



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 06:47 PM UTC

PDB ID : 8I9X / pdb_00008i9x
EMDB ID : EMD-35287
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- Ytm1-1
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 2.80 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

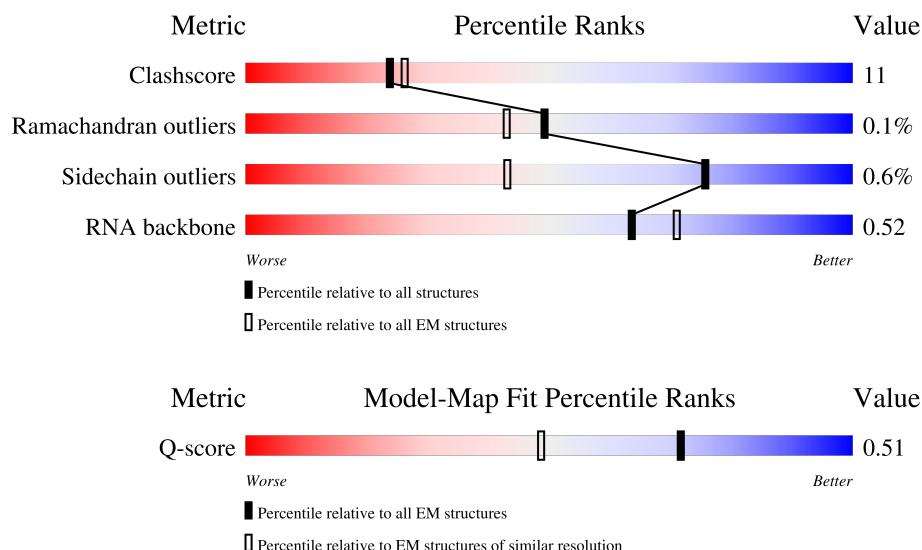
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



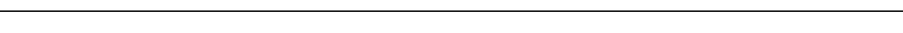
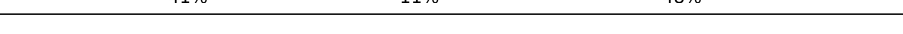
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	C1	3341	
2	C2	319	
3	CA	316	

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Mol	Chain	Length	Quality of chain
4	CB	391	
5	CC	801	
6	CD	495	
7	CE	598	
8	CF	270	
9	CG	184	
10	CH	661	
11	CI	414	
12	CJ	679	
13	CK	261	
14	CL	558	
15	CM	249	
15	LF	249	
16	CN	246	
17	CO	120	
18	CP	751	
19	CQ	225	
20	CR	237	
21	CS	834	
22	CT	688	
23	CU	451	
24	CV	147	
25	CX	203	
26	CY	788	
27	Cb	924	

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Mol	Chain	Length	Quality of chain
28	Cz	123	
29	LB	392	
30	LC	365	
31	LE	200	
32	LG	262	
33	LH	192	
34	LK	165	
35	LL	213	
36	LM	142	
37	LN	203	
38	LO	204	
39	LP	187	
40	LQ	213	
41	LR	2898	
42	LS	174	
43	LT	160	
44	LU	127	
45	LV	139	
46	LX	156	
47	LY	138	
48	LZ	135	
49	Lc	108	
50	Ld	120	
51	Le	131	
52	Lf	109	

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Mol	Chain	Length	Quality of chain
53	Lg	119	
54	Lh	935	
55	Li	110	
56	Lj	95	
57	Lk	81	
58	Ll	51	
59	Lq	217	

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 162633 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA (3341-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	2658	Total	C	N	O	P	0	0
			56864	25379	10296	18531	2658		

- Molecule 2 is a RNA chain called RNA (319-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	256	Total	C	N	O	P	0	0
			5456	2435	974	1791	256		

- Molecule 3 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CA	251	Total	C	N	O	S	0	0
			2069	1324	381	357	7		

- Molecule 4 is a protein called Ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CB	260	Total	C	N	O	S	0	0
			2063	1322	367	371	3		

- Molecule 5 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	CC	658	Total	C	N	O	P	S	0	0
			5297	3368	931	983	2	13		

- Molecule 6 is a protein called Ribosome biogenesis protein YTM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CD	460	Total	C	N	O	S	0	0
			3468	2173	610	679	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CD	88	ASP	GLU	conflict	UNP G0SFB5

- Molecule 7 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CE	462	Total	C	N	O	S	0	0
			3669	2350	642	666	11		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	543	LYS	-	insertion	UNP G0RYU9
CE	544	SER	-	insertion	UNP G0RYU9
CE	545	PHE	-	insertion	UNP G0RYU9
CE	546	GLY	-	insertion	UNP G0RYU9
CE	547	PHE	-	insertion	UNP G0RYU9
CE	548	SER	-	insertion	UNP G0RYU9
CE	549	THR	-	insertion	UNP G0RYU9
CE	550	PRO	-	insertion	UNP G0RYU9
CE	551	PRO	-	insertion	UNP G0RYU9
CE	552	ARG	-	insertion	UNP G0RYU9
CE	553	VAL	-	insertion	UNP G0RYU9
CE	554	ASP	-	insertion	UNP G0RYU9
CE	555	ILE	-	insertion	UNP G0RYU9
CE	556	THR	-	insertion	UNP G0RYU9
CE	557	LEU	-	insertion	UNP G0RYU9
CE	558	SER	-	insertion	UNP G0RYU9
CE	559	ALA	-	insertion	UNP G0RYU9
CE	560	SER	-	insertion	UNP G0RYU9
CE	561	LEU	-	insertion	UNP G0RYU9
CE	562	SER	-	insertion	UNP G0RYU9
CE	563	ARG	-	insertion	UNP G0RYU9
CE	564	ASP	-	insertion	UNP G0RYU9
CE	565	LYS	-	insertion	UNP G0RYU9
CE	566	LYS	-	insertion	UNP G0RYU9
CE	567	PRO	-	insertion	UNP G0RYU9
CE	568	GLN	-	insertion	UNP G0RYU9
CE	569	GLY	-	insertion	UNP G0RYU9
CE	570	ARG	-	insertion	UNP G0RYU9
CE	571	ARG	-	insertion	UNP G0RYU9
CE	572	ALA	-	insertion	UNP G0RYU9

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Chain	Residue	Modelled	Actual	Comment	Reference
CE	573	TYR	-	insertion	UNP G0RYU9
CE	574	GLY	-	insertion	UNP G0RYU9
CE	575	SER	-	insertion	UNP G0RYU9
CE	576	GLN	-	insertion	UNP G0RYU9
CE	577	PRO	-	insertion	UNP G0RYU9
CE	578	ARG	-	insertion	UNP G0RYU9
CE	579	GLN	-	insertion	UNP G0RYU9
CE	580	GLY	-	insertion	UNP G0RYU9
CE	581	GLY	-	insertion	UNP G0RYU9
CE	582	ARG	-	insertion	UNP G0RYU9
CE	583	TYR	-	insertion	UNP G0RYU9
CE	584	LYS	-	insertion	UNP G0RYU9

- Molecule 8 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CF	245	Total	C	N	O	S	0	0
			1945	1222	352	362	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CF	13	ILE	THR	conflict	UNP G0S616
CF	139	THR	PRO	conflict	UNP G0S616
CF	228	ASN	SER	conflict	UNP G0S616
CF	259	ILE	MET	conflict	UNP G0S616

- Molecule 9 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CG	177	Total	C	N	O	S	0	0
			1396	884	247	253	12		

- Molecule 10 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CH	542	Total	C	N	O	S	0	0
			4388	2784	770	818	16		

- Molecule 11 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CI	146	Total	C	N	O	S	0	0
			1196	763	224	204	5		

- Molecule 12 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CJ	494	Total	C	N	O	S	0	0
			4040	2575	719	734	12		

- Molecule 13 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CK	238	Total	C	N	O	S	0	0
			1908	1199	375	330	4		

- Molecule 14 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	CL	397	Total	C	N	O	0	0
			2239	1350	459	430		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CL	69	ARG	ILE	conflict	UNP G0SEW3

- Molecule 15 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CM	223	Total	C	N	O	S	0	0
			1820	1169	340	308	3		
15	LF	247	Total	C	N	O	S	0	0
			2017	1294	376	344	3		

- Molecule 16 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CN	246	Total	C	N	O	S	0	0
			1856	1158	322	369	7		

- Molecule 17 is a protein called DUF2423 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CO	62	Total	C	N	O	S	0	0
			468	290	94	82	2		

- Molecule 18 is a protein called RNA methyltransferase nop2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CP	356	Total	C	N	O	S	0	0
			2798	1777	495	510	16		

- Molecule 19 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CQ	179	Total	C	N	O	S	0	0
			1485	926	304	245	10		

- Molecule 20 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CR	167	Total	C	N	O	S	0	0
			1354	827	278	247	2		

- Molecule 21 is a protein called AdoMet-dependent rRNA methyltransferase SPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CS	262	Total	C	N	O	S	0	0
			2105	1322	399	377	7		

- Molecule 22 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CT	488	Total	C	N	O	S	0	0
			3911	2486	690	719	16		

- Molecule 23 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CU	178	Total	C	N	O	S	0	0
			1415	876	265	271	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
24	CV	139	Total	C	N	O		
			1073	672	213	188	0	0

- Molecule 25 is a protein called 60S ribosomal subunit-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	CX	88	Total	C	N	O	S	
			701	435	128	135	3	0

- Molecule 26 is a protein called Putative NOC2 family protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	CY	410	Total	C	N	O	S	
			3313	2127	597	577	12	0

- Molecule 27 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Cb	642	Total	C	N	O	S	
			5058	3216	918	911	13	0

- Molecule 28 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Cz	70	Total	C	N	O	S	
			592	368	120	101	3	0

- Molecule 29 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	LB	356	Total	C	N	O	S	
			2829	1798	518	501	12	0

- Molecule 30 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	LC	362	Total	C	N	O	S	
			2752	1738	526	479	9	0

- Molecule 31 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LE	179	Total	C	N	O	S	0	0
			1403	898	255	247	3		

- Molecule 32 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LG	204	Total	C	N	O	S	0	0
			1644	1060	297	282	5		

- Molecule 33 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LH	190	Total	C	N	O	S	0	0
			1496	950	268	272	6		

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	TYR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5

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Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LEU	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

- Molecule 34 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LK	145	Total	C	N	O	S	0	0
			1103	695	201	205	2		

- Molecule 35 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LL	117	Total	C	N	O	S	0	0
			964	608	206	148	2		

- Molecule 36 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LM	137	Total	C	N	O	S	0	0
			1101	699	211	190	1		

- Molecule 37 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LN	183	Total	C	N	O	S	0	0
			1563	974	332	253	4		

- Molecule 38 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LO	204	Total	C	N	O	S	0	0
			1618	1039	306	267	6		

- Molecule 39 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LP	169	Total	C	N	O	S	0	0
			1345	835	273	234	3		

- Molecule 40 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LQ	129	Total	C	N	O	S	0	0
			1021	646	200	173	2		

- Molecule 41 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LR	118	Total	C	N	O	S	0	0
			964	607	195	158	4		

- Molecule 42 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LS	174	Total	C	N	O	S	0	0
			1433	922	267	239	5		

- Molecule 43 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LT	126	Total	C	N	O	S	0	0
			1014	643	196	173	2		

- Molecule 44 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LU	105	Total	C	N	O	S	0	0
			850	551	147	151	1		

- Molecule 45 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LV	135	Total	C	N	O	S	0	0
			995	633	185	170	7		

- Molecule 46 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LX	137	Total	C	N	O	S	0	0
			1062	678	194	190			

- Molecule 47 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LY	134	Total	C	N	O	S	0	0
			1065	664	215	184	2		

- Molecule 48 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LZ	135	Total	C	N	O	S	0	0
			1112	713	207	188	4		

- Molecule 49 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lc	98	Total	C	N	O	S	0	0
			731	463	126	137	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ld	109	Total	C	N	O	S	0	0
			890	563	171	155	1		

- Molecule 51 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Le	127	Total	C	N	O	S	0	0
			1025	645	209	164	7		

- Molecule 52 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Lf	108	Total	C	N	O	S	0	0
			862	546	171	144	1		

- Molecule 53 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Lg	117	Total	C	N	O	S	0	0
			930	578	189	159	4		

- Molecule 54 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Lh	121	Total	C	N	O	S	0	0
			995	633	196	166			

- Molecule 55 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Li	88	Total	C	N	O	S	0	0
			731	449	162	119	1		

- Molecule 56 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lj	74	Total	C	N	O	S	0	0
			595	365	132	93	5		

- Molecule 57 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Lk	75	Total	C	N	O	S	0	0
			620	394	117	107	2		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lk	?	-	SER	deletion	UNP G0SG89
Lk	?	-	LYS	deletion	UNP G0SG89
Lk	?	-	ILE	deletion	UNP G0SG89
Lk	?	-	LEU	deletion	UNP G0SG89
Lk	?	-	THR	deletion	UNP G0SG89
Lk	?	-	ILE	deletion	UNP G0SG89

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Chain	Residue	Modelled	Actual	Comment	Reference
Lk	?	-	ALA	deletion	UNP G0SG89
Lk	?	-	PHE	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	LEU	deletion	UNP G0SG89
Lk	?	-	THR	deletion	UNP G0SG89

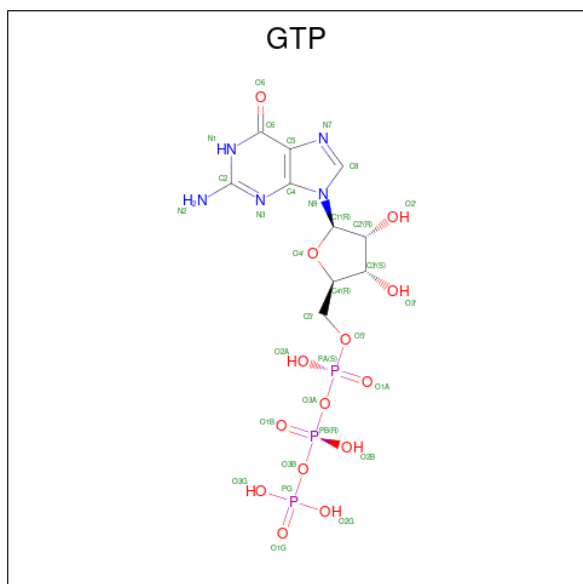
- Molecule 58 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	Ll	38	Total	C	N	O	0	0
			322	204	68	50		

- Molecule 59 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Lq	207	Total	C	N	O	S	0	0
			1600	1016	285	291	8		

- Molecule 60 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
60	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	

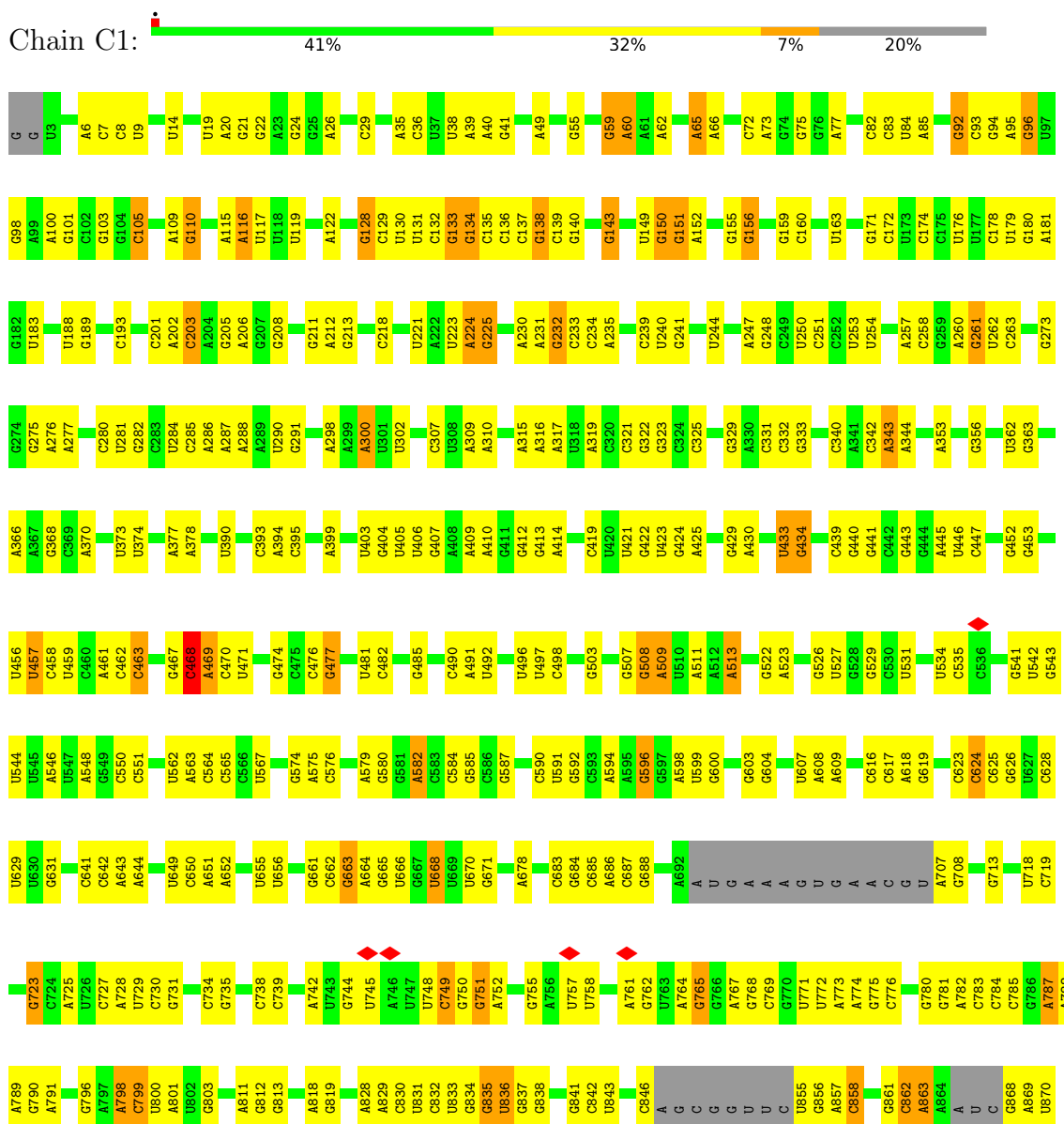
- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	CQ	1	Total 1	Zn 1	0
61	Lj	1	Total 1	Zn 1	0

3 Residue-property plots

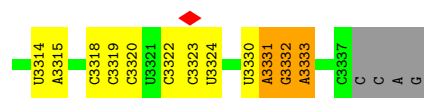
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: RNA (3341-MER)

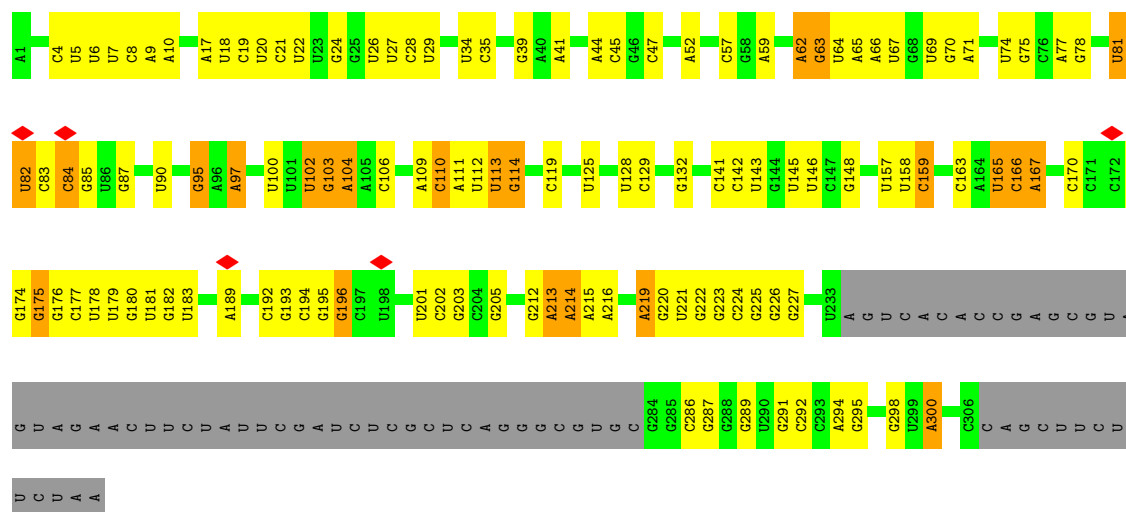




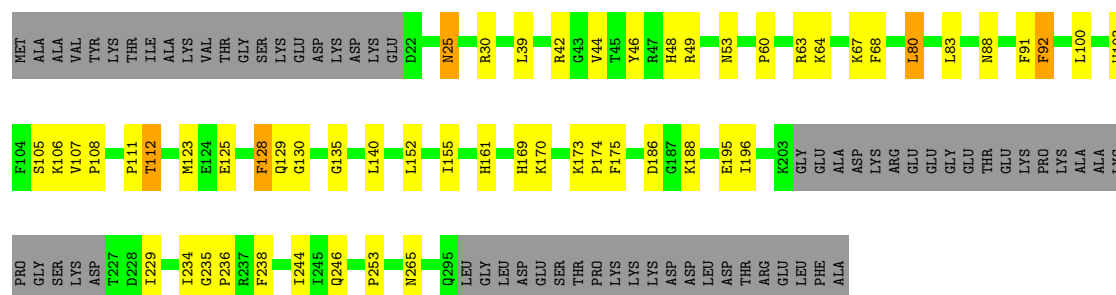
U3217	A3136	G3042	C2768	U	C	G	A2447	U2372	C2300	C	G	A
A3218	A3137	A3043	A2769	A	C	U	A2448	U2373	C2301	A	A	U
G3226	U3138	C3049	C2847	C2941	A	G	U2449	A2374	U2302	A	A	G
A3139	G3140	C3050	A2776	C2942	G	G	A2450	A2375	A2303	A	A	G
G3140	U3064	U3065	A2777	C2943	U	A	C2451	C2381	U2304	U	A	C
C3144	G3066	G3067	A2778	G2948	G	U	C2452	C2382	C2305	G	A	C
C3145	C3067	U2965	U2779	U2941	A	U	A2453	A2385	U2306	C	A	A
G3146	U3068	C2966	U2780	U2942	A	U	A2456	A2386	A2307	U	U	G
G3147	G3069	U2967	U2781	U2943	C	U	U2458	A2387	U2308	U	U	A
U3153	A3070	A2968	G2782	U2944	A	A	U2461	U2388	U2309	G	A	A
A3154	A3071	U2969	C2783	U2945	A	A	A2462	U2389	U2310	U	C	G
U3155	C3072	U2970	U2784	U2946	C	C	U2463	U2390	U2311	C	C	U
G3156	G3073	U2971	U2785	U2947	C	U	U2464	U2391	A2314	A	C	G
C3157	C3074	U2972	G2786	U2948	C	U	G2465	C2392	C2315	U	A	U
U3158	U3075	C2973	U2787	U2949	U	U	U2466	U2393	C2316	C	A	U
A3159	U3076	U2974	G2788	U2950	C	C	U2467	U2394	A2319	U	C	U
C3160	C3077	U2975	U2789	U2951	A	A	U2468	G2395	A2320	A	C	G
C3161	U3078	U2976	C2790	U2952	A	A	U2469	U2396	A2325	U	G	A
A3162	A3079	U2977	U2791	U2953	C	C	U2470	U2397	C2326	C	C	A
G3163	C3084	U2978	U2792	U2954	C	C	U2471	U2398	C2327	G	G	G
G3164	A3085	U2979	U2793	U2955	C	C	U2472	U2399	A2328	U	U	C
C3170	A3086	U2980	C2794	U2956	C	C	U2473	A2400	A2329	G	A	A
C3171	A3087	U2981	A2795	U2957	C	U	U2474	G2401	A2330	A	A	A
C3172	U3088	A2982	A2796	U2958	C	U	U2475	U2413	G2331	C	C	U
C3173	A3089	U2983	U2797	U2959	C	C	U2476	G2414	G2332	C	C	G
G3176	C3100	C2991	U2798	U2960	C	C	U2477	U2415	U2333	G	G	G
G3178	G3101	C2992	U2799	U2961	C	C	U2478	U2416	A2334	G	G	U
C3180	C3102	U2993	U2799	U2962	C	C	U2479	U2417	A2335	C	C	A
U3181	U3103	C3000	U2799	U2963	C	C	U2480	U2418	A2336	C	C	U
U3182	C3104	A3001	U2799	U2964	C	C	U2481	G2419	G2337	U	U	U
C3183	U3111	U2999	U2799	U2965	C	C	U2482	A2420	G2338	G	G	U
G3184	A3112	C3006	U2799	U2966	C	C	U2483	A2421	G2339	A	A	C
A3185	C3113	U2999	U2799	U2967	C	C	U2484	U2422	C2340	U	U	G
U3188	C3114	U3014	U2799	U2968	C	C	U2485	U2423	U2341	G	U	G
G3189	C3115	U3015	U2799	U2969	C	C	U2486	G2424	U2342	G	A	C
G3190	C3116	U3016	U2799	U2970	C	C	U2487	G2425	U2343	G	A	C
C3191	C3117	U3017	U2799	U2971	C	C	U2488	U2426	U2344	G	A	C
A3199	A3118	U3018	U2799	U2972	C	C	U2489	G2427	A2347	U	U	A
C3203	C3119	U3019	U2799	U2973	C	C	U2490	G2428	U2350	U	U	G
G3204	G3120	U3020	U2799	U2974	C	C	U2491	U2429	A2351	A	U	C
C3205	U3121	U3021	U2799	U2975	C	C	U2492	A2430	G2352	C	U	C
G3206	U3122	U3022	U2799	U2976	C	C	U2493	G2431	G2353	U	U	C
U3207	C3123	U3023	U2799	U2977	C	C	U2494	U2432	G2354	C	U	C
U3208	U3124	U3024	U2799	U2978	C	C	U2495	U2433	G2355	C	U	C
U3209	A3125	U3025	U2799	U2979	C	C	U2496	U2434	G2356	C	U	C
U3210	C3126	U3026	U2799	U2980	C	C	U2497	C2435	G2357	C	U	C
A3211	A3127	U3027	U2799	U2981	C	C	U2498	U2436	A2288	U	U	G
C3212	U3130	U3028	U2799	U2982	C	C	U2499	A2359	U2289	C	A	A
A3213	A3131	U3029	U2799	U2983	C	C	U2500	A2360	U2290	C	U	U
U3214	U3132	U3030	U2799	U2984	C	C	U2501	A2361	C2291	C	U	U
U3215	A3133	U3031	U2799	U2985	C	C	U2502	A2362	C2292	A	A	G
U3216	A3134	U3032	U2799	U2986	C	C	U2503	A2363	C2293	A	A	G
G3288	U3281	U3033	U2799	U2987	C	C	U2504	A2364	C2294	C	C	C
C3289	C3182	U3034	U2799	U2988	C	C	U2505	A2365	A2284	C	A	A
C3290	G3183	U3035	U2799	U2989	C	C	U2506	A2366	U2285	C	A	A
U3291	A3184	U3036	U2799	U2990	C	C	U2507	U2370	U2286	C	A	A
U3292	C3185	U3037	U2799	U2991	C	C	U2508	G2371	C2299	C	G	U
G3293	U3186	U3038	U2799	U2992	C	C	U2509					
U3294	C3187	U3039	U2799	U2993	C	C	U2510					
U3295	U3188	U3040	U2799	U2994	C	C	U2511					
G3296	A3189	U3041	U2799	U2995	C	C	U2512					
U3297	C3190	U3042	U2799	U2996	C	C	U2513					
U3298	G3191	U3043	U2799	U2997	C	C	U2514					
A3299	U3192	U3044	U2799	U2998	C	C	U2515					
U3302	C3193	U3045	U2799	U2999	C	C	U2516					
U3303	A3194	U3046	U2799	U3000	C	C	U2517					
C3304	U3195	U3047	U2799	U3001	C	C	U2518					
U3305	C3196	U3048	U2799	U3002	C	C	U2519					
G3306	U3197	U3049	U2799	U3003	C	C	U2520					
C3307	A3198	U3050	U2799	U3004	C	C	U2521					
G3309	U3199	U3051	U2799	U3005	C	C	U2522					



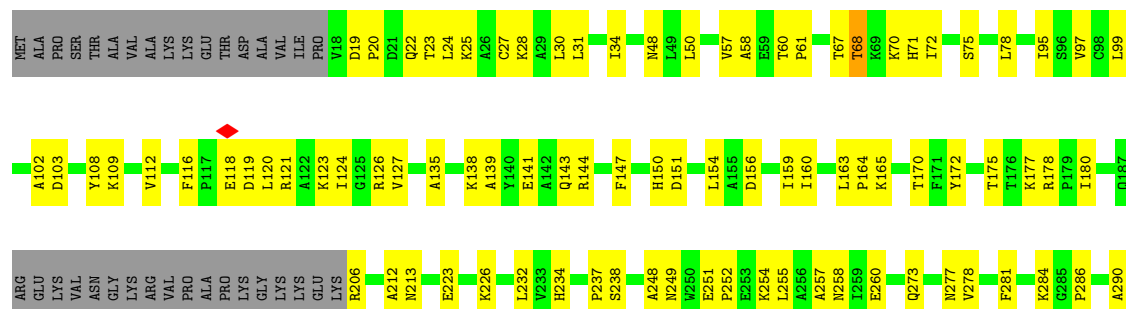
• Molecule 2: RNA (319-MER)



• Molecule 3: Brix domain-containing protein



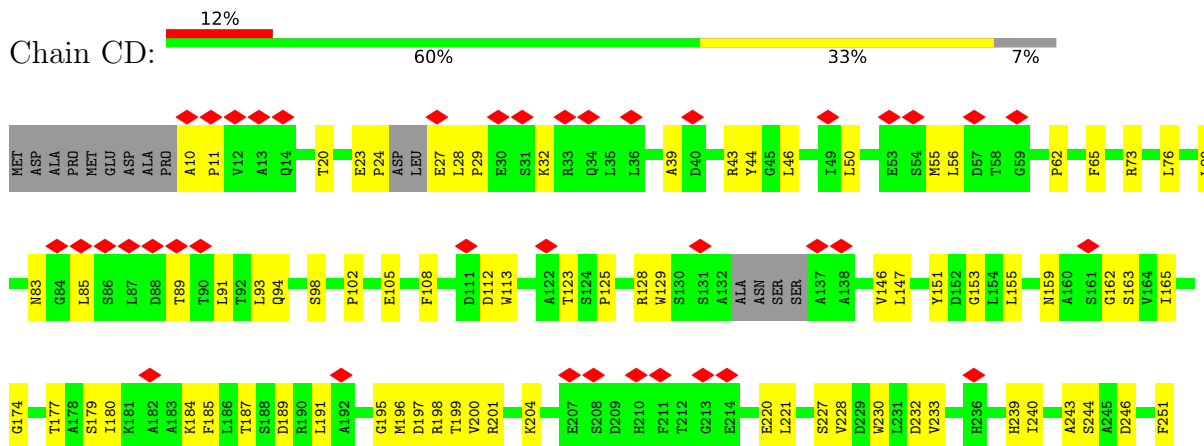
• Molecule 4: Ribosome biogenesis protein C8F11.04

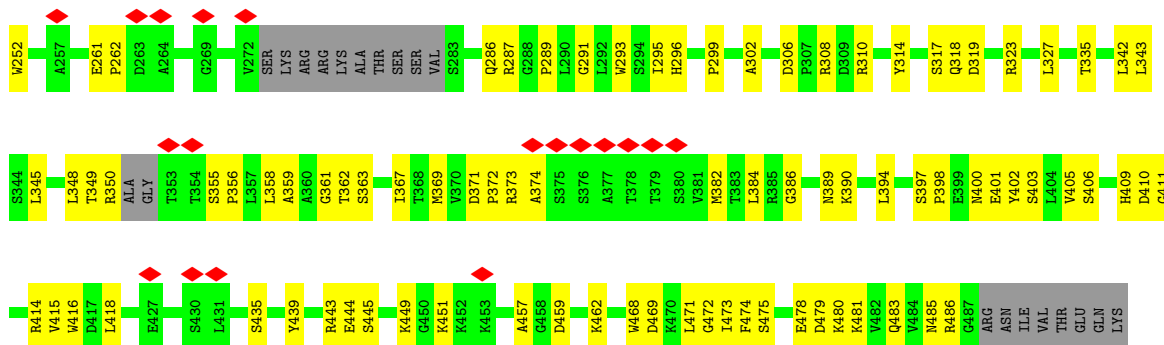


- Molecule 5: Ribosome biogenesis protein ERB1

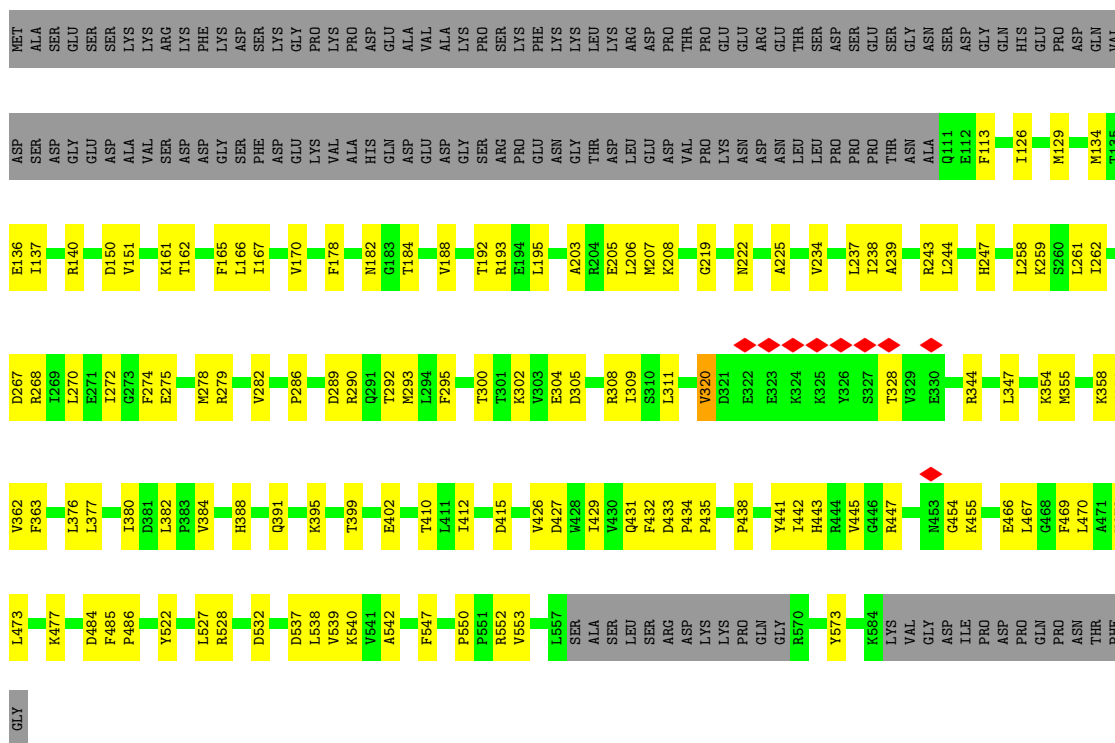


- Molecule 6: Ribosome biogenesis protein YTM1

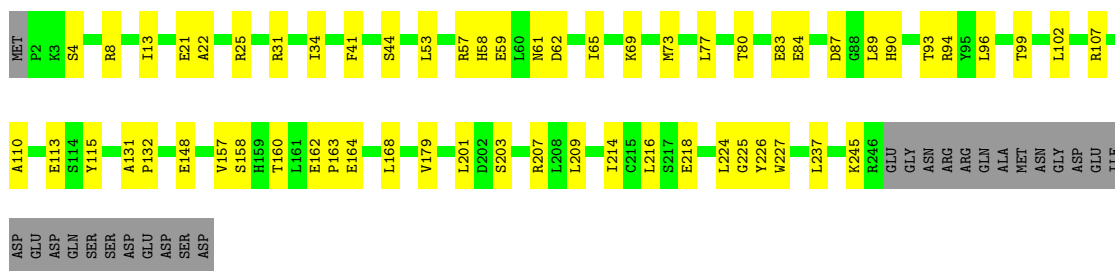




- Molecule 7: RNA helicase

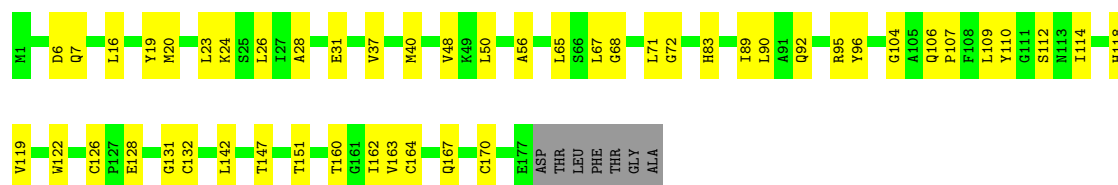


- Molecule 8: Ribosome assembly factor mrt4



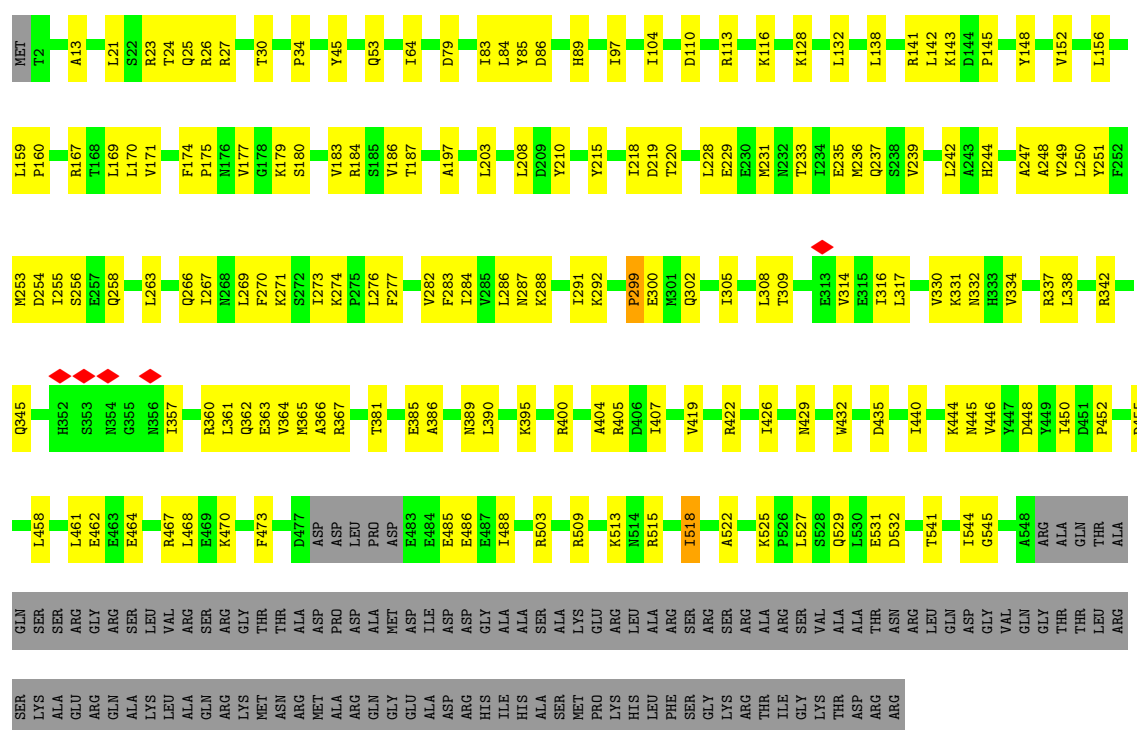
- Molecule 9: 60S ribosome subunit biogenesis protein NIP7

Chain CG:  70% 27%



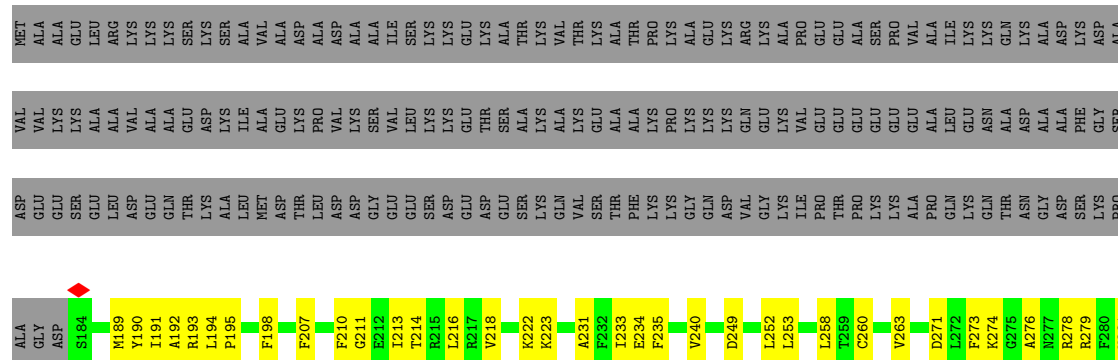
• Molecule 10: Nucleolar GTP-binding protein 1

Chain CH:  56% 25% 18%



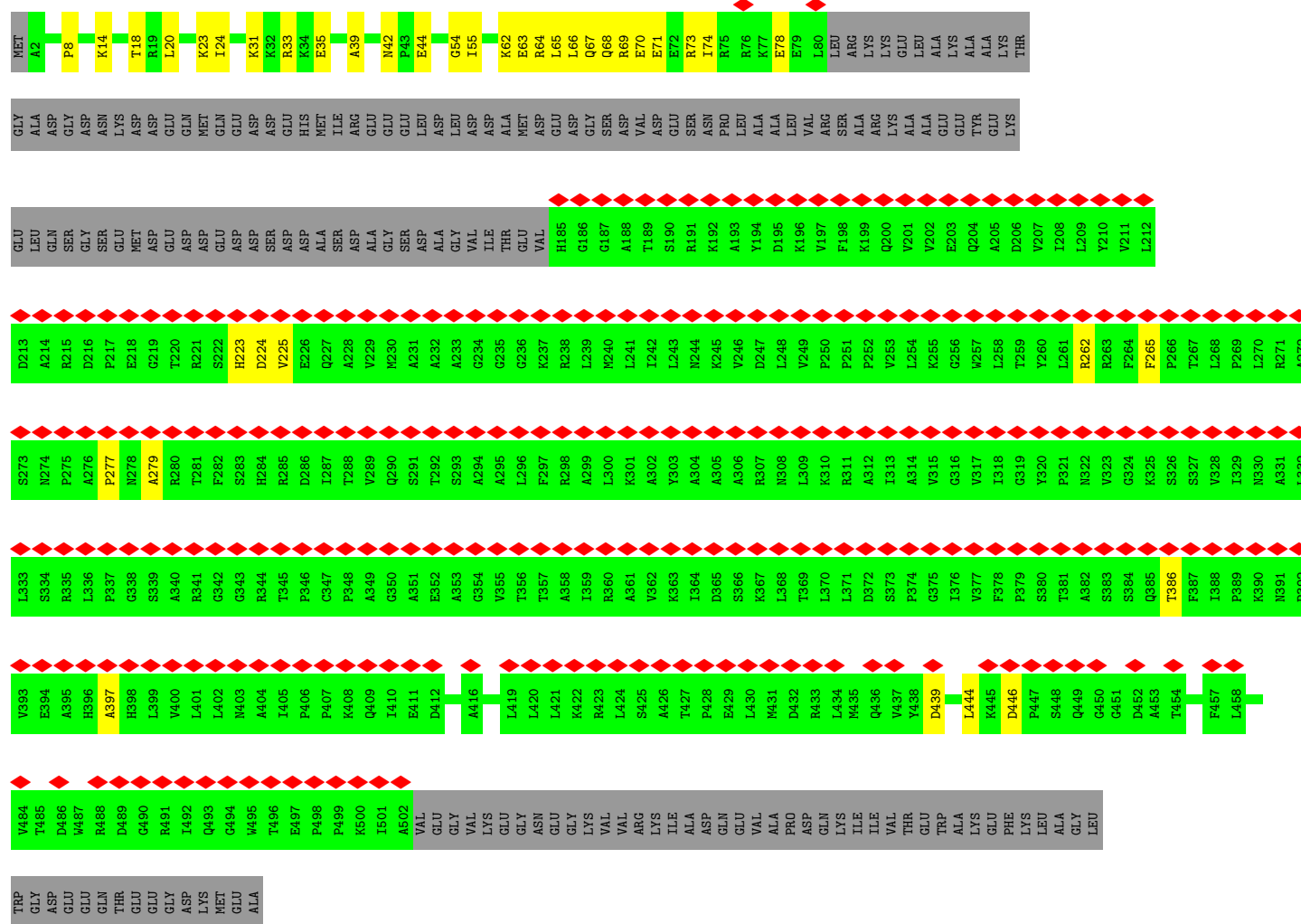
• Molecule 11: Putative RNA-binding protein

Chain CI:  21% 14% 65%

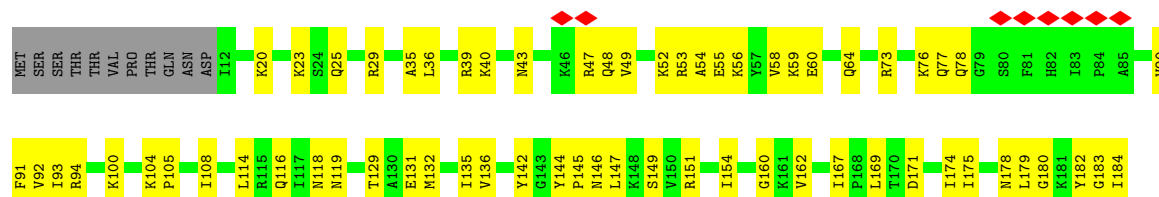


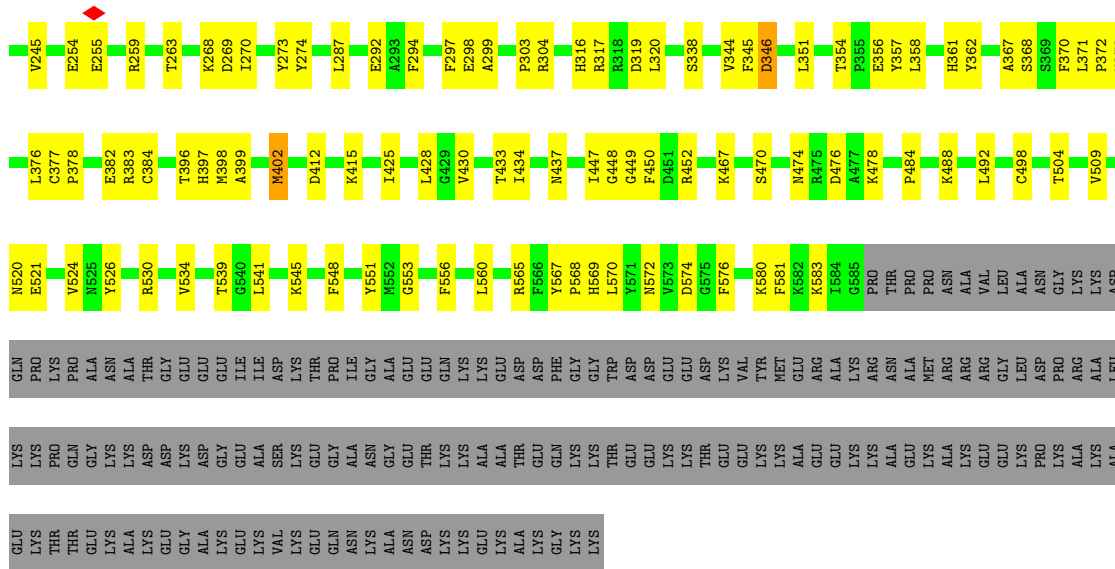


• Molecule 14: Putative GTP binding protein

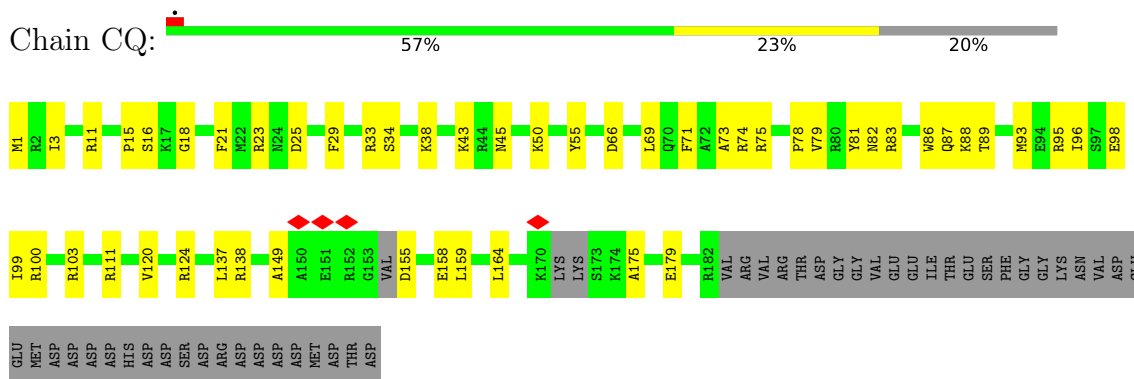


• Molecule 15: 60S ribosomal protein l7-like protein

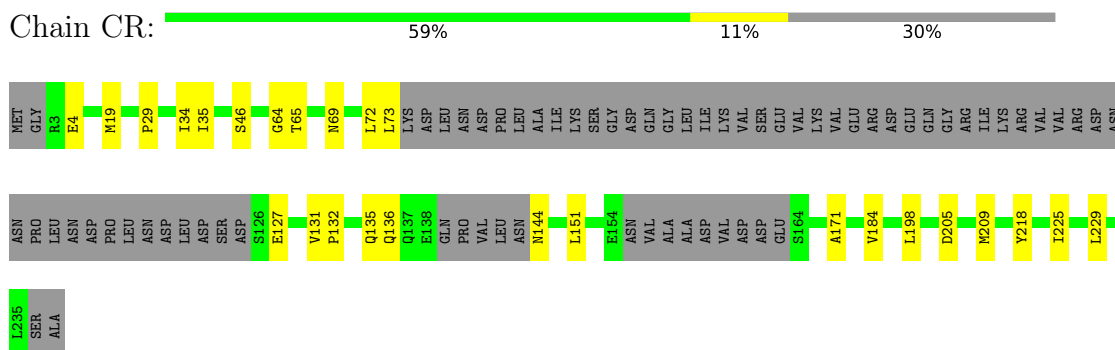




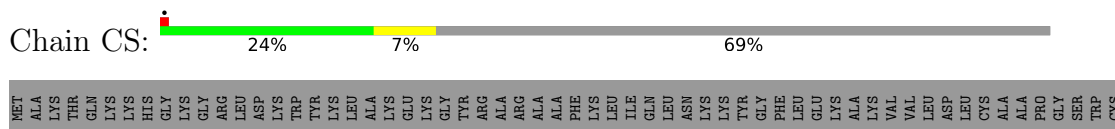
- Molecule 19: Ribosome biogenesis protein RLP24

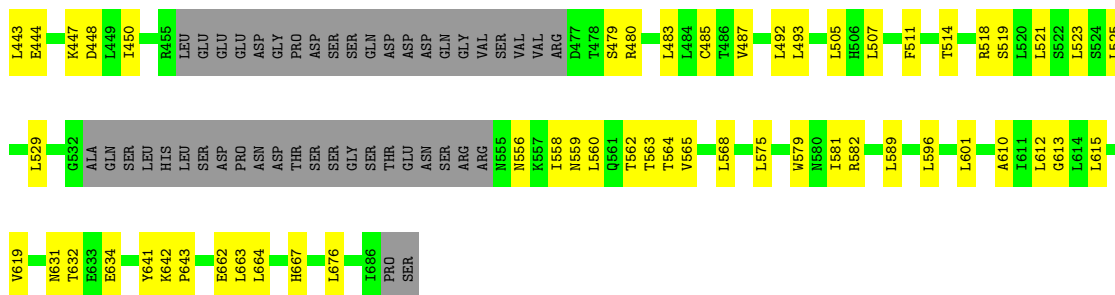


- Molecule 20: Nucleolar protein 16

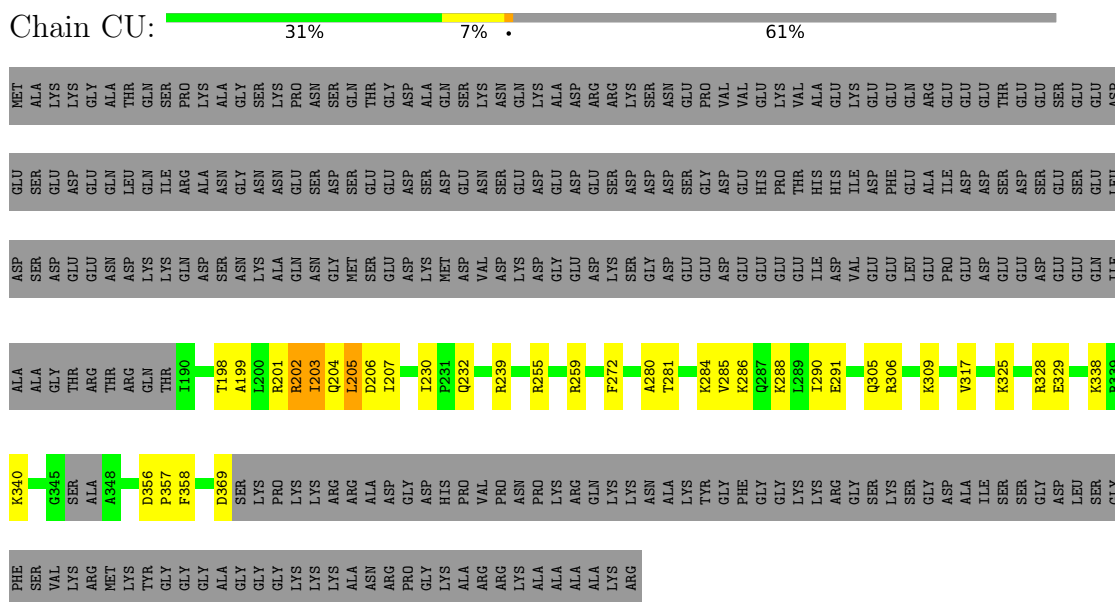


- Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1

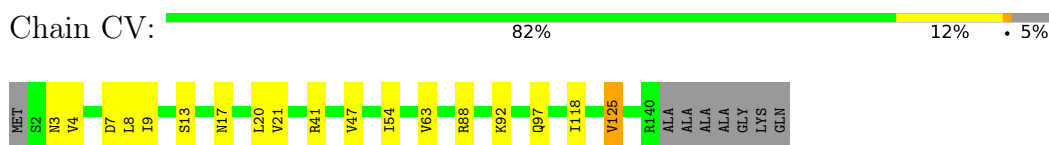




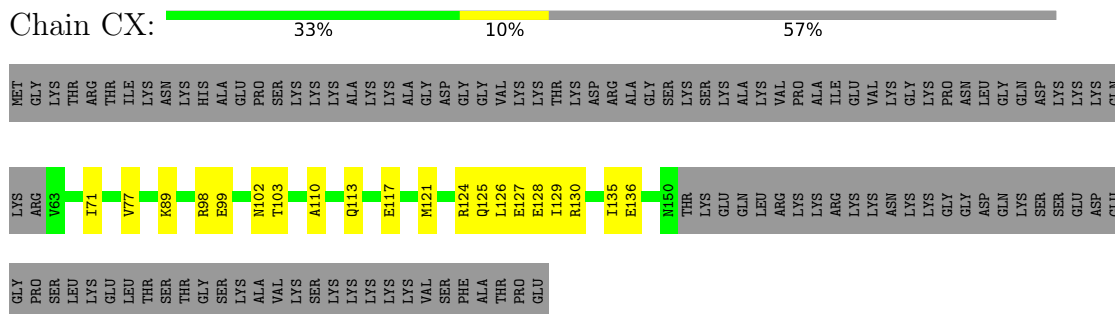
- Molecule 23: rRNA-processing protein EBP2



- Molecule 24: Putative 60S ribosomal protein

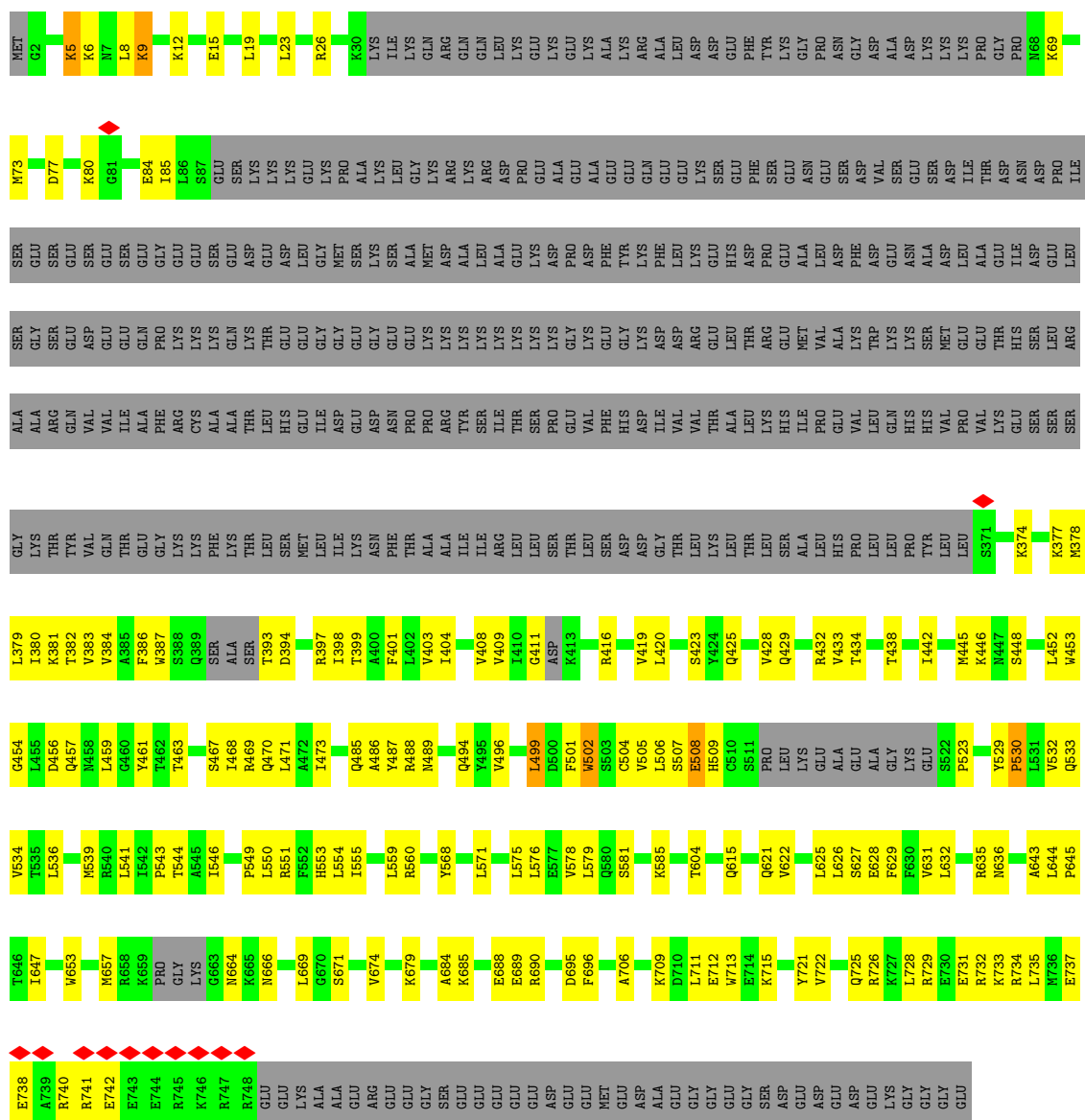


- Molecule 25: 60S ribosomal subunit-like protein



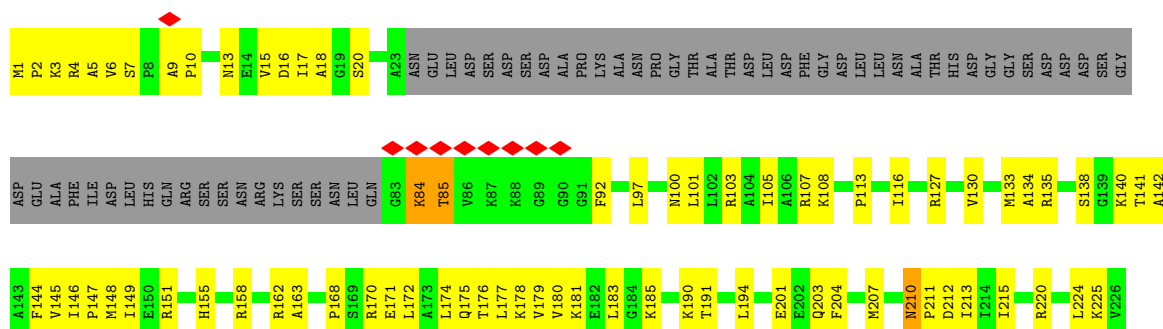
- Molecule 26: Putative NOC2 family protein

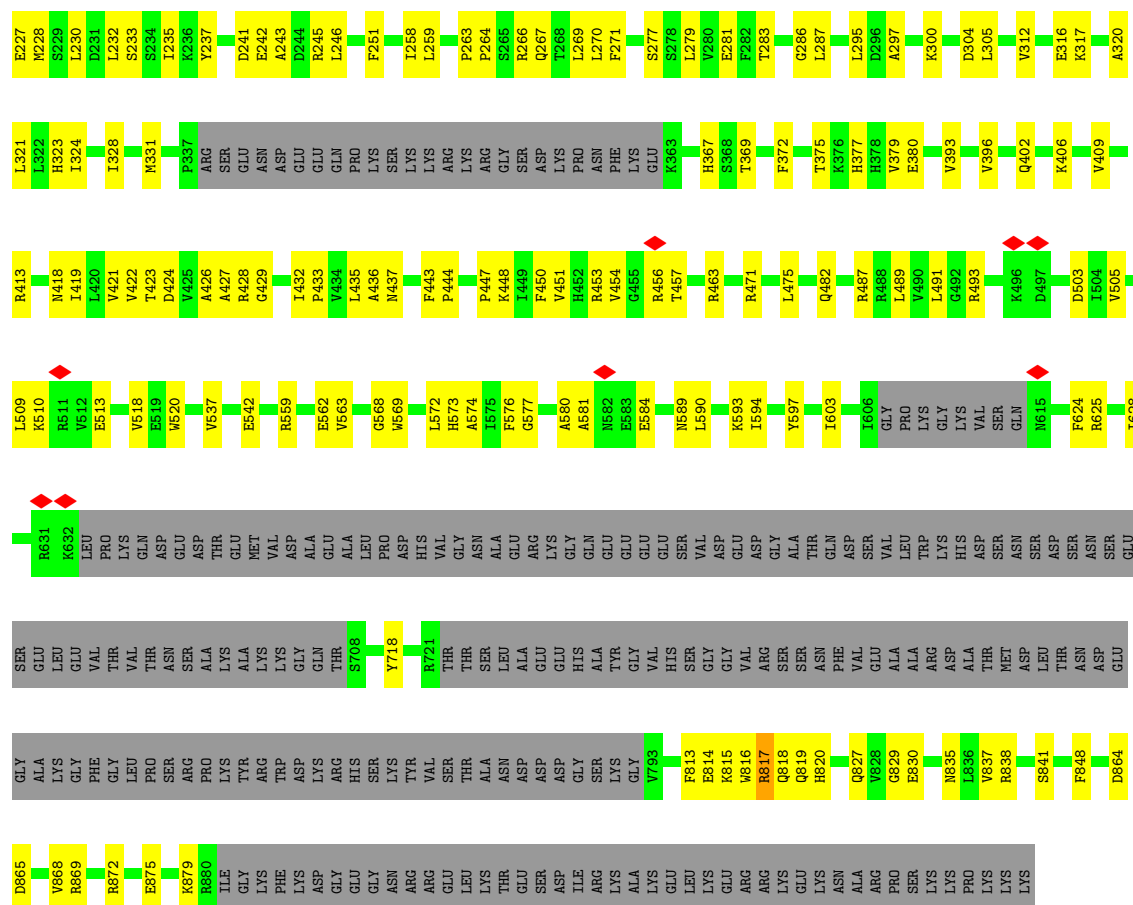
Chain CY:  31% 20% 48%



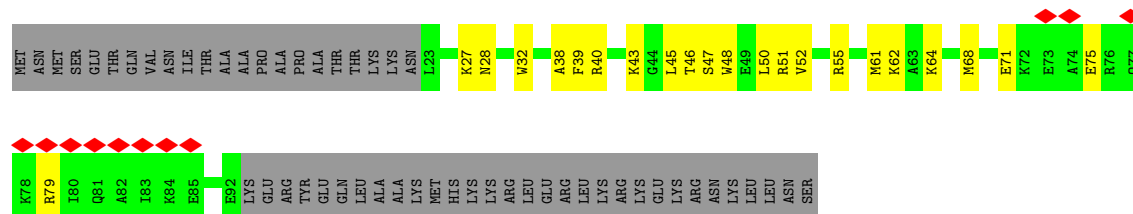
• Molecule 27: ATP-dependent RNA helicase DBP10

Chain Cb:  46% 23% 31%

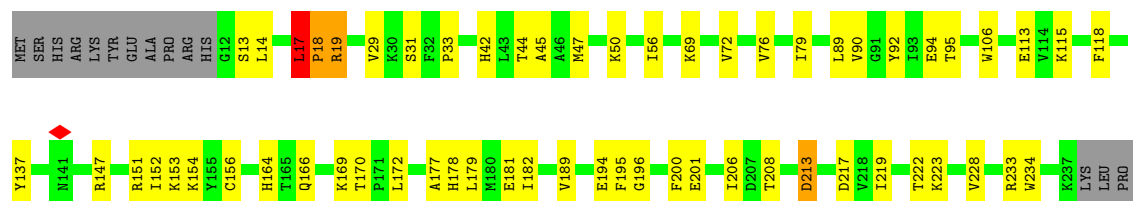


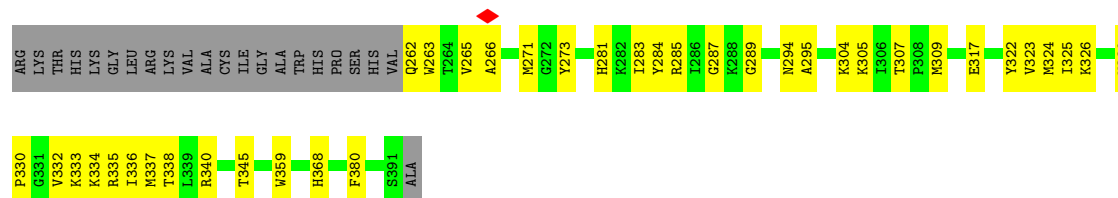


• Molecule 28: rRNA-processing protein



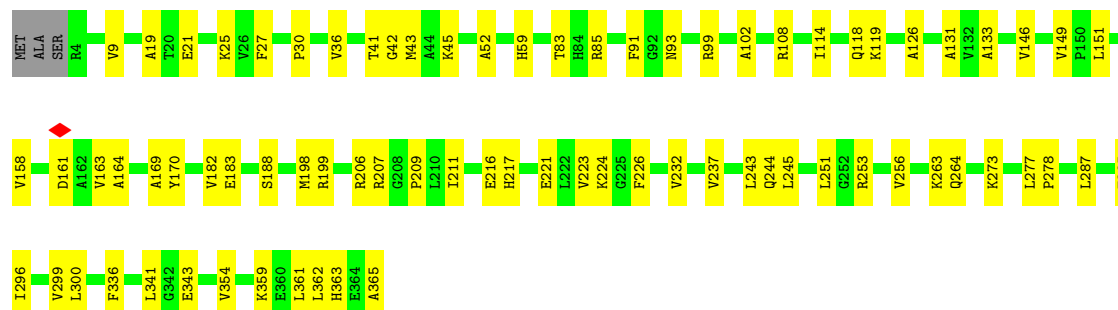
• Molecule 29: 60S ribosomal protein L3-like protein





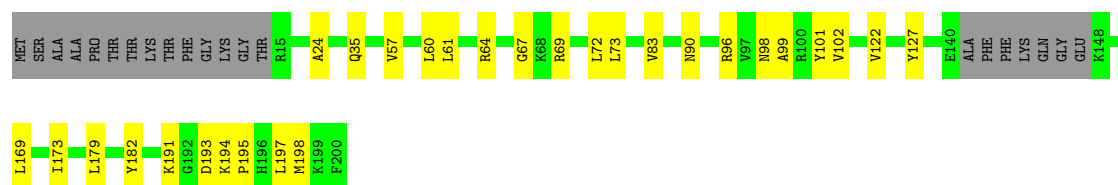
- Molecule 30: 60S ribosomal protein L4-like protein

Chain LC: 78% 21%



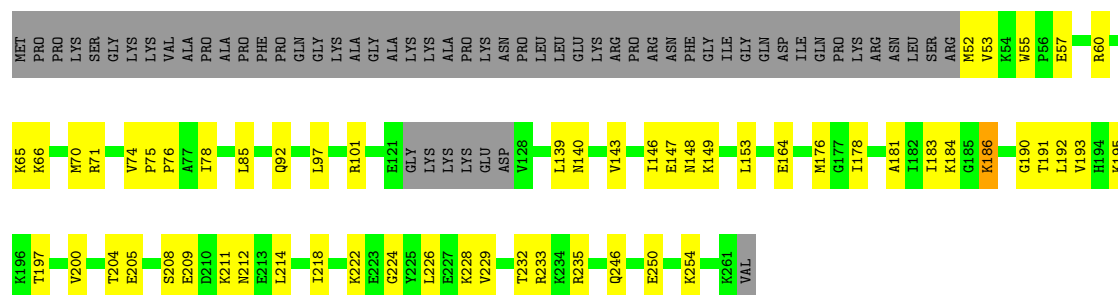
- Molecule 31: 60S ribosomal protein L6

Chain LE: 75% 14% 10%



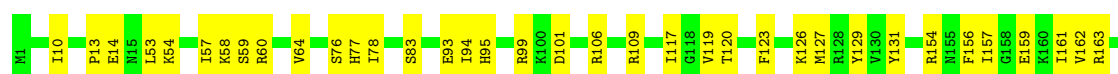
- Molecule 32: 60S ribosomal protein L8

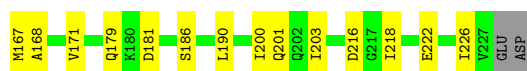
Chain LG: 56% 22% 22%



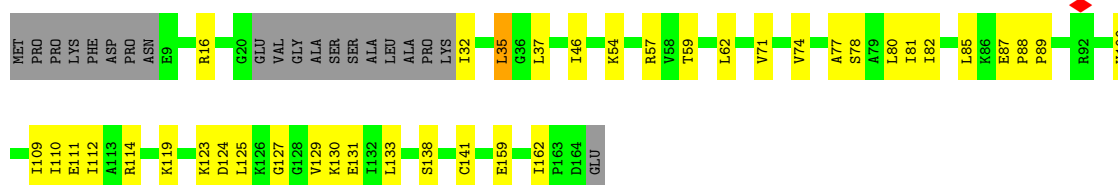
- Molecule 33: 60S ribosomal protein I9-like protein

Chain LH: 73% 26%

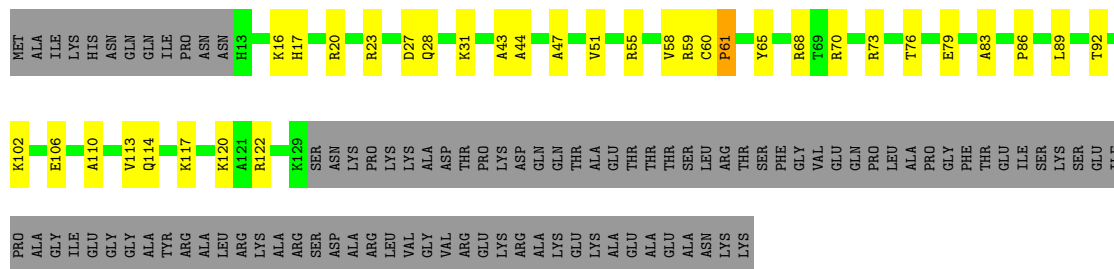




- Molecule 34: 60S ribosomal protein L12-like protein



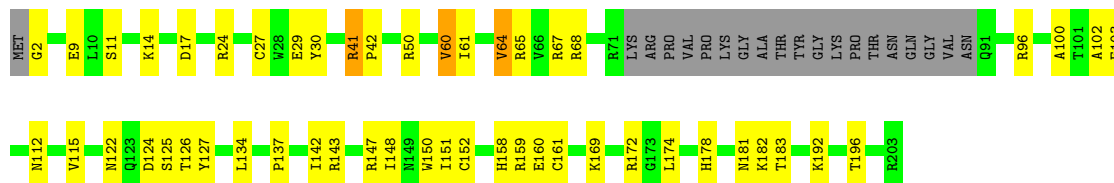
- Molecule 35: 60S ribosomal protein L13



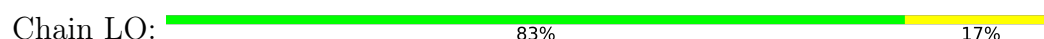
- Molecule 36: 60S ribosomal protein L14-like protein



- Molecule 37: Ribosomal protein L15



- Molecule 38: 60S ribosomal protein L16-like protein







ARG
ASN
ALA
LEU
LEU
GLY
GLU
GLU
GLU
SER
SER
LYS

- Molecule 42: 60S ribosomal protein L20

Chain LS: 71% 29%

M1 Q5 E6 Y7 Q8 H13 M27 R28 I29 F30 F41 F44 L45 R46 K50 T55 N62 V63 I64 H68 P69 K73 I77 W78 L79 R80 R84 N89 K92 V100 V103 M110 A111 A112 R115 A116 R117 F118 R119 L124 K125

V126 E133 Y139 I140 K141 Q142 V144 F150 P151 L152 R155 T161 K162 R169 P170 S171 T172 F173 S174

- Molecule 43: 60S ribosomal protein l21-like protein

Chain LT: 60% 19% 21%

MET GLY HIS ALA ALA GLY LEU ARG SER THR ARG TYR ALA PHE SER ARG GLY PHE ARG LYS HIS GLY GLN ILE PRO LEU SER THR TYR LEU R32 K43 V44 M45 G46 A47 V48 Q49 K50 F56 G59 K60 V64 K69 S70 A71 V74 R79 H82 R83 Y84

R92 I93 E94 H95 W96 K97 R100 S101 S102 E103 L106 R107 R108 M112 L128 M134 P135 R136 P148 Y156 F157 THR THR ILE

- Molecule 44: 60S ribosomal protein L22-like protein

Chain LU: 65% 18% 17%

MET ALA PRO LYS VAL ALA LYS LYS SER GLY ALA LYS GLY LYS GLY PRO K16 I22 K41 E45 L56 V59 I60 I65 G66 K69 L78 R81 K84 K89 F90 N94 D98 V99 L100 R101 V102 S106 V109 K113 F114 Y115 M116 I117 V118

H119 D120 ALA ALA GLU GLU GLU ASP

- Molecule 45: 60S ribosomal protein l23-like protein

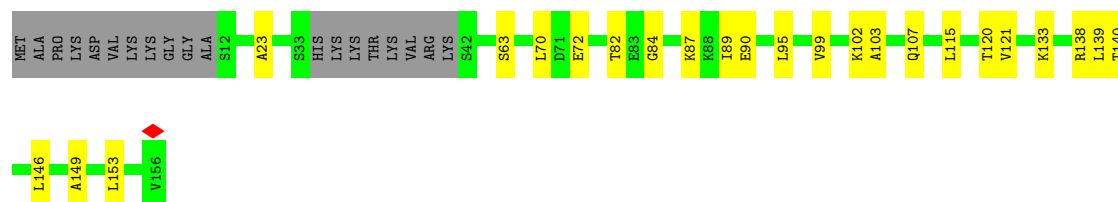
Chain LV: 72% 25%

MET ALA LYS GLN K5 L19 P20 V21 G22 M25 A28 R34 N35 L36 Y37 I38 V41 A44 R47 L48 M49 R50 A53 V56 V60 V64 K65 K66 L71 R72 K73 K74 V75 V79 I80 V81 R82 Q83 R89 F90 D91 G92 N100 V105

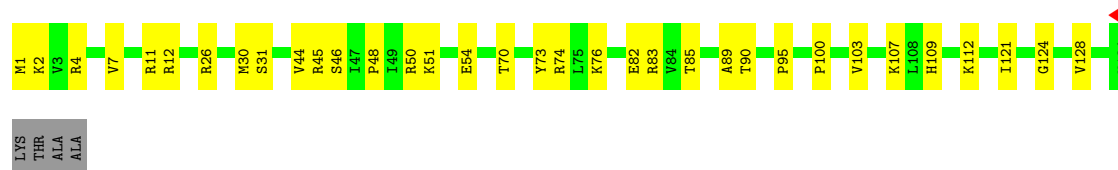
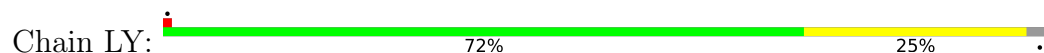
T117 V120 R130 V137 V138 M139

- Molecule 46: 60S ribosomal protein L25-like protein

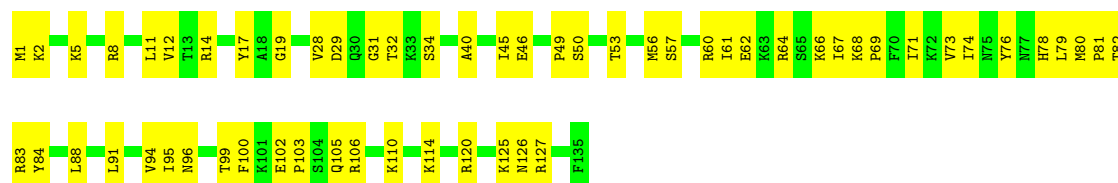
Chain LX: 72% 15% 12%



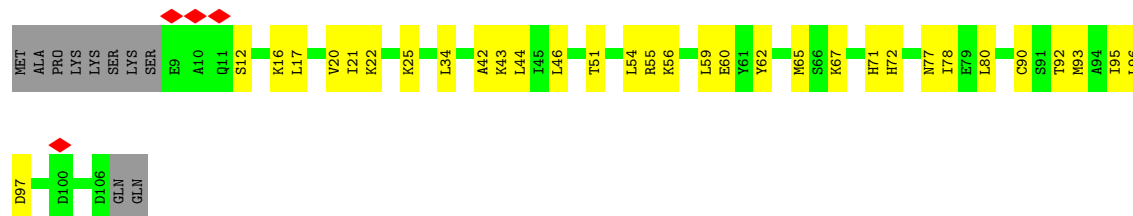
- Molecule 47: 60S ribosomal protein L26-like protein



- Molecule 48: 60S ribosomal protein L27



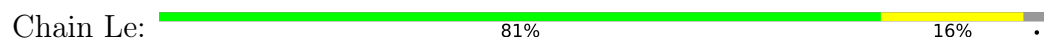
- Molecule 49: 60S ribosomal protein l30-like protein

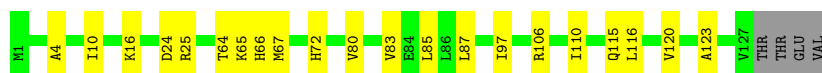


- Molecule 50: Putative 60S ribosomal protein



- Molecule 51: 60S ribosomal protein L32-like protein





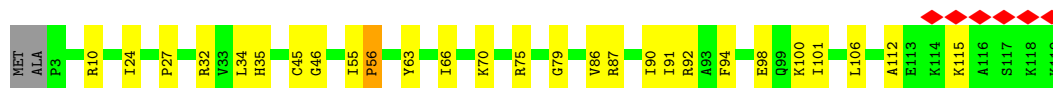
- Molecule 52: 60S ribosomal protein l33-like protein

Chain Lf: 81% 18%



- Molecule 53: Ribosomal protein l34-like protein

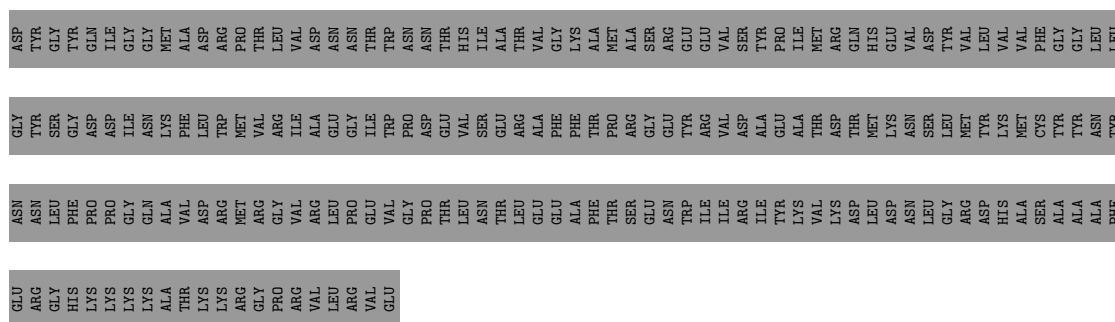
Chain Lg: 5% 76% 22%



- Molecule 54: dolichyl-diphosphooligosaccharide--protein glycotransferase

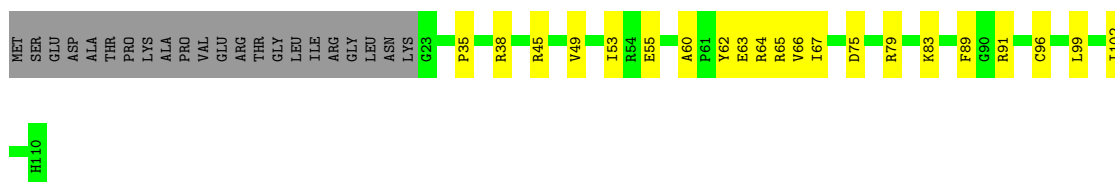
Chain Lh: 10% 87%





- Molecule 55: 60S ribosomal protein L36

Chain Li: 61% 19% 20%



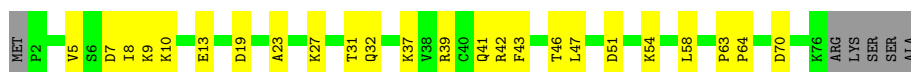
- Molecule 56: Ribosomal protein L37

Chain Lj: 58% 20% 22%



- Molecule 57: 60S ribosomal protein L38-like protein

Chain Lk: 63% 30% 7%



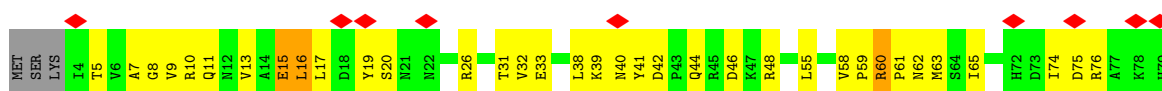
- Molecule 58: 60S ribosomal protein L39

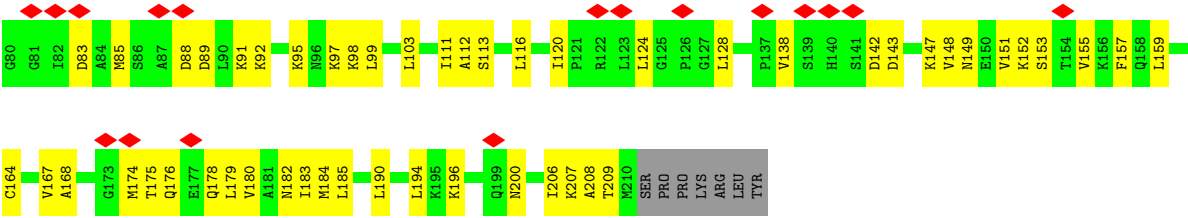
Chain Ll: 53% 22% 25%



- Molecule 59: Ribosomal protein

Chain Lq: 12% 56% 38% 5%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	77844	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.706	Depositor
Minimum map value	-0.294	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	438.9, 438.9, 438.9	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	C1	0.21	0/63619	0.35	2/99165 (0.0%)
2	C2	0.15	0/6097	0.27	0/9499
3	CA	0.58	0/2115	0.96	5/2840 (0.2%)
4	CB	0.28	0/2109	0.58	0/2866
5	CC	0.33	0/5423	0.60	3/7380 (0.0%)
6	CD	0.17	0/3543	0.49	0/4824
7	CE	0.20	0/3739	0.50	1/5040 (0.0%)
8	CF	0.30	0/1982	0.57	0/2671
9	CG	0.31	0/1422	0.59	0/1920
10	CH	0.33	0/4468	0.63	2/6029 (0.0%)
11	CI	0.19	0/1225	0.53	0/1645
12	CJ	0.24	0/4125	0.55	1/5548 (0.0%)
13	CK	0.22	0/1940	0.48	0/2601
14	CL	0.20	0/2247	0.49	0/3076
15	CM	0.20	0/1851	0.51	0/2481
15	LF	0.32	0/2055	0.60	0/2758
16	CN	0.32	0/1881	0.61	0/2560
17	CO	0.17	0/470	0.40	0/619
18	CP	0.34	0/2859	0.63	0/3870
19	CQ	0.24	0/1507	0.52	1/1996 (0.1%)
20	CR	0.28	0/1369	0.50	0/1828
21	CS	0.20	0/2127	0.49	0/2817
22	CT	0.21	0/3974	0.51	0/5357
23	CU	0.47	4/1428 (0.3%)	0.64	4/1910 (0.2%)
24	CV	0.42	0/1091	0.75	2/1468 (0.1%)
25	CX	0.17	0/705	0.47	0/938
26	CY	0.33	0/3368	0.72	2/4525 (0.0%)
27	Cb	0.19	0/5150	0.51	5/6936 (0.1%)
28	Cz	0.17	0/598	0.43	0/785
29	LB	0.36	0/2885	0.63	2/3872 (0.1%)
30	LC	0.18	0/2809	0.40	0/3787
31	LE	0.38	0/1428	0.65	0/1921

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LG	0.33	0/1667	0.61	1/2230 (0.0%)
33	LH	0.20	0/1516	0.47	0/2038
34	LK	0.45	0/1115	0.76	1/1496 (0.1%)
35	LL	0.45	0/983	0.72	0/1318
36	LM	0.18	0/1120	0.41	0/1507
37	LN	0.35	0/1595	0.57	0/2132
38	LO	0.37	0/1652	0.59	0/2215
39	LP	0.15	0/1367	0.38	0/1838
40	LQ	0.19	0/1033	0.42	0/1391
41	LR	0.20	0/980	0.46	0/1311
42	LS	0.24	0/1468	0.49	0/1975
43	LT	0.12	0/1033	0.36	0/1389
44	LU	0.24	0/863	0.52	0/1155
45	LV	0.20	0/1013	0.47	0/1361
46	LX	0.14	0/1078	0.34	0/1451
47	LY	0.16	0/1079	0.40	0/1443
48	LZ	0.16	0/1135	0.41	0/1519
49	Lc	0.14	0/740	0.41	0/995
50	Ld	0.16	0/904	0.35	0/1209
51	Le	0.26	0/1043	0.51	0/1389
52	Lf	0.40	0/883	0.58	0/1187
53	Lg	0.35	0/943	0.55	0/1258
54	Lh	0.15	0/1006	0.37	0/1338
55	Li	0.22	0/738	0.46	0/971
56	Lj	0.33	0/606	0.65	0/803
57	Lk	0.19	0/628	0.54	0/835
58	Ll	0.16	0/329	0.37	0/440
59	Lq	0.25	0/1621	0.63	1/2180 (0.0%)
All	All	0.26	4/171747 (0.0%)	0.48	33/245906 (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
29	LB	0	1
59	Lq	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CU	204	GLN	C-O	-6.90	1.15	1.24
23	CU	202	ARG	C-O	-6.60	1.15	1.24
23	CU	204	GLN	CA-C	-6.28	1.45	1.52
23	CU	201	ARG	C-N	-5.41	1.26	1.33

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CU	201	ARG	O-C-N	-7.34	114.34	122.12
7	CE	320	VAL	N-CA-C	-7.05	105.74	113.43
1	C1	3257	U	C2'-C3'-O3'	6.82	119.72	109.50
1	C1	468	C	C2'-C3'-O3'	6.51	119.27	109.50
29	LB	213	ASP	CB-CA-C	6.42	119.74	110.04
24	CV	125	VAL	CA-C-N	6.19	129.28	120.49
24	CV	125	VAL	C-N-CA	6.19	129.28	120.49
34	LK	54	LYS	CB-CA-C	-6.17	108.83	117.23
5	CC	435	PRO	N-CA-C	-6.11	105.40	113.65
26	CY	85	ILE	N-CA-C	-6.04	107.40	113.20
5	CC	733	PHE	CA-CB-CG	6.04	119.84	113.80
10	CH	299	PRO	CA-N-CD	-6.02	103.58	112.00
3	CA	238	PHE	CA-CB-CG	5.90	119.70	113.80
23	CU	202	ARG	CA-C-O	-5.80	112.25	119.38
29	LB	281	HIS	CB-CA-C	5.74	119.68	110.16
3	CA	128	PHE	CA-C-O	-5.66	114.85	120.80
27	Cb	817	ARG	CB-CG-CD	5.65	124.30	111.30
5	CC	441	PHE	CA-CB-CG	5.64	119.44	113.80
12	CJ	585	LEU	CA-CB-CG	5.62	135.96	116.30
3	CA	125	GLU	CB-CA-C	5.52	118.72	109.89
32	LG	186	LYS	N-CA-C	-5.46	106.46	113.23
27	Cb	817	ARG	CA-CB-CG	5.38	124.85	114.10
27	Cb	819	GLN	N-CA-CB	5.34	117.81	110.07
23	CU	204	GLN	CA-C-O	-5.25	114.96	120.58
19	CQ	18	GLY	CA-C-O	-5.25	118.67	122.45
23	CU	203	ILE	N-CA-CB	-5.24	105.34	112.16
27	Cb	84	LYS	CA-C-N	5.24	131.55	121.54
27	Cb	84	LYS	C-N-CA	5.24	131.55	121.54
3	CA	92	PHE	CA-CB-CG	5.13	118.93	113.80
26	CY	502	TRP	N-CA-C	-5.09	106.33	112.54
10	CH	532	ASP	CA-CB-CG	5.08	117.68	112.60
59	Lq	206	ILE	N-CA-C	-5.07	107.77	112.43
3	CA	25	ASN	N-CA-C	-5.03	106.44	112.58

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	LB	17	LEU	Peptide
59	Lq	60	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C1	56864	0	28664	897	0
2	C2	5456	0	2762	105	0
3	CA	2069	0	2109	40	0
4	CB	2063	0	2131	70	0
5	CC	5297	0	5220	141	0
6	CD	3468	0	3428	134	0
7	CE	3669	0	3775	94	0
8	CF	1945	0	1965	39	0
9	CG	1396	0	1420	38	0
10	CH	4388	0	4454	136	0
11	CI	1196	0	1202	47	0
12	CJ	4040	0	4087	110	0
13	CK	1908	0	2019	50	0
14	CL	2239	0	1495	28	0
15	CM	1820	0	1938	58	0
15	LF	2017	0	2130	48	0
16	CN	1856	0	1856	45	0
17	CO	468	0	503	14	0
18	CP	2798	0	2812	75	0
19	CQ	1485	0	1549	39	0
20	CR	1354	0	1400	22	0
21	CS	2105	0	2183	54	0
22	CT	3911	0	4023	112	0
23	CU	1415	0	1457	26	0
24	CV	1073	0	1130	13	0
25	CX	701	0	742	15	0
26	CY	3313	0	3449	150	0
27	Cb	5058	0	5223	181	0
28	Cz	592	0	640	22	0
29	LB	2829	0	2933	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	LC	2752	0	2878	61	0
31	LE	1403	0	1503	21	0
32	LG	1644	0	1793	41	0
33	LH	1496	0	1575	37	0
34	LK	1103	0	1177	25	0
35	LL	964	0	1041	33	0
36	LM	1101	0	1170	27	0
37	LN	1563	0	1618	37	0
38	LO	1618	0	1714	24	0
39	LP	1345	0	1389	34	0
40	LQ	1021	0	1118	29	0
41	LR	964	0	1022	24	0
42	LS	1433	0	1496	45	0
43	LT	1014	0	1073	20	0
44	LU	850	0	894	18	0
45	LV	995	0	1055	23	0
46	LX	1062	0	1145	17	0
47	LY	1065	0	1156	31	0
48	LZ	1112	0	1181	55	0
49	Lc	731	0	772	21	0
50	Ld	890	0	940	19	0
51	Le	1025	0	1104	15	0
52	Lf	862	0	891	13	0
53	Lg	930	0	1011	26	0
54	Lh	995	0	1110	19	0
55	Li	731	0	797	20	0
56	Lj	595	0	625	18	0
57	Lk	620	0	680	18	0
58	Ll	322	0	346	8	0
59	Lq	1600	0	1703	63	0
60	CH	32	0	12	1	0
61	CQ	1	0	0	0	0
61	Lj	1	0	0	0	0
All	All	162633	0	134688	3208	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (3208) 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)
42:LS:6:GLU:HB2	42:LS:64:ILE:O	1.48	1.13
1:C1:891:G:H1	1:C1:898:A:N6	1.57	1.01
1:C1:1156:G:H21	1:C1:1157:C:H41	1.01	1.00
1:C1:529:G:O6	1:C1:543:G:C2	2.16	0.99
6:CD:369:MET:HB2	6:CD:382:MET:HB3	1.45	0.95
1:C1:407:G:H21	1:C1:1381:A:N6	1.63	0.95
1:C1:2091:U:H3	1:C1:2285:G:H1	1.02	0.95
1:C1:856:G:N1	1:C1:875:A:N6	2.16	0.94
1:C1:2404:G:H1	1:C1:2467:U:H3	1.06	0.93
1:C1:2848:A:H61	1:C1:2871:C:H42	0.94	0.93
1:C1:407:G:H21	1:C1:1381:A:H61	0.94	0.93
1:C1:1046:A:N6	1:C1:1074:C:C2	2.38	0.91
40:LQ:106:LYS:O	40:LQ:127:GLU:HB2	1.70	0.91
1:C1:1457:G:H4'	50:Ld:65:LYS:HE3	1.53	0.90
1:C1:2735:G:H1	1:C1:2741:U:H3	0.92	0.89
1:C1:2414:G:H1	1:C1:2456:A:H2	1.20	0.88
1:C1:2848:A:N6	1:C1:2871:C:H42	1.70	0.88
33:LH:60:ARG:HE	33:LH:76:SER:HA	1.39	0.88
1:C1:958:A:H61	1:C1:1087:C:N4	1.70	0.88
13:CK:148:LYS:HE3	13:CK:150:ILE:HD11	1.56	0.87
27:Cb:201:GLU:HA	27:Cb:204:PHE:HD2	1.40	0.86
1:C1:2848:A:H61	1:C1:2871:C:N4	1.73	0.85
3:CA:170:LYS:HA	5:CC:190:ILE:HD11	1.59	0.85
26:CY:635:ARG:HH22	26:CY:713:TRP:HA	1.39	0.85
1:C1:891:G:H1	1:C1:898:A:H61	0.86	0.85
47:LY:31:SER:HA	47:LY:48:PRO:HA	1.58	0.85
1:C1:3288:G:H1	1:C1:3297:U:H3	1.25	0.85
1:C1:1885:G:H1	45:LV:65:LYS:HG2	1.42	0.84
4:CB:68:THR:HG21	4:CB:72:ILE:HD11	1.59	0.84
52:Lf:44:ASN:HA	52:Lf:47:LEU:HD13	1.58	0.84
12:CJ:585:LEU:HD23	12:CJ:589:ARG:HH22	1.43	0.83
10:CH:86:ASP:OD1	10:CH:89:HIS:ND1	2.11	0.82
28:Cz:45:LEU:HB3	42:LS:141:LYS:HE3	1.60	0.82
1:C1:670:U:O4	1:C1:684:G:O6	1.97	0.82
12:CJ:458:PRO:HB2	12:CJ:462:TRP:HZ3	1.41	0.82
1:C1:874:C:N3	1:C1:875:A:N6	2.27	0.82
6:CD:473:ILE:HB	6:CD:485:ASN:HB2	1.60	0.81
12:CJ:187:LYS:HE3	12:CJ:488:PRO:HB2	1.62	0.81
11:CI:214:THR:OG1	11:CI:234:GLU:OE1	1.98	0.81
26:CY:579:LEU:HD21	26:CY:622:VAL:HG11	1.61	0.81
42:LS:27:MET:HE1	42:LS:44:PHE:HB2	1.62	0.81
6:CD:443:ARG:NH1	6:CD:479:ASP:OD2	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CR:198:LEU:HB3	20:CR:209:MET:HE3	1.63	0.81
7:CE:328:THR:HA	7:CE:447:ARG:HH21	1.45	0.80
26:CY:432:ARG:HA	26:CY:494:GLN:HE21	1.44	0.80
32:LG:229:VAL:O	32:LG:233:ARG:HB3	1.82	0.80
1:C1:974:G:H1	1:C1:1038:U:H3	0.83	0.80
1:C1:1526:G:H5'	37:LN:67:ARG:HE	1.46	0.79
1:C1:3208:A:OP1	31:LE:64:ARG:NH2	2.15	0.79
1:C1:2736:A:OP1	18:CP:530:ARG:NH1	2.15	0.79
30:LC:362:LEU:HG	42:LS:64:ILE:HD12	1.63	0.79
1:C1:2387:G:O6	1:C1:2563:G:C2	2.36	0.79
1:C1:2848:A:N1	1:C1:2871:C:N3	2.31	0.79
14:CL:63:GLU:HB3	28:Cz:61:MET:HE1	1.64	0.79
27:Cb:101:LEU:HD13	27:Cb:149:ILE:HD11	1.65	0.78
1:C1:1156:G:N2	1:C1:1157:C:H41	1.79	0.78
6:CD:367:ILE:HB	6:CD:384:LEU:HB2	1.65	0.78
33:LH:93:GLU:OE2	33:LH:95:HIS:NE2	2.17	0.78
1:C1:958:A:N6	1:C1:1087:C:H42	1.82	0.78
1:C1:2361:A:N6	1:C1:2900:C:C4	2.52	0.78
56:Lj:15:THR:O	56:Lj:28:HIS:HA	1.84	0.78
18:CP:377:CYS:O	18:CP:452:ARG:NH1	2.17	0.78
27:Cb:17:ILE:HG12	27:Cb:448:LYS:HZ1	1.49	0.78
1:C1:856:G:H1	1:C1:875:A:N6	1.78	0.78
1:C1:1157:C:N4	38:LO:89:MET:SD	2.57	0.78
1:C1:2433:U:O2	1:C1:2436:G:O6	2.02	0.78
29:LB:106:TRP:O	29:LB:137:TYR:OH	2.02	0.78
20:CR:35:ILE:HG21	35:LL:47:ALA:HB1	1.66	0.77
12:CJ:669:ARG:HD2	12:CJ:672:LYS:HZ3	1.47	0.77
57:Lk:42:ARG:HH11	57:Lk:43:PHE:HE1	1.32	0.77
6:CD:405:VAL:HG12	6:CD:415:VAL:HG12	1.67	0.77
15:CM:91:PHE:HB2	15:CM:145:PRO:HG3	1.66	0.77
1:C1:889:G:H1	1:C1:900:U:H3	1.28	0.77
1:C1:2759:A:H5'	25:CX:89:LYS:HG3	1.67	0.77
1:C1:3115:C:H2'	1:C1:3116:G:H8	1.50	0.77
27:Cb:837:VAL:O	27:Cb:841:SER:HB3	1.85	0.77
1:C1:116:A:OP1	55:Li:45:ARG:NH1	2.17	0.76
1:C1:213:G:C6	1:C1:1371:G:C2	2.73	0.76
1:C1:974:G:O6	1:C1:1038:U:O4	2.04	0.76
29:LB:45:ALA:H	29:LB:182:ILE:HG23	1.49	0.76
1:C1:273:G:N7	37:LN:182:LYS:NZ	2.32	0.76
29:LB:222:THR:HG22	29:LB:330:PRO:HB3	1.68	0.76
33:LH:129:TYR:HB3	33:LH:218:ILE:HG13	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:529:G:O6	1:C1:543:G:N3	2.19	0.76
1:C1:2782:G:OP1	14:CL:23:LYS:NZ	2.19	0.76
6:CD:443:ARG:HH21	6:CD:444:GLU:HB3	1.50	0.76
59:Lq:174:MET:HB2	59:Lq:178:GLN:HE21	1.51	0.76
21:CS:681:TYR:HD2	55:Li:65:ARG:HB2	1.50	0.75
2:C2:71:A:N6	2:C2:85:G:N2	2.35	0.75
1:C1:2414:G:O6	1:C1:2456:A:N1	2.20	0.75
17:CO:37:LEU:HB3	29:LB:195:PHE:HZ	1.49	0.75
42:LS:5:GLN:NE2	42:LS:7:TYR:OH	2.20	0.75
1:C1:2432:C:H5''	59:Lq:26:ARG:HE	1.52	0.74
12:CJ:458:PRO:HB2	12:CJ:462:TRP:CZ3	2.21	0.74
22:CT:525:LEU:HD11	26:CY:645:PRO:HB2	1.69	0.74
10:CH:527:LEU:HD22	44:LU:117:ILE:HG22	1.69	0.74
11:CI:252:LEU:HD22	32:LG:92:GLN:HG3	1.69	0.74
12:CJ:9:LYS:O	12:CJ:14:ARG:NH1	2.20	0.74
1:C1:1046:A:N1	1:C1:1074:C:C4	2.54	0.74
2:C2:132:G:H4'	46:LX:107:GLN:HE21	1.52	0.74
18:CP:556:PHE:HB3	18:CP:560:LEU:HD12	1.68	0.74
5:CC:361:LEU:O	12:CJ:666:LYS:NZ	2.18	0.74
5:CC:367:ARG:HH22	5:CC:385:THR:HA	1.52	0.74
24:CV:54:ILE:HG12	24:CV:63:VAL:HG22	1.70	0.74
1:C1:1869:U:H2'	1:C1:1870:A:H8	1.53	0.74
2:C2:71:A:C6	2:C2:85:G:N2	2.56	0.74
10:CH:288:LYS:HB3	10:CH:291:ILE:HD13	1.69	0.74
47:LY:1:MET:HE3	47:LY:2:LYS:HG2	1.70	0.74
1:C1:745:U:O2	1:C1:749:C:N3	2.21	0.73
27:Cb:589:ASN:OD1	27:Cb:590:LEU:N	2.20	0.73
9:CG:96:TYR:O	9:CG:132:CYS:HA	1.88	0.73
27:Cb:105:ILE:HG13	27:Cb:108:LYS:NZ	2.03	0.73
6:CD:80:LEU:HD12	6:CD:85:LEU:HB2	1.70	0.73
7:CE:192:THR:HB	7:CE:195:LEU:HG	1.70	0.73
10:CH:23:ARG:HD2	10:CH:27:ARG:HE	1.54	0.73
48:LZ:50:SER:HB2	48:LZ:64:ARG:HB3	1.70	0.73
52:Lf:47:LEU:HD11	52:Lf:76:PRO:HD3	1.70	0.73
3:CA:39:LEU:HD21	3:CA:68:PHE:HB2	1.69	0.73
48:LZ:46:GLU:OE1	48:LZ:68:LYS:NZ	2.21	0.73
1:C1:3216:U:O2'	1:C1:3218:A:N6	2.19	0.73
48:LZ:81:PRO:HB2	49:Lc:65:MET:HE1	1.71	0.73
1:C1:2433:U:O2	1:C1:2436:G:C6	2.42	0.73
3:CA:123:MET:HG2	3:CA:235:GLY:HA2	1.71	0.73
13:CK:126:GLY:HA3	13:CK:161:PHE:HB2	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:230:A:H2'	1:C1:231:A:C8	2.24	0.72
15:LF:116:GLN:H	15:LF:119:ASN:HD22	1.37	0.72
1:C1:789:A:H2'	1:C1:790:G:C8	2.24	0.72
1:C1:1156:G:H21	1:C1:1157:C:N4	1.84	0.72
12:CJ:147:MET:HG3	12:CJ:234:TYR:HD2	1.53	0.72
1:C1:529:G:O6	1:C1:543:G:N2	2.22	0.72
5:CC:270:PRO:HB3	32:LG:148:ASN:HA	1.71	0.72
1:C1:567:U:OP1	15:LF:246:ARG:NH2	2.22	0.72
22:CT:436:GLN:HG2	22:CT:505:LEU:HD21	1.72	0.72
18:CP:236:ARG:NH2	18:CP:298:GLU:OE1	2.23	0.72
1:C1:642:C:H2'	1:C1:643:A:H8	1.54	0.71
1:C1:958:A:H61	1:C1:1087:C:H42	1.36	0.71
1:C1:1868:G:H2'	1:C1:1869:U:C6	2.24	0.71
5:CC:479:VAL:HG12	5:CC:489:TRP:HB3	1.71	0.71
7:CE:259:LYS:NZ	7:CE:289:ASP:OD2	2.23	0.71
11:CI:279:ARG:HH21	11:CI:281:LYS:HD3	1.55	0.71
12:CJ:390:PHE:HD2	12:CJ:465:ILE:HD12	1.56	0.71
22:CT:581:ILE:HG23	22:CT:582:ARG:HD3	1.72	0.71
18:CP:396:THR:HG21	18:CP:428:LEU:HD13	1.71	0.71
2:C2:75:G:OP2	47:LY:73:TYR:OH	2.09	0.71
16:CN:106:ASN:ND2	16:CN:150:SER:OG	2.24	0.71
58:LI:15:LYS:O	58:LI:19:GLN:NE2	2.23	0.71
1:C1:7:C:OP1	12:CJ:93:ARG:NH2	2.24	0.71
26:CY:738:GLU:HA	26:CY:741:ARG:HD2	1.72	0.71
37:LN:178:HIS:O	37:LN:181:ASN:ND2	2.24	0.71
1:C1:663:G:O2'	1:C1:665:G:O2'	2.09	0.71
24:CV:7:ASP:OD1	24:CV:41:ARG:NH1	2.23	0.71
34:LK:129:VAL:HG11	34:LK:162:ILE:HG12	1.73	0.70
5:CC:531:VAL:HA	5:CC:535:LEU:HD23	1.72	0.70
1:C1:1216:G:H5''	34:LK:119:LYS:HE2	1.73	0.70
2:C2:196:G:H1	2:C2:201:U:H3	1.39	0.70
6:CD:295:ILE:O	6:CD:323:ARG:NH1	2.24	0.70
1:C1:683:C:H1'	20:CR:64:GLY:H	1.57	0.70
6:CD:123:THR:O	6:CD:128:ARG:NH1	2.24	0.70
10:CH:395:LYS:O	10:CH:400:ARG:NH1	2.25	0.70
27:Cb:4:ARG:NH2	27:Cb:537:VAL:O	2.25	0.70
1:C1:130:U:O2	1:C1:133:G:N2	2.24	0.70
10:CH:284:ILE:HB	10:CH:316:ILE:HD13	1.73	0.70
4:CB:71:HIS:ND1	4:CB:237:PRO:O	2.23	0.70
30:LC:133:ALA:HB2	30:LC:149:VAL:HG21	1.74	0.70
59:Lq:194:LEU:HD21	59:Lq:200:ASN:HD22	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CA:130:GLY:HA3	3:CA:234:ILE:HG22	1.73	0.69
12:CJ:585:LEU:HG	12:CJ:589:ARG:HH12	1.56	0.69
38:LO:127:ARG:HG3	38:LO:131:LEU:HD12	1.73	0.69
1:C1:1305:C:H4'	42:LS:1:MET:HB2	1.72	0.69
12:CJ:147:MET:HG3	12:CJ:234:TYR:CD2	2.28	0.69
29:LB:217:ASP:OD2	29:LB:340:ARG:NH1	2.26	0.69
21:CS:673:LYS:O	21:CS:677:ILE:HD12	1.92	0.69
27:Cb:2:PRO:HA	27:Cb:5:ALA:HB2	1.75	0.69
37:LN:2:GLY:HA3	55:Li:45:ARG:HH22	1.58	0.69
42:LS:6:GLU:HB3	42:LS:64:ILE:HG23	1.75	0.69
27:Cb:142:ALA:HA	27:Cb:145:VAL:HG12	1.75	0.69
1:C1:3072:C:OP2	33:LH:99:ARG:NH2	2.25	0.69
26:CY:15:GLU:HA	26:CY:19:LEU:HB2	1.74	0.69
31:LE:193:ASP:HB3	31:LE:198:MET:HE1	1.73	0.69
33:LH:58:LYS:HG3	33:LH:59:SER:H	1.57	0.69
6:CD:180:ILE:HA	6:CD:195:GLY:HA3	1.74	0.68
47:LY:100:PRO:HA	47:LY:103:VAL:HG22	1.76	0.68
1:C1:796:G:H1	1:C1:906:A:H61	1.41	0.68
6:CD:50:LEU:HA	6:CD:55:MET:HG2	1.75	0.68
8:CF:31:ARG:HA	8:CF:34:ILE:HD12	1.74	0.68
9:CG:96:TYR:HB2	9:CG:131:GLY:O	1.93	0.68
29:LB:47:MET:HE2	29:LB:336:ILE:HD11	1.75	0.68
49:Lc:44:LEU:HD23	49:Lc:95:ILE:HD12	1.74	0.68
15:CM:182:TYR:HE2	15:CM:203:GLN:HG2	1.58	0.68
32:LG:65:LYS:NZ	37:LN:29:GLU:OE1	2.25	0.68
1:C1:356:G:N7	56:Lj:56:ARG:NH2	2.41	0.68
1:C1:781:G:H22	30:LC:102:ALA:HA	1.59	0.68
1:C1:813:G:H1	1:C1:843:U:H3	1.40	0.68
5:CC:593:ALA:HB3	5:CC:606:VAL:HB	1.74	0.68
1:C1:55:G:OP1	56:Lj:43:LYS:NZ	2.26	0.68
6:CD:65:PHE:HD1	6:CD:93:LEU:HD21	1.58	0.68
26:CY:581:SER:O	26:CY:585:LYS:NZ	2.26	0.68
37:LN:41:ARG:HG3	37:LN:42:PRO:HD2	1.76	0.68
4:CB:50:LEU:HD12	7:CE:486:PRO:HD2	1.75	0.68
22:CT:184:ILE:HD13	22:CT:207:GLU:HB3	1.75	0.68
1:C1:1239:C:OP1	34:LK:123:LYS:NZ	2.24	0.68
10:CH:317:LEU:HD22	10:CH:330:VAL:HG23	1.76	0.68
15:LF:155:TYR:OH	15:LF:188:GLU:OE1	2.12	0.68
32:LG:224:GLY:O	32:LG:228:LYS:NZ	2.23	0.68
48:LZ:82:THR:HG23	53:Lg:94:PHE:HZ	1.59	0.68
1:C1:407:G:N2	1:C1:1381:A:H61	1.79	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CM:76:LYS:HD2	15:CM:77:GLN:HG2	1.75	0.68
26:CY:529:TYR:HB3	26:CY:530:PRO:HD3	1.76	0.68
27:Cb:814:GLU:HA	27:Cb:817:ARG:HH11	1.59	0.68
21:CS:505:GLU:OE2	32:LG:254:LYS:NZ	2.26	0.67
48:LZ:74:ILE:HG23	48:LZ:79:LEU:HD11	1.76	0.67
1:C1:3159:A:OP2	36:LM:125:LYS:NZ	2.23	0.67
27:Cb:180:VAL:HG11	27:Cb:191:THR:HG21	1.74	0.67
5:CC:449:PHE:HB2	5:CC:797:ALA:HB3	1.77	0.67
12:CJ:141:LEU:HD23	12:CJ:206:ILE:HD13	1.76	0.67
13:CK:218:GLY:N	13:CK:245:ILE:O	2.25	0.67
26:CY:711:LEU:HG	26:CY:715:LYS:HD2	1.76	0.67
10:CH:85:TYR:O	10:CH:148:TYR:OH	2.12	0.67
10:CH:183:VAL:HG21	10:CH:219:ASP:HB2	1.76	0.67
15:CM:154:ILE:HD12	15:CM:191:ILE:HG12	1.77	0.67
26:CY:486:ALA:HA	26:CY:489:ASN:ND2	2.10	0.67
1:C1:1071:G:H2'	1:C1:1072:G:C8	2.29	0.67
15:LF:148:LYS:HB3	15:LF:246:ARG:HH22	1.60	0.67
1:C1:958:A:N1	1:C1:1087:C:N3	2.43	0.67
2:C2:182:G:OP1	15:CM:73:ARG:NH1	2.28	0.67
10:CH:283:PHE:HZ	10:CH:337:ARG:HD3	1.60	0.67
11:CI:207:PHE:HB3	11:CI:235:PHE:HZ	1.58	0.67
18:CP:425:ILE:HG23	18:CP:430:VAL:HB	1.77	0.67
22:CT:145:TYR:HB3	22:CT:148:HIS:ND1	2.09	0.67
1:C1:1548:C:H5''	15:CM:29:ARG:HD3	1.75	0.67
27:Cb:493:ARG:HH11	27:Cb:581:ALA:HB2	1.59	0.67
1:C1:75:G:H5''	35:LL:58:VAL:HB	1.75	0.66
1:C1:2387:G:O6	1:C1:2563:G:N2	2.29	0.66
15:CM:182:TYR:HB3	15:CM:200:ASN:HD22	1.60	0.66
12:CJ:511:GLU:OE1	12:CJ:664:ARG:NH1	2.29	0.66
48:LZ:49:PRO:HD3	48:LZ:67:ILE:HG12	1.78	0.66
22:CT:667:HIS:HA	26:CY:568:TYR:HB3	1.77	0.66
26:CY:485:GLN:HB3	26:CY:488:ARG:HB3	1.77	0.66
32:LG:226:LEU:HA	32:LG:229:VAL:HG22	1.76	0.66
1:C1:2780:U:H4'	10:CH:34:PRO:HB2	1.78	0.66
2:C2:29:U:H5''	35:LL:27:ASP:HB3	1.76	0.66
26:CY:69:LYS:HG3	26:CY:73:MET:HE2	1.77	0.66
59:Lq:39:LYS:HD2	59:Lq:40:ASN:HB2	1.76	0.66
27:Cb:241:ASP:OD1	27:Cb:242:GLU:HG3	1.94	0.66
47:LY:30:MET:HE1	47:LY:74:ARG:HA	1.77	0.66
1:C1:562:U:H2'	1:C1:563:A:H8	1.61	0.66
5:CC:446:GLN:HE22	6:CD:389:ASN:HA	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CG:109:LEU:HD13	18:CP:358:LEU:HD12	1.77	0.66
10:CH:527:LEU:HD23	44:LU:119:ASN:HA	1.78	0.66
52:Lf:22:ARG:HG3	52:Lf:23:ARG:HD2	1.77	0.66
48:LZ:71:ILE:HD11	48:LZ:106:ARG:HB2	1.77	0.66
18:CP:304:ARG:HG3	18:CP:574:ASP:OD1	1.96	0.66
46:LX:72:GLU:HG3	46:LX:115:LEU:HD21	1.78	0.66
56:Lj:76:ASN:HB3	56:Lj:79:ARG:HE	1.61	0.66
59:Lq:5:THR:HG23	59:Lq:8:GLY:H	1.61	0.66
1:C1:796:G:H1	1:C1:906:A:N6	1.94	0.66
3:CA:46:TYR:HA	3:CA:49:ARG:HE	1.61	0.66
12:CJ:614:LEU:HG	12:CJ:618:LYS:NZ	2.11	0.66
41:LR:99:GLN:NE2	41:LR:127:ALA:O	2.26	0.66
27:Cb:155:HIS:ND1	27:Cb:212:ASP:OD2	2.27	0.65
27:Cb:180:VAL:HG21	27:Cb:215:ILE:HD11	1.78	0.65
1:C1:979:A:H5'	42:LS:50:LYS:HE2	1.78	0.65
2:C2:192:C:O2'	4:CB:284:LYS:NZ	2.23	0.65
26:CY:544:THR:HG22	26:CY:546:ILE:H	1.61	0.65
41:LR:105:LEU:HD22	41:LR:135:LYS:HG3	1.77	0.65
15:CM:35:ALA:HB1	15:CM:39:ARG:HH12	1.61	0.65
26:CY:386:PHE:O	26:CY:397:ARG:NH2	2.29	0.65
27:Cb:101:LEU:O	27:Cb:105:ILE:HD12	1.96	0.65
1:C1:2818:U:O4	10:CH:141:ARG:NH2	2.29	0.65
19:CQ:95:ARG:NH1	19:CQ:98:GLU:OE2	2.29	0.65
26:CY:536:LEU:HD13	26:CY:539:MET:HE2	1.79	0.65
1:C1:404:G:N3	39:LP:118:GLN:NE2	2.45	0.65
1:C1:1430:U:H5''	39:LP:66:SER:HB2	1.79	0.65
22:CT:487:VAL:HG12	22:CT:558:ILE:HD13	1.77	0.65
22:CT:601:LEU:HD23	22:CT:664:LEU:HG	1.78	0.65
30:LC:161:ASP:HA	30:LC:164:ALA:HB3	1.78	0.65
31:LE:173:ILE:HG23	31:LE:179:LEU:HD23	1.77	0.65
7:CE:441:TYR:O	7:CE:445:VAL:HG12	1.95	0.65
26:CY:420:LEU:HD11	26:CY:463:THR:HG21	1.79	0.65
7:CE:267:ASP:OD1	7:CE:268:ARG:N	2.30	0.65
29:LB:153:LYS:NZ	29:LB:194:GLU:OE2	2.29	0.65
42:LS:6:GLU:CB	42:LS:64:ILE:HG23	2.27	0.65
1:C1:887:G:H2'	1:C1:888:G:C8	2.32	0.65
22:CT:613:GLY:HA3	26:CY:73:MET:HE1	1.78	0.65
54:Lh:34:LEU:HA	54:Lh:37:GLN:HG2	1.78	0.65
10:CH:110:ASP:OD1	10:CH:113:ARG:NH2	2.29	0.65
22:CT:161:LEU:HG	22:CT:165:LYS:HE3	1.78	0.65
42:LS:5:GLN:HA	42:LS:100:VAL:HG11	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:648:PHE:HB2	5:CC:661:LEU:HD21	1.78	0.64
59:Lq:60:ARG:O	59:Lq:62:ASN:N	2.30	0.64
3:CA:53:ASN:HA	3:CA:64:LYS:HZ1	1.61	0.64
27:Cb:816:TRP:NE1	27:Cb:820:HIS:CE1	2.65	0.64
30:LC:36:VAL:HG21	30:LC:251:LEU:HD21	1.78	0.64
1:C1:1842:G:N2	1:C1:1845:C:OP2	2.30	0.64
10:CH:255:ILE:HD11	10:CH:286:LEU:HD22	1.79	0.64
10:CH:282:VAL:HB	10:CH:314:VAL:HG12	1.79	0.64
18:CP:484:PRO:O	18:CP:488:LYS:HG2	1.96	0.64
26:CY:454:GLY:O	26:CY:457:GLN:NE2	2.29	0.64
27:Cb:509:LEU:HD23	27:Cb:576:PHE:HZ	1.62	0.64
3:CA:112:THR:HG22	3:CA:246:GLN:HG2	1.80	0.64
27:Cb:482:GLN:HG3	27:Cb:489:LEU:HB2	1.79	0.64
47:LY:73:TYR:CD2	47:LY:76:LYS:HG2	2.32	0.64
1:C1:642:C:H2'	1:C1:643:A:C8	2.33	0.64
4:CB:99:LEU:HB3	4:CB:127:VAL:HG12	1.80	0.64
15:CM:93:ILE:HG21	15:CM:248:MET:HE1	1.80	0.64
1:C1:2813:C:H2'	1:C1:2814:G:H8	1.63	0.64
41:LR:17:CYS:HB3	41:LR:52:LYS:HE2	1.80	0.64
1:C1:1784:C:H2'	1:C1:1785:G:H8	1.63	0.64
7:CE:377:LEU:HD13	7:CE:382:LEU:HD11	1.80	0.64
10:CH:174:PHE:HE2	10:CH:266:GLN:HA	1.63	0.64
1:C1:119:U:OP1	5:CC:280:ARG:NE	2.31	0.64
1:C1:1622:A:H5'	1:C1:1801:C:H5'	1.79	0.64
1:C1:1765:G:H2'	1:C1:1766:A:C8	2.33	0.64
10:CH:156:LEU:HD23	10:CH:159:LEU:HD12	1.78	0.64
20:CR:127:GLU:OE2	20:CR:135:GLN:NE2	2.25	0.64
47:LY:51:LYS:NZ	47:LY:70:THR:O	2.30	0.64
48:LZ:71:ILE:HD12	48:LZ:100:PHE:HE1	1.62	0.64
5:CC:693:SER:OG	5:CC:695:ASP:OD1	2.15	0.64
10:CH:208:LEU:HD22	10:CH:331:LYS:HD2	1.79	0.64
10:CH:445:ASN:HB2	10:CH:448:ASP:HB2	1.80	0.64
1:C1:3144:C:OP1	38:LO:178:ARG:NH1	2.31	0.63
4:CB:139:ALA:HB2	32:LG:212:ASN:HD22	1.62	0.63
1:C1:298:A:OP2	3:CA:265:ASN:ND2	2.28	0.63
2:C2:110:C:H42	56:Lj:27:LEU:HD22	1.63	0.63
27:Cb:505:VAL:HG13	27:Cb:573:HIS:HE2	1.63	0.63
31:LE:61:LEU:HD21	52:Lf:104:LEU:HB2	1.80	0.63
6:CD:147:LEU:HD22	6:CD:191:LEU:HD22	1.80	0.63
23:CU:325:LYS:NZ	23:CU:329:GLU:OE2	2.30	0.63
26:CY:728:LEU:O	26:CY:731:GLU:HG3	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:649:MET:O	12:CJ:653:ASN:ND2	2.31	0.63
20:CR:19:MET:HE1	56:Lj:75:LYS:HB2	1.81	0.63
22:CT:294:GLU:O	22:CT:393:ARG:NH1	2.32	0.63
1:C1:353:A:O3'	56:Lj:45:ARG:NH2	2.30	0.63
1:C1:403:U:H2'	1:C1:404:G:H8	1.63	0.63
11:CI:195:PRO:HG2	11:CI:253:LEU:HD23	1.81	0.63
15:CM:244:LEU:HG	15:CM:248:MET:HE2	1.81	0.63
59:Lq:111:ILE:HD13	59:Lq:151:VAL:HG11	1.81	0.63
1:C1:65:A:H1'	1:C1:77:A:H1'	1.79	0.63
1:C1:1458:G:N7	10:CH:515:ARG:NH2	2.46	0.63
12:CJ:614:LEU:HG	12:CJ:618:LYS:HZ1	1.63	0.63
17:CO:18:LYS:NZ	29:LB:345:THR:O	2.29	0.63
21:CS:436:MET:HE2	48:LZ:126:ASN:HA	1.80	0.63
48:LZ:99:THR:HG22	48:LZ:105:GLN:HB3	1.79	0.63
1:C1:1418:U:OP2	21:CS:818:ARG:NH1	2.31	0.63
1:C1:2350:U:H4'	39:LP:80:ARG:HH12	1.64	0.63
16:CN:107:VAL:HG23	16:CN:108:ILE:HG13	1.79	0.63
32:LG:222:LYS:O	32:LG:226:LEU:HB2	1.99	0.63
5:CC:489:TRP:CZ3	5:CC:526:PRO:HA	2.34	0.63
6:CD:306:ASP:O	6:CD:310:ARG:NH2	2.32	0.63
26:CY:631:VAL:HG21	26:CY:722:VAL:HG11	1.81	0.63
1:C1:98:G:OP1	35:LL:16:LYS:NZ	2.30	0.62
1:C1:1263:U:H2'	1:C1:1264:G:H8	1.64	0.62
3:CA:60:PRO:HG3	3:CA:135:GLY:HA2	1.80	0.62
22:CT:283:ARG:HD3	22:CT:320:SER:HB3	1.81	0.62
15:LF:162:VAL:HG22	15:LF:178:ASN:HD21	1.63	0.62
5:CC:180:TYR:O	5:CC:197:ARG:NH2	2.31	0.62
7:CE:359:LYS:HE3	7:CE:426:VAL:HG12	1.80	0.62
5:CC:501:THR:HG22	5:CC:516:ALA:HB3	1.81	0.62
29:LB:307:THR:HG21	29:LB:317:GLU:HG3	1.80	0.62
1:C1:1672:C:HO2'	1:C1:1751:U:HO2'	1.47	0.62
12:CJ:380:ARG:HD2	12:CJ:401:LEU:HB3	1.80	0.62
15:CM:94:ARG:HB2	15:CM:114:LEU:HB3	1.81	0.62
27:Cb:151:ARG:NH1	27:Cb:267:GLN:OE1	2.33	0.62
28:Cz:50:LEU:HD11	42:LS:133:GLU:HG3	1.80	0.62
32:LG:143:VAL:O	32:LG:147:GLU:HG3	1.99	0.62
1:C1:2456:A:H2'	1:C1:2457:C:H6	1.64	0.62
6:CD:102:PRO:HB2	6:CD:485:ASN:HB3	1.82	0.62
15:CM:108:ILE:HD12	15:CM:132:MET:HG2	1.81	0.62
1:C1:83:C:HO2'	1:C1:687:C:HO2'	1.40	0.62
1:C1:284:U:OP2	37:LN:68:ARG:NH2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1332:A:H2	1:C1:1335:C:H41	1.45	0.62
12:CJ:93:ARG:NH1	12:CJ:97:ARG:HD2	2.15	0.62
28:Cz:46:THR:HG21	28:Cz:51:ARG:HG3	1.82	0.62
34:LK:59:THR:OG1	34:LK:74:VAL:HG13	1.99	0.62
45:LV:79:VAL:HG23	45:LV:105:VAL:HG21	1.80	0.62
46:LX:63:SER:HB2	54:Lh:71:LEU:HD13	1.81	0.62
1:C1:2456:A:H2'	1:C1:2457:C:C6	2.34	0.62
10:CH:299:PRO:HD2	10:CH:300:GLU:H	1.64	0.62
12:CJ:177:HIS:HB3	12:CJ:273:LEU:HD11	1.82	0.62
20:CR:132:PRO:HG2	35:LL:106:GLU:HB3	1.82	0.62
1:C1:115:A:N6	1:C1:149:U:C2	2.68	0.62
1:C1:1550:C:OP2	15:CM:29:ARG:NH1	2.33	0.62
1:C1:1614:G:N2	1:C1:1617:A:OP2	2.26	0.62
48:LZ:45:ILE:HA	48:LZ:69:PRO:HA	1.82	0.62
1:C1:95:A:C5	1:C1:96:G:H1'	2.34	0.62
1:C1:1046:A:C6	1:C1:1074:C:C2	2.87	0.62
5:CC:699:LEU:HD23	5:CC:709:PRO:HG3	1.82	0.62
7:CE:234:VAL:HG11	7:CE:237:LEU:HD13	1.82	0.62
10:CH:381:THR:OG1	16:CN:157:GLN:OE1	2.15	0.62
26:CY:15:GLU:HG2	26:CY:19:LEU:HD22	1.82	0.62
27:Cb:428:ARG:HG2	27:Cb:428:ARG:HH11	1.65	0.62
1:C1:2091:U:O4	1:C1:2285:G:O6	2.17	0.61
44:LU:106:SER:HB3	44:LU:109:VAL:HB	1.82	0.61
1:C1:231:A:H2'	1:C1:232:G:C8	2.36	0.61
1:C1:2307:A:H2'	1:C1:2308:C:C6	2.36	0.61
12:CJ:251:LEU:HD23	12:CJ:273:LEU:HB3	1.82	0.61
1:C1:2350:U:O2'	39:LP:80:ARG:NH1	2.32	0.61
1:C1:2973:A:H2'	1:C1:2974:G:H8	1.64	0.61
8:CF:53:LEU:O	8:CF:57:ARG:HG3	2.00	0.61
9:CG:37:VAL:HG11	9:CG:50:LEU:HD13	1.83	0.61
11:CI:320:LEU:HD23	11:CI:323:MET:HG3	1.81	0.61
27:Cb:84:LYS:O	27:Cb:85:THR:HG23	1.99	0.61
27:Cb:140:LYS:HD3	27:Cb:271:PHE:HB3	1.81	0.61
44:LU:22:ILE:HB	44:LU:109:VAL:HG22	1.81	0.61
54:Lh:101:ASP:OD1	54:Lh:104:ARG:NH2	2.33	0.61
1:C1:1336:G:N2	1:C1:1338:U:O2'	2.29	0.61
1:C1:1765:G:H2'	1:C1:1766:A:H8	1.64	0.61
1:C1:2428:G:H21	59:Lq:209:THR:HG23	1.66	0.61
7:CE:305:ASP:OD1	7:CE:308:ARG:NH2	2.32	0.61
26:CY:555:ILE:HG23	26:CY:571:LEU:HD13	1.82	0.61
27:Cb:225:LYS:HD3	27:Cb:232:LEU:HD11	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Cb:432:ILE:HD13	27:Cb:456:ARG:HD2	1.82	0.61
1:C1:181:A:OP2	47:LY:45:ARG:NH1	2.31	0.61
3:CA:44:VAL:HG13	3:CA:48:HIS:HB2	1.81	0.61
5:CC:232:SER:OG	5:CC:234:ASP:OD1	2.19	0.61
6:CD:233:VAL:HG12	6:CD:240:ILE:HG12	1.80	0.61
1:C1:958:A:N6	1:C1:1087:C:N4	2.40	0.61
5:CC:477:VAL:HG11	5:CC:524:MET:HE1	1.81	0.61
21:CS:497:GLN:NE2	21:CS:498:GLU:O	2.33	0.61
27:Cb:331:MET:HE1	27:Cb:418:ASN:HB3	1.82	0.61
33:LH:54:LYS:HE2	36:LM:3:GLU:HB3	1.82	0.61
49:Lc:56:LYS:O	49:Lc:60:GLU:HG3	2.00	0.61
59:Lq:175:THR:H	59:Lq:178:GLN:NE2	1.99	0.61
1:C1:1044:A:O2'	43:LT:108:ARG:NH2	2.34	0.61
18:CP:238:ARG:NH2	18:CP:269:ASP:OD1	2.32	0.61
18:CP:521:GLU:OE2	18:CP:548:PHE:HB2	2.01	0.61
1:C1:542:U:H2'	1:C1:543:G:O4'	2.01	0.61
1:C1:2736:A:H5''	18:CP:526:TYR:HE1	1.66	0.61
7:CE:150:ASP:HB3	7:CE:311:LEU:HD22	1.83	0.61
10:CH:249:VAL:HG11	10:CH:277:PHE:CZ	2.36	0.61
10:CH:366:ALA:HA	16:CN:167:ILE:HD11	1.83	0.61
27:Cb:174:LEU:HB3	27:Cb:178:LYS:NZ	2.16	0.61
1:C1:1157:C:N4	38:LO:22:SER:OG	2.34	0.61
5:CC:367:ARG:HH12	5:CC:385:THR:HG1	1.47	0.61
5:CC:523:LEU:HD12	5:CC:583:LEU:HD23	1.82	0.61
26:CY:666:ASN:HD21	26:CY:669:LEU:HD13	1.66	0.61
36:LM:59:LEU:HD13	42:LS:152:LEU:HD11	1.82	0.61
5:CC:138:ARG:NH1	5:CC:140:GLU:OE2	2.30	0.61
5:CC:489:TRP:NE1	5:CC:491:VAL:HB	2.16	0.61
16:CN:15:VAL:HA	16:CN:61:ARG:HG2	1.83	0.61
27:Cb:203:GLN:HE22	27:Cb:220:ARG:HE	1.47	0.61
59:Lq:97:LYS:HG3	59:Lq:98:LYS:HD3	1.82	0.61
1:C1:780:G:H2'	1:C1:782:A:H62	1.66	0.60
1:C1:3164:G:C6	1:C1:3206:G:N1	2.69	0.60
5:CC:403:ARG:HD2	12:CJ:147:MET:HE1	1.83	0.60
26:CY:408:VAL:HG11	26:CY:452:LEU:HG	1.83	0.60
29:LB:222:THR:O	29:LB:273:TYR:HA	2.01	0.60
48:LZ:82:THR:HG23	53:Lg:94:PHE:CZ	2.36	0.60
21:CS:804:ARG:HD3	21:CS:805:PRO:HD2	1.83	0.60
22:CT:610:ALA:HA	26:CY:73:MET:SD	2.42	0.60
40:LQ:107:THR:HA	40:LQ:127:GLU:O	2.01	0.60
59:Lq:48:ARG:NH2	59:Lq:159:LEU:O	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1046:A:N1	1:C1:1074:C:N3	2.50	0.60
1:C1:2408:U:H2'	1:C1:2409:A:C8	2.37	0.60
1:C1:3319:C:O2'	29:LB:317:GLU:OE2	2.18	0.60
16:CN:67:ARG:HG2	16:CN:112:ASP:OD1	2.01	0.60
22:CT:322:LEU:HD12	22:CT:419:LEU:HD22	1.82	0.60
41:LR:89:MET:HE1	41:LR:97:ARG:HH12	1.65	0.60
1:C1:363:G:N1	1:C1:366:A:OP2	2.33	0.60
1:C1:567:U:OP1	15:LF:146:ASN:ND2	2.25	0.60
17:CO:37:LEU:HB3	29:LB:195:PHE:CZ	2.34	0.60
48:LZ:2:LYS:NZ	48:LZ:29:ASP:OD2	2.34	0.60
1:C1:2992:C:H4'	33:LH:161:ILE:HD13	1.82	0.60
5:CC:459:VAL:HG12	5:CC:778:ASP:HB3	1.83	0.60
14:CL:223:HIS:O	14:CL:225:VAL:N	2.34	0.60
23:CU:255:ARG:HE	23:CU:259:ARG:HH21	1.48	0.60
1:C1:405:U:OP1	39:LP:34:GLN:NE2	2.33	0.60
1:C1:1171:C:N3	1:C1:1297:U:O2	2.35	0.60
1:C1:1880:A:OP1	45:LV:37:TYR:OH	2.19	0.60
1:C1:2955:U:H2'	1:C1:2956:C:C6	2.37	0.60
2:C2:84:C:O2'	47:LY:112:LYS:NZ	2.34	0.60
4:CB:19:ASP:HB3	4:CB:22:GLN:OE1	2.02	0.60
4:CB:143:GLN:HG3	4:CB:170:THR:HG21	1.83	0.60
8:CF:21:GLU:OE1	8:CF:25:ARG:NH1	2.34	0.60
10:CH:45:TYR:HD2	10:CH:128:LYS:HD3	1.67	0.60
13:CK:164:ARG:HH21	13:CK:168:TYR:HB3	1.65	0.60
26:CY:438:THR:O	26:CY:442:ILE:HG12	2.02	0.60
29:LB:89:LEU:HD13	29:LB:196:GLY:HA3	1.83	0.60
33:LH:14:GLU:HA	36:LM:2:ALA:HB2	1.83	0.60
38:LO:139:THR:HG23	38:LO:142:ARG:H	1.67	0.60
8:CF:84:GLU:OE1	8:CF:90:HIS:ND1	2.28	0.60
16:CN:61:ARG:HD3	16:CN:106:ASN:HD21	1.67	0.60
26:CY:380:ILE:HG21	26:CY:419:VAL:HG22	1.82	0.60
26:CY:549:PRO:O	26:CY:553:HIS:ND1	2.28	0.60
27:Cb:141:THR:HA	27:Cb:144:PHE:CE1	2.37	0.60
39:LP:125:GLN:O	39:LP:140:MET:HA	2.01	0.60
1:C1:3132:U:O4	31:LE:191:LYS:NZ	2.33	0.60
12:CJ:585:LEU:CG	12:CJ:589:ARG:HH12	2.14	0.60
1:C1:476:C:H2'	1:C1:477:G:H8	1.66	0.60
1:C1:662:C:O2'	1:C1:666:U:OP1	2.19	0.60
1:C1:2432:C:OP2	59:Lq:26:ARG:NH2	2.35	0.60
1:C1:2816:U:OP2	1:C1:2817:U:O2'	2.20	0.60
2:C2:102:U:O2'	2:C2:103:G:OP1	2.18	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CS:488:ALA:HB1	22:CT:381:MET:HE1	1.84	0.60
22:CT:568:LEU:HD21	22:CT:610:ALA:HB1	1.82	0.60
27:Cb:108:LYS:HD3	27:Cb:183:LEU:HD21	1.84	0.60
42:LS:161:THR:HG23	42:LS:162:LYS:HD2	1.83	0.60
1:C1:835:G:O2'	1:C1:836:U:OP1	2.19	0.59
2:C2:132:G:H4'	46:LX:107:GLN:NE2	2.17	0.59
21:CS:700:GLU:O	21:CS:704:ASP:HB2	2.02	0.59
30:LC:287:LEU:HD11	40:LQ:60:LEU:HB2	1.83	0.59
37:LN:9:GLU:HG3	55:Li:49:VAL:HG12	1.84	0.59
39:LP:85:VAL:O	39:LP:89:GLN:HG3	2.02	0.59
1:C1:2799:G:O2'	14:CL:44:GLU:OE1	2.20	0.59
1:C1:3269:U:H5''	29:LB:309:MET:HE2	1.83	0.59
7:CE:438:PRO:HG2	7:CE:527:LEU:HD12	1.85	0.59
8:CF:80:THR:OG1	8:CF:83:GLU:OE1	2.19	0.59
48:LZ:73:VAL:HG23	48:LZ:100:PHE:CD2	2.37	0.59
51:Le:120:VAL:HB	51:Le:123:ALA:HB2	1.84	0.59
1:C1:789:A:H2'	1:C1:790:G:H8	1.64	0.59
4:CB:30:LEU:HB2	4:CB:291:LEU:HD11	1.85	0.59
5:CC:327:TRP:HB3	5:CC:330:GLU:HB2	1.85	0.59
5:CC:449:PHE:HB3	5:CC:480:TRP:CZ3	2.37	0.59
6:CD:108:PHE:HE1	6:CD:162:GLY:HA2	1.67	0.59
9:CG:104:GLY:HA3	9:CG:118:HIS:HB3	1.83	0.59
22:CT:601:LEU:HD22	22:CT:663:LEU:HD23	1.84	0.59
59:Lq:63:MET:SD	59:Lq:152:LYS:NZ	2.73	0.59
1:C1:1372:A:N6	1:C1:1400:A:O2'	2.35	0.59
5:CC:489:TRP:HE1	5:CC:491:VAL:HB	1.65	0.59
12:CJ:97:ARG:NH2	32:LG:195:LYS:O	2.33	0.59
29:LB:289:GLY:O	29:LB:305:LYS:NZ	2.35	0.59
1:C1:891:G:N2	1:C1:898:A:N1	2.43	0.59
1:C1:909:C:H2'	1:C1:910:A:C8	2.37	0.59
1:C1:1237:C:H2'	1:C1:1238:G:H8	1.67	0.59
26:CY:539:MET:HB2	26:CY:551:ARG:HG3	1.83	0.59
1:C1:251:C:OP1	20:CR:144:ASN:ND2	2.36	0.59
1:C1:897:G:H2'	1:C1:898:A:H8	1.68	0.59
8:CF:94:ARG:HD3	8:CF:245:LYS:HD3	1.83	0.59
10:CH:174:PHE:CE2	10:CH:266:GLN:HA	2.37	0.59
42:LS:68:HIS:O	42:LS:73:LYS:NZ	2.35	0.59
1:C1:151:G:OP2	55:Li:35:PRO:HG2	2.03	0.59
2:C2:220:G:N7	11:CI:278:ARG:NH2	2.51	0.59
8:CF:132:PRO:HD2	8:CF:216:LEU:HD23	1.85	0.59
10:CH:180:SER:O	10:CH:184:ARG:HG3	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:119:PRO:HB3	12:CJ:232:GLU:HB3	1.85	0.59
27:Cb:227:GLU:OE2	27:Cb:813:PHE:N	2.34	0.59
32:LG:204:THR:HG22	32:LG:205:GLU:HG3	1.84	0.59
59:Lq:59:PRO:C	59:Lq:61:PRO:HD3	2.28	0.59
1:C1:975:G:H4'	1:C1:976:U:H5'	1.84	0.59
4:CB:154:LEU:HD23	4:CB:180:ILE:HB	1.85	0.59
1:C1:319:A:OP1	35:LL:23:ARG:NH2	2.36	0.59
1:C1:405:U:H5''	39:LP:34:GLN:HE22	1.67	0.59
22:CT:431:ALA:HA	22:CT:434:ILE:HG12	1.85	0.59
30:LC:169:ALA:HB1	30:LC:226:PHE:CE1	2.38	0.59
36:LM:94:TRP:O	36:LM:97:THR:OG1	2.20	0.59
1:C1:785:C:OP1	30:LC:99:ARG:NH2	2.36	0.59
1:C1:3076:U:P	28:Cz:28:ASN:HD21	2.25	0.59
2:C2:214:A:H5'	11:CI:193:ARG:HG2	1.84	0.59
9:CG:20:MET:O	9:CG:95:ARG:NH2	2.36	0.59
13:CK:11:ARG:HH12	13:CK:16:ARG:HD2	1.68	0.59
16:CN:161:VAL:HG21	16:CN:181:LEU:HD23	1.84	0.59
22:CT:134:ILE:HG23	22:CT:148:HIS:HB3	1.83	0.59
26:CY:504:CYS:HA	26:CY:560:ARG:HH12	1.68	0.59
27:Cb:116:ILE:HB	27:Cb:295:LEU:HD21	1.85	0.59
27:Cb:471:ARG:NH1	27:Cb:542:GLU:OE2	2.35	0.59
1:C1:103:G:OP1	35:LL:70:ARG:NH1	2.36	0.58
1:C1:2294:A:H2'	1:C1:2295:C:C6	2.38	0.58
21:CS:438:MET:HE1	48:LZ:127:ARG:HB2	1.83	0.58
27:Cb:97:LEU:HB3	27:Cb:101:LEU:HD23	1.84	0.58
1:C1:440:G:H2'	1:C1:441:G:H8	1.68	0.58
4:CB:290:ALA:O	11:CI:319:LYS:NZ	2.36	0.58
10:CH:250:LEU:HD21	10:CH:334:VAL:HG21	1.85	0.58
1:C1:890:G:H2'	1:C1:891:G:C8	2.38	0.58
1:C1:1841:U:O2'	1:C1:3023:U:OP1	2.21	0.58
11:CI:216:LEU:HD13	11:CI:233:ILE:HG12	1.85	0.58
33:LH:94:ILE:HD13	33:LH:101:ASP:HB3	1.85	0.58
40:LQ:138:ARG:NH1	40:LQ:148:THR:HG21	2.18	0.58
1:C1:966:U:H2'	1:C1:967:U:C6	2.38	0.58
2:C2:219:A:N6	11:CI:218:VAL:O	2.36	0.58
4:CB:50:LEU:HA	7:CE:354:LYS:HE2	1.86	0.58
4:CB:147:PHE:O	4:CB:177:LYS:NZ	2.32	0.58
5:CC:142:ASP:HB2	5:CC:146:GLY:H	1.68	0.58
10:CH:422:ARG:NH1	10:CH:435:ASP:O	2.33	0.58
27:Cb:297:ALA:HB1	27:Cb:300:LYS:HB2	1.85	0.58
27:Cb:493:ARG:HE	27:Cb:574:ALA:HA	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LB:262:GLN:HB2	29:LB:265:VAL:HG23	1.86	0.58
5:CC:731:PRO:HB2	5:CC:746:HIS:CD2	2.39	0.58
15:CM:78:GLN:NE2	15:CM:131:GLU:OE2	2.30	0.58
15:CM:93:ILE:HA	15:CM:119:ASN:O	2.04	0.58
16:CN:82:GLN:HG3	16:CN:86:ASN:HD21	1.68	0.58
20:CR:209:MET:HE1	20:CR:229:LEU:HD11	1.84	0.58
26:CY:433:VAL:HG23	26:CY:434:THR:H	1.69	0.58
27:Cb:312:VAL:HG21	27:Cb:320:ALA:HB2	1.84	0.58
33:LH:64:VAL:HG23	33:LH:119:VAL:HG21	1.84	0.58
1:C1:894:A:C6	21:CS:727:ALA:HB1	2.39	0.58
1:C1:1618:C:OP2	53:Lg:75:ARG:NH1	2.31	0.58
1:C1:2847:C:H5'	10:CH:27:ARG:HH12	1.69	0.58
1:C1:3184:G:N7	29:LB:151:ARG:NH1	2.52	0.58
1:C1:3212:C:OP2	31:LE:96:ARG:NH1	2.36	0.58
3:CA:48:HIS:CE1	3:CA:100:LEU:HB2	2.39	0.58
6:CD:348:LEU:HD23	6:CD:350:ARG:H	1.67	0.58
18:CP:520:ASN:O	18:CP:521:GLU:HG2	2.02	0.58
22:CT:200:VAL:HG23	22:CT:201:LYS:HD3	1.86	0.58
1:C1:1097:G:H4'	1:C1:1098:G:H5''	1.86	0.58
1:C1:2320:A:H5'	39:LP:135:ARG:HH12	1.68	0.58
13:CK:248:ASN:ND2	13:CK:250:GLU:OE2	2.34	0.58
17:CO:106:ILE:HG23	17:CO:107:VAL:HG13	1.85	0.58
7:CE:362:VAL:HB	7:CE:412:ILE:HG22	1.85	0.58
10:CH:267:ILE:HG23	10:CH:308:LEU:HD11	1.85	0.58
27:Cb:17:ILE:HG12	27:Cb:448:LYS:NZ	2.18	0.58
1:C1:457:U:O4	24:CV:97:GLN:HG3	2.04	0.58
26:CY:446:LYS:HD3	26:CY:501:PHE:HD2	1.69	0.58
15:LF:133:ILE:HA	15:LF:136:VAL:HG12	1.86	0.58
33:LH:123:PHE:CZ	33:LH:190:LEU:HD12	2.39	0.58
49:Lc:54:LEU:HD13	53:Lg:92:ARG:HG2	1.85	0.58
1:C1:1452:U:H2'	1:C1:1453:U:H6	1.68	0.57
1:C1:3118:A:H2'	1:C1:3119:C:O4'	2.04	0.57
4:CB:97:VAL:HG22	4:CB:124:ILE:HA	1.85	0.57
7:CE:193:ARG:NH1	7:CE:219:GLY:O	2.37	0.57
15:CM:94:ARG:O	15:CM:118:ASN:N	2.37	0.57
34:LK:78:SER:O	34:LK:82:ILE:HG12	2.03	0.57
36:LM:113:THR:OG1	36:LM:116:ASP:OD1	2.21	0.57
3:CA:91:PHE:HB3	3:CA:103:TRP:HB2	1.85	0.57
6:CD:65:PHE:CD1	6:CD:93:LEU:HD21	2.39	0.57
6:CD:449:LYS:HB3	6:CD:451:LYS:NZ	2.19	0.57
7:CE:178:PHE:HA	7:CE:182:ASN:HD22	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CQ:137:LEU:HD22	19:CQ:164:LEU:HD13	1.85	0.57
35:LL:60:CYS:HA	35:LL:70:ARG:HH12	1.68	0.57
48:LZ:12:VAL:O	48:LZ:19:GLY:N	2.37	0.57
1:C1:407:G:N2	1:C1:1381:A:N6	2.44	0.57
1:C1:3205:C:N4	1:C1:3206:G:O6	2.37	0.57
5:CC:697:ARG:NH1	5:CC:714:ARG:HB2	2.20	0.57
7:CE:290:ARG:NH1	7:CE:292:THR:OG1	2.38	0.57
9:CG:31:GLU:HG3	22:CT:642:LYS:HD2	1.86	0.57
10:CH:419:VAL:O	29:LB:69:LYS:NZ	2.31	0.57
12:CJ:644:LYS:O	12:CJ:648:GLN:HG3	2.04	0.57
13:CK:98:THR:O	13:CK:102:LEU:HD12	2.05	0.57
26:CY:387:TRP:HZ2	26:CY:404:ILE:HD13	1.70	0.57
39:LP:115:LYS:HB2	39:LP:151:THR:HG22	1.86	0.57
1:C1:979:A:H2'	1:C1:980:G:C8	2.39	0.57
1:C1:1869:U:H2'	1:C1:1870:A:C8	2.36	0.57
1:C1:2975:C:H4'	16:CN:8:GLU:OE1	2.05	0.57
7:CE:466:GLU:OE2	7:CE:522:TYR:OH	2.19	0.57
10:CH:231:MET:HB3	10:CH:235:GLU:HG3	1.87	0.57
10:CH:251:TYR:HE1	10:CH:273:ILE:HD11	1.70	0.57
42:LS:140:ILE:HA	42:LS:143:LEU:HD12	1.86	0.57
48:LZ:94:VAL:HG23	48:LZ:95:ILE:HG23	1.86	0.57
54:Lh:68:ARG:HH22	54:Lh:84:ASP:HB3	1.68	0.57
1:C1:1171:C:N3	1:C1:1297:U:C2	2.73	0.57
4:CB:61:PRO:HD2	4:CB:286:PRO:HG3	1.86	0.57
7:CE:376:LEU:O	7:CE:380:ILE:HG12	2.04	0.57
59:Lq:88:ASP:OD1	59:Lq:91:LYS:NZ	2.37	0.57
1:C1:218:C:OP1	47:LY:46:SER:OG	2.21	0.57
1:C1:1181:C:H5''	14:CL:31:LYS:HD3	1.86	0.57
2:C2:298:G:H2'	11:CI:291:ARG:HH22	1.70	0.57
5:CC:238:LEU:HD22	21:CS:673:LYS:HG3	1.87	0.57
10:CH:525:LYS:NZ	44:LU:98:ASP:HB3	2.19	0.57
15:CM:193:GLU:O	15:CM:197:VAL:HA	2.05	0.57
21:CS:665:GLN:OE1	21:CS:671:LYS:NZ	2.35	0.57
22:CT:171:GLN:HA	22:CT:174:VAL:HG12	1.84	0.57
33:LH:10:ILE:HG13	33:LH:109:ARG:HG2	1.85	0.57
48:LZ:67:ILE:O	48:LZ:114:LYS:NZ	2.28	0.57
5:CC:459:VAL:HB	5:CC:791:ALA:HB2	1.85	0.57
7:CE:539:VAL:HA	7:CE:550:PRO:HG3	1.86	0.57
10:CH:89:HIS:CD2	27:Cb:625:ARG:HE	2.22	0.57
30:LC:42:GLY:HA3	30:LC:114:ILE:HD11	1.87	0.57
36:LM:35:ASP:OD2	36:LM:38:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:LN:96:ARG:HH21	37:LN:100:ALA:HB1	1.69	0.57
1:C1:603:G:H2'	1:C1:604:G:C8	2.40	0.57
1:C1:1787:G:OP2	1:C1:1787:G:N2	2.37	0.57
1:C1:2361:A:C6	1:C1:2900:C:C4	2.93	0.57
2:C2:175:G:H2'	2:C2:176:G:C8	2.39	0.57
6:CD:384:LEU:HD22	6:CD:416:TRP:CE3	2.40	0.57
10:CH:267:ILE:HG22	10:CH:271:LYS:NZ	2.20	0.57
15:CM:116:GLN:O	15:CM:119:ASN:ND2	2.38	0.57
16:CN:81:LEU:HD22	16:CN:96:ARG:HD3	1.86	0.57
37:LN:172:ARG:O	37:LN:183:THR:OG1	2.23	0.57
59:Lq:55:LEU:HD23	59:Lq:153:SER:HB2	1.87	0.57
1:C1:281:U:H2'	1:C1:282:G:H8	1.69	0.57
1:C1:1046:A:N6	1:C1:1074:C:O2	2.38	0.57
5:CC:571:ARG:HD3	5:CC:572:PRO:HD2	1.86	0.57
6:CD:177:THR:OG1	6:CD:197:ASP:OD1	2.22	0.57
7:CE:239:ALA:HB1	7:CE:244:LEU:HB2	1.86	0.57
26:CY:432:ARG:HD2	26:CY:494:GLN:NE2	2.19	0.57
32:LG:186:LYS:HB2	32:LG:197:THR:HG23	1.87	0.57
2:C2:83:C:O2	47:LY:109:HIS:NE2	2.28	0.57
6:CD:462:LYS:HG2	6:CD:478:GLU:OE2	2.05	0.57
7:CE:275:GLU:OE1	7:CE:279:ARG:NH1	2.38	0.57
9:CG:16:LEU:HD11	9:CG:71:LEU:HD21	1.87	0.57
31:LE:72:LEU:HA	31:LE:83:VAL:HG12	1.87	0.57
1:C1:143:G:N7	32:LG:140:ASN:ND2	2.53	0.56
1:C1:935:U:OP1	1:C1:1098:G:N2	2.38	0.56
1:C1:975:G:N2	1:C1:976:U:O4	2.38	0.56
1:C1:2747:U:O4	1:C1:2748:A:N6	2.38	0.56
10:CH:13:ALA:HB2	10:CH:143:LYS:HA	1.86	0.56
10:CH:236:MET:HA	10:CH:239:VAL:HG22	1.87	0.56
12:CJ:411:SER:HA	12:CJ:450:TYR:HE2	1.69	0.56
18:CP:498:CYS:O	18:CP:583:LYS:NZ	2.31	0.56
29:LB:285:ARG:NH1	29:LB:294:ASN:O	2.38	0.56
34:LK:59:THR:OG1	34:LK:74:VAL:O	2.14	0.56
47:LY:2:LYS:HE2	47:LY:7:VAL:HG13	1.86	0.56
59:Lq:16:LEU:HA	59:Lq:20:SER:H	1.70	0.56
1:C1:231:A:H2'	1:C1:232:G:H8	1.70	0.56
1:C1:663:G:O6	40:LQ:89:PRO:HB3	2.05	0.56
1:C1:2788:G:H2'	1:C1:2789:G:C8	2.40	0.56
12:CJ:461:VAL:O	12:CJ:465:ILE:HG12	2.04	0.56
18:CP:565:ARG:HD3	18:CP:567:TYR:OH	2.05	0.56
1:C1:749:C:H2'	1:C1:750:G:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:863:A:H5'	22:CT:582:ARG:HB2	1.87	0.56
1:C1:1272:U:H2'	1:C1:1273:A:C8	2.40	0.56
1:C1:1625:G:N2	1:C1:1787:G:O2'	2.38	0.56
1:C1:3288:G:O6	1:C1:3297:U:O4	2.23	0.56
5:CC:759:ILE:HG22	12:CJ:637:MET:HE1	1.86	0.56
10:CH:271:LYS:HA	10:CH:274:LYS:HE2	1.87	0.56
13:CK:175:MET:HE3	13:CK:175:MET:HA	1.87	0.56
15:CM:149:SER:OG	15:CM:246:ARG:NH1	2.38	0.56
18:CP:425:ILE:HG21	18:CP:433:THR:HG21	1.87	0.56
24:CV:9:ILE:HG22	24:CV:47:VAL:HG22	1.87	0.56
27:Cb:396:VAL:HG12	27:Cb:426:ALA:HB1	1.87	0.56
29:LB:17:LEU:HA	29:LB:19:ARG:H	1.70	0.56
37:LN:27:CYS:SG	37:LN:124:ASP:HB2	2.46	0.56
37:LN:192:LYS:O	37:LN:196:THR:HG23	2.05	0.56
48:LZ:60:ARG:O	48:LZ:64:ARG:HG3	2.05	0.56
1:C1:3029:C:O2	10:CH:503:ARG:NH2	2.33	0.56
3:CA:42:ARG:HD2	3:CA:67:LYS:HB2	1.87	0.56
16:CN:217:VAL:HA	16:CN:233:ILE:HD11	1.87	0.56
25:CX:127:GLU:OE2	25:CX:130:ARG:NH1	2.38	0.56
26:CY:379:LEU:O	26:CY:382:THR:OG1	2.20	0.56
26:CY:379:LEU:O	26:CY:383:VAL:HG23	2.05	0.56
26:CY:635:ARG:HH21	26:CY:711:LEU:HD23	1.70	0.56
27:Cb:145:VAL:HA	27:Cb:148:MET:HG2	1.87	0.56
45:LV:41:VAL:HG12	45:LV:60:VAL:HG12	1.86	0.56
47:LY:54:GLU:HB2	47:LY:107:LYS:HB3	1.87	0.56
1:C1:1263:U:H5''	8:CF:69:LYS:HG3	1.88	0.56
1:C1:1360:U:H2'	1:C1:1361:G:H8	1.70	0.56
1:C1:3305:U:H2'	1:C1:3306:G:C8	2.40	0.56
2:C2:100:U:O4	56:Lj:65:ARG:NH2	2.37	0.56
9:CG:48:VAL:HG12	9:CG:68:GLY:HA3	1.87	0.56
32:LG:232:THR:HB	32:LG:235:ARG:HH21	1.71	0.56
6:CD:73:ARG:HA	6:CD:73:ARG:NH1	2.21	0.56
17:CO:13:ASN:OD1	17:CO:16:ARG:NH2	2.39	0.56
26:CY:84:GLU:H	26:CY:533:GLN:HE22	1.53	0.56
32:LG:214:LEU:O	32:LG:218:ILE:HG12	2.06	0.56
39:LP:27:LYS:HG2	39:LP:63:TYR:CG	2.40	0.56
46:LX:90:GLU:HG3	46:LX:146:LEU:HD21	1.87	0.56
1:C1:2562:U:H2'	1:C1:2563:G:O4'	2.06	0.56
1:C1:3136:A:H2'	1:C1:3137:A:H8	1.71	0.56
5:CC:403:ARG:HD2	12:CJ:147:MET:CE	2.34	0.56
27:Cb:375:THR:HG22	27:Cb:377:HIS:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1171:C:H42	1:C1:1297:U:H1'	1.70	0.56
1:C1:2907:U:H2'	1:C1:2908:G:C8	2.40	0.56
48:LZ:103:PRO:HA	48:LZ:106:ARG:HD3	1.88	0.56
56:Lj:45:ARG:O	56:Lj:57:LYS:NZ	2.26	0.56
1:C1:1263:U:OP1	8:CF:69:LYS:HD2	2.06	0.56
2:C2:63:G:O2'	54:Lh:54:LYS:NZ	2.39	0.56
6:CD:62:PRO:HB2	6:CD:98:SER:HB2	1.86	0.56
22:CT:130:GLU:O	22:CT:134:ILE:HG12	2.06	0.56
15:LF:162:VAL:HG22	15:LF:178:ASN:ND2	2.21	0.56
59:Lq:194:LEU:HD23	59:Lq:196:LYS:H	1.71	0.56
1:C1:1103:U:P	14:CL:33:ARG:HH22	2.28	0.56
1:C1:1386:G:N2	1:C1:1389:A:OP2	2.30	0.56
1:C1:1665:U:O4	44:LU:89:LYS:NZ	2.39	0.56
1:C1:2407:A:H2'	1:C1:2408:U:C6	2.41	0.56
1:C1:2461:U:H2'	1:C1:2462:A:C8	2.40	0.56
27:Cb:444:PRO:HD3	27:Cb:453:ARG:HH22	1.71	0.56
27:Cb:559:ARG:HA	27:Cb:562:GLU:HG2	1.88	0.56
37:LN:148:ILE:O	37:LN:151:ILE:HG22	2.06	0.56
1:C1:213:G:C6	1:C1:1371:G:N2	2.74	0.55
5:CC:270:PRO:O	7:CE:552:ARG:HD3	2.05	0.55
6:CD:384:LEU:HD23	6:CD:435:SER:HB3	1.89	0.55
27:Cb:625:ARG:HH21	27:Cb:628:ILE:HD12	1.71	0.55
29:LB:325:ILE:HD11	29:LB:329:VAL:HG21	1.87	0.55
44:LU:59:VAL:HG23	44:LU:60:ILE:HG12	1.88	0.55
59:Lq:99:LEU:HD23	59:Lq:103:LEU:HD23	1.87	0.55
1:C1:133:G:O2'	1:C1:134:G:O4'	2.22	0.55
1:C1:768:G:H2'	1:C1:769:C:C6	2.42	0.55
8:CF:131:ALA:HB2	8:CF:201:LEU:HD11	1.87	0.55
9:CG:72:GLY:HA2	9:CG:83:HIS:ND1	2.22	0.55
9:CG:147:THR:HA	9:CG:164:CYS:HA	1.88	0.55
22:CT:483:LEU:HD21	22:CT:523:LEU:HD11	1.87	0.55
27:Cb:409:VAL:O	27:Cb:413:ARG:HG3	2.06	0.55
1:C1:476:C:H2'	1:C1:477:G:C8	2.41	0.55
1:C1:978:A:H2'	1:C1:979:A:C8	2.41	0.55
1:C1:1332:A:O2'	1:C1:1334:A:OP1	2.23	0.55
1:C1:1429:G:N7	39:LP:25:SER:OG	2.37	0.55
1:C1:1594:C:H2'	1:C1:1595:U:C6	2.42	0.55
1:C1:2088:A:H4'	19:CQ:43:LYS:HE3	1.89	0.55
1:C1:2387:G:C6	1:C1:2563:G:N2	2.75	0.55
1:C1:2777:A:H4'	1:C1:2778:A:OP1	2.06	0.55
6:CD:355:SER:HB2	6:CD:373:ARG:HH12	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CK:207:PRO:HA	13:CK:210:THR:HG22	1.87	0.55
27:Cb:228:MET:HB2	27:Cb:230:LEU:HG	1.87	0.55
27:Cb:444:PRO:HG3	27:Cb:450:PHE:HB2	1.87	0.55
28:Cz:61:MET:SD	28:Cz:64:LYS:NZ	2.79	0.55
1:C1:36:C:O2'	1:C1:915:G:N3	2.33	0.55
1:C1:2087:A:OP1	27:Cb:869:ARG:NH2	2.40	0.55
13:CK:241:ARG:HB2	13:CK:259:LEU:HD11	1.87	0.55
18:CP:371:LEU:HD12	18:CP:541:LEU:HD11	1.88	0.55
22:CT:596:LEU:HB3	22:CT:615:LEU:HD11	1.89	0.55
15:LF:23:LYS:HA	15:LF:26:GLU:HG2	1.89	0.55
1:C1:6:A:H5'	12:CJ:93:ARG:HG2	1.89	0.55
1:C1:1289:G:O4'	38:LO:61:LYS:NZ	2.40	0.55
1:C1:3305:U:H2'	1:C1:3306:G:H8	1.72	0.55
10:CH:250:LEU:HD23	10:CH:283:PHE:HB2	1.89	0.55
10:CH:385:GLU:O	10:CH:389:ASN:ND2	2.31	0.55
27:Cb:163:ALA:HB3	27:Cb:213:ILE:HG12	1.88	0.55
27:Cb:422:VAL:HG21	27:Cb:427:ALA:HB2	1.87	0.55
39:LP:16:ARG:HG2	39:LP:149:ILE:HG13	1.89	0.55
1:C1:247:A:H2'	1:C1:248:G:H8	1.72	0.55
1:C1:1087:C:H2'	1:C1:1088:G:H8	1.71	0.55
2:C2:159:C:C5	15:CM:55:GLU:HG2	2.41	0.55
6:CD:44:TYR:HB2	12:CJ:592:GLU:HG2	1.88	0.55
10:CH:467:ARG:O	10:CH:470:LYS:HG2	2.07	0.55
15:CM:64:GLN:HG3	15:CM:100:LYS:HD3	1.89	0.55
15:LF:94:ARG:O	15:LF:118:ASN:N	2.39	0.55
35:LL:43:ALA:O	35:LL:47:ALA:HA	2.06	0.55
51:Le:80:VAL:HA	51:Le:83:VAL:HG22	1.89	0.55
1:C1:651:A:H2'	1:C1:652:A:C8	2.42	0.55
1:C1:895:A:O2'	1:C1:896:A:O5'	2.24	0.55
1:C1:1157:C:O2'	1:C1:1158:C:O5'	2.21	0.55
6:CD:159:ASN:ND2	6:CD:163:SER:OG	2.40	0.55
27:Cb:105:ILE:HG13	27:Cb:108:LYS:HZ3	1.70	0.55
15:LF:104:LYS:HB3	15:LF:105:PRO:HD3	1.88	0.55
48:LZ:83:ARG:HH11	48:LZ:83:ARG:HG2	1.72	0.55
52:Lf:18:TYR:OH	52:Lf:91:LEU:O	2.23	0.55
1:C1:1108:G:O3'	23:CU:328:ARG:NH1	2.39	0.55
1:C1:1576:C:H2'	1:C1:1577:G:H8	1.72	0.55
1:C1:1615:C:O2'	48:LZ:78:HIS:ND1	2.37	0.55
1:C1:2980:U:H2'	1:C1:2981:A:H8	1.72	0.55
5:CC:461:ILE:HG21	5:CC:783:PRO:HD3	1.89	0.55
11:CI:286:ASN:OD1	11:CI:287:LYS:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CI:302:TRP:O	11:CI:306:VAL:HG23	2.07	0.55
26:CY:442:ILE:HA	26:CY:445:MET:HE2	1.87	0.55
27:Cb:827:GLN:N	27:Cb:830:GLU:OE1	2.40	0.55
1:C1:745:U:H3	1:C1:749:C:N4	2.04	0.55
1:C1:1176:G:H2'	1:C1:1177:A:C8	2.41	0.55
4:CB:103:ASP:HB2	4:CB:108:TYR:HE2	1.71	0.55
12:CJ:390:PHE:CD2	12:CJ:465:ILE:HD12	2.40	0.55
18:CP:317:ARG:NH2	18:CP:338:SER:O	2.37	0.55
18:CP:524:VAL:HG13	18:CP:581:PHE:CZ	2.42	0.55
27:Cb:243:ALA:HA	27:Cb:246:LEU:HD12	1.89	0.55
27:Cb:493:ARG:NH1	27:Cb:581:ALA:HB2	2.22	0.55
27:Cb:816:TRP:CD1	27:Cb:820:HIS:CE1	2.95	0.55
29:LB:29:VAL:HG12	29:LB:31:SER:H	1.71	0.55
29:LB:166:GLN:OE1	29:LB:169:LYS:HD2	2.07	0.55
48:LZ:80:MET:HE1	53:Lg:94:PHE:CD1	2.41	0.55
5:CC:516:ALA:HB2	5:CC:594:ILE:HD11	1.88	0.55
26:CY:706:ALA:HA	26:CY:709:LYS:NZ	2.22	0.55
15:LF:46:LYS:HA	15:LF:49:VAL:HG22	1.88	0.55
40:LQ:99:LEU:HD11	40:LQ:108:VAL:HG21	1.89	0.55
1:C1:725:A:OP1	40:LQ:94:ARG:NH1	2.40	0.54
1:C1:1777:A:H2'	1:C1:1778:A:C8	2.42	0.54
1:C1:2091:U:H2'	1:C1:2092:G:C8	2.42	0.54
1:C1:3188:U:H2'	1:C1:3189:G:C8	2.42	0.54
3:CA:63:ARG:HH11	5:CC:163:TPO:P	2.28	0.54
5:CC:742:LEU:HB2	5:CC:765:LEU:HB2	1.88	0.54
12:CJ:188:SER:HG	12:CJ:462:TRP:CD1	2.25	0.54
17:CO:30:LEU:HD11	29:LB:42:HIS:CG	2.42	0.54
22:CT:276:ASP:H	22:CT:279:PHE:HB3	1.71	0.54
15:LF:62:ARG:O	15:LF:66:ARG:HG2	2.06	0.54
33:LH:186:SER:HB2	33:LH:226:ILE:HD11	1.89	0.54
59:Lq:89:ASP:OD1	59:Lq:92:LYS:HE3	2.07	0.54
3:CA:196:ILE:HG23	3:CA:229:ILE:HG23	1.89	0.54
6:CD:398:PRO:HG2	6:CD:469:ASP:HA	1.89	0.54
16:CN:186:VAL:HG22	16:CN:193:ILE:HD13	1.88	0.54
18:CP:545:LYS:HD2	18:CP:570:LEU:HD21	1.89	0.54
26:CY:387:TRP:CZ2	26:CY:404:ILE:HD13	2.42	0.54
1:C1:649:U:H2'	1:C1:650:C:C6	2.42	0.54
1:C1:671:G:OP2	35:LL:28:GLN:NE2	2.41	0.54
1:C1:684:G:OP2	30:LC:273:LYS:NZ	2.40	0.54
1:C1:765:G:O2'	40:LQ:97:ARG:NH1	2.39	0.54
2:C2:175:G:H2'	2:C2:176:G:H8	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:190:LEU:HD11	12:CJ:462:TRP:CD2	2.42	0.54
15:LF:213:LEU:HB3	15:LF:248:MET:HB3	1.88	0.54
1:C1:2814:G:H21	13:CK:192:THR:HG21	1.72	0.54
4:CB:118:GLU:OE2	4:CB:121:ARG:NH1	2.41	0.54
6:CD:80:LEU:O	6:CD:83:ASN:C	2.50	0.54
15:CM:151:ARG:HD2	15:CM:191:ILE:HD13	1.90	0.54
20:CR:136:GLN:HE22	35:LL:114:GLN:HB2	1.72	0.54
27:Cb:100:ASN:OD1	27:Cb:101:LEU:N	2.40	0.54
48:LZ:1:MET:HE1	49:Lc:67:LYS:HD2	1.90	0.54
2:C2:286:C:H2'	2:C2:287:G:H8	1.72	0.54
5:CC:215:GLU:OE2	5:CC:233:ARG:NH1	2.40	0.54
5:CC:258:THR:HG23	32:LG:76:PRO:HG2	1.90	0.54
10:CH:215:TYR:HE1	10:CH:338:LEU:HD23	1.71	0.54
12:CJ:266:ALA:HB3	12:CJ:270:ALA:HB2	1.90	0.54
13:CK:44:GLY:C	13:CK:46:ARG:H	2.15	0.54
26:CY:635:ARG:HH22	26:CY:713:TRP:CA	2.18	0.54
35:LL:76:THR:HB	35:LL:79:GLU:HG2	1.89	0.54
36:LM:96:GLU:O	36:LM:101:LYS:NZ	2.41	0.54
47:LY:54:GLU:OE1	47:LY:54:GLU:N	2.41	0.54
53:Lg:55:ILE:HD11	53:Lg:79:GLY:HA2	1.89	0.54
1:C1:1646:G:H5'	1:C1:1722:G:H4'	1.89	0.54
2:C2:44:A:H2'	2:C2:45:C:C6	2.42	0.54
2:C2:166:C:H2'	2:C2:167:A:H8	1.72	0.54
4:CB:175:THR:HA	4:CB:178:ARG:HG3	1.88	0.54
4:CB:273:GLN:HB2	4:CB:277:ASN:HB2	1.89	0.54
5:CC:524:MET:HG2	5:CC:581:VAL:HA	1.90	0.54
6:CD:371:ASP:HB3	6:CD:374:ALA:HB2	1.89	0.54
7:CE:377:LEU:HD22	7:CE:382:LEU:HD21	1.89	0.54
12:CJ:178:TYR:CD2	12:CJ:245:LEU:HD23	2.42	0.54
19:CQ:120:VAL:O	19:CQ:124:ARG:HG2	2.08	0.54
23:CU:288:LYS:HA	23:CU:291:GLU:HG2	1.88	0.54
27:Cb:130:VAL:HB	27:Cb:269:LEU:HD22	1.89	0.54
1:C1:522:G:H2'	1:C1:523:A:C8	2.43	0.54
1:C1:819:G:H1	1:C1:836:U:H3	1.55	0.54
1:C1:2973:A:H2'	1:C1:2974:G:C8	2.42	0.54
6:CD:323:ARG:HG2	6:CD:335:THR:HG22	1.89	0.54
6:CD:415:VAL:HG22	6:CD:439:TYR:HB3	1.90	0.54
10:CH:305:ILE:O	10:CH:309:THR:HG23	2.07	0.54
15:CM:35:ALA:HB1	15:CM:39:ARG:NH1	2.21	0.54
29:LB:228:VAL:HG21	29:LB:271:MET:HE3	1.90	0.54
33:LH:127:MET:HE1	33:LH:200:ILE:HD12	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LR:134:HIS:CE1	41:LR:136:ARG:HB2	2.43	0.54
1:C1:812:G:H5''	26:CY:6:LYS:HG2	1.89	0.54
2:C2:97:A:OP1	54:Lh:72:ARG:NH2	2.41	0.54
5:CC:390:LEU:HD21	12:CJ:190:LEU:HD23	1.90	0.54
11:CI:306:VAL:HA	11:CI:309:GLU:HG3	1.89	0.54
27:Cb:835:ASN:OD1	27:Cb:838:ARG:NH2	2.41	0.54
34:LK:125:LEU:O	34:LK:129:VAL:HG12	2.07	0.54
59:Lq:155:VAL:HG11	59:Lq:167:VAL:HG22	1.88	0.54
1:C1:727:C:H2'	1:C1:728:A:H8	1.71	0.54
1:C1:3298:U:H2'	1:C1:3299:A:H8	1.73	0.54
7:CE:388:HIS:CE1	7:CE:391:GLN:HG3	2.43	0.54
9:CG:114:ILE:HB	9:CG:164:CYS:HB3	1.89	0.54
10:CH:522:ALA:HB1	41:LR:51:ILE:HD13	1.90	0.54
15:CM:131:GLU:O	15:CM:135:ILE:HG12	2.08	0.54
48:LZ:17:TYR:HE1	48:LZ:46:GLU:HG2	1.72	0.54
51:Le:106:ARG:O	51:Le:110:ILE:HG13	2.07	0.54
1:C1:920:U:O2	21:CS:818:ARG:NH2	2.41	0.54
2:C2:95:G:C4	56:Lj:79:ARG:NH1	2.76	0.54
10:CH:274:LYS:O	10:CH:277:PHE:N	2.41	0.54
27:Cb:148:MET:HE1	27:Cb:237:TYR:CD1	2.43	0.54
28:Cz:52:VAL:HG22	28:Cz:55:ARG:HH21	1.73	0.54
31:LE:60:LEU:O	31:LE:67:GLY:N	2.41	0.54
32:LG:66:LYS:HG2	32:LG:70:MET:HE2	1.90	0.54
1:C1:2073:G:O5'	27:Cb:107:ARG:NH2	2.40	0.53
1:C1:2361:A:C6	1:C1:2900:C:N3	2.76	0.53
1:C1:3183:C:H42	17:CO:93:ARG:HE	1.56	0.53
3:CA:123:MET:HE3	3:CA:236:PRO:HD3	1.90	0.53
7:CE:358:LYS:HE3	7:CE:427:ASP:OD2	2.09	0.53
1:C1:2076:C:H2'	1:C1:2077:G:H8	1.73	0.53
1:C1:2404:G:O6	1:C1:2467:U:O4	2.26	0.53
3:CA:53:ASN:HA	3:CA:64:LYS:NZ	2.24	0.53
4:CB:135:ALA:O	4:CB:138:LYS:NZ	2.41	0.53
5:CC:489:TRP:CD1	5:CC:490:SER:N	2.77	0.53
5:CC:606:VAL:HG22	5:CC:615:VAL:HG12	1.89	0.53
6:CD:345:LEU:HA	6:CD:359:ALA:O	2.08	0.53
8:CF:44:SER:HB2	8:CF:224:LEU:HD11	1.90	0.53
22:CT:323:ASN:O	22:CT:327:HIS:ND1	2.40	0.53
26:CY:539:MET:HB3	26:CY:554:LEU:HD21	1.90	0.53
29:LB:72:VAL:HG12	45:LV:90:PHE:HD2	1.73	0.53
36:LM:59:LEU:O	42:LS:155:ARG:NH2	2.39	0.53
37:LN:2:GLY:HA3	55:Li:45:ARG:NH2	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:LY:73:TYR:HD2	47:LY:76:LYS:HG2	1.73	0.53
1:C1:1120:U:H2'	1:C1:1121:G:H8	1.73	0.53
1:C1:2795:A:H1'	1:C1:2809:A:N6	2.23	0.53
2:C2:213:A:OP2	4:CB:144:ARG:NH2	2.41	0.53
3:CA:25:ASN:O	3:CA:169:HIS:HA	2.09	0.53
12:CJ:36:LEU:HB3	12:CJ:72:LEU:HD21	1.89	0.53
26:CY:374:LYS:HA	26:CY:377:LYS:HZ1	1.72	0.53
26:CY:579:LEU:HD22	26:CY:653:TRP:CZ3	2.43	0.53
26:CY:657:MET:CE	26:CY:664:ASN:H	2.20	0.53
48:LZ:56:MET:HE3	48:LZ:61:ILE:HD13	1.89	0.53
1:C1:1479:C:H2'	1:C1:1480:A:C8	2.43	0.53
13:CK:147:TRP:C	13:CK:170:ARG:HH21	2.16	0.53
18:CP:373:VAL:HG21	18:CP:397:HIS:HB3	1.90	0.53
21:CS:469:GLU:OE2	32:LG:71:ARG:NH2	2.40	0.53
22:CT:127:ALA:O	22:CT:131:LEU:HG	2.08	0.53
26:CY:429:GLN:HA	26:CY:432:ARG:HB3	1.91	0.53
26:CY:579:LEU:HD22	26:CY:653:TRP:CH2	2.44	0.53
30:LC:146:VAL:HG21	30:LC:151:LEU:HD11	1.91	0.53
39:LP:11:PRO:HA	39:LP:16:ARG:HH12	1.73	0.53
1:C1:2970:U:H2'	1:C1:2971:U:C6	2.43	0.53
7:CE:203:ALA:O	7:CE:207:MET:HG2	2.07	0.53
16:CN:14:GLY:O	16:CN:61:ARG:NH1	2.42	0.53
21:CS:552:LEU:HD13	49:Lc:16:LYS:HD2	1.90	0.53
27:Cb:493:ARG:NH2	27:Cb:573:HIS:O	2.37	0.53
47:LY:85:THR:HG22	47:LY:95:PRO:HA	1.89	0.53
1:C1:208:G:H5''	47:LY:11:ARG:HG3	1.88	0.53
1:C1:405:U:H5''	39:LP:34:GLN:NE2	2.24	0.53
1:C1:933:A:N3	1:C1:1096:U:O2'	2.38	0.53
1:C1:1219:G:N2	34:LK:138:SER:O	2.34	0.53
2:C2:57:C:H4'	2:C2:63:G:N7	2.24	0.53
6:CD:462:LYS:HG2	6:CD:478:GLU:CD	2.34	0.53
13:CK:203:ASN:H	13:CK:210:THR:HB	1.74	0.53
22:CT:277:ARG:HG3	22:CT:281:LYS:NZ	2.24	0.53
47:LY:82:GLU:HG2	47:LY:83:ARG:HG3	1.91	0.53
49:Lc:46:LEU:HD12	49:Lc:93:MET:HE3	1.90	0.53
1:C1:1464:A:N6	26:CY:15:GLU:OE1	2.41	0.53
1:C1:3332:G:O2'	1:C1:3333:A:H8	1.92	0.53
2:C2:45:C:O2'	58:Ll:11:GLN:OE1	2.22	0.53
2:C2:223:G:O2'	2:C2:300:A:OP2	2.26	0.53
5:CC:213:VAL:HG21	21:CS:721:LYS:HD2	1.91	0.53
7:CE:470:LEU:HD23	7:CE:473:LEU:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CI:295:ARG:HH11	11:CI:296:PRO:HD2	1.73	0.53
39:LP:88:ALA:O	39:LP:92:ILE:HG13	2.08	0.53
1:C1:119:U:H5''	5:CC:280:ARG:HG2	1.90	0.53
1:C1:399:A:C2	2:C2:17:A:H1'	2.44	0.53
1:C1:424:G:H2'	1:C1:425:A:C8	2.44	0.53
1:C1:972:G:N2	43:LT:59:GLY:O	2.42	0.53
1:C1:1199:A:OP2	28:Cz:62:LYS:NZ	2.34	0.53
5:CC:531:VAL:N	6:CD:198:ARG:HH22	2.07	0.53
9:CG:6:ASP:OD1	9:CG:7:GLN:N	2.41	0.53
10:CH:97:ILE:HD13	10:CH:142:LEU:HD13	1.90	0.53
10:CH:446:VAL:O	10:CH:450:ILE:HG12	2.09	0.53
12:CJ:380:ARG:HB2	12:CJ:401:LEU:HD12	1.91	0.53
27:Cb:201:GLU:HA	27:Cb:204:PHE:CD2	2.32	0.53
29:LB:92:TYR:OH	29:LB:181:GLU:OE2	2.20	0.53
30:LC:363:HIS:ND1	42:LS:64:ILE:HD11	2.24	0.53
32:LG:85:LEU:HD23	32:LG:181:ALA:HB1	1.91	0.53
54:Lh:48:LYS:O	54:Lh:52:LEU:HD12	2.08	0.53
1:C1:423:U:H2'	1:C1:424:G:C8	2.43	0.53
1:C1:650:C:H2'	1:C1:651:A:H8	1.73	0.53
1:C1:1213:A:H5''	1:C1:1214:C:H5'	1.90	0.53
1:C1:2414:G:H3'	1:C1:2415:U:H5'	1.91	0.53
1:C1:3180:C:H2'	1:C1:3181:C:O4'	2.09	0.53
6:CD:443:ARG:HE	6:CD:444:GLU:N	2.07	0.53
9:CG:112:SER:HB3	13:CK:136:VAL:HA	1.90	0.53
18:CP:569:HIS:CE1	18:CP:570:LEU:HD12	2.44	0.53
21:CS:818:ARG:O	21:CS:822:GLU:HG2	2.08	0.53
33:LH:60:ARG:NE	33:LH:76:SER:HA	2.18	0.53
38:LO:170:TYR:CE2	38:LO:174:LYS:HD2	2.44	0.53
1:C1:628:C:H2'	1:C1:629:U:C6	2.44	0.53
1:C1:1516:A:H2'	1:C1:1517:A:C8	2.43	0.53
1:C1:2091:U:H2'	1:C1:2092:G:H8	1.74	0.53
4:CB:70:LYS:HG3	11:CI:294:GLU:OE2	2.08	0.53
6:CD:343:LEU:HD13	6:CD:363:SER:HB3	1.90	0.53
21:CS:425:THR:HG22	21:CS:427:ALA:H	1.74	0.53
30:LC:336:PHE:HA	30:LC:341:LEU:HD23	1.91	0.53
42:LS:141:LYS:HA	42:LS:144:VAL:HG22	1.91	0.53
1:C1:861:G:OP1	1:C1:862:C:N4	2.39	0.52
5:CC:408:MET:O	5:CC:412:LEU:HB2	2.09	0.52
5:CC:416:VAL:HG21	15:CM:20:LYS:HE3	1.91	0.52
6:CD:197:ASP:O	6:CD:199:THR:HG23	2.10	0.52
9:CG:56:ALA:HB2	18:CP:434:ILE:HD13	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CS:681:TYR:CD2	55:Li:65:ARG:HB2	2.40	0.52
15:LF:95:ILE:HD11	15:LF:234:LEU:HD23	1.90	0.52
41:LR:44:LEU:HD22	41:LR:49:LEU:HD22	1.91	0.52
59:Lq:89:ASP:O	59:Lq:92:LYS:HG3	2.09	0.52
1:C1:507:G:OP1	15:LF:73:ARG:NH2	2.42	0.52
1:C1:2817:U:H4'	1:C1:2818:U:O5'	2.09	0.52
1:C1:3115:C:H2'	1:C1:3116:G:C8	2.38	0.52
1:C1:3172:U:H2'	1:C1:3173:C:C6	2.44	0.52
2:C2:192:C:H2'	2:C2:193:G:H8	1.74	0.52
6:CD:230:TRP:HB3	6:CD:243:ALA:HB3	1.92	0.52
12:CJ:376:ARG:HA	12:CJ:401:LEU:HD21	1.90	0.52
14:CL:70:GLU:O	14:CL:74:ILE:HD12	2.08	0.52
18:CP:354:THR:HG22	18:CP:356:GLU:H	1.74	0.52
19:CQ:66:ASP:OD1	19:CQ:66:ASP:N	2.42	0.52
27:Cb:15:VAL:HG13	27:Cb:448:LYS:HE3	1.89	0.52
34:LK:124:ASP:OD1	34:LK:125:LEU:N	2.42	0.52
1:C1:1158:C:H4'	38:LO:91:PRO:HD3	1.90	0.52
1:C1:1696:C:H2'	1:C1:1697:A:C8	2.44	0.52
1:C1:2778:A:H2'	1:C1:2779:C:O4'	2.09	0.52
21:CS:725:LEU:HD23	22:CT:401:LEU:HB3	1.91	0.52
40:LQ:120:LEU:O	40:LQ:140:ARG:NH2	2.39	0.52
51:Le:97:ILE:HG21	51:Le:106:ARG:HG2	1.91	0.52
1:C1:403:U:H2'	1:C1:404:G:C8	2.44	0.52
1:C1:764:A:H5''	1:C1:765:G:H5'	1.91	0.52
3:CA:253:PRO:HG2	5:CC:142:ASP:HB3	1.91	0.52
12:CJ:99:ASP:OD2	12:CJ:102:ASN:ND2	2.42	0.52
26:CY:679:LYS:HG3	26:CY:721:TYR:CD1	2.44	0.52
30:LC:151:LEU:HD12	30:LC:256:VAL:HG12	1.91	0.52
1:C1:433:U:H2'	1:C1:434:G:H8	1.75	0.52
5:CC:363:THR:HG23	5:CC:366:GLU:H	1.74	0.52
10:CH:360:ARG:NE	27:Cb:520:TRP:HE1	2.07	0.52
10:CH:452:PRO:HD3	19:CQ:79:VAL:HG21	1.89	0.52
12:CJ:412:ASP:OD1	12:CJ:414:ARG:HG2	2.10	0.52
18:CP:488:LYS:O	18:CP:492:LEU:HD23	2.10	0.52
18:CP:530:ARG:HH21	59:Lq:44:GLN:HG2	1.75	0.52
19:CQ:23:ARG:NE	19:CQ:25:ASP:OD1	2.40	0.52
22:CT:443:LEU:HD11	22:CT:493:LEU:HD21	1.91	0.52
40:LQ:82:MET:O	40:LQ:87:ARG:NH1	2.43	0.52
42:LS:80:ARG:HG2	42:LS:124:LEU:HD11	1.90	0.52
59:Lq:31:THR:O	59:Lq:209:THR:OG1	2.22	0.52
1:C1:409:A:H2'	1:C1:410:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2293:C:H3'	1:C1:2294:A:H5'	1.92	0.52
1:C1:2341:U:C2'	1:C1:2342:U:H5'	2.40	0.52
4:CB:68:THR:HG21	4:CB:72:ILE:CD1	2.37	0.52
17:CO:40:ILE:HD12	29:LB:208:THR:HG21	1.92	0.52
27:Cb:324:ILE:HD12	27:Cb:328:ILE:HD13	1.92	0.52
27:Cb:491:LEU:HB3	27:Cb:568:GLY:HA3	1.91	0.52
43:LT:100:ARG:HB2	43:LT:103:GLU:HB3	1.91	0.52
1:C1:1576:C:H2'	1:C1:1577:G:C8	2.45	0.52
2:C2:298:G:H2'	11:CI:291:ARG:NH2	2.25	0.52
6:CD:85:LEU:HD23	6:CD:89:THR:HB	1.90	0.52
10:CH:242:LEU:HB3	10:CH:277:PHE:HE1	1.73	0.52
14:CL:277:PRO:O	14:CL:279:ALA:N	2.42	0.52
22:CT:318:ASP:O	22:CT:319:GLU:HG3	2.09	0.52
29:LB:56:ILE:HG21	29:LB:324:MET:CE	2.40	0.52
30:LC:158:VAL:HA	30:LC:163:VAL:HG21	1.92	0.52
53:Lg:10:ARG:HH21	53:Lg:35:HIS:HB2	1.74	0.52
1:C1:874:C:N4	1:C1:875:A:H62	2.07	0.52
1:C1:1072:G:H2'	1:C1:1073:G:C8	2.45	0.52
1:C1:2737:A:H2'	1:C1:2738:A:O4'	2.10	0.52
1:C1:3297:U:O2'	1:C1:3298:U:OP1	2.24	0.52
2:C2:203:G:H5'	11:CI:223:LYS:HZ2	1.75	0.52
6:CD:468:TRP:HA	6:CD:472:GLY:O	2.10	0.52
21:CS:439:LEU:HD13	53:Lg:100:LYS:HB3	1.91	0.52
26:CY:539:MET:HB3	26:CY:554:LEU:HD11	1.92	0.52
40:LQ:150:THR:OG1	40:LQ:153:GLN:NE2	2.28	0.52
43:LT:82:HIS:O	43:LT:83:ARG:NE	2.41	0.52
49:Lc:42:ALA:HA	49:Lc:96:LEU:HD13	1.92	0.52
58:Ll:9:ILE:O	58:Ll:13:LEU:HG	2.09	0.52
1:C1:377:A:H2'	1:C1:378:A:C8	2.45	0.52
1:C1:433:U:H2'	1:C1:434:G:C8	2.45	0.52
1:C1:574:G:H2'	1:C1:575:A:H8	1.74	0.52
1:C1:1778:A:H2'	1:C1:1779:A:H8	1.73	0.52
1:C1:2832:G:OP2	10:CH:116:LYS:NZ	2.42	0.52
2:C2:286:C:H2'	2:C2:287:G:C8	2.45	0.52
8:CF:73:MET:HE3	8:CF:102:LEU:HG	1.91	0.52
10:CH:186:VAL:HG23	10:CH:187:THR:HG23	1.90	0.52
12:CJ:411:SER:HA	12:CJ:450:TYR:CE2	2.44	0.52
18:CP:254:GLU:HG3	18:CP:255:GLU:H	1.74	0.52
22:CT:480:ARG:HG3	22:CT:563:THR:HG22	1.92	0.52
22:CT:519:SER:O	22:CT:523:LEU:HG	2.09	0.52
22:CT:632:THR:HG21	26:CY:695:ASP:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LF:99:ASN:OD1	15:LF:100:LYS:NZ	2.40	0.52
3:CA:130:GLY:CA	3:CA:234:ILE:HG22	2.39	0.52
5:CC:235:GLU:O	5:CC:239:ILE:HG12	2.10	0.52
5:CC:352:LEU:HB3	12:CJ:191:SER:HB2	1.92	0.52
10:CH:145:PRO:HG3	27:Cb:624:PHE:CZ	2.44	0.52
10:CH:263:LEU:O	10:CH:267:ILE:HD12	2.10	0.52
12:CJ:467:ASP:OD2	12:CJ:471:LYS:NZ	2.30	0.52
18:CP:467:LYS:NZ	18:CP:574:ASP:OD2	2.42	0.52
31:LE:194:LYS:HD2	31:LE:197:LEU:HD12	1.92	0.52
1:C1:643:A:H2'	1:C1:644:A:C8	2.45	0.51
1:C1:651:A:H2'	1:C1:652:A:H8	1.73	0.51
5:CC:282:ILE:HD12	20:CR:218:TYR:HD1	1.75	0.51
8:CF:58:HIS:O	8:CF:61:ASN:ND2	2.43	0.51
10:CH:357:ILE:HG23	10:CH:361:LEU:HD22	1.92	0.51
11:CI:287:LYS:HE3	11:CI:291:ARG:NH2	2.25	0.51
12:CJ:88:GLU:OE2	12:CJ:120:ARG:NH2	2.41	0.51
20:CR:136:GLN:O	35:LL:117:LYS:NZ	2.43	0.51
34:LK:109:ILE:HG21	34:LK:133:LEU:HD22	1.93	0.51
47:LY:44:VAL:HG13	47:LY:121:ILE:HG21	1.92	0.51
54:Lh:37:GLN:O	54:Lh:45:LYS:NZ	2.33	0.51
58:Ll:18:LYS:O	58:Ll:21:ARG:HG2	2.10	0.51
59:Lq:38:LEU:HD23	59:Lq:39:LYS:N	2.25	0.51
1:C1:461:A:H2'	1:C1:462:C:C6	2.45	0.51
1:C1:603:G:H2'	1:C1:604:G:H8	1.75	0.51
1:C1:926:C:H2'	1:C1:927:C:C6	2.45	0.51
1:C1:1438:A:P	50:Ld:34:LYS:HD3	2.50	0.51
1:C1:1545:G:H2'	1:C1:1546:C:H6	1.75	0.51
4:CB:251:GLU:HB3	4:CB:254:LYS:HG2	1.93	0.51
10:CH:273:ILE:O	10:CH:276:LEU:HB2	2.11	0.51
14:CL:31:LYS:NZ	14:CL:35:GLU:OE2	2.31	0.51
21:CS:422:ILE:O	21:CS:428:LEU:HB2	2.10	0.51
25:CX:103:THR:HG21	25:CX:136:GLU:OE1	2.09	0.51
27:Cb:190:LYS:HB2	27:Cb:211:PRO:HA	1.92	0.51
1:C1:1046:A:C6	1:C1:1074:C:N3	2.78	0.51
2:C2:128:U:OP1	2:C2:129:C:N4	2.36	0.51
5:CC:177:LEU:HD21	5:CC:223:PRO:HA	1.92	0.51
6:CD:189:ASP:HB2	6:CD:204:LYS:NZ	2.26	0.51
8:CF:22:ALA:HA	8:CF:25:ARG:NH1	2.26	0.51
16:CN:66:ASN:HB2	16:CN:112:ASP:OD1	2.10	0.51
27:Cb:178:LYS:HA	27:Cb:181:LYS:HG2	1.91	0.51
15:LF:90:VAL:HG23	15:LF:125:VAL:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LH:53:LEU:HD21	33:LH:120:THR:HG22	1.92	0.51
33:LH:168:ALA:O	33:LH:171:VAL:HG12	2.10	0.51
35:LL:61:PRO:HD3	35:LL:70:ARG:HH12	1.75	0.51
48:LZ:40:ALA:HB2	48:LZ:76:TYR:HE1	1.75	0.51
50:Ld:89:ASP:OD1	50:Ld:90:GLU:N	2.39	0.51
59:Lq:85:MET:HG3	59:Lq:89:ASP:OD2	2.11	0.51
1:C1:919:C:H4'	21:CS:829:LEU:HD11	1.92	0.51
1:C1:1191:G:H5'	8:CF:4:SER:HB2	1.92	0.51
1:C1:2329:A:H2'	1:C1:2330:A:H8	1.75	0.51
1:C1:2361:A:N6	1:C1:2900:C:C5	2.79	0.51
1:C1:3203:C:H2'	1:C1:3204:G:H8	1.75	0.51
5:CC:654:ARG:HE	5:CC:675:LYS:HA	1.76	0.51
7:CE:137:ILE:HD13	7:CE:161:LYS:HB3	1.92	0.51
7:CE:354:LYS:NZ	7:CE:355:MET:HE3	2.25	0.51
10:CH:525:LYS:HZ3	44:LU:98:ASP:HB3	1.74	0.51
16:CN:118:HIS:CD2	16:CN:146:VAL:HG22	2.46	0.51
17:CO:37:LEU:HD22	29:LB:208:THR:HG22	1.91	0.51
29:LB:50:LYS:HB2	29:LB:337:MET:SD	2.51	0.51
54:Lh:43:GLY:O	54:Lh:46:LEU:N	2.44	0.51
57:Lk:8:ILE:HG23	57:Lk:58:LEU:HD12	1.91	0.51
59:Lq:75:ASP:OD1	59:Lq:76:ARG:N	2.43	0.51
1:C1:1094:A:H2'	1:C1:1095:G:C8	2.45	0.51
1:C1:2407:A:H2'	1:C1:2408:U:H6	1.76	0.51
1:C1:2569:U:H2'	1:C1:2570:U:C6	2.46	0.51
1:C1:3190:G:H2'	1:C1:3191:C:C6	2.45	0.51
2:C2:52:A:O5'	58:Ll:21:ARG:HD3	2.11	0.51
8:CF:57:ARG:HG2	8:CF:65:ILE:HG21	1.92	0.51
12:CJ:398:ASP:HB2	12:CJ:401:LEU:HD23	1.92	0.51
18:CP:270:ILE:HG13	18:CP:274:TYR:HD1	1.76	0.51
19:CQ:155:ASP:O	19:CQ:158:GLU:HG3	2.11	0.51
26:CY:684:ALA:O	26:CY:688:GLU:HG2	2.10	0.51
34:LK:16:ARG:HB3	34:LK:57:ARG:HD2	1.93	0.51
35:LL:60:CYS:HA	35:LL:70:ARG:NH1	2.25	0.51
41:LR:102:LEU:HD22	41:LR:138:LEU:HD22	1.93	0.51
43:LT:71:ALA:HA	43:LT:92:ARG:HA	1.91	0.51
59:Lq:113:SER:HA	59:Lq:138:VAL:HG22	1.92	0.51
1:C1:983:A:N1	1:C1:1032:U:O2'	2.43	0.51
1:C1:1263:U:H2'	1:C1:1264:G:C8	2.44	0.51
1:C1:1700:U:OP2	41:LR:124:TYR:OH	2.25	0.51
1:C1:1870:A:H2'	1:C1:1871:G:H8	1.76	0.51
1:C1:2882:U:H2'	1:C1:2883:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CM:160:GLY:N	15:CM:167:ILE:O	2.39	0.51
26:CY:69:LYS:HG3	26:CY:73:MET:CE	2.38	0.51
27:Cb:493:ARG:NE	27:Cb:574:ALA:HA	2.26	0.51
30:LC:296:ILE:O	30:LC:300:LEU:HB2	2.10	0.51
40:LQ:49:SER:OG	40:LQ:54:LEU:HD23	2.11	0.51
51:Le:64:THR:O	51:Le:67:MET:HG2	2.10	0.51
1:C1:1575:C:H2'	1:C1:1576:C:H6	1.75	0.51
1:C1:1885:G:H2'	1:C1:1886:C:C5	2.46	0.51
1:C1:2078:G:H2'	1:C1:2079:A:C8	2.45	0.51
1:C1:2445:G:N1	1:C1:2448:A:OP2	2.44	0.51
1:C1:2999:U:H5''	45:LV:47:ARG:HD2	1.92	0.51
2:C2:26:U:H2'	2:C2:27:U:C6	2.46	0.51
6:CD:29:PRO:HG2	6:CD:32:LYS:HG2	1.92	0.51
7:CE:137:ILE:HB	7:CE:320:VAL:HG21	1.93	0.51
10:CH:203:LEU:HD23	10:CH:220:THR:HA	1.93	0.51
10:CH:228:LEU:HD21	27:Cb:594:ILE:HD13	1.92	0.51
11:CI:315:ALA:O	11:CI:318:GLU:HG3	2.10	0.51
15:CM:182:TYR:HB3	15:CM:200:ASN:ND2	2.24	0.51
21:CS:732:LYS:HA	21:CS:735:GLU:HG2	1.93	0.51
26:CY:502:TRP:HE3	26:CY:505:VAL:HG21	1.75	0.51
40:LQ:99:LEU:HD11	40:LQ:108:VAL:CG2	2.41	0.51
41:LR:38:ARG:O	41:LR:42:ARG:HG3	2.10	0.51
1:C1:508:G:H3'	1:C1:509:A:H3'	1.92	0.51
1:C1:1900:A:H2'	1:C1:1901:A:C8	2.45	0.51
2:C2:119:C:OP1	12:CJ:70:GLN:NE2	2.41	0.51
2:C2:219:A:OP1	11:CI:222:LYS:NZ	2.39	0.51
3:CA:161:HIS:CE1	23:CU:205:LEU:HD22	2.46	0.51
6:CD:125:PRO:HD3	6:CD:128:ARG:NH2	2.25	0.51
10:CH:299:PRO:HA	10:CH:302:GLN:HB2	1.93	0.51
31:LE:195:PRO:HA	31:LE:198:MET:HG2	1.93	0.51
15:LF:114:LEU:HD21	15:LF:121:VAL:HG22	1.92	0.51
33:LH:13:PRO:HD2	33:LH:53:LEU:HD12	1.93	0.51
35:LL:86:PRO:HG2	35:LL:89:LEU:HB3	1.93	0.51
37:LN:124:ASP:OD1	37:LN:125:SER:N	2.41	0.51
53:Lg:86:VAL:O	53:Lg:90:ILE:HG13	2.11	0.51
1:C1:745:U:N3	1:C1:749:C:N4	2.59	0.51
1:C1:917:A:O2'	1:C1:918:G:H2'	2.10	0.51
1:C1:1066:A:H2'	1:C1:1067:A:C8	2.46	0.51
1:C1:1575:C:H2'	1:C1:1576:C:C6	2.46	0.51
1:C1:1795:A:H2'	1:C1:1796:A:C8	2.45	0.51
6:CD:358:LEU:HD13	6:CD:372:PRO:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CF:77:LEU:HB3	8:CF:89:LEU:HG	1.92	0.51
10:CH:360:ARG:NH2	16:CN:246:TYR:O	2.44	0.51
19:CQ:179:GLU:OE1	50:Ld:86:ARG:NH1	2.44	0.51
24:CV:92:LYS:HE3	15:LF:11:ASP:OD2	2.11	0.51
26:CY:377:LYS:C	26:CY:381:LYS:HZ2	2.18	0.51
29:LB:90:VAL:HG11	29:LB:181:GLU:OE2	2.11	0.51
30:LC:341:LEU:HD12	15:LF:62:ARG:NH2	2.25	0.51
32:LG:190:GLY:HA2	32:LG:193:VAL:HG22	1.92	0.51
54:Lh:34:LEU:O	54:Lh:38:LYS:HB2	2.10	0.51
56:Lj:54:LYS:O	56:Lj:58:VAL:HB	2.11	0.51
1:C1:976:U:O2	1:C1:1036:A:N7	2.44	0.51
1:C1:1233:A:H2'	1:C1:1234:A:C8	2.46	0.51
6:CD:28:LEU:HD11	6:CD:55:MET:HE3	1.92	0.51
9:CG:122:TRP:CH2	9:CG:163:VAL:HG11	2.45	0.51
21:CS:436:MET:HA	48:LZ:84:TYR:CE1	2.46	0.51
22:CT:232:ASP:HB3	22:CT:234:LYS:NZ	2.26	0.51
22:CT:437:ASP:HB3	25:CX:117:GLU:HG2	1.92	0.51
23:CU:356:ASP:HB2	23:CU:357:PRO:HD2	1.93	0.51
27:Cb:9:ALA:HB3	27:Cb:10:PRO:HD3	1.92	0.51
43:LT:102:ARG:O	43:LT:106:LEU:HG	2.11	0.51
1:C1:38:U:H2'	1:C1:39:A:C8	2.46	0.50
1:C1:2078:G:H2'	1:C1:2079:A:H8	1.76	0.50
12:CJ:372:PHE:CE1	12:CJ:417:HIS:HB2	2.46	0.50
12:CJ:373:PHE:HB3	12:CJ:418:GLN:HG2	1.93	0.50
16:CN:81:LEU:HG	19:CQ:78:PRO:HB3	1.92	0.50
22:CT:161:LEU:O	22:CT:165:LYS:HG3	2.11	0.50
22:CT:448:ASP:OD1	25:CX:124:ARG:NH1	2.34	0.50
39:LP:60:MET:HE3	39:LP:82:ARG:HD2	1.92	0.50
46:LX:120:THR:HA	46:LX:139:LEU:HA	1.93	0.50
59:Lq:39:LYS:HD2	59:Lq:40:ASN:N	2.26	0.50
1:C1:631:G:H5'	1:C1:1099:G:H1'	1.93	0.50
1:C1:631:G:H5''	1:C1:1098:G:C8	2.46	0.50
5:CC:445:GLN:HG3	6:CD:457:ALA:HB2	1.93	0.50
8:CF:41:PHE:CD2	8:CF:226:TYR:HB3	2.46	0.50
10:CH:167:ARG:HB3	10:CH:215:TYR:CE1	2.46	0.50
10:CH:171:VAL:HG23	10:CH:219:ASP:HA	1.92	0.50
15:CM:48:GLN:HG2	15:CM:49:VAL:H	1.77	0.50
16:CN:71:LEU:HD23	16:CN:97:ILE:HG21	1.91	0.50
30:LC:361:LEU:HD11	43:LT:148:PRO:HG2	1.93	0.50
34:LK:46:ILE:HD11	34:LK:62:LEU:HD21	1.93	0.50
35:LL:17:HIS:HB3	35:LL:20:ARG:HG2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:LP:17:ALA:HB3	39:LP:148:LEU:HD21	1.93	0.50
44:LU:84:LYS:HE3	44:LU:102:VAL:HG13	1.93	0.50
50:Ld:22:ILE:HB	50:Ld:79:ILE:HG22	1.93	0.50
1:C1:1171:C:C4	1:C1:1297:U:O2	2.64	0.50
1:C1:2433:U:H5	59:Lq:26:ARG:HH12	1.59	0.50
2:C2:83:C:N3	47:LY:50:ARG:NH2	2.59	0.50
11:CI:207:PHE:HB3	11:CI:235:PHE:CZ	2.42	0.50
27:Cb:435:LEU:O	27:Cb:457:THR:OG1	2.29	0.50
34:LK:62:LEU:HG	34:LK:71:VAL:HG22	1.93	0.50
36:LM:72:LEU:HD23	36:LM:72:LEU:H	1.75	0.50
1:C1:307:C:OP1	35:LL:102:LYS:NZ	2.40	0.50
1:C1:790:G:H2'	1:C1:791:A:H8	1.77	0.50
1:C1:1674:U:O2'	1:C1:1728:A:N1	2.38	0.50
6:CD:468:TRP:HB2	6:CD:473:ILE:HD13	1.93	0.50
9:CG:162:ILE:HG13	13:CK:141:LYS:HD3	1.94	0.50
19:CQ:45:ASN:ND2	27:Cb:864:ASP:OD1	2.42	0.50
29:LB:76:VAL:HG21	29:LB:324:MET:HE3	1.94	0.50
29:LB:164:HIS:HB3	29:LB:179:LEU:HD23	1.94	0.50
30:LC:299:VAL:HG21	40:LQ:159:PRO:HG2	1.93	0.50
37:LN:115:VAL:O	37:LN:159:ARG:NH1	2.45	0.50
48:LZ:5:LYS:HE2	48:LZ:8:ARG:HH21	1.77	0.50
1:C1:729:U:H2'	1:C1:730:C:C6	2.47	0.50
1:C1:1157:C:N3	38:LO:22:SER:HA	2.27	0.50
1:C1:1595:U:H2'	1:C1:1596:G:C8	2.47	0.50
1:C1:2779:C:H2'	1:C1:2780:U:C6	2.46	0.50
1:C1:2907:U:H2'	1:C1:2908:G:H8	1.76	0.50
5:CC:478:ARG:HD3	5:CC:487:GLN:HE22	1.76	0.50
6:CD:367:ILE:HD12	6:CD:394:LEU:HD21	1.92	0.50
10:CH:104:ILE:HG13	10:CH:138:LEU:HD22	1.94	0.50
21:CS:666:LEU:HD13	21:CS:676:LEU:HD11	1.93	0.50
26:CY:575:LEU:O	26:CY:578:VAL:HG22	2.11	0.50
36:LM:22:LEU:O	36:LM:25:GLY:N	2.42	0.50
45:LV:25:MET:HE3	45:LV:36:LEU:HD13	1.91	0.50
56:Lj:76:ASN:HB3	56:Lj:79:ARG:NE	2.27	0.50
1:C1:333:G:C6	30:LC:198:MET:HE2	2.47	0.50
1:C1:650:C:H2'	1:C1:651:A:C8	2.47	0.50
1:C1:1600:G:H2'	1:C1:1601:U:C6	2.46	0.50
1:C1:1899:U:H2'	1:C1:1900:A:C8	2.47	0.50
2:C2:47:C:O2'	2:C2:62:A:OP2	2.25	0.50
7:CE:347:LEU:HD21	7:CE:485:PHE:CD1	2.46	0.50
13:CK:19:ASP:OD2	33:LH:201:GLN:NE2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CK:68:HIS:HA	13:CK:71:ARG:HG2	1.92	0.50
17:CO:92:GLY:H	29:LB:147:ARG:HD2	1.77	0.50
18:CP:383:ARG:HH21	18:CP:449:GLY:C	2.19	0.50
18:CP:524:VAL:HG13	18:CP:581:PHE:HZ	1.76	0.50
26:CY:543:PRO:HB3	26:CY:551:ARG:HH22	1.77	0.50
27:Cb:372:PHE:CG	27:Cb:453:ARG:HD2	2.46	0.50
38:LO:15:HIS:CE1	38:LO:121:VAL:HG23	2.47	0.50
41:LR:105:LEU:HD23	41:LR:138:LEU:HD23	1.93	0.50
1:C1:404:G:H2'	1:C1:405:U:C6	2.47	0.50
1:C1:909:C:H2'	1:C1:910:A:H8	1.75	0.50
1:C1:2451:C:N4	1:C1:2452:C:N4	2.59	0.50
1:C1:2841:U:H2'	1:C1:2842:C:H6	1.77	0.50
5:CC:474:ASP:O	5:CC:492:LYS:NZ	2.45	0.50
6:CD:356:PRO:HG2	6:CD:372:PRO:HG2	1.94	0.50
10:CH:363:GLU:O	10:CH:367:ARG:HG3	2.12	0.50
15:LF:13:LEU:HD12	15:LF:13:LEU:O	2.12	0.50
1:C1:1291:U:OP2	14:CL:14:LYS:N	2.39	0.50
1:C1:3203:C:H2'	1:C1:3204:G:C8	2.47	0.50
2:C2:142:C:H2'	2:C2:143:U:C6	2.47	0.50
6:CD:415:VAL:CG2	6:CD:439:TYR:HB3	2.42	0.50
8:CF:162:GLU:HB3	8:CF:163:PRO:HD3	1.93	0.50
9:CG:24:LYS:O	9:CG:28:ALA:HB2	2.12	0.50
11:CI:249:ASP:HA	11:CI:260:CYS:HB2	1.94	0.50
12:CJ:267:GLU:HB2	12:CJ:380:ARG:HH12	1.76	0.50
16:CN:180:PRO:HG2	16:CN:230:PRO:HG2	1.93	0.50
22:CT:412:LEU:HG	22:CT:423:VAL:HG11	1.94	0.50
28:Cz:48:TRP:O	28:Cz:52:VAL:HG23	2.10	0.50
36:LM:44:PRO:HD2	36:LM:85:TRP:CE3	2.47	0.50
55:Li:63:GLU:O	55:Li:67:ILE:HG12	2.11	0.50
59:Lq:180:VAL:HA	59:Lq:183:ILE:HG12	1.94	0.50
1:C1:734:C:H2'	1:C1:735:G:H8	1.77	0.50
11:CI:190:TYR:CZ	11:CI:192:ALA:HB2	2.47	0.50
15:CM:169:LEU:HD22	15:CM:175:ILE:HD11	1.94	0.50
22:CT:172:MET:SD	22:CT:245:CYS:HA	2.51	0.50
22:CT:663:LEU:HD12	26:CY:636:ASN:HD22	1.75	0.50
26:CY:377:LYS:HA	26:CY:380:ILE:HG12	1.94	0.50
1:C1:947:U:C2	1:C1:948:A:C8	2.99	0.49
1:C1:1545:G:H2'	1:C1:1546:C:C6	2.47	0.49
1:C1:2472:U:H2'	1:C1:2473:A:H8	1.77	0.49
6:CD:296:HIS:ND1	6:CD:319:ASP:OD1	2.45	0.49
14:CL:262:ARG:HA	14:CL:265:PHE:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CM:182:TYR:CE2	15:CM:203:GLN:HG2	2.43	0.49
26:CY:728:LEU:HD23	26:CY:732:ARG:HE	1.77	0.49
49:Lc:25:LYS:H	49:Lc:97:ASP:HB3	1.75	0.49
1:C1:1448:G:N2	1:C1:1492:G:H5'	2.26	0.49
4:CB:116:PHE:CZ	4:CB:120:LEU:HD22	2.47	0.49
10:CH:79:ASP:OD1	10:CH:244:HIS:NE2	2.45	0.49
10:CH:253:MET:HE2	10:CH:284:ILE:HG21	1.94	0.49
26:CY:722:VAL:O	26:CY:726:ARG:HG3	2.11	0.49
27:Cb:475:LEU:HD21	27:Cb:563:VAL:HG23	1.93	0.49
33:LH:154:ARG:HG2	33:LH:162:VAL:HG22	1.92	0.49
39:LP:29:THR:HG22	39:LP:119:VAL:HG21	1.94	0.49
1:C1:72:C:H1'	35:LL:61:PRO:O	2.11	0.49
1:C1:404:G:OP1	39:LP:62:ARG:NH1	2.45	0.49
1:C1:422:G:H2'	1:C1:423:U:C6	2.47	0.49
1:C1:2431:G:N2	1:C1:2439:G:H1'	2.27	0.49
1:C1:3273:G:N2	1:C1:3309:G:O2'	2.45	0.49
5:CC:231:LEU:HD11	21:CS:663:ALA:HB1	1.93	0.49
5:CC:269:MET:HE1	7:CE:553:VAL:HG12	1.94	0.49
7:CE:136:GLU:OE2	7:CE:140:ARG:NE	2.33	0.49
10:CH:283:PHE:CZ	10:CH:337:ARG:HD3	2.42	0.49
10:CH:404:ALA:HA	10:CH:407:ILE:HD12	1.94	0.49
19:CQ:11:ARG:HA	29:LB:380:PHE:CZ	2.47	0.49
23:CU:281:THR:O	23:CU:285:VAL:HG23	2.12	0.49
27:Cb:380:GLU:HG2	45:LV:73:LYS:HD3	1.94	0.49
48:LZ:120:ARG:NH2	48:LZ:126:ASN:OD1	2.44	0.49
52:Lf:32:ILE:HD12	52:Lf:100:VAL:HG21	1.93	0.49
57:Lk:42:ARG:NH1	57:Lk:43:PHE:HE1	2.06	0.49
1:C1:881:G:H1'	1:C1:1568:A:N6	2.27	0.49
1:C1:895:A:HO2'	1:C1:896:A:H8	1.61	0.49
1:C1:1576:C:H5'	1:C1:1675:A:H1'	1.94	0.49
1:C1:1768:G:H2'	1:C1:1769:U:C6	2.48	0.49
1:C1:2302:U:C2	1:C1:2303:A:C8	3.01	0.49
1:C1:2425:G:N2	59:Lq:164:CYS:SG	2.85	0.49
5:CC:269:MET:HB3	7:CE:552:ARG:HD2	1.94	0.49
5:CC:529:PRO:HA	6:CD:198:ARG:HH21	1.77	0.49
5:CC:587:VAL:HG22	5:CC:591:ILE:HD11	1.94	0.49
11:CI:207:PHE:HB2	11:CI:213:ILE:HD11	1.93	0.49
12:CJ:134:PHE:HZ	12:CJ:245:LEU:HD12	1.78	0.49
13:CK:25:ARG:HD2	28:Cz:27:LYS:HE2	1.94	0.49
22:CT:631:ASN:ND2	22:CT:634:GLU:HG3	2.28	0.49
26:CY:394:ASP:O	26:CY:398:ILE:HD12	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:CY:502:TRP:HA	26:CY:505:VAL:HG22	1.94	0.49
34:LK:77:ALA:O	34:LK:81:ILE:HG12	2.12	0.49
50:Ld:20:TYR:HD2	50:Ld:83:ILE:HD12	1.77	0.49
54:Lh:31:LEU:HD11	54:Lh:49:ILE:HG23	1.94	0.49
1:C1:2385:U:H2'	1:C1:2386:A:H8	1.76	0.49
4:CB:139:ALA:HB1	4:CB:141:GLU:HG3	1.93	0.49
7:CE:467:LEU:HD13	7:CE:470:LEU:HD12	1.95	0.49
10:CH:299:PRO:HD2	10:CH:300:GLU:N	2.26	0.49
18:CP:259:ARG:O	18:CP:263:THR:HG23	2.11	0.49
19:CQ:21:PHE:HB3	19:CQ:29:PHE:HB2	1.93	0.49
22:CT:124:ILE:O	22:CT:128:GLN:HG3	2.13	0.49
47:LY:73:TYR:CE2	47:LY:76:LYS:HG2	2.48	0.49
1:C1:29:C:H4'	1:C1:62:A:H4'	1.95	0.49
1:C1:1205:A:N6	1:C1:1267:G:H21	2.10	0.49
1:C1:1636:C:HO2'	1:C1:1775:G:HO2'	1.57	0.49
1:C1:2414:G:N1	1:C1:2456:A:C2	2.70	0.49
2:C2:71:A:N6	2:C2:85:G:C2	2.81	0.49
5:CC:780:ASP:OD1	5:CC:781:TRP:N	2.46	0.49
6:CD:184:LYS:HD2	6:CD:232:ASP:HA	1.94	0.49
22:CT:246:ALA:O	22:CT:250:VAL:HG23	2.12	0.49
26:CY:453:TRP:HA	26:CY:456:ASP:OD2	2.12	0.49
42:LS:152:LEU:HD13	42:LS:155:ARG:NH1	2.27	0.49
59:Lq:38:LEU:HD22	59:Lq:41:TYR:HB3	1.93	0.49
1:C1:40:A:O2'	1:C1:92:G:N2	2.46	0.49
1:C1:115:A:N6	1:C1:149:U:N3	2.61	0.49
1:C1:2083:G:C4	27:Cb:848:PHE:HD1	2.30	0.49
1:C1:2898:A:O2'	1:C1:2899:A:OP2	2.24	0.49
1:C1:3265:A:H2'	1:C1:3266:G:H8	1.77	0.49
4:CB:156:ASP:O	4:CB:160:ILE:HG12	2.12	0.49
12:CJ:582:GLU:O	12:CJ:585:LEU:HB3	2.13	0.49
23:CU:230:ILE:HD13	23:CU:239:ARG:HG3	1.95	0.49
27:Cb:624:PHE:CE2	27:Cb:628:ILE:HD11	2.48	0.49
31:LE:98:ASN:HB3	31:LE:101:TYR:HD2	1.77	0.49
36:LM:17:GLY:CA	36:LM:72:LEU:HD21	2.43	0.49
49:Lc:60:GLU:OE2	49:Lc:72:HIS:NE2	2.40	0.49
54:Lh:22:LYS:NZ	54:Lh:26:GLU:OE2	2.41	0.49
55:Li:60:ALA:O	55:Li:64:ARG:HG3	2.13	0.49
59:Lq:76:ARG:NH1	59:Lq:142:ASP:O	2.46	0.49
1:C1:727:C:H2'	1:C1:728:A:C8	2.48	0.49
2:C2:182:G:O3'	4:CB:165:LYS:NZ	2.46	0.49
4:CB:109:LYS:HA	4:CB:112:VAL:HG12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:317:SER:OG	6:CD:318:GLN:N	2.45	0.49
7:CE:528:ARG:O	7:CE:532:ASP:HB3	2.12	0.49
24:CV:88:ARG:HD3	31:LE:24:ALA:HB3	1.95	0.49
25:CX:126:LEU:O	25:CX:130:ARG:HG3	2.13	0.49
26:CY:628:GLU:O	26:CY:632:LEU:HB2	2.13	0.49
27:Cb:443:PHE:CG	27:Cb:444:PRO:HD2	2.48	0.49
28:Cz:32:TRP:CE2	33:LH:190:LEU:HD11	2.47	0.49
29:LB:200:PHE:HB3	29:LB:201:GLU:OE1	2.12	0.49
33:LH:157:ILE:HG22	33:LH:157:ILE:O	2.12	0.49
1:C1:707:A:H5''	1:C1:708:G:H5'	1.95	0.49
1:C1:2336:C:H2'	1:C1:2337:G:C2	2.48	0.49
1:C1:2736:A:H5''	18:CP:526:TYR:CE1	2.46	0.49
1:C1:3159:A:H61	36:LM:122:ARG:HH21	1.60	0.49
5:CC:458:SER:HB2	5:CC:501:THR:HA	1.95	0.49
5:CC:493:LEU:HB3	5:CC:522:PHE:CE2	2.48	0.49
11:CI:194:LEU:HD22	11:CI:198:PHE:HD2	1.78	0.49
18:CP:382:GLU:HG2	18:CP:504:THR:HG21	1.95	0.49
22:CT:160:ILE:HD11	22:CT:163:ILE:HD12	1.94	0.49
23:CU:286:LYS:O	23:CU:290:ILE:HG12	2.13	0.49
29:LB:219:ILE:HB	29:LB:338:THR:HB	1.94	0.49
38:LO:90:ILE:HD11	38:LO:101:LEU:CD2	2.43	0.49
1:C1:105:C:H5'	1:C1:684:G:N2	2.28	0.49
1:C1:424:G:H2'	1:C1:425:A:H8	1.78	0.49
1:C1:713:G:C6	1:C1:723:G:C2	3.01	0.49
1:C1:978:A:H2'	1:C1:979:A:H8	1.77	0.49
1:C1:1344:G:H2'	1:C1:1345:A:C8	2.48	0.49
2:C2:8:C:H2'	2:C2:9:A:H8	1.77	0.49
5:CC:645:ARG:HB3	5:CC:647:LEU:HD13	1.95	0.49
21:CS:789:VAL:HG13	21:CS:811:ARG:HG3	1.93	0.49
26:CY:459:LEU:O	26:CY:463:THR:HG23	2.13	0.49
29:LB:323:VAL:HG12	29:LB:325:ILE:HG23	1.94	0.49
30:LC:296:ILE:HD13	40:LQ:159:PRO:HB3	1.94	0.49
15:LF:179:LEU:HB3	15:LF:184:ILE:HB	1.94	0.49
37:LN:126:THR:HG23	37:LN:127:TYR:CD1	2.48	0.49
51:Le:24:ASP:OD1	51:Le:25:ARG:N	2.46	0.49
1:C1:1272:U:H2'	1:C1:1273:A:H8	1.78	0.48
1:C1:2433:U:C2	1:C1:2436:G:O6	2.65	0.48
1:C1:2453:A:OP1	59:Lq:207:LYS:NZ	2.27	0.48
1:C1:3307:C:OP1	19:CQ:111:ARG:NH1	2.45	0.48
6:CD:159:ASN:HB3	6:CD:165:ILE:HD11	1.95	0.48
7:CE:477:LYS:HD2	7:CE:477:LYS:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CF:148:GLU:HG3	8:CF:214:ILE:HD12	1.94	0.48
9:CG:20:MET:HE1	9:CG:89:ILE:HG22	1.95	0.48
10:CH:210:TYR:HE1	10:CH:332:ASN:HD22	1.60	0.48
10:CH:251:TYR:CE1	10:CH:273:ILE:HD11	2.48	0.48
18:CP:299:ALA:HB1	18:CP:568:PRO:HB2	1.95	0.48
35:LL:60:CYS:HB2	35:LL:65:TYR:O	2.13	0.48
49:Lc:43:LYS:NZ	49:Lc:96:LEU:O	2.27	0.48
51:Le:10:ILE:HG12	51:Le:64:THR:HG23	1.94	0.48
1:C1:490:C:H2'	1:C1:491:A:H8	1.78	0.48
1:C1:2329:A:H2'	1:C1:2330:A:C8	2.48	0.48
10:CH:231:MET:HE2	10:CH:235:GLU:HG3	1.95	0.48
15:CM:104:LYS:HB3	15:CM:105:PRO:HD3	1.95	0.48
19:CQ:15:PRO:HB2	29:LB:359:TRP:HZ2	1.78	0.48
19:CQ:69:LEU:HD21	19:CQ:100:ARG:HE	1.77	0.48
22:CT:250:VAL:HG21	22:CT:266:LEU:HD11	1.94	0.48
27:Cb:210:ASN:O	27:Cb:210:ASN:ND2	2.44	0.48
27:Cb:572:LEU:HD22	27:Cb:584:GLU:HG3	1.95	0.48
43:LT:43:LYS:HB2	43:LT:97:LYS:NZ	2.28	0.48
49:Lc:12:SER:C	49:Lc:16:LYS:HZ2	2.21	0.48
55:Li:83:LYS:HE2	55:Li:89:PHE:CE1	2.48	0.48
59:Lq:32:VAL:HG23	59:Lq:208:ALA:HA	1.95	0.48
1:C1:1576:C:OP1	53:Lg:32:ARG:HD2	2.14	0.48
1:C1:1870:A:H2'	1:C1:1871:G:C8	2.48	0.48
4:CB:116:PHE:HD2	4:CB:121:ARG:HG3	1.78	0.48
6:CD:147:LEU:HD11	6:CD:155:LEU:HD13	1.95	0.48
6:CD:468:TRP:CD1	6:CD:473:ILE:HD13	2.48	0.48
8:CF:168:LEU:HD21	8:CF:207:ARG:HD3	1.95	0.48
10:CH:229:GLU:HB3	27:Cb:593:LYS:NZ	2.28	0.48
18:CP:530:ARG:NH2	59:Lq:44:GLN:HG2	2.28	0.48
26:CY:470:GLN:HE21	26:CY:471:LEU:HD22	1.78	0.48
48:LZ:62:GLU:HG3	48:LZ:66:LYS:HE2	1.95	0.48
1:C1:497:U:H2'	1:C1:498:C:C6	2.48	0.48
1:C1:670:U:H2'	1:C1:671:G:O4'	2.13	0.48
1:C1:1158:C:OP2	1:C1:1159:G:H3'	2.13	0.48
1:C1:1768:G:H2'	1:C1:1769:U:H6	1.76	0.48
6:CD:24:PRO:HA	6:CD:27:GLU:HG2	1.96	0.48
10:CH:467:ARG:O	10:CH:470:LYS:N	2.46	0.48
16:CN:118:HIS:CE1	16:CN:120:ASP:HB2	2.48	0.48
26:CY:615:GLN:NE2	26:CY:664:ASN:HD22	2.11	0.48
26:CY:666:ASN:ND2	26:CY:669:LEU:HD13	2.28	0.48
27:Cb:1:MET:HB2	27:Cb:2:PRO:HD3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:LN:60:VAL:HG22	37:LN:134:LEU:HB2	1.94	0.48
48:LZ:83:ARG:NH2	48:LZ:84:TYR:OH	2.47	0.48
54:Lh:34:LEU:HD22	54:Lh:49:ILE:HG13	1.95	0.48
1:C1:750:G:H2'	1:C1:751:G:C4	2.48	0.48
1:C1:1453:U:H2'	1:C1:1454:G:H8	1.78	0.48
4:CB:22:GLN:HA	4:CB:25:LYS:HG2	1.95	0.48
4:CB:27:CYS:O	4:CB:31:LEU:HD23	2.14	0.48
8:CF:157:VAL:HG22	8:CF:158:SER:H	1.78	0.48
13:CK:2:PRO:HB2	13:CK:6:TYR:CD1	2.48	0.48
17:CO:91:ILE:HA	29:LB:147:ARG:HG3	1.95	0.48
20:CR:205:ASP:O	20:CR:209:MET:HG3	2.14	0.48
27:Cb:233:SER:HA	27:Cb:263:PRO:HG3	1.94	0.48
15:LF:171:ASP:HB3	15:LF:174:ILE:HG13	1.94	0.48
32:LG:146:ILE:HG23	32:LG:178:ILE:HD12	1.94	0.48
50:Ld:19:GLU:HB3	50:Ld:80:ARG:HH21	1.78	0.48
59:Lq:116:LEU:O	59:Lq:120:ILE:HG23	2.14	0.48
59:Lq:175:THR:HG22	59:Lq:178:GLN:HE22	1.79	0.48
1:C1:115:A:H2'	1:C1:257:A:H2'	1.96	0.48
1:C1:223:U:H2'	1:C1:224:A:C8	2.48	0.48
1:C1:247:A:H2'	1:C1:248:G:C8	2.49	0.48
1:C1:861:G:H1'	1:C1:869:A:N6	2.27	0.48
1:C1:1595:U:H2'	1:C1:1596:G:H8	1.77	0.48
1:C1:1787:G:H1'	1:C1:1788:A:C8	2.49	0.48
1:C1:3134:A:OP2	38:LO:173:LYS:NZ	2.46	0.48
5:CC:473:ASP:C	5:CC:475:GLY:H	2.21	0.48
6:CD:125:PRO:HD3	6:CD:128:ARG:HH22	1.78	0.48
7:CE:399:THR:HA	7:CE:402:GLU:HG2	1.95	0.48
12:CJ:46:GLU:HG3	15:CM:20:LYS:HD2	1.95	0.48
13:CK:193:VAL:HG21	13:CK:228:LEU:HD11	1.96	0.48
22:CT:175:TYR:HA	22:CT:178:VAL:HG22	1.96	0.48
32:LG:139:LEU:HD23	32:LG:200:VAL:HG12	1.95	0.48
36:LM:19:VAL:O	36:LM:65:THR:OG1	2.30	0.48
48:LZ:106:ARG:O	48:LZ:110:LYS:HG3	2.13	0.48
1:C1:421:U:O2'	52:Lf:90:PRO:O	2.29	0.48
1:C1:1537:U:H5	1:C1:1539:A:N7	2.11	0.48
1:C1:2432:C:OP1	59:Lq:26:ARG:NE	2.47	0.48
4:CB:147:PHE:CZ	4:CB:177:LYS:HD3	2.49	0.48
5:CC:489:TRP:HD1	5:CC:490:SER:N	2.11	0.48
5:CC:576:LEU:HB3	5:CC:581:VAL:HB	1.96	0.48
6:CD:342:LEU:HD13	6:CD:362:THR:HG22	1.94	0.48
11:CI:211:GLY:HA3	11:CI:240:VAL:HG11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CM:147:LEU:O	15:CM:151:ARG:HG2	2.13	0.48
15:LF:166:ARG:HG3	15:LF:209:TRP:CD2	2.49	0.48
35:LL:110:ALA:HA	35:LL:113:VAL:HG22	1.96	0.48
1:C1:585:G:H1	1:C1:596:G:H5''	1.79	0.48
1:C1:1810:U:O2'	2:C2:114:G:OP1	2.31	0.48
1:C1:2887:C:O2'	27:Cb:3:LYS:O	2.32	0.48
1:C1:3136:A:H2'	1:C1:3137:A:C8	2.48	0.48
7:CE:344:ARG:NH2	7:CE:433:ASP:OD1	2.47	0.48
10:CH:64:ILE:HD11	10:CH:97:ILE:HB	1.96	0.48
13:CK:221:ILE:HD13	13:CK:245:ILE:HD11	1.96	0.48
26:CY:508:GLU:C	26:CY:509:HIS:HD2	2.21	0.48
27:Cb:144:PHE:C	27:Cb:147:PRO:HD2	2.39	0.48
30:LC:108:ARG:O	30:LC:108:ARG:HG2	2.14	0.48
15:LF:86:GLU:OE2	43:LT:136:ARG:NH1	2.44	0.48
48:LZ:17:TYR:CE1	48:LZ:46:GLU:HG2	2.49	0.48
49:Lc:46:LEU:HD23	49:Lc:71:HIS:HB3	1.96	0.48
51:Le:4:ALA:HB2	51:Le:72:HIS:CE1	2.49	0.48
1:C1:139:C:H2'	1:C1:140:G:O4'	2.14	0.48
1:C1:683:C:H1'	20:CR:64:GLY:N	2.28	0.48
5:CC:647:LEU:HD23	5:CC:658:CYS:SG	2.54	0.48
6:CD:125:PRO:HB3	6:CD:129:TRP:HZ3	1.79	0.48
6:CD:350:ARG:HG2	6:CD:401:GLU:HG3	1.96	0.48
7:CE:165:PHE:HB2	7:CE:262:ILE:HD13	1.96	0.48
12:CJ:263:ASP:HB3	15:CM:146:ASN:HD22	1.78	0.48
17:CO:91:ILE:HD13	29:LB:154:LYS:HD2	1.96	0.48
18:CP:344:VAL:HG11	18:CP:351:LEU:HD11	1.95	0.48
27:Cb:176:THR:O	27:Cb:179:VAL:HG12	2.14	0.48
29:LB:170:THR:HG22	29:LB:172:LEU:HG	1.95	0.48
35:LL:55:ARG:NH1	35:LL:73:ARG:O	2.46	0.48
37:LN:143:ARG:HE	54:Lh:97:LEU:HD23	1.78	0.48
59:Lq:15:GLU:O	59:Lq:19:TYR:HB3	2.14	0.48
1:C1:117:U:O2'	1:C1:119:U:OP2	2.29	0.48
1:C1:2408:U:H2'	1:C1:2409:A:H8	1.79	0.48
1:C1:3235:A:H2'	1:C1:3236:A:C8	2.48	0.48
3:CA:161:HIS:HE1	23:CU:205:LEU:HD22	1.77	0.48
5:CC:787:TRP:CG	5:CC:801:MET:HG2	2.48	0.48
6:CD:146:VAL:HG11	6:CD:474:PHE:CE2	2.49	0.48
6:CD:386:GLY:C	6:CD:414:ARG:HH12	2.22	0.48
6:CD:400:ASN:OD1	6:CD:401:GLU:N	2.47	0.48
14:CL:444:LEU:HA	15:LF:49:VAL:HG11	1.96	0.48
18:CP:357:TYR:HB2	18:CP:362:TYR:CZ	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CU:305:GLN:O	23:CU:309:LYS:HG3	2.14	0.48
27:Cb:379:VAL:HG13	27:Cb:421:VAL:HG13	1.95	0.48
1:C1:8:C:H2'	1:C1:9:U:C6	2.49	0.47
1:C1:468:C:H4'	1:C1:469:A:O5'	2.13	0.47
1:C1:643:A:H2'	1:C1:644:A:H8	1.80	0.47
1:C1:1268:A:OP1	28:Cz:40:ARG:NH2	2.47	0.47
1:C1:2470:U:H2'	1:C1:2471:U:C6	2.49	0.47
1:C1:3130:U:O2'	1:C1:3131:A:OP1	2.29	0.47
10:CH:128:LYS:HZ3	10:CH:132:LEU:HD22	1.79	0.47
19:CQ:33:ARG:HG2	29:LB:368:HIS:HB3	1.96	0.47
19:CQ:82:ASN:O	19:CQ:86:TRP:HE3	1.97	0.47
20:CR:151:LEU:HD22	35:LL:120:LYS:HE3	1.96	0.47
26:CY:378:MET:HA	26:CY:381:LYS:HG2	1.96	0.47
27:Cb:17:ILE:O	27:Cb:20:SER:OG	2.16	0.47
33:LH:131:TYR:HA	33:LH:216:ASP:HB3	1.96	0.47
1:C1:1757:G:O2'	1:C1:1759:G:OP2	2.22	0.47
1:C1:2319:A:H2'	1:C1:2320:A:H8	1.79	0.47
3:CA:111:PRO:HG3	23:CU:199:ALA:HB1	1.96	0.47
6:CD:252:TRP:CH2	6:CD:289:PRO:HG3	2.49	0.47
10:CH:444:LYS:HE2	19:CQ:93:MET:HE2	1.96	0.47
18:CP:376:LEU:HB2	18:CP:509:VAL:HG21	1.94	0.47
26:CY:729:ARG:C	26:CY:733:LYS:HZ3	2.21	0.47
30:LC:93:ASN:HA	30:LC:99:ARG:O	2.14	0.47
35:LL:92:THR:HG23	54:Lh:118:GLN:HA	1.96	0.47
42:LS:8:GLN:HG2	42:LS:62:ASN:HB2	1.96	0.47
1:C1:409:A:H2'	1:C1:410:A:C8	2.48	0.47
1:C1:897:G:H2'	1:C1:898:A:C8	2.48	0.47
1:C1:1780:U:H2'	1:C1:1781:C:C6	2.50	0.47
1:C1:2300:C:H2'	1:C1:2301:C:H6	1.78	0.47
1:C1:2452:C:O2'	1:C1:2453:A:H8	1.97	0.47
1:C1:2727:A:H2'	1:C1:2728:G:C8	2.49	0.47
1:C1:2796:A:H2'	1:C1:2797:G:O4'	2.13	0.47
1:C1:3162:A:H4'	1:C1:3163:G:O5'	2.14	0.47
1:C1:3272:U:H2'	1:C1:3273:G:O4'	2.14	0.47
3:CA:128:PHE:O	3:CA:129:GLN:HB2	2.15	0.47
5:CC:724:ARG:NH1	5:CC:725:PHE:O	2.48	0.47
15:CM:179:LEU:HB3	15:CM:184:ILE:HB	1.96	0.47
18:CP:268:LYS:HA	18:CP:268:LYS:HD3	1.67	0.47
19:CQ:89:THR:O	19:CQ:93:MET:HG3	2.13	0.47
22:CT:664:LEU:HB3	22:CT:676:LEU:HD11	1.96	0.47
27:Cb:283:THR:HA	27:Cb:287:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LC:9:VAL:HB	30:LC:19:ALA:HB3	1.96	0.47
41:LR:11:ALA:HA	41:LR:14:VAL:HG12	1.96	0.47
41:LR:15:LEU:HD22	41:LR:52:LYS:HB2	1.96	0.47
41:LR:103:ARG:NH1	41:LR:124:TYR:OH	2.46	0.47
52:Lf:27:PRO:O	52:Lf:90:PRO:HB3	2.14	0.47
1:C1:128:G:OP1	54:Lh:80:TYR:OH	2.18	0.47
1:C1:205:G:OP2	47:LY:1:MET:N	2.33	0.47
1:C1:771:U:H2'	1:C1:772:U:H6	1.79	0.47
1:C1:830:C:H2'	1:C1:831:U:C6	2.49	0.47
1:C1:1075:A:H5''	1:C1:1078:C:H5	1.80	0.47
1:C1:1157:C:HO2'	1:C1:1158:C:P	2.37	0.47
6:CD:200:VAL:HB	6:CD:221:LEU:HB2	1.97	0.47
7:CE:361:ILE:HB	7:CE:429:ILE:HD13	1.96	0.47
7:CE:384:VAL:HG23	7:CE:410:THR:HG23	1.95	0.47
16:CN:118:HIS:HB3	16:CN:121:LEU:CD1	2.44	0.47
26:CY:409:VAL:O	26:CY:416:ARG:NH2	2.47	0.47
28:Cz:68:MET:O	28:Cz:71:GLU:HG3	2.15	0.47
33:LH:163:ARG:HD3	33:LH:203:ILE:HG12	1.96	0.47
37:LN:30:TYR:O	37:LN:65:ARG:NH1	2.48	0.47
48:LZ:120:ARG:HH21	48:LZ:125:LYS:HG3	1.80	0.47
53:Lg:112:ALA:O	53:Lg:115:LYS:HG3	2.13	0.47
59:Lq:7:ALA:O	59:Lq:10:ARG:HB3	2.14	0.47
1:C1:234:C:H2'	1:C1:235:A:O4'	2.14	0.47
5:CC:423:ILE:HD11	12:CJ:649:MET:HE1	1.95	0.47
5:CC:696:LYS:O	5:CC:714:ARG:HG3	2.13	0.47
7:CE:377:LEU:HD23	7:CE:380:ILE:HD11	1.96	0.47
11:CI:316:ARG:O	11:CI:319:LYS:HG3	2.14	0.47
12:CJ:390:PHE:CE2	12:CJ:465:ILE:HG23	2.50	0.47
12:CJ:508:THR:HG23	12:CJ:511:GLU:H	1.79	0.47
23:CU:340:LYS:NZ	23:CU:369:ASP:HA	2.30	0.47
26:CY:731:GLU:HA	26:CY:734:ARG:CD	2.43	0.47
27:Cb:168:PRO:HG3	27:Cb:246:LEU:HG	1.95	0.47
27:Cb:203:GLN:NE2	27:Cb:220:ARG:HE	2.12	0.47
27:Cb:872:ARG:HG2	27:Cb:872:ARG:HH11	1.79	0.47
30:LC:211:ILE:HG12	30:LC:256:VAL:CG2	2.45	0.47
32:LG:75:PRO:HB3	37:LN:17:ASP:OD2	2.15	0.47
32:LG:208:SER:HA	32:LG:211:LYS:HG3	1.96	0.47
39:LP:59:PRO:HD3	39:LP:76:TRP:CE2	2.49	0.47
57:Lk:7:ASP:N	57:Lk:7:ASP:OD1	2.47	0.47
1:C1:765:G:H21	40:LQ:119:ARG:HB3	1.79	0.47
1:C1:2076:C:H2'	1:C1:2077:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2427:G:H2'	1:C1:2428:G:C8	2.50	0.47
1:C1:2848:A:H2'	1:C1:2849:U:C6	2.50	0.47
1:C1:2874:U:H2'	1:C1:2875:G:O4'	2.15	0.47
1:C1:3215:U:C2	1:C1:3217:U:H5'	2.50	0.47
1:C1:3289:C:C4	1:C1:3290:C:N4	2.82	0.47
1:C1:3304:C:H2'	1:C1:3305:U:C6	2.50	0.47
2:C2:129:C:OP1	12:CJ:11:GLY:N	2.38	0.47
5:CC:117:ILE:HD13	7:CE:472:HIS:CE1	2.50	0.47
5:CC:566:PRO:O	5:CC:625:THR:HB	2.14	0.47
9:CG:65:LEU:HD21	18:CP:415:LYS:HG3	1.95	0.47
10:CH:169:LEU:HD23	10:CH:248:ALA:HB3	1.95	0.47
23:CU:280:ALA:O	23:CU:284:LYS:HG3	2.13	0.47
29:LB:263:TRP:CD1	29:LB:263:TRP:H	2.32	0.47
32:LG:97:LEU:HB3	32:LG:192:LEU:HD11	1.96	0.47
41:LR:103:ARG:NH1	41:LR:124:TYR:CZ	2.83	0.47
42:LS:110:MET:HA	42:LS:110:MET:HE2	1.97	0.47
51:Le:65:LYS:HG2	51:Le:66:HIS:CD2	2.49	0.47
1:C1:19:U:H2'	1:C1:20:A:C8	2.50	0.47
1:C1:440:G:H2'	1:C1:441:G:C8	2.47	0.47
1:C1:836:U:H4'	41:LR:95:TRP:CD1	2.50	0.47
1:C1:1237:C:H2'	1:C1:1238:G:C8	2.49	0.47
1:C1:1657:G:O6	44:LU:81:ARG:NH2	2.48	0.47
1:C1:1692:G:N1	1:C1:1709:G:N3	2.63	0.47
1:C1:3086:A:C6	1:C1:3088:U:H1'	2.50	0.47
2:C2:9:A:H2'	2:C2:10:A:C8	2.50	0.47
4:CB:139:ALA:HB2	32:LG:212:ASN:ND2	2.28	0.47
4:CB:151:ASP:O	4:CB:177:LYS:HE3	2.14	0.47
5:CC:573:GLY:O	5:CC:576:LEU:HB2	2.15	0.47
7:CE:126:ILE:HD11	7:CE:167:ILE:HD11	1.96	0.47
9:CG:106:GLN:HG3	9:CG:110:TYR:CE2	2.49	0.47
18:CP:287:LEU:HD21	18:CP:567:TYR:OH	2.14	0.47
18:CP:551:TYR:O	18:CP:553:GLY:N	2.48	0.47
22:CT:448:ASP:OD2	25:CX:124:ARG:NH2	2.39	0.47
22:CT:612:LEU:HD21	22:CT:676:LEU:N	2.29	0.47
27:Cb:174:LEU:HB3	27:Cb:178:LYS:HZ1	1.80	0.47
29:LB:33:PRO:HD2	29:LB:44:THR:HG21	1.95	0.47
30:LC:237:VAL:HG11	30:LC:264:GLN:HB2	1.97	0.47
33:LH:129:TYR:O	33:LH:181:ASP:HB3	2.14	0.47
34:LK:127:GLY:HA2	34:LK:130:LYS:HG2	1.97	0.47
37:LN:137:PRO:O	37:LN:143:ARG:HD3	2.15	0.47
45:LV:28:ALA:O	45:LV:117:THR:N	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:LZ:17:TYR:OH	48:LZ:46:GLU:OE2	2.30	0.47
48:LZ:53:THR:H	48:LZ:56:MET:HE2	1.80	0.47
53:Lg:45:CYS:SG	53:Lg:46:GLY:N	2.87	0.47
55:Li:35:PRO:HA	55:Li:38:ARG:HB2	1.96	0.47
59:Lq:10:ARG:HH22	59:Lq:176:GLN:HG3	1.79	0.47
1:C1:155:G:H2'	1:C1:156:G:C8	2.50	0.47
1:C1:2414:G:C6	1:C1:2456:A:N1	2.83	0.47
1:C1:3283:G:H21	1:C1:3302:A:H2	1.63	0.47
2:C2:174:G:H1'	2:C2:175:G:C8	2.50	0.47
5:CC:704:ASP:OD1	57:Lk:9:LYS:HD3	2.15	0.47
6:CD:174:GLY:O	6:CD:201:ARG:NH2	2.42	0.47
10:CH:291:ILE:HD11	60:CH:1001:GTP:N2	2.30	0.47
12:CJ:228:GLY:O	12:CJ:232:GLU:HG3	2.14	0.47
16:CN:74:THR:OG1	19:CQ:74:ARG:NH2	2.43	0.47
21:CS:499:VAL:O	22:CT:183:ARG:NH1	2.48	0.47
22:CT:443:LEU:HD23	22:CT:443:LEU:HA	1.80	0.47
23:CU:205:LEU:HG	23:CU:207:ILE:HD11	1.96	0.47
24:CV:54:ILE:HG22	24:CV:118:ILE:HD12	1.96	0.47
26:CY:496:VAL:HG11	26:CY:550:LEU:HG	1.97	0.47
26:CY:546:ILE:HA	26:CY:604:THR:HG22	1.96	0.47
27:Cb:475:LEU:HD21	27:Cb:563:VAL:CG2	2.45	0.47
39:LP:176:ARG:O	39:LP:180:ILE:HG12	2.15	0.47
45:LV:56:VAL:HG23	45:LV:83:GLN:HB2	1.97	0.47
1:C1:288:A:N3	1:C1:291:G:O2'	2.46	0.47
1:C1:429:G:C4	1:C1:430:A:C8	3.03	0.47
1:C1:1636:C:O2'	1:C1:1775:G:O2'	2.27	0.47
1:C1:1880:A:H2'	1:C1:1881:G:H8	1.80	0.47
1:C1:3113:C:H2'	1:C1:3114:C:C6	2.50	0.47
1:C1:3189:G:H2'	1:C1:3190:G:H8	1.80	0.47
5:CC:500:ASN:N	5:CC:516:ALA:O	2.45	0.47
7:CE:170:VAL:HG21	7:CE:206:LEU:HD22	1.97	0.47
9:CG:19:TYR:OH	9:CG:167:GLN:NE2	2.44	0.47
15:CM:180:GLY:C	15:CM:183:GLY:H	2.23	0.47
20:CR:34:ILE:HD13	20:CR:171:ALA:HB1	1.97	0.47
37:LN:64:VAL:HG11	37:LN:102:ALA:HB1	1.97	0.47
48:LZ:28:VAL:HG12	48:LZ:31:GLY:H	1.80	0.47
1:C1:203:C:C2	30:LC:224:LYS:HD2	2.50	0.47
1:C1:1049:C:H5'	1:C1:1050:C:OP2	2.15	0.47
1:C1:3026:G:C2	1:C1:3027:A:C8	3.03	0.47
5:CC:772:ASN:HB3	48:LZ:105:GLN:HE21	1.79	0.47
6:CD:262:PRO:HG2	6:CD:286:GLN:OE1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:361:LEU:HA	10:CH:364:VAL:HG12	1.97	0.47
12:CJ:515:ALA:HB2	12:CJ:668:ARG:HH12	1.80	0.47
15:CM:52:LYS:HG3	15:CM:56:LYS:HD2	1.96	0.47
15:CM:129:THR:HA	15:CM:132:MET:HE2	1.97	0.47
26:CY:433:VAL:HG23	26:CY:434:THR:N	2.29	0.47
26:CY:579:LEU:HB3	26:CY:653:TRP:CZ3	2.50	0.47
26:CY:671:SER:HA	26:CY:674:VAL:HG12	1.96	0.47
36:LM:4:ILE:HG22	36:LM:6:VAL:HG23	1.96	0.47
45:LV:41:VAL:HG23	45:LV:44:ALA:HB2	1.97	0.47
57:Lk:5:VAL:HG12	57:Lk:47:LEU:HD13	1.97	0.47
1:C1:862:C:C2	22:CT:579:TRP:HE3	2.33	0.46
1:C1:2072:G:H2'	1:C1:2073:G:C8	2.49	0.46
1:C1:2326:G:H22	1:C1:2358:G:H1'	1.80	0.46
1:C1:2725:U:H3	1:C1:2749:G:H1	1.63	0.46
1:C1:2780:U:H2'	1:C1:2781:G:O4'	2.15	0.46
1:C1:3228:G:O2'	1:C1:3229:G:H8	1.99	0.46
6:CD:32:LYS:NZ	6:CD:55:MET:O	2.39	0.46
11:CI:290:GLY:O	11:CI:293:LEU:N	2.48	0.46
13:CK:225:VAL:HG21	13:CK:241:ARG:HG2	1.97	0.46
15:CM:36:LEU:O	15:CM:40:LYS:HG2	2.15	0.46
18:CP:270:ILE:HD11	18:CP:297:PHE:CD2	2.50	0.46
19:CQ:50:LYS:HG3	19:CQ:55:TYR:CE2	2.50	0.46
22:CT:171:GLN:O	22:CT:175:TYR:HD1	1.97	0.46
26:CY:467:SER:O	26:CY:471:LEU:HD23	2.15	0.46
26:CY:504:CYS:HA	26:CY:560:ARG:NH1	2.29	0.46
48:LZ:91:LEU:HD22	48:LZ:94:VAL:HG21	1.96	0.46
1:C1:423:U:H2'	1:C1:424:G:H8	1.77	0.46
1:C1:933:A:H4'	1:C1:949:G:H21	1.80	0.46
1:C1:1205:A:H62	1:C1:1267:G:H21	1.61	0.46
1:C1:2365:G:C2	1:C1:2366:A:H1'	2.50	0.46
1:C1:3069:G:O6	1:C1:3077:C:H5''	2.15	0.46
2:C2:216:A:H2	11:CI:263:VAL:HG22	1.80	0.46
4:CB:30:LEU:O	4:CB:34:ILE:HG12	2.14	0.46
5:CC:367:ARG:NH2	5:CC:384:PRO:O	2.48	0.46
5:CC:443:THR:N	5:CC:801:MET:O	2.43	0.46
5:CC:493:LEU:HB3	5:CC:522:PHE:HE2	1.79	0.46
5:CC:694:TYR:CD2	48:LZ:103:PRO:HG2	2.50	0.46
10:CH:160:PRO:HB3	13:CK:3:GLN:HB2	1.98	0.46
10:CH:386:ALA:O	10:CH:390:LEU:HG	2.15	0.46
16:CN:82:GLN:HG3	16:CN:86:ASN:ND2	2.31	0.46
16:CN:104:LEU:HA	16:CN:107:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:CY:731:GLU:O	26:CY:734:ARG:HD3	2.15	0.46
27:Cb:413:ARG:HE	27:Cb:433:PRO:HD3	1.80	0.46
27:Cb:423:THR:OG1	27:Cb:424:ASP:N	2.47	0.46
49:Lc:77:ASN:OD1	49:Lc:78:ILE:N	2.49	0.46
56:Lj:70:VAL:HA	56:Lj:73:ARG:HH11	1.80	0.46
59:Lq:124:LEU:HD23	59:Lq:124:LEU:H	1.80	0.46
1:C1:422:G:H2'	1:C1:423:U:H6	1.80	0.46
1:C1:1438:A:OP1	50:Ld:34:LYS:HD3	2.15	0.46
1:C1:1455:A:H5''	41:LR:23:TRP:CD1	2.50	0.46
1:C1:1634:G:N2	1:C1:1780:U:O4	2.49	0.46
1:C1:1682:U:H3	1:C1:1720:A:H62	1.63	0.46
1:C1:1901:A:H61	1:C1:2073:G:H1	1.63	0.46
1:C1:3064:U:H2'	1:C1:3065:G:H8	1.80	0.46
2:C2:4:C:H2'	2:C2:5:U:C6	2.50	0.46
5:CC:788:CYS:SG	5:CC:800:TRP:HB2	2.55	0.46
6:CD:28:LEU:HD12	6:CD:29:PRO:HD2	1.98	0.46
6:CD:291:GLY:HA3	6:CD:293:TRP:CH2	2.51	0.46
7:CE:188:VAL:HG23	7:CE:262:ILE:HB	1.97	0.46
10:CH:255:ILE:HG22	10:CH:292:LYS:HE3	1.96	0.46
10:CH:269:LEU:O	10:CH:273:ILE:HG12	2.15	0.46
10:CH:488:ILE:HD13	19:CQ:124:ARG:HD3	1.96	0.46
18:CP:292:GLU:HG2	18:CP:569:HIS:CE1	2.51	0.46
22:CT:562:THR:HG22	22:CT:564:THR:HG22	1.97	0.46
27:Cb:207:MET:HG3	27:Cb:224:LEU:HD21	1.96	0.46
27:Cb:510:LYS:HE2	27:Cb:576:PHE:CD1	2.50	0.46
31:LE:73:LEU:HD21	31:LE:169:LEU:HD11	1.97	0.46
37:LN:158:HIS:HB3	37:LN:161:CYS:HB2	1.97	0.46
39:LP:59:PRO:HB3	39:LP:78:VAL:HG11	1.98	0.46
51:Le:87:LEU:HD13	51:Le:116:LEU:HD22	1.97	0.46
1:C1:233:C:H2'	1:C1:234:C:C6	2.51	0.46
1:C1:772:U:H2'	1:C1:773:A:H8	1.80	0.46
1:C1:889:G:H2'	1:C1:890:G:C8	2.51	0.46
1:C1:1862:A:H2'	1:C1:1863:A:C8	2.50	0.46
1:C1:3264:A:OP1	50:Ld:27:ARG:NH1	2.49	0.46
2:C2:102:U:HO2'	2:C2:103:G:P	2.37	0.46
3:CA:130:GLY:C	3:CA:234:ILE:HG22	2.41	0.46
5:CC:778:ASP:OD1	5:CC:779:ILE:N	2.48	0.46
22:CT:514:THR:O	22:CT:518:ARG:HG3	2.15	0.46
22:CT:560:LEU:HD13	22:CT:565:VAL:HG12	1.96	0.46
30:LC:207:ARG:HH21	30:LC:253:ARG:HH12	1.63	0.46
15:LF:244:LEU:O	15:LF:248:MET:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:Lg:10:ARG:HE	53:Lg:35:HIS:CG	2.33	0.46
1:C1:738:C:OP1	23:CU:232:GLN:NE2	2.35	0.46
1:C1:2898:A:H2'	1:C1:2903:G:O4'	2.15	0.46
1:C1:3138:U:HO2'	42:LS:172:THR:HG1	1.56	0.46
1:C1:3265:A:H2'	1:C1:3266:G:C8	2.51	0.46
2:C2:223:G:H2'	2:C2:224:C:C6	2.50	0.46
5:CC:450:ARG:NH2	6:CD:459:ASP:OD1	2.35	0.46
5:CC:543:LEU:HD23	5:CC:620:LEU:HD21	1.97	0.46
9:CG:48:VAL:HG11	9:CG:67:LEU:HG	1.97	0.46
11:CI:271:ASP:OD1	11:CI:271:ASP:N	2.43	0.46
19:CQ:81:TYR:HA	19:CQ:86:TRP:CZ3	2.50	0.46
27:Cb:270:LEU:HD21	27:Cb:279:LEU:HD11	1.98	0.46
27:Cb:367:HIS:O	27:Cb:436:ALA:HB3	2.16	0.46
1:C1:322:G:C2	1:C1:323:G:C8	3.04	0.46
1:C1:662:C:H2'	1:C1:663:G:O4'	2.16	0.46
1:C1:1275:U:H2'	1:C1:1276:A:H8	1.80	0.46
2:C2:226:G:H2'	2:C2:227:G:H8	1.80	0.46
4:CB:19:ASP:OD1	4:CB:20:PRO:HD2	2.16	0.46
5:CC:672:PRO:HB2	5:CC:677:ILE:HD11	1.97	0.46
6:CD:348:LEU:HD23	6:CD:350:ARG:N	2.30	0.46
6:CD:475:SER:OG	6:CD:483:GLN:HB2	2.15	0.46
7:CE:293:MET:HE2	7:CE:295:PHE:HZ	1.80	0.46
15:CM:171:ASP:O	15:CM:174:ILE:HG22	2.16	0.46
30:LC:188:SER:OG	30:LC:206:ARG:NH1	2.49	0.46
32:LG:101:ARG:HG2	32:LG:192:LEU:O	2.16	0.46
36:LM:76:ALA:HB1	36:LM:80:ALA:HB3	1.98	0.46
44:LU:60:ILE:HD12	44:LU:78:LEU:HD22	1.96	0.46
47:LY:73:TYR:CE2	47:LY:76:LYS:HE3	2.51	0.46
1:C1:260:A:OP1	37:LN:50:ARG:NH1	2.49	0.46
1:C1:830:C:H2'	1:C1:831:U:H6	1.80	0.46
1:C1:1377:G:O2'	2:C2:18:U:O2	2.33	0.46
1:C1:3131:A:H62	31:LE:191:LYS:HE2	1.80	0.46
1:C1:3320:C:H5'	29:LB:317:GLU:OE1	2.16	0.46
2:C2:71:A:C5	2:C2:85:G:N2	2.83	0.46
5:CC:499:VAL:HA	5:CC:517:ALA:HB2	1.97	0.46
8:CF:87:ASP:O	8:CF:227:TRP:NE1	2.49	0.46
12:CJ:144:CYS:SG	12:CJ:238:LEU:HB2	2.56	0.46
19:CQ:99:ILE:O	19:CQ:103:ARG:HG2	2.15	0.46
22:CT:174:VAL:O	22:CT:178:VAL:HG22	2.16	0.46
23:CU:290:ILE:HD13	25:CX:71:ILE:HG13	1.97	0.46
32:LG:57:GLU:HG2	32:LG:60:ARG:NH2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:LK:110:ILE:O	34:LK:114:ARG:HG3	2.15	0.46
45:LV:19:LEU:HD21	45:LV:100:ASN:HB3	1.97	0.46
58:Ll:26:TRP:HZ3	58:Ll:30:ARG:HE	1.64	0.46
1:C1:221:U:OP1	47:LY:4:ARG:NH2	2.49	0.46
1:C1:343:A:N6	58:Ll:37:TYR:O	2.35	0.46
1:C1:933:A:H4'	1:C1:949:G:N2	2.31	0.46
1:C1:1178:C:H41	1:C1:1302:C:H5''	1.80	0.46
1:C1:1243:G:H4'	1:C1:1260:A:H2	1.80	0.46
1:C1:2304:U:H2'	1:C1:2305:C:C6	2.51	0.46
7:CE:261:LEU:O	7:CE:292:THR:HA	2.16	0.46
7:CE:292:THR:HB	7:CE:311:LEU:HD23	1.98	0.46
8:CF:158:SER:OG	8:CF:160:THR:HG22	2.16	0.46
9:CG:23:LEU:HD22	9:CG:26:LEU:HD12	1.98	0.46
16:CN:96:ARG:HH21	19:CQ:74:ARG:CZ	2.29	0.46
27:Cb:2:PRO:HD2	45:LV:75:VAL:HG21	1.97	0.46
30:LC:170:TYR:OH	30:LC:183:GLU:OE2	2.34	0.46
59:Lq:176:GLN:HA	59:Lq:179:LEU:HG	1.98	0.46
1:C1:213:G:O6	1:C1:1371:G:C2	2.69	0.46
1:C1:332:C:H2'	1:C1:333:G:O4'	2.15	0.46
1:C1:1054:G:H2'	1:C1:1055:U:C6	2.51	0.46
1:C1:1323:U:H2'	1:C1:1324:C:C6	2.51	0.46
1:C1:1548:C:C2	5:CC:408:MET:HE1	2.50	0.46
2:C2:7:U:H2'	2:C2:8:C:H6	1.81	0.46
2:C2:194:C:H5'	4:CB:67:THR:HG21	1.97	0.46
6:CD:113:TRP:CD1	6:CD:478:GLU:HB2	2.51	0.46
7:CE:222:ASN:HB3	7:CE:225:ALA:HB3	1.98	0.46
8:CF:218:GLU:HA	8:CF:218:GLU:OE1	2.16	0.46
10:CH:170:LEU:HD12	10:CH:247:ALA:HB3	1.98	0.46
10:CH:364:VAL:HG21	16:CN:242:VAL:HA	1.98	0.46
10:CH:513:LYS:HG3	10:CH:513:LYS:O	2.16	0.46
12:CJ:97:ARG:NH2	32:LG:191:THR:HA	2.31	0.46
16:CN:81:LEU:HD22	16:CN:96:ARG:CD	2.46	0.46
24:CV:21:VAL:HG11	51:Le:85:LEU:HD21	1.98	0.46
29:LB:333:LYS:O	29:LB:334:LYS:HG2	2.16	0.46
43:LT:43:LYS:HB2	43:LT:97:LYS:HZ1	1.81	0.46
1:C1:857:A:H2'	1:C1:858:C:O4'	2.16	0.46
1:C1:886:U:O2'	1:C1:887:G:OP1	2.27	0.46
1:C1:1151:A:H2'	1:C1:1152:A:C8	2.50	0.46
1:C1:3137:A:N3	1:C1:3140:G:O2'	2.48	0.46
6:CD:228:VAL:HA	6:CD:244:SER:HA	1.97	0.46
8:CF:164:GLU:OE2	8:CF:207:ARG:NH2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:236:MET:HE3	27:Cb:597:TYR:CD1	2.51	0.46
18:CP:367:ALA:HA	18:CP:370:PHE:CD2	2.51	0.46
18:CP:376:LEU:HD11	18:CP:452:ARG:HB3	1.97	0.46
26:CY:456:ASP:HB2	26:CY:459:LEU:HD21	1.97	0.46
27:Cb:158:ARG:HB3	27:Cb:829:GLY:HA2	1.97	0.46
27:Cb:443:PHE:CD2	27:Cb:444:PRO:HD2	2.51	0.46
33:LH:83:SER:HA	36:LM:6:VAL:HG11	1.98	0.46
37:LN:103:GLU:HB3	37:LN:160:GLU:HB2	1.97	0.46
43:LT:112:ASN:HB3	43:LT:128:LEU:HD12	1.98	0.46
53:Lg:56:PRO:HD2	53:Lg:70:LYS:O	2.16	0.46
57:Lk:10:LYS:O	57:Lk:13:GLU:HG3	2.15	0.46
1:C1:861:G:H1'	1:C1:869:A:H61	1.82	0.45
1:C1:1210:A:H5''	8:CF:203:SER:HB2	1.98	0.45
1:C1:1502:G:O3'	46:LX:82:THR:HG21	2.17	0.45
1:C1:1598:A:N1	1:C1:1805:C:N3	2.63	0.45
4:CB:57:VAL:O	4:CB:248:ALA:HB3	2.16	0.45
7:CE:258:LEU:HB3	7:CE:286:PRO:HG2	1.97	0.45
7:CE:344:ARG:HB3	7:CE:432:PHE:CE1	2.50	0.45
10:CH:79:ASP:O	10:CH:83:ILE:HG12	2.16	0.45
12:CJ:65:TYR:CE2	12:CJ:67:LYS:HB2	2.52	0.45
14:CL:66:LEU:HD12	28:Cz:68:MET:HE1	1.98	0.45
15:CM:43:ASN:O	15:CM:47:ARG:HG2	2.16	0.45
17:CO:14:HIS:O	17:CO:18:LYS:HG3	2.15	0.45
18:CP:539:THR:HA	18:CP:580:LYS:HD3	1.99	0.45
32:LG:153:LEU:HB2	32:LG:218:ILE:HD11	1.98	0.45
40:LQ:129:ALA:HB2	40:LQ:149:LEU:HD23	1.98	0.45
45:LV:34:ARG:HB3	45:LV:66:LYS:HG3	1.97	0.45
46:LX:121:VAL:N	46:LX:138:ARG:O	2.49	0.45
1:C1:370:A:H1'	47:LY:89:ALA:O	2.15	0.45
1:C1:831:U:H2'	1:C1:832:C:C6	2.51	0.45
1:C1:1322:C:H2'	1:C1:1323:U:C6	2.50	0.45
1:C1:1344:G:H2'	1:C1:1345:A:H8	1.81	0.45
1:C1:3204:G:O2'	1:C1:3205:C:OP1	2.31	0.45
5:CC:528:HIS:CG	5:CC:529:PRO:HD2	2.52	0.45
7:CE:184:THR:HA	7:CE:234:VAL:O	2.17	0.45
12:CJ:491:LYS:HA	12:CJ:491:LYS:HD2	1.81	0.45
14:CL:8:PRO:O	38:LO:60:ARG:HD2	2.17	0.45
15:CM:237:ARG:NH1	15:CM:244:LEU:HD22	2.32	0.45
22:CT:444:GLU:OE2	25:CX:121:MET:HG2	2.15	0.45
27:Cb:172:LEU:O	27:Cb:175:GLN:HG3	2.16	0.45
27:Cb:815:LYS:HA	27:Cb:818:GLN:OE1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LC:216:GLU:HG3	30:LC:217:HIS:ND1	2.31	0.45
30:LC:354:VAL:HG21	30:LC:359:LYS:HD3	1.98	0.45
42:LS:6:GLU:HB2	42:LS:64:ILE:HG23	1.98	0.45
1:C1:529:G:C6	1:C1:543:G:N3	2.84	0.45
1:C1:574:G:H2'	1:C1:575:A:C8	2.50	0.45
1:C1:835:G:HO2'	1:C1:836:U:P	2.40	0.45
1:C1:1259:C:H2'	1:C1:1260:A:H8	1.81	0.45
1:C1:1426:G:H2'	1:C1:1427:U:O4'	2.17	0.45
1:C1:2390:U:H5''	18:CP:383:ARG:HH12	1.80	0.45
1:C1:2963:A:H2'	1:C1:2964:U:O4'	2.16	0.45
1:C1:3112:A:H1'	1:C1:3113:C:H5	1.81	0.45
10:CH:440:ILE:HD12	19:CQ:3:ILE:HG13	1.98	0.45
11:CI:189:MET:HE1	11:CI:207:PHE:CE1	2.52	0.45
12:CJ:175:PHE:CE2	12:CJ:179:LEU:HD11	2.50	0.45
13:CK:245:ILE:HD13	13:CK:257:ALA:HB2	1.98	0.45
16:CN:237:MET:O	16:CN:241:ILE:HG12	2.17	0.45
22:CT:370:LEU:O	22:CT:373:ALA:N	2.49	0.45
27:Cb:402:GLN:HG3	27:Cb:406:LYS:NZ	2.31	0.45
33:LH:94:ILE:CD1	33:LH:101:ASP:HB3	2.44	0.45
36:LM:17:GLY:HA2	36:LM:72:LEU:HD21	1.97	0.45
43:LT:45:ASN:H	43:LT:95:HIS:CE1	2.34	0.45
46:LX:84:GLY:O	46:LX:87:LYS:HG3	2.16	0.45
1:C1:224:A:H2'	1:C1:225:G:O4'	2.16	0.45
1:C1:575:A:H2'	1:C1:576:C:C6	2.52	0.45
1:C1:920:U:H2'	1:C1:921:G:C8	2.52	0.45
1:C1:2457:C:C2	1:C1:2458:U:C5	3.04	0.45
1:C1:2478:U:H2'	1:C1:2479:U:H6	1.82	0.45
1:C1:2874:U:C6	1:C1:2893:U:H2'	2.51	0.45
4:CB:160:ILE:HA	4:CB:163:LEU:HD13	1.98	0.45
5:CC:721:ARG:NH1	48:LZ:102:GLU:OE1	2.49	0.45
7:CE:162:THR:HA	7:CE:165:PHE:CZ	2.51	0.45
10:CH:45:TYR:CD2	10:CH:128:LYS:HD3	2.48	0.45
10:CH:177:VAL:O	10:CH:287:ASN:ND2	2.50	0.45
11:CI:234:GLU:HB2	11:CI:273:PHE:CZ	2.52	0.45
14:CL:63:GLU:HG2	14:CL:64:ARG:N	2.31	0.45
26:CY:380:ILE:O	26:CY:384:VAL:HG13	2.16	0.45
29:LB:283:ILE:HA	29:LB:325:ILE:HG22	1.99	0.45
15:LF:150:VAL:O	15:LF:154:ILE:HG12	2.16	0.45
49:Lc:54:LEU:HD11	53:Lg:91:ILE:HG22	1.99	0.45
55:Li:67:ILE:CD1	55:Li:99:LEU:HB3	2.46	0.45
1:C1:137:C:H2'	1:C1:138:G:O4'	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:370:A:H4'	47:LY:90:THR:HG22	1.98	0.45
1:C1:497:U:H2'	1:C1:498:C:H6	1.81	0.45
1:C1:1454:G:H2'	1:C1:1455:A:H8	1.82	0.45
1:C1:1715:G:H5'	5:CC:612:ARG:HG3	1.98	0.45
1:C1:1763:U:H2'	1:C1:1764:C:C6	2.52	0.45
1:C1:1769:U:H2'	1:C1:1770:C:H6	1.82	0.45
1:C1:2371:G:H2'	1:C1:2372:U:C6	2.51	0.45
1:C1:2751:G:H2'	1:C1:2752:G:C8	2.51	0.45
1:C1:3078:U:H1'	1:C1:3079:A:H5''	1.97	0.45
7:CE:113:PHE:CZ	7:CE:134:MET:HG2	2.52	0.45
10:CH:444:LYS:HE2	10:CH:444:LYS:HB2	1.74	0.45
12:CJ:136:ASP:OD1	12:CJ:139:ARG:NH1	2.49	0.45
13:CK:167:LYS:HG2	13:CK:168:TYR:CE2	2.52	0.45
13:CK:239:TRP:CZ2	18:CP:470:SER:HA	2.51	0.45
20:CR:46:SER:HB3	20:CR:69:ASN:ND2	2.32	0.45
21:CS:691:GLY:O	32:LG:71:ARG:HB3	2.16	0.45
27:Cb:245:ARG:HH21	27:Cb:429:GLY:HA2	1.81	0.45
36:LM:112:LEU:HD11	36:LM:120:VAL:HG21	1.99	0.45
41:LR:14:VAL:HG21	41:LR:42:ARG:HG2	1.97	0.45
1:C1:531:U:N3	1:C1:541:G:N1	2.64	0.45
1:C1:886:U:HO2'	1:C1:887:G:P	2.37	0.45
1:C1:910:A:O2'	56:Lj:49:TRP:O	2.31	0.45
1:C1:1318:C:H2'	1:C1:1319:G:H8	1.81	0.45
2:C2:26:U:O2'	30:LC:52:ALA:O	2.34	0.45
5:CC:489:TRP:HZ3	5:CC:526:PRO:HA	1.80	0.45
5:CC:724:ARG:HH22	5:CC:727:LYS:HG3	1.82	0.45
6:CD:246:ASP:OD1	6:CD:246:ASP:N	2.48	0.45
6:CD:410:ASP:OD1	6:CD:410:ASP:N	2.49	0.45
11:CI:191:ILE:HD11	11:CI:258:LEU:HD23	1.98	0.45
12:CJ:258:ASP:OD2	12:CJ:261:LYS:HB2	2.17	0.45
13:CK:147:TRP:O	13:CK:170:ARG:NH2	2.50	0.45
22:CT:280:VAL:HG12	22:CT:283:ARG:HH22	1.82	0.45
26:CY:486:ALA:HA	26:CY:489:ASN:HD21	1.81	0.45
26:CY:502:TRP:CE3	26:CY:505:VAL:HG21	2.51	0.45
27:Cb:245:ARG:HE	27:Cb:428:ARG:HH12	1.65	0.45
31:LE:122:VAL:HG13	31:LE:127:TYR:CE1	2.52	0.45
34:LK:80:LEU:HB3	34:LK:112:ILE:HG12	1.98	0.45
34:LK:82:ILE:HD12	34:LK:100:HIS:CE1	2.52	0.45
37:LN:147:ARG:O	37:LN:150:TRP:NE1	2.48	0.45
39:LP:60:MET:HE2	39:LP:82:ARG:HB3	1.97	0.45
43:LT:48:VAL:HG12	43:LT:50:LYS:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:745:U:C2	1:C1:749:C:N3	2.84	0.45
1:C1:765:G:N2	40:LQ:119:ARG:HB3	2.32	0.45
1:C1:1103:U:H2'	1:C1:1104:U:C6	2.52	0.45
2:C2:216:A:C2	11:CI:263:VAL:HG22	2.52	0.45
3:CA:106:LYS:HD3	3:CA:161:HIS:HD2	1.81	0.45
18:CP:294:PHE:O	18:CP:298:GLU:HG2	2.17	0.45
18:CP:398:MET:O	18:CP:402:MET:HG2	2.17	0.45
18:CP:412:ASP:O	18:CP:437:ASN:HA	2.16	0.45
26:CY:627:SER:O	26:CY:631:VAL:HG12	2.17	0.45
26:CY:657:MET:HE3	26:CY:664:ASN:H	1.80	0.45
27:Cb:245:ARG:NH2	27:Cb:429:GLY:HA2	2.32	0.45
27:Cb:453:ARG:O	27:Cb:456:ARG:HB2	2.17	0.45
30:LC:170:TYR:HE2	30:LC:182:VAL:HG11	1.81	0.45
37:LN:169:LYS:HG2	37:LN:174:LEU:HD22	1.99	0.45
42:LS:46:ARG:HG2	42:LS:46:ARG:HH11	1.81	0.45
1:C1:452:G:H2'	1:C1:453:G:H8	1.82	0.45
1:C1:599:U:H2'	1:C1:600:G:H8	1.81	0.45
1:C1:833:U:H2'	1:C1:834:G:H8	1.80	0.45
1:C1:1483:U:H2'	1:C1:1484:G:C8	2.51	0.45
1:C1:3073:G:C2	28:Cz:38:ALA:HB2	2.52	0.45
9:CG:20:MET:HE3	9:CG:90:LEU:HD23	1.98	0.45
12:CJ:78:LEU:O	12:CJ:82:ARG:HG3	2.16	0.45
26:CY:381:LYS:HA	26:CY:384:VAL:HG22	1.98	0.45
26:CY:555:ILE:HG22	26:CY:625:LEU:HD12	1.98	0.45
27:Cb:396:VAL:HB	27:Cb:422:VAL:HG12	1.98	0.45
29:LB:233:ARG:HA	29:LB:271:MET:HG3	1.99	0.45
48:LZ:11:LEU:HD21	48:LZ:80:MET:HE3	1.99	0.45
48:LZ:32:THR:OG1	48:LZ:34:SER:O	2.29	0.45
48:LZ:103:PRO:O	48:LZ:106:ARG:HG2	2.17	0.45
53:Lg:87:ARG:O	53:Lg:91:ILE:HG12	2.17	0.45
1:C1:834:G:H2'	1:C1:835:G:O4'	2.17	0.45
1:C1:1436:A:N6	1:C1:1858:A:O2'	2.50	0.45
1:C1:1667:U:H2'	1:C1:1668:U:C6	2.52	0.45
1:C1:2291:C:C2	1:C1:2292:C:C5	3.05	0.45
1:C1:3304:C:H2'	1:C1:3305:U:H6	1.81	0.45
6:CD:409:HIS:C	6:CD:411:GLY:H	2.25	0.45
10:CH:270:PHE:O	10:CH:274:LYS:HG3	2.17	0.45
11:CI:308:LYS:O	11:CI:311:GLN:HG2	2.17	0.45
11:CI:317:ALA:O	11:CI:321:LYS:HG2	2.17	0.45
12:CJ:260:VAL:O	12:CJ:264:GLN:HG3	2.17	0.45
13:CK:149:ARG:NH1	13:CK:170:ARG:HH12	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:447:ILE:HG23	18:CP:448:GLY:H	1.82	0.45
20:CR:4:GLU:CD	20:CR:4:GLU:H	2.24	0.45
20:CR:209:MET:HE2	20:CR:225:ILE:HG21	1.99	0.45
21:CS:508:SER:HB2	22:CT:215:HIS:CE1	2.51	0.45
22:CT:124:ILE:H	22:CT:124:ILE:HD12	1.81	0.45
26:CY:383:VAL:HA	26:CY:386:PHE:HD2	1.81	0.45
26:CY:507:SER:C	26:CY:509:HIS:N	2.74	0.45
27:Cb:103:ARG:HH21	27:Cb:107:ARG:HH22	1.65	0.45
27:Cb:237:TYR:OH	27:Cb:269:LEU:HD11	2.16	0.45
27:Cb:323:HIS:ND1	27:Cb:509:LEU:HD22	2.32	0.45
30:LC:365:ALA:HB3	42:LS:28:ARG:HD3	1.98	0.45
42:LS:112:ALA:O	42:LS:115:ARG:NH1	2.49	0.45
42:LS:139:TYR:O	42:LS:142:GLN:HG2	2.16	0.45
48:LZ:14:ARG:HH21	53:Lg:87:ARG:NH1	2.14	0.45
48:LZ:96:ASN:O	48:LZ:99:THR:OG1	2.29	0.45
1:C1:1303:G:H2'	1:C1:1304:U:C6	2.52	0.45
1:C1:2360:A:H2'	1:C1:2901:G:H1	1.82	0.45
1:C1:3156:C:H2'	1:C1:3157:C:O4'	2.17	0.45
1:C1:3283:G:N2	1:C1:3303:U:O4	2.50	0.45
4:CB:150:HIS:O	4:CB:177:LYS:NZ	2.42	0.45
8:CF:59:GLU:HG2	8:CF:115:TYR:CZ	2.52	0.45
10:CH:251:TYR:HB3	10:CH:284:ILE:HD13	1.99	0.45
12:CJ:376:ARG:NE	15:CM:189:ASP:OD2	2.49	0.45
21:CS:475:MET:HE1	32:LG:55:TRP:CZ3	2.52	0.45
22:CT:280:VAL:HG12	22:CT:283:ARG:NH2	2.32	0.45
26:CY:425:GLN:O	26:CY:428:VAL:HB	2.17	0.45
26:CY:469:ARG:O	26:CY:473:ILE:HG12	2.17	0.45
27:Cb:300:LYS:HA	27:Cb:300:LYS:HD2	1.80	0.45
29:LB:94:GLU:OE1	38:LO:157:ARG:NH2	2.49	0.45
46:LX:121:VAL:HG23	46:LX:140:THR:HA	1.99	0.45
1:C1:171:G:H2'	1:C1:172:C:H6	1.82	0.44
1:C1:263:C:O2	55:Li:91:ARG:NH2	2.34	0.44
1:C1:340:C:O2	1:C1:344:A:O2'	2.34	0.44
1:C1:584:C:H2'	1:C1:596:G:O6	2.17	0.44
1:C1:687:C:H2'	1:C1:688:G:H8	1.82	0.44
1:C1:1215:G:N2	34:LK:131:GLU:OE2	2.43	0.44
1:C1:2290:U:H2'	1:C1:2291:C:H6	1.82	0.44
1:C1:2794:C:H2'	1:C1:2795:A:O4'	2.16	0.44
2:C2:44:A:H2'	2:C2:45:C:H6	1.82	0.44
5:CC:761:PRO:HD3	12:CJ:637:MET:HE3	1.98	0.44
5:CC:765:LEU:HD13	5:CC:800:TRP:CE3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:299:PRO:HG2	6:CD:318:GLN:HG3	1.98	0.44
8:CF:93:THR:HA	8:CF:96:LEU:HD13	1.98	0.44
12:CJ:371:THR:O	12:CJ:416:THR:OG1	2.25	0.44
16:CN:26:VAL:HG13	16:CN:34:PHE:HD2	1.81	0.44
16:CN:117:ILE:HD11	16:CN:139:ARG:HG2	1.98	0.44
20:CR:29:PRO:HG3	35:LL:44:ALA:HA	1.99	0.44
23:CU:288:LYS:HG3	23:CU:291:GLU:OE2	2.16	0.44
26:CY:532:VAL:O	26:CY:533:GLN:C	2.60	0.44
39:LP:32:THR:HG21	39:LP:87:SER:HB3	1.99	0.44
1:C1:84:U:OP2	1:C1:85:A:O2'	2.27	0.44
1:C1:405:U:H2'	1:C1:406:U:C6	2.53	0.44
1:C1:855:U:H2'	1:C1:856:G:C8	2.52	0.44
1:C1:1089:A:H2'	1:C1:1090:C:H6	1.82	0.44
1:C1:2381:A:H2'	1:C1:2382:C:H6	1.82	0.44
4:CB:206:ARG:HH22	4:CB:212:ALA:HA	1.81	0.44
5:CC:455:ARG:HD2	5:CC:777:LEU:HD21	1.99	0.44
6:CD:108:PHE:HE2	6:CD:474:PHE:HE2	1.64	0.44
6:CD:179:SER:O	6:CD:196:MET:N	2.48	0.44
7:CE:243:ARG:HG3	7:CE:247:HIS:HD2	1.81	0.44
12:CJ:123:LEU:HD22	12:CJ:126:ILE:HD12	2.00	0.44
13:CK:4:ASN:O	13:CK:6:TYR:N	2.50	0.44
14:CL:69:ARG:O	14:CL:73:ARG:HD3	2.16	0.44
15:CM:92:VAL:HG22	15:CM:142:TYR:HB3	1.97	0.44
22:CT:276:ASP:OD2	22:CT:277:ARG:N	2.50	0.44
24:CV:3:ASN:O	24:CV:8:LEU:HD22	2.17	0.44
26:CY:621:GLN:O	26:CY:625:LEU:HD23	2.17	0.44
26:CY:685:LYS:HA	26:CY:688:GLU:HG2	1.99	0.44
29:LB:284:TYR:OH	29:LB:326:LYS:HD2	2.17	0.44
45:LV:20:PRO:HA	45:LV:53:ALA:HA	1.98	0.44
46:LX:70:LEU:HD22	46:LX:102:LYS:HB2	1.98	0.44
57:Lk:23:ALA:HA	57:Lk:37:LYS:O	2.17	0.44
1:C1:452:G:H2'	1:C1:453:G:C8	2.52	0.44
1:C1:934:G:H3'	1:C1:1098:G:N2	2.33	0.44
1:C1:1038:U:H2'	1:C1:1039:A:C8	2.52	0.44
1:C1:2340:C:C2	1:C1:2341:U:C5	3.05	0.44
1:C1:2342:U:O2'	1:C1:2343:G:H8	2.00	0.44
1:C1:2370:U:H2'	1:C1:2371:G:H8	1.81	0.44
1:C1:2768:C:H2'	1:C1:2769:A:H8	1.82	0.44
9:CG:110:TYR:CD1	13:CK:132:MET:HE3	2.52	0.44
11:CI:299:GLU:HB3	11:CI:302:TRP:HB3	1.98	0.44
12:CJ:241:VAL:O	12:CJ:245:LEU:HD13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CN:18:THR:OG1	16:CN:60:GLY:HA2	2.17	0.44
16:CN:186:VAL:HG12	16:CN:218:ILE:HD11	1.99	0.44
26:CY:487:TYR:HA	26:CY:541:LEU:HD21	1.99	0.44
27:Cb:16:ASP:OD2	27:Cb:18:ALA:HB3	2.17	0.44
27:Cb:127:ARG:HA	27:Cb:267:GLN:NE2	2.32	0.44
15:LF:70:ARG:O	15:LF:74:ILE:HG12	2.18	0.44
32:LG:74:VAL:HG12	32:LG:78:ILE:HB	1.99	0.44
33:LH:156:PHE:O	33:LH:159:GLU:HG2	2.16	0.44
37:LN:142:ILE:HG22	37:LN:152:CYS:SG	2.57	0.44
38:LO:11:ASP:OD2	42:LS:169:ARG:NH2	2.50	0.44
40:LQ:158:LYS:HD3	40:LQ:162:ALA:O	2.17	0.44
49:Lc:21:ILE:HG13	49:Lc:22:LYS:N	2.32	0.44
55:Li:99:LEU:HD23	55:Li:102:ILE:HD12	1.98	0.44
57:Lk:63:PRO:HA	57:Lk:64:PRO:HD3	1.85	0.44
1:C1:316:A:H2'	1:C1:317:A:C8	2.52	0.44
1:C1:625:C:C2	1:C1:626:G:C8	3.06	0.44
1:C1:836:U:H4'	41:LR:95:TRP:NE1	2.32	0.44
1:C1:1251:U:H1'	1:C1:1254:C:H5	1.83	0.44
1:C1:1715:G:H4'	5:CC:611:GLN:OE1	2.16	0.44
1:C1:1822:C:H2'	1:C1:1823:C:C6	2.52	0.44
1:C1:2337:G:N2	1:C1:2337:G:OP2	2.48	0.44
1:C1:2468:U:H2'	1:C1:2469:U:H6	1.83	0.44
2:C2:81:U:O2	2:C2:82:U:O2'	2.35	0.44
5:CC:622:LYS:O	5:CC:623:HIS:C	2.61	0.44
7:CE:354:LYS:O	7:CE:355:MET:HE2	2.18	0.44
10:CH:450:ILE:HD13	19:CQ:89:THR:HG21	2.00	0.44
14:CL:65:LEU:O	14:CL:69:ARG:HG2	2.18	0.44
20:CR:65:THR:HG22	20:CR:72:LEU:HD12	1.98	0.44
22:CT:164:GLN:O	22:CT:168:ILE:HG12	2.17	0.44
22:CT:632:THR:HG21	26:CY:696:PHE:H	1.82	0.44
24:CV:3:ASN:OD1	24:CV:4:VAL:HG13	2.17	0.44
26:CY:729:ARG:O	26:CY:733:LYS:HG3	2.18	0.44
27:Cb:100:ASN:HA	27:Cb:103:ARG:HG2	2.00	0.44
1:C1:579:A:H8	1:C1:580:G:C8	2.36	0.44
1:C1:1602:G:H2'	1:C1:1603:G:O4'	2.17	0.44
1:C1:1674:U:O2	53:Lg:27:PRO:HB3	2.17	0.44
1:C1:2867:U:H2'	1:C1:2868:A:O4'	2.18	0.44
1:C1:3040:G:H2'	1:C1:3041:C:C6	2.52	0.44
4:CB:20:PRO:HA	4:CB:23:THR:OG1	2.18	0.44
5:CC:248:PRO:HB2	21:CS:681:TYR:HE1	1.82	0.44
6:CD:240:ILE:HB	6:CD:252:TRP:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:308:ARG:HH22	6:CD:355:SER:H	1.64	0.44
6:CD:468:TRP:HD1	6:CD:472:GLY:C	2.25	0.44
8:CF:62:ASP:OD1	8:CF:107:ARG:NH2	2.50	0.44
9:CG:20:MET:CE	9:CG:90:LEU:HD23	2.48	0.44
13:CK:247:ASN:O	13:CK:249:PRO:HD3	2.18	0.44
18:CP:367:ALA:HA	18:CP:370:PHE:HD2	1.83	0.44
18:CP:534:VAL:CG2	18:CP:581:PHE:HB3	2.47	0.44
22:CT:152:LEU:HA	22:CT:155:ILE:HG22	2.00	0.44
26:CY:734:ARG:NH1	26:CY:735:LEU:HG	2.32	0.44
27:Cb:177:LEU:HG	27:Cb:181:LYS:NZ	2.33	0.44
27:Cb:393:VAL:HA	27:Cb:419:ILE:HB	1.99	0.44
29:LB:152:ILE:HA	29:LB:156:CYS:SG	2.58	0.44
30:LC:43:MET:HG2	30:LC:243:LEU:HD11	1.98	0.44
42:LS:30:PHE:CE2	42:LS:103:VAL:HG21	2.52	0.44
45:LV:64:VAL:HG21	45:LV:71:LEU:HB3	1.99	0.44
1:C1:100:A:H2'	1:C1:101:G:N3	2.32	0.44
1:C1:1322:C:H2'	1:C1:1323:U:H6	1.81	0.44
1:C1:2356:G:H5''	1:C1:2904:A:H4'	2.00	0.44
1:C1:2480:C:H2'	1:C1:2481:A:H8	1.83	0.44
1:C1:3164:G:C6	1:C1:3206:G:C2	3.06	0.44
4:CB:78:LEU:HD22	4:CB:172:TYR:HD1	1.83	0.44
5:CC:269:MET:HE3	7:CE:538:LEU:HD13	1.99	0.44
7:CE:188:VAL:HG13	7:CE:238:ILE:HG23	2.00	0.44
8:CF:209:LEU:HD13	8:CF:216:LEU:HD13	2.00	0.44
10:CH:267:ILE:HG22	10:CH:271:LYS:HZ2	1.82	0.44
13:CK:129:GLU:OE2	13:CK:178:ARG:NH2	2.51	0.44
18:CP:344:VAL:HG21	18:CP:351:LEU:HD11	1.99	0.44
21:CS:700:GLU:OE2	37:LN:24:ARG:NE	2.49	0.44
21:CS:825:ALA:HA	21:CS:828:ARG:HG2	1.99	0.44
27:Cb:487:ARG:HH21	27:Cb:503:ASP:N	2.15	0.44
27:Cb:580:ALA:O	27:Cb:584:GLU:HG2	2.16	0.44
36:LM:129:PHE:CZ	36:LM:133:LYS:HD2	2.53	0.44
40:LQ:72:PHE:CE1	40:LQ:109:VAL:HG11	2.52	0.44
40:LQ:133:PHE:CE2	40:LQ:148:THR:HG23	2.53	0.44
41:LR:99:GLN:O	41:LR:103:ARG:HG3	2.18	0.44
43:LT:92:ARG:NH1	43:LT:94:GLU:HB2	2.32	0.44
52:Lf:16:LEU:HD11	52:Lf:33:LYS:HB2	1.99	0.44
57:Lk:19:ASP:OD1	57:Lk:19:ASP:N	2.51	0.44
1:C1:285:C:H2'	1:C1:286:A:O4'	2.18	0.44
1:C1:668:U:O4	30:LC:119:LYS:NZ	2.43	0.44
1:C1:745:U:O2	1:C1:749:C:C4	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1736:G:H2'	1:C1:1737:A:H8	1.83	0.44
1:C1:2404:G:H2'	1:C1:2405:A:C8	2.52	0.44
1:C1:2471:U:H2'	1:C1:2472:U:C6	2.52	0.44
1:C1:3185:A:H4'	29:LB:95:THR:HG22	2.00	0.44
1:C1:3210:U:O4	39:LP:181:ARG:HD3	2.17	0.44
2:C2:95:G:C5	56:Lj:79:ARG:NH1	2.83	0.44
4:CB:251:GLU:HG2	4:CB:252:PRO:HD2	2.00	0.44
5:CC:696:LYS:HG2	5:CC:718:GLU:C	2.43	0.44
6:CD:262:PRO:HG3	6:CD:287:ARG:C	2.43	0.44
9:CG:104:GLY:C	9:CG:107:PRO:HD2	2.43	0.44
9:CG:119:VAL:HG11	9:CG:122:TRP:CE2	2.53	0.44
11:CI:301:GLN:HA	11:CI:304:VAL:HG22	1.99	0.44
15:CM:23:LYS:HA	15:CM:23:LYS:HD2	1.86	0.44
21:CS:500:ASP:OD2	21:CS:502:GLU:HG3	2.18	0.44
27:Cb:264:PRO:HA	27:Cb:266:ARG:HH11	1.81	0.44
15:LF:90:VAL:HG23	15:LF:125:VAL:CG2	2.47	0.44
15:LF:92:VAL:O	15:LF:120:GLY:HA2	2.18	0.44
34:LK:85:LEU:HD11	34:LK:141:CYS:HB3	2.00	0.44
49:Lc:80:LEU:HD22	49:Lc:90:CYS:HB3	1.98	0.44
53:Lg:94:PHE:O	53:Lg:98:GLU:HG2	2.17	0.44
57:Lk:5:VAL:O	57:Lk:47:LEU:HD12	2.17	0.44
1:C1:513:A:O2'	42:LS:69:PRO:HD2	2.17	0.44
1:C1:775:G:H2'	1:C1:776:C:H6	1.82	0.44
1:C1:1187:A:H5'	1:C1:1187:A:H8	1.83	0.44
1:C1:1228:G:N2	1:C1:1246:C:HO2'	2.16	0.44
1:C1:1774:U:H5''	1:C1:1775:G:C8	2.52	0.44
1:C1:1842:G:H1	1:C1:1845:C:P	2.41	0.44
1:C1:1899:U:H2'	1:C1:1900:A:H8	1.82	0.44
1:C1:2845:A:N6	10:CH:30:THR:OG1	2.51	0.44
1:C1:3274:U:H4'	1:C1:3275:A:H5'	1.99	0.44
1:C1:3298:U:H2'	1:C1:3299:A:C8	2.53	0.44
4:CB:112:VAL:HG21	4:CB:124:ILE:HD13	2.00	0.44
6:CD:105:GLU:OE2	6:CD:486:ARG:HB2	2.18	0.44
6:CD:371:ASP:OD2	6:CD:373:ARG:HD3	2.18	0.44
7:CE:274:PHE:O	7:CE:278:MET:HG2	2.16	0.44
10:CH:84:LEU:HD22	27:Cb:603:ILE:HG13	2.00	0.44
10:CH:485:GLU:HG2	10:CH:486:GLU:N	2.33	0.44
13:CK:236:LYS:HB3	18:CP:474:ASN:ND2	2.32	0.44
26:CY:374:LYS:CA	26:CY:377:LYS:HZ1	2.31	0.44
27:Cb:101:LEU:HD21	27:Cb:146:ILE:HG23	1.99	0.44
29:LB:287:GLY:HA3	29:LB:322:TYR:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:LU:90:PHE:O	44:LU:94:MET:HG2	2.18	0.44
57:Lk:39:ARG:HH12	57:Lk:41:GLN:C	2.26	0.44
1:C1:981:C:H5''	1:C1:982:G:H5'	1.99	0.44
1:C1:1171:C:N4	1:C1:1297:U:H1'	2.32	0.44
1:C1:1201:C:N3	28:Cz:51:ARG:NH2	2.66	0.44
1:C1:1227:A:H2'	1:C1:1254:C:OP1	2.17	0.44
1:C1:2980:U:H2'	1:C1:2981:A:C8	2.53	0.44
1:C1:3014:U:H5'	1:C1:3043:A:H61	1.83	0.44
1:C1:3076:U:OP2	28:Cz:28:ASN:ND2	2.41	0.44
5:CC:402:GLU:OE1	12:CJ:193:LYS:NZ	2.48	0.44
5:CC:460:ALA:O	5:CC:468:LEU:HD12	2.18	0.44
7:CE:431:GLN:HG2	7:CE:435:PRO:HG3	1.99	0.44
9:CG:122:TRP:HH2	9:CG:163:VAL:HG11	1.81	0.44
10:CH:276:LEU:HD22	27:Cb:590:LEU:HD11	2.00	0.44
12:CJ:12:ALA:HB1	12:CJ:53:VAL:HG22	1.99	0.44
29:LB:113:GLU:HB2	29:LB:177:ALA:HB2	1.99	0.44
31:LE:99:ALA:HA	31:LE:102:VAL:HG22	1.99	0.44
32:LG:149:LYS:NZ	32:LG:176:MET:O	2.51	0.44
38:LO:63:THR:OG1	38:LO:71:GLY:HA2	2.18	0.44
46:LX:89:ILE:HG12	46:LX:95:LEU:HD23	2.00	0.44
50:Ld:20:TYR:CD2	50:Ld:83:ILE:HD12	2.52	0.44
1:C1:419:C:OP1	51:Le:16:LYS:HD3	2.18	0.43
1:C1:968:U:H2'	1:C1:969:U:C6	2.53	0.43
1:C1:1363:A:H2'	1:C1:1364:G:H8	1.83	0.43
1:C1:3021:U:H2'	1:C1:3022:G:H8	1.83	0.43
2:C2:6:U:C2	2:C2:7:U:C5	3.06	0.43
2:C2:192:C:H2'	2:C2:193:G:C8	2.52	0.43
4:CB:95:ILE:HG23	4:CB:123:LYS:HD2	2.00	0.43
5:CC:793:ALA:C	5:CC:795:GLY:H	2.25	0.43
6:CD:471:LEU:HG	6:CD:486:ARG:NH2	2.33	0.43
7:CE:293:MET:HE2	7:CE:295:PHE:CZ	2.53	0.43
9:CG:106:GLN:HB3	9:CG:107:PRO:HD3	2.00	0.43
15:CM:132:MET:O	15:CM:136:VAL:HG22	2.17	0.43
16:CN:82:GLN:O	16:CN:86:ASN:ND2	2.51	0.43
16:CN:109:VAL:HG13	16:CN:149:GLY:HA2	1.99	0.43
18:CP:320:LEU:HD13	18:CP:361:HIS:HB3	2.00	0.43
21:CS:475:MET:HE1	32:LG:55:TRP:CE3	2.53	0.43
23:CU:272:PHE:HB3	25:CX:77:VAL:HG12	1.98	0.43
30:LC:21:GLU:OE2	30:LC:263:LYS:NZ	2.47	0.43
30:LC:223:VAL:O	30:LC:226:PHE:C	2.61	0.43
51:Le:10:ILE:HA	51:Le:64:THR:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:550:C:H2'	1:C1:551:C:H6	1.83	0.43
1:C1:790:G:H2'	1:C1:791:A:C8	2.53	0.43
1:C1:1533:C:H2'	1:C1:1534:G:O4'	2.18	0.43
2:C2:41:A:O2'	56:Lj:59:THR:HG22	2.17	0.43
2:C2:74:U:C4	47:LY:73:TYR:HD1	2.36	0.43
2:C2:201:U:H2'	2:C2:202:C:C6	2.52	0.43
4:CB:50:LEU:CA	7:CE:354:LYS:HE2	2.47	0.43
8:CF:89:LEU:O	8:CF:93:THR:HG23	2.18	0.43
9:CG:128:GLU:O	9:CG:147:THR:HG23	2.18	0.43
9:CG:160:THR:C	13:CK:141:LYS:HE2	2.42	0.43
10:CH:455:ASP:OD1	19:CQ:88:LYS:HD2	2.18	0.43
12:CJ:460:TRP:CD1	12:CJ:471:LYS:HB2	2.53	0.43
13:CK:132:MET:O	13:CK:136:VAL:HG22	2.18	0.43
21:CS:729:PRO:HD2	21:CS:732:LYS:HD2	2.00	0.43
22:CT:290:PHE:HB3	22:CT:328:LEU:HA	2.00	0.43
22:CT:615:LEU:O	22:CT:619:VAL:HG23	2.18	0.43
24:CV:13:SER:HB2	24:CV:17:ASN:OD1	2.18	0.43
26:CY:393:THR:O	26:CY:397:ARG:HG2	2.18	0.43
27:Cb:135:ARG:HB2	27:Cb:456:ARG:HH22	1.82	0.43
31:LE:169:LEU:O	31:LE:173:ILE:HG13	2.17	0.43
40:LQ:126:MET:HG2	40:LQ:128:VAL:HG23	2.00	0.43
1:C1:421:U:C2	1:C1:422:G:C8	3.06	0.43
1:C1:868:G:H2'	1:C1:869:A:H8	1.84	0.43
1:C1:1285:A:H2'	1:C1:1286:A:C4	2.54	0.43
1:C1:1883:C:H41	27:Cb:251:PHE:HZ	1.66	0.43
1:C1:2077:G:H2'	1:C1:2078:G:H8	1.84	0.43
2:C2:178:U:H2'	2:C2:179:U:C6	2.53	0.43
6:CD:146:VAL:HG11	6:CD:474:PHE:CZ	2.53	0.43
7:CE:151:VAL:HB	7:CE:293:MET:HG2	2.00	0.43
7:CE:542:ALA:HB1	7:CE:547:PHE:HB2	2.01	0.43
10:CH:529:GLN:HG3	44:LU:99:TRP:CH2	2.53	0.43
18:CP:367:ALA:O	18:CP:371:LEU:HD23	2.18	0.43
25:CX:98:ARG:NH1	25:CX:102:ASN:OD1	2.52	0.43
26:CY:401:PHE:CD1	26:CY:448:SER:HB2	2.53	0.43
27:Cb:92:PHE:CE1	27:Cb:113:PRO:HB3	2.53	0.43
31:LE:57:VAL:HG11	31:LE:182:TYR:HE2	1.82	0.43
50:Ld:70:GLN:HB2	50:Ld:74:GLY:O	2.18	0.43
53:Lg:24:ILE:HG21	53:Lg:34:LEU:HD12	2.00	0.43
1:C1:254:U:O2	5:CC:275:PRO:HG3	2.18	0.43
1:C1:895:A:O2'	1:C1:896:A:H8	1.99	0.43
1:C1:975:G:H22	1:C1:1035:A:H2'	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2762:A:H2'	1:C1:2763:G:H8	1.83	0.43
1:C1:2786:G:H8	10:CH:25:GLN:OE1	2.02	0.43
1:C1:3022:G:H2'	1:C1:3023:U:C6	2.54	0.43
2:C2:7:U:H2'	2:C2:8:C:C6	2.54	0.43
6:CD:20:THR:O	6:CD:94:GLN:HA	2.18	0.43
7:CE:126:ILE:O	7:CE:129:MET:HB2	2.18	0.43
26:CY:8:LEU:HD12	26:CY:8:LEU:HA	1.79	0.43
26:CY:470:GLN:NE2	26:CY:471:LEU:HD22	2.33	0.43
29:LB:263:TRP:HD1	38:LO:65:TYR:O	2.01	0.43
30:LC:211:ILE:HD13	30:LC:226:PHE:CE2	2.53	0.43
37:LN:169:LYS:HA	37:LN:174:LEU:HD13	2.00	0.43
39:LP:125:GLN:HB2	39:LP:141:SER:OG	2.19	0.43
59:Lq:65:ILE:HG21	59:Lq:148:VAL:HG21	2.01	0.43
1:C1:481:U:H2'	1:C1:482:C:C6	2.53	0.43
1:C1:1538:C:C2	32:LG:60:ARG:NH1	2.87	0.43
1:C1:1673:U:O2'	1:C1:1674:U:H5'	2.18	0.43
1:C1:2470:U:H2'	1:C1:2471:U:H6	1.82	0.43
2:C2:224:C:H2'	2:C2:225:G:C8	2.53	0.43
7:CE:208:LYS:HB2	7:CE:208:LYS:HE2	1.78	0.43
11:CI:273:PHE:HB3	11:CI:276:ALA:HB2	2.00	0.43
12:CJ:372:PHE:CD1	12:CJ:417:HIS:HB2	2.54	0.43
13:CK:133:PHE:CE2	13:CK:148:LYS:HD2	2.53	0.43
16:CN:190:SER:OG	45:LV:130:ARG:NH2	2.51	0.43
27:Cb:590:LEU:O	27:Cb:594:ILE:HG12	2.19	0.43
30:LC:244:GLN:O	30:LC:253:ARG:HD3	2.19	0.43
15:LF:94:ARG:HD3	15:LF:116:GLN:O	2.19	0.43
15:LF:116:GLN:H	15:LF:119:ASN:ND2	2.10	0.43
33:LH:57:ILE:CG2	36:LM:6:VAL:HG22	2.49	0.43
37:LN:27:CYS:HB2	37:LN:122:ASN:HD21	1.82	0.43
38:LO:99:ALA:O	38:LO:103:ARG:HG3	2.19	0.43
39:LP:22:LEU:HD13	39:LP:90:PHE:HD2	1.84	0.43
1:C1:624:C:C2	1:C1:625:C:C5	3.06	0.43
1:C1:1055:U:H2'	1:C1:1056:U:C6	2.53	0.43
1:C1:1272:U:OP1	8:CF:8:ARG:HD3	2.19	0.43
1:C1:1599:U:H2'	1:C1:1600:G:C8	2.54	0.43
1:C1:1624:U:HO2'	1:C1:1798:U:HO2'	1.58	0.43
1:C1:2077:G:H2'	1:C1:2078:G:C8	2.53	0.43
1:C1:2340:C:H2'	1:C1:2341:U:H6	1.83	0.43
1:C1:3160:G:O4'	1:C1:3199:A:N6	2.52	0.43
2:C2:69:U:H2'	2:C2:70:G:O4'	2.18	0.43
2:C2:177:C:H2'	2:C2:178:U:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:205:G:H4'	4:CB:238:SER:HB2	2.00	0.43
4:CB:75:SER:C	4:CB:237:PRO:HG3	2.43	0.43
4:CB:223:GLU:HA	4:CB:226:LYS:HG2	2.01	0.43
5:CC:121:PHE:CE2	7:CE:472:HIS:HB3	2.53	0.43
5:CC:121:PHE:HA	7:CE:472:HIS:HD2	1.84	0.43
7:CE:454:GLY:O	7:CE:455:LYS:HE2	2.19	0.43
16:CN:223:ARG:HA	16:CN:228:ALA:CB	2.49	0.43
18:CP:232:LEU:HD22	18:CP:273:TYR:HD2	1.84	0.43
22:CT:330:LEU:HD12	22:CT:330:LEU:HA	1.90	0.43
22:CT:664:LEU:CB	22:CT:676:LEU:HD11	2.49	0.43
25:CX:113:GLN:OE1	25:CX:125:GLN:NE2	2.52	0.43
26:CY:706:ALA:HA	26:CY:709:LYS:HZ3	1.84	0.43
27:Cb:135:ARG:HB2	27:Cb:456:ARG:NH2	2.34	0.43
27:Cb:372:PHE:HB3	27:Cb:453:ARG:HH11	1.82	0.43
33:LH:126:LYS:HB3	33:LH:222:GLU:HB2	2.00	0.43
52:Lf:20:ARG:HB2	52:Lf:25:THR:HG22	1.99	0.43
1:C1:110:G:OP2	35:LL:73:ARG:NH2	2.51	0.43
1:C1:1726:G:O3'	57:Lk:46:THR:HG21	2.19	0.43
1:C1:2299:C:H2'	1:C1:2300:C:H6	1.84	0.43
1:C1:2374:G:H2'	1:C1:2375:A:C8	2.53	0.43
1:C1:2414:G:C2	1:C1:2424:G:H1'	2.53	0.43
1:C1:2738:A:H4'	1:C1:2739:U:OP1	2.17	0.43
3:CA:92:PHE:HB3	3:CA:100:LEU:HD11	2.00	0.43
5:CC:742:LEU:HD11	5:CC:779:ILE:HG13	2.01	0.43
6:CD:371:ASP:OD1	6:CD:373:ARG:NH1	2.52	0.43
6:CD:449:LYS:HB3	6:CD:451:LYS:HZ1	1.83	0.43
10:CH:342:ARG:HA	10:CH:345:GLN:HG2	2.00	0.43
12:CJ:377:GLU:CD	12:CJ:422:ARG:HG3	2.44	0.43
12:CJ:503:LEU:O	12:CJ:507:GLN:HB3	2.18	0.43
12:CJ:628:ALA:O	12:CJ:632:GLU:OE1	2.36	0.43
13:CK:174:PRO:O	13:CK:178:ARG:HG3	2.18	0.43
13:CK:218:GLY:CA	13:CK:245:ILE:O	2.67	0.43
19:CQ:34:SER:O	19:CQ:38:LYS:HG3	2.19	0.43
21:CS:476:TYR:CE1	21:CS:480:LYS:HD2	2.54	0.43
22:CT:321:VAL:HA	22:CT:324:LEU:HD12	2.01	0.43
27:Cb:432:ILE:HG22	27:Cb:433:PRO:O	2.19	0.43
29:LB:295:ALA:HB3	29:LB:304:LYS:HG3	2.00	0.43
30:LC:59:HIS:HA	30:LC:91:PHE:HE1	1.83	0.43
15:LF:67:GLU:HA	15:LF:70:ARG:HG2	2.01	0.43
36:LM:19:VAL:HG12	36:LM:29:ALA:HB2	2.00	0.43
40:LQ:91:SER:O	40:LQ:95:ILE:HG13	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:LV:47:ARG:HD3	45:LV:50:ARG:HE	1.84	0.43
52:Lf:15:HIS:HA	52:Lf:32:ILE:HD13	2.00	0.43
1:C1:462:C:H2'	1:C1:463:C:C6	2.53	0.43
1:C1:599:U:H2'	1:C1:600:G:C8	2.54	0.43
1:C1:894:A:C8	21:CS:728:ARG:HG2	2.53	0.43
1:C1:1088:G:H2'	1:C1:1089:A:H8	1.83	0.43
1:C1:1276:A:OP1	42:LS:84:ARG:NH1	2.51	0.43
1:C1:1303:G:H2'	1:C1:1304:U:H6	1.84	0.43
1:C1:1600:G:H2'	1:C1:1601:U:H6	1.84	0.43
1:C1:2902:U:H5''	1:C1:2903:G:OP1	2.18	0.43
1:C1:3103:G:H2'	1:C1:3104:A:H8	1.84	0.43
1:C1:3204:G:HO2'	1:C1:3205:C:P	2.42	0.43
2:C2:21:C:O2'	2:C2:22:U:H5'	2.19	0.43
2:C2:63:G:H22	2:C2:97:A:H2	1.66	0.43
2:C2:166:C:OP2	4:CB:213:ASN:ND2	2.43	0.43
3:CA:44:VAL:HG12	3:CA:49:ARG:HG3	2.01	0.43
3:CA:174:PRO:HG2	3:CA:175:PHE:CD2	2.54	0.43
4:CB:135:ALA:HB1	32:LG:209:GLU:HG3	2.01	0.43
6:CD:125:PRO:O	6:CD:129:TRP:HE3	2.02	0.43
6:CD:251:PHE:CE2	6:CD:327:LEU:HD21	2.53	0.43
6:CD:306:ASP:OD1	6:CD:314:TYR:OH	2.24	0.43
6:CD:308:ARG:HH22	6:CD:355:SER:N	2.17	0.43
10:CH:175:PRO:HB3	10:CH:197:ALA:O	2.18	0.43
10:CH:254:ASP:CG	10:CH:288:LYS:HD3	2.44	0.43
15:CM:25:GLN:O	15:CM:29:ARG:HG3	2.19	0.43
19:CQ:69:LEU:HD21	19:CQ:100:ARG:HH21	1.83	0.43
19:CQ:71:PHE:CD1	19:CQ:96:ILE:HD11	2.53	0.43
21:CS:504:TRP:CD2	22:CT:186:PRO:HG3	2.54	0.43
25:CX:125:GLN:O	25:CX:128:GLU:HG2	2.19	0.43
26:CY:411:GLY:HA3	26:CY:416:ARG:CZ	2.48	0.43
27:Cb:181:LYS:O	27:Cb:185:LYS:HG2	2.19	0.43
15:LF:93:ILE:HA	15:LF:120:GLY:HA2	2.01	0.43
42:LS:117:ARG:HD2	42:LS:119:ARG:HH12	1.84	0.43
44:LU:113:LYS:HE3	44:LU:113:LYS:HB3	1.79	0.43
45:LV:22:GLY:N	45:LV:38:ILE:O	2.47	0.43
45:LV:89:ARG:O	45:LV:92:GLY:N	2.52	0.43
1:C1:35:A:H2'	1:C1:36:C:H6	1.84	0.43
1:C1:529:G:C6	1:C1:543:G:N2	2.86	0.43
1:C1:1041:G:H4'	43:LT:60:LYS:HE3	2.00	0.43
1:C1:1293:G:H1'	1:C1:2343:G:OP1	2.19	0.43
1:C1:2942:C:H2'	1:C1:2943:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3001:A:H4'	29:LB:13:SER:HB2	2.01	0.43
2:C2:65:A:C4	2:C2:66:A:C8	3.07	0.43
2:C2:141:C:H1'	37:LN:112:ASN:OD1	2.19	0.43
2:C2:165:U:O2	4:CB:102:ALA:HB1	2.19	0.43
2:C2:176:G:H2'	2:C2:177:C:H6	1.84	0.43
11:CI:210:PHE:HD1	46:LX:23:ALA:HB1	1.84	0.43
12:CJ:28:LEU:HD22	12:CJ:32:ASP:HB3	2.01	0.43
12:CJ:119:PRO:HD3	12:CJ:235:MET:HE2	2.01	0.43
12:CJ:503:LEU:HA	12:CJ:506:GLN:HG2	2.00	0.43
25:CX:110:ALA:HB2	25:CX:129:ILE:HD11	2.01	0.43
26:CY:394:ASP:OD1	26:CY:394:ASP:N	2.52	0.43
27:Cb:171:GLU:OE1	27:Cb:171:GLU:N	2.33	0.43
27:Cb:277:SER:O	27:Cb:281:GLU:HG3	2.19	0.43
27:Cb:304:ASP:HB3	27:Cb:463:ARG:HA	2.01	0.43
35:LL:59:ARG:HE	35:LL:59:ARG:HB3	1.70	0.43
42:LS:27:MET:CE	42:LS:41:PHE:HA	2.48	0.43
43:LT:64:VAL:HA	43:LT:74:VAL:HA	2.00	0.43
1:C1:250:U:H2'	1:C1:251:C:C6	2.54	0.43
1:C1:490:C:H2'	1:C1:491:A:C8	2.54	0.43
1:C1:491:A:H2'	1:C1:492:U:C6	2.54	0.43
1:C1:1205:A:N7	1:C1:1268:A:C6	2.87	0.43
1:C1:1321:C:H2'	1:C1:1322:C:C6	2.54	0.43
1:C1:1668:U:H2'	1:C1:1669:C:C6	2.54	0.43
2:C2:4:C:H2'	2:C2:5:U:H6	1.84	0.43
2:C2:22:U:OP2	30:LC:198:MET:HG2	2.19	0.43
4:CB:232:LEU:HD13	4:CB:234:HIS:NE2	2.34	0.43
5:CC:375:PRO:HA	5:CC:378:ARG:NH1	2.34	0.43
5:CC:713:MET:HE2	5:CC:713:MET:HB2	1.85	0.43
7:CE:363:PHE:HB3	7:CE:415:ASP:OD1	2.18	0.43
15:CM:90:VAL:HG12	15:CM:144:TYR:HD1	1.83	0.43
22:CT:521:LEU:HD22	26:CY:645:PRO:HB3	2.01	0.43
26:CY:559:LEU:HD12	26:CY:625:LEU:HD12	2.01	0.43
27:Cb:145:VAL:HG11	27:Cb:179:VAL:HG22	2.00	0.43
27:Cb:316:GLU:HG2	27:Cb:518:VAL:HG21	2.01	0.43
27:Cb:509:LEU:HD23	27:Cb:576:PHE:CZ	2.48	0.43
30:LC:209:PRO:HG2	30:LC:232:VAL:HG22	2.01	0.43
38:LO:144:SER:HA	38:LO:147:VAL:HG22	2.01	0.43
55:Li:79:ARG:HD2	55:Li:96:CYS:SG	2.58	0.43
1:C1:707:A:C6	1:C1:764:A:H4'	2.54	0.42
1:C1:2371:G:H2'	1:C1:2372:U:H6	1.84	0.42
4:CB:257:ALA:O	4:CB:260:GLU:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:56:LEU:HD23	6:CD:56:LEU:O	2.18	0.42
7:CE:429:ILE:HG21	7:CE:445:VAL:HG21	2.01	0.42
7:CE:442:ILE:HD11	7:CE:469:PHE:HZ	1.84	0.42
18:CP:476:ASP:OD1	18:CP:478:LYS:HG2	2.18	0.42
19:CQ:83:ARG:O	19:CQ:87:GLN:HG2	2.19	0.42
22:CT:632:THR:CG2	26:CY:696:PHE:H	2.32	0.42
29:LB:47:MET:HE1	29:LB:178:HIS:HB3	2.00	0.42
30:LC:295:GLU:O	30:LC:299:VAL:HG22	2.19	0.42
15:LF:46:LYS:O	15:LF:50:ILE:HG12	2.18	0.42
32:LG:52:MET:HB3	32:LG:53:VAL:H	1.63	0.42
38:LO:8:VAL:CG1	38:LO:34:ILE:HD13	2.49	0.42
43:LT:79:ARG:HG3	43:LT:84:TYR:CE2	2.54	0.42
49:Lc:59:LEU:CD1	49:Lc:92:THR:HG21	2.49	0.42
50:Ld:32:THR:O	50:Ld:36:ARG:HG3	2.19	0.42
1:C1:261:G:H5''	37:LN:14:LYS:HE2	2.00	0.42
1:C1:1333:A:OP1	15:LF:21:LYS:HD3	2.19	0.42
1:C1:1452:U:H2'	1:C1:1453:U:C6	2.51	0.42
1:C1:1874:A:C2	27:Cb:815:LYS:HD3	2.55	0.42
1:C1:2340:C:H2'	1:C1:2341:U:C6	2.54	0.42
1:C1:2446:A:H2'	1:C1:2447:A:O4'	2.19	0.42
1:C1:2991:C:H5''	17:CO:9:ARG:HH12	1.83	0.42
1:C1:3162:A:H5''	1:C1:3163:G:C4	2.55	0.42
2:C2:145:U:H2'	2:C2:146:U:C6	2.55	0.42
5:CC:742:LEU:HD21	5:CC:776:VAL:HG11	2.01	0.42
6:CD:39:ALA:HA	6:CD:76:LEU:HD12	2.00	0.42
7:CE:182:ASN:OD1	20:CR:131:VAL:HG11	2.19	0.42
16:CN:61:ARG:HD3	16:CN:106:ASN:ND2	2.34	0.42
18:CP:368:SER:O	18:CP:372:PRO:HD3	2.19	0.42
21:CS:675:ASP:O	21:CS:679:GLU:HG3	2.19	0.42
26:CY:399:THR:O	26:CY:403:VAL:HG23	2.19	0.42
26:CY:507:SER:O	26:CY:509:HIS:N	2.52	0.42
27:Cb:13:ASN:HD21	27:Cb:428:ARG:HD3	1.84	0.42
27:Cb:259:LEU:HD21	27:Cb:286:GLY:HA3	2.01	0.42
15:LF:182:TYR:CZ	15:LF:203:GLN:HG2	2.54	0.42
35:LL:113:VAL:O	35:LL:117:LYS:HG2	2.20	0.42
42:LS:1:MET:HE3	42:LS:118:PHE:HD1	1.84	0.42
59:Lq:42:ASP:OD1	59:Lq:42:ASP:N	2.51	0.42
1:C1:213:G:C6	1:C1:1371:G:N1	2.86	0.42
1:C1:798:A:O2'	1:C1:799:C:O5'	2.29	0.42
1:C1:1188:G:H3'	1:C1:1189:G:H5''	2.01	0.42
1:C1:1727:G:OP1	57:Lk:37:LYS:HE2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:170:ASN:ND2	5:CC:223:PRO:O	2.52	0.42
5:CC:222:ASP:HA	5:CC:229:LEU:HD23	2.02	0.42
5:CC:248:PRO:HB2	21:CS:681:TYR:CE1	2.54	0.42
5:CC:370:TRP:NE1	5:CC:378:ARG:HD3	2.33	0.42
8:CF:225:GLY:HA2	8:CF:237:LEU:HD13	2.02	0.42
9:CG:170:CYS:HB3	18:CP:358:LEU:HB3	2.00	0.42
10:CH:228:LEU:O	10:CH:228:LEU:HD23	2.19	0.42
12:CJ:395:ILE:HD12	12:CJ:397:TRP:HZ3	1.85	0.42
12:CJ:419:ILE:HA	12:CJ:456:VAL:O	2.18	0.42
13:CK:149:ARG:CZ	13:CK:170:ARG:HH12	2.32	0.42
20:CR:73:LEU:HD13	35:LL:122:ARG:HH12	1.83	0.42
26:CY:530:PRO:O	26:CY:534:VAL:HG23	2.19	0.42
28:Cz:46:THR:HG22	28:Cz:47:SER:O	2.19	0.42
30:LC:25:LYS:NZ	30:LC:277:LEU:HD12	2.34	0.42
38:LO:28:LEU:HD11	38:LO:104:LEU:HB2	2.01	0.42
38:LO:124:GLN:NE2	42:LS:161:THR:O	2.53	0.42
45:LV:120:VAL:HG12	45:LV:137:VAL:O	2.19	0.42
59:Lq:58:VAL:HG21	59:Lq:149:ASN:OD1	2.18	0.42
1:C1:686:A:O5'	35:LL:68:ARG:NH1	2.53	0.42
1:C1:1365:G:H5''	30:LC:207:ARG:HD3	2.02	0.42
1:C1:1736:G:H2'	1:C1:1737:A:C8	2.54	0.42
1:C1:2746:C:H2'	1:C1:2747:U:C6	2.54	0.42
5:CC:750:PRO:HG2	5:CC:755:GLU:HB2	2.01	0.42
6:CD:43:ARG:HA	6:CD:46:LEU:HG	2.00	0.42
6:CD:80:LEU:HD21	6:CD:91:LEU:HD11	2.00	0.42
12:CJ:50:ARG:HG3	12:CJ:63:PHE:CE2	2.54	0.42
12:CJ:616:ALA:O	12:CJ:620:LEU:HD23	2.19	0.42
13:CK:186:HIS:CD2	13:CK:230:ILE:HD11	2.55	0.42
14:CL:39:ALA:O	14:CL:42:ASN:HB2	2.19	0.42
26:CY:5:LYS:HB2	26:CY:5:LYS:HE2	1.38	0.42
26:CY:579:LEU:HD23	26:CY:579:LEU:HA	1.86	0.42
27:Cb:170:ARG:O	27:Cb:174:LEU:HG	2.20	0.42
27:Cb:369:THR:HG23	27:Cb:419:ILE:HD13	2.01	0.42
29:LB:206:ILE:HG12	29:LB:323:VAL:CG2	2.49	0.42
49:Lc:51:THR:HG23	49:Lc:55:ARG:HD2	2.00	0.42
1:C1:280:C:H2'	1:C1:281:U:C6	2.54	0.42
1:C1:684:G:H2'	1:C1:685:C:C6	2.55	0.42
1:C1:773:A:H2'	1:C1:774:A:H8	1.85	0.42
1:C1:1160:G:O2'	1:C1:1310:C:H4'	2.20	0.42
1:C1:1162:G:C4	1:C1:1164:G:C8	3.08	0.42
1:C1:1509:C:H5''	53:Lg:10:ARG:HH12	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1809:G:N3	12:CJ:3:LYS:NZ	2.66	0.42
1:C1:1822:C:H2'	1:C1:1823:C:H6	1.84	0.42
1:C1:2389:U:H2'	1:C1:2390:U:C6	2.55	0.42
1:C1:2764:U:O2'	1:C1:2765:U:H5'	2.18	0.42
1:C1:2764:U:H2'	1:C1:2765:U:C6	2.54	0.42
2:C2:64:U:C2	2:C2:65:A:C8	3.08	0.42
6:CD:112:ASP:HA	6:CD:480:LYS:NZ	2.35	0.42
9:CG:109:LEU:HD11	9:CG:142:LEU:HD11	2.00	0.42
12:CJ:379:PRO:HB2	12:CJ:382:PRO:HD2	2.00	0.42
12:CJ:515:ALA:HB2	12:CJ:668:ARG:NH1	2.34	0.42
12:CJ:585:LEU:HD23	12:CJ:589:ARG:NH2	2.22	0.42
13:CK:38:ASN:O	13:CK:42:LEU:HG	2.20	0.42
14:CL:67:GLN:HA	14:CL:70:GLU:OE1	2.19	0.42
15:CM:162:VAL:HG12	15:CM:178:ASN:OD1	2.20	0.42
21:CS:487:ASP:C	21:CS:489:LYS:H	2.26	0.42
22:CT:288:LYS:HA	22:CT:291:GLN:HG2	2.02	0.42
22:CT:318:ASP:C	22:CT:320:SER:H	2.27	0.42
22:CT:372:LYS:O	22:CT:375:LYS:HB2	2.20	0.42
26:CY:432:ARG:HA	26:CY:494:GLN:NE2	2.24	0.42
27:Cb:162:ARG:HA	27:Cb:235:ILE:HA	2.01	0.42
27:Cb:447:PRO:O	27:Cb:451:VAL:HG23	2.18	0.42
28:Cz:32:TRP:HB2	33:LH:117:ILE:CD1	2.49	0.42
30:LC:164:ALA:HB2	30:LC:221:GLU:HG2	2.00	0.42
31:LE:98:ASN:O	31:LE:102:VAL:HG13	2.18	0.42
33:LH:200:ILE:O	33:LH:203:ILE:HG22	2.20	0.42
35:LL:83:ALA:HA	35:LL:117:LYS:HE3	2.01	0.42
39:LP:32:THR:HG23	39:LP:91:LEU:HD11	2.00	0.42
46:LX:149:ALA:HA	46:LX:153:LEU:HB2	2.01	0.42
59:Lq:46:ASP:OD1	59:Lq:46:ASP:N	2.49	0.42
1:C1:20:A:H2'	1:C1:21:G:C8	2.55	0.42
1:C1:171:G:H2'	1:C1:172:C:C6	2.54	0.42
1:C1:188:U:H2'	1:C1:189:G:O4'	2.20	0.42
1:C1:362:U:H2'	1:C1:363:G:O4'	2.20	0.42
1:C1:509:A:C8	30:LC:359:LYS:HE3	2.54	0.42
1:C1:771:U:C2	1:C1:772:U:C5	3.08	0.42
1:C1:926:C:H2'	1:C1:927:C:H6	1.84	0.42
1:C1:1089:A:H2'	1:C1:1090:C:C6	2.54	0.42
1:C1:1610:C:H5''	1:C1:1611:G:H5''	2.00	0.42
1:C1:2440:C:H2'	1:C1:2441:C:O4'	2.20	0.42
1:C1:3131:A:O2'	1:C1:3132:U:OP1	2.34	0.42
1:C1:3188:U:H2'	1:C1:3189:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:39:G:H1'	2:C2:104:A:N6	2.35	0.42
2:C2:203:G:H5'	11:CI:223:LYS:NZ	2.33	0.42
2:C2:219:A:H5''	11:CI:222:LYS:HE3	2.00	0.42
6:CD:23:GLU:HA	6:CD:24:PRO:HD3	1.89	0.42
6:CD:261:GLU:HA	6:CD:262:PRO:HD3	1.92	0.42
8:CF:99:THR:HG23	8:CF:99:THR:O	2.19	0.42
10:CH:21:LEU:HA	10:CH:24:THR:HG22	2.00	0.42
12:CJ:135:GLN:O	12:CJ:139:ARG:HG3	2.19	0.42
13:CK:260:LEU:HD23	23:CU:338:LYS:HB2	2.01	0.42
21:CS:654:ILE:HG23	21:CS:659:ALA:HB3	2.00	0.42
22:CT:145:TYR:HB3	22:CT:148:HIS:CE1	2.54	0.42
22:CT:367:GLN:O	22:CT:371:LEU:HD12	2.18	0.42
22:CT:371:LEU:O	22:CT:375:LYS:HG2	2.19	0.42
22:CT:525:LEU:HD23	26:CY:576:LEU:HG	2.01	0.42
22:CT:562:THR:HB	22:CT:565:VAL:HG23	2.02	0.42
26:CY:539:MET:SD	26:CY:554:LEU:HD11	2.60	0.42
26:CY:685:LYS:O	26:CY:689:GLU:OE1	2.37	0.42
27:Cb:134:ALA:HB3	27:Cb:140:LYS:HZ3	1.85	0.42
27:Cb:379:VAL:HG22	27:Cb:421:VAL:HG22	2.00	0.42
41:LR:96:MET:O	41:LR:100:ARG:HG3	2.20	0.42
1:C1:783:C:H2'	1:C1:784:C:H6	1.85	0.42
1:C1:832:C:H2'	1:C1:833:U:C6	2.55	0.42
1:C1:1490:C:H5''	1:C1:2316:C:H1'	2.02	0.42
1:C1:2418:A:H2'	1:C1:2419:G:O4'	2.20	0.42
1:C1:2768:C:H2'	1:C1:2769:A:C8	2.54	0.42
1:C1:2841:U:H2'	1:C1:2842:C:C6	2.52	0.42
1:C1:3331:A:H3'	1:C1:3332:G:H8	1.83	0.42
3:CA:173:LYS:HD3	5:CC:171:THR:HG22	2.02	0.42
3:CA:186:ASP:C	3:CA:188:LYS:H	2.27	0.42
4:CB:48:ASN:HA	7:CE:484:ASP:HB2	2.01	0.42
5:CC:447:THR:HB	5:CC:799:LEU:HB3	2.00	0.42
6:CD:108:PHE:CE1	6:CD:162:GLY:HA2	2.50	0.42
6:CD:361:GLY:HA2	6:CD:367:ILE:HD13	2.00	0.42
13:CK:220:ILE:HG21	23:CU:358:PHE:CE1	2.55	0.42
14:CL:54:GLY:O	42:LS:89:ASN:ND2	2.52	0.42
15:CM:242:ASN:O	15:CM:246:ARG:HG2	2.19	0.42
26:CY:579:LEU:HD11	26:CY:622:VAL:HG11	2.00	0.42
29:LB:234:TRP:CD1	29:LB:266:ALA:HB1	2.54	0.42
30:LC:277:LEU:HD23	30:LC:277:LEU:HA	1.87	0.42
15:LF:148:LYS:HB3	15:LF:246:ARG:NH2	2.30	0.42
36:LM:19:VAL:HG23	36:LM:65:THR:OG1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:Lh:38:LYS:HE3	54:Lh:38:LYS:HB3	1.95	0.42
59:Lq:92:LYS:HA	59:Lq:95:LYS:NZ	2.34	0.42
1:C1:65:A:C1'	1:C1:77:A:H1'	2.47	0.42
1:C1:531:U:O4	1:C1:541:G:O6	2.37	0.42
1:C1:862:C:H4'	1:C1:863:A:O5'	2.20	0.42
1:C1:1046:A:C2	1:C1:1074:C:C4	3.07	0.42
1:C1:1323:U:H2'	1:C1:1324:C:H6	1.82	0.42
1:C1:1594:C:H2'	1:C1:1595:U:H6	1.82	0.42
1:C1:1598:A:C2	1:C1:1805:C:C2	3.08	0.42
1:C1:2882:U:H2'	1:C1:2883:C:H6	1.81	0.42
1:C1:3070:A:H2'	1:C1:3071:A:O4'	2.19	0.42
1:C1:3157:C:OP1	36:LM:132:ARG:NH2	2.45	0.42
1:C1:3314:U:OP1	50:Ld:23:HIS:NE2	2.38	0.42
2:C2:224:C:H2'	2:C2:225:G:H8	1.84	0.42
4:CB:159:ILE:O	4:CB:163:LEU:HD12	2.19	0.42
8:CF:162:GLU:OE1	8:CF:179:VAL:HG13	2.19	0.42
9:CG:89:ILE:HA	9:CG:92:GLN:OE1	2.20	0.42
10:CH:426:ILE:HG13	10:CH:426:ILE:O	2.20	0.42
10:CH:429:ASN:HB3	10:CH:432:TRP:CD2	2.55	0.42
11:CI:218:VAL:HG12	11:CI:231:ALA:HB2	2.01	0.42
12:CJ:459:GLN:HG2	12:CJ:463:ASP:OD2	2.20	0.42
15:CM:54:ALA:O	15:CM:58:VAL:HG23	2.20	0.42
15:CM:174:ILE:HG13	15:CM:178:ASN:ND2	2.34	0.42
18:CP:235:LEU:O	18:CP:239:ILE:HG13	2.20	0.42
18:CP:241:ASP:O	18:CP:245:VAL:HG23	2.20	0.42
18:CP:399:ALA:HA	18:CP:402:MET:HG2	2.02	0.42
18:CP:572:ASN:ND2	27:Cb:718:TYR:CE2	2.88	0.42
21:CS:546:LYS:HD3	21:CS:547:PRO:HD2	2.01	0.42
21:CS:666:LEU:HD12	21:CS:666:LEU:HA	1.86	0.42
22:CT:428:ALA:HA	22:CT:492:LEU:HD21	2.02	0.42
27:Cb:225:LYS:HZ1	27:Cb:258:ILE:HA	1.84	0.42
28:Cz:40:ARG:HH21	28:Cz:43:LYS:HZ1	1.67	0.42
29:LB:18:PRO:O	29:LB:19:ARG:C	2.62	0.42
32:LG:246:GLN:O	32:LG:250:GLU:OE1	2.37	0.42
37:LN:96:ARG:NH2	37:LN:100:ALA:HB1	2.34	0.42
44:LU:65:ILE:HB	44:LU:69:LYS:HB2	2.02	0.42
52:Lf:39:ASP:OD1	52:Lf:39:ASP:N	2.53	0.42
1:C1:655:U:H2'	1:C1:656:U:C6	2.55	0.42
1:C1:772:U:C2	1:C1:773:A:C8	3.08	0.42
1:C1:1864:C:H3'	1:C1:1865:A:H5''	2.02	0.42
1:C1:2341:U:H2'	1:C1:2342:U:H5'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2977:U:H2'	1:C1:2990:A:N6	2.35	0.42
1:C1:2990:A:H2'	1:C1:2991:C:H6	1.84	0.42
3:CA:152:LEU:HD23	3:CA:155:ILE:HD12	2.02	0.42
4:CB:126:ARG:HG2	4:CB:150:HIS:CE1	2.55	0.42
5:CC:540:ARG:NH1	5:CC:582:LEU:HD11	2.35	0.42
10:CH:467:ARG:HA	10:CH:470:LYS:HG2	2.02	0.42
22:CT:123:GLN:H	22:CT:123:GLN:CD	2.27	0.42
23:CU:198:THR:O	23:CU:202:ARG:HG3	2.20	0.42
26:CY:635:ARG:HH21	26:CY:711:LEU:CD2	2.31	0.42
26:CY:690:ARG:HG2	26:CY:690:ARG:O	2.19	0.42
26:CY:721:TYR:CE1	26:CY:725:GLN:NE2	2.87	0.42
27:Cb:475:LEU:HD13	27:Cb:569:TRP:CZ3	2.54	0.42
30:LC:126:ALA:HB1	30:LC:245:LEU:HB3	2.02	0.42
33:LH:167:MET:HB3	33:LH:171:VAL:HG13	2.01	0.42
59:Lq:33:GLU:HA	59:Lq:168:ALA:HA	2.01	0.42
59:Lq:74:ILE:H	59:Lq:74:ILE:HD12	1.85	0.42
1:C1:159:G:H2'	1:C1:160:C:C6	2.54	0.42
1:C1:564:C:H2'	1:C1:565:C:C6	2.55	0.42
1:C1:768:G:H2'	1:C1:769:C:H6	1.84	0.42
1:C1:941:U:C4	23:CU:306:ARG:HG3	2.55	0.42
1:C1:1103:U:H2'	1:C1:1104:U:H6	1.83	0.42
1:C1:1722:G:C2	1:C1:1723:G:C8	3.08	0.42
1:C1:2549:A:H2'	1:C1:2550:G:O4'	2.20	0.42
1:C1:2846:U:OP1	10:CH:26:ARG:HD3	2.20	0.42
2:C2:201:U:H2'	2:C2:202:C:H6	1.85	0.42
6:CD:10:ALA:HA	6:CD:11:PRO:HD3	1.86	0.42
7:CE:270:LEU:HD13	7:CE:302:LYS:HB3	2.01	0.42
10:CH:233:THR:O	10:CH:237:GLN:HG3	2.20	0.42
12:CJ:189:PHE:HB3	12:CJ:196:TYR:HB2	2.01	0.42
13:CK:53:GLN:O	13:CK:57:GLN:HG3	2.20	0.42
14:CL:68:GLN:O	14:CL:71:GLU:HG3	2.20	0.42
24:CV:17:ASN:HB2	24:CV:20:LEU:HB2	2.00	0.42
26:CY:453:TRP:CZ3	26:CY:501:PHE:HZ	2.38	0.42
27:Cb:865:ASP:HB2	27:Cb:868:VAL:CG1	2.50	0.42
29:LB:79:ILE:HD12	29:LB:337:MET:SD	2.59	0.42
30:LC:83:THR:HG23	30:LC:85:ARG:H	1.85	0.42
34:LK:111:GLU:HA	34:LK:114:ARG:HG3	2.02	0.42
39:LP:64:ALA:HB1	39:LP:80:ARG:HE	1.85	0.42
40:LQ:130:ALA:HB3	40:LQ:133:PHE:CE1	2.55	0.42
45:LV:81:VAL:CG1	45:LV:120:VAL:HA	2.50	0.42
1:C1:976:U:C2	1:C1:1036:A:N7	2.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1260:A:H4'	8:CF:13:ILE:HD13	2.02	0.41
1:C1:1441:U:H2'	1:C1:1442:C:C6	2.55	0.41
1:C1:1557:C:H2'	1:C1:1558:G:C8	2.55	0.41
1:C1:1724:C:H2'	1:C1:1725:C:H6	1.85	0.41
1:C1:1776:A:H2'	1:C1:1777:A:C8	2.55	0.41
1:C1:2876:G:H2'	1:C1:2877:A:H8	1.84	0.41
2:C2:113:U:H5'	2:C2:114:G:OP1	2.20	0.41
6:CD:409:HIS:HD1	6:CD:462:LYS:HE3	1.85	0.41
7:CE:359:LYS:O	7:CE:427:ASP:HB3	2.20	0.41
8:CF:110:ALA:HA	8:CF:113:GLU:HG2	2.02	0.41
10:CH:179:LYS:HZ3	10:CH:179:LYS:HB2	1.85	0.41
10:CH:249:VAL:HG11	10:CH:277:PHE:CE2	2.54	0.41
10:CH:253:MET:HE2	10:CH:284:ILE:CG2	2.50	0.41
10:CH:361:LEU:O	10:CH:365:MET:HG2	2.20	0.41
12:CJ:376:ARG:HD2	15:CM:192:HIS:HB2	2.02	0.41
13:CK:157:VAL:HG21	13:CK:178:ARG:NE	2.35	0.41
15:CM:53:ARG:HB3	15:CM:55:GLU:OE1	2.20	0.41
15:CM:56:LYS:O	15:CM:60:GLU:OE1	2.38	0.41
15:CM:197:VAL:HG12	15:CM:201:PHE:CD1	2.55	0.41
19:CQ:73:ALA:HB3	19:CQ:75:ARG:HH12	1.84	0.41
22:CT:283:ARG:CD	22:CT:320:SER:HB3	2.49	0.41
27:Cb:243:ALA:HA	27:Cb:246:LEU:HB2	2.02	0.41
27:Cb:369:THR:CG2	27:Cb:419:ILE:HD13	2.50	0.41
35:LL:27:ASP:OD2	35:LL:31:LYS:HE2	2.19	0.41
39:LP:51:VAL:HA	39:LP:56:GLU:O	2.20	0.41
59:Lq:9:VAL:O	59:Lq:13:VAL:HG22	2.19	0.41
1:C1:174:C:N4	1:C1:230:A:H61	2.17	0.41
1:C1:332:C:OP2	30:LC:199:ARG:NH1	2.49	0.41
1:C1:661:G:O6	40:LQ:84:ARG:NH2	2.47	0.41
1:C1:818:A:N6	1:C1:837:G:H1'	2.36	0.41
1:C1:1215:G:C6	1:C1:1238:G:C6	3.08	0.41
1:C1:1260:A:H4'	8:CF:13:ILE:HG21	2.02	0.41
2:C2:19:C:C4	2:C2:20:U:C4	3.08	0.41
4:CB:50:LEU:C	7:CE:354:LYS:HE2	2.44	0.41
6:CD:220:GLU:O	6:CD:286:GLN:HA	2.20	0.41
6:CD:397:SER:HB3	6:CD:400:ASN:O	2.20	0.41
7:CE:429:ILE:HG21	7:CE:445:VAL:CG2	2.50	0.41
10:CH:461:LEU:O	10:CH:464:GLU:HG3	2.20	0.41
10:CH:518:ILE:H	10:CH:518:ILE:HG13	1.64	0.41
12:CJ:190:LEU:HD11	12:CJ:462:TRP:CE2	2.55	0.41
15:CM:187:ILE:O	15:CM:191:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CN:159:GLY:O	16:CN:181:LEU:HA	2.20	0.41
21:CS:499:VAL:HB	21:CS:503:GLU:OE2	2.20	0.41
21:CS:793:LYS:HG3	21:CS:795:THR:HG23	2.02	0.41
22:CT:318:ASP:O	22:CT:320:SER:N	2.53	0.41
26:CY:457:GLN:O	26:CY:461:TYR:N	2.51	0.41
26:CY:468:ILE:O	26:CY:471:LEU:N	2.53	0.41
26:CY:643:ALA:O	26:CY:647:ILE:HD12	2.20	0.41
26:CY:737:GLU:O	26:CY:740:ARG:HG2	2.20	0.41
27:Cb:141:THR:OG1	27:Cb:179:VAL:HG11	2.20	0.41
27:Cb:204:PHE:HE1	27:Cb:813:PHE:HB2	1.84	0.41
27:Cb:305:LEU:HD11	27:Cb:454:VAL:HB	2.02	0.41
30:LC:41:THR:O	30:LC:45:LYS:HG3	2.20	0.41
30:LC:133:ALA:CB	30:LC:149:VAL:HG21	2.45	0.41
31:LE:69:ARG:O	31:LE:90:ASN:ND2	2.53	0.41
33:LH:77:HIS:ND1	33:LH:78:ILE:HG13	2.35	0.41
37:LN:9:GLU:HB2	55:Li:53:ILE:HG13	2.02	0.41
40:LQ:96:ALA:O	40:LQ:100:LYS:HG2	2.20	0.41
40:LQ:107:THR:O	40:LQ:164:THR:HA	2.20	0.41
49:Lc:34:LEU:HD11	49:Lc:62:TYR:CZ	2.55	0.41
1:C1:7:C:H2'	1:C1:8:C:C6	2.55	0.41
1:C1:962:U:H2'	1:C1:963:C:O4'	2.20	0.41
1:C1:1479:C:H2'	1:C1:1480:A:H8	1.82	0.41
1:C1:3140:G:OP1	33:LH:60:ARG:HG3	2.19	0.41
2:C2:177:C:H2'	2:C2:178:U:C6	2.56	0.41
4:CB:58:ALA:HA	4:CB:249:ASN:HD22	1.85	0.41
5:CC:744:ILE:O	5:CC:762:VAL:HG22	2.19	0.41
6:CD:185:PHE:HA	6:CD:191:LEU:HD23	2.03	0.41
6:CD:355:SER:HB2	6:CD:373:ARG:NH1	2.33	0.41
6:CD:403:SER:HA	6:CD:416:TRP:O	2.20	0.41
7:CE:129:MET:HE1	7:CE:205:GLU:HB3	2.02	0.41
21:CS:729:PRO:HD2	21:CS:732:LYS:HB2	2.02	0.41
22:CT:662:GLU:C	26:CY:636:ASN:HD21	2.27	0.41
26:CY:499:LEU:HD13	26:CY:499:LEU:HA	1.89	0.41
26:CY:550:LEU:HD23	26:CY:554:LEU:HD23	2.02	0.41
26:CY:657:MET:HE1	26:CY:664:ASN:H	1.85	0.41
27:Cb:321:LEU:O	27:Cb:324:ILE:HG22	2.20	0.41
15:LF:14:VAL:HA	15:LF:15:PRO:HD3	1.89	0.41
15:LF:102:PRO:HB2	15:LF:105:PRO:HD2	2.01	0.41
15:LF:126:THR:HG22	15:LF:127:LYS:N	2.35	0.41
40:LQ:95:ILE:HG23	40:LQ:108:VAL:HG11	2.02	0.41
44:LU:41:LYS:O	44:LU:45:GLU:OE1	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:LX:99:VAL:O	46:LX:133:LYS:HB3	2.20	0.41
46:LX:103:ALA:HA	46:LX:107:GLN:OE1	2.20	0.41
56:Lj:15:THR:HG23	56:Lj:16:HIS:ND1	2.35	0.41
59:Lq:196:LYS:HE3	59:Lq:200:ASN:HB2	2.01	0.41
1:C1:1121:G:H2'	1:C1:1122:G:H8	1.84	0.41
1:C1:1453:U:P	41:LR:5:ARG:HH21	2.43	0.41
1:C1:1722:G:C2	1:C1:1723:G:N7	2.88	0.41
1:C1:1774:U:O3'	22:CT:368:ARG:HD2	2.19	0.41
1:C1:2291:C:O2'	1:C1:2292:C:H5'	2.21	0.41
1:C1:2869:A:H4'	1:C1:2870:G:C8	2.56	0.41
2:C2:4:C:C2	2:C2:5:U:C5	3.09	0.41
2:C2:24:G:N7	47:LY:12:ARG:NH1	2.69	0.41
2:C2:66:A:H2'	2:C2:67:U:C6	2.55	0.41
3:CA:105:SER:HB2	3:CA:112:THR:OG1	2.20	0.41
3:CA:108:PRO:HB3	7:CE:573:TYR:CE2	2.54	0.41
3:CA:195:GLU:HB2	3:CA:234:ILE:HG21	2.02	0.41
5:CC:262:PHE:HB3	55:Li:55:GLU:OE1	2.20	0.41
6:CD:108:PHE:O	6:CD:481:LYS:HA	2.21	0.41
6:CD:474:PHE:HA	6:CD:483:GLN:O	2.20	0.41
18:CP:368:SER:HB2	18:CP:576:PHE:CD2	2.56	0.41
22:CT:270:LEU:HD12	22:CT:286:LEU:HD12	2.02	0.41
22:CT:364:THR:OG1	22:CT:367:GLN:HG3	2.20	0.41
22:CT:404:VAL:O	22:CT:407:THR:HG22	2.20	0.41
22:CT:493:LEU:HD11	22:CT:507:LEU:HB3	2.01	0.41
22:CT:575:LEU:HD22	22:CT:589:LEU:HD23	2.02	0.41
22:CT:612:LEU:HD11	22:CT:676:LEU:HD23	2.02	0.41
26:CY:401:PHE:HA	26:CY:404:ILE:HG12	2.03	0.41
27:Cb:428:ARG:HG2	27:Cb:428:ARG:NH1	2.31	0.41
30:LC:27:PHE:CD1	30:LC:131:ALA:HB2	2.55	0.41
15:LF:20:LYS:O	15:LF:23:LYS:HG2	2.19	0.41
36:LM:27:LEU:HD11	36:LM:94:TRP:CG	2.55	0.41
40:LQ:110:VAL:HG12	40:LQ:167:LEU:HB2	2.02	0.41
49:Lc:17:LEU:HA	49:Lc:20:VAL:HG12	2.02	0.41
52:Lf:54:VAL:HG13	52:Lf:66:ILE:CG2	2.51	0.41
59:Lq:11:GLN:O	59:Lq:15:GLU:N	2.53	0.41
1:C1:404:G:H2'	1:C1:405:U:H6	1.85	0.41
1:C1:1438:A:C2	50:Ld:72:ILE:HD12	2.55	0.41
1:C1:1645:G:H2'	1:C1:1646:G:H8	1.85	0.41
1:C1:1877:G:H2'	1:C1:1878:G:H8	1.85	0.41
1:C1:2319:A:H2'	1:C1:2320:A:C8	2.55	0.41
1:C1:2883:C:H2'	1:C1:2884:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CB:19:ASP:HB3	4:CB:22:GLN:CD	2.45	0.41
4:CB:163:LEU:N	4:CB:164:PRO:HD2	2.35	0.41
5:CC:697:ARG:HD2	5:CC:712:THR:HB	2.01	0.41
6:CD:308:ARG:NH2	6:CD:349:THR:O	2.53	0.41
6:CD:402:TYR:O	6:CD:418:LEU:N	2.50	0.41
10:CH:529:GLN:HG3	44:LU:99:TRP:HH2	1.84	0.41
13:CK:239:TRP:CE2	18:CP:470:SER:HA	2.55	0.41
19:CQ:1:MET:SD	29:LB:359:TRP:CD1	3.14	0.41
22:CT:377:ALA:O	22:CT:381:MET:HG2	2.21	0.41
22:CT:436:GLN:HG2	22:CT:505:LEU:HD11	2.02	0.41
22:CT:556:ASN:HD22	22:CT:559:ASN:HB3	1.85	0.41
26:CY:635:ARG:NH2	26:CY:712:GLU:C	2.78	0.41
29:LB:332:VAL:HG22	29:LB:335:ARG:HE	1.85	0.41
32:LG:164:GLU:H	32:LG:164:GLU:HG3	1.54	0.41
35:LL:43:ALA:HB2	35:LL:51:VAL:HG11	2.03	0.41
57:Lk:27:LYS:NZ	57:Lk:70:ASP:OD2	2.41	0.41
59:Lq:9:VAL:HG21	59:Lq:184:MET:HE3	2.02	0.41
1:C1:155:G:H2'	1:C1:156:G:H8	1.85	0.41
1:C1:174:C:N3	1:C1:230:A:N1	2.68	0.41
1:C1:201:C:H2'	1:C1:202:A:O4'	2.20	0.41
1:C1:966:U:H2'	1:C1:967:U:H6	1.81	0.41
1:C1:1196:U:H2'	1:C1:1197:A:C8	2.56	0.41
1:C1:1442:C:H5'	50:Ld:59:LEU:O	2.20	0.41
1:C1:2288:A:H2'	1:C1:2289:U:H6	1.86	0.41
1:C1:2478:U:H2'	1:C1:2479:U:C6	2.56	0.41
5:CC:479:VAL:O	5:CC:488:VAL:HB	2.21	0.41
7:CE:268:ARG:O	7:CE:272:ILE:HG12	2.20	0.41
7:CE:278:MET:O	7:CE:282:VAL:HG22	2.21	0.41
7:CE:395:LYS:O	7:CE:399:THR:HG23	2.20	0.41
14:CL:74:ILE:O	14:CL:78:GLU:HG2	2.21	0.41
14:CL:386:THR:HA	14:CL:397:ALA:HB3	2.01	0.41
22:CT:479:SER:O	22:CT:483:LEU:HD23	2.19	0.41
26:CY:23:LEU:HD23	26:CY:26:ARG:HH12	1.86	0.41
27:Cb:133:MET:O	27:Cb:295:LEU:HD23	2.21	0.41
29:LB:115:LYS:HA	29:LB:118:PHE:CD2	2.55	0.41
29:LB:222:THR:O	29:LB:273:TYR:CA	2.67	0.41
34:LK:88:PRO:HA	34:LK:89:PRO:HD3	1.89	0.41
38:LO:115:ASP:OD1	38:LO:116:LYS:HG3	2.21	0.41
53:Lg:101:ILE:HD13	53:Lg:101:ILE:HA	1.91	0.41
57:Lk:31:THR:C	57:Lk:32:GLN:HG3	2.45	0.41
57:Lk:51:ASP:HB3	57:Lk:54:LYS:HE2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:582:A:H5'	31:LE:35:GLN:O	2.20	0.41
1:C1:787:A:H2'	1:C1:788:A:C2	2.56	0.41
1:C1:881:G:H1'	1:C1:1568:A:H62	1.85	0.41
1:C1:2421:A:N6	1:C1:2448:A:N6	2.69	0.41
2:C2:220:G:OP2	11:CI:274:LYS:NZ	2.54	0.41
5:CC:745:PHE:CE1	5:CC:761:PRO:HB3	2.56	0.41
6:CD:221:LEU:HD12	6:CD:252:TRP:CE3	2.56	0.41
6:CD:293:TRP:HB3	6:CD:295:ILE:HG23	2.02	0.41
7:CE:166:LEU:O	7:CE:170:VAL:HG23	2.21	0.41
7:CE:305:ASP:O	7:CE:309:ILE:HG23	2.21	0.41
7:CE:354:LYS:HZ2	7:CE:355:MET:HE3	1.86	0.41
10:CH:468:LEU:HD13	10:CH:473:PHE:CD2	2.56	0.41
12:CJ:584:THR:O	12:CJ:588:GLN:HB2	2.20	0.41
14:CL:55:ILE:HG12	42:LS:78:TRP:CH2	2.55	0.41
16:CN:123:ARG:O	16:CN:127:GLU:OE1	2.38	0.41
18:CP:383:ARG:HG2	18:CP:450:PHE:CD1	2.56	0.41
22:CT:450:ILE:HD11	22:CT:485:CYS:HB2	2.02	0.41
26:CY:575:LEU:O	26:CY:579:LEU:HG	2.20	0.41
29:LB:156:CYS:O	29:LB:189:VAL:HG21	2.20	0.41
29:LB:223:LYS:HB2	29:LB:332:VAL:HG13	2.01	0.41
15:LF:181:LYS:HE2	15:LF:182:TYR:CZ	2.56	0.41
43:LT:134:MET:HE3	43:LT:135:PRO:HD2	2.03	0.41
47:LY:26:ARG:HD3	47:LY:74:ARG:O	2.20	0.41
48:LZ:73:VAL:HG23	48:LZ:100:PHE:HD2	1.82	0.41
48:LZ:82:THR:HG22	48:LZ:84:TYR:HD2	1.85	0.41
50:Ld:24:LEU:O	50:Ld:28:LEU:HB2	2.21	0.41
59:Lq:128:LEU:O	59:Lq:128:LEU:HD23	2.20	0.41
1:C1:82:C:H2'	1:C1:83:C:C6	2.55	0.41
1:C1:1036:A:C5	1:C1:1037:A:C8	3.09	0.41
1:C1:1045:G:N7	1:C1:1079:G:H2'	2.35	0.41
1:C1:1120:U:H2'	1:C1:1121:G:C8	2.53	0.41
1:C1:3041:C:H2'	1:C1:3042:G:O4'	2.21	0.41
1:C1:3206:G:O2'	1:C1:3207:U:H5'	2.21	0.41
2:C2:159:C:H5''	15:CM:59:LYS:HD2	2.01	0.41
3:CA:174:PRO:HD3	5:CC:171:THR:HG21	2.01	0.41
4:CB:24:LEU:HG	4:CB:28:LYS:NZ	2.35	0.41
4:CB:292:PRO:C	4:CB:293:ILE:HG12	2.45	0.41
5:CC:121:PHE:HE2	7:CE:472:HIS:HB3	1.86	0.41
6:CD:159:ASN:ND2	6:CD:163:SER:HG	2.17	0.41
6:CD:306:ASP:OD2	6:CD:308:ARG:N	2.46	0.41
12:CJ:148:LEU:HD23	12:CJ:148:LEU:HA	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:369:ASN:C	12:CJ:370:PHE:HD1	2.28	0.41
14:CL:62:LYS:O	14:CL:66:LEU:HD23	2.20	0.41
21:CS:422:ILE:HD12	53:Lg:106:LEU:HD21	2.02	0.41
26:CY:738:GLU:O	26:CY:742:GLU:OE1	2.39	0.41
41:LR:134:HIS:CE1	41:LR:137:ALA:H	2.39	0.41
42:LS:77:ILE:HG12	42:LS:126:VAL:HG22	2.03	0.41
48:LZ:88:LEU:HD12	48:LZ:91:LEU:HD12	2.02	0.41
1:C1:179:U:H1'	47:LY:128:VAL:HG21	2.03	0.41
1:C1:300:A:C8	3:CA:244:ILE:HD13	2.55	0.41
1:C1:835:G:C4	1:C1:836:U:C5	3.09	0.41
1:C1:1087:C:H2'	1:C1:1088:G:C8	2.52	0.41
1:C1:1090:C:H2'	1:C1:1091:A:H8	1.86	0.41
1:C1:1238:G:H5'	34:LK:130:LYS:HD2	2.02	0.41
1:C1:1470:G:H5''	1:C1:1817:C:H42	1.86	0.41
1:C1:1476:U:H2'	58:Ll:17:GLN:NE2	2.36	0.41
1:C1:1897:C:H2'	1:C1:1898:G:C8	2.54	0.41
2:C2:27:U:H2'	2:C2:28:C:C6	2.55	0.41
2:C2:77:A:H2'	2:C2:78:G:C8	2.56	0.41
3:CA:112:THR:HG21	3:CA:246:GLN:HE21	1.86	0.41
4:CB:119:ASP:OD1	4:CB:119:ASP:N	2.54	0.41
4:CB:255:LEU:HA	4:CB:258:ASN:HD22	1.85	0.41
5:CC:505:ARG:NH1	5:CC:507:THR:OG1	2.54	0.41
5:CC:643:PRO:O	5:CC:644:LEU:HD23	2.21	0.41
6:CD:445:SER:O	6:CD:449:LYS:HG2	2.21	0.41
9:CG:126:CYS:H	9:CG:151:THR:HG23	1.85	0.41
10:CH:256:SER:C	10:CH:258:GLN:H	2.29	0.41
10:CH:488:ILE:CD1	19:CQ:124:ARG:HD3	2.51	0.41
12:CJ:39:TRP:O	12:CJ:130:ARG:HD2	2.21	0.41
12:CJ:382:PRO:O	12:CJ:386:ILE:HG12	2.20	0.41
16:CN:59:ILE:HG13	16:CN:60:GLY:N	2.35	0.41
18:CP:316:HIS:CD2	18:CP:319:ASP:H	2.39	0.41
22:CT:160:ILE:HD11	22:CT:163:ILE:CD1	2.50	0.41
22:CT:392:GLU:O	22:CT:396:ILE:HG12	2.21	0.41
22:CT:641:TYR:CE2	22:CT:643:PRO:HG3	2.56	0.41
26:CY:622:VAL:O	26:CY:626:LEU:HD23	2.20	0.41
27:Cb:264:PRO:HA	27:Cb:266:ARG:NH1	2.36	0.41
27:Cb:323:HIS:CD2	27:Cb:513:GLU:HG2	2.56	0.41
27:Cb:816:TRP:CD1	27:Cb:820:HIS:HE1	2.39	0.41
29:LB:332:VAL:H	29:LB:335:ARG:HE	1.69	0.41
39:LP:124:LYS:O	39:LP:126:ARG:NH1	2.54	0.41
42:LS:13:HIS:CE1	42:LS:55:THR:HB	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:LS:92:LYS:NZ	42:LS:110:MET:HE3	2.36	0.41
44:LU:101:ARG:HB3	44:LU:115:TYR:CZ	2.55	0.41
46:LX:90:GLU:HA	46:LX:146:LEU:HD21	2.03	0.41
50:Ld:37:ALA:HB3	50:Ld:38:PRO:HD3	2.03	0.41
53:Lg:63:TYR:HA	53:Lg:66:ILE:HG12	2.02	0.41
54:Lh:52:LEU:O	54:Lh:56:ILE:HG13	2.21	0.41
59:Lq:157:PHE:CD1	59:Lq:190:LEU:HD13	2.56	0.41
1:C1:618:A:H2'	1:C1:619:G:C8	2.56	0.41
1:C1:783:C:H2'	1:C1:784:C:C6	2.56	0.41
1:C1:1172:A:N3	1:C1:1172:A:H2'	2.36	0.41
1:C1:1316:C:H2'	1:C1:1317:C:H6	1.86	0.41
1:C1:1409:U:H5'	30:LC:45:LYS:HE2	2.02	0.41
1:C1:1795:A:H2'	1:C1:1796:A:H8	1.86	0.41
1:C1:2381:A:H2'	1:C1:2382:C:C6	2.55	0.41
1:C1:2436:G:O2'	1:C1:2437:G:O5'	2.37	0.41
4:CB:60:THR:HA	4:CB:61:PRO:HD3	1.87	0.41
4:CB:120:LEU:HA	4:CB:123:LYS:HB3	2.03	0.41
5:CC:186:ILE:O	5:CC:186:ILE:HG23	2.21	0.41
7:CE:537:ASP:CG	7:CE:540:LYS:HG3	2.46	0.41
19:CQ:137:LEU:HB3	19:CQ:138:ARG:H	1.50	0.41
22:CT:318:ASP:C	22:CT:319:GLU:HG3	2.46	0.41
22:CT:447:LYS:HG2	22:CT:511:PHE:CD2	2.56	0.41
24:CV:125:VAL:HG21	51:Le:115:GLN:HA	2.03	0.41
27:Cb:6:VAL:HG23	27:Cb:7:SER:N	2.36	0.41
27:Cb:92:PHE:CD2	27:Cb:105:ILE:HG12	2.56	0.41
27:Cb:103:ARG:NH2	27:Cb:107:ARG:HH12	2.19	0.41
27:Cb:194:LEU:HD21	27:Cb:207:MET:HE3	2.03	0.41
28:Cz:39:PHE:HA	33:LH:106:ARG:HH22	1.86	0.41
15:LF:229:ILE:HG13	15:LF:230:GLU:HG3	2.02	0.41
34:LK:35:LEU:H	34:LK:35:LEU:HG	1.59	0.41
37:LN:11:SER:O	37:LN:14:LYS:HG3	2.21	0.41
39:LP:47:PHE:O	39:LP:51:VAL:HG23	2.21	0.41
42:LS:152:LEU:HD13	42:LS:155:ARG:HH11	1.86	0.41
43:LT:64:VAL:HG12	43:LT:74:VAL:HG22	2.03	0.41
48:LZ:80:MET:HG3	53:Lg:91:ILE:HD12	2.03	0.41
57:Lk:5:VAL:O	57:Lk:47:LEU:HA	2.21	0.41
1:C1:24:G:H5'	56:Lj:59:THR:HG23	2.02	0.40
1:C1:178:C:O2'	47:LY:124:GLY:HA3	2.20	0.40
1:C1:373:U:H2'	1:C1:374:U:C6	2.56	0.40
1:C1:812:G:H4'	1:C1:1845:C:H42	1.86	0.40
1:C1:889:G:N2	1:C1:900:U:O2	2.45	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1599:U:OP2	12:CJ:48:ARG:HD3	2.21	0.40
1:C1:1697:A:H2'	1:C1:1698:G:H8	1.85	0.40
1:C1:2477:A:N1	1:C1:2552:C:N4	2.64	0.40
3:CA:30:ARG:NH1	23:CU:206:ASP:OD2	2.52	0.40
6:CD:151:TYR:C	6:CD:153:GLY:H	2.30	0.40
6:CD:406:SER:OG	6:CD:416:TRP:NE1	2.37	0.40
7:CE:328:THR:HG21	7:CE:443:HIS:CG	2.56	0.40
9:CG:89:ILE:HD12	9:CG:89:ILE:H	1.86	0.40
12:CJ:381:GLN:HB2	12:CJ:382:PRO:HD3	2.03	0.40
13:CK:175:MET:HE1	13:CK:178:ARG:HH11	1.86	0.40
16:CN:85:ARG:NH2	16:CN:89:PRO:O	2.54	0.40
18:CP:384:CYS:HA	18:CP:452:ARG:O	2.21	0.40
21:CS:702:LYS:HZ1	21:CS:703:HIS:CE1	2.38	0.40
22:CT:375:LYS:HD3	22:CT:378:GLN:NE2	2.35	0.40
26:CY:77:ASP:HA	26:CY:80:LYS:HE3	2.03	0.40
27:Cb:369:THR:HB	27:Cb:437:ASN:HB2	2.02	0.40
27:Cb:493:ARG:HH12	27:Cb:577:GLY:C	2.24	0.40
1:C1:59:G:H4'	1:C1:60:A:H4'	2.01	0.40
1:C1:503:G:N2	30:LC:343:GLU:OE2	2.54	0.40
1:C1:1045:G:N2	1:C1:1048:G:H21	2.17	0.40
1:C1:1208:G:H2'	1:C1:1209:C:C6	2.57	0.40
1:C1:2350:U:H4'	39:LP:80:ARG:NH1	2.35	0.40
1:C1:2722:C:H2'	1:C1:2723:C:C6	2.56	0.40
1:C1:2883:C:H2'	1:C1:2884:A:H8	1.84	0.40
1:C1:2986:A:O5'	1:C1:2986:A:H8	2.04	0.40
2:C2:8:C:H2'	2:C2:9:A:C8	2.55	0.40
6:CD:187:THR:OG1	6:CD:189:ASP:OD1	2.31	0.40
6:CD:230:TRP:CB	6:CD:302:ALA:HA	2.51	0.40
10:CH:148:TYR:O	10:CH:152:VAL:HG23	2.20	0.40
10:CH:357:ILE:HG22	10:CH:362:GLN:HG3	2.02	0.40
12:CJ:141:LEU:HA	12:CJ:144:CYS:HB3	2.02	0.40
12:CJ:237:LEU:O	12:CJ:241:VAL:HG23	2.21	0.40
14:CL:69:ARG:NH2	43:LT:156:TYR:O	2.54	0.40
16:CN:72:VAL:O	16:CN:96:ARG:HA	2.21	0.40
18:CP:377:CYS:HA	18:CP:378:PRO:HD3	1.93	0.40
25:CX:99:GLU:HG2	25:CX:135:ILE:HG22	2.02	0.40
26:CY:9:LYS:HA	26:CY:12:LYS:HE2	2.01	0.40
26:CY:559:LEU:HD21	26:CY:629:PHE:CD1	2.57	0.40
27:Cb:103:ARG:NH2	27:Cb:107:ARG:HH22	2.19	0.40
27:Cb:312:VAL:HG13	27:Cb:317:LYS:HD2	2.02	0.40
27:Cb:875:GLU:HG2	27:Cb:879:LYS:HE3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LC:30:PRO:HD2	30:LC:278:PRO:HG2	2.03	0.40
30:LC:118:GLN:HE21	30:LC:118:GLN:HB3	1.78	0.40
15:LF:46:LYS:NZ	15:LF:172:ASN:HB3	2.36	0.40
34:LK:85:LEU:O	34:LK:87:GLU:HG2	2.22	0.40
38:LO:129:LEU:HD11	42:LS:170:PRO:HG2	2.02	0.40
48:LZ:57:SER:O	48:LZ:61:ILE:HG12	2.22	0.40
48:LZ:83:ARG:NH1	53:Lg:98:GLU:OE1	2.54	0.40
54:Lh:107:GLU:H	54:Lh:107:GLU:CD	2.28	0.40
55:Li:67:ILE:HD11	55:Li:99:LEU:HD22	2.03	0.40
59:Lq:76:ARG:HH22	59:Lq:143:ASP:HA	1.85	0.40
1:C1:1231:G:C2	1:C1:1232:G:N7	2.90	0.40
1:C1:2314:A:H2'	1:C1:2315:G:H8	1.86	0.40
1:C1:2354:C:H4'	1:C1:2355:G:C2	2.57	0.40
1:C1:2396:U:OP1	1:C1:2477:A:O2'	2.27	0.40
1:C1:3297:U:HO2'	1:C1:3298:U:P	2.41	0.40
2:C2:166:C:H2'	2:C2:167:A:C8	2.54	0.40
3:CA:80:LEU:HD13	3:CA:80:LEU:HA	1.89	0.40
4:CB:156:ASP:N	4:CB:156:ASP:OD1	2.49	0.40
7:CE:300:THR:O	7:CE:304:GLU:HG2	2.20	0.40
10:CH:405:ARG:HG3	16:CN:36:SER:CB	2.52	0.40
12:CJ:497:TYR:OH	12:CJ:667:ARG:HD2	2.21	0.40
18:CP:345:PHE:O	18:CP:346:ASP:HB3	2.22	0.40
23:CU:288:LYS:HB3	23:CU:288:LYS:HE3	1.94	0.40
26:CY:507:SER:C	26:CY:509:HIS:H	2.29	0.40
26:CY:507:SER:OG	26:CY:560:ARG:NH1	2.55	0.40
27:Cb:204:PHE:HE1	27:Cb:228:MET:HE1	1.86	0.40
33:LH:157:ILE:HD13	33:LH:157:ILE:HG21	1.81	0.40
36:LM:14:VAL:HG22	42:LS:150:PHE:O	2.21	0.40
48:LZ:83:ARG:HG2	48:LZ:83:ARG:NH1	2.36	0.40
59:Lq:83:ASP:OD1	59:Lq:83:ASP:N	2.54	0.40
59:Lq:112:ALA:O	59:Lq:138:VAL:HG13	2.22	0.40
59:Lq:182:ASN:O	59:Lq:185:LEU:HG	2.21	0.40
1:C1:496:U:H2'	1:C1:497:U:O4'	2.21	0.40
1:C1:729:U:H2'	1:C1:730:C:H6	1.84	0.40
1:C1:961:U:H3'	1:C1:962:U:O4'	2.21	0.40
1:C1:1099:G:H2'	1:C1:1100:C:C6	2.57	0.40
1:C1:1437:U:HO2'	1:C1:1438:A:P	2.43	0.40
1:C1:1599:U:H2'	1:C1:1600:G:H8	1.87	0.40
1:C1:2413:G:H2'	1:C1:2414:G:C8	2.56	0.40
1:C1:2769:A:H2'	1:C1:2770:C:C6	2.56	0.40
1:C1:3138:U:O2'	42:LS:172:THR:OG1	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3183:C:H5'	1:C1:3184:G:OP2	2.21	0.40
5:CC:742:LEU:HD21	5:CC:779:ILE:HD11	2.04	0.40
10:CH:170:LEU:HD23	10:CH:218:ILE:HB	2.03	0.40
10:CH:458:LEU:O	10:CH:462:GLU:OE1	2.40	0.40
10:CH:531:GLU:HG3	10:CH:541:THR:HG21	2.04	0.40
13:CK:131:GLU:O	13:CK:135:VAL:HG23	2.21	0.40
19:CQ:175:ALA:HA	50:Ld:104:VAL:HA	2.04	0.40
21:CS:427:ALA:O	21:CS:431:ILE:HG12	2.21	0.40
22:CT:363:ARG:NH1	22:CT:371:LEU:HD22	2.35	0.40
22:CT:523:LEU:O	22:CT:529:LEU:HD21	2.21	0.40
26:CY:509:HIS:N	26:CY:509:HIS:CD2	2.90	0.40
27:Cb:135:ARG:NH1	27:Cb:138:SER:OG	2.54	0.40
30:LC:188:SER:OG	30:LC:206:ARG:HG2	2.21	0.40
41:LR:136:ARG:O	41:LR:140:GLU:OE1	2.40	0.40
51:Le:64:THR:HA	51:Le:67:MET:HE3	2.03	0.40
55:Li:62:TYR:O	55:Li:66:VAL:HG23	2.22	0.40
59:Lq:143:ASP:O	59:Lq:147:LYS:HG3	2.20	0.40
1:C1:150:G:H1'	55:Li:35:PRO:HB2	2.03	0.40
1:C1:378:A:O5'	1:C1:378:A:H8	2.03	0.40
1:C1:616:C:H2'	1:C1:617:C:H6	1.85	0.40
1:C1:641:C:H2'	1:C1:642:C:C6	2.56	0.40
1:C1:829:A:O5'	1:C1:829:A:H8	2.03	0.40
1:C1:1116:G:H4'	23:CU:317:VAL:HG11	2.03	0.40
1:C1:1179:A:H1'	14:CL:24:ILE:HD12	2.04	0.40
1:C1:1453:U:H2'	1:C1:1454:G:C8	2.57	0.40
1:C1:1697:A:H2'	1:C1:1698:G:C8	2.57	0.40
1:C1:1885:G:H22	45:LV:35:ASN:HD21	1.67	0.40
1:C1:3031:G:O2'	50:Ld:70:GLN:OE1	2.21	0.40
1:C1:3067:C:H2'	1:C1:3068:U:C6	2.56	0.40
1:C1:3164:G:O6	1:C1:3206:G:C6	2.75	0.40
2:C2:41:A:H61	2:C2:103:G:C2'	2.34	0.40
5:CC:138:ARG:HH11	5:CC:138:ARG:HG3	1.87	0.40
5:CC:529:PRO:O	6:CD:227:SER:N	2.54	0.40
5:CC:726:HIS:CD2	5:CC:781:TRP:HB3	2.56	0.40
5:CC:731:PRO:HB2	5:CC:746:HIS:HD2	1.83	0.40
6:CD:239:HIS:CE1	6:CD:251:PHE:HZ	2.39	0.40
6:CD:390:LYS:NZ	6:CD:409:HIS:CE1	2.90	0.40
7:CE:434:PRO:HA	7:CE:435:PRO:HD3	1.91	0.40
11:CI:234:GLU:HB2	11:CI:273:PHE:CE2	2.57	0.40
12:CJ:65:TYR:O	12:CJ:69:ILE:HG12	2.21	0.40
13:CK:101:ALA:O	13:CK:105:GLN:HG3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CL:223:HIS:C	14:CL:225:VAL:H	2.30	0.40
16:CN:63:THR:HG22	16:CN:72:VAL:HG12	2.04	0.40
19:CQ:149:ALA:HB2	19:CQ:159:LEU:HD22	2.02	0.40
22:CT:276:ASP:O	22:CT:280:VAL:HG22	2.22	0.40
26:CY:644:LEU:N	26:CY:645:PRO:HD2	2.36	0.40
27:Cb:444:PRO:HD3	27:Cb:453:ARG:NH2	2.35	0.40
28:Cz:75:GLU:OE2	28:Cz:79:ARG:NE	2.55	0.40
15:LF:214:SER:OG	15:LF:248:MET:O	2.37	0.40
48:LZ:62:GLU:O	48:LZ:66:LYS:HG2	2.22	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	CA	247/316 (78%)	233 (94%)	14 (6%)	0	100	100
4	CB	256/391 (66%)	241 (94%)	15 (6%)	0	100	100
5	CC	648/801 (81%)	611 (94%)	35 (5%)	2 (0%)	36	66
6	CD	450/495 (91%)	426 (95%)	24 (5%)	0	100	100
7	CE	458/598 (77%)	441 (96%)	17 (4%)	0	100	100
8	CF	243/270 (90%)	232 (96%)	11 (4%)	0	100	100
9	CG	175/184 (95%)	168 (96%)	7 (4%)	0	100	100
10	CH	538/661 (81%)	514 (96%)	23 (4%)	1 (0%)	43	72
11	CI	144/414 (35%)	134 (93%)	10 (7%)	0	100	100
12	CJ	484/679 (71%)	470 (97%)	14 (3%)	0	100	100
13	CK	234/261 (90%)	222 (95%)	11 (5%)	1 (0%)	30	60
14	CL	393/558 (70%)	362 (92%)	28 (7%)	3 (1%)	16	44
15	CM	219/249 (88%)	209 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	LF	245/249 (98%)	239 (98%)	6 (2%)	0	100	100
16	CN	244/246 (99%)	230 (94%)	14 (6%)	0	100	100
17	CO	56/120 (47%)	54 (96%)	2 (4%)	0	100	100
18	CP	354/751 (47%)	336 (95%)	17 (5%)	1 (0%)	36	66
19	CQ	173/225 (77%)	165 (95%)	7 (4%)	1 (1%)	21	51
20	CR	159/237 (67%)	157 (99%)	2 (1%)	0	100	100
21	CS	246/834 (30%)	238 (97%)	8 (3%)	0	100	100
22	CT	478/688 (70%)	460 (96%)	18 (4%)	0	100	100
23	CU	174/451 (39%)	173 (99%)	1 (1%)	0	100	100
24	CV	137/147 (93%)	133 (97%)	4 (3%)	0	100	100
25	CX	86/203 (42%)	85 (99%)	1 (1%)	0	100	100
26	CY	396/788 (50%)	365 (92%)	29 (7%)	2 (0%)	24	55
27	Cb	630/924 (68%)	604 (96%)	25 (4%)	1 (0%)	43	72
28	Cz	68/123 (55%)	66 (97%)	2 (3%)	0	100	100
29	LB	352/392 (90%)	332 (94%)	18 (5%)	2 (1%)	21	51
30	LC	360/365 (99%)	342 (95%)	18 (5%)	0	100	100
31	LE	175/200 (88%)	165 (94%)	10 (6%)	0	100	100
32	LG	200/262 (76%)	191 (96%)	9 (4%)	0	100	100
33	LH	188/192 (98%)	183 (97%)	5 (3%)	0	100	100
34	LK	141/165 (86%)	127 (90%)	13 (9%)	1 (1%)	18	47
35	LL	115/213 (54%)	107 (93%)	7 (6%)	1 (1%)	14	41
36	LM	135/142 (95%)	127 (94%)	8 (6%)	0	100	100
37	LN	179/203 (88%)	171 (96%)	8 (4%)	0	100	100
38	LO	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
39	LP	165/187 (88%)	161 (98%)	4 (2%)	0	100	100
40	LQ	127/213 (60%)	121 (95%)	6 (5%)	0	100	100
41	LR	114/2898 (4%)	114 (100%)	0	0	100	100
42	LS	172/174 (99%)	167 (97%)	5 (3%)	0	100	100
43	LT	124/160 (78%)	118 (95%)	5 (4%)	1 (1%)	16	44
44	LU	103/127 (81%)	101 (98%)	2 (2%)	0	100	100
45	LV	133/139 (96%)	128 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	LX	133/156 (85%)	129 (97%)	4 (3%)	0	100	100
47	LY	132/138 (96%)	127 (96%)	5 (4%)	0	100	100
48	LZ	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
49	Lc	96/108 (89%)	96 (100%)	0	0	100	100
50	Ld	107/120 (89%)	105 (98%)	2 (2%)	0	100	100
51	Le	125/131 (95%)	120 (96%)	5 (4%)	0	100	100
52	Lf	106/109 (97%)	103 (97%)	3 (3%)	0	100	100
53	Lg	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
54	Lh	119/935 (13%)	114 (96%)	5 (4%)	0	100	100
55	Li	86/110 (78%)	85 (99%)	1 (1%)	0	100	100
56	Lj	72/95 (76%)	70 (97%)	2 (3%)	0	100	100
57	Lk	73/81 (90%)	68 (93%)	5 (7%)	0	100	100
58	Ll	36/51 (71%)	34 (94%)	2 (6%)	0	100	100
59	Lq	205/217 (94%)	179 (87%)	26 (13%)	0	100	100
All	All	12458/20604 (60%)	11891 (95%)	550 (4%)	17 (0%)	49	77

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	CY	523	PRO
27	Cb	85	THR
26	CY	508	GLU
14	CL	224	ASP
14	CL	439	ASP
29	LB	18	PRO
29	LB	19	ARG
34	LK	159	GLU
35	LL	61	PRO
14	CL	446	ASP
18	CP	346	ASP
19	CQ	16	SER
10	CH	545	GLY
43	LT	44	VAL
5	CC	440	PRO
13	CK	122	PRO
5	CC	251	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CA	223/276 (81%)	217 (97%)	6 (3%)	39	74
4	CB	222/329 (68%)	217 (98%)	5 (2%)	44	78
5	CC	578/708 (82%)	569 (98%)	9 (2%)	55	83
6	CD	381/410 (93%)	381 (100%)	0	100	100
7	CE	398/517 (77%)	398 (100%)	0	100	100
8	CF	214/236 (91%)	214 (100%)	0	100	100
9	CG	150/155 (97%)	149 (99%)	1 (1%)	76	91
10	CH	481/575 (84%)	477 (99%)	4 (1%)	73	90
11	CI	121/336 (36%)	121 (100%)	0	100	100
12	CJ	428/579 (74%)	427 (100%)	1 (0%)	87	96
13	CK	204/225 (91%)	204 (100%)	0	100	100
14	CL	72/458 (16%)	70 (97%)	2 (3%)	38	73
15	CM	191/215 (89%)	191 (100%)	0	100	100
15	LF	213/215 (99%)	211 (99%)	2 (1%)	70	89
16	CN	206/206 (100%)	205 (100%)	1 (0%)	81	93
17	CO	48/99 (48%)	48 (100%)	0	100	100
18	CP	302/632 (48%)	300 (99%)	2 (1%)	76	91
19	CQ	150/192 (78%)	150 (100%)	0	100	100
20	CR	144/206 (70%)	143 (99%)	1 (1%)	76	91
21	CS	209/716 (29%)	209 (100%)	0	100	100
22	CT	427/600 (71%)	427 (100%)	0	100	100
23	CU	149/376 (40%)	147 (99%)	2 (1%)	61	86
24	CV	109/112 (97%)	109 (100%)	0	100	100
25	CX	76/172 (44%)	76 (100%)	0	100	100
26	CY	355/686 (52%)	349 (98%)	6 (2%)	53	83
27	Cb	540/779 (69%)	539 (100%)	1 (0%)	87	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	Cz	60/107 (56%)	60 (100%)	0	100	100
29	LB	301/331 (91%)	298 (99%)	3 (1%)	68	88
30	LC	283/285 (99%)	283 (100%)	0	100	100
31	LE	151/166 (91%)	151 (100%)	0	100	100
32	LG	175/222 (79%)	173 (99%)	2 (1%)	65	87
33	LH	167/169 (99%)	166 (99%)	1 (1%)	78	92
34	LK	120/136 (88%)	117 (98%)	3 (2%)	42	76
35	LL	99/176 (56%)	99 (100%)	0	100	100
36	LM	115/117 (98%)	115 (100%)	0	100	100
37	LN	164/180 (91%)	160 (98%)	4 (2%)	43	77
38	LO	163/163 (100%)	161 (99%)	2 (1%)	63	87
39	LP	137/152 (90%)	137 (100%)	0	100	100
40	LQ	110/178 (62%)	110 (100%)	0	100	100
41	LR	104/2396 (4%)	104 (100%)	0	100	100
42	LS	154/154 (100%)	154 (100%)	0	100	100
43	LT	109/135 (81%)	109 (100%)	0	100	100
44	LU	93/108 (86%)	93 (100%)	0	100	100
45	LV	99/102 (97%)	99 (100%)	0	100	100
46	LX	114/129 (88%)	114 (100%)	0	100	100
47	LY	117/119 (98%)	117 (100%)	0	100	100
48	LZ	121/121 (100%)	121 (100%)	0	100	100
49	Lc	79/88 (90%)	79 (100%)	0	100	100
50	Ld	95/105 (90%)	95 (100%)	0	100	100
51	Le	110/114 (96%)	110 (100%)	0	100	100
52	Lf	89/90 (99%)	89 (100%)	0	100	100
53	Lg	101/102 (99%)	100 (99%)	1 (1%)	68	88
54	Lh	108/781 (14%)	108 (100%)	0	100	100
55	Li	75/93 (81%)	74 (99%)	1 (1%)	61	86
56	Lj	61/78 (78%)	60 (98%)	1 (2%)	55	83
57	Lk	71/76 (93%)	71 (100%)	0	100	100
58	Ll	34/46 (74%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	Lq	179/189 (95%)	176 (98%)	3 (2%)	53	83
All	All	10549/17418 (61%)	10485 (99%)	64 (1%)	76	92

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	CA	80	LEU
3	CA	83	LEU
3	CA	88	ASN
3	CA	107	VAL
3	CA	112	THR
3	CA	140	LEU
4	CB	68	THR
4	CB	278	VAL
4	CB	281	PHE
4	CB	293	ILE
4	CB	295	GLN
5	CC	154	ILE
5	CC	428	LEU
5	CC	429	LEU
5	CC	431	LYS
5	CC	434	SER
5	CC	438	LEU
5	CC	439	LYS
5	CC	615	VAL
5	CC	730	LEU
9	CG	40	MET
10	CH	53	GLN
10	CH	509	ARG
10	CH	518	ILE
10	CH	544	ILE
12	CJ	644	LYS
14	CL	18	THR
14	CL	20	LEU
16	CN	216	SER
18	CP	303	PRO
18	CP	402	MET
20	CR	184	VAL
23	CU	203	ILE
23	CU	205	LEU
26	CY	5	LYS
26	CY	9	LYS

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Mol	Chain	Res	Type
26	CY	423	SER
26	CY	499	LEU
26	CY	506	LEU
26	CY	530	PRO
27	Cb	210	ASN
29	LB	14	LEU
29	LB	17	LEU
29	LB	213	ASP
15	LF	107	LYS
15	LF	222	PRO
32	LG	183	ILE
32	LG	184	LYS
33	LH	179	GLN
34	LK	32	ILE
34	LK	35	LEU
34	LK	37	LEU
37	LN	41	ARG
37	LN	60	VAL
37	LN	61	ILE
37	LN	64	VAL
38	LO	34	ILE
38	LO	102	GLU
53	Lg	56	PRO
55	Li	75	ASP
56	Lj	20	ARG
59	Lq	15	GLU
59	Lq	16	LEU
59	Lq	17	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (128) such sidechains are listed below:

Mol	Chain	Res	Type
3	CA	48	HIS
3	CA	109	ASN
3	CA	119	ASN
3	CA	161	HIS
3	CA	167	GLN
3	CA	246	GLN
4	CB	87	HIS
4	CB	105	GLN
4	CB	240	ASN
4	CB	280	ASN

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Mol	Chain	Res	Type
5	CC	166	ASN
5	CC	191	ASN
5	CC	244	GLN
5	CC	426	ASN
5	CC	500	ASN
5	CC	528	HIS
5	CC	618	HIS
5	CC	662	GLN
5	CC	753	GLN
6	CD	331	GLN
6	CD	409	HIS
6	CD	483	GLN
6	CD	485	ASN
7	CE	257	ASN
7	CE	388	HIS
7	CE	394	GLN
7	CE	472	HIS
7	CE	494	GLN
8	CF	58	HIS
8	CF	121	GLN
9	CG	41	GLN
9	CG	106	GLN
9	CG	118	HIS
10	CH	53	GLN
10	CH	126	GLN
10	CH	176	ASN
10	CH	232	ASN
10	CH	332	ASN
10	CH	411	ASN
11	CI	185	GLN
11	CI	201	HIS
11	CI	256	HIS
13	CK	4	ASN
13	CK	186	HIS
13	CK	244	GLN
14	CL	42	ASN
15	CM	119	ASN
16	CN	82	GLN
16	CN	86	ASN
17	CO	14	HIS
18	CP	265	GLN
18	CP	437	ASN

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Mol	Chain	Res	Type
18	CP	487	GLN
19	CQ	130	ASN
20	CR	136	GLN
20	CR	137	GLN
20	CR	220	GLN
22	CT	141	ASN
22	CT	148	HIS
22	CT	215	HIS
22	CT	251	ASN
22	CT	378	GLN
22	CT	622	HIS
22	CT	667	HIS
23	CU	204	GLN
23	CU	245	ASN
23	CU	336	GLN
24	CV	38	GLN
24	CV	48	ASN
26	CY	497	HIS
26	CY	509	HIS
26	CY	615	GLN
27	Cb	175	GLN
27	Cb	203	GLN
27	Cb	437	ASN
27	Cb	446	GLN
27	Cb	571	GLN
27	Cb	820	HIS
28	Cz	28	ASN
29	LB	280	ASN
29	LB	281	HIS
30	LC	60	GLN
30	LC	88	GLN
30	LC	111	HIS
30	LC	284	GLN
30	LC	297	GLN
31	LE	25	GLN
31	LE	53	GLN
15	LF	9	GLN
15	LF	82	HIS
15	LF	118	ASN
15	LF	178	ASN
32	LG	62	GLN
32	LG	64	GLN

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Mol	Chain	Res	Type
32	LG	141	HIS
32	LG	212	ASN
33	LH	113	ASN
33	LH	179	GLN
34	LK	14	HIS
34	LK	65	GLN
37	LN	156	HIS
39	LP	34	GLN
39	LP	118	GLN
40	LQ	101	ASN
40	LQ	103	ASN
40	LQ	122	GLN
41	LR	141	HIS
42	LS	5	GLN
43	LT	45	ASN
43	LT	131	GLN
43	LT	146	ASN
44	LU	44	ASN
46	LX	32	HIS
46	LX	107	GLN
50	Ld	64	ASN
51	Le	41	ASN
51	Le	90	ASN
52	Lf	15	HIS
52	Lf	24	ASN
53	Lg	15	ASN
53	Lg	84	ASN
54	Lh	50	HIS
54	Lh	67	GLN
57	Lk	60	GLN
58	Ll	19	GLN
58	Ll	20	ASN
59	Lq	40	ASN
59	Lq	200	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2640/3341 (79%)	537 (20%)	36 (1%)
2	C2	254/319 (79%)	52 (20%)	1 (0%)
All	All	2894/3660 (79%)	589 (20%)	37 (1%)

All (589) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	14	U
1	C1	22	G
1	C1	26	A
1	C1	41	G
1	C1	49	A
1	C1	59	G
1	C1	60	A
1	C1	65	A
1	C1	66	A
1	C1	73	A
1	C1	92	G
1	C1	93	C
1	C1	94	G
1	C1	96	G
1	C1	105	C
1	C1	109	A
1	C1	110	G
1	C1	116	A
1	C1	122	A
1	C1	128	G
1	C1	129	C
1	C1	131	U
1	C1	132	C
1	C1	133	G
1	C1	134	G
1	C1	135	C
1	C1	136	C
1	C1	138	G
1	C1	143	G
1	C1	150	G
1	C1	151	G
1	C1	152	A
1	C1	156	G
1	C1	163	U
1	C1	176	U
1	C1	180	G
1	C1	183	U
1	C1	193	C
1	C1	203	C
1	C1	206	A
1	C1	211	G
1	C1	212	A

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Mol	Chain	Res	Type
1	C1	224	A
1	C1	225	G
1	C1	232	G
1	C1	239	C
1	C1	240	U
1	C1	244	U
1	C1	253	U
1	C1	258	C
1	C1	261	G
1	C1	262	U
1	C1	275	G
1	C1	276	A
1	C1	277	A
1	C1	287	A
1	C1	290	U
1	C1	300	A
1	C1	302	U
1	C1	309	A
1	C1	310	A
1	C1	315	A
1	C1	321	C
1	C1	325	C
1	C1	329	G
1	C1	331	C
1	C1	342	C
1	C1	343	A
1	C1	368	G
1	C1	390	U
1	C1	393	C
1	C1	394	A
1	C1	395	C
1	C1	412	G
1	C1	413	G
1	C1	414	A
1	C1	433	U
1	C1	434	G
1	C1	439	C
1	C1	443	G
1	C1	445	A
1	C1	446	U
1	C1	447	C
1	C1	456	U

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Mol	Chain	Res	Type
1	C1	457	U
1	C1	458	C
1	C1	459	U
1	C1	463	C
1	C1	467	G
1	C1	468	C
1	C1	469	A
1	C1	470	C
1	C1	471	U
1	C1	474	G
1	C1	477	G
1	C1	485	G
1	C1	508	G
1	C1	509	A
1	C1	511	A
1	C1	513	A
1	C1	526	G
1	C1	527	U
1	C1	534	U
1	C1	535	C
1	C1	544	U
1	C1	546	A
1	C1	548	A
1	C1	582	A
1	C1	587	G
1	C1	590	C
1	C1	591	U
1	C1	592	G
1	C1	594	A
1	C1	596	G
1	C1	598	A
1	C1	607	U
1	C1	608	A
1	C1	609	A
1	C1	623	C
1	C1	624	C
1	C1	663	G
1	C1	664	A
1	C1	668	U
1	C1	678	A
1	C1	718	U
1	C1	719	C

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Mol	Chain	Res	Type
1	C1	723	G
1	C1	731	G
1	C1	739	C
1	C1	742	A
1	C1	744	G
1	C1	748	U
1	C1	749	C
1	C1	751	G
1	C1	752	A
1	C1	755	G
1	C1	757	U
1	C1	758	U
1	C1	761	A
1	C1	762	G
1	C1	765	G
1	C1	767	A
1	C1	787	A
1	C1	798	A
1	C1	799	C
1	C1	800	U
1	C1	801	A
1	C1	803	G
1	C1	811	A
1	C1	828	A
1	C1	835	G
1	C1	836	U
1	C1	838	G
1	C1	841	G
1	C1	842	C
1	C1	846	C
1	C1	858	C
1	C1	862	C
1	C1	863	A
1	C1	871	C
1	C1	877	A
1	C1	878	U
1	C1	887	G
1	C1	889	G
1	C1	896	A
1	C1	898	A
1	C1	925	A
1	C1	932	A

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Mol	Chain	Res	Type
1	C1	933	A
1	C1	934	G
1	C1	941	U
1	C1	942	C
1	C1	943	A
1	C1	944	G
1	C1	960	C
1	C1	964	A
1	C1	974	G
1	C1	975	G
1	C1	976	U
1	C1	982	G
1	C1	983	A
1	C1	1031	C
1	C1	1033	U
1	C1	1039	A
1	C1	1046	A
1	C1	1047	A
1	C1	1048	G
1	C1	1049	C
1	C1	1050	C
1	C1	1054	G
1	C1	1057	A
1	C1	1058	C
1	C1	1063	C
1	C1	1064	U
1	C1	1065	G
1	C1	1073	G
1	C1	1074	C
1	C1	1079	G
1	C1	1080	A
1	C1	1085	A
1	C1	1086	U
1	C1	1095	G
1	C1	1097	G
1	C1	1098	G
1	C1	1117	A
1	C1	1124	G
1	C1	1125	A
1	C1	1126	U
1	C1	1135	A
1	C1	1141	A

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Mol	Chain	Res	Type
1	C1	1142	C
1	C1	1143	G
1	C1	1157	C
1	C1	1158	C
1	C1	1159	G
1	C1	1163	U
1	C1	1164	G
1	C1	1172	A
1	C1	1174	C
1	C1	1175	A
1	C1	1178	C
1	C1	1179	A
1	C1	1180	C
1	C1	1186	A
1	C1	1187	A
1	C1	1189	G
1	C1	1190	C
1	C1	1191	G
1	C1	1203	U
1	C1	1204	G
1	C1	1218	G
1	C1	1227	A
1	C1	1228	G
1	C1	1234	A
1	C1	1240	U
1	C1	1245	A
1	C1	1247	U
1	C1	1254	C
1	C1	1268	A
1	C1	1269	A
1	C1	1271	G
1	C1	1272	U
1	C1	1286	A
1	C1	1287	U
1	C1	1289	G
1	C1	1291	U
1	C1	1295	G
1	C1	1312	A
1	C1	1314	A
1	C1	1330	A
1	C1	1331	G
1	C1	1332	A

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Mol	Chain	Res	Type
1	C1	1333	A
1	C1	1334	A
1	C1	1335	C
1	C1	1336	G
1	C1	1337	A
1	C1	1368	A
1	C1	1381	A
1	C1	1400	A
1	C1	1401	A
1	C1	1416	G
1	C1	1419	C
1	C1	1434	A
1	C1	1437	U
1	C1	1438	A
1	C1	1457	G
1	C1	1463	A
1	C1	1465	G
1	C1	1466	U
1	C1	1470	G
1	C1	1489	G
1	C1	1490	C
1	C1	1535	U
1	C1	1537	U
1	C1	1538	C
1	C1	1541	A
1	C1	1548	C
1	C1	1549	U
1	C1	1551	G
1	C1	1552	U
1	C1	1553	G
1	C1	1556	C
1	C1	1560	G
1	C1	1561	U
1	C1	1562	G
1	C1	1566	A
1	C1	1568	A
1	C1	1575	C
1	C1	1584	A
1	C1	1607	U
1	C1	1608	U
1	C1	1609	G
1	C1	1610	C

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Mol	Chain	Res	Type
1	C1	1618	C
1	C1	1621	A
1	C1	1622	A
1	C1	1623	C
1	C1	1624	U
1	C1	1637	G
1	C1	1662	C
1	C1	1693	A
1	C1	1695	A
1	C1	1696	C
1	C1	1709	G
1	C1	1715	G
1	C1	1722	G
1	C1	1729	A
1	C1	1730	G
1	C1	1741	U
1	C1	1742	U
1	C1	1744	U
1	C1	1749	G
1	C1	1759	G
1	C1	1760	C
1	C1	1774	U
1	C1	1775	G
1	C1	1776	A
1	C1	1791	G
1	C1	1794	U
1	C1	1795	A
1	C1	1798	U
1	C1	1800	U
1	C1	1813	U
1	C1	1819	U
1	C1	1820	A
1	C1	1821	A
1	C1	1822	C
1	C1	1825	C
1	C1	1828	C
1	C1	1829	A
1	C1	1837	A
1	C1	1842	G
1	C1	1843	A
1	C1	1845	C
1	C1	1857	G

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Mol	Chain	Res	Type
1	C1	1858	A
1	C1	1859	U
1	C1	1861	G
1	C1	1864	C
1	C1	1865	A
1	C1	1866	A
1	C1	1867	U
1	C1	1874	A
1	C1	1875	A
1	C1	1883	C
1	C1	1886	C
1	C1	1897	C
1	C1	1900	A
1	C1	1901	A
1	C1	2075	A
1	C1	2088	A
1	C1	2287	G
1	C1	2288	A
1	C1	2292	C
1	C1	2294	A
1	C1	2297	G
1	C1	2302	U
1	C1	2310	A
1	C1	2311	U
1	C1	2325	A
1	C1	2327	C
1	C1	2332	G
1	C1	2335	A
1	C1	2338	G
1	C1	2339	G
1	C1	2342	U
1	C1	2343	G
1	C1	2347	A
1	C1	2355	G
1	C1	2356	G
1	C1	2359	A
1	C1	2361	A
1	C1	2362	G
1	C1	2363	A
1	C1	2364	A
1	C1	2396	U
1	C1	2397	G

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Mol	Chain	Res	Type
1	C1	2399	G
1	C1	2407	A
1	C1	2409	A
1	C1	2414	G
1	C1	2415	U
1	C1	2419	G
1	C1	2422	U
1	C1	2424	G
1	C1	2425	G
1	C1	2428	G
1	C1	2430	A
1	C1	2432	C
1	C1	2433	U
1	C1	2434	U
1	C1	2435	C
1	C1	2436	G
1	C1	2437	G
1	C1	2438	C
1	C1	2439	G
1	C1	2443	G
1	C1	2444	U
1	C1	2449	U
1	C1	2453	A
1	C1	2456	A
1	C1	2464	U
1	C1	2465	G
1	C1	2467	U
1	C1	2484	G
1	C1	2551	A
1	C1	2560	G
1	C1	2564	G
1	C1	2730	C
1	C1	2738	A
1	C1	2740	U
1	C1	2749	G
1	C1	2758	G
1	C1	2759	A
1	C1	2760	A
1	C1	2761	A
1	C1	2767	C
1	C1	2775	A
1	C1	2777	A

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Mol	Chain	Res	Type
1	C1	2778	A
1	C1	2782	G
1	C1	2783	C
1	C1	2784	U
1	C1	2786	G
1	C1	2806	G
1	C1	2818	U
1	C1	2819	U
1	C1	2820	U
1	C1	2845	A
1	C1	2846	U
1	C1	2847	C
1	C1	2856	G
1	C1	2857	C
1	C1	2862	U
1	C1	2869	A
1	C1	2874	U
1	C1	2875	G
1	C1	2876	G
1	C1	2889	C
1	C1	2893	U
1	C1	2894	A
1	C1	2899	A
1	C1	2902	U
1	C1	2917	C
1	C1	2925	A
1	C1	2926	G
1	C1	2936	U
1	C1	2942	C
1	C1	2948	G
1	C1	2954	C
1	C1	2955	U
1	C1	2956	C
1	C1	2969	A
1	C1	3005	A
1	C1	3006	A
1	C1	3016	G
1	C1	3035	G
1	C1	3043	A
1	C1	3049	C
1	C1	3050	C
1	C1	3070	A

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Mol	Chain	Res	Type
1	C1	3074	C
1	C1	3079	A
1	C1	3084	A
1	C1	3086	A
1	C1	3087	A
1	C1	3088	U
1	C1	3098	A
1	C1	3099	A
1	C1	3100	C
1	C1	3101	G
1	C1	3111	U
1	C1	3112	A
1	C1	3113	C
1	C1	3117	C
1	C1	3118	A
1	C1	3119	C
1	C1	3121	U
1	C1	3122	U
1	C1	3124	U
1	C1	3125	A
1	C1	3126	G
1	C1	3127	A
1	C1	3130	U
1	C1	3131	A
1	C1	3132	U
1	C1	3134	A
1	C1	3139	A
1	C1	3140	G
1	C1	3145	C
1	C1	3146	G
1	C1	3147	G
1	C1	3153	U
1	C1	3154	A
1	C1	3161	C
1	C1	3162	A
1	C1	3163	G
1	C1	3170	C
1	C1	3171	C
1	C1	3178	G
1	C1	3181	C
1	C1	3183	C
1	C1	3185	A

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Mol	Chain	Res	Type
1	C1	3188	U
1	C1	3199	A
1	C1	3205	C
1	C1	3210	U
1	C1	3213	A
1	C1	3217	U
1	C1	3226	G
1	C1	3228	G
1	C1	3229	G
1	C1	3230	G
1	C1	3244	C
1	C1	3253	U
1	C1	3256	A
1	C1	3258	G
1	C1	3259	U
1	C1	3280	G
1	C1	3281	U
1	C1	3282	A
1	C1	3285	G
1	C1	3291	U
1	C1	3293	G
1	C1	3295	U
1	C1	3298	U
1	C1	3309	G
1	C1	3315	A
1	C1	3318	C
1	C1	3322	C
1	C1	3323	C
1	C1	3324	U
1	C1	3330	U
1	C1	3331	A
1	C1	3332	G
1	C1	3333	A
2	C2	34	U
2	C2	35	C
2	C2	59	A
2	C2	62	A
2	C2	63	G
2	C2	81	U
2	C2	82	U
2	C2	84	C
2	C2	87	G

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Mol	Chain	Res	Type
2	C2	90	U
2	C2	95	G
2	C2	97	A
2	C2	103	G
2	C2	104	A
2	C2	106	C
2	C2	109	A
2	C2	110	C
2	C2	111	A
2	C2	112	U
2	C2	113	U
2	C2	114	G
2	C2	125	U
2	C2	148	G
2	C2	157	U
2	C2	158	U
2	C2	159	C
2	C2	163	C
2	C2	165	U
2	C2	166	C
2	C2	167	A
2	C2	170	C
2	C2	173	U
2	C2	175	G
2	C2	180	G
2	C2	181	U
2	C2	183	U
2	C2	189	A
2	C2	195	G
2	C2	196	G
2	C2	212	G
2	C2	213	A
2	C2	214	A
2	C2	215	A
2	C2	219	A
2	C2	221	U
2	C2	222	G
2	C2	289	G
2	C2	291	G
2	C2	292	C
2	C2	294	A
2	C2	295	G

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Mol	Chain	Res	Type
2	C2	300	A

All (37) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	150	G
1	C1	241	G
1	C1	467	G
1	C1	468	C
1	C1	526	G
1	C1	590	C
1	C1	835	G
1	C1	862	C
1	C1	870	U
1	C1	886	U
1	C1	897	G
1	C1	1063	C
1	C1	1085	A
1	C1	1124	G
1	C1	1142	C
1	C1	1475	G
1	C1	1584	A
1	C1	1820	A
1	C1	2301	C
1	C1	2333	G
1	C1	2360	A
1	C1	2777	A
1	C1	2817	U
1	C1	2898	A
1	C1	2925	A
1	C1	3005	A
1	C1	3078	U
1	C1	3124	U
1	C1	3125	A
1	C1	3131	A
1	C1	3162	A
1	C1	3204	G
1	C1	3209	U
1	C1	3229	G
1	C1	3257	U
1	C1	3297	U
2	C2	102	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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
5	TPO	CC	163	5	8,10,11	0.68	0	10,14,16	1.04	1 (10%)
5	SEP	CC	160	5	8,9,10	0.64	0	7,12,14	0.73	0

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
5	TPO	CC	163	5	-	1/9/11/13	-
5	SEP	CC	160	5	-	0/6/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CC	163	TPO	O-C-CA	-2.56	118.19	124.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	CC	163	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	CC	163	TPO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
60	GTP	CH	1001	-	33,34,34	0.52	0	50,54,54	0.69	0

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
60	GTP	CH	1001	-	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

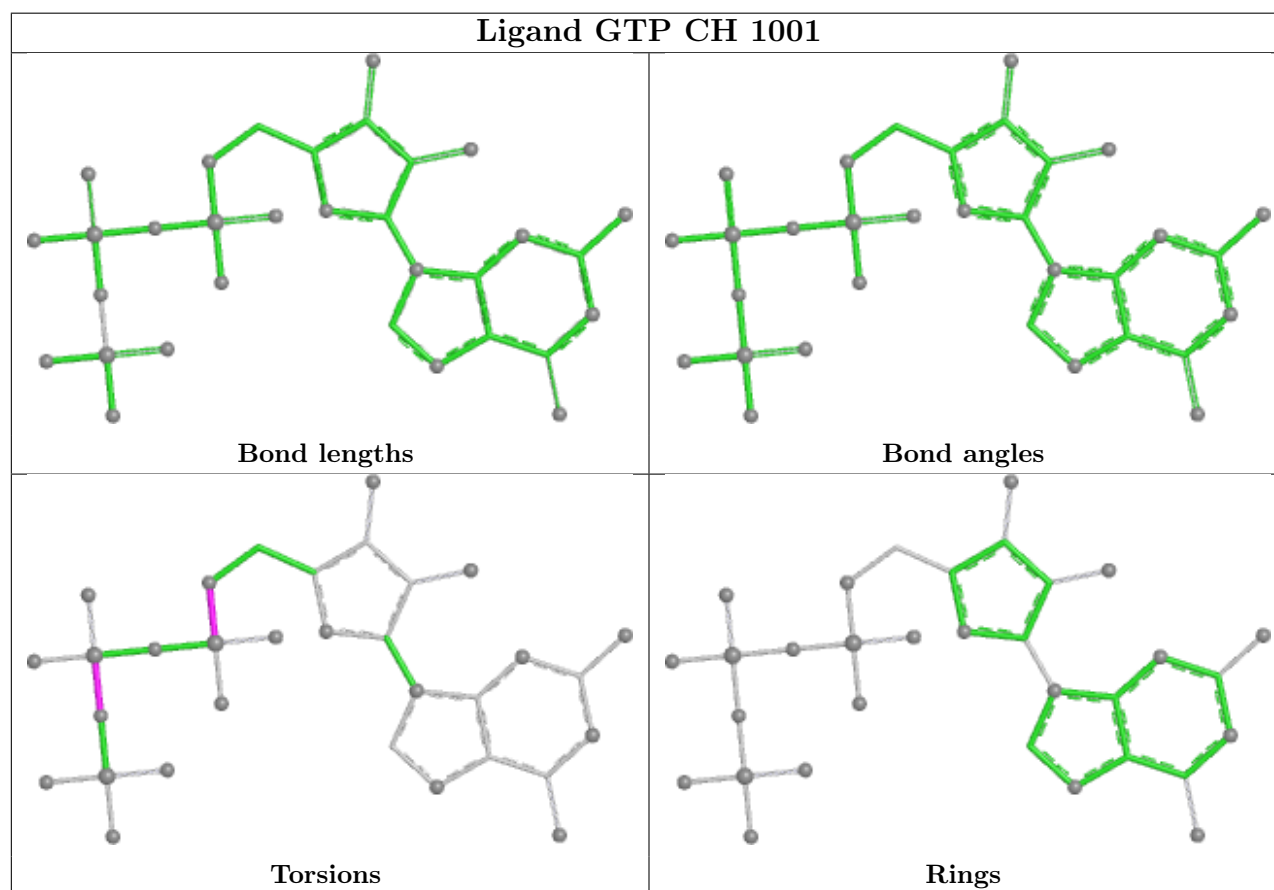
Mol	Chain	Res	Type	Atoms
60	CH	1001	GTP	PG-O3B-PB-O1B
60	CH	1001	GTP	C5'-O5'-PA-O1A
60	CH	1001	GTP	PG-O3B-PB-O2B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	CH	1001	GTP	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

There are no chain breaks in this entry.

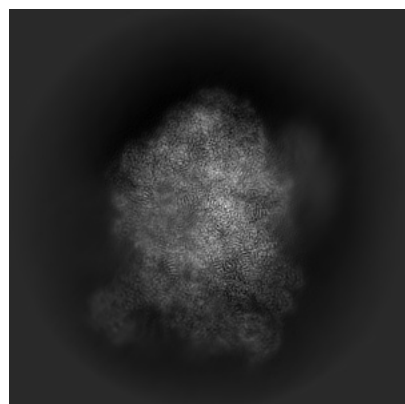
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35287. These allow visual inspection of the internal detail of the map and identification of artifacts.

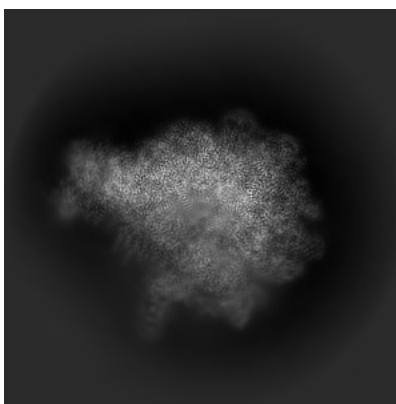
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

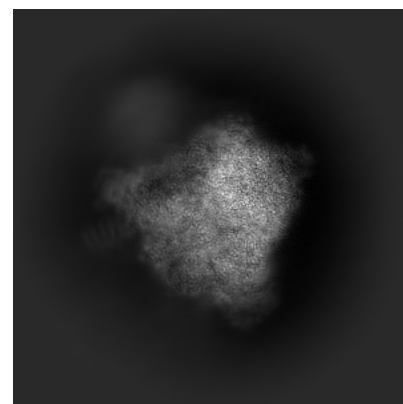
6.1.1 Primary map



X

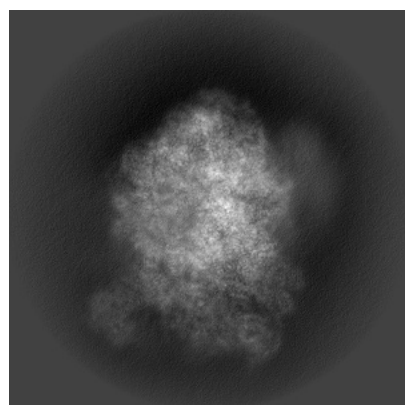


Y

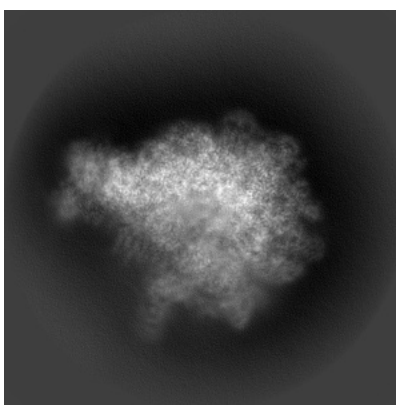


Z

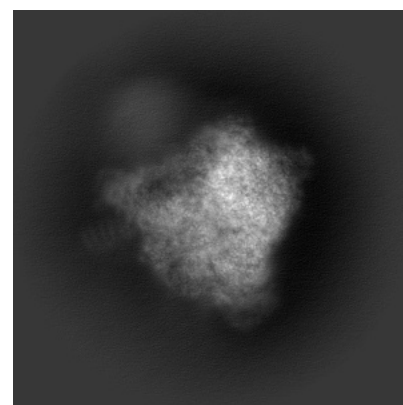
6.1.2 Raw map



X



Y

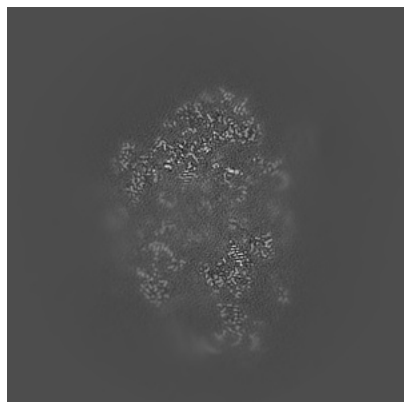


Z

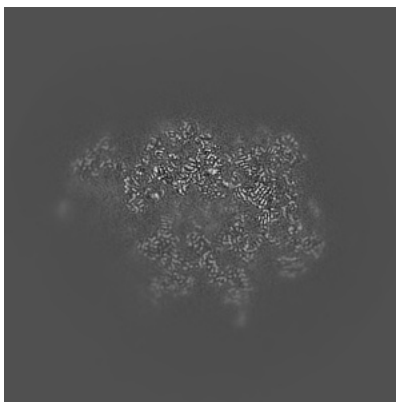
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

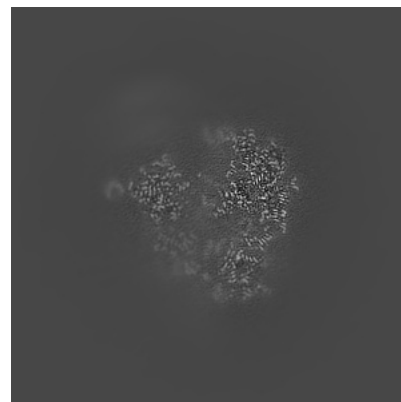
6.2.1 Primary map



X Index: 210

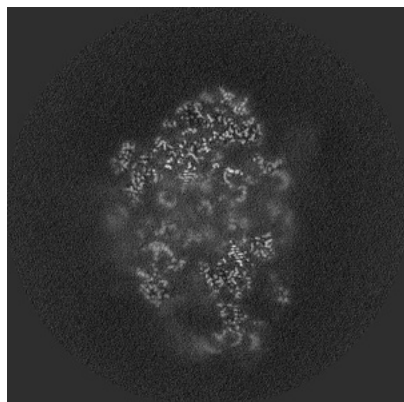


Y Index: 210

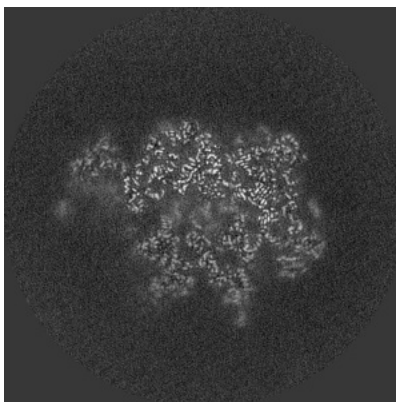


Z Index: 210

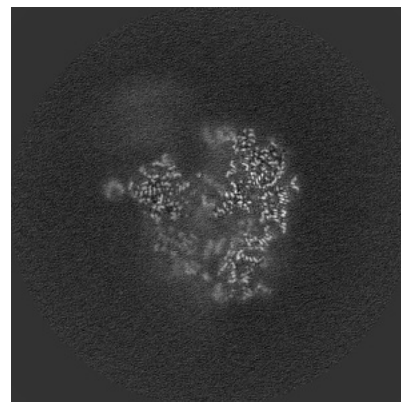
6.2.2 Raw map



X Index: 210



Y Index: 210

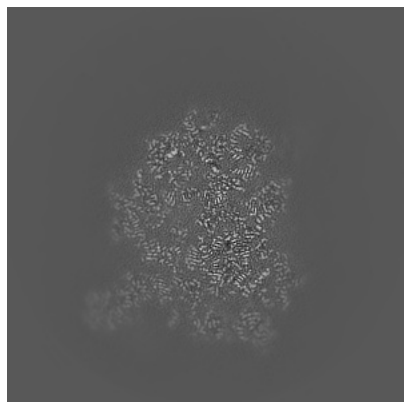


Z Index: 210

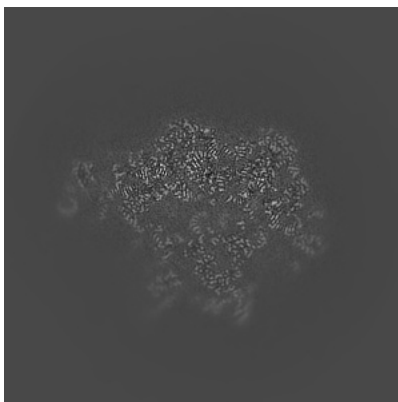
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

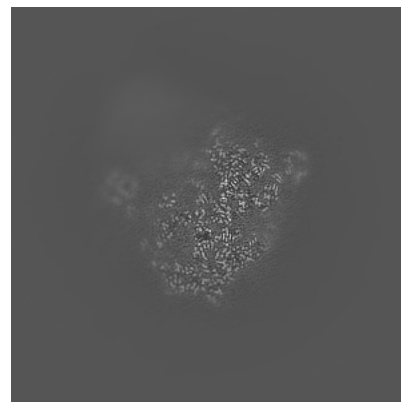
6.3.1 Primary map



X Index: 244

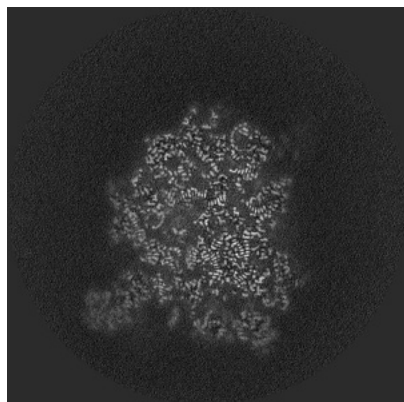


Y Index: 220

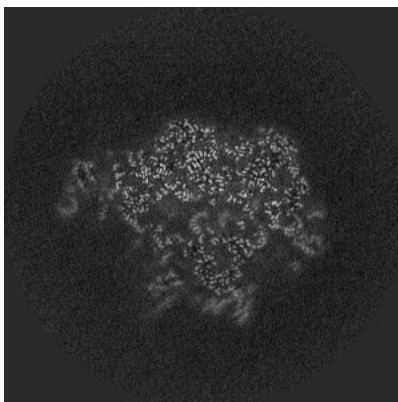


Z Index: 259

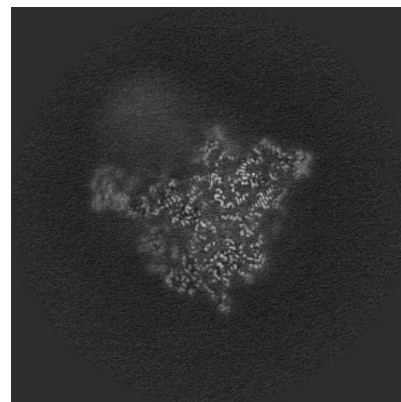
6.3.2 Raw map



X Index: 243



Y Index: 220

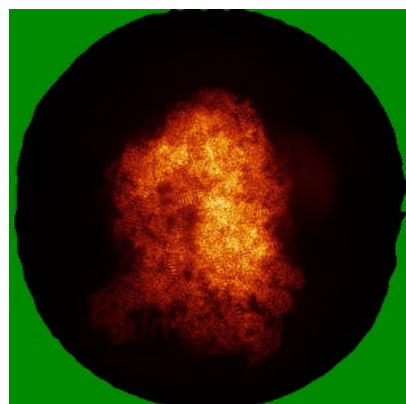


Z Index: 248

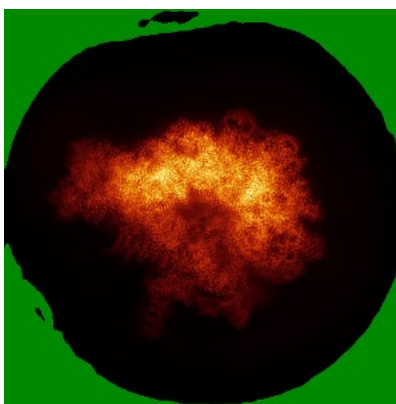
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

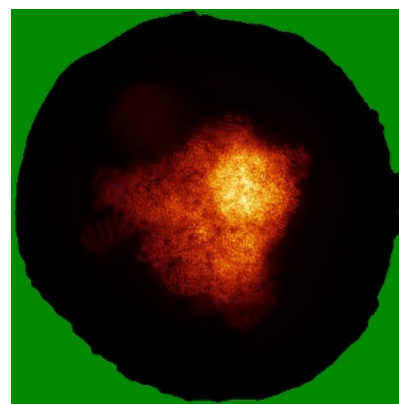
6.4.1 Primary map



X

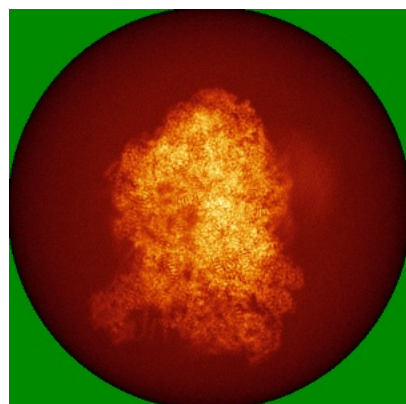


Y

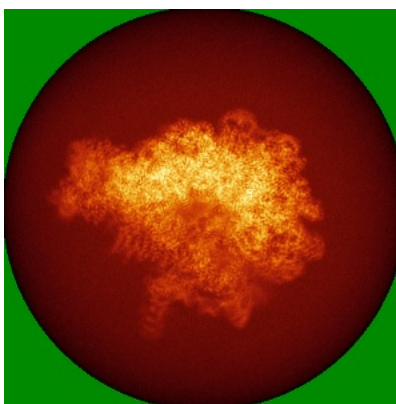


Z

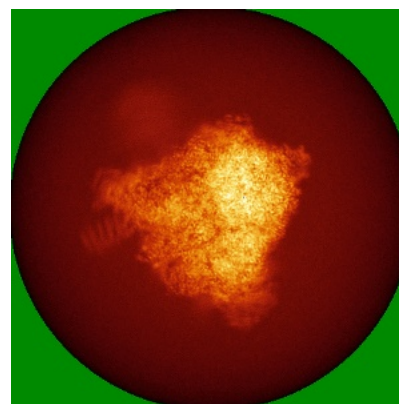
6.4.2 Raw map



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



X



Y



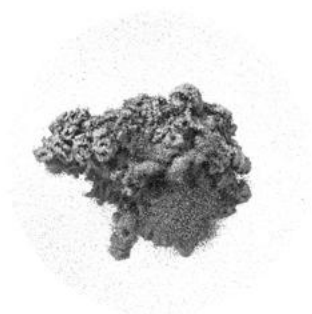
Z

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.

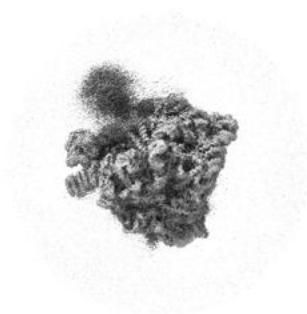
6.5.2 Raw map



X



Y



Z

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.

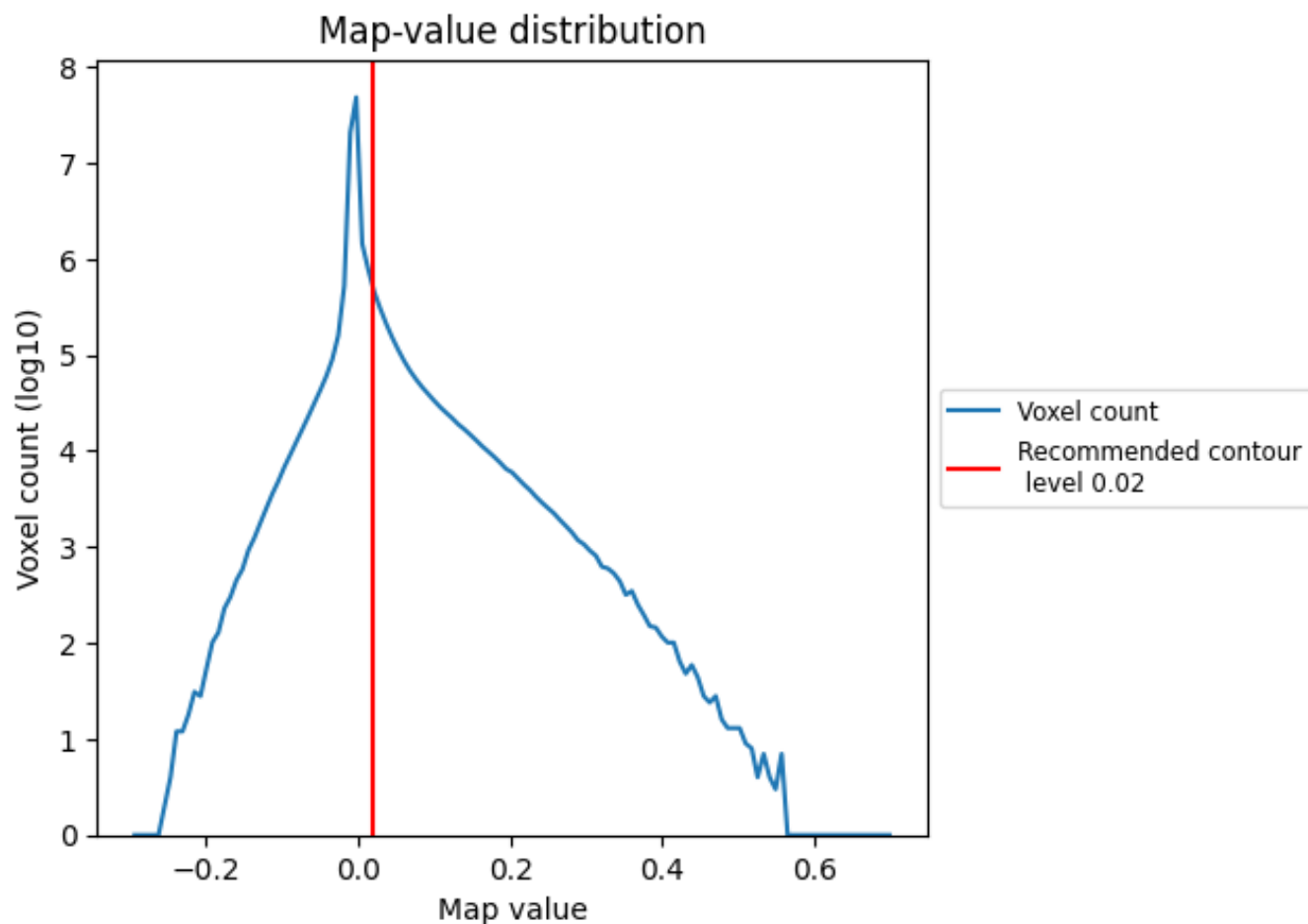
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

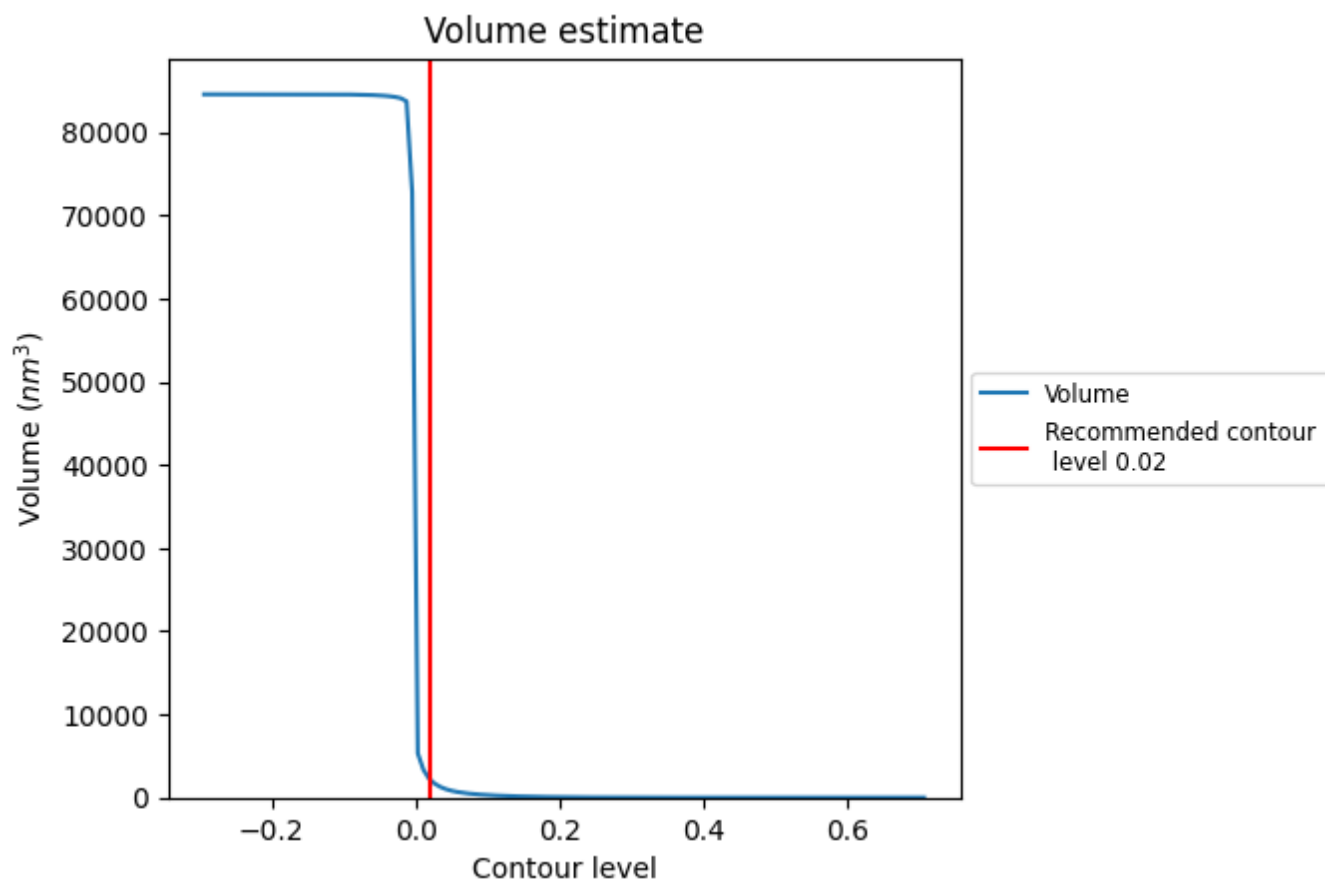
This section contains the results of statistical analysis of the map.

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.

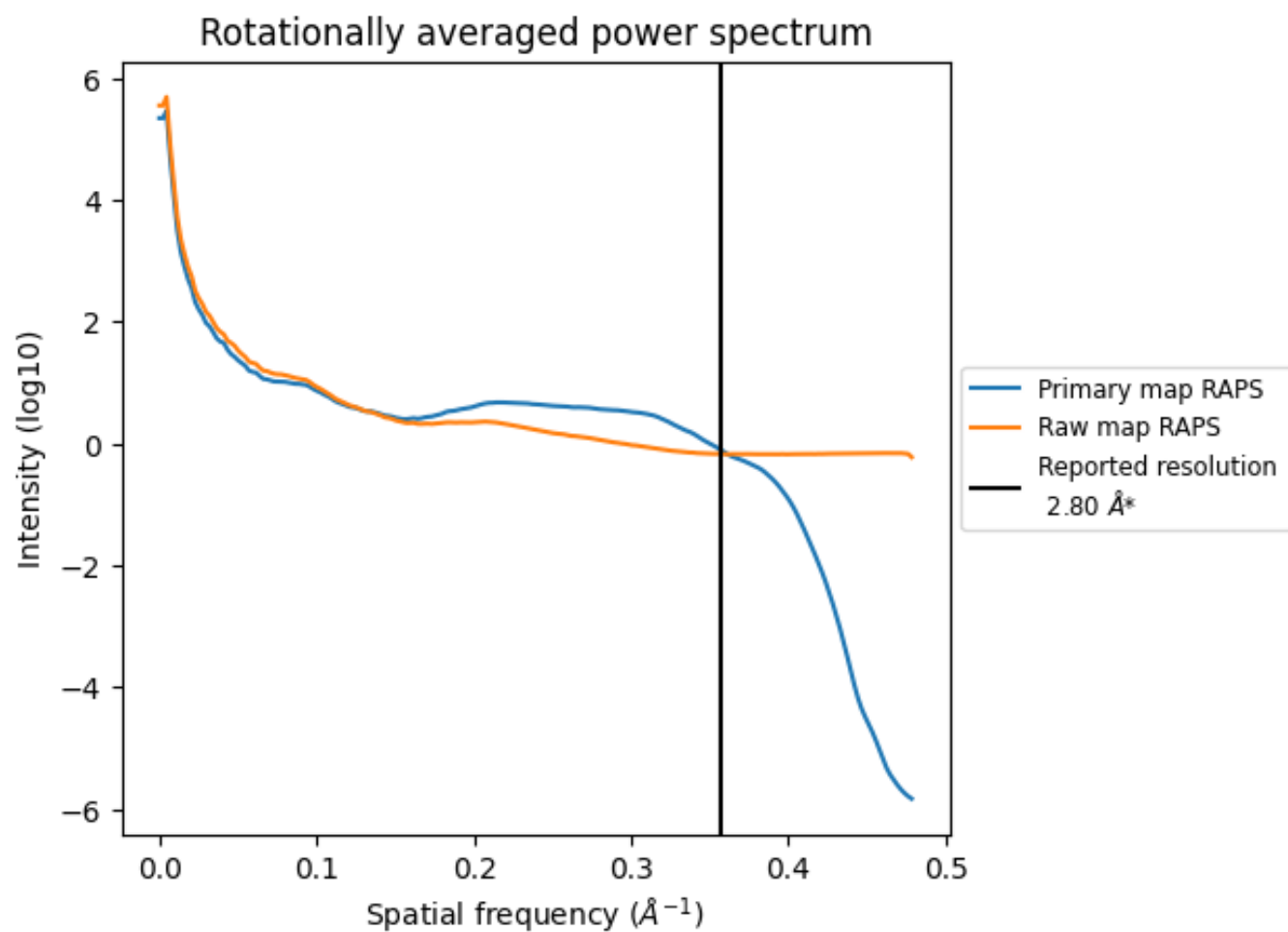
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2160 nm^3 ; this corresponds to an approximate mass of 1951 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 ⓘ

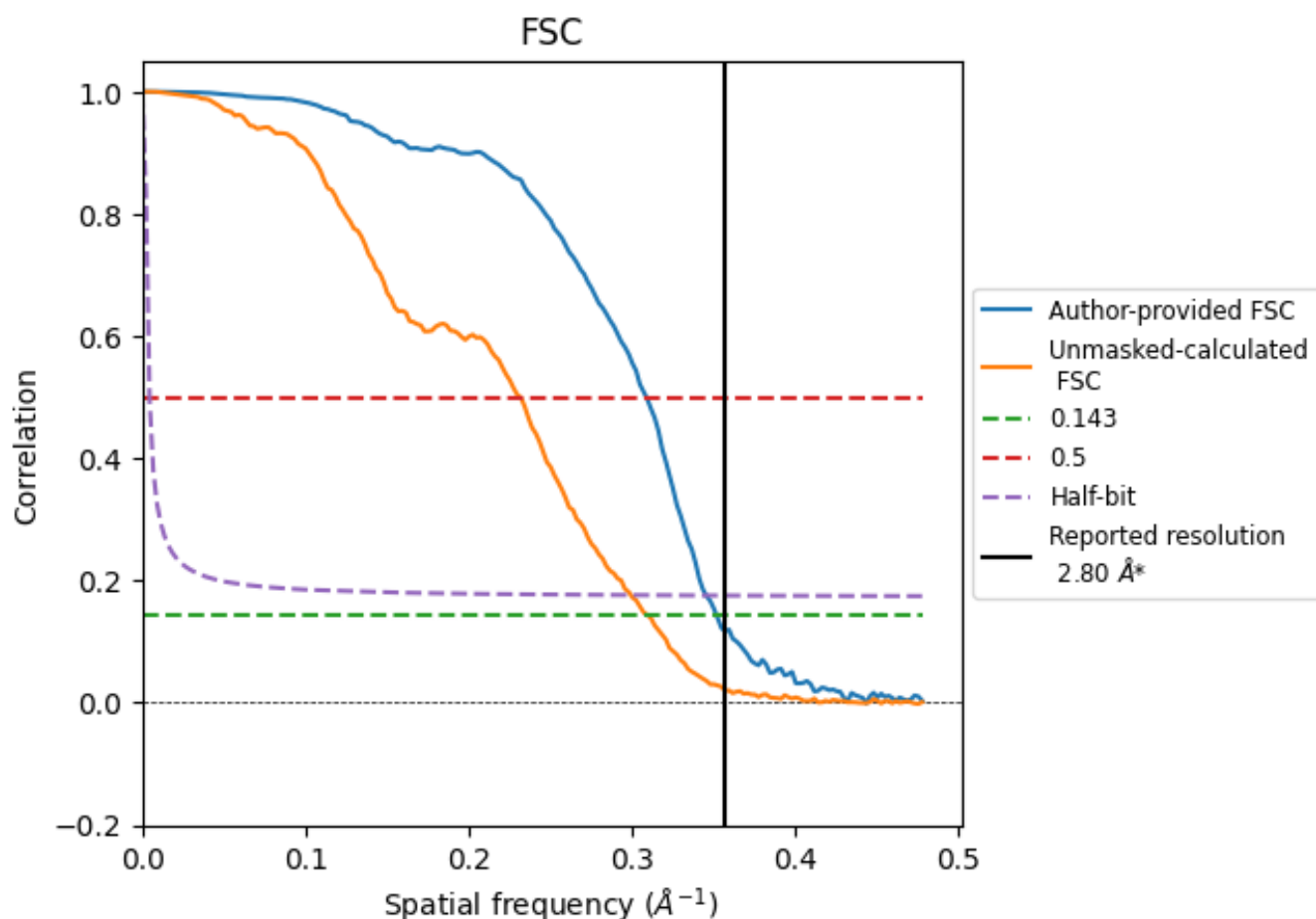


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

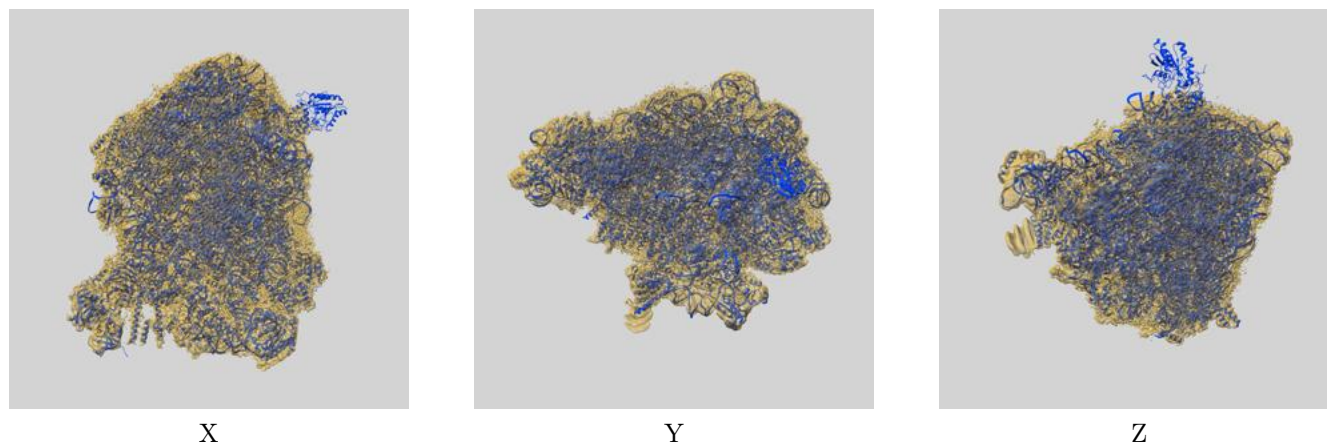
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.84	3.23	2.89
Unmasked-calculated*	3.22	4.31	3.34

*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 3.22 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

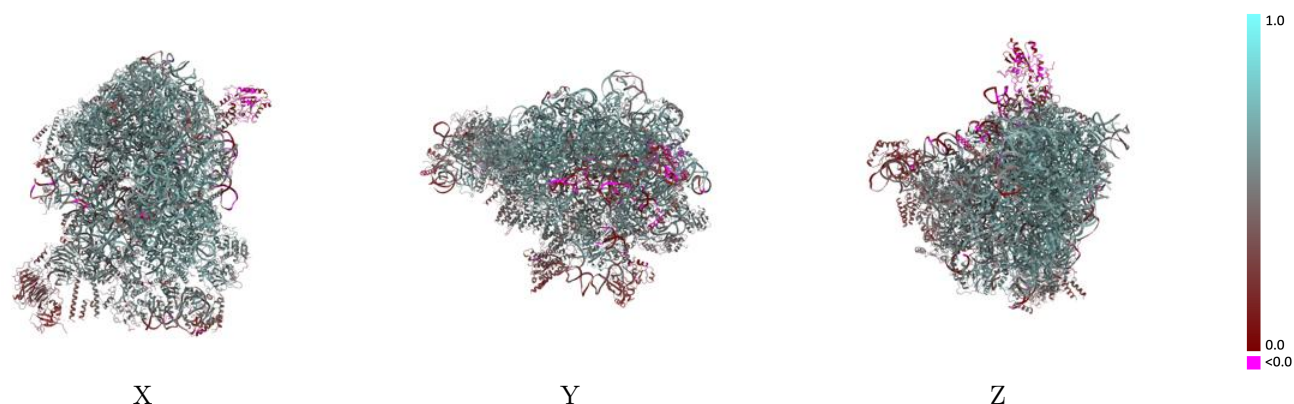
This section contains information regarding the fit between EMDB map EMD-35287 and PDB model 8I9X. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



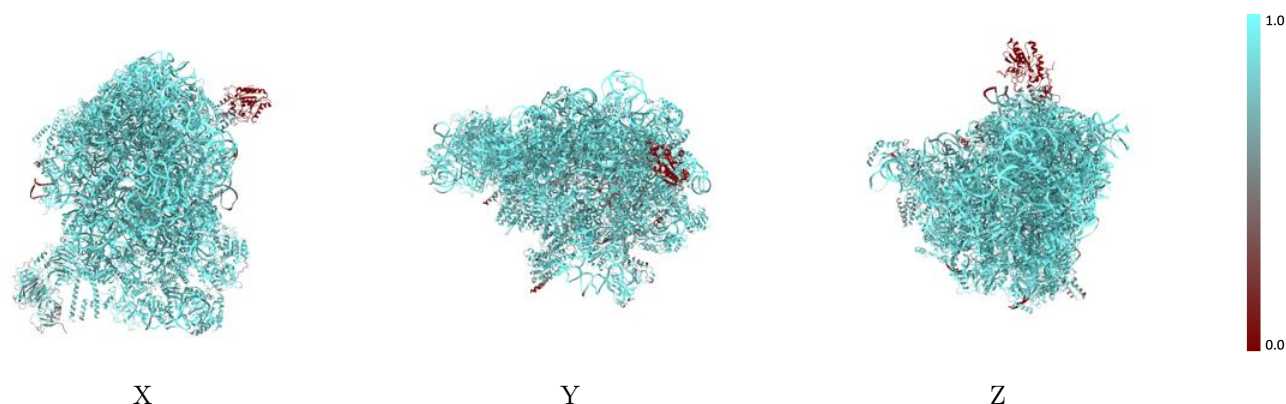
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



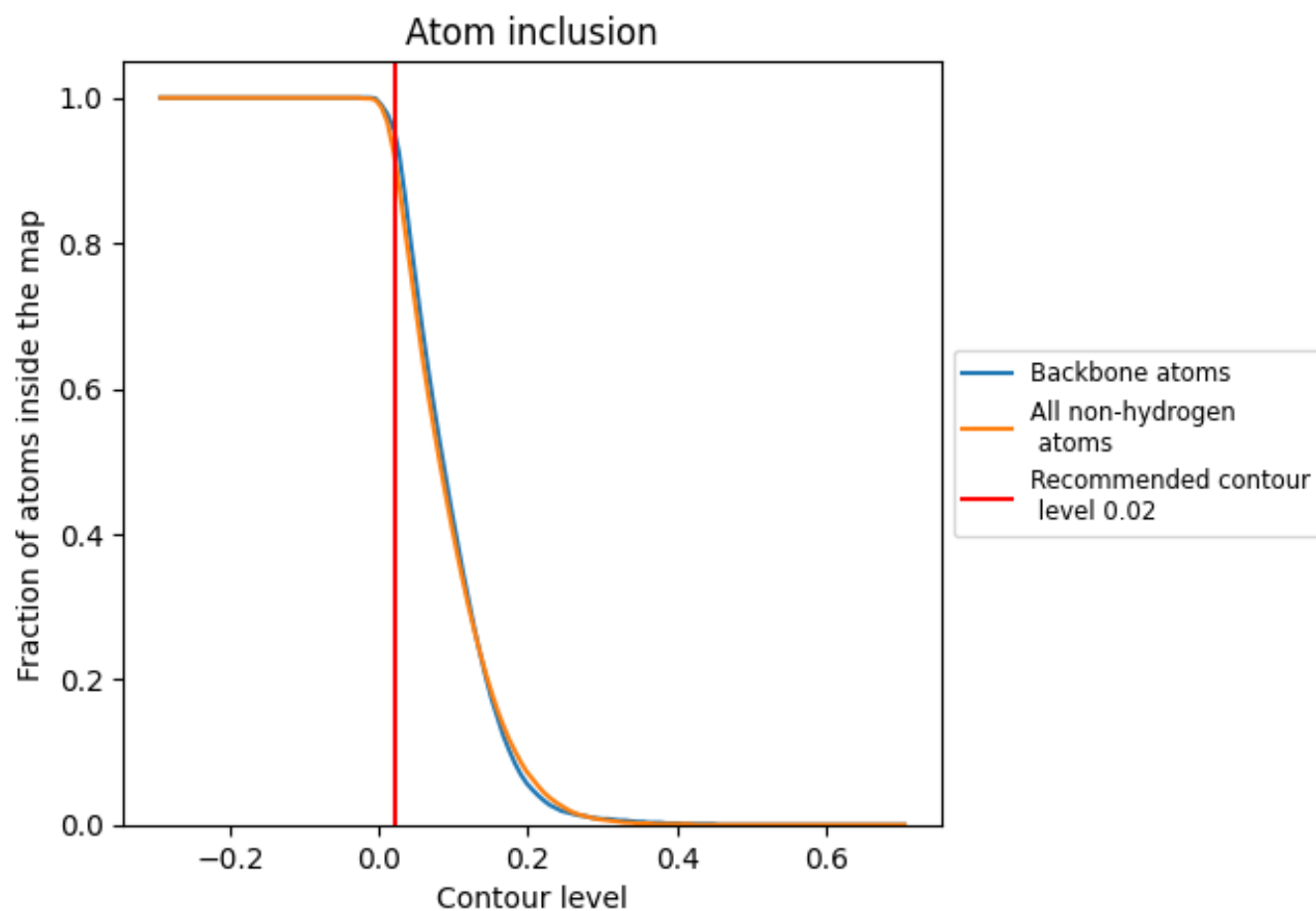
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 96% of all backbone atoms, 92% 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	 0.9230	 0.5100
C1	 0.9620	 0.5330
C2	 0.9560	 0.5250
CA	 0.9650	 0.5880
CB	 0.8770	 0.4350
CC	 0.9190	 0.4980
CD	 0.7160	 0.2940
CE	 0.9120	 0.5220
CF	 0.9180	 0.4920
CG	 0.9590	 0.5500
CH	 0.9210	 0.5160
CI	 0.8830	 0.4590
CJ	 0.9080	 0.4920
CK	 0.9420	 0.5280
CL	 0.3510	 0.2110
CM	 0.8870	 0.4600
CN	 0.9580	 0.5610
CO	 0.9630	 0.5830
CP	 0.9490	 0.5390
CQ	 0.9110	 0.5060
CR	 0.9460	 0.5800
CS	 0.8710	 0.4630
CT	 0.9210	 0.4850
CU	 0.9440	 0.5460
CV	 0.9680	 0.6000
CX	 0.9210	 0.5140
CY	 0.8150	 0.3390
Cb	 0.8500	 0.3790
Cz	 0.7450	 0.3270
LB	 0.9520	 0.5710
LC	 0.9640	 0.6040
LE	 0.9470	 0.5630
LF	 0.9600	 0.5880
LG	 0.9470	 0.5890
LH	 0.9480	 0.5600



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Chain	Atom inclusion	Q-score
LK	 0.8580	 0.3800
LL	 0.9830	 0.6150
LM	 0.9690	 0.5910
LN	 0.9850	 0.6500
LO	 0.9760	 0.6200
LP	 0.9550	 0.5550
LQ	 0.9570	 0.5560
LR	 0.9330	 0.4670
LS	 0.9640	 0.5760
LT	 0.8440	 0.3240
LU	 0.9140	 0.4990
LV	 0.9420	 0.5230
LX	 0.9430	 0.5510
LY	 0.9470	 0.5760
LZ	 0.9240	 0.4980
Lc	 0.8540	 0.4250
Ld	 0.9380	 0.5570
Le	 0.9720	 0.6150
Lf	 0.9830	 0.6290
Lg	 0.9060	 0.5300
Lh	 0.9410	 0.5440
Li	 0.9520	 0.5620
Lj	 0.9820	 0.6330
Lk	 0.8810	 0.4580
Ll	 0.9480	 0.4850
Lq	 0.7320	 0.2120