



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:04 AM UTC

PDB ID : 8K2B / pdb_00008k2b
EMDB ID : EMD-36837
Title : Cryo-EM structure of the human 39S mitoribosome with Tigecycline
Authors : Li, X.; Wang, M.; Cheng, J.
Deposited on : 2023-07-12
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

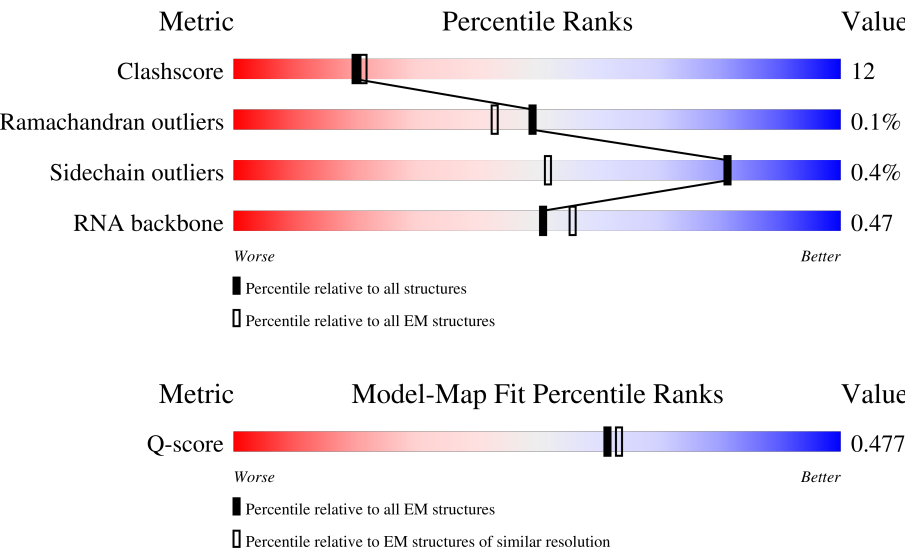
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

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

Mol	Chain	Length	Quality of chain
1	L1	1559	44% 42% 10%
2	L2	69	28% 23% 46% 12% 19%
3	LB	305	5% 63% 14% 22%

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Mol	Chain	Length	Quality of chain
4	LC	348	
5	LD	311	
6	LI	267	
7	LJ	261	
8	LK	192	
9	LM	178	
10	LN	145	
11	LO	296	
12	LP	251	
13	LQ	175	
14	LR	179	
15	LS	292	
16	LT	149	
17	LU	205	
18	LV	212	
19	LW	153	
20	LX	216	
21	La	148	
22	Lb	256	
23	Lu	250	
24	Ld	161	
25	Lf	188	
26	Lg	65	
27	Lh	92	
28	Li	188	

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Mol	Chain	Length	Quality of chain
29	Lj	103	
30	Lk	423	
31	Ll	380	
32	Lm	338	
33	Ln	206	
34	Lo	137	
35	Lp	142	
36	Lq	215	
37	Lr	332	
38	Ls	306	
39	Lt	279	
40	Lv	212	
41	Lw	166	
42	Lx	158	
43	Ly	128	
44	Lz	123	
45	L3	112	
46	L4	138	
47	L5	128	
48	L6	102	
49	L7	206	
50	L8	222	
51	SR	196	
52	Sf	439	
53	u	234	

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Mol	Chain	Length	Quality of chain
54	v	70	99% 49% 50%
55	w	156	51% 24% 26% 49%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 102269 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L1	1500	Total	C	N	O	P	0	0
			31847	14290	5750	10307	1500		

- Molecule 2 is a RNA chain called Val tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L2	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

- Molecule 3 is a protein called Large ribosomal subunit protein uL2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LB	237	Total	C	N	O	S	0	0
			1851	1151	375	316	9		

- Molecule 4 is a protein called Large ribosomal subunit protein uL3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LC	304	Total	C	N	O	S	0	0
			2393	1538	415	429	11		

- Molecule 5 is a protein called Large ribosomal subunit protein uL4m.

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

- Molecule 6 is a protein called Large ribosomal subunit protein bL9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LI	95	Total	C	N	O		0	0
			784	498	152	134			

- Molecule 7 is a protein called Large ribosomal subunit protein uL10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LJ	158	Total	C	N	O	S	0	0
			1283	828	235	210	10		

- Molecule 8 is a protein called Large ribosomal subunit protein uL11m.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL13m.

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

- Molecule 10 is a protein called Large ribosomal subunit protein uL14m.

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

- Molecule 11 is a protein called Large ribosomal subunit protein uL15m.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LP	221	Total	C	N	O	S	0	0
			1779	1138	325	306	10		

- Molecule 13 is a protein called Large ribosomal subunit protein bL17m.

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

- Molecule 14 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LR	146	Total	C	N	O	S	0	0
			1189	743	226	215	5		

- Molecule 15 is a protein called Large ribosomal subunit protein bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LS	219	Total	C	N	O	S	0	0
			1822	1168	322	323	9		

- Molecule 16 is a protein called Large ribosomal subunit protein bL20m.

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

- Molecule 17 is a protein called Large ribosomal subunit protein bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LU	160	Total	C	N	O	S	0	0
			1284	829	226	225	4		

- Molecule 18 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 19 is a protein called Large ribosomal subunit protein uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LW	143	Total	C	N	O	S	0	0
			1188	752	224	208	4		

- Molecule 20 is a protein called Large ribosomal subunit protein uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LX	202	Total	C	N	O	S	0	0
			1652	1053	294	297	8		

- Molecule 21 is a protein called Large ribosomal subunit protein bL27m.

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

- Molecule 22 is a protein called Large ribosomal subunit protein bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Lb	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 23 is a protein called Large ribosomal subunit protein uL29m.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL30m.

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

- Molecule 25 is a protein called Large ribosomal subunit protein bL32m.

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

- Molecule 26 is a protein called Large ribosomal subunit protein bL33m.

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

- Molecule 27 is a protein called Large ribosomal subunit protein bL34m.

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

- Molecule 28 is a protein called Large ribosomal subunit protein bL35m.

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

- Molecule 29 is a protein called Large ribosomal subunit protein bL36m.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lj	38	Total	C	N	O	S	0	0
			341	217	72	48	4		

- Molecule 30 is a protein called Large ribosomal subunit protein mL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lk	394	Total	C	N	O	S	0	0
			3210	2073	560	566	11		

- Molecule 31 is a protein called Large ribosomal subunit protein mL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ll	354	Total	C	N	O	S	0	0
			2947	1881	525	532	9		

- Molecule 32 is a protein called Large ribosomal subunit protein mL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lm	293	Total	C	N	O	S	0	0
			2382	1525	404	435	18		

- Molecule 33 is a protein called Large ribosomal subunit protein mL40.

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

- Molecule 34 is a protein called Large ribosomal subunit protein mL41.

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

- Molecule 35 is a protein called Large ribosomal subunit protein mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lp	97	Total	C	N	O	S	0	0
			815	514	147	149	5		

- Molecule 36 is a protein called Large ribosomal subunit protein mL43.

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

- Molecule 37 is a protein called Large ribosomal subunit protein mL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lr	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

- Molecule 38 is a protein called Large ribosomal subunit protein mL45.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ls	214	Total	C	N	O	S	0	0
			1754	1117	304	320	13		

- Molecule 39 is a protein called Large ribosomal subunit protein mL46.

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

- Molecule 40 is a protein called Large ribosomal subunit protein mL48.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lv	131	Total	C	N	O	S	0	0
			1039	663	169	203	4		

- Molecule 41 is a protein called Large ribosomal subunit protein mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lw	132	Total	C	N	O	S	0	0
			1097	710	191	194	2		

- Molecule 42 is a protein called Large ribosomal subunit protein mL50.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lx	110	Total	C	N	O	S	0	0
			895	568	156	168	3		

- Molecule 43 is a protein called Large ribosomal subunit protein mL51.

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

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lz	92	Total	C	N	O	S	0	0
			732	454	142	134	2		

- Molecule 45 is a protein called Large ribosomal subunit protein mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	L3	96	Total	C	N	O	S	0	0
			743	462	143	133	5		

- Molecule 46 is a protein called Large ribosomal subunit protein mL54.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	L4	83	Total	C	N	O	S	0	0
			703	446	124	130	3		

- Molecule 47 is a protein called Large ribosomal subunit protein mL55.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	L5	45	Total	C	N	O	S	0	0
			372	232	76	62	2		

- Molecule 48 is a protein called Large ribosomal subunit protein mL63.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	L6	94	Total	C	N	O	S	0	0
			797	501	165	128	3		

- Molecule 49 is a protein called Large ribosomal subunit protein mL62.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	L7	127	Total	C	N	O	S	0	0
			1058	661	201	192	4		

- Molecule 50 is a protein called Large ribosomal subunit protein mL64.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	L8	128	Total	C	N	O	S	0	0
			1076	671	208	192	5		

- Molecule 51 is a protein called Large ribosomal subunit protein mL66.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SR	146	Total	C	N	O	S	0	0
			1203	764	232	199	8		

- Molecule 52 is a protein called Large ribosomal subunit protein mL65.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Sf	370	Total	C	N	O	S	0	0
			3036	1946	542	534	14		

- Molecule 53 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	111	Total	C	N	O	S	0	0
			927	595	155	167	10		

- Molecule 54 is a protein called Mitochondrial ribosome and complex I assembly factor Alt-MIEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	69	Total	C	N	O	S	0	0
			588	372	116	100			

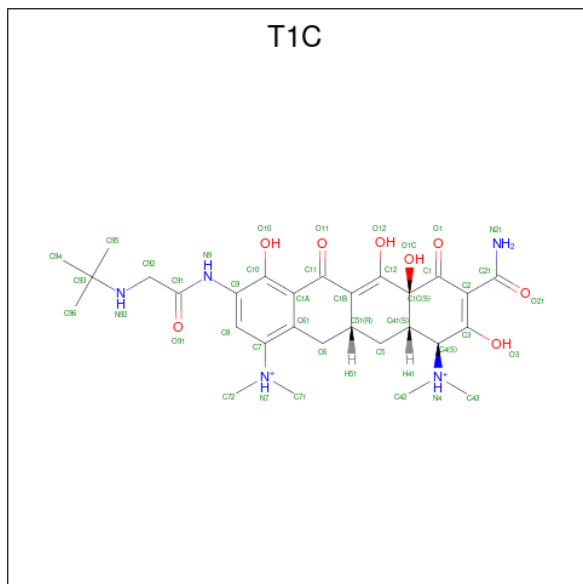
- Molecule 55 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	79	Total	C	N	O	S	0	0
			638	410	95	128	5		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	L1	93	Total	Mg	0
			93	93	
56	LB	1	Total	Mg	0
			1	1	
56	Lw	1	Total	Mg	0
			1	1	

- Molecule 57 is TIGECYCLINE (CCD ID: T1C) (formula: $C_{29}H_{41}N_5O_8$).

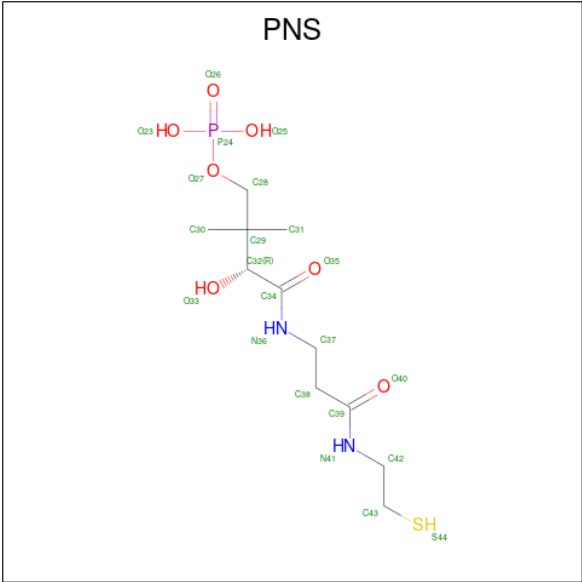


Mol	Chain	Residues	Atoms				AltConf
57	L1	1	Total	C	N	O	0
			42	29	5	8	

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

Mol	Chain	Residues	Atoms		AltConf
58	Lf	1	Total	Zn	0
			1	1	
58	Lj	1	Total	Zn	0
			1	1	
58	SR	1	Total	Zn	0
			1	1	

- Molecule 59 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: $C_{11}H_{23}N_2O_7PS$).

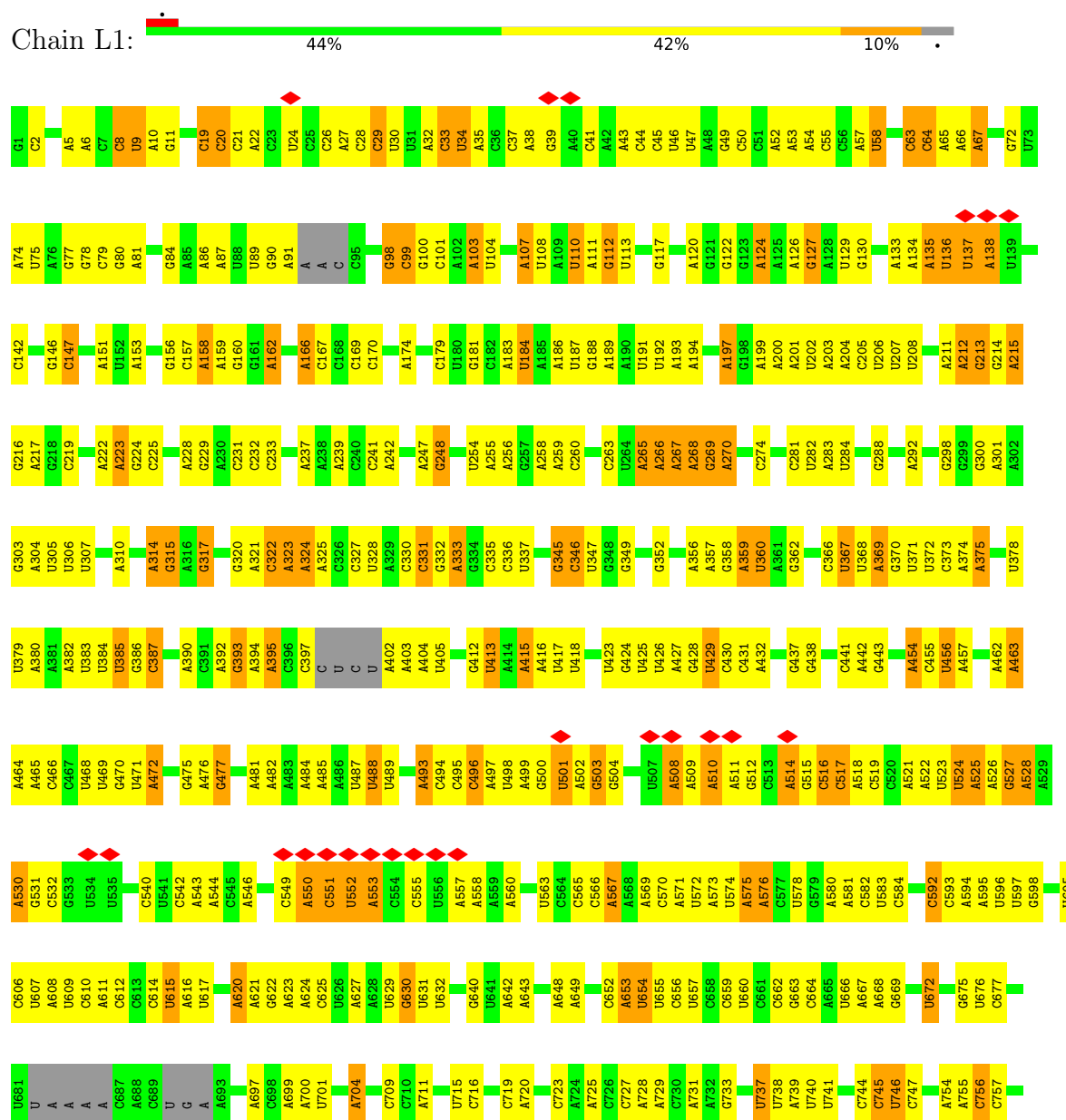


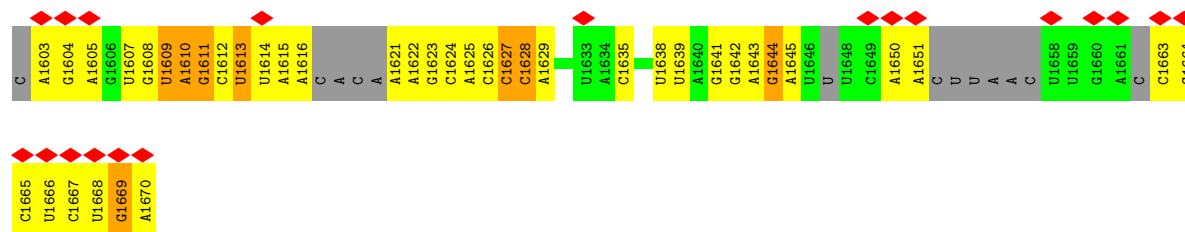
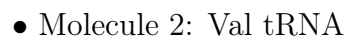
Mol	Chain	Residues	Atoms						AltConf
59	v	1	Total	C	N	O	P	S	0
			21	11	2	6	1	1	

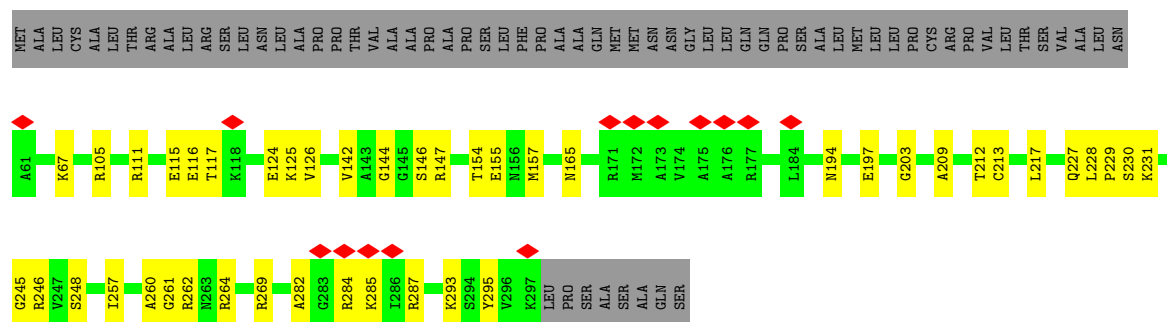
3 Residue-property plots

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

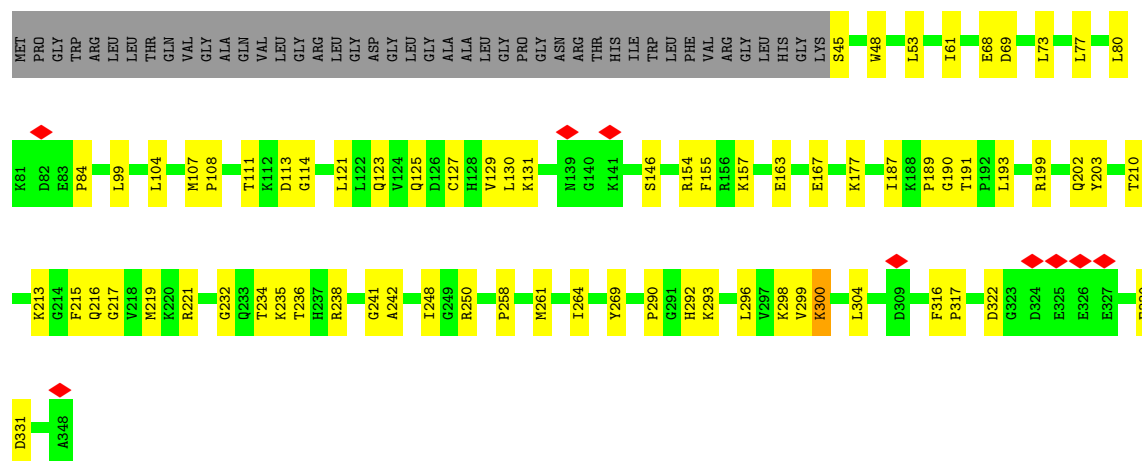






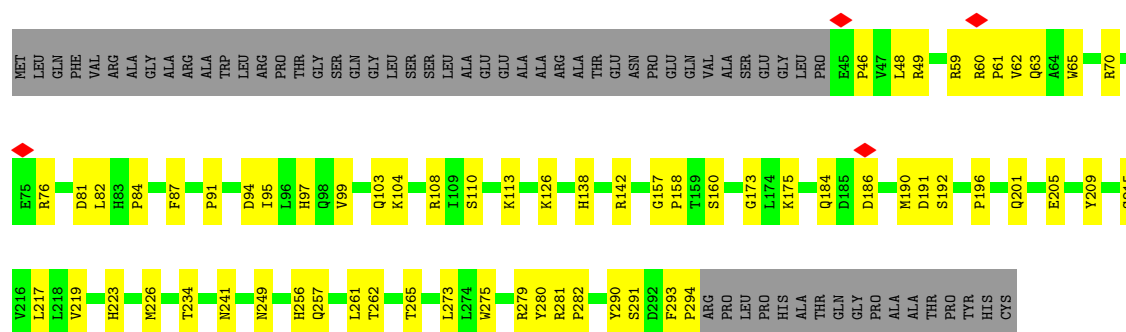
- Molecule 4: Large ribosomal subunit protein uL3m

Chain LC: 67% 20% 13%



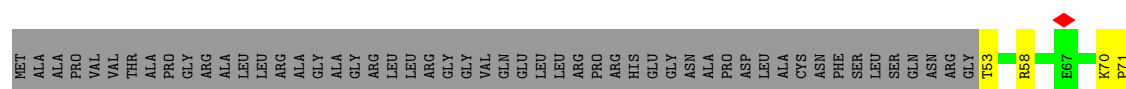
- Molecule 5: Large ribosomal subunit protein uL4m

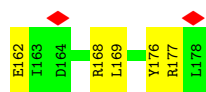
Chain LD: 59% 21% 20%



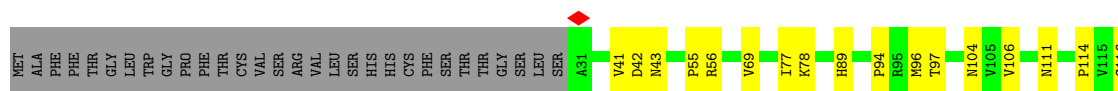
- Molecule 6: Large ribosomal subunit protein bL9m

Chain LI: 7% 24% 12% 64%

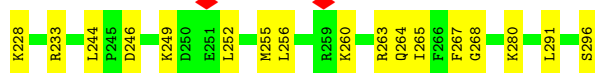
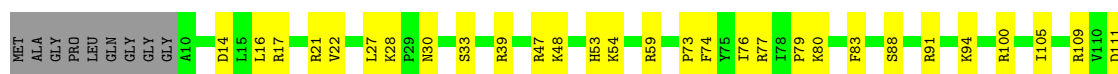




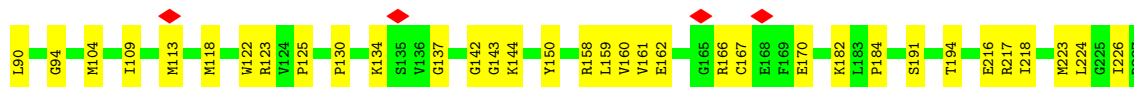
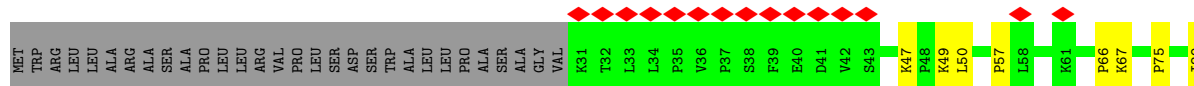
- Molecule 10: Large ribosomal subunit protein uL14m



- Molecule 11: Large ribosomal subunit protein uL15m

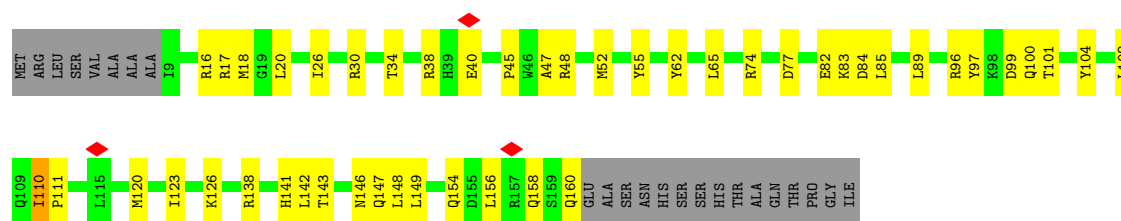


- Molecule 12: Large ribosomal subunit protein uL16m

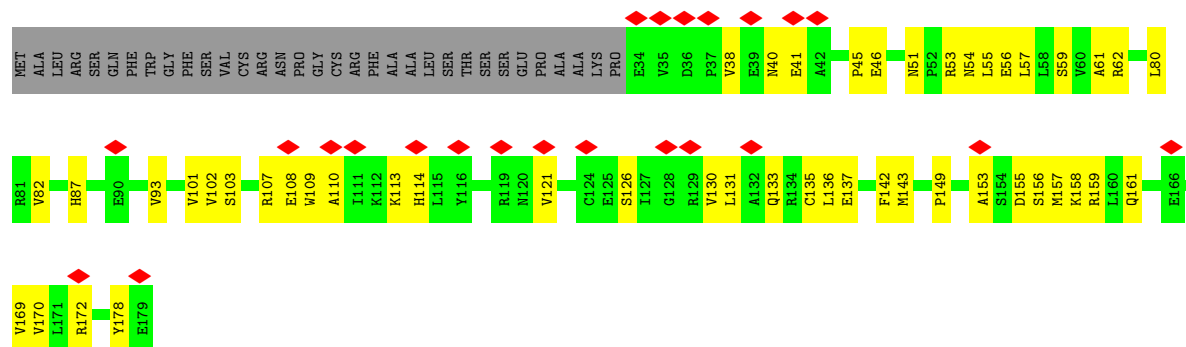


- Molecule 13: Large ribosomal subunit protein bL17m

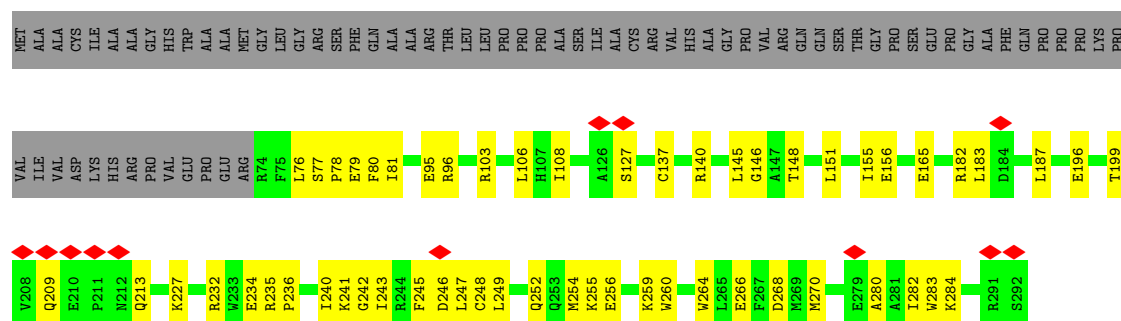




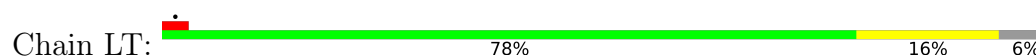
- Molecule 14: Mitochondrial ribosomal protein L18, isoform CRA_b



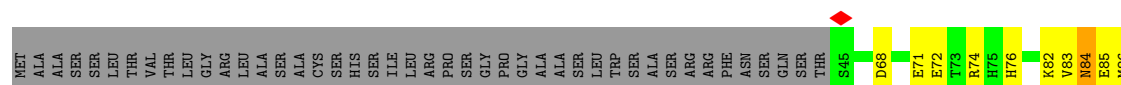
- Molecule 15: Large ribosomal subunit protein bL19m



- Molecule 16: Large ribosomal subunit protein bL20m

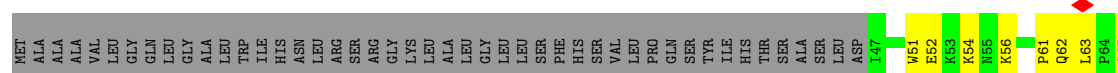


- Molecule 17: Large ribosomal subunit protein bL21m

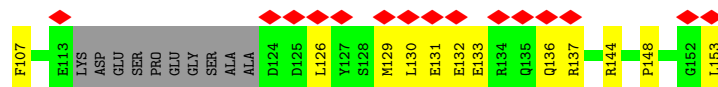
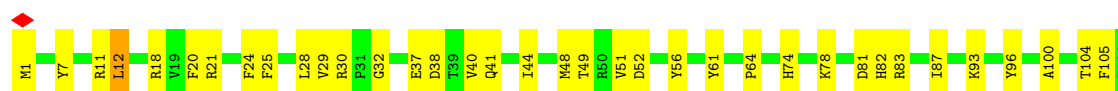




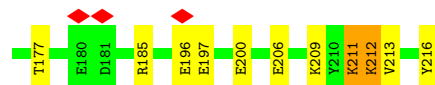
- Molecule 18: 39S ribosomal protein L22, mitochondrial



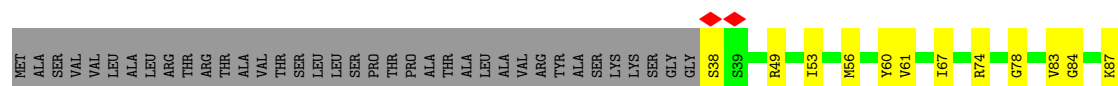
- Molecule 19: Large ribosomal subunit protein uL23m

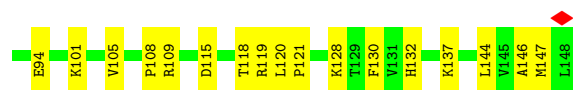


- Molecule 20: Large ribosomal subunit protein uL24m

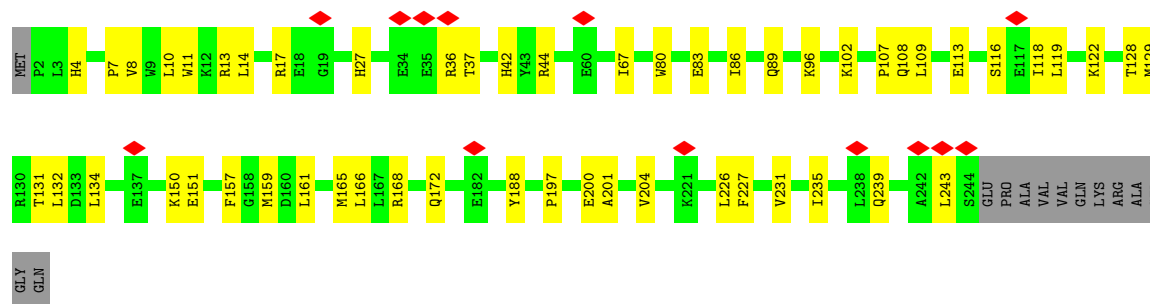
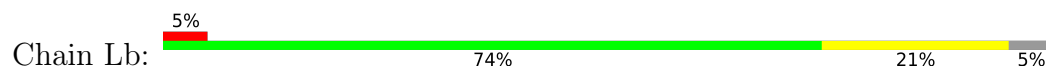


- Molecule 21: Large ribosomal subunit protein bL27m

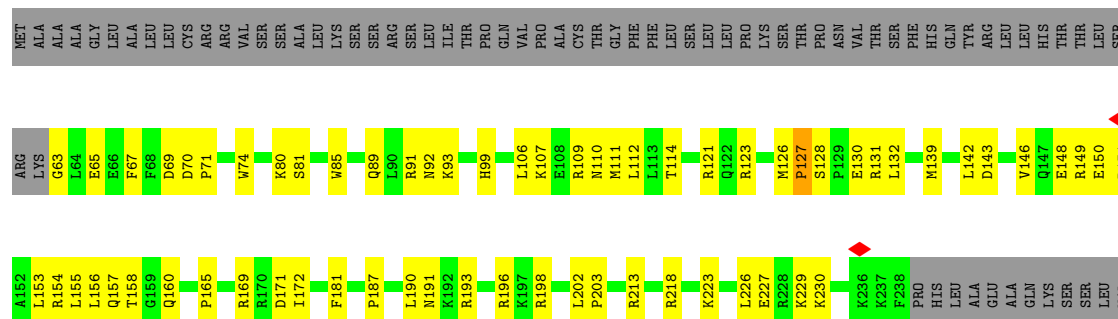




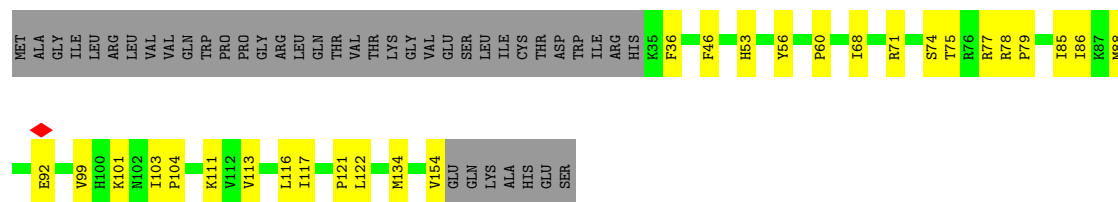
- Molecule 22: Large ribosomal subunit protein bL28m



- Molecule 23: Large ribosomal subunit protein uL29m



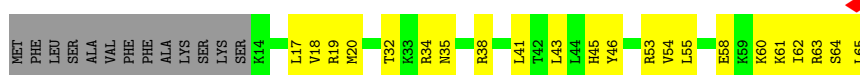
- Molecule 24: Large ribosomal subunit protein uL30m



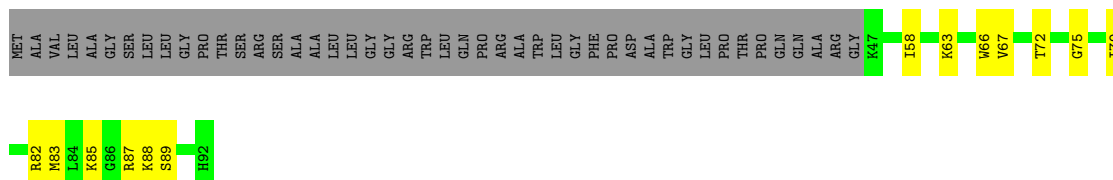
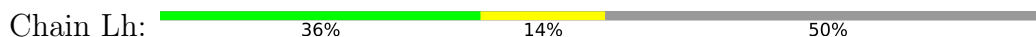
- Molecule 25: Large ribosomal subunit protein bL32m



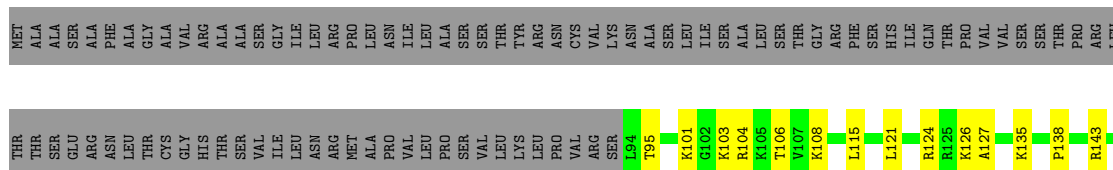
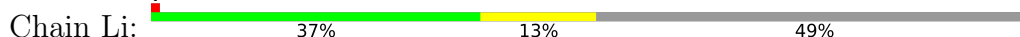
- Molecule 26: Large ribosomal subunit protein bL33m



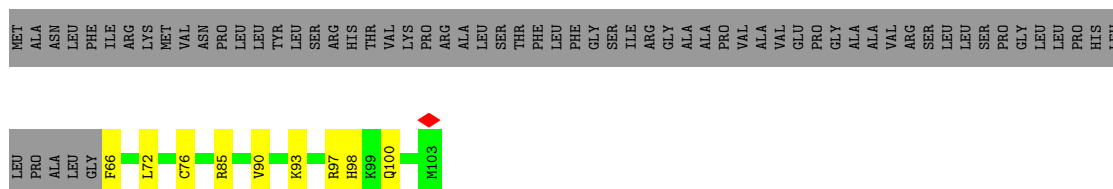
- Molecule 27: Large ribosomal subunit protein bL34m



- Molecule 28: Large ribosomal subunit protein bL35m

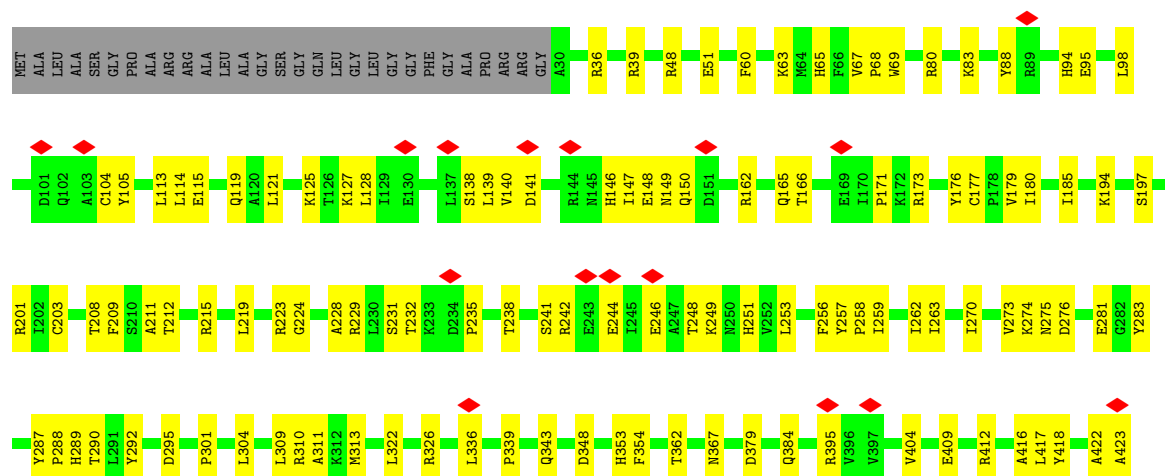


- Molecule 29: Large ribosomal subunit protein bL36m

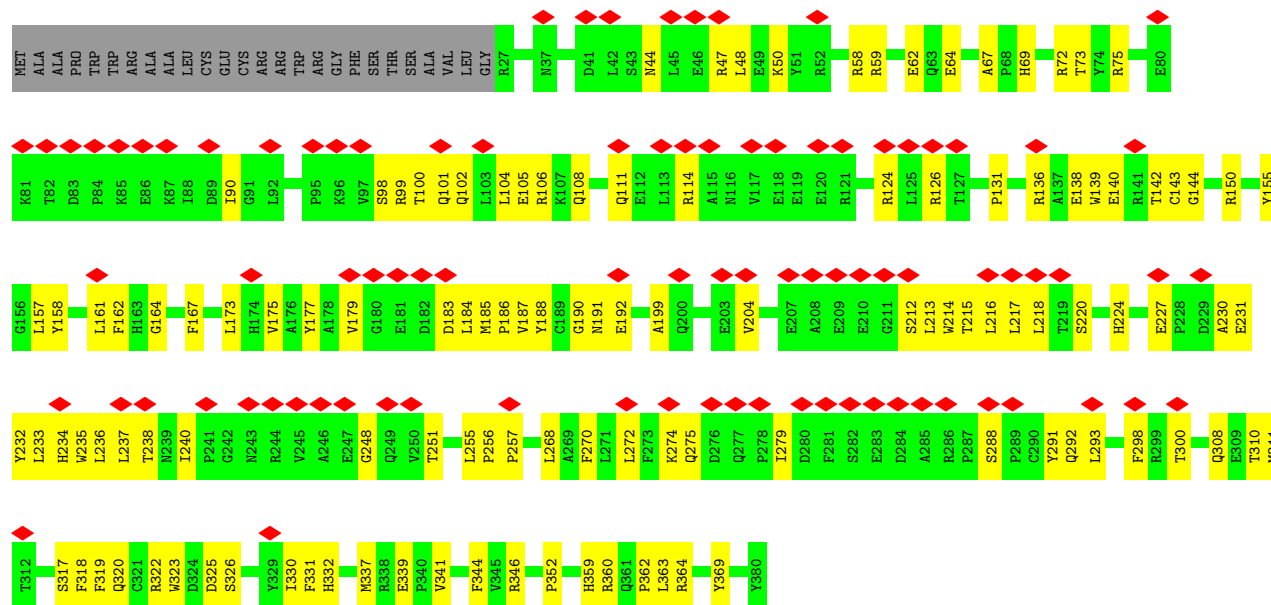


- Molecule 30: Large ribosomal subunit protein mL37

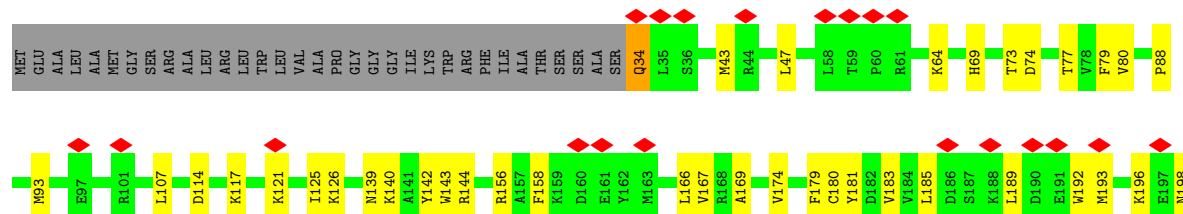


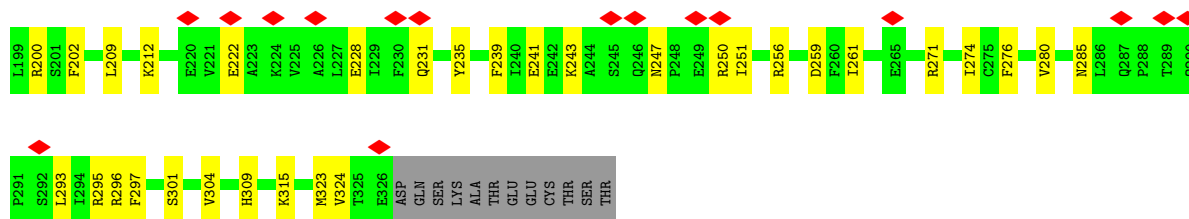


• Molecule 31: Large ribosomal subunit protein mL38

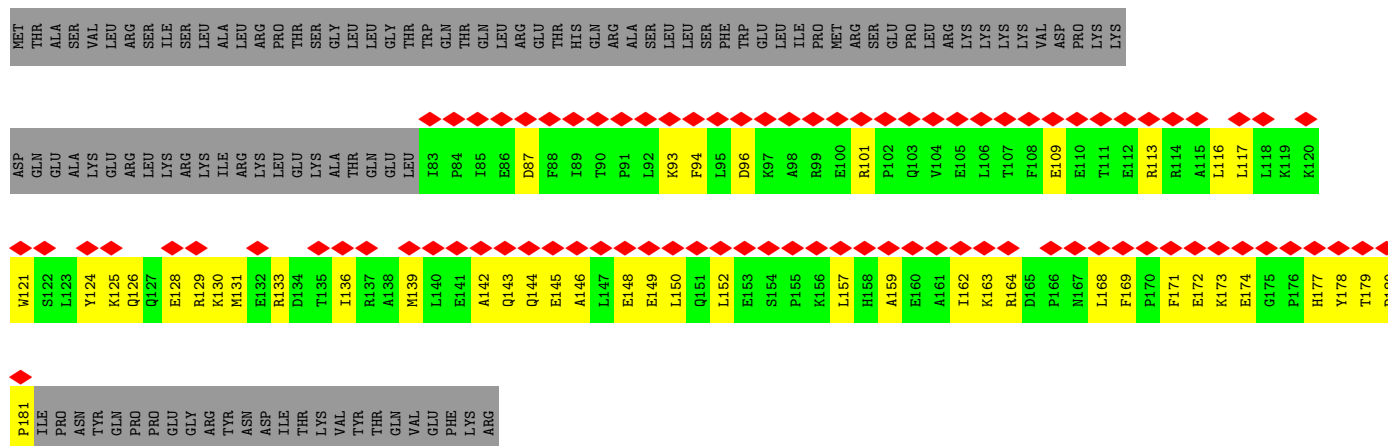
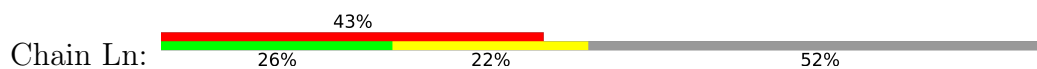


• Molecule 32: Large ribosomal subunit protein mL39

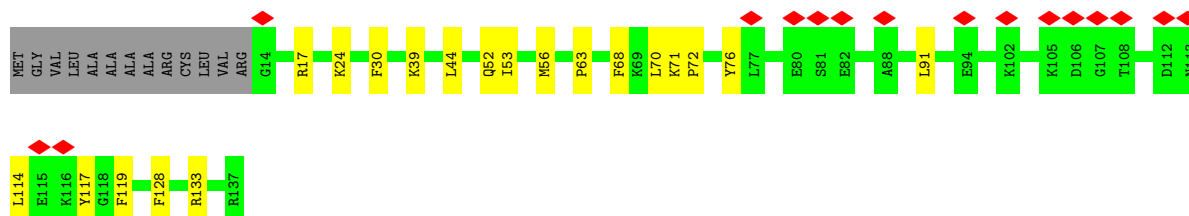
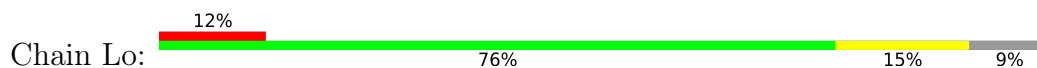




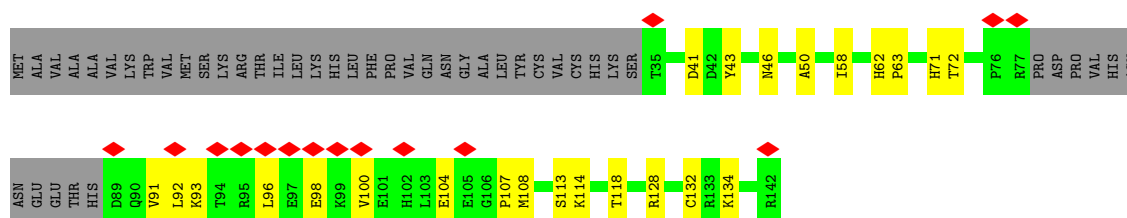
• Molecule 33: Large ribosomal subunit protein mL40



• Molecule 34: Large ribosomal subunit protein mL41

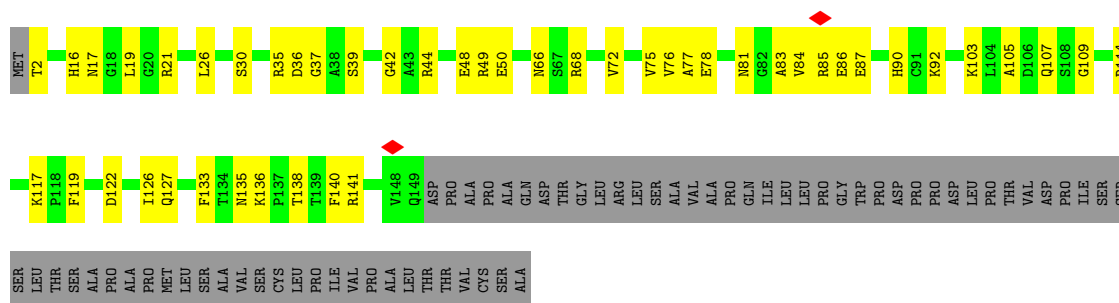


• Molecule 35: Large ribosomal subunit protein mL42

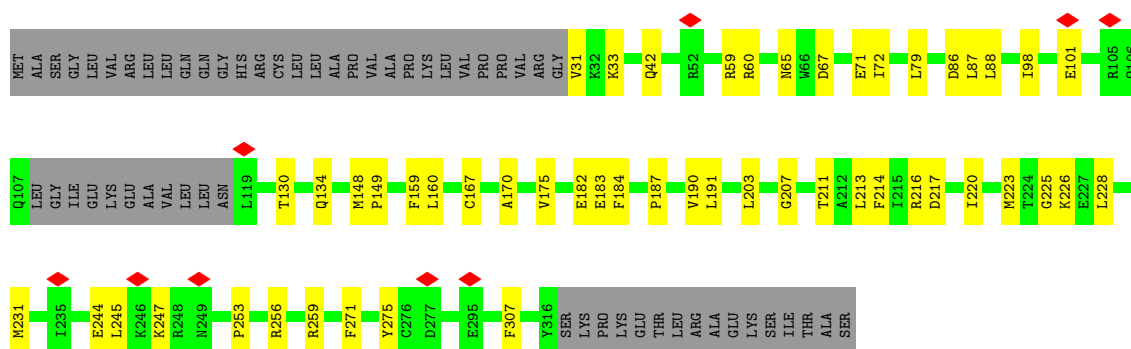


• Molecule 36: Large ribosomal subunit protein mL43

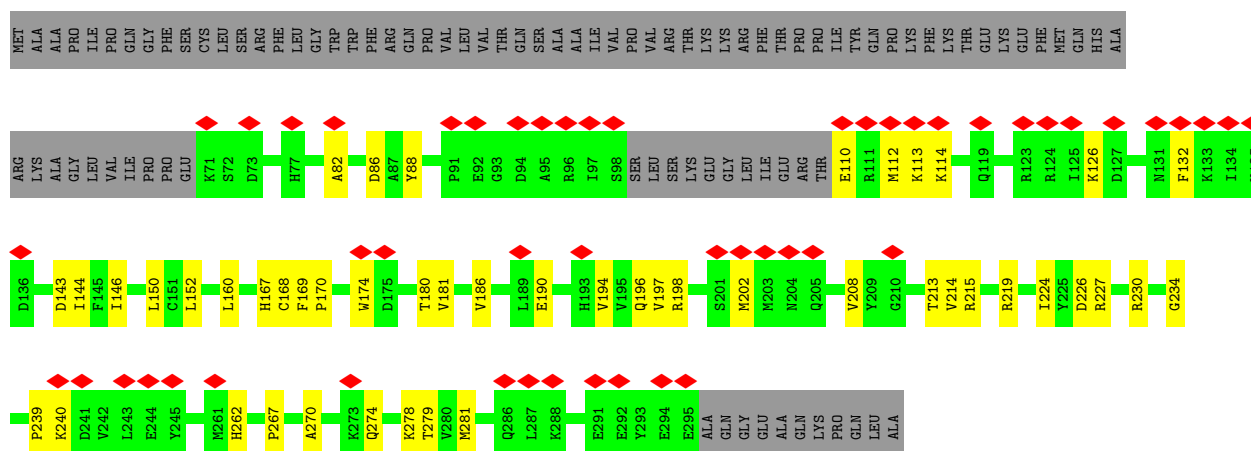




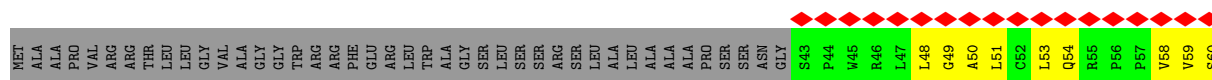
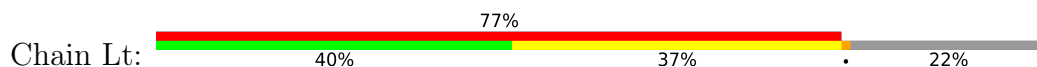
• Molecule 37: Large ribosomal subunit protein mL44

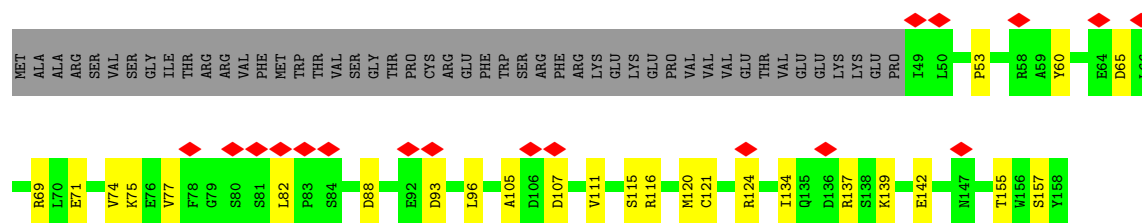


• Molecule 38: Large ribosomal subunit protein mL45

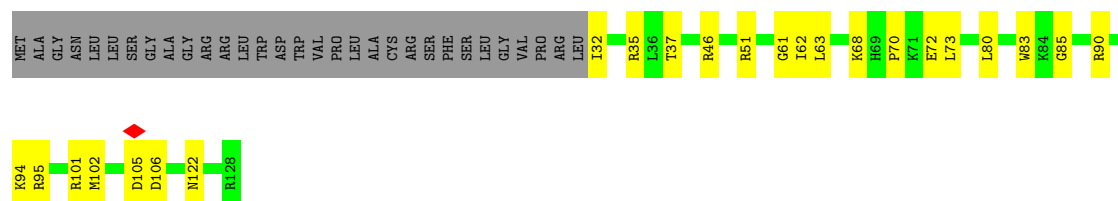


• Molecule 39: Large ribosomal subunit protein mL46

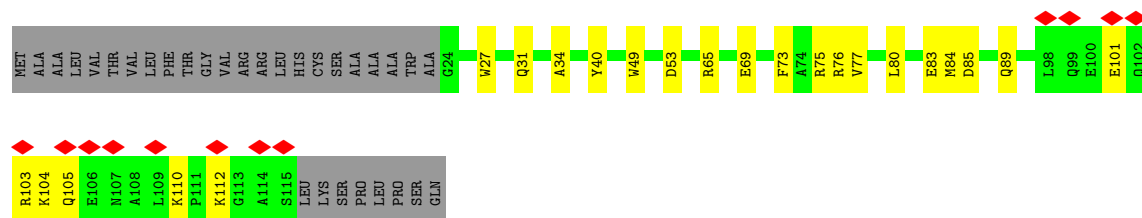




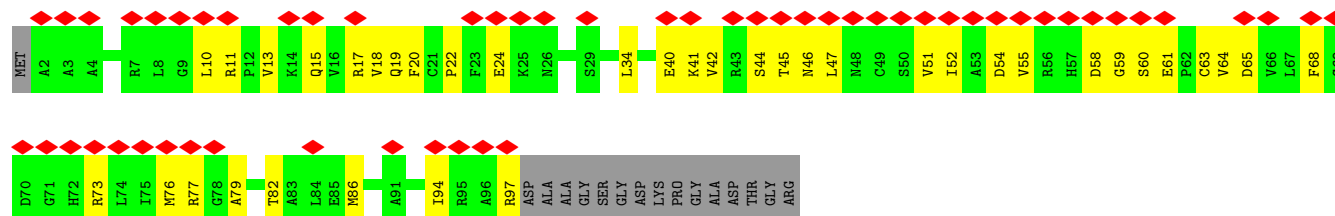
- Molecule 43: Large ribosomal subunit protein mL51



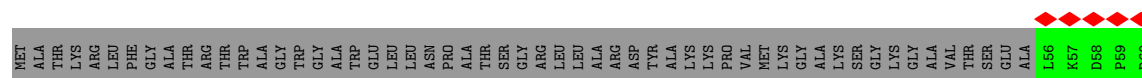
- Molecule 44: 39S ribosomal protein L52, mitochondrial

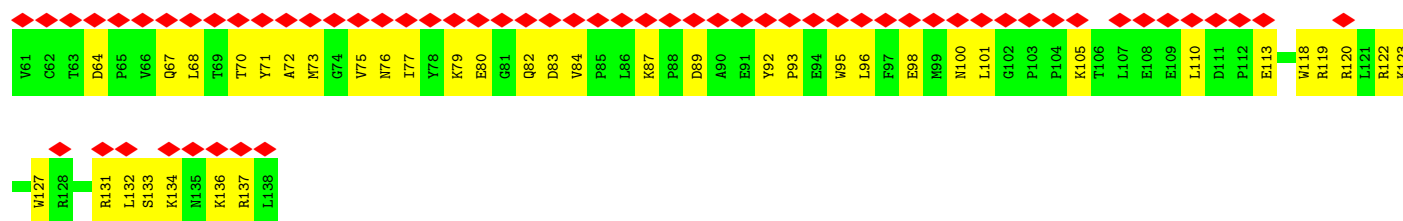


- Molecule 45: Large ribosomal subunit protein mL53

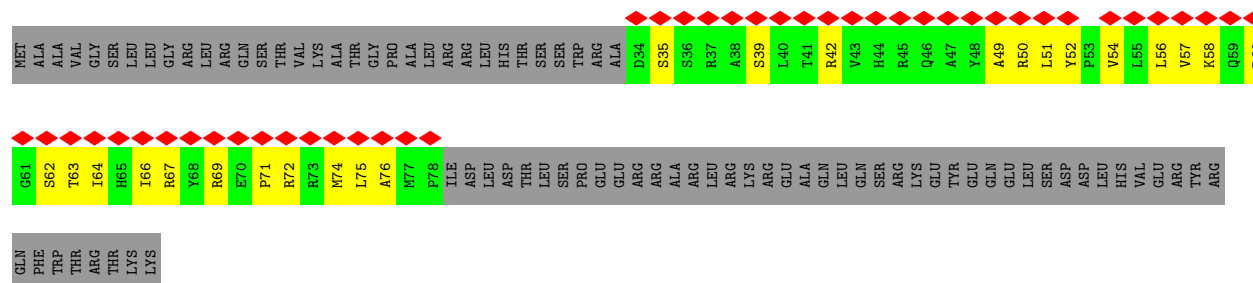


- Molecule 46: Large ribosomal subunit protein mL54

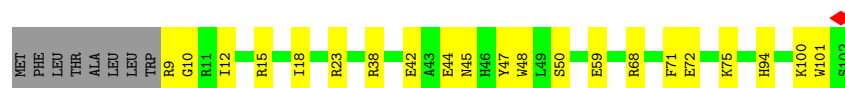




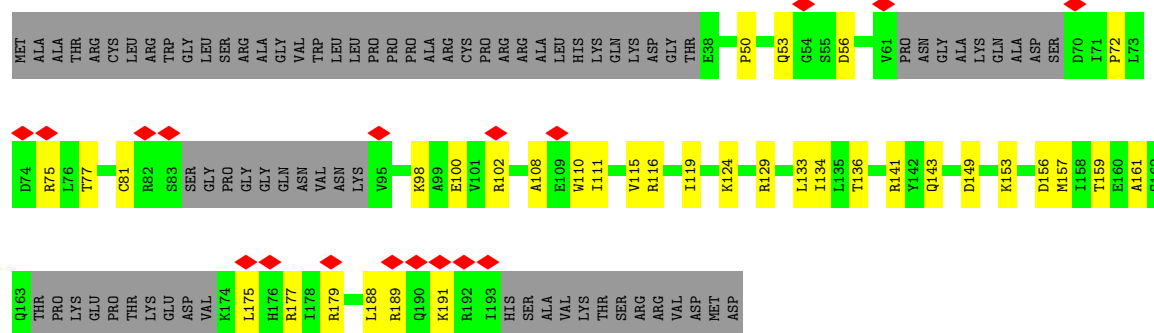
- Molecule 47: Large ribosomal subunit protein mL55



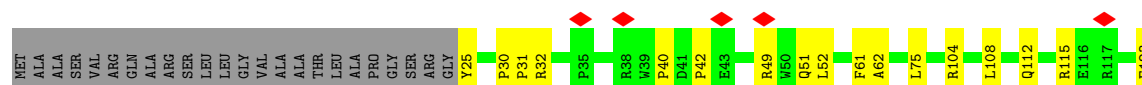
- Molecule 48: Large ribosomal subunit protein mL63



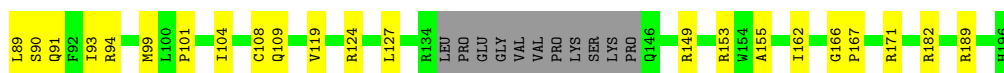
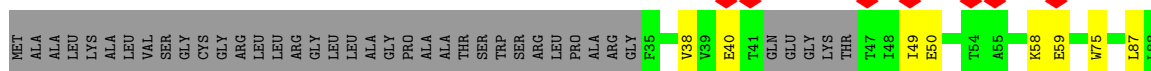
- Molecule 49: Large ribosomal subunit protein mL62



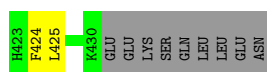
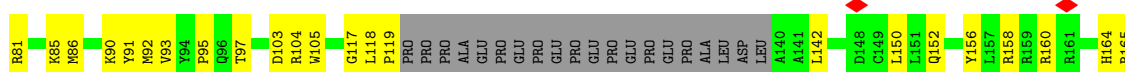
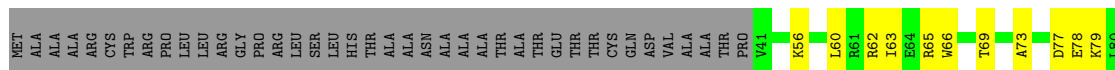
- Molecule 50: Large ribosomal subunit protein mL64



- Molecule 51: Large ribosomal subunit protein mL66

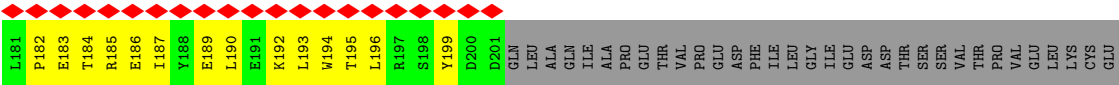


- Molecule 52: Large ribosomal subunit protein mL65

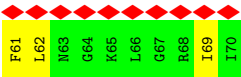
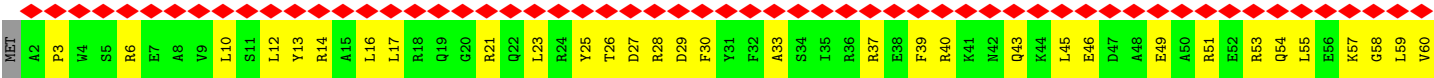


- Molecule 53: Mitochondrial assembly of ribosomal large subunit protein 1

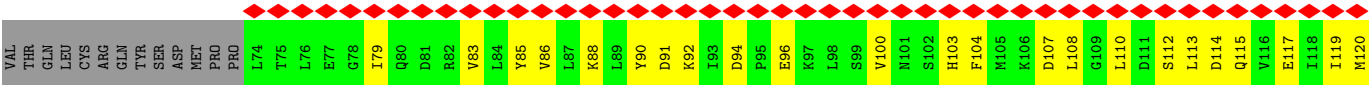
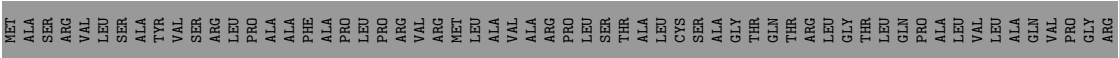
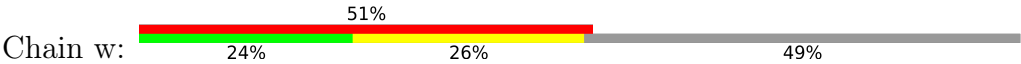




• Molecule 54: Mitochondrial ribosome and complex I assembly factor AltMIEF1



• Molecule 55: Acyl carrier protein, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12156	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.084	Depositor
Minimum map value	-0.030	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	499.80002, 499.80002, 499.80002	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, T1C, ZN, PNS

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	L1	0.25	0/35628	0.36	1/55448 (0.0%)
2	L2	0.15	0/1328	0.28	0/2056
3	LB	0.23	0/1888	0.42	0/2538
4	LC	0.32	0/2462	0.57	0/3340
5	LD	0.27	0/2071	0.43	0/2817
6	LI	0.26	0/798	0.52	0/1073
7	LJ	0.26	0/1308	0.57	0/1761
8	LK	0.18	0/1348	0.41	0/1813
9	LM	0.28	0/1495	0.45	0/2029
10	LN	0.40	0/904	0.70	1/1218 (0.1%)
11	LO	0.26	0/2359	0.42	0/3185
12	LP	0.23	0/1826	0.41	0/2458
13	LQ	0.26	0/1269	0.46	0/1708
14	LR	0.35	0/1215	0.54	0/1645
15	LS	0.28	0/1863	0.47	0/2509
16	LT	0.39	0/1174	0.66	0/1572
17	LU	0.27	0/1311	0.47	0/1778
18	LV	0.27	0/1402	0.43	0/1886
19	LW	0.36	0/1217	0.54	0/1644
20	LX	0.28	0/1697	0.46	0/2302
21	La	0.29	0/893	0.41	0/1204
22	Lb	0.24	0/2090	0.41	0/2825
23	Lu	0.25	0/1552	0.44	2/2079 (0.1%)
24	Ld	0.27	0/1003	0.44	0/1354
25	Lf	0.33	0/895	0.48	0/1201
26	Lg	0.25	0/438	0.40	0/583
27	Lh	0.28	0/382	0.37	0/507
28	Li	0.28	0/852	0.42	0/1136
29	Lj	0.21	0/349	0.33	0/461
30	Lk	0.25	0/3305	0.41	0/4502
31	Ll	0.24	0/3042	0.48	0/4140
32	Lm	0.22	0/2439	0.41	0/3299

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ln	0.25	0/855	0.56	0/1152
34	Lo	0.25	0/1025	0.45	0/1379
35	Lp	0.24	0/839	0.45	0/1136
36	Lq	0.26	0/1202	0.43	0/1626
37	Lr	0.25	0/2264	0.43	0/3059
38	Ls	0.20	0/1800	0.40	0/2436
39	Lt	0.20	0/1797	0.54	0/2422
40	Lv	0.23	0/1055	0.47	0/1427
41	Lw	0.38	0/1134	0.66	1/1547 (0.1%)
42	Lx	0.23	0/918	0.37	0/1249
43	Ly	0.32	0/849	0.46	0/1135
44	Lz	0.26	0/747	0.44	0/1005
45	L3	0.22	0/754	0.48	0/1017
46	L4	0.23	0/722	0.56	0/978
47	L5	0.20	0/379	0.52	0/510
48	L6	0.28	0/818	0.43	0/1097
49	L7	0.22	0/1071	0.40	0/1433
50	L8	0.21	0/1107	0.40	0/1498
51	SR	0.37	0/1238	0.61	0/1676
52	Sf	0.26	0/3114	0.42	0/4225
53	u	0.29	0/949	0.61	0/1281
54	v	0.33	0/597	0.65	0/796
55	w	0.20	0/647	0.52	0/871
All	All	0.26	0/107684	0.43	5/153026 (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
13	LQ	0	1
31	Ll	0	1
All	All	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	LN	129	LYS	N-CA-C	-7.34	103.28	111.28
23	Lu	127	PRO	CA-C-N	-6.30	116.73	122.28
23	Lu	127	PRO	C-N-CA	-6.30	116.73	122.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L1	840	U	C4'-C3'-O3'	-6.00	104.00	113.00
41	Lw	67	PRO	N-CA-C	-5.32	101.52	112.47

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	LQ	110	ILE	Peptide
31	Ll	288	SER	Peptide

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	L1	31847	0	16179	562	0
2	L2	1191	0	607	41	0
3	LB	1851	0	1909	32	0
4	LC	2393	0	2398	57	0
5	LD	2013	0	2044	52	0
6	LI	784	0	832	32	0
7	LJ	1283	0	1370	53	0
8	LK	1330	0	1407	58	0
9	LM	1451	0	1448	30	0
10	LN	889	0	941	31	0
11	LO	2305	0	2378	64	0
12	LP	1779	0	1808	37	0
13	LQ	1245	0	1283	40	0
14	LR	1189	0	1180	50	0
15	LS	1822	0	1859	42	0
16	LT	1153	0	1214	17	0
17	LU	1284	0	1354	44	0
18	LV	1368	0	1410	35	0
19	LW	1188	0	1180	46	0
20	LX	1652	0	1658	57	0
21	La	871	0	898	21	0
22	Lb	2035	0	2054	44	0
23	Lu	1517	0	1561	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	Ld	978	0	1030	28	0
25	Lf	880	0	902	16	0
26	Lg	433	0	475	22	0
27	Lh	376	0	406	14	0
28	Li	831	0	883	22	0
29	Lj	341	0	361	8	0
30	Lk	3210	0	3206	83	0
31	Ll	2947	0	2841	108	0
32	Lm	2382	0	2393	57	0
33	Ln	836	0	844	70	0
34	Lo	997	0	987	22	0
35	Lp	815	0	792	24	0
36	Lq	1178	0	1180	48	0
37	Lr	2217	0	2220	37	0
38	Ls	1754	0	1732	39	0
39	Lt	1762	0	1767	94	0
40	Lv	1039	0	1044	65	0
41	Lw	1097	0	1085	37	0
42	Lx	895	0	881	25	0
43	Ly	827	0	857	18	0
44	Lz	732	0	730	17	0
45	L3	743	0	758	37	0
46	L4	703	0	693	44	0
47	L5	372	0	387	31	0
48	L6	797	0	804	21	0
49	L7	1058	0	1083	31	0
50	L8	1076	0	1049	26	0
51	SR	1203	0	1219	29	0
52	Sf	3036	0	3022	82	0
53	u	927	0	921	69	0
54	v	588	0	604	45	0
55	w	638	0	637	38	0
56	L1	93	0	0	0	0
56	LB	1	0	0	0	0
56	Lw	1	0	0	0	0
57	L1	42	0	38	1	0
58	Lf	1	0	0	0	0
58	Lj	1	0	0	0	0
58	SR	1	0	0	0	0
59	v	21	0	21	3	0
All	All	102269	0	86824	2316	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 12.

All (2316) 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)
36:Lq:75:VAL:O	36:Lq:86:GLU:HA	1.38	1.19
9:LM:81:THR:O	9:LM:86:GLY:HA3	1.51	1.09
29:Lj:76:CYS:SG	29:Lj:98:HIS:CE1	2.45	1.09
35:Lp:71:HIS:HD1	36:Lq:138:THR:HG1	0.99	0.95
31:Ll:214:TRP:HB2	31:Ll:240:ILE:HB	1.51	0.91
39:Lt:264:LEU:HD22	39:Lt:269:LEU:HB3	1.55	0.87
46:L4:132:LEU:O	46:L4:136:LYS:HB2	1.74	0.87
8:LK:73:LYS:HD3	8:LK:74:PRO:HD2	1.58	0.86
1:L1:412:G:N2	24:Ld:88:MET:SD	2.49	0.85
3:LB:154:THR:H	3:LB:157:MET:HE3	1.42	0.85
54:v:3:PRO:HA	54:v:51:ARG:HG2	1.56	0.85
1:L1:575:A:H2'	51:SR:189:ARG:HE	1.42	0.84
33:Ln:173:LYS:HB3	40:Lv:175:GLN:NE2	1.91	0.84
52:Sf:165:ARG:HA	52:Sf:168:GLU:HG3	1.60	0.84
40:Lv:96:THR:HB	40:Lv:154:GLU:HG2	1.62	0.81
12:LP:218:ILE:HG23	12:LP:223:MET:HB2	1.63	0.81
27:Lh:72:THR:HG23	27:Lh:75:GLY:H	1.44	0.81
2:L2:1642:G:H2'	2:L2:1643:A:C8	2.16	0.81
23:Lu:128:SER:OG	23:Lu:131:ARG:NE	2.12	0.80
9:LM:168:ARG:NE	51:SR:58:LYS:O	2.15	0.80
18:LV:62:GLN:NE2	18:LV:67:PRO:O	2.15	0.80
45:L3:17:ARG:HH22	45:L3:19:GLN:HB2	1.47	0.80
1:L1:107:A:N6	1:L1:110:U:OP2	2.14	0.79
32:Lm:158:PHE:O	35:Lp:93:LYS:NZ	2.16	0.79
39:Lt:273:ARG:HA	39:Lt:276:VAL:HG12	1.63	0.79
1:L1:973:G:O2'	1:L1:975:G:OP2	2.00	0.79
20:LX:177:THR:HG22	34:Lo:71:LYS:H	1.46	0.79
47:L5:57:VAL:HA	47:L5:62:SER:O	1.83	0.79
1:L1:438:G:N7	12:LP:67:LYS:NZ	2.31	0.78
29:Lj:76:CYS:SG	29:Lj:98:HIS:HE1	1.95	0.78
32:Lm:34:GLN:N	32:Lm:34:GLN:HE21	1.80	0.78
52:Sf:319:GLN:HA	52:Sf:322:VAL:HB	1.65	0.78
16:LT:111:LYS:NZ	17:LU:139:ASP:OD1	2.16	0.78
10:LN:96:MET:HE1	15:LS:165:GLU:H	1.48	0.78
36:Lq:77:ALA:HB3	36:Lq:85:ARG:HB2	1.65	0.78
13:LQ:55:TYR:OH	15:LS:268:ASP:OD1	2.01	0.77
1:L1:496:C:O2	1:L1:544:A:N6	2.18	0.77
10:LN:42:ASP:OD1	10:LN:43:ASN:N	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LC:234:THR:HG22	4:LC:235:LYS:H	1.50	0.77
33:Ln:171:PHE:HD1	39:Lt:203:LYS:HZ3	1.31	0.77
5:LD:223:HIS:HA	5:LD:226:MET:HE3	1.66	0.76
39:Lt:122:ASP:O	39:Lt:126:GLN:NE2	2.19	0.76
37:Lr:259:ARG:HB2	37:Lr:271:PHE:HB2	1.67	0.76
40:Lv:137:LEU:HB2	40:Lv:145:LEU:HG	1.68	0.76
20:LX:105:ARG:HD3	38:Ls:174:TRP:CG	2.20	0.76
33:Ln:169:PHE:CZ	40:Lv:91:LEU:HD12	2.22	0.75
1:L1:64:C:OP2	6:LI:72:ARG:NE	2.20	0.75
32:Lm:247:ASN:ND2	32:Lm:251:ILE:O	2.19	0.75
39:Lt:162:ARG:HG2	39:Lt:251:HIS:HB2	1.69	0.75
7:LJ:93:ASN:HD21	7:LJ:155:VAL:HB	1.51	0.75
39:Lt:151:ARG:HH21	39:Lt:152:LYS:HZ1	1.35	0.74
47:L5:52:TYR:HD2	47:L5:71:PRO:HA	1.52	0.74
14:LR:62:ARG:NH2	21:La:137:LYS:O	2.19	0.74
1:L1:8:C:N4	1:L1:103:A:OP2	2.20	0.74
31:Ll:124:ARG:HH12	33:Ln:116:LEU:HD23	1.52	0.74
1:L1:911:A:O2'	1:L1:912:A:N7	2.20	0.74
15:LS:95:GLU:OE2	15:LS:145:LEU:N	2.19	0.74
1:L1:394:A:OP1	21:La:101:LYS:NZ	2.21	0.74
33:Ln:117:LEU:HD11	39:Lt:70:MET:SD	2.27	0.74
1:L1:219:C:OP1	11:LO:133:LYS:NZ	2.20	0.74
30:Lk:121:LEU:HD21	30:Lk:128:LEU:HB2	1.70	0.74
1:L1:197:A:H62	1:L1:625:C:H5	1.36	0.73
1:L1:829:U:OP2	1:L1:834:A:N6	2.17	0.73
55:w:83:VAL:HG21	55:w:145:VAL:HG22	1.70	0.73
4:LC:80:LEU:HA	4:LC:84:PRO:HG3	1.68	0.73
14:LR:38:VAL:HB	14:LR:41:GLU:HG3	1.69	0.73
35:Lp:104:GLU:HG2	35:Lp:107:PRO:HD2	1.69	0.73
7:LJ:188:ARG:HD2	45:L3:55:VAL:HG13	1.69	0.73
45:L3:15:GLN:HE21	45:L3:52:ILE:HD12	1.53	0.73
7:LJ:113:ARG:HH22	8:LK:133:GLN:HA	1.54	0.73
30:Lk:275:ASN:HD21	30:Lk:326:ARG:HH11	1.36	0.73
31:Ll:44:ASN:HB2	31:Ll:47:ARG:HB2	1.69	0.73
46:L4:76:ASN:ND2	46:L4:80:GLU:O	2.20	0.73
1:L1:475:G:H21	17:LU:104:ARG:HH12	1.34	0.73
1:L1:800:G:N2	1:L1:803:A:N6	2.36	0.73
40:Lv:80:ILE:HG22	40:Lv:89:GLY:HA2	1.71	0.72
46:L4:75:VAL:HG11	46:L4:84:VAL:HG22	1.70	0.72
1:L1:113:U:H5''	27:Lh:88:LYS:HD3	1.71	0.72
19:LW:137:ARG:CZ	20:LX:105:ARG:HH12	2.02	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lt:138:THR:OG1	39:Lt:150:ASN:O	2.07	0.72
40:Lv:127:MET:HB2	40:Lv:154:GLU:HB3	1.69	0.72
10:LN:55:PRO:HB3	10:LN:77:ILE:HG22	1.72	0.72
19:LW:133:GLU:OE1	20:LX:104:TYR:OH	2.07	0.72
33:Ln:109:GLU:OE1	33:Ln:113:ARG:NH1	2.22	0.72
33:Ln:174:GLU:HA	40:Lv:183:ARG:HH22	1.50	0.72
11:LO:143:GLU:OE2	49:L7:141:ARG:NH2	2.20	0.72
7:LJ:95:MET:HG3	7:LJ:181:ILE:HG13	1.72	0.71
54:v:6:ARG:HH11	54:v:10:LEU:HD21	1.54	0.71
6:LI:70:LYS:HE3	6:LI:71:PRO:HD2	1.73	0.71
30:Lk:354:PHE:HB3	30:Lk:417:LEU:HD11	1.73	0.71
1:L1:397:C:H5'	40:Lv:60:LYS:HD2	1.72	0.71
6:LI:115:LYS:O	6:LI:118:LEU:C	2.34	0.71
1:L1:263:C:H5''	30:Lk:395:ARG:HH12	1.56	0.71
17:LU:125:GLY:N	17:LU:160:VAL:O	2.23	0.71
37:Lr:160:LEU:HD21	37:Lr:223:MET:HB3	1.71	0.71
1:L1:1393:G:O2'	1:L1:1396:C:OP2	2.09	0.71
53:u:100:LEU:HD13	53:u:103:GLN:HE21	1.55	0.71
1:L1:429:U:H2'	1:L1:430:C:C6	2.26	0.71
1:L1:1002:A:OP1	18:LV:111:LYS:NZ	2.22	0.71
6:LI:53:THR:N	6:LI:86:THR:OG1	2.24	0.71
54:v:6:ARG:NH1	54:v:10:LEU:HD21	2.06	0.71
42:Lx:88:ASP:OD1	42:Lx:124:ARG:NH2	2.23	0.71
13:LQ:82:GLU:OE2	13:LQ:85:LEU:HD12	1.90	0.70
52:Sf:73:ALA:O	52:Sf:79:LYS:NZ	2.24	0.70
21:La:101:LYS:HD3	40:Lv:56:ILE:HG21	1.71	0.70
31:Ll:136:ARG:NH1	31:Ll:140:GLU:OE2	2.24	0.70
1:L1:991:U:H2'	1:L1:992:A:H8	1.56	0.70
15:LS:78:PRO:HA	15:LS:81:ILE:HG12	1.74	0.70
37:Lr:182:GLU:HG3	37:Lr:183:GLU:HG3	1.74	0.70
1:L1:609:U:OP2	43:Ly:46:ARG:NH1	2.24	0.70
6:LI:115:LYS:O	6:LI:118:LEU:O	2.09	0.70
40:Lv:92:ASN:ND2	40:Lv:192:GLU:OE2	2.24	0.70
1:L1:746:U:H4'	34:Lo:52:GLN:HB3	1.73	0.70
47:L5:57:VAL:HG12	47:L5:63:THR:HG22	1.74	0.70
23:Lu:109:ARG:HD3	23:Lu:139:MET:HE2	1.73	0.70
31:Ll:323:TRP:NE1	31:Ll:339:GLU:OE2	2.25	0.69
5:LD:280:TYR:HE1	41:Lw:57:ILE:HA	1.57	0.69
14:LR:108:GLU:HG3	14:LR:110:ALA:H	1.56	0.69
39:Lt:177:GLU:O	39:Lt:190:ARG:NH2	2.23	0.69
51:SR:101:PRO:HG2	51:SR:104:ILE:HD13	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:385:U:H2'	1:L1:386:G:H8	1.56	0.69
1:L1:1412:G:N2	1:L1:1415:A:OP2	2.22	0.69
8:LK:71:LEU:HB2	8:LK:79:GLU:HB2	1.73	0.69
36:Lq:75:VAL:O	36:Lq:86:GLU:CA	2.30	0.69
48:L6:68:ARG:O	48:L6:72:GLU:HG2	1.93	0.69
11:LO:14:ASP:OD1	11:LO:17:ARG:NH1	2.23	0.69
27:Lh:79:ILE:O	27:Lh:83:MET:HG3	1.93	0.69
8:LK:109:ALA:O	8:LK:171:ARG:NH1	2.25	0.69
10:LN:136:LYS:HD2	53:u:167:TRP:CG	2.27	0.69
40:Lv:122:GLU:N	40:Lv:158:GLN:O	2.26	0.69
42:Lx:105:ALA:HB1	42:Lx:111:VAL:HG22	1.74	0.69
45:L3:15:GLN:HE22	45:L3:17:ARG:HB3	1.57	0.69
54:v:46:GLU:OE1	54:v:46:GLU:N	2.26	0.69
8:LK:86:THR:HG23	8:LK:89:TYR:H	1.56	0.69
26:Lg:35:ASN:HB3	26:Lg:38:ARG:HG2	1.75	0.69
6:LI:53:THR:N	6:LI:86:THR:HG1	1.91	0.68
24:Ld:134:MET:HE3	44:Lz:75:ARG:HG2	1.74	0.68
41:Lw:37:ARG:HE	41:Lw:38:PHE:H	1.41	0.68
42:Lx:65:ASP:O	42:Lx:69:ARG:HG3	1.93	0.68
4:LC:213:LYS:HB3	4:LC:216:GLN:HE21	1.58	0.68
5:LD:241:ASN:HD22	50:L8:25:TYR:HB2	1.57	0.68
45:L3:76:MET:HG2	51:SR:49:ILE:HD11	1.75	0.68
50:L8:112:GLN:OE1	50:L8:115:ARG:NH2	2.27	0.68
14:LR:101:VAL:HG12	14:LR:102:VAL:HG23	1.76	0.68
33:Ln:172:GLU:OE2	40:Lv:183:ARG:NH2	2.26	0.68
40:Lv:175:GLN:OE1	40:Lv:175:GLN:HA	1.92	0.68
1:L1:135:A:O2'	1:L1:136:U:OP1	2.11	0.68
39:Lt:74:LEU:HD23	39:Lt:77:ILE:HD11	1.76	0.68
1:L1:524:U:C2	7:LJ:125:VAL:HG11	2.29	0.68
2:L2:1622:A:H4'	14:LR:107:ARG:HH12	1.58	0.68
4:LC:219:MET:HG3	4:LC:238:ARG:HG3	1.74	0.68
26:Lg:54:VAL:HB	50:L8:128:MET:HE2	1.76	0.68
1:L1:1450:C:H5''	53:u:147:LYS:HZ2	1.57	0.68
42:Lx:116:ARG:HB3	42:Lx:120:MET:HE3	1.76	0.67
18:LV:135:GLU:OE1	38:Ls:278:LYS:HB2	1.95	0.67
33:Ln:93:LYS:HE3	39:Lt:84:TYR:HD2	1.59	0.67
1:L1:1156:G:OP1	21:La:49:ARG:NH1	2.23	0.67
1:L1:1473:U:H2'	1:L1:1474:A:H8	1.58	0.67
8:LK:48:GLN:NE2	8:LK:52:GLU:OE2	2.27	0.67
36:Lq:49:ARG:HG3	36:Lq:50:GLU:HG2	1.74	0.67
38:Ls:190:GLU:OE2	38:Ls:215:ARG:NH2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:v:46:GLU:CD	54:v:46:GLU:H	2.01	0.67
17:LU:118:ASN:HD22	17:LU:118:ASN:C	2.02	0.67
3:LB:228:LEU:O	3:LB:231:LYS:N	2.28	0.67
18:LV:157:ARG:HB2	18:LV:167:MET:HG3	1.76	0.67
43:Ly:105:ASP:OD1	43:Ly:106:ASP:N	2.27	0.67
53:u:93:ASP:H	53:u:96:MET:HE2	1.59	0.67
1:L1:346:C:OP2	11:LO:59:ARG:NH1	2.27	0.67
23:Lu:151:ASP:OD1	23:Lu:154:ARG:NH2	2.24	0.67
5:LD:175:LYS:HG2	5:LD:273:LEU:HD13	1.77	0.67
30:Lk:276:ASP:OD1	52:Sf:158:ARG:NH1	2.28	0.67
1:L1:310:A:H5'	27:Lh:58:ILE:HD11	1.77	0.66
1:L1:1474:A:H2'	1:L1:1475:A:H8	1.60	0.66
20:LX:196:GLU:HG3	34:Lo:128:PHE:HD2	1.59	0.66
53:u:135:LEU:HD22	53:u:179:LEU:HB3	1.76	0.66
1:L1:1074:U:O2'	1:L1:1076:U:O4	2.12	0.66
9:LM:67:PHE:HZ	9:LM:103:ILE:HG21	1.58	0.66
30:Lk:336:LEU:HD21	30:Lk:362:THR:HG23	1.77	0.66
41:Lw:47:PHE:HA	41:Lw:50:ARG:HD3	1.75	0.66
2:L2:1626:C:O2'	33:Ln:133:ARG:NH2	2.29	0.66
13:LQ:142:LEU:HA	13:LQ:147:GLN:HE21	1.61	0.66
31:Ll:255:LEU:HD12	31:Ll:256:PRO:HD2	1.77	0.66
4:LC:129:VAL:HB	4:LC:191:THR:HG22	1.76	0.66
11:LO:252:LEU:HD13	11:LO:255:MET:HE3	1.78	0.66
1:L1:551:C:O2'	1:L1:553:A:N6	2.29	0.66
1:L1:608:A:OP1	43:Ly:51:ARG:NH1	2.28	0.66
1:L1:849:G:O3'	3:LB:293:LYS:NZ	2.24	0.66
11:LO:142:GLU:HB2	11:LO:162:LEU:HD23	1.78	0.66
1:L1:395:A:OP1	40:Lv:48:TYR:N	2.29	0.66
1:L1:1070:A:H2'	1:L1:1071:A:C8	2.31	0.66
23:Lu:169:ARG:NH2	30:Lk:63:LYS:O	2.28	0.66
3:LB:217:LEU:HD11	3:LB:227:GLN:HB2	1.76	0.66
12:LP:90:LEU:HD13	12:LP:159:LEU:HD23	1.78	0.66
53:u:151:CYS:HB3	53:u:154:ASP:HB3	1.78	0.66
1:L1:738:U:H2'	1:L1:739:A:H8	1.59	0.65
5:LD:282:PRO:O	5:LD:290:TYR:OH	2.13	0.65
11:LO:109:ARG:CZ	41:Lw:91:MET:HE1	2.26	0.65
46:L4:93:PRO:HD2	46:L4:96:LEU:HD13	1.77	0.65
47:L5:72:ARG:NE	47:L5:74:MET:O	2.28	0.65
1:L1:861:U:O4	3:LB:246:ARG:NH2	2.28	0.65
7:LJ:47:LEU:HD22	12:LP:226:ILE:HG12	1.79	0.65
8:LK:122:ARG:O	8:LK:126:GLN:NE2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lq:77:ALA:O	36:Lq:84:VAL:HA	1.95	0.65
1:L1:567:A:OP1	51:SR:171:ARG:NH2	2.23	0.65
40:Lv:133:GLU:HG2	40:Lv:149:VAL:HG12	1.78	0.65
18:LV:136:PHE:CD2	32:Lm:93:MET:HE3	2.32	0.65
42:Lx:69:ARG:NH2	42:Lx:107:ASP:OD2	2.28	0.65
1:L1:787:A:N3	13:LQ:17:ARG:NH2	2.44	0.65
19:LW:18:ARG:NH2	20:LX:206:GLU:OE1	2.30	0.65
26:Lg:20:MET:HG2	26:Lg:58:GLU:HA	1.79	0.65
39:Lt:260:LEU:HG	39:Lt:264:LEU:HD12	1.79	0.65
4:LC:213:LYS:HG3	4:LC:261:MET:HE3	1.78	0.65
53:u:108:ASP:HB3	53:u:128:SER:HB3	1.78	0.65
54:v:6:ARG:O	54:v:10:LEU:HD23	1.97	0.65
55:w:90:TYR:HE1	55:w:92:LYS:HG2	1.61	0.65
12:LP:89:ILE:HB	12:LP:161:VAL:HG22	1.78	0.65
30:Lk:223:ARG:NH1	52:Sf:160:ARG:HH12	1.94	0.65
46:L4:105:LYS:O	46:L4:120:ARG:NH1	2.30	0.65
14:LR:38:VAL:HG12	14:LR:40:ASN:H	1.61	0.65
51:SR:90:SER:HA	51:SR:93:ILE:HG12	1.77	0.65
1:L1:179:C:OP2	11:LO:53:HIS:NE2	2.30	0.65
1:L1:1343:G:HO2'	29:Lj:66:PHE:N	1.94	0.65
52:Sf:212:ARG:HD2	52:Sf:379:LEU:HB3	1.79	0.64
8:LK:26:ALA:HB3	8:LK:63:GLY:H	1.62	0.64
8:LK:87:VAL:HG23	8:LK:124:LYS:HE2	1.79	0.64
22:Lb:118:ILE:O	22:Lb:168:ARG:NH1	2.30	0.64
1:L1:187:U:H2'	1:L1:188:G:C8	2.32	0.64
13:LQ:82:GLU:N	13:LQ:82:GLU:OE1	2.29	0.64
30:Lk:241:SER:OG	30:Lk:244:GLU:OE1	2.11	0.64
1:L1:1354:U:H2'	1:L1:1355:A:H8	1.62	0.64
11:LO:149:THR:HA	11:LO:170:ASN:ND2	2.12	0.64
1:L1:746:U:OP2	52:Sf:165:ARG:NH2	2.26	0.64
20:LX:64:ILE:O	20:LX:71:GLY:N	2.30	0.64
45:L3:65:ASP:OD2	45:L3:73:ARG:NH2	2.28	0.64
49:L7:111:ILE:O	49:L7:116:ARG:NH2	2.31	0.64
5:LD:241:ASN:ND2	50:L8:25:TYR:HB2	2.12	0.64
32:Lm:114:ASP:HB2	32:Lm:117:LYS:HB2	1.78	0.64
17:LU:175:ARG:HB2	17:LU:180:PHE:HB3	1.80	0.64
38:Ls:126:LYS:NZ	38:Ls:132:PHE:O	2.24	0.64
6:LI:115:LYS:HD2	6:LI:118:LEU:H	1.62	0.64
8:LK:118:TYR:HB2	46:L4:96:LEU:HD11	1.80	0.64
9:LM:73:GLU:OE2	51:SR:149:ARG:NH2	2.30	0.64
54:v:12:LEU:HD12	54:v:59:LEU:HD22	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:L1:233:LEU:HD21	31:L1:236:LEU:HB2	1.80	0.63
46:L4:100:ASN:HD22	46:L4:105:LYS:HD2	1.61	0.63
1:L1:745:C:H3'	52:Sf:165:ARG:NH2	2.12	0.63
1:L1:819:C:O2'	1:L1:951:G:OP1	2.15	0.63
9:LM:28:PRO:HG3	9:LM:65:ILE:HD12	1.79	0.63
23:Lu:187:PRO:HD2	23:Lu:190:LEU:HD12	1.81	0.63
13:LQ:45:PRO:HG2	13:LQ:48:ARG:HH11	1.62	0.63
25:Lf:160:TYR:N	25:Lf:163:GLU:OE2	2.32	0.63
33:Ln:177:HIS:CE1	47:L5:62:SER:HB3	2.33	0.63
1:L1:1504:U:H2'	1:L1:1505:A:H8	1.63	0.63
11:LO:263:ARG:NH1	11:LO:296:SER:O	2.31	0.63
49:L7:108:ALA:O	49:L7:116:ARG:NH2	2.22	0.63
30:Lk:212:THR:HG21	30:Lk:273:VAL:HG13	1.80	0.63
31:L1:352:PRO:O	31:L1:369:TYR:OH	2.13	0.63
52:Sf:201:ASP:OD2	52:Sf:242:ARG:NH1	2.31	0.63
54:v:45:LEU:N	54:v:46:GLU:OE1	2.32	0.63
1:L1:265:A:O2'	1:L1:266:A:O5'	2.16	0.63
2:L2:1621:A:O5'	31:L1:99:ARG:NH2	2.31	0.63
1:L1:1182:C:HO2'	26:Lg:45:HIS:HD1	1.45	0.63
46:L4:67:GLN:HE22	46:L4:71:TYR:HB2	1.63	0.63
1:L1:800:G:N2	1:L1:803:A:C6	2.67	0.63
2:L2:1609:U:O2	2:L2:1616:A:N6	2.32	0.63
33:Ln:113:ARG:O	33:Ln:117:LEU:HB2	1.99	0.63
53:u:196:LEU:HD23	53:u:199:TYR:HB2	1.81	0.63
14:LR:114:HIS:ND1	31:L1:131:PRO:HD2	2.14	0.62
1:L1:166:A:N7	35:Lp:134:LYS:HE2	2.14	0.62
5:LD:241:ASN:OD1	5:LD:256:HIS:NE2	2.22	0.62
46:L4:76:ASN:HD22	46:L4:82:GLN:H	1.46	0.62
39:Lt:51:LEU:HD11	39:Lt:188:ALA:HA	1.80	0.62
1:L1:117:G:N2	1:L1:120:A:OP2	2.27	0.62
7:LJ:105:SER:N	45:L3:40:GLU:OE2	2.32	0.62
8:LK:155:VAL:HB	46:L4:101:LEU:HD11	1.82	0.62
30:Lk:228:ALA:HB3	30:Lk:292:TYR:HB2	1.80	0.62
31:L1:190:GLY:HA2	31:L1:319:PHE:HA	1.80	0.62
2:L2:1627:C:O4'	33:Ln:129:ARG:NH1	2.30	0.62
17:LU:76:HIS:ND1	35:Lp:50:ALA:HA	2.15	0.62
1:L1:19:C:N4	22:Lb:14:LEU:HB3	2.14	0.62
1:L1:130:G:N1	1:L1:133:A:OP2	2.33	0.62
1:L1:1088:G:OP1	6:LI:122:ARG:NH2	2.25	0.62
18:LV:133:ASN:ND2	38:Ls:226:ASP:OD2	2.32	0.62
20:LX:60:ASP:OD2	20:LX:145:ARG:NH1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:648:A:H2'	1:L1:649:A:C8	2.34	0.62
30:Lk:203:CYS:O	52:Sf:179:GLN:NE2	2.31	0.62
53:u:167:TRP:CZ3	53:u:180:MET:HE2	2.35	0.62
31:Ll:212:SER:HB2	31:Ll:274:LYS:HZ2	1.64	0.62
45:L3:13:VAL:HA	45:L3:68:PHE:HA	1.81	0.62
45:L3:20:PHE:HB2	45:L3:55:VAL:HA	1.82	0.62
47:L5:66:ILE:HD11	47:L5:75:LEU:HD12	1.80	0.62
51:SR:40:GLU:HG2	51:SR:49:ILE:HG22	1.82	0.62
1:L1:37:C:O2	30:Lk:80:ARG:NH2	2.32	0.62
1:L1:320:G:OP1	3:LB:269:ARG:NH1	2.32	0.62
1:L1:1474:A:H2'	1:L1:1475:A:C8	2.35	0.62
15:LS:240:ILE:HG22	15:LS:242:GLY:H	1.65	0.62
49:L7:133:LEU:HD21	49:L7:157:MET:HE1	1.82	0.62
1:L1:347:U:OP2	11:LO:59:ARG:NH2	2.30	0.61
1:L1:652:C:H4'	1:L1:653:A:H5''	1.81	0.61
13:LQ:26:ILE:HG13	15:LS:264:TRP:CD1	2.35	0.61
36:Lq:44:ARG:HD2	48:L6:101:TRP:CD1	2.35	0.61
6:LI:58:ARG:HH21	22:Lb:67:ILE:HD13	1.65	0.61
8:LK:116:HIS:CE1	46:L4:72:ALA:HA	2.35	0.61
12:LP:123:ARG:NH1	12:LP:162:GLU:OE1	2.29	0.61
13:LQ:52:MET:HE1	13:LQ:123:ILE:HG21	1.82	0.61
30:Lk:229:ARG:NH1	30:Lk:231:SER:OG	2.33	0.61
31:Ll:212:SER:HB2	31:Ll:274:LYS:NZ	2.15	0.61
11:LO:190:PRO:HB2	41:Lw:51:LEU:HD21	1.82	0.61
26:Lg:60:LYS:HE3	26:Lg:61:LYS:H	1.65	0.61
37:Lr:245:LEU:HD12	37:Lr:253:PRO:HD3	1.81	0.61
1:L1:875:U:H5''	1:L1:876:G:H5'	1.82	0.61
33:Ln:174:GLU:HA	40:Lv:183:ARG:HH12	1.65	0.61
1:L1:622:G:C8	16:LT:11:ARG:HG2	2.34	0.61
8:LK:59:ASP:OD1	46:L4:77:ILE:HG13	1.99	0.61
17:LU:162:GLU:HB3	17:LU:192:VAL:HB	1.83	0.61
18:LV:77:ARG:HB3	18:LV:80:ILE:HD11	1.81	0.61
35:Lp:128:ARG:NH1	35:Lp:132:CYS:SG	2.74	0.61
20:LX:86:VAL:HG21	20:LX:120:VAL:HG21	1.83	0.61
30:Lk:409:GLU:HA	30:Lk:412:ARG:HH11	1.64	0.61
14:LR:40:ASN:HB3	31:Ll:337:MET:HE1	1.82	0.61
30:Lk:274:LYS:NZ	30:Lk:275:ASN:O	2.29	0.61
9:LM:176:TYR:OH	51:SR:94:ARG:NH2	2.34	0.61
22:Lb:129:MET:SD	22:Lb:132:LEU:HD12	2.41	0.61
47:L5:51:LEU:HB3	47:L5:67:ARG:HB3	1.83	0.61
1:L1:1078:A:H2'	1:L1:1079:A:H8	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LR:53:ARG:NH1	31:Ll:155:TYR:OH	2.33	0.61
52:Sf:259:ILE:O	52:Sf:260:GLU:HG3	2.01	0.61
9:LM:67:PHE:HB3	9:LM:71:LYS:HB2	1.83	0.61
17:LU:194:ARG:NE	36:Lq:17:ASN:O	2.34	0.61
1:L1:551:C:H4'	1:L1:552:U:OP1	2.00	0.60
5:LD:59:ARG:HH21	5:LD:84:PRO:HB2	1.66	0.60
46:L4:87:LYS:HB2	46:L4:92:TYR:CZ	2.35	0.60
1:L1:122:G:OP2	27:Lh:85:LYS:NZ	2.32	0.60
4:LC:202:GLN:HG2	4:LC:203:TYR:H	1.66	0.60
55:w:112:SER:HA	55:w:115:GLN:OE1	2.00	0.60
1:L1:265:A:O2'	1:L1:266:A:O4'	2.17	0.60
20:LX:101:THR:HG23	20:LX:102:MET:H	1.65	0.60
41:Lw:154:ASP:OD1	41:Lw:155:GLN:N	2.34	0.60
26:Lg:55:LEU:H	50:L8:128:MET:CE	2.15	0.60
31:Ll:215:THR:OG1	31:Ll:275:GLN:NE2	2.33	0.60
37:Lr:226:LYS:HB2	37:Lr:231:MET:HE2	1.84	0.60
1:L1:1134:A:H2'	1:L1:1135:A:H8	1.66	0.60
4:LC:131:LYS:HG2	4:LC:146:SER:HB2	1.83	0.60
17:LU:95:LEU:HD23	17:LU:138:ALA:HB2	1.83	0.60
25:Lf:155:GLU:HB2	25:Lf:172:LYS:HG2	1.83	0.60
32:Lm:34:GLN:N	32:Lm:34:GLN:NE2	2.50	0.60
36:Lq:21:ARG:HG2	37:Lr:217:ASP:OD2	2.01	0.60
1:L1:416:A:H2'	1:L1:417:U:C6	2.36	0.60
1:L1:466:C:OP2	24:Ld:77:ARG:NH2	2.34	0.60
52:Sf:369:PHE:HB3	52:Sf:424:PHE:CE2	2.35	0.60
8:LK:122:ARG:HG2	8:LK:137:LEU:HD21	1.82	0.60
11:LO:203:ARG:O	11:LO:263:ARG:HD3	2.02	0.60
27:Lh:58:ILE:HG22	34:Lo:30:PHE:CZ	2.36	0.60
32:Lm:193:MET:HE1	32:Lm:285:ASN:HD21	1.65	0.60
1:L1:282:U:H2'	1:L1:283:A:H8	1.66	0.60
1:L1:345:G:H5'	1:L1:346:C:H5	1.67	0.60
2:L2:1628:C:HO2'	33:Ln:121:TRP:CD1	2.19	0.60
31:Ll:236:LEU:O	31:Ll:251:THR:OG1	2.20	0.60
54:v:29:ASP:OD1	54:v:30:PHE:N	2.33	0.60
12:LP:109:ILE:HG22	12:LP:113:MET:HE2	1.84	0.60
53:u:169:CYS:SG	53:u:170:VAL:N	2.75	0.60
55:w:91:ASP:OD1	55:w:92:LYS:N	2.35	0.60
4:LC:99:LEU:HB2	4:LC:127:CYS:SG	2.42	0.60
5:LD:126:LYS:NZ	5:LD:138:HIS:O	2.29	0.60
20:LX:131:THR:HG22	20:LX:149:ARG:HE	1.67	0.60
24:Ld:99:VAL:HG11	44:Lz:77:VAL:HG22	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:58:U:O2'	22:Lb:96:LYS:O	2.14	0.59
21:La:60:TYR:OH	21:La:94:GLU:OE2	2.20	0.59
23:Lu:171:ASP:OD1	23:Lu:172:ILE:N	2.33	0.59
41:Lw:144:THR:O	41:Lw:146:THR:N	2.35	0.59
52:Sf:152:GLN:HA	52:Sf:156:TYR:HB2	1.82	0.59
1:L1:1445:U:H2'	1:L1:1446:C:H6	1.67	0.59
21:La:84:GLY:O	21:La:87:LYS:N	2.35	0.59
1:L1:216:G:H1	43:Ly:61:GLY:HA3	1.67	0.59
1:L1:402:A:H2'	1:L1:403:A:C8	2.37	0.59
33:Ln:169:PHE:O	33:Ln:171:PHE:N	2.36	0.59
4:LC:127:CYS:HB2	4:LC:193:LEU:HB2	1.83	0.59
28:Li:106:THR:HG23	28:Li:162:THR:HA	1.84	0.59
39:Lt:199:ASN:ND2	39:Lt:242:ASP:OD1	2.21	0.59
1:L1:1078:A:H2'	1:L1:1079:A:C8	2.38	0.59
6:LI:146:LEU:HD23	6:LI:147:ARG:HG2	1.84	0.59
30:Lk:127:LYS:HG3	30:Lk:251:HIS:ND1	2.18	0.59
54:v:13:TYR:CD2	54:v:17:LEU:HD11	2.38	0.59
54:v:46:GLU:N	54:v:46:GLU:CD	2.60	0.59
1:L1:469:U:H3'	24:Ld:74:SER:OG	2.02	0.59
1:L1:725:A:O2'	30:Lk:384:GLN:NE2	2.35	0.59
7:LJ:93:ASN:ND2	7:LJ:155:VAL:HB	2.15	0.59
10:LN:139:ALA:HA	53:u:194:TRP:HH2	1.67	0.59
17:LU:130:LEU:HB2	17:LU:156:VAL:HB	1.84	0.59
28:Li:101:LYS:HB3	28:Li:103:LYS:HD3	1.83	0.59
46:L4:67:GLN:NE2	46:L4:71:TYR:HB2	2.18	0.59
30:Lk:201:ARG:HG2	30:Lk:232:THR:HG22	1.83	0.59
33:Ln:168:LEU:HD21	39:Lt:206:GLY:HA2	1.85	0.59
54:v:23:LEU:O	54:v:28:ARG:NH2	2.35	0.59
4:LC:248:ILE:HG22	4:LC:250:ARG:HG2	1.85	0.59
30:Lk:201:ARG:NH1	30:Lk:418:TYR:O	2.28	0.59
31:Ll:279:ILE:HG12	31:Ll:310:THR:HB	1.83	0.59
11:LO:91:ARG:NH2	11:LO:209:GLU:OE2	2.33	0.59
12:LP:166:ARG:O	46:L4:131:ARG:NH1	2.35	0.59
37:Lr:86:ASP:OD1	37:Lr:87:LEU:N	2.36	0.59
38:Ls:160:LEU:HD23	38:Ls:169:PHE:CE2	2.37	0.59
1:L1:156:G:H4'	1:L1:158:A:H2	1.68	0.59
1:L1:791:A:H4'	4:LC:235:LYS:HB3	1.85	0.59
1:L1:1332:G:H2'	1:L1:1333:A:H8	1.68	0.59
4:LC:69:ASP:OD1	4:LC:154:ARG:NH1	2.36	0.59
6:LI:79:VAL:HA	22:Lb:89:GLN:HB2	1.84	0.59
15:LS:246:ASP:OD1	15:LS:247:LEU:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LT:122:ARG:NH2	17:LU:72:GLU:OE2	2.36	0.59
52:Sf:77:ASP:OD1	52:Sf:78:GLU:N	2.36	0.59
54:v:13:TYR:O	54:v:17:LEU:HG	2.03	0.59
3:LB:146:SER:HA	30:Lk:263:ILE:HD12	1.84	0.58
39:Lt:267:LYS:HA	39:Lt:271:GLN:HG2	1.85	0.58
1:L1:802:A:O2'	1:L1:808:G:N7	2.25	0.58
1:L1:1302:A:H5''	12:LP:184:PRO:HA	1.85	0.58
1:L1:1408:C:H2'	1:L1:1409:G:H8	1.68	0.58
39:Lt:198:ASN:HB2	39:Lt:200:MET:HE2	1.84	0.58
1:L1:8:C:O2	20:LX:42:ARG:NH1	2.35	0.58
5:LD:184:GLN:HE22	11:LO:22:VAL:H	1.51	0.58
13:LQ:97:TYR:OH	13:LQ:126:LYS:O	2.16	0.58
13:LQ:154:GLN:O	13:LQ:158:GLN:HG2	2.03	0.58
14:LR:93:VAL:HG21	14:LR:135:CYS:SG	2.43	0.58
30:Lk:290:THR:HG22	30:Lk:343:GLN:HB2	1.85	0.58
46:L4:95:TRP:HA	46:L4:98:GLU:HG2	1.84	0.58
1:L1:475:G:N2	17:LU:104:ARG:HH12	2.00	0.58
2:L2:1607:U:H3	2:L2:1664:G:H1	1.51	0.58
5:LD:94:ASP:OD1	5:LD:95:ILE:N	2.35	0.58
6:LI:141:GLU:HA	6:LI:144:LYS:HE3	1.85	0.58
13:LQ:26:ILE:HG13	15:LS:264:TRP:HD1	1.67	0.58
15:LS:240:ILE:HG21	15:LS:243:ILE:HD12	1.85	0.58
23:Lu:69:ASP:OD1	23:Lu:70:ASP:N	2.34	0.58
39:Lt:51:LEU:HB2	39:Lt:174:PRO:HG2	1.85	0.58
1:L1:1519:C:O2'	51:SR:155:ALA:N	2.31	0.58
14:LR:137:GLU:HB2	31:Ll:188:TYR:HD2	1.67	0.58
22:Lb:231:VAL:HG21	34:Lo:114:LEU:HD21	1.83	0.58
33:Ln:178:TYR:O	39:Lt:136:ARG:HD3	2.02	0.58
42:Lx:75:LYS:HZ3	42:Lx:82:LEU:HB3	1.68	0.58
31:Ll:187:VAL:HG13	31:Ll:319:PHE:HB3	1.85	0.58
39:Lt:178:TRP:NE1	39:Lt:182:GLU:O	2.30	0.58
1:L1:772:U:OP1	52:Sf:81:ARG:NH2	2.26	0.58
4:LC:111:THR:O	4:LC:114:GLY:N	2.34	0.58
31:Ll:177:TYR:HB2	31:Ll:185:MET:HB3	1.84	0.58
1:L1:211:A:OP1	41:Lw:90:ARG:N	2.36	0.58
1:L1:1473:U:H2'	1:L1:1474:A:C8	2.37	0.58
5:LD:291:SER:N	41:Lw:53:PRO:O	2.35	0.58
11:LO:197:GLY:HA3	50:L8:62:ALA:HB2	1.85	0.58
37:Lr:59:ARG:HH21	37:Lr:184:PHE:HB2	1.69	0.58
40:Lv:125:TYR:HE2	40:Lv:127:MET:SD	2.27	0.58
1:L1:1504:U:H2'	1:L1:1505:A:C8	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L2:1627:C:H2'	2:L2:1628:C:H6	1.68	0.58
10:LN:94:PRO:O	10:LN:97:THR:OG1	2.20	0.58
31:L1:179:VAL:O	31:L1:183:ASP:HB3	2.03	0.58
37:Lr:159:PHE:CD2	37:Lr:231:MET:HG2	2.38	0.58
46:L4:76:ASN:ND2	46:L4:82:GLN:H	2.02	0.58
53:u:167:TRP:HZ3	53:u:180:MET:HE2	1.68	0.58
1:L1:33:C:O2'	1:L1:34:U:OP2	2.22	0.58
39:Lt:120:LEU:HD13	39:Lt:123:MET:HE2	1.85	0.58
53:u:97:MET:HE2	53:u:125:VAL:HG21	1.86	0.58
55:w:138:LEU:HD13	55:w:144:ILE:HG12	1.84	0.58
1:L1:323:A:N3	1:L1:324:A:H5''	2.18	0.57
1:L1:1125:U:H2'	1:L1:1126:G:H8	1.68	0.57
2:L2:1644:G:O6	14:LR:87:HIS:NE2	2.36	0.57
10:LN:41:VAL:HG11	10:LN:104:ASN:HD22	1.69	0.57
40:Lv:60:LYS:HA	40:Lv:63:ILE:HG22	1.85	0.57
1:L1:488:U:OP1	51:SR:182:ARG:NH2	2.37	0.57
1:L1:1480:U:H2'	1:L1:1481:A:C8	2.40	0.57
28:Li:146:GLU:OE2	31:L1:362:PRO:HB3	2.04	0.57
34:Lo:53:ILE:HD12	34:Lo:56:MET:HE2	1.86	0.57
49:L7:102:ARG:HG2	49:L7:134:ILE:HG12	1.85	0.57
53:u:135:LEU:HD23	53:u:138:MET:HE2	1.86	0.57
1:L1:77:G:OP2	1:L1:79:C:N4	2.37	0.57
1:L1:99:C:C4	5:LD:108:ARG:HD2	2.39	0.57
7:LJ:120:LYS:NZ	7:LJ:157:GLU:OE1	2.37	0.57
39:Lt:197:GLU:HG3	39:Lt:244:SER:OG	2.03	0.57
50:L8:42:PRO:HA	50:L8:52:LEU:HD11	1.86	0.57
17:LU:194:ARG:HD3	36:Lq:19:LEU:HD23	1.85	0.57
20:LX:80:ILE:HB	20:LX:85:TRP:HB2	1.86	0.57
40:Lv:149:VAL:HG23	47:L5:69:ARG:NH2	2.19	0.57
53:u:150:LYS:HG3	53:u:151:CYS:H	1.69	0.57
1:L1:305:U:H2'	1:L1:306:U:C6	2.40	0.57
1:L1:578:U:OP1	16:LT:99:ARG:NH2	2.30	0.57
18:LV:212:LEU:HA	36:Lq:119:PHE:HE1	1.68	0.57
20:LX:54:TRP:NE1	20:LX:56:LEU:O	2.38	0.57
30:Lk:104:CYS:HA	30:Lk:219:LEU:O	2.04	0.57
33:Ln:96:ASP:N	39:Lt:84:TYR:OH	2.27	0.57
40:Lv:175:GLN:OE1	40:Lv:184:LEU:HD23	2.04	0.57
53:u:183:GLU:O	53:u:186:GLU:HG2	2.04	0.57
3:LB:126:VAL:HA	3:LB:142:VAL:HG12	1.87	0.57
8:LK:140:VAL:O	8:LK:144:ILE:HG12	2.05	0.57
16:LT:85:ALA:O	16:LT:89:ASN:ND2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LT:112:THR:HG1	36:Lq:127:GLN:HE22	1.50	0.57
20:LX:19:TYR:OH	20:LX:31:ASP:OD2	2.23	0.57
23:Lu:223:LYS:NZ	23:Lu:227:GLU:OE2	2.36	0.57
33:Ln:131:MET:HA	33:Ln:131:MET:HE3	1.86	0.57
39:Lt:49:GLY:HA2	39:Lt:232:PHE:HB3	1.87	0.57
20:LX:57:PHE:HD1	20:LX:145:ARG:HH21	1.53	0.57
20:LX:105:ARG:HD3	38:Ls:174:TRP:CD2	2.39	0.57
30:Lk:139:LEU:HD11	30:Lk:423:ALA:HB3	1.87	0.57
1:L1:282:U:H2'	1:L1:283:A:C8	2.39	0.57
7:LJ:86:ILE:HA	7:LJ:89:VAL:HG22	1.86	0.57
24:Ld:53:HIS:CE1	24:Ld:60:PRO:HG3	2.40	0.57
24:Ld:117:ILE:O	48:L6:45:ASN:ND2	2.38	0.57
31:Ll:192:GLU:OE1	31:Ll:322:ARG:NH1	2.38	0.57
39:Lt:97:ARG:HA	39:Lt:100:LYS:HE2	1.86	0.57
53:u:132:THR:O	53:u:136:HIS:ND1	2.28	0.57
1:L1:1007:A:H2'	1:L1:1008:A:C8	2.38	0.57
8:LK:70:ILE:HG23	8:LK:80:ILE:HG13	1.87	0.57
8:LK:114:LEU:HA	8:LK:117:VAL:HG12	1.87	0.57
18:LV:63:LEU:HD23	18:LV:65:GLY:H	1.70	0.57
30:Lk:60:PHE:HB3	30:Lk:67:VAL:HG12	1.87	0.57
36:Lq:122:ASP:OD2	37:Lr:225:GLY:HA3	2.05	0.57
52:Sf:165:ARG:HA	52:Sf:168:GLU:CG	2.33	0.57
1:L1:849:G:N7	3:LB:230:SER:OG	2.38	0.56
7:LJ:60:ILE:HG22	7:LJ:60:ILE:O	2.04	0.56
11:LO:233:ARG:HB3	11:LO:244:LEU:HD11	1.87	0.56
45:L3:77:ARG:NH1	51:SR:50:GLU:OE2	2.38	0.56
53:u:184:THR:HA	53:u:187:ILE:HG22	1.87	0.56
1:L1:283:A:O2'	1:L1:793:A:OP1	2.23	0.56
7:LJ:95:MET:N	7:LJ:95:MET:SD	2.78	0.56
20:LX:63:GLU:OE1	20:LX:73:GLN:NE2	2.38	0.56
31:Ll:233:LEU:HD11	31:Ll:236:LEU:HD22	1.85	0.56
32:Lm:139:ASN:O	32:Lm:143:TRP:HD1	1.88	0.56
39:Lt:151:ARG:HH22	39:Lt:157:LEU:HD11	1.70	0.56
9:LM:27:PRO:HG2	9:LM:30:LYS:HB2	1.87	0.56
17:LU:155:ARG:NH2	17:LU:157:GLU:OE2	2.38	0.56
31:Ll:240:ILE:HD13	31:Ll:248:GLY:HA3	1.87	0.56
39:Lt:82:SER:OG	39:Lt:83:LEU:N	2.35	0.56
54:v:43:GLN:HG3	59:v:101:PNS:H422	1.87	0.56
1:L1:1499:C:H2'	1:L1:1500:C:C6	2.41	0.56
2:L2:1622:A:H2'	2:L2:1623:G:C8	2.39	0.56
8:LK:39:LEU:HB3	8:LK:44:VAL:HB	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LR:103:SER:OG	31:Ll:150:ARG:NH2	2.32	0.56
30:Lk:146:HIS:O	30:Lk:194:LYS:NZ	2.38	0.56
37:Lr:220:ILE:HA	37:Lr:223:MET:HG2	1.87	0.56
42:Lx:137:ARG:NH1	42:Lx:142:GLU:HA	2.21	0.56
55:w:104:PHE:O	55:w:110:LEU:N	2.36	0.56
1:L1:476:A:C4	16:LT:64:MET:HE3	2.41	0.56
9:LM:136:ASP:OD1	9:LM:137:ILE:N	2.38	0.56
15:LS:256:GLU:HA	15:LS:259:LYS:HD2	1.86	0.56
28:Li:172:TYR:HB2	28:Li:175:ASP:HB2	1.88	0.56
33:Ln:149:GLU:HB3	39:Lt:212:HIS:CD2	2.41	0.56
40:Lv:96:THR:HG22	40:Lv:183:ARG:HB2	1.87	0.56
53:u:166:ASP:OD1	53:u:167:TRP:N	2.38	0.56
54:v:39:PHE:HA	54:v:43:GLN:OE1	2.06	0.56
1:L1:371:U:H2'	1:L1:372:U:C6	2.40	0.56
10:LN:128:ARG:HH22	53:u:120:TYR:HD1	1.54	0.56
12:LP:57:PRO:HD2	12:LP:150:TYR:CD2	2.39	0.56
31:Ll:90:ILE:HA	44:Lz:112:LYS:HB2	1.87	0.56
31:Ll:199:ALA:HA	31:Ll:256:PRO:HB3	1.88	0.56
3:LB:293:LYS:HE3	3:LB:295:TYR:CE1	2.40	0.56
5:LD:97:HIS:HD2	11:LO:27:LEU:HB3	1.69	0.56
53:u:107:ARG:NH1	53:u:130:THR:HA	2.21	0.56
53:u:190:LEU:HD23	53:u:190:LEU:H	1.70	0.56
1:L1:1354:U:H2'	1:L1:1355:A:C8	2.41	0.56
14:LR:110:ALA:HA	31:Ll:138:GLU:OE2	2.06	0.56
32:Lm:189:LEU:O	32:Lm:295:ARG:NH2	2.39	0.56
33:Ln:178:TYR:HD2	33:Ln:179:THR:HG23	1.71	0.56
1:L1:1238:U:H4'	26:Lg:62:ILE:HG21	1.87	0.56
19:LW:49:THR:HB	19:LW:52:ASP:OD1	2.06	0.56
54:v:40:ARG:HH21	55:w:113:LEU:HD23	1.70	0.56
1:L1:985:G:N2	1:L1:989:C:O2'	2.39	0.56
1:L1:1124:C:O2	22:Lb:108:GLN:NE2	2.25	0.56
5:LD:280:TYR:CE1	41:Lw:57:ILE:HA	2.39	0.55
32:Lm:74:ASP:OD1	32:Lm:77:THR:OG1	2.20	0.55
1:L1:508:A:H2'	1:L1:509:A:C8	2.42	0.55
1:L1:1064:A:H2'	1:L1:1065:G:H8	1.72	0.55
9:LM:143:GLU:OE1	36:Lq:136:LYS:HD2	2.06	0.55
20:LX:170:TRP:HZ3	23:Lu:80:LYS:HZ3	1.53	0.55
33:Ln:149:GLU:HB3	39:Lt:212:HIS:HD2	1.71	0.55
45:L3:61:GLU:HG2	45:L3:79:ALA:HB2	1.88	0.55
48:L6:15:ARG:HB3	48:L6:18:ILE:HG12	1.87	0.55
1:L1:1445:U:H2'	1:L1:1446:C:C6	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LS:96:ARG:NH1	15:LS:282:ILE:HG12	2.21	0.55
15:LS:148:THR:HG22	15:LS:165:GLU:HG2	1.87	0.55
30:Lk:242:ARG:O	30:Lk:246:GLU:HG2	2.06	0.55
53:u:180:MET:SD	53:u:184:THR:OG1	2.46	0.55
55:w:133:ILE:O	55:w:136:GLU:HG3	2.05	0.55
1:L1:1397:U:OP1	4:LC:234:THR:OG1	2.23	0.55
8:LK:58:LYS:HB3	46:L4:79:LYS:NZ	2.22	0.55
40:Lv:154:GLU:OE1	40:Lv:156:VAL:HG23	2.07	0.55
52:Sf:150:LEU:HD22	52:Sf:405:ILE:HD11	1.88	0.55
1:L1:883:G:H2'	1:L1:884:A:H8	1.71	0.55
1:L1:889:U:H4'	1:L1:890:G:O5'	2.07	0.55
20:LX:102:MET:SD	20:LX:104:TYR:HB2	2.47	0.55
30:Lk:223:ARG:HD2	52:Sf:160:ARG:HH22	1.70	0.55
42:Lx:116:ARG:O	42:Lx:120:MET:HG2	2.07	0.55
1:L1:211:A:OP2	41:Lw:111:ARG:NH2	2.39	0.55
30:Lk:229:ARG:HH21	30:Lk:288:PRO:HG3	1.72	0.55
31:L1:326:SER:O	31:L1:330:ILE:HD12	2.06	0.55
50:L8:147:GLN:HA	50:L8:150:LYS:HG2	1.89	0.55
1:L1:2:C:O2'	18:LV:149:ARG:O	2.21	0.55
7:LJ:116:LEU:HG	7:LJ:121:ILE:HD11	1.88	0.55
19:LW:81:ASP:HB3	19:LW:87:ILE:HD11	1.87	0.55
1:L1:304:A:H5'	3:LB:261:GLY:HA2	1.87	0.55
1:L1:648:A:H2'	1:L1:649:A:H8	1.70	0.55
1:L1:929:U:OP2	1:L1:955:C:N4	2.40	0.55
1:L1:1488:A:H2'	1:L1:1489:A:H8	1.71	0.55
12:LP:218:ILE:HA	12:LP:223:MET:HG3	1.88	0.55
33:Ln:113:ARG:HH21	33:Ln:116:LEU:HD12	1.71	0.55
46:L4:136:LYS:HE2	46:L4:136:LYS:HA	1.89	0.55
1:L1:360:U:O4	1:L1:428:G:C5	2.60	0.55
1:L1:616:A:H2'	1:L1:617:U:C6	2.41	0.55
1:L1:1070:A:N3	1:L1:1251:A:O2'	2.34	0.55
8:LK:179:LYS:HA	8:LK:182:ASP:OD2	2.05	0.55
10:LN:42:ASP:OD1	10:LN:116:GLY:HA3	2.07	0.55
50:L8:128:MET:HE3	50:L8:132:ILE:HD11	1.89	0.55
1:L1:487:U:OP1	51:SR:182:ARG:NH1	2.40	0.55
1:L1:801:G:O2'	1:L1:984:U:O4	2.19	0.55
1:L1:991:U:H2'	1:L1:992:A:C8	2.41	0.55
1:L1:1408:C:H2'	1:L1:1409:G:C8	2.42	0.55
10:LN:117:THR:O	10:LN:140:ILE:HB	2.07	0.55
33:Ln:174:GLU:HA	40:Lv:183:ARG:NH2	2.21	0.55
40:Lv:122:GLU:HB2	40:Lv:158:GLN:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LD:60:ARG:NH2	42:Lx:121:CYS:SG	2.80	0.54
14:LR:82:VAL:HG11	14:LR:157:MET:HE1	1.89	0.54
22:Lb:7:PRO:HD2	22:Lb:10:LEU:HD12	1.89	0.54
41:Lw:96:VAL:HG22	41:Lw:110:ILE:HG12	1.87	0.54
1:L1:697:A:N3	23:Lu:123:ARG:NH2	2.55	0.54
1:L1:928:A:H3'	1:L1:955:C:H42	1.72	0.54
13:LQ:108:LEU:HD13	25:Lf:122:LEU:HD11	1.89	0.54
17:LU:119:GLU:CD	17:LU:121:ASP:H	2.16	0.54
30:Lk:232:THR:HG23	30:Lk:289:HIS:HB2	1.89	0.54
36:Lq:30:SER:O	36:Lq:75:VAL:HA	2.08	0.54
39:Lt:188:ALA:O	39:Lt:191:THR:OG1	2.23	0.54
44:Lz:85:ASP:O	44:Lz:89:GLN:OE1	2.24	0.54
45:L3:64:VAL:HB	45:L3:76:MET:HB2	1.88	0.54
1:L1:475:G:H21	17:LU:104:ARG:NH1	2.04	0.54
8:LK:187:GLU:HG2	8:LK:191:LYS:HE3	1.90	0.54
10:LN:136:LYS:HD2	53:u:167:TRP:CD2	2.43	0.54
30:Lk:215:ARG:NH2	30:Lk:367:ASN:OD1	2.39	0.54
32:Lm:139:ASN:HB3	32:Lm:174:VAL:HG21	1.89	0.54
39:Lt:54:GLN:HA	39:Lt:157:LEU:O	2.06	0.54
42:Lx:75:LYS:NZ	42:Lx:82:LEU:HB3	2.22	0.54
49:L7:81:CYS:SG	49:L7:98:LYS:HB3	2.47	0.54
1:L1:63:C:O2'	1:L1:64:C:OP1	2.24	0.54
1:L1:259:A:H2'	1:L1:260:C:C6	2.43	0.54
1:L1:570:C:H5'	9:LM:29:GLY:HA3	1.88	0.54
1:L1:847:U:OP1	3:LB:287:ARG:NE	2.40	0.54
1:L1:1280:U:H2'	1:L1:1281:A:H8	1.72	0.54
2:L2:1603:A:N6	2:L2:1669:G:O6	2.41	0.54
8:LK:44:VAL:HA	8:LK:78:PHE:HZ	1.71	0.54
30:Lk:211:ALA:HB1	30:Lk:322:LEU:HD22	1.89	0.54
37:Lr:216:ARG:HA	37:Lr:220:ILE:HG12	1.90	0.54
7:LJ:160:LYS:HG3	7:LJ:163:GLU:HB3	1.89	0.54
30:Lk:223:ARG:HD2	52:Sf:160:ARG:NH2	2.22	0.54
33:Ln:174:GLU:CA	40:Lv:183:ARG:HH22	2.21	0.54
38:Ls:196:GLN:HE21	38:Ls:198:ARG:HH11	1.54	0.54
49:L7:175:LEU:HB3	49:L7:179:ARG:HH12	1.73	0.54
52:Sf:142:LEU:HD13	52:Sf:422:VAL:HG21	1.88	0.54
1:L1:314:A:H8	1:L1:317:G:H21	1.55	0.54
1:L1:530:A:H5'	46:L4:134:LYS:HE3	1.90	0.54
2:L2:1611:G:H2'	2:L2:1612:C:C6	2.42	0.54
5:LD:49:ARG:NH1	5:LD:81:ASP:O	2.40	0.54
5:LD:103:GLN:HE22	5:LD:249:ASN:HB2	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Lb:200:GLU:N	22:Lb:200:GLU:OE1	2.40	0.54
39:Lt:160:LEU:HG	39:Lt:171:TRP:HB3	1.88	0.54
45:L3:24:GLU:OE1	45:L3:24:GLU:N	2.41	0.54
9:LM:80:HIS:HA	9:LM:86:GLY:O	2.08	0.54
9:LM:138:LEU:HD23	9:LM:141:LEU:HD12	1.89	0.54
15:LS:232:ARG:HD3	15:LS:235:ARG:NH2	2.23	0.54
19:LW:40:VAL:HG22	19:LW:105:PHE:CD2	2.43	0.54
32:Lm:192:TRP:O	32:Lm:193:MET:HE2	2.08	0.54
32:Lm:285:ASN:HD22	32:Lm:293:LEU:HD21	1.73	0.54
33:Ln:150:LEU:HD11	33:Ln:157:LEU:HB3	1.90	0.54
44:Lz:65:ARG:HG2	44:Lz:69:GLU:OE2	2.08	0.54
1:L1:412:G:H2'	1:L1:413:U:O4'	2.08	0.54
1:L1:457:A:H4'	1:L1:581:A:C5	2.43	0.54
4:LC:234:THR:O	4:LC:236:THR:N	2.39	0.54
14:LR:93:VAL:HG22	14:LR:143:MET:HE1	1.90	0.54
14:LR:178:TYR:O	31:Ll:346:ARG:NH1	2.40	0.54
22:Lb:8:VAL:O	22:Lb:11:TRP:HB2	2.07	0.54
24:Ld:68:ILE:HD11	24:Ld:122:LEU:HD13	1.88	0.54
39:Lt:183:THR:HG22	39:Lt:185:ARG:H	1.72	0.54
43:Ly:68:LYS:HZ2	50:L8:32:ARG:N	2.06	0.54
46:L4:137:ARG:NE	46:L4:137:ARG:HA	2.21	0.54
1:L1:605:U:H2'	1:L1:606:C:H6	1.72	0.54
9:LM:28:PRO:HG2	9:LM:67:PHE:CE1	2.43	0.54
13:LQ:99:ASP:OD1	13:LQ:100:GLN:N	2.41	0.54
31:Ll:217:LEU:HD13	31:Ll:236:LEU:HD13	1.89	0.54
36:Lq:133:PHE:CG	37:Lr:259:ARG:HD2	2.43	0.54
45:L3:58:ASP:OD1	45:L3:60:SER:N	2.40	0.54
54:v:6:ARG:NH2	55:w:112:SER:HG	2.05	0.54
8:LK:73:LYS:CD	8:LK:74:PRO:HD2	2.36	0.54
18:LV:51:TRP:CD1	18:LV:74:TYR:HB3	2.43	0.54
19:LW:20:PHE:O	23:Lu:99:HIS:NE2	2.42	0.54
31:Ll:233:LEU:HB2	31:Ll:298:PHE:HB2	1.88	0.54
33:Ln:164:ARG:HB3	40:Lv:86:TYR:HB3	1.89	0.54
1:L1:86:A:H2'	1:L1:87:A:C8	2.43	0.53
1:L1:336:C:H2'	1:L1:337:U:C6	2.43	0.53
10:LN:69:VAL:HG23	10:LN:89:HIS:CE1	2.42	0.53
13:LQ:141:HIS:O	13:LQ:147:GLN:NE2	2.41	0.53
41:Lw:107:MET:HE1	41:Lw:148:ARG:HE	1.74	0.53
1:L1:169:C:H2'	1:L1:170:C:C6	2.43	0.53
1:L1:605:U:H2'	1:L1:606:C:C6	2.44	0.53
1:L1:1198:C:H2'	1:L1:1199:A:O4'	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LC:177:LYS:HB3	4:LC:298:LYS:HE3	1.90	0.53
13:LQ:34:THR:HG23	13:LQ:82:GLU:OE2	2.08	0.53
14:LR:53:ARG:HH21	14:LR:57:LEU:HD21	1.71	0.53
45:L3:42:VAL:O	45:L3:45:THR:OG1	2.25	0.53
7:LJ:113:ARG:NH2	8:LK:133:GLN:HA	2.23	0.53
31:Ll:175:VAL:HG11	31:Ll:270:PHE:CE2	2.43	0.53
39:Lt:168:GLN:HB3	39:Lt:170:VAL:HG22	1.89	0.53
54:v:54:GLN:O	54:v:57:LYS:HG2	2.08	0.53
1:L1:1239:G:H5'	1:L1:1240:A:OP1	2.07	0.53
1:L1:1263:G:N2	1:L1:1266:U:O2	2.34	0.53
1:L1:1444:U:H2'	1:L1:1445:U:C6	2.43	0.53
14:LR:153:ALA:O	14:LR:158:LYS:HE2	2.09	0.53
54:v:51:ARG:HH21	54:v:55:LEU:N	2.07	0.53
1:L1:437:G:OP1	12:LP:144:LYS:HE3	2.08	0.53
4:LC:187:ILE:CG2	4:LC:191:THR:HG21	2.39	0.53
7:LJ:134:PHE:O	7:LJ:138:SER:OG	2.23	0.53
51:SR:124:ARG:NH1	51:SR:153:ARG:O	2.42	0.53
1:L1:516:C:O2'	1:L1:517:C:OP1	2.22	0.53
1:L1:761:C:O2'	1:L1:762:A:H5'	2.09	0.53
33:Ln:101:ARG:HG2	39:Lt:80:GLU:HA	1.89	0.53
38:Ls:196:GLN:HB3	38:Ls:213:THR:HB	1.90	0.53
39:Lt:70:MET:SD	39:Lt:70:MET:N	2.82	0.53
45:L3:18:VAL:HG23	45:L3:64:VAL:HG22	1.91	0.53
54:v:16:LEU:HD11	54:v:61:PHE:HD1	1.73	0.53
55:w:115:GLN:O	55:w:119:ILE:HG12	2.08	0.53
22:Lb:235:ILE:O	22:Lb:239:GLN:HG2	2.08	0.53
37:Lr:60:ARG:NH2	37:Lr:65:ASN:O	2.42	0.53
1:L1:970:C:H2'	1:L1:971:A:C8	2.44	0.53
1:L1:1134:A:H2'	1:L1:1135:A:C8	2.44	0.53
2:L2:1664:G:H2'	2:L2:1665:C:C6	2.43	0.53
7:LJ:78:LEU:HG	7:LJ:82:LEU:HG	1.91	0.53
15:LS:96:ARG:HH11	15:LS:282:ILE:HG12	1.74	0.53
20:LX:129:LYS:HG2	20:LX:130:PRO:HD2	1.90	0.53
26:Lg:19:ARG:HB2	26:Lg:62:ILE:HD11	1.90	0.53
39:Lt:260:LEU:HD11	39:Lt:272:VAL:HG23	1.91	0.53
44:Lz:53:ASP:OD1	44:Lz:53:ASP:N	2.42	0.53
48:L6:71:PHE:CE2	48:L6:75:LYS:HD2	2.43	0.53
52:Sf:91:TYR:OH	52:Sf:269:ASP:OD2	2.26	0.53
53:u:149:LEU:HD23	53:u:150:LYS:HB2	1.90	0.53
1:L1:1438:U:OP2	4:LC:221:ARG:NH2	2.35	0.53
15:LS:127:SER:OG	53:u:115:PRO:O	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:481:A:H2'	1:L1:482:A:C8	2.43	0.52
1:L1:704:A:N1	52:Sf:97:THR:OG1	2.36	0.52
1:L1:883:G:H2'	1:L1:884:A:C8	2.44	0.52
6:LI:102:VAL:HG22	6:LI:103:GLU:OE1	2.08	0.52
6:LI:115:LYS:HB3	6:LI:118:LEU:HB3	1.90	0.52
8:LK:118:TYR:O	8:LK:122:ARG:HG3	2.09	0.52
10:LN:114:PRO:HD2	10:LN:136:LYS:HE3	1.91	0.52
17:LU:118:ASN:C	17:LU:118:ASN:ND2	2.67	0.52
36:Lq:78:GLU:HA	36:Lq:83:ALA:O	2.09	0.52
1:L1:1159:C:OP2	1:L1:1160:A:O2'	2.24	0.52
2:L2:1622:A:H4'	14:LR:107:ARG:NH1	2.22	0.52
3:LB:284:ARG:NH1	3:LB:285:LYS:O	2.41	0.52
7:LJ:147:PHE:HZ	7:LJ:153:LEU:HD21	1.74	0.52
11:LO:260:LYS:NZ	11:LO:265:ILE:O	2.38	0.52
1:L1:86:A:H2'	1:L1:87:A:H8	1.74	0.52
1:L1:1018:C:H2'	1:L1:1019:C:C6	2.44	0.52
1:L1:1024:A:N3	1:L1:1272:C:O2'	2.33	0.52
4:LC:123:GLN:OE1	4:LC:125:GLN:NE2	2.43	0.52
4:LC:221:ARG:HA	4:LC:261:MET:SD	2.49	0.52
22:Lb:166:LEU:HD12	22:Lb:204:VAL:HG11	1.92	0.52
52:Sf:178:ASP:OD1	52:Sf:179:GLN:N	2.42	0.52
1:L1:156:G:H4'	1:L1:158:A:C2	2.44	0.52
1:L1:188:G:H2'	1:L1:189:A:C8	2.45	0.52
1:L1:395:A:C5	21:La:74:ARG:HD2	2.44	0.52
1:L1:516:C:H2'	1:L1:517:C:C6	2.44	0.52
7:LJ:167:ILE:O	7:LJ:170:THR:OG1	2.21	0.52
19:LW:30:ARG:HB2	19:LW:107:PHE:CG	2.44	0.52
28:Li:151:ASN:ND2	31:Ll:359:HIS:ND1	2.58	0.52
32:Lm:143:TRP:CE3	32:Lm:179:PHE:HD2	2.28	0.52
51:SR:162:ILE:O	51:SR:162:ILE:HG13	2.09	0.52
53:u:96:MET:O	53:u:100:LEU:HD23	2.09	0.52
1:L1:992:A:H2'	1:L1:993:C:C6	2.44	0.52
1:L1:1184:U:H4'	28:Li:138:PRO:HG2	1.91	0.52
1:L1:1488:A:H2'	1:L1:1489:A:C8	2.45	0.52
18:LV:82:TYR:CD2	18:LV:87:MET:HE2	2.44	0.52
20:LX:185:ARG:HA	23:Lu:92:ASN:OD1	2.09	0.52
38:Ls:197:VAL:O	38:Ls:198:ARG:HD2	2.08	0.52
52:Sf:92:MET:HE3	52:Sf:276:ARG:HE	1.74	0.52
1:L1:75:U:O4	28:Li:108:LYS:NZ	2.43	0.52
1:L1:549:C:O2'	1:L1:550:A:O5'	2.27	0.52
1:L1:1057:C:H2'	1:L1:1058:C:H6	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:1152:C:O2'	1:L1:1245:C:OP2	2.27	0.52
1:L1:1371:U:H2'	1:L1:1372:U:H6	1.74	0.52
2:L2:1628:C:HO2'	33:Ln:121:TRP:HD1	1.55	0.52
12:LP:104:MET:HE2	12:LP:182:LYS:HB3	1.92	0.52
39:Lt:116:LEU:HG	39:Lt:117:ALA:H	1.75	0.52
50:L8:140:ARG:O	50:L8:144:GLU:HG2	2.09	0.52
7:LJ:188:ARG:CD	45:L3:55:VAL:HG13	2.37	0.52
31:Ll:100:THR:O	31:Ll:104:LEU:HG	2.10	0.52
31:Ll:183:ASP:OD2	49:L7:189:ARG:NH1	2.35	0.52
38:Ls:168:CYS:HB2	38:Ls:262:HIS:O	2.10	0.52
40:Lv:127:MET:HE3	40:Lv:128:PRO:HD2	1.92	0.52
47:L5:57:VAL:HG22	47:L5:76:ALA:HA	1.92	0.52
1:L1:475:G:N2	17:LU:104:ARG:HH22	2.08	0.52
1:L1:668:A:C4	1:L1:669:G:C8	2.98	0.52
32:Lm:196:LYS:HB3	32:Lm:200:ARG:NH2	2.24	0.52
39:Lt:146:ARG:NH2	39:Lt:259:GLU:HG3	2.24	0.52
55:w:86:VAL:HG21	55:w:122:MET:HG3	1.92	0.52
1:L1:181:G:OP1	1:L1:454:A:O2'	2.27	0.52
1:L1:1374:A:H2'	1:L1:1375:A:C8	2.45	0.52
2:L2:1628:C:H4'	33:Ln:121:TRP:CD1	2.45	0.52
5:LD:262:THR:O	5:LD:265:THR:OG1	2.24	0.52
10:LN:117:THR:HG22	10:LN:118:ARG:CZ	2.40	0.52
13:LQ:156:LEU:O	13:LQ:160:GLN:HG3	2.09	0.52
15:LS:196:GLU:HA	15:LS:199:THR:HG22	1.90	0.52
18:LV:133:ASN:HD22	38:Ls:226:ASP:CG	2.18	0.52
30:Lk:138:SER:HA	30:Lk:141:ASP:HB2	1.92	0.52
31:Ll:325:ASP:OD2	49:L7:124:LYS:NZ	2.32	0.52
32:Lm:276:PHE:HB2	32:Lm:304:VAL:HG22	1.91	0.52
52:Sf:103:ASP:OD1	52:Sf:104:ARG:N	2.43	0.52
1:L1:214:G:N3	1:L1:225:C:O2'	2.42	0.52
5:LD:191:ASP:OD1	5:LD:192:SER:N	2.43	0.52
10:LN:94:PRO:HG2	10:LN:97:THR:HG21	1.92	0.52
11:LO:180:ASP:HB2	11:LO:204:MET:HB2	1.92	0.52
13:LQ:101:THR:O	13:LQ:104:TYR:OH	2.25	0.52
14:LR:121:VAL:HG12	14:LR:156:SER:OG	2.10	0.52
17:LU:125:GLY:CA	17:LU:160:VAL:O	2.58	0.52
24:Ld:46:PHE:CZ	24:Ld:111:LYS:HG2	2.45	0.52
31:Ll:64:GLU:O	31:Ll:69:HIS:NE2	2.43	0.52
31:Ll:175:VAL:HG22	31:Ll:204:VAL:HG13	1.92	0.52
39:Lt:243:PHE:HE2	39:Lt:248:ASN:HB2	1.75	0.52
50:L8:134:ASN:O	50:L8:137:GLN:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:779:G:OP2	52:Sf:225:ARG:NH2	2.39	0.51
7:LJ:40:MET:HE1	7:LJ:48:MET:HE3	1.92	0.51
31:Ll:67:ALA:O	31:Ll:75:ARG:NH2	2.43	0.51
42:Lx:71:GLU:O	42:Lx:74:VAL:HG12	2.09	0.51
51:SR:166:GLY:O	51:SR:171:ARG:NH1	2.43	0.51
53:u:108:ASP:HB3	53:u:128:SER:CB	2.40	0.51
54:v:46:GLU:OE2	59:v:101:PNS:H421	2.09	0.51
15:LS:182:ARG:HD2	15:LS:187:LEU:HD11	1.91	0.51
33:Ln:177:HIS:CD2	47:L5:64:ILE:HD12	2.45	0.51
39:Lt:198:ASN:HB3	39:Lt:243:PHE:CD1	2.46	0.51
1:L1:80:G:H2'	1:L1:81:A:C8	2.45	0.51
1:L1:191:U:H2'	1:L1:192:U:C6	2.45	0.51
1:L1:201:A:N3	28:Li:104:ARG:NH2	2.59	0.51
1:L1:1202:C:O2'	21:La:88:CYS:SG	2.67	0.51
8:LK:166:ALA:O	8:LK:169:LYS:HG3	2.10	0.51
47:L5:58:LYS:HE2	47:L5:60:ASP:HB3	1.92	0.51
52:Sf:369:PHE:HB3	52:Sf:424:PHE:HE2	1.75	0.51
1:L1:237:A:N3	1:L1:1260:U:O2'	2.38	0.51
1:L1:1085:A:H5''	22:Lb:129:MET:HE2	1.92	0.51
30:Lk:223:ARG:HH11	52:Sf:160:ARG:HH12	1.56	0.51
31:Ll:218:LEU:HD13	31:Ll:270:PHE:CE1	2.45	0.51
53:u:95:ASP:N	53:u:95:ASP:OD1	2.40	0.51
1:L1:802:A:OP1	10:LN:56:ARG:NH2	2.42	0.51
4:LC:330:GLU:HG3	4:LC:331:ASP:OD1	2.10	0.51
7:LJ:108:ASP:HA	7:LJ:111:LEU:HG	1.93	0.51
10:LN:42:ASP:HB2	10:LN:106:VAL:HG23	1.91	0.51
19:LW:29:VAL:HG23	19:LW:41:GLN:HB3	1.91	0.51
1:L1:914:C:H2'	1:L1:915:G:H8	1.75	0.51
9:LM:177:ARG:HH21	51:SR:38:VAL:HB	1.75	0.51
14:LR:40:ASN:OD1	31:Ll:293:LEU:HG	2.09	0.51
31:Ll:138:GLU:O	31:Ll:142:THR:HG22	2.10	0.51
39:Lt:51:LEU:H	39:Lt:174:PRO:HD2	1.76	0.51
40:Lv:183:ARG:HA	40:Lv:183:ARG:NE	2.25	0.51
42:Lx:60:TYR:HB3	42:Lx:134:ILE:HG22	1.93	0.51
52:Sf:239:ASN:HB2	52:Sf:299:PHE:HB2	1.91	0.51
53:u:98:VAL:HG11	54:v:25:TYR:HD2	1.76	0.51
1:L1:269:G:H5'	1:L1:270:A:H5''	1.92	0.51
1:L1:269:G:O2'	1:L1:303:G:H4'	2.11	0.51
1:L1:727:C:H2'	1:L1:728:A:C8	2.45	0.51
1:L1:733:G:OP2	3:LB:105:ARG:NH2	2.35	0.51
1:L1:1030:G:H2'	1:L1:1031:G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LU:112:ASP:OD1	17:LU:113:LEU:N	2.42	0.51
18:LV:69:ARG:O	38:Ls:230:ARG:NH2	2.41	0.51
19:LW:61:TYR:CE2	23:Lu:67:PHE:HE1	2.28	0.51
21:La:146:ALA:HB3	31:Ll:341:VAL:HB	1.92	0.51
30:Lk:125:LYS:HA	30:Lk:253:LEU:HD11	1.93	0.51
33:Ln:171:PHE:HE2	40:Lv:175:GLN:HE21	1.59	0.51
39:Lt:82:SER:OG	47:L5:50:ARG:N	2.44	0.51
49:L7:72:PRO:HB2	49:L7:75:ARG:HB2	1.92	0.51
17:LU:94:ARG:O	36:Lq:126:ILE:HD13	2.11	0.51
18:LV:197:LYS:O	18:LV:201:GLN:HG2	2.11	0.51
24:Ld:121:PRO:HG3	48:L6:48:TRP:CH2	2.45	0.51
32:Lm:88:PRO:HB3	32:Lm:125:ILE:HD11	1.92	0.51
43:Ly:94:LYS:HE2	43:Ly:102:MET:HE3	1.92	0.51
45:L3:17:ARG:HH11	45:L3:17:ARG:HG3	1.76	0.51
52:Sf:92:MET:CE	52:Sf:276:ARG:HE	2.24	0.51
1:L1:181:G:H2'	1:L1:1023:A:N7	2.26	0.51
1:L1:501:U:C2	1:L1:503:G:H4'	2.46	0.51
2:L2:1611:G:H2'	2:L2:1612:C:H6	1.76	0.51
20:LX:76:VAL:HA	20:LX:88:VAL:HA	1.92	0.51
21:La:119:ARG:O	31:Ll:50:LYS:HE3	2.10	0.51
1:L1:725:A:OP1	30:Lk:173:ARG:NH1	2.44	0.51
1:L1:998:A:H2'	1:L1:999:A:C8	2.46	0.51
1:L1:1058:C:H2'	1:L1:1059:U:H6	1.76	0.51
1:L1:1141:G:H2'	1:L1:1142:U:C6	2.45	0.51
6:Li:115:LYS:NZ	6:Li:117:SER:HB3	2.26	0.51
16:LT:122:ARG:HE	16:LT:142:PHE:HD2	1.58	0.51
28:Li:124:ARG:HG3	28:Li:148:VAL:HG23	1.92	0.51
35:Lp:41:ASP:OD1	35:Lp:46:ASN:ND2	2.33	0.51
36:Lq:35:ARG:HG3	48:L6:101:TRP:HB2	1.92	0.51
47:L5:52:TYR:HE2	47:L5:71:PRO:HG3	1.76	0.51
47:L5:56:LEU:HD22	47:L5:66:ILE:HD13	1.92	0.51
52:Sf:152:GLN:NE2	52:Sf:179:GLN:HG2	2.26	0.51
55:w:114:ASP:O	55:w:117:GLU:HG3	2.10	0.51
1:L1:386:G:H2'	1:L1:387:C:H6	1.75	0.50
1:L1:1004:U:H2'	1:L1:1005:G:O4'	2.10	0.50
17:LU:170:ILE:HD13	17:LU:185:ILE:HG12	1.93	0.50
31:Ll:185:MET:CE	49:L7:189:ARG:HG3	2.41	0.50
31:Ll:186:PRO:HB2	31:Ll:188:TYR:CE1	2.46	0.50
37:Lr:203:LEU:HD13	37:Lr:211:THR:HG21	1.93	0.50
40:Lv:106:TYR:OH	40:Lv:174:ILE:O	2.29	0.50
1:L1:359:A:O2'	1:L1:454:A:N6	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:676:U:H2'	1:L1:677:C:C6	2.46	0.50
5:LD:62:VAL:HG23	5:LD:82:LEU:HB2	1.93	0.50
7:LJ:108:ASP:HB3	7:LJ:112:MET:HE1	1.93	0.50
20:LX:140:ALA:HB3	20:LX:142:GLU:OE1	2.12	0.50
24:Ld:101:LYS:HE3	44:Lz:80:LEU:HD22	1.93	0.50
30:Lk:94:HIS:ND1	30:Lk:95:GLU:HG3	2.25	0.50
32:Lm:143:TRP:CD1	32:Lm:174:VAL:HG22	2.47	0.50
52:Sf:299:PHE:HZ	52:Sf:425:LEU:HD11	1.76	0.50
1:L1:197:A:N1	1:L1:349:G:O2'	2.41	0.50
1:L1:345:G:H5'	1:L1:346:C:C5	2.46	0.50
1:L1:993:C:H2'	1:L1:994:U:H6	1.76	0.50
1:L1:1398:G:OP2	1:L1:1398:G:N2	2.43	0.50
4:LC:292:HIS:ND1	4:LC:293:LYS:O	2.37	0.50
12:LP:142:GLY:O	21:La:38:SER:OG	2.27	0.50
31:Ll:257:PRO:HB3	31:Ll:268:LEU:HD21	1.93	0.50
33:Ln:129:ARG:HG3	33:Ln:130:LYS:N	2.26	0.50
38:Ls:267:PRO:HG2	38:Ls:270:ALA:HB2	1.94	0.50
45:L3:40:GLU:O	45:L3:44:SER:OG	2.28	0.50
52:Sf:119:PRO:HG3	52:Sf:394:TRP:CD2	2.47	0.50
1:L1:162:A:H5'	36:Lq:114:ARG:NH1	2.26	0.50
1:L1:166:A:C8	35:Lp:134:LYS:HE2	2.46	0.50
1:L1:300:G:H2'	1:L1:301:A:O4'	2.12	0.50
11:LO:280:LYS:HD3	41:Lw:45:TYR:HE2	1.77	0.50
17:LU:68:ASP:OD1	17:LU:71:GLU:HB3	2.11	0.50
37:Lr:148:MET:HE1	37:Lr:307:PHE:HB2	1.94	0.50
40:Lv:122:GLU:HB2	40:Lv:158:GLN:CB	2.41	0.50
1:L1:672:U:H5''	19:LW:78:LYS:HB2	1.93	0.50
1:L1:719:C:H5''	30:Lk:301:PRO:HB3	1.92	0.50
1:L1:853:C:H4'	1:L1:854:A:OP1	2.11	0.50
11:LO:182:ARG:O	11:LO:186:ILE:HG12	2.10	0.50
11:LO:225:ASP:HB3	11:LO:228:LYS:HB2	1.94	0.50
17:LU:160:VAL:HA	17:LU:193:LEU:HD23	1.92	0.50
28:Li:168:ARG:NH1	28:Li:170:ASN:OD1	2.45	0.50
36:Lq:37:GLY:O	36:Lq:44:ARG:NH1	2.31	0.50
40:Lv:95:LEU:HD13	40:Lv:184:LEU:HD13	1.93	0.50
1:L1:1280:U:H2'	1:L1:1281:A:C8	2.46	0.50
18:LV:82:TYR:HD2	18:LV:87:MET:HE2	1.76	0.50
26:Lg:20:MET:HE1	26:Lg:43:LEU:HD12	1.92	0.50
33:Ln:177:HIS:ND1	33:Ln:179:THR:O	2.44	0.50
41:Lw:107:MET:CE	41:Lw:148:ARG:HE	2.25	0.50
52:Sf:119:PRO:HG2	52:Sf:250:PHE:HD2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:496:C:H2'	1:L1:497:A:C8	2.46	0.50
1:L1:738:U:H2'	1:L1:739:A:C8	2.44	0.50
10:LN:139:ALA:HB1	53:u:190:LEU:CD1	2.42	0.50
17:LU:144:LEU:HB2	35:Lp:58:ILE:HB	1.94	0.50
53:u:100:LEU:HD13	53:u:103:GLN:NE2	2.24	0.50
54:v:51:ARG:HA	59:v:101:PNS:S44	2.51	0.50
1:L1:314:A:H8	1:L1:317:G:N2	2.09	0.50
1:L1:788:A:O2'	4:LC:215:PHE:O	2.25	0.50
1:L1:1133:A:H2'	1:L1:1134:A:O4'	2.12	0.50
1:L1:1177:C:C5	1:L1:1224:U:H2'	2.47	0.50
5:LD:113:LYS:HD2	5:LD:157:GLY:HA2	1.94	0.50
14:LR:41:GLU:HG2	31:Ll:337:MET:SD	2.51	0.50
14:LR:51:ASN:HD21	31:Ll:320:GLN:HE22	1.60	0.50
1:L1:120:A:OP1	27:Lh:82:ARG:NH1	2.44	0.50
1:L1:1448:U:H2'	1:L1:1449:C:H6	1.77	0.50
11:LO:17:ARG:NH2	42:Lx:115:SER:O	2.45	0.50
14:LR:51:ASN:HB3	14:LR:54:ASN:HB2	1.93	0.50
19:LW:28:LEU:HD12	23:Lu:67:PHE:HD2	1.77	0.50
22:Lb:17:ARG:HH11	22:Lb:17:ARG:HG3	1.77	0.50
30:Lk:105:TYR:CZ	30:Lk:262:ILE:HD12	2.47	0.50
32:Lm:183:VAL:HB	32:Lm:297:PHE:HE1	1.77	0.50
33:Ln:171:PHE:HE2	40:Lv:175:GLN:NE2	2.09	0.50
38:Ls:186:VAL:HG21	38:Ls:239:PRO:HB3	1.93	0.50
42:Lx:74:VAL:HA	42:Lx:77:VAL:HG12	1.94	0.50
55:w:79:ILE:O	55:w:83:VAL:HG23	2.12	0.50
1:L1:508:A:H8	1:L1:508:A:OP1	1.95	0.49
1:L1:552:U:H2'	1:L1:553:A:N3	2.27	0.49
1:L1:1447:C:H2'	1:L1:1448:U:H6	1.77	0.49
7:LJ:105:SER:HB2	45:L3:40:GLU:HG2	1.93	0.49
10:LN:128:ARG:O	10:LN:131:GLU:HB2	2.12	0.49
15:LS:280:ALA:O	15:LS:284:LYS:HG2	2.12	0.49
18:LV:157:ARG:N	18:LV:165:GLY:O	2.42	0.49
20:LX:121:LYS:HD2	20:LX:130:PRO:HB2	1.94	0.49
23:Lu:71:PRO:HA	23:Lu:74:TRP:CE2	2.47	0.49
23:Lu:169:ARG:NH2	30:Lk:65:HIS:HD2	2.10	0.49
36:Lq:26:LEU:HD22	36:Lq:105:ALA:HA	1.94	0.49
45:L3:44:SER:HA	45:L3:47:LEU:HD22	1.92	0.49
49:L7:115:VAL:O	49:L7:119:ILE:HG12	2.11	0.49
52:Sf:237:PRO:HB3	52:Sf:300:HIS:CE1	2.47	0.49
1:L1:305:U:H2'	1:L1:306:U:H6	1.77	0.49
1:L1:1167:A:H2'	1:L1:1168:A:N3	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LK:20:ILE:HD11	8:LK:42:ARG:HG2	1.94	0.49
53:u:192:LYS:O	53:u:196:LEU:HB2	2.12	0.49
54:v:17:LEU:HD13	55:w:120:MET:SD	2.52	0.49
1:L1:663:G:H2'	1:L1:664:C:C6	2.46	0.49
1:L1:992:A:H2'	1:L1:993:C:H6	1.76	0.49
1:L1:1384:G:H2'	1:L1:1385:U:C6	2.47	0.49
14:LR:80:LEU:HB2	14:LR:143:MET:SD	2.53	0.49
14:LR:178:TYR:C	31:Ll:346:ARG:HH12	2.20	0.49
30:Lk:83:LYS:HD2	30:Lk:88:TYR:HD1	1.77	0.49
30:Lk:289:HIS:ND1	30:Lk:290:THR:HG23	2.28	0.49
40:Lv:121:VAL:HG22	40:Lv:159:ILE:HG22	1.93	0.49
52:Sf:93:VAL:HB	52:Sf:233:ILE:HG12	1.94	0.49
4:LC:269:TYR:HB3	4:LC:304:LEU:HD11	1.93	0.49
15:LS:183:LEU:O	15:LS:241:LYS:HE2	2.12	0.49
23:Lu:158:THR:HG23	23:Lu:160:GLN:H	1.76	0.49
40:Lv:131:THR:HG22	40:Lv:151:THR:HG22	1.94	0.49
49:L7:110:TRP:CD1	49:L7:110:TRP:H	2.29	0.49
53:u:97:MET:CE	53:u:125:VAL:HG21	2.42	0.49
8:LK:52:GLU:HB3	8:LK:56:ARG:HE	1.78	0.49
9:LM:39:LEU:HD11	9:LM:125:LEU:HB2	1.94	0.49
12:LP:160:VAL:HG12	12:LP:161:VAL:HG13	1.95	0.49
14:LR:40:ASN:HD21	31:Ll:292:GLN:HA	1.77	0.49
22:Lb:150:LYS:HD3	22:Lb:159:MET:HG3	1.93	0.49
29:Lj:90:VAL:HB	29:Lj:100:GLN:HB2	1.93	0.49
30:Lk:244:GLU:O	30:Lk:248:THR:HG23	2.12	0.49
31:Ll:231:GLU:OE2	31:Ll:300:THR:HG23	2.12	0.49
45:L3:17:ARG:NH2	45:L3:19:GLN:HB2	2.21	0.49
1:L1:441:C:H2'	1:L1:442:A:C8	2.46	0.49
2:L2:1638:U:H2'	2:L2:1639:U:C6	2.48	0.49
5:LD:160:SER:HB2	43:Ly:80:LEU:HD22	1.95	0.49
21:La:61:VAL:HG21	21:La:67:ILE:HD11	1.95	0.49
39:Lt:75:GLN:O	39:Lt:79:ILE:HG12	2.12	0.49
45:L3:82:THR:O	45:L3:86:MET:HG3	2.12	0.49
52:Sf:296:HIS:ND1	52:Sf:297:THR:OG1	2.35	0.49
54:v:16:LEU:HD21	54:v:62:LEU:HB2	1.95	0.49
1:L1:560:A:H61	1:L1:1280:U:H1'	1.78	0.49
22:Lb:226:LEU:HD12	23:Lu:155:LEU:HB3	1.94	0.49
39:Lt:265:LYS:HB2	39:Lt:266:PRO:HD3	1.95	0.49
50:L8:134:ASN:HA	50:L8:137:GLN:HG3	1.94	0.49
52:Sf:297:THR:HG23	52:Sf:358:GLN:HG3	1.95	0.49
53:u:168:LEU:HB2	53:u:179:LEU:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:129:U:H2'	1:L1:130:G:O4'	2.12	0.49
1:L1:283:A:OP1	4:LC:232:GLY:HA2	2.13	0.49
1:L1:456:U:H5'	17:LU:175:ARG:NH2	2.27	0.49
1:L1:844:C:H2'	1:L1:845:U:H6	1.77	0.49
17:LU:96:PHE:HB3	36:Lq:126:ILE:HD12	1.94	0.49
19:LW:25:PHE:CE1	23:Lu:139:MET:HE1	2.48	0.49
19:LW:49:THR:HG22	19:LW:51:VAL:H	1.78	0.49
30:Lk:140:VAL:HB	30:Lk:416:ALA:HB2	1.93	0.49
33:Ln:126:GLN:HG3	33:Ln:129:ARG:CZ	2.42	0.49
54:v:12:LEU:HD11	54:v:58:GLY:HA3	1.95	0.49
55:w:148:ILE:HA	55:w:151:LYS:HE3	1.95	0.49
1:L1:583:U:H2'	1:L1:584:C:H6	1.78	0.49
1:L1:1477:G:H5''	4:LC:210:THR:HG21	1.94	0.49
3:LB:285:LYS:HB2	3:LB:287:ARG:NH2	2.27	0.49
5:LD:219:VAL:HB	5:LD:261:LEU:HD23	1.94	0.49
8:LK:182:ASP:O	8:LK:186:GLN:HG2	2.13	0.49
13:LQ:38:ARG:HB2	13:LQ:85:LEU:HD11	1.95	0.49
30:Lk:235:PRO:HG3	30:Lk:287:TYR:CE1	2.48	0.49
33:Ln:101:ARG:HH21	39:Lt:82:SER:C	2.20	0.49
43:Ly:68:LYS:HZ2	50:L8:31:PRO:C	2.21	0.49
43:Ly:83:TRP:CH2	43:Ly:85:GLY:HA3	2.48	0.49
44:Lz:27:TRP:O	44:Lz:31:GLN:HG2	2.13	0.49
49:L7:156:ASP:HA	49:L7:159:THR:HG22	1.94	0.49
52:Sf:164:HIS:HB2	52:Sf:167:GLU:OE1	2.12	0.49
53:u:124:PHE:HZ	53:u:190:LEU:HD11	1.78	0.49
7:LJ:93:ASN:OD1	7:LJ:156:SER:N	2.45	0.49
19:LW:129:MET:HA	19:LW:129:MET:HE2	1.94	0.49
24:Ld:78:ARG:HD2	24:Ld:116:LEU:HD21	1.94	0.49
27:Lh:58:ILE:HG22	34:Lo:30:PHE:CE1	2.48	0.49
31:Ll:59:ARG:O	31:Ll:62:GLU:HG3	2.13	0.49
31:Ll:186:PRO:HD3	49:L7:191:LYS:HD3	1.94	0.49
33:Ln:142:ALA:HB2	39:Lt:274:ARG:HG2	1.94	0.49
46:L4:83:ASP:N	46:L4:83:ASP:OD1	2.44	0.49
49:L7:50:PRO:HA	49:L7:53:GLN:HE22	1.77	0.49
1:L1:1448:U:H2'	1:L1:1449:C:C6	2.48	0.48
5:LD:91:PRO:HB3	11:LO:16:LEU:HD11	1.94	0.48
8:LK:141:VAL:O	8:LK:145:ILE:HG12	2.13	0.48
12:LP:228:LYS:HD2	24:Ld:78:ARG:HH21	1.78	0.48
31:Ll:183:ASP:C	31:Ll:184:LEU:HD12	2.38	0.48
32:Lm:185:LEU:HD12	32:Lm:295:ARG:HH11	1.77	0.48
38:Ls:146:ILE:O	38:Ls:150:LEU:HG	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lv:77:VAL:HG12	40:Lv:80:ILE:HB	1.94	0.48
41:Lw:46:GLN:HA	41:Lw:49:GLU:CD	2.37	0.48
1:L1:543:A:H2'	1:L1:544:A:H5'	1.95	0.48
1:L1:676:U:OP1	52:Sf:223:ARG:NH2	2.47	0.48
1:L1:1364:U:H2'	1:L1:1365:C:C6	2.48	0.48
3:LB:257:ILE:O	3:LB:262:ARG:HD2	2.13	0.48
8:LK:44:VAL:HA	8:LK:78:PHE:CZ	2.47	0.48
8:LK:60:ILE:HG12	8:LK:61:LYS:H	1.77	0.48
22:Lb:107:PRO:HG2	22:Lb:109:LEU:HD21	1.94	0.48
22:Lb:227:PHE:CD2	34:Lo:119:PHE:HB2	2.48	0.48
31:Ll:173:LEU:HD13	31:Ll:272:LEU:HD22	1.95	0.48
33:Ln:146:ALA:HB1	39:Lt:209:PRO:HB2	1.95	0.48
50:L8:40:PRO:HG3	50:L8:51:GLN:HB3	1.96	0.48
52:Sf:142:LEU:HD21	52:Sf:187:LEU:HD22	1.94	0.48
54:v:3:PRO:CA	54:v:51:ARG:HG2	2.36	0.48
55:w:83:VAL:HG22	55:w:122:MET:CE	2.43	0.48
1:L1:29:C:N4	23:Lu:198:ARG:O	2.45	0.48
1:L1:493:A:N3	1:L1:551:C:N4	2.60	0.48
1:L1:1311:A:O2'	12:LP:137:GLY:HA2	2.13	0.48
30:Lk:173:ARG:HH21	30:Lk:348:ASP:HB2	1.78	0.48
33:Ln:162:ILE:HG22	33:Ln:162:ILE:O	2.13	0.48
52:Sf:363:ASP:OD1	52:Sf:366:TYR:N	2.40	0.48
1:L1:423:U:O2	1:L1:596:U:O2'	2.31	0.48
1:L1:923:G:N2	1:L1:962:A:OP2	2.36	0.48
1:L1:1239:G:OP1	26:Lg:63:ARG:NH1	2.34	0.48
2:L2:1644:G:N7	14:LR:87:HIS:HE1	2.11	0.48
5:LD:113:LYS:HG3	5:LD:157:GLY:H	1.78	0.48
8:LK:74:PRO:HA	8:LK:76:ARG:HH22	1.78	0.48
22:Lb:36:ARG:NH1	22:Lb:37:THR:O	2.45	0.48
41:Lw:45:TYR:CD1	41:Lw:48:VAL:HB	2.48	0.48
49:L7:77:THR:HG22	49:L7:102:ARG:O	2.13	0.48
1:L1:79:C:OP2	1:L1:1229:C:O2'	2.24	0.48
1:L1:258:A:H2'	1:L1:259:A:C8	2.49	0.48
1:L1:258:A:H2'	1:L1:259:A:H8	1.78	0.48
4:LC:322:ASP:OD1	4:LC:322:ASP:N	2.45	0.48
15:LS:209:GLN:O	15:LS:213:GLN:NE2	2.46	0.48
23:Lu:218:ARG:NH2	43:Ly:105:ASP:OD2	2.46	0.48
31:Ll:217:LEU:HD12	31:Ll:235:TRP:O	2.14	0.48
36:Lq:30:SER:HB2	36:Lq:76:VAL:HB	1.96	0.48
38:Ls:196:GLN:HE21	38:Ls:198:ARG:HD3	1.77	0.48
39:Lt:201:GLU:H	39:Lt:241:GLY:HA3	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lv:129:THR:HA	40:Lv:152:THR:O	2.14	0.48
53:u:110:CYS:HA	54:v:26:THR:HG23	1.96	0.48
55:w:83:VAL:HG22	55:w:122:MET:HE3	1.95	0.48
1:L1:359:A:H1'	1:L1:360:U:O2	2.13	0.48
1:L1:472:A:O2'	1:L1:592:C:OP1	2.24	0.48
31:Ll:237:LEU:HG	31:Ll:240:ILE:HD11	1.95	0.48
40:Lv:92:ASN:OD1	40:Lv:158:GLN:HG3	2.13	0.48
44:Lz:76:ARG:O	44:Lz:80:LEU:HG	2.13	0.48
52:Sf:66:TRP:O	52:Sf:69:THR:OG1	2.22	0.48
53:u:91:LYS:HB3	53:u:92:PHE:H	1.50	0.48
1:L1:1254:U:H2'	1:L1:1255:U:C6	2.49	0.48
7:LJ:160:LYS:HA	7:LJ:160:LYS:HD2	1.64	0.48
9:LM:67:PHE:HD2	9:LM:72:TRP:CE2	2.31	0.48
11:LO:83:PHE:CG	28:Li:115:LEU:HB2	2.49	0.48
31:Ll:213:LEU:HB3	31:Ll:275:GLN:HB2	1.95	0.48
33:Ln:171:PHE:CE2	40:Lv:175:GLN:NE2	2.80	0.48
39:Lt:151:ARG:NH1	39:Lt:254:TRP:O	2.46	0.48
43:Ly:68:LYS:HG2	43:Ly:72:GLU:OE2	2.13	0.48
45:L3:63:CYS:SG	45:L3:64:VAL:N	2.87	0.48
52:Sf:63:ILE:HA	52:Sf:66:TRP:CD1	2.49	0.48
1:L1:429:U:H2'	1:L1:430:C:H6	1.77	0.48
2:L2:1622:A:H2'	2:L2:1623:G:H8	1.78	0.48
7:LJ:119:HIS:HB3	7:LJ:160:LYS:HG2	1.96	0.48
18:LV:135:GLU:OE2	38:Ls:279:THR:N	2.33	0.48
23:Lu:112:LEU:HD13	23:Lu:132:LEU:HA	1.94	0.48
23:Lu:202:LEU:HB3	23:Lu:203:PRO:HD2	1.96	0.48
32:Lm:69:HIS:HB2	32:Lm:79:PHE:HE2	1.79	0.48
53:u:150:LYS:CG	53:u:151:CYS:H	2.27	0.48
1:L1:215:A:H5''	1:L1:216:G:OP2	2.14	0.48
1:L1:994:U:H2'	1:L1:995:U:H6	1.78	0.48
1:L1:1058:C:H2'	1:L1:1059:U:C6	2.49	0.48
1:L1:1330:A:H2'	1:L1:1331:G:C8	2.49	0.48
7:LJ:44:ARG:NH1	12:LP:234:ASP:OD2	2.32	0.48
14:LR:137:GLU:HB2	31:Ll:188:TYR:CD2	2.46	0.48
14:LR:137:GLU:HA	49:L7:188:LEU:HD11	1.96	0.48
15:LS:137:CYS:HA	15:LS:151:LEU:HD23	1.96	0.48
31:Ll:187:VAL:O	31:Ll:317:SER:OG	2.32	0.48
31:Ll:190:GLY:N	31:Ll:318:PHE:O	2.46	0.48
33:Ln:159:ALA:O	33:Ln:163:LYS:NZ	2.42	0.48
38:Ls:112:MET:SD	38:Ls:113:LYS:N	2.86	0.48
40:Lv:183:ARG:HA	40:Lv:183:ARG:CZ	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:L4:64:ASP:O	46:L4:68:LEU:HG	2.13	0.48
48:L6:10:GLY:HA3	51:SR:167:PRO:HG3	1.96	0.48
49:L7:149:ASP:O	49:L7:153:LYS:HG3	2.13	0.48
53:u:180:MET:HG3	53:u:185:ARG:NH2	2.29	0.48
1:L1:241:C:H2'	1:L1:242:A:H8	1.79	0.48
1:L1:321:A:H5''	1:L1:322:C:OP1	2.14	0.48
1:L1:499:A:H1'	1:L1:522:A:C2	2.49	0.48
1:L1:892:U:O2'	3:LB:284:ARG:O	2.21	0.48
1:L1:928:A:H1'	1:L1:957:G:N2	2.29	0.48
6:LI:107:VAL:HG23	6:LI:108:ARG:H	1.79	0.48
8:LK:165:ALA:HA	8:LK:168:GLN:HG2	1.95	0.48
20:LX:125:PRO:HD2	20:LX:152:ARG:HD2	1.95	0.48
23:Lu:130:GLU:HG2	23:Lu:131:ARG:N	2.29	0.48
24:Ld:71:ARG:HD3	24:Ld:86:ILE:HD12	1.96	0.48
26:Lg:17:LEU:HD12	26:Lg:32:THR:O	2.14	0.48
31:Ll:108:GLN:HA	31:Ll:111:GLN:OE1	2.13	0.48
32:Lm:156:ARG:HH12	32:Lm:259:ASP:HB2	1.79	0.48
39:Lt:184:LEU:HB3	39:Lt:234:PHE:CZ	2.48	0.48
46:L4:100:ASN:OD1	46:L4:101:LEU:N	2.46	0.48
49:L7:119:ILE:HD11	49:L7:161:ALA:HB2	1.96	0.48
52:Sf:316:CYS:HB3	52:Sf:319:GLN:HB2	1.96	0.48
53:u:93:ASP:OD2	53:u:94:ILE:HG22	2.13	0.48
1:L1:67:A:N6	1:L1:90:G:H1'	2.28	0.47
1:L1:755:A:OP1	52:Sf:221:HIS:ND1	2.47	0.47
2:L2:1638:U:H2'	2:L2:1639:U:H6	1.78	0.47
2:L2:1664:G:H2'	2:L2:1665:C:H6	1.79	0.47
7:LJ:62:PRO:HA	7:LJ:65:LEU:HB2	1.96	0.47
14:LR:121:VAL:HG11	14:LR:155:ASP:OD2	2.14	0.47
18:LV:136:PHE:CE2	32:Lm:93:MET:HE3	2.49	0.47
19:LW:28:LEU:H	23:Lu:114:THR:HG22	1.79	0.47
19:LW:61:TYR:CZ	23:Lu:107:LYS:HG2	2.49	0.47
30:Lk:309:LEU:O	30:Lk:313:MET:HG3	2.12	0.47
32:Lm:198:ASN:HD22	35:Lp:92:LEU:HD11	1.79	0.47
41:Lw:37:ARG:HE	41:Lw:38:PHE:N	2.11	0.47
46:L4:119:ARG:HD2	46:L4:122:ARG:HH21	1.79	0.47
1:L1:575:A:H4'	1:L1:576:A:OP1	2.13	0.47
6:LI:107:VAL:HG23	6:LI:108:ARG:N	2.30	0.47
12:LP:228:LYS:HD2	24:Ld:78:ARG:NH2	2.28	0.47
20:LX:170:TRP:HH2	23:Lu:81:SER:O	1.96	0.47
28:Li:143:ARG:O	28:Li:146:GLU:HB3	2.14	0.47
40:Lv:125:TYR:C	40:Lv:155:ARG:HH21	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:L5:72:ARG:NH1	47:L5:75:LEU:HD23	2.29	0.47
54:v:21:ARG:HH21	54:v:28:ARG:HH11	1.61	0.47
1:L1:201:A:H2'	1:L1:202:U:C6	2.50	0.47
1:L1:523:U:H2'	1:L1:525:A:H62	1.79	0.47
19:LW:133:GLU:OE2	19:LW:137:ARG:NH1	2.47	0.47
20:LX:197:GLU:O	20:LX:200:GLU:HG3	2.14	0.47
32:Lm:143:TRP:CZ3	32:Lm:179:PHE:HD2	2.32	0.47
50:L8:123:GLU:O	50:L8:127:LYS:HG2	2.14	0.47
52:Sf:266:CYS:SG	52:Sf:270:LYS:HG2	2.54	0.47
53:u:180:MET:SD	53:u:185:ARG:N	2.87	0.47
55:w:104:PHE:HB3	55:w:110:LEU:HB2	1.96	0.47
1:L1:136:U:H1'	1:L1:137:U:OP2	2.14	0.47
1:L1:745:C:H3'	52:Sf:165:ARG:HH21	1.80	0.47
3:LB:115:GLU:OE2	3:LB:147:ARG:NH2	2.47	0.47
4:LC:210:THR:HG22	4:LC:290:PRO:HB3	1.97	0.47
9:LM:62:THR:OG1	9:LM:101:VAL:HG12	2.14	0.47
13:LQ:85:LEU:O	13:LQ:89:LEU:N	2.37	0.47
21:La:147:MET:HE2	21:La:147:MET:HA	1.97	0.47
22:Lb:172:GLN:OE1	22:Lb:188:TYR:HD2	1.96	0.47
24:Ld:99:VAL:HG13	44:Lz:73:PHE:CZ	2.49	0.47
30:Lk:36:ARG:HG2	30:Lk:39:ARG:HH21	1.79	0.47
1:L1:514:A:C4	1:L1:515:G:C8	3.03	0.47
1:L1:652:C:OP1	25:Lf:139:ARG:NH2	2.44	0.47
6:LI:103:GLU:HG2	6:LI:104:ASN:OD1	2.14	0.47
7:LJ:166:ARG:O	7:LJ:170:THR:HG23	2.15	0.47
14:LR:159:ARG:HH22	31:Ll:126:ARG:HB3	1.78	0.47
14:LR:170:VAL:HG12	14:LR:172:ARG:H	1.78	0.47
20:LX:58:CYS:C	20:LX:159:PHE:HZ	2.23	0.47
23:Lu:153:LEU:HD11	23:Lu:157:GLN:NE2	2.30	0.47
40:Lv:149:VAL:HG23	47:L5:69:ARG:HH22	1.79	0.47
41:Lw:44:GLU:N	41:Lw:44:GLU:OE1	2.47	0.47
46:L4:131:ARG:O	46:L4:134:LYS:HB2	2.15	0.47
47:L5:52:TYR:CD2	47:L5:71:PRO:HA	2.41	0.47
1:L1:247:A:OP1	27:Lh:63:LYS:HE3	2.14	0.47
1:L1:640:G:O2'	1:L1:1005:G:O6	2.26	0.47
1:L1:1325:G:O2'	1:L1:1371:U:O2'	2.32	0.47
4:LC:68:GLU:OE1	32:Lm:315:LYS:NZ	2.46	0.47
22:Lb:239:GLN:O	22:Lb:243:LEU:HD23	2.15	0.47
25:Lf:133:GLU:O	25:Lf:137:ILE:HG12	2.14	0.47
25:Lf:177:ARG:NH2	25:Lf:179:ARG:HD3	2.30	0.47
28:Li:121:LEU:HD23	28:Li:149:PHE:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lq:42:GLY:HA3	36:Lq:92:LYS:O	2.15	0.47
37:Lr:72:ILE:HG23	37:Lr:88:LEU:HD23	1.96	0.47
38:Ls:196:GLN:HE21	38:Ls:198:ARG:NH1	2.12	0.47
39:Lt:122:ASP:C	39:Lt:126:GLN:HE22	2.23	0.47
53:u:108:ASP:OD1	53:u:109:ILE:N	2.48	0.47
55:w:134:ASP:O	55:w:138:LEU:HG	2.14	0.47
1:L1:608:A:P	43:Ly:51:ARG:HH12	2.37	0.47
1:L1:709:C:H4'	34:Lo:44:LEU:HD23	1.97	0.47
1:L1:1021:U:H2'	1:L1:1022:G:C8	2.50	0.47
3:LB:155:GLU:HA	3:LB:248:SER:HA	1.96	0.47
4:LC:187:ILE:HG22	4:LC:191:THR:HG21	1.97	0.47
11:LO:280:LYS:HD3	41:Lw:45:TYR:CE2	2.49	0.47
26:Lg:64:SER:C	26:Lg:65:LEU:HD22	2.40	0.47
30:Lk:148:GLU:OE1	30:Lk:149:ASN:ND2	2.47	0.47
30:Lk:310:ARG:HA	30:Lk:313:MET:HE2	1.95	0.47
31:Ll:157:LEU:HB3	31:Ll:161:LEU:HD12	1.95	0.47
31:Ll:344:PHE:HE2	31:Ll:346:ARG:HE	1.61	0.47
33:Ln:125:LYS:O	33:Ln:125:LYS:HD3	2.15	0.47
36:Lq:117:LYS:O	36:Lq:119:PHE:N	2.38	0.47
37:Lr:228:LEU:HB2	37:Lr:307:PHE:CD1	2.49	0.47
39:Lt:178:TRP:CH2	39:Lt:180:PRO:HA	2.50	0.47
47:L5:74:MET:HA	47:L5:74:MET:HE3	1.95	0.47
51:SR:87:LEU:O	51:SR:91:GLN:HG3	2.15	0.47
52:Sf:85:LYS:HE3	52:Sf:86:MET:HE2	1.97	0.47
53:u:170:VAL:HG12	53:u:177:ILE:HB	1.97	0.47
53:u:183:GLU:HA	53:u:186:GLU:CD	2.39	0.47
1:L1:431:C:H2'	1:L1:432:A:H8	1.80	0.47
2:L2:1628:C:C2	2:L2:1629:A:C8	3.02	0.47
2:L2:1663:C:H2'	2:L2:1664:G:H8	1.80	0.47
23:Lu:169:ARG:HH21	30:Lk:65:HIS:HD2	1.63	0.47
31:Ll:185:MET:HE2	31:Ll:185:MET:HA	1.96	0.47
35:Lp:114:LYS:HA	35:Lp:114:LYS:HD3	1.70	0.47
44:Lz:34:ALA:HB2	44:Lz:40:TYR:CE2	2.50	0.47
52:Sf:119:PRO:HG2	52:Sf:250:PHE:CD2	2.50	0.47
1:L1:35:A:C8	34:Lo:39:LYS:HD2	2.50	0.47
1:L1:378:U:H2'	1:L1:379:U:C6	2.50	0.47
4:LC:199:ARG:HA	4:LC:199:ARG:HD3	1.73	0.47
8:LK:31:PRO:O	8:LK:36:GLY:HA3	2.15	0.47
17:LU:82:LYS:O	17:LU:85:GLU:HG3	2.15	0.47
20:LX:59:GLY:HA3	20:LX:159:PHE:CZ	2.50	0.47
32:Lm:143:TRP:NE1	32:Lm:174:VAL:HG13	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:L3:22:PRO:HG3	45:L3:55:VAL:HG23	1.96	0.47
1:L1:1040:C:O2'	1:L1:1550:A:N1	2.44	0.47
1:L1:1057:C:H2'	1:L1:1058:C:C6	2.49	0.47
1:L1:1070:A:H2'	1:L1:1071:A:H8	1.79	0.47
1:L1:1219:C:H2'	1:L1:1220:U:H6	1.79	0.47
2:L2:1603:A:H2'	2:L2:1604:G:C8	2.50	0.47
5:LD:186:ASP:OD1	11:LO:21:ARG:NH2	2.48	0.47
7:LJ:96:ILE:HA	7:LJ:155:VAL:HG12	1.96	0.47
8:LK:74:PRO:HA	8:LK:76:ARG:NH2	2.30	0.47
9:LM:168:ARG:HH21	51:SR:58:LYS:HD2	1.79	0.47
12:LP:191:SER:N	12:LP:194:THR:OG1	2.34	0.47
15:LS:245:PHE:HA	15:LS:248:CYS:SG	2.55	0.47
25:Lf:179:ARG:HH21	25:Lf:182:PRO:HD3	1.80	0.47
31:Ll:233:LEU:HD12	31:Ll:298:PHE:CG	2.50	0.47
54:v:57:LYS:HA	54:v:60:VAL:HG22	1.96	0.47
1:L1:9:U:O2'	1:L1:10:A:O5'	2.30	0.46
1:L1:241:C:H2'	1:L1:242:A:C8	2.50	0.46
1:L1:500:G:C5	1:L1:501:U:H5	2.33	0.46
1:L1:833:A:H5'	1:L1:1425:G:H4'	1.97	0.46
1:L1:1141:G:H2'	1:L1:1142:U:H6	1.80	0.46
7:LJ:86:ILE:HG22	7:LJ:126:PHE:CD2	2.49	0.46
19:LW:133:GLU:OE2	19:LW:137:ARG:CZ	2.63	0.46
32:Lm:180:CYS:HA	32:Lm:297:PHE:O	2.15	0.46
36:Lq:103:LYS:O	36:Lq:107:GLN:HG2	2.15	0.46
39:Lt:119:ASP:N	39:Lt:119:ASP:OD1	2.47	0.46
39:Lt:173:LEU:HD12	39:Lt:233:PHE:CE1	2.50	0.46
45:L3:11:ARG:HA	45:L3:46:ASN:ND2	2.30	0.46
51:SR:89:LEU:HD23	51:SR:119:VAL:HA	1.97	0.46
52:Sf:174:LEU:HB3	52:Sf:175:PRO:HD3	1.97	0.46
1:L1:382:A:H5''	41:Lw:150:LYS:HE3	1.97	0.46
1:L1:993:C:H2'	1:L1:994:U:C6	2.49	0.46
2:L2:1603:A:H2'	2:L2:1604:G:H8	1.80	0.46
13:LQ:18:MET:CE	13:LQ:48:ARG:HG2	2.45	0.46
20:LX:101:THR:HG23	20:LX:102:MET:N	2.30	0.46
20:LX:161:ARG:HG3	20:LX:162:ALA:N	2.30	0.46
33:Ln:87:ASP:OD2	40:Lv:153:HIS:HE1	1.97	0.46
40:Lv:95:LEU:HD21	40:Lv:106:TYR:CD2	2.49	0.46
54:v:16:LEU:HD22	54:v:62:LEU:HD13	1.96	0.46
55:w:79:ILE:HG23	55:w:126:PHE:HE2	1.80	0.46
1:L1:126:A:O2'	1:L1:127:G:H5'	2.15	0.46
1:L1:1087:A:H5'	6:LI:122:ARG:NH2	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:1459:A:H2'	1:L1:1460:A:C8	2.50	0.46
1:L1:1483:U:C2	1:L1:1484:U:C5	3.03	0.46
2:L2:1665:C:H2'	2:L2:1666:U:C6	2.50	0.46
20:LX:54:TRP:CD1	20:LX:81:ARG:HD3	2.50	0.46
33:Ln:177:HIS:HD2	47:L5:64:ILE:HD12	1.80	0.46
36:Lq:39:SER:HB2	36:Lq:90:HIS:CD2	2.50	0.46
36:Lq:66:ASN:OD1	42:Lx:155:THR:OG1	2.31	0.46
39:Lt:253:VAL:HG21	39:Lt:263:TYR:CZ	2.51	0.46
45:L3:11:ARG:HA	45:L3:46:ASN:HD22	1.79	0.46
1:L1:247:A:N1	1:L1:327:C:H1'	2.31	0.46
1:L1:1045:A:O2'	4:LC:248:ILE:O	2.31	0.46
8:LK:119:GLU:HG2	46:L4:84:VAL:HG21	1.97	0.46
11:LO:105:ILE:HG23	11:LO:112:PRO:HG3	1.98	0.46
15:LS:106:LEU:O	15:LS:108:ILE:HG12	2.15	0.46
20:LX:36:PRO:HD2	20:LX:39:ILE:HB	1.96	0.46
22:Lb:80:TRP:CE2	22:Lb:109:LEU:HD11	2.50	0.46
31:Ll:183:ASP:OD1	31:Ll:184:LEU:N	2.48	0.46
31:Ll:236:LEU:O	31:Ll:238:THR:HG23	2.15	0.46
37:Lr:170:ALA:HB1	37:Lr:175:VAL:HB	1.97	0.46
40:Lv:96:THR:CG2	40:Lv:183:ARG:HB2	2.45	0.46
40:Lv:125:TYR:HE1	40:Lv:158:GLN:OE1	1.99	0.46
52:Sf:253:LEU:HD21	52:Sf:389:ARG:CZ	2.45	0.46
1:L1:931:A:O2'	1:L1:932:U:H5''	2.15	0.46
15:LS:79:GLU:OE1	15:LS:140:ARG:NH2	2.49	0.46
15:LS:103:ARG:O	15:LS:106:LEU:C	2.58	0.46
18:LV:62:GLN:HE22	18:LV:68:ARG:HA	1.81	0.46
33:Ln:124:TYR:O	33:Ln:128:GLU:HG2	2.15	0.46
36:Lq:44:ARG:HB3	48:L6:101:TRP:NE1	2.29	0.46
52:Sf:62:ARG:HG2	52:Sf:65:ARG:HH21	1.80	0.46
52:Sf:369:PHE:HZ	52:Sf:417:VAL:HG13	1.81	0.46
1:L1:124:A:OP1	5:LD:142:ARG:NH2	2.26	0.46
1:L1:379:U:H2'	1:L1:380:A:H8	1.80	0.46
1:L1:503:G:H2'	1:L1:504:G:C8	2.51	0.46
3:LB:260:ALA:O	3:LB:264:ARG:HG2	2.16	0.46
5:LD:65:TRP:CE3	5:LD:76:ARG:HG2	2.50	0.46
7:LJ:79:ILE:HD12	7:LJ:79:ILE:H	1.81	0.46
12:LP:130:PRO:HB3	12:LP:150:TYR:HE1	1.81	0.46
13:LQ:110:ILE:HG13	13:LQ:120:MET:HB3	1.96	0.46
14:LR:136:LEU:HD12	14:LR:169:VAL:HG13	1.98	0.46
19:LW:1:MET:HE1	34:Lo:39:LYS:HB2	1.97	0.46
26:Lg:34:ARG:NH1	26:Lg:38:ARG:O	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:L1:234:HIS:CE1	31:L1:257:PRO:HA	2.50	0.46
33:Ln:87:ASP:OD2	40:Lv:153:HIS:CE1	2.69	0.46
39:Lt:94:GLU:HA	39:Lt:97:ARG:HG2	1.97	0.46
45:L3:10:LEU:H	45:L3:10:LEU:HD23	1.79	0.46
45:L3:17:ARG:HG2	45:L3:65:ASP:HB3	1.98	0.46
47:L5:52:TYR:HD2	47:L5:71:PRO:CA	2.26	0.46
54:v:17:LEU:HD22	55:w:120:MET:SD	2.55	0.46
55:w:147:TYR:CE1	55:w:151:LYS:HE2	2.51	0.46
1:L1:213:G:O2'	1:L1:214:G:H5'	2.15	0.46
1:L1:462:A:H5'	1:L1:463:A:OP2	2.16	0.46
1:L1:574:U:H2'	16:LT:128:PHE:CE1	2.51	0.46
1:L1:994:U:H2'	1:L1:995:U:C6	2.50	0.46
1:L1:1075:A:O2'	22:Lb:102:LYS:O	2.29	0.46
1:L1:1281:A:H2'	1:L1:1282:U:C6	2.51	0.46
5:LD:61:PRO:HA	5:LD:84:PRO:HD3	1.96	0.46
7:LJ:113:ARG:NH1	8:LK:134:ASP:OD1	2.48	0.46
10:LN:128:ARG:CZ	53:u:120:TYR:HA	2.45	0.46
10:LN:136:LYS:HD2	53:u:167:TRP:CD1	2.51	0.46
12:LP:216:GLU:HG2	12:LP:217:ARG:N	2.30	0.46
14:LR:157:MET:O	14:LR:161:GLN:HG3	2.16	0.46
31:L1:224:HIS:CE1	31:L1:227:GLU:H	2.34	0.46
31:L1:275:GLN:HG2	31:L1:311:MET:HB3	1.98	0.46
32:Lm:256:ARG:HD3	32:Lm:261:ILE:HG12	1.98	0.46
52:Sf:346:TRP:CH2	52:Sf:348:GLU:HB2	2.50	0.46
1:L1:192:U:H2'	1:L1:193:A:H8	1.80	0.46
5:LD:275:TRP:O	5:LD:279:ARG:HB2	2.16	0.46
8:LK:49:PHE:CE1	8:LK:80:ILE:HG12	2.51	0.46
11:LO:204:MET:HE3	11:LO:204:MET:HB3	1.62	0.46
20:LX:170:TRP:NE1	34:Lo:76:TYR:H	2.14	0.46
41:Lw:52:LEU:HD12	41:Lw:53:PRO:HD2	1.98	0.46
52:Sf:81:ARG:O	52:Sf:85:LYS:HB3	2.15	0.46
53:u:93:ASP:CG	53:u:94:ILE:H	2.23	0.46
1:L1:212:A:H4'	1:L1:213:G:H5'	1.98	0.46
1:L1:1339:C:O2'	1:L1:1445:U:OP1	2.27	0.46
2:L2:1621:A:H61	2:L2:1645:A:H2'	1.81	0.46
38:Ls:202:MET:HA	38:Ls:208:VAL:HG22	1.97	0.46
40:Lv:90:VAL:C	40:Lv:91:LEU:HD22	2.40	0.46
53:u:138:MET:O	53:u:142:VAL:HG13	2.16	0.46
1:L1:266:A:H4'	1:L1:267:A:N7	2.30	0.46
1:L1:315:G:OP1	1:L1:317:G:O2'	2.34	0.46
1:L1:785:U:H2'	1:L1:786:U:H6	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LJ:86:ILE:HG22	7:LJ:126:PHE:HD2	1.80	0.46
9:LM:154:ARG:NH2	9:LM:157:GLU:OE2	2.49	0.46
10:LN:111:ASN:HB3	53:u:164:THR:HB	1.97	0.46
20:LX:196:GLU:HG3	34:Lo:128:PHE:CD2	2.47	0.46
26:Lg:38:ARG:HG2	26:Lg:38:ARG:HH11	1.81	0.46
42:Lx:71:GLU:O	42:Lx:75:LYS:HG2	2.16	0.46
46:L4:123:LYS:HE2	46:L4:127:TRP:CZ2	2.50	0.46
50:L8:137:GLN:HA	50:L8:140:ARG:HG2	1.96	0.46
1:L1:8:C:HO2'	1:L1:9:U:H6	1.64	0.45
1:L1:89:U:H2'	1:L1:90:G:C8	2.51	0.45
4:LC:113:ASP:N	4:LC:113:ASP:OD1	2.45	0.45
30:Lk:105:TYR:CE1	30:Lk:262:ILE:HD12	2.51	0.45
31:Ll:332:HIS:O	49:L7:129:ARG:NH2	2.49	0.45
32:Lm:121:LYS:HD3	32:Lm:121:LYS:HA	1.69	0.45
35:Lp:96:LEU:CD1	35:Lp:98:GLU:HB2	2.45	0.45
36:Lq:72:VAL:HG13	36:Lq:90:HIS:HB2	1.98	0.45
38:Ls:219:ARG:HG2	38:Ls:239:PRO:HB2	1.98	0.45
39:Lt:50:ALA:C	39:Lt:51:LEU:HD12	2.41	0.45
39:Lt:151:ARG:NH2	39:Lt:157:LEU:HD11	2.31	0.45
5:LD:234:THR:O	50:L8:25:TYR:N	2.50	0.45
31:Ll:220:SER:O	31:Ll:231:GLU:HB2	2.16	0.45
37:Lr:148:MET:HG3	37:Lr:149:PRO:HD2	1.98	0.45
50:L8:108:LEU:O	50:L8:112:GLN:HG2	2.16	0.45
1:L1:542:C:H2'	1:L1:543:A:H8	1.81	0.45
1:L1:1531:A:H2'	1:L1:1532:U:O4'	2.16	0.45
4:LC:316:PHE:HB3	4:LC:317:PRO:HD3	1.98	0.45
5:LD:281:ARG:HG2	11:LO:125:ARG:HD3	1.99	0.45
22:Lb:197:PRO:HB2	22:Lb:200:GLU:OE1	2.16	0.45
23:Lu:91:ARG:O	23:Lu:149:ARG:NH2	2.48	0.45
32:Lm:139:ASN:O	32:Lm:143:TRP:CD1	2.69	0.45
32:Lm:180:CYS:HB3	32:Lm:296:ARG:HG3	1.97	0.45
33:Ln:149:GLU:HG3	39:Lt:230:LYS:HE2	1.98	0.45
38:Ls:86:ASP:O	38:Ls:196:GLN:NE2	2.40	0.45
41:Lw:46:GLN:HG3	41:Lw:47:PHE:N	2.30	0.45
45:L3:19:GLN:HA	45:L3:54:ASP:HB3	1.98	0.45
46:L4:79:LYS:H	46:L4:79:LYS:HD3	1.80	0.45
52:Sf:152:GLN:HE22	52:Sf:179:GLN:HG2	1.81	0.45
54:v:16:LEU:HD11	54:v:61:PHE:CD1	2.52	0.45
54:v:49:GLU:O	54:v:53:ARG:HG2	2.16	0.45
55:w:130:ILE:HG12	55:w:151:LYS:NZ	2.32	0.45
1:L1:333:A:OP2	1:L1:1064:A:O2'	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:623:A:C4	11:LO:39:ARG:NH1	2.84	0.45
7:LJ:121:ILE:HG22	7:LJ:156:SER:HB3	1.99	0.45
9:LM:153:LYS:HE3	9:LM:158:TYR:CD1	2.51	0.45
10:LN:132:GLY:O	53:u:160:GLU:HG2	2.16	0.45
18:LV:52:GLU:OE1	18:LV:52:GLU:N	2.40	0.45
19:LW:64:PRO:HB2	19:LW:100:ALA:HB3	1.99	0.45
22:Lb:157:PHE:CD1	30:Lk:48:ARG:HG2	2.52	0.45
30:Lk:173:ARG:HG2	30:Lk:176:TYR:OH	2.16	0.45
33:Ln:177:HIS:N	39:Lt:58:VAL:O	2.50	0.45
38:Ls:194:VAL:HA	38:Ls:214:VAL:HG22	1.98	0.45
40:Lv:94:HIS:HB2	40:Lv:185:SER:O	2.15	0.45
47:L5:52:TYR:O	47:L5:54:VAL:HG23	2.17	0.45
47:L5:72:ARG:CZ	47:L5:75:LEU:HD23	2.47	0.45
1:L1:191:U:H2'	1:L1:192:U:H6	1.81	0.45
2:L2:1627:C:O2'	2:L2:1628:C:H5'	2.17	0.45
14:LR:53:ARG:NH2	14:LR:57:LEU:HD21	2.31	0.45
20:LX:51:ASP:OD1	20:LX:51:ASP:N	2.47	0.45
20:LX:211:LYS:HB3	20:LX:212:LYS:H	1.66	0.45
22:Lb:201:ALA:O	22:Lb:204:VAL:HG12	2.16	0.45
25:Lf:159:LEU:HD23	25:Lf:174:ILE:HG23	1.98	0.45
26:Lg:20:MET:HG2	26:Lg:58:GLU:CA	2.44	0.45
30:Lk:257:TYR:CD1	30:Lk:258:PRO:HA	2.51	0.45
36:Lq:77:ALA:O	36:Lq:84:VAL:CA	2.63	0.45
41:Lw:108:THR:HG21	41:Lw:157:LEU:HD12	1.99	0.45
53:u:93:ASP:N	53:u:96:MET:HE2	2.29	0.45
55:w:104:PHE:HD2	55:w:115:GLN:HG3	1.80	0.45
55:w:140:CYS:SG	55:w:143:GLU:HG2	2.56	0.45
1:L1:882:U:C2	1:L1:883:G:C8	3.04	0.45
10:LN:118:ARG:HA	10:LN:118:ARG:HD3	1.57	0.45
13:LQ:38:ARG:HH21	13:LQ:82:GLU:HG3	1.82	0.45
19:LW:56:TYR:OH	23:Lu:106:LEU:HD21	2.16	0.45
20:LX:69:ASP:O	20:LX:72:LYS:HB2	2.15	0.45
21:La:105:VAL:HG11	31:Ll:58:ARG:HD2	1.99	0.45
23:Lu:193:ARG:HG2	23:Lu:196:ARG:HH12	1.82	0.45
30:Lk:353:HIS:CE1	30:Lk:379:ASP:H	2.34	0.45
52:Sf:63:ILE:HD13	52:Sf:66:TRP:HE1	1.81	0.45
1:L1:207:U:O3'	11:LO:30:ASN:ND2	2.49	0.45
1:L1:360:U:C4	1:L1:428:G:N7	2.85	0.45
1:L1:367:U:H4'	1:L1:370:G:C6	2.52	0.45
1:L1:378:U:H2'	1:L1:379:U:H6	1.81	0.45
1:L1:837:A:H2'	1:L1:838:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:1554:G:H2'	1:L1:1555:G:H8	1.81	0.45
15:LS:76:LEU:HD22	15:LS:283:TRP:NE1	2.32	0.45
25:Lf:182:PRO:HG2	25:Lf:185:PHE:CB	2.46	0.45
30:Lk:114:LEU:HB3	30:Lk:263:ILE:HG21	1.98	0.45
30:Lk:176:TYR:HA	30:Lk:179:VAL:HG22	1.98	0.45
32:Lm:142:TYR:OH	32:Lm:301:SER:OG	2.34	0.45
32:Lm:202:PHE:HB3	32:Lm:280:VAL:HG21	1.99	0.45
39:Lt:133:LEU:HD23	39:Lt:133:LEU:H	1.81	0.45
1:L1:32:A:OP2	27:Lh:67:VAL:HG22	2.17	0.45
1:L1:417:U:H2'	1:L1:418:U:C6	2.51	0.45
1:L1:666:U:H2'	1:L1:667:A:H8	1.82	0.45
1:L1:1005:G:H4'	18:LV:167:MET:HE3	1.98	0.45
2:L2:1643:A:OP1	31:Ll:114:ARG:NH2	2.37	0.45
5:LD:82:LEU:HB3	5:LD:87:PHE:CD1	2.52	0.45
7:LJ:168:LEU:HD13	7:LJ:176:LEU:HB2	1.99	0.45
8:LK:113:THR:HG23	8:LK:115:LYS:H	1.82	0.45
19:LW:131:GLU:HG3	19:LW:132:GLU:N	2.32	0.45
22:Lb:13:ARG:HB3	22:Lb:17:ARG:HH12	1.81	0.45
22:Lb:113:GLU:HG2	22:Lb:122:LYS:HE3	1.98	0.45
22:Lb:116:SER:OG	22:Lb:119:LEU:HB2	2.16	0.45
46:L4:100:ASN:ND2	46:L4:105:LYS:HD2	2.29	0.45
46:L4:133:SER:HA	46:L4:136:LYS:HB3	1.98	0.45
1:L1:560:A:N6	1:L1:1280:U:H1'	2.32	0.45
1:L1:657:U:H4'	13:LQ:30:ARG:HH21	1.82	0.45
1:L1:1064:A:H2'	1:L1:1065:G:C8	2.52	0.45
1:L1:1384:G:H2'	1:L1:1385:U:H6	1.82	0.45
1:L1:1404:A:N6	1:L1:1425:G:H1'	2.30	0.45
18:LV:61:PRO:HG3	38:Ls:180:THR:HG21	1.97	0.45
19:LW:28:LEU:N	23:Lu:114:THR:HG22	2.32	0.45
21:La:120:LEU:HD12	21:La:121:PRO:HD2	1.99	0.45
23:Lu:89:GLN:O	23:Lu:93:LYS:HG2	2.16	0.45
30:Lk:173:ARG:HA	30:Lk:176:TYR:CE2	2.52	0.45
30:Lk:197:SER:OG	30:Lk:422:ALA:HB1	2.17	0.45
39:Lt:187:THR:HA	39:Lt:190:ARG:HG2	1.99	0.45
1:L1:267:A:HO2'	1:L1:268:A:C5'	2.28	0.45
1:L1:417:U:H2'	1:L1:418:U:H6	1.82	0.45
1:L1:728:A:H2'	1:L1:729:A:O4'	2.16	0.45
11:LO:111:ASP:O	11:LO:116:ILE:HD11	2.17	0.45
14:LR:59:SER:OG	49:L7:177:ARG:NH1	2.50	0.45
20:LX:44:VAL:HG11	20:LX:83:ARG:CZ	2.47	0.45
20:LX:105:ARG:NH1	38:Ls:170:PRO:HB2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Lb:83:GLU:HG2	22:Lb:107:PRO:HB3	1.99	0.45
23:Lu:63:GLY:N	23:Lu:65:GLU:OE2	2.50	0.45
31:Ll:362:PRO:HB2	31:Ll:364:ARG:HG3	1.99	0.45
51:SR:89:LEU:O	51:SR:93:ILE:HG23	2.17	0.45
52:Sf:178:ASP:HB2	52:Sf:202:TYR:CE1	2.52	0.45
1:L1:415:A:H2'	1:L1:416:A:C8	2.52	0.44
1:L1:1083:A:O2'	6:LI:88:HIS:ND1	2.47	0.44
1:L1:1450:C:H5''	53:u:147:LYS:NZ	2.31	0.44
2:L2:1663:C:H2'	2:L2:1664:G:C8	2.52	0.44
7:LJ:49:ALA:HA	7:LJ:52:GLU:OE2	2.17	0.44
9:LM:158:TYR:HD1	9:LM:162:GLU:OE2	1.99	0.44
13:LQ:110:ILE:HG13	13:LQ:120:MET:CB	2.47	0.44
17:LU:96:PHE:HB3	36:Lq:126:ILE:CD1	2.47	0.44
23:Lu:110:ASN:O	23:Lu:114:THR:HG23	2.16	0.44
24:Ld:101:LYS:NZ	44:Lz:83:GLU:OE1	2.31	0.44
31:Ll:157:LEU:O	31:Ll:161:LEU:N	2.50	0.44
32:Lm:47:LEU:HD21	32:Lm:228:GLU:HG3	1.99	0.44
32:Lm:169:ALA:HB2	32:Lm:181:TYR:CD1	2.52	0.44
40:Lv:77:VAL:HG22	40:Lv:78:ARG:H	1.83	0.44
43:Ly:83:TRP:HZ3	43:Ly:90:ARG:HG2	1.81	0.44
49:L7:50:PRO:HA	49:L7:53:GLN:NE2	2.32	0.44
51:SR:58:LYS:HD2	51:SR:59:GLU:O	2.17	0.44
52:Sf:251:VAL:HG11	52:Sf:255:TYR:CD2	2.51	0.44
1:L1:503:G:H2'	1:L1:504:G:H8	1.82	0.44
1:L1:1286:A:C6	1:L1:1299:A:C8	3.06	0.44
1:L1:1447:C:H2'	1:L1:1448:U:C6	2.52	0.44
3:LB:116:GLU:OE1	3:LB:117:THR:HG23	2.17	0.44
4:LC:234:THR:HG22	4:LC:235:LYS:N	2.26	0.44
8:LK:113:THR:HG21	8:LK:115:LYS:HE2	1.99	0.44
9:LM:147:GLN:NE2	9:LM:151:ILE:HD11	2.32	0.44
20:LX:100:LYS:HD2	20:LX:104:TYR:O	2.16	0.44
23:Lu:111:MET:HE3	23:Lu:111:MET:HB3	1.82	0.44
31:Ll:98:SER:HB3	31:Ll:101:GLN:HG3	1.99	0.44
36:Lq:85:ARG:NH2	36:Lq:87:GLU:OE2	2.50	0.44
37:Lr:59:ARG:NH2	37:Lr:184:PHE:HB2	2.32	0.44
39:Lt:116:LEU:HG	39:Lt:117:ALA:N	2.32	0.44
52:Sf:374:LEU:HD12	52:Sf:391:ASN:ND2	2.32	0.44
1:L1:74:A:OP2	28:Li:108:LYS:NZ	2.41	0.44
1:L1:430:C:H2'	1:L1:431:C:H6	1.81	0.44
1:L1:845:U:O2'	3:LB:282:ALA:O	2.35	0.44
1:L1:1042:G:H2'	1:L1:1043:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:1229:C:H5''	11:LO:80:LYS:HD3	2.00	0.44
1:L1:1328:U:O2	4:LC:241:GLY:HA3	2.17	0.44
8:LK:44:VAL:HG13	8:LK:78:PHE:CE2	2.52	0.44
15:LS:76:LEU:HD12	15:LS:76:LEU:HA	1.74	0.44
20:LX:163:ASP:OD1	20:LX:165:ILE:HG22	2.16	0.44
30:Lk:165:GLN:OE1	30:Lk:166:THR:HG23	2.17	0.44
31:Ll:158:TYR:O	31:Ll:164:GLY:N	2.34	0.44
32:Lm:166:LEU:HB3	32:Lm:181:TYR:CE2	2.52	0.44
33:Ln:136:ILE:HD11	40:Lv:173:ILE:HG13	1.99	0.44
35:Lp:43:TYR:HD1	36:Lq:135:ASN:HA	1.81	0.44
36:Lq:140:PHE:HE2	36:Lq:141:ARG:NH1	2.14	0.44
39:Lt:255:VAL:HG23	39:Lt:259:GLU:HB2	1.99	0.44
52:Sf:95:PRO:HG2	52:Sf:235:ASP:CG	2.43	0.44
53:u:190:LEU:HA	53:u:193:LEU:HD23	1.99	0.44
1:L1:283:A:H2'	1:L1:284:U:H6	1.82	0.44
1:L1:676:U:H2'	1:L1:677:C:H6	1.82	0.44
1:L1:785:U:H2'	1:L1:786:U:C6	2.52	0.44
1:L1:1125:U:H2'	1:L1:1126:G:C8	2.49	0.44
1:L1:1301:A:O2'	12:LP:182:LYS:O	2.33	0.44
5:LD:59:ARG:HE	5:LD:84:PRO:HB2	1.82	0.44
7:LJ:113:ARG:NH2	8:LK:132:LEU:O	2.51	0.44
10:LN:118:ARG:CZ	53:u:193:LEU:HD21	2.47	0.44
12:LP:94:GLY:O	12:LP:244:LYS:HD2	2.17	0.44
17:LU:84:ASN:O	17:LU:88:VAL:HG23	2.17	0.44
17:LU:94:ARG:HG3	36:Lq:126:ILE:HD13	1.99	0.44
19:LW:24:PHE:CE2	19:LW:48:MET:HG2	2.52	0.44
22:Lb:17:ARG:HG3	22:Lb:17:ARG:NH1	2.32	0.44
27:Lh:89:SER:OG	34:Lo:17:ARG:NE	2.43	0.44
35:Lp:46:ASN:O	35:Lp:63:PRO:HD2	2.16	0.44
39:Lt:266:PRO:O	39:Lt:270:ALA:HB3	2.17	0.44
42:Lx:71:GLU:HA	42:Lx:74:VAL:HG12	1.99	0.44
52:Sf:321:GLU:OE2	52:Sf:398:SER:OG	2.25	0.44
55:w:103:HIS:O	55:w:107:ASP:HB2	2.17	0.44
1:L1:99:C:N3	5:LD:104:LYS:NZ	2.65	0.44
1:L1:402:A:H2'	1:L1:403:A:H8	1.82	0.44
1:L1:770:G:H2'	1:L1:771:C:C6	2.52	0.44
1:L1:837:A:O2'	1:L1:838:C:OP1	2.29	0.44
15:LS:227:LYS:NZ	15:LS:234:GLU:OE1	2.50	0.44
33:Ln:148:GLU:O	33:Ln:152:LEU:HG	2.17	0.44
37:Lr:79:LEU:HD13	37:Lr:214:PHE:HE2	1.81	0.44
41:Lw:46:GLN:HA	41:Lw:49:GLU:OE1	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:L5:72:ARG:NH2	47:L5:75:LEU:HA	2.33	0.44
53:u:112:ILE:HD13	54:v:69:ILE:HD13	1.99	0.44
1:L1:9:U:H2'	1:L1:10:A:H8	1.83	0.44
1:L1:356:A:H2'	1:L1:357:A:C8	2.52	0.44
1:L1:386:G:H2'	1:L1:387:C:C6	2.52	0.44
1:L1:583:U:H2'	1:L1:584:C:C6	2.52	0.44
1:L1:848:A:H2'	1:L1:860:A:H61	1.82	0.44
1:L1:879:C:N4	1:L1:892:U:H2'	2.33	0.44
1:L1:1364:U:H2'	1:L1:1365:C:H6	1.83	0.44
4:LC:217:GLY:HA2	4:LC:258:PRO:HB3	1.99	0.44
4:LC:300:LYS:HE3	4:LC:300:LYS:HB2	1.63	0.44
10:LN:118:ARG:NH1	53:u:193:LEU:HG	2.33	0.44
12:LP:226:ILE:O	12:LP:230:LEU:HG	2.17	0.44
13:LQ:55:TYR:CD2	15:LS:270:MET:HE1	2.52	0.44
19:LW:132:GLU:O	19:LW:136:GLN:HG3	2.17	0.44
19:LW:153:LEU:HD11	38:Ls:240:LYS:HB2	1.98	0.44
25:Lf:180:LYS:HD3	25:Lf:181:ARG:O	2.17	0.44
25:Lf:184:TRP:CD1	25:Lf:184:TRP:H	2.34	0.44
42:Lx:69:ARG:NH1	42:Lx:69:ARG:HB3	2.32	0.44
1:L1:20:C:O2	23:Lu:213:ARG:HG3	2.17	0.44
1:L1:335:C:H2'	1:L1:336:C:C6	2.53	0.44
1:L1:552:U:H2'	1:L1:553:A:C2	2.53	0.44
1:L1:580:A:H2'	1:L1:582:C:H5	1.82	0.44
1:L1:778:G:OP1	52:Sf:222:ARG:HD2	2.18	0.44
1:L1:940:U:H2'	1:L1:941:C:C6	2.53	0.44
1:L1:1085:A:H5''	22:Lb:129:MET:CE	2.47	0.44
1:L1:1281:A:H2'	1:L1:1282:U:H6	1.83	0.44
4:LC:104:LEU:HD23	4:LC:121:LEU:HD23	2.00	0.44
9:LM:68:SER:O	9:LM:71:LYS:HG3	2.18	0.44
13:LQ:55:TYR:CG	15:LS:270:MET:HE1	2.53	0.44
17:LU:104:ARG:HB2	17:LU:106:TRP:NE1	2.33	0.44
18:LV:75:HIS:HD2	18:LV:120:VAL:HG13	1.82	0.44
18:LV:113:GLY:O	18:LV:117:ILE:HG13	2.17	0.44
20:LX:59:GLY:N	20:LX:76:VAL:HG23	2.33	0.44
30:Lk:246:GLU:O	30:Lk:249:LYS:HB2	2.18	0.44
32:Lm:192:TRP:HE3	32:Lm:295:ARG:HH12	1.64	0.44
33:Ln:136:ILE:CD1	40:Lv:173:ILE:HG13	2.48	0.44
34:Lo:68:PHE:CZ	34:Lo:70:LEU:HD12	2.53	0.44
35:Lp:41:ASP:OD1	35:Lp:46:ASN:HA	2.18	0.44
43:Ly:70:PRO:HA	43:Ly:73:LEU:HD12	2.00	0.44
54:v:12:LEU:O	54:v:16:LEU:HD23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:v:14:ARG:NH1	55:w:132:ASP:HB2	2.32	0.44
1:L1:9:U:O2'	1:L1:10:A:O4'	2.36	0.44
1:L1:103:A:OP1	37:Lr:31:VAL:N	2.51	0.44
1:L1:153:A:H2	1:L1:1036:A:C2	2.35	0.44
1:L1:430:C:H2'	1:L1:431:C:C6	2.53	0.44
1:L1:910:U:H2'	1:L1:911:A:C8	2.51	0.44
1:L1:940:U:H2'	1:L1:941:C:H6	1.83	0.44
1:L1:1269:C:H2'	1:L1:1270:A:C8	2.52	0.44
1:L1:1444:U:H2'	1:L1:1445:U:H6	1.83	0.44
4:LC:80:LEU:HD12	4:LC:322:ASP:O	2.18	0.44
7:LJ:107:GLU:O	7:LJ:110:LEU:HG	2.18	0.44
9:LM:169:LEU:HD13	51:SR:75:TRP:CD1	2.52	0.44
11:LO:28:LYS:HB2	48:L6:94:HIS:CD2	2.53	0.44
11:LO:148:PHE:O	11:LO:170:ASN:ND2	2.48	0.44
13:LQ:62:TYR:O	13:LQ:65:LEU:HB2	2.18	0.44
19:LW:12:LEU:H	19:LW:12:LEU:HG	1.46	0.44
19:LW:37:GLU:HB3	19:LW:104:THR:HG23	1.99	0.44
19:LW:41:GLN:OE1	19:LW:96:TYR:HE1	2.00	0.44
19:LW:132:GLU:OE2	38:Ls:82:ALA:HB3	2.18	0.44
30:Lk:147:ILE:HB	30:Lk:150:GLN:HG3	2.00	0.44
31:Ll:139:TRP:CZ2	31:Ll:144:GLY:HA2	2.53	0.44
32:Lm:185:LEU:HD23	32:Lm:185:LEU:HA	1.83	0.44
35:Lp:100:VAL:HG23	35:Lp:100:VAL:O	2.17	0.44
39:Lt:184:LEU:O	39:Lt:187:THR:OG1	2.21	0.44
46:L4:82:GLN:O	46:L4:82:GLN:HG2	2.17	0.44
46:L4:89:ASP:OD1	46:L4:89:ASP:N	2.51	0.44
53:u:167:TRP:O	53:u:168:LEU:HD12	2.18	0.44
55:w:100:VAL:HB	55:w:142:GLN:HB3	1.99	0.44
1:L1:122:G:N7	27:Lh:87:ARG:NH2	2.66	0.44
1:L1:248:G:N2	1:L1:328:U:O4	2.48	0.44
1:L1:374:A:C4	1:L1:375:A:C8	3.05	0.44
1:L1:1039:A:H5'	25:Lf:93:ARG:HG3	2.00	0.44
1:L1:1142:U:H2'	1:L1:1143:U:O4'	2.17	0.44
2:L2:1666:U:H2'	2:L2:1667:C:C6	2.53	0.44
5:LD:70:ARG:HA	5:LD:196:PRO:HD3	2.00	0.44
5:LD:190:MET:HE2	5:LD:190:MET:HB2	1.89	0.44
11:LO:291:LEU:HD23	11:LO:291:LEU:HA	1.87	0.44
20:LX:177:THR:HG21	23:Lu:85:TRP:CZ2	2.53	0.44
23:Lu:165:PRO:HB2	23:Lu:181:PHE:CD2	2.53	0.44
31:Ll:105:GLU:O	31:Ll:108:GLN:HG3	2.18	0.44
31:Ll:204:VAL:HG11	31:Ll:216:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Ln:178:TYR:HB2	40:Lv:180:GLU:OE2	2.17	0.44
36:Lq:78:GLU:HG2	36:Lq:84:VAL:HG22	1.99	0.44
38:Ls:234:GLY:H	38:Ls:274:GLN:HE22	1.66	0.44
40:Lv:95:LEU:HD21	40:Lv:106:TYR:HD2	1.83	0.44
1:L1:49:G:H2'	1:L1:50:C:H6	1.82	0.43
1:L1:837:A:H2'	1:L1:838:C:H6	1.82	0.43
1:L1:1177:C:C6	1:L1:1224:U:H2'	2.53	0.43
6:LI:108:ARG:N	6:LI:110:ASP:OD1	2.50	0.43
24:Ld:85:ILE:HA	24:Ld:88:MET:HE3	2.00	0.43
52:Sf:421:ILE:O	52:Sf:425:LEU:HD13	2.18	0.43
53:u:185:ARG:O	53:u:189:GLU:HG3	2.18	0.43
1:L1:424:G:H2'	1:L1:425:U:H6	1.83	0.43
1:L1:528:A:N6	8:LK:150:SER:HB3	2.32	0.43
8:LK:109:ALA:HB3	8:LK:153:ILE:HD13	2.00	0.43
11:LO:264:GLN:NE2	11:LO:267:PHE:O	2.50	0.43
14:LR:133:GLN:NE2	31:LI:136:ARG:HD2	2.33	0.43
16:LT:149:HIS:HD2	24:Ld:154:VAL:HG22	1.84	0.43
17:LU:71:GLU:O	17:LU:74:ARG:HG2	2.18	0.43
37:Lr:130:THR:O	37:Lr:134:GLN:HG2	2.18	0.43
48:L6:12:ILE:HG13	48:L6:23:ARG:HB2	2.00	0.43
49:L7:100:GLU:HG2	49:L7:136:THR:HG22	2.01	0.43
1:L1:372:U:H2'	1:L1:373:C:H6	1.83	0.43
1:L1:575:A:C4	51:SR:189:ARG:HG2	2.53	0.43
7:LJ:181:ILE:O	7:LJ:184:THR:HG22	2.19	0.43
9:LM:22:ASP:OD1	9:LM:23:GLY:N	2.51	0.43
18:LV:54:LYS:O	38:Ls:227:ARG:NH2	2.52	0.43
21:La:128:LYS:HB2	21:La:130:PHE:CE1	2.54	0.43
29:Lj:93:LYS:HB2	29:Lj:93:LYS:HE2	1.88	0.43
30:Lk:115:GLU:HB2	30:Lk:119:GLN:HB2	2.00	0.43
32:Lm:69:HIS:HB2	32:Lm:79:PHE:CE2	2.53	0.43
42:Lx:69:ARG:NH1	42:Lx:107:ASP:OD2	2.51	0.43
47:L5:66:ILE:HD11	47:L5:75:LEU:CD1	2.48	0.43
1:L1:183:A:H5''	1:L1:184:U:OP2	2.18	0.43
1:L1:624:A:OP2	11:LO:39:ARG:NH2	2.51	0.43
1:L1:1329:C:H1'	4:LC:242:ALA:O	2.18	0.43
4:LC:61:ILE:HD11	13:LQ:149:LEU:HD13	2.01	0.43
11:LO:30:ASN:O	11:LO:33:SER:OG	2.29	0.43
11:LO:88:SER:HA	11:LO:134:ARG:HE	1.82	0.43
12:LP:47:LYS:NZ	12:LP:49:LYS:HB2	2.33	0.43
16:LT:65:ARG:HA	16:LT:68:TRP:CE3	2.53	0.43
33:Ln:126:GLN:HG3	33:Ln:129:ARG:NH2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Lr:79:LEU:HD23	37:Lr:79:LEU:HA	1.79	0.43
41:Lw:141:ASN:HB3	41:Lw:146:THR:HG22	2.00	0.43
49:L7:153:LYS:O	49:L7:157:MET:HG3	2.18	0.43
52:Sf:90:LYS:HD2	52:Sf:232:GLN:HB2	1.99	0.43
1:L1:477:G:H1'	17:LU:104:ARG:HH21	1.84	0.43
1:L1:740:U:H2'	1:L1:741:U:C6	2.53	0.43
1:L1:940:U:H3	1:L1:952:G:H1	1.66	0.43
1:L1:1256:A:O2'	1:L1:1417:C:OP1	2.29	0.43
3:LB:213:CYS:HB3	3:LB:246:ARG:HG2	2.01	0.43
4:LC:129:VAL:O	4:LC:190:GLY:N	2.48	0.43
6:LI:84:GLU:OE2	22:Lb:44:ARG:NH2	2.51	0.43
12:LP:57:PRO:HD2	12:LP:150:TYR:CE2	2.53	0.43
22:Lb:4:HIS:O	43:Ly:101:ARG:NH1	2.48	0.43
30:Lk:295:ASP:OD2	30:Lk:304:LEU:N	2.52	0.43
32:Lm:271:ARG:O	32:Lm:274:ILE:HG12	2.18	0.43
54:v:40:ARG:NH2	55:w:113:LEU:HD23	2.32	0.43
1:L1:192:U:H2'	1:L1:193:A:C8	2.54	0.43
1:L1:1272:C:H2'	1:L1:1273:G:H8	1.84	0.43
5:LD:63:GLN:NE2	5:LD:81:ASP:OD1	2.51	0.43
7:LJ:84:ARG:NH1	46:L4:113:GLU:OE2	2.49	0.43
11:LO:47:ARG:HB3	11:LO:48:LYS:H	1.66	0.43
13:LQ:143:THR:OG1	13:LQ:146:ASN:ND2	2.51	0.43
21:La:144:LEU:HD11	21:La:147:MET:HE3	2.00	0.43
22:Lb:27:HIS:CD2	22:Lb:200:GLU:HG3	2.54	0.43
28:Li:180:TYR:CE1	31:LI:363:LEU:HB3	2.54	0.43
30:Lk:177:CYS:O	30:Lk:180:ILE:HG22	2.19	0.43
30:Lk:283:TYR:OH	52:Sf:152:GLN:OE1	2.28	0.43
32:Lm:323:MET:HE3	32:Lm:324:VAL:O	2.19	0.43
39:Lt:161:VAL:HG12	39:Lt:252:HIS:CD2	2.53	0.43
52:Sf:105:TRP:CG	52:Sf:271:LEU:HD13	2.53	0.43
53:u:195:THR:C	53:u:196:LEU:HD12	2.44	0.43
1:L1:28:C:O2'	1:L1:32:A:N3	2.42	0.43
1:L1:98:G:O6	23:Lu:229:LYS:NZ	2.48	0.43
1:L1:281:C:H2'	1:L1:282:U:C6	2.53	0.43
8:LK:19:VAL:HG22	8:LK:71:LEU:HG	2.00	0.43
12:LP:50:LEU:HD22	12:LP:122:TRP:CE2	2.53	0.43
13:LQ:148:LEU:HD11	32:Lm:143:TRP:CZ2	2.53	0.43
16:LT:96:GLU:O	17:LU:105:GLN:NE2	2.49	0.43
25:Lf:120:HIS:CD2	25:Lf:120:HIS:H	2.36	0.43
26:Lg:55:LEU:HD21	50:L8:135:TRP:CD2	2.54	0.43
31:LI:359:HIS:CD2	31:LI:360:ARG:HG2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lo:68:PHE:CE2	34:Lo:70:LEU:HB2	2.53	0.43
35:Lp:113:SER:OG	35:Lp:118:THR:O	2.36	0.43
36:Lq:36:ASP:O	48:L6:100:LYS:HE3	2.18	0.43
44:Lz:80:LEU:O	44:Lz:84:MET:HG3	2.18	0.43
46:L4:110:LEU:HD23	46:L4:110:LEU:HA	1.85	0.43
50:L8:144:GLU:O	50:L8:147:GLN:HG3	2.18	0.43
1:L1:52:A:H2'	1:L1:53:A:O4'	2.19	0.43
1:L1:213:G:OP2	11:LO:100:ARG:NH2	2.46	0.43
1:L1:610:C:H2'	1:L1:611:A:O4'	2.18	0.43
1:L1:655:U:H2'	1:L1:656:C:H6	1.84	0.43
1:L1:659:C:H2'	1:L1:660:U:O4'	2.19	0.43
1:L1:1128:A:H2'	1:L1:1129:U:H6	1.84	0.43
1:L1:1418:C:O2'	1:L1:1419:A:H2	2.01	0.43
10:LN:118:ARG:NH2	53:u:193:LEU:HD21	2.34	0.43
10:LN:139:ALA:HA	53:u:194:TRP:CH2	2.49	0.43
11:LO:216:ASP:OD1	11:LO:217:ALA:N	2.52	0.43
13:LQ:74:ARG:NH1	15:LS:266:GLU:OE2	2.52	0.43
17:LU:140:ASN:HA	35:Lp:62:HIS:O	2.19	0.43
19:LW:144:ARG:HD2	19:LW:144:ARG:HA	1.74	0.43
21:La:83:VAL:HA	21:La:88:CYS:O	2.19	0.43
27:Lh:82:ARG:NH2	27:Lh:87:ARG:HD2	2.34	0.43
31:Ll:44:ASN:O	31:Ll:48:LEU:HG	2.19	0.43
31:Ll:73:THR:HG22	31:Ll:75:ARG:H	1.84	0.43
33:Ln:143:GLN:OE1	33:Ln:144:GLN:NE2	2.50	0.43
39:Lt:212:HIS:HB3	39:Lt:230:LYS:HZ1	1.82	0.43
41:Lw:45:TYR:O	41:Lw:49:GLU:OE1	2.37	0.43
1:L1:739:A:H2'	1:L1:740:U:C6	2.54	0.43
1:L1:899:C:H2'	1:L1:923:G:H5''	2.01	0.43
1:L1:1086:C:H2'	1:L1:1087:A:C8	2.54	0.43
5:LD:184:GLN:HE22	11:LO:22:VAL:HG23	1.84	0.43
8:LK:175:LEU:HD23	8:LK:175:LEU:HA	1.85	0.43
10:LN:139:ALA:HB1	53:u:190:LEU:HD13	2.01	0.43
12:LP:75:PRO:HB3	12:LP:241:TYR:OH	2.19	0.43
16:LT:94:GLN:OE1	16:LT:145:VAL:HG13	2.19	0.43
22:Lb:128:THR:O	22:Lb:131:THR:HG22	2.18	0.43
30:Lk:209:PHE:CZ	30:Lk:224:GLY:HA3	2.54	0.43
32:Lm:64:LYS:HD2	32:Lm:80:VAL:HG12	2.00	0.43
33:Ln:144:GLN:O	33:Ln:148:GLU:OE1	2.37	0.43
35:Lp:91:VAL:HG23	35:Lp:92:LEU:HG	2.01	0.43
40:Lv:102:LEU:HD11	47:L5:39:SER:HA	2.01	0.43
45:L3:18:VAL:HG11	45:L3:34:LEU:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L6:47:TYR:O	48:L6:50:SER:OG	2.31	0.43
50:L8:30:PRO:HA	50:L8:31:PRO:HD3	1.93	0.43
1:L1:160:G:H5''	36:Lq:2:THR:HG21	2.01	0.43
1:L1:551:C:HO2'	1:L1:553:A:N6	2.17	0.43
1:L1:596:U:H2'	1:L1:597:U:C6	2.54	0.43
1:L1:832:C:O2	1:L1:1425:G:O2'	2.33	0.43
2:L2:1668:U:H2'	2:L2:1669:G:H5'	2.00	0.43
5:LD:99:VAL:HG21	5:LD:173:GLY:HA3	1.99	0.43
7:LJ:95:MET:HE3	7:LJ:159:PRO:N	2.34	0.43
22:Lb:36:ARG:NH1	22:Lb:151:GLU:OE2	2.50	0.43
32:Lm:107:LEU:HB2	32:Lm:126:LYS:HB3	2.01	0.43
32:Lm:192:TRP:CD1	35:Lp:91:VAL:HG11	2.54	0.43
33:Ln:126:GLN:HA	33:Ln:129:ARG:HG2	2.01	0.43
33:Ln:145:GLU:HA	33:Ln:148:GLU:OE1	2.18	0.43
39:Lt:199:ASN:ND2	39:Lt:242:ASP:H	2.16	0.43
39:Lt:264:LEU:HB3	39:Lt:269:LEU:O	2.19	0.43
50:L8:147:GLN:HA	50:L8:150:LYS:HZ2	1.84	0.43
55:w:133:ILE:O	55:w:137:LYS:HG2	2.19	0.43
1:L1:19:C:H42	22:Lb:14:LEU:HB3	1.84	0.42
1:L1:20:C:H2'	1:L1:21:C:C6	2.53	0.42
1:L1:32:A:C8	27:Lh:66:TRP:CG	3.07	0.42
1:L1:179:C:H5''	1:L1:1265:A:N1	2.33	0.42
1:L1:477:G:H4'	16:LT:98:ASN:ND2	2.34	0.42
1:L1:1137:U:H2'	1:L1:1138:U:C6	2.54	0.42
57:L1:1692:T1C:H432	57:L1:1692:T1C:H41	1.76	0.42
5:LD:110:SER:O	5:LD:158:PRO:HA	2.19	0.42
11:LO:74:PHE:HA	11:LO:77:ARG:HG2	2.01	0.42
15:LS:79:GLU:HG2	15:LS:80:PHE:N	2.33	0.42
26:Lg:46:TYR:HA	26:Lg:53:ARG:HA	2.01	0.42
29:Lj:97:ARG:HG3	29:Lj:98:HIS:CD2	2.54	0.42
30:Lk:48:ARG:HD3	30:Lk:51:GLU:CD	2.43	0.42
39:Lt:53:LEU:HD22	39:Lt:236:ALA:HB3	2.00	0.42
39:Lt:186:GLY:O	39:Lt:189:GLU:HG3	2.19	0.42
53:u:100:LEU:O	53:u:104:GLU:HG2	2.18	0.42
54:v:6:ARG:NH2	55:w:112:SER:OG	2.52	0.42
1:L1:72:G:N2	1:L1:84:G:H2'	2.34	0.42
1:L1:138:A:O2'	18:LV:56:LYS:HD3	2.19	0.42
1:L1:254:U:H2'	1:L1:255:A:C8	2.54	0.42
1:L1:470:G:OP2	24:Ld:74:SER:OG	2.19	0.42
1:L1:1226:G:OP2	28:Li:135:LYS:NZ	2.46	0.42
1:L1:1371:U:H4'	1:L1:1372:U:OP1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:1394:A:H5''	1:L1:1395:U:H5'	2.01	0.42
1:L1:1443:A:H2'	1:L1:1444:U:C6	2.54	0.42
2:L2:1635:C:H5''	40:Lv:112:ASN:OD1	2.18	0.42
9:LM:20:LEU:HB2	9:LM:141:LEU:HD22	2.01	0.42
10:LN:131:GLU:O	10:LN:132:GLY:C	2.62	0.42
11:LO:207:PRO:O	11:LO:211:VAL:HG23	2.19	0.42
17:LU:160:VAL:HG22	17:LU:193:LEU:HD21	2.02	0.42
18:LV:94:ILE:HD11	18:LV:117:ILE:HG21	2.01	0.42
20:LX:44:VAL:HG11	20:LX:83:ARG:NH2	2.34	0.42
22:Lb:161:LEU:O	22:Lb:165:MET:HG3	2.19	0.42
34:Lo:114:LEU:HA	34:Lo:117:TYR:HD2	1.84	0.42
1:L1:358:G:N1	1:L1:594:A:OP2	2.33	0.42
1:L1:383:U:OP2	41:Lw:150:LYS:NZ	2.45	0.42
1:L1:844:C:H2'	1:L1:845:U:C6	2.55	0.42
1:L1:993:C:C2	1:L1:994:U:C5	3.07	0.42
1:L1:1082:C:C2	1:L1:1083:A:C8	3.07	0.42
1:L1:1473:U:O4	1:L1:1474:A:N6	2.52	0.42
4:LC:107:MET:SD	15:LS:145:LEU:HD12	2.59	0.42
6:LI:70:LYS:CE	6:LI:71:PRO:HD2	2.47	0.42
8:LK:60:ILE:O	8:LK:61:LYS:C	2.62	0.42
8:LK:162:GLU:HG2	8:LK:163:GLU:N	2.34	0.42
11:LO:123:ASN:CG	41:Lw:53:PRO:HB3	2.44	0.42
12:LP:223:MET:HB3	48:L6:42:GLU:OE2	2.20	0.42
13:LQ:16:ARG:NE	13:LQ:47:ALA:HB1	2.35	0.42
16:LT:87:ILE:O	16:LT:91:VAL:HG23	2.18	0.42
20:LX:177:THR:HG21	23:Lu:85:TRP:HZ2	1.83	0.42
31:Ll:218:LEU:HD13	31:Ll:270:PHE:CD1	2.54	0.42
31:Ll:308:GLN:NE2	44:Lz:110:LYS:HG2	2.34	0.42
53:u:112:ILE:CG2	53:u:124:PHE:HB3	2.50	0.42
55:w:85:TYR:HD1	55:w:88:LYS:HZ3	1.66	0.42
1:L1:328:U:OP1	1:L1:331:C:N4	2.36	0.42
1:L1:1481:A:H2'	1:L1:1482:C:H6	1.84	0.42
2:L2:1612:C:H2'	2:L2:1613:U:C6	2.54	0.42
7:LJ:123:MET:HA	7:LJ:153:LEU:O	2.19	0.42
8:LK:171:ARG:HE	8:LK:175:LEU:HG	1.84	0.42
9:LM:154:ARG:HG2	51:SR:127:LEU:HA	2.01	0.42
14:LR:93:VAL:HG23	14:LR:131:LEU:HD21	2.01	0.42
15:LS:103:ARG:O	15:LS:106:LEU:O	2.37	0.42
15:LS:155:ILE:HG22	15:LS:156:GLU:HG2	2.01	0.42
15:LS:227:LYS:HD3	15:LS:249:LEU:HD21	2.01	0.42
15:LS:235:ARG:NH1	15:LS:260:TRP:CZ3	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LV:63:LEU:HD23	18:LV:65:GLY:N	2.33	0.42
18:LV:94:ILE:HD13	18:LV:106:LEU:HD11	2.01	0.42
23:Lu:99:HIS:CE1	34:Lo:63:PRO:HD3	2.54	0.42
30:Lk:185:ILE:HD11	30:Lk:292:TYR:CZ	2.54	0.42
32:Lm:239:PHE:O	32:Lm:243:LYS:HG2	2.19	0.42
33:Ln:94:PHE:HA	39:Lt:84:TYR:CE2	2.54	0.42
33:Ln:178:TYR:HB3	47:L5:63:THR:O	2.20	0.42
49:L7:98:LYS:NZ	49:L7:100:GLU:OE2	2.51	0.42
1:L1:179:C:P	11:LO:53:HIS:HE2	2.42	0.42
1:L1:704:A:N6	52:Sf:272:PRO:O	2.50	0.42
1:L1:999:A:H2'	1:L1:1000:C:C6	2.55	0.42
1:L1:1460:A:H8	1:L1:1460:A:O5'	2.02	0.42
3:LB:257:ILE:O	3:LB:262:ARG:NH1	2.46	0.42
18:LV:125:GLN:NE2	18:LV:137:ARG:O	2.34	0.42
31:Ll:162:PHE:HE2	31:Ll:167:PHE:CE1	2.38	0.42
31:Ll:224:HIS:CD2	31:Ll:230:ALA:HB3	2.55	0.42
33:Ln:174:GLU:OE1	33:Ln:174:GLU:N	2.48	0.42
36:Lq:81:ASN:OD1	36:Lq:109:GLY:HA3	2.19	0.42
37:Lr:98:ILE:O	37:Lr:101:GLU:HG3	2.19	0.42
38:Ls:226:ASP:OD2	38:Ls:230:ARG:HG3	2.19	0.42
39:Lt:59:VAL:O	39:Lt:154:ASP:HA	2.19	0.42
39:Lt:182:GLU:OE2	39:Lt:190:ARG:NH1	2.52	0.42
49:L7:191:LYS:HB3	49:L7:191:LYS:HE3	1.76	0.42
1:L1:26:C:H2'	1:L1:27:A:C8	2.55	0.42
1:L1:367:U:O2'	1:L1:368:U:O4'	2.32	0.42
1:L1:754:A:C6	1:L1:756:C:C2	3.08	0.42
1:L1:1404:A:H61	1:L1:1425:G:H1'	1.85	0.42
7:LJ:84:ARG:HH22	46:L4:113:GLU:HG2	1.84	0.42
11:LO:28:LYS:HB3	11:LO:28:LYS:HE2	1.80	0.42
17:LU:98:VAL:HB	17:LU:135:LEU:HB3	2.02	0.42
19:LW:29:VAL:O	19:LW:41:GLN:HB3	2.19	0.42
26:Lg:60:LYS:HE3	26:Lg:61:LYS:N	2.32	0.42
31:Ll:142:THR:HG23	31:Ll:143:CYS:N	2.34	0.42
38:Ls:143:ASP:O	38:Ls:144:ILE:C	2.63	0.42
52:Sf:189:SER:OG	52:Sf:190:PRO:HD3	2.19	0.42
1:L1:393:G:H5'	31:Ll:72:ARG:HG3	2.02	0.42
1:L1:484:A:O2'	1:L1:485:A:H5'	2.19	0.42
1:L1:642:A:H2'	1:L1:643:A:O4'	2.19	0.42
1:L1:929:U:H4'	1:L1:930:A:OP2	2.20	0.42
1:L1:1128:A:H2'	1:L1:1129:U:C6	2.55	0.42
1:L1:1146:G:C4	1:L1:1147:G:C8	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L2:1628:C:O2'	33:Ln:121:TRP:HD1	2.02	0.42
2:L2:1665:C:H2'	2:L2:1666:U:H6	1.85	0.42
7:LJ:168:LEU:CD1	7:LJ:176:LEU:HB2	2.50	0.42
12:LP:224:LEU:HD22	48:L6:38:ARG:CZ	2.49	0.42
13:LQ:84:ASP:OD2	25:Lf:149:PHE:HA	2.20	0.42
13:LQ:110:ILE:O	13:LQ:120:MET:HB2	2.19	0.42
18:LV:91:ALA:O	18:LV:95:ARG:HG3	2.19	0.42
20:LX:170:TRP:HZ3	23:Lu:80:LYS:NZ	2.17	0.42
24:Ld:75:THR:O	24:Ld:78:ARG:HB2	2.20	0.42
25:Lf:182:PRO:HG2	25:Lf:185:PHE:HB2	2.01	0.42
30:Lk:384:GLN:N	30:Lk:404:VAL:O	2.53	0.42
33:Ln:149:GLU:HA	33:Ln:152:LEU:HD12	2.02	0.42
36:Lq:68:ARG:HB3	42:Lx:157:SER:HB2	2.01	0.42
37:Lr:226:LYS:CB	37:Lr:231:MET:HE2	2.48	0.42
41:Lw:125:GLU:O	41:Lw:129:SER:OG	2.30	0.42
42:Lx:93:ASP:OD2	42:Lx:96:LEU:HD23	2.19	0.42
45:L3:76:MET:HE1	45:L3:86:MET:O	2.19	0.42
54:v:33:ALA:O	54:v:37:ARG:HD3	2.20	0.42
1:L1:223:A:H4'	1:L1:224:G:H5'	2.01	0.42
1:L1:437:G:OP1	12:LP:66:PRO:HA	2.19	0.42
1:L1:857:A:C5	3:LB:67:LYS:HB3	2.55	0.42
1:L1:1186:C:H2'	1:L1:1187:U:O4'	2.20	0.42
5:LD:280:TYR:CD1	41:Lw:57:ILE:HG13	2.55	0.42
6:LI:122:ARG:O	6:LI:126:GLN:HB2	2.20	0.42
9:LM:93:ALA:O	9:LM:97:LEU:HD23	2.20	0.42
11:LO:94:LYS:HG3	11:LO:129:ILE:HD13	2.02	0.42
17:LU:94:ARG:O	36:Lq:126:ILE:HG21	2.19	0.42
19:LW:28:LEU:HD12	23:Lu:67:PHE:CD2	2.54	0.42
19:LW:126:LEU:O	19:LW:129:MET:HB3	2.20	0.42
20:LX:84:ASN:HB3	20:LX:117:HIS:ND1	2.35	0.42
26:Lg:41:LEU:HD23	26:Lg:41:LEU:HA	1.84	0.42
30:Lk:219:LEU:HD12	30:Lk:219:LEU:HA	1.76	0.42
33:Ln:180:PRO:HD3	39:Lt:59:VAL:HG22	2.01	0.42
38:Ls:110:GLU:O	38:Ls:114:LYS:HG2	2.19	0.42
39:Lt:266:PRO:HB2	39:Lt:267:LYS:H	1.54	0.42
45:L3:10:LEU:HA	45:L3:94:ILE:HD13	2.01	0.42
54:v:54:GLN:HA	54:v:57:LYS:HG2	2.01	0.42
1:L1:67:A:H61	1:L1:90:G:H1'	1.84	0.42
1:L1:255:A:H2'	1:L1:256:A:C8	2.55	0.42
1:L1:782:A:C2	13:LQ:20:LEU:HG	2.54	0.42
3:LB:209:ALA:O	3:LB:212:THR:OG1	2.26	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LC:155:PHE:HA	32:Lm:309:HIS:CE1	2.55	0.42
4:LC:236:THR:HG23	4:LC:236:THR:O	2.19	0.42
6:LI:85:ASP:HB3	6:LI:87:LYS:O	2.20	0.42
12:LP:170:GLU:H	12:LP:170:GLU:CD	2.28	0.42
13:LQ:82:GLU:OE2	13:LQ:85:LEU:CD1	2.65	0.42
15:LS:235:ARG:HA	15:LS:236:PRO:HD3	1.88	0.42
17:LU:122:LEU:HD21	44:Lz:49:TRP:CH2	2.55	0.42
19:LW:74:HIS:HB2	34:Lo:24:LYS:HE3	2.02	0.42
21:La:53:ILE:HG21	21:La:56:MET:SD	2.60	0.42
31:Ll:331:PHE:O	31:Ll:337:MET:HB3	2.19	0.42
32:Lm:69:HIS:HE1	32:Lm:73:THR:O	2.02	0.42
33:Ln:162:ILE:O	40:Lv:86:TYR:HD2	2.02	0.42
35:Lp:43:TYR:CD1	36:Lq:135:ASN:HA	2.55	0.42
38:Ls:88:TYR:HB2	38:Ls:196:GLN:OE1	2.20	0.42
38:Ls:152:LEU:HD22	38:Ls:181:VAL:HG11	2.00	0.42
39:Lt:75:GLN:O	39:Lt:78:GLU:HG3	2.20	0.42
52:Sf:377:LEU:HA	52:Sf:377:LEU:HD23	1.81	0.42
54:v:39:PHE:O	54:v:43:GLN:OE1	2.37	0.42
55:w:94:ASP:HB2	55:w:96:GLU:HG3	2.01	0.42
1:L1:136:U:H4'	1:L1:137:U:C5'	2.49	0.42
1:L1:292:A:N7	1:L1:831:C:C2	2.88	0.42
1:L1:347:U:OP1	11:LO:54:LYS:NZ	2.42	0.42
1:L1:494:C:H2'	1:L1:495:C:C6	2.55	0.42
1:L1:566:C:N4	1:L1:1018:C:O2	2.53	0.42
1:L1:837:A:HO2'	1:L1:838:C:P	2.40	0.42
4:LC:202:GLN:HG2	4:LC:203:TYR:N	2.32	0.42
5:LD:215:SER:OG	5:LD:257:GLN:N	2.42	0.42
6:LI:138:LYS:HA	6:LI:141:GLU:HG3	2.02	0.42
14:LR:55:LEU:HB3	14:LR:61:ALA:HB2	2.02	0.42
15:LS:77:SER:OG	15:LS:80:PHE:HD2	2.02	0.42
23:Lu:142:LEU:O	23:Lu:146:VAL:HG23	2.20	0.42
28:Li:126:LYS:HB3	28:Li:126:LYS:HE3	1.81	0.42
30:Lk:68:PRO:HG2	30:Lk:69:TRP:CE3	2.55	0.42
39:Lt:65:PRO:O	39:Lt:68:GLU:HG3	2.20	0.42
39:Lt:74:LEU:HD22	47:L5:42:ARG:HB3	2.02	0.42
39:Lt:214:THR:HB	39:Lt:230:LYS:CD	2.50	0.42
44:Lz:101:GLU:OE1	44:Lz:104:LYS:HE3	2.20	0.42
45:L3:68:PHE:CG	45:L3:97:ARG:HD2	2.55	0.42
1:L1:146:G:H2'	1:L1:147:C:O4'	2.20	0.41
1:L1:211:A:H62	41:Lw:111:ARG:HD3	1.84	0.41
1:L1:222:A:C6	28:Li:182:ASP:OD2	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:346:C:OP1	1:L1:369:A:O2'	2.29	0.41
1:L1:379:U:H2'	1:L1:380:A:C8	2.54	0.41
1:L1:510:A:C5	1:L1:514:A:C5	3.08	0.41
1:L1:524:U:O2	7:LJ:125:VAL:HG11	2.18	0.41
3:LB:194:ASN:ND2	3:LB:245:GLY:O	2.51	0.41
5:LD:46:PRO:HB2	5:LD:48:LEU:CD2	2.50	0.41
5:LD:280:TYR:HD1	41:Lw:57:ILE:HG13	1.85	0.41
11:LO:118:LEU:HD11	11:LO:157:GLN:NE2	2.35	0.41
11:LO:246:ASP:OD2	11:LO:249:LYS:NZ	2.47	0.41
14:LR:45:PRO:HG2	14:LR:46:GLU:OE1	2.19	0.41
17:LU:137:GLY:HA2	17:LU:142:THR:HA	2.02	0.41
18:LV:190:LYS:HE2	18:LV:195:HIS:CE1	2.54	0.41
19:LW:148:PRO:HD2	38:Ls:224:ILE:HD13	2.02	0.41
20:LX:156:LYS:HB3	20:LX:156:LYS:HE2	1.69	0.41
24:Ld:103:ILE:HB	48:L6:59:GLU:OE1	2.20	0.41
31:Ll:99:ARG:HA	31:Ll:99:ARG:HD2	1.87	0.41
32:Lm:241:GLU:OE1	32:Lm:250:ARG:NH2	2.48	0.41
34:Lo:71:LYS:HB3	34:Lo:72:PRO:HD2	2.02	0.41
39:Lt:202:ALA:HA	39:Lt:239:LEU:H	1.85	0.41
49:L7:119:ILE:CD1	49:L7:161:ALA:HB2	2.50	0.41
1:L1:153:A:H2	1:L1:1036:A:H2	1.68	0.41
1:L1:228:A:H2'	1:L1:229:G:H8	1.86	0.41
1:L1:382:A:H5'	41:Lw:105:ARG:HG3	2.01	0.41
4:LC:53:LEU:O	13:LQ:138:ARG:HD3	2.20	0.41
4:LC:187:ILE:HG21	4:LC:191:THR:HG21	2.01	0.41
6:Li:133:SER:C	6:Li:137:LYS:HZ3	2.28	0.41
7:LJ:95:MET:HE1	7:LJ:157:GLU:C	2.45	0.41
11:LO:184:LEU:HA	11:LO:187:VAL:HG12	2.02	0.41
22:Lb:134:LEU:HD23	22:Lb:134:LEU:HA	1.91	0.41
40:Lv:179:PRO:HA	47:L5:35:SER:OG	2.20	0.41
41:Lw:160:TRP:CE2	41:Lw:164:LYS:HD2	2.55	0.41
49:L7:175:LEU:HB3	49:L7:179:ARG:NH1	2.33	0.41
54:v:16:LEU:HD13	54:v:16:LEU:HA	1.91	0.41
1:L1:267:A:H4'	1:L1:268:A:OP1	2.19	0.41
1:L1:405:U:O2'	1:L1:1163:A:N7	2.40	0.41
1:L1:424:G:O2'	1:L1:595:A:N3	2.47	0.41
1:L1:495:C:H2'	1:L1:496:C:C6	2.54	0.41
1:L1:747:C:H2'	52:Sf:310:ARG:NH2	2.35	0.41
1:L1:1255:U:O2'	1:L1:1257:C:OP1	2.27	0.41
7:LJ:78:LEU:HA	46:L4:118:TRP:CZ3	2.55	0.41
10:LN:78:LYS:HE2	10:LN:78:LYS:HB3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LX:216:TYR:HE1	23:Lu:191:ASN:HD22	1.68	0.41
28:Li:108:LYS:HD3	28:Li:108:LYS:HA	1.88	0.41
31:Ll:102:GLN:OE1	31:Ll:106:ARG:NH1	2.54	0.41
32:Lm:285:ASN:ND2	32:Lm:293:LEU:HD21	2.34	0.41
34:Lo:91:LEU:HD12	34:Lo:91:LEU:HA	1.88	0.41
36:Lq:48:GLU:OE2	42:Lx:139:LYS:HD2	2.20	0.41
37:Lr:207:GLY:O	37:Lr:211:THR:HG22	2.20	0.41
43:Ly:62:ILE:HG13	43:Ly:63:LEU:HD12	2.01	0.41
46:L4:79:LYS:HE2	46:L4:79:LYS:HB2	1.87	0.41
53:u:169:CYS:SG	53:u:178:HIS:HD2	2.44	0.41
55:w:138:LEU:HD22	55:w:144:ILE:HA	2.02	0.41
1:L1:423:U:C2	1:L1:424:G:C8	3.09	0.41
1:L1:620:A:H2'	1:L1:621:A:C8	2.55	0.41
1:L1:927:C:H4'	1:L1:967:C:O3'	2.20	0.41
1:L1:1472:A:H2'	1:L1:1473:U:C6	2.54	0.41
7:LJ:173:PHE:HB3	45:L3:51:VAL:HG13	2.01	0.41
8:LK:58:LYS:HB3	46:L4:79:LYS:HZ2	1.86	0.41
12:LP:118:MET:HE3	12:LP:167:CYS:SG	2.61	0.41
14:LR:142:PHE:CD1	14:LR:170:VAL:HB	2.55	0.41
17:LU:83:VAL:HA	17:LU:86:MET:HE3	2.01	0.41
19:LW:61:TYR:CZ	23:Lu:67:PHE:HE1	2.38	0.41
23:Lu:150:GLU:OE1	34:Lo:133:ARG:NH2	2.54	0.41
26:Lg:18:VAL:HG11	26:Lg:58:GLU:OE2	2.21	0.41
30:Lk:208:THR:HA	30:Lk:224:GLY:O	2.21	0.41
33:Ln:174:GLU:HA	40:Lv:183:ARG:NH1	2.31	0.41
36:Lq:19:LEU:HD23	36:Lq:19:LEU:HA	1.80	0.41
38:Ls:82:ALA:HB1	38:Ls:167:HIS:ND1	2.35	0.41
39:Lt:267:LYS:HD2	39:Lt:271:GLN:HG3	2.00	0.41
45:L3:41:LYS:O	45:L3:45:THR:HG23	2.21	0.41
50:L8:104:ARG:O	50:L8:108:LEU:HD23	2.20	0.41
51:SR:108:CYS:O	51:SR:109:GLN:C	2.64	0.41
1:L1:386:G:C4	1:L1:387:C:C5	3.08	0.41
1:L1:500:G:N2	1:L1:521:A:H1'	2.36	0.41
1:L1:527:G:H3'	1:L1:527:G:OP2	2.20	0.41
1:L1:880:A:H2'	1:L1:880:A:N3	2.35	0.41
1:L1:925:A:H2'	1:L1:926:G:O4'	2.20	0.41
1:L1:1230:C:H2'	1:L1:1231:A:H8	1.85	0.41
5:LD:209:TYR:CE1	42:Lx:53:PRO:HG2	2.55	0.41
8:LK:46:ILE:H	8:LK:46:ILE:HG13	1.73	0.41
13:LQ:77:ASP:O	13:LQ:83:LYS:NZ	2.54	0.41
15:LS:252:GLN:HA	15:LS:255:LYS:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Lu:226:LEU:O	23:Lu:230:LYS:HG2	2.20	0.41
39:Lt:185:ARG:HD3	39:Lt:204:PHE:CD2	2.56	0.41
50:L8:61:PHE:CD2	50:L8:75:LEU:HD11	2.55	0.41
1:L1:266:A:OP1	1:L1:267:A:N6	2.53	0.41
1:L1:347:U:H1'	1:L1:1262:G:OP1	2.20	0.41
1:L1:356:A:H2'	1:L1:357:A:H8	1.85	0.41
1:L1:497:A:N6	1:L1:542:C:OP2	2.49	0.41
1:L1:597:U:H2'	1:L1:598:G:H8	1.86	0.41
1:L1:615:U:H2'	1:L1:616:A:H8	1.85	0.41
1:L1:715:U:H2'	1:L1:716:C:H6	1.86	0.41
1:L1:1083:A:H1'	6:LI:88:HIS:CE1	2.55	0.41
1:L1:1300:C:H2'	1:L1:1301:A:O4'	2.21	0.41
7:LJ:83:ARG:HA	7:LJ:86:ILE:HG12	2.02	0.41
8:LK:70:ILE:HA	8:LK:80:ILE:HA	2.02	0.41
8:LK:155:VAL:O	46:L4:101:LEU:HD21	2.20	0.41
12:LP:125:PRO:HD3	12:LP:158:ARG:HH22	1.85	0.41
14:LR:38:VAL:HG12	14:LR:40:ASN:HB2	2.03	0.41
18:LV:192:ALA:N	35:Lp:108:MET:HE3	2.35	0.41
22:Lb:227:PHE:HB2	23:Lu:156:LEU:O	2.20	0.41
31:Ll:191:ASN:OD1	31:Ll:191:ASN:N	2.51	0.41
31:Ll:217:LEU:O	31:Ll:270:PHE:HA	2.20	0.41
31:Ll:237:LEU:CG	31:Ll:240:ILE:HD11	2.51	0.41
33:Ln:139:MET:HE2	40:Lv:169:ILE:HG23	2.01	0.41
37:Lr:67:ASP:O	37:Lr:71:GLU:HG2	2.21	0.41
46:L4:67:GLN:HA	46:L4:70:THR:HG22	2.03	0.41
53:u:107:ARG:HD3	53:u:130:THR:HB	2.02	0.41
1:L1:516:C:C2	1:L1:517:C:C5	3.09	0.41
1:L1:565:C:O3'	48:L6:9:ARG:NH1	2.54	0.41
1:L1:999:A:H2'	1:L1:1000:C:H6	1.86	0.41
3:LB:124:GLU:HG2	3:LB:144:GLY:HA3	2.03	0.41
4:LC:127:CYS:CB	4:LC:193:LEU:HB2	2.49	0.41
6:LI:97:ILE:HB	6:LI:130:VAL:HG23	2.03	0.41
14:LR:109:TRP:CE2	14:LR:113:LYS:HB3	2.56	0.41
19:LW:32:GLY:HA2	23:Lu:121:ARG:HH22	1.84	0.41
20:LX:55:TYR:CD1	20:LX:133:ILE:HG13	2.56	0.41
23:Lu:126:MET:HG3	23:Lu:127:PRO:HD2	2.02	0.41
26:Lg:38:ARG:HG2	26:Lg:38:ARG:NH1	2.36	0.41
30:Lk:256:PHE:HD1	30:Lk:259:ILE:HB	1.86	0.41
39:Lt:248:ASN:ND2	39:Lt:250:GLY:O	2.53	0.41
51:SR:99:MET:HE3	51:SR:99:MET:HB3	1.90	0.41
52:Sf:415:ASP:OD1	52:Sf:415:ASP:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:265:A:HO2'	1:L1:266:A:C4'	2.32	0.41
1:L1:567:A:P	51:SR:171:ARG:HH22	2.38	0.41
1:L1:606:C:H2'	1:L1:607:U:C6	2.55	0.41
1:L1:996:U:H2'	1:L1:997:U:O4'	2.21	0.41
1:L1:1030:G:H2'	1:L1:1031:G:H8	1.85	0.41
1:L1:1548:A:H2'	1:L1:1549:G:C8	2.55	0.41
4:LC:130:LEU:O	4:LC:189:PRO:HB3	2.20	0.41
5:LD:190:MET:O	5:LD:262:THR:HA	2.21	0.41
5:LD:201:GLN:HG3	5:LD:205:GLU:OE1	2.21	0.41
7:LJ:117:ARG:HG2	8:LK:134:ASP:OD2	2.21	0.41
7:LJ:158:GLU:HA	7:LJ:159:PRO:HD3	1.94	0.41
8:LK:130:PHE:O	8:LK:133:GLN:C	2.63	0.41
11:LO:252:LEU:HD12	11:LO:256:LEU:HG	2.03	0.41
13:LQ:40:GLU:OE2	13:LQ:96:ARG:NH2	2.46	0.41
16:LT:57:ARG:HE	17:LU:169:ARG:NH2	2.18	0.41
37:Lr:213:LEU:HD23	37:Lr:213:LEU:HA	1.88	0.41
40:Lv:125:TYR:HE1	40:Lv:158:GLN:CD	2.28	0.41
46:L4:75:VAL:HG13	46:L4:76:ASN:N	2.36	0.41
1:L1:108:U:C2	1:L1:112:G:C6	3.09	0.41
1:L1:373:C:C2	1:L1:374:A:C8	3.08	0.41
1:L1:385:U:C2	48:L6:71:PHE:CZ	3.09	0.41
1:L1:468:U:O2'	1:L1:481:A:N3	2.51	0.41
1:L1:542:C:H2'	1:L1:543:A:C8	2.55	0.41
1:L1:737:U:H2'	1:L1:738:U:C6	2.56	0.41
1:L1:800:G:C2	1:L1:803:A:N6	2.87	0.41
1:L1:986:U:H2'	1:L1:987:C:O4'	2.21	0.41
2:L2:1611:G:N2	2:L2:1625:A:H1'	2.36	0.41
4:LC:157:LYS:HA	4:LC:157:LYS:HD3	1.83	0.41
5:LD:65:TRP:CD2	5:LD:76:ARG:HG2	2.55	0.41
5:LD:293:PHE:HA	5:LD:294:PRO:HD2	1.88	0.41
6:LI:58:ARG:HA	6:LI:80:TYR:HA	2.02	0.41
11:LO:149:THR:HA	11:LO:170:ASN:HD21	1.81	0.41
11:LO:180:ASP:OD1	11:LO:181:PRO:HD2	2.21	0.41
11:LO:268:GLY:HA3	41:Lw:47:PHE:CD2	2.56	0.41
14:LR:53:ARG:NE	14:LR:56:GLU:OE1	2.32	0.41
18:LV:94:ILE:O	18:LV:94:ILE:HG13	2.19	0.41
19:LW:126:LEU:O	19:LW:130:LEU:HD23	2.21	0.41
20:LX:58:CYS:C	20:LX:159:PHE:CZ	2.98	0.41
23:Lu:91:ARG:HH21	23:Lu:148:GLU:CD	2.27	0.41
26:Lg:20:MET:HE2	26:Lg:32:THR:OG1	2.21	0.41
30:Lk:113:LEU:HD12	30:Lk:311:ALA:HB1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Lk:238:THR:HG21	30:Lk:339:PRO:HD2	2.02	0.41
31:Ll:220:SER:OG	31:Ll:232:TYR:HB2	2.21	0.41
31:Ll:291:TYR:O	31:Ll:292:GLN:NE2	2.54	0.41
32:Lm:140:LYS:HB3	32:Lm:144:ARG:NH2	2.36	0.41
33:Ln:177:HIS:O	39:Lt:60:SER:N	2.52	0.41
37:Lr:33:LYS:HB2	37:Lr:33:LYS:HE2	1.94	0.41
37:Lr:167:CYS:HB3	37:Lr:191:LEU:HD23	2.02	0.41
40:Lv:88:TYR:HE1	40:Lv:164:ALA:HA	1.85	0.41
40:Lv:192:GLU:O	40:Lv:192:GLU:HG2	2.21	0.41
49:L7:56:ASP:OD1	49:L7:56:ASP:C	2.64	0.41
50:L8:49:ARG:HA	50:L8:52:LEU:HB2	2.03	0.41
52:Sf:266:CYS:SG	52:Sf:267:LYS:N	2.93	0.41
53:u:91:LYS:HD2	53:u:150:LYS:HG2	2.02	0.41
54:v:27:ASP:OD1	54:v:27:ASP:N	2.53	0.41
1:L1:605:U:C2	1:L1:606:C:C5	3.09	0.41
1:L1:1199:A:P	28:Li:124:ARG:HH22	2.43	0.41
1:L1:1273:G:C6	1:L1:1274:C:C4	3.09	0.41
1:L1:1369:U:C2	1:L1:1371:U:H5'	2.56	0.41
2:L2:1623:G:H2'	2:L2:1624:C:O4'	2.20	0.41
4:LC:73:LEU:O	4:LC:77:LEU:HG	2.21	0.41
9:LM:159:THR:O	9:LM:162:GLU:HG2	2.21	0.41
19:LW:21:ARG:NH1	23:Lu:143:ASP:OD1	2.49	0.41
19:LW:28:LEU:CD1	23:Lu:67:PHE:HD2	2.34	0.41
30:Lk:253:LEU:HD23	30:Lk:253:LEU:HA	1.82	0.41
31:Ll:139:TRP:HA	31:Ll:142:THR:HG22	2.03	0.41
32:Lm:43:MET:HE2	32:Lm:231:GLN:HE22	1.86	0.41
37:Lr:244:GLU:HA	37:Lr:247:LYS:HG2	2.03	0.41
39:Lt:48:LEU:HB3	39:Lt:175:GLN:NE2	2.36	0.41
39:Lt:184:LEU:HA	39:Lt:187:THR:HG23	2.03	0.41
42:Lx:139:LYS:HB3	42:Lx:139:LYS:HE3	1.92	0.41
46:L4:67:GLN:HG3	46:L4:73:MET:CE	2.50	0.41
1:L1:306:U:H2'	1:L1:307:U:C6	2.56	0.40
1:L1:995:U:OP2	13:LQ:17:ARG:HD2	2.21	0.40
1:L1:1076:U:H2'	1:L1:1077:U:C6	2.56	0.40
6:LI:138:LYS:HE3	6:LI:138:LYS:HB3	1.93	0.40
11:LO:163:ALA:O	11:LO:167:ILE:HG12	2.20	0.40
15:LS:249:LEU:HB2	15:LS:254:MET:HE3	2.02	0.40
20:LX:56:LEU:HD11	20:LX:120:VAL:HG23	2.02	0.40
20:LX:75:LYS:HE3	20:LX:75:LYS:HB2	1.79	0.40
21:La:78:GLY:HA3	21:La:132:HIS:ND1	2.37	0.40
28:Li:95:THR:HG23	43:Ly:122:ASN:ND2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Lj:72:LEU:HD22	29:Lj:100:GLN:HB3	2.02	0.40
32:Lm:209:LEU:HD23	32:Lm:212:LYS:HE3	2.03	0.40
38:Ls:196:GLN:NE2	38:Ls:198:ARG:HH11	2.19	0.40
39:Lt:122:ASP:C	39:Lt:126:GLN:NE2	2.76	0.40
47:L5:57:VAL:CG1	47:L5:63:THR:HG22	2.49	0.40
52:Sf:56:LYS:O	52:Sf:60:LEU:HG	2.21	0.40
52:Sf:299:PHE:CD1	52:Sf:360:VAL:HB	2.57	0.40
52:Sf:309:GLU:O	52:Sf:313:ARG:HG3	2.21	0.40
55:w:139:MET:HE3	55:w:139:MET:HB3	1.92	0.40
1:L1:323:A:C5	1:L1:325:A:H1'	2.57	0.40
1:L1:868:C:H5''	1:L1:965:G:OP2	2.21	0.40
3:LB:111:ARG:NH2	3:LB:165:ASN:OD1	2.54	0.40
3:LB:125:LYS:HE3	3:LB:125:LYS:HB3	1.93	0.40
3:LB:197:GLU:HG2	3:LB:203:GLY:C	2.46	0.40
4:LC:163:GLU:O	4:LC:167:GLU:HG2	2.20	0.40
4:LC:296:LEU:HD23	4:LC:296:LEU:HA	1.86	0.40
5:LD:217:LEU:HB2	5:LD:256:HIS:CG	2.57	0.40
19:LW:44:ILE:HG13	19:LW:93:LYS:HB3	2.04	0.40
20:LX:129:LYS:O	20:LX:131:THR:HG23	2.21	0.40
22:Lb:157:PHE:CE1	30:Lk:48:ARG:HG2	2.57	0.40
24:Ld:56:TYR:CE1	48:L6:44:GLU:HG3	2.55	0.40
25:Lf:167:GLU:O	25:Lf:170:GLN:HG2	2.21	0.40
30:Lk:98:LEU:O	30:Lk:270:ILE:HG13	2.21	0.40
33:Ln:181:PRO:HB3	47:L5:60:ASP:OD2	2.21	0.40
36:Lq:16:HIS:HB3	36:Lq:19:LEU:HD12	2.03	0.40
41:Lw:127:PHE:CD2	41:Lw:128:LEU:HD22	2.57	0.40
44:Lz:103:ARG:O	44:Lz:105:GLN:HG2	2.22	0.40
46:L4:93:PRO:HB3	46:L4:95:TRP:CE2	2.56	0.40
55:w:104:PHE:CB	55:w:115:GLN:HE21	2.34	0.40
55:w:108:LEU:HB2	55:w:110:LEU:HG	2.02	0.40
1:L1:55:C:H4'	1:L1:1062:G:OP1	2.22	0.40
1:L1:72:G:H22	1:L1:84:G:H2'	1.86	0.40
1:L1:371:U:H2'	1:L1:372:U:H6	1.86	0.40
1:L1:385:U:H2'	1:L1:386:G:C8	2.46	0.40
1:L1:846:C:H2'	1:L1:847:U:C6	2.56	0.40
14:LR:109:TRP:CZ2	14:LR:113:LYS:HB3	2.57	0.40
20:LX:135:TRP:HB3	20:LX:143:ARG:NH1	2.37	0.40
22:Lb:42:HIS:CG	22:Lb:86:ILE:HD11	2.57	0.40
23:Lu:153:LEU:HD12	23:Lu:153:LEU:HA	1.88	0.40
30:Lk:162:ARG:O	30:Lk:171:PRO:HD2	2.21	0.40
30:Lk:281:GLU:CD	30:Lk:281:GLU:H	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Lp:72:THR:OG1	37:Lr:256:ARG:NE	2.43	0.40
39:Lt:172:ILE:HG22	39:Lt:269:LEU:HD11	2.03	0.40
42:Lx:65:ASP:OD1	42:Lx:65:ASP:N	2.48	0.40
45:L3:58:ASP:OD1	45:L3:59:GLY:N	2.54	0.40
53:u:107:ARG:HH22	53:u:182:PRO:HD3	1.85	0.40
54:v:14:ARG:HA	54:v:17:LEU:HD12	2.04	0.40
1:L1:63:C:H5'	43:Ly:95:ARG:CZ	2.51	0.40
1:L1:206:U:H2'	1:L1:207:U:C6	2.57	0.40
1:L1:383:U:H2'	1:L1:384:U:C6	2.56	0.40
1:L1:629:U:H5''	1:L1:630:G:H5''	2.03	0.40
1:L1:654:U:H2'	1:L1:655:U:C6	2.57	0.40
1:L1:962:A:O2'	1:L1:965:G:N3	2.44	0.40
1:L1:1083:A:HO2'	6:LI:88:HIS:CE1	2.39	0.40
1:L1:1446:C:H2'	1:L1:1447:C:H6	1.87	0.40
1:L1:1495:C:H2'	1:L1:1496:U:C6	2.57	0.40
1:L1:1519:C:P	29:Lj:85:ARG:H	2.43	0.40
8:LK:26:ALA:O	8:LK:63:GLY:N	2.55	0.40
11:LO:73:PRO:HG2	11:LO:76:ILE:HB	2.04	0.40
11:LO:79:PRO:HD3	28:Li:127:ALA:HA	2.03	0.40
12:LP:109:ILE:HG22	12:LP:113:MET:CE	2.50	0.40
14:LR:40:ASN:HB3	31:Ll:337:MET:CE	2.49	0.40
14:LR:93:VAL:CG2	14:LR:143:MET:HE1	2.52	0.40
14:LR:126:SER:O	14:LR:130:VAL:HG23	2.22	0.40
17:LU:112:ASP:O	17:LU:194:ARG:HA	2.21	0.40
19:LW:1:MET:HA	19:LW:7:TYR:OH	2.21	0.40
19:LW:82:HIS:CE1	19:LW:83:ARG:HG3	2.56	0.40
21:La:115:ASP:HA	21:La:118:THR:HG22	2.03	0.40
24:Ld:36:PHE:HE2	24:Ld:79:PRO:HG3	1.86	0.40
24:Ld:86:ILE:HG12	24:Ld:113:VAL:HG21	2.03	0.40
24:Ld:104:PRO:HD2	48:L6:59:GLU:OE1	2.21	0.40
32:Lm:167:VAL:HG13	32:Lm:235:TYR:CD1	2.57	0.40
32:Lm:222:GLU:HA	32:Lm:251:ILE:HD13	2.03	0.40
36:Lq:133:PHE:HB3	37:Lr:259:ARG:NH1	2.37	0.40
39:Lt:187:THR:O	39:Lt:191:THR:HG23	2.22	0.40
40:Lv:125:TYR:HE1	40:Lv:158:GLN:NE2	2.20	0.40
40:Lv:169:ILE:O	40:Lv:173:ILE:HG12	2.20	0.40
52:Sf:117:GLY:O	52:Sf:118:LEU:HD23	2.21	0.40
52:Sf:251:VAL:HG13	52:Sf:252:PRO:HD2	2.04	0.40
55:w:130:ILE:HG12	55:w:151:LYS:HZ2	1.86	0.40
1:L1:193:A:H2'	1:L1:194:A:C8	2.56	0.40
1:L1:204:A:C4	1:L1:205:C:C5	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:622:G:C6	16:LT:10:LEU:N	2.90	0.40
1:L1:631:U:H2'	1:L1:632:U:C6	2.57	0.40
1:L1:941:C:H2'	1:L1:942:C:H6	1.86	0.40
1:L1:1481:A:H4'	15:LS:146:GLY:O	2.21	0.40
2:L2:1610:A:H2'	2:L2:1644:G:H21	1.87	0.40
3:LB:229:PRO:C	3:LB:231:LYS:H	2.28	0.40
4:LC:107:MET:SD	4:LC:108:PRO:O	2.79	0.40
8:LK:134:ASP:OD1	8:LK:134:ASP:N	2.55	0.40
11:LO:146:ASP:CG	49:L7:143:GLN:HG2	2.47	0.40
12:LP:134:LYS:NZ	12:LP:143:GLY:O	2.51	0.40
19:LW:38:ASP:OD1	19:LW:38:ASP:N	2.53	0.40
23:Lu:156:LEU:HA	23:Lu:156:LEU:HD23	1.91	0.40
24:Ld:68:ILE:HG12	24:Ld:122:LEU:HB2	2.02	0.40
24:Ld:71:ARG:NH2	24:Ld:92:GLU:O	2.53	0.40
32:Lm:79:PHE:CD1	38:Ls:281:MET:HG3	2.56	0.40
35:Lp:72:THR:HG21	37:Lr:275:TYR:CE1	2.56	0.40
37:Lr:187:PRO:HB2	37:Lr:190:VAL:HG23	2.04	0.40
39:Lt:83:LEU:O	47:L5:49:ALA:HA	2.22	0.40
39:Lt:214:THR:HB	39:Lt:230:LYS:HD2	2.02	0.40
48:L6:44:GLU:HG2	48:L6:48:TRP:CD1	2.56	0.40
52:Sf:187:LEU:O	52:Sf:190:PRO:HD2	2.22	0.40
52:Sf:273:LEU:HD12	52:Sf:273:LEU:HA	1.94	0.40
52:Sf:378:ALA:HB1	52:Sf:383:ALA:HB1	2.04	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	LB	235/305 (77%)	228 (97%)	7 (3%)	0	100	100
4	LC	302/348 (87%)	279 (92%)	23 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	LD	248/311 (80%)	233 (94%)	15 (6%)	0	100	100
6	LI	93/267 (35%)	87 (94%)	6 (6%)	0	100	100
7	LJ	154/261 (59%)	134 (87%)	20 (13%)	0	100	100
8	LK	173/192 (90%)	165 (95%)	8 (5%)	0	100	100
9	LM	175/178 (98%)	164 (94%)	11 (6%)	0	100	100
10	LN	113/145 (78%)	106 (94%)	6 (5%)	1 (1%)	14	42
11	LO	285/296 (96%)	275 (96%)	10 (4%)	0	100	100
12	LP	219/251 (87%)	214 (98%)	5 (2%)	0	100	100
13	LQ	150/175 (86%)	142 (95%)	7 (5%)	1 (1%)	18	47
14	LR	144/179 (80%)	138 (96%)	6 (4%)	0	100	100
15	LS	217/292 (74%)	198 (91%)	19 (9%)	0	100	100
16	LT	138/149 (93%)	134 (97%)	4 (3%)	0	100	100
17	LU	158/205 (77%)	151 (96%)	7 (4%)	0	100	100
18	LV	164/212 (77%)	151 (92%)	13 (8%)	0	100	100
19	LW	139/153 (91%)	137 (99%)	2 (1%)	0	100	100
20	LX	200/216 (93%)	182 (91%)	17 (8%)	1 (0%)	24	54
21	La	109/148 (74%)	103 (94%)	5 (5%)	1 (1%)	14	42
22	Lb	241/256 (94%)	233 (97%)	8 (3%)	0	100	100
23	Lu	174/250 (70%)	169 (97%)	5 (3%)	0	100	100
24	Ld	118/161 (73%)	116 (98%)	2 (2%)	0	100	100
25	Lf	106/188 (56%)	101 (95%)	5 (5%)	0	100	100
26	Lg	50/65 (77%)	50 (100%)	0	0	100	100
27	Lh	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
28	Li	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
29	Lj	36/103 (35%)	36 (100%)	0	0	100	100
30	Lk	392/423 (93%)	383 (98%)	9 (2%)	0	100	100
31	Ll	352/380 (93%)	321 (91%)	31 (9%)	0	100	100
32	Lm	291/338 (86%)	280 (96%)	11 (4%)	0	100	100
33	Ln	97/206 (47%)	84 (87%)	13 (13%)	0	100	100
34	Lo	122/137 (89%)	116 (95%)	6 (5%)	0	100	100
35	Lp	93/142 (66%)	88 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Lq	146/215 (68%)	133 (91%)	13 (9%)	0	100	100
37	Lr	271/332 (82%)	264 (97%)	7 (3%)	0	100	100
38	Ls	210/306 (69%)	204 (97%)	6 (3%)	0	100	100
39	Lt	211/279 (76%)	189 (90%)	20 (10%)	2 (1%)	14	42
40	Lv	125/212 (59%)	121 (97%)	4 (3%)	0	100	100
41	Lw	130/166 (78%)	119 (92%)	10 (8%)	1 (1%)	16	44
42	Lx	108/158 (68%)	105 (97%)	3 (3%)	0	100	100
43	Ly	95/128 (74%)	91 (96%)	4 (4%)	0	100	100
44	Lz	90/123 (73%)	85 (94%)	5 (6%)	0	100	100
45	L3	94/112 (84%)	89 (95%)	5 (5%)	0	100	100
46	L4	81/138 (59%)	74 (91%)	7 (9%)	0	100	100
47	L5	43/128 (34%)	40 (93%)	3 (7%)	0	100	100
48	L6	92/102 (90%)	90 (98%)	2 (2%)	0	100	100
49	L7	119/206 (58%)	112 (94%)	7 (6%)	0	100	100
50	L8	126/222 (57%)	124 (98%)	2 (2%)	0	100	100
51	SR	140/196 (71%)	136 (97%)	4 (3%)	0	100	100
52	Sf	366/439 (83%)	350 (96%)	15 (4%)	1 (0%)	36	65
53	u	109/234 (47%)	103 (94%)	4 (4%)	2 (2%)	6	26
54	v	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
55	w	77/156 (49%)	71 (92%)	6 (8%)	0	100	100
All	All	8325/11134 (75%)	7894 (95%)	421 (5%)	10 (0%)	49	78

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	Lt	266	PRO
39	Lt	270	ALA
10	LN	132	GLY
52	Sf	260	GLU
53	u	120	TYR
20	LX	211	LYS
53	u	119	ARG
21	La	108	PRO
41	Lw	69	PRO
13	LQ	111	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	LB	191/245 (78%)	191 (100%)	0	100	100
4	LC	258/290 (89%)	253 (98%)	5 (2%)	50	66
5	LD	217/262 (83%)	217 (100%)	0	100	100
6	LI	86/228 (38%)	86 (100%)	0	100	100
7	LJ	145/232 (62%)	145 (100%)	0	100	100
8	LK	138/150 (92%)	138 (100%)	0	100	100
9	LM	155/156 (99%)	155 (100%)	0	100	100
10	LN	98/124 (79%)	94 (96%)	4 (4%)	27	52
11	LO	245/249 (98%)	245 (100%)	0	100	100
12	LP	188/211 (89%)	188 (100%)	0	100	100
13	LQ	133/150 (89%)	133 (100%)	0	100	100
14	LR	128/154 (83%)	127 (99%)	1 (1%)	73	77
15	LS	201/256 (78%)	201 (100%)	0	100	100
16	LT	118/126 (94%)	115 (98%)	3 (2%)	42	62
17	LU	145/180 (81%)	143 (99%)	2 (1%)	59	70
18	LV	146/182 (80%)	146 (100%)	0	100	100
19	LW	128/135 (95%)	126 (98%)	2 (2%)	55	68
20	LX	180/191 (94%)	177 (98%)	3 (2%)	53	67
21	La	91/119 (76%)	90 (99%)	1 (1%)	65	74
22	Lb	219/229 (96%)	219 (100%)	0	100	100
23	Lu	159/223 (71%)	159 (100%)	0	100	100
24	Ld	111/147 (76%)	111 (100%)	0	100	100
25	Lf	97/164 (59%)	97 (100%)	0	100	100
26	Lg	49/60 (82%)	49 (100%)	0	100	100
27	Lh	40/72 (56%)	40 (100%)	0	100	100
28	Li	88/166 (53%)	88 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Lj	37/89 (42%)	37 (100%)	0	100	100
30	Lk	353/368 (96%)	353 (100%)	0	100	100
31	Ll	313/332 (94%)	313 (100%)	0	100	100
32	Lm	269/303 (89%)	268 (100%)	1 (0%)	84	83
33	Ln	91/190 (48%)	91 (100%)	0	100	100
34	Lo	104/112 (93%)	104 (100%)	0	100	100
35	Lp	93/133 (70%)	93 (100%)	0	100	100
36	Lq	130/186 (70%)	130 (100%)	0	100	100
37	Lr	241/288 (84%)	240 (100%)	1 (0%)	84	83
38	Ls	196/274 (72%)	196 (100%)	0	100	100
39	Lt	188/236 (80%)	188 (100%)	0	100	100
40	Lv	117/188 (62%)	117 (100%)	0	100	100
41	Lw	122/148 (82%)	121 (99%)	1 (1%)	73	77
42	Lx	104/148 (70%)	104 (100%)	0	100	100
43	Ly	86/110 (78%)	83 (96%)	3 (4%)	32	56
44	Lz	73/97 (75%)	73 (100%)	0	100	100
45	L3	81/90 (90%)	81 (100%)	0	100	100
46	L4	78/116 (67%)	78 (100%)	0	100	100
47	L5	40/113 (35%)	40 (100%)	0	100	100
48	L6	80/87 (92%)	80 (100%)	0	100	100
49	L7	117/181 (65%)	117 (100%)	0	100	100
50	L8	110/178 (62%)	110 (100%)	0	100	100
51	SR	133/169 (79%)	133 (100%)	0	100	100
52	Sf	326/381 (86%)	325 (100%)	1 (0%)	86	84
53	u	105/200 (52%)	102 (97%)	3 (3%)	37	60
54	v	59/60 (98%)	59 (100%)	0	100	100
55	w	73/136 (54%)	73 (100%)	0	100	100
All	All	7473/9614 (78%)	7442 (100%)	31 (0%)	81	83

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LC	45	SER

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Mol	Chain	Res	Type
4	LC	48	TRP
4	LC	264	ILE
4	LC	299	VAL
4	LC	300	LYS
10	LN	127	LEU
10	LN	128	ARG
10	LN	129	LYS
10	LN	130	ARG
14	LR	149	PRO
16	LT	17	ARG
16	LT	44	ARG
16	LT	51	VAL
17	LU	84	ASN
17	LU	118	ASN
19	LW	11	ARG
19	LW	12	LEU
20	LX	209	LYS
20	LX	212	LYS
20	LX	213	VAL
21	La	109	ARG
32	Lm	34	GLN
37	Lr	42	GLN
41	Lw	66	TYR
43	Ly	32	ILE
43	Ly	35	ARG
43	Ly	37	THR
52	Sf	408	ASN
53	u	118	MET
53	u	119	ARG
53	u	121	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (72) such sidechains are listed below:

Mol	Chain	Res	Type
3	LB	168	HIS
4	LC	216	GLN
5	LD	103	GLN
5	LD	105	ASN
5	LD	184	GLN
7	LJ	101	ASN
7	LJ	119	HIS
8	LK	84	GLN

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Mol	Chain	Res	Type
8	LK	116	HIS
8	LK	178	GLN
9	LM	89	GLN
10	LN	89	HIS
10	LN	142	GLN
11	LO	102	GLN
12	LP	117	ASN
12	LP	202	GLN
13	LQ	91	GLN
13	LQ	147	GLN
15	LS	213	GLN
15	LS	239	ASN
17	LU	75	HIS
18	LV	62	GLN
18	LV	195	HIS
20	LX	117	HIS
23	Lu	189	HIS
25	Lf	105	ASN
25	Lf	118	GLN
25	Lf	120	HIS
26	Lg	15	ASN
26	Lg	31	ASN
28	Li	151	ASN
30	Lk	149	ASN
30	Lk	150	GLN
30	Lk	221	GLN
30	Lk	269	ASN
30	Lk	275	ASN
30	Lk	420	HIS
31	Ll	101	GLN
31	Ll	275	GLN
31	Ll	354	GLN
32	Lm	285	ASN
37	Lr	48	GLN
37	Lr	69	HIS
37	Lr	73	GLN
37	Lr	80	GLN
37	Lr	123	GLN
37	Lr	155	ASN
38	Ls	196	GLN
39	Lt	67	GLN
39	Lt	75	GLN

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Mol	Chain	Res	Type
39	Lt	87	HIS
39	Lt	126	GLN
39	Lt	252	HIS
40	Lv	115	ASN
40	Lv	153	HIS
42	Lx	67	GLN
45	L3	15	GLN
45	L3	35	GLN
46	L4	67	GLN
49	L7	104	HIS
50	L8	120	HIS
50	L8	138	GLN
50	L8	139	GLN
51	SR	79	HIS
51	SR	123	HIS
52	Sf	107	GLN
52	Sf	164	HIS
52	Sf	343	GLN
52	Sf	373	GLN
52	Sf	420	GLN
53	u	103	GLN
53	u	178	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L1	1491/1559 (95%)	364 (24%)	19 (1%)
2	L2	51/69 (73%)	16 (31%)	0
All	All	1542/1628 (94%)	380 (24%)	19 (1%)

All (380) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L1	5	A
1	L1	6	A
1	L1	8	C
1	L1	9	U
1	L1	11	G
1	L1	19	C
1	L1	20	C
1	L1	22	A

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Mol	Chain	Res	Type
1	L1	24	U
1	L1	29	C
1	L1	30	U
1	L1	34	U
1	L1	38	A
1	L1	39	G
1	L1	41	C
1	L1	43	A
1	L1	44	C
1	L1	45	C
1	L1	46	U
1	L1	47	U
1	L1	54	A
1	L1	57	A
1	L1	58	U
1	L1	63	C
1	L1	64	C
1	L1	65	A
1	L1	66	A
1	L1	67	A
1	L1	78	G
1	L1	91	A
1	L1	98	G
1	L1	99	C
1	L1	100	G
1	L1	101	C
1	L1	103	A
1	L1	104	U
1	L1	107	A
1	L1	110	U
1	L1	111	A
1	L1	112	G
1	L1	124	A
1	L1	127	G
1	L1	134	A
1	L1	135	A
1	L1	136	U
1	L1	137	U
1	L1	138	A
1	L1	142	C
1	L1	147	C
1	L1	151	A

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Mol	Chain	Res	Type
1	L1	157	C
1	L1	158	A
1	L1	159	A
1	L1	162	A
1	L1	166	A
1	L1	167	C
1	L1	174	A
1	L1	184	U
1	L1	186	A
1	L1	197	A
1	L1	199	A
1	L1	200	A
1	L1	203	A
1	L1	208	U
1	L1	212	A
1	L1	213	G
1	L1	215	A
1	L1	217	A
1	L1	223	A
1	L1	231	C
1	L1	232	C
1	L1	233	C
1	L1	239	A
1	L1	248	G
1	L1	265	A
1	L1	266	A
1	L1	267	A
1	L1	268	A
1	L1	269	G
1	L1	270	A
1	L1	274	C
1	L1	288	G
1	L1	298	G
1	L1	314	A
1	L1	315	G
1	L1	317	G
1	L1	322	C
1	L1	323	A
1	L1	324	A
1	L1	330	C
1	L1	331	C
1	L1	332	G

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Mol	Chain	Res	Type
1	L1	333	A
1	L1	345	G
1	L1	346	C
1	L1	352	G
1	L1	359	A
1	L1	360	U
1	L1	362	G
1	L1	366	C
1	L1	367	U
1	L1	369	A
1	L1	375	A
1	L1	385	U
1	L1	387	C
1	L1	390	A
1	L1	392	A
1	L1	393	G
1	L1	395	A
1	L1	404	A
1	L1	413	U
1	L1	415	A
1	L1	426	U
1	L1	427	A
1	L1	429	U
1	L1	443	G
1	L1	454	A
1	L1	455	C
1	L1	456	U
1	L1	463	A
1	L1	464	A
1	L1	465	A
1	L1	471	U
1	L1	472	A
1	L1	477	G
1	L1	488	U
1	L1	489	U
1	L1	493	A
1	L1	496	C
1	L1	498	U
1	L1	501	U
1	L1	502	A
1	L1	503	G
1	L1	508	A

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Mol	Chain	Res	Type
1	L1	510	A
1	L1	511	A
1	L1	512	G
1	L1	514	A
1	L1	517	C
1	L1	518	A
1	L1	519	C
1	L1	524	U
1	L1	525	A
1	L1	526	A
1	L1	527	G
1	L1	528	A
1	L1	530	A
1	L1	531	G
1	L1	532	C
1	L1	540	C
1	L1	546	A
1	L1	550	A
1	L1	551	C
1	L1	552	U
1	L1	553	A
1	L1	555	C
1	L1	557	A
1	L1	558	A
1	L1	563	U
1	L1	567	A
1	L1	569	A
1	L1	571	A
1	L1	572	U
1	L1	573	A
1	L1	575	A
1	L1	576	A
1	L1	592	C
1	L1	593	C
1	L1	612	C
1	L1	614	C
1	L1	615	U
1	L1	620	A
1	L1	627	A
1	L1	630	G
1	L1	653	A
1	L1	654	U

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Mol	Chain	Res	Type
1	L1	662	C
1	L1	672	U
1	L1	675	G
1	L1	699	A
1	L1	700	A
1	L1	701	U
1	L1	704	A
1	L1	711	A
1	L1	720	A
1	L1	723	C
1	L1	731	A
1	L1	737	U
1	L1	744	C
1	L1	745	C
1	L1	746	U
1	L1	756	C
1	L1	757	C
1	L1	762	A
1	L1	771	C
1	L1	773	C
1	L1	774	A
1	L1	775	U
1	L1	777	A
1	L1	779	G
1	L1	794	G
1	L1	808	G
1	L1	809	C
1	L1	814	C
1	L1	823	C
1	L1	830	A
1	L1	832	C
1	L1	834	A
1	L1	836	A
1	L1	837	A
1	L1	838	C
1	L1	841	C
1	L1	850	C
1	L1	851	A
1	L1	853	C
1	L1	854	A
1	L1	857	A
1	L1	860	A

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Mol	Chain	Res	Type
1	L1	861	U
1	L1	869	A
1	L1	870	C
1	L1	874	C
1	L1	887	C
1	L1	888	A
1	L1	889	U
1	L1	890	G
1	L1	900	C
1	L1	904	G
1	L1	907	C
1	L1	911	A
1	L1	912	A
1	L1	913	C
1	L1	918	C
1	L1	922	G
1	L1	923	G
1	L1	930	A
1	L1	931	A
1	L1	932	U
1	L1	933	C
1	L1	934	A
1	L1	936	U
1	L1	948	U
1	L1	956	U
1	L1	957	G
1	L1	958	U
1	L1	959	A
1	L1	960	U
1	L1	962	A
1	L1	963	A
1	L1	964	U
1	L1	965	G
1	L1	975	G
1	L1	984	U
1	L1	985	G
1	L1	986	U
1	L1	990	U
1	L1	1013	C
1	L1	1014	C
1	L1	1016	G
1	L1	1024	A

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Mol	Chain	Res	Type
1	L1	1026	A
1	L1	1027	G
1	L1	1028	G
1	L1	1029	C
1	L1	1032	G
1	L1	1036	A
1	L1	1039	A
1	L1	1048	C
1	L1	1049	G
1	L1	1053	A
1	L1	1054	G
1	L1	1055	A
1	L1	1056	C
1	L1	1060	A
1	L1	1062	G
1	L1	1069	U
1	L1	1073	U
1	L1	1074	U
1	L1	1075	A
1	L1	1087	A
1	L1	1088	G
1	L1	1140	G
1	L1	1161	G
1	L1	1162	A
1	L1	1163	A
1	L1	1177	C
1	L1	1184	U
1	L1	1191	A
1	L1	1194	U
1	L1	1195	C
1	L1	1222	A
1	L1	1223	A
1	L1	1225	U
1	L1	1236	C
1	L1	1240	A
1	L1	1241	C
1	L1	1242	C
1	L1	1243	A
1	L1	1246	G
1	L1	1247	G
1	L1	1252	A
1	L1	1256	A

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Mol	Chain	Res	Type
1	L1	1258	C
1	L1	1262	G
1	L1	1265	A
1	L1	1286	A
1	L1	1293	A
1	L1	1304	A
1	L1	1308	U
1	L1	1309	U
1	L1	1311	A
1	L1	1319	G
1	L1	1320	A
1	L1	1322	G
1	L1	1323	U
1	L1	1324	U
1	L1	1330	A
1	L1	1335	A
1	L1	1337	C
1	L1	1346	G
1	L1	1351	C
1	L1	1352	G
1	L1	1371	U
1	L1	1372	U
1	L1	1379	U
1	L1	1383	A
1	L1	1384	G
1	L1	1386	C
1	L1	1389	A
1	L1	1393	G
1	L1	1416	U
1	L1	1419	A
1	L1	1426	U
1	L1	1430	U
1	L1	1432	U
1	L1	1438	U
1	L1	1439	U
1	L1	1442	A
1	L1	1444	U
1	L1	1452	U
1	L1	1461	G
1	L1	1471	A
1	L1	1480	U
1	L1	1485	C

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Mol	Chain	Res	Type
1	L1	1487	C
1	L1	1488	A
1	L1	1492	C
1	L1	1498	C
1	L1	1499	C
1	L1	1502	C
1	L1	1506	A
1	L1	1510	A
1	L1	1513	U
1	L1	1520	A
1	L1	1522	C
1	L1	1536	C
1	L1	1537	A
1	L1	1539	A
1	L1	1540	C
1	L1	1542	C
1	L1	1547	A
1	L1	1548	A
1	L1	1550	A
1	L1	1558	U
2	L2	1605	A
2	L2	1608	G
2	L2	1609	U
2	L2	1610	A
2	L2	1611	G
2	L2	1613	U
2	L2	1614	U
2	L2	1615	A
2	L2	1627	C
2	L2	1628	C
2	L2	1641	G
2	L2	1644	G
2	L2	1650	A
2	L2	1651	A
2	L2	1669	G
2	L2	1670	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L1	33	C
1	L1	63	C

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Mol	Chain	Res	Type
1	L1	135	A
1	L1	136	U
1	L1	137	U
1	L1	267	A
1	L1	393	G
1	L1	516	C
1	L1	551	C
1	L1	575	A
1	L1	837	A
1	L1	853	C
1	L1	860	A
1	L1	889	U
1	L1	930	A
1	L1	1235	A
1	L1	1319	G
1	L1	1371	U
1	L1	1536	C

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 100 ligands modelled in this entry, 98 are monoatomic - leaving 2 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	PNS	v	101	-	14,20,21	2.34	4 (28%)	18,26,29	3.01	7 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	T1C	L1	1692	56	45,45,45	1.14	4 (8%)	56,72,72	1.04	5 (8%)

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	PNS	v	101	-	-	12/24/26/27	-
57	T1C	L1	1692	56	-	11/22/80/80	0/4/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	v	101	PNS	C39-N41	5.72	1.46	1.33
57	L1	1692	T1C	C21-N21	5.02	1.47	1.33
59	v	101	PNS	C34-N36	5.01	1.45	1.33
59	v	101	PNS	O40-C39	-2.78	1.17	1.23
57	L1	1692	T1C	C4-N4	2.30	1.52	1.47
57	L1	1692	T1C	O11-C11	2.24	1.27	1.23
59	v	101	PNS	O35-C34	-2.20	1.19	1.23
57	L1	1692	T1C	C7-N7	2.15	1.48	1.42

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	v	101	PNS	C38-C39-N41	7.21	129.47	116.34
59	v	101	PNS	O40-C39-C38	-6.01	111.13	122.02
59	v	101	PNS	C42-N41-C39	4.24	130.72	122.82
59	v	101	PNS	C37-N36-C34	-3.92	115.51	122.55
59	v	101	PNS	C32-C34-N36	3.19	122.54	116.48
57	L1	1692	T1C	C1-C1C-C12	3.14	113.56	109.88
59	v	101	PNS	C37-C38-C39	2.96	117.33	112.39
59	v	101	PNS	C30-C29-C28	2.95	113.09	108.22
57	L1	1692	T1C	C11-C1B-C12	2.88	121.08	118.80
57	L1	1692	T1C	O1C-C1C-C12	-2.75	105.75	110.14
57	L1	1692	T1C	C1C-C41-C4	2.68	115.31	111.64
57	L1	1692	T1C	C1C-C1-C2	2.14	119.14	115.75

There are no chirality outliers.

All (23) torsion outliers are listed below:

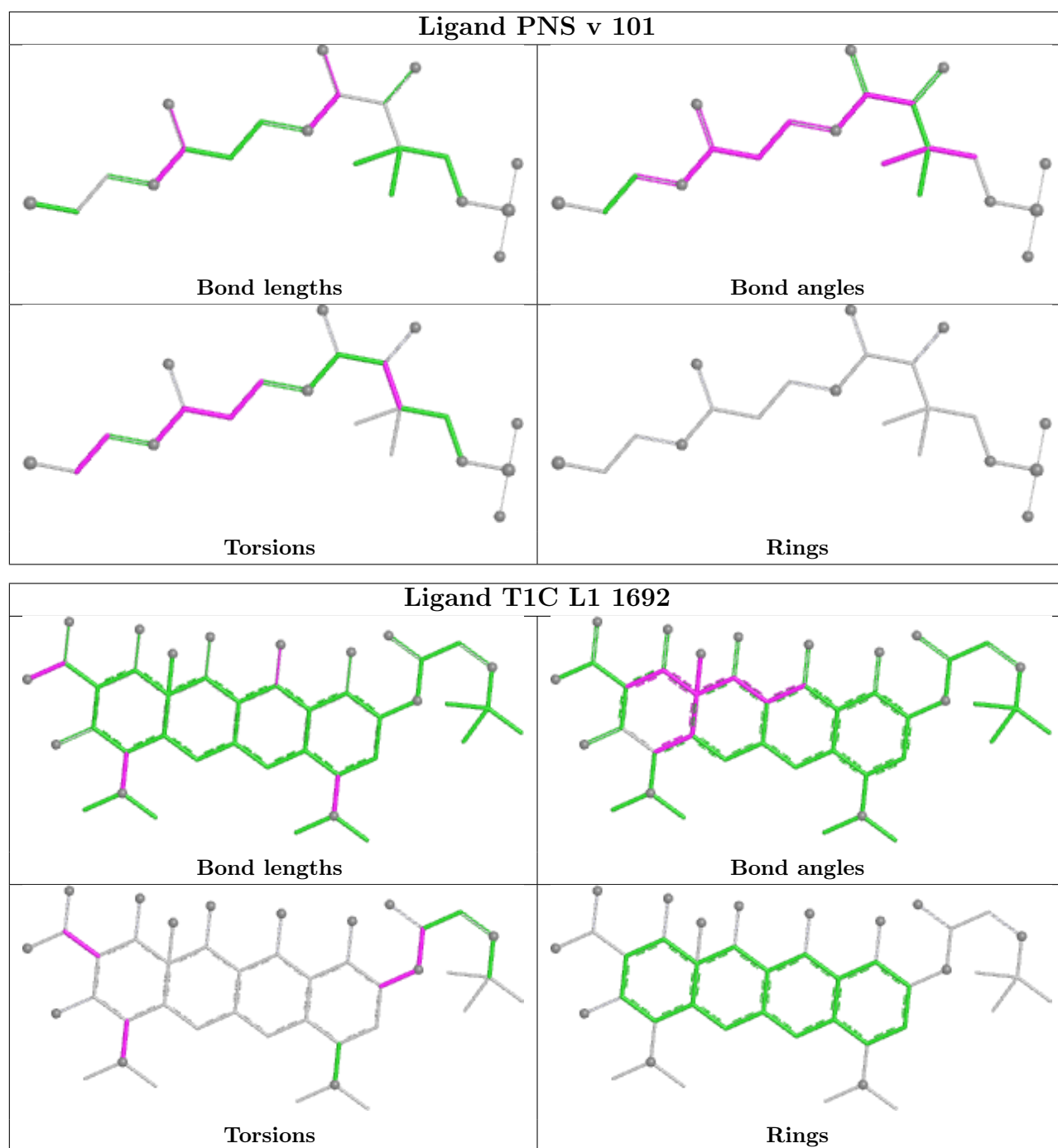
Mol	Chain	Res	Type	Atoms
57	L1	1692	T1C	C92-C91-N9-C9
57	L1	1692	T1C	C41-C4-N4-C43
57	L1	1692	T1C	C3-C4-N4-C43
57	L1	1692	T1C	C3-C4-N4-C42
57	L1	1692	T1C	C3-C2-C21-O21
57	L1	1692	T1C	C3-C2-C21-N21
57	L1	1692	T1C	C1-C2-C21-O21
59	v	101	PNS	C28-C29-C32-O33
59	v	101	PNS	C28-C29-C32-C34
59	v	101	PNS	C30-C29-C32-O33
59	v	101	PNS	C30-C29-C32-C34
59	v	101	PNS	C31-C29-C32-O33
59	v	101	PNS	C31-C29-C32-C34
59	v	101	PNS	N41-C42-C43-S44
57	L1	1692	T1C	O91-C91-N9-C9
59	v	101	PNS	C38-C39-N41-C42
59	v	101	PNS	O40-C39-N41-C42
59	v	101	PNS	N36-C37-C38-C39
57	L1	1692	T1C	C41-C4-N4-C42
57	L1	1692	T1C	C1-C2-C21-N21
59	v	101	PNS	C37-C38-C39-O40
57	L1	1692	T1C	C10-C9-N9-C91
59	v	101	PNS	C37-C38-C39-N41

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	v	101	PNS	3	0
57	L1	1692	T1C	1	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](#)

There are no chain breaks in this entry.

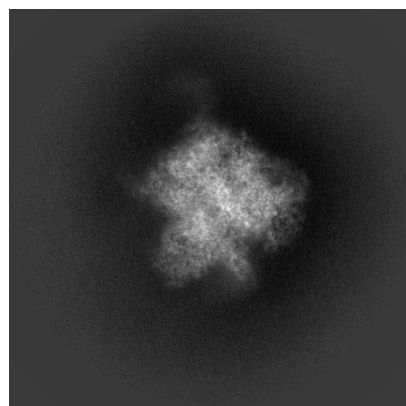
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36837. These allow visual inspection of the internal detail of the map and identification of artifacts.

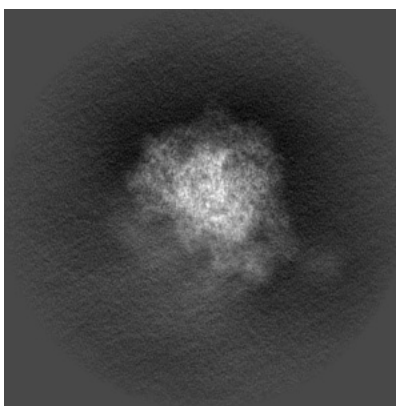
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

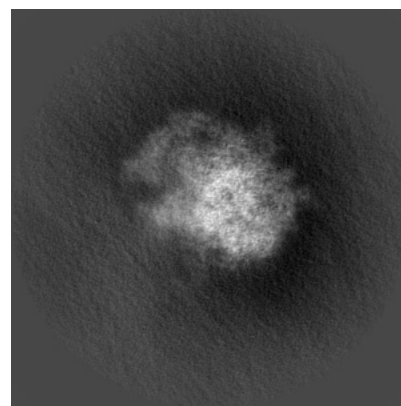
6.1.1 Primary map



X

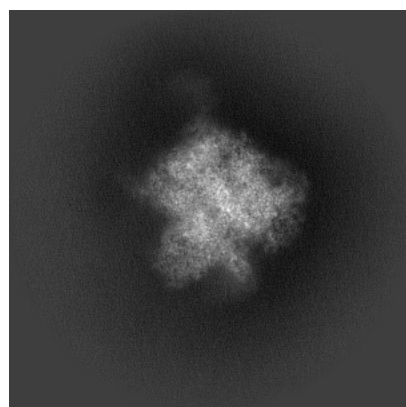


Y

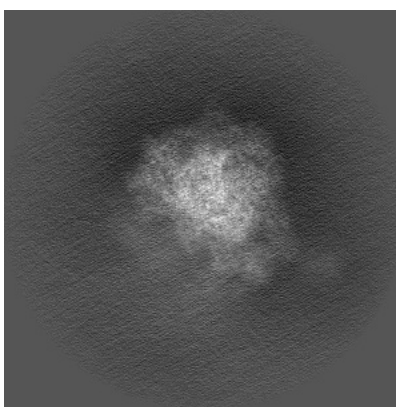


Z

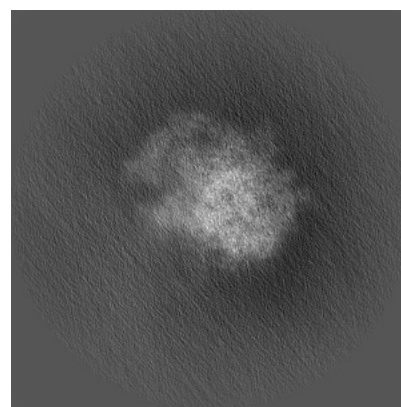
6.1.2 Raw map



X



Y

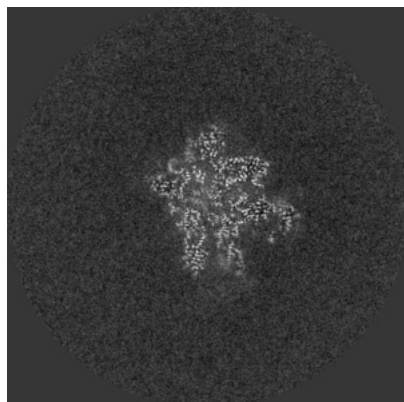


Z

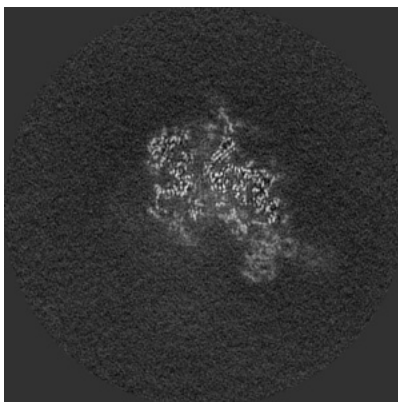
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

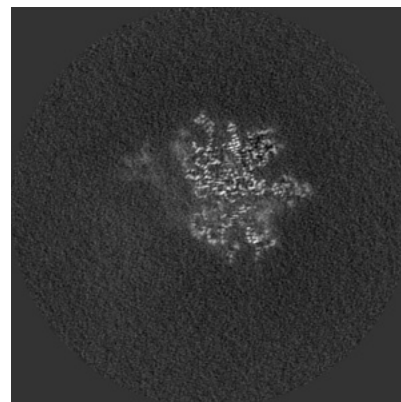
6.2.1 Primary map



X Index: 210

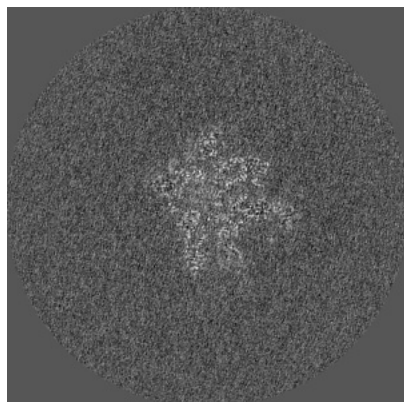


Y Index: 210

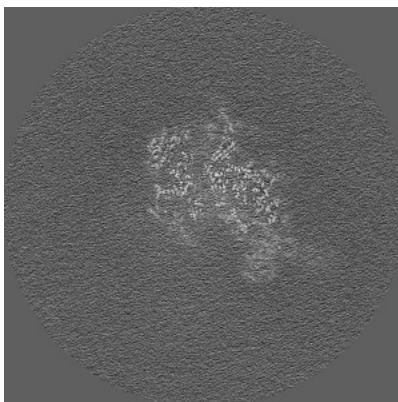


Z Index: 210

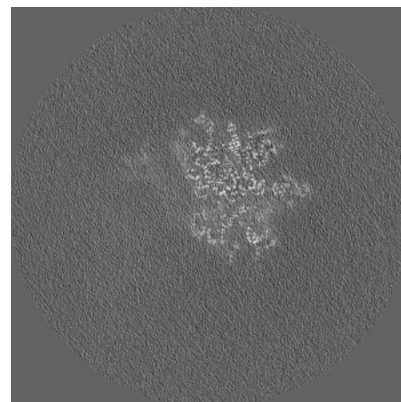
6.2.2 Raw map



X Index: 210



Y Index: 210

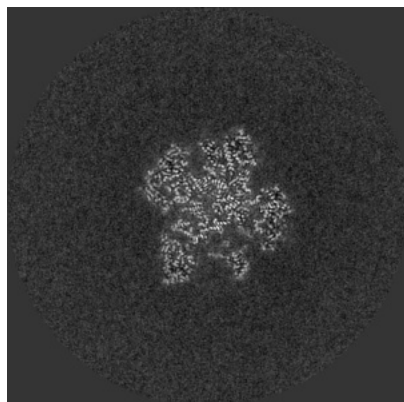


Z Index: 210

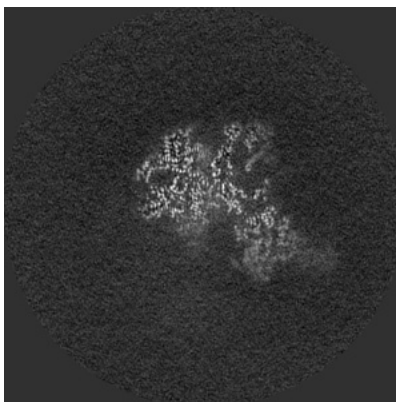
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

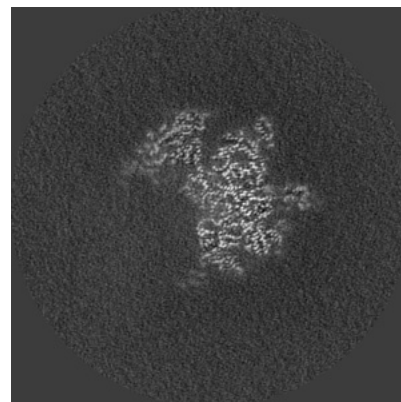
6.3.1 Primary map



X Index: 234

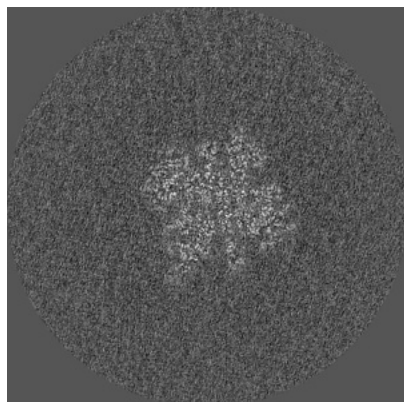


Y Index: 201

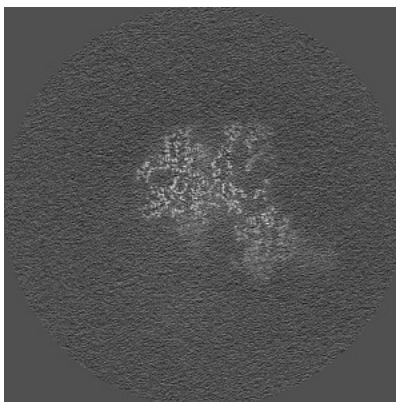


Z Index: 226

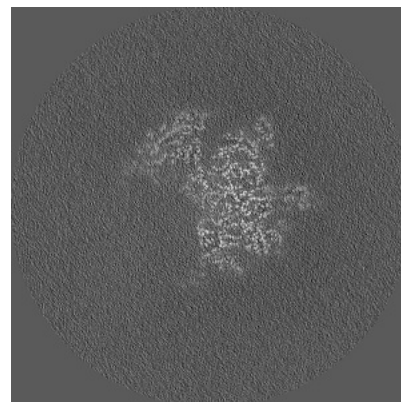
6.3.2 Raw map



X Index: 228



Y Index: 201

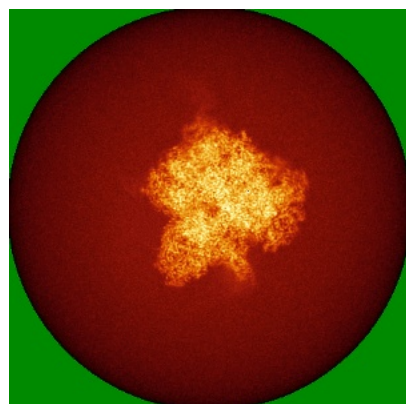


Z Index: 226

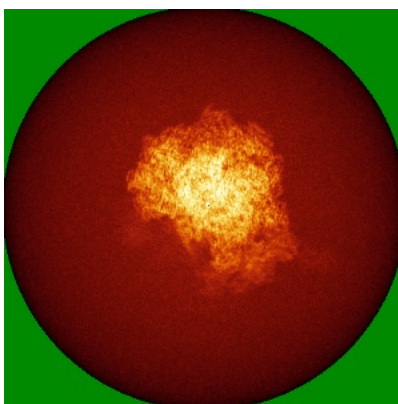
The images above show the largest variance slices of the map in three orthogonal directions.

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

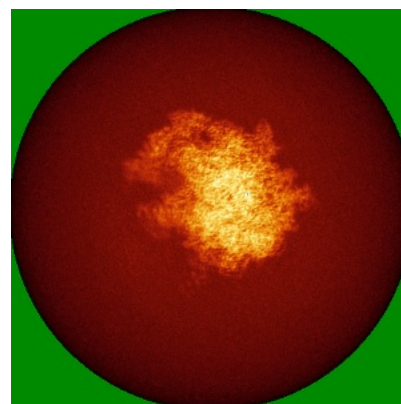
6.4.1 Primary map



X

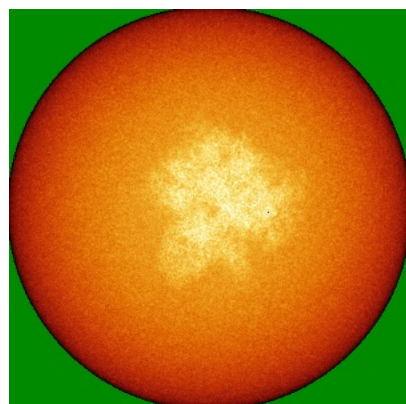


Y

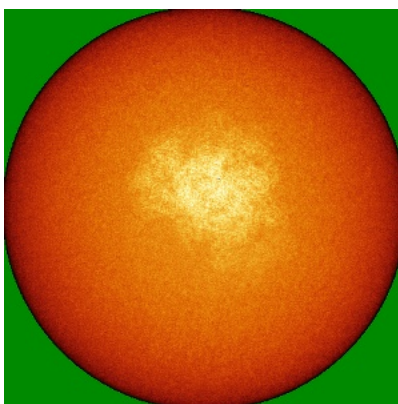


Z

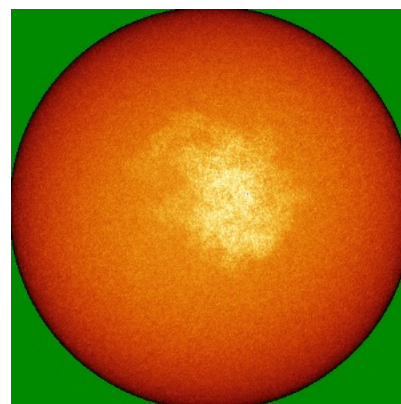
6.4.2 Raw map



X



Y



Z

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

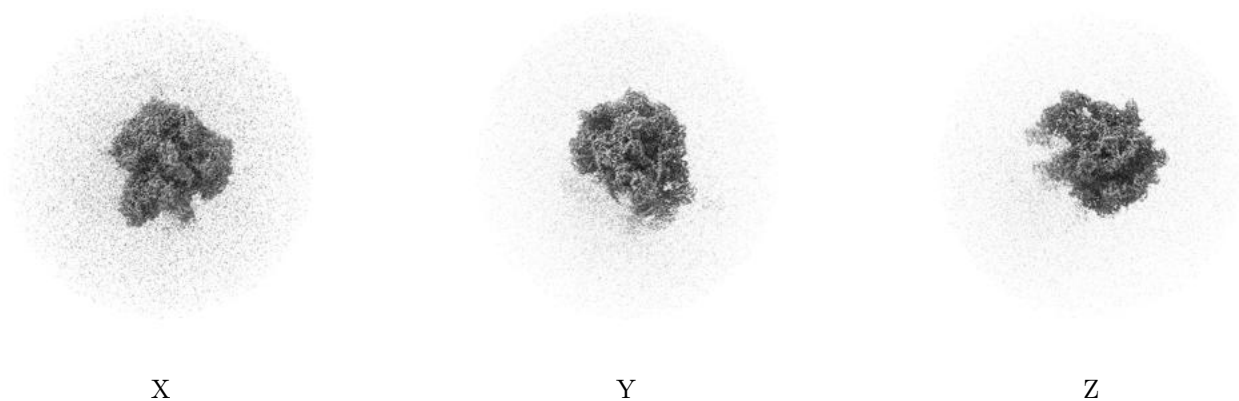
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

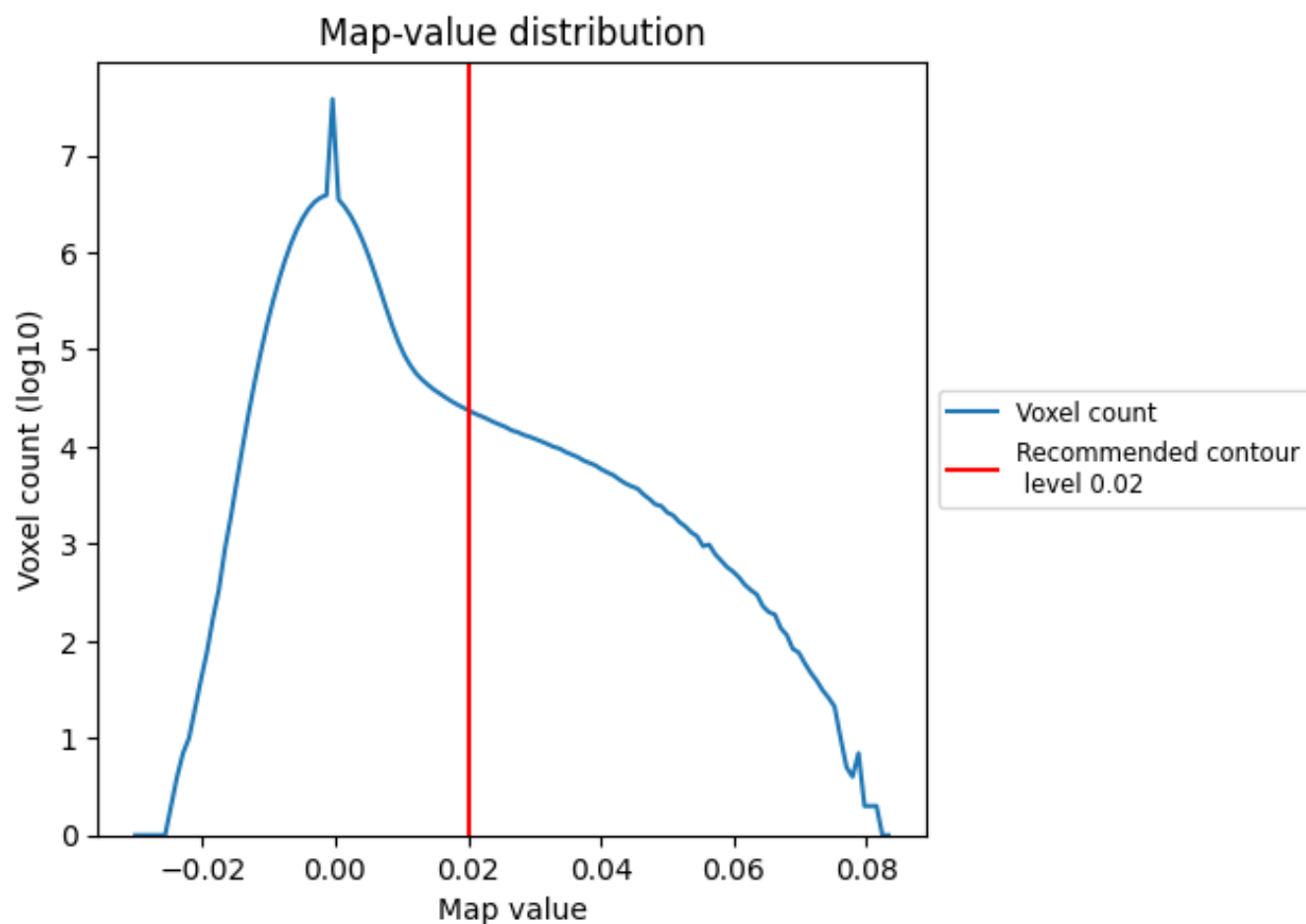
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

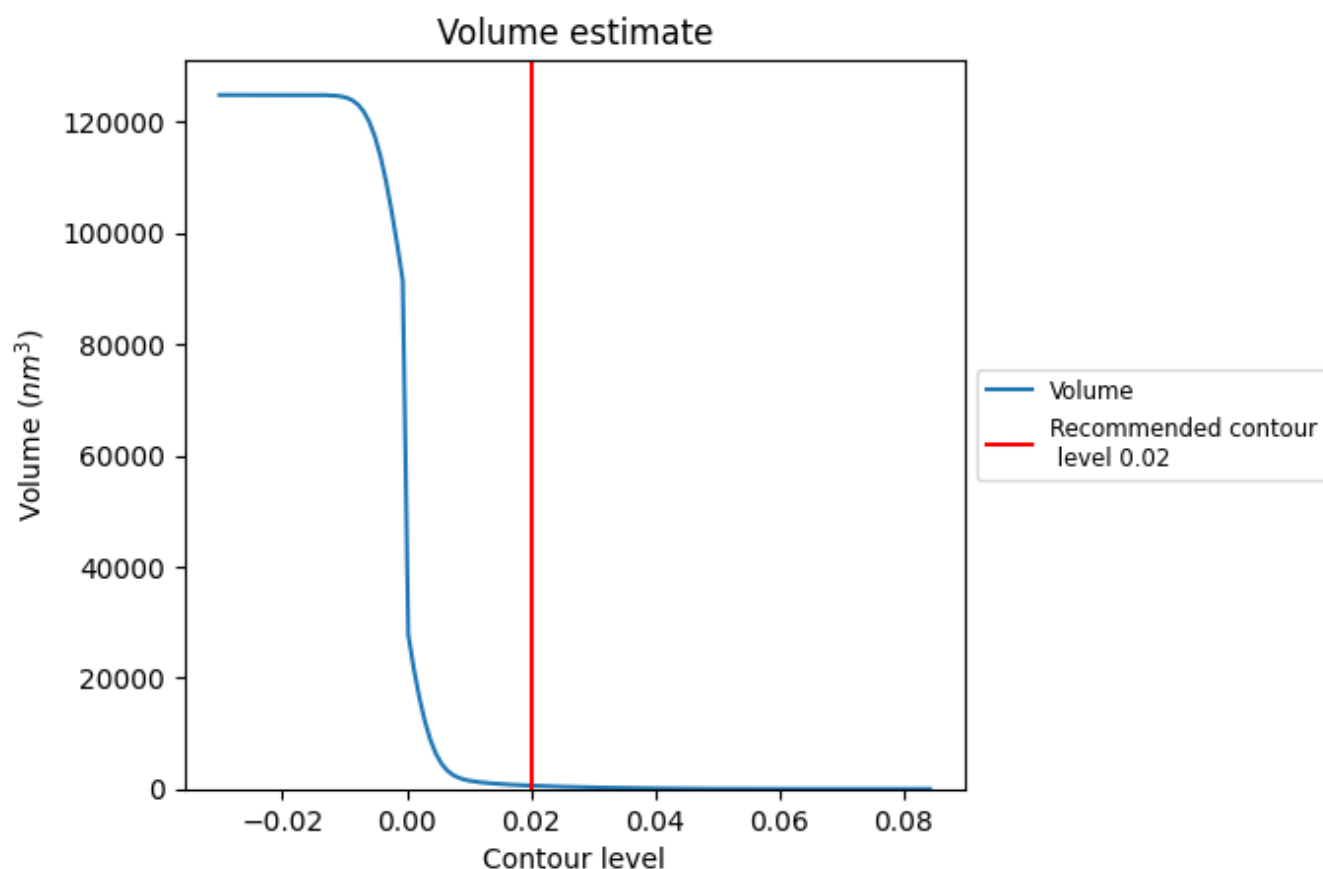
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

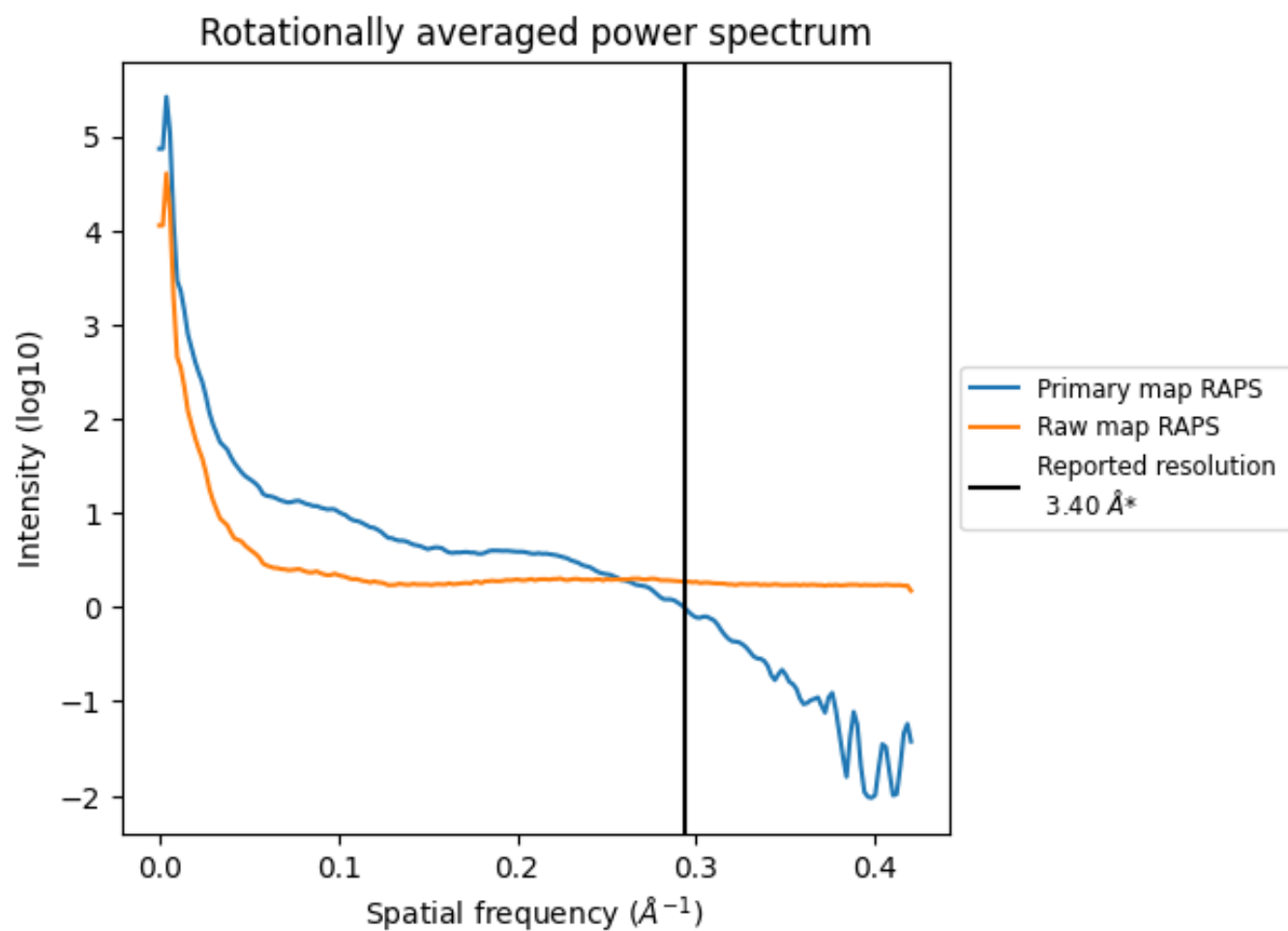
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 603 nm^3 ; this corresponds to an approximate mass of 544 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

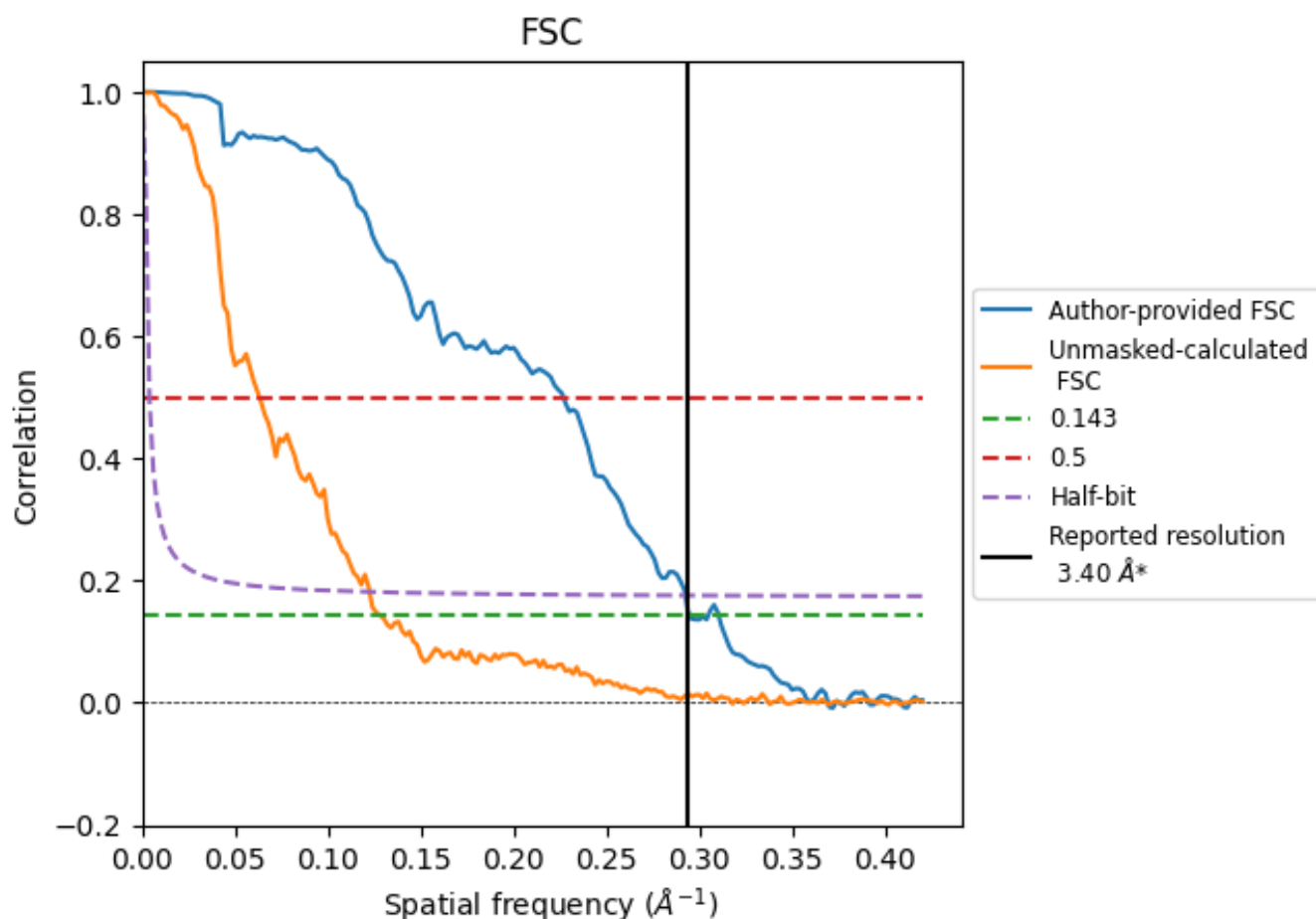


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

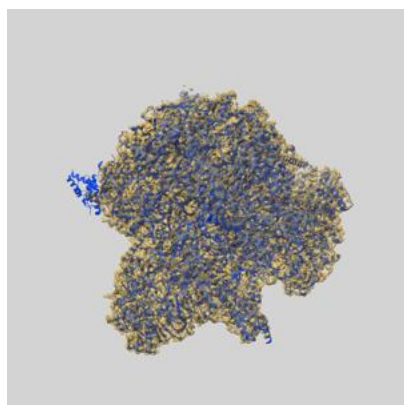
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.39	4.41	3.42
Unmasked-calculated*	7.81	15.82	8.16

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.81 differs from the reported value 3.4 by more than 10 %

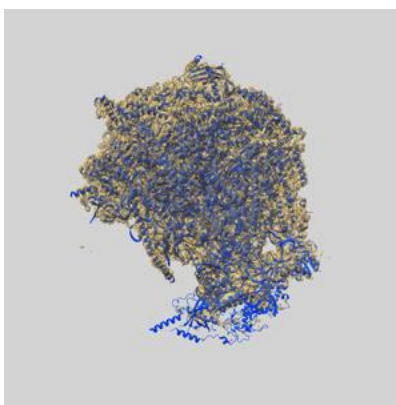
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-36837 and PDB model 8K2B. Per-residue inclusion information can be found in section [3](#) on page [16](#).

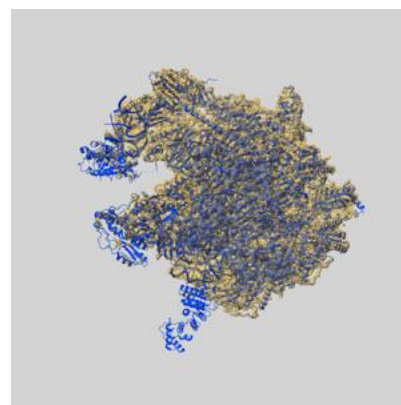
9.1 Map-model overlay [i](#)



X



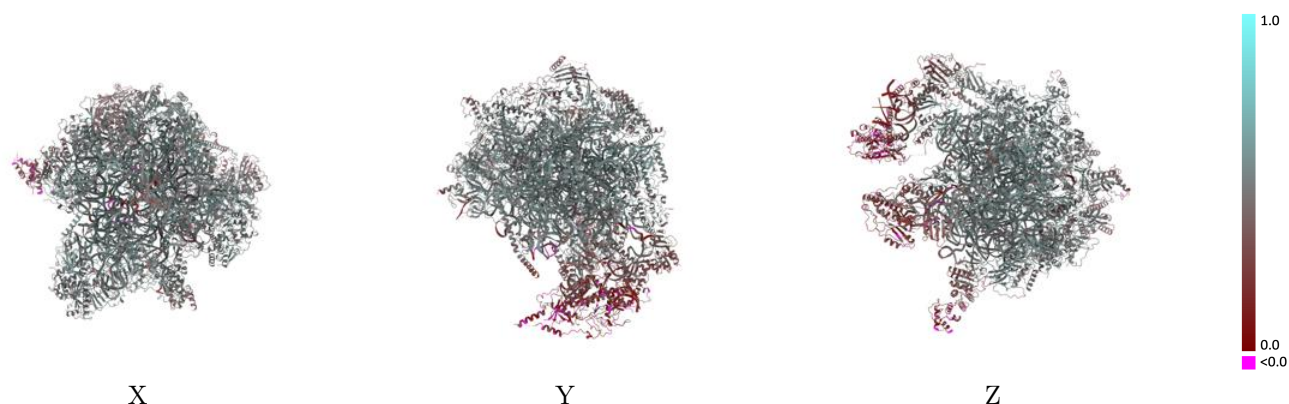
Y



Z

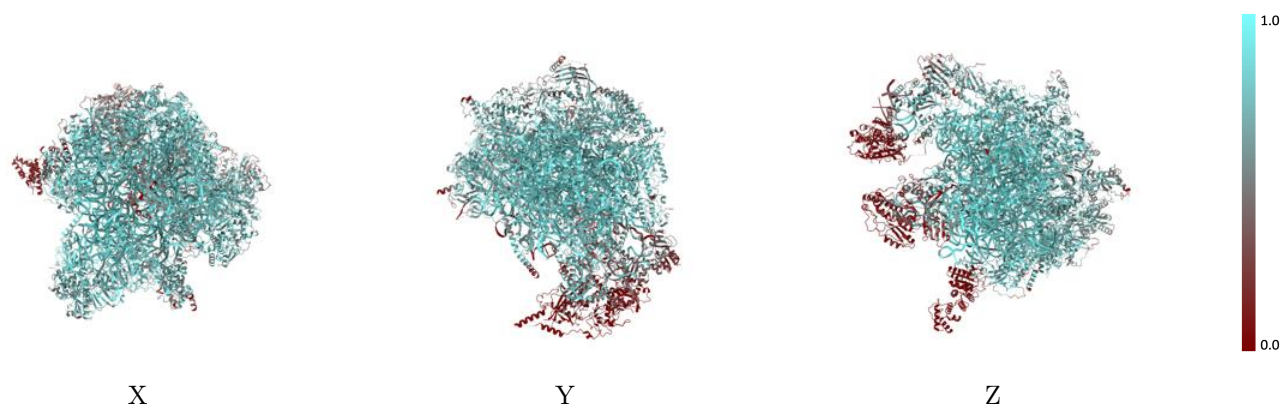
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



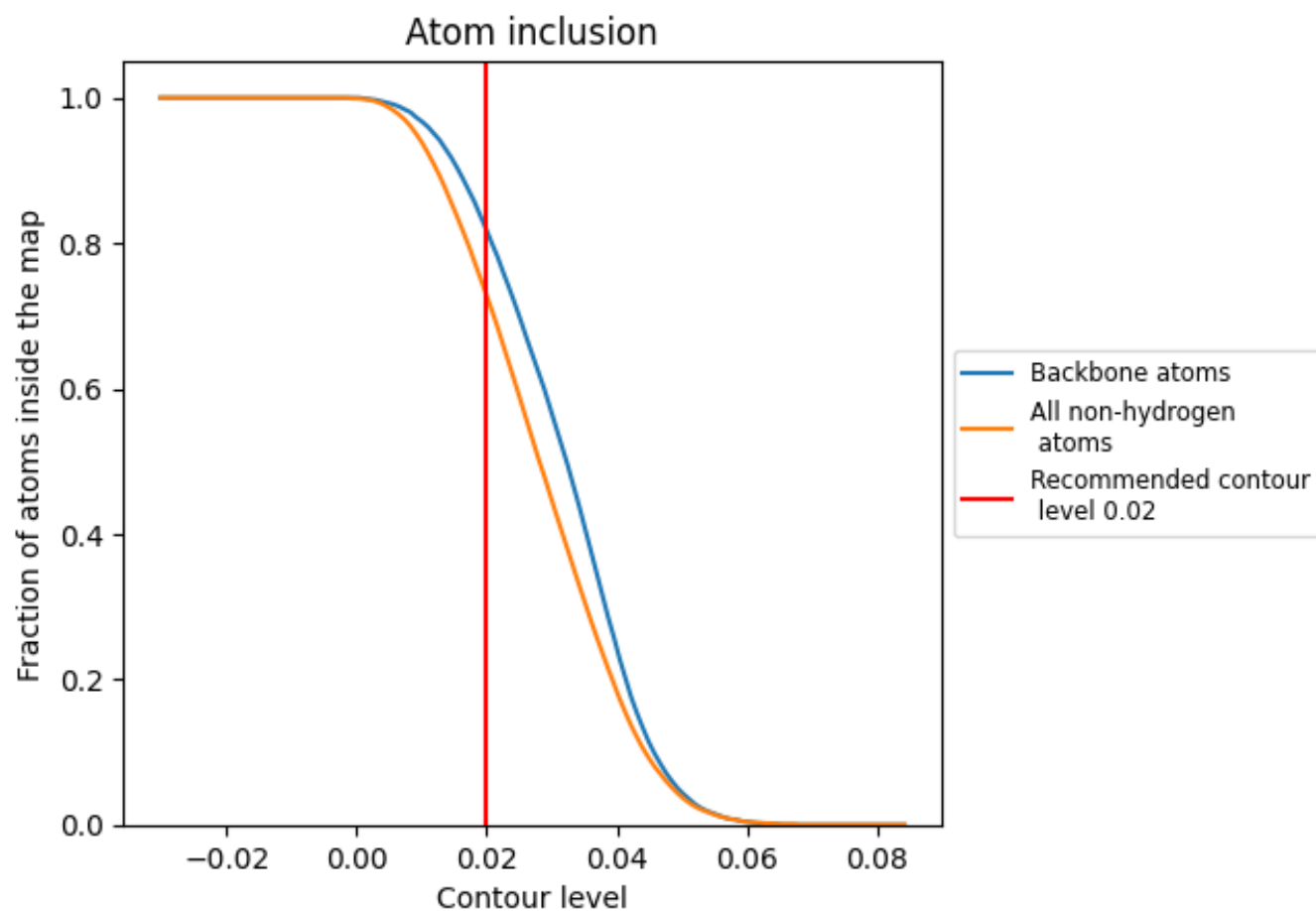
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 73% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7280	 0.4770
L1	 0.9020	 0.5070
L2	 0.5800	 0.2490
L3	 0.3620	 0.3780
L4	 0.1990	 0.2850
L5	 0.0170	 0.1300
L6	 0.8520	 0.5340
L7	 0.6160	 0.4660
L8	 0.6470	 0.4470
LB	 0.7580	 0.5260
LC	 0.7910	 0.5200
LD	 0.8090	 0.5400
LI	 0.6210	 0.4830
LJ	 0.4010	 0.3640
LK	 0.0920	 0.2550
LM	 0.8410	 0.5380
LN	 0.7400	 0.5080
LO	 0.8020	 0.5340
LP	 0.7110	 0.5020
LQ	 0.8140	 0.5250
LR	 0.6630	 0.4390
LS	 0.7280	 0.4940
LT	 0.8370	 0.5390
LU	 0.7760	 0.5290
LV	 0.8150	 0.5320
LW	 0.7460	 0.5160
LX	 0.6110	 0.4560
La	 0.8260	 0.5460
Lb	 0.7190	 0.5050
Ld	 0.8100	 0.5390
Lf	 0.7670	 0.5210
Lg	 0.7450	 0.5150
Lh	 0.9140	 0.5600
Li	 0.8680	 0.5580
Lj	 0.8130	 0.5440



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Chain	Atom inclusion	Q-score
Lk	 0.7370	 0.5060
Ll	 0.5870	 0.3940
Lm	 0.6430	 0.4750
Ln	 0.1080	 0.1920
Lo	 0.7060	 0.5000
Lp	 0.6960	 0.5030
Lq	 0.8240	 0.5470
Lr	 0.7280	 0.5100
Ls	 0.5500	 0.4530
Lt	 0.0310	 0.1460
Lu	 0.7720	 0.5110
Lv	 0.1820	 0.2530
Lw	 0.7670	 0.5210
Lx	 0.6200	 0.4770
Ly	 0.8470	 0.5480
Lz	 0.6980	 0.4890
SR	 0.7860	 0.5210
Sf	 0.7790	 0.5200
u	 0.0520	 0.3420
v	 0.0000	 0.2490
w	 0.0000	 0.1360