



Full wwPDB EM Validation Report ⓘ

Mar 15, 2026 – 03:27 AM UTC

PDB ID : 8ETG / pdb_00008etg
EMDB ID : EMD-24397
Title : Fkbp39 associated 60S nascent ribosome State 3
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-17
Resolution : 3.40 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:

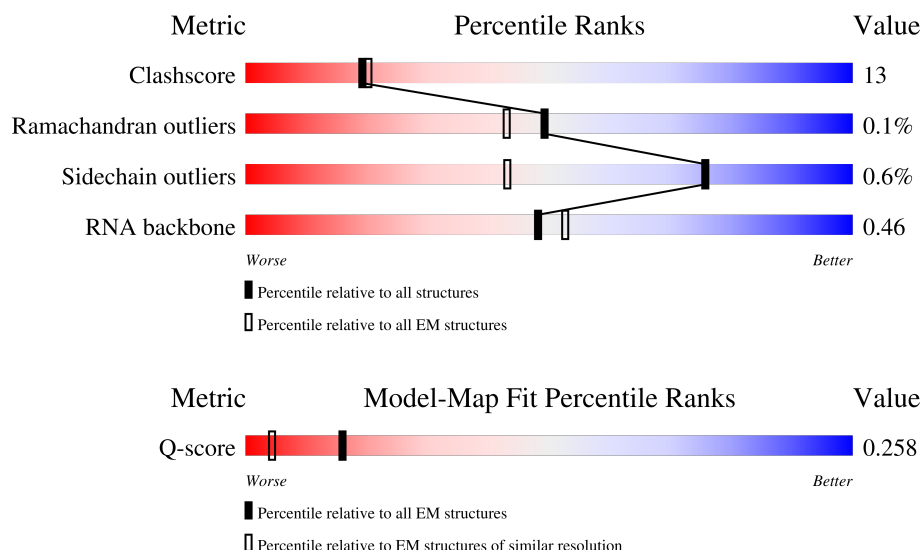
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 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.



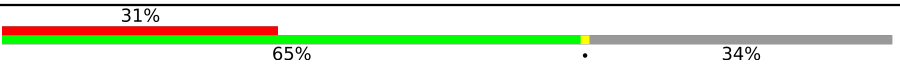
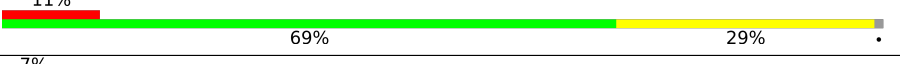
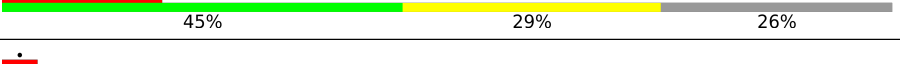
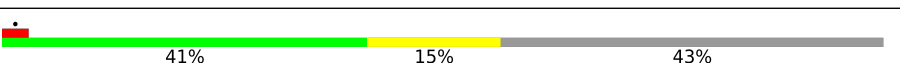
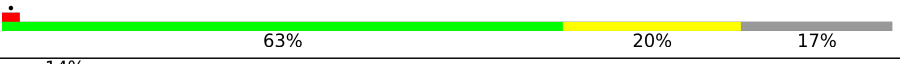
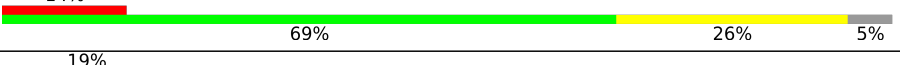
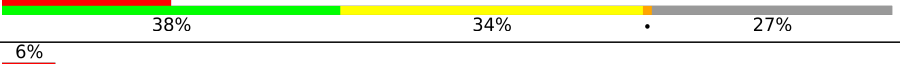
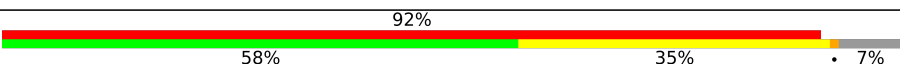
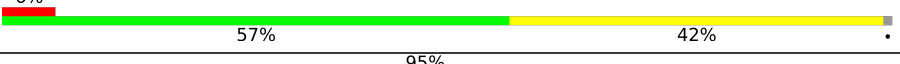
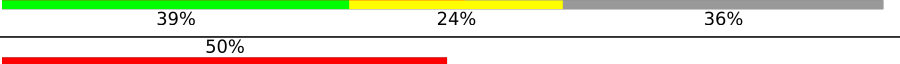
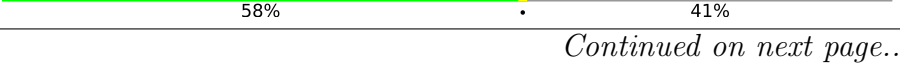
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	3497	
2	2	165	
3	3	302	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	A	295	
5	B	388	
6	C	363	
7	D	578	
8	E	195	
9	F	250	
10	G	259	
11	H	190	
12	K	373	
13	L	208	
14	M	134	
15	N	201	
16	O	197	
17	P	187	
18	Q	187	
19	R	193	
20	S	176	
21	U	117	
22	V	139	
23	W	241	
24	X	141	
25	Y	126	
26	Z	136	
27	a	148	
28	b	642	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	c	117	
30	d	113	
31	e	127	
32	f	108	
33	g	112	
34	h	122	
35	i	99	
36	j	91	
37	k	74	
38	m	740	
39	n	607	
40	o	276	
41	p	440	
42	r	260	
43	t	249	
44	u	192	
45	v	209	
46	y	244	
47	T	160	
48	6	300	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 99257 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 RNA (1912-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2018	Total	C	N	O	P	0	0
			43202	19298	7842	14044	2018		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	3196	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	146	Total	C	N	O	P	0	0
			3102	1388	547	1021	146		

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	S	0	0
			1015	642	190	177	6		

- Molecule 4 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	A	196	Total	C	N	O	0	0
			1015	610	201	204		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	334	Total	C	N	O	S	0	0
			2653	1682	491	471	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	359	Total	C	N	O	S	0	0
			2795	1765	536	491	3		

- Molecule 7 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	D	82	Total	C	N	O	0	0
			408	244	82	82		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	145	Total	C	N	O	S	0	0
			1126	723	208	192	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	214	Total	C	N	O	S	0	0
			1745	1124	320	298	3		

- Molecule 10 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	184	Total	C	N	O	S	0	0
			1452	934	262	254	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	183	Total	C	N	O	S	0	0
			1451	914	266	265	6		

- Molecule 12 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	K	231	Total	C	N	O	0	0
			1145	683	231	231		

- Molecule 13 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	118	Total	C	N	O	S	0	0
			962	603	204	154	1		

- Molecule 14 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	124	Total	C	N	O	S	0	0
			1000	639	190	167	4		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	166	Total	C	N	O	S	0	0
			1406	883	291	229	3		

- Molecule 16 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	187	Total	C	N	O	S	0	0
			1483	956	281	242	4		

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	136	Total	C	N	O	S	0	0
			1080	690	196	191	3		

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	130	Total	C	N	O	S	0	0
			1020	646	196	177	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	57	Total	C	N	O	S	0	0
			456	282	93	78	3		

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	174	Total	C	N	O	S	0	0
			1434	925	269	235	5		

- Molecule 21 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	98	Total	C	N	O	0	0
			484	288	98	98		

- Molecule 22 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	129	Total	C	N	O	S	0	0
			976	617	179	172	8		

- Molecule 23 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	193	Total	C	N	O	0	0
			948	562	193	193		

- Molecule 24 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	130	Total	C	N	O	S	0	0
			1032	658	192	181	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Z	129	Total	C	N	O	0	0
			637	378	129	130		

- Molecule 27 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	a	94	Total	C	N	O	0	0
			747	474	142	131		

- Molecule 28 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	b	378	Total	C	N	O	0	0
			1875	1119	378	378		

- Molecule 29 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	c	66	Total	C	N	O	0	0
			325	193	66	66		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	94	Total	C	N	O	S	0	0
			787	500	156	128	3		

- Molecule 31 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	117	Total	C	N	O	S	0	0
			939	588	190	156	5		

- Molecule 32 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
33	g	87	Total	C	N	O	0	0
			428	254	87	87		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
34	h	121	Total	C	N	O	0	0
			999	629	194	176		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
35	i	78	Total	C	N	O	S	0
			637	394	135	107	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
36	j	71	Total	C	N	O	S	0
			563	346	121	90	6	0

- Molecule 37 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	k	70	Total	C	N	O		0
			349	209	70	70		0

- Molecule 38 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	m	484	Total	C	N	O	S	0
			2881	1757	557	566	1	0

- Molecule 39 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	n	416	Total	C	N	O	S	0
			3389	2186	587	604	12	0

- Molecule 40 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	o	109	Total	C	N	O	S	0
			897	579	162	150	6	0

- Molecule 41 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	p	287	Total	C	N	O	0	0
			1416	842	287	287		

- Molecule 42 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	154	Total	C	N	O	S	0	0
			1009	613	208	187	1		

- Molecule 43 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	235	Total	C	N	O	S	0	0
			1948	1242	367	334	5		

- Molecule 44 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	u	99	Total	C	N	O	0	0
			491	293	99	99		

- Molecule 45 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	140	Total	C	N	O	S	0	0
			1143	721	220	199	3		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	y	225	Total	C	N	O	0	0
			1107	657	225	225		

- Molecule 47 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	T	19	Total	C	N	O	0	0
			147	93	26	28		

- Molecule 48 is a RNA chain called RNA (62-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
48	6	62	Total	C	N	O	P	0	0
			1315	590	229	434	62		

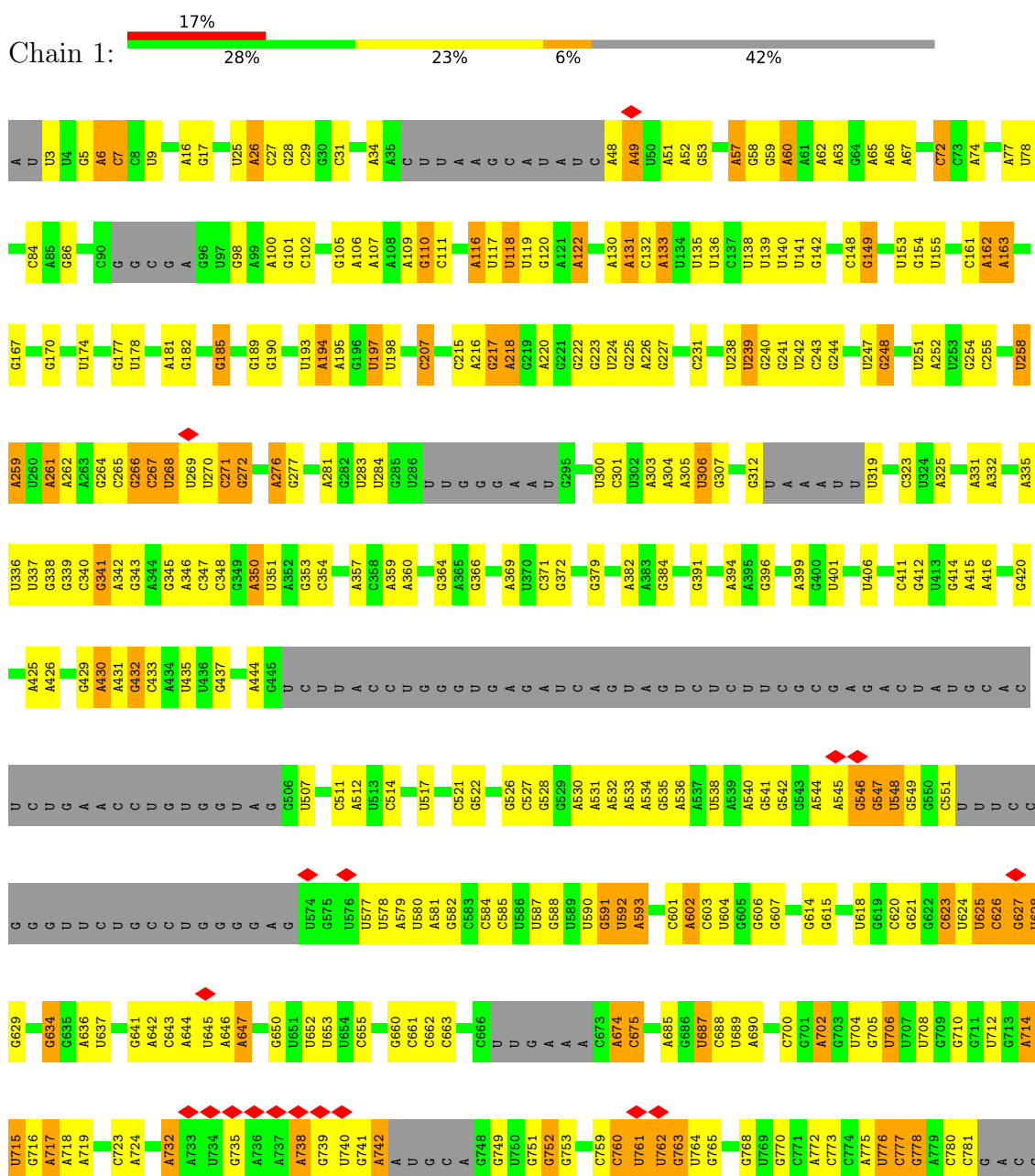
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

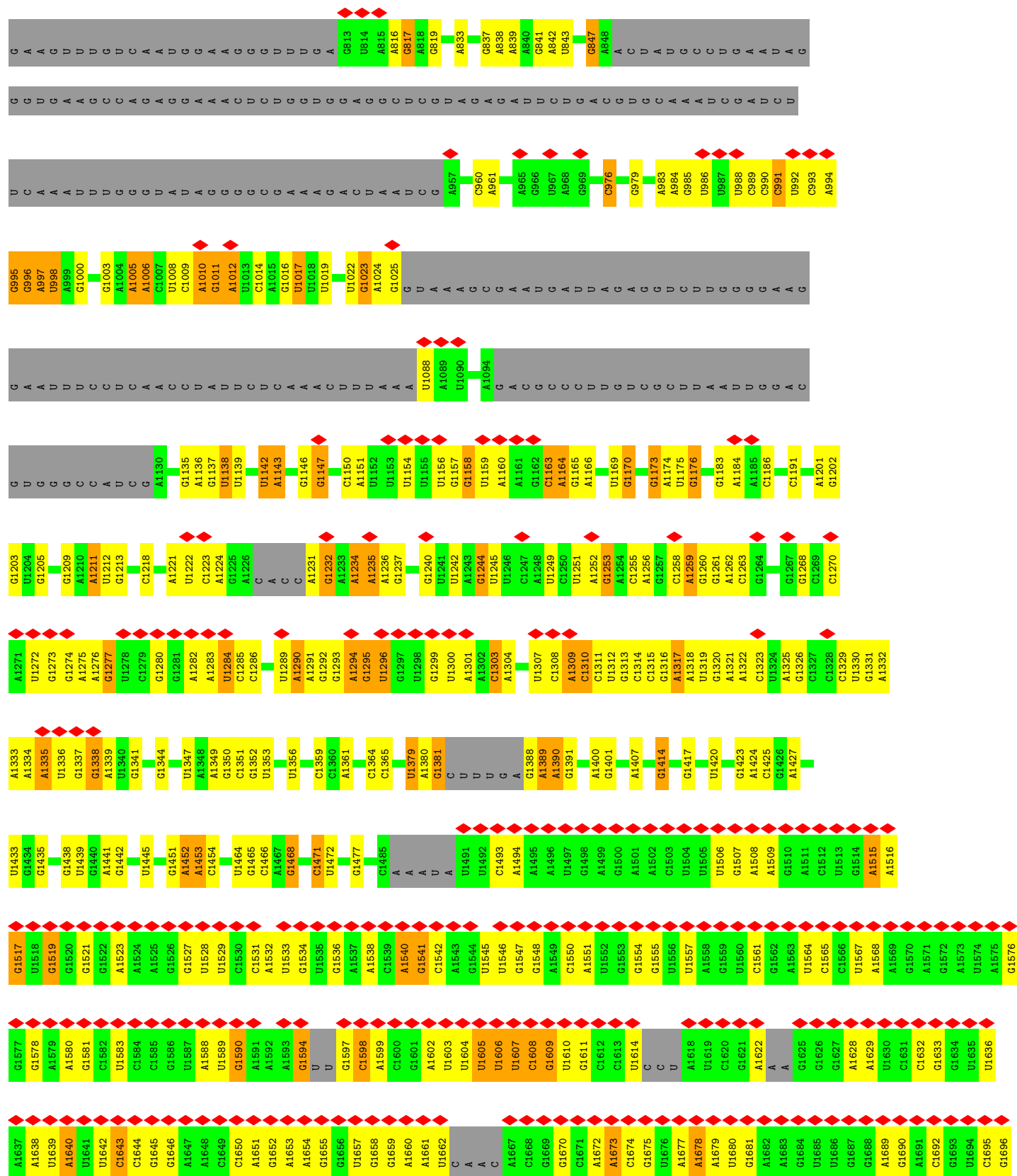
Mol	Chain	Residues	Atoms		AltConf
49	j	1	Total	Zn	0
			1	1	

3 Residue-property plots [i](#)

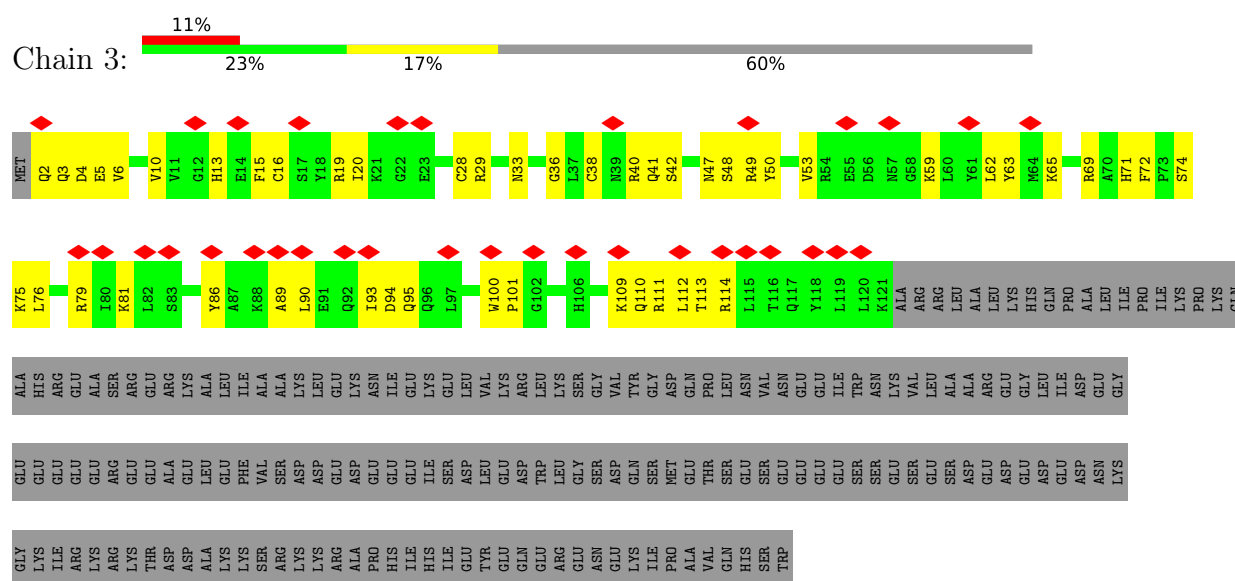
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: RNA (1912-MER)

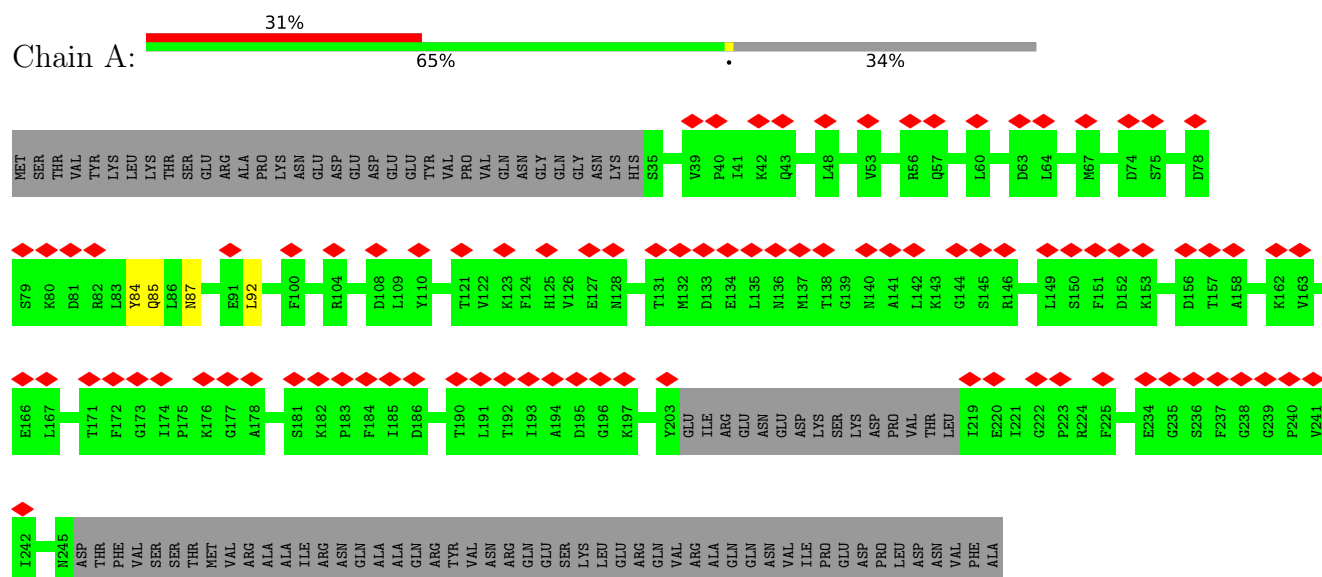




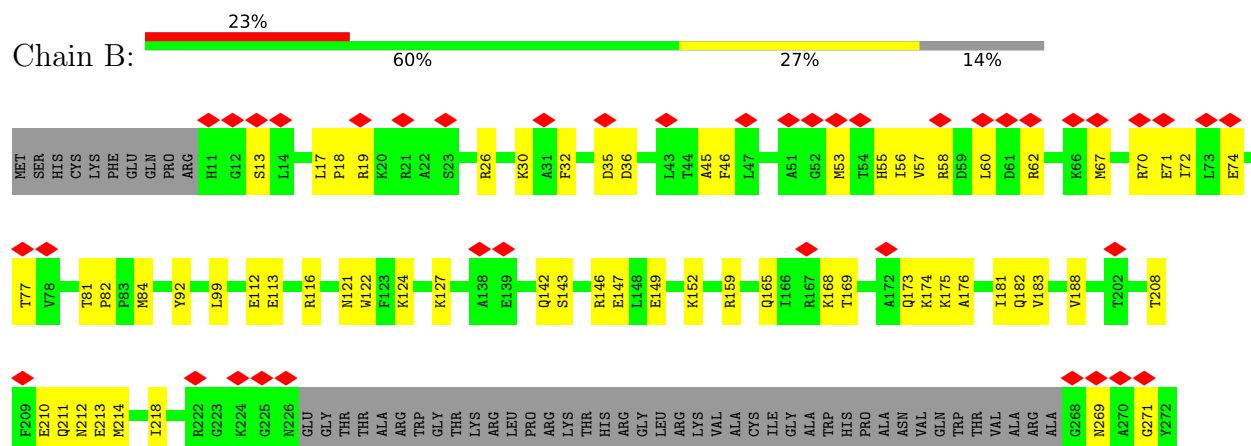




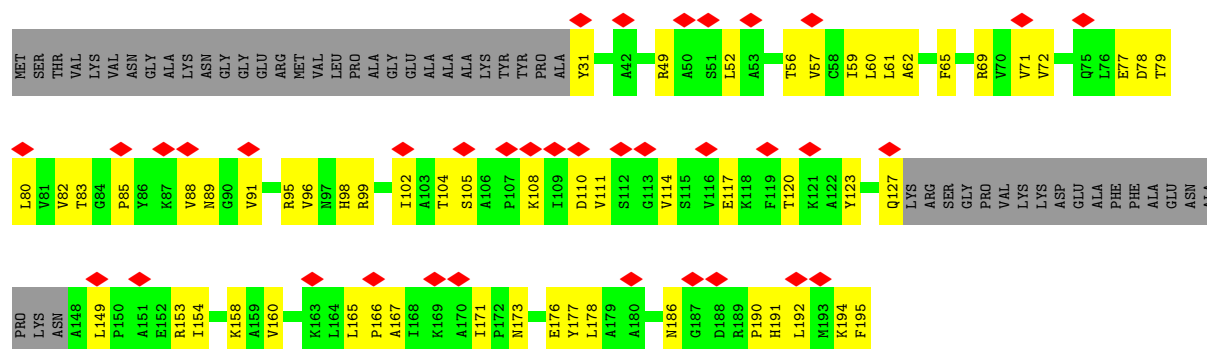
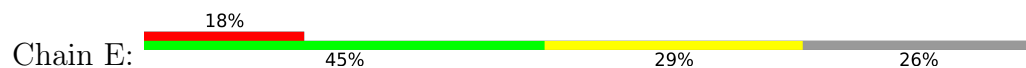
- Molecule 4: Ribosome biogenesis protein brx1



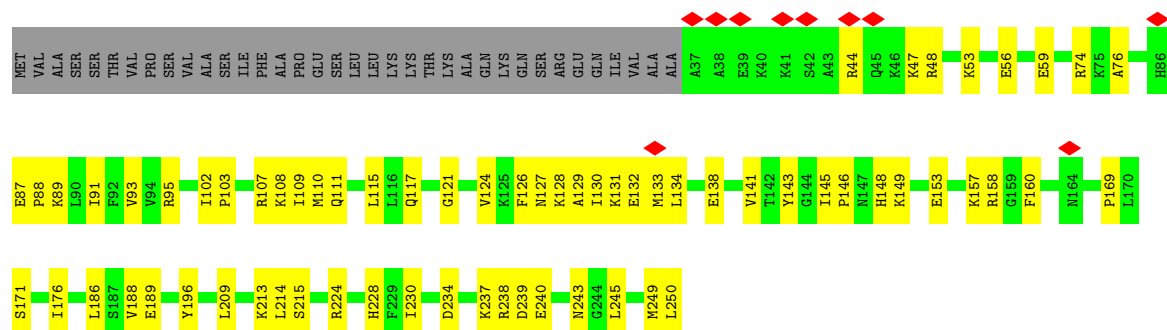
- Molecule 5: 60S ribosomal protein L3-A



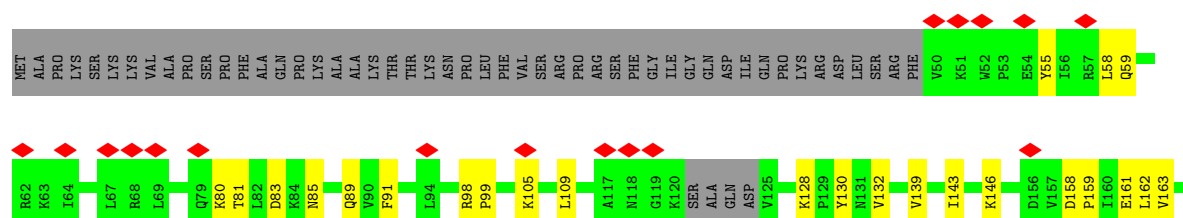
- Molecule 8: 60S ribosomal protein L6

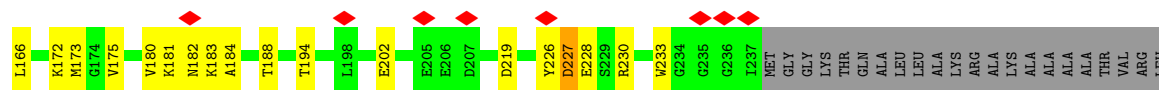


- Molecule 9: 60S ribosomal protein L7-B



- Molecule 10: 60S ribosomal protein L8

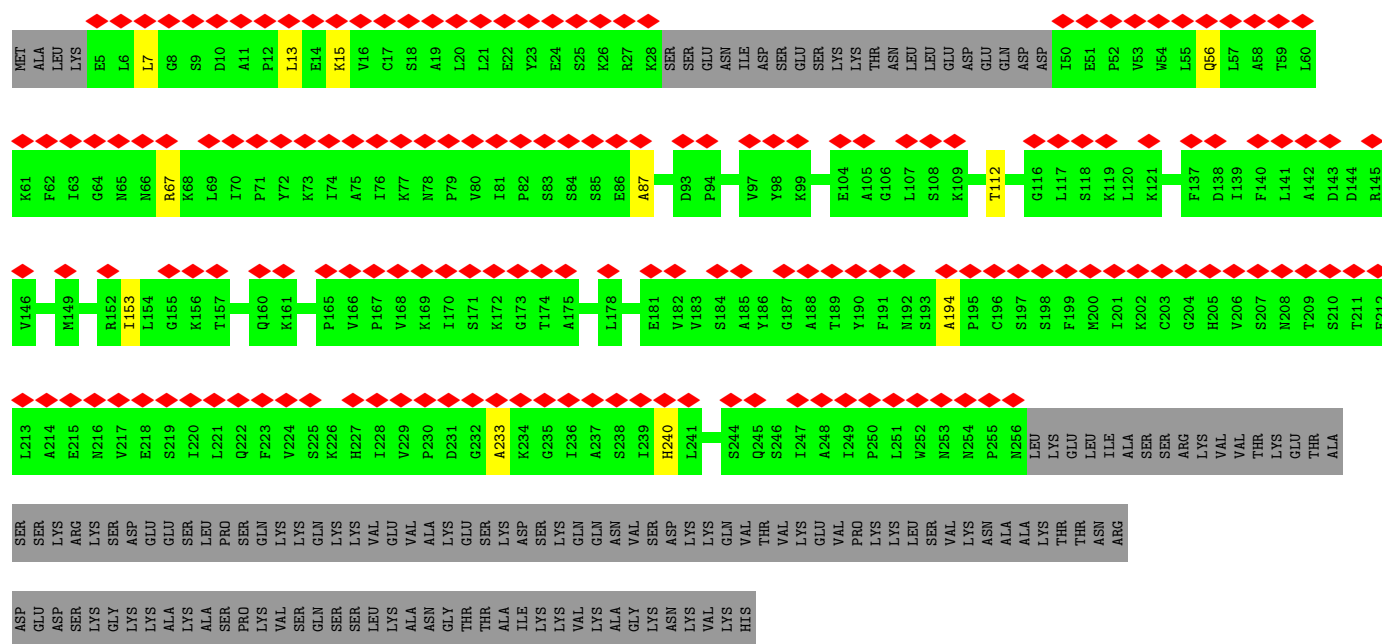




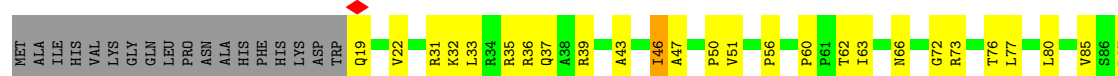
• Molecule 11: 60S ribosomal protein L9-A

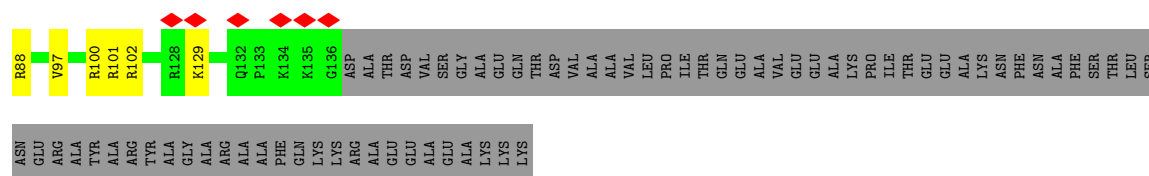


• Molecule 12: Putative ribosome biogenesis protein C8F11.04

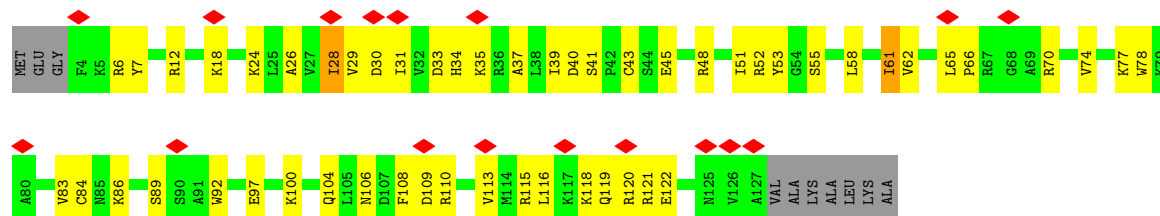


• Molecule 13: 60S ribosomal protein L13

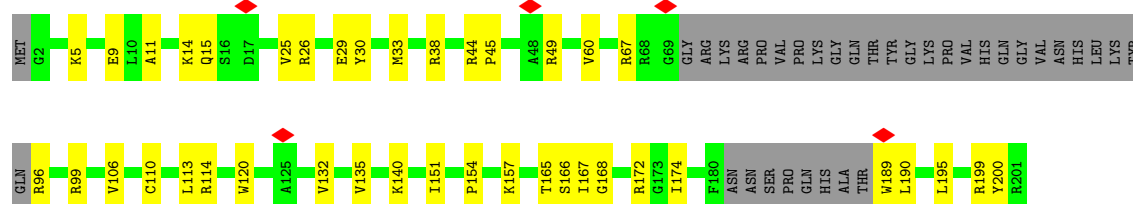




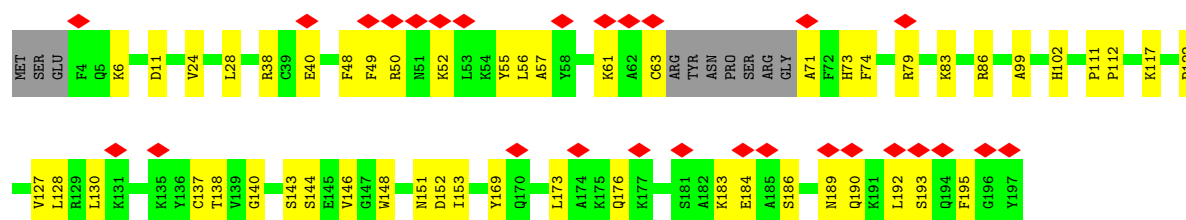
- Molecule 14: 60S ribosomal protein L14



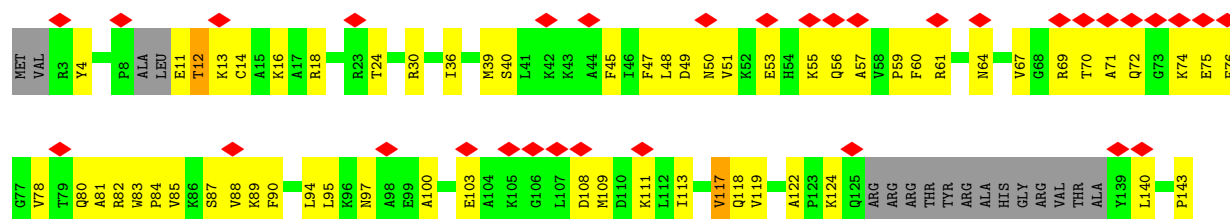
- Molecule 15: 60S ribosomal protein L15-A

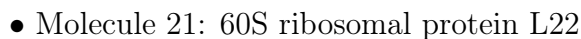
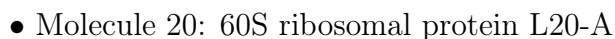
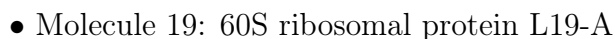


- Molecule 16: 60S ribosomal protein L16-B



- Molecule 17: 60S ribosomal protein L17-A







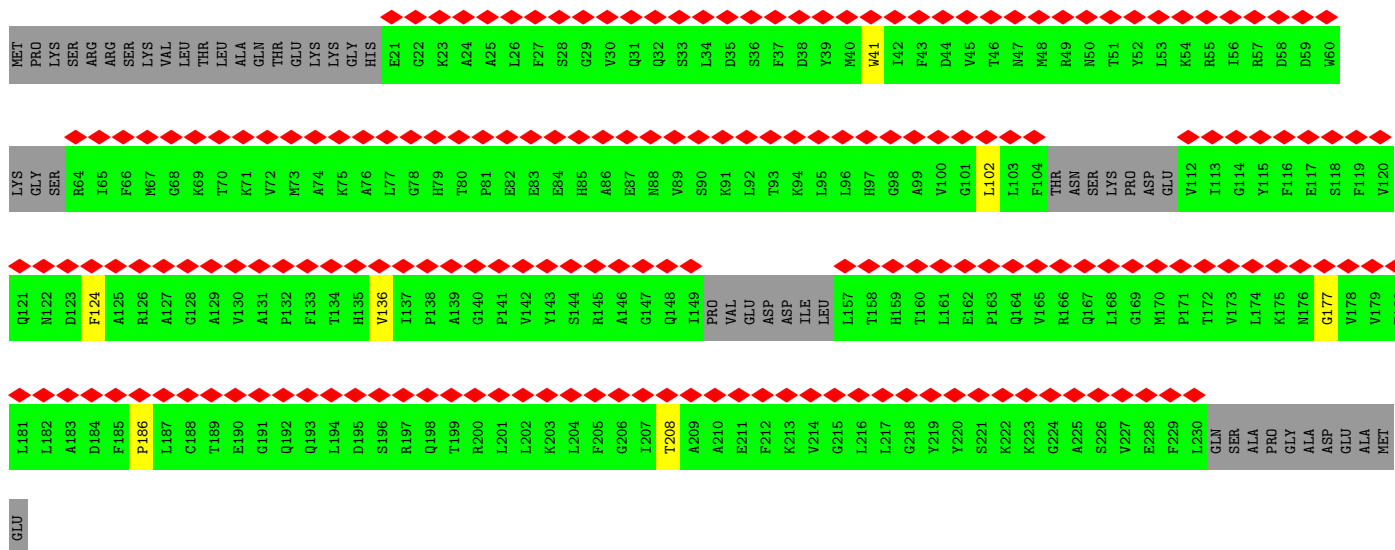
• Molecule 22: 60S ribosomal protein L23-A

Chain V:



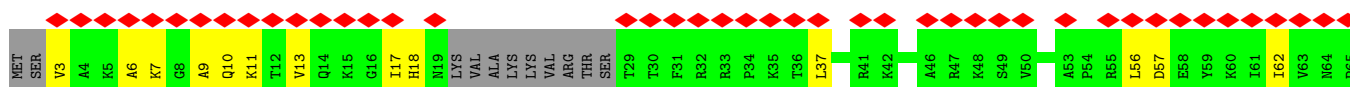
• Molecule 23: Ribosome assembly factor mrt4

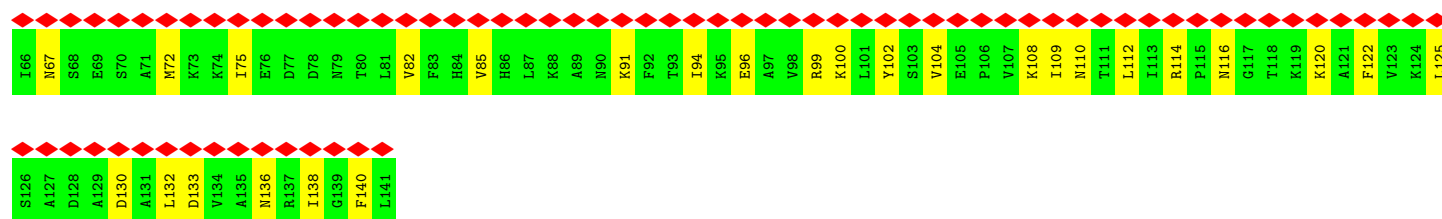
Chain W:



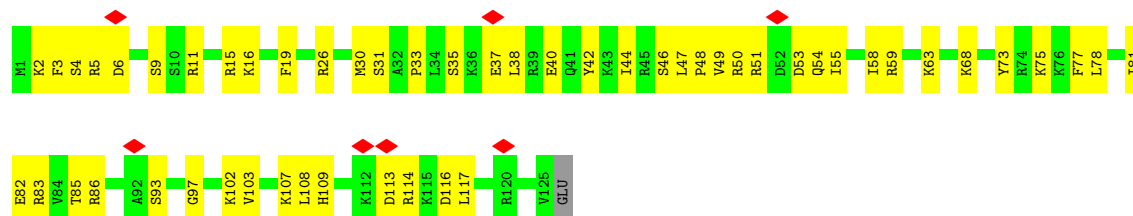
• Molecule 24: 60S ribosomal protein L25-A

Chain X:

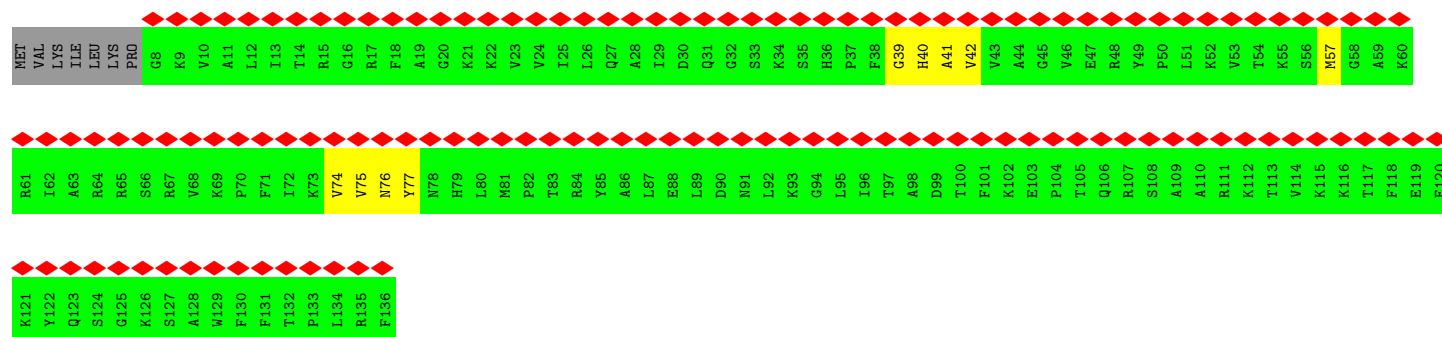
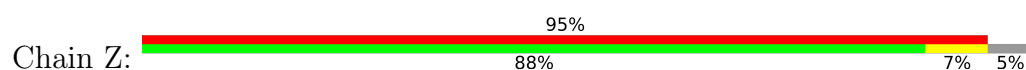




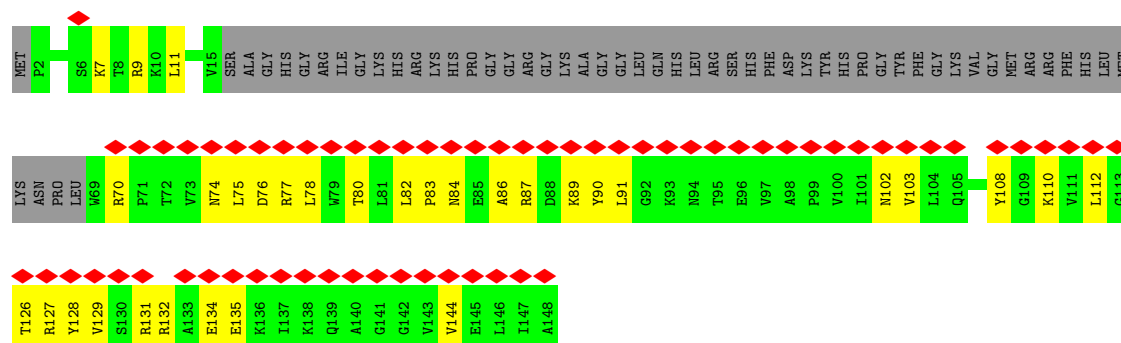
• Molecule 25: 60S ribosomal protein L26



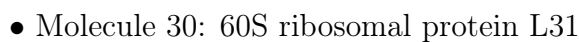
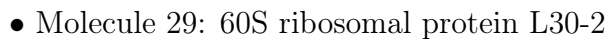
• Molecule 26: 60S ribosomal protein L27-A

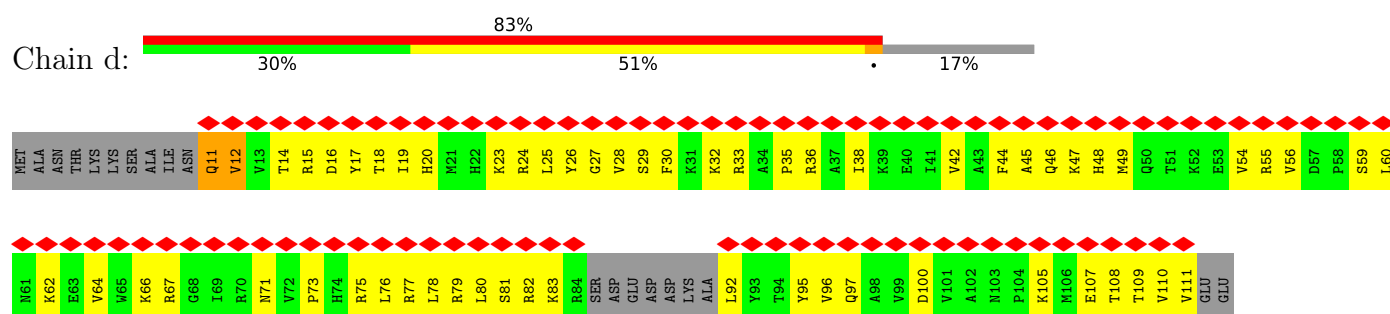


• Molecule 27: 60S ribosomal protein L28-A

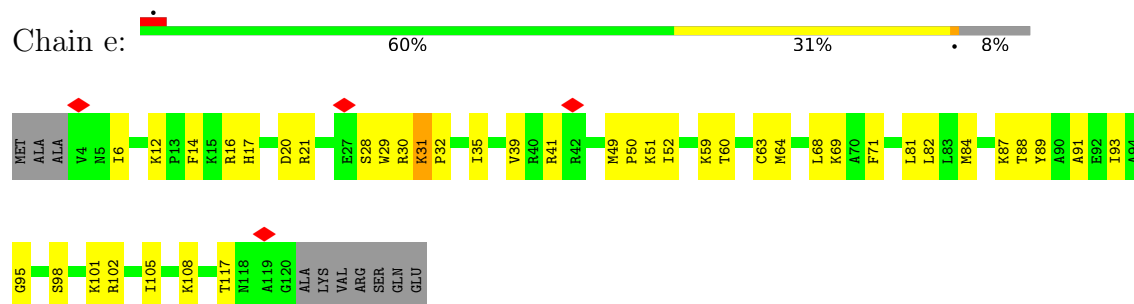


• Molecule 28: Probable nucleolar GTP-binding protein 1

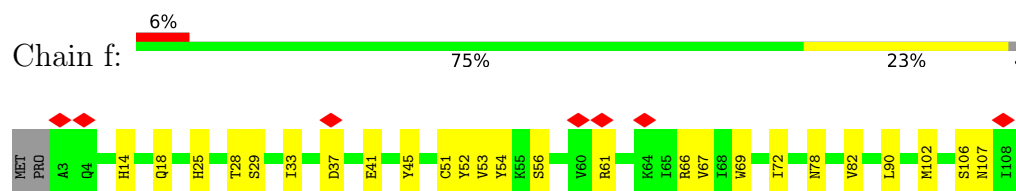




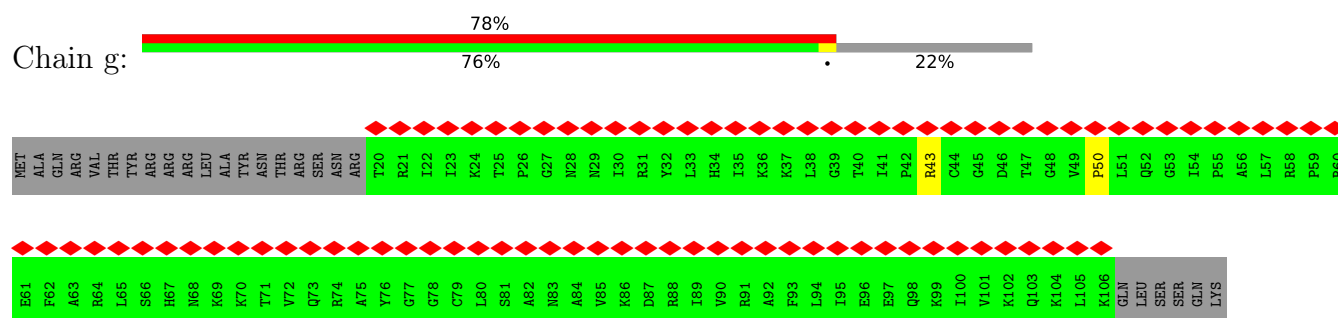
- Molecule 31: 60S ribosomal protein L32-A



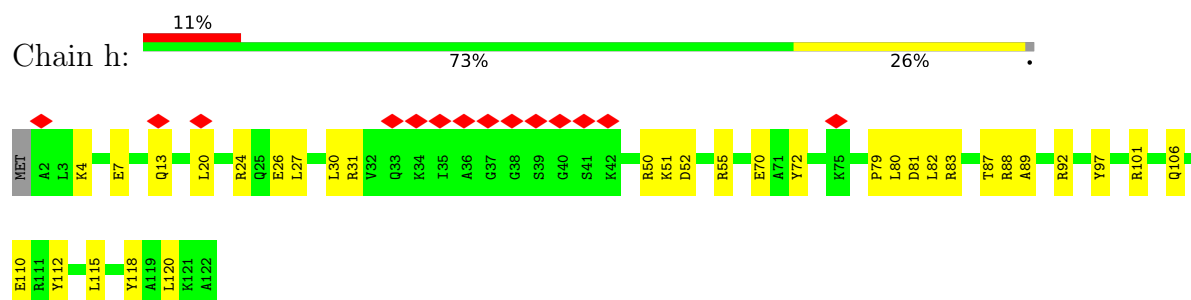
- Molecule 32: 60S ribosomal protein L33-B



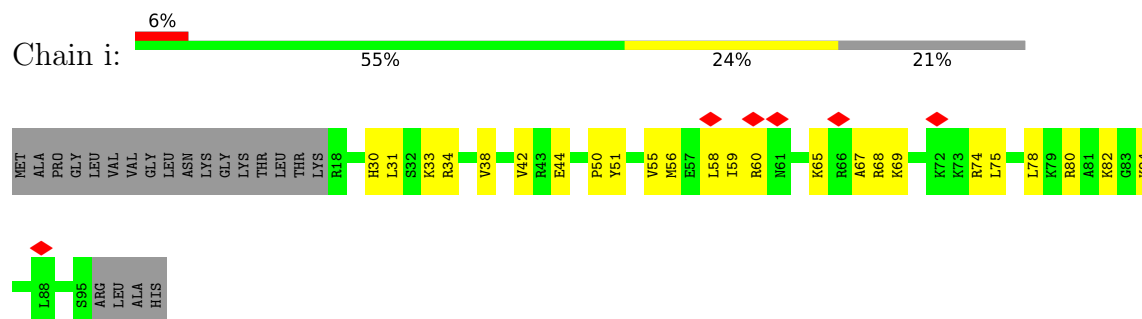
- Molecule 33: 60S ribosomal protein L34-A



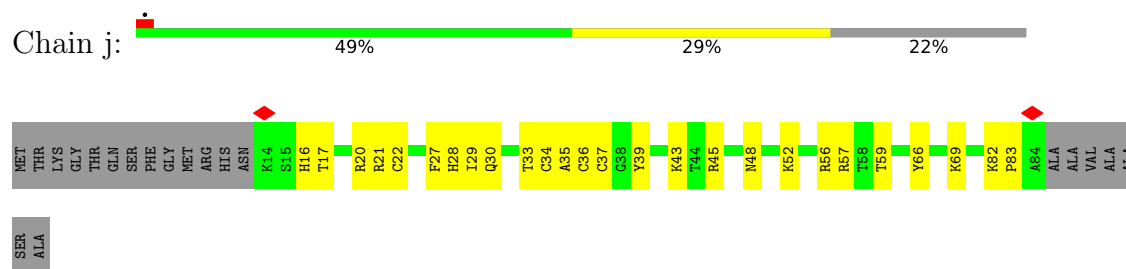
- Molecule 34: 60S ribosomal protein L35



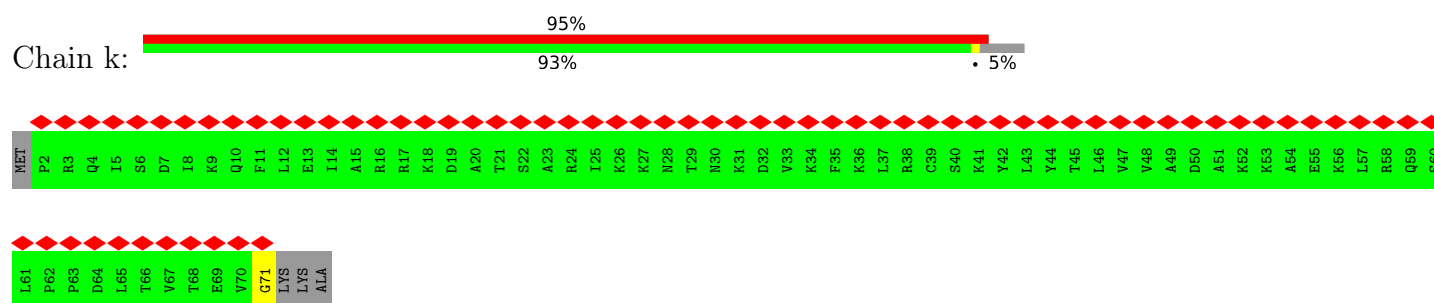
- Molecule 35: 60S ribosomal protein L36-B



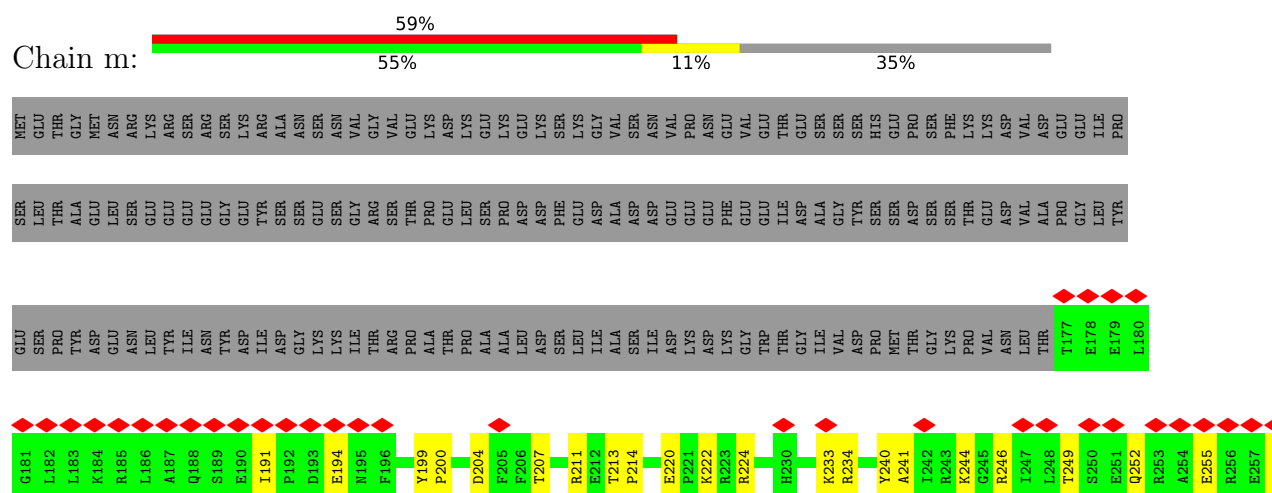
- Molecule 36: 60S ribosomal protein L37-B

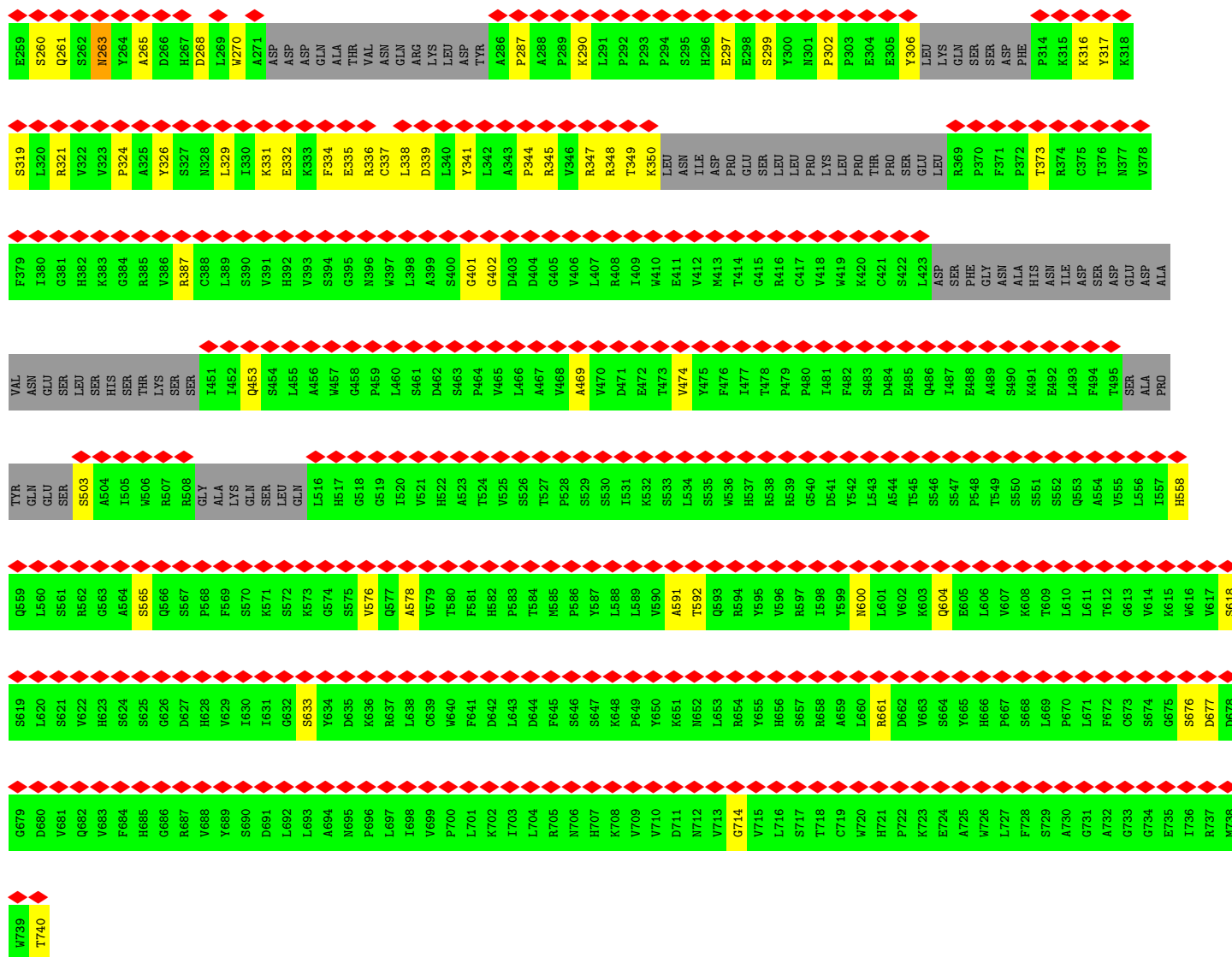


- Molecule 37: 60S ribosomal protein L38-1

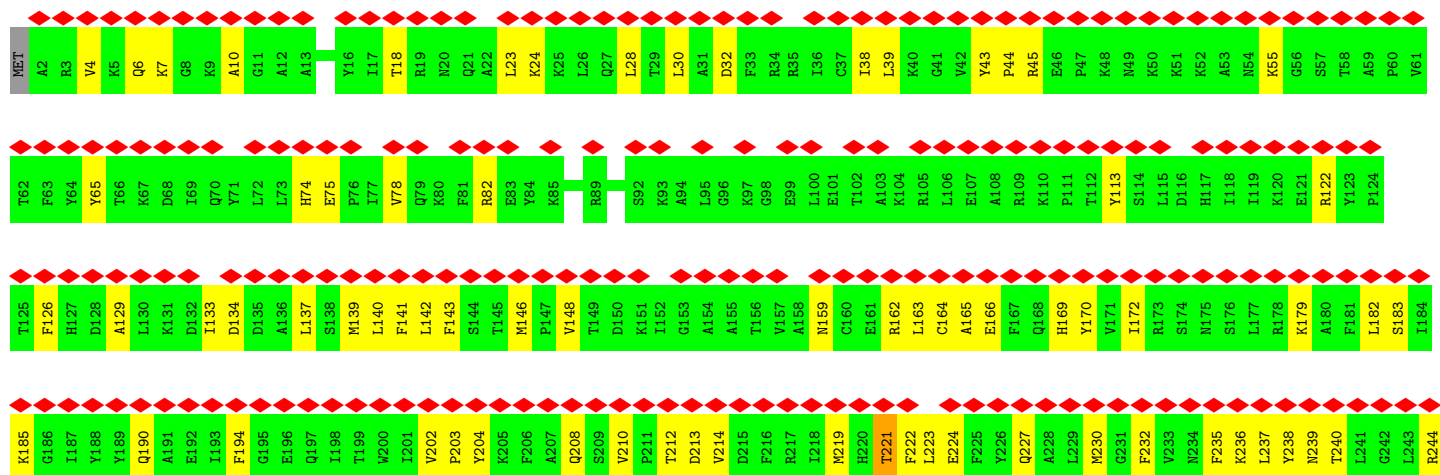


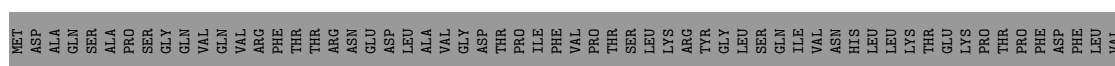
- Molecule 38: Ribosome biogenesis protein erbl1

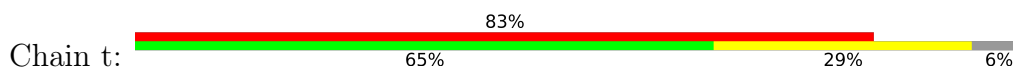
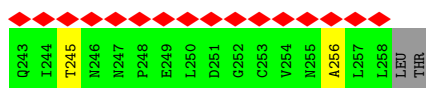


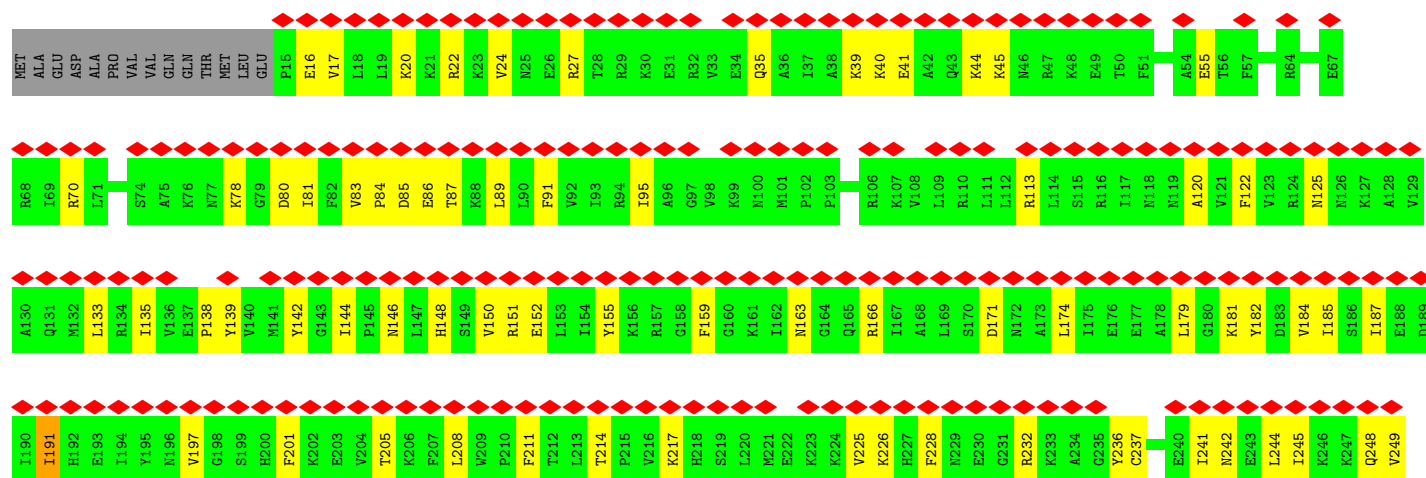


• Molecule 39: Pescadillo homolog

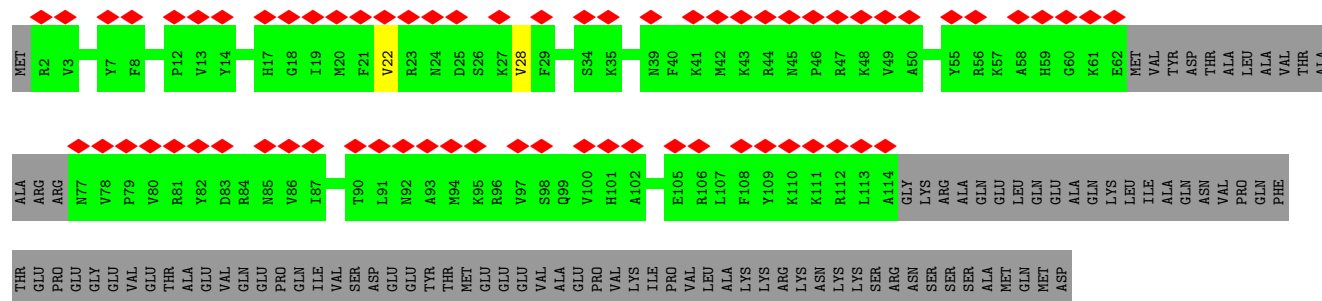




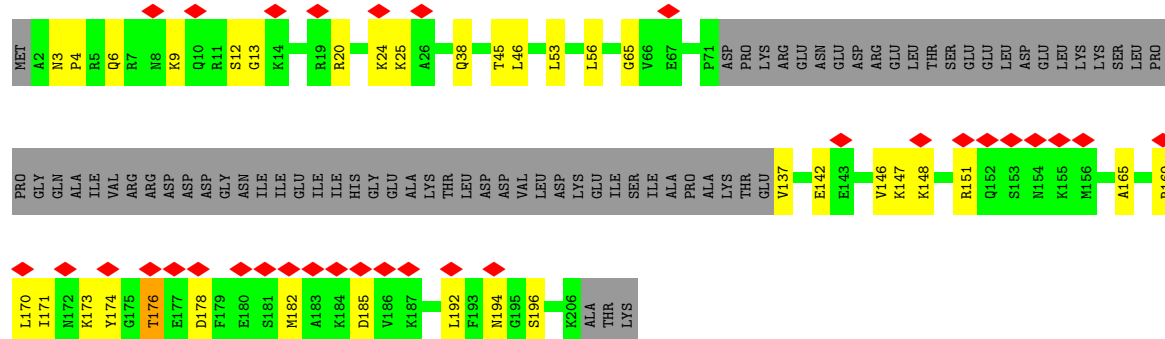




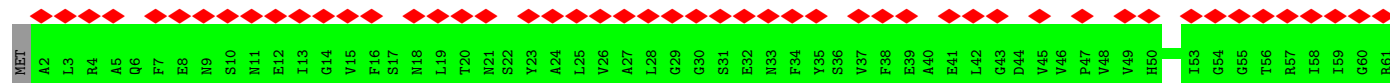
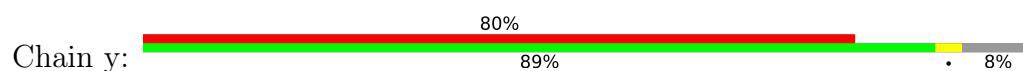
• Molecule 44: Ribosome biogenesis protein rlp24



• Molecule 45: Nucleolar protein 16



• Molecule 46: Eukaryotic translation initiation factor 6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.532	Depositor
Minimum map value	-0.304	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.17	0/48337	0.26	0/75284
2	2	0.23	0/3465	0.31	0/5390
3	3	0.18	0/1037	0.40	0/1396
4	A	0.06	0/1015	0.23	0/1406
5	B	0.15	0/2706	0.33	0/3635
6	C	0.22	0/2848	0.39	0/3842
7	D	0.06	0/404	0.16	0/558
8	E	0.14	0/1146	0.34	0/1545
9	F	0.19	0/1781	0.34	0/2389
10	G	0.22	0/1474	0.34	0/1987
11	H	0.15	0/1470	0.36	0/1982
12	K	0.10	0/1143	0.25	0/1591
13	L	0.33	1/980 (0.1%)	0.42	0/1314
14	M	0.17	0/1017	0.32	0/1365
15	N	0.27	0/1436	0.35	0/1920
16	O	0.17	0/1511	0.30	0/2023
17	P	0.16	0/1101	0.34	0/1475
18	Q	0.18	0/1031	0.33	0/1384
19	R	0.23	0/460	0.43	0/614
20	S	0.17	0/1470	0.35	0/1977
21	U	0.05	0/483	0.19	0/671
22	V	0.12	0/992	0.33	0/1337
23	W	0.06	0/944	0.23	0/1305
24	X	0.18	0/1048	0.39	0/1406
25	Y	0.22	0/1008	0.37	0/1341
26	Z	0.05	0/636	0.16	0/882
27	a	0.26	0/760	0.47	0/1026
28	b	0.05	0/1870	0.18	0/2601
29	c	0.06	0/323	0.18	0/446
30	d	0.30	0/801	0.52	0/1075
31	e	0.21	0/953	0.32	0/1271
32	f	0.20	0/859	0.34	0/1152

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.05	0/427	0.18	0/592
34	h	0.20	0/1008	0.29	0/1340
35	i	0.15	0/643	0.32	0/852
36	j	0.22	0/575	0.35	0/761
37	k	0.05	0/348	0.18	0/485
38	m	0.19	0/2910	0.27	0/3993
39	n	0.15	0/3468	0.29	0/4670
40	o	0.18	0/919	0.42	0/1232
41	p	0.07	0/1411	0.20	0/1956
42	r	0.15	0/1014	0.38	0/1361
43	t	0.14	0/1979	0.31	0/2645
44	u	0.06	0/489	0.19	0/679
45	v	0.19	0/1161	0.39	0/1552
46	y	0.05	0/1106	0.19	0/1536
47	T	0.14	0/151	0.39	0/207
48	6	0.09	0/1466	0.16	0/2270
All	All	0.17	1/105584 (0.0%)	0.29	0/153721

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	L	60	PRO	CA-C	-6.40	1.48	1.51

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	43202	0	21751	685	0
2	2	3102	0	1570	32	0
3	3	1015	0	1015	46	0
4	A	1015	0	495	6	0
5	B	2653	0	2736	86	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	2795	0	2918	105	0
7	D	408	0	181	1	0
8	E	1126	0	1207	52	0
9	F	1745	0	1818	56	0
10	G	1452	0	1557	31	0
11	H	1451	0	1511	72	0
12	K	1145	0	504	5	0
13	L	962	0	1033	28	0
14	M	1000	0	1063	46	0
15	N	1406	0	1441	34	0
16	O	1483	0	1584	41	0
17	P	1080	0	1095	53	0
18	Q	1020	0	1114	30	0
19	R	456	0	493	25	0
20	S	1434	0	1497	70	0
21	U	484	0	222	1	0
22	V	976	0	1026	41	0
23	W	948	0	440	4	0
24	X	1032	0	1102	37	0
25	Y	998	0	1090	44	0
26	Z	637	0	296	5	0
27	a	747	0	790	32	0
28	b	1875	0	831	6	0
29	c	325	0	154	2	0
30	d	787	0	837	66	0
31	e	939	0	1000	39	0
32	f	839	0	866	23	0
33	g	428	0	193	1	0
34	h	999	0	1092	23	0
35	i	637	0	696	20	0
36	j	563	0	578	19	0
37	k	349	0	156	1	0
38	m	2881	0	1917	80	0
39	n	3389	0	3436	98	0
40	o	897	0	914	47	0
41	p	1416	0	627	27	0
42	r	1009	0	791	33	0
43	t	1948	0	2066	62	0
44	u	491	0	217	1	0
45	v	1143	0	1192	30	0
46	y	1107	0	514	4	0
47	T	147	0	140	6	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	6	1315	0	666	20	0
49	j	1	0	0	0	0
All	All	99257	0	70432	1928	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 13.

All (1928) 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)
30:d:49:MET:HE1	30:d:82:ARG:HE	1.15	1.05
5:B:331:PRO:HD2	5:B:334:ARG:HE	1.33	0.91
1:1:607:G:H4'	32:f:107:ASN:HD21	1.36	0.88
38:m:249:THR:HG23	38:m:252:GLN:HE22	1.36	0.88
11:H:93:VAL:HB	11:H:178:TYR:HE1	1.40	0.86
1:1:3352:A:H3'	1:1:3353:U:H5''	1.60	0.84
1:1:238:U:H5'	1:1:240:G:H5'	1.60	0.83
17:P:30:ARG:HA	17:P:119:VAL:HG21	1.60	0.83
36:j:36:CYS:SG	36:j:57:ARG:NH2	2.53	0.82
30:d:25:LEU:HD21	30:d:33:ARG:HD2	1.62	0.81
1:1:621:G:H5''	9:F:44:ARG:HH21	1.45	0.80
27:a:82:LEU:HD21	27:a:86:ALA:HB3	1.63	0.80
1:1:1010:A:H4'	1:1:1011:G:H5'	1.65	0.79
39:n:139:MET:HE1	39:n:219:MET:SD	2.23	0.79
14:M:33:ASP:OD1	14:M:34:HIS:N	2.15	0.79
6:C:101:MET:HE2	6:C:104:PRO:HA	1.64	0.79
1:1:1879:C:H2'	1:1:1880:A:H8	1.48	0.79
18:Q:92:GLU:OE1	18:Q:92:GLU:N	2.14	0.78
2:2:49:A:HO2'	36:j:59:THR:HG1	1.31	0.78
24:X:13:VAL:HG13	24:X:17:ILE:HG22	1.66	0.78
1:1:1605:U:H3	1:1:1607:U:H2'	1.49	0.78
30:d:49:MET:HE1	30:d:82:ARG:NE	1.98	0.77
42:r:149:MET:HA	42:r:171:ILE:H	1.50	0.77
6:C:7:THR:OG1	6:C:21:THR:HB	1.85	0.77
19:R:20:ARG:HG3	19:R:21:LYS:HD3	1.68	0.76
42:r:55:ARG:HH22	42:r:56:LYS:HG3	1.50	0.76
34:h:4:LYS:HB2	34:h:7:GLU:HG3	1.68	0.76
1:1:2931:C:H3'	1:1:2932:A:H8	1.50	0.76
40:o:187:HIS:H	40:o:190:MET:HE1	1.52	0.75
5:B:92:TYR:HB3	5:B:99:LEU:HD12	1.68	0.75
5:B:218:ILE:HD11	5:B:339:ARG:HH12	1.52	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:45:LYS:HZ3	20:S:51:LYS:HA	1.52	0.75
1:1:312:G:H1	1:1:319:U:H3	1.31	0.74
1:1:533:A:OP1	6:C:350:LYS:NZ	2.20	0.74
5:B:285:ILE:HG22	5:B:322:VAL:HG12	1.69	0.74
17:P:61:ARG:O	17:P:64:ASN:ND2	2.20	0.74
31:e:21:ARG:NH1	31:e:21:ARG:O	2.20	0.74
1:1:27:C:H3'	1:1:28:G:H21	1.51	0.74
1:1:760:C:N4	1:1:763:G:OP2	2.20	0.74
1:1:1730:U:O2'	1:1:1789:A:N1	2.20	0.74
11:H:93:VAL:HB	11:H:178:TYR:CE1	2.22	0.74
22:V:42:PHE:CE1	22:V:61:LEU:HD11	2.23	0.74
22:V:24:ILE:HD11	22:V:35:ASN:HB3	1.69	0.74
11:H:90:MET:HB3	11:H:142:ILE:HB	1.69	0.74
19:R:21:LYS:HA	19:R:53:LYS:HZ1	1.53	0.73
1:1:3196:U:H3	1:1:3230:G:H1	1.36	0.73
39:n:4:VAL:O	39:n:6:GLN:NE2	2.21	0.73
17:P:70:THR:HG22	17:P:72:GLN:H	1.52	0.73
36:j:30:GLN:OE1	36:j:30:GLN:N	2.21	0.73
20:S:44:LEU:HD21	20:S:50:VAL:HB	1.70	0.73
35:i:75:LEU:HD23	35:i:80:ARG:HB3	1.71	0.73
1:1:366:G:N2	1:1:369:A:OP2	2.20	0.73
1:1:3092:U:H3'	1:1:3093:G:H5'	1.69	0.73
5:B:211:GLN:NE2	5:B:283:TYR:O	2.20	0.73
11:H:104:THR:OG1	11:H:105:GLU:OE1	2.07	0.72
38:m:306:TYR:HB3	38:m:316:LYS:HD2	1.70	0.72
1:1:190:G:H1	1:1:242:U:H3	1.37	0.72
25:Y:54:GLN:HB3	25:Y:107:LYS:HB3	1.70	0.72
22:V:106:ASN:HD21	22:V:110:GLU:HB3	1.54	0.72
1:1:26:A:N3	1:1:336:U:O2'	2.23	0.72
1:1:1692:C:N4	1:1:1839:A:OP2	2.21	0.72
15:N:5:LYS:HG3	35:i:38:VAL:HG11	1.69	0.72
5:B:375:GLU:HA	5:B:378:GLN:HE22	1.54	0.72
1:1:116:A:OP1	35:i:34:ARG:NH2	2.23	0.71
1:1:3027:U:H5'	22:V:43:GLY:HA2	1.72	0.71
1:1:1270:C:H42	1:1:1280:G:H1	1.37	0.71
5:B:281:LYS:O	5:B:325:ASN:ND2	2.22	0.71
6:C:140:ARG:HG3	6:C:140:ARG:HH11	1.55	0.71
6:C:5:ARG:HD2	6:C:23:ALA:HB1	1.71	0.71
38:m:249:THR:H	38:m:252:GLN:HE22	1.38	0.71
1:1:31:C:O2'	15:N:96:ARG:NH1	2.23	0.71
1:1:1930:G:N7	19:R:20:ARG:NH1	2.37	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:607:G:H4'	32:f:107:ASN:ND2	2.05	0.71
19:R:8:LYS:HD2	19:R:22:VAL:HG21	1.71	0.71
39:n:23:LEU:HD11	39:n:30:LEU:HD13	1.72	0.71
1:1:2933:A:N6	1:1:2945:G:O2'	2.24	0.71
38:m:334:PHE:HD1	39:n:219:MET:HE1	1.54	0.71
1:1:2423:G:N2	1:1:2427:C:O2'	2.23	0.71
6:C:338:LYS:NZ	6:C:341:VAL:HG12	2.06	0.71
40:o:188:GLU:OE2	40:o:188:GLU:N	2.21	0.71
6:C:179:ASP:OD1	6:C:182:LYS:NZ	2.21	0.71
1:1:401:U:O3'	25:Y:86:ARG:NH2	2.22	0.70
1:1:1175:U:OP2	31:e:41:ARG:NH1	2.24	0.70
43:t:55:GLU:OE1	43:t:55:GLU:N	2.23	0.70
1:1:3480:C:H4'	5:B:315:GLY:HA2	1.71	0.70
2:2:137:A:H5''	39:n:10:ALA:HB1	1.72	0.70
39:n:141:PHE:HD2	39:n:202:VAL:HG22	1.56	0.70
1:1:3138:U:H5''	22:V:47:ARG:HD2	1.73	0.70
3:3:100:TRP:CD1	3:3:101:PRO:HD2	2.27	0.70
6:C:37:VAL:HG21	6:C:246:LEU:HD21	1.74	0.70
42:r:21:GLU:OE1	42:r:21:GLU:N	2.20	0.70
42:r:52:GLU:HB2	42:r:55:ARG:HH21	1.57	0.70
36:j:21:ARG:NH2	36:j:43:LYS:O	2.25	0.70
42:r:9:GLU:N	42:r:9:GLU:OE2	2.24	0.70
3:3:114:ARG:HH21	31:e:84:MET:HE1	1.56	0.69
17:P:109:MET:HE2	17:P:109:MET:HA	1.74	0.69
34:h:27:LEU:HD11	34:h:50:ARG:HG3	1.72	0.69
1:1:1531:C:H2'	1:1:1532:A:H8	1.56	0.69
6:C:302:VAL:HG23	18:Q:38:ARG:HB3	1.72	0.69
45:v:173:LYS:NZ	45:v:174:TYR:CE2	2.60	0.69
1:1:3012:G:H1	1:1:3024:C:H5	1.39	0.69
5:B:58:ARG:NH1	5:B:74:GLU:OE2	2.24	0.69
11:H:92:LEU:HB3	11:H:140:ASP:HB2	1.75	0.69
20:S:78:ILE:HD11	20:S:109:MET:HE2	1.74	0.69
6:C:338:LYS:HZ3	6:C:341:VAL:HG12	1.58	0.69
18:Q:21:GLU:N	18:Q:21:GLU:OE2	2.26	0.69
1:1:1639:U:O2	1:1:1639:U:H2'	1.92	0.69
20:S:78:ILE:CD1	20:S:109:MET:HE2	2.23	0.69
20:S:80:TYR:CD2	20:S:109:MET:HE3	2.27	0.69
31:e:63:CYS:SG	31:e:69:LYS:NZ	2.64	0.69
1:1:1598:C:OP2	39:n:24:LYS:NZ	2.26	0.69
32:f:53:VAL:HG22	32:f:67:VAL:HG22	1.73	0.69
1:1:3209:A:H4'	11:H:69:ARG:HB3	1.75	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:52:LYS:O	16:O:56:LEU:HD22	1.93	0.68
35:i:78:LEU:HG	35:i:82:LYS:HE2	1.76	0.68
16:O:117:LYS:NZ	20:S:169:PRO:O	2.27	0.68
3:3:20:ILE:HD11	3:3:29:ARG:HB2	1.75	0.68
15:N:114:ARG:NH1	15:N:151:ILE:O	2.26	0.68
1:1:1438:G:N2	1:1:1441:A:OP2	2.22	0.68
45:v:194:ASN:ND2	45:v:196:SER:OG	2.27	0.68
16:O:63:CYS:HG	16:O:71:ALA:N	1.91	0.68
40:o:112:LEU:HD12	40:o:116:PHE:HB3	1.74	0.67
40:o:122:ARG:HG3	40:o:134:LEU:HD13	1.77	0.67
17:P:119:VAL:HG12	17:P:146:ILE:HG12	1.76	0.67
18:Q:92:GLU:H	18:Q:92:GLU:CD	2.00	0.67
39:n:159:ASN:OD1	39:n:162:ARG:NH2	2.27	0.67
5:B:383:LEU:HD23	5:B:384:LYS:H	1.59	0.67
10:G:161:GLU:OE2	15:N:26:ARG:NH2	2.27	0.67
1:1:1244:G:H5'	20:S:136:ARG:HH21	1.59	0.67
1:1:2947:C:H1'	42:r:59:ILE:HD13	1.76	0.67
17:P:4:TYR:HE1	17:P:18:ARG:HE	1.41	0.67
24:X:3:VAL:HG12	40:o:158:VAL:HG23	1.75	0.67
38:m:290:LYS:HG3	43:t:17:VAL:HG23	1.77	0.67
1:1:1284:U:H5''	1:1:1285:C:H5'	1.77	0.67
30:d:25:LEU:HD23	30:d:25:LEU:O	1.95	0.67
5:B:284:ARG:NH1	5:B:294:ALA:O	2.28	0.66
3:3:110:GLN:HB3	3:3:114:ARG:HH22	1.59	0.66
18:Q:94:MET:O	18:Q:114:ARG:NH2	2.26	0.66
1:1:1218:C:H5	1:1:1350:G:H1	1.43	0.66
3:3:16:CYS:HB3	3:3:19:ARG:HG2	1.78	0.66
10:G:163:VAL:HG12	10:G:166:LEU:HD12	1.77	0.66
43:t:171:ASP:HB2	43:t:174:LEU:HG	1.77	0.66
1:1:3272:U:O2	16:O:6:LYS:NZ	2.28	0.66
1:1:3435:U:N3	1:1:3470:G:O2'	2.27	0.66
9:F:87:GLU:OE2	9:F:89:LYS:HG3	1.95	0.66
16:O:127:VAL:HG23	16:O:128:LEU:HD12	1.78	0.66
48:6:6:C:N3	48:6:48:G:O2'	2.29	0.66
1:1:847:G:OP1	36:j:16:HIS:NE2	2.26	0.66
20:S:7:GLN:OE1	20:S:61:ASN:ND2	2.23	0.66
9:F:245:LEU:HD21	9:F:249:MET:HE3	1.76	0.66
1:1:1146:G:N2	1:1:1146:G:OP2	2.27	0.66
1:1:3315:A:N1	8:E:176:GLU:HB2	2.10	0.66
30:d:24:ARG:HG2	30:d:24:ARG:HH11	1.61	0.66
38:m:191:ILE:H	38:m:191:ILE:HD12	1.62	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:239:U:O4	45:v:25:LYS:NZ	2.20	0.65
25:Y:5:ARG:HG3	45:v:24:LYS:HG3	1.78	0.65
1:1:1242:U:O2'	20:S:112:ARG:NH1	2.29	0.65
36:j:20:ARG:NH2	36:j:39:TYR:OH	2.28	0.65
2:2:79:A:O2'	25:Y:51:ARG:NH2	2.29	0.65
9:F:234:ASP:OD2	9:F:238:ARG:NH2	2.28	0.65
17:P:67:VAL:O	17:P:80:GLN:NE2	2.29	0.65
25:Y:55:ILE:HD11	25:Y:81:ILE:HG12	1.79	0.65
18:Q:53:GLN:O	18:Q:58:ARG:NH1	2.30	0.65
38:m:249:THR:CG2	38:m:252:GLN:HE22	2.09	0.65
1:1:1379:U:OP2	18:Q:37:ARG:NH1	2.30	0.65
4:A:92:LEU:HD11	35:i:69:LYS:HB3	1.78	0.65
5:B:146:ARG:NH1	5:B:149:GLU:OE1	2.30	0.65
24:X:72:MET:HE3	24:X:72:MET:HA	1.77	0.65
2:2:71:G:O2'	34:h:51:LYS:NZ	2.30	0.65
3:3:3:GLN:HG3	3:3:4:ASP:H	1.61	0.65
5:B:116:ARG:O	5:B:175:LYS:NZ	2.29	0.65
24:X:6:ALA:HA	24:X:10:GLN:HB2	1.79	0.64
1:1:3315:A:OP2	14:M:118:LYS:NZ	2.29	0.64
14:M:65:LEU:HD12	14:M:66:PRO:HD2	1.78	0.64
22:V:28:ALA:O	22:V:117:THR:HG23	1.98	0.64
1:1:3203:C:H2'	1:1:3204:G:H8	1.63	0.64
39:n:146:MET:HA	39:n:208:GLN:HE22	1.61	0.64
1:1:3285:G:H1	1:1:3302:U:H3	1.45	0.64
1:1:3475:U:OP2	30:d:75:ARG:NH2	2.29	0.64
9:F:130:ILE:HA	9:F:133:MET:HB2	1.78	0.64
38:m:334:PHE:HD1	39:n:219:MET:CE	2.10	0.64
13:L:87:ARG:HH21	13:L:88:ARG:HH12	1.46	0.64
20:S:11:ARG:HD2	20:S:21:PRO:HG2	1.79	0.64
39:n:258:ALA:HB1	39:n:261:ALA:HB3	1.79	0.64
40:o:187:HIS:N	40:o:190:MET:HE1	2.12	0.64
40:o:189:ASN:HB2	40:o:192:LYS:HB2	1.80	0.64
1:1:372:G:OP2	36:j:52:LYS:NZ	2.30	0.64
11:H:23:ALA:O	11:H:40:ARG:NH2	2.31	0.64
24:X:85:VAL:HG11	24:X:94:ILE:HD11	1.78	0.64
10:G:162:LEU:HD11	15:N:45:PRO:HG3	1.79	0.64
11:H:116:LEU:HD23	11:H:116:LEU:O	1.97	0.64
1:1:252:A:OP1	45:v:148:LYS:NZ	2.30	0.64
1:1:528:G:OP1	9:F:74:ARG:NH2	2.31	0.64
1:1:712:U:OP2	13:L:36:ARG:NH2	2.31	0.64
3:3:19:ARG:NH1	3:3:28:CYS:SG	2.71	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:7:LYS:HE3	40:o:161:VAL:HG22	1.80	0.64
35:i:51:TYR:OH	35:i:84:LYS:NZ	2.31	0.63
39:n:137:LEU:HD22	39:n:230:MET:HE1	1.80	0.63
3:3:69:ARG:HD2	3:3:75:LYS:HD2	1.80	0.63
8:E:89:ASN:ND2	8:E:178:LEU:O	2.30	0.63
20:S:65:GLU:OE2	20:S:72:LYS:NZ	2.30	0.63
39:n:75:GLU:HB3	39:n:78:VAL:HG23	1.80	0.63
1:1:396:G:H1'	17:P:97:ASN:HD21	1.63	0.63
1:1:1009:C:N4	1:1:1136:A:N1	2.47	0.63
14:M:31:ILE:O	20:S:94:ARG:NH2	2.30	0.63
1:1:732:A:N6	1:1:742:A:OP2	2.31	0.63
10:G:172:LYS:HE3	38:m:211:ARG:HB2	1.79	0.63
1:1:1417:G:OP1	6:C:205:ARG:NH1	2.27	0.63
17:P:16:LYS:HG2	17:P:149:ILE:HG12	1.80	0.63
1:1:351:U:H1'	6:C:97:ARG:HG3	1.80	0.62
5:B:378:GLN:N	5:B:378:GLN:OE1	2.32	0.62
6:C:147:ILE:HD11	6:C:152:LEU:HB2	1.79	0.62
18:Q:92:GLU:HB2	27:a:80:THR:HG21	1.81	0.62
28:b:404:ALA:HA	28:b:408:GLY:HA2	1.79	0.62
30:d:47:LYS:HZ2	30:d:48:HIS:HA	1.64	0.62
1:1:174:U:O2'	1:1:259:A:N6	2.29	0.62
39:n:142:LEU:HA	39:n:203:PRO:HG3	1.82	0.62
10:G:146:LYS:NZ	10:G:173:MET:O	2.33	0.62
43:t:81:ILE:HG13	43:t:83:VAL:H	1.64	0.62
14:M:24:LYS:HE2	14:M:45:GLU:HG3	1.81	0.62
38:m:335:GLU:O	43:t:22:ARG:NH2	2.32	0.62
40:o:112:LEU:HD23	40:o:148:TYR:HA	1.80	0.62
45:v:171:ILE:HD11	45:v:176:THR:HA	1.81	0.62
1:1:650:G:N2	1:1:1435:G:OP1	2.26	0.62
1:1:3040:G:N2	1:1:3044:U:OP2	2.33	0.62
39:n:366:ARG:NH2	39:n:386:LEU:O	2.32	0.62
1:1:262:A:N3	34:h:112:TYR:OH	2.30	0.62
17:P:11:GLU:O	17:P:13:LYS:N	2.33	0.62
42:r:16:ARG:HD3	42:r:17:ARG:H	1.64	0.62
1:1:48:A:H4'	1:1:49:A:H5'	1.81	0.62
1:1:1222:U:OP2	16:O:50:ARG:NH1	2.33	0.62
6:C:183:VAL:HG21	6:C:226:GLY:HA3	1.81	0.62
1:1:1636:U:OP1	19:R:42:ARG:NH2	2.30	0.62
20:S:57:ILE:HG21	20:S:60:ILE:HD11	1.82	0.62
22:V:137:THR:HG22	46:y:101:LEU:HA	1.82	0.62
31:e:88:THR:HG23	31:e:89:TYR:HD1	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:m:576:VAL:HA	38:m:592:THR:HA	1.82	0.61
43:t:245:ILE:O	43:t:249:VAL:N	2.30	0.61
1:1:2993:G:OP2	1:1:2994:C:N4	2.30	0.61
27:a:132:ARG:HA	27:a:135:GLU:OE2	2.00	0.61
36:j:27:PHE:HA	36:j:34:CYS:HA	1.82	0.61
1:1:1390:A:N7	3:3:13:HIS:NE2	2.48	0.61
1:1:1536:G:N2	1:1:1547:G:N7	2.47	0.61
6:C:329:ARG:NH1	9:F:171:SER:O	2.33	0.61
22:V:82:ARG:HD3	22:V:97:PHE:HD2	1.65	0.61
38:m:344:PRO:HG2	43:t:20:LYS:HB2	1.82	0.61
1:1:163:A:N6	1:1:272:G:O2'	2.32	0.61
1:1:223:G:OP1	25:Y:15:ARG:NH1	2.34	0.61
1:1:1424:A:N6	1:1:1452:A:O2'	2.34	0.61
1:1:2972:G:H1	1:1:3044:U:H3	1.48	0.61
11:H:11:LEU:HB2	11:H:72:TYR:HE1	1.66	0.61
1:1:216:A:OP1	6:C:163:LYS:NZ	2.34	0.61
1:1:3145:A:H4'	5:B:364:LYS:HE3	1.83	0.61
1:1:3203:C:H2'	1:1:3204:G:C8	2.36	0.61
42:r:16:ARG:HD3	42:r:17:ARG:N	2.15	0.61
1:1:1379:U:OP1	18:Q:38:ARG:NH1	2.33	0.61
1:1:3133:U:OP1	5:B:348:ARG:NH1	2.33	0.61
1:1:3318:A:O2'	1:1:3319:G:OP2	2.17	0.61
2:2:45:A:OP2	34:h:88:ARG:NH1	2.33	0.60
43:t:78:LYS:NZ	43:t:80:ASP:O	2.33	0.60
1:1:63:A:N3	1:1:78:U:O2'	2.31	0.60
6:C:228:GLU:HG3	6:C:248:ARG:HH22	1.66	0.60
27:a:132:ARG:HA	27:a:135:GLU:CD	2.26	0.60
30:d:16:ASP:OD2	30:d:77:ARG:NE	2.35	0.60
40:o:122:ARG:NH2	40:o:195:ASP:OD2	2.30	0.60
42:r:55:ARG:NH2	42:r:56:LYS:HG3	2.16	0.60
1:1:587:U:H2'	1:1:588:G:H8	1.66	0.60
15:N:11:ALA:O	15:N:14:LYS:NZ	2.27	0.60
16:O:52:LYS:HG3	16:O:56:LEU:HD21	1.83	0.60
17:P:117:VAL:HG22	17:P:148:ILE:HG12	1.82	0.60
20:S:62:GLU:OE1	20:S:62:GLU:N	2.34	0.60
1:1:1364:C:OP1	9:F:117:GLN:NE2	2.33	0.60
6:C:285:SER:N	18:Q:126:ASP:OD2	2.34	0.60
34:h:52:ASP:OD1	34:h:55:ARG:NH1	2.35	0.60
19:R:38:ARG:HB3	19:R:42:ARG:HH12	1.65	0.60
31:e:84:MET:HA	31:e:84:MET:HE2	1.83	0.60
40:o:153:PHE:HD2	40:o:159:ALA:HA	1.65	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1454:C:OP2	6:C:195:LYS:NZ	2.34	0.60
1:1:1700:G:H1	1:1:1825:U:H3	1.50	0.60
3:3:5:GLU:CD	6:C:289:VAL:H	2.08	0.60
1:1:1578:G:H1	1:1:1583:U:H3	1.50	0.60
19:R:24:MET:N	19:R:24:MET:SD	2.75	0.60
38:m:249:THR:HG23	38:m:252:GLN:NE2	2.12	0.60
1:1:197:U:O4	25:Y:102:LYS:NZ	2.34	0.60
1:1:749:G:H1	1:1:776:U:H3	1.48	0.60
5:B:124:LYS:HD2	5:B:124:LYS:H	1.65	0.60
16:O:52:LYS:HG3	16:O:56:LEU:CD2	2.31	0.60
1:1:3107:A:H62	5:B:13:SER:HA	1.65	0.60
41:p:313:LEU:HA	41:p:329:SER:HA	1.82	0.60
1:1:1332:A:N7	42:r:45:ILE:HD11	2.17	0.59
11:H:124:ILE:HD11	11:H:162:ILE:HD13	1.83	0.59
42:r:22:GLU:OE2	42:r:22:GLU:N	2.28	0.59
1:1:741:G:N7	27:a:110:LYS:NZ	2.40	0.59
2:2:101:U:H2'	2:2:102:C:O4'	2.02	0.59
24:X:114:ARG:HH21	24:X:116:ASN:HD21	1.50	0.59
1:1:960:C:H2'	1:1:961:A:C8	2.38	0.59
22:V:111:MET:N	22:V:111:MET:SD	2.75	0.59
1:1:371:C:OP2	36:j:56:ARG:NH2	2.36	0.59
1:1:674:A:H2'	1:1:675:C:C6	2.37	0.59
18:Q:90:ASP:OD1	18:Q:91:ASP:N	2.35	0.59
1:1:742:A:H8	27:a:114:LYS:HD3	1.68	0.59
1:1:1016:G:N2	1:1:1170:G:OP1	2.28	0.59
5:B:112:GLU:HG3	5:B:122:TRP:CH2	2.36	0.59
10:G:226:TYR:O	10:G:228:GLU:N	2.36	0.59
17:P:4:TYR:HE2	17:P:16:LYS:HB3	1.67	0.59
1:1:1244:G:OP1	20:S:138:TYR:OH	2.20	0.59
15:N:135:VAL:HG21	15:N:151:ILE:HG21	1.84	0.59
35:i:30:HIS:CG	35:i:31:LEU:H	2.20	0.59
1:1:1025:G:H22	1:1:1088:U:H3	1.49	0.59
1:1:3314:U:OP2	14:M:121:ARG:NH2	2.34	0.59
8:E:99:ARG:NH1	32:f:106:SER:O	2.34	0.59
13:L:36:ARG:HH22	45:v:45:THR:HG21	1.66	0.59
1:1:1262:A:H4'	1:1:1292:G:H8	1.68	0.59
1:1:1598:C:H2'	1:1:1599:A:H8	1.68	0.59
39:n:555:LYS:NZ	39:n:556:GLU:OE2	2.35	0.59
1:1:1606:U:H3	39:n:221:THR:HG22	1.67	0.59
9:F:157:LYS:HD3	9:F:250:LEU:HD22	1.84	0.59
38:m:249:THR:H	38:m:252:GLN:NE2	2.01	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:n:574:SER:O	39:n:578:ASN:ND2	2.36	0.59
1:1:1681:G:N2	1:1:1849:G:O2'	2.32	0.59
8:E:71:VAL:HG13	8:E:178:LEU:HD11	1.85	0.59
8:E:77:GLU:OE1	8:E:78:ASP:N	2.17	0.59
26:Z:40:HIS:HA	26:Z:76:ASN:HA	1.85	0.59
39:n:140:LEU:HD22	39:n:230:MET:HG3	1.85	0.59
39:n:179:LYS:HE3	39:n:190:GLN:HG2	1.85	0.59
1:1:252:A:OP1	45:v:151:ARG:NH2	2.36	0.58
1:1:379:G:N1	1:1:382:A:OP2	2.36	0.58
5:B:301:THR:HG23	28:b:437:ASP:H	1.66	0.58
10:G:83:ASP:OD1	10:G:85:ASN:N	2.36	0.58
14:M:61:ILE:HD11	14:M:83:VAL:HG22	1.84	0.58
15:N:38:ARG:HH12	15:N:60:VAL:HG22	1.68	0.58
16:O:74:PHE:HB3	16:O:79:ARG:HB3	1.85	0.58
1:1:1517:G:H2'	1:1:1519:G:C8	2.38	0.58
1:1:1714:A:H2'	1:1:1715:G:H8	1.67	0.58
13:L:80:LEU:HD11	13:L:97:VAL:HG22	1.84	0.58
17:P:40:SER:HA	17:P:113:ILE:HG22	1.85	0.58
1:1:369:A:O3'	36:j:45:ARG:NH2	2.35	0.58
4:A:84:TYR:O	4:A:87:ASN:ND2	2.35	0.58
13:L:63:ILE:HD12	13:L:66:ASN:HD21	1.69	0.58
25:Y:116:ASP:OD1	25:Y:117:LEU:N	2.37	0.58
36:j:82:LYS:HD3	36:j:83:PRO:HD2	1.84	0.58
43:t:159:PHE:HB3	43:t:166:ARG:HH12	1.69	0.58
1:1:984:A:O2'	1:1:1000:G:N2	2.37	0.58
2:2:128:U:P	39:n:74:HIS:HE2	2.26	0.58
39:n:349:ASN:ND2	39:n:431:GLY:O	2.36	0.58
1:1:1803:U:OP1	1:1:1805:A:N6	2.36	0.58
1:1:3217:U:H1'	1:1:3218:A:H5''	1.86	0.58
1:1:3306:C:O2	14:M:6:ARG:NH1	2.34	0.58
27:a:103:VAL:HG12	27:a:108:TYR:HB2	1.86	0.58
39:n:113:TYR:OH	39:n:224:GLU:OE1	2.20	0.58
1:1:194:A:N3	1:1:215:C:O2'	2.35	0.58
3:3:47:ASN:OD1	3:3:48:SER:N	2.36	0.58
6:C:288:ASP:CG	6:C:291:ARG:HB2	2.28	0.58
6:C:314:HIS:CE1	9:F:169:PRO:HG2	2.38	0.58
11:H:88:TYR:HB3	11:H:144:LEU:HB2	1.85	0.58
14:M:86:LYS:O	14:M:89:SER:OG	2.20	0.58
31:e:17:HIS:CG	31:e:39:VAL:HG21	2.38	0.58
1:1:764:U:H3'	1:1:765:G:H8	1.69	0.58
1:1:1527:G:N2	1:1:1527:G:OP2	2.36	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:79:THR:HG21	8:E:95:ARG:HD2	1.85	0.58
39:n:244:ARG:NH1	39:n:266:GLU:OE1	2.37	0.58
41:p:222:GLY:HA2	41:p:264:LEU:HA	1.86	0.58
43:t:41:GLU:OE1	43:t:45:LYS:NZ	2.32	0.58
1:1:364:G:O2'	6:C:83:GLY:O	2.22	0.58
1:1:1739:A:OP2	1:1:1780:G:N1	2.30	0.58
38:m:387:ARG:H	38:m:402:GLY:HA2	1.69	0.58
1:1:717:A:OP2	6:C:48:LYS:NZ	2.36	0.58
1:1:1472:U:OP1	6:C:78:ARG:NH2	2.36	0.58
3:3:74:SER:HB3	6:C:148:PRO:HA	1.85	0.58
19:R:20:ARG:HE	19:R:21:LYS:HE3	1.69	0.58
40:o:106:VAL:HG13	40:o:181:ILE:HG23	1.85	0.58
1:1:1557:U:OP1	1:1:1642:U:N3	2.35	0.57
25:Y:58:ILE:HG22	25:Y:59:ARG:HG2	1.85	0.57
38:m:578:ALA:HB3	38:m:591:ALA:HB3	1.86	0.57
1:1:3210:A:N1	42:r:33:HIS:NE2	2.47	0.57
6:C:156:ASP:OD2	6:C:255:SER:OG	2.22	0.57
1:1:34:A:N3	1:1:842:A:O2'	2.37	0.57
14:M:12:ARG:HG3	14:M:62:VAL:HG22	1.85	0.57
18:Q:90:ASP:OD2	18:Q:110:SER:OG	2.22	0.57
27:a:82:LEU:HD23	27:a:83:PRO:N	2.19	0.57
40:o:148:TYR:OH	48:6:98:G:OP1	2.20	0.57
40:o:183:GLU:HA	40:o:186:VAL:HG13	1.85	0.57
41:p:97:TYR:HA	41:p:431:ASN:HA	1.85	0.57
1:1:3135:G:OP1	5:B:62:ARG:NH1	2.37	0.57
1:1:3172:C:OP1	30:d:71:ASN:ND2	2.28	0.57
5:B:159:ARG:NE	5:B:182:GLN:OE1	2.28	0.57
22:V:17:LEU:HB3	22:V:53:ALA:HB3	1.86	0.57
25:Y:2:LYS:HD3	25:Y:9:SER:HB2	1.86	0.57
30:d:18:THR:HB	30:d:77:ARG:HH11	1.69	0.57
42:r:184:THR:HA	42:r:191:THR:HA	1.86	0.57
1:1:614:G:OP1	31:e:59:LYS:NZ	2.33	0.57
33:g:43:ARG:HA	33:g:50:PRO:HA	1.87	0.57
45:v:174:TYR:HE2	45:v:185:ASP:HB2	1.69	0.57
6:C:97:ARG:NH1	6:C:98:SER:OG	2.38	0.57
20:S:13:VAL:N	20:S:54:THR:O	2.33	0.57
43:t:214:THR:O	43:t:248:GLN:NE2	2.37	0.57
1:1:444:A:H61	1:1:647:A:H62	1.52	0.57
5:B:274:HIS:O	5:B:275:ARG:NH1	2.35	0.57
1:1:2428:U:H2'	1:1:2429:A:H8	1.70	0.57
1:1:3318:A:OP2	1:1:3319:G:N2	2.38	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:153:HIS:O	20:S:156:THR:OG1	2.23	0.57
22:V:42:PHE:CD1	22:V:61:LEU:HD21	2.40	0.57
40:o:104:LYS:HE3	40:o:152:GLU:OE1	2.04	0.57
40:o:133:ARG:NH2	40:o:191:PHE:HB2	2.19	0.57
1:1:58:G:H5''	15:N:154:PRO:HB2	1.85	0.57
1:1:2993:G:H22	42:r:5:GLU:HA	1.70	0.57
2:2:95:G:OP1	34:h:4:LYS:NZ	2.38	0.57
16:O:152:ASP:OD2	16:O:153:ILE:N	2.37	0.57
24:X:72:MET:HE3	24:X:75:ILE:HD11	1.87	0.57
39:n:594:LYS:HA	39:n:597:ILE:HD12	1.87	0.57
8:E:78:ASP:OD1	8:E:79:THR:N	2.38	0.56
9:F:110:MET:HE3	9:F:115:LEU:HB2	1.87	0.56
20:S:157:GLY:C	20:S:159:VAL:H	2.12	0.56
35:i:58:LEU:HB3	35:i:67:ALA:HB2	1.87	0.56
1:1:1731:A:OP2	1:1:1789:A:N6	2.33	0.56
11:H:78:MET:N	11:H:78:MET:SD	2.78	0.56
26:Z:39:GLY:O	26:Z:77:TYR:N	2.38	0.56
38:m:249:THR:N	38:m:252:GLN:OE1	2.38	0.56
38:m:348:ARG:N	43:t:16:GLU:O	2.34	0.56
47:T:143:THR:OG1	47:T:147:GLU:OE2	2.23	0.56
1:1:27:C:N4	1:1:57:A:H61	2.04	0.56
8:E:60:LEU:HD23	8:E:65:PHE:HB2	1.88	0.56
8:E:120:THR:HG23	8:E:123:TYR:H	1.70	0.56
11:H:95:ALA:H	11:H:175:ASP:HB2	1.70	0.56
42:r:52:GLU:OE1	42:r:52:GLU:N	2.39	0.56
1:1:1515:A:N6	1:1:1927:C:O2	2.38	0.56
9:F:47:LYS:HE3	9:F:186:LEU:HD13	1.85	0.56
27:a:131:ARG:NH1	27:a:134:GLU:OE2	2.39	0.56
1:1:710:G:OP1	13:L:39:ARG:NH2	2.32	0.56
11:H:90:MET:HE1	11:H:179:VAL:HA	1.88	0.56
1:1:1142:U:O2'	1:1:1143:A:O5'	2.21	0.56
1:1:1338:G:H5'	16:O:61:LYS:HE3	1.86	0.56
1:1:3175:U:C5	30:d:30:PHE:HE2	2.23	0.56
8:E:52:LEU:HD13	8:E:80:LEU:HD11	1.86	0.56
30:d:100:ASP:OD1	30:d:100:ASP:N	2.35	0.56
31:e:20:ASP:OD1	31:e:21:ARG:N	2.39	0.56
41:p:372:ALA:HA	41:p:382:VAL:HA	1.88	0.56
1:1:216:A:N3	6:C:223:ASN:ND2	2.54	0.56
1:1:1011:G:H2'	1:1:1012:A:H4'	1.87	0.56
1:1:3225:A:N6	1:1:3227:U:O2	2.38	0.56
10:G:109:LEU:HD23	38:m:234:ARG:HG2	1.86	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:36:ILE:HA	17:P:39:MET:SD	2.46	0.56
39:n:235:PHE:O	39:n:239:ASN:ND2	2.39	0.56
42:r:55:ARG:O	42:r:59:ILE:HG22	2.05	0.56
1:1:1202:G:P	9:F:224:ARG:HH22	2.29	0.56
1:1:1557:U:O2'	24:X:110:ASN:OD1	2.22	0.56
1:1:1567:U:H2'	1:1:1568:A:H8	1.70	0.56
1:1:3477:A:C4	30:d:26:TYR:HD2	2.24	0.56
14:M:65:LEU:HD21	14:M:74:VAL:HG22	1.88	0.56
25:Y:78:LEU:HD13	25:Y:97:GLY:HA3	1.88	0.56
30:d:24:ARG:HG2	30:d:24:ARG:NH1	2.21	0.56
38:m:319:SER:OG	39:n:405:ASP:OD2	2.24	0.56
40:o:174:LYS:NZ	48:6:94:A:OP2	2.33	0.56
13:L:62:THR:HG22	13:L:63:ILE:H	1.71	0.56
25:Y:85:THR:HG21	25:Y:93:SER:HB3	1.86	0.56
45:v:9:LYS:HA	45:v:12:SER:HB3	1.88	0.56
8:E:72:VAL:HA	8:E:82:VAL:HG23	1.87	0.56
27:a:127:ARG:HH21	27:a:128:TYR:HE2	1.53	0.56
45:v:3:ASN:OD1	45:v:4:PRO:HD2	2.06	0.56
1:1:1658:G:OP1	39:n:566:SER:OG	2.23	0.55
1:1:3316:G:N1	1:1:3359:U:O2	2.39	0.55
1:1:1201:A:H5''	9:F:224:ARG:HH21	1.71	0.55
43:t:138:PRO:HG2	43:t:139:TYR:CE1	2.41	0.55
1:1:741:G:O6	27:a:70:ARG:NH1	2.39	0.55
1:1:1531:C:H2'	1:1:1532:A:C8	2.39	0.55
1:1:1640:A:O2'	1:1:1642:U:OP2	2.23	0.55
1:1:2477:C:H1'	17:P:69:ARG:HH12	1.72	0.55
1:1:3193:U:H4'	5:B:279:ASN:HB3	1.88	0.55
3:3:49:ARG:HG3	3:3:100:TRP:HE1	1.69	0.55
6:C:108:TRP:CD1	13:L:22:VAL:HG21	2.41	0.55
45:v:38:GLN:OE1	45:v:38:GLN:HA	2.06	0.55
1:1:347:C:OP1	1:1:1414:G:O2'	2.25	0.55
1:1:545:A:N6	1:1:547:G:N3	2.53	0.55
1:1:991:C:O2'	1:1:994:A:N6	2.40	0.55
1:1:1643:C:OP1	24:X:108:LYS:NZ	2.29	0.55
1:1:2925:G:H2'	1:1:2926:G:C8	2.41	0.55
8:E:77:GLU:CD	8:E:78:ASP:H	2.12	0.55
23:W:136:VAL:HA	23:W:186:PRO:HA	1.89	0.55
39:n:39:LEU:O	39:n:122:ARG:NH1	2.39	0.55
6:C:283:ILE:HD11	18:Q:106:ARG:HE	1.71	0.55
8:E:105:SER:N	8:E:195:PHE:O	2.38	0.55
9:F:108:LYS:NZ	9:F:111:GLN:OE1	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:132:ARG:HA	27:a:135:GLU:OE1	2.06	0.55
42:r:6:TYR:HA	42:r:9:GLU:OE1	2.06	0.55
1:1:425:A:H2'	1:1:426:A:C8	2.41	0.55
1:1:718:A:N1	2:2:36:C:O2'	2.39	0.55
1:1:1352:G:H21	20:S:111:ALA:HB2	1.71	0.55
1:1:3210:A:O3'	11:H:62:ARG:NH1	2.40	0.55
2:2:83:G:H2'	2:2:84:C:C6	2.41	0.55
6:C:14:ASP:OD1	6:C:16:SER:N	2.29	0.55
14:M:43:CYS:HB3	14:M:45:GLU:CD	2.32	0.55
39:n:437:ASP:OD1	39:n:438:LEU:N	2.40	0.55
1:1:1262:A:O2'	1:1:1292:G:H1'	2.07	0.55
1:1:1546:U:H2'	1:1:1547:G:H8	1.71	0.55
1:1:1701:G:H2'	1:1:1702:A:C8	2.42	0.55
1:1:3147:U:H2'	1:1:3148:G:H8	1.71	0.55
6:C:140:ARG:HG3	6:C:140:ARG:NH1	2.19	0.55
11:H:87:ARG:HE	11:H:89:LYS:HE3	1.71	0.55
41:p:231:GLU:HA	41:p:259:ARG:HA	1.89	0.55
1:1:3416:A:N6	5:B:121:ASN:OD1	2.40	0.55
1:1:3426:G:H2'	1:1:3427:G:H8	1.72	0.55
3:3:16:CYS:HA	6:C:139:ALA:HB1	1.88	0.55
5:B:283:TYR:CZ	5:B:325:ASN:HB3	2.41	0.55
6:C:283:ILE:HG22	6:C:284:ILE:HG23	1.89	0.55
14:M:7:TYR:O	14:M:12:ARG:NE	2.40	0.55
15:N:110:CYS:HB3	15:N:113:LEU:HD12	1.89	0.55
1:1:3039:U:H2'	1:1:3042:G:N7	2.22	0.55
10:G:130:TYR:HE1	10:G:202:GLU:HG2	1.72	0.55
13:L:77:LEU:HD22	13:L:87:ARG:HD3	1.89	0.55
24:X:112:LEU:HD21	24:X:120:LYS:HD2	1.88	0.55
1:1:1353:U:OP1	20:S:116:ARG:NH1	2.30	0.55
1:1:3222:C:O2'	11:H:158:ASN:OD1	2.25	0.55
3:3:10:VAL:HG22	6:C:34:PRO:HG3	1.89	0.55
18:Q:61:ILE:HD11	18:Q:65:LYS:HG2	1.88	0.55
25:Y:31:SER:HA	25:Y:48:PRO:HA	1.88	0.55
27:a:89:LYS:HG3	27:a:90:TYR:CD2	2.42	0.55
30:d:42:VAL:HG23	30:d:54:VAL:HG21	1.89	0.55
39:n:591:ARG:HA	39:n:594:LYS:HE3	1.88	0.55
1:1:985:G:H21	1:1:1147:G:H1	1.54	0.54
1:1:1231:A:O2'	1:1:1232:G:N2	2.40	0.54
1:1:1701:G:H2'	1:1:1702:A:H8	1.72	0.54
1:1:3033:G:H2'	1:1:3034:G:C8	2.42	0.54
20:S:162:ALA:HB3	20:S:165:LYS:HB2	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d:19:ILE:HG21	30:d:76:LEU:HD13	1.88	0.54
1:1:985:G:N2	1:1:1147:G:H1	2.04	0.54
1:1:3244:C:H2'	1:1:3245:G:C8	2.42	0.54
11:H:115:PHE:HE2	11:H:163:CYS:HA	1.71	0.54
38:m:618:SER:H	38:m:633:SER:HA	1.71	0.54
1:1:1696:G:H2'	1:1:1697:G:C8	2.42	0.54
8:E:89:ASN:HB3	8:E:91:VAL:HG23	1.88	0.54
19:R:38:ARG:HB3	19:R:42:ARG:NH1	2.22	0.54
39:n:141:PHE:CD2	39:n:202:VAL:HG22	2.41	0.54
1:1:1156:U:H2'	1:1:1157:G:H8	1.72	0.54
1:1:1715:G:H1	1:1:1723:U:H3	1.56	0.54
1:1:1780:G:H4'	1:1:1781:G:H21	1.72	0.54
2:2:131:G:H2'	2:2:132:G:C8	2.43	0.54
32:f:37:ASP:OD1	32:f:37:ASP:N	2.41	0.54
39:n:166:GLU:O	39:n:238:TYR:OH	2.25	0.54
39:n:183:SER:O	39:n:204:TYR:OH	2.20	0.54
41:p:106:TRP:O	41:p:122:TYR:N	2.40	0.54
2:2:54:G:O2'	2:2:69:A:N1	2.35	0.54
6:C:228:GLU:OE1	6:C:239:GLN:NE2	2.41	0.54
14:M:120:ARG:HD2	16:O:183:LYS:HD2	1.89	0.54
18:Q:63:ILE:HG22	18:Q:90:ASP:HA	1.89	0.54
25:Y:37:GLU:HA	25:Y:40:GLU:OE2	2.08	0.54
1:1:58:G:N2	1:1:60:A:N3	2.56	0.54
1:1:1827:G:H2'	1:1:1828:A:C8	2.43	0.54
1:1:3351:U:H2'	1:1:3352:A:C8	2.43	0.54
32:f:51:CYS:SG	32:f:102:MET:HE3	2.48	0.54
32:f:56:SER:OG	32:f:66:ARG:NE	2.32	0.54
38:m:373:THR:N	38:m:740:THR:O	2.39	0.54
8:E:194:LYS:O	14:M:110:ARG:NH2	2.40	0.54
22:V:51:LEU:H	22:V:51:LEU:HD12	1.73	0.54
24:X:130:ASP:OD1	24:X:132:LEU:N	2.41	0.54
38:m:339:ASP:OD1	43:t:22:ARG:NH1	2.38	0.54
1:1:167:G:H5'	38:m:222:LYS:HD2	1.89	0.54
3:3:49:ARG:HA	3:3:65:LYS:HG3	1.90	0.54
27:a:77:ARG:O	27:a:80:THR:OG1	2.24	0.54
4:A:92:LEU:HD13	35:i:68:ARG:HE	1.72	0.54
9:F:149:LYS:HE2	9:F:153:GLU:OE2	2.08	0.54
20:S:78:ILE:HB	20:S:120:ILE:HD11	1.90	0.54
25:Y:35:SER:OG	25:Y:37:GLU:OE2	2.25	0.54
1:1:178:U:H3	1:1:254:G:H1	1.56	0.54
1:1:1262:A:H5''	1:1:1263:C:H5'	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1299:G:H1'	1:1:1304:A:H61	1.73	0.54
1:1:3033:G:H2'	1:1:3034:G:H8	1.74	0.54
2:2:29:C:OP1	6:C:195:LYS:HE2	2.08	0.54
14:M:51:ILE:HD12	14:M:52:ARG:H	1.73	0.54
14:M:97:GLU:HA	14:M:100:LYS:HB3	1.89	0.54
46:y:109:ALA:HB2	46:y:149:GLY:HA2	1.90	0.54
1:1:1915:G:H2'	1:1:1916:G:H8	1.73	0.53
38:m:339:ASP:CG	43:t:22:ARG:HH22	2.16	0.53
39:n:164:CYS:SG	39:n:165:ALA:N	2.81	0.53
41:p:201:GLU:H	41:p:216:SER:HA	1.73	0.53
42:r:19:ASP:OD2	42:r:19:ASP:N	2.33	0.53
1:1:995:G:H2'	1:1:996:G:H8	1.73	0.53
1:1:1644:C:N4	1:1:1645:G:O6	2.41	0.53
1:1:2925:G:H2'	1:1:2926:G:H8	1.74	0.53
1:1:3284:G:H2'	1:1:3285:G:H8	1.73	0.53
11:H:11:LEU:HD23	11:H:12:THR:C	2.34	0.53
20:S:78:ILE:HD11	20:S:109:MET:CE	2.38	0.53
12:K:56:GLN:N	12:K:240:HIS:O	2.40	0.53
14:M:97:GLU:H	14:M:97:GLU:CD	2.17	0.53
22:V:70:ASP:OD1	22:V:71:LEU:N	2.41	0.53
30:d:78:LEU:HD12	30:d:96:VAL:CG2	2.37	0.53
38:m:241:ALA:HB1	38:m:246:ARG:HB2	1.89	0.53
39:n:134:ASP:OD1	39:n:134:ASP:N	2.40	0.53
1:1:276:A:N6	1:1:304:A:OP2	2.34	0.53
1:1:323:C:P	13:L:102:ARG:HH22	2.31	0.53
5:B:372:THR:HG23	5:B:375:GLU:H	1.74	0.53
1:1:1277:G:H1'	1:1:1295:G:H2'	1.91	0.53
1:1:1941:A:H2'	1:1:1942:A:C8	2.43	0.53
1:1:3208:G:O6	1:1:3216:C:H5''	2.09	0.53
1:1:3373:C:H4'	8:E:62:ALA:HB1	1.90	0.53
6:C:289:VAL:O	6:C:293:ILE:HG12	2.08	0.53
8:E:57:VAL:O	8:E:104:THR:OG1	2.22	0.53
8:E:114:VAL:HG21	8:E:160:VAL:HG13	1.91	0.53
11:H:48:LYS:NZ	11:H:50:GLY:O	2.37	0.53
30:d:67:ARG:HG3	30:d:73:PRO:HD3	1.91	0.53
1:1:283:U:H2'	1:1:284:U:H6	1.73	0.53
2:2:31:U:H1'	25:Y:16:LYS:HG3	1.89	0.53
11:H:90:MET:HE2	11:H:90:MET:HA	1.90	0.53
20:S:121:ARG:NH1	47:T:154:VAL:O	2.41	0.53
22:V:82:ARG:HB2	22:V:101:ALA:H	1.74	0.53
31:e:6:ILE:HD13	31:e:60:THR:HB	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:n:194:PHE:HZ	39:n:240:THR:HG21	1.73	0.53
39:n:399:ILE:HB	39:n:416:ARG:HD3	1.89	0.53
1:1:1739:A:N6	1:1:1780:G:O4'	2.42	0.53
1:1:3123:A:H2'	1:1:3124:G:O4'	2.09	0.53
14:M:26:ALA:HB3	14:M:39:ILE:HD12	1.89	0.53
1:1:1253:G:H21	1:1:1317:A:H2	1.55	0.53
1:1:2931:C:H5	1:1:2947:C:H41	1.56	0.53
1:1:3235:A:OP2	5:B:30:LYS:NZ	2.32	0.53
11:H:29:THR:HG22	11:H:34:THR:HG23	1.90	0.53
19:R:12:ALA:HA	19:R:15:LEU:HB3	1.90	0.53
43:t:144:ILE:O	43:t:242:ASN:ND2	2.40	0.53
1:1:1826:C:H2'	1:1:1827:G:H8	1.74	0.53
17:P:50:ASN:HB3	17:P:55:LYS:HB2	1.90	0.53
20:S:80:TYR:OH	20:S:113:HIS:O	2.26	0.53
25:Y:6:ASP:OD1	45:v:20:ARG:HG3	2.09	0.53
38:m:299:SER:H	38:m:302:PRO:HG3	1.74	0.53
40:o:119:LYS:O	40:o:123:MET:HG3	2.09	0.53
1:1:1365:C:H5''	9:F:213:LYS:HB3	1.90	0.53
1:1:3247:U:H4'	1:1:3395:G:H1'	1.90	0.53
5:B:299:ASP:O	5:B:301:THR:OG1	2.24	0.53
10:G:158:ASP:HB3	10:G:159:PRO:HD3	1.91	0.53
30:d:77:ARG:HH22	30:d:108:THR:HA	1.74	0.53
1:1:641:G:H2'	1:1:642:A:H8	1.73	0.52
1:1:761:U:H1'	1:1:762:U:H5'	1.91	0.52
13:L:31:ARG:HD3	13:L:35:ARG:NH1	2.24	0.52
39:n:357:THR:O	39:n:400:THR:N	2.40	0.52
40:o:202:PRO:HB2	40:o:205:THR:OG1	2.09	0.52
1:1:714:A:H5'	1:1:717:A:N7	2.24	0.52
14:M:40:ASP:OD1	14:M:41:SER:N	2.41	0.52
41:p:273:MET:H	41:p:288:GLY:HA2	1.74	0.52
48:6:87:A:H2'	48:6:88:G:O4'	2.08	0.52
1:1:530:A:N1	20:S:64:SER:N	2.57	0.52
1:1:1695:C:H2'	1:1:1696:G:H8	1.74	0.52
1:1:3104:G:H2'	1:1:3105:G:H8	1.75	0.52
1:1:3423:A:H2'	1:1:3424:A:C8	2.43	0.52
3:3:62:LEU:HD22	3:3:93:ILE:HD12	1.91	0.52
8:E:83:THR:OG1	8:E:91:VAL:O	2.28	0.52
8:E:117:GLU:OE1	8:E:117:GLU:N	2.24	0.52
24:X:37:LEU:HD11	39:n:82:ARG:NH1	2.24	0.52
39:n:141:PHE:CE1	39:n:164:CYS:HB2	2.45	0.52
39:n:369:LEU:HA	39:n:372:VAL:HG12	1.90	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:227:ASP:HA	10:G:230:ARG:HH11	1.75	0.52
27:a:102:ASN:HA	27:a:125:GLN:HB2	1.92	0.52
41:p:296:TRP:HA	41:p:303:ASN:HA	1.91	0.52
1:1:216:A:H4'	1:1:218:A:N7	2.25	0.52
1:1:837:G:H4'	6:C:75:ARG:HB2	1.91	0.52
1:1:1308:C:O2'	1:1:1309:A:O5'	2.24	0.52
6:C:314:HIS:ND1	6:C:314:HIS:O	2.43	0.52
13:L:50:PRO:HD2	34:h:118:TYR:CE2	2.44	0.52
17:P:48:LEU:HD12	17:P:88:VAL:HB	1.90	0.52
25:Y:30:MET:HE3	25:Y:77:PHE:HA	1.91	0.52
16:O:184:GLU:OE1	16:O:184:GLU:N	2.38	0.52
19:R:17:CYS:SG	19:R:52:ARG:NH1	2.79	0.52
30:d:66:LYS:HB3	30:d:67:ARG:HH21	1.75	0.52
38:m:337:CYS:HB3	39:n:222:PHE:CE2	2.44	0.52
1:1:1918:G:H1	1:1:1921:C:P	2.32	0.52
38:m:503:SER:N	38:m:565:SER:O	2.42	0.52
1:1:2931:C:H3'	1:1:2932:A:C8	2.37	0.52
1:1:3284:G:H2'	1:1:3285:G:C8	2.45	0.52
1:1:3417:A:H1'	1:1:3490:A:H4'	1.92	0.52
41:p:192:LEU:O	41:p:258:ALA:N	2.43	0.52
1:1:621:G:H5''	9:F:44:ARG:NH2	2.21	0.52
1:1:1714:A:H2'	1:1:1715:G:C8	2.45	0.52
1:1:3112:A:O2'	1:1:3113:A:H8	1.93	0.52
32:f:72:ILE:HD12	32:f:82:VAL:HG21	1.92	0.52
38:m:338:LEU:HB2	43:t:22:ARG:NH2	2.25	0.52
39:n:357:THR:HG22	39:n:379:LYS:HB3	1.92	0.52
41:p:151:TRP:HA	41:p:158:PHE:HA	1.91	0.52
1:1:1260:G:H2'	1:1:1261:G:H8	1.74	0.52
2:2:111:G:OP2	2:2:113:A:O2'	2.28	0.52
3:3:71:HIS:C	3:3:72:PHE:HD2	2.18	0.52
3:3:110:GLN:O	3:3:113:THR:OG1	2.27	0.52
40:o:200:ARG:NH1	48:6:181:C:O4'	2.43	0.52
1:1:522:G:H1	1:1:604:U:H3	1.58	0.51
1:1:1773:A:H2'	1:1:1774:G:H8	1.74	0.51
3:3:19:ARG:NH2	3:3:38:CYS:SG	2.77	0.51
1:1:700:C:O2'	1:1:704:U:OP1	2.23	0.51
1:1:1389:A:H4'	1:1:1390:A:O5'	2.10	0.51
8:E:165:LEU:HG	8:E:166:PRO:HD3	1.92	0.51
9:F:138:GLU:OE2	9:F:228:HIS:NE2	2.43	0.51
9:F:237:LYS:HD2	9:F:239:ASP:H	1.76	0.51
31:e:35:ILE:O	31:e:41:ARG:NH2	2.34	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:h:26:GLU:O	34:h:30:LEU:N	2.38	0.51
43:t:89:LEU:HD11	43:t:122:PHE:HB3	1.92	0.51
43:t:179:LEU:HB3	43:t:184:VAL:HB	1.92	0.51
6:C:281:GLU:OE1	18:Q:112:ARG:NE	2.43	0.51
8:E:59:ILE:HG12	8:E:69:ARG:HG2	1.93	0.51
20:S:41:TRP:HH2	20:S:55:GLY:HA3	1.75	0.51
1:1:174:U:HO2'	1:1:259:A:H61	1.59	0.51
1:1:391:G:N2	1:1:394:A:OP2	2.30	0.51
1:1:1277:G:N3	1:1:1295:G:O2'	2.38	0.51
17:P:4:TYR:CE2	17:P:16:LYS:HB3	2.46	0.51
25:Y:26:ARG:O	25:Y:30:MET:HG3	2.10	0.51
27:a:7:LYS:HG2	27:a:11:LEU:HD12	1.93	0.51
42:r:154:THR:HA	42:r:213:VAL:HA	1.92	0.51
1:1:1695:C:H2'	1:1:1696:G:C8	2.45	0.51
1:1:3147:U:H2'	1:1:3148:G:C8	2.45	0.51
5:B:82:PRO:HG2	5:B:169:THR:HG22	1.91	0.51
38:m:331:LYS:NZ	39:n:213:ASP:OD2	2.37	0.51
41:p:109:GLY:HA3	41:p:148:SER:HA	1.91	0.51
1:1:118:U:N3	1:1:122:A:OP2	2.22	0.51
1:1:1259:A:H2'	1:1:1260:G:C8	2.46	0.51
1:1:1605:U:O4	1:1:1608:C:H5''	2.10	0.51
1:1:2925:G:H5'	28:b:135:GLY:HA3	1.92	0.51
1:1:3148:G:H2'	1:1:3149:G:H8	1.76	0.51
13:L:80:LEU:HB3	13:L:85:VAL:HG23	1.91	0.51
16:O:122:PRO:HG3	20:S:168:ALA:HB2	1.92	0.51
21:U:51:VAL:HA	21:U:65:ALA:HA	1.93	0.51
30:d:14:THR:HG23	30:d:81:SER:HB3	1.93	0.51
30:d:59:SER:O	30:d:62:LYS:HB2	2.09	0.51
40:o:110:GLY:N	40:o:177:GLN:O	2.39	0.51
1:1:601:C:OP2	9:F:149:LYS:HE3	2.10	0.51
1:1:1156:U:H2'	1:1:1157:G:C8	2.45	0.51
1:1:1183:G:OP2	1:1:1183:G:N2	2.25	0.51
1:1:1309:A:HO2'	1:1:1310:C:P	2.34	0.51
1:1:1312:U:H2'	1:1:1313:G:H8	1.76	0.51
1:1:1629:A:H1'	1:1:1650:C:H1'	1.93	0.51
1:1:2432:U:H2'	1:1:2433:A:C8	2.46	0.51
1:1:3000:U:H2'	1:1:3001:C:C6	2.46	0.51
24:X:132:LEU:O	24:X:136:ASN:ND2	2.42	0.51
41:p:363:ALA:HA	41:p:371:PHE:HA	1.92	0.51
42:r:182:ASN:HA	42:r:193:GLN:HA	1.92	0.51
1:1:1710:G:H1	1:1:1728:U:H3	1.59	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:28:CYS:N	3:3:36:GLY:O	2.43	0.51
8:E:31:TYR:HB2	31:e:87:LYS:HB3	1.93	0.51
17:P:4:TYR:CE2	17:P:16:LYS:HD2	2.45	0.51
18:Q:41:SER:OG	18:Q:134:THR:O	2.27	0.51
24:X:62:ILE:HD13	24:X:85:VAL:HG23	1.93	0.51
30:d:49:MET:HG3	30:d:80:LEU:HD21	1.92	0.51
34:h:87:THR:HG22	34:h:89:ALA:H	1.76	0.51
38:m:326:TYR:CE2	39:n:185:LYS:HD3	2.46	0.51
48:6:58:A:H2'	48:6:59:A:C8	2.46	0.51
1:1:59:G:H4'	1:1:60:A:OP1	2.11	0.51
1:1:715:U:H4'	25:Y:3:PHE:CE1	2.46	0.51
1:1:997:A:O2'	1:1:998:U:OP1	2.24	0.51
1:1:1341:G:O2'	1:1:2468:A:O2'	2.21	0.51
1:1:2454:C:H2'	1:1:2455:U:H6	1.75	0.51
20:S:157:GLY:O	20:S:159:VAL:N	2.44	0.51
39:n:260:LEU:HD12	39:n:374:ARG:HH21	1.76	0.51
1:1:1213:G:N2	1:1:1356:U:O2	2.44	0.51
1:1:1915:G:H2'	1:1:1916:G:C8	2.46	0.51
5:B:306:THR:HG21	5:B:316:VAL:HG22	1.93	0.51
6:C:159:GLN:O	6:C:215:THR:OG1	2.29	0.51
8:E:49:ARG:NH1	8:E:98:HIS:O	2.35	0.51
23:W:124:PHE:HA	23:W:208:THR:HA	1.93	0.51
24:X:9:ALA:HA	24:X:13:VAL:HG23	1.91	0.51
38:m:260:SER:OG	38:m:261:GLN:N	2.43	0.51
1:1:526:G:OP1	6:C:342:LYS:NZ	2.44	0.50
1:1:1564:U:OP2	1:1:1565:C:N4	2.40	0.50
1:1:1598:C:H2'	1:1:1599:A:C8	2.46	0.50
20:S:31:PRO:HD2	20:S:35:VAL:HG11	1.93	0.50
42:r:199:VAL:HA	42:r:220:ILE:HA	1.94	0.50
1:1:1674:C:H2'	1:1:1675:G:H8	1.75	0.50
1:1:3276:A:H2'	1:1:3277:A:O4'	2.10	0.50
1:1:3337:A:H2'	1:1:3338:A:C8	2.46	0.50
1:1:3425:C:H4'	30:d:18:THR:HG23	1.93	0.50
2:2:20:A:H4'	17:P:4:TYR:O	2.12	0.50
5:B:143:SER:O	5:B:147:GLU:HG2	2.11	0.50
41:p:383:TRP:HA	41:p:392:ILE:H	1.75	0.50
1:1:531:A:C2	6:C:349:PRO:HD2	2.47	0.50
1:1:1674:C:H2'	1:1:1675:G:C8	2.46	0.50
1:1:1826:C:H2'	1:1:1827:G:C8	2.46	0.50
1:1:1917:U:H3	1:1:1923:G:H1	1.58	0.50
5:B:281:LYS:NZ	5:B:352:GLU:O	2.40	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:137:LEU:HD23	6:C:144:ILE:HD13	1.93	0.50
30:d:47:LYS:HG3	30:d:48:HIS:CD2	2.47	0.50
34:h:20:LEU:O	34:h:24:ARG:HG2	2.12	0.50
34:h:106:GLN:O	34:h:110:GLU:HG2	2.11	0.50
6:C:338:LYS:HZ3	6:C:341:VAL:HA	1.75	0.50
10:G:81:THR:HG1	10:G:181:LYS:HZ3	1.52	0.50
24:X:114:ARG:NH2	24:X:116:ASN:HD21	2.08	0.50
42:r:61:MET:HE2	42:r:61:MET:HA	1.93	0.50
1:1:1017:U:O2'	9:F:109:ILE:HD11	2.11	0.50
1:1:1580:A:O2'	15:N:96:ARG:NH2	2.44	0.50
1:1:717:A:N6	45:v:25:LYS:HE2	2.26	0.50
1:1:764:U:H3'	1:1:765:G:C8	2.46	0.50
1:1:1941:A:H2'	1:1:1942:A:H8	1.76	0.50
1:1:3117:A:N6	1:1:3129:A:OP2	2.39	0.50
3:3:3:GLN:CG	3:3:4:ASP:H	2.23	0.50
9:F:158:ARG:NH1	9:F:214:LEU:HA	2.26	0.50
16:O:57:ALA:O	16:O:61:LYS:HG2	2.12	0.50
17:P:14:CYS:O	17:P:16:LYS:HG3	2.11	0.50
20:S:174:THR:O	20:S:174:THR:HG22	2.11	0.50
43:t:146:ASN:O	43:t:150:VAL:HG23	2.11	0.50
1:1:735:G:N2	1:1:738:A:OP2	2.43	0.50
1:1:995:G:H2'	1:1:996:G:C8	2.47	0.50
1:1:1005:A:N6	1:1:1006:A:N6	2.59	0.50
1:1:1309:A:O2'	1:1:1310:C:O5'	2.30	0.50
5:B:331:PRO:HD2	5:B:334:ARG:NE	2.15	0.50
17:P:108:ASP:OD1	17:P:109:MET:N	2.45	0.50
1:1:258:U:H3'	1:1:259:A:H5'	1.94	0.50
20:S:11:ARG:NH1	20:S:56:GLU:OE2	2.44	0.50
22:V:54:ALA:HB2	22:V:60:VAL:HG11	1.94	0.50
26:Z:57:MET:HA	43:t:27:ARG:HH12	1.77	0.50
36:j:28:HIS:CE1	36:j:30:GLN:HB2	2.47	0.50
38:m:302:PRO:O	38:m:316:LYS:NZ	2.45	0.50
1:1:702:A:O2'	27:a:77:ARG:NH1	2.45	0.50
1:1:1533:U:H2'	1:1:1534:G:C8	2.47	0.50
1:1:1879:C:H2'	1:1:1880:A:C8	2.38	0.50
11:H:106:ASN:ND2	11:H:106:ASN:O	2.45	0.50
17:P:12:THR:OG1	17:P:13:LYS:N	2.43	0.50
20:S:59:ALA:C	20:S:60:ILE:HD13	2.37	0.50
35:i:55:VAL:O	35:i:59:ILE:HG12	2.12	0.50
1:1:155:U:OP2	15:N:49:ARG:NH2	2.43	0.49
5:B:208:THR:O	5:B:340:LYS:NZ	2.45	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:15:LEU:CD2	19:R:17:CYS:HB2	2.41	0.49
31:e:14:PHE:CG	31:e:50:PRO:HG3	2.47	0.49
39:n:373:ILE:HG22	39:n:378:GLY:HA3	1.94	0.49
41:p:96:ALA:O	41:p:432:GLN:N	2.43	0.49
1:1:1274:G:N3	1:1:1301:A:O2'	2.45	0.49
44:u:22:VAL:HA	44:u:28:VAL:HA	1.95	0.49
48:6:7:U:N3	48:6:47:U:OP1	2.32	0.49
1:1:620:C:O2	6:C:329:ARG:HD3	2.11	0.49
1:1:3421:G:H2'	1:1:3422:G:H8	1.77	0.49
8:E:69:ARG:HD3	8:E:177:TYR:CE1	2.46	0.49
1:1:1509:A:H5'	30:d:62:LYS:HZ2	1.77	0.49
1:1:1610:U:H2'	1:1:1611:G:H8	1.77	0.49
1:1:1670:G:N2	1:1:1673:A:OP2	2.25	0.49
5:B:293:ASN:OD1	5:B:294:ALA:N	2.44	0.49
6:C:190:ARG:HB3	6:C:195:LYS:HB3	1.94	0.49
9:F:91:ILE:HG23	9:F:124:VAL:HB	1.93	0.49
24:X:112:LEU:HD23	24:X:112:LEU:H	1.78	0.49
39:n:406:ARG:HH12	39:n:409:ILE:HG23	1.77	0.49
1:1:372:G:OP1	6:C:62:THR:HG23	2.13	0.49
1:1:511:C:H2'	1:1:512:A:C8	2.47	0.49
1:1:742:A:OP2	27:a:112:LEU:HB3	2.11	0.49
1:1:1533:U:H2'	1:1:1534:G:H8	1.77	0.49
1:1:1632:C:H2'	1:1:1633:G:C8	2.47	0.49
1:1:2454:C:H2'	1:1:2455:U:C6	2.47	0.49
27:a:76:ASP:OD1	27:a:77:ARG:N	2.45	0.49
1:1:1262:A:N6	1:1:1307:U:OP2	2.45	0.49
1:1:1321:A:H2'	1:1:1322:A:H8	1.77	0.49
1:1:3024:C:O2'	1:1:3025:A:O5'	2.27	0.49
1:1:3099:G:O2'	5:B:92:TYR:OH	2.30	0.49
1:1:3160:U:H2'	1:1:3161:G:H8	1.77	0.49
6:C:319:ASN:HD22	6:C:322:LYS:HE2	1.77	0.49
9:F:91:ILE:HD11	9:F:143:TYR:HD2	1.78	0.49
9:F:103:PRO:O	9:F:107:ARG:HG3	2.12	0.49
15:N:99:ARG:HB3	15:N:167:ILE:HG12	1.95	0.49
20:S:80:TYR:CD2	20:S:109:MET:CE	2.93	0.49
22:V:14:ARG:HD2	22:V:15:MET:N	2.27	0.49
22:V:76:MET:HE1	22:V:104:ILE:HG23	1.95	0.49
1:1:620:C:H2'	1:1:621:G:O4'	2.12	0.49
1:1:646:A:HO2'	1:1:647:A:H8	1.60	0.49
1:1:1164:A:H2'	1:1:1165:G:C8	2.48	0.49
1:1:1424:A:OP1	1:1:1425:C:O2'	2.17	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1608:C:H1'	1:1:1609:G:C8	2.47	0.49
1:1:3131:C:O4'	11:H:120:ILE:HD11	2.13	0.49
9:F:127:ASN:OD1	9:F:129:ALA:N	2.46	0.49
17:P:57:ALA:HB3	17:P:81:ALA:HB1	1.93	0.49
19:R:44:LEU:HD21	19:R:49:LEU:HB3	1.95	0.49
30:d:15:ARG:HG2	30:d:110:VAL:HA	1.95	0.49
30:d:26:TYR:HD1	30:d:27:GLY:N	2.11	0.49
43:t:113:ARG:NH1	43:t:205:THR:O	2.46	0.49
1:1:3306:C:N4	14:M:92:TRP:HB2	2.27	0.49
6:C:239:GLN:O	6:C:248:ARG:HD3	2.12	0.49
16:O:11:ASP:OD2	16:O:38:ARG:NH2	2.46	0.49
16:O:61:LYS:O	16:O:73:HIS:NE2	2.40	0.49
38:m:326:TYR:HE2	39:n:185:LYS:HD3	1.78	0.49
41:p:203:VAL:HA	41:p:214:SER:HA	1.95	0.49
1:1:189:G:H1	1:1:243:C:H41	1.60	0.49
1:1:216:A:O2'	1:1:218:A:OP2	2.21	0.49
1:1:1471:C:O2'	6:C:95:MET:HE1	2.13	0.49
1:1:1713:G:H2'	1:1:1714:A:C8	2.48	0.49
6:C:333:TYR:HE2	9:F:59:GLU:HG2	1.78	0.49
11:H:109:VAL:HG22	11:H:125:LYS:HA	1.93	0.49
19:R:25:ASP:HB2	19:R:28:GLU:OE1	2.13	0.49
24:X:85:VAL:HG21	24:X:94:ILE:HG12	1.95	0.49
39:n:38:ILE:HD12	39:n:222:PHE:CZ	2.48	0.49
1:1:3:U:O4	24:X:18:HIS:ND1	2.39	0.49
1:1:306:U:H4'	1:1:307:G:H5'	1.94	0.49
1:1:340:C:OP2	45:v:6:GLN:NE2	2.42	0.49
1:1:538:U:O2	1:1:588:G:N2	2.42	0.49
1:1:1778:A:H2'	1:1:1779:U:C6	2.48	0.49
1:1:1946:A:H2'	1:1:1947:G:C8	2.48	0.49
1:1:3025:A:H2'	1:1:3026:C:C6	2.48	0.49
6:C:140:ARG:HH21	6:C:242:PRO:HG2	1.77	0.49
6:C:288:ASP:O	6:C:288:ASP:OD2	2.31	0.49
8:E:56:THR:OG1	8:E:108:LYS:NZ	2.33	0.49
11:H:44:ILE:HD12	11:H:68:ILE:HD11	1.94	0.49
24:X:96:GLU:HA	24:X:96:GLU:OE2	2.13	0.49
38:m:336:ARG:O	38:m:339:ASP:HB2	2.13	0.49
43:t:133:LEU:HD11	43:t:142:TYR:CG	2.48	0.49
1:1:271:C:H2'	1:1:272:G:H8	1.78	0.48
1:1:2927:C:H42	1:1:2951:G:H1	1.61	0.48
1:1:2951:G:O2'	42:r:191:THR:N	2.32	0.48
16:O:24:VAL:O	16:O:28:LEU:HD23	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:7:GLN:NE2	19:R:35:ALA:O	2.32	0.48
38:m:334:PHE:CD1	39:n:219:MET:CE	2.93	0.48
39:n:379:LYS:HG3	39:n:392:PHE:HZ	1.78	0.48
39:n:438:LEU:HG	39:n:446:PRO:HG3	1.95	0.48
43:t:87:THR:OG1	43:t:89:LEU:O	2.31	0.48
1:1:1439:U:H1'	31:e:51:LYS:O	2.13	0.48
1:1:2432:U:H2'	1:1:2433:A:H8	1.79	0.48
5:B:81:THR:O	5:B:81:THR:OG1	2.24	0.48
6:C:147:ILE:HG13	6:C:152:LEU:HD22	1.96	0.48
8:E:149:LEU:HD23	8:E:149:LEU:H	1.78	0.48
16:O:40:GLU:CD	16:O:40:GLU:H	2.20	0.48
41:p:146:LEU:HA	41:p:162:SER:HA	1.95	0.48
43:t:55:GLU:HG2	48:6:2:C:C6	2.49	0.48
1:1:139:U:P	1:1:140:U:H3	2.36	0.48
1:1:182:G:N2	1:1:251:U:O2	2.46	0.48
1:1:1011:G:H21	1:1:1136:A:H1'	1.78	0.48
8:E:59:ILE:HB	8:E:102:ILE:HB	1.95	0.48
9:F:146:PRO:HA	9:F:243:ASN:OD1	2.13	0.48
10:G:143:ILE:HG23	10:G:175:VAL:HG21	1.95	0.48
11:H:88:TYR:CE1	11:H:182:ARG:HG3	2.48	0.48
17:P:122:ALA:HB3	17:P:143:PRO:HB2	1.94	0.48
1:1:623:C:H2'	1:1:624:U:O4'	2.12	0.48
1:1:687:U:H2'	1:1:688:C:C6	2.48	0.48
1:1:994:A:H2'	1:1:995:G:O4'	2.13	0.48
1:1:3113:A:H2'	1:1:3114:C:C6	2.49	0.48
19:R:15:LEU:O	19:R:15:LEU:HD23	2.13	0.48
30:d:49:MET:O	30:d:49:MET:HE3	2.14	0.48
38:m:252:GLN:HA	38:m:255:GLU:HG2	1.95	0.48
38:m:321:ARG:HD2	43:t:185:ILE:HG22	1.94	0.48
38:m:677:ASP:HA	38:m:714:GLY:H	1.78	0.48
43:t:225:VAL:HG23	43:t:228:PHE:HB2	1.94	0.48
45:v:147:LYS:NZ	45:v:151:ARG:HE	2.11	0.48
1:1:1824:C:H2'	1:1:1825:U:C6	2.48	0.48
1:1:3174:A:OP1	1:1:3176:G:H5'	2.14	0.48
17:P:57:ALA:HB2	17:P:83:TRP:NE1	2.28	0.48
18:Q:84:VAL:HB	18:Q:141:VAL:HG23	1.95	0.48
20:S:80:TYR:HB3	20:S:87:HIS:HB2	1.96	0.48
25:Y:4:SER:OG	25:Y:6:ASP:HB2	2.13	0.48
29:c:56:ILE:O	29:c:82:HIS:N	2.45	0.48
30:d:20:HIS:O	30:d:24:ARG:HG3	2.14	0.48
38:m:349:THR:O	38:m:349:THR:OG1	2.30	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:86:G:O2'	1:1:98:G:O6	2.30	0.48
1:1:433:C:N3	1:1:660:G:N2	2.61	0.48
1:1:644:A:H4'	1:1:645:U:OP2	2.14	0.48
1:1:705:G:H2'	1:1:706:U:H5'	1.96	0.48
1:1:1380:A:H3'	1:1:1380:A:N3	2.27	0.48
1:1:1658:G:H2'	1:1:1659:G:H8	1.78	0.48
1:1:1784:U:O2	1:1:1784:U:H2'	2.12	0.48
1:1:3118:G:H22	1:1:3127:G:H3'	1.78	0.48
5:B:17:LEU:HD13	5:B:18:PRO:HA	1.94	0.48
8:E:173:ASN:ND2	8:E:176:GLU:OE2	2.37	0.48
10:G:91:PHE:CZ	10:G:180:VAL:HG11	2.48	0.48
10:G:98:ARG:NH2	10:G:188:THR:O	2.47	0.48
11:H:15:LYS:NZ	11:H:16:GLY:O	2.37	0.48
22:V:19:LEU:HD21	22:V:100:ASN:HD22	1.78	0.48
24:X:102:TYR:CE1	24:X:138:ILE:HD11	2.49	0.48
30:d:67:ARG:HG3	30:d:73:PRO:CD	2.44	0.48
31:e:88:THR:HG23	31:e:89:TYR:CD1	2.46	0.48
38:m:341:TYR:CD1	39:n:38:ILE:HD11	2.48	0.48
40:o:103:LYS:HG3	40:o:156:LEU:HD23	1.94	0.48
40:o:107:LEU:HB3	40:o:151:ILE:HG13	1.95	0.48
41:p:145:SER:O	41:p:163:LEU:N	2.43	0.48
1:1:261:A:O2'	38:m:233:LYS:NZ	2.24	0.48
3:3:40:ARG:O	3:3:50:TYR:OH	2.30	0.48
17:P:57:ALA:HB2	17:P:83:TRP:CE2	2.49	0.48
25:Y:58:ILE:O	25:Y:63:LYS:HG3	2.13	0.48
32:f:33:ILE:H	32:f:33:ILE:HD12	1.79	0.48
1:1:546:G:C6	20:S:143:LEU:HD13	2.49	0.48
1:1:1234:A:H4'	1:1:1235:A:O5'	2.13	0.48
1:1:1466:C:O2'	1:1:1468:G:OP2	2.28	0.48
1:1:1516:A:OP2	1:1:1913:A:O2'	2.23	0.48
1:1:3195:C:H42	1:1:3231:U:H3	1.61	0.48
11:H:90:MET:SD	11:H:177:ILE:HG13	2.54	0.48
20:S:56:GLU:OE1	20:S:56:GLU:N	2.46	0.48
22:V:82:ARG:HB2	22:V:101:ALA:N	2.29	0.48
22:V:82:ARG:NH2	22:V:117:THR:O	2.27	0.48
29:c:53:ALA:HA	29:c:107:ILE:HA	1.95	0.48
30:d:75:ARG:NH1	30:d:105:LYS:HE3	2.28	0.48
38:m:469:ALA:HA	38:m:474:VAL:HA	1.96	0.48
41:p:211:VAL:HA	41:p:225:ASP:HA	1.95	0.48
1:1:3188:U:O3'	22:V:50:ARG:NH2	2.47	0.48
1:1:3369:A:H4'	1:1:3370:U:H5'	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:338:LYS:HZ3	6:C:341:VAL:CG1	2.23	0.48
12:K:87:ALA:O	12:K:112:THR:N	2.42	0.48
20:S:116:ARG:O	20:S:120:ILE:HG22	2.13	0.48
43:t:181:LYS:CG	43:t:182:TYR:CE1	2.96	0.48
48:6:50:U:H2'	48:6:51:G:C8	2.49	0.48
3:3:114:ARG:HH21	31:e:84:MET:CE	2.23	0.48
4:A:92:LEU:HD12	35:i:65:LYS:HG2	1.96	0.48
6:C:36:LEU:O	6:C:40:VAL:HG23	2.14	0.48
8:E:177:TYR:HE2	14:M:108:PHE:HA	1.79	0.48
16:O:40:GLU:O	16:O:140:GLY:N	2.45	0.48
40:o:185:GLN:N	40:o:185:GLN:OE1	2.47	0.48
1:1:251:U:H2'	1:1:252:A:H8	1.79	0.47
1:1:341:G:OP2	45:v:9:LYS:HE3	2.14	0.47
1:1:548:U:H2'	1:1:549:G:H8	1.79	0.47
1:1:1321:A:H2'	1:1:1322:A:C8	2.49	0.47
1:1:1678:A:H2'	1:1:1679:A:N3	2.29	0.47
1:1:3332:U:H2'	1:1:3333:G:C8	2.49	0.47
4:A:92:LEU:HD13	35:i:68:ARG:NE	2.29	0.47
17:P:47:PHE:HD2	17:P:48:LEU:HD22	1.78	0.47
31:e:16:ARG:HB2	31:e:28:SER:O	2.14	0.47
43:t:85:ASP:CG	43:t:86:GLU:N	2.71	0.47
1:1:1236:A:N1	1:1:1330:U:H5	2.11	0.47
1:1:3123:A:H8	28:b:209:HIS:H	1.61	0.47
5:B:183:VAL:HG23	5:B:183:VAL:O	2.14	0.47
11:H:124:ILE:HD11	11:H:162:ILE:HG21	1.96	0.47
14:M:78:TRP:HE1	14:M:84:CYS:H	1.61	0.47
39:n:126:PHE:CG	39:n:236:LYS:HD3	2.49	0.47
41:p:273:MET:N	41:p:287:VAL:O	2.47	0.47
42:r:60:GLN:O	42:r:64:THR:HG23	2.14	0.47
1:1:339:G:P	45:v:6:GLN:HE21	2.37	0.47
1:1:3333:G:H1	1:1:3354:U:H3	1.62	0.47
2:2:141:A:H2'	2:2:142:A:C8	2.49	0.47
8:E:191:HIS:CD2	8:E:192:LEU:HG	2.49	0.47
11:H:127:LEU:H	11:H:127:LEU:HD12	1.79	0.47
38:m:194:GLU:CD	38:m:194:GLU:H	2.23	0.47
1:1:1295:G:N2	1:1:1296:U:O4	2.40	0.47
1:1:1465:G:N7	27:a:9:ARG:NH1	2.63	0.47
1:1:1540:A:O2'	1:1:1541:G:OP1	2.29	0.47
1:1:1652:G:H2'	1:1:1653:A:H8	1.78	0.47
1:1:2995:A:H4'	11:H:172:LYS:HD3	1.96	0.47
2:2:95:G:N1	25:Y:113:ASP:OD2	2.26	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:291:ARG:HH11	6:C:291:ARG:HG3	1.79	0.47
10:G:80:LYS:HB3	10:G:226:TYR:CZ	2.50	0.47
14:M:119:GLN:HA	14:M:122:GLU:OE1	2.13	0.47
20:S:12:LYS:HG2	20:S:21:PRO:HB3	1.95	0.47
22:V:79:ILE:HD13	22:V:128:TRP:CD1	2.48	0.47
27:a:124:VAL:HG22	27:a:126:THR:HG23	1.95	0.47
32:f:14:HIS:CD2	32:f:29:SER:HB3	2.49	0.47
43:t:148:HIS:NE2	43:t:152:GLU:OE2	2.47	0.47
1:1:3099:G:P	5:B:26:ARG:HH22	2.37	0.47
5:B:122:TRP:HE1	5:B:127:LYS:HG3	1.78	0.47
8:E:85:PRO:HB2	8:E:88:VAL:HB	1.97	0.47
17:P:84:PRO:HB2	17:P:87:SER:HB2	1.96	0.47
20:S:76:ILE:HG23	20:S:125:VAL:HG22	1.97	0.47
1:1:3331:U:H3	1:1:3356:A:N6	2.11	0.47
3:3:29:ARG:HA	31:e:81:LEU:HD11	1.97	0.47
5:B:92:TYR:HE2	5:B:159:ARG:HD2	1.79	0.47
6:C:312:ARG:NH2	6:C:315:VAL:HG23	2.29	0.47
8:E:117:GLU:H	8:E:117:GLU:CD	2.15	0.47
9:F:133:MET:HE2	9:F:133:MET:HA	1.94	0.47
32:f:18:GLN:HB3	32:f:28:THR:HG23	1.96	0.47
34:h:79:PRO:HD2	34:h:82:LEU:HD12	1.96	0.47
39:n:172:ILE:HD11	39:n:371:PHE:HA	1.96	0.47
43:t:120:ALA:HB3	43:t:211:PHE:HD2	1.80	0.47
1:1:27:C:H2'	1:1:28:G:H5'	1.95	0.47
1:1:527:C:H5''	6:C:343:ILE:HD11	1.96	0.47
1:1:1209:G:N3	1:1:1359:C:O2'	2.47	0.47
1:1:1260:G:H2'	1:1:1261:G:C8	2.50	0.47
1:1:1594:G:O2'	1:1:1597:G:H5''	2.14	0.47
1:1:2952:C:O2'	1:1:2953:U:H5'	2.14	0.47
2:2:83:G:OP2	25:Y:73:TYR:OH	2.31	0.47
3:3:47:ASN:HB3	3:3:50:TYR:CE2	2.49	0.47
3:3:79:ARG:NH1	3:3:81:LYS:HB2	2.30	0.47
6:C:74:ALA:O	6:C:78:ARG:NH1	2.36	0.47
10:G:80:LYS:HB3	10:G:226:TYR:CE1	2.48	0.47
10:G:183:LYS:HB2	10:G:194:THR:HG23	1.95	0.47
31:e:29:TRP:CZ2	31:e:50:PRO:HD2	2.49	0.47
34:h:13:GLN:NE2	34:h:13:GLN:O	2.47	0.47
43:t:181:LYS:HG3	43:t:182:TYR:CE1	2.49	0.47
1:1:3333:G:H2'	1:1:3334:A:C8	2.49	0.47
1:1:3359:U:O4	14:M:115:ARG:NH2	2.43	0.47
5:B:35:ASP:OD1	5:B:36:ASP:N	2.48	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:311:PHE:N	5:B:315:GLY:O	2.45	0.47
22:V:11:THR:OG1	22:V:12:LYS:N	2.47	0.47
48:6:1:A:O2'	48:6:3:A:N7	2.39	0.47
10:G:55:TYR:O	10:G:59:GLN:HG3	2.14	0.47
11:H:145:GLU:OE1	11:H:145:GLU:N	2.48	0.47
34:h:80:LEU:HA	34:h:83:ARG:HD2	1.97	0.47
45:v:45:THR:HG22	45:v:46:LEU:H	1.79	0.47
1:1:58:G:OP1	15:N:157:LYS:NZ	2.34	0.47
1:1:207:C:OP2	25:Y:59:ARG:NH2	2.38	0.47
1:1:420:G:N3	17:P:118:GLN:NE2	2.63	0.47
1:1:548:U:H2'	1:1:549:G:C8	2.50	0.47
1:1:590:U:O5'	1:1:591:G:H5''	2.15	0.47
1:1:1201:A:H5''	9:F:224:ARG:NH2	2.29	0.47
1:1:1658:G:H2'	1:1:1659:G:C8	2.50	0.47
1:1:1672:A:O2'	1:1:1749:C:O2'	2.28	0.47
1:1:3043:C:H2'	1:1:3044:U:C6	2.50	0.47
5:B:53:MET:HB3	5:B:77:THR:HA	1.96	0.47
11:H:150:GLU:OE1	11:H:150:GLU:N	2.48	0.47
17:P:45:PHE:HE1	17:P:95:LEU:HB3	1.80	0.47
18:Q:94:MET:SD	18:Q:114:ARG:NH2	2.88	0.47
38:m:270:TRP:CH2	39:n:129:ALA:HB2	2.49	0.47
1:1:222:G:OP1	25:Y:11:ARG:NH1	2.46	0.46
1:1:752:G:H3'	1:1:753:G:H8	1.80	0.46
1:1:1222:U:C4	16:O:49:PHE:HD1	2.33	0.46
11:H:148:SER:O	11:H:152:VAL:HG23	2.15	0.46
13:L:129:LYS:HD3	13:L:129:LYS:HA	1.77	0.46
14:M:78:TRP:HE1	14:M:84:CYS:N	2.14	0.46
18:Q:95:LEU:HD13	27:a:91:LEU:HD21	1.97	0.46
40:o:106:VAL:HG23	40:o:191:PHE:HZ	1.80	0.46
42:r:20:HIS:CE1	42:r:24:LYS:HD3	2.50	0.46
1:1:1388:G:OP1	3:3:41:GLN:NE2	2.48	0.46
1:1:1791:G:H21	37:k:71:GLY:HA3	1.79	0.46
11:H:71:VAL:O	11:H:75:ILE:HG12	2.15	0.46
14:M:12:ARG:O	14:M:28:ILE:HG22	2.15	0.46
20:S:33:GLU:HG2	20:S:34:SER:N	2.30	0.46
30:d:19:ILE:HD13	30:d:44:PHE:CE2	2.49	0.46
30:d:38:ILE:HD11	30:d:64:VAL:HG11	1.97	0.46
43:t:155:TYR:HE1	43:t:187:ILE:HB	1.79	0.46
1:1:1262:A:H4'	1:1:1292:G:C8	2.48	0.46
5:B:32:PHE:CG	5:B:182:GLN:HG3	2.51	0.46
5:B:57:VAL:HG13	5:B:71:GLU:CD	2.41	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:132:GLU:OE1	9:F:132:GLU:N	2.46	0.46
11:H:5:ILE:HG21	14:M:34:HIS:CE1	2.50	0.46
17:P:60:PHE:O	17:P:64:ASN:HB3	2.16	0.46
38:m:347:ARG:HA	43:t:17:VAL:HA	1.96	0.46
41:p:157:SER:HA	41:p:171:VAL:HA	1.98	0.46
48:6:11:C:H2'	48:6:12:A:C8	2.50	0.46
1:1:283:U:H2'	1:1:284:U:C6	2.49	0.46
1:1:1008:U:N3	1:1:1009:C:N3	2.63	0.46
6:C:285:SER:OG	6:C:286:ASN:N	2.48	0.46
16:O:86:ARG:HG2	16:O:86:ARG:HH11	1.81	0.46
20:S:25:ARG:HH22	20:S:27:ARG:HD2	1.80	0.46
24:X:6:ALA:HB1	40:o:161:VAL:HG11	1.98	0.46
25:Y:2:LYS:O	25:Y:2:LYS:HG3	2.15	0.46
30:d:16:ASP:OD2	30:d:16:ASP:C	2.59	0.46
1:1:742:A:C8	27:a:114:LYS:HD3	2.48	0.46
1:1:1606:U:N3	39:n:221:THR:HG22	2.29	0.46
3:3:63:TYR:CE1	3:3:79:ARG:HB2	2.51	0.46
11:H:36:LYS:HE3	11:H:36:LYS:HB2	1.81	0.46
11:H:127:LEU:HB2	11:H:151:ASN:OD1	2.15	0.46
20:S:11:ARG:HH12	20:S:14:PRO:HD3	1.81	0.46
31:e:71:PHE:HD2	31:e:82:LEU:HD11	1.81	0.46
38:m:249:THR:O	38:m:252:GLN:OE1	2.33	0.46
39:n:55:LYS:HA	39:n:55:LYS:HD3	1.84	0.46
40:o:117:TYR:O	40:o:121:MET:HG3	2.16	0.46
1:1:353:G:O2'	2:2:33:G:N3	2.49	0.46
1:1:740:U:H2'	1:1:741:G:O4'	2.16	0.46
5:B:46:PHE:CE1	5:B:84:MET:HE1	2.49	0.46
9:F:53:LYS:O	9:F:56:GLU:HG2	2.15	0.46
10:G:139:VAL:O	10:G:143:ILE:HD12	2.15	0.46
17:P:71:ALA:O	17:P:74:LYS:HG2	2.15	0.46
18:Q:29:VAL:O	18:Q:33:ARG:N	2.47	0.46
30:d:11:GLN:O	30:d:12:VAL:C	2.59	0.46
30:d:19:ILE:HD13	30:d:44:PHE:HE2	1.81	0.46
30:d:19:ILE:N	30:d:76:LEU:O	2.44	0.46
34:h:97:TYR:O	34:h:101:ARG:HG2	2.15	0.46
38:m:334:PHE:CD1	39:n:214:VAL:HG23	2.50	0.46
1:1:1344:G:OP1	16:O:83:LYS:NZ	2.41	0.46
1:1:1347:U:OP1	16:O:130:LEU:HA	2.15	0.46
1:1:1509:A:O3'	30:d:66:LYS:NZ	2.48	0.46
1:1:1712:A:H2'	1:1:1713:G:C8	2.51	0.46
1:1:1914:A:H2'	1:1:1915:G:C8	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3148:G:H2'	1:1:3149:G:C8	2.50	0.46
1:1:3333:G:H2'	1:1:3334:A:H8	1.80	0.46
3:3:65:LYS:HE3	3:3:76:LEU:HD21	1.96	0.46
6:C:140:ARG:NH2	6:C:242:PRO:HG2	2.30	0.46
6:C:312:ARG:CZ	6:C:315:VAL:HG23	2.44	0.46
11:H:74:ILE:O	11:H:78:MET:HE1	2.15	0.46
13:L:36:ARG:NH2	45:v:45:THR:HG21	2.31	0.46
15:N:165:THR:HG22	15:N:166:SER:H	1.79	0.46
16:O:48:PHE:HA	16:O:137:CYS:HB2	1.97	0.46
22:V:42:PHE:CZ	22:V:61:LEU:HD11	2.50	0.46
24:X:96:GLU:HG3	24:X:100:LYS:NZ	2.31	0.46
30:d:82:ARG:HG2	30:d:92:LEU:HD22	1.98	0.46
38:m:204:ASP:OD1	38:m:204:ASP:N	2.47	0.46
1:1:976:C:N4	27:a:9:ARG:O	2.41	0.46
1:1:1284:U:O2'	1:1:1294:A:N3	2.41	0.46
1:1:1842:U:H2'	1:1:1843:C:C6	2.51	0.46
1:1:3160:U:H2'	1:1:3161:G:C8	2.50	0.46
1:1:3203:C:N3	1:1:3224:G:N2	2.64	0.46
3:3:109:LYS:HA	3:3:112:LEU:HD12	1.97	0.46
8:E:110:ASP:OD2	8:E:110:ASP:C	2.58	0.46
39:n:143:PHE:CD1	39:n:223:LEU:HD21	2.50	0.46
39:n:169:HIS:CD2	39:n:260:LEU:HD22	2.51	0.46
40:o:103:LYS:HG3	40:o:156:LEU:CD2	2.46	0.46
1:1:1234:A:H5'	1:1:1235:A:C4	2.51	0.46
1:1:1381:G:H3'	3:3:41:GLN:HG2	1.98	0.46
1:1:1951:A:H61	1:1:2427:C:H42	1.64	0.46
1:1:3141:G:OP1	5:B:19:ARG:NH2	2.49	0.46
3:3:94:ASP:OD1	3:3:95:GLN:N	2.49	0.46
6:C:332:PRO:HB3	9:F:48:ARG:CZ	2.46	0.46
11:H:11:LEU:HD23	11:H:11:LEU:C	2.40	0.46
19:R:15:LEU:HD13	19:R:22:VAL:HG12	1.97	0.46
20:S:79:ARG:NH2	20:S:86:THR:OG1	2.48	0.46
30:d:77:ARG:NH2	30:d:107:GLU:O	2.48	0.46
42:r:245:THR:H	42:r:256:ALA:HA	1.81	0.46
43:t:236:TYR:HD1	43:t:237:CYS:N	2.14	0.46
1:1:167:G:N2	1:1:268:U:O2	2.48	0.46
1:1:1325:A:H2'	1:1:1326:G:C8	2.51	0.46
1:1:1707:U:H3	1:1:1816:G:H1	1.63	0.46
1:1:1874:U:H2'	1:1:1875:U:C6	2.50	0.46
1:1:3349:U:H2'	1:1:3350:U:C6	2.51	0.46
1:1:3403:U:H1'	1:1:3414:U:O2	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:80:TYR:HD1	20:S:81:ASP:N	2.14	0.46
39:n:163:LEU:HD13	39:n:230:MET:HB2	1.98	0.46
47:T:141:VAL:HG23	47:T:141:VAL:O	2.16	0.46
1:1:240:G:O2'	1:1:241:G:H5''	2.16	0.45
1:1:674:A:O2'	1:1:675:C:OP1	2.33	0.45
1:1:1319:U:H2'	1:1:1320:G:H8	1.80	0.45
1:1:1494:A:H5''	30:d:55:ARG:HE	1.81	0.45
1:1:1567:U:H1'	1:1:1839:A:H2	1.80	0.45
1:1:1740:U:N3	1:1:1827:G:O2'	2.43	0.45
1:1:3200:U:H2'	1:1:3201:A:H8	1.81	0.45
1:1:3217:U:N3	1:1:3220:G:N7	2.64	0.45
8:E:60:LEU:HD11	8:E:96:VAL:HG21	1.97	0.45
11:H:9:GLU:HB3	11:H:55:PHE:HD1	1.81	0.45
18:Q:100:LEU:HB3	18:Q:102:ILE:HD11	1.97	0.45
20:S:98:ARG:NH2	20:S:127:GLU:OE2	2.49	0.45
38:m:558:HIS:HA	38:m:565:SER:HA	1.98	0.45
1:1:1918:G:N2	1:1:1921:C:OP2	2.40	0.45
1:1:2971:C:O2'	1:1:2972:G:H5'	2.17	0.45
7:D:529:PRO:O	38:m:214:PRO:HD3	2.16	0.45
11:H:11:LEU:HB3	11:H:53:ILE:HB	1.97	0.45
15:N:189:TRP:CE3	15:N:190:LEU:HG	2.52	0.45
17:P:94:LEU:HB3	17:P:148:ILE:HD12	1.98	0.45
30:d:83:LYS:NZ	30:d:95:TYR:HB3	2.31	0.45
45:v:53:LEU:HD22	45:v:137:VAL:HG21	1.98	0.45
45:v:171:ILE:CD1	45:v:176:THR:HA	2.45	0.45
1:1:1508:A:O3'	30:d:62:LYS:NZ	2.47	0.45
1:1:1702:A:H2'	1:1:1703:G:C8	2.51	0.45
1:1:3004:U:H2'	1:1:3005:A:O4'	2.17	0.45
9:F:76:ALA:HB2	47:T:140:PHE:HE2	1.81	0.45
9:F:176:ILE:HD11	9:F:188:VAL:HG22	1.98	0.45
16:O:28:LEU:HD12	16:O:99:ALA:O	2.15	0.45
28:b:290:LYS:H	28:b:323:CYS:H	1.63	0.45
31:e:29:TRP:CE2	31:e:50:PRO:HD2	2.52	0.45
35:i:30:HIS:O	35:i:31:LEU:HB2	2.17	0.45
39:n:129:ALA:O	39:n:133:ILE:HB	2.16	0.45
1:1:1445:U:OP1	31:e:95:GLY:N	2.40	0.45
1:1:1653:A:OP2	39:n:7:LYS:NZ	2.50	0.45
1:1:1827:G:H2'	1:1:1828:A:H8	1.81	0.45
1:1:3367:A:OP1	1:1:3368:A:N6	2.50	0.45
3:3:100:TRP:O	3:3:101:PRO:C	2.60	0.45
8:E:105:SER:HB3	14:M:106:ASN:HD22	1.80	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:174:LEU:N	11:H:174:LEU:HD12	2.31	0.45
31:e:82:LEU:HD13	31:e:91:ALA:HB2	1.98	0.45
46:y:187:ASN:HA	46:y:210:THR:HA	1.99	0.45
1:1:185:G:C2	1:1:248:G:C8	3.04	0.45
1:1:414:G:H1'	2:2:24:G:N2	2.31	0.45
1:1:3351:U:H2'	1:1:3352:A:H8	1.82	0.45
16:O:169:TYR:O	16:O:173:LEU:N	2.38	0.45
17:P:124:LYS:HD3	17:P:140:LEU:HD13	1.99	0.45
30:d:78:LEU:HD12	30:d:96:VAL:HG22	1.97	0.45
43:t:87:THR:HG21	43:t:144:ILE:HG12	1.98	0.45
43:t:236:TYR:HD1	43:t:237:CYS:H	1.64	0.45
45:v:12:SER:OG	45:v:13:GLY:N	2.49	0.45
1:1:343:G:N2	2:2:37:U:O2	2.50	0.45
1:1:1740:U:H3	1:1:1827:G:HO2'	1.61	0.45
1:1:1847:C:H3'	1:1:1848:G:H8	1.81	0.45
1:1:1880:A:H2'	1:1:1881:U:H5'	1.98	0.45
1:1:3271:G:H2'	8:E:186:ASN:ND2	2.31	0.45
9:F:239:ASP:OD2	9:F:240:GLU:N	2.50	0.45
14:M:116:LEU:HD23	16:O:192:LEU:HD22	1.98	0.45
25:Y:37:GLU:OE2	25:Y:38:LEU:HD23	2.17	0.45
30:d:11:GLN:HB3	30:d:12:VAL:H	1.59	0.45
48:6:103:G:H2'	48:6:104:U:C6	2.52	0.45
1:1:53:G:OP2	36:j:48:ASN:ND2	2.48	0.45
1:1:817:G:N2	18:Q:91:ASP:OD1	2.50	0.45
1:1:3100:C:O2'	5:B:99:LEU:O	2.20	0.45
1:1:3173:A:H5''	1:1:3174:A:H5'	1.99	0.45
1:1:3419:G:H1'	1:1:3421:G:O4'	2.17	0.45
5:B:122:TRP:CD1	5:B:122:TRP:C	2.93	0.45
13:L:43:ALA:HB2	13:L:51:VAL:HG22	1.99	0.45
30:d:25:LEU:HD21	30:d:33:ARG:CD	2.39	0.45
38:m:287:PRO:HD2	39:n:43:TYR:OH	2.17	0.45
1:1:1352:G:N2	20:S:111:ALA:HB2	2.32	0.45
1:1:1509:A:C4'	30:d:62:LYS:HZ3	2.29	0.45
1:1:1547:G:H4'	1:1:1548:G:H21	1.82	0.45
1:1:2428:U:H2'	1:1:2429:A:C8	2.51	0.45
1:1:3022:C:H2'	1:1:3023:C:O4'	2.17	0.45
6:C:14:ASP:OD1	6:C:15:GLY:N	2.50	0.45
11:H:24:ARG:HH11	11:H:24:ARG:HB2	1.81	0.45
13:L:19:GLN:HA	15:N:195:LEU:HD21	1.98	0.45
17:P:85:VAL:O	17:P:89:LYS:HG2	2.17	0.45
22:V:87:TRP:HZ3	22:V:89:ARG:HB2	1.82	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:75:LEU:HD23	27:a:78:LEU:HD13	1.98	0.45
30:d:47:LYS:NZ	30:d:48:HIS:HA	2.30	0.45
1:1:542:G:H1	1:1:584:C:H42	1.63	0.45
1:1:1025:G:N2	1:1:1088:U:H3	2.15	0.45
1:1:1672:A:H2'	1:1:1673:A:C4	2.52	0.45
1:1:1707:U:H2'	1:1:1708:G:H8	1.82	0.45
5:B:67:MET:CE	5:B:70:ARG:HB3	2.47	0.45
6:C:314:HIS:CD2	9:F:171:SER:HB3	2.51	0.45
9:F:145:ILE:O	9:F:243:ASN:ND2	2.45	0.45
14:M:18:LYS:HB2	14:M:55:SER:HB2	1.98	0.45
14:M:109:ASP:HB3	16:O:195:PHE:CE1	2.52	0.45
30:d:79:ARG:HD3	30:d:111:VAL:HG21	1.97	0.45
38:m:220:GLU:OE1	38:m:224:ARG:NH1	2.48	0.45
40:o:105:GLY:O	40:o:153:PHE:N	2.27	0.45
1:1:1150:C:H2'	1:1:1151:A:C8	2.52	0.45
1:1:1417:G:H21	3:3:15:PHE:HE1	1.65	0.45
1:1:1717:U:O2'	1:1:1720:C:N4	2.43	0.45
3:3:111:ARG:HG2	31:e:84:MET:HE1	1.98	0.45
41:p:108:SER:N	41:p:120:SER:O	2.50	0.45
48:6:56:A:H2'	48:6:57:A:C8	2.51	0.45
15:N:44:ARG:NH2	15:N:120:TRP:O	2.31	0.44
17:P:67:VAL:HG13	17:P:82:ARG:HG3	1.98	0.44
18:Q:126:ASP:OD1	18:Q:126:ASP:N	2.42	0.44
20:S:79:ARG:HD3	20:S:88:ASN:OD1	2.16	0.44
22:V:25:MET:SD	22:V:26:ASN:N	2.90	0.44
39:n:403:ILE:HD12	39:n:419:ILE:HG13	1.98	0.44
41:p:408:LEU:HA	41:p:423:GLY:HA3	1.99	0.44
2:2:19:C:H2'	2:2:20:A:O4'	2.16	0.44
6:C:58:ALA:C	6:C:60:HIS:H	2.26	0.44
6:C:279:LEU:HD23	6:C:280:PRO:HD2	1.98	0.44
15:N:38:ARG:HH11	15:N:60:VAL:HG13	1.81	0.44
22:V:26:ASN:OD1	22:V:27:CYS:N	2.50	0.44
38:m:339:ASP:HA	43:t:22:ARG:HH12	1.82	0.44
1:1:138:U:N3	34:h:70:GLU:OE1	2.35	0.44
1:1:1019:U:O3'	9:F:128:LYS:NZ	2.42	0.44
1:1:1523:A:N6	1:1:1893:C:O2	2.50	0.44
1:1:1547:G:O2'	1:1:1548:G:N3	2.50	0.44
1:1:1554:G:H2'	1:1:1555:G:H8	1.81	0.44
1:1:1644:C:H2'	1:1:1645:G:C8	2.52	0.44
1:1:3239:A:H4'	1:1:3240:G:O5'	2.17	0.44
5:B:212:ASN:HD21	5:B:354:VAL:H	1.66	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:131:LYS:HB3	9:F:131:LYS:HE2	1.77	0.44
14:M:51:ILE:HD12	14:M:52:ARG:N	2.31	0.44
14:M:78:TRP:CD1	14:M:83:VAL:HB	2.53	0.44
15:N:38:ARG:NH1	15:N:60:VAL:HG13	2.32	0.44
17:P:24:THR:HB	17:P:90:PHE:CE2	2.53	0.44
20:S:11:ARG:HH21	47:T:141:VAL:HG12	1.83	0.44
31:e:101:LYS:O	31:e:105:ILE:HG13	2.17	0.44
48:6:92:G:O2'	48:6:93:A:H5'	2.16	0.44
1:1:254:G:H2'	1:1:255:C:C6	2.53	0.44
1:1:266:G:H5'	1:1:267:C:OP2	2.16	0.44
1:1:335:A:OP1	13:L:31:ARG:NH2	2.49	0.44
1:1:587:U:H2'	1:1:588:G:C8	2.50	0.44
1:1:625:U:O2'	1:1:626:C:O5'	2.32	0.44
1:1:1400:A:H2'	1:1:1401:G:O4'	2.17	0.44
1:1:1506:U:H2'	1:1:1507:G:H8	1.82	0.44
5:B:269:ASN:ND2	5:B:271:GLY:O	2.48	0.44
10:G:80:LYS:HE2	10:G:80:LYS:HB2	1.70	0.44
11:H:45:GLU:OE2	11:H:47:LYS:HB2	2.17	0.44
13:L:62:THR:HG22	13:L:63:ILE:N	2.31	0.44
15:N:140:LYS:HD3	15:N:140:LYS:HA	1.73	0.44
20:S:24:PHE:HB3	47:T:151:LEU:HD22	1.99	0.44
20:S:41:TRP:CH2	20:S:55:GLY:HA3	2.51	0.44
30:d:42:VAL:O	30:d:46:GLN:N	2.50	0.44
31:e:31:LYS:HE3	31:e:49:MET:CE	2.46	0.44
32:f:18:GLN:O	32:f:25:HIS:HB2	2.17	0.44
32:f:69:TRP:CH2	32:f:102:MET:HE1	2.52	0.44
1:1:615:G:N2	1:1:637:U:OP1	2.48	0.44
1:1:1259:A:H2'	1:1:1260:G:H8	1.83	0.44
1:1:1330:U:H2'	1:1:1331:G:H8	1.83	0.44
1:1:1506:U:P	19:R:8:LYS:HZ1	2.41	0.44
1:1:1508:A:C2'	30:d:62:LYS:HZ1	2.30	0.44
1:1:1645:G:H2'	1:1:1646:G:C8	2.53	0.44
1:1:1659:G:O2'	1:1:1678:A:N1	2.46	0.44
9:F:93:VAL:O	9:F:121:GLY:HA2	2.18	0.44
14:M:35:LYS:HA	14:M:53:TYR:HD2	1.82	0.44
26:Z:41:ALA:N	26:Z:75:VAL:O	2.50	0.44
42:r:45:ILE:HD13	42:r:45:ILE:N	2.31	0.44
1:1:723:C:O2'	1:1:724:A:O5'	2.32	0.44
1:1:1164:A:H2'	1:1:1165:G:H8	1.82	0.44
1:1:1389:A:H5''	1:1:1391:G:H1'	1.99	0.44
5:B:210:GLU:C	5:B:212:ASN:H	2.25	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:296:THR:HG23	5:B:303:LYS:HZ3	1.83	0.44
5:B:323:MET:HE2	5:B:323:MET:HB2	1.89	0.44
6:C:5:ARG:NH1	6:C:26:PHE:CZ	2.82	0.44
8:E:191:HIS:HD2	8:E:192:LEU:HG	1.83	0.44
11:H:47:LYS:HA	11:H:47:LYS:HD3	1.68	0.44
16:O:55:TYR:CD1	16:O:146:VAL:HG11	2.53	0.44
16:O:74:PHE:HD2	16:O:79:ARG:HG3	1.83	0.44
24:X:56:LEU:HD12	24:X:56:LEU:HA	1.78	0.44
38:m:345:ARG:HD2	39:n:43:TYR:CG	2.52	0.44
38:m:387:ARG:N	38:m:401:GLY:O	2.51	0.44
43:t:22:ARG:HB2	43:t:24:VAL:HG22	2.00	0.44
1:1:517:U:OP1	6:C:319:ASN:HB2	2.18	0.44
1:1:585:C:OP1	20:S:70:LYS:NZ	2.43	0.44
1:1:984:A:C6	1:1:985:G:C4	3.06	0.44
1:1:1163:C:H2'	1:1:1164:A:H8	1.83	0.44
1:1:1427:A:N3	1:1:1453:A:O2'	2.46	0.44
1:1:1590:G:OP2	1:1:1590:G:H4'	2.17	0.44
1:1:1786:U:H2'	1:1:1787:G:C8	2.53	0.44
3:3:53:VAL:HG11	3:3:112:LEU:HD21	1.99	0.44
10:G:173:MET:HE1	38:m:211:ARG:HD3	1.99	0.44
14:M:29:VAL:HG11	14:M:48:ARG:HH12	1.83	0.44
16:O:190:GLN:O	16:O:193:SER:OG	2.29	0.44
24:X:67:ASN:HB3	24:X:140:PHE:HD2	1.82	0.44
25:Y:2:LYS:NZ	25:Y:4:SER:O	2.51	0.44
30:d:60:LEU:HD21	30:d:97:GLN:HA	2.00	0.44
43:t:217:LYS:HG2	43:t:228:PHE:CE2	2.53	0.44
43:t:226:LYS:NZ	48:6:1:A:OP2	2.43	0.44
1:1:426:A:O2'	1:1:655:C:OP1	2.29	0.44
1:1:592:U:H1'	6:C:346:GLU:O	2.18	0.44
1:1:723:C:H1'	45:v:65:GLY:HA3	1.99	0.44
1:1:841:G:H2'	1:1:842:A:C8	2.53	0.44
1:1:1023:G:H2'	1:1:1024:A:C8	2.53	0.44
1:1:1843:C:H2'	1:1:1844:C:C6	2.52	0.44
1:1:1936:A:H2'	1:1:1937:G:H8	1.83	0.44
19:R:7:GLN:HE22	19:R:33:SER:C	2.25	0.44
27:a:74:ASN:HB3	27:a:114:LYS:HB2	2.00	0.44
27:a:129:VAL:HG21	27:a:144:VAL:HG11	1.99	0.44
39:n:45:ARG:HD3	39:n:65:TYR:CD1	2.53	0.44
45:v:170:LEU:HD12	45:v:182:MET:HB3	2.00	0.44
1:1:271:C:H2'	1:1:272:G:C8	2.52	0.44
1:1:621:G:OP2	9:F:44:ARG:NE	2.51	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:777:C:H2'	1:1:778:G:H5''	1.99	0.44
1:1:1557:U:P	1:1:1642:U:H3	2.40	0.44
1:1:1712:A:H2'	1:1:1713:G:H8	1.83	0.44
1:1:2932:A:H2	1:1:2945:G:H3'	1.83	0.44
1:1:3137:U:H2'	1:1:3138:U:C6	2.53	0.44
1:1:3435:U:H3	1:1:3470:G:HO2'	1.63	0.44
5:B:122:TRP:HE1	5:B:127:LYS:CG	2.31	0.44
9:F:189:GLU:OE2	9:F:189:GLU:HA	2.18	0.44
17:P:75:GLU:OE1	17:P:75:GLU:N	2.50	0.44
20:S:135:ARG:HB2	20:S:136:ARG:HH11	1.82	0.44
24:X:109:ILE:C	24:X:110:ASN:HD22	2.26	0.44
32:f:51:CYS:HB2	32:f:67:VAL:HG13	2.00	0.44
32:f:52:TYR:CE2	32:f:54:TYR:CD1	3.06	0.44
1:1:130:A:H2'	1:1:131:A:O4'	2.18	0.43
1:1:148:C:H2'	1:1:149:G:O4'	2.18	0.43
1:1:674:A:H2'	1:1:675:C:H6	1.79	0.43
3:3:5:GLU:OE2	6:C:289:VAL:N	2.29	0.43
8:E:123:TYR:OH	8:E:153:ARG:NE	2.51	0.43
16:O:74:PHE:CD2	16:O:79:ARG:HG3	2.53	0.43
20:S:51:LYS:HB2	20:S:54:THR:HG22	2.00	0.43
22:V:40:SER:HB3	22:V:61:LEU:HD23	2.00	0.43
30:d:83:LYS:HZ3	30:d:95:TYR:HB3	1.83	0.43
35:i:33:LYS:HE2	35:i:33:LYS:HB2	1.71	0.43
38:m:578:ALA:O	38:m:591:ALA:N	2.46	0.43
1:1:841:G:H2'	1:1:842:A:H8	1.82	0.43
1:1:1423:G:OP1	31:e:98:SER:OG	2.24	0.43
1:1:1550:C:H2'	1:1:1551:A:H8	1.83	0.43
3:3:29:ARG:HG3	31:e:81:LEU:HD21	2.00	0.43
15:N:15:GLN:HB3	35:i:50:PRO:HD2	2.00	0.43
17:P:100:ALA:HA	17:P:103:GLU:OE2	2.18	0.43
34:h:72:TYR:CE2	34:h:79:PRO:HD3	2.53	0.43
38:m:661:ARG:H	38:m:676:SER:HA	1.83	0.43
40:o:166:MET:HB2	40:o:178:CYS:SG	2.57	0.43
48:6:88:G:H2'	48:6:89:U:O4'	2.18	0.43
1:1:102:C:HO2'	13:L:62:THR:HG1	1.51	0.43
1:1:107:A:O2'	1:1:332:A:N3	2.50	0.43
1:1:993:C:H2'	1:1:994:A:N9	2.33	0.43
1:1:1332:A:N7	1:1:2922:U:N3	2.65	0.43
1:1:3332:U:H2'	1:1:3333:G:H8	1.83	0.43
17:P:4:TYR:HE2	17:P:16:LYS:HD2	1.82	0.43
19:R:7:GLN:NE2	19:R:32:ILE:O	2.51	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:61:ARG:HA	32:f:61:ARG:HD2	1.59	0.43
34:h:88:ARG:O	34:h:92:ARG:HD2	2.18	0.43
38:m:344:PRO:HA	39:n:44:PRO:O	2.18	0.43
8:E:167:ALA:O	8:E:171:ILE:HG12	2.19	0.43
8:E:194:LYS:NZ	14:M:104:GLN:O	2.36	0.43
10:G:99:PRO:HD3	10:G:132:VAL:HG12	2.00	0.43
10:G:158:ASP:HB3	10:G:159:PRO:CD	2.49	0.43
11:H:17:VAL:HB	11:H:29:THR:OG1	2.18	0.43
38:m:265:ALA:HA	39:n:232:PHE:CE1	2.53	0.43
40:o:136:MET:HE2	40:o:145:SER:HB3	2.00	0.43
40:o:181:ILE:CD1	40:o:185:GLN:HE21	2.31	0.43
40:o:203:HIS:NE2	48:6:83:A:H5'	2.34	0.43
43:t:197:VAL:HA	43:t:201:PHE:CD1	2.53	0.43
48:6:93:A:H4'	48:6:94:A:C2	2.54	0.43
1:1:546:G:O3'	20:S:145:PRO:HB3	2.18	0.43
1:1:838:A:H2'	1:1:839:A:N3	2.34	0.43
1:1:1773:A:H2'	1:1:1774:G:C8	2.51	0.43
1:1:2337:G:H2'	1:1:2338:G:H8	1.83	0.43
1:1:3368:A:N1	8:E:154:ILE:HG23	2.33	0.43
1:1:3477:A:N3	30:d:23:LYS:HA	2.33	0.43
3:3:2:GLN:HB2	3:3:6:VAL:HG11	1.99	0.43
6:C:158:VAL:HG23	6:C:161:PHE:CZ	2.53	0.43
11:H:28:VAL:HG11	11:H:78:MET:HG2	2.01	0.43
15:N:30:TYR:HA	15:N:33:MET:HE3	2.01	0.43
15:N:168:GLY:O	15:N:172:ARG:HG2	2.18	0.43
30:d:15:ARG:HB3	30:d:17:TYR:CE2	2.53	0.43
39:n:419:ILE:HA	39:n:440:ALA:HA	2.00	0.43
40:o:200:ARG:HG3	40:o:200:ARG:O	2.18	0.43
41:p:200:VAL:HA	41:p:216:SER:HA	2.00	0.43
1:1:77:A:H5'	13:L:100:ARG:NH2	2.33	0.43
1:1:641:G:H2'	1:1:642:A:C8	2.51	0.43
1:1:1240:G:OP1	42:r:36:SER:OG	2.24	0.43
1:1:2474:A:H61	1:1:3088:G:H2'	1.83	0.43
14:M:115:ARG:HA	14:M:115:ARG:HD3	1.80	0.43
15:N:189:TRP:HE3	15:N:190:LEU:HG	1.83	0.43
16:O:144:SER:HB2	16:O:151:ASN:HB2	2.01	0.43
40:o:199:LYS:HD2	40:o:199:LYS:O	2.18	0.43
1:1:1157:G:H2'	1:1:1158:G:O4'	2.18	0.43
1:1:1442:G:P	31:e:30:ARG:HH22	2.42	0.43
1:1:1493:C:H2'	1:1:1494:A:C8	2.53	0.43
1:1:1739:A:H2	1:1:1781:G:H1	1.65	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3026:C:H2'	1:1:3027:U:O4'	2.18	0.43
1:1:3470:G:H1	5:B:381:GLY:N	2.16	0.43
5:B:45:ALA:HB3	5:B:181:ILE:HG23	1.99	0.43
9:F:88:PRO:O	9:F:126:PHE:HB3	2.19	0.43
10:G:233:TRP:NE1	38:m:200:PRO:O	2.52	0.43
17:P:13:LYS:H	17:P:13:LYS:HG2	1.64	0.43
22:V:108:LYS:HE2	22:V:108:LYS:HB2	1.85	0.43
30:d:32:LYS:C	30:d:35:PRO:HD2	2.44	0.43
30:d:45:ALA:O	30:d:49:MET:HB2	2.19	0.43
38:m:317:TYR:CE2	38:m:324:PRO:HD3	2.54	0.43
40:o:135:ARG:HH22	48:6:98:G:H5'	1.83	0.43
42:r:54:ARG:HD2	42:r:57:GLU:OE1	2.18	0.43
1:1:110:G:OP2	13:L:73:ARG:NH2	2.34	0.43
1:1:430:A:H2'	1:1:431:A:C8	2.54	0.43
1:1:643:C:H2'	1:1:644:A:C8	2.53	0.43
1:1:1211:A:H5''	32:f:78:ASN:HB2	2.01	0.43
1:1:1417:G:H4'	6:C:242:PRO:HB2	2.01	0.43
5:B:297:ASP:N	5:B:297:ASP:OD1	2.51	0.43
8:E:127:GLN:H	8:E:127:GLN:CD	2.25	0.43
11:H:13:ILE:HG22	11:H:14:PRO:O	2.18	0.43
18:Q:50:ARG:HB3	18:Q:85:VAL:HG21	2.01	0.43
38:m:297:GLU:OE2	39:n:449:LEU:HD13	2.18	0.43
38:m:334:PHE:HA	39:n:219:MET:HE1	2.01	0.43
39:n:166:GLU:OE2	39:n:247:PRO:HD2	2.19	0.43
40:o:160:ASN:C	40:o:160:ASN:OD1	2.61	0.43
40:o:185:GLN:CD	40:o:185:GLN:H	2.27	0.43
43:t:237:CYS:SG	43:t:241:ILE:HB	2.59	0.43
1:1:9:U:O2	2:2:158:G:N2	2.51	0.43
1:1:162:A:H8	1:1:162:A:OP1	2.01	0.43
1:1:372:G:O6	36:j:56:ARG:HD3	2.18	0.43
1:1:584:C:P	14:M:70:ARG:HE	2.42	0.43
1:1:593:A:OP1	6:C:348:THR:OG1	2.36	0.43
1:1:979:G:H5''	31:e:52:ILE:HB	2.01	0.43
1:1:3244:C:H2'	1:1:3245:G:H8	1.84	0.43
1:1:3354:U:H2'	1:1:3355:G:C8	2.54	0.43
13:L:76:THR:HG22	13:L:101:ARG:HB3	2.01	0.43
17:P:78:VAL:HG12	17:P:80:GLN:H	1.84	0.43
20:S:16:GLU:HG2	20:S:17:HIS:ND1	2.34	0.43
39:n:182:LEU:HD11	39:n:425:TYR:CD2	2.54	0.43
41:p:130:ASP:N	41:p:134:GLU:O	2.47	0.43
1:1:435:U:OP1	31:e:12:LYS:NZ	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3355:G:H2'	1:1:3356:A:O4'	2.18	0.43
5:B:60:LEU:HD23	5:B:67:MET:HB3	2.00	0.43
8:E:61:LEU:HD23	8:E:61:LEU:HA	1.78	0.43
9:F:95:ARG:NH1	9:F:115:LEU:O	2.49	0.43
17:P:61:ARG:HH21	17:P:76:PHE:HB3	1.84	0.43
20:S:15:THR:HG23	20:S:18:GLU:H	1.84	0.43
32:f:51:CYS:HB3	32:f:69:TRP:CZ3	2.53	0.43
38:m:600:ASN:O	38:m:604:GLN:N	2.52	0.43
39:n:210:VAL:HG12	39:n:212:THR:H	1.84	0.43
1:1:6:A:H5'	1:1:7:C:OP2	2.19	0.42
1:1:52:A:H1'	1:1:843:U:O2'	2.19	0.42
1:1:719:A:OP1	15:N:199:ARG:NH2	2.52	0.42
1:1:985:G:C6	1:1:1173:G:C5	3.07	0.42
1:1:1657:U:H2'	1:1:1658:G:C8	2.54	0.42
1:1:3175:U:C6	30:d:30:PHE:HE2	2.36	0.42
6:C:267:THR:OG1	6:C:281:GLU:HG2	2.19	0.42
12:K:67:ARG:HA	12:K:194:ALA:HA	2.00	0.42
17:P:49:ASP:O	17:P:53:GLU:HG2	2.19	0.42
20:S:131:LYS:NZ	20:S:140:LYS:O	2.52	0.42
27:a:82:LEU:HD23	27:a:82:LEU:C	2.42	0.42
32:f:90:LEU:HD23	32:f:90:LEU:HA	1.80	0.42
38:m:211:ARG:NH2	38:m:213:THR:OG1	2.52	0.42
39:n:30:LEU:HD12	39:n:30:LEU:HA	1.80	0.42
43:t:70:ARG:NH2	43:t:135:ILE:O	2.43	0.42
1:1:251:U:H2'	1:1:252:A:C8	2.54	0.42
1:1:264:G:C6	1:1:265:C:C4	3.07	0.42
1:1:1237:G:O3'	42:r:54:ARG:NH1	2.52	0.42
1:1:1335:A:C5	1:1:3034:G:H1'	2.54	0.42
1:1:1652:G:H2'	1:1:1653:A:C8	2.54	0.42
1:1:2338:G:H2'	1:1:2339:G:H8	1.83	0.42
1:1:3144:C:H5'	5:B:53:MET:HE2	2.01	0.42
1:1:3180:C:O2'	1:1:3433:U:OP1	2.31	0.42
5:B:67:MET:HE1	5:B:70:ARG:HB3	2.01	0.42
5:B:213:GLU:HG2	5:B:214:MET:H	1.83	0.42
8:E:177:TYR:CE2	14:M:108:PHE:HA	2.54	0.42
9:F:134:LEU:HB3	9:F:143:TYR:CE1	2.54	0.42
14:M:28:ILE:HD13	14:M:37:ALA:HB1	2.01	0.42
27:a:84:ASN:HA	27:a:87:ARG:HD3	2.01	0.42
30:d:80:LEU:HD23	30:d:81:SER:N	2.34	0.42
31:e:64:MET:HG3	31:e:68:LEU:O	2.17	0.42
40:o:124:TYR:CE1	40:o:166:MET:HE2	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:t:91:PHE:CZ	43:t:120:ALA:HB1	2.55	0.42
1:1:189:G:H1	1:1:243:C:N4	2.17	0.42
1:1:1651:A:H2'	1:1:1652:G:C8	2.54	0.42
1:1:1885:G:H5''	24:X:91:LYS:HD2	2.01	0.42
1:1:1929:A:P	19:R:21:LYS:HZ3	2.41	0.42
1:1:3120:A:H5''	11:H:96:HIS:CE1	2.54	0.42
1:1:3414:U:H4'	5:B:173:GLN:HG3	2.00	0.42
3:3:33:ASN:OD1	3:3:42:SER:HB2	2.18	0.42
10:G:105:LYS:HB2	10:G:105:LYS:HE3	1.75	0.42
20:S:73:VAL:HG22	20:S:94:ARG:HB2	2.01	0.42
24:X:96:GLU:OE2	24:X:99:ARG:HD2	2.19	0.42
40:o:118:GLU:OE2	40:o:138:ARG:NE	2.35	0.42
40:o:141:LYS:HD3	40:o:141:LYS:HA	1.84	0.42
43:t:217:LYS:HG2	43:t:228:PHE:HE2	1.84	0.42
45:v:178:ASP:O	45:v:182:MET:HG3	2.19	0.42
1:1:1506:U:H2'	1:1:1507:G:C8	2.54	0.42
1:1:1557:U:H1'	24:X:110:ASN:HB3	2.01	0.42
1:1:2455:U:N3	1:1:2456:G:N7	2.67	0.42
1:1:3433:U:H2'	1:1:3434:G:O4'	2.19	0.42
6:C:14:ASP:OD1	6:C:14:ASP:C	2.63	0.42
6:C:155:ASP:OD1	6:C:155:ASP:N	2.50	0.42
6:C:270:VAL:HG22	6:C:271:ALA:O	2.19	0.42
6:C:291:ARG:HG3	6:C:291:ARG:NH1	2.32	0.42
11:H:35:LEU:HB3	11:H:37:GLN:HE22	1.84	0.42
11:H:102:ASN:HB2	11:H:111:GLU:HG3	2.01	0.42
38:m:263:ASN:O	38:m:263:ASN:ND2	2.45	0.42
38:m:334:PHE:CG	39:n:214:VAL:HG23	2.54	0.42
39:n:170:TYR:CE1	39:n:237:LEU:HB3	2.55	0.42
1:1:135:U:O2	1:1:140:U:N3	2.53	0.42
1:1:305:A:C8	1:1:307:G:H1'	2.54	0.42
1:1:2477:C:H1'	17:P:69:ARG:NH1	2.33	0.42
1:1:3116:U:H4'	11:H:119:ARG:HH11	1.85	0.42
1:1:3217:U:H4'	1:1:3218:A:OP1	2.17	0.42
1:1:3331:U:H3	1:1:3356:A:H61	1.68	0.42
5:B:165:GLN:NE2	5:B:168:LYS:HG2	2.34	0.42
6:C:35:ASP:OD1	6:C:36:LEU:N	2.52	0.42
9:F:148:HIS:HB2	9:F:196:TYR:CE2	2.55	0.42
12:K:7:LEU:HA	12:K:233:ALA:HB1	2.01	0.42
16:O:28:LEU:CD1	16:O:102:HIS:HB2	2.49	0.42
25:Y:53:ASP:OD1	25:Y:109:HIS:N	2.52	0.42
45:v:165:ALA:O	45:v:169:ARG:HD3	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:535:G:H2'	1:1:536:A:C8	2.54	0.42
1:1:1307:U:H2'	1:1:1308:C:C6	2.55	0.42
1:1:1325:A:H2'	1:1:1326:G:H8	1.83	0.42
1:1:1929:A:N7	19:R:20:ARG:NH2	2.67	0.42
5:B:116:ARG:NE	5:B:122:TRP:CZ3	2.87	0.42
10:G:89:GLN:HG3	40:o:170:LEU:CD2	2.50	0.42
10:G:219:ASP:OD1	10:G:219:ASP:C	2.63	0.42
11:H:116:LEU:O	11:H:118:GLU:N	2.52	0.42
11:H:174:LEU:O	11:H:178:TYR:OH	2.37	0.42
14:M:77:LYS:HD3	14:M:77:LYS:HA	1.90	0.42
36:j:66:TYR:CE1	36:j:69:LYS:HD2	2.55	0.42
39:n:408:HIS:NE2	39:n:410:SER:HB3	2.35	0.42
43:t:35:GLN:HG2	43:t:39:LYS:HE2	2.02	0.42
43:t:133:LEU:HD21	43:t:142:TYR:CZ	2.55	0.42
1:1:84:C:O2'	1:1:101:G:O6	2.29	0.42
1:1:1300:U:H1'	1:1:1303:C:C5	2.55	0.42
1:1:1638:A:OP1	19:R:38:ARG:NH1	2.48	0.42
1:1:1786:U:H2'	1:1:1787:G:H8	1.85	0.42
1:1:1951:A:H61	1:1:2427:C:N4	2.17	0.42
1:1:2976:C:H2'	1:1:2977:U:C6	2.55	0.42
1:1:3096:G:H2'	1:1:3097:U:C6	2.55	0.42
1:1:3399:C:H2'	1:1:3400:C:C6	2.55	0.42
6:C:314:HIS:HD2	9:F:171:SER:HB3	1.84	0.42
8:E:56:THR:O	8:E:72:VAL:HG12	2.20	0.42
11:H:39:LEU:HA	11:H:41:HIS:CD2	2.55	0.42
14:M:30:ASP:OD2	14:M:31:ILE:N	2.52	0.42
15:N:25:VAL:O	15:N:29:GLU:HG3	2.19	0.42
18:Q:117:LYS:HB3	18:Q:117:LYS:HE3	1.79	0.42
20:S:26:MET:HB3	20:S:28:LEU:HD22	2.01	0.42
22:V:100:ASN:N	22:V:100:ASN:OD1	2.52	0.42
22:V:106:ASN:ND2	22:V:110:GLU:HB3	2.29	0.42
31:e:29:TRP:O	31:e:30:ARG:NH1	2.52	0.42
36:j:22:CYS:HB3	36:j:37:CYS:SG	2.59	0.42
38:m:339:ASP:HA	43:t:22:ARG:NH1	2.35	0.42
43:t:91:PHE:CE1	43:t:120:ALA:HB1	2.54	0.42
43:t:138:PRO:HG2	43:t:139:TYR:CD1	2.54	0.42
1:1:634:G:O2'	6:C:315:VAL:HG12	2.20	0.42
1:1:1202:G:H2'	1:1:1203:G:O4'	2.20	0.42
1:1:1329:C:N4	1:1:1330:U:O4	2.53	0.42
1:1:1420:U:OP2	6:C:143:ARG:NH2	2.53	0.42
1:1:1494:A:H5'	30:d:56:VAL:O	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1567:U:H1'	1:1:1839:A:C2	2.55	0.42
1:1:1726:U:H2'	1:1:1727:U:C6	2.54	0.42
1:1:2932:A:O2'	1:1:2946:A:N6	2.50	0.42
8:E:111:VAL:O	8:E:114:VAL:HG12	2.19	0.42
20:S:11:ARG:HB2	20:S:21:PRO:HB2	2.00	0.42
22:V:23:ALA:O	22:V:38:ILE:HG22	2.20	0.42
35:i:56:MET:HE1	35:i:60:ARG:HD2	2.02	0.42
38:m:255:GLU:HA	38:m:258:ARG:HE	1.84	0.42
39:n:568:LYS:O	39:n:571:LYS:NZ	2.28	0.42
1:1:993:C:H2'	1:1:994:A:C4	2.54	0.42
1:1:2477:C:H5'	17:P:80:GLN:NE2	2.35	0.42
1:1:3025:A:H2'	1:1:3026:C:H6	1.84	0.42
1:1:3485:U:H2'	1:1:3486:U:C6	2.55	0.42
2:2:114:C:H4'	2:2:115:G:H5''	2.01	0.42
5:B:152:LYS:HA	5:B:188:VAL:HG12	2.00	0.42
6:C:25:PRO:HB2	6:C:27:VAL:HG12	2.01	0.42
6:C:292:LEU:HD13	18:Q:31:LEU:HD22	2.02	0.42
11:H:68:ILE:HD13	11:H:68:ILE:HA	1.80	0.42
11:H:69:ARG:HA	11:H:69:ARG:HD2	1.79	0.42
14:M:58:LEU:HA	14:M:58:LEU:HD13	1.83	0.42
17:P:59:PRO:HD3	17:P:76:PHE:CE2	2.55	0.42
20:S:45:LYS:O	20:S:49:LYS:HD2	2.20	0.42
20:S:129:GLU:HG2	20:S:130:LYS:HG2	2.00	0.42
25:Y:42:TYR:HE1	25:Y:108:LEU:HD12	1.84	0.42
42:r:9:GLU:H	42:r:9:GLU:CD	2.26	0.42
43:t:95:ILE:HD12	43:t:232:ARG:HD3	2.01	0.42
43:t:232:ARG:NH2	43:t:244:LEU:HD11	2.34	0.42
1:1:27:C:H3'	1:1:28:G:N2	2.28	0.42
1:1:132:C:H2'	1:1:133:A:O4'	2.20	0.42
1:1:431:A:H2'	1:1:432:G:O4'	2.20	0.42
1:1:1255:C:H2'	1:1:1256:A:O4'	2.20	0.42
1:1:1493:C:H2'	1:1:1494:A:H8	1.85	0.42
1:1:1578:G:OP1	15:N:67:ARG:NH1	2.52	0.42
1:1:1689:A:H2'	1:1:1690:G:O4'	2.20	0.42
1:1:2984:C:HO2'	1:1:3029:A:HO2'	1.66	0.42
1:1:3195:C:N4	1:1:3231:U:H3	2.17	0.42
6:C:338:LYS:NZ	6:C:341:VAL:HA	2.35	0.42
11:H:6:TYR:HA	11:H:57:VAL:O	2.20	0.42
12:K:13:LEU:O	12:K:15:LYS:N	2.51	0.42
13:L:33:LEU:O	13:L:37:GLN:HG3	2.19	0.42
16:O:143:SER:OG	16:O:148:TRP:HB2	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:44:THR:HG21	22:V:52:PRO:HG3	2.01	0.42
25:Y:82:GLU:O	25:Y:83:ARG:HG2	2.19	0.42
30:d:28:VAL:HG11	30:d:36:ARG:HG3	2.02	0.42
40:o:183:GLU:HA	40:o:186:VAL:CG1	2.50	0.42
43:t:113:ARG:NH2	43:t:208:LEU:O	2.30	0.42
1:1:348:C:OP2	6:C:197:ARG:NH1	2.45	0.41
1:1:689:U:H2'	1:1:690:A:C8	2.55	0.41
1:1:1508:A:O2'	30:d:62:LYS:NZ	2.50	0.41
1:1:3204:G:H2'	1:1:3205:G:O4'	2.21	0.41
1:1:3281:A:O2'	11:H:44:ILE:N	2.53	0.41
2:2:79:A:C2	2:2:96:A:H1'	2.55	0.41
6:C:158:VAL:HA	6:C:161:PHE:CE1	2.56	0.41
9:F:108:LYS:HB2	9:F:108:LYS:HE2	1.91	0.41
15:N:174:ILE:HD13	15:N:174:ILE:HA	1.88	0.41
24:X:7:LYS:O	24:X:11:LYS:HB3	2.19	0.41
39:n:404:CYS:SG	39:n:418:TYR:HD2	2.42	0.41
43:t:84:PRO:O	43:t:125:ASN:ND2	2.48	0.41
1:1:141:U:H2'	1:1:142:G:O4'	2.19	0.41
1:1:197:U:O4'	1:1:231:C:H5'	2.20	0.41
1:1:1221:A:N3	1:1:1221:A:H2'	2.35	0.41
1:1:1643:C:OP2	1:1:1643:C:H3'	2.21	0.41
1:1:1845:A:H2'	1:1:1846:A:H8	1.85	0.41
1:1:2337:G:H2'	1:1:2338:G:C8	2.55	0.41
1:1:3187:A:O2'	1:1:3189:C:H2'	2.19	0.41
5:B:373:PRO:HA	5:B:376:ALA:HB3	2.01	0.41
6:C:293:ILE:HD11	18:Q:31:LEU:HA	2.02	0.41
8:E:190:PRO:HD2	32:f:45:TYR:OH	2.19	0.41
11:H:9:GLU:HB3	11:H:55:PHE:CD1	2.54	0.41
11:H:9:GLU:OE2	11:H:69:ARG:NH1	2.54	0.41
16:O:137:CYS:SG	16:O:138:THR:N	2.93	0.41
17:P:50:ASN:HB3	17:P:56:GLN:OE1	2.20	0.41
19:R:14:VAL:O	19:R:16:LYS:NZ	2.53	0.41
20:S:80:TYR:HD2	20:S:89:MET:HE1	1.85	0.41
25:Y:33:PRO:HD2	25:Y:103:VAL:O	2.20	0.41
31:e:31:LYS:HD2	31:e:32:PRO:HD2	2.02	0.41
38:m:453:GLN:N	38:m:469:ALA:O	2.53	0.41
43:t:151:ARG:HA	43:t:191:ILE:HD13	2.01	0.41
1:1:16:A:H2'	1:1:17:G:O4'	2.20	0.41
1:1:1245:U:P	20:S:136:ARG:HH22	2.43	0.41
1:1:1290:A:N3	1:1:1311:C:O2'	2.51	0.41
1:1:1713:G:H2'	1:1:1714:A:H8	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:321:LEU:HD11	9:F:153:GLU:HA	2.02	0.41
13:L:32:LYS:O	13:L:36:ARG:HG3	2.20	0.41
16:O:86:ARG:HG2	16:O:86:ARG:NH1	2.36	0.41
17:P:108:ASP:OD1	17:P:108:ASP:C	2.63	0.41
36:j:17:THR:HG23	36:j:29:ILE:HD11	2.02	0.41
39:n:159:ASN:ND2	39:n:227:GLN:HB3	2.35	0.41
39:n:435:ARG:HD3	39:n:437:ASP:H	1.84	0.41
1:1:1176:G:H4'	31:e:41:ARG:O	2.21	0.41
1:1:3245:G:C6	1:1:3246:A:C6	3.09	0.41
1:1:3352:A:N3	1:1:3352:A:H2'	2.36	0.41
3:3:59:LYS:NZ	3:3:81:LYS:HD3	2.35	0.41
6:C:231:ASN:HB3	6:C:234:ARG:HG2	2.02	0.41
11:H:41:HIS:CE1	11:H:42:VAL:HG22	2.54	0.41
20:S:160:GLY:O	20:S:165:LYS:NZ	2.41	0.41
22:V:42:PHE:CE1	22:V:61:LEU:HD21	2.55	0.41
27:a:75:LEU:HB3	27:a:117:LEU:HD21	2.03	0.41
31:e:64:MET:HE1	31:e:117:THR:HG22	2.02	0.41
39:n:423:TRP:HD1	39:n:439:TYR:CD1	2.38	0.41
1:1:1350:G:C6	1:1:1351:C:C4	3.09	0.41
1:1:2931:C:H5	1:1:2947:C:N4	2.17	0.41
1:1:3239:A:H4'	1:1:3240:G:C5'	2.51	0.41
3:3:93:ILE:HG13	3:3:112:LEU:HD21	2.01	0.41
5:B:165:GLN:HE22	5:B:168:LYS:NZ	2.18	0.41
8:E:158:LYS:HB2	8:E:158:LYS:HE3	1.78	0.41
16:O:186:SER:OG	16:O:189:ASN:OD1	2.36	0.41
22:V:60:VAL:O	22:V:78:ALA:N	2.47	0.41
31:e:108:LYS:HE2	31:e:108:LYS:HB2	1.81	0.41
39:n:403:ILE:HD11	39:n:420:GLN:C	2.45	0.41
42:r:198:GLY:O	42:r:221:GLU:N	2.53	0.41
43:t:40:LYS:HB3	43:t:44:LYS:NZ	2.36	0.41
1:1:223:G:H2'	1:1:224:U:O4'	2.20	0.41
1:1:652:U:H2'	1:1:653:U:C6	2.56	0.41
1:1:985:G:N3	1:1:1147:G:N1	2.69	0.41
1:1:1005:A:N6	1:1:1138:U:O4	2.54	0.41
1:1:1642:U:O2'	1:1:1643:C:H5'	2.20	0.41
1:1:3044:U:H2'	1:1:3045:G:C8	2.56	0.41
1:1:3206:C:H2'	1:1:3207:U:C6	2.56	0.41
3:3:86:TYR:O	3:3:90:LEU:HG	2.21	0.41
5:B:116:ARG:HG2	5:B:122:TRP:CE3	2.55	0.41
6:C:130:ALA:HB1	6:C:136:LEU:HD12	2.02	0.41
11:H:87:ARG:HG3	11:H:143:ILE:HG23	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:107:GLY:HA3	11:H:132:VAL:O	2.20	0.41
11:H:173:PHE:C	11:H:174:LEU:HD12	2.45	0.41
24:X:96:GLU:O	24:X:100:LYS:NZ	2.46	0.41
25:Y:47:LEU:HD23	25:Y:47:LEU:HA	1.86	0.41
30:d:15:ARG:HB3	30:d:17:TYR:HE2	1.85	0.41
39:n:439:TYR:CZ	39:n:446:PRO:HG2	2.56	0.41
46:y:65:GLY:HA3	46:y:70:LEU:HA	2.02	0.41
1:1:29:C:H4'	1:1:62:A:H4'	2.01	0.41
1:1:1319:U:H2'	1:1:1320:G:C8	2.55	0.41
1:1:3271:G:H2'	8:E:186:ASN:HD22	1.84	0.41
9:F:95:ARG:HA	9:F:141:VAL:HG12	2.02	0.41
11:H:31:PRO:HD2	11:H:83:THR:HA	2.01	0.41
11:H:63:LYS:HE3	11:H:63:LYS:HB2	1.89	0.41
14:M:12:ARG:HD2	14:M:58:LEU:HD12	2.02	0.41
16:O:173:LEU:O	16:O:176:GLN:NE2	2.53	0.41
20:S:79:ARG:HG3	20:S:121:ARG:NH1	2.36	0.41
24:X:57:ASP:OD1	24:X:57:ASP:N	2.42	0.41
26:Z:42:VAL:HA	26:Z:74:VAL:HA	2.02	0.41
31:e:87:LYS:HA	31:e:87:LYS:HD3	1.67	0.41
1:1:72:C:H5'	13:L:63:ILE:HD13	2.02	0.41
1:1:120:G:C8	10:G:128:LYS:HG3	2.56	0.41
1:1:1916:G:H2'	1:1:1917:U:C6	2.55	0.41
1:1:2473:A:C5	1:1:3239:A:H8	2.39	0.41
2:2:163:A:C6	2:2:164:U:C4	3.08	0.41
5:B:149:GLU:HA	5:B:152:LYS:HG2	2.03	0.41
8:E:191:HIS:CD2	32:f:41:GLU:OE2	2.74	0.41
18:Q:18:PRO:HD3	18:Q:52:PHE:CE1	2.55	0.41
20:S:22:LYS:HZ2	20:S:24:PHE:HA	1.85	0.41
23:W:41:TRP:O	23:W:102:LEU:HA	2.21	0.41
30:d:78:LEU:HD13	30:d:97:GLN:O	2.21	0.41
43:t:155:TYR:CE1	43:t:187:ILE:HD12	2.56	0.41
1:1:541:G:H2'	1:1:542:G:H8	1.86	0.41
1:1:990:C:C2	1:1:996:G:C2	3.09	0.41
1:1:1268:G:H1'	1:1:1294:A:N6	2.36	0.41
1:1:1320:G:H2'	1:1:1321:A:H8	1.86	0.41
1:1:1823:U:H2'	1:1:1824:C:C6	2.56	0.41
1:1:3346:U:H5'	1:1:3347:G:O4'	2.21	0.41
2:2:44:G:C5	34:h:88:ARG:HD3	2.55	0.41
3:3:89:ALA:O	3:3:93:ILE:HG12	2.21	0.41
4:A:85:GLN:OE1	35:i:82:LYS:NZ	2.52	0.41
5:B:211:GLN:NE2	5:B:211:GLN:O	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:308:MET:HE3	5:B:308:MET:HB3	1.88	0.41
6:C:146:GLU:HG3	6:C:175:LYS:HG3	2.03	0.41
6:C:190:ARG:NH2	6:C:202:VAL:HG12	2.36	0.41
6:C:235:LEU:HD23	6:C:235:LEU:HA	1.87	0.41
6:C:324:LYS:HA	6:C:324:LYS:HD3	1.93	0.41
10:G:184:ALA:O	10:G:188:THR:HG23	2.21	0.41
10:G:233:TRP:CD2	38:m:199:TYR:HB3	2.56	0.41
13:L:46:ILE:H	13:L:46:ILE:HG13	1.66	0.41
14:M:113:VAL:HA	14:M:116:LEU:HB2	2.01	0.41
15:N:9:GLU:O	35:i:42:VAL:HG11	2.21	0.41
15:N:199:ARG:CZ	15:N:200:TYR:HE1	2.34	0.41
17:P:51:VAL:HG11	17:P:88:VAL:HG11	2.03	0.41
19:R:21:LYS:HA	19:R:53:LYS:NZ	2.29	0.41
25:Y:44:ILE:HD12	25:Y:44:ILE:HA	1.88	0.41
27:a:82:LEU:HD23	27:a:83:PRO:O	2.21	0.41
32:f:69:TRP:CZ3	32:f:102:MET:HE1	2.56	0.41
34:h:120:LEU:HB3	45:v:56:LEU:HB2	2.02	0.41
36:j:35:ALA:O	36:j:45:ARG:NE	2.54	0.41
38:m:329:LEU:O	38:m:332:GLU:HG3	2.21	0.41
39:n:24:LYS:HB2	39:n:24:LYS:HE3	1.97	0.41
39:n:143:PHE:CE2	39:n:223:LEU:HD11	2.56	0.41
39:n:208:GLN:OE1	39:n:208:GLN:N	2.54	0.41
40:o:134:LEU:HG	40:o:151:ILE:HG22	2.03	0.41
43:t:133:LEU:HD21	43:t:142:TYR:CE1	2.55	0.41
45:v:142:GLU:O	45:v:146:VAL:HG22	2.21	0.41
1:1:181:A:H2'	1:1:182:G:C8	2.55	0.41
1:1:541:G:H2'	1:1:542:G:C8	2.56	0.41
1:1:1274:G:H1	1:1:1275:A:H62	1.69	0.41
1:1:1825:U:H2'	1:1:1826:C:C6	2.56	0.41
1:1:1891:C:H2'	1:1:1892:U:C6	2.56	0.41
1:1:1911:C:H2'	1:1:1912:C:C6	2.56	0.41
1:1:2949:U:H2'	1:1:2950:U:C6	2.56	0.41
1:1:3106:U:O2'	1:1:3107:A:H2'	2.21	0.41
1:1:3301:C:H2'	1:1:3302:U:C6	2.55	0.41
5:B:116:ARG:HD2	5:B:174:LYS:O	2.21	0.41
5:B:343:LEU:H	5:B:343:LEU:HD23	1.86	0.41
8:E:60:LEU:HD12	8:E:60:LEU:HA	1.77	0.41
13:L:56:PRO:HG2	13:L:72:GLY:HA3	2.03	0.41
16:O:111:PRO:N	16:O:112:PRO:HD2	2.36	0.41
17:P:111:LYS:HB3	17:P:152:GLU:OE1	2.21	0.41
30:d:66:LYS:HD3	30:d:66:LYS:HA	1.91	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:h:27:LEU:HD21	34:h:31:ARG:HH12	1.86	0.41
36:j:33:THR:HA	36:j:39:TYR:O	2.21	0.41
45:v:192:LEU:HD23	45:v:192:LEU:HA	1.92	0.41
1:1:350:A:OP2	2:2:29:C:N4	2.54	0.40
1:1:627:G:H2'	1:1:628:U:H5'	2.02	0.40
1:1:1235:A:H61	1:1:1331:G:H1'	1.86	0.40
1:1:1610:U:H2'	1:1:1611:G:C8	2.56	0.40
1:1:3286:U:H2'	1:1:3287:A:C8	2.56	0.40
2:2:22:C:H2'	2:2:23:G:O4'	2.21	0.40
6:C:179:ASP:O	6:C:183:VAL:HG13	2.21	0.40
11:H:11:LEU:HD23	11:H:12:THR:N	2.36	0.40
25:Y:30:MET:O	25:Y:49:VAL:HG22	2.21	0.40
25:Y:48:PRO:O	25:Y:114:ARG:NH2	2.54	0.40
34:h:81:ASP:OD1	34:h:82:LEU:HG	2.21	0.40
38:m:268:ASP:OD1	38:m:270:TRP:HD1	2.04	0.40
38:m:270:TRP:CD1	38:m:270:TRP:H	2.38	0.40
38:m:350:LYS:HB3	43:t:16:GLU:HB2	2.03	0.40
39:n:249:ILE:HD12	39:n:263:TYR:CZ	2.56	0.40
1:1:301:C:O3'	35:i:74:ARG:NH1	2.55	0.40
1:1:602:A:H1'	6:C:334:ALA:HB1	2.03	0.40
1:1:983:A:H5''	1:1:1174:A:N6	2.36	0.40
1:1:3110:U:H2'	1:1:3111:C:C6	2.56	0.40
2:2:82:U:C3'	25:Y:75:LYS:HZ1	2.33	0.40
5:B:121:ASN:O	5:B:122:TRP:C	2.64	0.40
9:F:160:PHE:CE2	9:F:169:PRO:HG3	2.56	0.40
9:F:209:LEU:HD23	9:F:209:LEU:HA	1.97	0.40
11:H:89:LYS:HB2	11:H:180:SER:OG	2.21	0.40
22:V:110:GLU:HA	22:V:130:ARG:HD2	2.02	0.40
24:X:104:VAL:HG21	24:X:125:LEU:HD23	2.03	0.40
24:X:112:LEU:HD23	24:X:112:LEU:N	2.36	0.40
25:Y:15:ARG:O	25:Y:19:PHE:HD2	2.05	0.40
25:Y:46:SER:OG	25:Y:47:LEU:N	2.55	0.40
25:Y:50:ARG:HD2	25:Y:51:ARG:H	1.84	0.40
25:Y:68:LYS:H	25:Y:82:GLU:HG2	1.86	0.40
1:1:281:A:N1	1:1:300:U:H5	2.19	0.40
1:1:985:G:N2	1:1:1173:G:H2'	2.37	0.40
1:1:1365:C:H1'	9:F:215:SER:HB2	2.04	0.40
1:1:2985:A:H61	1:1:3008:C:H42	1.70	0.40
1:1:2994:C:H6	1:1:2994:C:H2'	1.73	0.40
1:1:3223:A:H2'	1:1:3224:G:O4'	2.21	0.40
5:B:301:THR:OG1	28:b:436:LEU:HA	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:308:SER:O	6:C:309:ARG:C	2.63	0.40
9:F:228:HIS:ND1	9:F:230:ILE:HG12	2.36	0.40
15:N:38:ARG:NH1	15:N:60:VAL:HG22	2.36	0.40
15:N:167:ILE:HA	15:N:167:ILE:HD12	1.85	0.40
20:S:116:ARG:HA	20:S:116:ARG:HD3	1.95	0.40
22:V:89:ARG:HG2	22:V:91:ASP:OD1	2.21	0.40
25:Y:9:SER:O	25:Y:9:SER:OG	2.35	0.40
32:f:51:CYS:SG	32:f:102:MET:CE	3.09	0.40
38:m:240:TYR:CZ	38:m:244:LYS:HG3	2.56	0.40
39:n:141:PHE:CD1	39:n:164:CYS:HB2	2.56	0.40
39:n:146:MET:HG2	39:n:208:GLN:NE2	2.36	0.40
40:o:204:ALA:O	40:o:208:ARG:HG2	2.21	0.40
43:t:163:ASN:O	43:t:163:ASN:CG	2.64	0.40
1:1:3145:A:O2'	5:B:55:HIS:ND1	2.50	0.40
1:1:3337:A:O2'	1:1:3338:A:P	2.80	0.40
5:B:72:ILE:HD11	22:V:90:LYS:HB3	2.02	0.40
5:B:142:GLN:HE21	5:B:142:GLN:C	2.23	0.40
6:C:169:ALA:O	6:C:173:GLU:HG2	2.21	0.40
17:P:64:ASN:HB2	17:P:80:GLN:OE1	2.22	0.40
18:Q:57:ASN:C	18:Q:59:PRO:HD3	2.46	0.40
20:S:11:ARG:HG3	20:S:56:GLU:OE2	2.21	0.40
22:V:91:ASP:OD1	22:V:92:GLY:N	2.54	0.40
22:V:111:MET:SD	22:V:130:ARG:HD2	2.62	0.40
24:X:82:VAL:HG22	24:X:122:PHE:HD1	1.86	0.40
35:i:44:GLU:OE2	38:m:207:THR:OG1	2.30	0.40
39:n:28:LEU:HD22	39:n:32:ASP:HB2	2.03	0.40
39:n:360:LEU:HB2	39:n:382:TRP:HA	2.03	0.40
1:1:217:G:OP2	6:C:163:LYS:HD3	2.22	0.40
1:1:415:A:C2	2:2:25:A:H1'	2.56	0.40
1:1:1303:C:H3'	1:1:1304:A:H8	1.86	0.40
1:1:2999:U:H2'	1:1:3000:U:H6	1.86	0.40
1:1:3204:G:H21	11:H:161:GLN:HE22	1.69	0.40
1:1:3207:U:O4	1:1:3216:C:H4'	2.21	0.40
1:1:3330:G:H1	1:1:3357:C:H42	1.69	0.40
3:3:50:TYR:HA	3:3:100:TRP:CZ2	2.56	0.40
5:B:56:ILE:HD12	5:B:356:LEU:HD22	2.03	0.40
5:B:57:VAL:HG13	5:B:71:GLU:OE2	2.22	0.40
5:B:113:GLU:HB2	5:B:176:ALA:HB2	2.03	0.40
15:N:106:VAL:HG21	15:N:132:VAL:HG21	2.04	0.40
22:V:19:LEU:HB2	22:V:54:ALA:O	2.21	0.40
23:W:177:GLY:N	42:r:13:LYS:O	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:133:ASP:OD2	24:X:133:ASP:C	2.64	0.40
25:Y:78:LEU:HD23	25:Y:78:LEU:HA	1.92	0.40
27:a:74:ASN:OD1	27:a:114:LYS:HB2	2.22	0.40
31:e:93:ILE:HG21	31:e:102:ARG:HG2	2.03	0.40
39:n:359:PHE:O	39:n:403:ILE:HG22	2.21	0.40
40:o:156:LEU:HA	40:o:159:ALA:HB3	2.04	0.40
40:o:206:ILE:C	40:o:206:ILE:HD12	2.46	0.40
41:p:117:ILE:N	41:p:129:TRP:O	2.52	0.40
41:p:337:HIS:HA	41:p:348:SER:HA	2.04	0.40
43:t:95:ILE:HD12	43:t:232:ARG:HB3	2.03	0.40
48:6:42:U:H2'	48:6:43:G:C8	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	118/302 (39%)	108 (92%)	10 (8%)	0	100	100
4	A	192/295 (65%)	188 (98%)	4 (2%)	0	100	100
5	B	330/388 (85%)	307 (93%)	23 (7%)	0	100	100
6	C	357/363 (98%)	329 (92%)	28 (8%)	0	100	100
7	D	74/578 (13%)	74 (100%)	0	0	100	100
8	E	141/195 (72%)	133 (94%)	8 (6%)	0	100	100
9	F	212/250 (85%)	202 (95%)	10 (5%)	0	100	100
10	G	180/259 (70%)	170 (94%)	8 (4%)	2 (1%)	11	38
11	H	181/190 (95%)	166 (92%)	15 (8%)	0	100	100
12	K	227/373 (61%)	213 (94%)	13 (6%)	1 (0%)	30	59
13	L	116/208 (56%)	108 (93%)	7 (6%)	1 (1%)	14	42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	M	122/134 (91%)	116 (95%)	6 (5%)	0	100	100
15	N	160/201 (80%)	147 (92%)	13 (8%)	0	100	100
16	O	183/197 (93%)	180 (98%)	3 (2%)	0	100	100
17	P	130/187 (70%)	115 (88%)	14 (11%)	1 (1%)	16	44
18	Q	126/187 (67%)	119 (94%)	7 (6%)	0	100	100
19	R	55/193 (28%)	51 (93%)	4 (7%)	0	100	100
20	S	172/176 (98%)	160 (93%)	10 (6%)	2 (1%)	10	35
21	U	96/117 (82%)	92 (96%)	4 (4%)	0	100	100
22	V	127/139 (91%)	124 (98%)	3 (2%)	0	100	100
23	W	185/241 (77%)	176 (95%)	9 (5%)	0	100	100
24	X	126/141 (89%)	121 (96%)	5 (4%)	0	100	100
25	Y	123/126 (98%)	117 (95%)	6 (5%)	0	100	100
26	Z	127/136 (93%)	125 (98%)	2 (2%)	0	100	100
27	a	90/148 (61%)	87 (97%)	3 (3%)	0	100	100
28	b	368/642 (57%)	360 (98%)	8 (2%)	0	100	100
29	c	62/117 (53%)	60 (97%)	2 (3%)	0	100	100
30	d	90/113 (80%)	82 (91%)	7 (8%)	1 (1%)	11	38
31	e	115/127 (91%)	109 (95%)	6 (5%)	0	100	100
32	f	104/108 (96%)	96 (92%)	8 (8%)	0	100	100
33	g	85/112 (76%)	84 (99%)	1 (1%)	0	100	100
34	h	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
35	i	76/99 (77%)	73 (96%)	3 (4%)	0	100	100
36	j	69/91 (76%)	67 (97%)	2 (3%)	0	100	100
37	k	68/74 (92%)	67 (98%)	1 (2%)	0	100	100
38	m	470/740 (64%)	450 (96%)	20 (4%)	0	100	100
39	n	410/607 (68%)	388 (95%)	22 (5%)	0	100	100
40	o	107/276 (39%)	102 (95%)	5 (5%)	0	100	100
41	p	277/440 (63%)	270 (98%)	7 (2%)	0	100	100
42	r	146/260 (56%)	143 (98%)	3 (2%)	0	100	100
43	t	233/249 (94%)	219 (94%)	14 (6%)	0	100	100
44	u	95/192 (50%)	90 (95%)	5 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	v	136/209 (65%)	127 (93%)	9 (7%)	0	100	100
46	y	223/244 (91%)	219 (98%)	4 (2%)	0	100	100
47	T	17/160 (11%)	17 (100%)	0	0	100	100
All	All	7220/10706 (67%)	6868 (95%)	344 (5%)	8 (0%)	49	78

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	P	12	THR
20	S	158	VAL
10	G	227	ASP
20	S	159	VAL
12	K	153	ILE
30	d	12	VAL
10	G	182	ASN
13	L	47	ALA

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	
3	3	109/271 (40%)	109 (100%)	0	100	100
4	A	11/266 (4%)	11 (100%)	0	100	100
5	B	283/326 (87%)	283 (100%)	0	100	100
6	C	296/297 (100%)	295 (100%)	1 (0%)	86	84
8	E	119/155 (77%)	119 (100%)	0	100	100
9	F	180/210 (86%)	179 (99%)	1 (1%)	78	80
10	G	154/212 (73%)	153 (99%)	1 (1%)	78	80
11	H	164/170 (96%)	162 (99%)	2 (1%)	63	72
13	L	99/167 (59%)	98 (99%)	1 (1%)	68	75
14	M	107/113 (95%)	105 (98%)	2 (2%)	50	66

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	N	146/176 (83%)	146 (100%)	0	100	100
16	O	153/162 (94%)	153 (100%)	0	100	100
17	P	112/149 (75%)	111 (99%)	1 (1%)	70	76
18	Q	111/159 (70%)	111 (100%)	0	100	100
19	R	51/162 (32%)	50 (98%)	1 (2%)	48	65
20	S	152/154 (99%)	152 (100%)	0	100	100
22	V	102/107 (95%)	101 (99%)	1 (1%)	68	75
24	X	112/122 (92%)	112 (100%)	0	100	100
25	Y	110/111 (99%)	110 (100%)	0	100	100
27	a	81/122 (66%)	81 (100%)	0	100	100
30	d	86/102 (84%)	83 (96%)	3 (4%)	32	56
31	e	100/107 (94%)	99 (99%)	1 (1%)	68	75
32	f	89/91 (98%)	89 (100%)	0	100	100
34	h	106/107 (99%)	105 (99%)	1 (1%)	70	76
35	i	68/84 (81%)	68 (100%)	0	100	100
36	j	58/71 (82%)	58 (100%)	0	100	100
38	m	132/659 (20%)	131 (99%)	1 (1%)	73	77
39	n	364/532 (68%)	361 (99%)	3 (1%)	73	77
40	o	96/246 (39%)	96 (100%)	0	100	100
42	r	59/224 (26%)	57 (97%)	2 (3%)	32	57
43	t	211/223 (95%)	210 (100%)	1 (0%)	81	81
45	v	120/181 (66%)	119 (99%)	1 (1%)	73	77
47	T	17/139 (12%)	17 (100%)	0	100	100
All	All	4158/6377 (65%)	4134 (99%)	24 (1%)	76	80

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	C	181	ILE
9	F	102	ILE
10	G	58	LEU
11	H	35	LEU
11	H	178	TYR
13	L	46	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
14	M	28	ILE
14	M	61	ILE
17	P	117	VAL
19	R	34	ASN
22	V	130	ARG
30	d	11	GLN
30	d	29	SER
30	d	109	THR
31	e	31	LYS
34	h	115	LEU
38	m	263	ASN
39	n	18	THR
39	n	148	VAL
39	n	221	THR
42	r	19	ASP
42	r	37	LEU
43	t	191	ILE
45	v	176	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	87	ASN
5	B	109	HIS
5	B	165	GLN
5	B	319	ASN
6	C	344	ASN
9	F	69	GLN
9	F	207	ASN
10	G	89	GLN
11	H	37	GLN
11	H	41	HIS
11	H	184	ASN
13	L	28	GLN
13	L	66	ASN
16	O	5	GLN
16	O	43	ASN
16	O	82	GLN
17	P	54	HIS
17	P	80	GLN
18	Q	53	GLN
19	R	55	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
24	X	86	HIS
27	a	4	HIS
30	d	48	HIS
32	f	43	GLN
35	i	63	GLN
39	n	239	ASN
39	n	349	ASN
39	n	411	GLN
39	n	580	ASN
39	n	585	ASN
42	r	3	GLN
42	r	4	ASN
42	r	40	GLN
43	t	163	ASN
45	v	37	GLN
47	T	139	HIS
47	T	152	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1981/3497 (56%)	472 (23%)	23 (1%)
2	2	143/165 (86%)	23 (16%)	2 (1%)
48	6	57/300 (19%)	24 (42%)	0
All	All	2181/3962 (55%)	519 (23%)	25 (1%)

All (519) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	6	A
1	1	7	C
1	1	25	U
1	1	26	A
1	1	49	A
1	1	51	A
1	1	57	A
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	72	C
1	1	74	A
1	1	100	A
1	1	105	G
1	1	106	A
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	117	U
1	1	118	U
1	1	119	U
1	1	122	A
1	1	131	A
1	1	133	A
1	1	136	U
1	1	149	G
1	1	153	U
1	1	154	G
1	1	161	C
1	1	162	A
1	1	163	A
1	1	170	G
1	1	177	G
1	1	185	G
1	1	193	U
1	1	194	A
1	1	195	A
1	1	197	U
1	1	198	U
1	1	207	C
1	1	217	G
1	1	218	A
1	1	220	A
1	1	225	G
1	1	226	A
1	1	227	G
1	1	239	U
1	1	244	G
1	1	247	U
1	1	248	G
1	1	258	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	259	A
1	1	261	A
1	1	266	G
1	1	267	C
1	1	268	U
1	1	269	U
1	1	271	C
1	1	272	G
1	1	276	A
1	1	277	G
1	1	303	A
1	1	306	U
1	1	325	A
1	1	331	A
1	1	337	U
1	1	338	G
1	1	341	G
1	1	342	A
1	1	345	G
1	1	346	A
1	1	350	A
1	1	354	C
1	1	357	A
1	1	359	A
1	1	360	A
1	1	384	G
1	1	399	A
1	1	406	U
1	1	411	C
1	1	412	G
1	1	416	A
1	1	429	G
1	1	430	A
1	1	432	G
1	1	437	G
1	1	507	U
1	1	514	C
1	1	521	C
1	1	532	A
1	1	534	A
1	1	540	A
1	1	544	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	546	G
1	1	547	G
1	1	548	U
1	1	551	C
1	1	577	U
1	1	578	U
1	1	579	A
1	1	580	U
1	1	581	A
1	1	582	G
1	1	591	G
1	1	592	U
1	1	593	A
1	1	602	A
1	1	603	C
1	1	606	G
1	1	618	U
1	1	623	C
1	1	625	U
1	1	626	C
1	1	627	G
1	1	628	U
1	1	629	G
1	1	634	G
1	1	636	A
1	1	647	A
1	1	661	C
1	1	662	C
1	1	663	C
1	1	674	A
1	1	675	C
1	1	685	A
1	1	687	U
1	1	702	A
1	1	706	U
1	1	708	U
1	1	714	A
1	1	715	U
1	1	716	G
1	1	717	A
1	1	732	A
1	1	738	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	739	G
1	1	742	A
1	1	751	G
1	1	752	G
1	1	759	C
1	1	760	C
1	1	761	U
1	1	762	U
1	1	763	G
1	1	768	G
1	1	770	G
1	1	772	A
1	1	773	C
1	1	775	A
1	1	776	U
1	1	777	C
1	1	778	G
1	1	780	C
1	1	781	C
1	1	816	A
1	1	817	G
1	1	819	G
1	1	833	A
1	1	847	G
1	1	976	C
1	1	986	U
1	1	988	U
1	1	989	C
1	1	991	C
1	1	992	U
1	1	995	G
1	1	996	G
1	1	997	A
1	1	998	U
1	1	1003	G
1	1	1005	A
1	1	1006	A
1	1	1010	A
1	1	1011	G
1	1	1012	A
1	1	1014	C
1	1	1017	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1022	U
1	1	1023	G
1	1	1135	G
1	1	1137	G
1	1	1138	U
1	1	1139	U
1	1	1142	U
1	1	1143	A
1	1	1147	G
1	1	1154	U
1	1	1158	G
1	1	1160	A
1	1	1163	C
1	1	1164	A
1	1	1166	A
1	1	1169	U
1	1	1170	G
1	1	1173	G
1	1	1176	G
1	1	1184	A
1	1	1186	C
1	1	1191	C
1	1	1205	G
1	1	1211	A
1	1	1212	U
1	1	1223	C
1	1	1224	A
1	1	1232	G
1	1	1235	A
1	1	1244	G
1	1	1249	U
1	1	1251	U
1	1	1252	A
1	1	1253	G
1	1	1258	C
1	1	1259	A
1	1	1273	G
1	1	1276	A
1	1	1277	G
1	1	1282	A
1	1	1283	A
1	1	1284	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1286	C
1	1	1289	U
1	1	1290	A
1	1	1291	A
1	1	1293	G
1	1	1294	A
1	1	1295	G
1	1	1296	U
1	1	1303	C
1	1	1309	A
1	1	1310	C
1	1	1315	C
1	1	1316	G
1	1	1317	A
1	1	1318	A
1	1	1323	C
1	1	1333	A
1	1	1334	A
1	1	1335	A
1	1	1336	U
1	1	1337	G
1	1	1338	G
1	1	1339	A
1	1	1349	A
1	1	1361	A
1	1	1379	U
1	1	1381	G
1	1	1389	A
1	1	1390	A
1	1	1407	A
1	1	1414	G
1	1	1433	U
1	1	1451	G
1	1	1452	A
1	1	1453	A
1	1	1464	U
1	1	1468	G
1	1	1471	C
1	1	1477	G
1	1	1515	A
1	1	1517	G
1	1	1519	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1521	G
1	1	1528	U
1	1	1529	U
1	1	1538	A
1	1	1541	G
1	1	1542	C
1	1	1545	U
1	1	1561	C
1	1	1576	G
1	1	1581	G
1	1	1588	A
1	1	1589	U
1	1	1590	G
1	1	1594	G
1	1	1598	C
1	1	1602	A
1	1	1603	U
1	1	1604	U
1	1	1605	U
1	1	1606	U
1	1	1607	U
1	1	1608	C
1	1	1609	G
1	1	1614	U
1	1	1622	A
1	1	1628	A
1	1	1640	A
1	1	1643	C
1	1	1654	A
1	1	1655	G
1	1	1660	A
1	1	1661	A
1	1	1662	U
1	1	1673	A
1	1	1677	A
1	1	1678	A
1	1	1680	U
1	1	1720	C
1	1	1736	A
1	1	1737	C
1	1	1738	C
1	1	1739	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1746	U
1	1	1753	A
1	1	1781	G
1	1	1782	U
1	1	1783	G
1	1	1784	U
1	1	1789	A
1	1	1790	A
1	1	1791	G
1	1	1801	C
1	1	1804	C
1	1	1805	A
1	1	1806	U
1	1	1811	A
1	1	1814	C
1	1	1816	G
1	1	1820	C
1	1	1821	G
1	1	1833	C
1	1	1849	G
1	1	1852	G
1	1	1874	U
1	1	1875	U
1	1	1876	U
1	1	1877	C
1	1	1881	U
1	1	1917	U
1	1	1920	A
1	1	1921	C
1	1	1924	C
1	1	1933	G
1	1	1935	U
1	1	1939	A
1	1	1940	C
1	1	1947	G
1	1	2423	G
1	1	2424	U
1	1	2452	G
1	1	2454	C
1	1	2464	G
1	1	2465	G
1	1	2471	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	2473	A
1	1	2476	U
1	1	2921	U
1	1	2925	G
1	1	2929	G
1	1	2931	C
1	1	2932	A
1	1	2946	A
1	1	2952	C
1	1	2953	U
1	1	2972	G
1	1	2973	G
1	1	2978	U
1	1	2982	A
1	1	2984	C
1	1	2993	G
1	1	3006	A
1	1	3011	U
1	1	3014	A
1	1	3024	C
1	1	3025	A
1	1	3028	A
1	1	3030	U
1	1	3031	A
1	1	3034	G
1	1	3036	A
1	1	3037	C
1	1	3038	G
1	1	3040	G
1	1	3041	A
1	1	3042	G
1	1	3046	G
1	1	3082	A
1	1	3083	C
1	1	3085	G
1	1	3087	U
1	1	3091	G
1	1	3093	G
1	1	3108	A
1	1	3113	A
1	1	3116	U
1	1	3117	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	3118	G
1	1	3119	U
1	1	3125	A
1	1	3126	G
1	1	3128	A
1	1	3144	C
1	1	3151	A
1	1	3152	U
1	1	3153	U
1	1	3170	G
1	1	3174	A
1	1	3175	U
1	1	3182	G
1	1	3188	U
1	1	3189	C
1	1	3190	A
1	1	3195	C
1	1	3196	U
1	1	3205	G
1	1	3209	A
1	1	3211	C
1	1	3218	A
1	1	3225	A
1	1	3226	A
1	1	3227	U
1	1	3238	A
1	1	3239	A
1	1	3240	G
1	1	3246	A
1	1	3271	G
1	1	3272	U
1	1	3273	A
1	1	3276	A
1	1	3282	G
1	1	3299	U
1	1	3307	U
1	1	3313	G
1	1	3315	A
1	1	3316	G
1	1	3317	A
1	1	3318	A
1	1	3319	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	3322	G
1	1	3324	G
1	1	3327	A
1	1	3329	G
1	1	3332	U
1	1	3335	U
1	1	3336	G
1	1	3337	A
1	1	3338	A
1	1	3343	A
1	1	3344	A
1	1	3345	G
1	1	3346	U
1	1	3347	G
1	1	3351	U
1	1	3352	A
1	1	3353	U
1	1	3358	U
1	1	3359	U
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3373	C
1	1	3396	A
1	1	3404	G
1	1	3405	C
1	1	3417	A
1	1	3418	U
1	1	3420	U
1	1	3431	A
1	1	3435	U
1	1	3440	A
1	1	3441	G
1	1	3470	G
1	1	3476	A
1	1	3477	A
1	1	3479	C
1	1	3490	A
1	1	3491	A
1	1	3492	G
2	2	31	U
2	2	42	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	43	C
2	2	46	U
2	2	59	G
2	2	67	A
2	2	68	U
2	2	70	C
2	2	71	G
2	2	98	U
2	2	99	C
2	2	103	G
2	2	112	A
2	2	113	A
2	2	114	C
2	2	115	G
2	2	124	G
2	2	132	G
2	2	133	U
2	2	134	U
2	2	135	C
2	2	136	U
2	2	159	U
48	6	2	C
48	6	3	A
48	6	5	U
48	6	6	C
48	6	7	U
48	6	9	C
48	6	45	G
48	6	47	U
48	6	49	U
48	6	55	G
48	6	56	A
48	6	57	A
48	6	60	U
48	6	89	U
48	6	92	G
48	6	94	A
48	6	96	U
48	6	97	C
48	6	105	G
48	6	106	A
48	6	108	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	6	178	U
48	6	181	C
48	6	182	C

All (25) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	270	U
1	1	674	A
1	1	716	G
1	1	761	U
1	1	995	G
1	1	997	A
1	1	1159	U
1	1	1234	A
1	1	1258	C
1	1	1272	U
1	1	1314	C
1	1	1333	A
1	1	1338	G
1	1	1389	A
1	1	1540	A
1	1	1851	A
1	1	1916	G
1	1	3217	U
1	1	3239	A
1	1	3318	A
1	1	3328	U
1	1	3337	A
1	1	3372	C
2	2	103	G
2	2	131	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

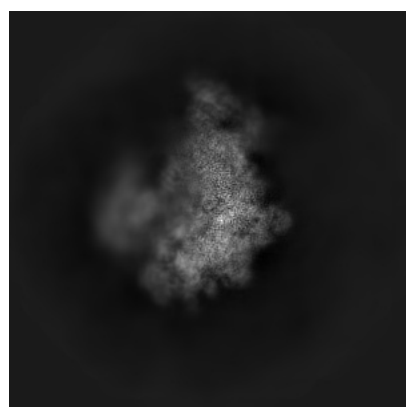
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24397. These allow visual inspection of the internal detail of the map and identification of artifacts.

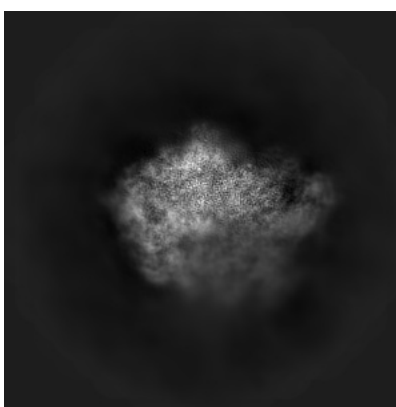
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

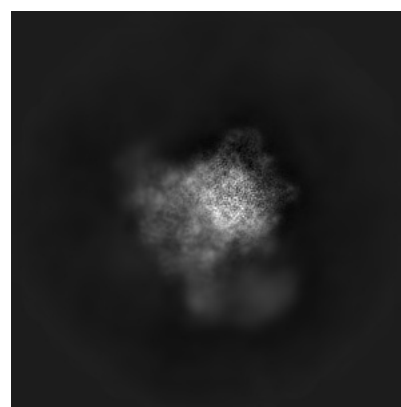
6.1.1 Primary map



X



Y

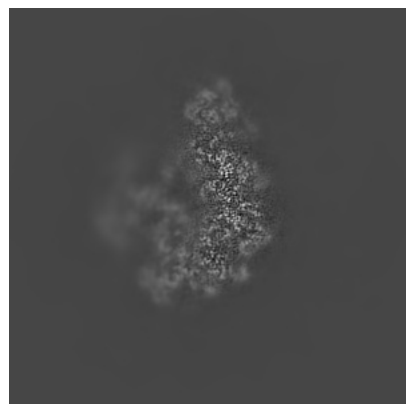


Z

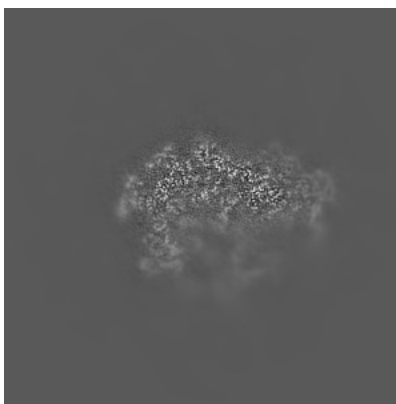
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

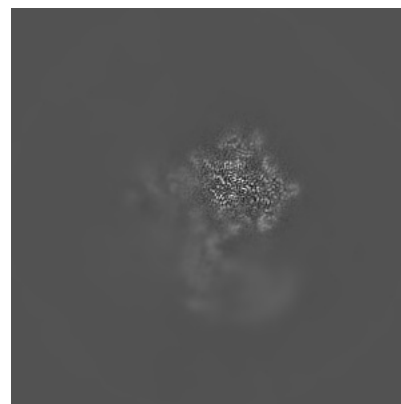
6.2.1 Primary map



X Index: 256



Y Index: 256

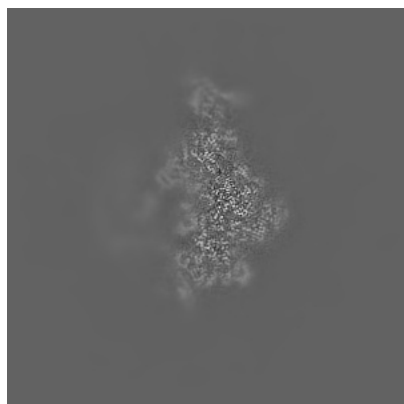


Z Index: 256

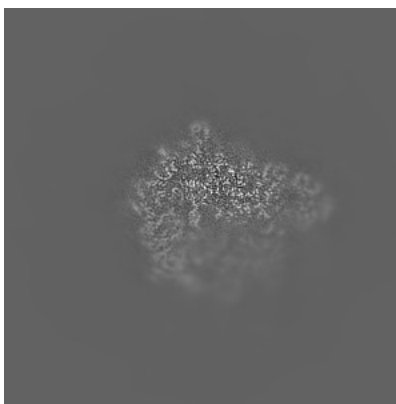
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

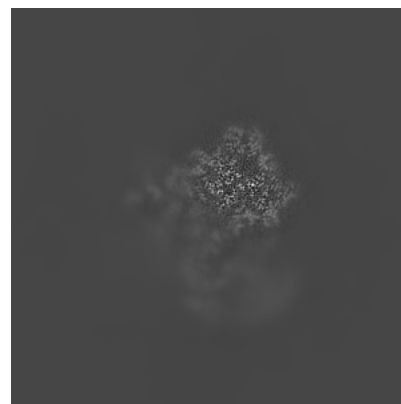
6.3.1 Primary map



X Index: 282



Y Index: 272

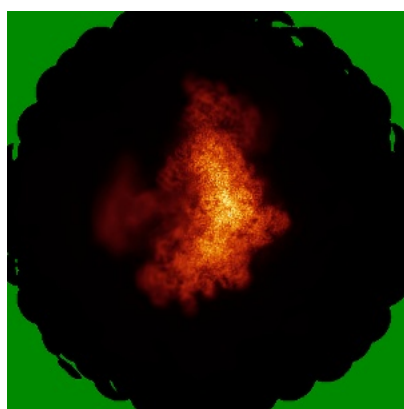


Z Index: 250

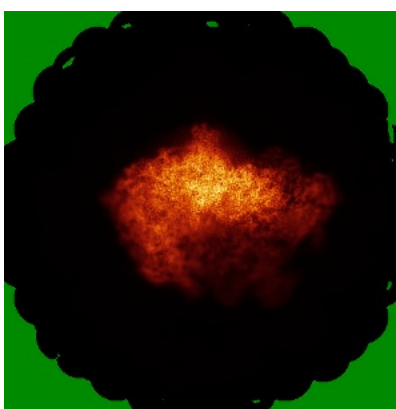
The images above show the largest variance slices of the map in three orthogonal directions.

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

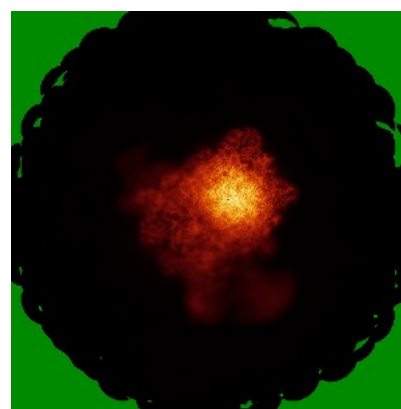
6.4.1 Primary map



X



Y

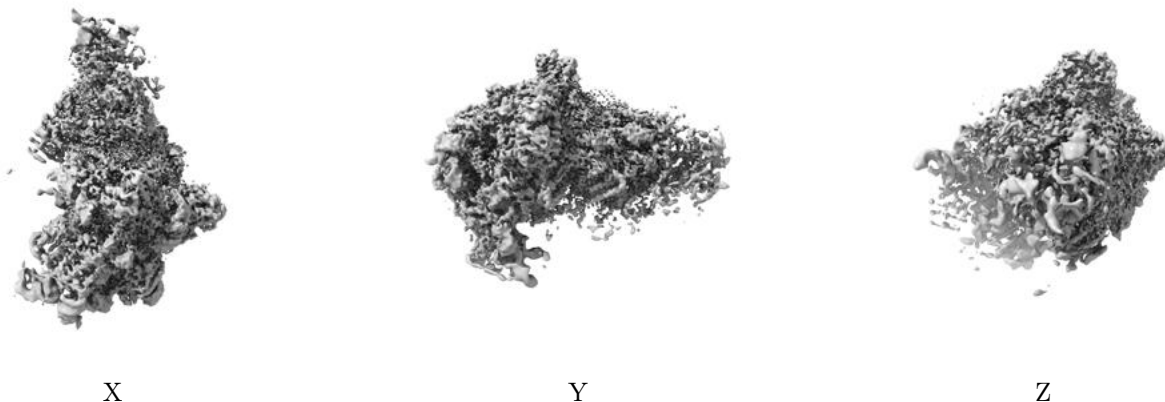


Z

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

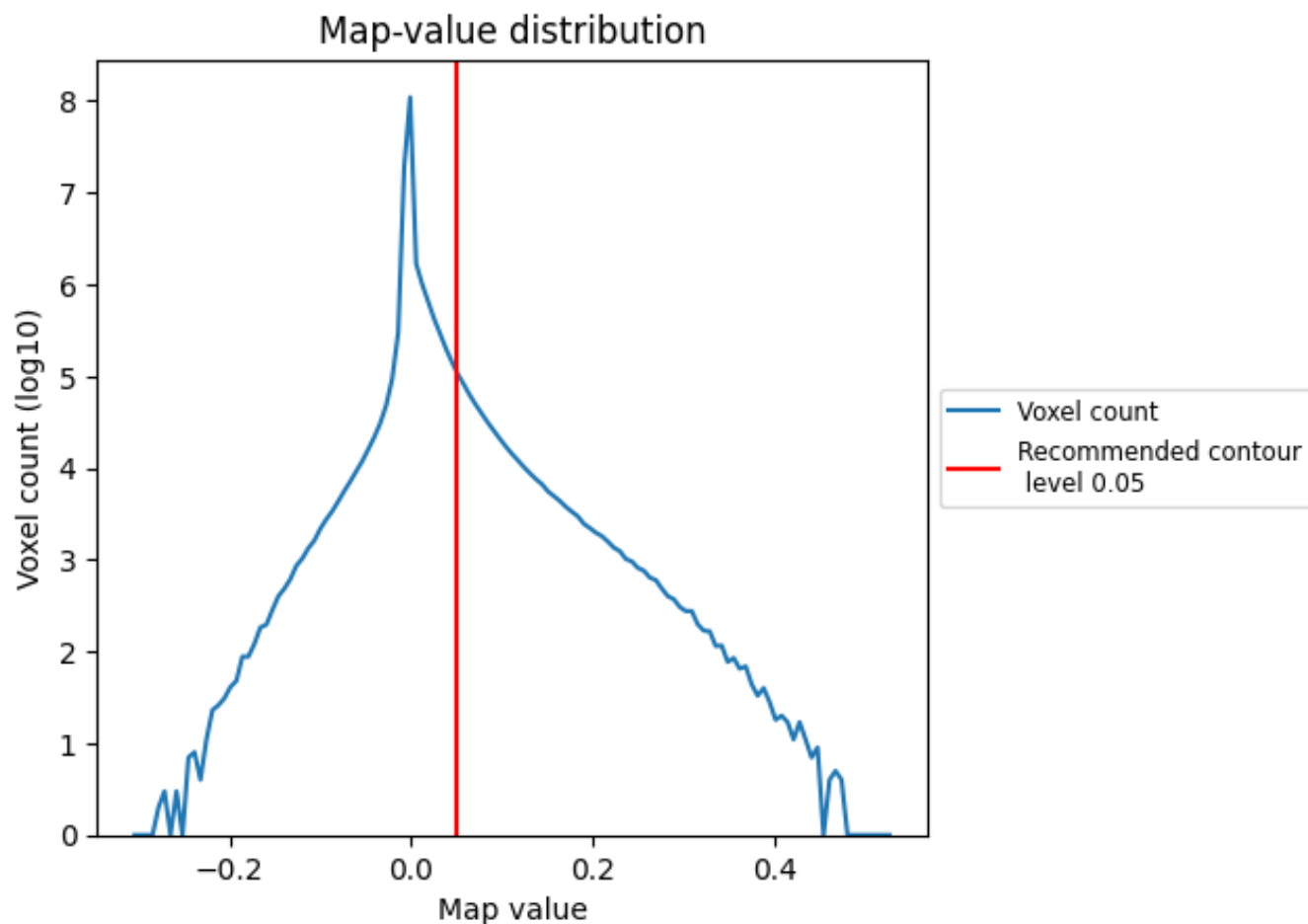
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

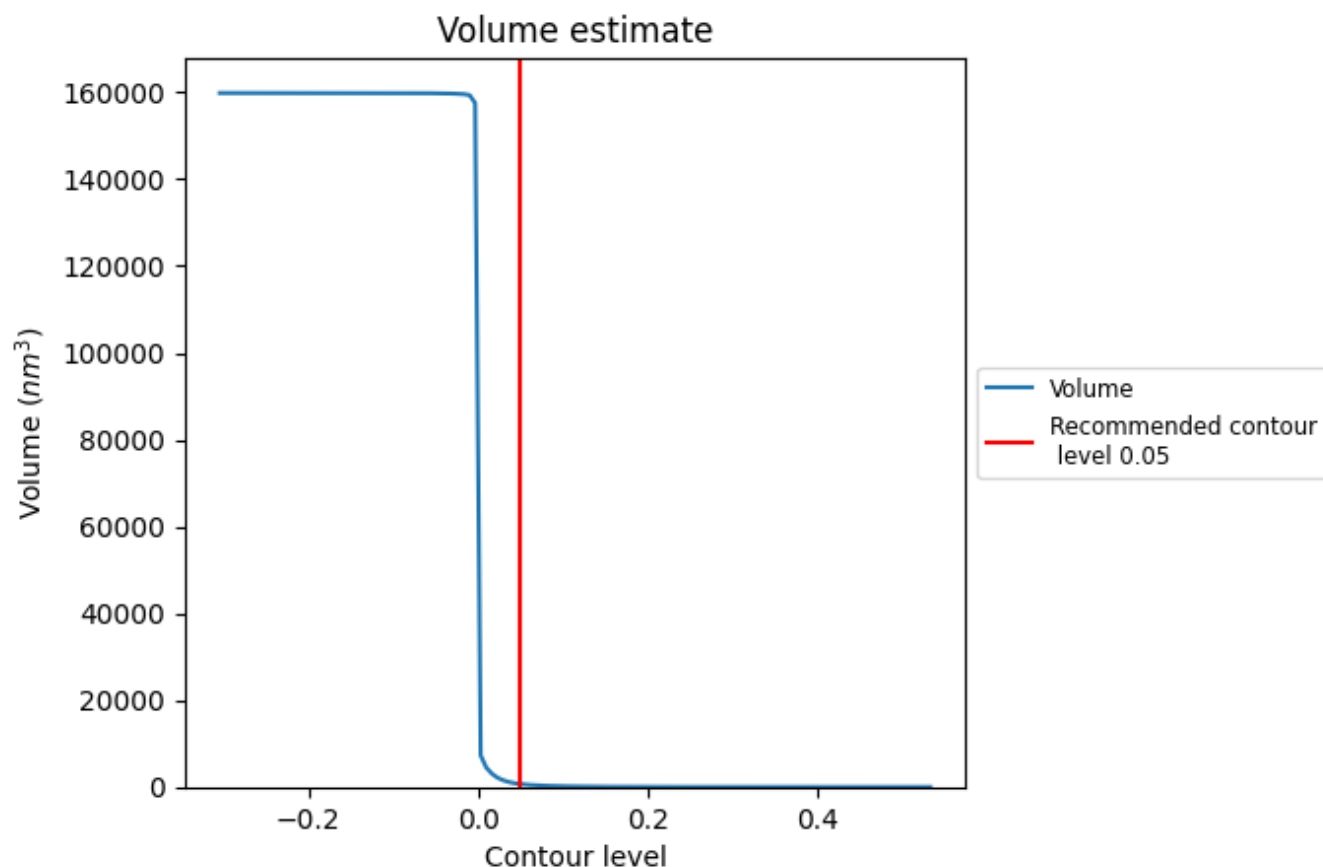
This section contains the results of statistical analysis of the map.

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.

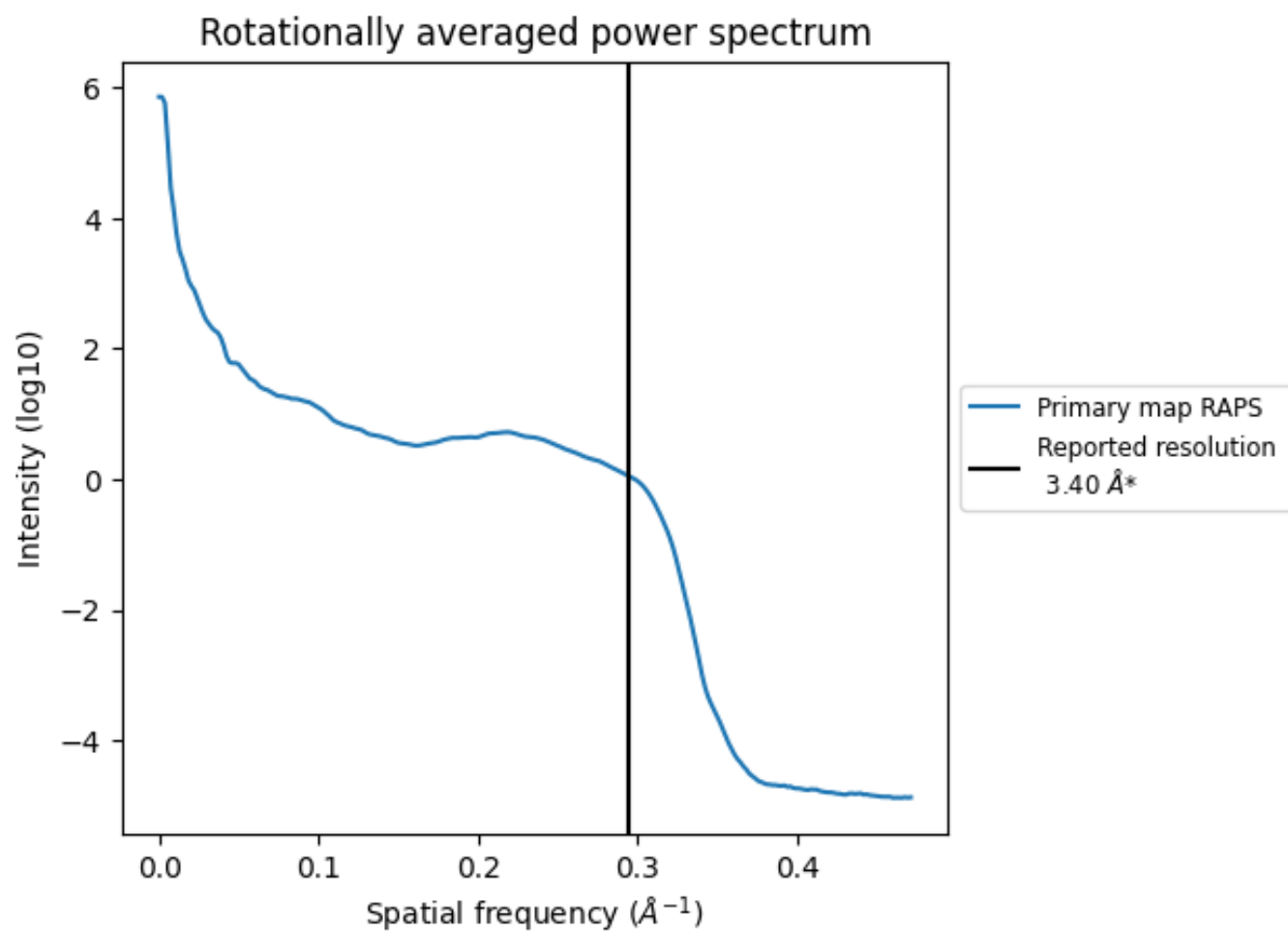
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 669 nm³; this corresponds to an approximate mass of 605 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 0.294 Å⁻¹

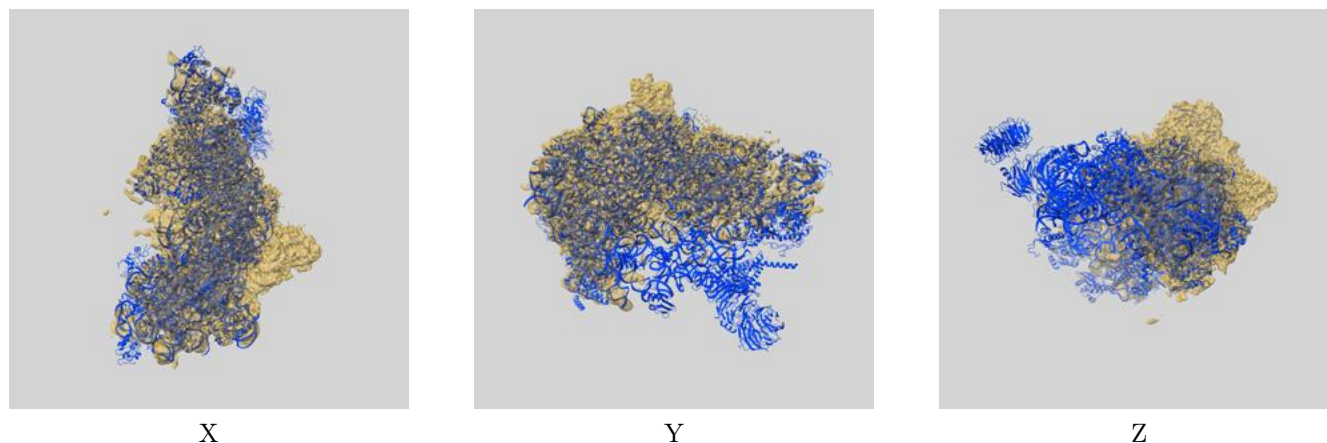
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

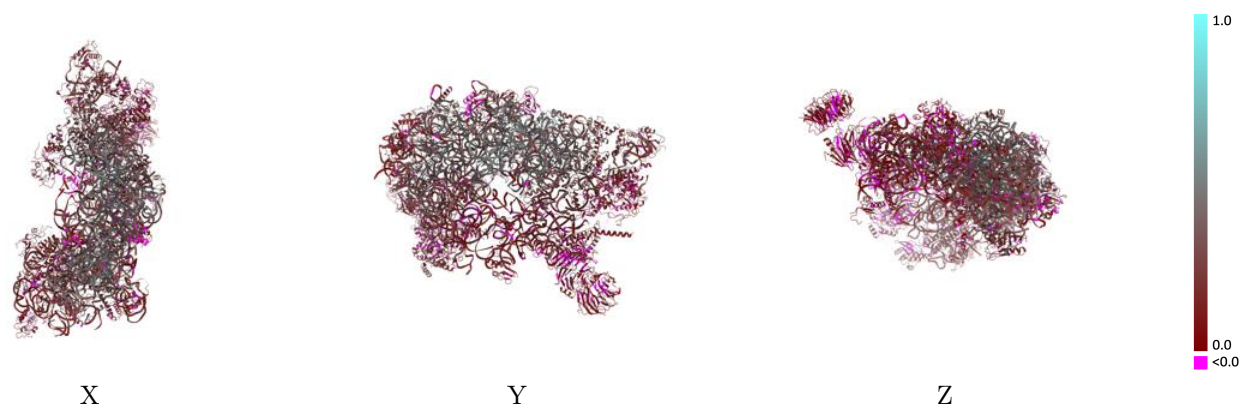
This section contains information regarding the fit between EMDB map EMD-24397 and PDB model 8ETG. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



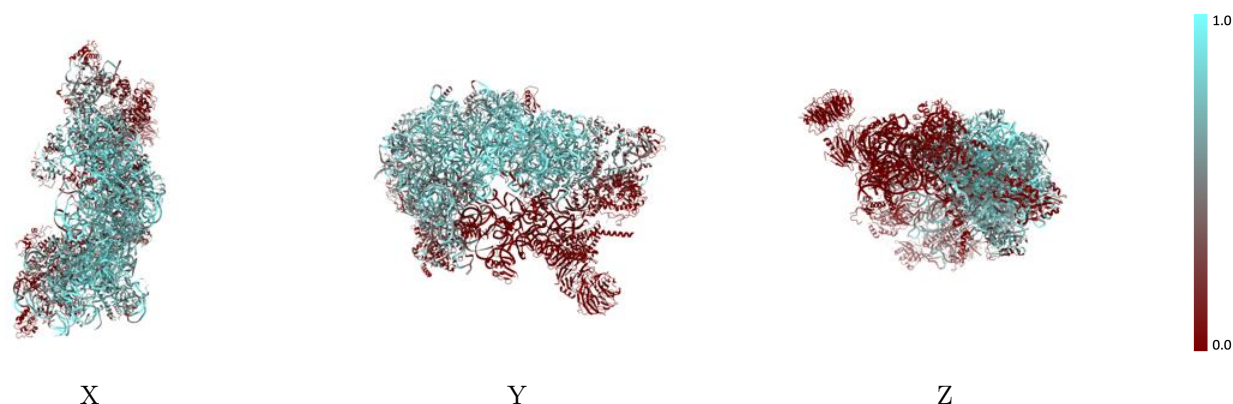
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



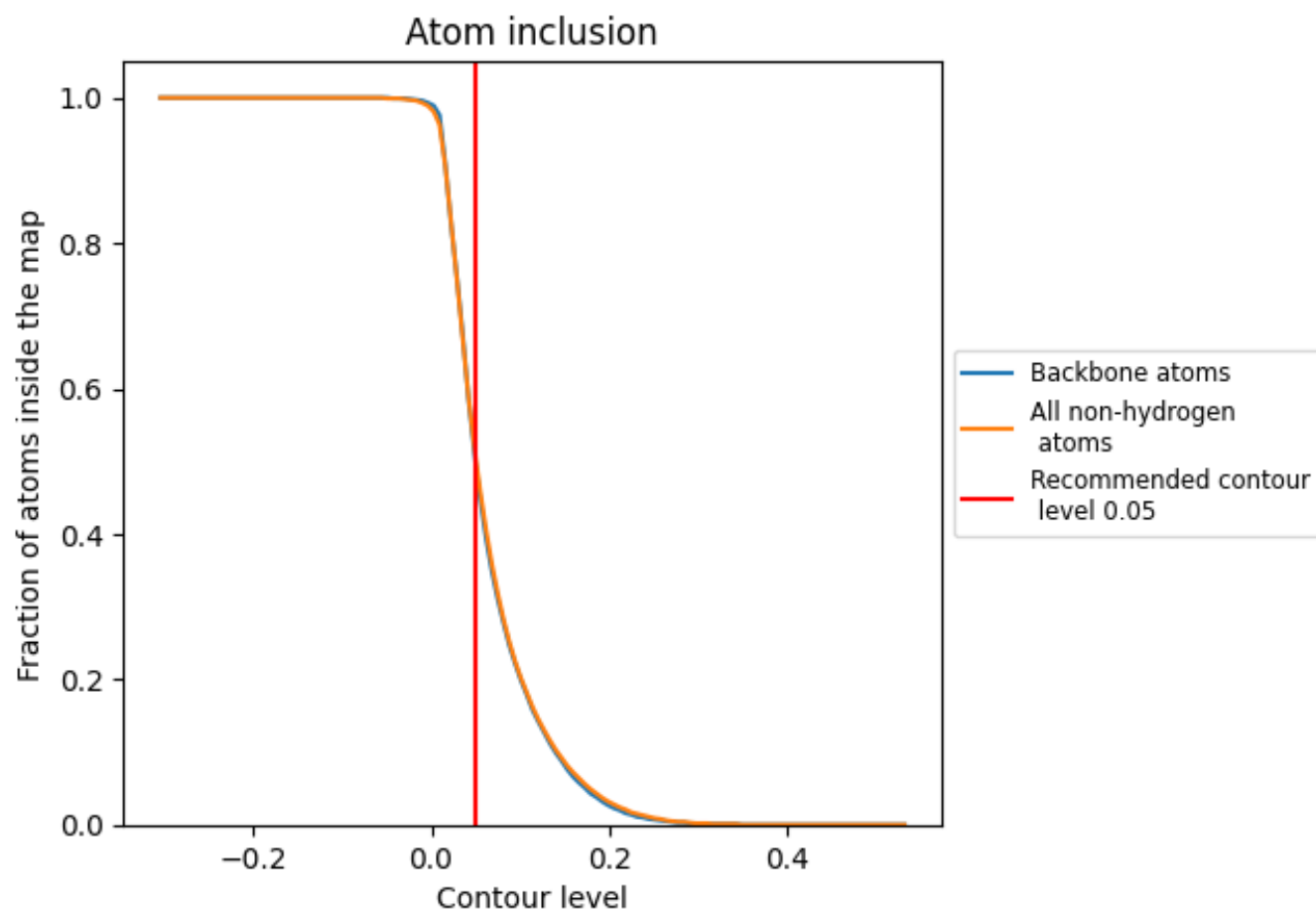
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 50% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5050	 0.2580
1	 0.6110	 0.2740
2	 0.7840	 0.3630
3	 0.5550	 0.1600
6	 0.4840	 0.2490
A	 0.4910	 0.2160
B	 0.5580	 0.2520
C	 0.7320	 0.3730
D	 0.4260	 0.3090
E	 0.5830	 0.2080
F	 0.7450	 0.3850
G	 0.6270	 0.2970
H	 0.3860	 0.1750
K	 0.2660	 0.2550
L	 0.8260	 0.4420
M	 0.6180	 0.2650
N	 0.7830	 0.4010
O	 0.6580	 0.3360
P	 0.5680	 0.2640
Q	 0.6910	 0.3180
R	 0.0000	 0.1510
S	 0.5210	 0.2810
T	 0.3470	 0.2810
U	 0.0000	 0.1600
V	 0.0400	 0.0870
W	 0.0040	 0.1490
X	 0.0990	 0.2120
Y	 0.7310	 0.3790
Z	 0.0000	 0.1140
a	 0.1530	 0.0820
b	 0.1630	 0.1630
c	 0.0000	 0.0820
d	 0.0040	 0.1560
e	 0.7730	 0.3970
f	 0.7740	 0.3980



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
g	 0.0000	 0.0670
h	 0.6860	 0.3740
i	 0.6880	 0.3140
j	 0.8280	 0.4290
k	 0.0000	 0.1790
m	 0.1130	 0.1280
n	 0.0820	 0.1570
o	 0.3330	 0.2010
p	 0.0000	 0.0760
r	 0.1450	 0.1580
t	 0.1370	 0.1360
u	 0.3460	 0.2140
v	 0.6180	 0.3110
y	 0.1400	 0.1250