



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 02:50 AM UTC

PDB ID : 7L20 / pdb_00007L20
EMDB ID : EMD-23121
Title : Cryo-EM structure of the human 39S mitoribosomal subunit in complex with RRFmt and EF-G2mt.
Authors : Agrawal, E.; Koripella, R.
Deposited on : 2020-12-15
Resolution : 3.15 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

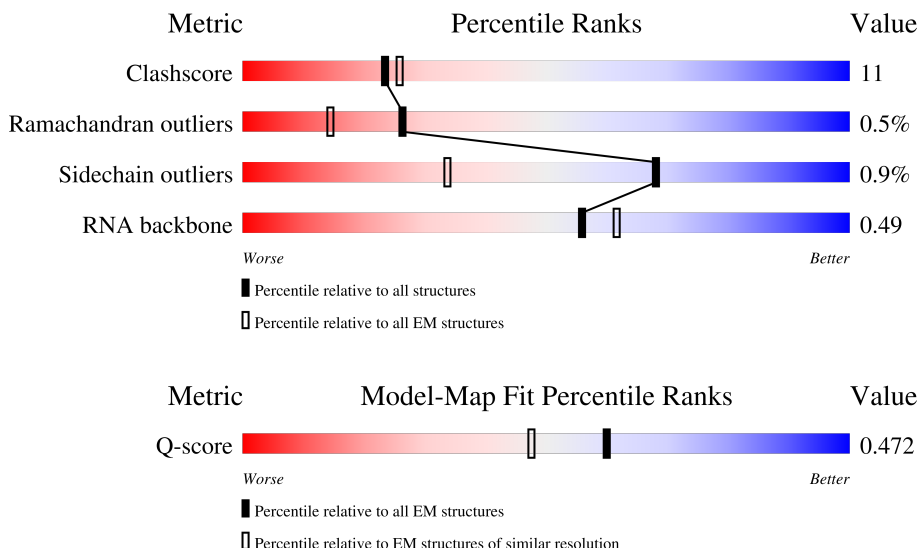
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.15 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	14486 (2.65 - 3.65)

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	A	1559	
2	B	73	
3	D	305	

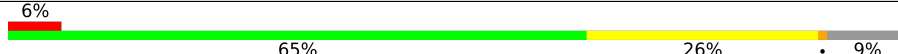
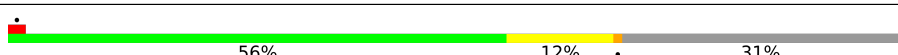
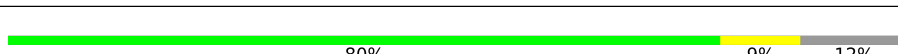
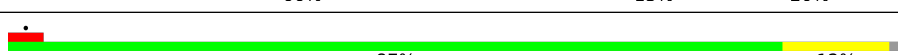
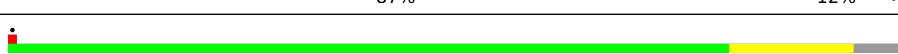
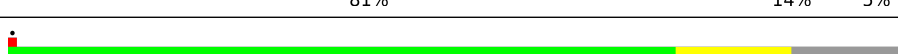
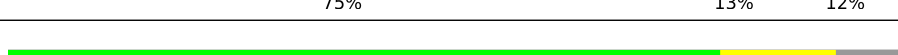
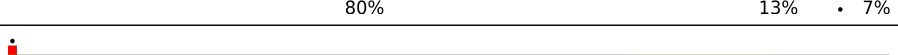
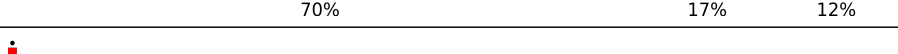
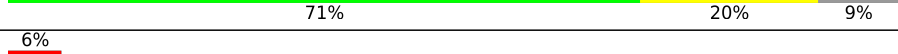
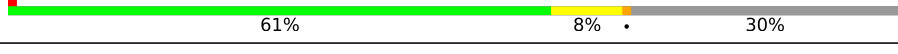
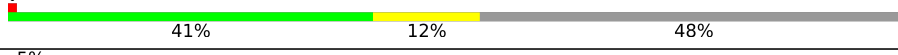
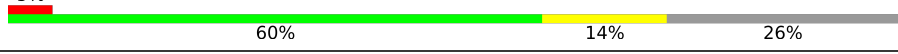
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	F	311	
5	H	267	
6	K	178	
7	L	145	
8	M	296	
9	O	175	
10	R	149	
11	S	205	
12	T	212	
13	W	148	
14	X	256	
15	Y	250	
16	Z	161	
17	0	188	
18	1	65	
19	2	92	
20	3	188	
21	4	103	
22	8	206	
23	b	155	
24	e	279	
25	g	166	
26	i	128	
27	j	123	
28	m	128	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	o	102	
30	q	222	
31	r	196	
32	J	192	
33	I	261	
34	N	251	
35	P	179	
36	U	153	
37	V	216	
38	E	348	
39	5	423	
40	6	380	
41	7	338	
42	9	137	
43	a	142	
44	c	332	
45	d	306	
46	f	194	
47	h	158	
48	k	112	
49	l	138	
50	p	206	
51	s	439	
52	Q	292	
53	u	65	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	TA	198	
54	TB	198	
54	TC	198	
55	z	204	
56	w	696	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
59	GCP	w	801	-	-	X	-

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 110234 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1527	Total	C	N	O	P	0	0
			32395	14536	5844	10488	1527		

- Molecule 2 is a RNA chain called tRNAval.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

- Molecule 3 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	239	Total	C	N	O	S	0	0
			1866	1162	377	318	9		

- Molecule 4 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 5 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	H	98	Total	C	N	O	0	0
			806	510	156	140		

- Molecule 6 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 7 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 8 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 9 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 10 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	R	140	Total	C	N	O	S	0	0
			1153	732	231	186	4		

- Molecule 11 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 12 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	T	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 13 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	W	111	Total	C	N	O	S	0	0
			871	558	164	146	3		

- Molecule 14 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	X	243	Total	C	N	O	S	0	0
			2027	1310	350	362	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	148	ALA	THR	variant	UNP Q13084
X	149	SER	PRO	variant	UNP Q13084
X	150	GLY	LYS	variant	UNP Q13084

- Molecule 15 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 16 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Z	120	Total	C	N	O	S	0	0
			978	626	183	166	3		

- Molecule 17 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 18 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 19 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	2	46	Total	C	N	O	S	0	0
			376	233	83	59	1		

- Molecule 20 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 21 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 22 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	8	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 23 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 24 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	217	Total	C	N	O	S	0	0
			1762	1124	310	323	5		

- Molecule 25 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	g	132	Total	C	N	O	S	0	0
			1096	709	191	194	2		

- Molecule 26 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 27 is a protein called cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	j	93	Total	C	N	O	S	0	0
			740	460	143	135	2		

- Molecule 28 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	m	45	Total	C	N	O	S	0	0
			372	232	76	62	2		

- Molecule 29 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	o	94	Total	C	N	O	S	0	0
			797	501	165	128	3		

- Molecule 30 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	q	168	Total	C	N	O	S	0	0
			1293	801	254	233	5		

- Molecule 31 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	r	162	Total	C	N	O	S	0	0
			1322	839	252	223	8		

- Molecule 32 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	175	Total	C	N	O	S	0	0
			1330	847	237	244	2		

- Molecule 33 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	179	Total	C	N	O	S	0	0
			1435	925	258	242	10		

- Molecule 34 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	N	222	Total	C	N	O	S	0	0
			1786	1143	326	307	10		

- Molecule 35 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	P	143	Total	C	N	O	S	0	0
			1165	729	223	208	5		

- Molecule 36 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	U	152	Total	C	N	O	S	0	0
			1222	773	233	213	3		

- Molecule 37 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	V	206	Total	C	N	O	S	0	0
			1682	1071	299	304	8		

- Molecule 38 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	E	306	Total	C	N	O	S	0	0
			2410	1547	419	433	11		

- Molecule 39 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5	393	Total	C	N	O	S	0	0
			3205	2070	559	565	11		

- Molecule 40 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 41 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	7	297	Total	C	N	O	S	0	0
			2410	1540	409	443	18		

- Molecule 42 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 43 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	a	108	Total	C	N	O	S	0	0
			896	560	162	169	5		

- Molecule 44 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	c	289	Total	C	N	O	S	0	0
			2322	1483	400	430	9		

- Molecule 45 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	d	257	Total	C	N	O	S	0	0
			2075	1326	363	372	14		

- Molecule 46 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	f	146	Total	C	N	O	S	0	0
			1126	714	186	222	4		

- Molecule 47 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	h	110	Total	C	N	O	S	0	0
			894	568	156	167	3		

- Molecule 48 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	k	96	Total	C	N	O	S	0	0
			743	462	143	133	5		

- Molecule 49 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	l	72	Total	C	N	O	S	0	0
			619	394	112	111	2		

- Molecule 50 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	152	Total	C	N	O	S	0	0
			1227	762	232	229	4		

- Molecule 51 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	393	Total	C	N	O	S	0	0
			3178	2036	565	563	14		

- Molecule 52 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Q	220	Total	C	N	O	S	0	0
			1834	1174	326	325	9		

- Molecule 53 is a protein called 39 S P-site finger.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	u	65	Total	C	N	O	0	0
			325	195	65	65		

- Molecule 54 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	TA	45	Total	C	N	O	0	0
			345	222	54	69		
54	TB	27	Total	C	N	O	0	0
			213	137	33	43		
54	TC	71	Total	C	N	O	0	0
			352	210	71	71		

- Molecule 55 is a protein called Ribosome-recycling factor, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	197	Total	C	N	O	S	0	0
			1525	942	274	301	8		

- Molecule 56 is a protein called Ribosome-releasing factor 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	w	696	Total	C	N	O	S	0	0
			5422	3424	932	1042	24		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	86	LEU	THR	conflict	UNP Q969S9
w	90	VAL	ILE	conflict	UNP Q969S9
w	94	THR	SER	conflict	UNP Q969S9
w	197	ASP	MET	conflict	UNP Q969S9
w	216	ARG	LYS	conflict	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	GLY	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	LYS	deletion	UNP Q969S9
w	?	-	LYS	deletion	UNP Q969S9
w	?	-	HIS	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	GLN	deletion	UNP Q969S9
w	?	-	ASN	deletion	UNP Q969S9
w	?	-	ASN	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9

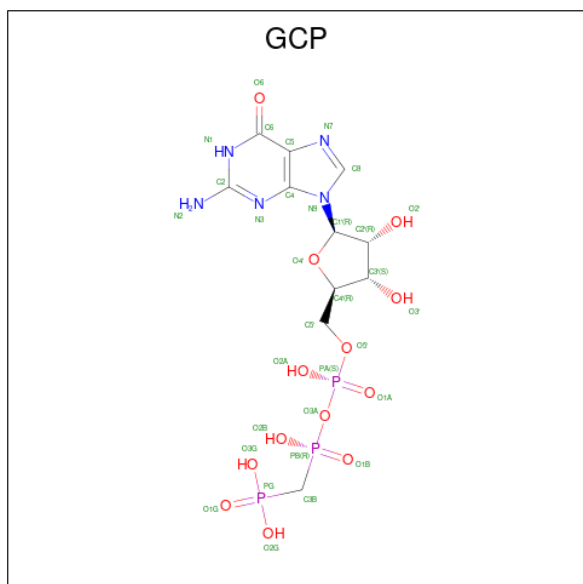
- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	A	97	Total	Mg	0
			97	97	
57	D	1	Total	Mg	0
			1	1	
57	W	1	Total	Mg	0
			1	1	
57	g	1	Total	Mg	0
			1	1	
57	E	1	Total	Mg	0
			1	1	
57	w	1	Total	Mg	0
			1	1	

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	0	1	Total	Zn	0
			1	1	
58	4	1	Total	Zn	0
			1	1	
58	r	1	Total	Zn	0
			1	1	

- Molecule 59 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

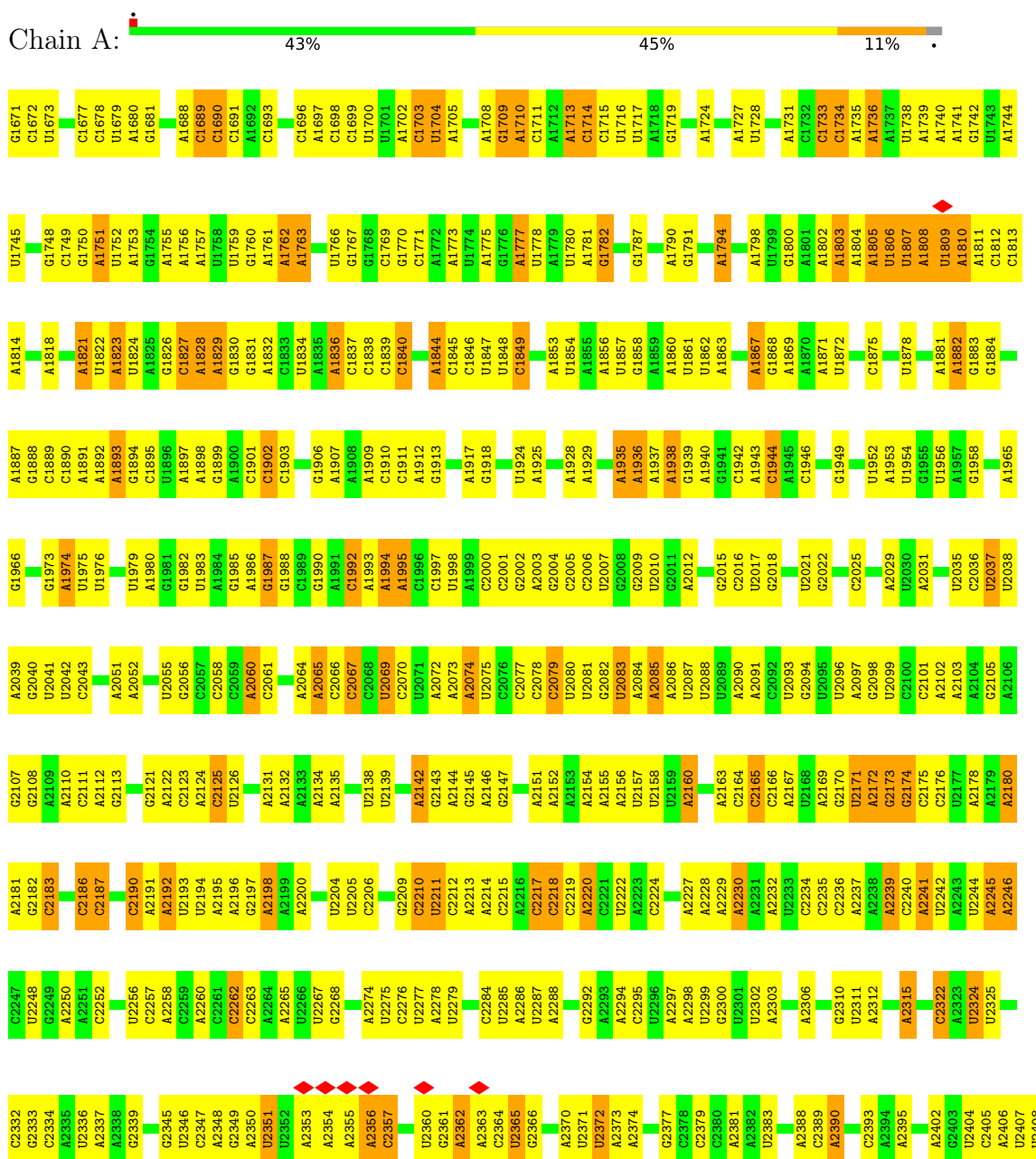


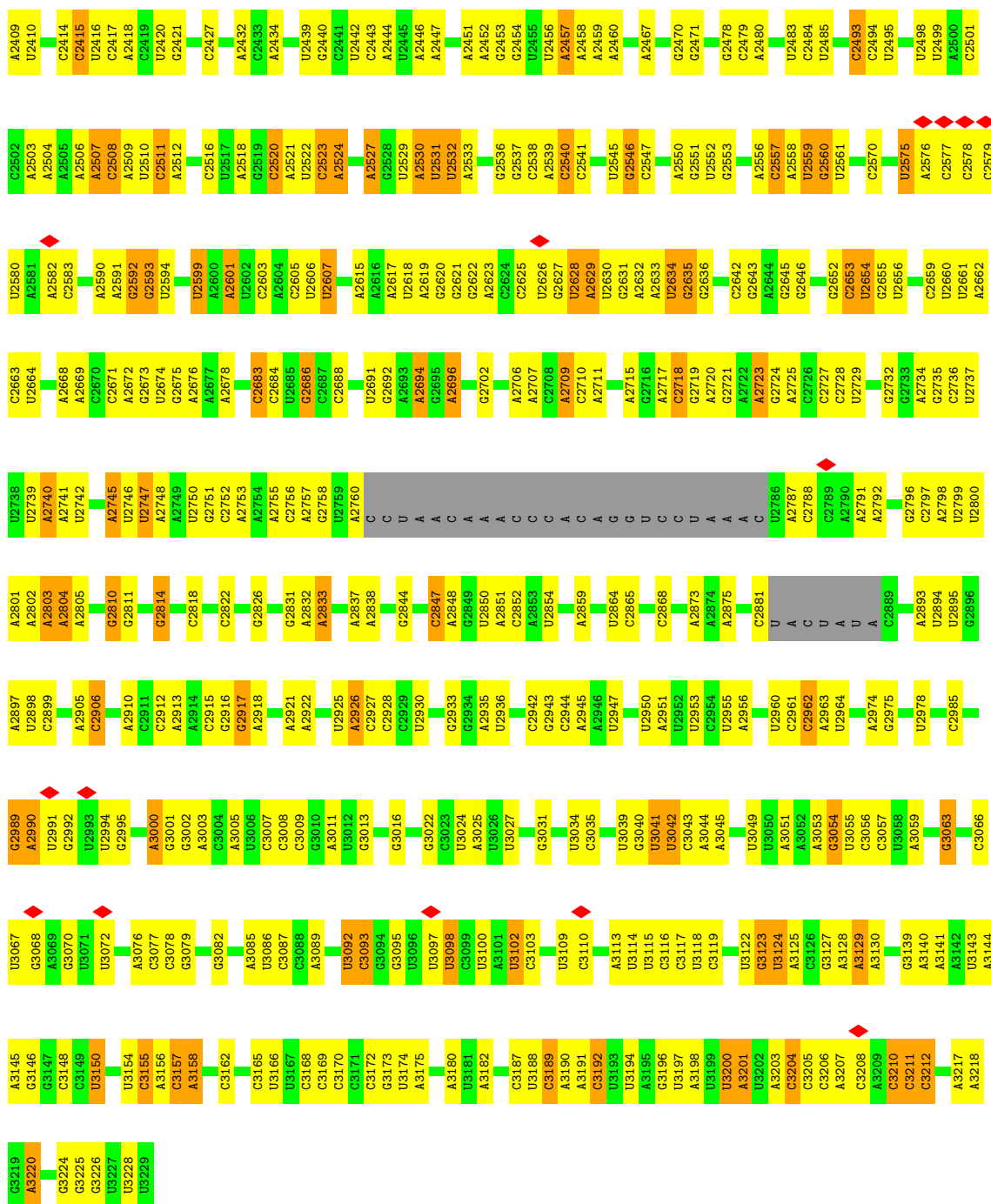
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
59	w	1	32	11	5	13	3	0

3 Residue-property plots

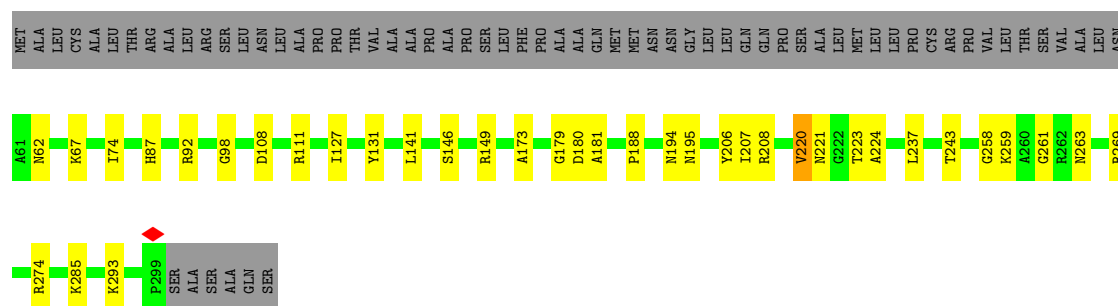
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S rRNA mitochondrial



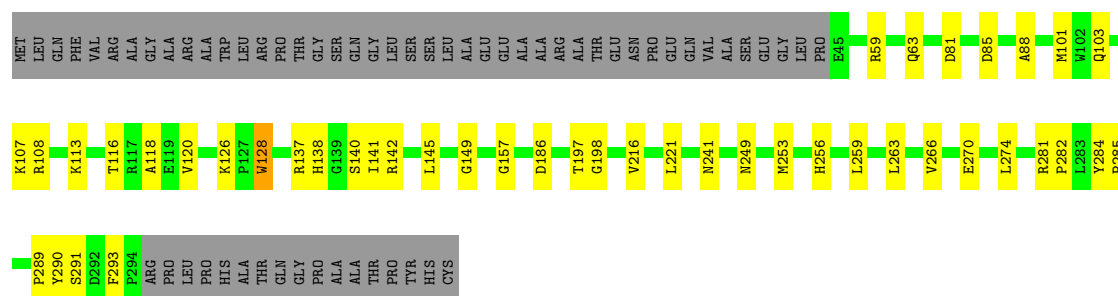


Chain D:  66% 12% 22%



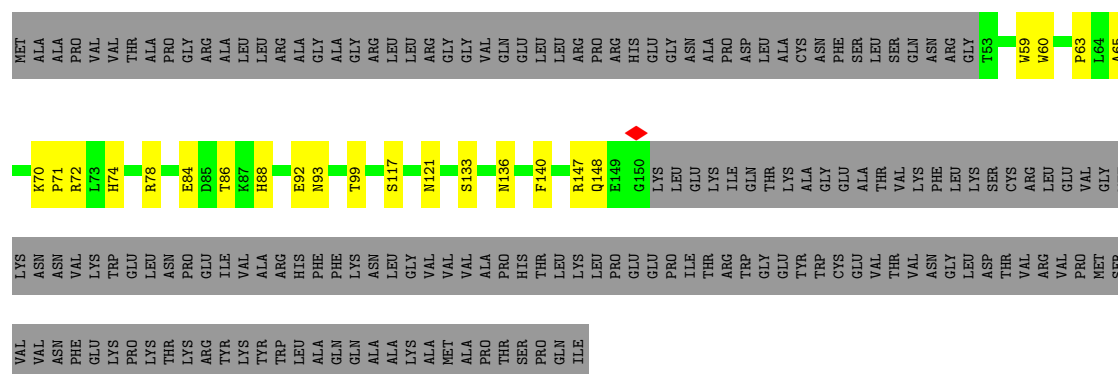
- Molecule 4: 39S ribosomal protein L4, mitochondrial

Chain F:  66% 14% 20%



- Molecule 5: 39S ribosomal protein L9, mitochondrial

Chain H:  28% 8% 63%



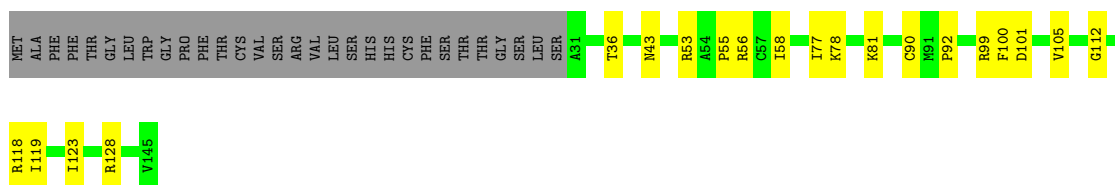
- Molecule 6: 39S ribosomal protein L13, mitochondrial

Chain K:  84% 15% ..



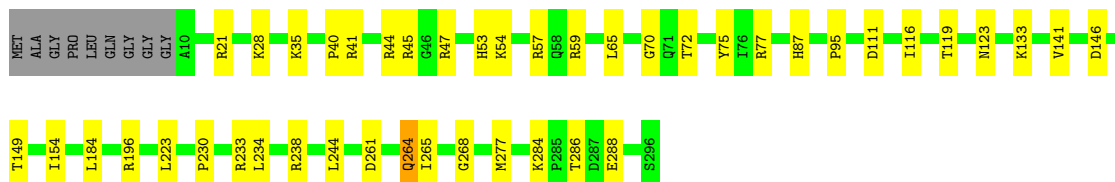
- Molecule 7: 39S ribosomal protein L14, mitochondrial

Chain L:  66% 14% 21%



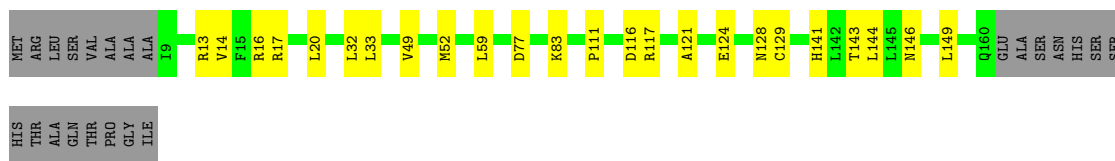
- Molecule 8: 39S ribosomal protein L15, mitochondrial

Chain M: 82% 15% .



- Molecule 9: 39S ribosomal protein L17, mitochondrial

Chain O: 73% 14% 13%



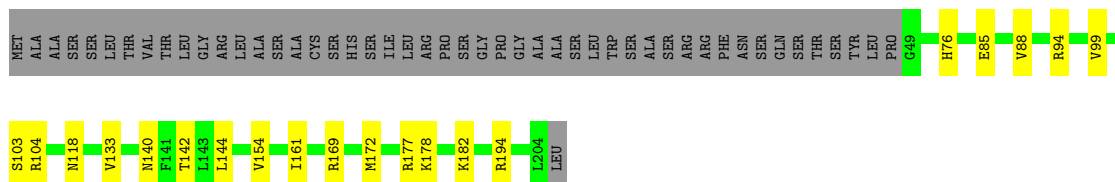
- Molecule 10: 39S ribosomal protein L20, mitochondrial

Chain R: 83% 11% 6%



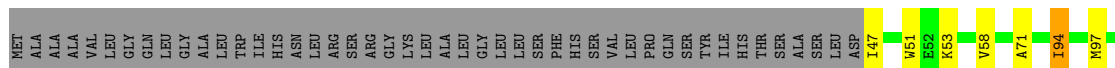
- Molecule 11: 39S ribosomal protein L21, mitochondrial

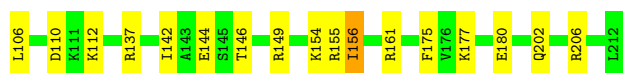
Chain S: 66% 10% 24%



- Molecule 12: 39S ribosomal protein L22, mitochondrial

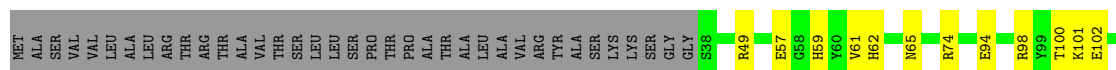
Chain T: 67% 10% 22%





- Molecule 13: 39S ribosomal protein L27, mitochondrial

Chain W: 65% 10% 25%



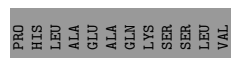
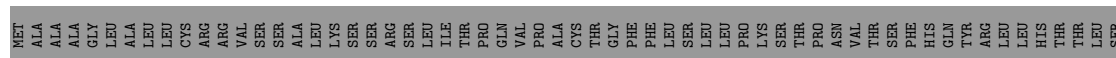
- Molecule 14: 39S ribosomal protein L28, mitochondrial

Chain X: 86% 9% 5%



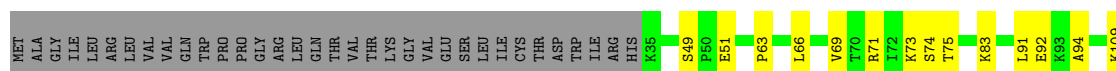
- Molecule 15: 39S ribosomal protein L47, mitochondrial

Chain Y: 58% 12% 30%



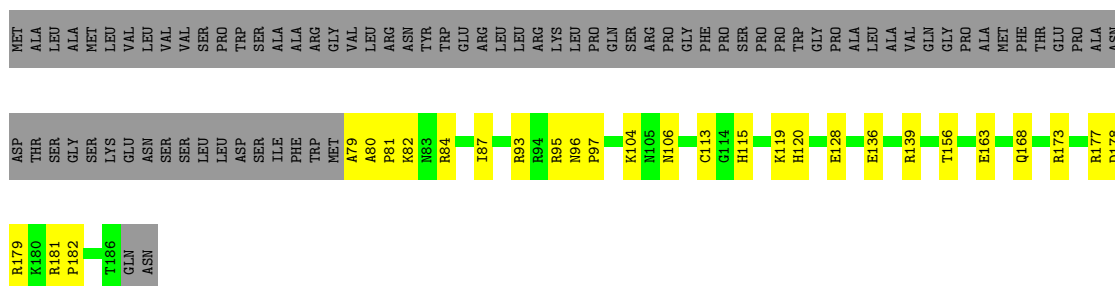
- Molecule 16: 39S ribosomal protein L30, mitochondrial

Chain Z: 62% 12% 25%



- Molecule 17: 39S ribosomal protein L32, mitochondrial

Chain 0: 43% 15% 43%



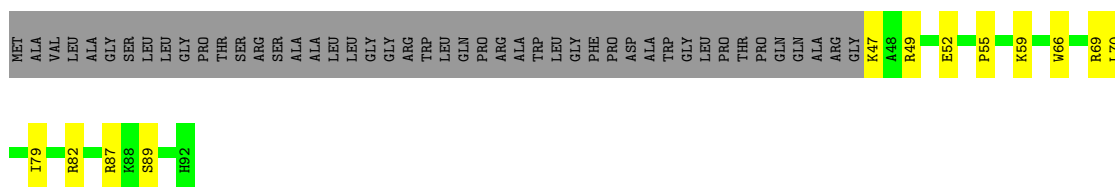
- Molecule 18: 39S ribosomal protein L33, mitochondrial

Chain 1: 66% 14% 20%



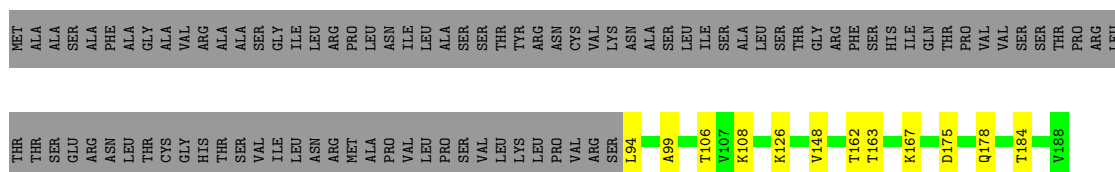
- Molecule 19: 39S ribosomal protein L34, mitochondrial

Chain 2: 37% 13% 50%



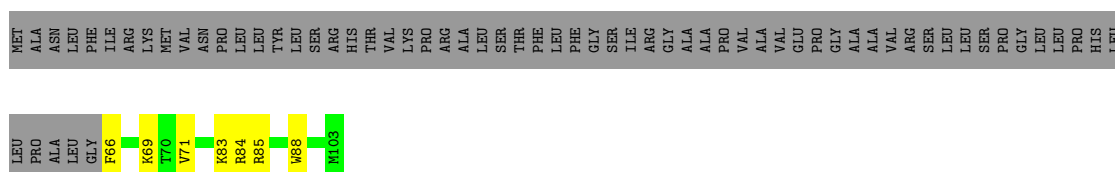
- Molecule 20: 39S ribosomal protein L35, mitochondrial

Chain 3: 44% 6% 49%



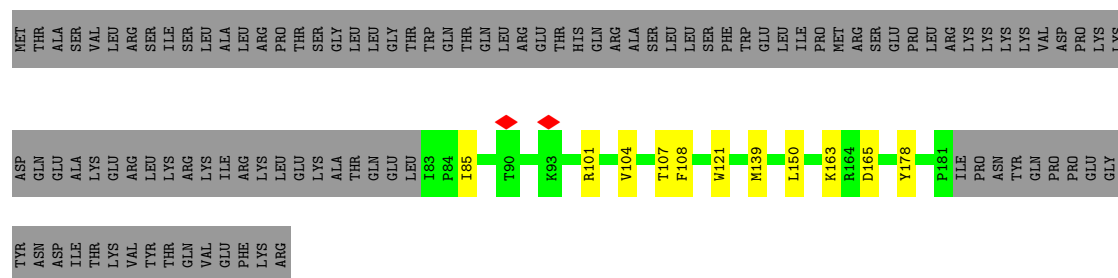
- Molecule 21: 39S ribosomal protein L36, mitochondrial

Chain 4: 30% 7% 63%



- Molecule 22: 39S ribosomal protein L40, mitochondrial

Chain 8: 43% 5% 52%



- Molecule 23: 39S ribosomal protein L43, mitochondrial

Chain b: 75% 21% 5%



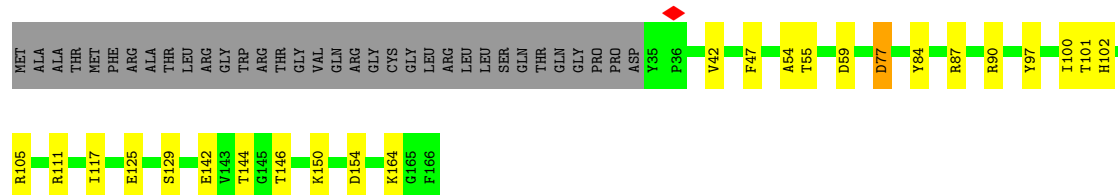
- Molecule 24: 39S ribosomal protein L46, mitochondrial

Chain e: 8% 57% 20% 22%



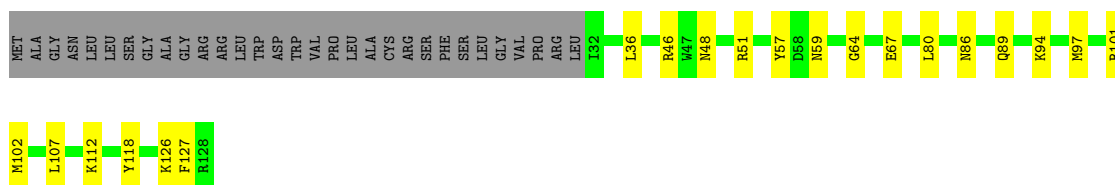
- Molecule 25: 39S ribosomal protein L49, mitochondrial

Chain g: 65% 14% 20%



- Molecule 26: 39S ribosomal protein L51, mitochondrial

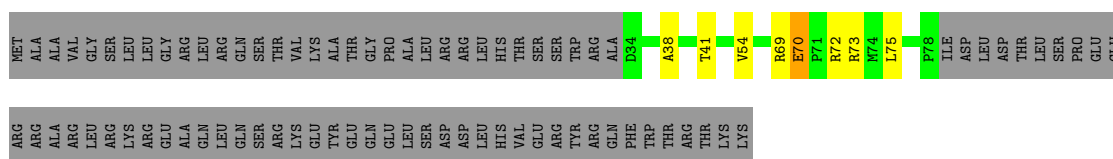
Chain i: 60% 16% 24%



- Molecule 27: cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA



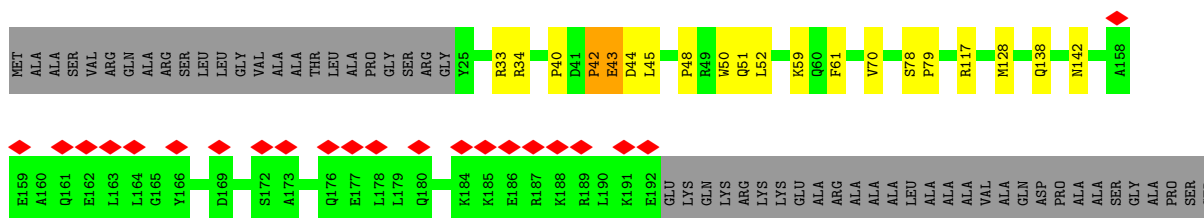
- Molecule 28: 39S ribosomal protein L55, mitochondrial



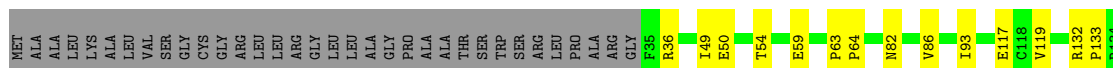
- Molecule 29: Ribosomal protein 63, mitochondrial



- Molecule 30: Growth arrest and DNA damage-inducible proteins-interacting protein 1

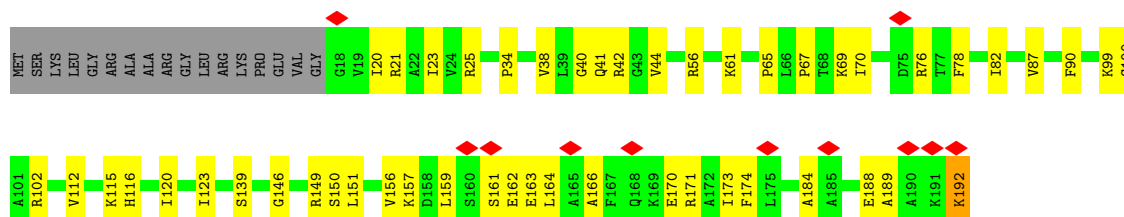


- Molecule 31: 39S ribosomal protein S18a, mitochondrial

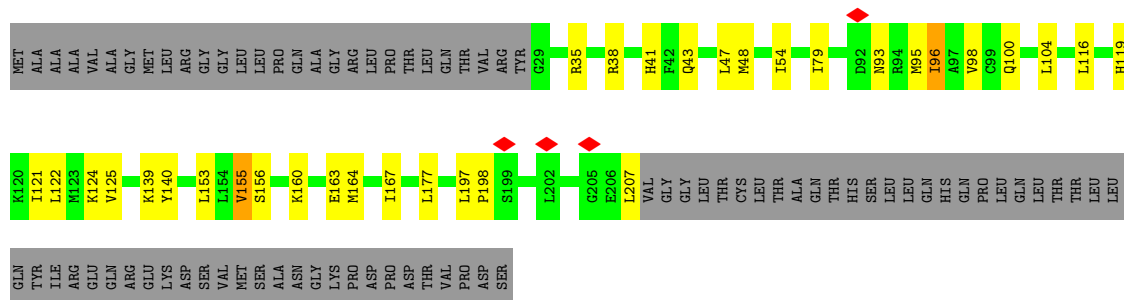




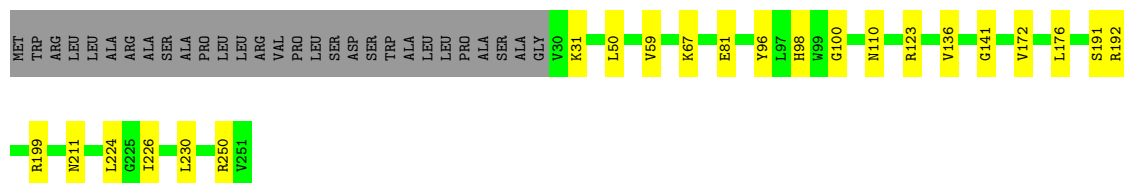
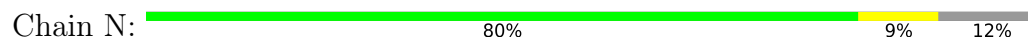
- Molecule 32: 39S ribosomal protein L11, mitochondrial



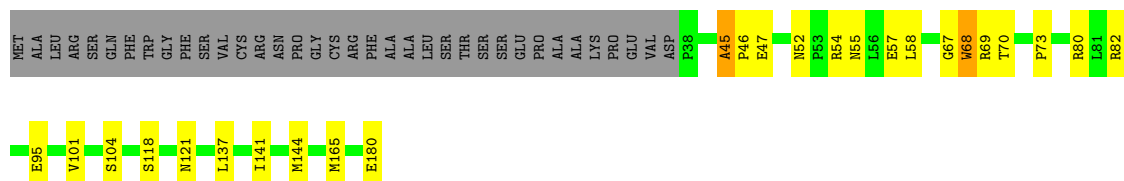
- Molecule 33: 39S ribosomal protein L10, mitochondrial



- Molecule 34: 39S ribosomal protein L16, mitochondrial



- Molecule 35: Mitochondrial ribosomal protein L18, isoform CRA_b



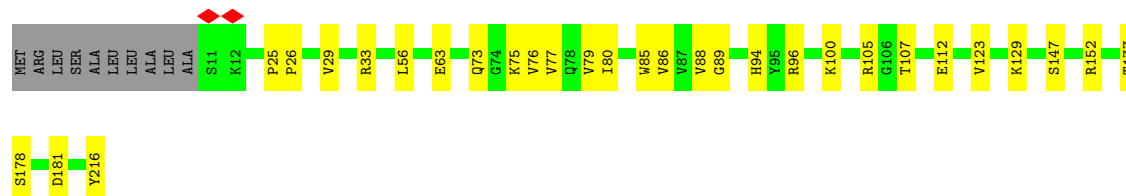
- Molecule 36: 39S ribosomal protein L23, mitochondrial

Chain U:  87% 12%



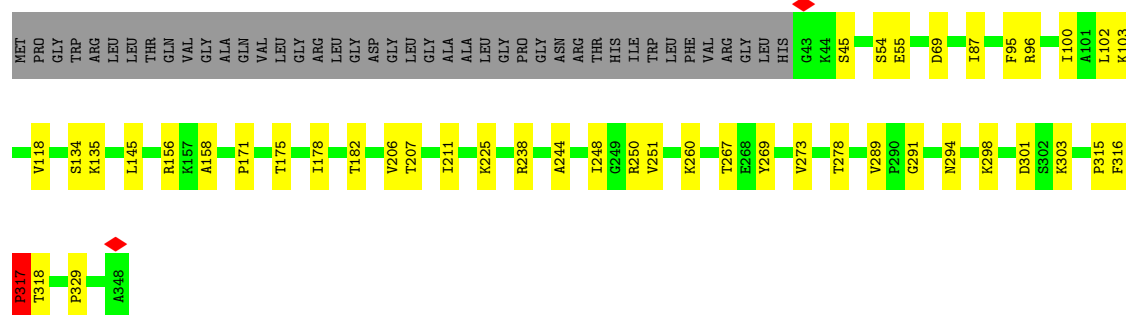
- Molecule 37: 39S ribosomal protein L24, mitochondrial

Chain V:  81% 14% 5%



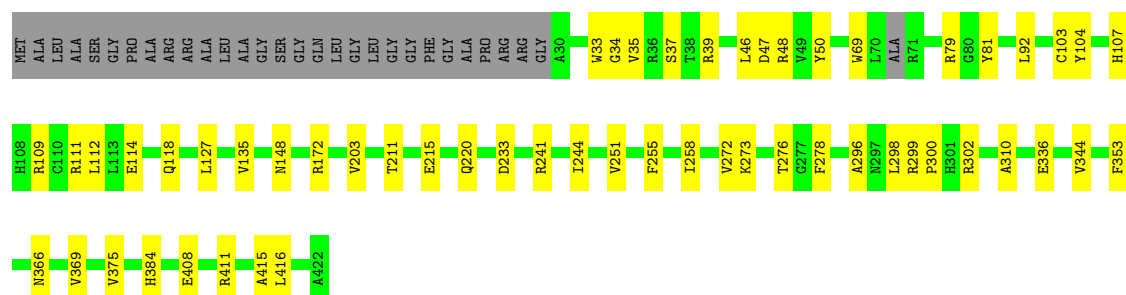
- Molecule 38: 39S ribosomal protein L3, mitochondrial

Chain E:  75% 13% 12%



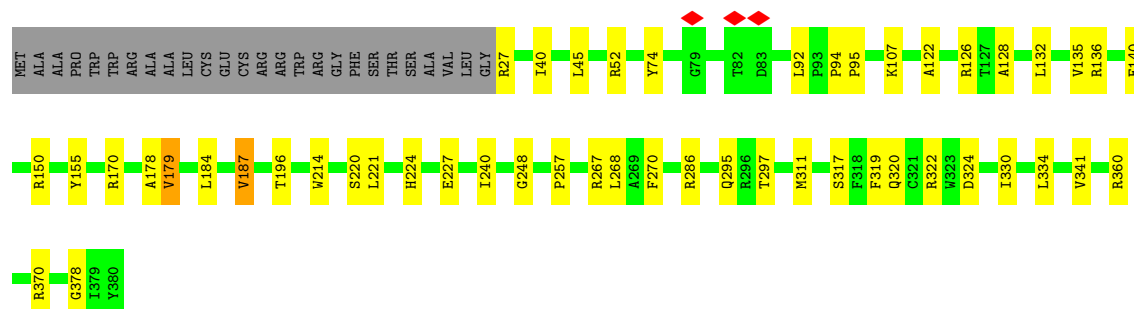
- Molecule 39: 39S ribosomal protein L37, mitochondrial

Chain 5:  80% 13% 7%

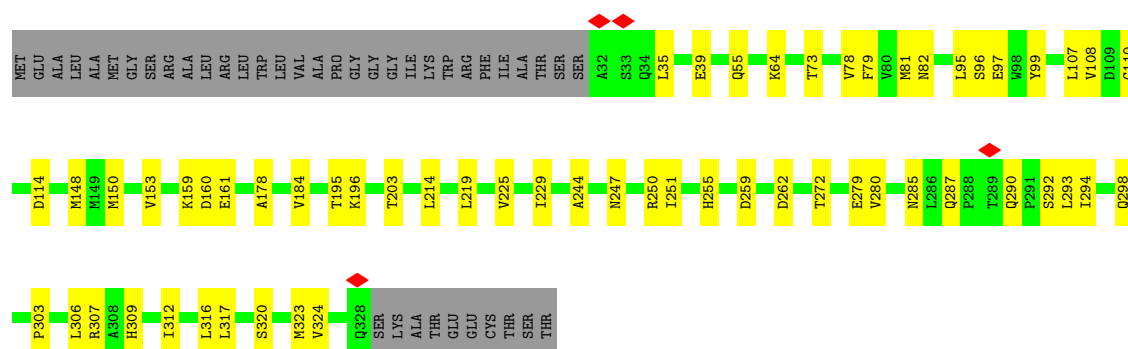


- Molecule 40: 39S ribosomal protein L38, mitochondrial

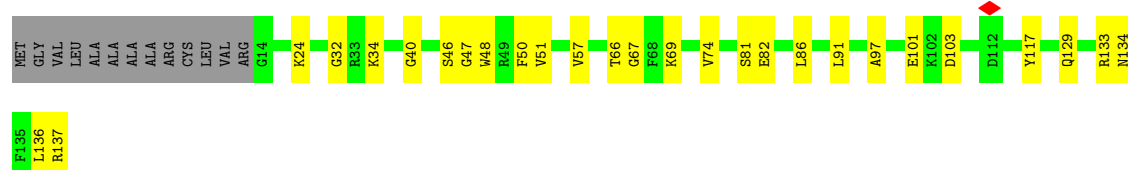
Chain 6:  80% 13% 7%



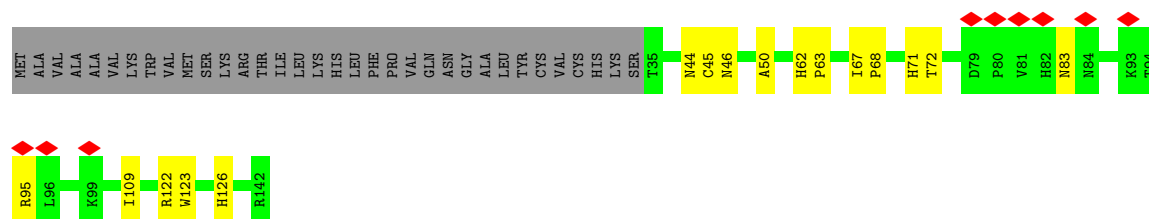
- Molecule 41: 39S ribosomal protein L39, mitochondrial



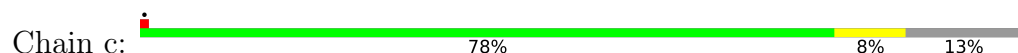
- Molecule 42: 39S ribosomal protein L41, mitochondrial

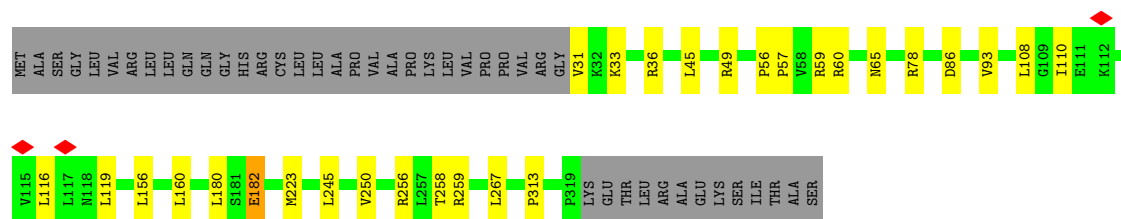


- Molecule 43: 39S ribosomal protein L42, mitochondrial

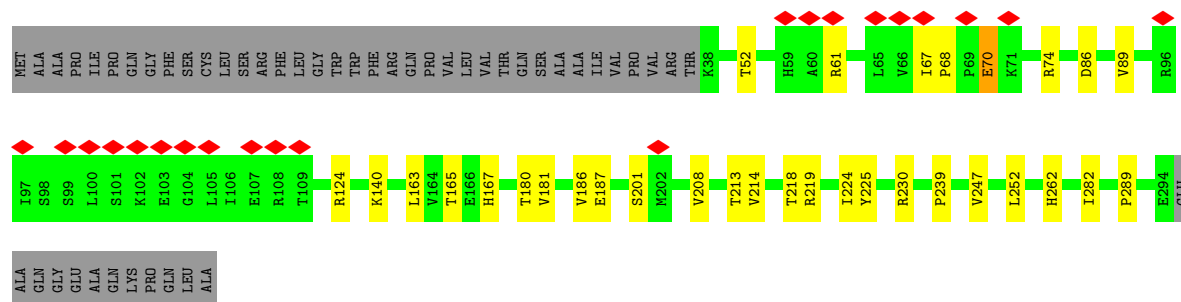
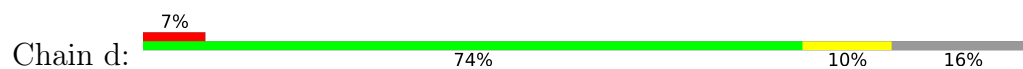


- Molecule 44: 39S ribosomal protein L44, mitochondrial

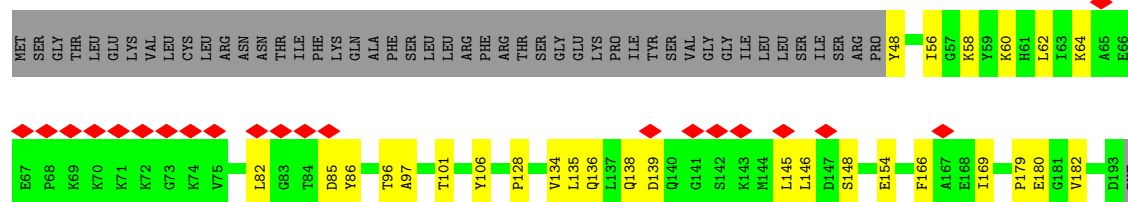




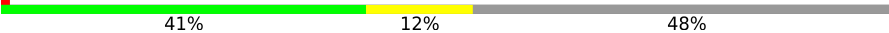
- Molecule 45: 39S ribosomal protein L45, mitochondrial



- Molecule 46: 39S ribosomal protein L48, mitochondrial



- Molecule 49: 39S ribosomal protein L54, mitochondrial

Chain l: 

MET ALA THR LYS ARG LEU PHE GLY THR TRP TRP ALA GLY TRP GLY ALA TRP GLU LEU LEU ASN PRO ALA THR SER GLY ARG LEU LEU ALA ARG ASP TYR ALA LYS LYS VAL MET LYS GLY LYS SER GLY LYS GLY ALA VAL THR SER GLU LEU LYS ASP PRO ASP

VAL CYS THR ASP PRO V66 Q67 L68 T69 T70 W73 G74 V75 N76 Y78 K79 E80 Y92 F97 L101 G102 S114 R115 E116 I126 H129 S133 R137 LEU

- Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p: 

MET ALA THR ARG CYS LEU ARG TRP GLY LEU SER ARG ALA GLY VAL TRP LEU LEU PRO PRO PRO ALA CYS ARG ALA LEU HIS LYS GLN LYS ASP GLY THR E98 Y49 P62 N63 G64 A65 K66 Q67 A68 D71 T78 I79 C82 R83 S84 S85 G86 PRO

GLY GLY GLN ASN VAL ASN K94 V95 K98 V101 H104 T107 L133 E138 L147 R155 D156 M157 E167 P168 T169 K170 E171 D172 R177 E181 N182 R185 Q190 K191 H194 S195 A196 VAL LYS THR SER ARG ARG VAL ASP MET ASP

- Molecule 51: 39S ribosomal protein S30, mitochondrial

Chain s: 

MET ALA ALA ALA ARG CYS TRP ARG PRO LEU LEU ARG GLY PRO ARG LEU SER THR HIS THR ALA ASN ALA ALA THR ALA THR THR GLU THR THR CYS GLN ASP VAL ALA THR P40 W66 T89 R81 T84 K85 Y91 Y94 D103 T112 A123 E124

P125 E126 P127 E128 N129 E130 P131 E132 P133 D138 Y156 R162 V163 H164 V171 D178 V181 L188 N192 R203 H207 L229 D234 N238 N239 C266 K267 K270 F274 N280 F299 L302 R310 L332 A349 D350 V356

A359 L374 N375 T376 L377 N391 E403 T404 I405 E406 D407 V410 K411 D416 V422 L426 E432 LYS SER GLN LEU LEU LEU ASN

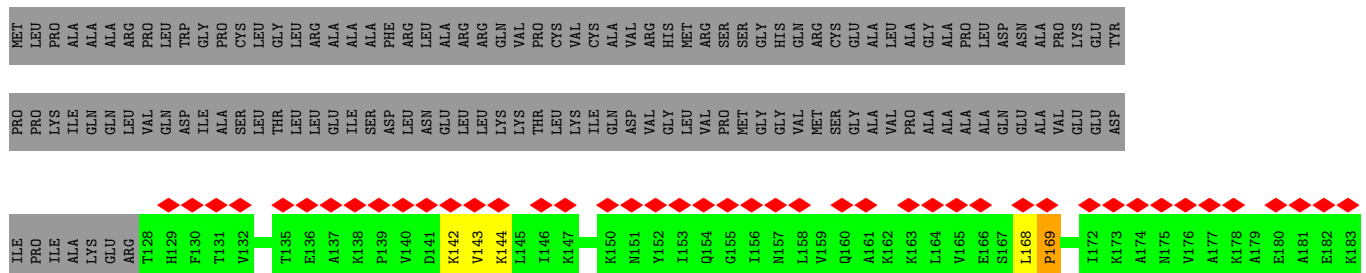
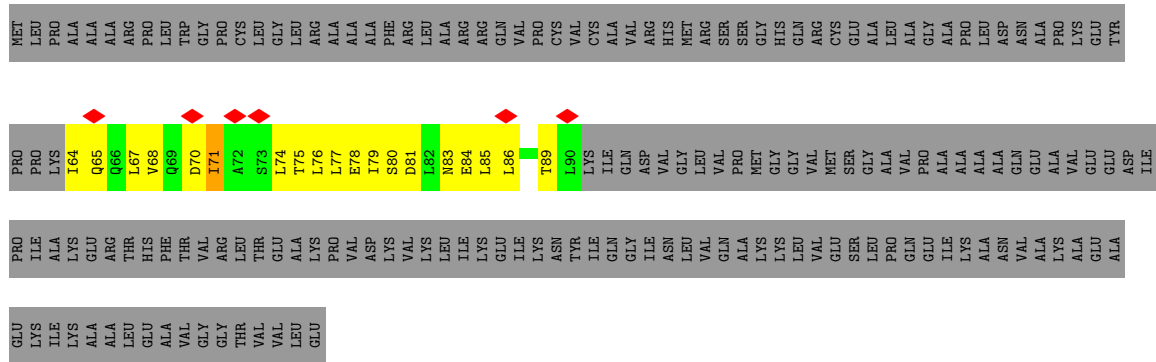
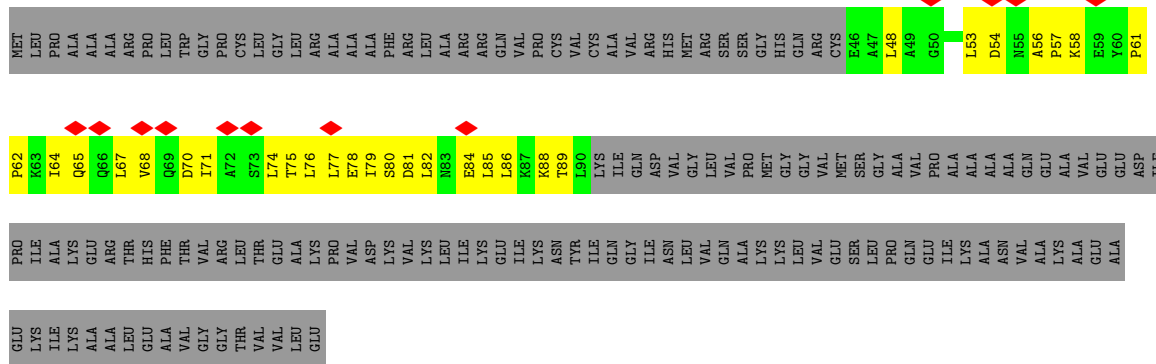
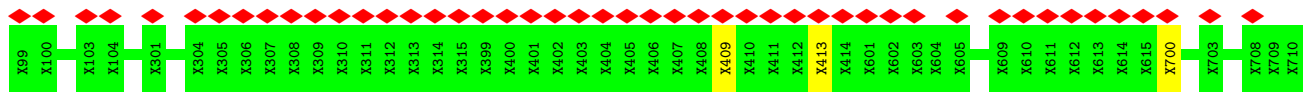
- Molecule 52: 39S ribosomal protein L19, mitochondrial

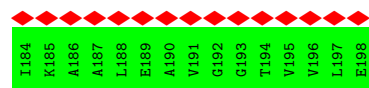
Chain Q: 

MET ALA ALA CYS ILE ALA GLY HIS TRP ALA MET GLY LEU LEU ARG SER PHE GLN ALA ARG LEU LEU PRO PRO PRO ALA ALA SER THR GLY PRO SER GLU PRO GLY PHE GLN PRO PRO PRO LYS PRO

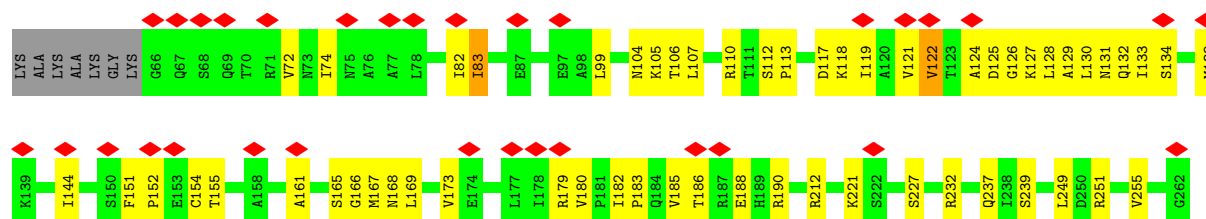
VAL ILE VAL ASP LYS HIS ARG PRO VAL GLU GLU R73 L76 R84 Q85 D88 F92 R96 L100 I108 L117 T120 Y125 Q132 L151 R152 Q158 E161 L166 S186 K205 K221 P228 K231 R244 L247

D268 K269 M270 E279 I282 K283 E285 I286 S292

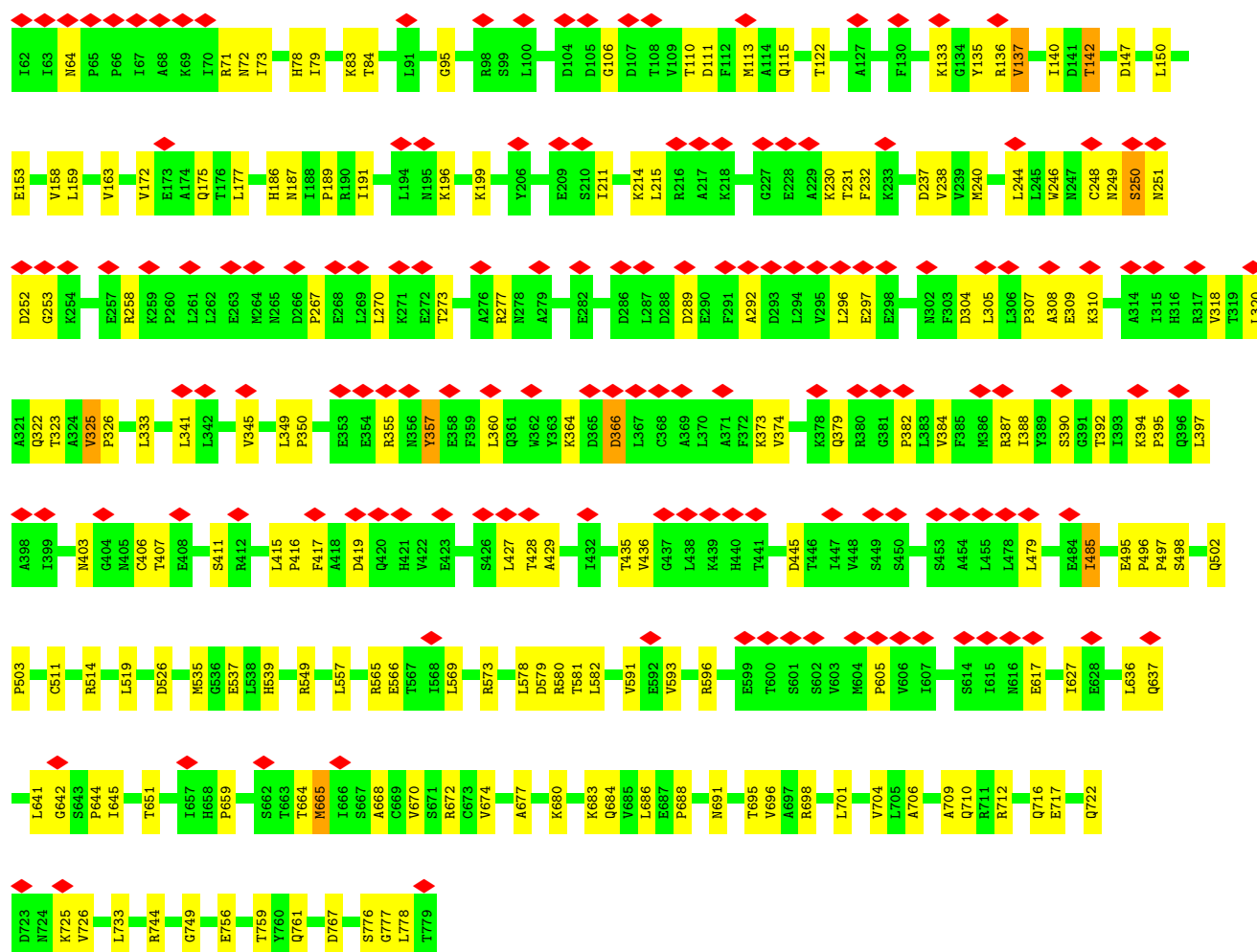
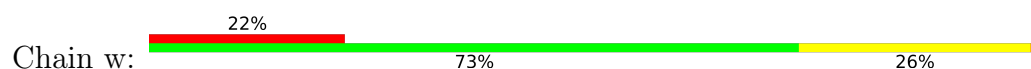




• Molecule 55: Ribosome-recycling factor, mitochondrial



• Molecule 56: Ribosome-releasing factor 2, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	132008	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	71	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-16 (4k x 4k)	Depositor
Maximum map value	3.217	Depositor
Minimum map value	-1.964	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.126	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	429.30002, 429.30002, 429.30002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07325, 1.07325, 1.07325	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, GCP, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.11	0/36245	0.27	0/56418
2	B	0.23	0/1328	0.41	0/2056
3	D	0.34	0/1904	0.59	0/2561
4	F	0.43	0/2071	0.69	3/2817 (0.1%)
5	H	0.34	0/820	0.69	0/1102
6	K	0.45	0/1495	0.63	0/2029
7	L	0.38	0/904	0.59	2/1218 (0.2%)
8	M	0.41	0/2359	0.70	0/3185
9	O	0.41	0/1269	0.66	0/1708
10	R	0.43	0/1174	0.67	0/1572
11	S	0.42	0/1276	0.62	0/1729
12	T	0.40	0/1402	0.59	1/1886 (0.1%)
13	W	0.42	0/893	0.62	0/1204
14	X	0.33	0/2081	0.64	2/2812 (0.1%)
15	Y	0.38	0/1552	0.57	0/2079
16	Z	0.41	0/1003	0.61	0/1354
17	0	0.38	0/895	0.69	0/1201
18	1	0.33	0/438	0.58	0/583
19	2	0.45	0/382	0.60	0/507
20	3	0.44	0/852	0.57	0/1136
21	4	0.44	0/350	0.60	0/461
22	8	0.26	0/855	0.56	0/1152
23	b	0.39	0/1202	0.60	0/1626
24	e	0.30	0/1797	0.67	0/2422
25	g	0.41	0/1132	0.63	2/1543 (0.1%)
26	i	0.42	0/849	0.69	2/1135 (0.2%)
27	j	0.36	0/755	0.57	0/1016
28	m	0.25	0/379	0.57	0/510
29	o	0.39	0/818	0.70	0/1097
30	q	0.29	0/1323	0.62	0/1794
31	r	0.41	0/1362	0.62	0/1846
32	J	0.40	2/1348 (0.1%)	0.63	0/1813

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.32	0/1467	0.69	0/1984
34	N	0.39	1/1833 (0.1%)	0.54	0/2468
35	P	0.34	0/1191	0.69	2/1611 (0.1%)
36	U	0.36	0/1252	0.54	0/1697
37	V	0.31	0/1727	0.57	0/2341
38	E	0.38	0/2479	0.59	2/3360 (0.1%)
39	5	0.33	0/3300	0.57	0/4495
40	6	0.32	0/3043	0.58	2/4140 (0.0%)
41	7	0.31	0/2467	0.56	2/3337 (0.1%)
42	9	0.33	0/1025	0.58	0/1379
43	a	0.34	0/923	0.57	0/1254
44	c	0.33	0/2371	0.57	0/3205
45	d	0.30	0/2132	0.63	0/2887
46	f	0.28	0/1144	0.62	0/1551
47	h	0.30	0/917	0.59	0/1249
48	k	0.29	0/754	0.65	1/1017 (0.1%)
49	l	0.27	0/636	0.50	0/860
50	p	0.30	0/1246	0.60	0/1675
51	s	0.39	1/3262 (0.0%)	0.58	1/4435 (0.0%)
52	Q	0.35	0/1875	0.53	0/2523
54	TA	0.22	0/349	0.62	0/475
54	TB	0.26	0/212	0.57	0/286
54	TC	0.08	0/351	0.18	0/488
55	z	0.17	0/1534	0.41	0/2063
56	w	0.16	0/5511	0.43	0/7479
All	All	0.29	4/115514 (0.0%)	0.50	22/163831 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	D	0	1
5	H	0	1
6	K	0	1
8	M	0	2
10	R	0	1
12	T	0	1
16	Z	0	1
17	0	0	1
26	i	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
27	j	0	1
28	m	0	1
30	q	0	1
35	P	0	2
38	E	0	1
41	7	0	1
45	d	0	1
47	h	0	3
50	p	0	2
51	s	0	2
56	w	0	1
All	All	0	26

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	J	188	GLU	C-N	8.19	1.45	1.34
34	N	230	LEU	C-N	-7.97	1.19	1.33
51	s	164	HIS	CE1-NE2	7.26	1.39	1.32
32	J	184	ALA	C-N	-6.68	1.25	1.33

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	112	GLY	CA-C-N	5.83	132.20	121.70
7	L	112	GLY	C-N-CA	5.83	132.20	121.70
4	F	221	LEU	CA-C-N	5.83	132.67	121.54
4	F	221	LEU	C-N-CA	5.83	132.67	121.54
14	X	126	THR	CA-C-N	5.72	128.30	120.35
14	X	126	THR	C-N-CA	5.72	128.30	120.35
12	T	161	ARG	N-CA-C	-5.67	100.40	108.23
4	F	128	TRP	CA-CB-CG	5.43	123.93	113.60
35	P	67	GLY	CA-C-N	5.28	131.63	121.54
35	P	67	GLY	C-N-CA	5.28	131.63	121.54
40	6	257	PRO	CA-C-N	-5.21	117.70	122.28
40	6	257	PRO	C-N-CA	-5.21	117.70	122.28
48	k	11	ARG	N-CA-C	5.15	121.19	109.81
41	7	108	VAL	CA-C-N	5.10	131.28	121.54
41	7	108	VAL	C-N-CA	5.10	131.28	121.54
26	i	64	GLY	CA-C-N	5.10	129.65	122.46
26	i	64	GLY	C-N-CA	5.10	129.65	122.46
51	s	164	HIS	CB-CG-CD2	-5.09	124.58	131.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	E	317	PRO	CA-C-N	5.03	131.15	121.54
38	E	317	PRO	C-N-CA	5.03	131.15	121.54
25	g	54	ALA	CA-C-N	5.00	131.09	121.54
25	g	54	ALA	C-N-CA	5.00	131.09	121.54

There are no chirality outliers.

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	0	177	ARG	Peptide
41	7	287	GLN	Peptide
3	D	206	TYR	Peptide
38	E	316	PHE	Peptide
5	H	86	THR	Peptide
6	K	3	SER	Peptide
8	M	264	GLN	Peptide
8	M	286	THR	Peptide
35	P	45	ALA	Peptide
35	P	68	TRP	Peptide
10	R	137	GLU	Peptide
12	T	94	ILE	Peptide
16	Z	141	SER	Peptide
45	d	70	GLU	Peptide
47	h	132	VAL	Peptide
47	h	52	CYS	Peptide
47	h	82	LEU	Peptide
26	i	57	TYR	Peptide
27	j	110	LYS	Peptide
28	m	70	GLU	Peptide
50	p	82	CYS	Peptide
50	p	83	ARG	Peptide
30	q	78	SER	Peptide
51	s	156	TYR	Peptide
51	s	349	ALA	Peptide
56	w	142	THR	Mainchain

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	A	32395	0	16443	1157	0
2	B	1191	0	607	6	0
3	D	1866	0	1927	44	0
4	F	2013	0	2044	30	0
5	H	806	0	849	24	0
6	K	1451	0	1448	29	0
7	L	889	0	941	19	0
8	M	2305	0	2378	43	0
9	O	1245	0	1283	22	0
10	R	1153	0	1214	19	0
11	S	1251	0	1322	20	0
12	T	1368	0	1410	26	0
13	W	871	0	898	22	0
14	X	2027	0	2040	17	0
15	Y	1517	0	1561	34	0
16	Z	978	0	1030	12	0
17	0	880	0	902	37	0
18	1	433	0	475	7	0
19	2	376	0	406	20	0
20	3	831	0	883	10	0
21	4	342	0	361	10	0
22	8	836	0	844	10	0
23	b	1178	0	1180	23	0
24	e	1762	0	1767	35	0
25	g	1096	0	1081	23	0
26	i	827	0	857	32	0
27	j	740	0	741	10	0
28	m	372	0	387	7	0
29	o	797	0	804	31	0
30	q	1293	0	1176	18	0
31	r	1322	0	1349	45	0
32	J	1330	0	1405	80	0
33	I	1435	0	1519	47	0
34	N	1786	0	1817	31	0
35	P	1165	0	1162	18	0
36	U	1222	0	1187	15	0
37	V	1682	0	1692	18	0
38	E	2410	0	2418	60	0
39	5	3205	0	3201	50	0
40	6	2948	0	2841	38	0
41	7	2410	0	2415	33	0
42	9	997	0	987	29	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	a	896	0	847	14	0
44	c	2322	0	2338	30	0
45	d	2075	0	2037	21	0
46	f	1126	0	1106	23	0
47	h	894	0	881	7	0
48	k	743	0	758	28	0
49	l	619	0	611	21	0
50	p	1227	0	1239	20	0
51	s	3178	0	3124	46	0
52	Q	1834	0	1872	27	0
53	u	325	0	75	2	0
54	TA	345	0	363	173	0
54	TB	213	0	234	134	0
54	TC	352	0	169	7	0
55	z	1525	0	1599	213	0
56	w	5422	0	5495	262	0
57	A	97	0	0	0	0
57	D	1	0	0	0	0
57	E	1	0	0	0	0
57	W	1	0	0	0	0
57	g	1	0	0	0	0
57	w	1	0	0	0	0
58	0	1	0	0	0	0
58	4	1	0	0	0	0
58	r	1	0	0	0	0
59	w	32	0	14	13	0
All	All	110234	0	94014	2232	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 11.

All (2232) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2172:A:H2'	32:J:23:ILE:CD1	1.26	1.62
54:TA:68:VAL:CG2	54:TB:85:LEU:HD23	1.21	1.57
55:z:138:MET:HE1	56:w:636:LEU:CD2	1.08	1.55
48:k:57:HIS:CB	54:TA:53:LEU:HD13	1.37	1.55
48:k:57:HIS:HB3	54:TA:53:LEU:CD1	1.42	1.48
1:A:2579:C:N4	55:z:119:ILE:CD1	1.74	1.47
1:A:3157:C:N4	9:O:14:VAL:HG21	1.20	1.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2493:C:N4	1:A:2540:C:C1'	1.76	1.46
1:A:2961:C:C4	1:A:2962:C:C4	2.04	1.45
54:TA:82:LEU:HA	54:TB:67:LEU:CD1	0.99	1.44
55:z:138:MET:CE	56:w:636:LEU:CD2	1.92	1.44
1:A:3203:A:C1'	38:E:303:LYS:HZ2	1.25	1.43
54:TA:82:LEU:CA	54:TB:67:LEU:CD1	1.94	1.42
1:A:3203:A:C1'	38:E:303:LYS:NZ	1.75	1.42
1:A:2178:A:N6	56:w:716:GLN:HA	1.33	1.41
54:TA:81:ASP:C	54:TB:64:ILE:HD12	1.45	1.40
55:z:251:ARG:NH2	56:w:778:LEU:HD13	1.37	1.39
1:A:2175:C:O2'	32:J:102:ARG:CG	1.69	1.39
54:TA:81:ASP:HA	54:TB:64:ILE:CD1	1.53	1.39
1:A:1834:U:C4	12:T:206:ARG:HA	1.58	1.37
1:A:2172:A:C2'	32:J:23:ILE:HD13	1.51	1.37
55:z:186:THR:CG2	56:w:495:GLU:O	1.71	1.36
54:TA:81:ASP:O	54:TB:64:ILE:HD12	1.20	1.35
55:z:134:SER:CA	56:w:664:THR:HG21	1.56	1.35
1:A:2578:C:N4	55:z:129:ALA:HA	1.42	1.35
1:A:2579:C:N4	55:z:119:ILE:CG1	1.89	1.34
54:TA:68:VAL:CB	54:TB:85:LEU:HD23	1.59	1.33
55:z:186:THR:CG2	56:w:495:GLU:C	1.89	1.33
1:A:1731:A:N6	26:i:118:TYR:CD1	1.95	1.33
33:I:139:LYS:O	54:TA:48:LEU:HG	1.28	1.33
55:z:105:LYS:HG3	56:w:637:GLN:OE1	1.15	1.31
1:A:2175:C:HO2'	32:J:102:ARG:CG	1.37	1.30
1:A:2582:A:N1	56:w:581:THR:O	1.61	1.30
1:A:2493:C:N4	1:A:2540:C:H1'	1.36	1.30
1:A:2178:A:N3	56:w:717:GLU:HG3	1.46	1.29
1:A:2577:C:C6	55:z:132:GLN:HG3	1.67	1.29
1:A:2178:A:C2	56:w:717:GLU:HA	1.67	1.29
54:TA:82:LEU:HD23	54:TB:67:LEU:CD2	1.60	1.29
54:TA:82:LEU:CD2	54:TB:67:LEU:HD22	1.59	1.29
55:z:132:GLN:HG2	56:w:668:ALA:CB	1.62	1.29
1:A:2578:C:N3	55:z:119:ILE:HA	1.44	1.28
1:A:2579:C:H42	55:z:119:ILE:CG1	1.45	1.28
54:TA:68:VAL:CB	54:TB:85:LEU:CD2	2.11	1.28
54:TA:68:VAL:HG21	54:TB:85:LEU:CD2	1.59	1.28
55:z:186:THR:HG22	56:w:496:PRO:C	1.58	1.28
55:z:186:THR:HG21	56:w:495:GLU:C	1.36	1.28
1:A:2577:C:C5	55:z:131:ASN:N	2.01	1.28
1:A:3089:A:N6	55:z:232:ARG:CZ	1.71	1.27

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:139:LYS:O	54:TA:48:LEU:CG	1.81	1.27
1:A:2578:C:O2	55:z:119:ILE:HB	1.23	1.27
55:z:190:ARG:NH2	56:w:495:GLU:OE2	1.63	1.26
55:z:251:ARG:HH22	56:w:778:LEU:CD1	1.48	1.25
55:z:186:THR:HG22	56:w:496:PRO:O	1.32	1.25
1:A:2576:A:O2'	56:w:578:LEU:CD2	1.86	1.24
54:TA:68:VAL:CG2	54:TB:85:LEU:CD2	2.16	1.23
1:A:2173:G:N2	32:J:150:SER:O	1.71	1.23
1:A:2178:A:N6	56:w:716:GLN:CA	2.00	1.22
1:A:2577:C:N1	55:z:132:GLN:HG3	1.53	1.22
6:K:155:LEU:O	6:K:158:TYR:CD2	1.85	1.22
1:A:2065:A:C8	13:W:74:ARG:HA	1.74	1.22
55:z:251:ARG:NH2	56:w:777:GLY:O	1.71	1.21
1:A:2175:C:O2'	32:J:102:ARG:HG3	1.04	1.21
54:TC:143:VAL:CB	56:w:292:ALA:HA	1.69	1.21
1:A:3110:C:N4	1:A:3203:A:H61	1.38	1.20
54:TA:85:LEU:CD1	54:TB:67:LEU:HB2	1.70	1.20
1:A:3157:C:N4	9:O:14:VAL:CG2	2.02	1.20
1:A:2493:C:C4	1:A:2540:C:C6	2.28	1.20
1:A:1939:G:N2	1:A:2495:U:C1'	2.05	1.19
54:TA:81:ASP:CA	54:TB:64:ILE:HD12	1.70	1.19
1:A:2178:A:C6	56:w:716:GLN:C	2.21	1.19
1:A:1939:G:N2	1:A:2495:U:H1'	1.58	1.18
33:I:207:LEU:HD13	54:TB:86:LEU:CD1	1.72	1.18
54:TA:68:VAL:HG11	54:TB:85:LEU:CD2	1.70	1.18
1:A:2578:C:N4	55:z:129:ALA:CA	2.05	1.18
1:A:3203:A:H1'	38:E:303:LYS:NZ	0.86	1.18
54:TA:85:LEU:HB2	54:TB:65:GLN:CA	1.74	1.18
1:A:2172:A:H2'	32:J:23:ILE:HD11	1.20	1.18
1:A:3110:C:H42	1:A:3203:A:N6	1.38	1.18
54:TA:68:VAL:HG11	54:TB:85:LEU:CG	1.73	1.18
1:A:3157:C:H41	9:O:14:VAL:CG2	1.57	1.17
34:N:136:VAL:HG11	55:z:72:VAL:CB	1.73	1.17
1:A:1809:U:O2	12:T:53:LYS:NZ	1.76	1.17
1:A:2961:C:C5	1:A:2962:C:N4	2.12	1.17
54:TA:85:LEU:HA	54:TA:88:LYS:HE3	1.27	1.16
54:TA:81:ASP:CA	54:TB:64:ILE:CD1	2.20	1.15
34:N:136:VAL:CG2	55:z:72:VAL:HG11	1.76	1.15
48:k:57:HIS:ND1	54:TA:53:LEU:HD22	1.59	1.15
55:z:138:MET:CE	56:w:636:LEU:HD23	1.64	1.15
1:A:2579:C:N4	55:z:119:ILE:HD11	1.42	1.14

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:TA:68:VAL:CG1	54:TB:85:LEU:CD2	2.25	1.14
1:A:2178:A:N1	56:w:716:GLN:O	1.80	1.14
1:A:2577:C:H42	55:z:129:ALA:C	1.54	1.14
1:A:2578:C:N4	55:z:128:LEU:O	1.81	1.14
1:A:1699:C:C6	15:Y:197:LYS:HG3	1.83	1.14
1:A:2493:C:C4	1:A:2540:C:N1	2.16	1.14
1:A:2577:C:N4	55:z:129:ALA:C	2.06	1.13
1:A:2818:C:O2	55:z:227:SER:OG	1.65	1.13
1:A:2961:C:C4	1:A:2962:C:N3	2.15	1.13
1:A:2961:C:N4	1:A:2962:C:N3	1.95	1.13
54:TA:88:LYS:NZ	54:TB:65:GLN:HB3	1.62	1.12
34:N:136:VAL:CG1	55:z:72:VAL:HB	1.78	1.12
55:z:105:LYS:CG	56:w:637:GLN:OE1	1.96	1.12
54:TA:82:LEU:CD2	54:TB:67:LEU:CD2	2.22	1.12
1:A:1939:G:C2	1:A:2495:U:H1'	1.83	1.12
1:A:2155:A:C2	29:o:26:PHE:CE1	2.38	1.12
1:A:2060:A:C5	1:A:2079:C:N3	2.18	1.11
1:A:2961:C:C5	1:A:2962:C:C4	2.36	1.11
1:A:2579:C:N4	55:z:119:ILE:HG12	1.51	1.11
54:TA:68:VAL:CG1	54:TB:85:LEU:HD21	1.81	1.11
55:z:134:SER:O	56:w:664:THR:HG22	1.50	1.11
1:A:2172:A:C2'	32:J:23:ILE:CD1	2.17	1.11
33:I:197:LEU:HD21	54:TB:76:LEU:HD21	1.33	1.11
54:TA:85:LEU:HB2	54:TB:65:GLN:HA	1.17	1.11
54:TA:82:LEU:HA	54:TB:67:LEU:HD11	1.18	1.10
1:A:2576:A:O4'	56:w:580:ARG:HB2	1.47	1.10
1:A:3203:A:C2'	38:E:303:LYS:HZ3	1.65	1.10
55:z:132:GLN:HG2	56:w:668:ALA:HB1	1.32	1.10
54:TA:88:LYS:HZ2	54:TB:65:GLN:CB	1.65	1.09
54:TA:85:LEU:HD11	54:TB:67:LEU:CB	1.82	1.09
55:z:190:ARG:HH21	56:w:495:GLU:CD	1.59	1.09
1:A:1699:C:H5	15:Y:197:LYS:HG2	1.11	1.09
1:A:2065:A:H8	13:W:74:ARG:HA	0.96	1.08
1:A:2178:A:N1	56:w:716:GLN:C	2.11	1.08
54:TA:88:LYS:HZ2	54:TB:65:GLN:HB3	1.08	1.08
55:z:251:ARG:NH2	56:w:778:LEU:HA	1.67	1.08
54:TA:81:ASP:HA	54:TB:64:ILE:HD13	1.14	1.08
55:z:251:ARG:HH21	56:w:777:GLY:C	1.61	1.08
1:A:2578:C:O2	55:z:119:ILE:CB	2.01	1.07
54:TA:81:ASP:O	54:TB:64:ILE:CD1	2.01	1.07
54:TA:82:LEU:HA	54:TB:67:LEU:HD12	1.15	1.07

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:TA:82:LEU:HD23	54:TB:67:LEU:HD22	1.07	1.07
54:TA:85:LEU:CA	54:TA:88:LYS:HE3	1.84	1.07
1:A:1834:U:O4	12:T:206:ARG:CB	2.02	1.07
1:A:2235:C:C5	6:K:78:SER:OG	2.05	1.06
33:I:207:LEU:HD13	54:TB:86:LEU:HD11	1.16	1.06
1:A:2493:C:N4	1:A:2540:C:N1	2.04	1.06
33:I:139:LYS:O	54:TA:48:LEU:CD1	2.04	1.06
54:TA:85:LEU:HA	54:TA:88:LYS:CE	1.85	1.06
55:z:134:SER:HA	56:w:664:THR:CG2	1.85	1.06
34:N:136:VAL:HG13	55:z:72:VAL:HG21	1.31	1.05
1:A:2194:U:O2	33:I:125:VAL:HG12	1.56	1.05
1:A:2578:C:N4	55:z:128:LEU:C	2.12	1.05
55:z:138:MET:CE	56:w:636:LEU:HD22	1.67	1.05
54:TA:85:LEU:HD12	54:TB:67:LEU:HB2	1.36	1.05
54:TA:84:GLU:HB3	54:TB:64:ILE:HD11	1.35	1.04
1:A:1811:A:N6	44:c:49:ARG:CZ	2.19	1.04
1:A:1699:C:C5	15:Y:197:LYS:CG	2.40	1.04
1:A:2577:C:N4	55:z:130:LEU:N	2.04	1.04
1:A:1731:A:C6	26:i:118:TYR:CD1	2.44	1.04
54:TA:68:VAL:HG11	54:TB:85:LEU:HG	1.37	1.04
1:A:1849:C:OP2	8:M:53:HIS:NE2	1.90	1.03
1:A:2582:A:H1'	55:z:125:ASP:HB3	1.32	1.03
1:A:1834:U:O4	12:T:206:ARG:HB2	1.58	1.03
54:TA:89:THR:HG21	54:TB:68:VAL:HG13	1.39	1.03
1:A:1699:C:C5	15:Y:197:LYS:HG2	1.93	1.03
54:TA:82:LEU:HA	54:TB:67:LEU:HD13	1.06	1.03
1:A:2388:A:N6	3:D:127:ILE:HG21	1.71	1.03
1:A:2576:A:O2'	56:w:578:LEU:HD21	1.27	1.02
1:A:1902:C:O2	26:i:127:PHE:HD2	1.39	1.02
1:A:1812:C:O2	44:c:45:LEU:HD22	1.59	1.02
1:A:2194:U:O2	33:I:125:VAL:CG1	2.08	1.02
1:A:2178:A:N6	56:w:716:GLN:C	2.18	1.01
55:z:138:MET:HE1	56:w:636:LEU:HD23	1.09	1.01
54:TB:75:THR:HG22	54:TB:78:GLU:HB2	1.37	1.01
1:A:2493:C:C5	1:A:2540:C:C2	2.49	1.01
54:TA:85:LEU:HB3	54:TB:64:ILE:HG13	1.43	1.01
1:A:1853:A:OP2	11:S:177:ARG:NH2	1.94	1.01
33:I:207:LEU:CD1	54:TB:86:LEU:CD1	2.39	1.00
38:E:207:THR:CG2	38:E:267:THR:HG23	1.91	1.00
1:A:2576:A:O2'	56:w:665:MET:CE	2.09	1.00
55:z:186:THR:CG2	56:w:496:PRO:C	2.33	1.00

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1834:U:N3	12:T:206:ARG:HA	1.74	1.00
1:A:1834:U:C4	12:T:206:ARG:CA	2.45	1.00
1:A:2579:C:C4	55:z:119:ILE:HG12	1.97	1.00
54:TA:82:LEU:CA	54:TB:67:LEU:HD13	1.71	1.00
54:TA:68:VAL:HG11	54:TB:85:LEU:HD21	1.41	1.00
55:z:134:SER:CA	56:w:664:THR:CG2	2.38	1.00
1:A:2579:C:H41	55:z:119:ILE:HD11	0.85	0.99
8:M:261:ASP:HB3	8:M:264:GLN:OE1	1.61	0.99
34:N:136:VAL:HG21	55:z:72:VAL:CG1	1.92	0.99
54:TA:68:VAL:HB	54:TB:85:LEU:CD2	1.91	0.99
55:z:134:SER:C	56:w:664:THR:HG22	1.88	0.99
2:B:1607:U:H3	2:B:1664:G:H1	1.09	0.99
1:A:2556:A:C5	1:A:2557:C:O2	2.16	0.98
55:z:255:VAL:HG11	56:w:776:SER:O	1.60	0.98
1:A:2175:C:O2'	32:J:102:ARG:CD	2.11	0.98
54:TA:88:LYS:NZ	54:TB:65:GLN:OE1	1.96	0.98
1:A:2175:C:H5''	32:J:99:LYS:HG3	1.45	0.98
54:TA:68:VAL:CB	54:TB:85:LEU:HD21	1.90	0.98
55:z:186:THR:CG2	56:w:496:PRO:O	2.11	0.98
55:z:134:SER:C	56:w:664:THR:CG2	2.37	0.98
38:E:269:TYR:HE1	38:E:303:LYS:HE2	1.27	0.97
1:A:2582:A:O4'	55:z:125:ASP:CG	2.06	0.97
1:A:2493:C:H42	1:A:2540:C:C1'	1.72	0.97
1:A:2576:A:H2'	55:z:132:GLN:OE1	1.64	0.97
1:A:3089:A:N6	55:z:232:ARG:NE	2.09	0.97
54:TC:143:VAL:CB	56:w:292:ALA:CA	2.43	0.97
1:A:2125:C:OP2	11:S:178:LYS:HD2	1.63	0.97
55:z:251:ARG:CZ	56:w:778:LEU:HD13	1.95	0.97
6:K:155:LEU:O	6:K:158:TYR:HD2	0.94	0.97
55:z:128:LEU:HB3	56:w:580:ARG:HH12	1.28	0.97
1:A:1811:A:H61	44:c:49:ARG:CZ	1.78	0.96
1:A:2170:G:O2'	32:J:87:VAL:HG21	1.65	0.96
55:z:134:SER:O	56:w:664:THR:CG2	2.11	0.96
34:N:136:VAL:HG13	55:z:72:VAL:CG2	1.95	0.96
1:A:2178:A:C2	56:w:717:GLU:CA	2.49	0.96
55:z:134:SER:HA	56:w:664:THR:HG21	0.96	0.96
34:N:136:VAL:HG21	55:z:72:VAL:HG11	1.43	0.96
54:TA:85:LEU:HA	54:TA:88:LYS:CD	1.95	0.96
1:A:1839:C:C2	1:A:1840:C:C5	2.53	0.95
1:A:1902:C:O2	26:i:127:PHE:CD2	2.19	0.95
1:A:2155:A:N1	29:o:26:PHE:CZ	2.34	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2178:A:H62	56:w:716:GLN:HA	1.27	0.95
54:TA:89:THR:HG21	54:TB:68:VAL:CG1	1.96	0.95
34:N:136:VAL:HG22	55:z:72:VAL:HG11	1.49	0.94
1:A:2065:A:C8	13:W:74:ARG:CA	2.49	0.94
1:A:2192:A:H4'	32:J:139:SER:OG	1.67	0.94
54:TA:81:ASP:CG	54:TB:64:ILE:HG21	1.91	0.94
1:A:2578:C:H41	55:z:129:ALA:N	1.66	0.94
54:TA:74:LEU:HD13	54:TA:78:GLU:HB3	1.50	0.94
54:TA:81:ASP:C	54:TB:64:ILE:CD1	2.39	0.94
1:A:2172:A:O2'	32:J:23:ILE:HD13	1.67	0.94
48:k:58:ASP:OD1	54:TA:56:ALA:HB2	1.66	0.94
1:A:2960:U:O2	56:w:709:ALA:HB3	1.67	0.94
55:z:185:VAL:CG1	56:w:497:PRO:O	2.16	0.94
33:I:207:LEU:CD1	54:TB:86:LEU:HD11	1.95	0.94
1:A:1939:G:N2	1:A:2495:U:O4'	2.01	0.94
1:A:1902:C:C2	26:i:127:PHE:HD2	1.85	0.94
1:A:2493:C:C5	1:A:2540:C:C6	2.56	0.93
1:A:1811:A:N6	44:c:49:ARG:NH2	2.15	0.93
1:A:2172:A:H2'	32:J:23:ILE:HD13	0.95	0.93
54:TA:89:THR:CG2	54:TB:68:VAL:HG13	1.99	0.93
54:TA:85:LEU:HD11	54:TB:67:LEU:HB2	1.41	0.93
1:A:2576:A:O2'	56:w:665:MET:HE2	1.69	0.93
1:A:2155:A:C2	29:o:26:PHE:CD1	2.57	0.92
1:A:2897:A:N1	1:A:2898:U:C5	2.36	0.92
38:E:269:TYR:CE1	38:E:303:LYS:HE2	2.04	0.92
55:z:186:THR:HG21	56:w:495:GLU:O	0.75	0.92
1:A:2678:A:N1	17:0:81:PRO:HD2	1.84	0.92
1:A:2493:C:C5	1:A:2540:C:C4	2.57	0.92
1:A:1699:C:O2	19:2:70:LEU:HD12	1.69	0.91
34:N:136:VAL:CG1	55:z:72:VAL:CB	2.43	0.91
1:A:2579:C:H42	55:z:119:ILE:HG12	1.08	0.91
1:A:2240:C:N4	31:r:196:HIS:HB2	1.86	0.91
1:A:2493:C:C6	1:A:2540:C:C5	2.59	0.91
1:A:2578:C:H42	55:z:129:ALA:HA	1.17	0.91
1:A:2493:C:H41	1:A:2540:C:H1'	1.18	0.90
1:A:2615:A:C6	7:L:58:ILE:HB	2.06	0.90
1:A:1699:C:C5	15:Y:197:LYS:HG3	2.04	0.90
1:A:3198:A:H2'	1:A:3201:A:H62	1.34	0.90
55:z:186:THR:HG22	56:w:496:PRO:N	1.86	0.90
55:z:186:THR:HG22	56:w:496:PRO:CA	2.02	0.90
1:A:2060:A:N7	1:A:2079:C:N3	2.20	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1731:A:N6	26:i:118:TYR:HD1	1.59	0.90
1:A:2578:C:N3	55:z:119:ILE:CA	2.34	0.90
1:A:1836:A:C6	1:A:1837:C:C5	2.60	0.89
1:A:2178:A:C2	56:w:717:GLU:HG3	2.06	0.89
1:A:3157:C:H1'	52:Q:84:ARG:HB3	1.54	0.89
1:A:3203:A:H1'	38:E:303:LYS:HZ3	1.21	0.89
1:A:2582:A:H1'	55:z:125:ASP:CB	2.02	0.89
1:A:1699:C:H5	15:Y:197:LYS:CG	1.82	0.88
1:A:2692:G:OP1	29:o:15:ARG:HA	1.73	0.88
55:z:186:THR:HG22	56:w:495:GLU:C	1.97	0.88
1:A:2577:C:H41	55:z:130:LEU:C	1.81	0.88
54:TA:85:LEU:CB	54:TB:65:GLN:HA	2.02	0.88
1:A:2493:C:C5	1:A:2540:C:C5	2.61	0.88
1:A:3157:C:H42	9:O:14:VAL:HG21	1.35	0.88
55:z:251:ARG:HH22	56:w:778:LEU:HD13	0.73	0.88
1:A:2578:C:C2	55:z:119:ILE:HB	2.07	0.88
1:A:2060:A:C2	1:A:2061:C:C5	2.62	0.87
1:A:3110:C:N3	1:A:3203:A:N1	2.21	0.87
14:X:143:PHE:O	14:X:147:LYS:HB2	1.74	0.87
54:TA:85:LEU:CB	54:TB:64:ILE:HG13	2.03	0.87
54:TA:82:LEU:HD21	54:TB:67:LEU:HD22	1.56	0.87
1:A:2582:A:H4'	55:z:125:ASP:OD2	1.73	0.87
1:A:3203:A:H1'	38:E:303:LYS:HZ1	1.36	0.87
54:TA:82:LEU:CA	54:TB:67:LEU:HD11	1.83	0.87
54:TA:85:LEU:CD1	54:TB:67:LEU:CB	2.44	0.87
48:k:58:ASP:OD1	54:TA:56:ALA:CB	2.22	0.87
1:A:1834:U:O4	12:T:206:ARG:CA	2.22	0.87
1:A:2493:C:C6	1:A:2540:C:C4	2.64	0.86
55:z:186:THR:CG2	56:w:496:PRO:N	2.38	0.86
38:E:207:THR:HG22	38:E:267:THR:CB	2.05	0.86
1:A:2132:A:H62	29:o:16:GLN:HE22	1.24	0.86
1:A:2577:C:C4	55:z:130:LEU:N	2.44	0.86
1:A:2579:C:H41	55:z:119:ILE:CD1	1.53	0.86
54:TA:81:ASP:OD1	54:TB:64:ILE:HG21	1.75	0.86
1:A:2582:A:O4'	55:z:125:ASP:OD1	1.93	0.85
33:I:140:TYR:HA	54:TA:48:LEU:HD12	1.56	0.85
1:A:1839:C:O2	1:A:1840:C:C5	2.29	0.85
1:A:2058:C:O2	16:Z:109:LYS:NZ	2.09	0.85
1:A:2388:A:H61	3:D:127:ILE:HG21	1.36	0.85
1:A:1790:A:OP1	19:2:82:ARG:NH1	2.09	0.85
1:A:2678:A:H2	17:0:80:ALA:CB	1.87	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:TA:85:LEU:HD11	54:TB:67:LEU:CG	2.06	0.85
54:TC:143:VAL:CB	56:w:292:ALA:CB	2.54	0.85
1:A:1731:A:C6	26:i:118:TYR:CG	2.65	0.85
1:A:3157:C:H41	9:O:14:VAL:HG21	1.07	0.85
55:z:105:LYS:HG3	56:w:637:GLN:CD	2.02	0.85
54:TA:89:THR:CG2	54:TB:68:VAL:CG1	2.54	0.84
1:A:2578:C:H41	55:z:128:LEU:C	1.82	0.84
1:A:2577:C:O5'	55:z:132:GLN:NE2	2.11	0.84
33:I:139:LYS:O	54:TA:48:LEU:HD12	1.75	0.84
34:N:136:VAL:CG1	55:z:72:VAL:CG2	2.55	0.84
1:A:2576:A:H5'	56:w:579:ASP:O	1.77	0.84
1:A:2174:G:H4'	32:J:151:LEU:CD1	2.07	0.84
1:A:2578:C:N4	55:z:129:ALA:N	2.21	0.84
1:A:2065:A:C8	13:W:74:ARG:CB	2.61	0.83
1:A:3189:C:O2	31:r:154:TRP:CG	2.32	0.83
1:A:2576:A:O4'	56:w:580:ARG:CB	2.26	0.83
1:A:2852:C:O2'	18:l:45:HIS:ND1	2.11	0.83
54:TA:82:LEU:HD23	54:TB:67:LEU:CD1	2.08	0.83
1:A:1731:A:OP1	5:H:74:HIS:NE2	2.11	0.83
1:A:2577:C:N1	55:z:132:GLN:CG	2.41	0.83
54:TA:85:LEU:CB	54:TA:88:LYS:HE3	2.09	0.83
54:TA:88:LYS:HZ2	54:TB:65:GLN:CA	1.90	0.83
55:z:124:ALA:HB3	56:w:582:LEU:HD21	1.58	0.83
55:z:251:ARG:NH2	56:w:778:LEU:CA	2.42	0.82
54:TA:85:LEU:CB	54:TB:65:GLN:N	2.43	0.82
1:A:2178:A:N1	56:w:717:GLU:HA	1.93	0.82
54:TB:74:LEU:HD23	54:TB:79:ILE:HG12	1.62	0.82
1:A:2499:U:OP2	1:A:2504:A:N6	2.12	0.82
54:TA:82:LEU:HD23	54:TB:67:LEU:CG	2.09	0.82
1:A:2897:A:C2	1:A:2898:U:C6	2.67	0.82
56:w:122:THR:H	59:w:801:GCP:PG	2.02	0.82
1:A:2178:A:H61	56:w:716:GLN:CA	1.93	0.82
1:A:2442:U:H5''	51:s:81:ARG:HH22	1.44	0.82
54:TA:85:LEU:HD13	54:TB:65:GLN:CA	2.10	0.82
54:TA:85:LEU:HA	54:TA:88:LYS:CG	2.10	0.82
54:TA:68:VAL:HB	54:TB:85:LEU:HD21	1.54	0.81
1:A:2178:A:C4	56:w:717:GLU:HG3	2.15	0.81
34:N:136:VAL:HG11	55:z:72:VAL:HB	0.89	0.81
1:A:1834:U:O4	12:T:206:ARG:HA	1.77	0.81
1:A:2215:C:OP1	34:N:31:LYS:HD2	1.80	0.81
55:z:138:MET:HE1	56:w:636:LEU:HD22	0.82	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2578:C:C2	55:z:119:ILE:HA	2.15	0.81
54:TA:85:LEU:HA	54:TA:88:LYS:HG3	1.62	0.81
1:A:2493:C:C4	1:A:2540:C:C1'	2.61	0.81
1:A:2493:C:H42	1:A:2540:C:H1'	1.37	0.81
1:A:1699:C:C6	15:Y:197:LYS:CG	2.59	0.81
1:A:2556:A:C6	1:A:2557:C:O2	2.34	0.81
1:A:2577:C:N4	55:z:130:LEU:CA	2.44	0.81
55:z:128:LEU:HB3	56:w:580:ARG:NH1	1.94	0.81
1:A:2582:A:C1'	55:z:125:ASP:CG	2.54	0.80
1:A:2961:C:C2	1:A:2962:C:C6	2.70	0.80
1:A:1939:G:C2	1:A:2495:U:C1'	2.58	0.80
1:A:2576:A:H5'	56:w:579:ASP:C	2.05	0.80
1:A:3203:A:C1'	38:E:303:LYS:HZ3	1.65	0.80
1:A:1744:A:OP1	8:M:87:HIS:HE1	1.65	0.80
54:TA:85:LEU:HB2	54:TB:65:GLN:N	1.92	0.80
1:A:2060:A:C5	1:A:2079:C:C2	2.66	0.79
1:A:2170:G:O2'	32:J:87:VAL:CG2	2.30	0.79
1:A:2470:G:O2'	7:L:36:THR:HG22	1.81	0.79
1:A:2796:G:H21	5:H:88:HIS:CE1	1.99	0.79
1:A:2379:C:C5	42:9:48:TRP:CE2	2.70	0.79
54:TA:82:LEU:HD21	54:TB:67:LEU:CD2	2.12	0.79
33:I:207:LEU:HD13	54:TB:86:LEU:HD13	1.65	0.79
54:TA:61:PRO:HB2	54:TA:64:ILE:HD13	1.64	0.79
55:z:138:MET:HE2	56:w:636:LEU:HD23	1.65	0.79
1:A:2577:C:OP2	56:w:672:ARG:NH1	2.15	0.79
54:TA:68:VAL:HG21	54:TB:85:LEU:HD23	0.80	0.79
1:A:1699:C:H6	15:Y:197:LYS:HG3	1.41	0.79
1:A:1813:C:H5	26:i:36:LEU:HD21	1.46	0.79
1:A:2559:U:H1'	1:A:2560:G:OP2	1.81	0.79
1:A:2577:C:C4	55:z:131:ASN:N	2.51	0.79
1:A:3011:A:O2'	1:A:3173:G:N2	2.15	0.79
1:A:1839:C:N3	1:A:1840:C:N4	2.31	0.79
1:A:2577:C:N4	55:z:130:LEU:C	2.41	0.79
1:A:2155:A:C2	29:o:26:PHE:CZ	2.70	0.79
38:E:207:THR:HG23	38:E:267:THR:HG23	1.64	0.78
1:A:2111:C:OP1	33:I:35:ARG:NH1	2.16	0.78
1:A:2017:U:OP2	8:M:59:ARG:NH2	2.12	0.78
1:A:3189:C:O2'	31:r:155:ALA:N	2.14	0.78
55:z:251:ARG:CZ	56:w:777:GLY:O	2.30	0.78
1:A:1672:C:O2'	12:T:149:ARG:O	2.01	0.78
1:A:2065:A:H8	13:W:74:ARG:CA	1.84	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2395:A:HI'	39:5:384:HIS:HB2	1.66	0.77
38:E:207:THR:CG2	38:E:267:THR:CG2	2.62	0.77
1:A:2578:C:C2	55:z:118:LYS:O	2.37	0.77
1:A:2493:C:N4	1:A:2540:C:O4'	2.17	0.77
1:A:2678:A:C2	17:0:80:ALA:CB	2.68	0.77
1:A:2897:A:C2	1:A:2898:U:C5	2.73	0.77
1:A:1702:A:C8	19:2:66:TRP:CG	2.73	0.77
1:A:2580:U:H3	55:z:127:LYS:HB2	1.50	0.77
1:A:2678:A:N1	17:0:81:PRO:CD	2.48	0.77
1:A:2577:C:C4	55:z:129:ALA:C	2.60	0.77
1:A:2582:A:C6	56:w:581:THR:O	2.36	0.77
38:E:207:THR:HG22	38:E:267:THR:OG1	1.85	0.77
54:TA:85:LEU:HD13	54:TB:65:GLN:C	2.10	0.77
1:A:1881:A:OP1	25:g:90:ARG:HG2	1.83	0.77
1:A:2961:C:N3	1:A:2962:C:C2	2.53	0.76
1:A:3154:U:OP1	52:Q:231:LYS:NZ	2.18	0.76
1:A:2577:C:C6	55:z:132:GLN:CG	2.61	0.76
33:I:197:LEU:CD2	54:TB:76:LEU:HD21	2.13	0.76
1:A:2275:U:HI'	10:R:12:ASN:HB3	1.66	0.76
1:A:2576:A:O2'	56:w:665:MET:SD	2.43	0.76
1:A:1818:A:OP1	17:0:95:ARG:NH2	2.18	0.76
1:A:3192:C:OP1	31:r:132:ARG:NH1	2.14	0.76
1:A:2582:A:C4'	55:z:125:ASP:OD2	2.34	0.76
1:A:2578:C:C2	55:z:119:ILE:CA	2.68	0.76
1:A:2383:U:O2'	39:5:92:LEU:CD2	2.34	0.76
1:A:2178:A:C6	56:w:716:GLN:O	2.34	0.76
1:A:1902:C:C2	26:i:127:PHE:CD2	2.74	0.76
1:A:2214:A:H5'	49:l:126:ILE:HD11	1.67	0.76
1:A:3157:C:O2'	52:Q:85:GLY:HA2	1.86	0.76
1:A:1738:U:O4	1:A:1760:G:N2	2.17	0.75
34:N:136:VAL:CG2	55:z:72:VAL:CG1	2.56	0.75
49:l:73:MET:SD	49:l:79:LYS:HE3	2.26	0.75
54:TA:76:LEU:HA	54:TA:79:ILE:HD12	1.68	0.75
1:A:3189:C:OP1	21:4:85:ARG:N	2.15	0.75
54:TA:68:VAL:CG1	54:TB:85:LEU:HG	2.15	0.75
1:A:1699:C:O2	19:2:70:LEU:CD1	2.35	0.75
56:w:84:THR:HG22	59:w:801:GCP:O2B	1.86	0.75
38:E:207:THR:CG2	38:E:267:THR:OG1	2.35	0.75
1:A:2178:A:H2	56:w:717:GLU:HA	1.49	0.74
1:A:2278:A:OP1	26:i:51:ARG:NH1	2.18	0.74
8:M:261:ASP:CB	8:M:264:GLN:OE1	2.35	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:z:132:GLN:HG2	56:w:668:ALA:HB3	1.66	0.74
1:A:2493:C:C5	1:A:2540:C:N3	2.53	0.74
1:A:3203:A:C2'	38:E:303:LYS:NZ	2.36	0.74
41:7:159:LYS:HD3	41:7:161:GLU:HB2	1.68	0.74
1:A:2615:A:N6	7:L:58:ILE:HB	2.03	0.74
1:A:3042:U:C5	1:A:3043:C:C6	2.75	0.74
1:A:3157:C:C1'	52:Q:84:ARG:HB3	2.16	0.74
1:A:3198:A:H2'	1:A:3201:A:N6	2.00	0.74
1:A:2240:C:OP2	6:K:71:LYS:NZ	2.20	0.74
1:A:2298:A:H61	4:F:145:LEU:HD22	1.52	0.74
54:TA:85:LEU:CA	54:TA:88:LYS:CE	2.57	0.74
1:A:2192:A:C4'	32:J:139:SER:OG	2.34	0.74
54:TA:85:LEU:CB	54:TA:88:LYS:CE	2.65	0.74
54:TA:81:ASP:CA	54:TB:64:ILE:HD13	1.98	0.74
55:z:186:THR:N	56:w:496:PRO:O	2.16	0.74
1:A:2079:C:C5	1:A:2080:U:C2	2.76	0.73
1:A:2578:C:H41	55:z:129:ALA:CA	1.85	0.73
1:A:2961:C:N4	1:A:2962:C:C4	2.42	0.73
54:TA:82:LEU:CB	54:TB:67:LEU:HD13	2.19	0.73
1:A:2172:A:N6	32:J:34:PRO:HG3	2.04	0.73
1:A:2493:C:C5	1:A:2540:C:N1	2.51	0.73
1:A:2559:U:C1'	1:A:2560:G:OP2	2.37	0.73
1:A:2578:C:O2	55:z:119:ILE:CA	2.35	0.73
33:I:207:LEU:CD1	54:TB:86:LEU:HD13	2.14	0.73
1:A:2579:C:C4	55:z:119:ILE:CD1	2.70	0.73
1:A:1809:U:O2'	1:A:1810:A:OP1	2.06	0.73
1:A:2578:C:C2	55:z:119:ILE:CB	2.68	0.73
54:TA:68:VAL:HG21	54:TB:85:LEU:CG	2.19	0.73
1:A:2524:A:N6	3:D:92:ARG:NH1	2.36	0.72
24:e:198:ASN:HD22	24:e:243:PHE:HA	1.54	0.72
1:A:2527:A:C6	39:5:33:TRP:HE3	2.08	0.72
38:E:207:THR:HG22	38:E:267:THR:HA	1.69	0.72
1:A:2193:U:O4	1:A:2196:A:C2	2.42	0.72
1:A:2961:C:C4	1:A:2962:C:C5	2.77	0.72
43:a:68:PRO:HG2	43:a:71:HIS:HD2	1.54	0.72
1:A:1794:A:OP1	4:F:142:ARG:NH2	2.22	0.72
1:A:1812:C:C2	44:c:45:LEU:HD22	2.24	0.72
1:A:1884:G:H1'	1:A:1895:C:H1'	1.71	0.72
54:TA:85:LEU:CD1	54:TB:67:LEU:H	2.03	0.72
55:z:251:ARG:HH22	56:w:778:LEU:CG	2.02	0.72
1:A:1808:A:H4'	1:A:1809:U:OP1	1.88	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1813:C:C5	26:i:36:LEU:HD21	2.25	0.72
1:A:2442:U:H5''	51:s:81:ARG:NH2	2.04	0.72
1:A:2578:C:N3	55:z:118:LYS:O	2.23	0.72
1:A:1787:G:N2	1:A:1790:A:OP2	2.21	0.72
1:A:2060:A:C6	1:A:2061:C:N4	2.58	0.72
54:TA:85:LEU:HD13	54:TB:65:GLN:HA	1.72	0.72
54:TA:85:LEU:HD11	54:TB:67:LEU:H	1.55	0.71
1:A:2265:A:OP1	8:M:47:ARG:NH2	2.22	0.71
1:A:2065:A:N9	13:W:74:ARG:HG3	2.04	0.71
55:z:251:ARG:NH1	56:w:778:LEU:HD13	2.06	0.71
1:A:2175:C:C2'	32:J:102:ARG:HG3	2.20	0.71
1:A:2576:A:O2'	56:w:578:LEU:HD23	1.85	0.71
54:TA:82:LEU:HD23	54:TB:67:LEU:HD13	1.72	0.71
1:A:2388:A:H61	3:D:127:ILE:CG2	2.03	0.71
1:A:2493:C:O2'	1:A:2494:C:H5'	1.90	0.71
1:A:1823:A:O2'	43:a:126:HIS:CE1	2.43	0.71
6:K:154:ARG:O	6:K:158:TYR:CE2	2.41	0.71
1:A:1902:C:O2'	26:i:126:LYS:HB2	1.90	0.71
33:I:139:LYS:HG3	54:TA:48:LEU:HD11	1.73	0.71
56:w:73:ILE:HD11	56:w:163:VAL:HG13	1.71	0.71
1:A:2171:U:H4'	1:A:2172:A:H3'	1.73	0.71
1:A:3203:A:O2'	38:E:303:LYS:NZ	2.22	0.71
1:A:2579:C:N4	55:z:119:ILE:HD13	1.96	0.70
1:A:2383:U:O2'	39:5:92:LEU:HD21	1.91	0.70
32:J:166:ALA:O	32:J:170:GLU:HB2	1.90	0.70
55:z:132:GLN:CG	56:w:668:ALA:CB	2.58	0.70
1:A:2172:A:C8	32:J:23:ILE:HD12	2.27	0.70
1:A:2190:C:H4'	32:J:149:ARG:HH21	1.54	0.70
32:J:41:GLN:N	56:w:698:ARG:NH1	2.24	0.70
1:A:2961:C:C4	1:A:2962:C:N4	2.41	0.70
1:A:2017:U:OP1	8:M:54:LYS:NZ	2.16	0.70
1:A:2753:A:H1'	5:H:88:HIS:CE1	2.27	0.70
1:A:2961:C:N3	1:A:2962:C:C4	2.57	0.70
1:A:3013:G:HO2'	21:4:66:PHE:N	1.89	0.70
1:A:2241:A:H61	31:r:82:ASN:CG	1.99	0.70
1:A:2745:A:H4'	14:X:102:LYS:O	1.92	0.70
1:A:3082:G:N2	1:A:3085:A:OP2	2.19	0.70
55:z:132:GLN:CG	56:w:668:ALA:HB1	2.18	0.70
1:A:2961:C:C2	1:A:2962:C:C5	2.80	0.69
1:A:2493:C:H5	1:A:2540:C:C2	2.07	0.69
38:E:207:THR:HG22	38:E:267:THR:HG23	1.71	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1848:U:OP1	8:M:53:HIS:HE1	1.74	0.69
1:A:2545:U:H5''	1:A:2546:G:H5'	1.73	0.69
23:b:49:ARG:HG3	23:b:50:GLU:HG3	1.74	0.69
1:A:2191:A:N6	1:A:2198:A:OP2	2.25	0.69
1:A:2493:C:N3	1:A:2540:C:C6	2.61	0.69
1:A:2818:C:O2	55:z:227:SER:CB	2.39	0.69
33:I:139:LYS:C	54:TA:48:LEU:HG	2.15	0.69
38:E:207:THR:HG22	38:E:267:THR:CG2	2.23	0.69
1:A:2155:A:C6	29:o:26:PHE:CZ	2.80	0.69
38:E:207:THR:HG22	38:E:267:THR:CA	2.22	0.69
1:A:2194:U:C2	33:I:125:VAL:HG12	2.27	0.69
1:A:2256:U:O2'	11:S:118:ASN:ND2	2.25	0.69
1:A:2579:C:N3	55:z:119:ILE:HG12	2.06	0.69
1:A:2052:A:H5''	25:g:150:LYS:HE3	1.75	0.69
1:A:3157:C:O2'	52:Q:85:GLY:CA	2.40	0.69
1:A:1939:G:H3'	1:A:1939:G:N3	2.08	0.69
54:TA:82:LEU:CD2	54:TB:67:LEU:HD21	2.19	0.69
1:A:2172:A:H8	32:J:23:ILE:HD12	1.57	0.68
1:A:2214:A:H5'	49:l:126:ILE:CD1	2.22	0.68
1:A:2577:C:C6	55:z:131:ASN:HB2	2.28	0.68
54:TA:84:GLU:O	54:TA:88:LYS:HG3	1.93	0.68
1:A:2240:C:H41	31:r:196:HIS:HB2	1.58	0.68
49:l:68:LEU:CD2	49:l:70:THR:HG23	2.23	0.68
55:z:190:ARG:NE	56:w:495:GLU:OE1	2.26	0.68
1:A:2298:A:N6	4:F:145:LEU:HD22	2.07	0.68
1:A:2373:A:C2	51:s:274:PHE:CB	2.77	0.68
1:A:2661:U:OP2	38:E:238:ARG:NH2	2.26	0.68
54:TA:88:LYS:HZ2	54:TB:65:GLN:N	1.92	0.68
55:z:138:MET:HE2	56:w:636:LEU:CD2	2.14	0.68
1:A:1813:C:C5	26:i:36:LEU:HD11	2.28	0.68
54:TA:82:LEU:CB	54:TB:67:LEU:CD1	2.69	0.68
1:A:1702:A:C8	19:2:66:TRP:CD2	2.82	0.68
1:A:2373:A:C2	51:s:274:PHE:HB2	2.29	0.68
54:TA:85:LEU:HD11	54:TB:67:LEU:HG	1.73	0.68
1:A:3129:A:OP1	56:w:79:ILE:HG12	1.93	0.68
54:TA:85:LEU:CD1	54:TB:67:LEU:N	2.57	0.68
1:A:2158:U:O2'	31:r:153:ARG:NH2	2.27	0.68
1:A:2577:C:C2	55:z:132:GLN:HG3	2.28	0.68
54:TA:85:LEU:CD1	54:TB:65:GLN:HA	2.23	0.68
55:z:185:VAL:CG1	56:w:498:SER:HA	2.24	0.68
1:A:2155:A:C6	29:o:26:PHE:CE2	2.81	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2580:U:O2	55:z:127:LYS:HD2	1.94	0.68
1:A:2599:U:OP2	1:A:2625:C:N4	2.26	0.68
1:A:3068:G:N2	1:A:3068:G:OP2	2.26	0.68
1:A:3210:C:N3	38:E:156:ARG:HA	2.10	0.67
55:z:251:ARG:HH12	56:w:778:LEU:CD1	2.07	0.67
56:w:83:LYS:N	59:w:801:GCP:O2A	2.26	0.67
1:A:2370:A:OP1	36:U:41:GLN:NE2	2.24	0.67
37:V:177:THR:HG22	42:9:74:VAL:HA	1.76	0.67
1:A:2575:U:O3'	56:w:579:ASP:O	2.12	0.67
48:k:57:HIS:HB2	54:TA:53:LEU:HD13	1.68	0.67
1:A:2065:A:C8	13:W:74:ARG:HG3	2.30	0.67
1:A:2421:G:H5''	42:9:24:LYS:HG2	1.75	0.67
1:A:2576:A:H5'	56:w:579:ASP:N	2.09	0.67
59:w:801:GCP:O2B	59:w:801:GCP:O3G	2.13	0.67
1:A:2678:A:H2	17:0:80:ALA:HB2	1.58	0.67
1:A:2483:U:H2'	1:A:2484:C:O4'	1.94	0.67
1:A:2576:A:C1'	56:w:580:ARG:HB2	2.24	0.67
1:A:2960:U:O4'	56:w:710:GLN:HA	1.95	0.67
4:F:59:ARG:NH1	4:F:88:ALA:O	2.27	0.67
41:7:73:THR:HG1	41:7:99:TYR:HH	1.42	0.67
1:A:1809:U:OP1	1:A:1809:U:H4'	1.95	0.67
55:z:185:VAL:HG12	56:w:497:PRO:O	1.94	0.67
1:A:3042:U:C5	1:A:3043:C:C5	2.83	0.67
34:N:50:LEU:H	34:N:110:ASN:HD21	1.43	0.67
1:A:2530:A:H4'	1:A:2531:U:H5'	1.77	0.66
1:A:2995:G:H1	1:A:3067:U:H3	1.43	0.66
1:A:1867:A:H62	1:A:2295:C:H5	1.44	0.66
55:z:251:ARG:NH2	56:w:778:LEU:CD1	2.25	0.66
55:z:105:LYS:HE2	56:w:637:GLN:HG2	1.77	0.66
1:A:2373:A:N1	51:s:274:PHE:CB	2.58	0.66
55:z:251:ARG:NE	56:w:777:GLY:O	2.29	0.66
4:F:293:PHE:HB2	25:g:55:THR:HG21	1.78	0.66
1:A:2025:C:OP2	11:S:182:LYS:NZ	2.26	0.66
1:A:2395:A:OP1	39:5:172:ARG:NH2	2.29	0.66
1:A:2178:A:N1	56:w:717:GLU:CA	2.58	0.66
1:A:2236:C:N4	1:A:2688:C:O2	2.29	0.66
1:A:2578:C:N3	55:z:119:ILE:HD12	2.11	0.66
1:A:2176:C:H5''	32:J:102:ARG:NH2	2.11	0.65
1:A:2560:G:OP2	1:A:2560:G:H8	1.79	0.65
1:A:2577:C:C1'	55:z:132:GLN:HG3	2.26	0.65
1:A:2694:A:N3	1:A:2942:C:O2'	2.29	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2822:C:O2'	1:A:2915:C:OP2	2.14	0.65
1:A:2144:A:OP1	10:R:57:ARG:HD3	1.96	0.65
1:A:2172:A:H61	32:J:34:PRO:HG3	1.62	0.65
1:A:2230:A:N7	1:A:2975:G:O2'	2.29	0.65
1:A:2523:C:O2	3:D:87:HIS:ND1	2.29	0.65
1:A:1836:A:N1	1:A:1837:C:C5	2.64	0.65
1:A:2065:A:C8	13:W:74:ARG:CG	2.80	0.65
56:w:566:GLU:HB2	56:w:645:ILE:HG12	1.78	0.65
1:A:2176:C:C5'	32:J:102:ARG:NH2	2.59	0.65
1:A:2248:U:OP1	10:R:99:ARG:NH2	2.29	0.65
32:J:159:LEU:O	32:J:163:GLU:N	2.30	0.65
56:w:211:ILE:HG23	56:w:215:LEU:HD12	1.77	0.65
1:A:1760:G:OP2	30:q:59:LYS:NZ	2.29	0.65
1:A:1811:A:N6	44:c:49:ARG:NE	2.45	0.65
1:A:2349:G:O2'	1:A:2351:U:O4	2.14	0.65
55:z:185:VAL:HG13	56:w:498:SER:HA	1.78	0.65
1:A:1974:A:H5'	3:D:261:GLY:HA2	1.79	0.65
1:A:2178:A:H61	56:w:716:GLN:C	2.01	0.65
1:A:2373:A:C2	51:s:274:PHE:CG	2.84	0.65
1:A:2520:C:OP2	3:D:293:LYS:NZ	2.30	0.65
1:A:2796:G:N2	5:H:88:HIS:HE1	1.95	0.65
1:A:1836:A:N1	1:A:1837:C:C6	2.65	0.65
1:A:2178:A:C6	56:w:716:GLN:CA	2.69	0.65
1:A:2961:C:C5	1:A:2962:C:C5	2.85	0.65
51:s:405:ILE:HG12	51:s:410:VAL:HG12	1.79	0.64
1:A:1777:A:N6	1:A:1780:U:OP2	2.29	0.64
6:K:27:PRO:HG2	6:K:30:LYS:HB2	1.79	0.64
54:TA:85:LEU:CG	54:TB:64:ILE:HG13	2.15	0.64
1:A:1702:A:N7	19:2:66:TRP:CE3	2.66	0.64
1:A:3122:U:OP1	1:A:3124:U:H1'	1.97	0.64
14:X:10:LEU:HD22	30:q:45:LEU:HD23	1.80	0.64
34:N:136:VAL:HG21	55:z:72:VAL:HG12	1.80	0.64
1:A:1698:C:O2'	1:A:1702:A:N3	2.30	0.64
1:A:1839:C:N3	1:A:1840:C:C4	2.66	0.64
1:A:2174:G:H4'	32:J:151:LEU:HD11	1.80	0.64
1:A:2175:C:H5''	32:J:99:LYS:CG	2.24	0.64
1:A:3089:A:N6	55:z:232:ARG:NH2	2.43	0.64
1:A:3210:C:OP1	38:E:158:ALA:HA	1.98	0.64
1:A:2178:A:C6	56:w:716:GLN:HA	2.24	0.63
1:A:1831:G:OP2	23:b:4:ARG:HG3	1.98	0.63
1:A:1881:A:H62	25:g:111:ARG:HD3	1.63	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2107:G:OP2	34:N:67:LYS:HG2	1.97	0.63
1:A:3150:U:N3	38:E:118:VAL:HG11	2.12	0.63
4:F:113:LYS:HG3	4:F:157:GLY:H	1.63	0.63
54:TB:75:THR:O	54:TB:79:ILE:HG13	1.98	0.63
1:A:1847:U:OP1	8:M:47:ARG:NE	2.24	0.63
36:U:120:GLY:HA3	36:U:124:ASP:HB2	1.80	0.63
1:A:2484:C:C5	1:A:2485:U:C4	2.86	0.63
1:A:2131:A:C4	31:r:168:ARG:NH1	2.67	0.63
1:A:2178:A:N6	56:w:716:GLN:O	2.29	0.63
1:A:2671:C:H2'	1:A:2672:A:H8	1.64	0.63
1:A:3204:C:H5'	38:E:298:LYS:NZ	2.13	0.63
4:F:103:GLN:HE22	4:F:249:ASN:HB2	1.62	0.63
55:z:212:ARG:HH12	55:z:239:SER:HA	1.63	0.63
1:A:2664:U:OP1	9:O:17:ARG:HD3	1.97	0.63
1:A:2373:A:N1	51:s:274:PHE:HB3	2.14	0.63
28:m:69:ARG:HG3	28:m:70:GLU:HG3	1.81	0.63
54:TA:85:LEU:HB3	54:TA:88:LYS:HE3	1.79	0.63
1:A:1893:A:H1'	1:A:1894:G:C8	2.34	0.63
1:A:2178:A:N1	56:w:717:GLU:N	2.46	0.62
1:A:1939:G:H21	1:A:2495:U:H1'	1.61	0.62
1:A:2175:C:O2'	32:J:102:ARG:NE	2.32	0.62
1:A:2388:A:C5	3:D:141:LEU:CD2	2.83	0.62
45:d:181:VAL:HG22	45:d:224:ILE:HG12	1.79	0.62
1:A:2145:G:N1	1:A:2256:U:O4	2.32	0.62
1:A:2508:C:H2'	1:A:2509:A:C8	2.34	0.62
1:A:2582:A:C4'	55:z:125:ASP:CG	2.73	0.62
1:A:3150:U:H3	38:E:118:VAL:HG11	1.65	0.62
54:TA:57:PRO:O	54:TA:58:LYS:HD3	1.99	0.62
1:A:1857:U:H2'	1:A:1858:G:C8	2.34	0.62
1:A:2111:C:H2'	1:A:2112:A:C8	2.34	0.62
17:O:119:LYS:O	17:O:120:HIS:ND1	2.33	0.62
23:b:72:VAL:HG13	23:b:90:HIS:HB2	1.80	0.62
55:z:134:SER:N	56:w:664:THR:HG21	2.14	0.62
56:w:122:THR:N	59:w:801:GCP:O1G	2.32	0.62
56:w:191:ILE:HG22	56:w:326:PRO:HD2	1.80	0.62
1:A:1672:C:OP1	12:T:51:TRP:HB2	1.98	0.62
1:A:2176:C:H5''	32:J:102:ARG:HH21	1.62	0.62
1:A:2388:A:C6	3:D:127:ILE:HG21	2.34	0.62
32:J:70:ILE:HD11	32:J:78:PHE:HB2	1.81	0.62
54:TB:70:ASP:OD1	54:TB:71:ILE:HD12	2.00	0.62
24:e:198:ASN:HD21	24:e:200:MET:HE2	1.63	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:7:214:LEU:H	41:7:272:THR:HG22	1.65	0.62
1:A:2178:A:N3	56:w:717:GLU:CG	2.42	0.62
1:A:3210:C:C4	38:E:156:ARG:HA	2.35	0.62
51:s:266:CYS:SG	51:s:267:LYS:N	2.72	0.62
1:A:1935:A:H2'	1:A:1938:A:H61	1.63	0.62
1:A:1935:A:H3'	1:A:1936:A:H5''	1.82	0.62
1:A:2442:U:H4'	51:s:85:LYS:HD2	1.80	0.62
1:A:2796:G:N2	5:H:88:HIS:CE1	2.67	0.62
1:A:1902:C:H2'	26:i:126:LYS:H	1.65	0.62
1:A:2333:G:N1	1:A:2442:U:O4	2.32	0.62
1:A:2960:U:C4	56:w:706:ALA:HB1	2.35	0.62
1:A:2961:C:C6	1:A:2962:C:C5	2.87	0.62
54:TA:64:ILE:HG12	54:TB:81:ASP:HB2	1.82	0.62
54:TA:88:LYS:NZ	54:TB:65:GLN:N	2.48	0.62
1:A:1713:A:N1	39:5:69:TRP:NE1	2.48	0.61
1:A:2493:C:N4	1:A:2540:C:C2	2.68	0.61
54:TA:86:LEU:HA	54:TB:68:VAL:HG22	1.82	0.61
1:A:1703:C:OP1	42:9:34:LYS:NZ	2.33	0.61
54:TC:142:LYS:CB	56:w:296:LEU:HD21	2.30	0.61
32:J:41:GLN:CD	56:w:698:ARG:HH21	1.81	0.61
51:s:112:THR:HG22	51:s:391:ASN:HB2	1.82	0.61
1:A:1800:G:N1	1:A:1803:A:OP2	2.30	0.61
40:6:178:ALA:HA	50:p:194:HIS:HD2	1.66	0.61
1:A:3194:U:OP1	31:r:141:PRO:HG2	2.01	0.61
24:e:203:LYS:HE3	24:e:239:LEU:HG	1.83	0.61
52:Q:92:PHE:O	52:Q:96:ARG:HB2	2.00	0.61
1:A:1698:C:OP1	15:Y:182:LYS:NZ	2.27	0.61
1:A:3009:C:C5	1:A:3031:G:N1	2.69	0.61
1:A:1811:A:H62	44:c:49:ARG:NH2	1.99	0.61
1:A:2064:A:C6	46:f:48:TYR:CE2	2.89	0.61
32:J:157:LYS:HE2	49:l:97:PHE:HB3	1.83	0.61
49:l:68:LEU:HD22	49:l:70:THR:HG23	1.83	0.61
1:A:2578:C:N3	55:z:119:ILE:CD1	2.64	0.61
54:TA:88:LYS:NZ	54:TB:65:GLN:CB	2.40	0.61
56:w:158:VAL:O	56:w:387:ARG:NH1	2.34	0.61
1:A:1836:A:C2	1:A:1837:C:C6	2.89	0.61
1:A:2362:A:N6	1:A:2432:A:O4'	2.33	0.61
1:A:2960:U:O4	56:w:706:ALA:HB1	2.00	0.61
24:e:173:LEU:HD12	24:e:174:PRO:HD2	1.81	0.61
1:A:1884:G:N3	1:A:1895:C:O2'	2.33	0.61
1:A:2215:C:OP1	34:N:31:LYS:CD	2.47	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:b:37:GLY:O	23:b:44:ARG:NH2	2.33	0.61
6:K:158:TYR:OH	31:r:86:VAL:CG2	2.49	0.60
52:Q:76:LEU:HD21	52:Q:282:ILE:HD11	1.82	0.60
1:A:1763:A:H5'	30:q:34:ARG:CZ	2.31	0.60
1:A:2241:A:N6	31:r:82:ASN:OD1	2.32	0.60
26:i:67:GLU:HG2	30:q:33:ARG:HE	1.65	0.60
56:w:297:GLU:OE1	56:w:310:LYS:NZ	2.34	0.60
1:A:1705:A:N6	42:9:40:GLY:O	2.34	0.60
1:A:2961:C:C4	1:A:2962:C:C2	2.89	0.60
15:Y:185:VAL:HG22	36:U:9:LEU:HD21	1.82	0.60
33:I:100:GLN:NE2	48:k:35:GLN:OE1	2.35	0.60
34:N:81:GLU:O	34:N:123:ARG:NH2	2.34	0.60
1:A:2339:G:H21	1:A:2427:C:H5'	1.65	0.60
1:A:2379:C:N4	42:9:48:TRP:CZ2	2.70	0.60
1:A:3129:A:OP2	56:w:79:ILE:HD11	2.01	0.60
1:A:1749:C:OP2	1:A:2899:C:O2'	2.19	0.60
1:A:2215:C:OP1	34:N:31:LYS:CG	2.49	0.60
56:w:767:ASP:N	56:w:767:ASP:OD1	2.34	0.60
15:Y:91:ARG:NH2	15:Y:148:GLU:OE1	2.35	0.60
1:A:1811:A:H61	44:c:49:ARG:NE	1.99	0.60
1:A:2155:A:N1	29:o:26:PHE:CE1	2.62	0.60
1:A:2155:A:N3	29:o:26:PHE:CG	2.70	0.60
28:m:72:ARG:HD3	28:m:75:LEU:HD21	1.84	0.60
56:w:677:ALA:HA	56:w:680:LYS:HE2	1.83	0.60
1:A:2406:A:O2'	39:5:109:ARG:NH1	2.35	0.60
1:A:2510:U:H5''	1:A:2511:C:OP1	2.02	0.60
56:w:320:LEU:HG	56:w:350:PRO:HB3	1.84	0.60
33:I:119:HIS:O	33:I:160:LYS:NZ	2.33	0.59
40:6:155:TYR:O	40:6:267:ARG:NH1	2.34	0.59
54:TA:89:THR:CG2	54:TB:68:VAL:HG11	2.30	0.59
1:A:1939:G:O2'	1:A:1973:G:H4'	2.01	0.59
1:A:2661:U:H2'	1:A:2662:A:H8	1.67	0.59
26:i:94:LYS:NZ	26:i:102:MET:SD	2.75	0.59
54:TA:85:LEU:HD11	54:TB:67:LEU:N	2.16	0.59
54:TA:88:LYS:CD	54:TB:65:GLN:HB3	2.31	0.59
56:w:596:ARG:NH1	56:w:651:THR:OG1	2.35	0.59
1:A:1839:C:O2	1:A:1840:C:C6	2.56	0.59
50:p:79:ILE:HG12	50:p:101:VAL:HG12	1.83	0.59
55:z:186:THR:CG2	56:w:496:PRO:CA	2.71	0.59
1:A:1769:C:C4	4:F:108:ARG:HD2	2.38	0.59
1:A:2195:A:H1'	1:A:2215:C:H1'	1.85	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2868:C:O2'	8:M:77:ARG:HD3	2.02	0.59
1:A:3200:U:H3	6:K:97:LEU:HB3	1.66	0.59
32:J:21:ARG:HG3	32:J:69:LYS:HE3	1.83	0.59
33:I:93:ASN:ND2	33:I:95:MET:O	2.34	0.59
1:A:1889:C:OP1	8:M:133:LYS:NZ	2.34	0.59
25:g:142:GLU:HB3	29:o:88:ILE:HG13	1.83	0.59
30:q:40:PRO:HG3	30:q:51:GLN:HB3	1.84	0.59
32:J:25:ARG:HA	32:J:65:PRO:HA	1.84	0.59
32:J:170:GLU:HA	32:J:173:ILE:HG12	1.83	0.59
1:A:2523:C:OP2	39:5:35:VAL:HG13	2.03	0.59
1:A:3189:C:O2	31:r:154:TRP:CD2	2.56	0.59
1:A:3210:C:H42	38:E:156:ARG:HG3	1.66	0.59
19:2:82:ARG:HE	19:2:87:ARG:HG3	1.67	0.59
32:J:189:ALA:O	32:J:192:LYS:HD3	2.03	0.59
56:w:511:CYS:SG	56:w:514:ARG:NH2	2.75	0.59
56:w:535:MET:O	56:w:744:ARG:NH2	2.35	0.59
5:H:84:GLU:OE1	14:X:44:ARG:NH2	2.35	0.59
15:Y:121:ARG:HH22	36:U:32:GLY:HA2	1.68	0.59
40:6:136:ARG:NH2	40:6:140:GLU:OE1	2.36	0.59
1:A:2470:G:HO2'	7:L:36:THR:HG22	1.66	0.59
1:A:2875:A:H5''	35:P:180:GLU:HB3	1.85	0.59
32:J:40:GLY:C	56:w:698:ARG:HH12	2.07	0.59
56:w:196:LYS:HE3	59:w:801:GCP:C2	2.33	0.59
1:A:1767:G:N7	15:Y:228:ARG:NH1	2.51	0.59
1:A:2131:A:C6	31:r:168:ARG:CZ	2.86	0.59
32:J:20:ILE:HB	32:J:70:ILE:HG23	1.84	0.59
51:s:163:VAL:HG21	51:s:171:VAL:HG21	1.85	0.59
54:TA:85:LEU:CA	54:TA:88:LYS:CD	2.75	0.58
1:A:2176:C:C5'	32:J:102:ARG:HH21	2.16	0.58
1:A:2193:U:O4	1:A:2196:A:H2	1.84	0.58
1:A:3127:G:N2	1:A:3130:A:OP2	2.33	0.58
6:K:158:TYR:OH	31:r:86:VAL:HG21	2.03	0.58
32:J:42:ARG:HG3	32:J:76:ARG:HH22	1.67	0.58
37:V:79:VAL:HG12	37:V:86:VAL:HG12	1.85	0.58
56:w:115:GLN:HE21	56:w:549:ARG:HH12	1.50	0.58
1:A:1821:A:H61	17:0:97:PRO:HD3	1.67	0.58
1:A:2132:A:H62	29:o:16:GLN:NE2	1.98	0.58
1:A:2212:C:H2'	1:A:2213:A:H8	1.68	0.58
1:A:2582:A:H1'	55:z:125:ASP:CG	2.26	0.58
20:3:126:LYS:HE2	20:3:148:VAL:HG21	1.86	0.58
40:6:224:HIS:HE1	40:6:297:THR:HG23	1.68	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2950:U:H2'	1:A:2951:A:H8	1.69	0.58
3:D:194:ASN:ND2	3:D:195:ASN:OD1	2.36	0.58
20:3:106:THR:HG22	20:3:163:THR:H	1.68	0.58
33:I:41:HIS:HD2	33:I:43:GLN:H	1.52	0.58
42:9:129:GLN:HG2	42:9:134:ASN:HB2	1.85	0.58
1:A:2576:A:C1'	56:w:580:ARG:CB	2.81	0.58
51:s:239:ASN:HB2	51:s:299:PHE:HB2	1.85	0.58
54:TB:83:ASN:HA	54:TB:86:LEU:CD2	2.34	0.58
1:A:1907:A:N3	1:A:2930:U:O2'	2.36	0.58
1:A:2537:G:O2'	1:A:2634:U:OP2	2.22	0.58
1:A:2578:C:C2	55:z:119:ILE:HD13	2.38	0.58
12:T:202:GLN:OE1	43:a:122:ARG:NH2	2.37	0.58
32:J:171:ARG:NH1	49:l:75:VAL:O	2.37	0.58
55:z:104:ASN:O	56:w:642:GLY:CA	2.52	0.58
50:p:86:GLY:HA2	50:p:95:VAL:HG22	1.86	0.58
1:A:3212:C:H4'	17:0:106:ASN:OD1	2.04	0.58
54:TA:62:PRO:O	54:TA:65:GLN:HB2	2.04	0.58
1:A:2388:A:N6	3:D:127:ILE:CG2	2.57	0.57
1:A:2389:C:H5''	39:5:300:PRO:HB3	1.85	0.57
1:A:2501:C:H41	19:2:49:ARG:HB3	1.69	0.57
39:5:408:GLU:OE2	39:5:411:ARG:NH1	2.37	0.57
55:z:104:ASN:O	56:w:642:GLY:HA2	2.04	0.57
56:w:712:ARG:NH2	56:w:767:ASP:OD2	2.35	0.57
1:A:2556:A:N7	1:A:2557:C:O2	2.36	0.57
5:H:78:ARG:NH1	14:X:87:LEU:O	2.37	0.57
27:j:36:ASN:ND2	27:j:38:SER:OG	2.35	0.57
1:A:1762:A:H62	30:q:33:ARG:HD2	1.69	0.57
1:A:1998:U:O2	19:2:52:GLU:HB3	2.04	0.57
1:A:2065:A:H1'	13:W:74:ARG:O	2.04	0.57
1:A:2085:A:H2'	1:A:2086:A:C8	2.38	0.57
55:z:251:ARG:HH22	56:w:778:LEU:CA	2.13	0.57
56:w:140:ILE:HD12	56:w:159:LEU:HD21	1.85	0.57
1:A:2577:C:N4	55:z:131:ASN:N	2.52	0.57
1:A:1887:A:O4'	4:F:285:PRO:HD3	2.03	0.57
1:A:2241:A:H61	31:r:82:ASN:ND2	2.03	0.57
1:A:2961:C:H5	1:A:2962:C:N4	1.98	0.57
1:A:3102:U:H2'	1:A:3103:C:H6	1.70	0.57
55:z:134:SER:O	56:w:664:THR:CB	2.52	0.57
1:A:1848:U:OP1	8:M:53:HIS:CE1	2.57	0.57
34:N:98:HIS:HD2	34:N:100:GLY:H	1.52	0.57
54:TA:85:LEU:CB	54:TA:88:LYS:NZ	2.67	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2172:A:C8	32:J:23:ILE:CD1	2.87	0.57
1:A:2214:A:C5'	49:I:126:ILE:HD11	2.33	0.57
1:A:3157:C:H1'	52:Q:84:ARG:CB	2.30	0.57
55:z:82:ILE:HG23	55:z:83:ILE:HG22	1.86	0.57
1:A:2155:A:C4	29:o:26:PHE:CD2	2.92	0.57
1:A:2180:A:O2'	1:A:2206:C:O3'	2.23	0.57
1:A:2576:A:C5'	56:w:579:ASP:N	2.68	0.57
10:R:95:VAL:HG11	11:S:144:LEU:HD23	1.86	0.57
55:z:138:MET:SD	56:w:636:LEU:HD22	2.45	0.57
56:w:71:ARG:HB2	56:w:137:VAL:HG12	1.87	0.57
7:L:92:PRO:HD3	7:L:99:ARG:HE	1.70	0.57
15:Y:128:SER:HB2	15:Y:131:ARG:HH11	1.70	0.57
33:I:116:LEU:HD22	33:I:121:ILE:HD11	1.87	0.57
40:6:220:SER:HA	40:6:268:LEU:HA	1.85	0.57
52:Q:96:ARG:NH1	52:Q:285:GLU:OE1	2.36	0.57
1:A:2065:A:C5	13:W:74:ARG:HD2	2.40	0.57
49:I:68:LEU:HD23	49:I:70:THR:HG23	1.87	0.57
1:A:2178:A:C2	56:w:717:GLU:CG	2.84	0.56
1:A:2529:U:OP2	3:D:208:ARG:NE	2.38	0.56
1:A:2734:A:H2'	1:A:2735:G:H8	1.69	0.56
45:d:67:ILE:HA	45:d:70:GLU:HG3	1.85	0.56
1:A:2235:C:H5	6:K:78:SER:OG	1.78	0.56
1:A:2960:U:OP2	56:w:710:GLN:HG3	2.04	0.56
33:I:207:LEU:HD11	54:TB:86:LEU:CD1	2.31	0.56
1:A:1992:C:C4	3:D:274:ARG:HB2	2.40	0.56
1:A:2085:A:H2'	1:A:2086:A:H8	1.69	0.56
1:A:2389:C:C5'	39:5:300:PRO:HB3	2.35	0.56
1:A:3188:U:OP2	21:4:84:ARG:NE	2.23	0.56
22:8:139:MET:HG2	24:e:275:PHE:HA	1.85	0.56
27:j:102:GLN:NE2	27:j:106:GLU:OE2	2.38	0.56
33:I:177:LEU:HB3	48:k:22:PRO:HB3	1.87	0.56
50:p:98:LYS:HG3	50:p:138:GLU:HG2	1.87	0.56
1:A:2933:G:N2	1:A:2936:U:O2	2.36	0.56
10:R:57:ARG:HE	11:S:169:ARG:HH21	1.52	0.56
33:I:139:LYS:O	54:TA:48:LEU:CB	2.51	0.56
1:A:2718:C:OP1	17:0:82:LYS:NZ	2.32	0.56
15:Y:115:LEU:HD21	15:Y:127:PRO:HD2	1.87	0.56
56:w:230:LYS:HD2	56:w:231:THR:HG23	1.87	0.56
1:A:1713:A:N1	39:5:69:TRP:CD1	2.74	0.56
1:A:2016:C:OP2	8:M:59:ARG:NH1	2.38	0.56
24:e:55:ARG:O	24:e:156:ASN:ND2	2.38	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5:296:ALA:HB3	39:5:302:ARG:HG3	1.86	0.56
1:A:2678:A:C2	17:0:80:ALA:HB1	2.39	0.56
38:E:248:ILE:HG22	38:E:250:ARG:HG2	1.86	0.56
39:5:114:GLU:H	39:5:118:GLN:HE21	1.53	0.56
42:9:103:ASP:OD2	42:9:117:TYR:CE1	2.58	0.56
48:k:58:ASP:OD1	54:TA:56:ALA:HB3	2.05	0.56
1:A:1733:C:N3	5:H:72:ARG:HB2	2.21	0.56
1:A:2536:G:H2'	1:A:2537:G:H8	1.70	0.56
1:A:3125:A:OP1	56:w:199:LYS:NZ	2.37	0.56
18:1:26:THR:O	30:q:117:ARG:NH2	2.39	0.56
37:V:33:ARG:NH2	45:d:61:ARG:O	2.39	0.56
54:TB:74:LEU:CD2	54:TB:79:ILE:HG12	2.35	0.56
15:Y:143:ASP:OD2	42:9:137:ARG:NH2	2.37	0.56
36:U:66:ALA:HB2	36:U:100:ALA:HA	1.88	0.56
1:A:1936:A:OP1	1:A:1938:A:N6	2.38	0.56
1:A:2234:C:HO2'	1:A:2688:C:HO2'	1.54	0.56
1:A:2508:C:H2'	1:A:2509:A:H8	1.70	0.56
10:R:134:ASP:O	10:R:136:LYS:NZ	2.39	0.56
12:T:94:ILE:HA	12:T:97:MET:HE2	1.87	0.56
35:P:104:SER:OG	40:6:150:ARG:NH2	2.35	0.56
37:V:112:GLU:OE1	45:d:74:ARG:NH1	2.38	0.56
54:TA:85:LEU:HB2	54:TA:88:LYS:HZ2	1.71	0.56
56:w:84:THR:HG22	59:w:801:GCP:O1A	2.05	0.56
1:A:1702:A:N7	19:2:66:TRP:CD2	2.74	0.55
1:A:2172:A:C2'	32:J:23:ILE:HD11	2.10	0.55
1:A:2176:C:H5'	32:J:102:ARG:CZ	2.36	0.55
1:A:2235:C:C6	6:K:78:SER:OG	2.56	0.55
1:A:2390:A:H5'	39:5:299:ARG:HB3	1.88	0.55
1:A:2740:A:N3	1:A:2921:A:O2'	2.38	0.55
1:A:3128:A:N6	56:w:744:ARG:HB2	2.22	0.55
20:3:148:VAL:HG13	40:6:360:ARG:HA	1.87	0.55
23:b:144:ARG:NH1	23:b:147:GLU:OE2	2.39	0.55
1:A:2146:A:N6	23:b:117:LYS:HB2	2.22	0.55
1:A:2484:C:C5	1:A:2485:U:C5	2.94	0.55
7:L:53:ARG:HH11	7:L:56:ARG:HH12	1.54	0.55
8:M:44:ARG:HG3	8:M:45:ARG:HG3	1.87	0.55
56:w:318:VAL:O	56:w:323:THR:OG1	2.23	0.55
1:A:1688:A:OP2	14:X:5:LYS:NZ	2.38	0.55
1:A:2065:A:C8	13:W:74:ARG:HB2	2.39	0.55
1:A:2178:A:C4	56:w:717:GLU:CG	2.89	0.55
1:A:2347:C:H2'	1:A:2348:A:C8	2.41	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:g:150:LYS:NZ	29:o:79:THR:O	2.38	0.55
40:6:184:LEU:HB3	50:p:191:LYS:HB2	1.87	0.55
56:w:345:VAL:HG13	56:w:349:LEU:HD12	1.89	0.55
1:A:1809:U:H2'	1:A:1810:A:H4'	1.88	0.55
1:A:1911:C:H2'	1:A:1912:A:H8	1.71	0.55
1:A:2615:A:C2	7:L:58:ILE:HD12	2.41	0.55
1:A:2906:C:N3	18:1:19:ARG:NH2	2.55	0.55
1:A:2964:U:O2	21:4:69:LYS:NZ	2.38	0.55
1:A:1805:A:OP2	37:V:94:HIS:NE2	2.35	0.55
1:A:2084:A:N6	29:o:71:PHE:HB2	2.21	0.55
1:A:2176:C:H5'	32:J:102:ARG:NH2	2.22	0.55
15:Y:198:ARG:NH2	19:2:70:LEU:O	2.39	0.55
45:d:124:ARG:NH1	45:d:201:SER:OG	2.40	0.55
54:TA:81:ASP:CB	54:TB:64:ILE:HG21	2.36	0.55
1:A:1990:G:OP1	3:D:269:ARG:NH2	2.39	0.55
1:A:2065:A:OP1	46:f:48:TYR:N	2.39	0.55
1:A:2960:U:O2	56:w:709:ALA:CB	2.47	0.55
11:S:161:ILE:HD11	11:S:194:ARG:HD2	1.89	0.55
29:o:55:THR:OG1	29:o:58:GLN:NE2	2.40	0.55
46:f:166:PHE:HA	46:f:169:ILE:HG22	1.89	0.55
54:TA:82:LEU:CD2	54:TB:67:LEU:CD1	2.82	0.55
55:z:251:ARG:HH12	56:w:778:LEU:HD13	1.69	0.55
1:A:3191:A:C2	31:r:133:PRO:HB3	2.42	0.55
24:e:211:GLY:H	24:e:233:PHE:HB2	1.72	0.55
36:U:130:LEU:HD12	37:V:107:THR:HG21	1.88	0.55
40:6:92:LEU:HB2	40:6:170:ARG:HG3	1.88	0.55
45:d:165:THR:HG23	45:d:167:HIS:H	1.71	0.55
46:f:138:GLN:HE21	46:f:139:ASP:H	1.53	0.55
54:TA:85:LEU:O	54:TA:88:LYS:HD2	2.06	0.55
56:w:573:ARG:O	56:w:680:LYS:NZ	2.40	0.55
1:A:1992:C:N3	3:D:274:ARG:HB2	2.20	0.55
1:A:2507:A:O2'	1:A:2508:C:OP1	2.23	0.55
1:A:2945:A:O2'	1:A:2947:U:O4	2.24	0.55
30:q:48:PRO:HG2	30:q:51:GLN:HG3	1.87	0.55
31:r:36:ARG:NH1	48:k:80:HIS:O	2.40	0.55
33:I:47:LEU:HD22	34:N:226:ILE:HG12	1.87	0.55
1:A:1939:G:C8	3:D:259:LYS:HD2	2.42	0.55
1:A:2060:A:O2'	1:A:2061:C:H5''	2.06	0.55
1:A:2390:A:H4'	39:5:300:PRO:HD3	1.87	0.55
1:A:2578:C:H42	55:z:129:ALA:CA	1.92	0.55
23:b:85:ARG:NH2	23:b:87:GLU:OE2	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1731:A:N1	26:i:118:TYR:CB	2.70	0.55
1:A:1731:A:N1	26:i:118:TYR:CG	2.73	0.55
1:A:1827:C:O2'	10:R:48:ARG:NH1	2.39	0.55
1:A:2372:U:O4	51:s:270:LYS:HD2	2.07	0.55
1:A:2852:C:H3'	18:l:44:LEU:O	2.07	0.55
1:A:3189:C:H5	21:4:83:LYS:HE2	1.72	0.55
32:J:90:PHE:HB3	32:J:120:ILE:HD13	1.87	0.55
35:P:118:SER:O	35:P:121:ASN:ND2	2.40	0.55
39:5:112:LEU:HD12	39:5:310:ALA:HB1	1.87	0.55
46:f:97:ALA:HB2	46:f:182:VAL:HG12	1.89	0.55
48:k:65:ASP:N	48:k:65:ASP:OD1	2.39	0.55
54:TB:83:ASN:O	54:TB:86:LEU:HD23	2.06	0.55
54:TC:143:VAL:CB	56:w:292:ALA:HB2	2.37	0.55
1:A:2075:U:O2'	1:A:2833:A:N7	2.30	0.54
1:A:2406:A:N1	39:5:111:ARG:NH1	2.54	0.54
1:A:3206:C:N3	38:E:178:ILE:HD12	2.22	0.54
20:3:175:ASP:HB3	20:3:178:GLN:HB2	1.89	0.54
38:E:134:SER:OG	38:E:135:LYS:N	2.41	0.54
56:w:72:ASN:HB3	56:w:159:LEU:HD12	1.89	0.54
25:g:59:ASP:N	25:g:59:ASP:OD1	2.41	0.54
48:k:14:LYS:HE3	48:k:69:GLY:HA2	1.88	0.54
50:p:133:LEU:HD21	50:p:157:MET:HE1	1.89	0.54
55:z:185:VAL:HG13	56:w:497:PRO:C	2.32	0.54
1:A:1822:U:O2	1:A:2707:A:O2'	2.25	0.54
1:A:2302:U:H2'	1:A:2303:A:H8	1.71	0.54
23:b:56:ARG:NH2	47:h:147:ASN:O	2.40	0.54
36:U:68:VAL:HG22	36:U:97:VAL:HG12	1.89	0.54
39:5:107:HIS:HD2	39:5:109:ARG:H	1.55	0.54
43:a:72:THR:O	44:c:256:ARG:NH2	2.41	0.54
50:p:79:ILE:HD13	50:p:147:LEU:HD11	1.89	0.54
1:A:1812:C:N4	26:i:36:LEU:HD12	2.21	0.54
2:B:1640:A:O3'	40:6:126:ARG:NH1	2.40	0.54
30:q:138:GLN:O	30:q:142:ASN:ND2	2.40	0.54
32:J:163:GLU:HA	32:J:166:ALA:HB3	1.89	0.54
36:U:19:VAL:HB	42:9:136:LEU:HD23	1.89	0.54
1:A:2193:U:O4	1:A:2196:A:N1	2.41	0.54
1:A:2205:U:O4	56:w:725:LYS:NZ	2.41	0.54
1:A:2719:G:H21	17:0:79:ALA:HA	1.73	0.54
1:A:3210:C:N4	38:E:156:ARG:C	2.65	0.54
6:K:61:ASN:HD22	6:K:64:HIS:HD2	1.54	0.54
22:8:85:ILE:HB	46:f:128:PRO:HG3	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:m:38:ALA:HB3	46:f:179:PRO:HB3	1.89	0.54
32:J:149:ARG:NH1	49:l:101:LEU:O	2.39	0.54
1:A:1857:U:H2'	1:A:1858:G:H8	1.73	0.54
1:A:2373:A:N3	51:s:274:PHE:CD2	2.76	0.54
1:A:2408:U:H2'	1:A:2409:A:H8	1.73	0.54
1:A:2536:G:H2'	1:A:2537:G:C8	2.43	0.54
1:A:2576:A:C2'	55:z:132:GLN:OE1	2.46	0.54
15:Y:113:LEU:HB3	36:U:27:GLN:HG2	1.89	0.54
54:TA:74:LEU:HD22	54:TA:78:GLU:OE1	2.08	0.54
1:A:3002:G:H2'	1:A:3003:A:H8	1.73	0.54
15:Y:191:ASN:ND2	37:V:216:TYR:OH	2.41	0.54
33:I:95:MET:HB3	33:I:156:SER:HB2	1.90	0.54
38:E:96:ARG:NH1	38:E:315:PRO:O	2.41	0.54
43:a:83:ASN:O	43:a:95:ARG:NH2	2.41	0.54
44:c:59:ARG:HH22	44:c:182:GLU:HA	1.73	0.54
44:c:86:ASP:OD1	44:c:86:ASP:N	2.41	0.54
54:TA:68:VAL:HG21	54:TB:85:LEU:CB	2.36	0.54
1:A:1994:A:O2'	1:A:1995:A:OP2	2.22	0.54
1:A:2546:G:C6	1:A:2547:C:N4	2.76	0.54
1:A:3189:C:C5	21:4:83:LYS:HE2	2.43	0.54
32:J:161:SER:HA	32:J:164:LEU:HG	1.89	0.54
54:TA:88:LYS:HZ3	54:TB:65:GLN:HB3	1.68	0.54
56:w:591:VAL:HG11	56:w:670:VAL:HG22	1.90	0.54
1:A:2079:C:C5	1:A:2080:U:O2	2.61	0.54
1:A:2655:G:N2	1:A:2659:C:O2'	2.40	0.54
35:P:58:LEU:HD23	50:p:177:ARG:HH21	1.72	0.54
56:w:277:ARG:NH1	56:w:304:ASP:O	2.40	0.54
1:A:3043:C:H2'	1:A:3043:C:O2	2.08	0.53
7:L:90:CYS:O	7:L:99:ARG:CZ	2.57	0.53
33:I:98:VAL:HG12	33:I:153:LEU:HD12	1.91	0.53
54:TA:85:LEU:CA	54:TA:88:LYS:HG3	2.36	0.53
55:z:124:ALA:HB3	56:w:582:LEU:CD2	2.33	0.53
1:A:1703:C:O2'	1:A:1704:U:OP2	2.22	0.53
1:A:1762:A:N7	30:q:33:ARG:HG3	2.23	0.53
1:A:1836:A:N6	1:A:1837:C:C5	2.76	0.53
1:A:1952:U:H2'	1:A:1953:A:H8	1.73	0.53
1:A:2175:C:HO2'	32:J:102:ARG:HG3	0.49	0.53
1:A:2577:C:C2	55:z:132:GLN:CG	2.90	0.53
1:A:2837:A:H2'	1:A:2838:A:C8	2.43	0.53
17:0:128:GLU:HG2	45:d:289:PRO:HG2	1.89	0.53
56:w:636:LEU:HD12	56:w:644:PRO:HB3	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1839:C:H2'	1:A:1840:C:C6	2.44	0.53
1:A:2479:C:C2	1:A:2480:A:C8	2.97	0.53
5:H:65:ALA:HB3	5:H:71:PRO:HA	1.90	0.53
55:z:251:ARG:HH21	56:w:778:LEU:CA	2.17	0.53
1:A:3129:A:H2	56:w:537:GLU:OE2	1.91	0.53
1:A:3189:C:H1'	31:r:154:TRP:HB3	1.90	0.53
54:TA:86:LEU:HD12	54:TB:71:ILE:HD13	1.91	0.53
1:A:1809:U:C5	1:A:1810:A:H1'	2.44	0.53
38:E:206:VAL:HG21	38:E:289:VAL:HG22	1.91	0.53
41:7:114:ASP:OD1	41:7:114:ASP:N	2.38	0.53
54:TA:64:ILE:HD12	54:TA:64:ILE:H	1.73	0.53
55:z:132:GLN:HG2	56:w:668:ALA:HB2	1.79	0.53
55:z:185:VAL:HG13	56:w:498:SER:CA	2.37	0.53
1:A:2479:C:H2'	1:A:2479:C:O2	2.08	0.53
1:A:2740:A:H2'	1:A:2741:A:H8	1.74	0.53
1:A:2961:C:O2	1:A:2961:C:H2'	2.09	0.53
12:T:94:ILE:HD11	12:T:106:LEU:HD11	1.89	0.53
23:b:135:ASN:OD1	43:a:44:ASN:ND2	2.39	0.53
49:l:68:LEU:HD22	49:l:70:THR:CG2	2.39	0.53
1:A:1839:C:O2	1:A:1839:C:H2'	2.08	0.53
1:A:2086:A:H2'	1:A:2087:U:H6	1.74	0.53
1:A:2302:U:H2'	1:A:2303:A:C8	2.44	0.53
1:A:2577:C:C1'	55:z:132:GLN:CG	2.86	0.53
1:A:2605:C:OP2	1:A:2606:U:O2'	2.22	0.53
1:A:2678:A:H2	17:0:80:ALA:CA	2.22	0.53
1:A:2719:G:N2	17:0:79:ALA:HA	2.23	0.53
1:A:3115:U:H2'	1:A:3116:C:C6	2.44	0.53
1:A:3144:A:H2'	1:A:3145:A:H8	1.72	0.53
14:X:64:ASP:OD1	14:X:64:ASP:N	2.42	0.53
51:s:375:ASN:H	51:s:391:ASN:HD22	1.56	0.53
52:Q:117:LEU:HD12	52:Q:151:LEU:HD21	1.90	0.53
1:A:2190:C:O2'	32:J:146:GLY:HA2	2.08	0.53
1:A:2578:C:C2	55:z:119:ILE:CD1	2.91	0.53
1:A:3042:U:H5	1:A:3043:C:C5	2.26	0.53
1:A:3198:A:C2'	1:A:3201:A:H62	2.16	0.53
35:P:68:TRP:O	35:P:70:THR:N	2.39	0.53
54:TA:82:LEU:CG	54:TB:67:LEU:HD11	2.39	0.53
55:z:251:ARG:NH2	56:w:778:LEU:HD22	2.24	0.53
1:A:1828:A:H4'	1:A:1829:A:C8	2.43	0.53
1:A:2240:C:N4	31:r:196:HIS:CB	2.66	0.53
9:O:143:THR:OG1	9:O:146:ASN:ND2	2.36	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Z:69:VAL:HG12	16:Z:119:ILE:HG12	1.91	0.53
45:d:180:THR:HG23	45:d:225:TYR:HB2	1.91	0.53
54:TA:82:LEU:CD2	54:TB:67:LEU:HD13	2.38	0.53
1:A:2796:G:H21	5:H:88:HIS:HE1	1.43	0.53
2:B:1607:U:O4	2:B:1664:G:O6	2.27	0.53
23:b:34:SER:OG	23:b:36:ASP:O	2.24	0.53
35:P:57:GLU:O	50:p:177:ARG:NH2	2.41	0.53
44:c:108:LEU:HG	44:c:110:ILE:HG13	1.90	0.53
45:d:187:GLU:O	45:d:218:THR:OG1	2.27	0.53
47:h:62:PRO:HD3	47:h:133:PRO:HB3	1.91	0.53
48:k:57:HIS:CG	54:TA:53:LEU:HD22	2.39	0.53
1:A:3063:G:O2'	1:A:3066:C:OP2	2.25	0.52
54:TA:82:LEU:CG	54:TB:67:LEU:CD1	2.87	0.52
56:w:411:SER:OG	56:w:436:VAL:O	2.26	0.52
1:A:2067:C:H4'	46:f:60:LYS:HB2	1.92	0.52
1:A:2678:A:C2	17:0:80:ALA:HB2	2.42	0.52
1:A:2850:U:H2'	1:A:2851:A:N3	2.25	0.52
24:e:162:ARG:HH21	24:e:164:LYS:HE2	1.73	0.52
55:z:251:ARG:NH2	56:w:777:GLY:C	2.46	0.52
22:8:101:ARG:NH1	24:e:82:SER:OG	2.41	0.52
33:I:93:ASN:HD21	33:I:156:SER:H	1.56	0.52
35:P:82:ARG:NH1	35:P:95:GLU:OE2	2.40	0.52
44:c:160:LEU:HD21	44:c:223:MET:HG3	1.91	0.52
45:d:208:VAL:HG23	45:d:252:LEU:HB2	1.90	0.52
48:k:27:VAL:HG12	48:k:62:PRO:HG3	1.90	0.52
55:z:251:ARG:NH1	56:w:778:LEU:CD1	2.67	0.52
1:A:1752:U:H2'	1:A:1753:A:H8	1.74	0.52
1:A:1773:A:OP2	44:c:31:VAL:N	2.42	0.52
1:A:1809:U:O2'	1:A:1810:A:P	2.67	0.52
1:A:1821:A:N6	17:0:97:PRO:HD3	2.23	0.52
1:A:2060:A:N1	1:A:2061:C:C5	2.76	0.52
1:A:3128:A:C6	56:w:744:ARG:CB	2.92	0.52
7:L:92:PRO:CD	7:L:99:ARG:HE	2.23	0.52
41:7:247:ASN:HD21	41:7:251:ILE:H	1.58	0.52
42:9:103:ASP:OD2	42:9:117:TYR:HE1	1.91	0.52
45:d:219:ARG:HD3	45:d:239:PRO:HB2	1.90	0.52
54:TB:74:LEU:HD12	54:TB:78:GLU:HG2	1.90	0.52
1:A:2355:A:H3'	1:A:2356:A:H4'	1.92	0.52
1:A:2961:C:N3	1:A:2962:C:C5	2.77	0.52
1:A:3044:A:H2'	1:A:3045:A:H8	1.74	0.52
1:A:3089:A:N6	55:z:232:ARG:CD	2.71	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:126:LYS:NZ	4:F:138:HIS:O	2.42	0.52
11:S:194:ARG:HE	23:b:19:LEU:HG	1.74	0.52
47:h:49:ILE:HG23	47:h:50:LEU:HD12	1.90	0.52
51:s:103:ASP:OD1	51:s:103:ASP:N	2.42	0.52
1:A:1736:A:N6	1:A:1761:A:O2'	2.43	0.52
1:A:2041:U:H2'	1:A:2042:U:C6	2.45	0.52
1:A:3051:A:C6	1:A:3115:U:H4'	2.45	0.52
13:W:61:VAL:HG13	13:W:65:ASN:HB2	1.92	0.52
37:V:178:SER:OG	37:V:181:ASP:OD1	2.27	0.52
40:6:187:VAL:HG23	40:6:319:PHE:HB3	1.91	0.52
40:6:286:ARG:NH1	40:6:295:GLN:O	2.43	0.52
47:h:105:ALA:HB1	47:h:111:VAL:HG22	1.92	0.52
1:A:2009:G:OP1	26:i:112:LYS:HD3	2.09	0.52
1:A:2257:C:OP1	27:j:61:LYS:HB2	2.10	0.52
55:z:117:ASP:OD1	55:z:131:ASN:ND2	2.42	0.52
1:A:2373:A:C2	51:s:274:PHE:CD2	2.98	0.52
1:A:2678:A:C2	17:0:80:ALA:HA	2.45	0.52
3:D:111:ARG:NH2	3:D:179:GLY:O	2.43	0.52
5:H:99:THR:HG22	5:H:140:PHE:HZ	1.74	0.52
23:b:26:LEU:HD22	23:b:105:ALA:HA	1.92	0.52
31:r:135:LEU:HD11	31:r:139:VAL:HB	1.92	0.52
40:6:45:LEU:HD23	46:f:64:LYS:HB2	1.90	0.52
48:k:63:CYS:HA	48:k:77:ARG:HA	1.92	0.52
1:A:1802:A:N7	1:A:1805:A:N6	2.57	0.52
1:A:2194:U:O2	33:I:125:VAL:HG11	2.05	0.52
14:X:4:HIS:O	26:i:101:ARG:NH1	2.42	0.52
41:7:64:LYS:NZ	41:7:82:ASN:OD1	2.38	0.52
41:7:203:THR:HG22	41:7:280:VAL:H	1.73	0.52
51:s:178:ASP:HA	51:s:181:VAL:HG12	1.91	0.52
54:TA:57:PRO:C	54:TA:58:LYS:HD3	2.35	0.52
55:z:138:MET:CE	56:w:636:LEU:HD21	2.25	0.52
1:A:1731:A:OP1	5:H:74:HIS:CE1	2.63	0.52
1:A:2377:G:H21	42:9:32:GLY:CA	2.23	0.52
1:A:2383:U:O2'	39:5:92:LEU:HD23	2.10	0.52
1:A:2577:C:C5	55:z:131:ASN:HB2	2.45	0.52
1:A:3210:C:N4	38:E:156:ARG:CA	2.73	0.52
9:O:124:GLU:OE1	9:O:128:ASN:ND2	2.43	0.52
11:S:94:ARG:HH21	44:c:313:PRO:HB3	1.75	0.52
14:X:23:ARG:NH2	14:X:219:GLU:OE2	2.43	0.52
27:j:45:GLU:HG2	27:j:63:GLN:HE22	1.75	0.52
51:s:403:GLU:HG3	51:s:404:THR:HG23	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:TA:89:THR:HG23	54:TB:68:VAL:HG13	1.90	0.52
55:z:251:ARG:HH22	56:w:778:LEU:HA	1.45	0.52
1:A:1709:G:H4'	1:A:1710:A:OP1	2.09	0.51
1:A:1939:G:N3	1:A:1939:G:C3'	2.73	0.51
1:A:2209:G:C2'	1:A:2210:C:OP1	2.57	0.51
56:w:364:LYS:HG2	56:w:366:ASP:H	1.73	0.51
1:A:1805:A:H5'	37:V:96:ARG:HD3	1.92	0.51
1:A:1939:G:H21	1:A:2495:U:C1'	2.11	0.51
1:A:3200:U:O4	6:K:97:LEU:HD22	2.11	0.51
15:Y:144:LYS:NZ	15:Y:148:GLU:OE2	2.42	0.51
27:j:112:LYS:NZ	40:6:311:MET:O	2.44	0.51
55:z:185:VAL:HG13	56:w:497:PRO:O	2.07	0.51
1:A:1745:U:O4	20:3:108:LYS:NZ	2.43	0.51
1:A:2086:A:H2'	1:A:2087:U:C6	2.45	0.51
1:A:2155:A:N3	29:o:26:PHE:CD1	2.78	0.51
1:A:3165:C:H2'	1:A:3166:U:C6	2.44	0.51
24:e:90:ARG:NH2	24:e:94:GLU:OE2	2.43	0.51
51:s:138:ASP:OD2	51:s:138:ASP:N	2.41	0.51
52:Q:108:ILE:HD13	52:Q:166:LEU:HD22	1.90	0.51
1:A:1829:A:H2'	1:A:1830:G:H8	1.74	0.51
1:A:2379:C:C4	42:9:48:TRP:CZ2	2.99	0.51
1:A:2493:C:C4	1:A:2540:C:C2	2.81	0.51
1:A:2797:C:H2'	1:A:2798:A:H8	1.75	0.51
40:6:214:TRP:HB2	40:6:240:ILE:HB	1.91	0.51
1:A:1814:A:N3	1:A:1862:U:O2'	2.41	0.51
1:A:2082:G:H2'	1:A:2083:U:O4'	2.10	0.51
1:A:2377:G:H21	42:9:32:GLY:HA2	1.75	0.51
1:A:2453:G:O6	1:A:2672:A:N6	2.42	0.51
35:P:73:PRO:HG3	35:P:80:ARG:HH22	1.75	0.51
54:TA:88:LYS:HD2	54:TB:68:VAL:HG21	1.92	0.51
56:w:163:VAL:HG12	56:w:191:ILE:HD11	1.92	0.51
1:A:2003:A:OP2	1:A:2734:A:O2'	2.27	0.51
1:A:2035:U:O2'	8:M:70:GLY:HA3	2.10	0.51
28:m:70:GLU:O	28:m:72:ARG:N	2.43	0.51
9:O:32:LEU:HB3	9:O:52:MET:HE2	1.93	0.51
41:7:148:MET:HE1	41:7:255:HIS:HB2	1.92	0.51
54:TA:82:LEU:CB	54:TB:67:LEU:HD11	2.39	0.51
1:A:2524:A:C6	3:D:92:ARG:CZ	2.94	0.51
24:e:122:ASP:O	24:e:126:GLN:NE2	2.44	0.51
32:J:149:ARG:NH1	49:l:102:GLY:O	2.44	0.51
33:I:139:LYS:C	54:TA:48:LEU:CD1	2.80	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5:278:PHE:HA	51:s:156:TYR:HE2	1.76	0.51
1:A:1868:G:H2'	8:M:40:PRO:HG3	1.93	0.51
1:A:1939:G:N3	1:A:1939:G:C2'	2.73	0.51
1:A:3210:C:H42	38:E:156:ARG:CG	2.24	0.51
4:F:263:LEU:HA	4:F:266:VAL:HG12	1.92	0.51
9:O:49:VAL:HG21	9:O:121:ALA:HB3	1.92	0.51
25:g:154:ASP:OD2	25:g:154:ASP:N	2.44	0.51
54:TA:53:LEU:HD23	54:TA:53:LEU:H	1.76	0.51
54:TA:74:LEU:CD1	54:TA:78:GLU:HB3	2.32	0.51
55:z:121:VAL:HG13	55:z:161:ALA:HB2	1.93	0.51
56:w:403:ASN:HD22	56:w:445:ASP:HA	1.76	0.51
1:A:1702:A:H8	19:2:66:TRP:CB	2.24	0.51
1:A:2292:G:OP1	10:R:11:ARG:HD3	2.11	0.51
1:A:2629:A:N3	1:A:3079:G:O2'	2.43	0.51
1:A:2719:G:H2'	1:A:2720:A:H8	1.76	0.51
16:Z:138:CYS:SG	16:Z:139:LEU:N	2.84	0.51
24:e:183:THR:HG23	24:e:186:GLY:H	1.76	0.51
32:J:120:ILE:HA	32:J:123:ILE:HG22	1.93	0.51
50:p:182:ASN:OD1	50:p:185:ARG:NH1	2.43	0.51
54:TA:77:LEU:O	54:TA:80:SER:OG	2.25	0.51
1:A:1693:C:H6	15:Y:178:TRP:CD1	2.29	0.50
1:A:1894:G:H2'	1:A:1895:C:H6	1.76	0.50
1:A:2155:A:C5	29:o:26:PHE:CE2	2.98	0.50
1:A:2157:U:H5'	31:r:182:ARG:NH1	2.26	0.50
1:A:3124:U:O2	1:A:3124:U:H2'	2.10	0.50
1:A:3189:C:C2	31:r:154:TRP:CD2	2.99	0.50
6:K:74:GLN:HA	31:r:161:PRO:HA	1.92	0.50
20:3:184:THR:HG21	40:6:370:ARG:HG3	1.93	0.50
33:I:54:ILE:HD12	34:N:211:ASN:HB3	1.93	0.50
1:A:1755:A:H4'	5:H:72:ARG:HH22	1.77	0.50
1:A:1791:G:OP2	19:2:82:ARG:HD3	2.11	0.50
1:A:2288:A:O2'	4:F:101:MET:HE3	2.12	0.50
17:0:163:GLU:OE2	17:0:181:ARG:NH1	2.44	0.50
54:TA:85:LEU:HB3	54:TA:88:LYS:CE	2.38	0.50
55:z:188:GLU:CD	56:w:498:SER:OG	2.54	0.50
1:A:1912:A:H2'	1:A:1913:G:C8	2.46	0.50
38:E:69:ASP:HB2	38:E:171:PRO:HB3	1.93	0.50
56:w:307:PRO:O	56:w:309:GLU:N	2.43	0.50
1:A:1813:C:H5	26:i:36:LEU:CD2	2.21	0.50
1:A:1979:U:H2'	1:A:1980:A:H8	1.77	0.50
1:A:2055:U:C4	29:o:71:PHE:CD2	2.99	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3115:U:H2'	1:A:3116:C:H6	1.75	0.50
39:5:103:CYS:SG	39:5:104:TYR:N	2.85	0.50
44:c:60:ARG:NH1	44:c:65:ASN:O	2.40	0.50
45:d:213:THR:HG23	45:d:247:VAL:HG12	1.94	0.50
54:TB:77:LEU:O	54:TB:77:LEU:HD23	2.11	0.50
1:A:1740:A:H5''	8:M:133:LYS:HZ1	1.76	0.50
1:A:2121:G:H2'	1:A:2122:A:H8	1.77	0.50
1:A:2388:A:C6	3:D:141:LEU:HD23	2.47	0.50
1:A:2395:A:C8	39:5:384:HIS:CE1	2.99	0.50
1:A:2740:A:H2'	1:A:2741:A:C8	2.47	0.50
1:A:3200:U:H4'	1:A:3201:A:H5''	1.93	0.50
44:c:93:VAL:HG12	44:c:180:LEU:HD12	1.93	0.50
1:A:1806:U:H1'	1:A:1807:U:OP2	2.11	0.50
1:A:2005:C:H2'	1:A:2006:C:C6	2.47	0.50
1:A:2108:G:N7	34:N:67:LYS:NZ	2.60	0.50
1:A:2373:A:C6	51:s:274:PHE:CD1	2.99	0.50
1:A:2590:A:H2'	1:A:2591:A:C8	2.45	0.50
1:A:3128:A:C6	56:w:744:ARG:HB2	2.47	0.50
1:A:3203:A:O2'	38:E:303:LYS:CE	2.60	0.50
24:e:119:ASP:OD2	24:e:119:ASP:N	2.42	0.50
54:TA:76:LEU:H	54:TA:76:LEU:HD12	1.76	0.50
56:w:189:PRO:HG2	56:w:350:PRO:HG3	1.93	0.50
1:A:1992:C:C2	3:D:274:ARG:HB2	2.47	0.50
38:E:207:THR:HG21	38:E:267:THR:OG1	2.08	0.50
39:5:353:PHE:HB3	39:5:416:LEU:HD11	1.93	0.50
43:a:109:ILE:HG12	43:a:123:TRP:HB2	1.94	0.50
1:A:1839:C:C2	1:A:1840:C:H5	2.25	0.50
1:A:2073:A:C5	1:A:2074:A:H1'	2.47	0.50
1:A:2174:G:O2'	32:J:100:GLY:HA3	2.12	0.50
1:A:2692:G:N1	1:A:2696:A:OP2	2.28	0.50
8:M:119:THR:O	8:M:123:ASN:ND2	2.45	0.50
11:S:133:VAL:HG11	11:S:154:VAL:HG11	1.94	0.50
1:A:1762:A:N7	30:q:33:ARG:CG	2.75	0.50
1:A:1939:G:N3	1:A:2495:U:H1'	2.22	0.50
3:D:108:ASP:OD2	3:D:149:ARG:NH1	2.44	0.50
4:F:284:TYR:O	4:F:290:TYR:OH	2.30	0.50
22:8:150:LEU:HB2	24:e:212:HIS:HE1	1.75	0.50
50:p:71:ASP:OD1	50:p:71:ASP:N	2.44	0.50
1:A:1713:A:O2'	1:A:1714:C:OP1	2.29	0.49
1:A:1939:G:N7	3:D:259:LYS:HB2	2.26	0.49
1:A:1952:U:H2'	1:A:1953:A:C8	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2439:U:H2'	1:A:2440:G:H8	1.77	0.49
1:A:2642:C:H2'	1:A:2643:G:C8	2.47	0.49
1:A:2673:G:H5''	12:T:112:LYS:HB2	1.94	0.49
24:e:177:GLU:O	24:e:190:ARG:NH2	2.45	0.49
28:m:54:VAL:HG21	28:m:75:LEU:HD23	1.93	0.49
46:f:96:THR:HB	46:f:154:GLU:HG3	1.94	0.49
54:TA:85:LEU:HD11	54:TB:67:LEU:CA	2.41	0.49
56:w:251:ASN:O	56:w:253:GLY:N	2.45	0.49
1:A:3144:A:H2'	1:A:3145:A:C8	2.46	0.49
39:5:215:GLU:OE2	39:5:366:ASN:ND2	2.45	0.49
54:TA:81:ASP:O	54:TA:85:LEU:HG	2.12	0.49
55:z:144:ILE:HB	55:z:180:VAL:HB	1.94	0.49
1:A:1823:A:O2'	43:a:126:HIS:ND1	2.46	0.49
1:A:1911:C:H2'	1:A:1912:A:C8	2.47	0.49
1:A:2142:A:O2'	1:A:2262:C:OP1	2.21	0.49
1:A:2213:A:H2'	49:l:126:ILE:HD12	1.95	0.49
1:A:3210:C:N4	38:E:156:ARG:O	2.45	0.49
11:S:103:SER:O	11:S:103:SER:OG	2.28	0.49
13:W:100:THR:OG1	13:W:132:HIS:NE2	2.39	0.49
13:W:101:LYS:HD3	46:f:56:ILE:HG21	1.94	0.49
33:I:93:ASN:HD22	33:I:96:ILE:HG23	1.77	0.49
1:A:2575:U:N3	1:A:2583:C:N4	2.60	0.49
1:A:2379:C:C5	42:9:48:TRP:CD2	3.01	0.49
1:A:2661:U:H2'	1:A:2662:A:C8	2.47	0.49
1:A:2810:G:H2'	1:A:2811:G:H8	1.77	0.49
1:A:2898:U:O2	1:A:2898:U:H3'	2.12	0.49
46:f:136:GLN:N	46:f:146:LEU:O	2.45	0.49
51:s:66:TRP:HA	51:s:69:THR:HG22	1.94	0.49
1:A:2995:G:O2'	1:A:3041:U:O2'	2.31	0.49
4:F:140:SER:OG	4:F:141:ILE:O	2.26	0.49
55:z:104:ASN:HB3	56:w:641:LEU:C	2.38	0.49
4:F:116:THR:HG23	4:F:118:ALA:H	1.78	0.49
33:I:207:LEU:HD11	54:TB:86:LEU:HD13	1.91	0.49
41:7:96:SER:OG	41:7:97:GLU:N	2.43	0.49
1:A:1744:A:OP1	8:M:87:HIS:CE1	2.56	0.49
1:A:2315:A:H1'	1:A:2357:C:N4	2.28	0.49
56:w:374:VAL:HG13	56:w:384:VAL:HG22	1.94	0.49
1:A:3173:G:H2'	1:A:3174:U:O4'	2.12	0.49
3:D:146:SER:O	3:D:146:SER:OG	2.29	0.49
32:J:38:VAL:HA	32:J:41:GLN:HE21	1.78	0.49
32:J:156:VAL:HG22	32:J:159:LEU:HD22	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:P:52:ASN:HB3	35:P:55:ASN:HB2	1.93	0.49
38:E:269:TYR:CE1	38:E:303:LYS:CE	2.88	0.49
1:A:1993:A:H8	1:A:2498:U:O2'	1.96	0.49
1:A:2388:A:N1	3:D:127:ILE:HG22	2.28	0.49
1:A:2727:C:H2'	1:A:2728:C:H6	1.78	0.49
7:L:100:PHE:HB3	52:Q:158:GLN:HE21	1.78	0.49
41:7:184:VAL:HG22	41:7:294:ILE:HG22	1.95	0.49
1:A:1762:A:N6	30:q:33:ARG:HD2	2.28	0.48
1:A:1771:C:OP1	44:c:33:LYS:NZ	2.46	0.48
1:A:1862:U:H2'	1:A:1863:A:H8	1.78	0.48
1:A:2178:A:C4	56:w:717:GLU:CD	2.91	0.48
1:A:2279:U:OP2	26:i:46:ARG:NH2	2.46	0.48
7:L:55:PRO:HB3	7:L:77:ILE:HG12	1.94	0.48
41:7:279:GLU:HG2	41:7:317:LEU:HD13	1.94	0.48
55:z:74:ILE:HG22	55:z:237:GLN:HG2	1.94	0.48
1:A:1943:A:H2'	1:A:1944:C:H5''	1.95	0.48
1:A:2577:C:C2	55:z:132:GLN:CD	2.91	0.48
1:A:3009:C:H5	1:A:3031:G:N1	2.11	0.48
1:A:3054:G:H2'	1:A:3055:U:C6	2.48	0.48
4:F:63:GLN:HA	4:F:81:ASP:HA	1.95	0.48
8:M:233:ARG:HB3	8:M:244:LEU:HD11	1.93	0.48
9:O:129:CYS:SG	17:O:156:THR:OG1	2.64	0.48
16:Z:75:THR:HB	16:Z:83:LYS:HG2	1.94	0.48
33:I:164:MET:HA	33:I:167:ILE:HG22	1.94	0.48
33:I:197:LEU:CD2	54:TB:76:LEU:CD2	2.89	0.48
56:w:83:LYS:NZ	56:w:142:THR:O	2.44	0.48
56:w:110:THR:OG1	56:w:417:PHE:O	2.30	0.48
56:w:565:ARG:O	56:w:686:LEU:N	2.46	0.48
1:A:1860:A:O2'	10:R:34:ARG:NH2	2.46	0.48
1:A:3117:C:H2'	1:A:3118:U:H6	1.77	0.48
1:A:3129:A:P	56:w:79:ILE:HG12	2.53	0.48
37:V:80:ILE:HB	37:V:85:TRP:HB2	1.96	0.48
52:Q:221:LYS:HB3	52:Q:244:ARG:HG3	1.95	0.48
54:TA:85:LEU:HB3	54:TA:88:LYS:NZ	2.28	0.48
1:A:1906:G:O2'	4:F:137:ARG:HD3	2.14	0.48
1:A:2286:A:H2'	1:A:2287:U:C6	2.48	0.48
1:A:2511:C:O2'	3:D:258:GLY:C	2.57	0.48
14:X:128:THR:OG1	14:X:129:MET:N	2.47	0.48
39:5:241:ARG:NH1	39:5:336:GLU:HA	2.28	0.48
40:6:221:LEU:HB2	40:6:267:ARG:HG3	1.95	0.48
1:A:2096:U:O4	8:M:57:ARG:NH1	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2178:A:N9	56:w:717:GLU:OE2	2.46	0.48
1:A:2961:C:N3	1:A:2962:C:C6	2.81	0.48
12:T:137:ARG:NH2	41:7:95:LEU:O	2.45	0.48
22:8:178:TYR:CZ	46:f:180:GLU:HG2	2.48	0.48
38:E:54:SER:OG	38:E:55:GLU:N	2.45	0.48
40:6:224:HIS:CD2	40:6:227:GLU:H	2.31	0.48
48:k:78:GLY:HA3	48:k:86:MET:HE1	1.95	0.48
1:A:2164:C:H2'	1:A:2165:C:C6	2.48	0.48
32:J:23:ILE:HA	32:J:67:PRO:HA	1.94	0.48
54:TA:85:LEU:CD1	54:TB:67:LEU:CA	2.91	0.48
56:w:270:LEU:HA	56:w:273:THR:HG22	1.96	0.48
1:A:2077:C:O2'	13:W:59:HIS:NE2	2.35	0.48
1:A:2079:C:C6	1:A:2080:U:O2	2.66	0.48
1:A:2493:C:H5	1:A:2540:C:N3	2.06	0.48
1:A:2499:U:O2	1:A:2499:U:H3'	2.14	0.48
1:A:2503:A:H5'	1:A:3095:G:H4'	1.94	0.48
1:A:2728:C:H2'	1:A:2729:U:H6	1.78	0.48
37:V:100:LYS:HE2	37:V:105:ARG:HD2	1.95	0.48
1:A:1837:C:O2	1:A:1837:C:H3'	2.14	0.48
1:A:1844:A:OP2	10:R:48:ARG:NH2	2.47	0.48
1:A:1881:A:OP2	25:g:111:ARG:NH2	2.46	0.48
1:A:1980:A:OP2	19:2:59:LYS:HE2	2.13	0.48
1:A:2069:U:H3'	1:A:2069:U:O2	2.14	0.48
1:A:2070:C:H3'	1:A:2070:C:O2	2.14	0.48
12:T:71:ALA:H	12:T:180:GLU:HG2	1.78	0.48
22:8:163:LYS:HA	46:f:86:TYR:HB2	1.95	0.48
48:k:40:GLU:O	48:k:44:SER:HB3	2.13	0.48
56:w:78:HIS:ND1	56:w:79:ILE:HG12	2.29	0.48
56:w:394:LYS:HB2	56:w:397:LEU:HD23	1.95	0.48
1:A:1834:U:N3	12:T:206:ARG:CA	2.62	0.48
1:A:2527:A:C6	39:5:33:TRP:CE3	2.95	0.48
1:A:2527:A:C1'	3:D:67:LYS:HD3	2.43	0.48
1:A:2552:U:C2	1:A:2553:G:C8	3.02	0.48
6:K:171:THR:HG22	31:r:59:GLU:H	1.79	0.48
20:3:162:THR:OG1	20:3:167:LYS:NZ	2.47	0.48
34:N:172:VAL:O	34:N:176:LEU:HB2	2.14	0.48
38:E:45:SER:O	41:7:307:ARG:NH2	2.46	0.48
45:d:86:ASP:OD1	45:d:86:ASP:N	2.46	0.48
54:TA:85:LEU:HB2	54:TA:88:LYS:NZ	2.28	0.48
1:A:2131:A:N1	31:r:168:ARG:CZ	2.77	0.48
1:A:2415:C:N3	42:9:51:VAL:HG11	2.29	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:223:THR:OG1	3:D:224:ALA:N	2.47	0.48
16:Z:49:SER:OG	16:Z:51:GLU:OE2	2.32	0.48
39:5:241:ARG:NH1	39:5:336:GLU:C	2.71	0.48
41:7:160:ASP:OD1	41:7:160:ASP:N	2.46	0.48
1:A:2087:U:H2'	1:A:2088:U:H6	1.78	0.47
1:A:3024:U:H2'	1:A:3025:A:H8	1.79	0.47
1:A:3128:A:C6	56:w:744:ARG:HB3	2.48	0.47
33:I:124:LYS:HD2	33:I:155:VAL:HG11	1.96	0.47
45:d:247:VAL:HG23	45:d:262:HIS:HB3	1.96	0.47
56:w:187:ASN:O	56:w:355:ARG:NH2	2.46	0.47
1:A:1829:A:H2'	1:A:1830:G:C8	2.49	0.47
1:A:2060:A:C2	1:A:2061:C:C6	3.02	0.47
1:A:2953:U:H5''	21:4:71:VAL:HG12	1.96	0.47
38:E:244:ALA:HB2	38:E:251:VAL:HG12	1.96	0.47
46:f:135:LEU:HD12	46:f:145:LEU:HD23	1.95	0.47
55:z:110:ARG:HD2	56:w:526:ASP:O	2.13	0.47
1:A:1831:G:OP1	23:b:3:ALA:HB3	2.15	0.47
1:A:2055:U:H2'	1:A:2056:G:H8	1.79	0.47
1:A:2131:A:C5	31:r:168:ARG:NH1	2.82	0.47
1:A:2197:G:O4'	49:l:126:ILE:HG21	2.14	0.47
1:A:2409:A:H2'	1:A:2410:U:C6	2.49	0.47
1:A:2787:A:H2'	1:A:2788:C:C6	2.49	0.47
23:b:80:LEU:HD21	44:c:78:ARG:HH11	1.80	0.47
24:e:116:LEU:HB3	24:e:117:ALA:H	1.49	0.47
31:r:93:ILE:HG21	31:r:119:VAL:HG21	1.97	0.47
32:J:115:LYS:HE3	49:l:92:TYR:HE2	1.79	0.47
33:I:122:LEU:HB3	33:I:155:VAL:HG13	1.95	0.47
33:I:197:LEU:HD12	33:I:198:PRO:HD2	1.96	0.47
40:6:330:ILE:HG23	40:6:334:LEU:HD12	1.95	0.47
56:w:83:LYS:HD3	59:w:801:GCP:H3B1	1.95	0.47
1:A:1805:A:H5'	37:V:96:ARG:CD	2.44	0.47
1:A:1808:A:C4'	1:A:1809:U:OP1	2.59	0.47
1:A:2556:A:H1'	1:A:2560:G:N2	2.29	0.47
1:A:2746:U:H2'	1:A:2747:U:C6	2.49	0.47
6:K:4:PHE:HB3	6:K:9:GLN:HB2	1.96	0.47
34:N:81:GLU:OE2	34:N:199:ARG:NH1	2.46	0.47
40:6:196:THR:OG1	40:6:324:ASP:OD2	2.29	0.47
51:s:203:ARG:NH2	51:s:238:ASN:OD1	2.47	0.47
54:TA:81:ASP:HB3	54:TB:64:ILE:HB	1.97	0.47
1:A:2347:C:H2'	1:A:2348:A:H8	1.78	0.47
1:A:2453:G:O2'	9:O:116:ASP:OD2	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2580:U:N3	55:z:127:LYS:HB2	2.25	0.47
1:A:2652:G:N7	1:A:2653:C:N4	2.62	0.47
1:A:2662:A:H2'	1:A:2663:C:H6	1.80	0.47
1:A:2673:G:H2'	1:A:2674:U:H6	1.80	0.47
2:B:1628:C:H2'	2:B:1629:A:H8	1.80	0.47
32:J:56:ARG:HB3	32:J:82:ILE:HD11	1.96	0.47
1:A:2192:A:C4'	32:J:139:SER:HG	2.27	0.47
8:M:28:LYS:HD3	29:o:94:HIS:CE1	2.50	0.47
41:7:178:ALA:HB2	41:7:320:SER:HB2	1.96	0.47
51:s:188:LEU:HD11	51:s:422:VAL:HG23	1.95	0.47
55:z:185:VAL:HG11	56:w:498:SER:HA	1.94	0.47
1:A:1809:U:H2'	1:A:1810:A:O5'	2.14	0.47
1:A:1813:C:O2	1:A:1813:C:H3'	2.15	0.47
1:A:1839:C:C2	1:A:1840:C:C4	3.02	0.47
1:A:2094:G:O2'	1:A:2265:A:N3	2.39	0.47
1:A:2192:A:C5'	32:J:139:SER:OG	2.63	0.47
1:A:2620:G:H2'	1:A:2621:G:H8	1.79	0.47
1:A:2751:G:H2'	1:A:2752:C:C6	2.50	0.47
1:A:2752:C:H2'	1:A:2753:A:H8	1.80	0.47
1:A:2803:A:H2'	1:A:2804:A:O4'	2.15	0.47
1:A:3175:A:OP2	1:A:3187:C:N4	2.43	0.47
8:M:95:PRO:HB3	8:M:141:VAL:HG21	1.95	0.47
13:W:62:HIS:HA	13:W:94:GLU:HG2	1.96	0.47
31:r:49:ILE:HD12	48:k:76:MET:HE2	1.96	0.47
39:5:34:GLY:HA3	39:5:39:ARG:HH21	1.79	0.47
39:5:34:GLY:HA3	39:5:39:ARG:HE	1.80	0.47
52:Q:244:ARG:HE	52:Q:247:LEU:HD13	1.79	0.47
55:z:151:PHE:HB2	55:z:154:CYS:SG	2.54	0.47
55:z:179:ARG:H	55:z:179:ARG:HD2	1.79	0.47
56:w:113:MET:N	56:w:113:MET:SD	2.87	0.47
56:w:415:LEU:HD12	56:w:416:PRO:HD2	1.97	0.47
1:A:2060:A:C6	1:A:2061:C:C4	3.03	0.47
1:A:2415:C:C2	42:9:51:VAL:HG11	2.50	0.47
1:A:2717:A:OP1	1:A:2718:C:O2'	2.28	0.47
1:A:3224:G:H2'	1:A:3225:G:H8	1.78	0.47
8:M:65:LEU:HB3	20:3:94:LEU:HD23	1.97	0.47
42:9:66:THR:OG1	42:9:67:GLY:N	2.48	0.47
54:TA:82:LEU:HG	54:TB:67:LEU:HD11	1.97	0.47
55:z:169:LEU:HA	55:z:182:ILE:HD11	1.96	0.47
1:A:1731:A:N3	20:3:99:ALA:HB1	2.29	0.47
1:A:2274:A:OP1	44:c:36:ARG:HD2	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2294:A:H4'	10:R:14:VAL:HG21	1.96	0.47
1:A:2471:G:O2'	1:A:2654:U:O4	2.32	0.47
1:A:2577:C:P	55:z:132:GLN:NE2	2.88	0.47
15:Y:170:ARG:HD3	15:Y:201:ALA:HB2	1.97	0.47
18:1:18:VAL:HG12	18:1:61:LYS:HB3	1.97	0.47
23:b:32:SER:O	23:b:32:SER:OG	2.31	0.47
34:N:191:SER:OG	34:N:192:ARG:N	2.46	0.47
40:6:322:ARG:NH2	50:p:181:GLU:OE1	2.47	0.47
1:A:2025:C:P	11:S:182:LYS:HZ2	2.38	0.47
1:A:2420:U:H2'	1:A:2421:G:H8	1.80	0.47
1:A:2621:G:C2	1:A:2622:G:C8	3.03	0.47
1:A:3009:C:O2	1:A:3009:C:H3'	2.15	0.47
1:A:3009:C:O2'	1:A:3115:U:OP1	2.23	0.47
1:A:3139:G:H2'	1:A:3140:A:C8	2.49	0.47
14:X:168:ARG:HH11	14:X:175:GLN:HG2	1.80	0.47
32:J:44:VAL:HB	32:J:76:ARG:HH21	1.79	0.47
52:Q:120:THR:HB	52:Q:132:GLN:HG3	1.96	0.47
1:A:2004:G:H2'	1:A:2005:C:C6	2.50	0.46
1:A:2006:C:H2'	1:A:2007:U:C6	2.49	0.46
12:T:180:GLU:OE2	45:d:230:ARG:NH1	2.48	0.46
24:e:203:LYS:N	24:e:237:LEU:O	2.47	0.46
38:E:103:LYS:NZ	38:E:291:GLY:O	2.47	0.46
55:z:251:ARG:HH21	56:w:778:LEU:N	2.07	0.46
1:A:1693:C:C6	15:Y:178:TRP:CD1	3.03	0.46
1:A:1979:U:H2'	1:A:1980:A:C8	2.50	0.46
1:A:2152:A:OP1	29:o:34:ASN:HB3	2.15	0.46
1:A:2960:U:H1'	56:w:709:ALA:C	2.39	0.46
1:A:3200:U:N3	6:K:97:LEU:HB3	2.30	0.46
16:Z:71:ARG:NH2	16:Z:92:GLU:O	2.48	0.46
56:w:695:THR:HG22	56:w:726:VAL:HG22	1.96	0.46
1:A:1982:G:H2'	1:A:1983:U:C6	2.50	0.46
1:A:2495:U:O4	1:A:2509:A:H2	1.99	0.46
1:A:2678:A:N1	17:0:81:PRO:HD3	2.30	0.46
1:A:3155:C:H2'	1:A:3156:A:C8	2.50	0.46
11:S:85:GLU:HA	11:S:88:VAL:HG12	1.96	0.46
38:E:207:THR:CG2	38:E:267:THR:CB	2.81	0.46
55:z:185:VAL:CG1	56:w:497:PRO:C	2.85	0.46
56:w:133:LYS:HB3	56:w:135:TYR:CE2	2.51	0.46
1:A:2439:U:H2'	1:A:2440:G:C8	2.50	0.46
3:D:181:ALA:HB2	3:D:243:THR:HG22	1.98	0.46
13:W:57:GLU:HG3	13:W:98:ARG:HA	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:e:125:GLU:OE2	28:m:73:ARG:NH2	2.49	0.46
42:9:86:LEU:HD21	42:9:91:LEU:HD12	1.97	0.46
54:TA:85:LEU:HD13	54:TB:67:LEU:N	2.29	0.46
54:TA:85:LEU:HG	54:TB:67:LEU:HD12	1.98	0.46
54:TA:88:LYS:CE	54:TB:65:GLN:HB3	2.40	0.46
56:w:84:THR:HG22	59:w:801:GCP:PA	2.55	0.46
1:A:2628:U:H4'	1:A:2629:A:O5'	2.15	0.46
1:A:3204:C:H5'	38:E:298:LYS:HZ3	1.80	0.46
4:F:107:LYS:HE3	4:F:107:LYS:HB2	1.75	0.46
5:H:117:SER:O	5:H:121:ASN:ND2	2.49	0.46
31:r:142:LYS:NZ	31:r:143:SER:O	2.49	0.46
1:A:2052:A:H5''	25:g:150:LYS:CE	2.43	0.46
1:A:2072:A:H2'	1:A:2073:A:C8	2.50	0.46
1:A:2245:A:H4'	1:A:2246:A:OP1	2.14	0.46
1:A:2324:U:H2'	1:A:2325:U:H6	1.81	0.46
1:A:3158:A:H8	9:O:13:ARG:HH22	1.64	0.46
1:A:2241:A:H8	31:r:194:LEU:HD23	1.80	0.46
1:A:2615:A:H1'	7:L:81:LYS:HD3	1.98	0.46
1:A:2960:U:C1'	56:w:710:GLN:HA	2.46	0.46
32:J:162:GLU:O	32:J:166:ALA:CB	2.64	0.46
56:w:756:GLU:OE1	56:w:756:GLU:N	2.49	0.46
1:A:1917:A:N1	1:A:1997:C:H1'	2.31	0.46
1:A:2311:U:H2'	1:A:2312:A:H8	1.80	0.46
1:A:2560:G:C6	1:A:2561:U:C4	3.04	0.46
1:A:2577:C:H6	55:z:131:ASN:HB2	1.78	0.46
6:K:11:TRP:HH2	44:c:267:LEU:HD22	1.80	0.46
15:Y:202:LEU:HD12	15:Y:202:LEU:HA	1.80	0.46
24:e:230:LYS:HG2	24:e:232:PHE:HE1	1.80	0.46
39:5:278:PHE:HA	51:s:156:TYR:CE2	2.51	0.46
1:A:2516:C:H5''	3:D:285:LYS:HG2	1.98	0.46
6:K:80:HIS:ND1	6:K:81:THR:O	2.49	0.46
37:V:76:VAL:HA	37:V:88:VAL:HA	1.97	0.46
39:5:276:THR:HG23	39:5:278:PHE:H	1.80	0.46
50:p:85:SER:OG	50:p:94:LYS:O	2.34	0.46
51:s:207:HIS:HD2	51:s:234:ASP:HA	1.81	0.46
1:A:2042:U:H2'	1:A:2043:C:C6	2.50	0.46
1:A:2579:C:C4	55:z:119:ILE:HD13	2.46	0.46
1:A:2926:A:O2'	1:A:3087:C:OP1	2.24	0.46
1:A:3051:A:C8	1:A:3116:C:H5'	2.50	0.46
6:K:153:LYS:O	6:K:158:TYR:CZ	2.69	0.46
13:W:102:GLU:OE2	40:6:74:TYR:N	2.49	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Y:118:GLU:HG2	36:U:110:LEU:HD12	1.97	0.46
24:e:91:ALA:O	24:e:95:ASN:ND2	2.49	0.46
28:m:41:THR:OG1	46:f:101:THR:OG1	2.25	0.46
56:w:150:LEU:HD13	56:w:485:ILE:HA	1.98	0.46
56:w:557:LEU:HD23	56:w:557:LEU:H	1.79	0.46
1:A:1696:C:OP2	15:Y:180:LYS:NZ	2.44	0.45
1:A:2139:U:OP1	16:Z:73:LYS:HA	2.17	0.45
1:A:2417:C:OP2	51:s:310:ARG:NH1	2.48	0.45
4:F:282:PRO:O	4:F:290:TYR:OH	2.18	0.45
11:S:140:ASN:HD22	43:a:63:PRO:HA	1.80	0.45
12:T:144:GLU:HG3	12:T:177:LYS:HD3	1.99	0.45
33:I:197:LEU:HD21	54:TB:76:LEU:CD2	2.23	0.45
54:TA:68:VAL:HG21	54:TB:85:LEU:HB3	1.98	0.45
1:A:1805:A:H2	1:A:1807:U:H3	1.63	0.45
1:A:1861:U:OP1	10:R:40:ARG:NH1	2.49	0.45
1:A:2082:G:OP2	29:o:67:ARG:HD2	2.15	0.45
1:A:2110:A:N6	34:N:96:TYR:HD2	2.14	0.45
1:A:2167:A:N6	1:A:2212:C:OP2	2.44	0.45
1:A:2213:A:H4'	49:l:129:HIS:CD2	2.51	0.45
1:A:2239:A:O2'	6:K:29:GLY:HA3	2.16	0.45
1:A:2674:U:H2'	1:A:2675:G:O4'	2.16	0.45
1:A:2917:G:O6	8:M:77:ARG:NH2	2.49	0.45
1:A:3008:C:O2'	1:A:3009:C:H5'	2.17	0.45
1:A:3117:C:H2'	1:A:3118:U:C6	2.51	0.45
1:A:3210:C:H42	38:E:156:ARG:CB	2.29	0.45
6:K:60:MET:HB3	6:K:133:ILE:HD11	1.97	0.45
23:b:65:VAL:HB	47:h:154:ILE:HG22	1.98	0.45
35:P:54:ARG:NH1	40:6:155:TYR:OH	2.49	0.45
1:A:1693:C:H3'	1:A:1693:C:O2	2.16	0.45
1:A:1912:A:H2'	1:A:1913:G:H8	1.81	0.45
1:A:1965:A:H2'	1:A:1966:G:C8	2.52	0.45
1:A:2453:G:H2'	1:A:2454:G:H8	1.80	0.45
1:A:2483:U:N3	1:A:2484:C:C6	2.85	0.45
6:K:154:ARG:C	6:K:158:TYR:CZ	2.85	0.45
24:e:245:GLN:O	24:e:248:ASN:ND2	2.49	0.45
52:Q:283:TRP:HA	52:Q:286:ILE:HG22	1.98	0.45
56:w:84:THR:CG2	59:w:801:GCP:O2B	2.62	0.45
1:A:1828:A:H2'	10:R:35:LYS:HE2	1.97	0.45
1:A:2174:G:H4'	32:J:151:LEU:HD12	1.92	0.45
1:A:2306:A:O2'	17:0:84:ARG:NH2	2.46	0.45
1:A:2550:A:C8	1:A:2590:A:C4	3.04	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:142:ARG:HA	4:F:149:GLY:HA2	1.99	0.45
7:L:43:ASN:HB2	7:L:118:ARG:HB3	1.97	0.45
14:X:125:VAL:HG22	14:X:157:PHE:HE2	1.82	0.45
32:J:164:LEU:HD22	49:I:77:ILE:HB	1.98	0.45
36:U:17:LEU:HD11	42:9:136:LEU:HD22	1.99	0.45
54:TA:64:ILE:HG12	54:TB:81:ASP:CB	2.47	0.45
56:w:196:LYS:HD2	59:w:801:GCP:C6	2.46	0.45
1:A:1756:A:C2	1:A:1757:A:C8	3.04	0.45
1:A:1839:C:N3	1:A:1840:C:C5	2.81	0.45
1:A:1949:G:OP2	19:2:47:LYS:HE3	2.15	0.45
1:A:2174:G:C4'	32:J:151:LEU:CD1	2.89	0.45
1:A:2579:C:C4	55:z:119:ILE:CG1	2.68	0.45
1:A:2961:C:N1	1:A:2962:C:C5	2.85	0.45
1:A:3198:A:H2'	1:A:3198:A:N3	2.31	0.45
7:L:128:ARG:HB2	52:Q:125:TYR:HB3	1.99	0.45
18:1:63:ARG:HG2	18:1:65:LEU:HD23	1.99	0.45
42:9:81:SER:OG	42:9:82:GLU:N	2.49	0.45
1:A:1673:U:OP1	12:T:47:ILE:HD13	2.17	0.45
1:A:1839:C:C4	1:A:1840:C:N4	2.83	0.45
1:A:1861:U:H2'	1:A:1862:U:C6	2.51	0.45
1:A:2310:G:N2	1:A:2676:A:OP2	2.38	0.45
8:M:72:THR:OG1	8:M:77:ARG:NH2	2.49	0.45
32:J:40:GLY:C	56:w:698:ARG:NH1	2.72	0.45
39:5:233:ASP:OD1	39:5:233:ASP:N	2.49	0.45
48:k:58:ASP:HB3	54:TA:53:LEU:HD21	1.98	0.45
52:Q:205:LYS:HD3	52:Q:205:LYS:HA	1.83	0.45
52:Q:268:ASP:O	52:Q:270:MET:N	2.50	0.45
53:u:409:UNK:O	53:u:413:UNK:CB	2.64	0.45
55:z:105:LYS:HG2	56:w:637:GLN:OE1	2.07	0.45
56:w:406:CYS:SG	56:w:407:THR:N	2.90	0.45
1:A:1734:C:H42	26:i:107:LEU:CD2	2.30	0.45
1:A:1763:A:H5'	30:q:34:ARG:NE	2.31	0.45
1:A:2010:U:O4'	1:A:2012:A:H5'	2.16	0.45
1:A:2578:C:C4	55:z:119:ILE:HD12	2.50	0.45
1:A:2606:U:H4'	1:A:2607:U:H3'	1.99	0.45
1:A:2810:G:H2'	1:A:2811:G:C8	2.52	0.45
32:J:116:HIS:NE2	49:l:80:GLU:O	2.44	0.45
32:J:159:LEU:HG	32:J:163:GLU:HB3	1.99	0.45
38:E:87:ILE:HG12	38:E:317:PRO:HG3	1.97	0.45
45:d:140:LYS:HE2	45:d:140:LYS:HB3	1.73	0.45
45:d:186:VAL:HG21	45:d:239:PRO:HB3	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:l:73:MET:SD	49:l:79:LYS:HG3	2.56	0.45
56:w:115:GLN:HG2	56:w:549:ARG:HH22	1.82	0.45
56:w:388:ILE:HG23	56:w:429:ALA:HA	1.99	0.45
56:w:691:ASN:ND2	56:w:756:GLU:OE2	2.49	0.45
1:A:1755:A:O2'	5:H:63:PRO:O	2.34	0.45
1:A:2124:A:OP1	1:A:2125:C:H3'	2.16	0.45
1:A:2826:G:OP1	13:W:49:ARG:NE	2.50	0.45
8:M:284:LYS:HE3	25:g:42:VAL:HG11	1.98	0.45
11:S:76:HIS:ND1	43:a:50:ALA:HA	2.32	0.45
35:P:54:ARG:HH22	35:P:141:ILE:HA	1.81	0.45
55:z:133:ILE:C	56:w:664:THR:HG21	2.41	0.45
56:w:240:MET:SD	56:w:258:ARG:NH2	2.90	0.45
1:A:1898:A:H2'	1:A:1899:G:C8	2.52	0.45
1:A:2176:C:H5'	32:J:102:ARG:NE	2.31	0.45
1:A:2379:C:C5	42:9:48:TRP:CZ2	3.04	0.45
1:A:2559:U:H4'	1:A:2560:G:O5'	2.17	0.45
5:H:133:SER:OG	5:H:136:ASN:ND2	2.50	0.45
6:K:177:ARG:NE	48:k:85:GLU:OE2	2.50	0.45
16:Z:71:ARG:HH21	16:Z:94:ALA:HB2	1.82	0.45
22:8:165:ASP:OD1	22:8:165:ASP:N	2.50	0.45
33:I:139:LYS:HB2	54:TA:48:LEU:HG	1.98	0.45
48:k:57:HIS:HB3	54:TA:53:LEU:CG	2.36	0.45
1:A:2051:A:H2'	1:A:2052:A:C8	2.52	0.45
37:V:75:LYS:O	37:V:89:GLY:N	2.41	0.45
56:w:78:HIS:CD2	56:w:175:GLN:HB2	2.52	0.45
1:A:1965:A:H2'	1:A:1966:G:H8	1.81	0.44
1:A:2241:A:H61	31:r:82:ASN:HD21	1.64	0.44
1:A:2524:A:C2	3:D:92:ARG:HG2	2.52	0.44
10:R:17:ARG:HE	10:R:17:ARG:HB2	1.49	0.44
10:R:108:TYR:HD1	23:b:125:SER:HB2	1.82	0.44
26:i:86:ASN:H	26:i:89:GLN:HB2	1.83	0.44
33:I:160:LYS:HE3	33:I:160:LYS:HB2	1.70	0.44
38:E:294:ASN:HD21	52:Q:88:ASP:HB2	1.82	0.44
46:f:82:LEU:HB2	46:f:85:ASP:HB3	1.98	0.44
48:k:57:HIS:CB	54:TA:53:LEU:CD1	2.34	0.44
51:s:192:ASN:HB2	51:s:426:LEU:HD23	1.98	0.44
1:A:1719:G:O2'	1:A:1910:C:O2	2.34	0.44
1:A:1894:G:H2'	1:A:1895:C:C6	2.52	0.44
1:A:2077:C:H2'	1:A:2078:C:O4'	2.17	0.44
1:A:2131:A:C6	31:r:168:ARG:NE	2.86	0.44
1:A:2178:A:C6	56:w:717:GLU:N	2.77	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2220:A:C2	1:A:3182:A:H5'	2.52	0.44
3:D:194:ASN:OD1	3:D:243:THR:OG1	2.33	0.44
7:L:78:LYS:HE2	7:L:78:LYS:HB2	1.77	0.44
8:M:238:ARG:O	50:p:155:ARG:NH2	2.37	0.44
26:i:48:ASN:HB3	26:i:51:ARG:H	1.81	0.44
41:7:285:ASN:HB3	41:7:293:LEU:HD11	1.97	0.44
1:A:1807:U:HO2'	1:A:1808:A:C5'	2.28	0.44
1:A:2523:C:O2	3:D:87:HIS:CG	2.69	0.44
12:T:110:ASP:OD1	12:T:110:ASP:N	2.46	0.44
17:0:179:ARG:HH12	17:0:182:PRO:HD3	1.83	0.44
22:8:178:TYR:HA	24:e:59:VAL:HG23	2.00	0.44
31:r:50:GLU:OE1	48:k:77:ARG:NH1	2.45	0.44
37:V:129:LYS:HD3	37:V:129:LYS:HA	1.69	0.44
39:5:127:LEU:HD11	39:5:375:VAL:HG12	1.99	0.44
41:7:148:MET:HE3	41:7:262:ASP:HB3	1.98	0.44
55:z:122:VAL:HG23	55:z:126:GLY:H	1.82	0.44
55:z:134:SER:O	56:w:664:THR:HB	2.17	0.44
56:w:110:THR:HA	56:w:419:ASP:HA	1.98	0.44
1:A:1759:U:H2'	1:A:1760:G:C8	2.53	0.44
1:A:1898:A:H2'	1:A:1899:G:H8	1.82	0.44
1:A:2550:A:C5	1:A:2590:A:C6	3.06	0.44
1:A:2678:A:H2	17:0:80:ALA:HA	1.81	0.44
15:Y:110:ASN:O	15:Y:114:THR:HG23	2.18	0.44
39:5:241:ARG:HA	39:5:244:ILE:HB	1.98	0.44
40:6:179:VAL:H	50:p:194:HIS:CD2	2.36	0.44
41:7:150:MET:HA	41:7:153:VAL:HG12	1.98	0.44
54:TB:86:LEU:HA	54:TB:89:THR:OG1	2.17	0.44
55:z:128:LEU:CB	56:w:580:ARG:HH12	2.03	0.44
1:A:2155:A:C2	29:o:26:PHE:CG	3.03	0.44
1:A:2346:U:H2'	1:A:2347:C:C6	2.52	0.44
39:5:79:ARG:HE	39:5:79:ARG:HB3	1.67	0.44
41:7:244:ALA:HB1	41:7:250:ARG:HD3	1.99	0.44
54:TA:71:ILE:O	54:TA:74:LEU:HG	2.18	0.44
1:A:1778:U:OP1	4:F:120:VAL:HG13	2.18	0.44
1:A:1868:G:OP2	8:M:41:ARG:NH1	2.43	0.44
1:A:1939:G:N3	1:A:1939:G:H2'	2.33	0.44
1:A:2373:A:N1	51:s:274:PHE:CG	2.86	0.44
1:A:2727:C:H2'	1:A:2728:C:C6	2.53	0.44
1:A:3041:U:H2'	1:A:3042:U:C6	2.53	0.44
1:A:3118:U:H2'	1:A:3119:C:H6	1.81	0.44
9:O:77:ASP:O	9:O:83:LYS:NZ	2.51	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:e:139:GLU:HG2	24:e:151:ARG:O	2.18	0.44
40:6:40:ILE:HD11	46:f:62:LEU:HD22	2.00	0.44
43:a:45:CYS:SG	43:a:46:ASN:N	2.90	0.44
43:a:68:PRO:HG2	43:a:71:HIS:CD2	2.43	0.44
50:p:104:HIS:CD2	50:p:107:THR:HG22	2.53	0.44
1:A:1731:A:N6	26:i:118:TYR:CE1	2.70	0.44
1:A:1953:A:H2'	1:A:1954:U:H6	1.83	0.44
1:A:2186:C:O2'	1:A:2187:C:OP1	2.32	0.44
1:A:2355:A:H4'	1:A:2363:A:C8	2.53	0.44
3:D:173:ALA:HB1	3:D:188:PRO:HG3	2.00	0.44
8:M:111:ASP:OD2	8:M:111:ASP:N	2.50	0.44
24:e:50:ALA:N	24:e:232:PHE:O	2.51	0.44
29:o:101:TRP:CE3	47:h:139:LYS:HG2	2.53	0.44
39:5:135:VAL:HB	39:5:415:ALA:HB1	2.00	0.44
41:7:55:GLN:HG3	41:7:219:LEU:HD11	1.99	0.44
1:A:2145:G:H1'	11:S:104:ARG:NH1	2.32	0.44
1:A:2155:A:O2'	1:A:2156:A:O4'	2.34	0.44
1:A:2277:U:H2'	1:A:2278:A:H8	1.83	0.44
1:A:2550:A:C5	1:A:2551:G:C8	3.05	0.44
1:A:2635:G:H2'	1:A:2636:G:H8	1.82	0.44
1:A:3102:U:C2	17:0:81:PRO:HA	2.53	0.44
4:F:253:MET:HG2	4:F:259:LEU:HD22	2.00	0.44
9:O:33:LEU:HD21	9:O:59:LEU:HD22	1.99	0.44
35:P:95:GLU:HG2	35:P:101:VAL:HG12	1.99	0.44
41:7:298:GLN:HE22	41:7:323:MET:HA	1.83	0.44
48:k:38:SER:O	48:k:38:SER:OG	2.32	0.44
51:s:84:THR:HB	51:s:280:ASN:HB2	1.98	0.44
56:w:64:ASN:OD1	56:w:136:ARG:NH2	2.48	0.44
56:w:593:VAL:HG21	56:w:674:VAL:HG12	2.00	0.44
1:A:1671:G:C6	1:A:1818:A:N1	2.86	0.44
1:A:2121:G:H2'	1:A:2122:A:C8	2.53	0.44
35:P:45:ALA:O	35:P:47:GLU:N	2.51	0.44
49:l:114:SER:OG	49:l:116:GLU:OE1	2.35	0.44
1:A:1804:A:C6	45:d:68:PRO:HB3	2.53	0.43
1:A:1846:C:H2'	1:A:1847:U:C6	2.53	0.43
1:A:1975:U:H2'	1:A:1976:U:C6	2.53	0.43
1:A:2275:U:H2'	1:A:2276:C:C6	2.53	0.43
1:A:2523:C:H6	39:5:37:SER:HB2	1.83	0.43
1:A:2747:U:H2'	1:A:2748:A:H8	1.83	0.43
1:A:3220:A:OP1	38:E:260:LYS:NZ	2.51	0.43
3:D:180:ASP:OD1	3:D:180:ASP:N	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:O:129:CYS:HG	17:O:156:THR:HG1	1.60	0.43
9:O:141:HIS:HD2	9:O:146:ASN:HB3	1.83	0.43
35:P:58:LEU:HD23	35:P:58:LEU:HA	1.85	0.43
40:6:184:LEU:HD23	50:p:190:GLN:H	1.83	0.43
49:l:133:SER:O	49:l:133:SER:OG	2.33	0.43
55:z:221:LYS:HE3	55:z:221:LYS:HB3	1.87	0.43
1:A:2065:A:C1'	13:W:74:ARG:HG3	2.48	0.43
1:A:2131:A:C6	31:r:168:ARG:HD2	2.53	0.43
1:A:2532:U:H2'	1:A:2533:A:H8	1.83	0.43
1:A:2577:C:O2	1:A:2577:C:H3'	2.18	0.43
1:A:2804:A:H2'	1:A:2805:A:H8	1.84	0.43
1:A:3092:U:H2'	1:A:3093:C:C6	2.53	0.43
8:M:223:LEU:O	50:p:49:TYR:OH	2.30	0.43
25:g:117:ILE:HD13	25:g:142:GLU:HG2	2.00	0.43
38:E:301:ASP:N	38:E:301:ASP:OD1	2.51	0.43
54:TA:62:PRO:HA	54:TA:65:GLN:CD	2.44	0.43
54:TA:62:PRO:HA	54:TA:65:GLN:CG	2.48	0.43
56:w:696:VAL:HG21	56:w:704:VAL:HG11	1.98	0.43
1:A:1699:C:C2	19:2:70:LEU:HD12	2.50	0.43
1:A:1882:A:OP2	25:g:97:TYR:HE1	2.01	0.43
1:A:2577:C:H41	55:z:131:ASN:N	2.14	0.43
1:A:2753:A:H1'	5:H:88:HIS:HE1	1.80	0.43
3:D:62:ASN:OD1	3:D:62:ASN:N	2.50	0.43
8:M:230:PRO:HB2	50:p:62:PRO:HG3	2.00	0.43
10:R:47:ILE:HG12	11:S:172:MET:HE1	1.99	0.43
11:S:142:THR:HG23	43:a:62:HIS:CE1	2.53	0.43
14:X:238:LEU:HD21	42:9:101:GLU:HG3	2.00	0.43
17:0:104:LYS:HB3	17:0:104:LYS:HE2	1.75	0.43
30:q:42:PRO:O	30:q:44:ASP:N	2.51	0.43
32:J:170:GLU:O	32:J:174:PHE:HB2	2.18	0.43
52:Q:152:ARG:HG3	52:Q:161:GLU:HG2	1.99	0.43
54:TC:168:LEU:HA	54:TC:169:PRO:HA	1.78	0.43
55:z:190:ARG:NH2	56:w:495:GLU:CD	2.41	0.43
1:A:1741:A:H4'	1:A:1742:G:H4'	2.01	0.43
1:A:2064:A:N6	46:f:48:TYR:CE2	2.87	0.43
1:A:2365:U:H2'	1:A:2366:G:C8	2.54	0.43
1:A:2402:A:C8	3:D:131:TYR:CE2	3.07	0.43
1:A:2493:C:H3'	1:A:2493:C:O2	2.19	0.43
1:A:3143:U:C2	1:A:3144:A:C8	3.06	0.43
1:A:3206:C:O2	1:A:3206:C:H3'	2.18	0.43
4:F:270:GLU:O	4:F:274:LEU:HB2	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:e:132:LYS:HE2	24:e:132:LYS:HB3	1.85	0.43
36:U:112:PRO:HA	36:U:113:GLU:HA	1.80	0.43
55:z:105:LYS:HE2	56:w:637:GLN:CG	2.45	0.43
56:w:191:ILE:HA	56:w:325:VAL:HG23	2.00	0.43
56:w:691:ASN:HB3	56:w:756:GLU:CD	2.44	0.43
56:w:744:ARG:O	56:w:749:GLY:N	2.52	0.43
1:A:2073:A:OP2	40:6:27:ARG:HB2	2.18	0.43
1:A:2302:U:C2	1:A:2303:A:C8	3.06	0.43
1:A:2336:U:C2	1:A:2337:A:C8	3.06	0.43
1:A:2379:C:O2	1:A:2379:C:H3'	2.19	0.43
1:A:2388:A:OP2	3:D:74:ILE:HG23	2.18	0.43
1:A:2897:A:C6	1:A:2898:U:C4	3.06	0.43
1:A:3188:U:O2'	1:A:3192:C:N4	2.50	0.43
4:F:197:THR:OG1	4:F:198:GLY:N	2.51	0.43
56:w:237:ASP:OD1	56:w:238:VAL:N	2.51	0.43
56:w:333:LEU:HD22	59:w:801:GCP:C2	2.49	0.43
1:A:1680:A:H61	1:A:1775:A:H61	1.66	0.43
1:A:1689:C:O2	1:A:1689:C:H3'	2.19	0.43
1:A:2178:A:C4	56:w:717:GLU:OE2	2.71	0.43
1:A:2673:G:H2'	1:A:2674:U:C6	2.53	0.43
1:A:2702:G:OP1	6:K:114:LYS:HE3	2.17	0.43
8:M:234:LEU:HD13	50:p:62:PRO:HG2	2.01	0.43
23:b:27:GLN:HG2	44:c:78:ARG:HH12	1.83	0.43
39:5:273:LYS:HA	39:5:273:LYS:HD2	1.66	0.43
54:TA:88:LYS:NZ	54:TB:65:GLN:H	2.17	0.43
55:z:185:VAL:HG11	56:w:497:PRO:O	2.14	0.43
1:A:1690:C:N3	15:Y:213:ARG:NH2	2.55	0.43
1:A:1782:G:N2	1:A:1794:A:OP2	2.38	0.43
1:A:1826:G:N2	1:A:2686:G:N7	2.67	0.43
1:A:2484:C:C6	1:A:2485:U:C5	3.07	0.43
1:A:3139:G:H2'	1:A:3140:A:H8	1.83	0.43
24:e:255:VAL:HG12	24:e:260:LEU:HG	2.00	0.43
39:5:211:THR:HG22	39:5:220:GLN:HB2	1.99	0.43
46:f:134:VAL:HG23	46:f:148:SER:HB2	2.01	0.43
52:Q:76:LEU:HD23	52:Q:279:GLU:HG2	1.99	0.43
56:w:569:LEU:HD11	56:w:684:GLN:HG2	2.00	0.43
1:A:1937:A:O2'	1:A:1938:A:O4'	2.36	0.43
1:A:1987:G:H2'	1:A:1988:G:H8	1.84	0.43
1:A:2060:A:C2	1:A:2061:C:C4	3.05	0.43
1:A:2067:C:OP1	46:f:58:LYS:HA	2.19	0.43
1:A:2241:A:N6	31:r:82:ASN:HD21	2.17	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2418:A:C8	42:9:50:PHE:CD2	3.07	0.43
1:A:2859:A:N6	1:A:2873:A:O2'	2.52	0.43
1:A:2961:C:N4	1:A:2962:C:N4	2.58	0.43
1:A:3056:C:H2'	1:A:3057:C:C6	2.54	0.43
1:A:3092:U:H2'	1:A:3093:C:H6	1.83	0.43
1:A:3189:C:H5	21:4:83:LYS:CE	2.32	0.43
7:L:101:ASP:OD2	52:Q:152:ARG:NH2	2.52	0.43
8:M:35:LYS:HB3	8:M:35:LYS:HE2	1.76	0.43
8:M:268:GLY:HA3	25:g:47:PHE:CG	2.53	0.43
15:Y:98:LEU:HD22	15:Y:142:LEU:HG	2.00	0.43
15:Y:128:SER:HB2	15:Y:131:ARG:HD3	2.00	0.43
15:Y:232:LYS:HD3	15:Y:232:LYS:HA	1.72	0.43
19:2:89:SER:O	19:2:89:SER:OG	2.35	0.43
36:U:143:ARG:HG2	45:d:282:ILE:HD11	2.00	0.43
40:6:94:PRO:HA	40:6:95:PRO:HD3	1.94	0.43
46:f:136:GLN:OE1	53:u:700:UNK:N	2.52	0.43
54:TA:67:LEU:O	54:TA:70:ASP:HB3	2.19	0.43
1:A:2275:U:H2'	1:A:2276:C:H6	1.83	0.43
1:A:2333:G:H2'	1:A:2334:C:C6	2.54	0.43
1:A:2537:G:H2'	1:A:2538:C:C6	2.54	0.43
1:A:2545:U:H1'	1:A:2635:G:N2	2.34	0.43
1:A:3076:A:H2'	1:A:3077:C:H6	1.84	0.43
8:M:146:ASP:N	8:M:146:ASP:OD1	2.50	0.43
12:T:154:LYS:O	12:T:155:ARG:NH1	2.48	0.43
25:g:105:ARG:HH12	29:o:83:PRO:HD3	1.84	0.43
32:J:162:GLU:O	32:J:166:ALA:HB2	2.18	0.43
35:P:137:LEU:HD23	35:P:137:LEU:HA	1.91	0.43
39:5:203:VAL:HG11	39:5:278:PHE:HZ	1.83	0.43
39:5:241:ARG:NH2	39:5:244:ILE:HD13	2.34	0.43
39:5:255:PHE:HD2	39:5:258:ILE:HB	1.84	0.43
1:A:2065:A:N7	13:W:74:ARG:HB2	2.34	0.43
1:A:2101:C:H2'	1:A:2102:A:H8	1.84	0.43
1:A:2578:C:C2	55:z:118:LYS:C	2.97	0.43
1:A:2662:A:H2'	1:A:2663:C:C6	2.54	0.43
15:Y:163:ALA:HB1	42:9:133:ARG:HB2	2.01	0.43
16:Z:63:PRO:HG2	29:o:53:TYR:HD1	1.83	0.43
23:b:66:ASN:HD22	23:b:68:ARG:HH11	1.66	0.43
24:e:58:VAL:HB	24:e:153:LEU:HB2	2.00	0.43
24:e:176:ALA:HA	24:e:191:THR:HG21	2.00	0.43
24:e:210:CYS:HB2	24:e:233:PHE:HB3	2.01	0.43
39:5:46:LEU:HD13	39:5:50:TYR:HB2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:7:35:LEU:HD22	41:7:39:GLU:HG3	2.01	0.43
43:a:67:ILE:HG21	44:c:258:THR:HG23	2.01	0.43
44:c:116:LEU:HA	44:c:119:LEU:HG	2.01	0.43
52:Q:186:SER:O	52:Q:186:SER:OG	2.34	0.43
54:TA:85:LEU:HD13	54:TB:67:LEU:H	1.81	0.43
1:A:1677:C:O5'	44:c:31:VAL:HG12	2.19	0.42
1:A:2192:A:H2'	1:A:2193:U:C6	2.54	0.42
1:A:2456:U:H2'	1:A:2457:A:C8	2.54	0.42
1:A:2467:A:O2'	1:A:3154:U:H4'	2.19	0.42
1:A:2593:G:O2'	1:A:2631:G:O6	2.30	0.42
1:A:3044:A:H2'	1:A:3045:A:C8	2.53	0.42
1:A:3054:G:H2'	1:A:3055:U:H6	1.84	0.42
1:A:3210:C:N4	38:E:156:ARG:HA	2.33	0.42
23:b:17:ASN:HD21	23:b:25:GLN:HE21	1.67	0.42
25:g:84:TYR:OH	25:g:164:LYS:NZ	2.40	0.42
25:g:101:THR:OG1	25:g:102:HIS:N	2.52	0.42
25:g:144:THR:O	25:g:146:THR:N	2.50	0.42
27:j:53:ASP:OD2	27:j:55:ARG:NH2	2.52	0.42
31:r:132:ARG:HA	31:r:132:ARG:HD3	1.82	0.42
42:9:69:LYS:HE2	42:9:69:LYS:HB3	1.90	0.42
48:k:62:PRO:HD2	48:k:79:ALA:HB2	2.01	0.42
54:TA:85:LEU:CA	54:TA:88:LYS:HD2	2.48	0.42
1:A:1759:U:H5''	8:M:196:ARG:HD3	2.01	0.42
1:A:2081:U:OP1	29:o:63:ALA:HB3	2.19	0.42
1:A:2138:U:O2'	1:A:2151:A:N3	2.42	0.42
1:A:2170:G:H2'	1:A:2171:U:C2	2.54	0.42
17:0:113:CYS:O	17:0:115:HIS:ND1	2.52	0.42
18:1:23:GLU:HB2	30:q:128:MET:HE1	2.01	0.42
23:b:8:SER:OG	23:b:116:ARG:NH1	2.50	0.42
25:g:125:GLU:O	25:g:129:SER:HB3	2.19	0.42
40:6:132:LEU:HA	40:6:135:VAL:HG12	2.02	0.42
56:w:683:LYS:HE2	56:w:683:LYS:HB2	1.89	0.42
1:A:1696:C:H2'	1:A:1697:A:H8	1.83	0.42
1:A:1733:C:N3	5:H:72:ARG:HD2	2.35	0.42
1:A:1733:C:H42	5:H:72:ARG:CD	2.33	0.42
1:A:1811:A:C6	44:c:49:ARG:NE	2.86	0.42
1:A:1924:U:H2'	1:A:1925:A:H8	1.84	0.42
1:A:2405:C:H2'	39:5:298:LEU:HD11	2.01	0.42
1:A:2523:C:H5''	39:5:35:VAL:HG11	2.00	0.42
1:A:2576:A:H5''	56:w:578:LEU:HA	2.01	0.42
4:F:249:ASN:OD1	4:F:249:ASN:N	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:92:GLU:H	5:H:92:GLU:HG2	1.65	0.42
8:M:149:THR:O	8:M:149:THR:OG1	2.35	0.42
41:7:298:GLN:HE22	41:7:324:VAL:H	1.67	0.42
41:7:309:HIS:HB3	41:7:312:ILE:HD12	2.01	0.42
54:TA:81:ASP:OD1	54:TB:64:ILE:HD13	2.19	0.42
1:A:1897:A:H2'	1:A:1898:A:H8	1.85	0.42
1:A:2373:A:C4	51:s:274:PHE:CD2	3.08	0.42
1:A:2511:C:O5'	3:D:263:ASN:ND2	2.53	0.42
1:A:2540:C:H2'	1:A:2541:C:O4'	2.19	0.42
15:Y:72:LYS:HE2	15:Y:72:LYS:HB3	1.82	0.42
38:E:95:PHE:H	38:E:182:THR:HG22	1.84	0.42
40:6:240:ILE:HD13	40:6:248:GLY:HA3	1.99	0.42
56:w:248:CYS:O	56:w:250:SER:N	2.53	0.42
56:w:304:ASP:CG	56:w:307:PRO:HG3	2.45	0.42
56:w:688:PRO:HG2	56:w:733:LEU:HB3	2.01	0.42
1:A:1731:A:H61	26:i:118:TYR:HD1	1.53	0.42
1:A:2061:C:O2	1:A:2061:C:H3'	2.19	0.42
1:A:2160:A:H5'	21:4:88:TRP:CE2	2.54	0.42
1:A:2339:G:H4'	19:2:55:PRO:HG2	2.02	0.42
1:A:2459:A:C4	1:A:2460:A:C8	3.08	0.42
1:A:2578:C:O2	55:z:119:ILE:N	2.52	0.42
1:A:2668:A:H2'	1:A:2669:A:C8	2.54	0.42
1:A:2989:G:H5''	1:A:2990:A:H5'	2.01	0.42
1:A:3170:C:H3'	1:A:3170:C:O2	2.19	0.42
6:K:153:LYS:O	6:K:158:TYR:OH	2.29	0.42
13:W:145:VAL:HG23	40:6:341:VAL:HG23	2.01	0.42
42:9:46:SER:OG	42:9:47:GLY:N	2.50	0.42
54:TA:54:ASP:O	54:TA:57:PRO:HB3	2.19	0.42
1:A:1882:A:N1	1:A:1891:A:O2'	2.50	0.42
1:A:2094:G:P	8:M:57:ARG:HD3	2.60	0.42
1:A:2190:C:H2'	1:A:2191:A:O4'	2.20	0.42
1:A:2456:U:OP1	9:O:16:ARG:NE	2.38	0.42
1:A:2484:C:H3'	1:A:2484:C:O2	2.19	0.42
1:A:2710:C:H2'	1:A:2711:A:H8	1.85	0.42
1:A:3143:U:H2'	1:A:3144:A:H8	1.84	0.42
9:O:144:LEU:HD23	41:7:303:PRO:HD3	2.02	0.42
24:e:85:SER:HB3	24:e:88:GLU:HG2	2.02	0.42
38:E:145:LEU:HD23	38:E:145:LEU:HA	1.90	0.42
44:c:56:PRO:HA	44:c:57:PRO:HD3	1.89	0.42
56:w:187:ASN:ND2	56:w:322:GLN:HE22	2.18	0.42
1:A:1731:A:N3	20:3:99:ALA:CB	2.83	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2155:A:H2	29:o:26:PHE:CE1	2.24	0.42
1:A:2192:A:O3'	32:J:139:SER:OG	2.35	0.42
1:A:2267:U:H2'	1:A:2268:G:H8	1.84	0.42
1:A:2511:C:O2	1:A:2511:C:H3'	2.19	0.42
1:A:2518:A:H2'	1:A:2530:A:N6	2.34	0.42
1:A:2847:C:H2'	1:A:2848:A:O4'	2.20	0.42
1:A:3051:A:N7	1:A:3115:U:O2'	2.52	0.42
2:B:1621:A:N7	40:6:107:LYS:NZ	2.63	0.42
33:I:48:MET:HG2	34:N:250:ARG:HH21	1.85	0.42
41:7:303:PRO:HD2	41:7:306:LEU:HB2	2.02	0.42
54:TC:144:LYS:HA	56:w:289:ASP:OD1	2.20	0.42
56:w:627:ILE:HD12	56:w:670:VAL:HG21	2.01	0.42
1:A:1809:U:C2'	1:A:1810:A:O5'	2.67	0.42
1:A:2591:A:H2'	1:A:2592:G:O4'	2.19	0.42
1:A:2691:U:H2'	1:A:2692:G:C8	2.55	0.42
22:8:107:THR:OG1	22:8:108:PHE:N	2.53	0.42
29:o:80:SER:O	29:o:80:SER:OG	2.31	0.42
41:7:107:LEU:HD12	41:7:107:LEU:HA	1.91	0.42
41:7:225:VAL:O	41:7:229:ILE:HG12	2.20	0.42
51:s:267:LYS:HB3	51:s:267:LYS:HE2	1.72	0.42
1:A:1893:A:H4'	1:A:1894:G:H5'	2.01	0.42
1:A:2217:C:H2'	1:A:2218:C:C2	2.55	0.42
1:A:2346:U:H2'	1:A:2347:C:H6	1.85	0.42
1:A:2507:A:HO2'	1:A:2508:C:P	2.41	0.42
1:A:2511:C:O2	1:A:2512:A:C8	2.73	0.42
1:A:2646:G:H4'	1:A:3093:C:H4'	2.02	0.42
1:A:2653:C:H5''	52:Q:228:PRO:HG3	2.02	0.42
1:A:2736:C:H2'	1:A:2737:U:C6	2.55	0.42
1:A:2742:U:O2	14:X:99:LYS:HE2	2.19	0.42
1:A:3194:U:OP1	31:r:141:PRO:CG	2.66	0.42
3:D:237:LEU:HD23	3:D:237:LEU:HA	1.89	0.42
5:H:59:TRP:HD1	5:H:60:TRP:CD1	2.38	0.42
42:9:97:ALA:O	42:9:101:GLU:HB2	2.19	0.42
51:s:162:ARG:H	51:s:163:VAL:HA	1.85	0.42
51:s:332:LEU:HD21	51:s:359:ALA:HB2	2.01	0.42
54:TA:79:ILE:HA	54:TA:82:LEU:HD12	2.02	0.42
1:A:1739:A:O2'	1:A:1888:G:H1'	2.20	0.42
1:A:1884:G:OP2	4:F:281:ARG:HG2	2.20	0.42
1:A:2103:A:OP2	33:I:38:ARG:NH2	2.52	0.42
1:A:2167:A:N6	1:A:2211:U:H5''	2.35	0.42
1:A:2617:A:H1'	1:A:2619:A:N7	2.35	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2672:A:H5''	12:T:110:ASP:O	2.19	0.42
1:A:2709:A:C4'	17:O:96:ASN:HD21	2.33	0.42
1:A:3034:U:H2'	1:A:3035:C:C6	2.55	0.42
24:e:50:ALA:HA	24:e:175:GLN:HA	2.00	0.42
32:J:61:LYS:HE3	32:J:61:LYS:HB2	1.88	0.42
41:7:79:PHE:HB3	41:7:81:MET:HE2	2.01	0.42
56:w:502:GLN:HB3	56:w:503:PRO:HD3	2.01	0.42
1:A:1830:G:OP2	23:b:4:ARG:HD3	2.20	0.41
1:A:1956:U:O2'	1:A:3098:U:O2'	2.35	0.41
1:A:2016:C:H2'	1:A:2017:U:H6	1.85	0.41
1:A:2131:A:C5	31:r:168:ARG:HD2	2.54	0.41
1:A:2373:A:C5	51:s:274:PHE:CD1	3.08	0.41
1:A:2388:A:C6	3:D:127:ILE:CG2	3.01	0.41
1:A:2493:C:H41	1:A:2540:C:C1'	1.86	0.41
1:A:2797:C:H2'	1:A:2798:A:C8	2.54	0.41
1:A:3000:A:H2'	1:A:3001:G:C8	2.54	0.41
1:A:3041:U:H2'	1:A:3042:U:H6	1.85	0.41
1:A:3089:A:C6	55:z:232:ARG:HD3	2.55	0.41
1:A:3123:G:H2'	1:A:3124:U:OP2	2.20	0.41
6:K:138:LEU:HD23	6:K:138:LEU:HA	1.93	0.41
9:O:143:THR:HG1	9:O:146:ASN:HD22	1.61	0.41
37:V:63:GLU:HG3	37:V:73:GLN:HE21	1.86	0.41
1:A:1673:U:OP2	12:T:47:ILE:HA	2.20	0.41
1:A:1862:U:H2'	1:A:1863:A:C8	2.54	0.41
1:A:1875:C:OP1	25:g:101:THR:O	2.38	0.41
1:A:2683:C:OP1	10:R:34:ARG:HD3	2.21	0.41
1:A:2974:A:H2'	1:A:2975:G:C8	2.55	0.41
1:A:3189:C:C1'	31:r:158:SER:HG	2.33	0.41
3:D:220:VAL:HG12	3:D:221:ASN:H	1.85	0.41
16:Z:69:VAL:HG23	16:Z:91:LEU:HD21	2.00	0.41
19:2:69:ARG:HG3	19:2:79:ILE:HD11	2.02	0.41
24:e:47:LEU:HB3	24:e:178:TRP:CD1	2.55	0.41
25:g:77:ASP:OD1	25:g:77:ASP:N	2.53	0.41
26:i:97:MET:HE2	26:i:97:MET:HB3	1.87	0.41
37:V:25:PRO:HA	37:V:26:PRO:HD3	1.91	0.41
38:E:100:ILE:HD13	38:E:175:THR:HG23	2.02	0.41
40:6:170:ARG:HD3	40:6:170:ARG:HA	1.90	0.41
47:h:140:PHE:HB3	47:h:156:TRP:CE2	2.55	0.41
48:k:19:GLN:HB3	48:k:56:ARG:HH21	1.85	0.41
51:s:374:LEU:HD21	51:s:377:LEU:HD13	2.01	0.41
56:w:357:TYR:HE1	56:w:360:LEU:HD13	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1845:C:H2'	1:A:1846:C:H6	1.85	0.41
1:A:2814:G:N2	34:N:141:GLY:HA2	2.36	0.41
17:O:87:ILE:HD12	17:O:87:ILE:HA	1.91	0.41
17:O:168:GLN:HE21	17:O:168:GLN:HB2	1.66	0.41
24:e:97:ARG:HA	24:e:100:LYS:HB2	2.01	0.41
45:d:163:LEU:HD23	45:d:163:LEU:HA	1.93	0.41
1:A:1761:A:C8	30:q:50:TRP:CH2	3.08	0.41
1:A:1942:C:H2'	1:A:1943:A:O4'	2.20	0.41
1:A:2017:U:C2	1:A:2018:G:C8	3.08	0.41
1:A:2143:G:C6	1:A:2258:A:C2	3.08	0.41
1:A:2158:U:O2'	31:r:153:ARG:CZ	2.68	0.41
1:A:2576:A:H5''	56:w:578:LEU:HD12	0.98	0.41
1:A:2578:C:O2	55:z:118:LYS:C	2.63	0.41
1:A:2943:G:H2'	1:A:2944:C:H6	1.86	0.41
4:F:85:ASP:OD1	25:g:87:ARG:NH2	2.53	0.41
12:T:156:ILE:HG23	45:d:52:THR:HG21	2.02	0.41
30:q:61:PHE:HB2	30:q:70:VAL:HG22	2.02	0.41
35:P:144:MET:HE2	35:P:144:MET:HB3	1.90	0.41
39:5:47:ASP:OD1	39:5:47:ASP:N	2.53	0.41
1:A:2143:G:H2'	1:A:2144:A:H8	1.85	0.41
1:A:2257:C:OP1	27:j:61:LYS:N	2.46	0.41
1:A:2324:U:H2'	1:A:2325:U:C6	2.55	0.41
1:A:2374:A:C2	51:s:94:TYR:HB2	2.55	0.41
1:A:2524:A:H2'	1:A:2524:A:N3	2.35	0.41
1:A:2601:A:C6	1:A:3077:C:H1'	2.56	0.41
1:A:3078:C:H2'	1:A:3079:G:H8	1.85	0.41
1:A:3165:C:H2'	1:A:3166:U:H6	1.84	0.41
9:O:117:ARG:HD3	9:O:117:ARG:HA	1.92	0.41
10:R:34:ARG:HG3	10:R:37:ARG:HH21	1.85	0.41
11:S:99:VAL:HG22	11:S:133:VAL:HG22	2.01	0.41
31:r:117:GLU:HG3	31:r:180:LEU:HD12	2.03	0.41
40:6:270:PHE:N	40:6:317:SER:O	2.51	0.41
48:k:87:LEU:HD23	48:k:87:LEU:HA	1.86	0.41
1:A:1702:A:C8	19:2:66:TRP:CB	3.03	0.41
1:A:1731:A:N6	26:i:118:TYR:CG	2.67	0.41
1:A:1928:A:H2'	1:A:1929:A:C8	2.56	0.41
1:A:2388:A:C4	3:D:141:LEU:HD22	2.56	0.41
1:A:2575:U:H3	1:A:2583:C:N4	2.18	0.41
4:F:289:PRO:HG2	8:M:277:MET:HE2	2.02	0.41
5:H:93:ASN:OD1	5:H:93:ASN:N	2.48	0.41
15:Y:202:LEU:HA	15:Y:203:PRO:HD3	1.95	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:P:165:MET:HE2	35:P:165:MET:HB2	1.95	0.41
48:k:57:HIS:HB3	54:TA:53:LEU:HD13	0.53	0.41
51:s:302:LEU:HD23	51:s:302:LEU:HA	1.90	0.41
51:s:411:LYS:HA	51:s:411:LYS:HD2	1.77	0.41
56:w:759:THR:HG21	56:w:761:GLN:HE21	1.85	0.41
1:A:2017:U:O2'	1:A:2723:A:N1	2.51	0.41
1:A:2131:A:C2	31:r:168:ARG:CZ	3.03	0.41
1:A:2232:A:N6	1:A:2978:U:OP1	2.53	0.41
1:A:2310:G:O2'	1:A:2675:G:O6	2.38	0.41
1:A:2506:A:H1'	1:A:2601:A:N6	2.35	0.41
1:A:3039:U:N3	1:A:3041:U:H5'	2.36	0.41
1:A:3086:U:H2'	1:A:3087:C:H6	1.86	0.41
4:F:186:ASP:OD2	8:M:21:ARG:NH1	2.54	0.41
9:O:149:LEU:HD23	41:7:316:LEU:HD21	2.02	0.41
23:b:133:PHE:HB3	44:c:259:ARG:HD2	2.03	0.41
31:r:63:PRO:HA	31:r:64:PRO:HD3	1.93	0.41
54:TB:80:SER:O	54:TB:84:GLU:HG2	2.21	0.41
55:z:132:GLN:HB3	56:w:665:MET:CE	2.50	0.41
56:w:519:LEU:HD23	56:w:519:LEU:H	1.86	0.41
1:A:2090:A:H2'	1:A:2091:A:C8	2.55	0.41
1:A:2241:A:H2'	31:r:192:TRP:HE3	1.86	0.41
1:A:2353:A:H2'	1:A:2354:A:C8	2.56	0.41
1:A:2559:U:O4'	1:A:2560:G:OP2	2.39	0.41
1:A:2894:U:H5''	1:A:2895:U:O4'	2.21	0.41
1:A:2925:U:O2'	1:A:2927:C:OP1	2.30	0.41
1:A:3145:A:H2'	1:A:3146:G:C8	2.56	0.41
1:A:3225:G:H2'	1:A:3226:G:H8	1.84	0.41
4:F:241:ASN:OD1	4:F:256:HIS:NE2	2.40	0.41
17:0:136:GLU:OE2	17:0:139:ARG:NH1	2.53	0.41
24:e:48:LEU:HD21	24:e:175:GLN:HE21	1.85	0.41
25:g:144:THR:O	25:g:144:THR:OG1	2.32	0.41
27:j:46:LEU:HD23	27:j:46:LEU:HA	1.96	0.41
27:j:64:LEU:HD23	27:j:64:LEU:HA	1.89	0.41
38:E:278:THR:OG1	38:E:329:PRO:O	2.34	0.41
44:c:245:LEU:HD22	44:c:250:VAL:HB	2.02	0.41
1:A:1731:A:N1	26:i:118:TYR:HB3	2.36	0.41
1:A:1798:A:H8	1:A:1798:A:OP2	2.03	0.41
1:A:1807:U:O2'	1:A:1808:A:O5'	2.33	0.41
1:A:1892:A:C1'	40:6:378:GLY:HA3	2.50	0.41
1:A:2041:U:H2'	1:A:2042:U:H6	1.86	0.41
1:A:2081:U:OP1	29:o:63:ALA:N	2.45	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2123:C:H2'	1:A:2124:A:C8	2.56	0.41
1:A:2139:U:P	16:Z:74:SER:H	2.44	0.41
1:A:2198:A:N6	32:J:150:SER:HB3	2.35	0.41
1:A:2322:C:OP1	17:O:139:ARG:NE	2.53	0.41
1:A:2532:U:H2'	1:A:2533:A:C8	2.56	0.41
1:A:2801:A:H2'	1:A:2802:A:C8	2.55	0.41
1:A:3027:U:H4'	1:A:3173:G:H5'	2.03	0.41
1:A:3148:C:OP1	38:E:211:ILE:HG13	2.20	0.41
1:A:3211:C:H5'	1:A:3212:C:OP1	2.21	0.41
7:L:90:CYS:O	7:L:99:ARG:NE	2.53	0.41
12:T:146:THR:HG23	12:T:175:PHE:HD2	1.85	0.41
29:o:38:ARG:HB3	34:N:224:LEU:HD21	2.03	0.41
36:U:46:MET:HE3	36:U:46:MET:HB3	1.92	0.41
41:7:195:THR:OG1	41:7:196:LYS:N	2.54	0.41
51:s:91:TYR:HE1	51:s:229:LEU:HD22	1.86	0.41
1:A:1696:C:H2'	1:A:1697:A:C8	2.56	0.41
1:A:1751:A:OP1	8:M:75:TYR:OH	2.10	0.41
1:A:2037:U:H4'	1:A:2040:G:C6	2.56	0.41
1:A:2182:G:O2'	1:A:2183:C:OP1	2.39	0.41
1:A:2215:C:OP1	34:N:31:LYS:HG3	2.20	0.41
1:A:2960:U:N3	56:w:706:ALA:HB1	2.36	0.41
1:A:3122:U:H4'	1:A:3123:G:H4'	2.03	0.41
10:R:136:LYS:HA	10:R:137:GLU:HA	1.81	0.41
35:P:52:ASN:HD21	40:6:320:GLN:HE22	1.69	0.41
37:V:147:SER:HB3	37:V:152:ARG:H	1.86	0.41
38:E:225:LYS:HB3	38:E:225:LYS:HE3	1.79	0.41
56:w:244:LEU:HB3	56:w:246:TRP:HZ3	1.86	0.41
1:A:1837:C:H2'	1:A:1838:C:O4'	2.21	0.40
1:A:1893:A:O3'	1:A:1894:G:H8	2.04	0.40
1:A:1924:U:OP1	3:D:98:GLY:N	2.54	0.40
1:A:2131:A:N6	31:r:168:ARG:HD2	2.36	0.40
1:A:2160:A:H5'	21:4:88:TRP:CZ2	2.56	0.40
1:A:2511:C:O2'	3:D:258:GLY:CA	2.69	0.40
1:A:2538:C:H5''	1:A:2635:G:OP2	2.21	0.40
1:A:3040:G:H2'	1:A:3041:U:O4'	2.21	0.40
14:X:77:ARG:NH1	39:5:48:ARG:HE	2.20	0.40
17:O:178:ASP:OD2	17:O:178:ASP:N	2.55	0.40
22:8:121:TRP:CD2	24:e:70:MET:HE2	2.56	0.40
54:TA:85:LEU:CG	54:TB:65:GLN:HA	2.51	0.40
55:z:99:LEU:HD22	55:z:249:LEU:HD22	2.03	0.40
56:w:84:THR:CG2	59:w:801:GCP:O1A	2.68	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1731:A:C6	26:i:118:TYR:CE1	3.01	0.40
1:A:1808:A:N3	1:A:1809:U:O2'	2.54	0.40
1:A:2087:U:H2'	1:A:2088:U:C6	2.55	0.40
1:A:2538:C:H2'	1:A:2539:A:O4'	2.21	0.40
6:K:26:GLN:NE2	6:K:149:ARG:H	2.20	0.40
44:c:156:LEU:HD23	44:c:156:LEU:HA	1.91	0.40
52:Q:269:MET:HE2	52:Q:269:MET:HB3	1.86	0.40
54:TA:75:THR:O	54:TA:79:ILE:HG13	2.20	0.40
1:A:2420:U:H1'	42:9:32:GLY:HA2	2.03	0.40
1:A:2615:A:C4	7:L:58:ILE:HD12	2.55	0.40
1:A:2720:A:H2'	1:A:2721:G:H8	1.86	0.40
1:A:2799:U:H2'	1:A:2800:U:C6	2.57	0.40
1:A:3118:U:H2'	1:A:3119:C:C6	2.55	0.40
5:H:70:LYS:HE2	5:H:70:LYS:HB2	1.94	0.40
5:H:147:ARG:NH1	5:H:148:GLN:OE1	2.54	0.40
8:M:116:ILE:HB	8:M:154:ILE:HG13	2.04	0.40
32:J:116:HIS:O	32:J:120:ILE:HG13	2.21	0.40
41:7:259:ASP:OD1	41:7:259:ASP:N	2.52	0.40
46:f:106:TYR:CE1	46:f:179:PRO:HD3	2.56	0.40
51:s:416:ASP:OD1	51:s:416:ASP:N	2.54	0.40
52:Q:100:LEU:HD23	52:Q:100:LEU:HA	1.88	0.40
55:z:154:CYS:SG	55:z:155:THR:N	2.94	0.40
56:w:153:GLU:HG3	56:w:186:HIS:CE1	2.57	0.40
1:A:1690:C:H2'	1:A:1691:C:C6	2.57	0.40
1:A:2190:C:O2'	32:J:146:GLY:CA	2.69	0.40
1:A:2493:C:C2	1:A:2540:C:C6	3.10	0.40
1:A:2678:A:C2	17:0:80:ALA:CA	3.01	0.40
7:L:119:ILE:HG21	7:L:123:ILE:HD11	2.03	0.40
11:S:118:ASN:N	11:S:118:ASN:OD1	2.53	0.40
27:j:102:GLN:O	27:j:106:GLU:HG3	2.22	0.40
30:q:42:PRO:HB2	30:q:43:GLU:H	1.71	0.40
33:I:79:ILE:H	33:I:79:ILE:HG12	1.64	0.40
36:U:11:ARG:NH1	39:5:81:TYR:O	2.54	0.40
40:6:122:ALA:HB1	40:6:128:ALA:HB2	2.03	0.40
51:s:188:LEU:HD23	51:s:188:LEU:HA	1.93	0.40
1:A:2240:C:P	6:K:71:LYS:HZ2	2.44	0.40
1:A:2310:G:OP2	17:0:93:ARG:NH2	2.55	0.40
1:A:2373:A:C6	51:s:274:PHE:CG	3.09	0.40
1:A:2408:U:H2'	1:A:2409:A:C8	2.55	0.40
1:A:2523:C:H5''	39:5:35:VAL:CG1	2.52	0.40
1:A:2622:G:C2	1:A:2623:A:C8	3.10	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1637:C:H5'	40:6:52:ARG:HB3	2.03	0.40
14:X:7:PRO:HD2	14:X:10:LEU:HD12	2.04	0.40
14:X:39:THR:OG1	14:X:152:ASP:OD1	2.33	0.40
16:Z:66:LEU:HD12	16:Z:122:LEU:HD23	2.04	0.40
17:0:156:THR:HG21	17:0:173:ARG:HH21	1.86	0.40
41:7:290:GLN:NE2	41:7:292:SER:H	2.20	0.40
51:s:229:LEU:HD23	51:s:229:LEU:HA	1.94	0.40
55:z:113:PRO:HG2	55:z:138:MET:HE2	2.03	0.40
56:w:147:ASP:HB3	56:w:539:HIS:HB2	2.04	0.40
56:w:177:LEU:HD11	56:w:214:LYS:HE2	2.02	0.40
56:w:427:LEU:HD13	56:w:427:LEU:HA	1.99	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	D	237/305 (78%)	227 (96%)	9 (4%)	1 (0%)	30	59
4	F	248/311 (80%)	226 (91%)	20 (8%)	2 (1%)	16	46
5	H	96/267 (36%)	88 (92%)	8 (8%)	0	100	100
6	K	175/178 (98%)	153 (87%)	20 (11%)	2 (1%)	11	39
7	L	113/145 (78%)	102 (90%)	11 (10%)	0	100	100
8	M	285/296 (96%)	248 (87%)	35 (12%)	2 (1%)	18	49
9	O	150/175 (86%)	133 (89%)	16 (11%)	1 (1%)	18	49
10	R	138/149 (93%)	130 (94%)	8 (6%)	0	100	100
11	S	154/205 (75%)	143 (93%)	11 (7%)	0	100	100
12	T	164/212 (77%)	156 (95%)	8 (5%)	0	100	100
13	W	109/148 (74%)	102 (94%)	7 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	X	241/256 (94%)	221 (92%)	20 (8%)	0	100	100
15	Y	174/250 (70%)	165 (95%)	7 (4%)	2 (1%)	11	39
16	Z	118/161 (73%)	110 (93%)	8 (7%)	0	100	100
17	0	106/188 (56%)	92 (87%)	14 (13%)	0	100	100
18	1	50/65 (77%)	45 (90%)	5 (10%)	0	100	100
19	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
20	3	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
21	4	36/103 (35%)	34 (94%)	2 (6%)	0	100	100
22	8	97/206 (47%)	95 (98%)	2 (2%)	0	100	100
23	b	146/155 (94%)	135 (92%)	11 (8%)	0	100	100
24	e	211/279 (76%)	203 (96%)	8 (4%)	0	100	100
25	g	130/166 (78%)	122 (94%)	8 (6%)	0	100	100
26	i	95/128 (74%)	88 (93%)	7 (7%)	0	100	100
27	j	91/123 (74%)	84 (92%)	6 (7%)	1 (1%)	11	39
28	m	43/128 (34%)	37 (86%)	6 (14%)	0	100	100
29	o	92/102 (90%)	85 (92%)	7 (8%)	0	100	100
30	q	164/222 (74%)	153 (93%)	8 (5%)	3 (2%)	6	29
31	r	160/196 (82%)	148 (92%)	11 (7%)	1 (1%)	21	52
32	J	173/192 (90%)	163 (94%)	10 (6%)	0	100	100
33	I	177/261 (68%)	167 (94%)	10 (6%)	0	100	100
34	N	220/251 (88%)	215 (98%)	5 (2%)	0	100	100
35	P	141/179 (79%)	131 (93%)	8 (6%)	2 (1%)	9	34
36	U	150/153 (98%)	141 (94%)	9 (6%)	0	100	100
37	V	204/216 (94%)	194 (95%)	10 (5%)	0	100	100
38	E	304/348 (87%)	283 (93%)	20 (7%)	1 (0%)	36	64
39	5	391/423 (92%)	375 (96%)	16 (4%)	0	100	100
40	6	352/380 (93%)	328 (93%)	24 (7%)	0	100	100
41	7	295/338 (87%)	276 (94%)	18 (6%)	1 (0%)	36	64
42	9	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
43	a	106/142 (75%)	101 (95%)	5 (5%)	0	100	100
44	c	287/332 (86%)	269 (94%)	18 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	d	255/306 (83%)	235 (92%)	20 (8%)	0	100	100
46	f	144/194 (74%)	135 (94%)	9 (6%)	0	100	100
47	h	108/158 (68%)	98 (91%)	9 (8%)	1 (1%)	14	43
48	k	94/112 (84%)	88 (94%)	6 (6%)	0	100	100
49	l	70/138 (51%)	63 (90%)	7 (10%)	0	100	100
50	p	148/206 (72%)	139 (94%)	8 (5%)	1 (1%)	18	49
51	s	391/439 (89%)	361 (92%)	29 (7%)	1 (0%)	36	64
52	Q	218/292 (75%)	209 (96%)	9 (4%)	0	100	100
54	TA	43/198 (22%)	35 (81%)	8 (19%)	0	100	100
54	TB	25/198 (13%)	24 (96%)	1 (4%)	0	100	100
54	TC	69/198 (35%)	59 (86%)	9 (13%)	1 (1%)	9	34
55	z	195/204 (96%)	164 (84%)	23 (12%)	8 (4%)	2	14
56	w	692/696 (99%)	583 (84%)	93 (13%)	16 (2%)	5	24
All	All	9334/12090 (77%)	8605 (92%)	682 (7%)	47 (0%)	26	55

All (47) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	q	43	GLU
35	P	69	ARG
6	K	160	GLN
38	E	317	PRO
55	z	106	THR
55	z	183	PRO
56	w	111	ASP
56	w	379	GLN
56	w	605	PRO
4	F	291	SER
8	M	288	GLU
30	q	42	PRO
50	p	84	SER
56	w	250	SER
56	w	366	ASP
56	w	373	LYS
3	D	207	ILE
6	K	4	PHE
27	j	35	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	q	79	PRO
51	s	350	ASP
54	TC	169	PRO
55	z	168	ASN
56	w	249	ASN
56	w	252	ASP
8	M	265	ILE
15	Y	203	PRO
55	z	112	SER
55	z	165	SER
56	w	308	ALA
56	w	390	SER
41	7	110	GLY
55	z	166	GLY
55	z	167	MET
56	w	95	GLY
56	w	106	GLY
56	w	485	ILE
56	w	722	GLN
47	h	133	PRO
9	O	111	PRO
31	r	136	PRO
35	P	46	PRO
55	z	152	PRO
4	F	128	TRP
15	Y	202	LEU
56	w	395	PRO
56	w	659	PRO

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	D	193/245 (79%)	192 (100%)	1 (0%)	81	82
4	F	217/262 (83%)	216 (100%)	1 (0%)	81	82
5	H	88/228 (39%)	88 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	K	155/156 (99%)	155 (100%)	0	100	100
7	L	98/124 (79%)	97 (99%)	1 (1%)	68	76
8	M	245/249 (98%)	244 (100%)	1 (0%)	84	84
9	O	133/150 (89%)	132 (99%)	1 (1%)	73	78
10	R	118/126 (94%)	118 (100%)	0	100	100
11	S	141/180 (78%)	141 (100%)	0	100	100
12	T	146/182 (80%)	143 (98%)	3 (2%)	47	67
13	W	91/119 (76%)	90 (99%)	1 (1%)	65	75
14	X	217/227 (96%)	216 (100%)	1 (0%)	81	82
15	Y	159/223 (71%)	158 (99%)	1 (1%)	78	81
16	Z	111/147 (76%)	110 (99%)	1 (1%)	70	77
17	0	97/164 (59%)	97 (100%)	0	100	100
18	1	49/60 (82%)	49 (100%)	0	100	100
19	2	40/72 (56%)	40 (100%)	0	100	100
20	3	88/166 (53%)	88 (100%)	0	100	100
21	4	37/89 (42%)	37 (100%)	0	100	100
22	8	91/190 (48%)	90 (99%)	1 (1%)	65	75
23	b	130/135 (96%)	130 (100%)	0	100	100
24	e	188/236 (80%)	187 (100%)	1 (0%)	81	82
25	g	122/148 (82%)	120 (98%)	2 (2%)	55	71
26	i	86/110 (78%)	84 (98%)	2 (2%)	44	66
27	j	74/97 (76%)	74 (100%)	0	100	100
28	m	40/113 (35%)	40 (100%)	0	100	100
29	o	80/87 (92%)	80 (100%)	0	100	100
30	q	113/178 (64%)	112 (99%)	1 (1%)	70	77
31	r	147/169 (87%)	145 (99%)	2 (1%)	59	73
32	J	138/150 (92%)	136 (99%)	2 (1%)	59	73
33	I	164/232 (71%)	160 (98%)	4 (2%)	43	66
34	N	189/211 (90%)	188 (100%)	1 (0%)	81	82
35	P	125/154 (81%)	125 (100%)	0	100	100
36	U	125/135 (93%)	125 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	V	184/191 (96%)	180 (98%)	4 (2%)	45	67
38	E	260/290 (90%)	257 (99%)	3 (1%)	63	74
39	5	353/368 (96%)	348 (99%)	5 (1%)	59	73
40	6	313/332 (94%)	311 (99%)	2 (1%)	78	81
41	7	272/303 (90%)	271 (100%)	1 (0%)	84	84
42	9	104/112 (93%)	103 (99%)	1 (1%)	68	76
43	a	101/133 (76%)	101 (100%)	0	100	100
44	c	253/288 (88%)	252 (100%)	1 (0%)	84	84
45	d	224/274 (82%)	222 (99%)	2 (1%)	70	77
46	f	122/173 (70%)	122 (100%)	0	100	100
47	h	104/148 (70%)	104 (100%)	0	100	100
48	k	81/90 (90%)	80 (99%)	1 (1%)	63	74
49	l	67/116 (58%)	67 (100%)	0	100	100
50	p	134/181 (74%)	133 (99%)	1 (1%)	76	80
51	s	336/381 (88%)	335 (100%)	1 (0%)	86	85
52	Q	202/256 (79%)	202 (100%)	0	100	100
54	TA	39/158 (25%)	39 (100%)	0	100	100
54	TB	26/158 (16%)	25 (96%)	1 (4%)	29	58
55	z	175/179 (98%)	171 (98%)	4 (2%)	44	66
56	w	604/604 (100%)	588 (97%)	16 (3%)	40	64
All	All	8189/10249 (80%)	8118 (99%)	71 (1%)	68	77

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	220	VAL
4	F	216	VAL
7	L	105	VAL
8	M	184	LEU
9	O	20	LEU
12	T	58	VAL
12	T	142	ILE
12	T	156	ILE
13	W	125	VAL
14	X	238	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	Y	190	LEU
16	Z	110	LEU
22	8	104	VAL
24	e	98	LEU
25	g	77	ASP
25	g	100	ILE
26	i	59	ASN
26	i	80	LEU
30	q	52	LEU
31	r	54	THR
31	r	190	THR
32	J	112	VAL
32	J	192	LYS
33	I	96	ILE
33	I	104	LEU
33	I	155	VAL
33	I	163	GLU
34	N	59	VAL
37	V	29	VAL
37	V	56	LEU
37	V	77	VAL
37	V	123	VAL
38	E	102	LEU
38	E	273	VAL
38	E	318	THR
39	5	148	ASN
39	5	251	VAL
39	5	272	VAL
39	5	344	VAL
39	5	369	VAL
40	6	179	VAL
40	6	187	VAL
41	7	78	VAL
42	9	57	VAL
44	c	182	GLU
45	d	89	VAL
45	d	214	VAL
48	k	51	VAL
50	p	78	THR
51	s	356	VAL
54	TB	71	ILE
55	z	83	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
55	z	107	LEU
55	z	122	VAL
55	z	173	VAL
56	w	137	VAL
56	w	172	VAL
56	w	232	PHE
56	w	267	PRO
56	w	305	LEU
56	w	325	VAL
56	w	341	LEU
56	w	357	TYR
56	w	382	PRO
56	w	392	THR
56	w	428	THR
56	w	435	THR
56	w	479	LEU
56	w	617	GLU
56	w	665	MET
56	w	701	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (177) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	165	ASN
3	D	182	HIS
3	D	194	ASN
3	D	195	ASN
3	D	227	GLN
3	D	252	HIS
4	F	74	GLN
4	F	97	HIS
4	F	103	GLN
4	F	130	GLN
4	F	184	GLN
5	H	88	HIS
5	H	136	ASN
6	K	26	GLN
6	K	40	GLN
6	K	48	HIS
6	K	56	HIS
6	K	61	ASN
6	K	64	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	K	74	GLN
6	K	89	GLN
7	L	43	ASN
7	L	52	HIS
7	L	72	GLN
7	L	80	GLN
7	L	104	ASN
7	L	142	GLN
8	M	26	ASN
8	M	84	ASN
8	M	87	HIS
8	M	92	GLN
8	M	120	GLN
8	M	198	GLN
9	O	128	ASN
9	O	141	HIS
9	O	160	GLN
10	R	30	HIS
10	R	125	HIS
11	S	118	ASN
11	S	140	ASN
12	T	62	GLN
12	T	109	ASN
12	T	151	GLN
12	T	201	GLN
13	W	41	ASN
13	W	62	HIS
13	W	80	HIS
13	W	110	ASN
14	X	215	GLN
15	Y	73	ASN
15	Y	99	HIS
16	Z	67	HIS
16	Z	98	GLN
17	0	96	ASN
17	0	118	GLN
17	0	168	GLN
20	3	154	GLN
22	8	127	GLN
22	8	143	GLN
23	b	25	GLN
23	b	27	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
23	b	102	GLN
23	b	123	ASN
24	e	126	GLN
24	e	175	GLN
24	e	198	ASN
24	e	212	HIS
24	e	245	GLN
24	e	248	ASN
24	e	251	HIS
24	e	271	GLN
25	g	102	HIS
25	g	104	ASN
26	i	89	GLN
27	j	30	GLN
27	j	36	ASN
27	j	63	GLN
29	o	21	HIS
29	o	58	GLN
30	q	130	GLN
30	q	139	GLN
30	q	142	ASN
31	r	65	ASN
31	r	69	GLN
31	r	184	ASN
32	J	41	GLN
33	I	41	HIS
33	I	189	GLN
33	I	193	ASN
34	N	68	ASN
34	N	98	HIS
34	N	110	ASN
36	U	35	GLN
36	U	135	GLN
37	V	73	GLN
38	E	57	ASN
38	E	128	HIS
38	E	280	HIS
38	E	281	ASN
38	E	294	ASN
38	E	336	ASN
39	5	65	HIS
39	5	118	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
39	5	149	GLN
39	5	159	HIS
39	5	190	GLN
39	5	220	GLN
39	5	301	HIS
39	5	383	GLN
40	6	224	HIS
40	6	234	HIS
40	6	239	ASN
40	6	266	HIS
40	6	275	GLN
40	6	320	GLN
41	7	45	ASN
41	7	298	GLN
43	a	71	HIS
43	a	126	HIS
44	c	69	HIS
44	c	73	GLN
44	c	82	ASN
44	c	94	ASN
44	c	128	GLN
44	c	155	ASN
44	c	204	GLN
44	c	249	ASN
45	d	59	HIS
45	d	157	HIS
45	d	196	GLN
45	d	207	ASN
46	f	108	GLN
46	f	138	GLN
47	h	67	GLN
47	h	85	ASN
47	h	103	HIS
48	k	72	HIS
49	l	67	GLN
49	l	100	ASN
49	l	124	GLN
49	l	125	ASN
50	p	104	HIS
50	p	194	HIS
51	s	87	GLN
51	s	107	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	s	191	HIS
51	s	207	HIS
51	s	238	ASN
51	s	240	GLN
51	s	382	GLN
51	s	387	ASN
51	s	391	ASN
51	s	408	ASN
52	Q	212	ASN
55	z	84	ASN
55	z	131	ASN
55	z	184	GLN
55	z	189	HIS
55	z	202	ASN
55	z	252	HIS
56	w	72	ASN
56	w	78	HIS
56	w	115	GLN
56	w	138	ASN
56	w	145	HIS
56	w	182	GLN
56	w	187	ASN
56	w	249	ASN
56	w	278	ASN
56	w	283	GLN
56	w	400	HIS
56	w	403	ASN
56	w	420	GLN
56	w	507	HIS
56	w	544	HIS
56	w	761	GLN
56	w	766	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1522/1559 (97%)	349 (22%)	28 (1%)
2	B	51/73 (69%)	13 (25%)	1 (1%)
All	All	1573/1632 (96%)	362 (23%)	29 (1%)

All (362) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1678	C
1	A	1679	U
1	A	1681	G
1	A	1689	C
1	A	1690	C
1	A	1700	U
1	A	1704	U
1	A	1708	A
1	A	1709	G
1	A	1710	A
1	A	1711	C
1	A	1713	A
1	A	1714	C
1	A	1715	C
1	A	1716	U
1	A	1717	U
1	A	1724	A
1	A	1727	A
1	A	1728	U
1	A	1733	C
1	A	1734	C
1	A	1735	A
1	A	1736	A
1	A	1748	G
1	A	1750	G
1	A	1751	A
1	A	1762	A
1	A	1763	A
1	A	1766	U
1	A	1770	G
1	A	1777	A
1	A	1781	A
1	A	1782	G
1	A	1794	A
1	A	1803	A
1	A	1805	A
1	A	1806	U
1	A	1807	U
1	A	1808	A
1	A	1809	U
1	A	1810	A
1	A	1821	A
1	A	1823	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1824	U
1	A	1827	C
1	A	1828	A
1	A	1829	A
1	A	1832	A
1	A	1836	A
1	A	1840	C
1	A	1844	A
1	A	1849	C
1	A	1854	U
1	A	1856	A
1	A	1867	A
1	A	1869	A
1	A	1871	A
1	A	1872	U
1	A	1878	U
1	A	1882	A
1	A	1883	G
1	A	1890	C
1	A	1893	A
1	A	1901	C
1	A	1902	C
1	A	1903	C
1	A	1909	A
1	A	1918	G
1	A	1935	A
1	A	1936	A
1	A	1938	A
1	A	1940	A
1	A	1944	C
1	A	1946	C
1	A	1958	G
1	A	1974	A
1	A	1985	G
1	A	1986	A
1	A	1987	G
1	A	1992	C
1	A	1994	A
1	A	1995	A
1	A	2000	C
1	A	2001	C
1	A	2002	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2015	G
1	A	2021	U
1	A	2022	G
1	A	2029	A
1	A	2031	A
1	A	2036	C
1	A	2037	U
1	A	2038	U
1	A	2039	A
1	A	2060	A
1	A	2065	A
1	A	2066	C
1	A	2067	C
1	A	2069	U
1	A	2074	A
1	A	2079	C
1	A	2083	U
1	A	2085	A
1	A	2093	U
1	A	2097	A
1	A	2098	G
1	A	2099	U
1	A	2105	G
1	A	2113	G
1	A	2125	C
1	A	2126	U
1	A	2134	A
1	A	2135	A
1	A	2142	A
1	A	2147	G
1	A	2154	A
1	A	2160	A
1	A	2163	A
1	A	2165	C
1	A	2166	C
1	A	2169	A
1	A	2171	U
1	A	2172	A
1	A	2173	G
1	A	2174	G
1	A	2180	A
1	A	2181	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2183	C
1	A	2187	C
1	A	2190	C
1	A	2192	A
1	A	2198	A
1	A	2200	A
1	A	2204	U
1	A	2210	C
1	A	2211	U
1	A	2217	C
1	A	2218	C
1	A	2219	C
1	A	2220	A
1	A	2222	U
1	A	2224	C
1	A	2227	A
1	A	2228	A
1	A	2229	A
1	A	2230	A
1	A	2237	A
1	A	2239	A
1	A	2241	A
1	A	2242	U
1	A	2244	U
1	A	2245	A
1	A	2246	A
1	A	2250	A
1	A	2252	C
1	A	2260	A
1	A	2262	C
1	A	2263	C
1	A	2284	C
1	A	2285	U
1	A	2297	A
1	A	2299	U
1	A	2300	G
1	A	2315	A
1	A	2322	C
1	A	2324	U
1	A	2332	C
1	A	2345	G
1	A	2350	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2351	U
1	A	2356	A
1	A	2357	C
1	A	2360	U
1	A	2361	G
1	A	2362	A
1	A	2364	C
1	A	2365	U
1	A	2371	U
1	A	2372	U
1	A	2381	A
1	A	2390	A
1	A	2393	C
1	A	2404	U
1	A	2407	U
1	A	2414	C
1	A	2415	C
1	A	2416	U
1	A	2434	A
1	A	2443	C
1	A	2444	A
1	A	2446	A
1	A	2447	A
1	A	2451	A
1	A	2452	A
1	A	2458	A
1	A	2478	G
1	A	2493	C
1	A	2507	A
1	A	2508	C
1	A	2511	C
1	A	2520	C
1	A	2521	A
1	A	2522	U
1	A	2523	C
1	A	2524	A
1	A	2527	A
1	A	2530	A
1	A	2531	U
1	A	2532	U
1	A	2540	C
1	A	2546	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2557	C
1	A	2558	A
1	A	2559	U
1	A	2560	G
1	A	2570	C
1	A	2575	U
1	A	2592	G
1	A	2593	G
1	A	2594	U
1	A	2599	U
1	A	2601	A
1	A	2603	C
1	A	2607	U
1	A	2618	U
1	A	2626	U
1	A	2627	G
1	A	2629	A
1	A	2630	U
1	A	2632	A
1	A	2633	A
1	A	2634	U
1	A	2635	G
1	A	2645	G
1	A	2654	U
1	A	2656	U
1	A	2660	U
1	A	2683	C
1	A	2684	C
1	A	2686	G
1	A	2694	A
1	A	2696	A
1	A	2706	A
1	A	2709	A
1	A	2715	A
1	A	2718	C
1	A	2723	A
1	A	2724	G
1	A	2725	A
1	A	2732	G
1	A	2739	U
1	A	2740	A
1	A	2745	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2747	U
1	A	2750	U
1	A	2755	A
1	A	2756	C
1	A	2757	A
1	A	2758	G
1	A	2760	A
1	A	2791	A
1	A	2792	A
1	A	2803	A
1	A	2804	A
1	A	2810	G
1	A	2814	G
1	A	2831	G
1	A	2832	A
1	A	2833	A
1	A	2844	G
1	A	2847	C
1	A	2854	U
1	A	2864	U
1	A	2865	C
1	A	2881	C
1	A	2893	A
1	A	2906	C
1	A	2910	A
1	A	2912	C
1	A	2913	A
1	A	2916	G
1	A	2917	G
1	A	2918	A
1	A	2922	A
1	A	2926	A
1	A	2928	C
1	A	2935	A
1	A	2955	U
1	A	2956	A
1	A	2962	C
1	A	2963	A
1	A	2985	C
1	A	2990	A
1	A	2991	U
1	A	2992	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2994	U
1	A	3000	A
1	A	3005	A
1	A	3007	C
1	A	3016	G
1	A	3022	G
1	A	3041	U
1	A	3042	U
1	A	3049	U
1	A	3053	A
1	A	3054	G
1	A	3059	A
1	A	3063	G
1	A	3070	G
1	A	3072	U
1	A	3093	C
1	A	3097	U
1	A	3098	U
1	A	3100	U
1	A	3102	U
1	A	3109	U
1	A	3113	A
1	A	3114	U
1	A	3123	G
1	A	3124	U
1	A	3129	A
1	A	3141	A
1	A	3150	U
1	A	3155	C
1	A	3157	C
1	A	3158	A
1	A	3162	C
1	A	3168	C
1	A	3169	C
1	A	3172	C
1	A	3180	A
1	A	3189	C
1	A	3190	A
1	A	3192	C
1	A	3196	G
1	A	3197	U
1	A	3200	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	3201	A
1	A	3204	C
1	A	3205	C
1	A	3207	A
1	A	3208	C
1	A	3210	C
1	A	3211	C
1	A	3212	C
1	A	3217	A
1	A	3218	A
1	A	3220	A
1	A	3228	U
2	B	1607	U
2	B	1608	G
2	B	1609	U
2	B	1611	G
2	B	1613	U
2	B	1614	U
2	B	1615	A
2	B	1625	A
2	B	1644	G
2	B	1645	A
2	B	1651	A
2	B	1659	U
2	B	1669	G

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1703	C
1	A	1709	G
1	A	1713	A
1	A	1805	A
1	A	1806	U
1	A	1807	U
1	A	1808	A
1	A	1809	U
1	A	1823	A
1	A	1871	A
1	A	1994	A
1	A	2165	C
1	A	2172	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2186	C
1	A	2245	A
1	A	2361	G
1	A	2457	A
1	A	2507	A
1	A	2530	A
1	A	2559	U
1	A	2628	U
1	A	2653	C
1	A	2905	A
1	A	2989	G
1	A	3041	U
1	A	3092	U
1	A	3123	G
1	A	3196	G
2	B	1607	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 106 ligands modelled in this entry, 105 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	GCP	w	801	57,56	32,34,34	1.70	6 (18%)	49,54,54	1.90	10 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	GCP	w	801	57,56	-	5/19/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	w	801	GCP	PG-O1G	5.63	1.61	1.50
59	w	801	GCP	C5-C4	3.18	1.47	1.38
59	w	801	GCP	PG-O3G	3.07	1.61	1.55
59	w	801	GCP	PG-O2G	-2.58	1.49	1.55
59	w	801	GCP	C4-N9	-2.30	1.32	1.38
59	w	801	GCP	PB-O2B	2.26	1.61	1.56

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	w	801	GCP	PB-O3A-PA	-5.88	113.17	132.37
59	w	801	GCP	C2-N3-C4	4.95	120.82	112.30
59	w	801	GCP	C5-C4-N3	-4.77	120.79	128.39
59	w	801	GCP	C6-C5-N7	4.20	137.93	130.29
59	w	801	GCP	N9-C4-N3	3.37	132.69	125.95
59	w	801	GCP	O4'-C1'-N9	2.55	114.15	108.36
59	w	801	GCP	C6-C5-C4	-2.41	115.20	118.83
59	w	801	GCP	C4-C5-N7	-2.40	106.86	110.67
59	w	801	GCP	C1'-N9-C4	-2.28	119.76	126.49
59	w	801	GCP	O6-C6-C5	-2.14	120.89	126.53

There are no chirality outliers.

All (5) torsion outliers are listed below:

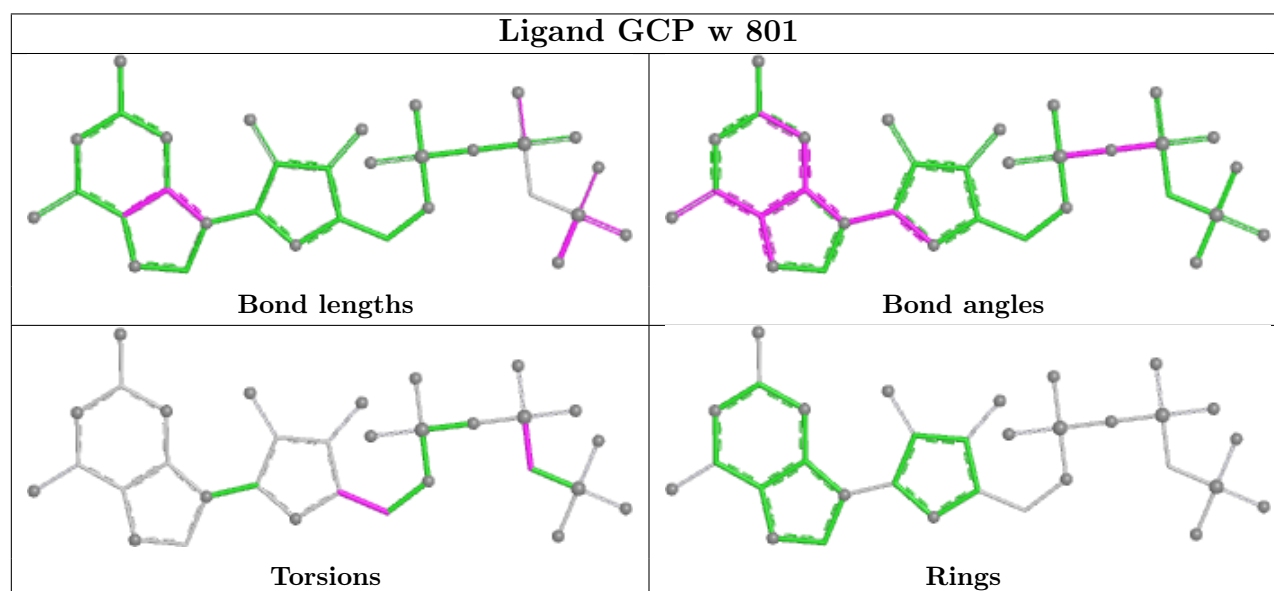
Mol	Chain	Res	Type	Atoms
59	w	801	GCP	PG-C3B-PB-O1B
59	w	801	GCP	PG-C3B-PB-O3A
59	w	801	GCP	O4'-C4'-C5'-O5'
59	w	801	GCP	C3'-C4'-C5'-O5'
59	w	801	GCP	PG-C3B-PB-O2B

There are no ring outliers.

1 monomer is involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	w	801	GCP	13	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
53	u	4

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
56	w	1
1	A	1
34	N	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	u	414:UNK	C	601:UNK	N	50.84
1	u	106:UNK	C	301:UNK	N	32.66
1	u	315:UNK	C	399:UNK	N	23.91
1	u	615:UNK	C	700:UNK	N	15.49
1	w	455:LEU	C	478:LEU	N	11.53
1	A	2580:U	O3'	2581:A	P	3.69
1	N	230:LEU	C	231:SER	N	1.19

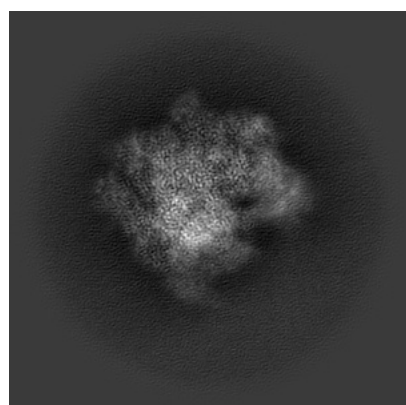
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23121. These allow visual inspection of the internal detail of the map and identification of artifacts.

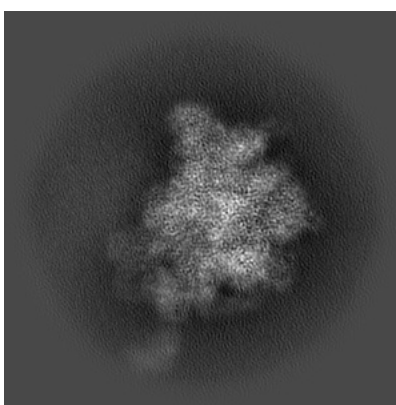
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

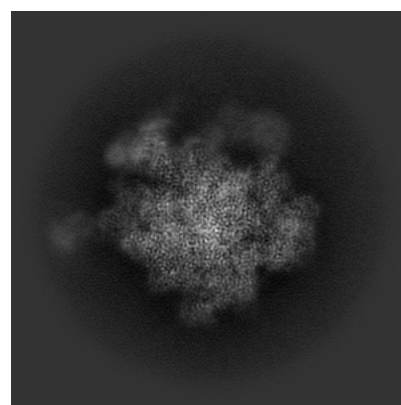
6.1.1 Primary map



X



Y

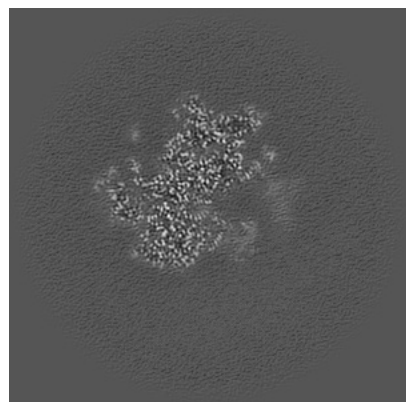


Z

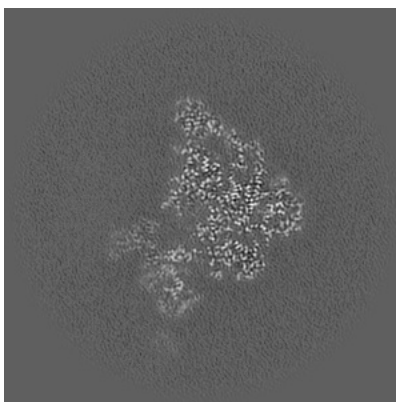
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

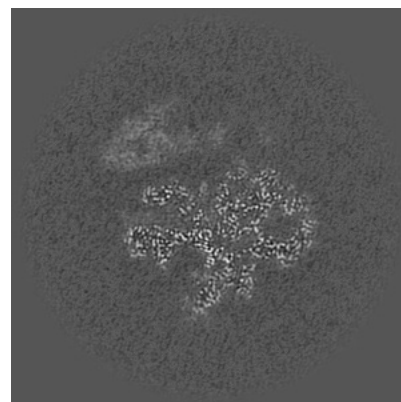
6.2.1 Primary map



X Index: 200



Y Index: 200

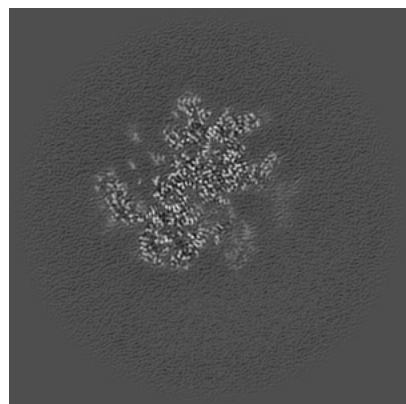


Z Index: 200

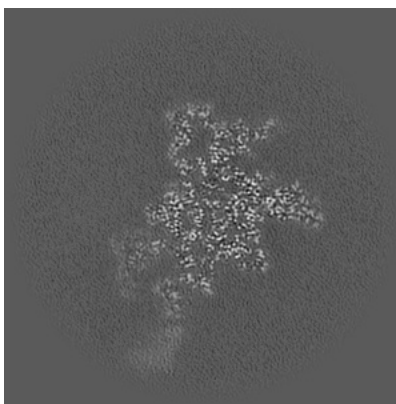
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

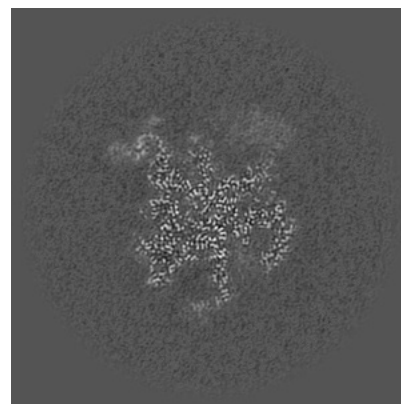
6.3.1 Primary map



X Index: 195



Y Index: 179

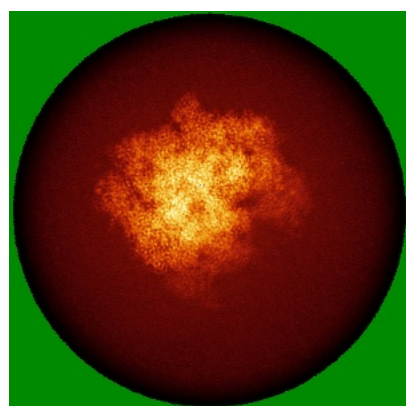


Z Index: 232

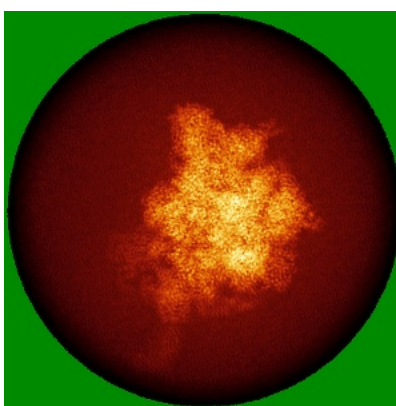
The images above show the largest variance slices of the map in three orthogonal directions.

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

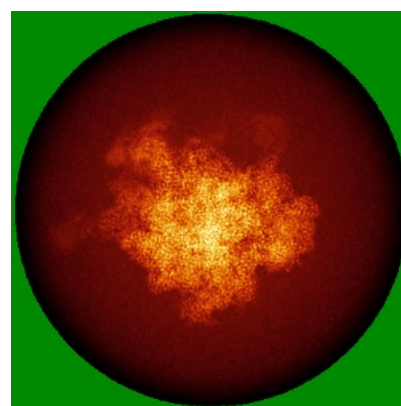
6.4.1 Primary map



X



Y

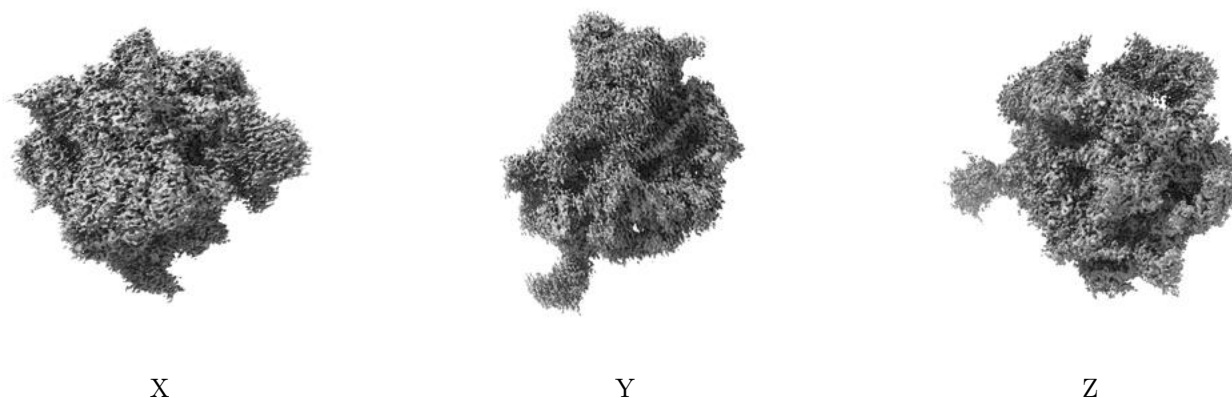


Z

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

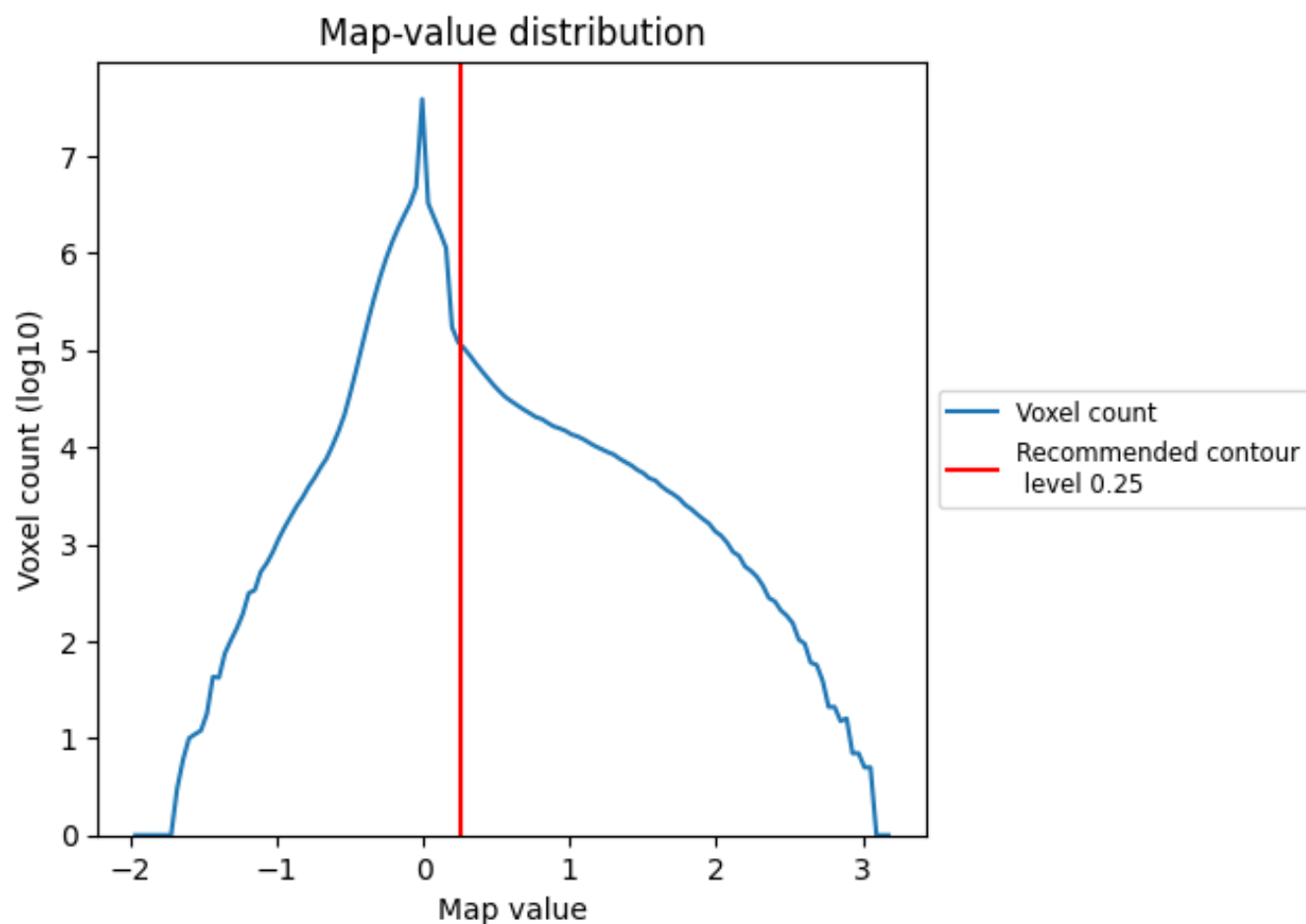
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

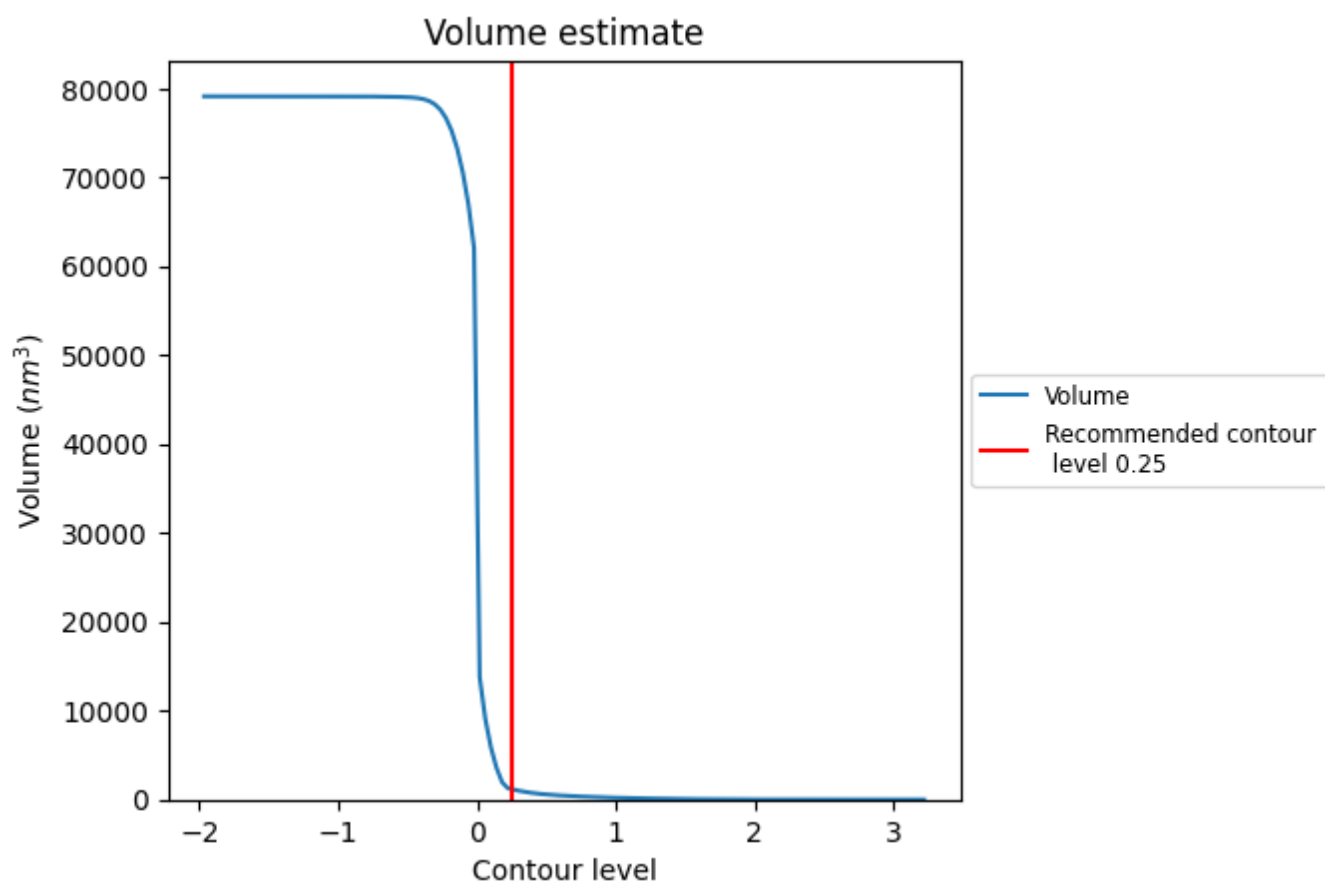
This section contains the results of statistical analysis of the map.

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.

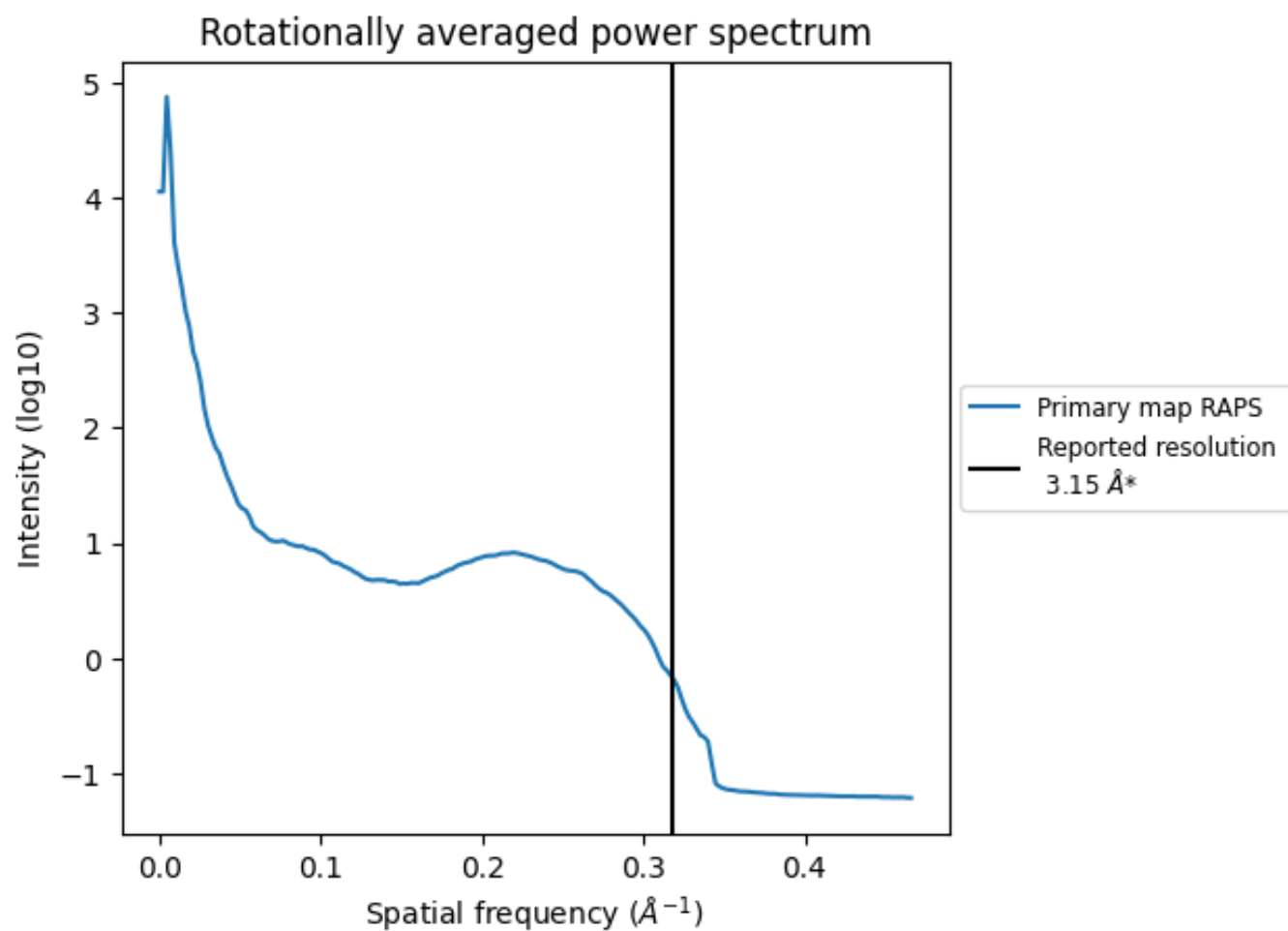
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1170 nm³; this corresponds to an approximate mass of 1057 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 0.317 Å⁻¹

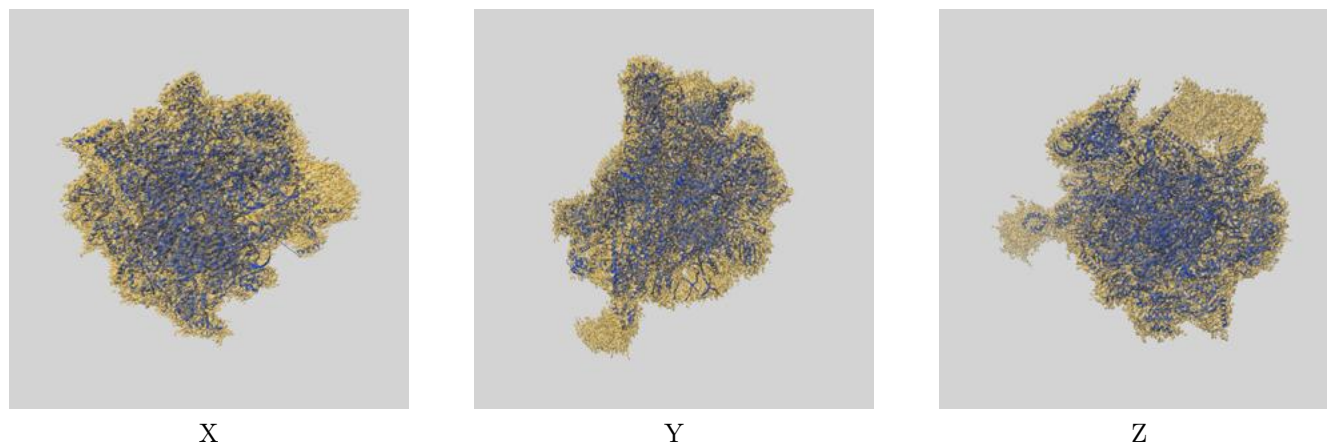
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

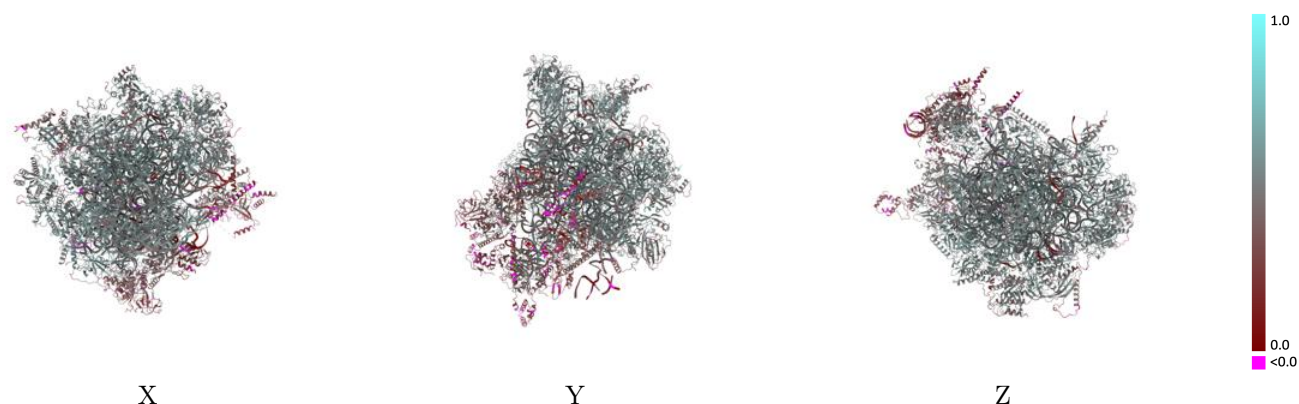
This section contains information regarding the fit between EMDB map EMD-23121 and PDB model 7L20. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



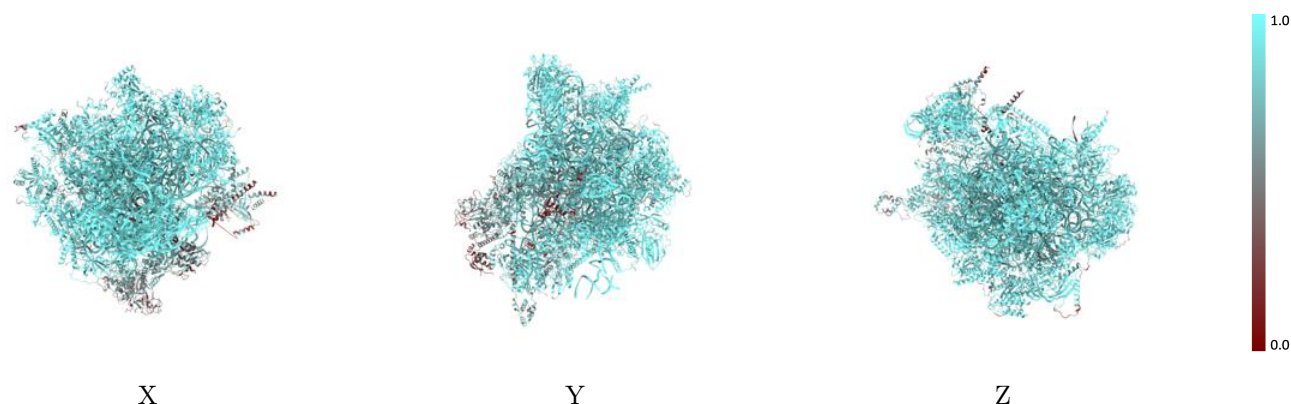
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



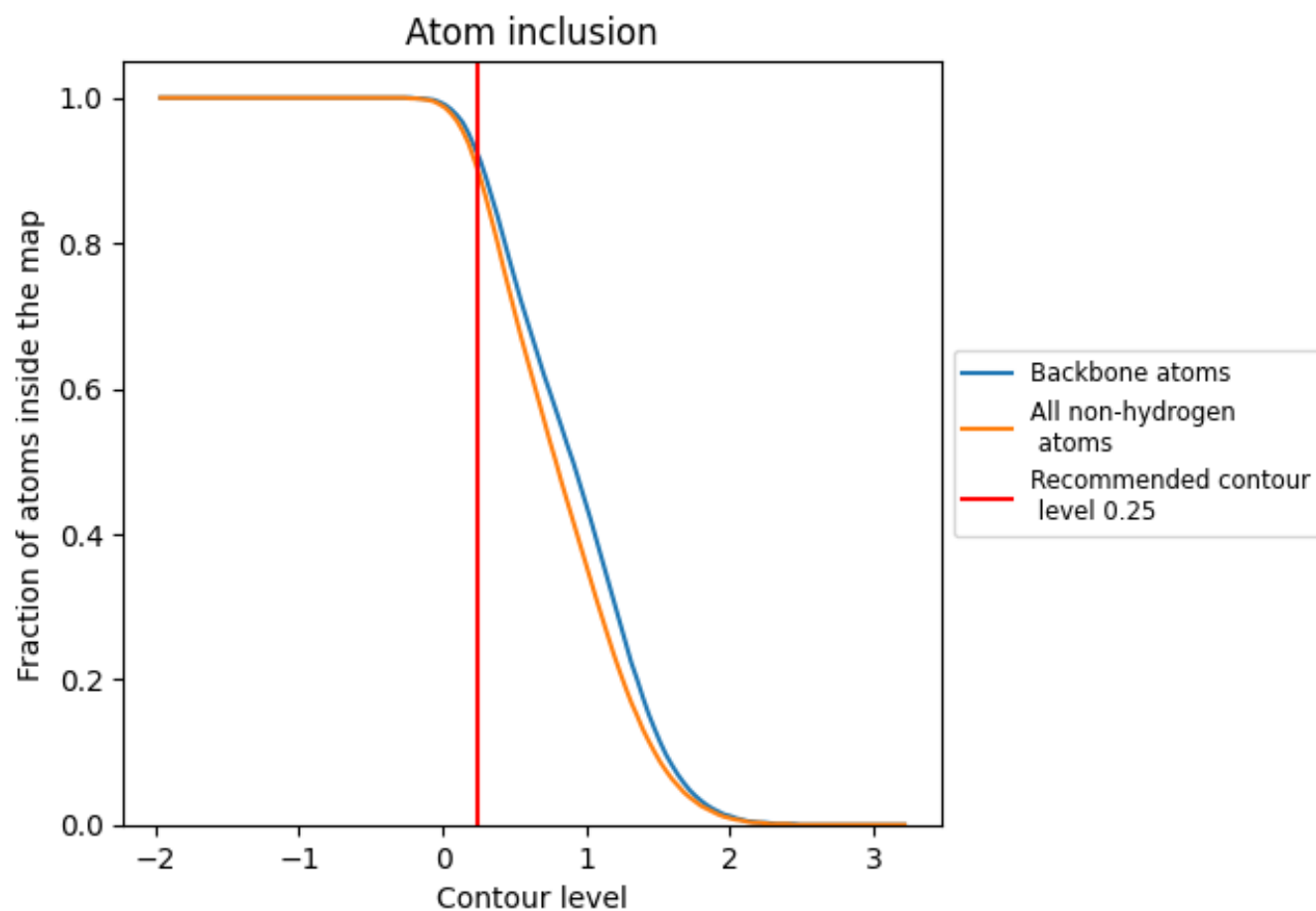
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8980	 0.4720
0	 0.9450	 0.5340
1	 0.9330	 0.5240
2	 0.9610	 0.5740
3	 0.9550	 0.5720
4	 0.9730	 0.5740
5	 0.9530	 0.5150
6	 0.9350	 0.4680
7	 0.9250	 0.4850
8	 0.7820	 0.3180
9	 0.9510	 0.5210
A	 0.9310	 0.4740
B	 0.9370	 0.3360
D	 0.9580	 0.5400
E	 0.9530	 0.5470
F	 0.9550	 0.5400
H	 0.9280	 0.4970
I	 0.8800	 0.4210
J	 0.7820	 0.3140
K	 0.9640	 0.5510
L	 0.9520	 0.5370
M	 0.9580	 0.5410
N	 0.9430	 0.5450
O	 0.9500	 0.5410
P	 0.9520	 0.5080
Q	 0.9480	 0.5380
R	 0.9370	 0.5510
S	 0.9570	 0.5510
T	 0.9480	 0.5530
TA	 0.6080	 0.1640
TB	 0.6010	 0.1610
TC	 0.2590	 0.1400
U	 0.9180	 0.5120
V	 0.9120	 0.4810
W	 0.9380	 0.5500



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
X	 0.9380	 0.5250
Y	 0.9510	 0.5320
Z	 0.9510	 0.5530
a	 0.8710	 0.4760
b	 0.9560	 0.5480
c	 0.9280	 0.5070
d	 0.8630	 0.4480
e	 0.7420	 0.2390
f	 0.7580	 0.3490
g	 0.9330	 0.5230
h	 0.9190	 0.4730
i	 0.9500	 0.5560
j	 0.9110	 0.5070
k	 0.9160	 0.4430
l	 0.8680	 0.4000
m	 0.8500	 0.3360
o	 0.9400	 0.5430
p	 0.8530	 0.4360
q	 0.8350	 0.4010
r	 0.9550	 0.5280
s	 0.9370	 0.5180
u	 0.3170	 0.0710
w	 0.5880	 0.2990
z	 0.6480	 0.3260