	0.50
9:5:4708:A:C2	9:5:4709:U:H5'	2.47	0.50
18:F:88:GLU:HB3	42:T:135:PRO:HB3	1.94	0.50
21:h:89:ARG:HD3	49:8:36:G:C5	2.46	0.50
22:H:106:GLN:HB3	22:H:111:LEU:HB3	1.93	0.50
30:M:17:PHE:CE1	30:M:54:CYS:HA	2.47	0.50
41:S:28:TYR:CD1	42:T:149:GLU:HB3	2.47	0.50
47:7:82:G:H2'	47:7:83:A:C8	2.47	0.50
9:5:657:C:H2'	9:5:658:C:C6	2.47	0.49
9:5:2447:U:H1'	9:5:2744:A:H2	1.77	0.49
9:5:4354:U:H3	51:a:60:HIS:CE1	2.30	0.49
21:h:48:ARG:NH2	49:8:63:U:OP1	2.39	0.49
22:H:97:ALA:HA	31:m:78:ILE:HD11	1.94	0.49
32:N:190:ALA:HA	32:N:193:ARG:CZ	2.42	0.49
38:Q:49:LYS:O	38:Q:53:MET:HG3	2.12	0.49
1:1:209:G:H2'	1:1:210:G:C8	2.46	0.49
6:x:48:LEU:HB3	6:x:86:LEU:HD11	1.95	0.49
9:5:327:U:O2'	23:i:30:ARG:NH1	2.43	0.49
9:5:710:G:H2'	9:5:711:A:H8	1.77	0.49
9:5:729:G:OP2	18:F:78:ARG:NE	2.43	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:2407:G:H2'	29:l:13:LEU:HD22	1.94	0.49
9:5:2848:G:O2'	9:5:3838:U:O4	2.24	0.49
9:5:3729:U:H2'	9:5:3730:U:C6	2.47	0.49
14:D:259:ARG:HG3	14:D:260:GLU:N	2.27	0.49
16:E:65:TYR:O	16:E:66:LYS:HG2	2.11	0.49
52:t:181:ILE:HG22	52:t:192:ARG:HD3	1.94	0.49
9:5:1198:G:H2'	9:5:1199:G:H8	1.76	0.49
9:5:2878:G:OP2	9:5:2879:A:O2'	2.26	0.49
9:5:2897:G:H4'	40:R:101:ILE:HD13	1.93	0.49
18:F:181:LEU:HB3	18:F:186:ILE:HB	1.92	0.49
22:H:66:GLU:O	22:H:69:THR:OG1	2.30	0.49
35:o:77:CYS:SG	35:o:79:SER:OG	2.62	0.49
39:r:61:VAL:HG22	39:r:81:THR:HG22	1.92	0.49
39:r:108:MET:O	39:r:112:ARG:HG2	2.13	0.49
1:l:95:U:H2'	1:l:96:A:C8	2.47	0.49
5:v:62:ILE:HD11	5:v:128:LEU:HD13	1.94	0.49
6:x:37:THR:HA	6:x:40:LEU:HD12	1.93	0.49
9:5:460:C:H2'	9:5:461:G:H8	1.76	0.49
9:5:944:A:H62	18:F:63:TYR:HE2	1.60	0.49
9:5:1098:G:H2'	9:5:1099:C:C6	2.47	0.49
9:5:4688:C:H2'	9:5:4689:U:C6	2.47	0.49
9:5:4933:C:H2'	9:5:4934:A:C8	2.46	0.49
12:C:177:TRP:CD1	12:C:181:LYS:HE3	2.47	0.49
14:D:259:ARG:HG3	14:D:260:GLU:H	1.77	0.49
2:q:66:LYS:HZ3	2:q:81:ARG:HE	1.60	0.49
7:A:20:VAL:HG12	7:A:23:ARG:HD2	1.94	0.49
9:5:658:C:H2'	9:5:659:G:C8	2.47	0.49
9:5:1733:G:N3	9:5:4214:A:H2'	2.27	0.49
9:5:4928:C:H5''	30:M:114:LYS:CD	2.39	0.49
1:l:250:U:O2'	1:l:251:G:O4'	2.25	0.49
9:5:1185:G:H21	14:D:278:ASP:CG	2.20	0.49
9:5:1352:C:H3'	38:Q:104:ARG:NH2	2.27	0.49
9:5:3783:A:H4'	9:5:3784:A:H5''	1.95	0.49
9:5:4274:A:H2'	9:5:4275:G:H8	1.77	0.49
9:5:4642:U:H2'	9:5:4643:G:H8	1.78	0.49
16:E:84:VAL:HG12	16:E:85:LEU:H	1.77	0.49
36:P:18:ARG:NH1	36:P:147:GLU:OE1	2.46	0.49
47:7:110:G:H2'	47:7:111:C:C6	2.47	0.49
9:5:1823:G:H5''	42:T:35:LYS:HE2	1.95	0.49
9:5:2079:G:H2'	9:5:2080:U:C6	2.48	0.49
9:5:2486:G:H2'	9:5:2487:G:C8	2.48	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:2635:U:H5'	40:R:55:VAL:HG21	1.95	0.49
9:5:2658:G:O2'	9:5:2675:G:N2	2.45	0.49
16:E:174:PRO:HG2	16:E:177:LEU:HD12	1.95	0.49
40:R:12:SER:OG	40:R:17:CYS:O	2.30	0.49
40:R:24:LEU:HA	40:R:50:ILE:HG22	1.94	0.49
52:t:172:ASP:HB3	52:t:200:LYS:NZ	2.27	0.49
6:x:384:ASP:HA	6:x:387:LEU:HD12	1.94	0.49
9:5:1769:G:H2'	9:5:1770:A:H8	1.78	0.49
24:I:49:CYS:SG	24:I:51:HIS:NE2	2.83	0.49
39:r:18:ILE:HD12	39:r:25:TYR:HB2	1.94	0.49
47:7:3:C:H2'	47:7:4:U:H6	1.77	0.49
9:5:422:C:H2'	9:5:423:G:C8	2.45	0.49
9:5:707:C:H2'	9:5:708:G:H8	1.78	0.49
9:5:1942:A:H2'	9:5:1943:A:C8	2.48	0.49
9:5:3871:A:H2'	9:5:3872:A:C8	2.48	0.49
9:5:3936:A:N6	9:5:4175:G:O6	2.46	0.49
9:5:4594:U:H2'	9:5:4595:G:C8	2.48	0.49
9:5:4748:U:O4	9:5:4952:G:O6	2.30	0.49
9:5:4949:G:N2	9:5:4950:U:H2'	2.27	0.49
14:D:65:ALA:HA	14:D:74:ILE:HA	1.95	0.49
14:D:76:CYS:SG	14:D:109:LEU:HD13	2.53	0.49
21:h:31:LEU:HB3	21:h:47:ILE:HG12	1.94	0.49
21:h:103:LYS:NZ	21:h:111:GLU:OE2	2.44	0.49
34:O:87:MET:HG2	34:O:87:MET:O	2.12	0.49
50:Z:88:ASP:OD1	50:Z:88:ASP:N	2.46	0.49
9:5:443:G:OP1	17:f:54:LYS:HB3	2.13	0.49
9:5:1855:G:O6	9:5:1880:G:N2	2.45	0.49
9:5:2253:A:H2'	9:5:2254:G:H4'	1.95	0.49
9:5:2753:G:H5'	50:Z:135:ARG:NH1	2.27	0.49
9:5:4738:C:H2'	9:5:4739:C:C6	2.48	0.49
30:M:105:THR:O	30:M:109:ARG:HG3	2.12	0.49
32:N:180:PHE:C	32:N:182:HIS:H	2.20	0.49
33:n:7:LYS:HE2	33:n:11:ARG:HH21	1.78	0.49
36:P:33:ALA:HA	36:P:36:ILE:HG22	1.95	0.49
47:7:64:G:H2'	47:7:65:G:C8	2.48	0.49
7:A:241:ARG:NH1	9:5:3659:G:OP1	2.46	0.48
9:5:1301:C:H5''	9:5:1302:U:H5	1.78	0.48
9:5:1333:A:H2'	9:5:1334:A:C8	2.48	0.48
21:h:9:LEU:HB3	21:h:60:VAL:HG11	1.93	0.48
32:N:68:ARG:NH1	32:N:124:ASP:O	2.36	0.48
6:x:413:SER:HB3	6:x:417:VAL:HG23	1.94	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:1456:C:O2'	38:Q:73:PRO:O	2.26	0.48
9:5:1822:U:H3'	9:5:1823:G:H8	1.79	0.48
9:5:2492:C:H2'	9:5:2493:G:C8	2.49	0.48
9:5:2597:G:H4'	19:g:43:LYS:HB3	1.96	0.48
24:I:52:MET:HB2	24:I:135:ILE:HB	1.95	0.48
25:j:64:MET:SD	25:j:67:LEU:HB3	2.53	0.48
40:R:21:LYS:NZ	40:R:55:VAL:HA	2.28	0.48
48:Y:22:PRO:O	48:Y:26:ARG:HG3	2.14	0.48
9:5:1646:A:O2'	25:j:49:TRP:O	2.28	0.48
9:5:1726:U:O4	9:5:1836:G:O6	2.31	0.48
9:5:1726:U:H5'	18:F:137:ILE:HD11	1.94	0.48
9:5:3890:A:N6	9:5:4571:A:O4'	2.47	0.48
9:5:5004:C:H2'	9:5:5005:G:O4'	2.13	0.48
40:R:38:ARG:C	40:R:40:GLN:H	2.20	0.48
2:q:107:TYR:O	2:q:111:MET:SD	2.70	0.48
8:b:38:LYS:HE2	9:5:1816:C:H4'	1.94	0.48
9:5:5019:A:H2'	9:5:5020:G:H8	1.79	0.48
12:C:166:GLU:O	12:C:170:LEU:HD23	2.13	0.48
14:D:288:LEU:O	14:D:292:GLU:HG2	2.14	0.48
30:M:11:ARG:HB3	30:M:27:ILE:HD12	1.95	0.48
48:Y:50:ARG:HG2	48:Y:51:LYS:H	1.78	0.48
50:Z:52:LYS:O	50:Z:65:ARG:NH2	2.45	0.48
9:5:163:A:H2'	9:5:164:G:H8	1.79	0.48
9:5:265:C:H4'	9:5:266:C:OP2	2.13	0.48
9:5:1431:C:H2'	9:5:1432:G:O4'	2.14	0.48
9:5:1434:G:H2'	9:5:1435:G:H8	1.77	0.48
9:5:1617:G:H1'	9:5:2513:A:N6	2.29	0.48
9:5:1669:A:H4'	9:5:1685:G:N2	2.27	0.48
6:x:288:GLN:HB3	6:x:289:PRO:HD3	1.94	0.48
6:x:332:MET:HE3	6:x:336:PHE:CZ	2.48	0.48
9:5:2589:C:H2'	9:5:2590:G:O4'	2.13	0.48
9:5:3904:G:HO2'	9:5:3905:A:P	2.35	0.48
9:5:4274:A:H2'	9:5:4275:G:C8	2.49	0.48
9:5:4923:C:H2'	9:5:4924:C:C6	2.49	0.48
9:5:5006:U:H4'	9:5:5007:A:H5'	1.94	0.48
19:g:64:LEU:HD23	19:g:67:LEU:HD12	1.94	0.48
48:Y:50:ARG:NH2	49:8:83:C:N3	2.61	0.48
49:8:107:C:H2'	49:8:108:A:C8	2.48	0.48
6:x:222:ASP:OD1	6:x:223:ALA:N	2.47	0.48
6:x:352:ILE:HG12	6:x:354:GLY:H	1.78	0.48
9:5:967:C:H5'	16:E:106:ARG:HH22	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:1407:C:O2'	9:5:1408:G:OP1	2.30	0.48
9:5:1516:G:O2'	28:L:18:TRP:NE1	2.37	0.48
9:5:2723:U:H2'	9:5:2724:G:C8	2.49	0.48
9:5:4871:C:H4'	9:5:4872:G:H5'	1.95	0.48
38:Q:25:LEU:O	38:Q:29:VAL:HG23	2.14	0.48
40:R:105:LEU:HD22	40:R:135:LYS:HG3	1.95	0.48
49:8:122:G:H21	49:8:128:C:N4	2.10	0.48
4:u:18:VAL:HG22	4:u:27:ARG:HB2	1.95	0.48
9:5:491:G:H1'	9:5:665:C:H42	1.79	0.48
9:5:1293:G:H2'	9:5:1294:A:C4	2.49	0.48
9:5:2386:U:H5''	40:R:24:LEU:HD12	1.96	0.48
9:5:2836:A:C2	9:5:3895:G:H4'	2.49	0.48
9:5:3595:U:H1'	40:R:114:LYS:HG2	1.95	0.48
9:5:4076:G:OP2	9:5:4163:U:N3	2.44	0.48
9:5:4704:C:H4'	22:H:129:ARG:HH21	1.78	0.48
9:5:4955:A:H2'	9:5:4956:A:C8	2.49	0.48
22:H:92:MET:CB	22:H:181:VAL:HA	2.43	0.48
26:J:35:ARG:HD2	26:J:123:ILE:HG13	1.95	0.48
26:J:95:ARG:H	26:J:98:ASN:HD22	1.61	0.48
30:M:5:ARG:HB3	30:M:57:LEU:HD11	1.95	0.48
34:O:46:ASN:OD1	34:O:49:ARG:HG3	2.13	0.48
41:S:74:ARG:O	41:S:76:LYS:NZ	2.46	0.48
47:7:58:A:H2'	47:7:59:G:H8	1.79	0.48
1:1:212:C:O2'	1:1:214:A:OP1	2.32	0.48
9:5:65:A:H61	9:5:75:G:H1'	1.77	0.48
9:5:1074:G:H2'	9:5:1075:G:C8	2.48	0.48
9:5:1079:C:N4	9:5:1080:C:H41	2.12	0.48
9:5:1440:U:H2'	9:5:1441:C:C6	2.49	0.48
9:5:1850:A:N3	9:5:2283:G:O2'	2.46	0.48
9:5:2400:G:N2	19:g:6:THR:HG22	2.29	0.48
9:5:2597:G:H5''	19:g:43:LYS:HB3	1.95	0.48
9:5:4188:U:H2'	9:5:4189:U:C6	2.49	0.48
9:5:4624:A:H2'	9:5:4625:C:C6	2.48	0.48
10:B:95:THR:HG22	10:B:97:ARG:H	1.77	0.48
17:f:45:LYS:HA	17:f:107:PRO:HG2	1.95	0.48
29:l:33:ASN:OD1	29:l:35:ILE:HG22	2.14	0.48
48:Y:10:ASP:OD1	48:Y:11:ARG:N	2.46	0.48
9:5:967:C:OP1	9:5:2254:G:N1	2.31	0.48
9:5:1238:A:N7	16:E:56:SER:OG	2.41	0.48
9:5:1338:G:H4'	9:5:1339:U:H6	1.79	0.48
9:5:1822:U:O2'	14:D:45:ASN:HB2	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:1912:G:H2'	9:5:1913:C:C6	2.48	0.48
16:E:170:LEU:HD11	16:E:182:LEU:HD12	1.96	0.48
21:h:117:ARG:HH12	28:L:129:ARG:HD2	1.79	0.48
44:V:57:VAL:HG21	44:V:122:ALA:HB3	1.95	0.48
51:a:76:ASP:N	51:a:114:LYS:O	2.47	0.48
52:t:177:GLU:CG	52:t:179:LYS:HG2	2.43	0.48
5:v:152:ARG:O	5:v:156:LEU:HG	2.14	0.47
9:5:7:C:H5''	32:N:41:ARG:NH2	2.29	0.47
9:5:65:A:N6	9:5:75:G:H1'	2.29	0.47
9:5:287:U:H2'	9:5:288:G:C8	2.49	0.47
9:5:1076:C:H42	9:5:1235:G:H22	1.62	0.47
9:5:1484:G:H1'	28:L:195:ARG:NH2	2.29	0.47
9:5:1645:C:H2'	9:5:1646:A:C8	2.49	0.47
9:5:2295:C:H2'	9:5:2296:G:H8	1.79	0.47
9:5:2778:G:N1	49:8:113:C:OP1	2.47	0.47
9:5:2836:A:H2	9:5:3895:G:H4'	1.78	0.47
10:B:163:LEU:HD22	10:B:180:LEU:HG	1.96	0.47
12:C:218:VAL:O	12:C:222:ARG:HG3	2.13	0.47
14:D:57:ASN:OD1	47:7:49:A:N6	2.47	0.47
19:g:86:CYS:O	19:g:90:ARG:HG2	2.14	0.47
6:x:107:VAL:HG23	6:x:219:TYR:HD1	1.79	0.47
9:5:907:C:H2'	9:5:908:G:C8	2.44	0.47
9:5:1237:C:H2'	18:F:53:TYR:CD2	2.48	0.47
9:5:2633:U:H2'	9:5:2634:C:C6	2.49	0.47
9:5:2809:G:O2'	9:5:4644:G:OP1	2.30	0.47
10:B:173:LEU:HD11	10:B:342:LYS:HB3	1.95	0.47
13:d:37:GLY:O	13:d:41:ARG:HG3	2.13	0.47
14:D:164:LYS:HG2	14:D:195:HIS:HE2	1.79	0.47
22:H:176:LEU:HD12	22:H:176:LEU:O	2.14	0.47
26:J:26:VAL:HG11	26:J:32:ARG:HB3	1.95	0.47
32:N:191:ALA:O	32:N:195:ARG:HD3	2.14	0.47
36:P:23:ARG:NH2	36:P:125:MET:SD	2.87	0.47
1:1:175:G:H5'	5:v:154:HIS:CD2	2.50	0.47
9:5:705:G:H2'	9:5:706:C:H6	1.79	0.47
9:5:741:C:H2'	9:5:742:G:C8	2.50	0.47
9:5:1486:C:H2'	9:5:1487:G:C8	2.50	0.47
9:5:1514:U:H2'	9:5:1515:A:H8	1.79	0.47
9:5:2362:U:H2'	9:5:2363:A:H8	1.80	0.47
9:5:2637:U:H2'	9:5:2719:C:H5	1.79	0.47
9:5:3738:G:O2'	9:5:4180:G:O2'	2.28	0.47
9:5:4069:U:O2'	9:5:4070:U:OP1	2.26	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:x:11:THR:HB	6:x:295:LEU:HG	1.96	0.47
6:x:459:ASN:OD1	6:x:481:GLN:HG2	2.14	0.47
7:A:147:ARG:HG2	7:A:157:VAL:HG22	1.94	0.47
9:5:1411:C:H2'	9:5:1412:G:C8	2.49	0.47
9:5:1450:C:H2'	9:5:1451:G:O4'	2.15	0.47
9:5:1548:G:O2'	9:5:2812:A:N3	2.44	0.47
9:5:1778:C:OP1	14:D:5:LYS:NZ	2.38	0.47
9:5:2411:C:H2'	9:5:2412:A:C8	2.49	0.47
9:5:2429:A:OP1	29:l:43:HIS:NE2	2.45	0.47
9:5:4740:G:H2'	9:5:4741:C:C6	2.49	0.47
14:D:64:ILE:HG13	14:D:105:LEU:HD21	1.96	0.47
16:E:266:TYR:OH	30:M:106:ASP:OD2	2.21	0.47
24:I:36:LEU:HD22	24:I:69:ARG:HD3	1.96	0.47
28:L:168:VAL:O	28:L:168:VAL:HG12	2.15	0.47
36:P:126:ARG:HB2	36:P:126:ARG:NH1	2.29	0.47
44:V:62:MET:HE3	44:V:76:VAL:HG12	1.97	0.47
9:5:68:U:OP1	32:N:178:HIS:ND1	2.36	0.47
9:5:3911:C:H2'	9:5:3912:U:H6	1.78	0.47
9:5:4937:C:H1'	16:E:181:PRO:HG3	1.96	0.47
38:Q:82:VAL:O	38:Q:102:ALA:HA	2.15	0.47
1:l:163:A:OP2	1:l:176:A:O2'	2.33	0.47
6:x:37:THR:O	6:x:41:GLU:HG3	2.15	0.47
9:5:226:G:OP2	48:Y:1:MET:N	2.37	0.47
9:5:1423:U:H2'	9:5:1424:G:H8	1.78	0.47
9:5:2652:G:N2	37:p:61:MET:SD	2.88	0.47
36:P:22:LEU:HD12	36:P:90:PHE:CD2	2.49	0.47
49:8:132:G:H2'	49:8:133:G:H8	1.80	0.47
51:a:36:GLY:O	51:a:41:HIS:HB2	2.15	0.47
6:x:47:LYS:H	6:x:47:LYS:HE3	1.79	0.47
9:5:268:G:H2'	9:5:269:G:C8	2.50	0.47
9:5:705:G:H2'	9:5:706:C:C6	2.50	0.47
9:5:712:C:H42	9:5:956:A:H61	1.63	0.47
9:5:1098:G:H2'	9:5:1099:C:H6	1.79	0.47
9:5:1207:C:H2'	9:5:1208:G:H8	1.80	0.47
9:5:2263:A:H1'	9:5:2264:C:H5	1.80	0.47
9:5:2295:C:O2'	12:C:45:ARG:NH2	2.48	0.47
9:5:2611:A:H2'	9:5:2612:G:C8	2.49	0.47
9:5:3589:G:H2'	9:5:3590:G:C8	2.49	0.47
9:5:3893:C:H2'	9:5:3894:A:C8	2.50	0.47
9:5:3945:A:H2'	9:5:3946:G:C8	2.50	0.47
9:5:4413:C:H41	9:5:4429:C:N4	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:4880:C:N4	9:5:4881:U:O4	2.47	0.47
17:f:33:VAL:HG23	17:f:38:GLU:HB2	1.96	0.47
17:f:50:VAL:HA	17:f:69:VAL:HG12	1.97	0.47
51:a:3:SER:HA	51:a:6:ARG:HH11	1.79	0.47
1:1:168:G:O2'	1:1:170:C:OP2	2.32	0.47
6:x:332:MET:HE1	6:x:427:PHE:CD2	2.49	0.47
9:5:2758:G:H2'	9:5:2759:G:C4	2.50	0.47
9:5:3708:C:H2'	9:5:3709:U:O2	2.15	0.47
9:5:3903:A:H2'	9:5:3904:G:H8	1.80	0.47
9:5:4220:A:OP2	42:T:2:THR:N	2.47	0.47
10:B:184:GLN:NE2	10:B:185:VAL:O	2.47	0.47
11:c:51:ASN:HD21	11:c:78:ASN:CG	2.23	0.47
7:A:180:LEU:HD22	37:p:18:TYR:HB3	1.96	0.47
9:5:1315:C:H2'	9:5:1316:G:H8	1.80	0.47
9:5:1398:A:H5'	9:5:1420:A:N1	2.29	0.47
9:5:2490:U:H3'	9:5:2491:C:C6	2.50	0.47
9:5:2664:G:H4'	9:5:2677:G:H4'	1.97	0.47
9:5:3786:U:OP1	9:5:4550:G:O2'	2.32	0.47
9:5:4323:A:H4'	14:D:176:SER:OG	2.15	0.47
9:5:4627:U:HO2'	10:B:55:HIS:HE2	1.51	0.47
9:5:4719:G:O2'	9:5:4720:C:O5'	2.30	0.47
38:Q:22:ASP:O	38:Q:26:ARG:HG3	2.15	0.47
9:5:664:G:N2	9:5:665:C:H41	2.13	0.47
9:5:1339:U:H2'	9:5:1340:C:C6	2.50	0.47
9:5:4134:C:H2'	9:5:4135:G:C8	2.47	0.47
9:5:4578:G:H2'	9:5:4579:U:C6	2.50	0.47
18:F:128:ASN:O	18:F:132:ILE:HG12	2.15	0.47
20:G:59:ARG:HG2	20:G:62:ARG:NH2	2.29	0.47
52:t:171:VAL:HA	52:t:197:ARG:HD2	1.96	0.47
1:1:194:G:H1	1:1:205:A:N6	2.10	0.46
3:s:77:UNK:HA	9:5:2794:C:H42	1.80	0.46
9:5:197:A:H2'	9:5:198:A:C8	2.49	0.46
9:5:218:A:H4'	9:5:219:G:O4'	2.14	0.46
9:5:1541:C:H1'	9:5:2448:G:H21	1.80	0.46
9:5:2492:C:H2'	9:5:2493:G:H8	1.79	0.46
9:5:2521:G:H2'	9:5:2522:G:H8	1.80	0.46
9:5:3633:C:H2'	9:5:3634:G:C8	2.50	0.46
9:5:4712:C:H2'	9:5:4713:G:H8	1.80	0.46
9:5:5061:A:H4'	9:5:5062:G:H5''	1.97	0.46
10:B:56:ILE:HD13	10:B:285:TYR:HD2	1.78	0.46
15:e:38:PRO:HB3	15:e:43:ASN:ND2	2.30	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:G:180:PRO:HG3	20:G:219:VAL:HB	1.97	0.46
24:I:83:ASP:OD1	24:I:83:ASP:N	2.47	0.46
45:W:47:ARG:HE	45:W:54:LEU:HB3	1.80	0.46
46:X:73:HIS:HA	46:X:76:ILE:HD12	1.97	0.46
49:8:124:U:H4'	49:8:125:C:O5'	2.13	0.46
50:Z:95:VAL:HG21	50:Z:113:GLU:HG2	1.96	0.46
9:5:1757:U:N3	9:5:1758:G:N7	2.63	0.46
9:5:2374:A:H2'	9:5:2375:A:H8	1.78	0.46
9:5:2859:G:N2	9:5:3837:C:O2	2.49	0.46
9:5:4304:A:OP1	42:T:81:LYS:NZ	2.37	0.46
22:H:90:TYR:HB2	22:H:146:LEU:HB2	1.98	0.46
27:k:24:LYS:HD3	27:k:69:LEU:HD21	1.96	0.46
48:Y:71:VAL:HG21	48:Y:96:HIS:CE1	2.51	0.46
9:5:1695:U:H2'	9:5:1696:C:O4'	2.15	0.46
9:5:2091:C:O2	9:5:2092:G:H2'	2.16	0.46
9:5:2485:U:H2'	9:5:2486:G:C8	2.50	0.46
9:5:2902:G:H2'	9:5:3592:G:H22	1.81	0.46
9:5:4080:C:H2'	9:5:4081:G:H8	1.80	0.46
9:5:4154:G:H2'	9:5:4155:C:H6	1.80	0.46
9:5:4888:U:N3	9:5:4889:G:N7	2.63	0.46
19:g:82:MET:HE3	19:g:87:VAL:HG22	1.97	0.46
20:G:184:LEU:HD21	20:G:189:ARG:HD3	1.97	0.46
34:O:75:ALA:HB3	34:O:78:ARG:HG2	1.98	0.46
40:R:10:LEU:HD21	40:R:38:ARG:N	2.30	0.46
47:7:108:G:H2'	47:7:109:U:C6	2.50	0.46
48:Y:74:TYR:CD2	48:Y:77:LYS:HG2	2.51	0.46
6:x:273:ILE:HG13	6:x:283:GLU:HB2	1.96	0.46
9:5:2755:A:OP2	50:Z:65:ARG:NH1	2.43	0.46
9:5:3916:G:H2'	9:5:3917:A:C8	2.50	0.46
9:5:4177:C:H2'	9:5:4178:A:H8	1.79	0.46
12:C:145:GLU:CD	12:C:145:GLU:H	2.23	0.46
26:J:142:ALA:HB2	26:J:151:ILE:HG23	1.98	0.46
36:P:16:LYS:HG2	36:P:149:ILE:HG12	1.96	0.46
1:1:220:C:H2'	1:1:221:C:C6	2.51	0.46
9:5:6:C:H2'	9:5:7:C:C6	2.50	0.46
9:5:1866:U:OP1	24:I:4:ARG:NH2	2.36	0.46
9:5:1942:A:H2'	9:5:1943:A:H8	1.79	0.46
9:5:2263:A:H5''	39:r:39:ARG:NH1	2.31	0.46
9:5:3700:C:O2'	9:5:3774:A:H1'	2.15	0.46
9:5:3774:A:H2'	9:5:3775:A:N3	2.31	0.46
9:5:4333:C:O2	42:T:8:ARG:NH1	2.49	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:4627:U:HO2'	10:B:55:HIS:CD2	2.32	0.46
18:F:107:VAL:HG13	18:F:138:VAL:HG12	1.98	0.46
36:P:31:GLU:HG3	36:P:60:PHE:CD1	2.50	0.46
40:R:95:TRP:HE3	40:R:98:ARG:HH21	1.63	0.46
49:8:67:U:H2'	49:8:68:G:H8	1.79	0.46
1:1:129:C:H2'	1:1:130:A:H8	1.80	0.46
1:1:219:C:H2'	1:1:220:C:H6	1.81	0.46
9:5:122:U:H2'	9:5:123:C:C6	2.51	0.46
9:5:371:A:O2'	9:5:372:A:O4'	2.27	0.46
9:5:396:A:H2'	9:5:397:G:C8	2.50	0.46
9:5:1089:G:H2'	9:5:1090:G:H8	1.81	0.46
9:5:1307:A:H2'	9:5:1308:C:C6	2.51	0.46
9:5:1870:C:H2'	9:5:1871:A:H8	1.81	0.46
9:5:2102:G:H2'	9:5:2103:G:C8	2.51	0.46
9:5:2673:G:O3'	11:c:30:GLY:HA2	2.14	0.46
9:5:3722:G:H2'	9:5:3723:A:C8	2.50	0.46
9:5:4635:A:O2'	9:5:4637:G:OP1	2.33	0.46
9:5:4966:A:H2'	9:5:4967:A:C8	2.51	0.46
9:5:5046:U:H2'	9:5:5050:C:H41	1.81	0.46
9:5:5061:A:C4'	9:5:5062:G:H5''	2.45	0.46
22:H:31:ARG:HH11	22:H:87:GLY:HA3	1.81	0.46
24:I:49:CYS:HG	24:I:168:SER:HG	1.61	0.46
30:M:10:GLY:HA2	30:M:64:PHE:HE1	1.81	0.46
52:t:185:MET:HE3	52:t:192:ARG:HH21	1.81	0.46
9:5:222:C:H2'	9:5:223:G:O4'	2.15	0.46
9:5:676:C:H5'	39:r:99:LYS:HD2	1.98	0.46
9:5:1184:A:H2'	9:5:1185:G:H8	1.81	0.46
9:5:3633:C:H2'	9:5:3634:G:H8	1.79	0.46
9:5:3916:G:H2'	9:5:3917:A:H8	1.80	0.46
9:5:5022:U:N3	9:5:5025:C:N4	2.64	0.46
21:h:104:THR:HG23	21:h:107:GLN:H	1.80	0.46
31:m:108:VAL:HG13	31:m:109:ASN:OD1	2.16	0.46
38:Q:39:THR:OG1	38:Q:44:ASN:ND2	2.47	0.46
6:x:349:LEU:HD22	6:x:355:PHE:HB2	1.97	0.46
9:5:273:U:H2'	9:5:274:C:C6	2.51	0.46
9:5:297:U:O2'	32:N:179:LYS:O	2.24	0.46
9:5:732:A:H8	9:5:732:A:OP2	1.98	0.46
9:5:1753:G:H2'	9:5:1755:C:H5''	1.97	0.46
9:5:2844:A:O2'	9:5:4631:G:H4'	2.15	0.46
9:5:4637:G:H2'	9:5:4638:U:C6	2.51	0.46
9:5:4678:G:N2	9:5:4713:G:H1'	2.31	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:5005:G:H22	9:5:5041:G:H1'	1.80	0.46
10:B:171:LEU:HB3	10:B:173:LEU:HD23	1.97	0.46
6:x:165:GLU:HB3	6:x:171:ILE:HD11	1.97	0.46
9:5:187:U:H4'	9:5:188:G:OP2	2.16	0.46
9:5:983:C:H2'	9:5:984:C:O4'	2.16	0.46
9:5:1364:U:H5''	28:L:36:ARG:HH21	1.81	0.46
9:5:3920:U:H2'	9:5:3921:U:C6	2.51	0.46
9:5:4081:G:H2'	9:5:4082:G:C8	2.51	0.46
9:5:4192:A:H2'	9:5:4193:C:H6	1.81	0.46
9:5:4452:U:O2'	9:5:4453:C:H5'	2.16	0.46
9:5:4906:C:H2'	9:5:4907:G:C8	2.49	0.46
10:B:322:HIS:O	10:B:342:LYS:NZ	2.37	0.46
17:f:8:LYS:HB3	17:f:100:ARG:NH1	2.30	0.46
30:M:16:SER:HB2	30:M:56:GLN:HE21	1.81	0.46
6:x:374:LYS:O	6:x:377:THR:HB	2.16	0.46
7:A:3:ARG:HD3	9:5:1628:C:H42	1.81	0.46
9:5:703:G:N2	9:5:705:G:OP2	2.49	0.46
9:5:1507:C:H5'	12:C:114:ARG:HH11	1.80	0.46
9:5:2745:A:H2'	9:5:2746:A:C8	2.50	0.46
9:5:2901:G:O2'	9:5:2902:G:H5'	2.16	0.46
9:5:4153:C:H2'	9:5:4154:G:C8	2.50	0.46
10:B:40:PRO:O	10:B:42:HIS:ND1	2.40	0.46
19:g:88:ARG:HG2	50:Z:14:LEU:HB3	1.97	0.46
24:I:55:ASP:OD2	24:I:164:LYS:NZ	2.39	0.46
30:M:100:ARG:HA	30:M:103:LYS:HE2	1.98	0.46
30:M:100:ARG:HA	30:M:103:LYS:HG2	1.98	0.46
46:X:102:VAL:HA	46:X:134:LYS:HD2	1.97	0.46
6:x:131:LYS:HD3	6:x:184:PHE:HA	1.98	0.45
9:5:7:C:H2'	9:5:8:U:C6	2.50	0.45
9:5:20:U:P	49:8:36:G:H22	2.38	0.45
9:5:673:C:H2'	9:5:674:G:C8	2.51	0.45
9:5:1817:U:H2'	9:5:1818:G:O4'	2.16	0.45
9:5:2485:U:H3	9:5:2493:G:H1	1.64	0.45
9:5:2594:C:H2'	9:5:2595:C:C6	2.51	0.45
12:C:31:PRO:HD3	12:C:282:HIS:CD2	2.51	0.45
21:h:99:GLU:HA	21:h:102:LEU:HB2	1.98	0.45
28:L:88:LYS:HG3	28:L:89:LYS:HG3	1.98	0.45
30:M:5:ARG:NE	30:M:59:ASP:OD1	2.48	0.45
41:S:34:ALA:HB1	41:S:39:VAL:HB	1.96	0.45
49:8:108:A:N1	49:8:112:G:C6	2.84	0.45
1:1:104:C:H5''	1:1:105:G:OP2	2.15	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:x:17:LEU:HB2	6:x:31:MET:HG3	1.97	0.45
9:5:292:G:O6	32:N:181:HIS:ND1	2.44	0.45
9:5:722:G:O3'	12:C:347:HIS:ND1	2.48	0.45
9:5:1423:U:H2'	9:5:1424:G:C8	2.51	0.45
9:5:1458:C:H3'	9:5:1459:A:H8	1.80	0.45
9:5:1735:U:H2'	9:5:1736:A:H8	1.81	0.45
9:5:2078:C:H2'	9:5:2079:G:H8	1.81	0.45
9:5:2262:G:O2'	9:5:2263:A:OP1	2.31	0.45
9:5:2521:G:H2'	9:5:2522:G:C8	2.51	0.45
9:5:4635:A:H3'	9:5:4636:U:H4'	1.99	0.45
14:D:167:VAL:HG21	14:D:175:HIS:CD2	2.51	0.45
16:E:189:PHE:HA	17:f:106:TYR:HB2	1.96	0.45
27:k:3:ARG:HB2	27:k:43:TYR:CE1	2.52	0.45
38:Q:75:ARG:HA	38:Q:78:LYS:HE2	1.99	0.45
41:S:53:LYS:HE3	47:7:74:A:O3'	2.15	0.45
46:X:56:ARG:HG2	46:X:58:PRO:HD3	1.97	0.45
52:t:184:VAL:HG13	52:t:210:ILE:HG12	1.98	0.45
6:x:109:LEU:HD12	6:x:225:ILE:HD11	1.98	0.45
6:x:325:GLY:HA3	6:x:432:LYS:HG2	1.99	0.45
9:5:184:U:O4	9:5:253:G:O6	2.34	0.45
9:5:668:C:H2'	9:5:669:C:H6	1.81	0.45
9:5:693:C:O2'	9:5:694:C:OP1	2.30	0.45
9:5:1879:C:H2'	9:5:1880:G:O4'	2.15	0.45
9:5:2837:U:H5'	10:B:249:ARG:HB2	1.98	0.45
9:5:4088:C:H4'	9:5:4166:G:OP1	2.17	0.45
9:5:4192:A:H2'	9:5:4193:C:C6	2.51	0.45
9:5:4454:G:HO2'	9:5:4500:U:HO2'	1.64	0.45
9:5:4939:C:H5''	9:5:4941:G:H5''	1.99	0.45
16:E:172:THR:HG21	16:E:249:VAL:HG11	1.97	0.45
9:5:479:G:H2'	9:5:480:C:C6	2.52	0.45
9:5:1072:C:HO2'	9:5:1073:G:H8	1.64	0.45
9:5:1340:C:H2'	9:5:1341:U:C6	2.52	0.45
9:5:1811:G:H2'	9:5:1812:C:C6	2.52	0.45
9:5:2552:G:P	9:5:2553:A:H5''	2.57	0.45
9:5:4459:U:H2'	9:5:4460:U:C6	2.52	0.45
24:I:91:LEU:HD12	24:I:135:ILE:HG23	1.99	0.45
31:m:97:ARG:HH21	31:m:122:ARG:HB3	1.80	0.45
32:N:31:ARG:NH1	32:N:124:ASP:OD2	2.49	0.45
6:x:81:LYS:HA	6:x:84:VAL:HG12	1.99	0.45
9:5:5032:C:H2'	9:5:5033:G:O4'	2.17	0.45
14:D:21:ARG:HG3	14:D:24:ARG:NH2	2.32	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:j:27:TYR:HA	25:j:34:CYS:HA	1.97	0.45
38:Q:18:PRO:HG3	38:Q:29:VAL:HG21	1.97	0.45
41:S:41:LYS:HD2	41:S:61:ILE:HG13	1.99	0.45
44:V:121:VAL:O	44:V:140:ALA:N	2.36	0.45
47:7:57:C:H2'	47:7:58:A:C8	2.51	0.45
6:x:260:LEU:HA	6:x:263:VAL:HG22	1.98	0.45
9:5:375:G:OP2	25:j:52:LYS:NZ	2.41	0.45
9:5:1277:G:H2'	9:5:1278:C:C6	2.51	0.45
9:5:1494:U:H2'	9:5:1495:G:C8	2.51	0.45
9:5:2333:G:H5''	12:C:195:LYS:HE3	1.97	0.45
9:5:2550:G:H2'	9:5:2551:A:H8	1.82	0.45
9:5:3595:U:O2	40:R:114:LYS:HA	2.15	0.45
9:5:4990:C:H41	10:B:176:LYS:HB3	1.81	0.45
9:5:5025:C:H2'	9:5:5028:G:C8	2.52	0.45
28:L:79:GLU:HG2	28:L:104:ASN:HD22	1.82	0.45
9:5:318:A:H2'	9:5:319:A:C8	2.52	0.45
9:5:1475:G:H2'	9:5:1476:C:C6	2.52	0.45
9:5:1916:G:O6	17:f:18:LEU:HB2	2.17	0.45
9:5:2274:C:OP1	12:C:312:ARG:N	2.50	0.45
9:5:3766:A:OP2	9:5:3767:C:N4	2.49	0.45
9:5:4122:G:N2	50:Z:135:ARG:O	2.36	0.45
9:5:4261:C:H2'	9:5:4262:C:C6	2.52	0.45
9:5:4746:C:N4	9:5:4955:A:H61	2.15	0.45
9:5:4770:U:H2'	9:5:4772:C:H41	1.82	0.45
16:E:164:LEU:HD12	16:E:168:LEU:HD11	1.98	0.45
30:M:86:TRP:O	30:M:89:THR:OG1	2.34	0.45
1:1:209:G:H2'	1:1:210:G:H8	1.81	0.45
6:x:112:SER:HB2	6:x:220:VAL:HG12	1.99	0.45
9:5:56:A:H2'	9:5:57:G:C8	2.52	0.45
9:5:136:C:H5'	21:h:96:ASN:OD1	2.17	0.45
9:5:1380:G:H4'	9:5:1381:U:OP1	2.16	0.45
9:5:1479:G:H2'	9:5:1480:C:C6	2.52	0.45
9:5:1504:G:H2'	9:5:1505:C:C6	2.52	0.45
9:5:2632:U:H2'	9:5:2633:U:C5	2.52	0.45
10:B:130:PHE:HD1	10:B:133:TYR:HB3	1.80	0.45
17:f:93:PRO:HB2	17:f:95:LYS:HG2	1.99	0.45
18:F:153:ASN:ND2	18:F:193:ILE:HD13	2.32	0.45
50:Z:96:VAL:HG12	50:Z:110:ALA:HB1	1.98	0.45
52:t:171:VAL:HG12	52:t:193:ALA:HA	1.97	0.45
6:x:346:SER:HB3	6:x:365:GLU:OE1	2.17	0.45
6:x:353:PRO:HD2	6:x:483:MET:HE1	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:x:458:LEU:O	6:x:462:MET:HG2	2.17	0.45
7:A:208:GLU:HG3	9:5:1631:A:H2	1.82	0.45
8:b:35:VAL:HG13	42:T:66:ASN:HD22	1.82	0.45
9:5:81:C:H1'	9:5:1359:G:N2	2.26	0.45
9:5:1369:C:H5''	9:5:1370:G:H3'	1.98	0.45
9:5:2376:A:H2'	9:5:2377:C:C6	2.52	0.45
9:5:2674:A:OP2	11:c:31:TYR:N	2.50	0.45
9:5:3895:G:N2	10:B:268:ARG:HH21	2.15	0.45
9:5:4082:G:H2'	9:5:4083:U:C6	2.52	0.45
9:5:4301:U:OP2	9:5:4303:C:N4	2.50	0.45
14:D:155:THR:O	47:7:35:U:O2'	2.32	0.45
15:e:99:ILE:HG21	15:e:108:ARG:HG2	1.99	0.45
17:f:71:TRP:HB2	17:f:89:ARG:HH12	1.81	0.45
24:I:140:THR:OG1	24:I:141:LYS:N	2.50	0.45
30:M:118:MET:HE2	30:M:122:ILE:HD11	1.99	0.45
34:O:110:PRO:HA	34:O:113:ASP:CG	2.42	0.45
41:S:82:LEU:N	41:S:93:MET:O	2.43	0.45
44:V:83:ARG:HB2	44:V:102:ALA:HB3	1.99	0.45
9:5:58:G:H4'	9:5:59:A:H4'	1.98	0.45
9:5:163:A:H2'	9:5:164:G:C8	2.51	0.45
9:5:455:C:H2'	9:5:456:C:O4'	2.17	0.45
9:5:1802:A:N3	42:T:130:ARG:NH2	2.59	0.45
9:5:2022:C:H2'	9:5:2023:C:H6	1.82	0.45
9:5:2045:G:O6	9:5:3870:C:O2'	2.35	0.45
9:5:3592:G:H2'	9:5:3593:C:H4'	1.99	0.45
9:5:4091:G:H2'	9:5:4092:G:N9	2.32	0.45
9:5:4412:C:H2'	9:5:4413:C:O2	2.17	0.45
9:5:4453:C:H2'	9:5:4454:G:O4'	2.17	0.45
9:5:4586:G:O6	9:5:4717:A:N6	2.49	0.45
26:J:18:ARG:HB3	26:J:133:VAL:HG12	1.99	0.45
26:J:27:GLY:HA2	26:J:68:ILE:HA	1.99	0.45
29:l:21:ARG:HD3	49:8:52:A:O5'	2.17	0.45
40:R:10:LEU:HD11	40:R:38:ARG:HB3	1.98	0.45
7:A:156:LYS:HG2	7:A:158:ILE:HG23	1.99	0.44
9:5:66:A:O2'	9:5:326:C:O2	2.28	0.44
9:5:122:U:H2'	9:5:123:C:H6	1.81	0.44
9:5:158:A:N1	9:5:276:C:O2'	2.42	0.44
9:5:318:A:H2'	9:5:319:A:H8	1.81	0.44
9:5:711:A:H2'	9:5:712:C:C6	2.52	0.44
9:5:1912:G:N2	34:O:87:MET:HE2	2.27	0.44
9:5:2078:C:H2'	9:5:2079:G:C8	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:4071:U:H2'	9:5:4072:C:C6	2.51	0.44
9:5:4699:U:H4'	9:5:4700:A:OP1	2.17	0.44
12:C:325:MET:O	12:C:329:ASN:N	2.49	0.44
14:D:215:ASP:OD1	14:D:215:ASP:N	2.48	0.44
15:e:100:ALA:O	15:e:108:ARG:NH2	2.50	0.44
38:Q:58:ARG:HH11	38:Q:84:GLY:HA2	1.82	0.44
44:V:83:ARG:HE	44:V:100:ASP:CG	2.25	0.44
1:1:106:G:OP1	1:1:106:G:H4'	2.18	0.44
6:x:410:SER:OG	6:x:413:SER:OG	2.29	0.44
9:5:101:A:O2'	28:L:63:THR:OG1	2.35	0.44
9:5:246:G:H2'	9:5:247:G:H8	1.82	0.44
9:5:1502:G:H22	51:a:77:LYS:HE3	1.82	0.44
9:5:1569:U:H2'	9:5:1570:G:H8	1.80	0.44
9:5:2437:C:H42	46:X:89:LYS:NZ	2.14	0.44
9:5:2692:U:H2'	9:5:2693:G:O4'	2.17	0.44
9:5:3716:C:H3'	9:5:3735:G:H22	1.82	0.44
9:5:3911:C:H2'	9:5:3912:U:C6	2.52	0.44
12:C:144:ILE:O	12:C:147:VAL:HG22	2.18	0.44
26:J:18:ARG:O	26:J:75:ARG:NH1	2.50	0.44
26:J:41:GLU:HG2	26:J:47:THR:HA	1.99	0.44
30:M:57:LEU:HD23	30:M:57:LEU:H	1.81	0.44
36:P:29:THR:HG21	36:P:146:ILE:HD11	1.98	0.44
6:x:34:GLU:HA	6:x:37:THR:HB	1.99	0.44
6:x:135:ILE:HB	6:x:189:VAL:HG22	1.99	0.44
9:5:152:U:P	32:N:49:ARG:HH12	2.41	0.44
9:5:307:A:OP1	23:i:45:ARG:NH2	2.50	0.44
9:5:394:G:N2	9:5:397:G:OP2	2.37	0.44
9:5:713:C:H2'	9:5:714:G:H8	1.83	0.44
9:5:982:U:OP1	16:E:69:TYR:HE2	2.00	0.44
9:5:1210:C:N3	18:F:68:ARG:NH2	2.65	0.44
9:5:2079:G:H2'	9:5:2080:U:H6	1.82	0.44
9:5:2088:A:OP2	38:Q:38:ARG:NH2	2.49	0.44
9:5:2374:A:H2'	9:5:2375:A:C8	2.51	0.44
9:5:2617:G:P	40:R:64:ARG:HH21	2.40	0.44
9:5:3812:C:OP1	9:5:3813:A:O2'	2.31	0.44
12:C:33:ARG:HG3	12:C:122:TYR:OH	2.17	0.44
14:D:50:ARG:HA	14:D:145:TYR:H	1.82	0.44
14:D:63:GLN:HB3	14:D:77:ALA:HA	1.98	0.44
14:D:74:ILE:HD11	47:7:115:A:C1'	2.44	0.44
24:I:63:GLU:CD	24:I:63:GLU:H	2.25	0.44
34:O:55:LEU:HD23	34:O:58:LEU:HD12	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:P:54:LYS:HA	36:P:83:TRP:CD1	2.52	0.44
39:r:97:ILE:HG22	39:r:104:PRO:HA	1.99	0.44
41:S:164:LYS:O	41:S:165:PRO:C	2.61	0.44
49:8:33:G:H4'	49:8:34:U:C5	2.51	0.44
51:a:134:GLU:HG2	51:a:138:LYS:HE2	1.98	0.44
52:t:192:ARG:O	52:t:196:VAL:HG23	2.18	0.44
1:1:172:A:N1	1:1:173:A:N6	2.66	0.44
7:A:6:ARG:HH12	7:A:199:VAL:H	1.64	0.44
9:5:6:C:H5''	20:G:197:LYS:HB3	1.99	0.44
9:5:75:G:C5	28:L:102:ARG:HA	2.53	0.44
9:5:1196:G:H2'	9:5:1197:C:C6	2.53	0.44
9:5:2536:A:OP2	27:k:37:ARG:NH1	2.50	0.44
9:5:4208:U:H2'	9:5:4209:G:H8	1.83	0.44
9:5:4922:C:H2'	9:5:4923:C:H6	1.80	0.44
10:B:317:LEU:HD22	10:B:382:VAL:HG13	1.99	0.44
15:e:107:ASN:O	15:e:111:ILE:HG13	2.18	0.44
24:I:46:PHE:HB2	24:I:139:ARG:NH1	2.32	0.44
30:M:10:GLY:HA3	30:M:62:LEU:O	2.17	0.44
2:q:67:MET:SD	2:q:79:ARG:HD3	2.58	0.44
6:x:52:LEU:HG	6:x:82:GLU:HB3	1.97	0.44
6:x:303:LEU:O	6:x:307:VAL:HG23	2.18	0.44
6:x:462:MET:HB3	6:x:466:MET:HE3	1.97	0.44
9:5:405:U:H5'	48:Y:87:ARG:HH22	1.83	0.44
9:5:1442:C:H2'	9:5:1443:A:C8	2.53	0.44
9:5:4066:U:H2'	9:5:4067:U:C6	2.52	0.44
9:5:4208:U:H2'	9:5:4209:G:C8	2.52	0.44
9:5:4729:A:OP2	9:5:4735:G:N2	2.47	0.44
15:e:91:CYS:O	15:e:95:TYR:N	2.48	0.44
18:F:48:ARG:O	18:F:52:ILE:HG12	2.17	0.44
26:J:151:ILE:HG13	26:J:151:ILE:O	2.18	0.44
28:L:150:LEU:HD23	28:L:154:VAL:HG22	1.98	0.44
29:l:38:ASN:HD22	29:l:41:ARG:HD2	1.81	0.44
40:R:38:ARG:O	40:R:39:GLN:HB3	2.17	0.44
42:T:147:GLU:OE2	42:T:147:GLU:N	2.50	0.44
1:1:205:A:H2'	1:1:206:G:O4'	2.17	0.44
7:A:70:LYS:HG2	9:5:2594:C:H5''	1.99	0.44
9:5:6:C:H2'	9:5:7:C:H6	1.83	0.44
9:5:1849:U:H3'	28:L:5:ARG:NH2	2.33	0.44
9:5:2558:C:H2'	9:5:2559:G:C8	2.52	0.44
9:5:3880:G:H2'	9:5:3881:G:C8	2.53	0.44
9:5:4472:G:H2'	9:5:4473:A:H5'	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:4565:C:OP1	34:O:65:ASN:ND2	2.44	0.44
9:5:4642:U:H2'	9:5:4643:G:C8	2.52	0.44
14:D:115:MET:HG2	14:D:115:MET:O	2.18	0.44
15:e:92:ASN:HB3	15:e:120:ILE:HG12	1.99	0.44
22:H:2:LYS:HD3	30:M:33:GLN:HE22	1.83	0.44
28:L:63:THR:O	28:L:65:ARG:N	2.50	0.44
1:1:129:C:H2'	1:1:130:A:C8	2.52	0.44
6:x:41:GLU:C	6:x:43:ASP:N	2.76	0.44
7:A:27:ALA:HB2	7:A:58:LEU:HD21	2.00	0.44
9:5:86:U:H2'	9:5:87:A:H8	1.83	0.44
9:5:2028:C:H2'	9:5:2029:A:C8	2.53	0.44
9:5:2485:U:H2'	9:5:2486:G:H8	1.82	0.44
9:5:2533:C:OP1	46:X:139:ARG:NH1	2.51	0.44
9:5:3855:C:H2'	9:5:3856:A:H8	1.83	0.44
9:5:4237:C:O3'	9:5:4326:G:N2	2.51	0.44
9:5:4238:G:H2'	9:5:4239:A:C8	2.52	0.44
9:5:4667:C:OP1	10:B:224:LYS:NZ	2.51	0.44
11:c:54:ALA:HA	11:c:57:LYS:HE2	2.00	0.44
16:E:142:PRO:HA	16:E:160:PHE:HD2	1.82	0.44
18:F:98:ARG:HG2	18:F:98:ARG:HH11	1.83	0.44
41:S:76:LYS:HE2	41:S:78:PHE:HZ	1.82	0.44
49:8:130:C:H2'	49:8:131:G:C8	2.53	0.44
50:Z:6:LYS:HB2	50:Z:9:LYS:HG2	2.00	0.44
6:x:467:ASP:O	6:x:470:VAL:HG22	2.16	0.44
7:A:183:GLY:CA	9:5:1613:A:H5''	2.48	0.44
9:5:298:G:H5'	32:N:179:LYS:O	2.17	0.44
9:5:1721:G:H2'	9:5:1722:C:C6	2.53	0.44
9:5:1728:U:H2'	9:5:1729:A:H8	1.83	0.44
9:5:4601:U:H2'	9:5:4602:A:H8	1.83	0.44
9:5:4681:A:H2'	9:5:4682:U:O4'	2.18	0.44
9:5:4918:C:N4	9:5:4919:G:O6	2.50	0.44
9:5:4961:G:H2'	9:5:4962:C:C6	2.52	0.44
9:5:5010:U:H2'	9:5:5011:A:C8	2.53	0.44
9:5:5053:U:H3'	9:5:5054:C:O4'	2.18	0.44
10:B:161:ARG:HG2	10:B:184:GLN:HA	2.00	0.44
18:F:229:PHE:N	18:F:235:ALA:O	2.51	0.44
1:1:105:G:O6	1:1:249:G:O2'	2.32	0.44
7:A:117:GLU:CG	7:A:162:ASN:HB2	2.44	0.44
9:5:115:C:O2'	9:5:276:C:OP1	2.36	0.44
9:5:308:G:H3'	23:i:33:LEU:HB2	2.00	0.44
9:5:1759:G:H2'	9:5:1760:G:H8	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:2779:C:OP1	46:X:106:LYS:N	2.50	0.44
9:5:4617:G:OP1	10:B:62:ARG:HD2	2.17	0.44
12:C:331:TYR:HA	18:F:53:TYR:CE1	2.53	0.44
34:O:110:PRO:N	34:O:111:PRO:HD2	2.32	0.44
41:S:48:VAL:HG12	41:S:54:MET:HB2	1.99	0.44
49:8:71:A:H4'	49:8:72:A:O5'	2.18	0.44
5:v:230:ALA:O	5:v:234:ASN:ND2	2.40	0.43
7:A:52:PRO:HB3	9:5:2741:U:OP1	2.18	0.43
8:b:36:ASP:OD1	8:b:36:ASP:N	2.51	0.43
9:5:8:U:OP1	32:N:40:PRO:HG2	2.18	0.43
9:5:696:C:H5''	9:5:697:G:H5'	2.00	0.43
9:5:943:A:OP1	18:F:247:ARG:NH2	2.48	0.43
9:5:956:A:H3'	9:5:957:G:C5	2.52	0.43
9:5:1601:A:OP1	25:j:5:THR:OG1	2.29	0.43
9:5:1603:C:H2'	9:5:1604:G:H8	1.83	0.43
9:5:1874:A:H2'	9:5:1875:C:C6	2.52	0.43
9:5:2570:U:H2'	9:5:2571:C:C6	2.53	0.43
9:5:4731:G:O2'	9:5:4733:C:OP2	2.34	0.43
10:B:222:VAL:O	10:B:343:ARG:NH1	2.51	0.43
12:C:305:PRO:HB3	38:Q:38:ARG:HH12	1.83	0.43
16:E:111:TYR:CE1	39:r:119:ARG:HD2	2.53	0.43
23:i:90:LEU:HA	23:i:93:VAL:HG22	2.00	0.43
28:L:70:VAL:N	28:L:159:ASN:HD21	2.15	0.43
36:P:22:LEU:HD12	36:P:90:PHE:CE2	2.53	0.43
48:Y:106:ILE:HG21	48:Y:109:LEU:HD23	1.99	0.43
6:x:338:ASN:OD1	6:x:339:ILE:N	2.51	0.43
6:x:345:PHE:HB3	6:x:365:GLU:HG3	2.00	0.43
9:5:748:G:H8	9:5:749:G:H5'	1.84	0.43
9:5:935:A:H4'	9:5:937:U:OP2	2.19	0.43
9:5:1434:G:H2'	9:5:1435:G:C8	2.52	0.43
9:5:1902:G:H2'	9:5:1903:G:H8	1.83	0.43
9:5:2810:U:H2'	9:5:2811:G:O4'	2.18	0.43
9:5:4950:U:O3'	9:5:4951:G:H3'	2.18	0.43
12:C:177:TRP:NE1	12:C:181:LYS:HE3	2.33	0.43
34:O:8:VAL:HG12	34:O:117:ARG:HG3	1.99	0.43
9:5:23:C:OP1	25:j:44:LYS:NZ	2.43	0.43
9:5:490:C:H2'	9:5:491:G:C8	2.54	0.43
9:5:1872:G:O2'	9:5:4219:A:N3	2.48	0.43
9:5:2817:C:H2'	9:5:2818:C:C6	2.53	0.43
9:5:3732:A:H2'	9:5:3733:A:H8	1.83	0.43
9:5:4303:C:H2'	9:5:4305:G:H8	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:4635:A:OP1	9:5:4636:U:O2'	2.36	0.43
9:5:4914:C:H2'	9:5:4915:G:H8	1.82	0.43
11:c:21:VAL:O	11:c:25:GLY:N	2.50	0.43
12:C:177:TRP:HA	12:C:180:ILE:HD13	2.00	0.43
21:h:80:PRO:HD2	21:h:83:LEU:HD12	1.99	0.43
37:p:39:CYS:SG	37:p:47:MET:HE2	2.58	0.43
41:S:113:MET:HE3	41:S:113:MET:HB3	1.81	0.43
7:A:112:ILE:H	37:p:83:ILE:HD11	1.84	0.43
9:5:185:C:O2'	9:5:188:G:OP2	2.35	0.43
9:5:363:A:N1	9:5:376:A:H5''	2.33	0.43
9:5:425:U:N3	9:5:426:A:N7	2.67	0.43
9:5:1314:C:C2	9:5:1315:C:C5	3.06	0.43
9:5:3615:G:H1'	45:W:44:ARG:NH1	2.34	0.43
9:5:3709:U:O2'	9:5:3710:G:H8	2.00	0.43
9:5:4524:G:N3	10:B:252:ALA:HB1	2.33	0.43
9:5:4618:G:H5'	44:V:15:ARG:HB3	2.00	0.43
9:5:4648:A:H2'	9:5:4649:G:H8	1.83	0.43
9:5:4914:C:H2'	9:5:4915:G:C8	2.53	0.43
10:B:212:GLY:O	10:B:284:ILE:HD11	2.18	0.43
14:D:146:LEU:HD22	14:D:163:LEU:HB2	2.00	0.43
20:G:57:TRP:HB3	20:G:61:ILE:HG21	2.00	0.43
22:H:88:PHE:CE1	22:H:151:ILE:HD12	2.54	0.43
40:R:8:LYS:HG3	40:R:19:LYS:HB2	2.00	0.43
41:S:85:ASP:O	41:S:123:SER:OG	2.34	0.43
47:7:70:G:H2'	47:7:71:G:H8	1.83	0.43
5:v:164:LYS:HA	5:v:167:GLU:HG2	1.99	0.43
6:x:33:LYS:C	6:x:35:VAL:H	2.27	0.43
8:b:20:GLY:O	8:b:22:LYS:HG2	2.19	0.43
9:5:1218:G:H3'	9:5:1219:G:H5''	2.00	0.43
9:5:2598:A:N3	19:g:61:PRO:HB3	2.33	0.43
9:5:3870:C:H2'	9:5:3871:A:C8	2.54	0.43
9:5:4458:C:H2'	9:5:4459:U:C6	2.53	0.43
10:B:56:ILE:HG22	10:B:74:GLU:O	2.18	0.43
10:B:84:MET:HG2	10:B:166:THR:HG22	2.00	0.43
22:H:67:LEU:O	22:H:70:VAL:HG12	2.18	0.43
29:l:8:ARG:HG2	29:l:11:ARG:HH21	1.84	0.43
32:N:128:LYS:HE3	32:N:130:PHE:CZ	2.53	0.43
49:8:131:G:H2'	49:8:132:G:H8	1.83	0.43
1:1:175:G:O2'	1:1:177:G:H5'	2.19	0.43
6:x:36:CYS:O	6:x:40:LEU:HG	2.18	0.43
9:5:173:C:H5'	28:L:129:ARG:NH2	2.34	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:263:G:N2	21:h:112:ARG:HH22	2.15	0.43
9:5:453:G:H2'	9:5:453:G:N3	2.33	0.43
9:5:755:C:H4'	22:H:54:ARG:HH22	1.84	0.43
9:5:1068:G:H2'	9:5:1069:G:H8	1.83	0.43
9:5:1285:U:O2'	9:5:1286:C:H5''	2.18	0.43
9:5:2502:G:H4'	9:5:2503:G:OP1	2.17	0.43
9:5:2577:C:OP1	50:Z:111:ARG:NH1	2.52	0.43
9:5:2581:A:H2'	9:5:2582:A:C4	2.53	0.43
9:5:2607:C:H2'	9:5:2608:G:C8	2.54	0.43
9:5:3769:C:H2'	9:5:3770:U:C6	2.54	0.43
9:5:4091:G:H2'	9:5:4092:G:C8	2.53	0.43
9:5:4964:C:H2'	9:5:4965:U:C2	2.54	0.43
9:5:5057:C:H2'	9:5:5058:A:C8	2.53	0.43
12:C:150:LEU:HB3	12:C:151:PRO:HD3	2.01	0.43
28:L:81:LEU:HD13	28:L:88:LYS:HA	2.00	0.43
34:O:58:LEU:HD11	34:O:145:VAL:HG13	1.99	0.43
35:o:89:LYS:HG3	35:o:90:HIS:ND1	2.33	0.43
36:P:15:CYS:SG	36:P:102:ALA:HB2	2.59	0.43
41:S:141:ALA:O	41:S:144:GLN:HG2	2.18	0.43
50:Z:89:ILE:HG12	50:Z:91:LEU:HG	2.00	0.43
6:x:375:LEU:HD12	6:x:375:LEU:HA	1.74	0.43
9:5:23:C:H2'	9:5:24:G:O4'	2.19	0.43
9:5:1364:U:OP2	28:L:36:ARG:NH2	2.51	0.43
9:5:1398:A:N6	9:5:1419:G:H1'	2.34	0.43
9:5:1755:C:N4	9:5:1778:C:O2'	2.31	0.43
9:5:2082:G:H21	18:F:167:LYS:HE2	1.83	0.43
9:5:2776:G:H2'	9:5:2777:G:C8	2.53	0.43
9:5:3727:A:H2'	9:5:3728:A:C8	2.54	0.43
9:5:4076:G:H5'	20:G:73:ARG:HG3	1.99	0.43
9:5:4158:C:H2'	9:5:4159:C:C6	2.54	0.43
9:5:4417:C:H2'	9:5:4418:G:O4'	2.19	0.43
9:5:4578:G:H2'	9:5:4579:U:H6	1.84	0.43
12:C:333:LYS:HE3	16:E:50:ILE:HA	2.00	0.43
14:D:177:THR:HA	14:D:180:PHE:HD2	1.84	0.43
15:e:91:CYS:HB2	15:e:95:TYR:CD1	2.51	0.43
28:L:46:ILE:O	28:L:149:GLN:NE2	2.51	0.43
49:8:144:U:H2'	49:8:145:C:C6	2.53	0.43
9:5:275:C:H2'	9:5:276:C:C6	2.53	0.43
9:5:1068:G:H2'	9:5:1069:G:C8	2.54	0.43
9:5:2607:C:H2'	9:5:2608:G:H8	1.83	0.43
9:5:2652:G:H22	37:p:59:SER:HA	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:3594:C:H1'	9:5:3597:G:N3	2.34	0.43
12:C:12:SER:OG	12:C:15:GLY:O	2.29	0.43
16:E:108:MET:O	39:r:87:ARG:NH1	2.51	0.43
20:G:167:VAL:HG23	20:G:167:VAL:O	2.18	0.43
24:I:153:ARG:O	24:I:156:LYS:HB2	2.19	0.43
50:Z:76:ASN:HB2	50:Z:79:HIS:HB2	2.01	0.43
1:1:104:C:C3'	1:1:105:G:C5'	2.90	0.43
9:5:228:C:H2'	9:5:229:G:C8	2.54	0.43
9:5:432:U:H4'	9:5:433:A:H5''	2.00	0.43
9:5:660:A:H2'	9:5:661:C:C6	2.54	0.43
9:5:909:A:H2'	9:5:910:G:C8	2.52	0.43
9:5:1315:C:H2'	9:5:1316:G:C8	2.54	0.43
9:5:1938:C:H4'	9:5:1939:A:O4'	2.19	0.43
9:5:2089:G:N3	12:C:307:LYS:HE3	2.34	0.43
9:5:2751:G:C2	9:5:2752:G:N7	2.86	0.43
9:5:4745:G:N2	9:5:4956:A:H61	2.14	0.43
9:5:4890:G:H2'	9:5:4891:G:C8	2.53	0.43
9:5:4966:A:H2'	9:5:4967:A:H8	1.83	0.43
12:C:56:GLU:HG3	12:C:57:LEU:HD22	2.00	0.43
18:F:231:GLU:HA	41:S:2:LYS:HA	2.00	0.43
22:H:162:GLN:NE2	22:H:181:VAL:H	2.16	0.43
24:I:200:ILE:HG13	24:I:200:ILE:O	2.18	0.43
26:J:10:ASN:HB3	26:J:13:ARG:HG2	2.01	0.43
36:P:21:ASN:H	36:P:145:HIS:CD2	2.37	0.43
43:U:23:LEU:HD21	43:U:83:LEU:HB3	2.01	0.43
48:Y:55:VAL:HG13	48:Y:104:VAL:HG13	2.00	0.43
49:8:60:G:H21	49:8:64:U:H1'	1.84	0.43
50:Z:76:ASN:HD22	50:Z:79:HIS:CE1	2.35	0.43
1:1:94:C:N3	1:1:257:C:N4	2.66	0.43
1:1:104:C:C2'	1:1:105:G:H5''	2.49	0.43
9:5:288:G:H2'	9:5:289:C:C6	2.54	0.43
9:5:684:G:O2'	9:5:685:C:O5'	2.35	0.43
9:5:1510:G:H2'	9:5:1511:U:C6	2.53	0.43
9:5:1633:G:H5'	9:5:1634:A:OP1	2.19	0.43
9:5:2375:A:H2'	9:5:2376:A:H8	1.83	0.43
9:5:4123:C:H2'	9:5:4124:G:C8	2.54	0.43
9:5:4525:C:H4'	10:B:244:THR:HG23	2.01	0.43
9:5:4572:U:H1'	9:5:4720:C:C4	2.54	0.43
9:5:4592:C:H2'	9:5:4593:C:C6	2.54	0.43
9:5:4670:C:O2'	9:5:4672:A:OP2	2.31	0.43
9:5:5005:G:N2	9:5:5041:G:O2'	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:297:LYS:HG3	10:B:299:ILE:HG23	2.00	0.43
12:C:35:ASP:OD1	12:C:35:ASP:N	2.52	0.43
18:F:93:PHE:HB2	18:F:147:PRO:HG3	2.01	0.43
18:F:163:LYS:HE2	18:F:208:ASN:O	2.19	0.43
24:I:46:PHE:HB3	24:I:140:THR:HA	2.00	0.43
26:J:79:ALA:O	26:J:83:LEU:HD23	2.19	0.43
36:P:118:GLN:NE2	36:P:147:GLU:OE2	2.52	0.43
1:1:105:G:O6	1:1:250:U:O4'	2.37	0.42
9:5:711:A:H2'	9:5:712:C:H6	1.84	0.42
9:5:1374:G:O2'	12:C:233:THR:O	2.34	0.42
9:5:1545:G:H2'	9:5:1546:C:C6	2.54	0.42
9:5:1569:U:H2'	9:5:1570:G:C8	2.53	0.42
9:5:1884:C:H2'	9:5:1885:G:H8	1.82	0.42
9:5:2654:C:H2'	9:5:2655:C:H6	1.84	0.42
9:5:3896:C:H1'	10:B:268:ARG:HH22	1.85	0.42
9:5:4911:A:H5'	10:B:97:ARG:NH2	2.34	0.42
9:5:4945:G:C6	17:f:60:PRO:HD3	2.53	0.42
12:C:26:ALA:HB3	12:C:266:THR:HA	2.01	0.42
14:D:13:PHE:O	47:7:11:A:N6	2.46	0.42
14:D:51:MET:HE1	14:D:166:ALA:HB2	2.00	0.42
22:H:26:ILE:HD12	22:H:35:ARG:HD3	2.00	0.42
26:J:40:LEU:HD12	26:J:70:VAL:HG13	2.01	0.42
28:L:164:GLU:HG3	51:a:100:ILE:HD13	2.01	0.42
41:S:27:LEU:HD12	42:T:143:THR:HB	2.01	0.42
43:U:42:PHE:CE1	43:U:46:ARG:HG3	2.53	0.42
49:8:131:G:H2'	49:8:132:G:C8	2.54	0.42
4:u:11:LEU:HD11	43:U:99:TRP:CD1	2.53	0.42
8:b:16:TRP:NE1	42:T:81:LYS:O	2.52	0.42
9:5:94:A:H5''	51:a:34:ASN:HB2	2.02	0.42
9:5:228:C:H2'	9:5:229:G:H8	1.84	0.42
9:5:252:C:H2'	9:5:253:G:C8	2.54	0.42
9:5:1351:G:H2'	9:5:1352:C:C6	2.53	0.42
9:5:2361:G:O2'	9:5:3859:G:O6	2.29	0.42
9:5:2591:A:H2'	9:5:2592:U:C6	2.53	0.42
9:5:4970:C:O3'	36:P:72:GLN:HG2	2.19	0.42
10:B:84:MET:HE1	10:B:183:ILE:HD11	2.02	0.42
18:F:90:LYS:HG2	42:T:135:PRO:HG2	2.02	0.42
22:H:16:VAL:HG13	22:H:27:VAL:HG13	2.01	0.42
22:H:110:SER:HA	22:H:128:MET:SD	2.59	0.42
36:P:118:GLN:OE1	36:P:120:ASN:ND2	2.44	0.42
48:Y:52:ASP:O	48:Y:110:LYS:HB2	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:244:C:H2'	1:1:245:G:C8	2.54	0.42
5:v:166:ALA:HB1	5:v:190:THR:HG22	2.02	0.42
6:x:47:LYS:HA	52:t:211:MET:SD	2.58	0.42
6:x:116:THR:HG22	6:x:120:LYS:HE3	2.00	0.42
6:x:402:ARG:O	6:x:406:VAL:HG23	2.19	0.42
6:x:403:ILE:HG23	6:x:417:VAL:HG11	2.01	0.42
9:5:301:G:N2	9:5:4176:C:O2'	2.46	0.42
9:5:417:G:N2	49:8:16:G:O2'	2.52	0.42
9:5:499:G:H2'	9:5:499:G:N3	2.34	0.42
9:5:1271:G:H5'	9:5:1272:C:C6	2.54	0.42
9:5:1865:G:N2	9:5:1868:A:OP2	2.33	0.42
9:5:2580:U:H5''	50:Z:73:LYS:HE2	2.01	0.42
10:B:235:TRP:CD1	10:B:267:ALA:HB1	2.55	0.42
12:C:146:GLU:CD	12:C:175:LYS:HD3	2.45	0.42
13:d:25:TYR:CE1	13:d:88:LEU:HD12	2.54	0.42
14:D:21:ARG:HA	14:D:24:ARG:CZ	2.49	0.42
20:G:97:LYS:C	20:G:97:LYS:HD3	2.44	0.42
28:L:57:PRO:HG3	28:L:76:PHE:CD1	2.54	0.42
39:r:7:TRP:HA	39:r:10:VAL:HG12	2.01	0.42
41:S:30:MET:HE2	41:S:30:MET:HB3	1.89	0.42
6:x:336:PHE:CE2	6:x:375:LEU:HD23	2.53	0.42
7:A:89:TYR:HB2	7:A:100:ASN:HD21	1.84	0.42
7:A:116:LEU:HD13	7:A:164:ALA:HB2	2.01	0.42
9:5:1400:G:H2'	9:5:1401:C:H6	1.84	0.42
9:5:1811:G:H2'	9:5:1812:C:H6	1.82	0.42
9:5:1952:G:OP1	41:S:139:ARG:HD2	2.19	0.42
9:5:2628:U:H2'	9:5:2629:C:C6	2.54	0.42
9:5:4946:U:H1'	16:E:154:ARG:HD2	2.01	0.42
11:c:64:ALA:O	11:c:68:LYS:N	2.52	0.42
12:C:218:VAL:HG12	12:C:229:LEU:HD22	2.00	0.42
16:E:110:ARG:NH1	39:r:87:ARG:HH21	2.17	0.42
23:i:29:ARG:O	23:i:29:ARG:HD3	2.19	0.42
34:O:50:ASN:HD22	34:O:136:ALA:HB3	1.84	0.42
49:8:19:C:H2'	49:8:20:A:C8	2.55	0.42
49:8:32:C:H2'	49:8:33:G:O4'	2.20	0.42
5:v:141:LEU:O	5:v:145:ALA:CB	2.61	0.42
6:x:393:ALA:HA	6:x:421:LEU:HD11	2.02	0.42
6:x:428:ALA:O	6:x:432:LYS:HG3	2.20	0.42
7:A:196:TRP:HB3	7:A:197:PRO:HD3	2.01	0.42
9:5:418:A:H4'	9:5:2311:C:H5'	2.01	0.42
9:5:976:G:H2'	9:5:977:C:C6	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:1876:U:H2'	9:5:1877:G:C8	2.54	0.42
9:5:1895:G:O2'	9:5:1907:A:N3	2.43	0.42
9:5:1917:A:H4'	17:f:79:GLY:HA3	2.01	0.42
9:5:2341:A:OP2	51:a:4:ARG:NH2	2.50	0.42
9:5:3664:G:H2'	9:5:3665:G:H8	1.83	0.42
9:5:3720:G:H22	9:5:3733:A:H2	1.67	0.42
9:5:4155:C:H2'	9:5:4156:G:O4'	2.20	0.42
10:B:304:SER:OG	10:B:310:SER:O	2.31	0.42
11:c:53:PRO:HG2	11:c:56:ARG:HB3	2.00	0.42
34:O:189:ILE:O	34:O:193:THR:N	2.52	0.42
38:Q:122:THR:OG1	38:Q:124:ASP:OD1	2.25	0.42
41:S:11:LYS:HD2	41:S:29:ARG:HH21	1.85	0.42
42:T:32:ARG:HG3	42:T:34:TYR:CE2	2.54	0.42
49:8:31:G:H2'	49:8:32:C:O4'	2.19	0.42
1:1:210:G:H2'	1:1:211:U:C6	2.55	0.42
6:x:113:GLY:O	6:x:117:THR:OG1	2.26	0.42
6:x:218:VAL:HG22	6:x:244:SER:HB2	2.01	0.42
6:x:441:PHE:CG	6:x:442:LYS:N	2.87	0.42
7:A:58:LEU:HD23	7:A:75:LEU:HG	2.02	0.42
9:5:381:U:H2'	9:5:382:G:O4'	2.20	0.42
9:5:1241:C:OP1	9:5:1242:G:N2	2.52	0.42
9:5:1939:A:H5'	9:5:1940:G:H4'	2.02	0.42
9:5:2352:U:H1'	12:C:96:CYS:HA	2.02	0.42
9:5:3856:A:H5''	36:P:83:TRP:O	2.20	0.42
9:5:4321:U:H2'	9:5:4322:G:C8	2.54	0.42
9:5:4873:G:C2	30:M:94:LYS:HD2	2.55	0.42
16:E:97:ASN:O	16:E:101:ARG:NH1	2.52	0.42
20:G:165:GLU:HG3	32:N:19:MET:HE1	2.00	0.42
24:I:59:GLN:HB3	24:I:126:VAL:HG11	2.02	0.42
40:R:18:GLY:C	40:R:20:LYS:H	2.27	0.42
42:T:80:VAL:O	42:T:82:GLY:N	2.49	0.42
47:7:23:A:H2'	47:7:24:C:C6	2.55	0.42
49:8:21:C:N4	49:8:22:U:O4	2.53	0.42
6:x:74:MET:SD	46:X:152:LYS:HD2	2.59	0.42
6:x:420:LEU:CA	6:x:423:GLN:HE21	2.25	0.42
9:5:131:C:H2'	9:5:132:G:C4	2.55	0.42
9:5:221:C:H2'	9:5:222:C:C6	2.55	0.42
9:5:425:U:C2	9:5:426:A:C8	3.08	0.42
9:5:1567:U:H2'	9:5:1568:C:C6	2.55	0.42
9:5:2725:A:H1'	40:R:93:VAL:HG21	2.01	0.42
9:5:4991:U:H2'	9:5:4992:G:H8	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:273:LEU:HD22	47:7:107:G:H5''	2.02	0.42
16:E:84:VAL:HG12	16:E:85:LEU:N	2.35	0.42
24:I:90:ARG:HG3	24:I:134:VAL:HG12	2.01	0.42
24:I:101:LYS:HB3	24:I:101:LYS:HE3	1.85	0.42
26:J:36:ALA:O	26:J:39:VAL:HG22	2.20	0.42
38:Q:61:LEU:HD21	38:Q:66:MET:HB2	2.02	0.42
5:v:155:LEU:HD23	5:v:159:LEU:HD23	2.01	0.42
5:v:159:LEU:HD13	5:v:197:LEU:HG	2.01	0.42
9:5:161:G:H2'	9:5:162:A:H8	1.84	0.42
9:5:1397:A:OP1	51:a:132:ARG:HB2	2.20	0.42
9:5:1440:U:HO2'	9:5:1441:C:P	2.42	0.42
9:5:2097:U:H2'	9:5:2098:G:O4'	2.19	0.42
9:5:2780:C:H2'	9:5:2781:G:H8	1.85	0.42
9:5:4094:G:H2'	9:5:4095:G:C8	2.54	0.42
9:5:4340:U:H5'	38:Q:178:ARG:HG3	2.01	0.42
9:5:4862:G:H2'	9:5:4863:G:C8	2.55	0.42
12:C:231:ASN:OD1	12:C:232:VAL:N	2.52	0.42
12:C:316:LYS:HB2	12:C:324:ILE:HG13	2.02	0.42
16:E:137:ARG:NH1	16:E:140:ILE:HD11	2.34	0.42
1:1:104:C:H3'	1:1:105:G:C5'	2.40	0.42
1:1:134:U:H2'	1:1:135:G:C8	2.55	0.42
7:A:103:PRO:HA	7:A:163:ARG:HA	2.01	0.42
9:5:496:G:H2'	9:5:497:G:C8	2.54	0.42
9:5:1553:A:O2'	37:p:9:GLY:O	2.33	0.42
9:5:2812:A:OP1	40:R:83:GLY:N	2.53	0.42
9:5:3910:C:H2'	9:5:3911:C:H6	1.85	0.42
9:5:4322:G:N2	9:5:4324:A:H3'	2.35	0.42
9:5:4870:G:H21	9:5:4870:G:P	2.43	0.42
9:5:4970:C:C2	9:5:4971:A:C8	3.08	0.42
9:5:5051:C:H2'	9:5:5052:C:C6	2.55	0.42
11:c:22:MET:HE3	11:c:85:CYS:HA	2.01	0.42
13:d:93:ASN:HB2	13:d:103:TYR:HD1	1.85	0.42
14:D:82:GLU:CD	14:D:108:ARG:HH22	2.28	0.42
16:E:134:ARG:NE	16:E:165:SER:O	2.51	0.42
16:E:156:LYS:HB3	16:E:178:ASN:HD21	1.85	0.42
19:g:23:SER:HB3	19:g:33:LEU:HD13	2.02	0.42
41:S:84:TYR:CE1	41:S:93:MET:HE3	2.54	0.42
47:7:38:U:H1'	47:7:42:A:H61	1.85	0.42
52:t:206:ILE:HG23	52:t:210:ILE:HD12	2.00	0.42
6:x:195:HIS:HD2	6:x:197:GLN:CG	2.32	0.42
9:5:86:U:H2'	9:5:87:A:C8	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:419:A:H62	49:8:15:G:H21	1.68	0.42
9:5:969:C:O2'	9:5:970:G:O4'	2.37	0.42
9:5:1370:G:H4'	9:5:1371:A:H5'	2.01	0.42
9:5:1449:C:H2'	9:5:1450:C:C6	2.55	0.42
9:5:2383:C:H5''	9:5:2384:U:H5	1.85	0.42
9:5:2626:U:O4	43:U:97:ARG:NH1	2.53	0.42
9:5:2753:G:H8	9:5:2753:G:OP2	2.03	0.42
9:5:4510:A:H2'	9:5:4511:A:C8	2.55	0.42
16:E:88:VAL:HG11	16:E:91:PRO:HG3	2.00	0.42
24:I:31:ILE:HG22	24:I:62:SER:HB2	2.01	0.42
27:k:3:ARG:HB2	27:k:43:TYR:CD1	2.55	0.42
31:m:97:ARG:NH2	31:m:122:ARG:HB3	2.35	0.42
32:N:46:ASP:OD1	32:N:46:ASP:N	2.53	0.42
44:V:87:SER:OG	44:V:95:PHE:HB3	2.20	0.42
45:W:56:ARG:HG2	45:W:61:LYS:HB2	2.00	0.42
46:X:107:HIS:CD2	49:8:130:C:H4'	2.55	0.42
50:Z:53:VAL:C	50:Z:55:ALA:H	2.28	0.42
1:1:162:C:H2'	1:1:163:A:C8	2.55	0.41
7:A:227:ARG:HH22	9:5:3659:G:H4'	1.84	0.41
9:5:424:U:H2'	9:5:425:U:H6	1.85	0.41
9:5:1728:U:C2	9:5:1729:A:C8	3.07	0.41
9:5:2052:G:O2'	9:5:2057:A:N1	2.45	0.41
9:5:2375:A:H2'	9:5:2376:A:C8	2.55	0.41
9:5:2394:G:O4'	9:5:2397:G:N2	2.53	0.41
9:5:2591:A:C6	9:5:2755:A:C5	3.08	0.41
9:5:2595:C:C2	9:5:2751:G:N2	2.88	0.41
9:5:3861:A:H2'	9:5:3862:A:C8	2.52	0.41
9:5:4299:U:H2'	9:5:4300:U:H6	1.85	0.41
26:J:35:ARG:O	26:J:39:VAL:HG13	2.20	0.41
32:N:17:ASP:OD1	32:N:17:ASP:N	2.53	0.41
32:N:84:PRO:HA	32:N:87:HIS:CG	2.55	0.41
41:S:14:GLY:HA2	41:S:62:VAL:HG23	2.02	0.41
50:Z:22:LYS:NZ	50:Z:129:TRP:O	2.53	0.41
1:1:134:U:H2'	1:1:135:G:H8	1.85	0.41
9:5:252:C:H2'	9:5:253:G:H8	1.85	0.41
9:5:1077:C:H5''	9:5:1215:C:OP1	2.21	0.41
9:5:1195:G:H2'	9:5:1196:G:H8	1.85	0.41
9:5:1368:A:O2'	9:5:1369:C:OP1	2.34	0.41
9:5:1922:G:O2'	9:5:1923:A:H5'	2.20	0.41
9:5:2610:G:H2'	9:5:2611:A:H8	1.85	0.41
9:5:2696:A:C5	27:k:69:LEU:HD13	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:3871:A:H2'	9:5:3872:A:H8	1.84	0.41
9:5:3910:C:H2'	9:5:3911:C:C6	2.55	0.41
9:5:4262:C:H2'	9:5:4263:C:H6	1.85	0.41
9:5:4420:U:O2	9:5:4420:U:H2'	2.19	0.41
9:5:4879:C:H2'	9:5:4880:C:C6	2.56	0.41
12:C:110:ARG:O	12:C:113:ARG:NH1	2.46	0.41
25:j:58:THR:OG1	25:j:59:THR:N	2.53	0.41
52:t:200:LYS:C	52:t:202:ASN:N	2.71	0.41
2:q:107:TYR:CG	2:q:111:MET:HE1	2.54	0.41
9:5:151:G:O6	20:G:139:GLY:HA3	2.21	0.41
9:5:229:G:H5''	48:Y:11:ARG:HD2	2.02	0.41
9:5:279:A:N6	9:5:307:A:N7	2.68	0.41
9:5:288:G:H2'	9:5:289:C:H6	1.85	0.41
9:5:436:C:H2'	9:5:437:G:H8	1.85	0.41
9:5:724:C:H2'	9:5:725:G:H8	1.85	0.41
9:5:1285:U:O2	16:E:126:ARG:NE	2.40	0.41
9:5:1392:A:H2'	9:5:1393:G:C8	2.55	0.41
9:5:2436:U:O4	46:X:130:PRO:HG3	2.20	0.41
9:5:2446:C:H2'	9:5:2447:U:C6	2.54	0.41
9:5:4324:A:H2'	9:5:4325:A:C8	2.55	0.41
9:5:4622:A:H4'	10:B:13:SER:HB2	2.01	0.41
10:B:220:ILE:HG13	10:B:278:THR:HG23	2.02	0.41
12:C:318:PRO:HB3	12:C:325:MET:HB2	2.02	0.41
18:F:192:LEU:HD21	18:F:210:LEU:HD11	2.02	0.41
21:h:118:LYS:HE3	28:L:127:PHE:CD2	2.54	0.41
28:L:46:ILE:HB	28:L:49:ARG:HB2	2.01	0.41
47:7:19:C:H2'	47:7:20:U:C6	2.55	0.41
48:Y:55:VAL:N	48:Y:68:GLY:O	2.45	0.41
49:8:12:G:C2	49:8:13:G:C8	3.08	0.41
49:8:108:A:N6	49:8:112:G:O6	2.52	0.41
9:5:1309:C:H2'	9:5:1310:C:C6	2.55	0.41
9:5:1345:A:H2'	9:5:1346:C:C6	2.56	0.41
9:5:1356:U:H2'	9:5:1357:C:C6	2.55	0.41
9:5:1461:C:H2'	9:5:1462:A:C8	2.55	0.41
9:5:4163:U:H5'	9:5:4164:C:H5''	2.02	0.41
9:5:4510:A:N6	9:5:4592:C:O2'	2.54	0.41
9:5:4627:U:H4'	10:B:373:LYS:HD2	2.01	0.41
9:5:4748:U:H2'	9:5:4749:C:O4'	2.20	0.41
9:5:4992:G:H2'	9:5:4993:G:H8	1.86	0.41
12:C:177:TRP:HE1	12:C:181:LYS:HE3	1.85	0.41
16:E:126:ARG:HA	16:E:126:ARG:HD3	1.75	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:F:96:ARG:CZ	18:F:111:LEU:HD13	2.51	0.41
23:i:80:HIS:O	23:i:84:LYS:HG3	2.20	0.41
24:I:181:PHE:O	24:I:185:VAL:HG12	2.20	0.41
26:J:17:ILE:O	26:J:17:ILE:HG13	2.19	0.41
26:J:95:ARG:H	26:J:98:ASN:ND2	2.18	0.41
30:M:109:ARG:HA	30:M:112:VAL:HG12	2.02	0.41
36:P:64:ASN:HB2	36:P:80:GLN:HG3	2.03	0.41
40:R:39:GLN:HA	40:R:42:ARG:HE	1.85	0.41
44:V:57:VAL:HG22	44:V:125:CYS:HB2	2.02	0.41
46:X:103:LYS:HB3	46:X:103:LYS:HE2	1.85	0.41
50:Z:97:ASN:OD1	50:Z:97:ASN:N	2.53	0.41
4:u:28:ARG:HH11	4:u:31:LYS:HG3	1.84	0.41
9:5:669:C:H2'	9:5:670:G:H8	1.85	0.41
9:5:1338:G:H4'	9:5:1339:U:C6	2.56	0.41
9:5:1494:U:H2'	9:5:1495:G:H8	1.86	0.41
9:5:2083:C:H4'	9:5:2084:C:OP2	2.20	0.41
9:5:2539:C:H2'	9:5:2540:C:C6	2.55	0.41
9:5:3751:G:H21	9:5:3775:A:H8	1.69	0.41
9:5:3934:G:H2'	9:5:3935:C:C6	2.56	0.41
9:5:4710:C:H2'	9:5:4711:C:C6	2.55	0.41
9:5:5061:A:H1'	9:5:5062:G:OP2	2.20	0.41
10:B:167:GLN:HE22	10:B:204:GLN:NE2	2.19	0.41
12:C:326:LEU:HD11	12:C:333:LYS:HB2	2.03	0.41
15:e:28:TYR:HB2	15:e:31:ILE:HG12	2.03	0.41
24:I:52:MET:HE2	24:I:152:LEU:HD12	2.02	0.41
29:l:26:TRP:CD1	29:l:26:TRP:H	2.38	0.41
30:M:23:LYS:HD2	30:M:43:THR:O	2.21	0.41
34:O:73:PHE:HB3	34:O:78:ARG:HB2	2.02	0.41
40:R:139:MET:HG2	40:R:143:HIS:NE2	2.35	0.41
41:S:32:ILE:HG21	41:S:40:ALA:HA	2.01	0.41
51:a:4:ARG:HA	51:a:9:ARG:HG3	2.02	0.41
1:1:148:G:O2'	2:q:15:PHE:O	2.29	0.41
6:x:316:GLU:HG2	6:x:317:ALA:N	2.35	0.41
9:5:1211:G:H2'	9:5:1212:G:C8	2.55	0.41
9:5:1497:A:H61	38:Q:175:GLU:HB2	1.85	0.41
9:5:1698:C:OP1	18:F:165:ASN:ND2	2.54	0.41
9:5:1740:C:C2	9:5:1786:A:N6	2.72	0.41
9:5:1786:A:O2'	9:5:1788:A:OP2	2.27	0.41
9:5:2328:G:H2'	9:5:2329:U:C6	2.56	0.41
9:5:5003:U:H2'	9:5:5004:C:C6	2.55	0.41
10:B:92:TYR:CE2	10:B:101:THR:HG22	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:C:46:LYS:HD2	12:C:113:ARG:HG3	2.01	0.41
12:C:264:TYR:HE1	12:C:274:LYS:HE3	1.86	0.41
13:d:85:ARG:HB3	13:d:109:VAL:O	2.19	0.41
20:G:64:GLN:HG3	20:G:67:ARG:NH2	2.36	0.41
30:M:29:ASP:OD1	30:M:30:VAL:N	2.51	0.41
36:P:3:ARG:NH1	49:8:12:G:OP1	2.54	0.41
36:P:91:LEU:HD23	36:P:91:LEU:HA	1.89	0.41
37:p:50:ARG:HB3	37:p:54:ILE:HG22	2.02	0.41
38:Q:81:VAL:HB	38:Q:138:LEU:HD23	2.03	0.41
39:r:66:ARG:C	39:r:68:SER:H	2.28	0.41
52:t:181:ILE:CD1	52:t:196:VAL:HA	2.36	0.41
52:t:194:LYS:HA	52:t:197:ARG:NH1	2.35	0.41
2:q:53:CYS:SG	2:q:60:VAL:HG11	2.61	0.41
7:A:9:ARG:HD2	9:5:1628:C:OP2	2.21	0.41
9:5:114:G:O6	9:5:157:U:N3	2.54	0.41
9:5:347:A:H2'	9:5:348:G:C8	2.55	0.41
9:5:1317:U:H2'	9:5:1318:C:C6	2.55	0.41
9:5:1440:U:O2'	9:5:1441:C:OP1	2.34	0.41
9:5:1455:G:H2'	9:5:1456:C:C6	2.56	0.41
9:5:1662:C:H2'	9:5:1663:C:C6	2.55	0.41
9:5:2640:G:H2'	9:5:2641:A:C8	2.56	0.41
9:5:4119:C:O2'	9:5:4120:U:N3	2.53	0.41
9:5:4290:U:H5''	35:o:9:ARG:O	2.21	0.41
9:5:4929:C:H5'	16:E:262:GLN:HG2	2.03	0.41
12:C:210:ILE:HD13	12:C:252:TRP:CE2	2.55	0.41
14:D:129:GLU:OE2	14:D:131:ASN:ND2	2.54	0.41
16:E:42:ARG:HG2	16:E:61:ARG:HG2	2.03	0.41
16:E:137:ARG:NH2	17:f:110:ILE:OXT	2.48	0.41
22:H:19:SER:O	22:H:26:ILE:HG22	2.20	0.41
34:O:24:ALA:HB1	34:O:88:LEU:HD21	2.02	0.41
34:O:193:THR:O	34:O:197:LYS:HG2	2.21	0.41
44:V:16:ILE:HD11	44:V:57:VAL:HG12	2.02	0.41
2:q:18:ILE:N	2:q:82:VAL:O	2.51	0.41
6:x:45:ASN:HB3	6:x:47:LYS:HE3	2.01	0.41
6:x:106:PHE:O	6:x:191:THR:OG1	2.25	0.41
9:5:1480:C:O2'	9:5:1482:G:OP2	2.33	0.41
9:5:1895:G:H2'	9:5:1896:A:O4'	2.20	0.41
9:5:1948:G:H2'	9:5:1949:U:O4'	2.21	0.41
9:5:2080:U:H2'	9:5:2081:C:H6	1.84	0.41
9:5:2876:G:P	37:p:6:LYS:H	2.43	0.41
9:5:3920:U:H2'	9:5:3921:U:H6	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:4263:C:H2'	9:5:4264:G:O4'	2.20	0.41
9:5:4268:A:H61	9:5:4281:A:H62	1.69	0.41
9:5:4875:G:O2'	41:S:170:LYS:NZ	2.33	0.41
20:G:106:THR:OG1	20:G:107:LYS:N	2.54	0.41
34:O:74:ARG:HD2	34:O:145:VAL:HG12	2.02	0.41
49:8:130:C:H2'	49:8:131:G:H8	1.85	0.41
52:t:187:GLN:HB2	52:t:210:ILE:HD13	2.03	0.41
6:x:428:ALA:HA	6:x:431:VAL:HG22	2.02	0.41
7:A:40:TYR:N	9:5:4117:U:O4	2.43	0.41
9:5:735:G:H2'	9:5:736:C:C6	2.56	0.41
9:5:1400:G:H2'	9:5:1401:C:C6	2.56	0.41
9:5:1769:G:H2'	9:5:1770:A:C8	2.56	0.41
9:5:1957:U:O2'	9:5:1958:A:H5'	2.21	0.41
9:5:2642:A:N6	9:5:2643:G:O6	2.54	0.41
9:5:2824:C:H2'	9:5:2825:A:C8	2.56	0.41
9:5:3611:A:N3	9:5:5016:A:H1'	2.35	0.41
9:5:4869:U:H3'	9:5:4870:G:N2	2.36	0.41
9:5:4925:U:H1'	9:5:4926:C:C5	2.56	0.41
12:C:195:LYS:HA	12:C:200:ARG:HA	2.01	0.41
15:e:82:VAL:HG13	15:e:114:ARG:HG2	2.02	0.41
16:E:92:VAL:HG12	16:E:105:LEU:HD11	2.03	0.41
16:E:125:GLY:C	16:E:126:ARG:HH11	2.28	0.41
16:E:222:ARG:HB2	16:E:229:PHE:CD1	2.56	0.41
16:E:228:ILE:HD12	16:E:228:ILE:HA	1.95	0.41
17:f:46:ARG:HB2	17:f:104:MET:HB2	2.02	0.41
26:J:82:ILE:HA	26:J:85:LYS:HG2	2.03	0.41
26:J:100:SER:OG	26:J:104:ASN:O	2.29	0.41
27:k:5:ILE:HD11	27:k:43:TYR:HB3	2.02	0.41
37:p:33:GLN:HG3	37:p:49:ARG:HD3	2.03	0.41
40:R:169:ALA:HA	40:R:172:ARG:HG2	2.03	0.41
6:x:134:LEU:HD23	6:x:188:ILE:HB	2.02	0.41
7:A:3:ARG:H	7:A:207:VAL:HG22	1.86	0.41
9:5:21:G:N2	49:8:40:A:H1'	2.36	0.41
9:5:286:U:H2'	9:5:287:U:C6	2.56	0.41
9:5:443:G:H5''	17:f:54:LYS:HG2	2.03	0.41
9:5:970:G:N2	16:E:122:LEU:HD11	2.35	0.41
9:5:980:U:H2'	9:5:981:C:C6	2.55	0.41
9:5:1340:C:H2'	9:5:1341:U:H6	1.86	0.41
9:5:1612:G:N3	9:5:1612:G:H2'	2.36	0.41
9:5:1633:G:H4'	9:5:1634:A:O5'	2.21	0.41
9:5:2594:C:H2'	9:5:2595:C:H6	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:3889:G:N7	9:5:4720:C:H2'	2.36	0.41
9:5:4736:C:H2'	9:5:4737:G:C8	2.56	0.41
16:E:142:PRO:HA	16:E:160:PHE:CD2	2.56	0.41
26:J:53:ALA:N	26:J:66:GLU:O	2.50	0.41
32:N:137:PRO:HG2	32:N:138:PHE:CD2	2.55	0.41
34:O:129:LEU:HD23	34:O:130:LYS:O	2.20	0.41
36:P:7:ASP:OD1	36:P:7:ASP:N	2.52	0.41
39:r:86:ALA:HA	39:r:118:LEU:HD13	2.02	0.41
7:A:58:LEU:HA	7:A:78:ALA:H	1.87	0.40
9:5:18:C:H2'	9:5:19:G:C8	2.56	0.40
9:5:423:G:H2'	9:5:424:U:H6	1.86	0.40
9:5:1211:G:HO2'	9:5:1212:G:P	2.44	0.40
9:5:1327:C:H2'	9:5:1328:G:C8	2.56	0.40
9:5:1804:A:H4'	9:5:1805:A:O5'	2.18	0.40
9:5:1846:G:H2'	9:5:1847:C:C6	2.57	0.40
9:5:2593:C:H42	9:5:2753:G:H1	1.69	0.40
9:5:4405:G:H4'	24:I:4:ARG:HD3	2.03	0.40
9:5:4448:G:H5''	9:5:4449:A:H5'	2.02	0.40
9:5:4616:A:H2'	9:5:4617:G:O4'	2.21	0.40
9:5:4674:C:O2'	10:B:282:LYS:NZ	2.51	0.40
9:5:4730:C:O5'	9:5:4731:G:N2	2.54	0.40
9:5:4745:G:H2'	9:5:4746:C:C6	2.56	0.40
10:B:17:LEU:HB3	10:B:235:TRP:HH2	1.86	0.40
10:B:62:ARG:NH2	10:B:361:GLU:OE1	2.52	0.40
12:C:11:TYR:CD2	12:C:17:SER:HB3	2.56	0.40
12:C:36:ILE:HD11	12:C:119:GLN:OE1	2.21	0.40
19:g:78:TYR:CG	19:g:82:MET:HE2	2.56	0.40
21:h:80:PRO:HG3	46:X:61:PRO:HG2	2.02	0.40
32:N:9:GLU:OE2	32:N:12:ARG:NH1	2.53	0.40
38:Q:159:PRO:HB2	38:Q:160:HIS:HD2	1.86	0.40
39:r:45:HIS:HB2	39:r:48:THR:HG22	2.02	0.40
42:T:75:VAL:HG12	42:T:88:ARG:HB3	2.03	0.40
9:5:234:G:H1	9:5:2304:U:H3	1.69	0.40
9:5:406:C:O2'	9:5:407:A:OP1	2.39	0.40
9:5:948:C:OP1	12:C:336:ARG:NH2	2.41	0.40
9:5:967:C:H42	9:5:2255:C:H41	1.70	0.40
9:5:1086:C:H2'	9:5:1087:A:H8	1.85	0.40
9:5:1455:G:H4'	9:5:1456:C:OP1	2.22	0.40
9:5:1511:U:H2'	9:5:1512:G:C8	2.57	0.40
9:5:1666:C:H2'	9:5:1667:G:O4'	2.22	0.40
9:5:1804:A:O2'	9:5:1833:G:N1	2.53	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:1823:G:H2'	9:5:1825:A:C8	2.55	0.40
9:5:2046:G:C2	34:O:60:LYS:HE2	2.56	0.40
9:5:2296:G:C6	9:5:2339:G:N1	2.90	0.40
9:5:2505:C:H1'	9:5:2506:G:C2	2.56	0.40
9:5:4346:U:O2'	35:o:80:LYS:O	2.39	0.40
9:5:4467:A:O2'	9:5:4510:A:H1'	2.21	0.40
9:5:4524:G:C2	10:B:252:ALA:HB1	2.56	0.40
9:5:4730:C:H5''	9:5:4965:U:C2	2.56	0.40
9:5:4874:A:C4	34:O:175:MET:HE2	2.56	0.40
12:C:237:ILE:HG23	12:C:238:LEU:HD22	2.02	0.40
18:F:128:ASN:HB2	42:T:132:PRO:HB2	2.03	0.40
21:h:21:LEU:HD11	21:h:54:ILE:HG23	2.02	0.40
23:i:44:ILE:HD12	32:N:10:LEU:HB2	2.03	0.40
28:L:26:PHE:HA	32:N:202:ARG:HD3	2.03	0.40
30:M:3:PHE:CE1	41:S:155:PRO:HA	2.55	0.40
36:P:48:LEU:O	36:P:52:THR:HG23	2.21	0.40
41:S:77:ASN:HB2	41:S:132:ILE:O	2.21	0.40
50:Z:11:VAL:HG21	50:Z:80:LEU:HB3	2.03	0.40
2:q:68:TYR:HB3	2:q:71:GLU:HB3	2.02	0.40
9:5:693:C:H2'	9:5:694:C:C6	2.56	0.40
9:5:1395:U:H2'	9:5:1396:G:O4'	2.21	0.40
9:5:1884:C:H4'	9:5:2070:U:C4	2.56	0.40
9:5:2102:G:H2'	9:5:2103:G:H8	1.84	0.40
9:5:2601:A:OP1	19:g:40:LYS:NZ	2.44	0.40
14:D:37:VAL:HG22	14:D:50:ARG:HD3	2.03	0.40
15:e:26:ASP:OD1	15:e:27:ARG:HG3	2.22	0.40
21:h:22:ASP:OD1	46:X:74:TYR:OH	2.35	0.40
28:L:163:LYS:HE3	28:L:163:LYS:HB2	1.90	0.40
39:r:46:ARG:O	39:r:65:LYS:HD2	2.21	0.40
44:V:40:ILE:HG12	44:V:62:MET:O	2.21	0.40
2:q:18:ILE:HD13	2:q:105:MET:HE1	2.03	0.40
7:A:177:LYS:HB2	37:p:29:ILE:HG21	2.03	0.40
7:A:180:LEU:HD23	7:A:180:LEU:HA	1.93	0.40
9:5:386:A:OP2	48:Y:89:LYS:HD3	2.21	0.40
9:5:490:C:N4	9:5:491:G:O6	2.55	0.40
9:5:1428:U:H5'	38:Q:42:THR:HB	2.04	0.40
9:5:1727:U:H2'	9:5:1728:U:H6	1.86	0.40
9:5:1845:U:H2'	9:5:1846:G:H8	1.86	0.40
9:5:2493:G:O2'	49:8:127:U:OP1	2.39	0.40
9:5:2554:U:O4	9:5:2762:G:O2'	2.30	0.40
9:5:3684:G:H2'	9:5:3685:C:C6	2.57	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:5:3788:C:N4	9:5:3812:C:O4'	2.55	0.40
9:5:4538:G:H2'	9:5:4539:U:C6	2.56	0.40
9:5:4709:U:H2'	9:5:4710:C:C6	2.57	0.40
9:5:4747:C:H2'	9:5:4748:U:C6	2.57	0.40
9:5:4921:C:H2'	9:5:4922:C:C6	2.56	0.40
9:5:5019:A:H2'	9:5:5020:G:C8	2.55	0.40
12:C:67:TRP:CE3	12:C:73:VAL:HG11	2.55	0.40
15:e:35:TRP:CZ2	15:e:56:PRO:HD2	2.56	0.40
19:g:68:SER:O	19:g:72:LYS:HE2	2.21	0.40
21:h:70:ARG:NH1	21:h:83:LEU:O	2.49	0.40
30:M:28:VAL:HG21	30:M:39:ASP:HB2	2.03	0.40
32:N:165:THR:O	32:N:169:ARG:N	2.50	0.40
35:o:24:THR:OG1	35:o:69:ARG:HB3	2.22	0.40
47:7:23:A:H2	47:7:118:C:H1'	1.87	0.40
2:q:68:TYR:CE2	2:q:70:ARG:HB3	2.57	0.40
6:x:426:LYS:HD2	6:x:465:MET:HB3	2.02	0.40
6:x:474:MET:SD	6:x:483:MET:HG3	2.61	0.40
8:b:5:LYS:HE3	8:b:8:THR:HB	2.03	0.40
9:5:2:G:H2'	9:5:3:C:C6	2.57	0.40
9:5:425:U:OP1	36:P:37:LYS:NZ	2.51	0.40
9:5:496:G:H2'	9:5:497:G:H8	1.86	0.40
9:5:701:G:O3'	15:e:8:VAL:HG23	2.22	0.40
9:5:1182:C:OP2	9:5:1183:C:N4	2.54	0.40
9:5:1295:C:O2	9:5:1296:G:N2	2.55	0.40
9:5:1739:G:H1'	9:5:1742:A:H62	1.87	0.40
9:5:2430:C:H2'	9:5:2431:A:H8	1.86	0.40
9:5:4478:G:O2'	9:5:4602:A:N1	2.44	0.40
9:5:4618:G:C2	9:5:4619:U:C5	3.09	0.40
9:5:5052:C:H2'	9:5:5053:U:O4'	2.21	0.40
10:B:92:TYR:HE2	10:B:101:THR:HG22	1.87	0.40
15:e:26:ASP:OD1	15:e:27:ARG:N	2.53	0.40
15:e:75:ARG:HB2	15:e:95:TYR:CD2	2.57	0.40
16:E:129:PHE:HA	16:E:132:HIS:CE1	2.57	0.40
34:O:21:ALA:HA	34:O:87:MET:SD	2.61	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	
2	q	103/144 (72%)	101 (98%)	2 (2%)	0	100	100
4	u	30/162 (18%)	30 (100%)	0	0	100	100
5	v	195/627 (31%)	192 (98%)	3 (2%)	0	100	100
6	x	486/504 (96%)	464 (96%)	20 (4%)	2 (0%)	30	48
7	A	242/244 (99%)	225 (93%)	17 (7%)	0	100	100
8	b	73/223 (33%)	70 (96%)	3 (4%)	0	100	100
10	B	392/403 (97%)	380 (97%)	12 (3%)	0	100	100
11	c	92/115 (80%)	91 (99%)	1 (1%)	0	100	100
12	C	360/413 (87%)	348 (97%)	12 (3%)	0	100	100
13	d	105/125 (84%)	102 (97%)	3 (3%)	0	100	100
14	D	290/297 (98%)	278 (96%)	12 (4%)	0	100	100
15	e	126/157 (80%)	119 (94%)	7 (6%)	0	100	100
16	E	232/291 (80%)	204 (88%)	28 (12%)	0	100	100
17	f	107/110 (97%)	101 (94%)	6 (6%)	0	100	100
18	F	223/225 (99%)	216 (97%)	7 (3%)	0	100	100
19	g	112/129 (87%)	112 (100%)	0	0	100	100
20	G	239/319 (75%)	222 (93%)	17 (7%)	0	100	100
21	h	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
22	H	188/192 (98%)	179 (95%)	9 (5%)	0	100	100
23	i	100/102 (98%)	94 (94%)	6 (6%)	0	100	100
24	I	200/214 (94%)	193 (96%)	7 (4%)	0	100	100
25	j	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
26	J	167/178 (94%)	155 (93%)	12 (7%)	0	100	100
27	k	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
28	L	208/210 (99%)	192 (92%)	16 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	l	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
30	M	136/218 (62%)	129 (95%)	7 (5%)	0	100	100
31	m	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
32	N	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
33	n	21/25 (84%)	21 (100%)	0	0	100	100
34	O	197/500 (39%)	194 (98%)	3 (2%)	0	100	100
35	o	102/141 (72%)	95 (93%)	7 (7%)	0	100	100
36	P	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
37	p	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
38	Q	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
39	r	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
40	R	178/196 (91%)	174 (98%)	4 (2%)	0	100	100
41	S	173/175 (99%)	165 (95%)	8 (5%)	0	100	100
42	T	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
43	U	100/102 (98%)	94 (94%)	6 (6%)	0	100	100
44	V	129/140 (92%)	125 (97%)	4 (3%)	0	100	100
45	W	61/157 (39%)	60 (98%)	1 (2%)	0	100	100
46	X	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
48	Y	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
50	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
51	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
52	t	45/215 (21%)	38 (84%)	6 (13%)	1 (2%)	5	11
All	All	7214/9239 (78%)	6881 (95%)	330 (5%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	x	42	ALA
52	t	201	ASN
6	x	450	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	
2	q	92/121 (76%)	92 (100%)	0	100	100
4	u	26/136 (19%)	26 (100%)	0	100	100
5	v	173/529 (33%)	173 (100%)	0	100	100
6	x	410/421 (97%)	409 (100%)	1 (0%)	87	95
7	A	187/187 (100%)	187 (100%)	0	100	100
8	b	62/170 (36%)	62 (100%)	0	100	100
10	B	336/348 (97%)	336 (100%)	0	100	100
11	c	79/98 (81%)	79 (100%)	0	100	100
12	C	302/337 (90%)	302 (100%)	0	100	100
13	d	98/110 (89%)	98 (100%)	0	100	100
14	D	247/250 (99%)	247 (100%)	0	100	100
15	e	114/141 (81%)	114 (100%)	0	100	100
16	E	208/251 (83%)	208 (100%)	0	100	100
17	f	88/89 (99%)	88 (100%)	0	100	100
18	F	194/195 (100%)	194 (100%)	0	100	100
19	g	98/109 (90%)	98 (100%)	0	100	100
20	G	206/273 (76%)	206 (100%)	0	100	100
21	h	109/110 (99%)	109 (100%)	0	100	100
22	H	169/171 (99%)	169 (100%)	0	100	100
23	i	86/86 (100%)	86 (100%)	0	100	100
24	I	174/181 (96%)	174 (100%)	0	100	100
25	j	73/80 (91%)	73 (100%)	0	100	100
26	J	142/149 (95%)	142 (100%)	0	100	100
27	k	64/64 (100%)	64 (100%)	0	100	100
28	L	176/176 (100%)	176 (100%)	0	100	100
29	l	47/48 (98%)	47 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	M	117/160 (73%)	117 (100%)	0	100	100
31	m	48/116 (41%)	48 (100%)	0	100	100
32	N	171/172 (99%)	171 (100%)	0	100	100
33	n	22/24 (92%)	22 (100%)	0	100	100
34	O	171/433 (40%)	171 (100%)	0	100	100
35	o	92/121 (76%)	92 (100%)	0	100	100
36	P	134/134 (100%)	134 (100%)	0	100	100
37	p	74/75 (99%)	74 (100%)	0	100	100
38	Q	163/163 (100%)	163 (100%)	0	100	100
39	r	109/121 (90%)	109 (100%)	0	100	100
40	R	159/175 (91%)	159 (100%)	0	100	100
41	S	156/156 (100%)	156 (100%)	0	100	100
42	T	139/140 (99%)	139 (100%)	0	100	100
43	U	92/92 (100%)	92 (100%)	0	100	100
44	V	101/107 (94%)	101 (100%)	0	100	100
45	W	55/126 (44%)	55 (100%)	0	100	100
46	X	107/134 (80%)	107 (100%)	0	100	100
48	Y	124/135 (92%)	124 (100%)	0	100	100
50	Z	117/118 (99%)	117 (100%)	0	100	100
51	a	119/120 (99%)	119 (100%)	0	100	100
52	t	41/183 (22%)	40 (98%)	1 (2%)	43	67
All	All	6271/7835 (80%)	6269 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	x	47	LYS
52	t	197	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (136) such sidechains are listed below:

Mol	Chain	Res	Type
2	q	88	GLN
5	v	71	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	v	72	GLN
5	v	165	HIS
6	x	102	ASN
6	x	126	GLN
6	x	195	HIS
6	x	227	GLN
6	x	232	GLN
6	x	326	GLN
6	x	347	GLN
6	x	385	GLN
6	x	404	GLN
6	x	423	GLN
6	x	473	HIS
7	A	132	ASN
7	A	162	ASN
8	b	6	ASN
8	b	11	ASN
8	b	42	ASN
8	b	49	HIS
10	B	109	HIS
10	B	203	GLN
10	B	204	GLN
10	B	209	GLN
10	B	271	GLN
10	B	302	ASN
10	B	376	HIS
11	c	51	ASN
12	C	41	HIS
12	C	187	GLN
12	C	212	ASN
12	C	245	HIS
12	C	329	ASN
12	C	346	ASN
13	d	34	HIS
13	d	118	GLN
14	D	9	ASN
14	D	122	GLN
14	D	131	ASN
14	D	138	GLN
14	D	191	ASN
14	D	229	ASN
15	e	34	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	e	43	ASN
15	e	68	HIS
15	e	101	HIS
16	E	131	GLN
16	E	280	HIS
17	f	55	ASN
17	f	56	ASN
18	F	58	HIS
18	F	65	GLN
18	F	112	GLN
18	F	121	ASN
18	F	153	ASN
18	F	165	ASN
18	F	208	ASN
18	F	250	ASN
20	G	29	ASN
20	G	85	GLN
20	G	112	GLN
20	G	141	ASN
21	h	62	ASN
21	h	63	GLN
22	H	79	ASN
22	H	156	ASN
22	H	162	GLN
23	i	12	ASN
23	i	36	HIS
23	i	80	HIS
24	I	73	ASN
24	I	144	ASN
24	I	147	HIS
25	j	13	ASN
26	J	110	GLN
26	J	112	HIS
26	J	155	HIS
28	L	19	GLN
28	L	104	ASN
28	L	149	GLN
28	L	159	ASN
29	l	4	HIS
29	l	19	GLN
29	l	38	ASN
30	M	33	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	M	48	GLN
31	m	84	GLN
31	m	119	ASN
32	N	99	GLN
32	N	149	GLN
32	N	158	HIS
34	O	50	ASN
34	O	63	ASN
34	O	143	HIS
35	o	36	GLN
36	P	25	HIS
36	P	34	GLN
36	P	56	GLN
36	P	72	GLN
36	P	80	GLN
36	P	97	ASN
36	P	116	HIS
36	P	133	HIS
36	P	137	ASN
36	P	145	HIS
37	p	72	ASN
38	Q	160	HIS
38	Q	188	ASN
39	r	30	ASN
39	r	31	ASN
39	r	45	HIS
39	r	100	ASN
40	R	39	GLN
40	R	58	HIS
40	R	86	ASN
41	S	50	GLN
41	S	108	GLN
42	T	3	ASN
42	T	54	HIS
42	T	66	ASN
42	T	127	GLN
43	U	50	ASN
43	U	94	ASN
43	U	116	GLN
44	V	36	ASN
45	W	48	GLN
46	X	93	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	X	94	ASN
48	Y	18	HIS
48	Y	20	ASN
48	Y	86	GLN
50	Z	76	ASN
51	a	34	ASN
51	a	60	HIS
51	a	66	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	166/167 (99%)	35 (21%)	2 (1%)
47	7	119/120 (99%)	11 (9%)	0
49	8	155/156 (99%)	31 (20%)	1 (0%)
9	5	3478/4754 (73%)	693 (19%)	70 (2%)
All	All	3918/5197 (75%)	770 (19%)	73 (1%)

All (770) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	99	C
1	1	100	C
1	1	101	G
1	1	102	A
1	1	105	G
1	1	106	G
1	1	109	G
1	1	111	C
1	1	114	C
1	1	120	G
1	1	144	C
1	1	151	C
1	1	174	G
1	1	175	G
1	1	177	G
1	1	184	A
1	1	185	C
1	1	187	G
1	1	191	C
1	1	212	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	213	A
1	1	215	A
1	1	227	G
1	1	230	C
1	1	231	A
1	1	233	U
1	1	235	G
1	1	236	U
1	1	237	G
1	1	245	G
1	1	246	C
1	1	247	C
1	1	249	G
1	1	251	G
1	1	252	A
9	5	2	G
9	5	8	U
9	5	12	A
9	5	13	U
9	5	21	G
9	5	25	A
9	5	39	A
9	5	42	A
9	5	48	G
9	5	49	U
9	5	59	A
9	5	64	A
9	5	65	A
9	5	66	A
9	5	73	A
9	5	76	A
9	5	91	G
9	5	109	G
9	5	110	C
9	5	116	G
9	5	119	G
9	5	126	C
9	5	134	G
9	5	135	G
9	5	136	C
9	5	143	C
9	5	144	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	159	C
9	5	164	G
9	5	165	A
9	5	169	G
9	5	171	U
9	5	172	C
9	5	173	C
9	5	183	C
9	5	184	U
9	5	185	C
9	5	186	G
9	5	187	U
9	5	188	G
9	5	189	G
9	5	197	A
9	5	200	U
9	5	201	C
9	5	205	C
9	5	210	C
9	5	216	C
9	5	217	C
9	5	218	A
9	5	220	C
9	5	224	U
9	5	227	A
9	5	233	U
9	5	246	G
9	5	262	G
9	5	265	C
9	5	266	C
9	5	267	G
9	5	274	C
9	5	276	C
9	5	278	G
9	5	280	G
9	5	297	U
9	5	306	A
9	5	309	C
9	5	315	G
9	5	316	U
9	5	334	A
9	5	335	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	340	C
9	5	350	C
9	5	363	A
9	5	373	G
9	5	386	A
9	5	387	G
9	5	407	A
9	5	409	G
9	5	412	G
9	5	431	G
9	5	432	U
9	5	446	C
9	5	449	C
9	5	450	G
9	5	451	C
9	5	452	A
9	5	453	G
9	5	454	U
9	5	455	C
9	5	456	C
9	5	468	U
9	5	485	C
9	5	486	C
9	5	487	G
9	5	654	C
9	5	664	G
9	5	666	G
9	5	667	A
9	5	668	C
9	5	683	C
9	5	684	G
9	5	685	C
9	5	686	A
9	5	694	C
9	5	696	C
9	5	697	G
9	5	703	G
9	5	704	C
9	5	707	C
9	5	729	G
9	5	730	G
9	5	732	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	737	C
9	5	746	A
9	5	747	A
9	5	748	G
9	5	749	G
9	5	914	U
9	5	918	G
9	5	920	C
9	5	925	C
9	5	927	G
9	5	928	C
9	5	929	A
9	5	930	G
9	5	931	C
9	5	932	A
9	5	933	G
9	5	934	C
9	5	936	C
9	5	938	C
9	5	939	G
9	5	940	C
9	5	942	G
9	5	944	A
9	5	945	U
9	5	946	C
9	5	957	G
9	5	958	G
9	5	960	A
9	5	961	G
9	5	962	C
9	5	963	G
9	5	964	A
9	5	965	G
9	5	966	A
9	5	967	C
9	5	968	C
9	5	969	C
9	5	970	G
9	5	971	U
9	5	973	G
9	5	976	G
9	5	978	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	982	U
9	5	984	C
9	5	1072	C
9	5	1076	C
9	5	1167	C
9	5	1177	U
9	5	1178	G
9	5	1183	C
9	5	1210	C
9	5	1211	G
9	5	1212	G
9	5	1214	C
9	5	1215	C
9	5	1219	G
9	5	1233	G
9	5	1236	C
9	5	1237	C
9	5	1238	A
9	5	1239	C
9	5	1242	G
9	5	1272	C
9	5	1273	G
9	5	1274	A
9	5	1275	G
9	5	1279	A
9	5	1280	C
9	5	1281	G
9	5	1285	U
9	5	1286	C
9	5	1288	G
9	5	1293	G
9	5	1295	C
9	5	1296	G
9	5	1297	U
9	5	1301	C
9	5	1304	C
9	5	1326	A
9	5	1330	A
9	5	1344	C
9	5	1354	A
9	5	1358	G
9	5	1366	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	1367	C
9	5	1369	C
9	5	1370	G
9	5	1371	A
9	5	1377	G
9	5	1378	C
9	5	1379	C
9	5	1380	G
9	5	1381	U
9	5	1387	A
9	5	1394	G
9	5	1397	A
9	5	1399	G
9	5	1407	C
9	5	1408	G
9	5	1409	C
9	5	1410	U
9	5	1411	C
9	5	1420	A
9	5	1429	C
9	5	1437	C
9	5	1440	U
9	5	1441	C
9	5	1445	U
9	5	1446	C
9	5	1448	G
9	5	1456	C
9	5	1457	G
9	5	1475	G
9	5	1478	C
9	5	1482	G
9	5	1483	C
9	5	1497	A
9	5	1498	G
9	5	1501	C
9	5	1504	G
9	5	1516	G
9	5	1523	A
9	5	1525	A
9	5	1534	A
9	5	1547	A
9	5	1553	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	1563	A
9	5	1564	A
9	5	1566	C
9	5	1568	C
9	5	1573	G
9	5	1574	G
9	5	1578	U
9	5	1591	U
9	5	1596	U
9	5	1602	U
9	5	1612	G
9	5	1613	A
9	5	1624	G
9	5	1625	G
9	5	1631	A
9	5	1633	G
9	5	1634	A
9	5	1638	A
9	5	1654	G
9	5	1661	C
9	5	1676	C
9	5	1677	U
9	5	1694	C
9	5	1697	G
9	5	1698	C
9	5	1720	C
9	5	1721	G
9	5	1724	G
9	5	1741	G
9	5	1742	A
9	5	1754	U
9	5	1755	C
9	5	1756	U
9	5	1757	U
9	5	1760	G
9	5	1761	G
9	5	1764	G
9	5	1768	C
9	5	1769	G
9	5	1772	C
9	5	1776	A
9	5	1781	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	1787	A
9	5	1803	G
9	5	1804	A
9	5	1805	A
9	5	1812	C
9	5	1815	G
9	5	1819	G
9	5	1822	U
9	5	1828	C
9	5	1833	G
9	5	1834	U
9	5	1835	G
9	5	1836	G
9	5	1840	G
9	5	1847	C
9	5	1848	C
9	5	1855	G
9	5	1869	G
9	5	1892	A
9	5	1897	A
9	5	1916	G
9	5	1918	U
9	5	1920	C
9	5	1921	C
9	5	1922	G
9	5	1923	A
9	5	1930	U
9	5	1931	C
9	5	1945	G
9	5	1956	A
9	5	1957	U
9	5	1958	A
9	5	1961	G
9	5	1962	A
9	5	2025	A
9	5	2026	A
9	5	2044	U
9	5	2047	A
9	5	2048	U
9	5	2055	G
9	5	2056	G
9	5	2062	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	2064	G
9	5	2069	A
9	5	2084	C
9	5	2089	G
9	5	2092	G
9	5	2093	A
9	5	2094	G
9	5	2095	A
9	5	2097	U
9	5	2107	C
9	5	2248	C
9	5	2250	C
9	5	2252	G
9	5	2253	A
9	5	2254	G
9	5	2255	C
9	5	2257	C
9	5	2258	C
9	5	2259	G
9	5	2260	C
9	5	2261	G
9	5	2263	A
9	5	2264	C
9	5	2265	G
9	5	2266	C
9	5	2267	U
9	5	2268	A
9	5	2269	C
9	5	2270	G
9	5	2275	G
9	5	2289	C
9	5	2300	A
9	5	2301	G
9	5	2306	G
9	5	2313	A
9	5	2316	G
9	5	2331	G
9	5	2332	A
9	5	2333	G
9	5	2348	G
9	5	2351	C
9	5	2360	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	2395	A
9	5	2396	A
9	5	2410	C
9	5	2417	A
9	5	2422	C
9	5	2425	U
9	5	2432	U
9	5	2433	G
9	5	2441	C
9	5	2469	C
9	5	2471	G
9	5	2475	G
9	5	2488	C
9	5	2489	C
9	5	2490	U
9	5	2491	C
9	5	2503	G
9	5	2504	C
9	5	2505	C
9	5	2506	G
9	5	2507	A
9	5	2512	A
9	5	2513	A
9	5	2517	A
9	5	2530	U
9	5	2537	A
9	5	2544	G
9	5	2546	G
9	5	2547	G
9	5	2552	G
9	5	2554	U
9	5	2555	G
9	5	2571	C
9	5	2575	U
9	5	2576	G
9	5	2582	A
9	5	2583	C
9	5	2586	G
9	5	2587	A
9	5	2589	C
9	5	2602	G
9	5	2618	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	2619	G
9	5	2620	G
9	5	2640	G
9	5	2662	G
9	5	2673	G
9	5	2686	G
9	5	2687	U
9	5	2695	A
9	5	2696	A
9	5	2708	U
9	5	2710	C
9	5	2711	G
9	5	2712	G
9	5	2715	G
9	5	2725	A
9	5	2726	G
9	5	2740	U
9	5	2743	A
9	5	2753	G
9	5	2754	G
9	5	2758	G
9	5	2760	G
9	5	2762	G
9	5	2767	U
9	5	2768	C
9	5	2769	U
9	5	2770	C
9	5	2772	C
9	5	2787	A
9	5	2788	U
9	5	2790	U
9	5	2798	A
9	5	2811	G
9	5	2814	C
9	5	2826	U
9	5	2828	U
9	5	2838	G
9	5	2842	G
9	5	2855	G
9	5	2905	C
9	5	3593	C
9	5	3594	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	3596	A
9	5	3597	G
9	5	3602	C
9	5	3605	C
9	5	3606	U
9	5	3618	C
9	5	3625	G
9	5	3626	G
9	5	3635	A
9	5	3662	A
9	5	3672	G
9	5	3673	C
9	5	3692	A
9	5	3698	G
9	5	3710	G
9	5	3711	A
9	5	3748	A
9	5	3753	G
9	5	3759	A
9	5	3760	A
9	5	3773	U
9	5	3776	G
9	5	3777	G
9	5	3784	A
9	5	3786	U
9	5	3810	C
9	5	3811	G
9	5	3812	C
9	5	3814	U
9	5	3817	A
9	5	3819	G
9	5	3840	U
9	5	3877	A
9	5	3878	C
9	5	3879	G
9	5	3889	G
9	5	3892	U
9	5	3897	G
9	5	3901	A
9	5	3905	A
9	5	3906	A
9	5	3907	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	3908	A
9	5	3915	U
9	5	3917	A
9	5	3926	C
9	5	3927	U
9	5	3938	G
9	5	3939	G
9	5	4069	U
9	5	4070	U
9	5	4076	G
9	5	4077	A
9	5	4085	A
9	5	4086	G
9	5	4088	C
9	5	4090	G
9	5	4094	G
9	5	4097	G
9	5	4114	C
9	5	4115	G
9	5	4116	C
9	5	4117	U
9	5	4119	C
9	5	4120	U
9	5	4122	G
9	5	4125	C
9	5	4127	A
9	5	4128	A
9	5	4143	G
9	5	4144	C
9	5	4145	C
9	5	4162	C
9	5	4163	U
9	5	4166	G
9	5	4170	A
9	5	4171	C
9	5	4183	G
9	5	4184	G
9	5	4191	G
9	5	4203	A
9	5	4212	A
9	5	4225	G
9	5	4229	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	4233	A
9	5	4234	A
9	5	4241	C
9	5	4249	G
9	5	4251	A
9	5	4254	G
9	5	4267	G
9	5	4268	A
9	5	4271	A
9	5	4273	A
9	5	4280	A
9	5	4289	U
9	5	4291	G
9	5	4297	G
9	5	4304	A
9	5	4305	G
9	5	4306	U
9	5	4314	C
9	5	4318	C
9	5	4319	C
9	5	4330	G
9	5	4332	C
9	5	4336	A
9	5	4349	C
9	5	4350	C
9	5	4354	U
9	5	4355	G
9	5	4377	G
9	5	4378	A
9	5	4380	A
9	5	4387	C
9	5	4394	A
9	5	4395	U
9	5	4396	A
9	5	4398	C
9	5	4401	G
9	5	4415	A
9	5	4419	U
9	5	4421	C
9	5	4422	A
9	5	4436	U
9	5	4437	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	4440	G
9	5	4444	C
9	5	4448	G
9	5	4449	A
9	5	4453	C
9	5	4464	A
9	5	4471	U
9	5	4473	A
9	5	4476	C
9	5	4500	U
9	5	4512	U
9	5	4513	A
9	5	4518	A
9	5	4524	G
9	5	4528	G
9	5	4529	G
9	5	4548	A
9	5	4549	G
9	5	4560	C
9	5	4567	G
9	5	4570	G
9	5	4575	G
9	5	4577	U
9	5	4586	G
9	5	4590	A
9	5	4599	A
9	5	4617	G
9	5	4627	U
9	5	4636	U
9	5	4637	G
9	5	4647	G
9	5	4652	G
9	5	4656	A
9	5	4657	U
9	5	4667	C
9	5	4670	C
9	5	4671	C
9	5	4672	A
9	5	4677	U
9	5	4678	G
9	5	4682	U
9	5	4695	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	4697	U
9	5	4700	A
9	5	4709	U
9	5	4719	G
9	5	4720	C
9	5	4730	C
9	5	4731	G
9	5	4732	G
9	5	4742	G
9	5	4743	G
9	5	4744	A
9	5	4745	G
9	5	4746	C
9	5	4750	G
9	5	4753	U
9	5	4756	C
9	5	4757	C
9	5	4758	U
9	5	4760	G
9	5	4764	A
9	5	4770	U
9	5	4771	C
9	5	4869	U
9	5	4871	C
9	5	4873	G
9	5	4876	U
9	5	4878	C
9	5	4883	C
9	5	4884	G
9	5	4886	C
9	5	4889	G
9	5	4890	G
9	5	4896	G
9	5	4901	G
9	5	4902	C
9	5	4903	G
9	5	4904	G
9	5	4911	A
9	5	4913	G
9	5	4919	G
9	5	4927	G
9	5	4929	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	4930	C
9	5	4933	C
9	5	4936	G
9	5	4937	C
9	5	4944	C
9	5	4945	G
9	5	4948	C
9	5	4949	G
9	5	4950	U
9	5	4951	G
9	5	4959	U
9	5	4963	G
9	5	4964	C
9	5	4965	U
9	5	4966	A
9	5	4976	U
9	5	4988	U
9	5	4989	U
9	5	4990	C
9	5	4991	U
9	5	5006	U
9	5	5007	A
9	5	5013	C
9	5	5017	G
9	5	5023	C
9	5	5024	C
9	5	5026	U
9	5	5027	C
9	5	5028	G
9	5	5041	G
9	5	5047	C
9	5	5050	C
9	5	5054	C
9	5	5060	A
9	5	5061	A
9	5	5062	G
47	7	22	A
47	7	40	U
47	7	51	G
47	7	53	U
47	7	63	C
47	7	64	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
47	7	89	G
47	7	100	A
47	7	110	G
47	7	111	C
47	7	120	U
49	8	2	G
49	8	23	C
49	8	34	U
49	8	38	U
49	8	39	G
49	8	59	A
49	8	62	A
49	8	63	U
49	8	71	A
49	8	77	A
49	8	79	G
49	8	82	A
49	8	83	C
49	8	84	A
49	8	85	U
49	8	86	U
49	8	90	C
49	8	94	G
49	8	103	A
49	8	105	C
49	8	108	A
49	8	110	U
49	8	111	U
49	8	114	G
49	8	115	G
49	8	123	U
49	8	124	U
49	8	125	C
49	8	126	C
49	8	127	U
49	8	128	C

All (73) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	234	A
1	1	236	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	12	A
9	5	47	A
9	5	48	G
9	5	125	C
9	5	134	G
9	5	170	C
9	5	216	C
9	5	226	G
9	5	265	C
9	5	275	C
9	5	385	A
9	5	406	C
9	5	454	U
9	5	684	G
9	5	693	C
9	5	917	A
9	5	930	G
9	5	943	A
9	5	957	G
9	5	1211	G
9	5	1232	G
9	5	1236	C
9	5	1238	A
9	5	1296	G
9	5	1329	G
9	5	1357	C
9	5	1368	A
9	5	1380	G
9	5	1407	C
9	5	1440	U
9	5	1455	G
9	5	1633	G
9	5	1720	C
9	5	1804	A
9	5	2046	G
9	5	2068	C
9	5	2083	C
9	5	2093	A
9	5	2251	G
9	5	2256	C
9	5	2257	C
9	5	2260	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	5	2262	G
9	5	2265	G
9	5	2502	G
9	5	2506	G
9	5	2639	U
9	5	2695	A
9	5	3625	G
9	5	3697	U
9	5	3888	G
9	5	4069	U
9	5	4170	A
9	5	4232	U
9	5	4448	G
9	5	4528	G
9	5	4656	A
9	5	4699	U
9	5	4719	G
9	5	4885	U
9	5	4888	U
9	5	4889	G
9	5	4935	C
9	5	4948	C
9	5	4965	U
9	5	5022	U
9	5	5027	C
9	5	5059	C
9	5	5060	A
9	5	5061	A
49	8	124	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 [i](#)

Of 102 ligands modelled in this entry, 102 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

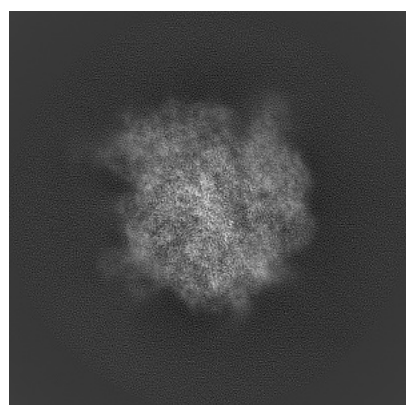
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14191. These allow visual inspection of the internal detail of the map and identification of artifacts.

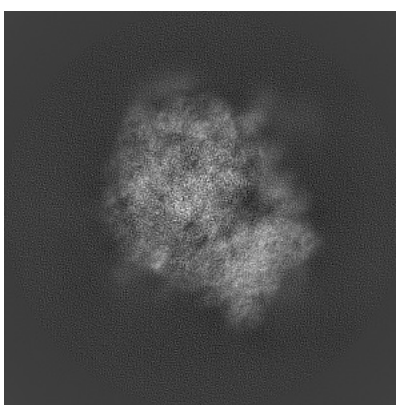
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

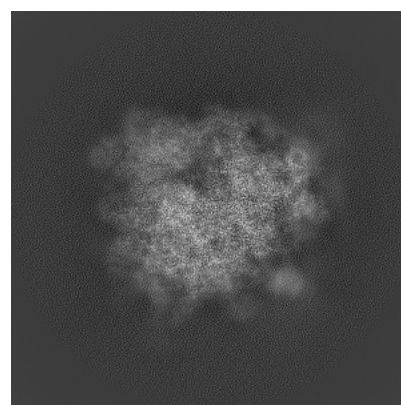
6.1.1 Primary map



X



Y

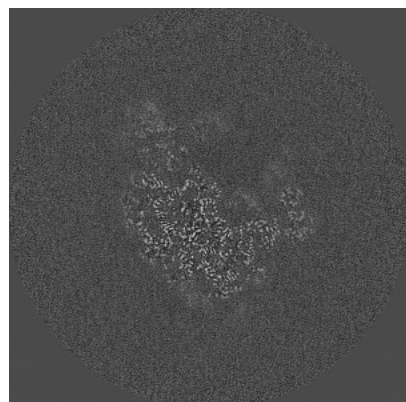


Z

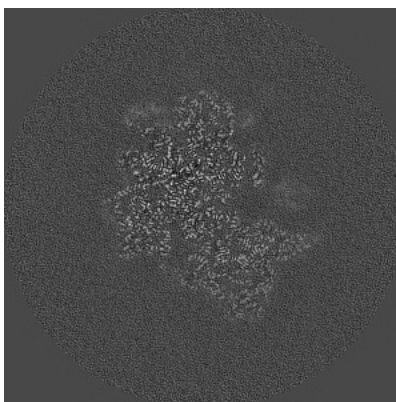
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

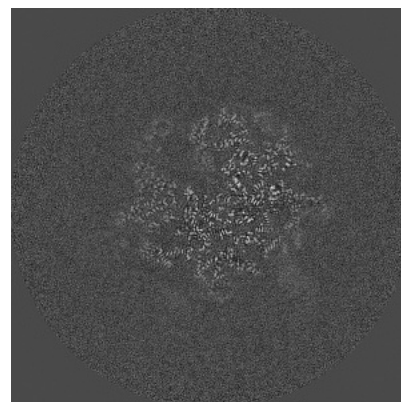
6.2.1 Primary map



X Index: 224



Y Index: 224

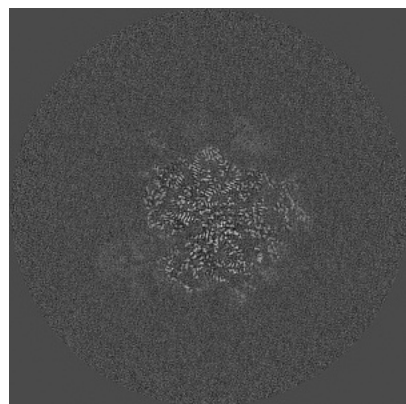


Z Index: 224

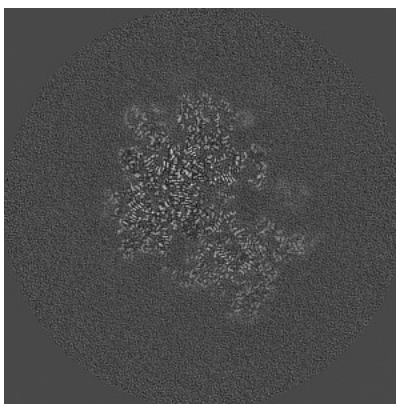
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

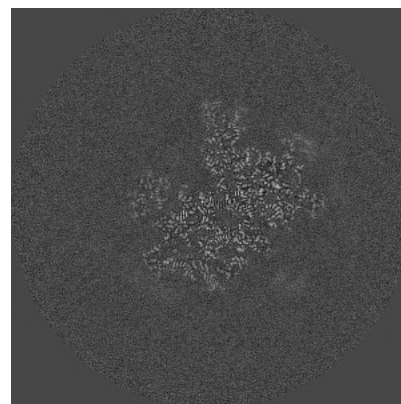
6.3.1 Primary map



X Index: 258



Y Index: 226

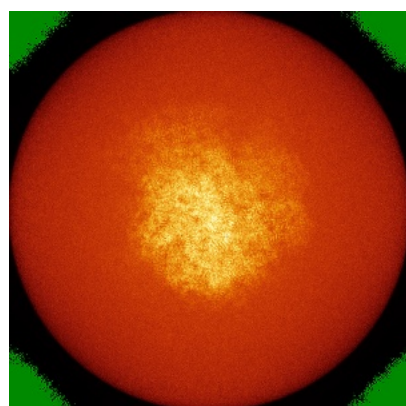


Z Index: 207

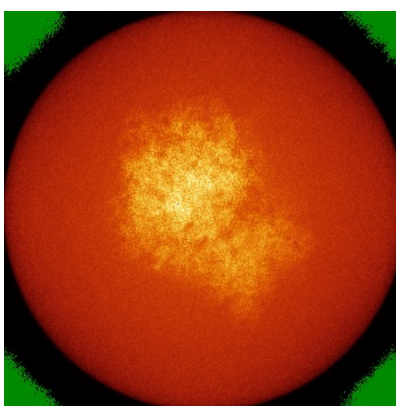
The images above show the largest variance slices of the map in three orthogonal directions.

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

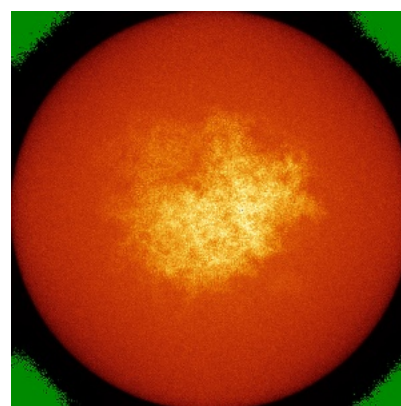
6.4.1 Primary map



X



Y

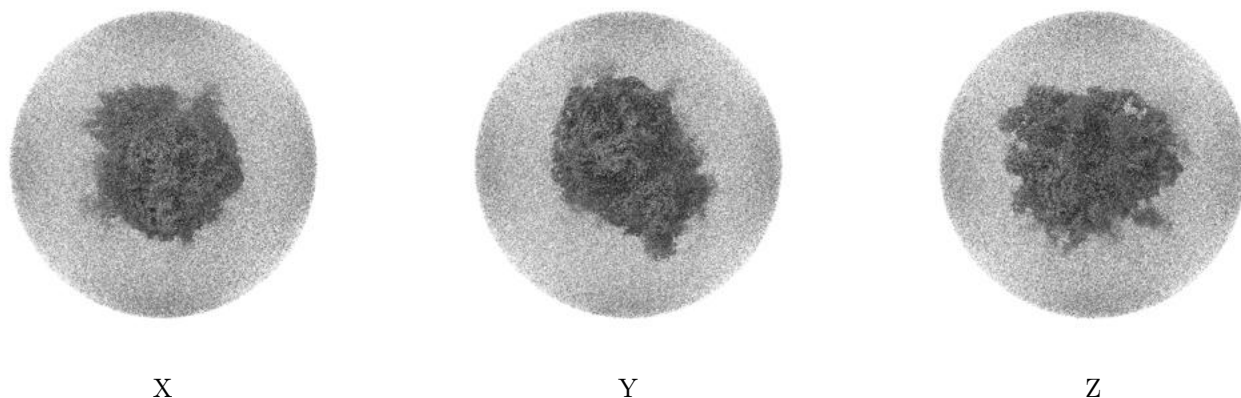


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.027. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

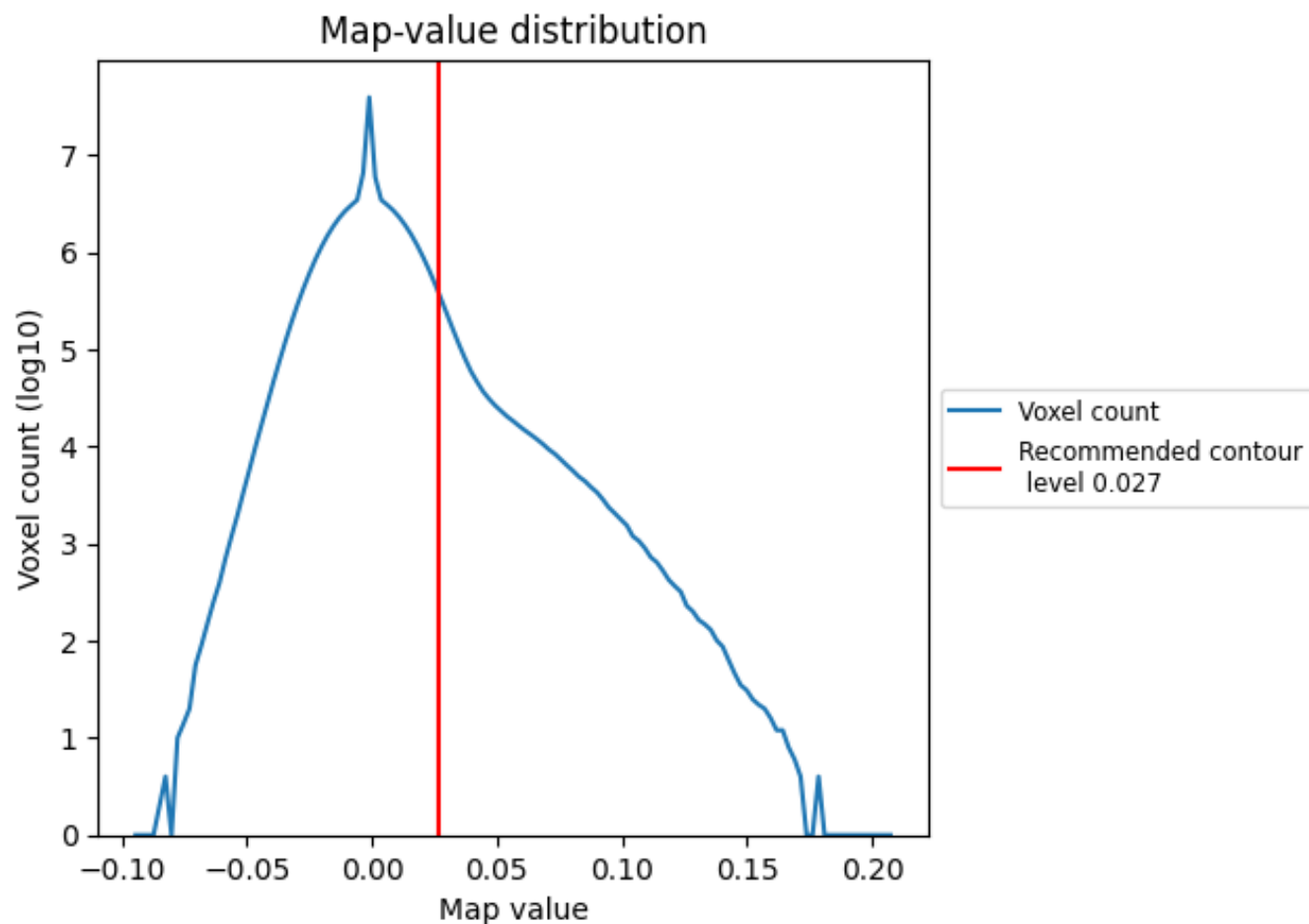
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

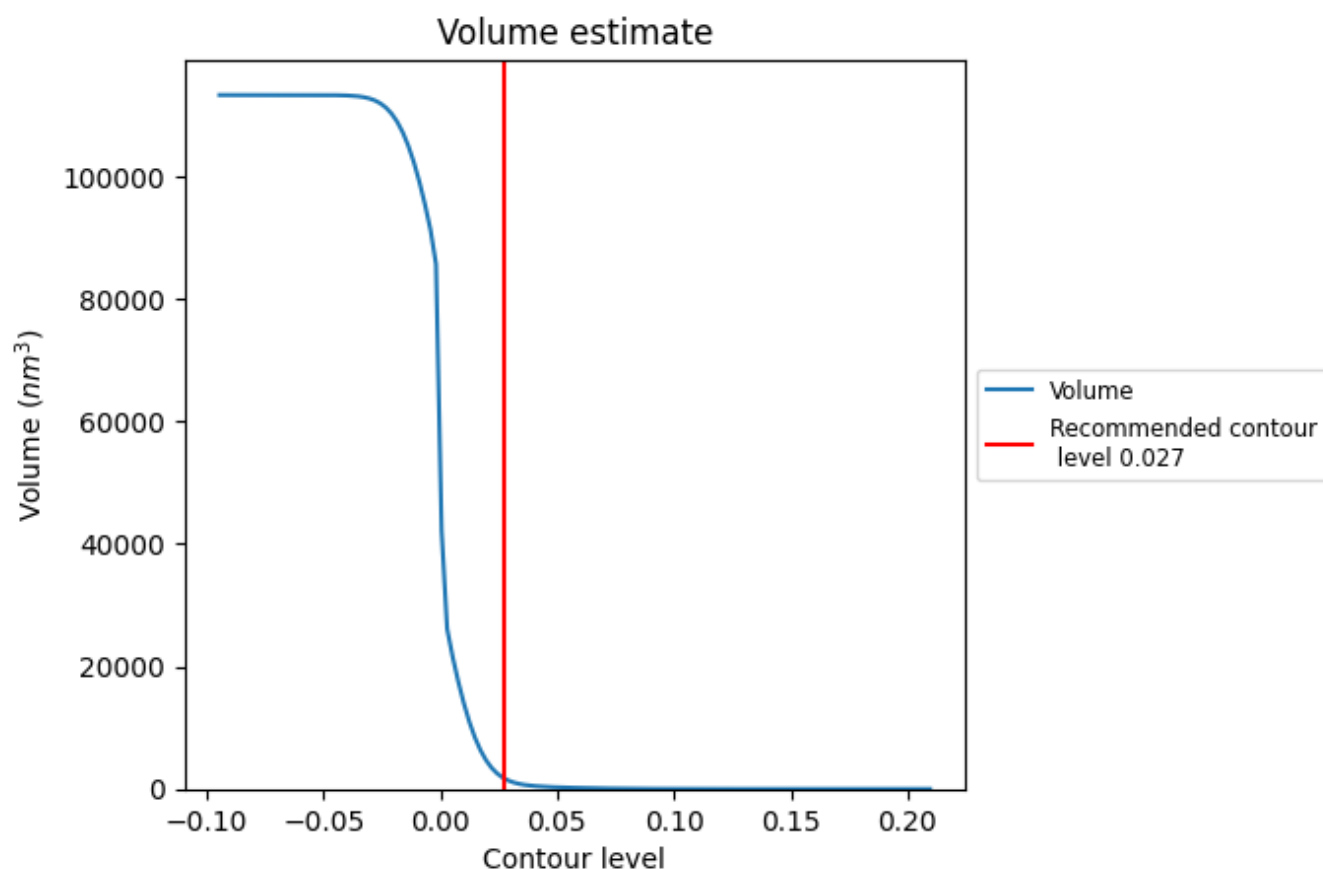
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

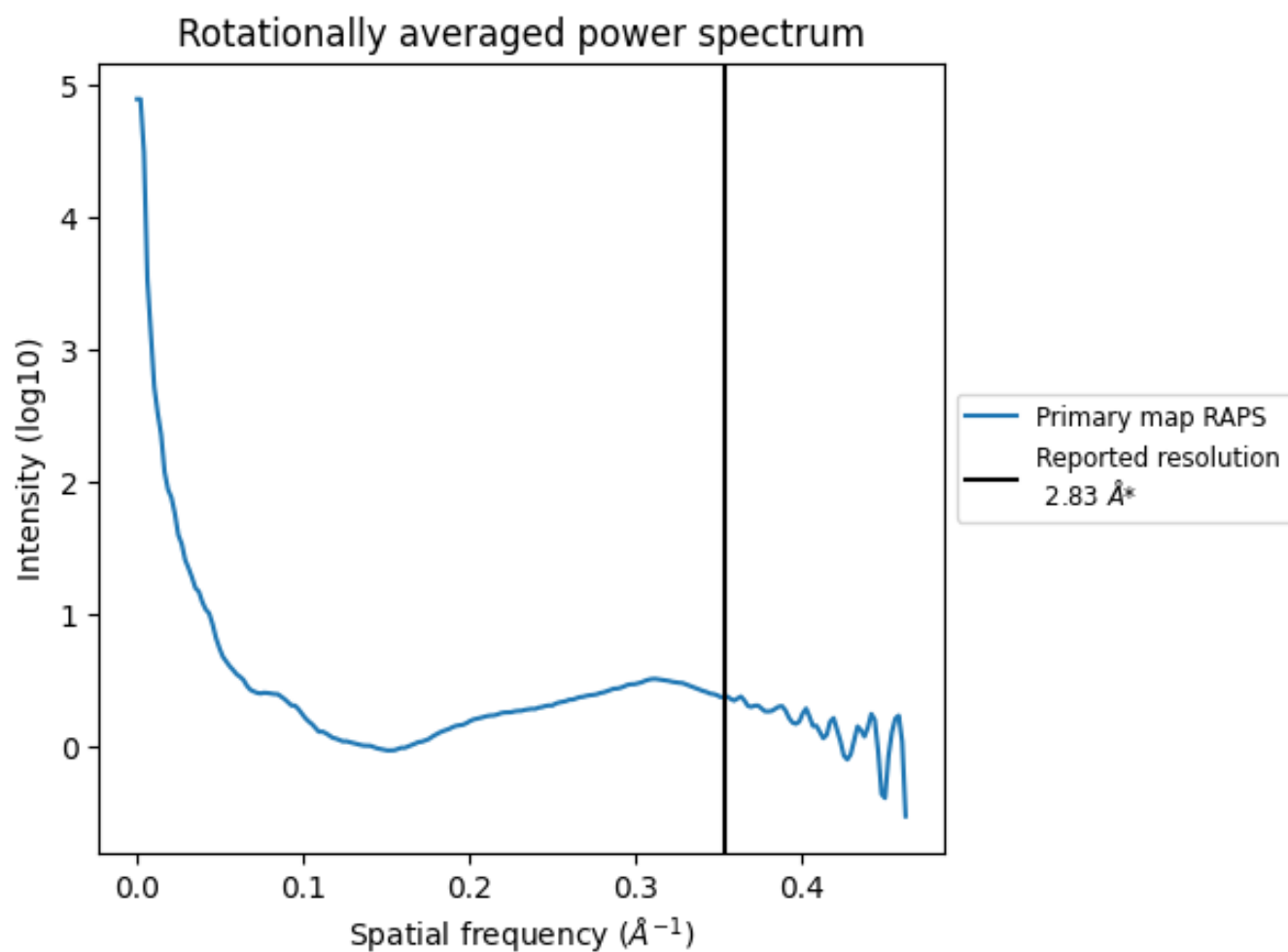
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1806 nm^3 ; this corresponds to an approximate mass of 1632 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 0.353 Å⁻¹

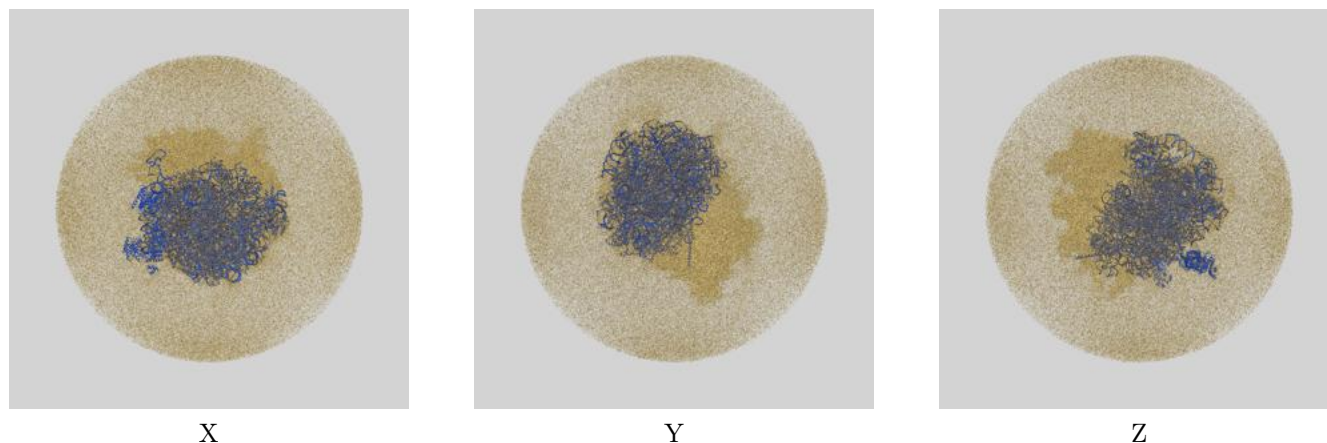
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

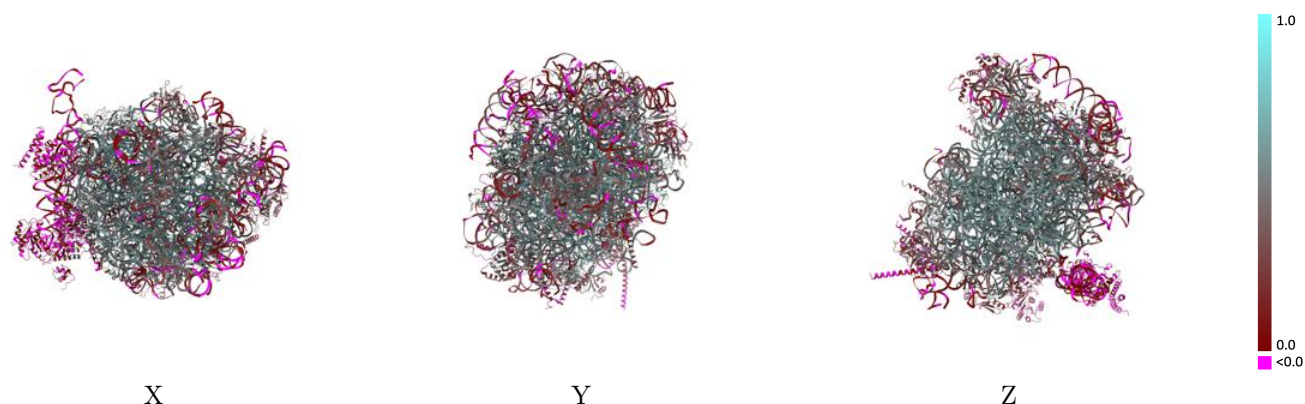
This section contains information regarding the fit between EMDB map EMD-14191 and PDB model 7QWQ. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

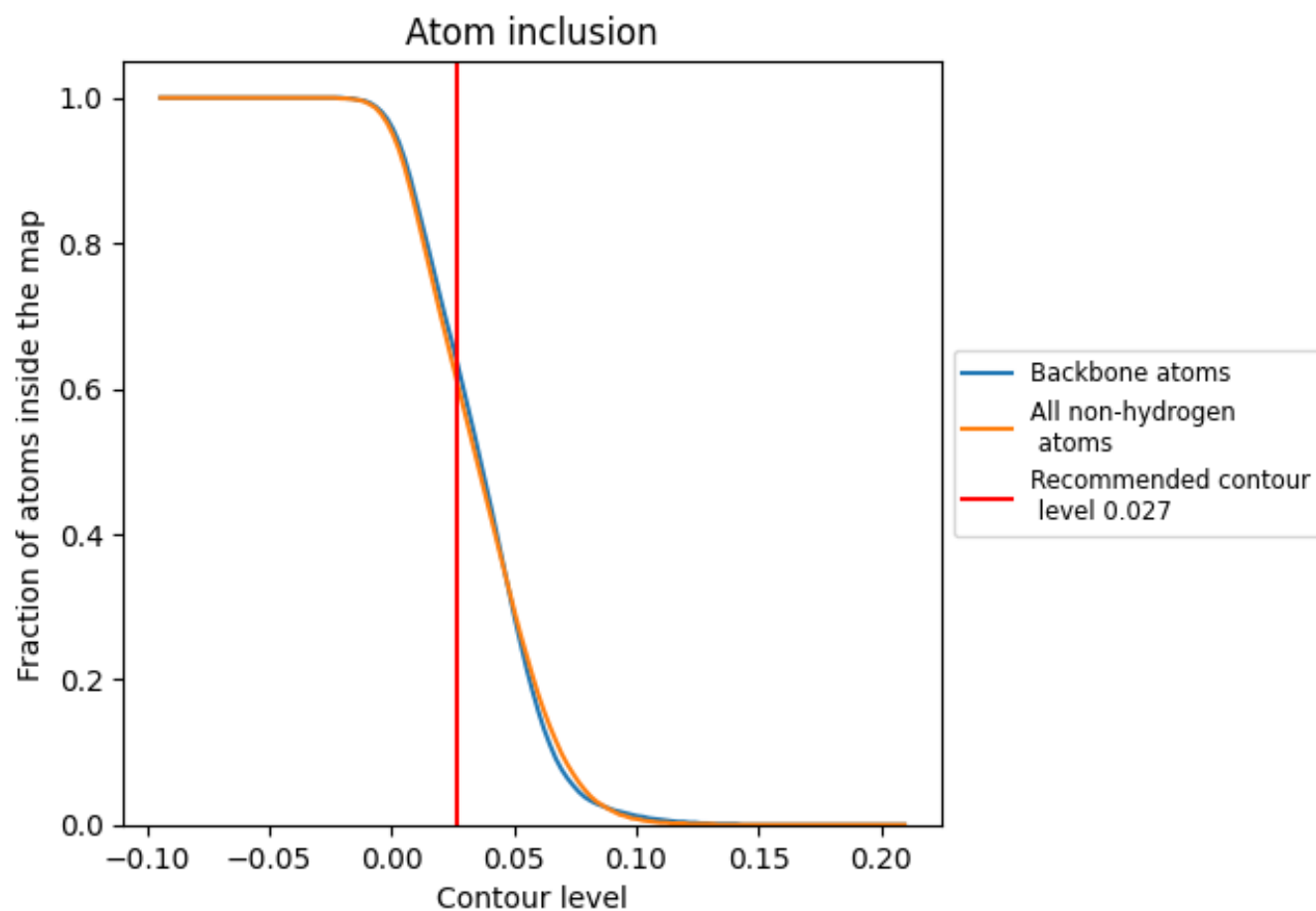


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6060	 0.4260
1	 0.0220	 0.0320
5	 0.6720	 0.4520
7	 0.6920	 0.4260
8	 0.7220	 0.4840
A	 0.7640	 0.5540
B	 0.7230	 0.5330
C	 0.7130	 0.5270
D	 0.4240	 0.3040
E	 0.4640	 0.3410
F	 0.7380	 0.5250
G	 0.4250	 0.3260
H	 0.5020	 0.3800
I	 0.6320	 0.4870
J	 0.3030	 0.2270
L	 0.5740	 0.4280
M	 0.5550	 0.3830
N	 0.7700	 0.5380
O	 0.7470	 0.5310
P	 0.7840	 0.5780
Q	 0.7570	 0.5580
R	 0.5450	 0.3790
S	 0.6970	 0.4990
T	 0.6160	 0.4770
U	 0.2170	 0.3430
V	 0.7220	 0.5260
W	 0.6400	 0.4820
X	 0.6120	 0.4690
Y	 0.6710	 0.5000
Z	 0.3710	 0.2430
a	 0.7590	 0.5320
b	 0.5160	 0.4270
c	 0.4010	 0.2660
d	 0.6300	 0.4740
e	 0.7950	 0.5870



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.7990	 0.5640
g	 0.5920	 0.4240
h	 0.6030	 0.4630
i	 0.5250	 0.4080
j	 0.8220	 0.5760
k	 0.3390	 0.2670
l	 0.6830	 0.5250
m	 0.5960	 0.4340
n	 0.4180	 0.3770
o	 0.6250	 0.4870
p	 0.6650	 0.4980
q	 0.0120	 0.0720
r	 0.6800	 0.4950
s	 0.0500	 0.1370
t	 0.0390	 0.0670
u	 0.0450	 0.2840
v	 0.0080	 0.0480
x	 0.0560	 0.1430