



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:01 AM UTC

PDB ID : 8I9T / pdb_00008i9t
EMDB ID : EMD-35283
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- State Dbp10-1
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

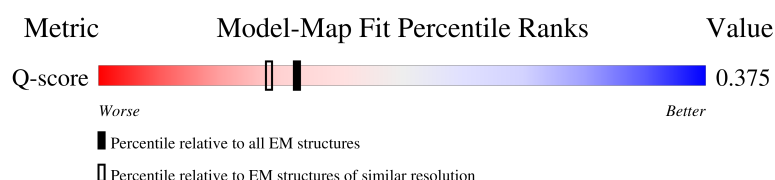
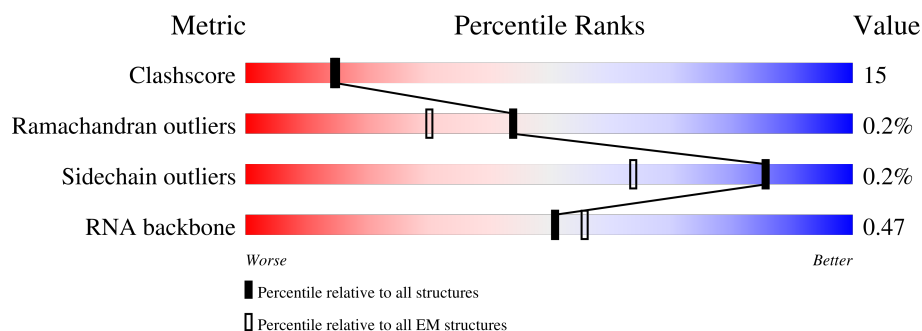
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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	 5% 25% 31% 7% 36%
2	C2	256	 5% 25% 29% 8% 38%
3	C3	161	 5% 22% 27% 12% 39%

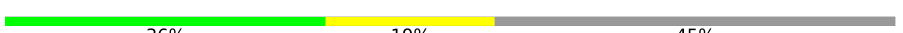
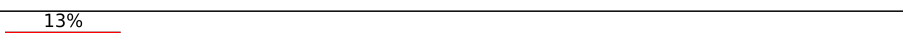
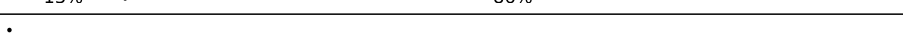
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Mol	Chain	Length	Quality of chain
4	CA	316	
5	CB	391	
6	CC	801	
7	CE	598	
8	CF	270	
9	CG	184	
10	CH	661	
11	CI	414	
12	CJ	679	
13	CK	261	
14	CL	558	
15	CM	249	
15	LF	249	
16	CN	246	
17	CO	120	
18	CP	751	
19	CQ	225	
20	CR	237	
21	CS	726	
22	CU	451	
23	CX	203	
24	Cz	123	
25	Cb	732	
26	Ch	354	
27	LB	392	

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Mol	Chain	Length	Quality of chain
28	LC	365	
29	LE	200	
30	LG	262	
31	LH	192	
32	LK	165	
33	LL	213	
34	LM	142	
35	LN	203	
36	LO	204	
37	LP	187	
38	LQ	213	
39	LS	174	
40	LT	160	
41	LV	139	
42	LX	156	
43	LY	138	
44	Le	131	
45	Lf	109	
46	Lh	935	
47	Li	110	
48	Lj	95	
49	Lq	217	
50	Cc	282	
51	Cd	436	
52	Ce	336	

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Mol	Chain	Length	Quality of chain
53	Cf	570	11%5%• 83%
54	Cg	478	14% 31%18%51%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 133790 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	2132	Total	C	N	O	P	0	0
			45600	20357	8256	14855	2132		

- Molecule 2 is a RNA chain called RNA (256-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	158	Total	C	N	O	P	0	0
			3359	1502	593	1106	158		

- Molecule 3 is a RNA chain called RNA (161-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	98	Total	C	N	O	P	0	0
			2097	933	381	685	98		

- Molecule 4 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CA	260	Total	C	N	O	S	0	0
			2144	1371	393	373	7		

- Molecule 5 is a protein called Ribosome biogenesis protein C8F11.04.

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

- Molecule 6 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CC	289	Total	C	N	O	S	0	0
			2388	1520	399	462	7		

- Molecule 7 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CE	463	Total	C	N	O	S	0	0
			3673	2352	643	667	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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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	476	Total	C	N	O	S	0	0
			3851	2451	669	716	15		

- 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	380	Total	C	N	O	S	0	0
			3109	2003	547	549	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CK	222	Total	C	N	O	S	0	0
			1778	1113	349	312	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CL	390	Total	C	N	O		0	0
			2173	1307	446	420			

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	187	Total	C	N	O	S	0	0
			1525	987	278	257	3		
15	LF	240	Total	C	N	O	S	0	0
			1967	1264	368	332	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	324	Total	C	N	O	S	0	0
			2535	1618	445	457	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CQ	112	Total	C	N	O	S	0	0
			960	607	195	148	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	90	Total	C	N	O	S	0	0
			734	463	124	145	2		

- Molecule 22 is a protein called rRNA-processing protein EBP2.

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

- Molecule 23 is a protein called 60S ribosomal subunit-like protein.

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

- Molecule 24 is a protein called rRNA-processing protein.

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

- Molecule 25 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Cb	560	Total	C	N	O	S	0	0
			4397	2797	791	800	9		

- Molecule 26 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ch	71	Total	C	N	O	S	0	0
			562	350	109	102	1		

- Molecule 27 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LB	341	Total	C	N	O	S	0	0
			2708	1721	493	482	12		

- Molecule 28 is a protein called 60S ribosomal protein L4-like protein.

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

- Molecule 29 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LE	170	Total	C	N	O	S	0	0
			1338	861	241	233	3		

- Molecule 30 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LG	195	Total	C	N	O	S	0	0
			1574	1015	285	269	5		

- Molecule 31 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	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
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 32 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LK	146	Total	C	N	O	S	0	0
			1112	701	203	206	2		

- Molecule 33 is a protein called 60S ribosomal protein L13.

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

- Molecule 34 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 35 is a protein called Ribosomal protein L15.

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

- Molecule 36 is a protein called 60S ribosomal protein L16-like protein.

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

- Molecule 37 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LP	154	Total	C	N	O	S	0	0
			1212	758	233	218	3		

- Molecule 38 is a protein called Ribosomal protein L18-like protein.

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

- Molecule 39 is a protein called 60S ribosomal protein L20.

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

- Molecule 40 is a protein called 60S ribosomal protein l21-like protein.

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

- Molecule 41 is a protein called 60S ribosomal protein l23-like protein.

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

- Molecule 42 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	LX	22	Total	C	N	O	0	0
			148	91	31	26		

- Molecule 43 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 44 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Le	131	Total	C	N	O	S	0	0
			1055	663	213	172	7		

- Molecule 45 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 46 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 47 is a protein called 60S ribosomal protein L36.

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

- Molecule 48 is a protein called Ribosomal protein L37.

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

- Molecule 49 is a protein called Ribosomal protein.

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

- Molecule 50 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Cc	236	Total	C	N	O	S	0	0
			1898	1208	337	343	10		

- Molecule 51 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Cd	342	Total	C	N	O	S	0	0
			2763	1743	533	483	4		

- Molecule 52 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ce	194	Total	C	N	O	S	0	0
			1609	1020	304	276	9		

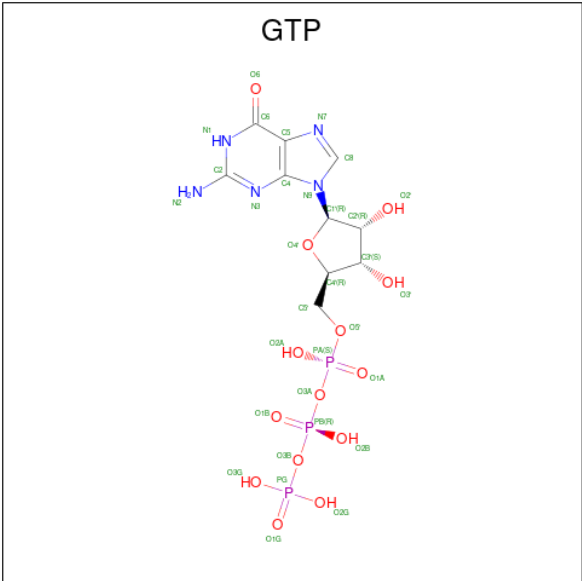
- Molecule 53 is a protein called 60S ribosome biogenesis protein Rrp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Cf	98	Total	C	N	O	S	0	0
			845	517	173	154	1		

- Molecule 54 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Cg	233	Total	C	N	O	S	0	0
			1850	1168	348	324	10		

- Molecule 55 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

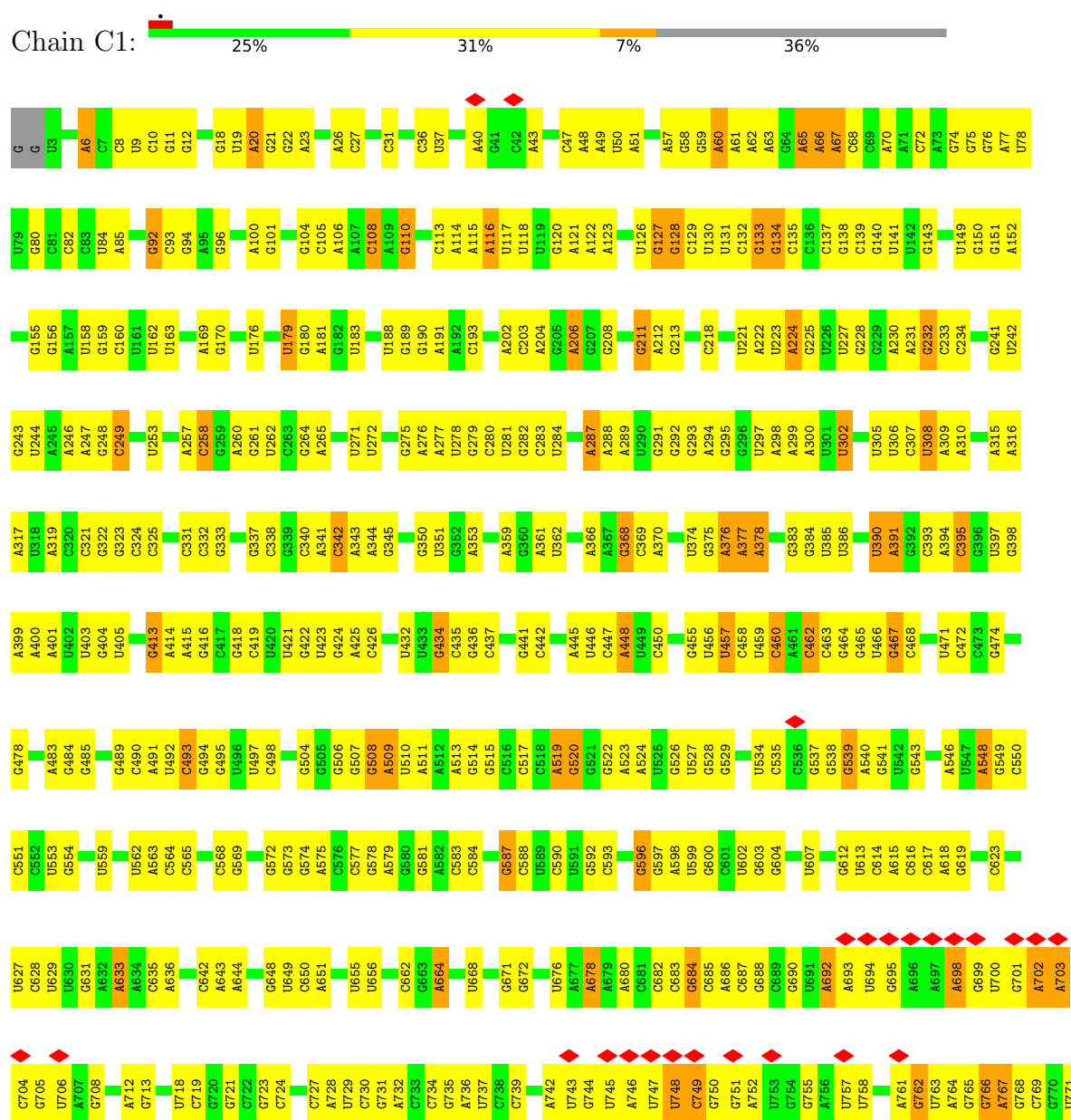
- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	CQ	1	Total	Zn	0
			1	1	
56	Lj	1	Total	Zn	0
			1	1	
56	Ce	1	Total	Zn	0
			1	1	

3 Residue-property plots

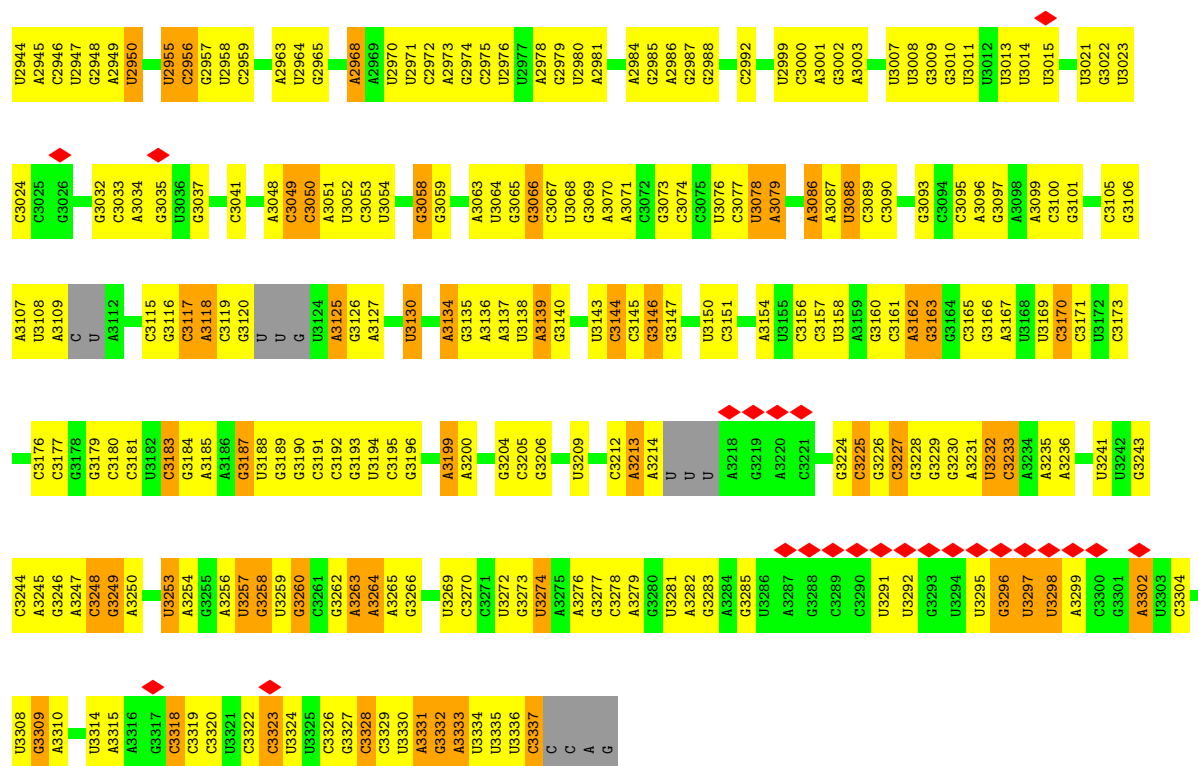
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: RNA (3341-MER)

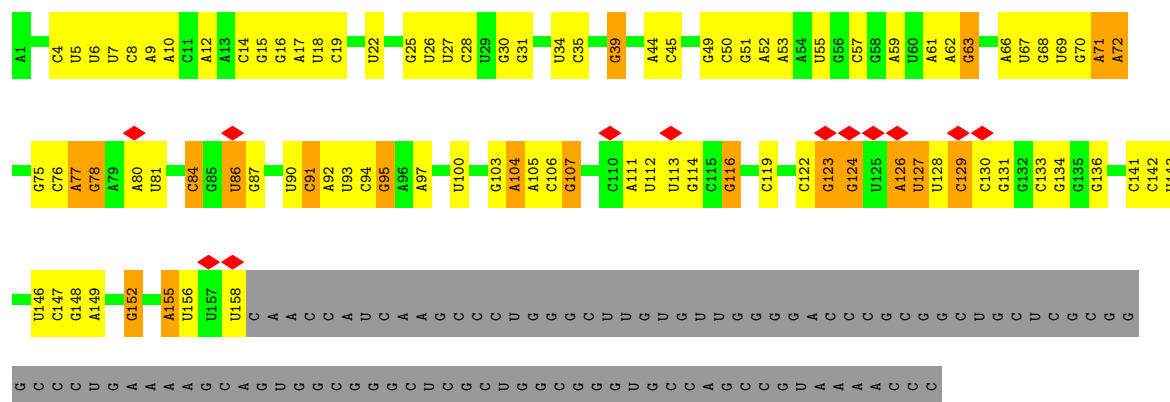
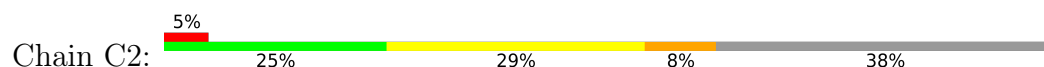




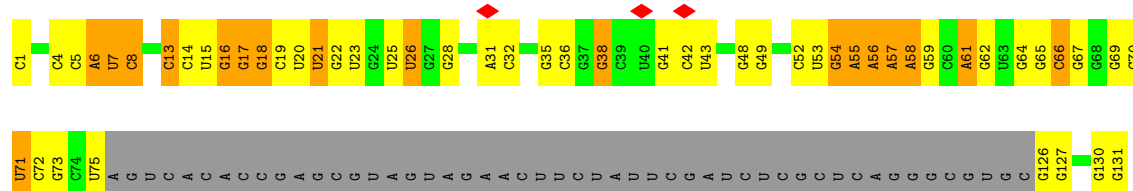
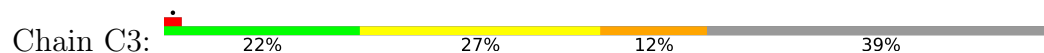




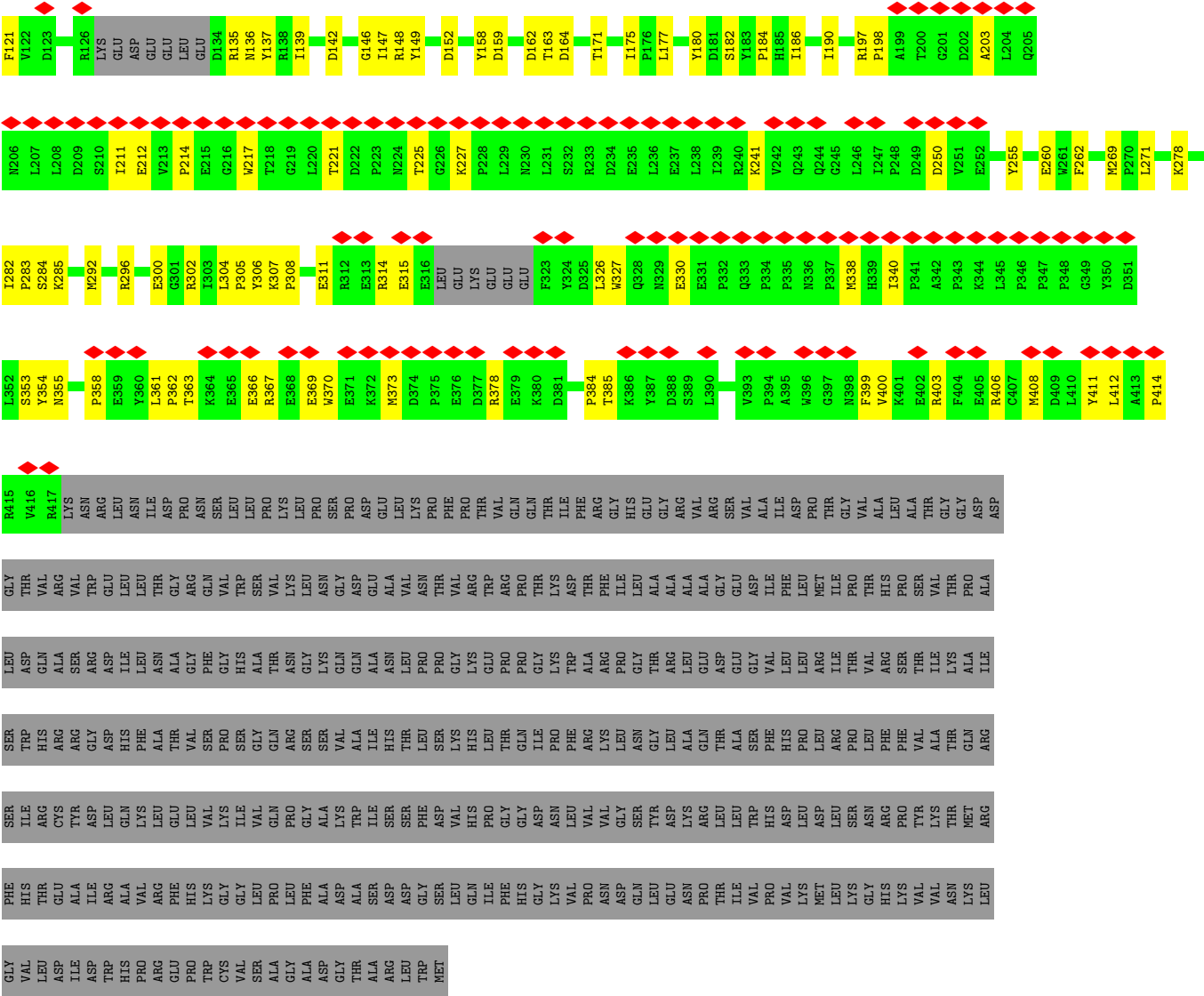
• Molecule 2: RNA (256-MER)



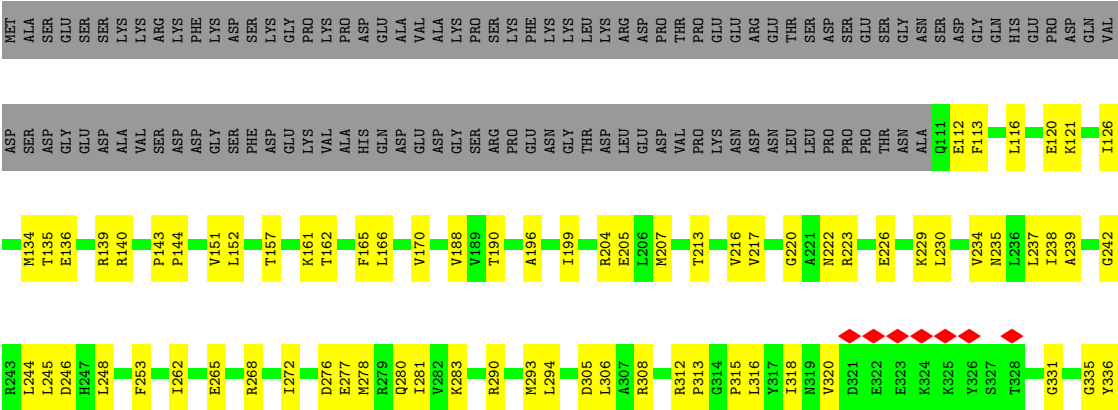
• Molecule 3: RNA (161-MER)

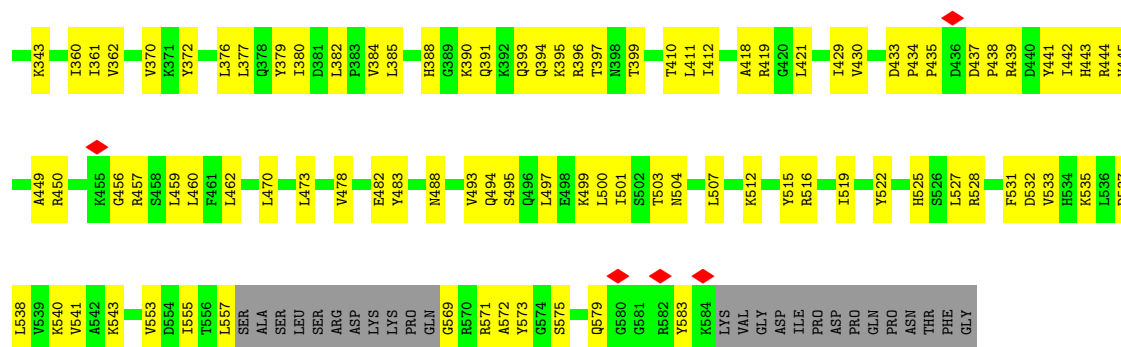






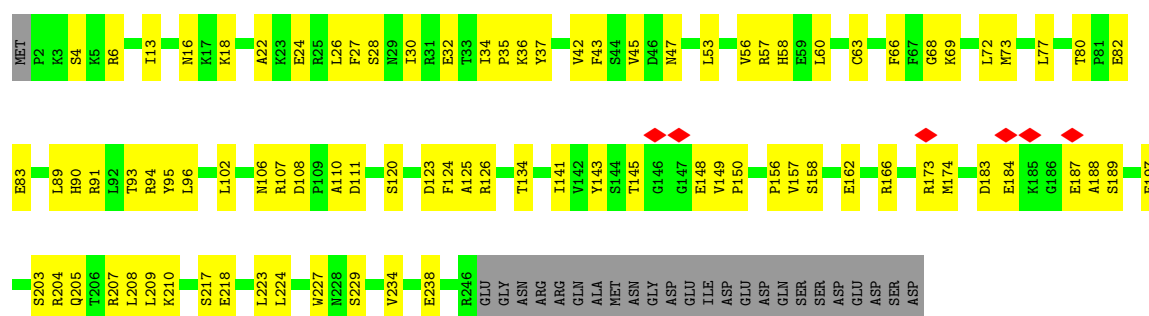
● Molecule 7: RNA helicase





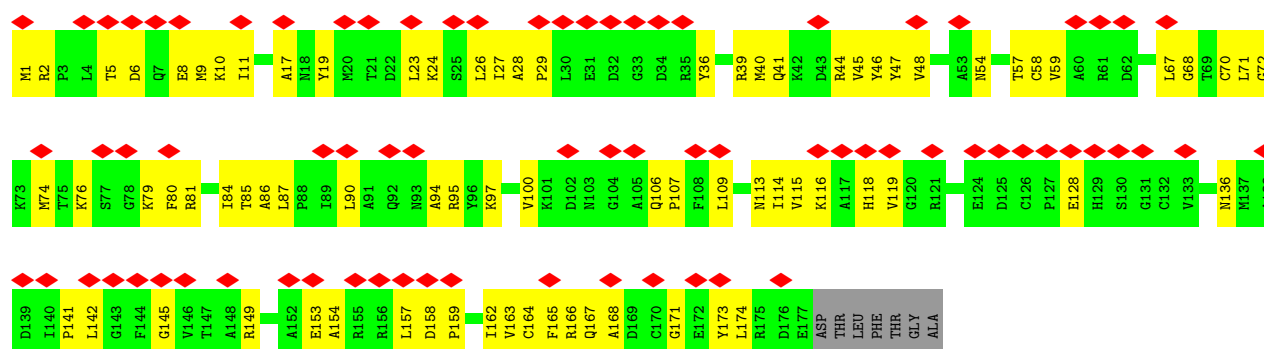
• Molecule 8: Ribosome assembly factor mrt4

Chain CF: 58% 33% 9%



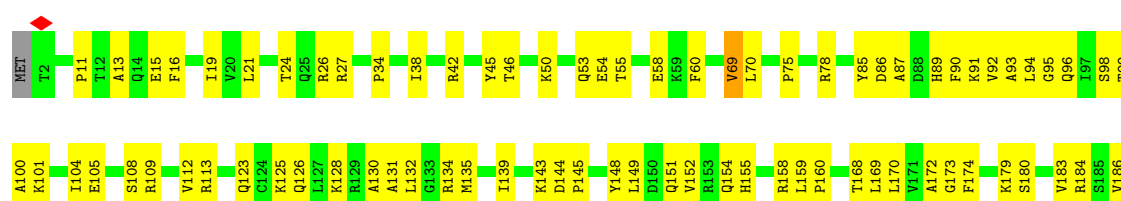
• Molecule 9: 60S ribosome subunit biogenesis protein NIP7

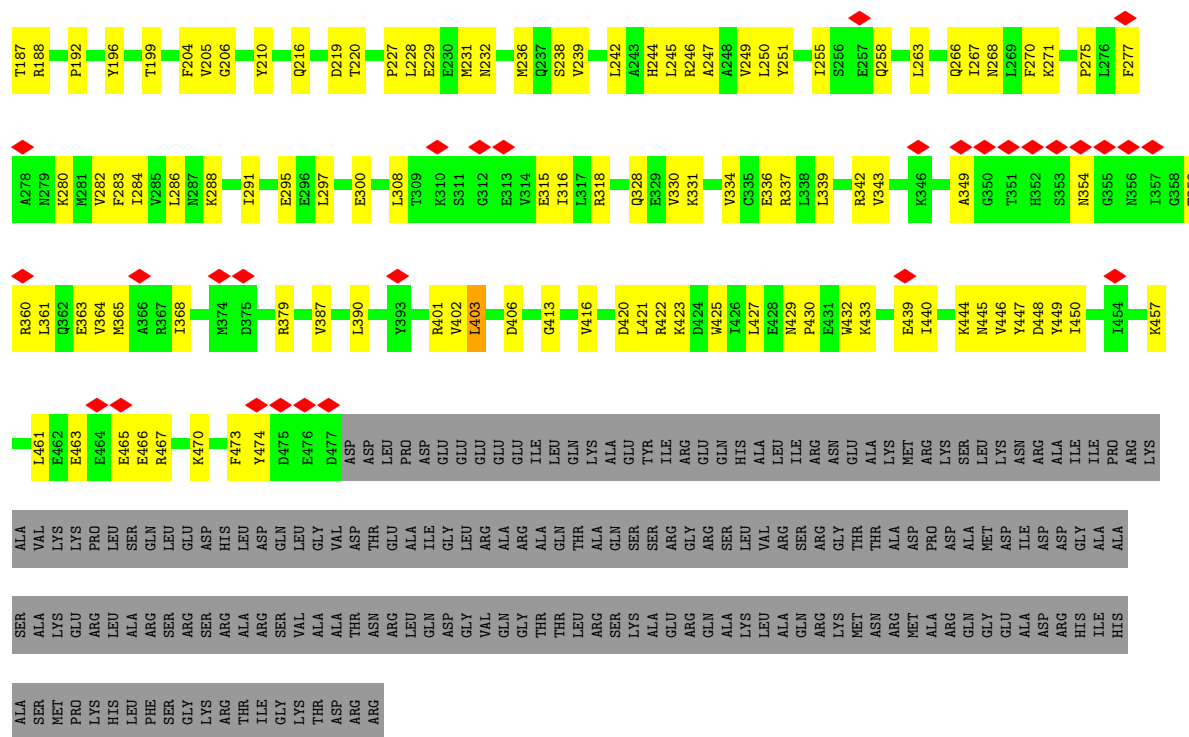
Chain CG: 41% 54% 42%



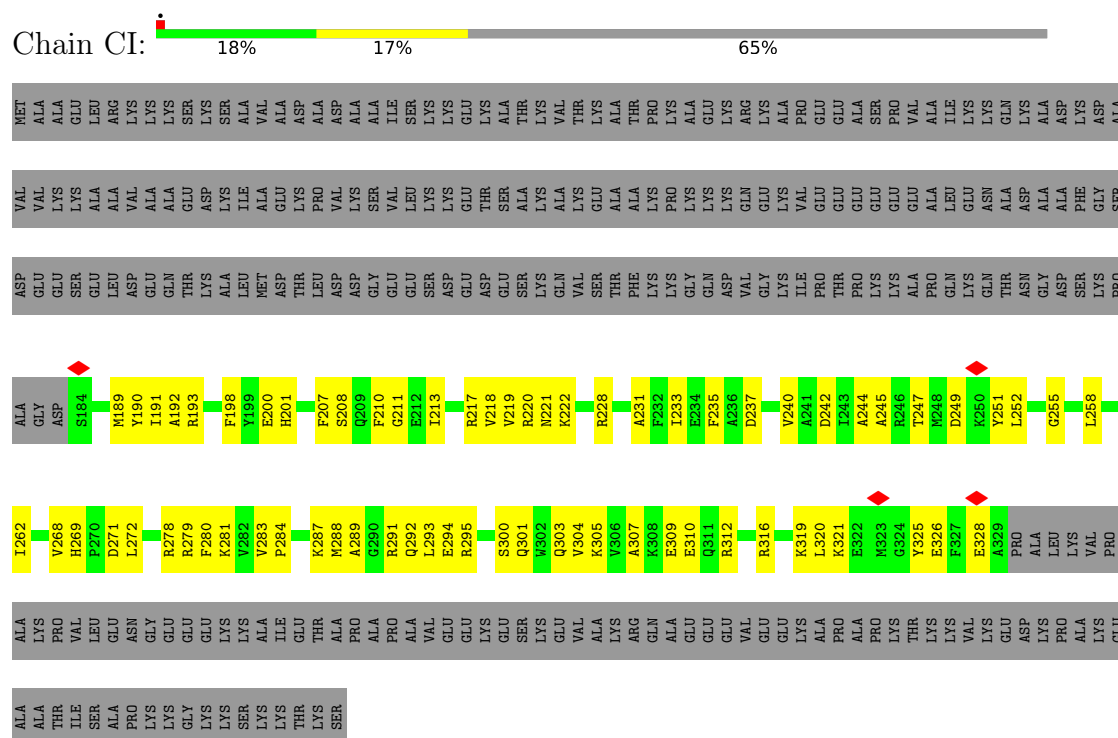
• Molecule 10: Nucleolar GTP-binding protein 1

Chain CH: 5% 44% 28% 28%





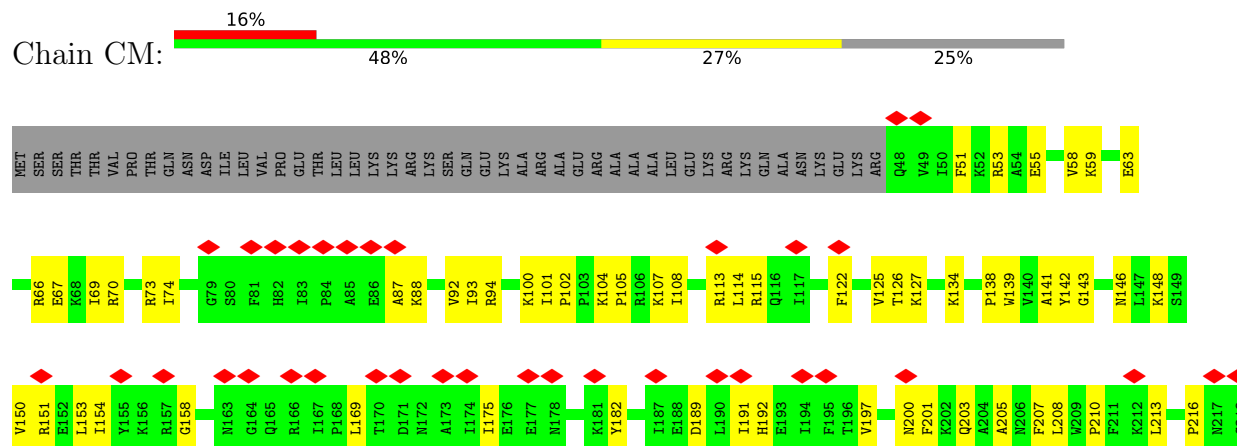
• Molecule 11: Putative RNA-binding protein



Chain CL:



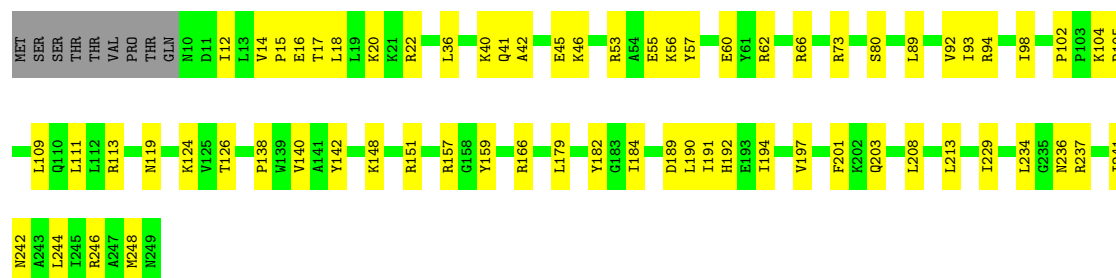
Chain CM:





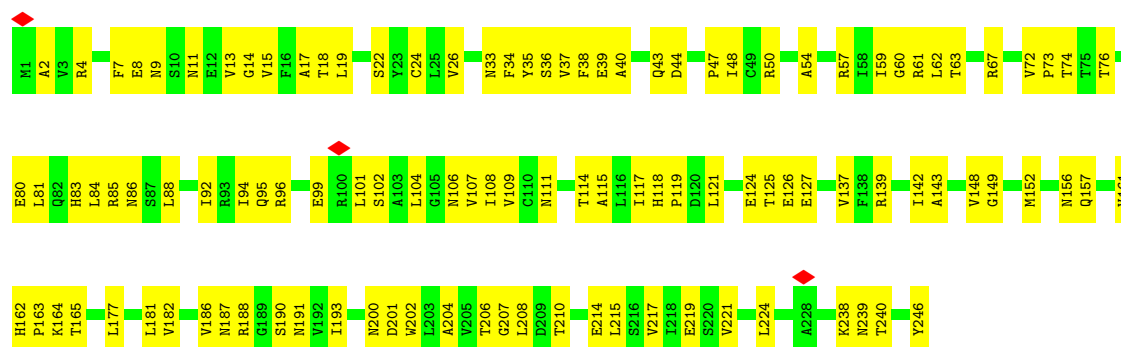
- Molecule 15: 60S ribosomal protein l7-like protein

Chain LF: 69% 27% .



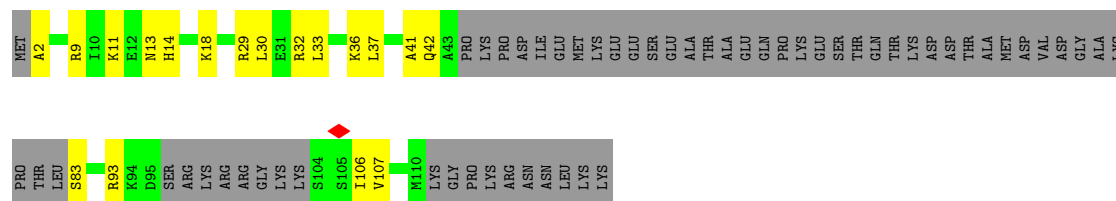
- Molecule 16: Eukaryotic translation initiation factor 6

Chain CN: 55% 45%



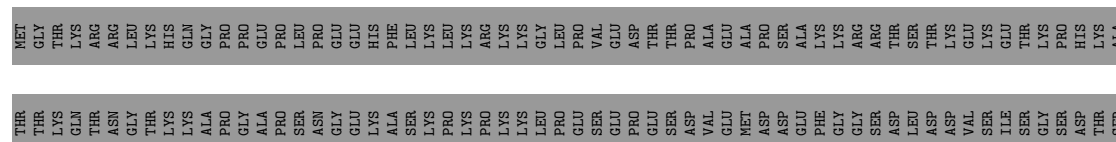
- Molecule 17: DUF2423 domain-containing protein

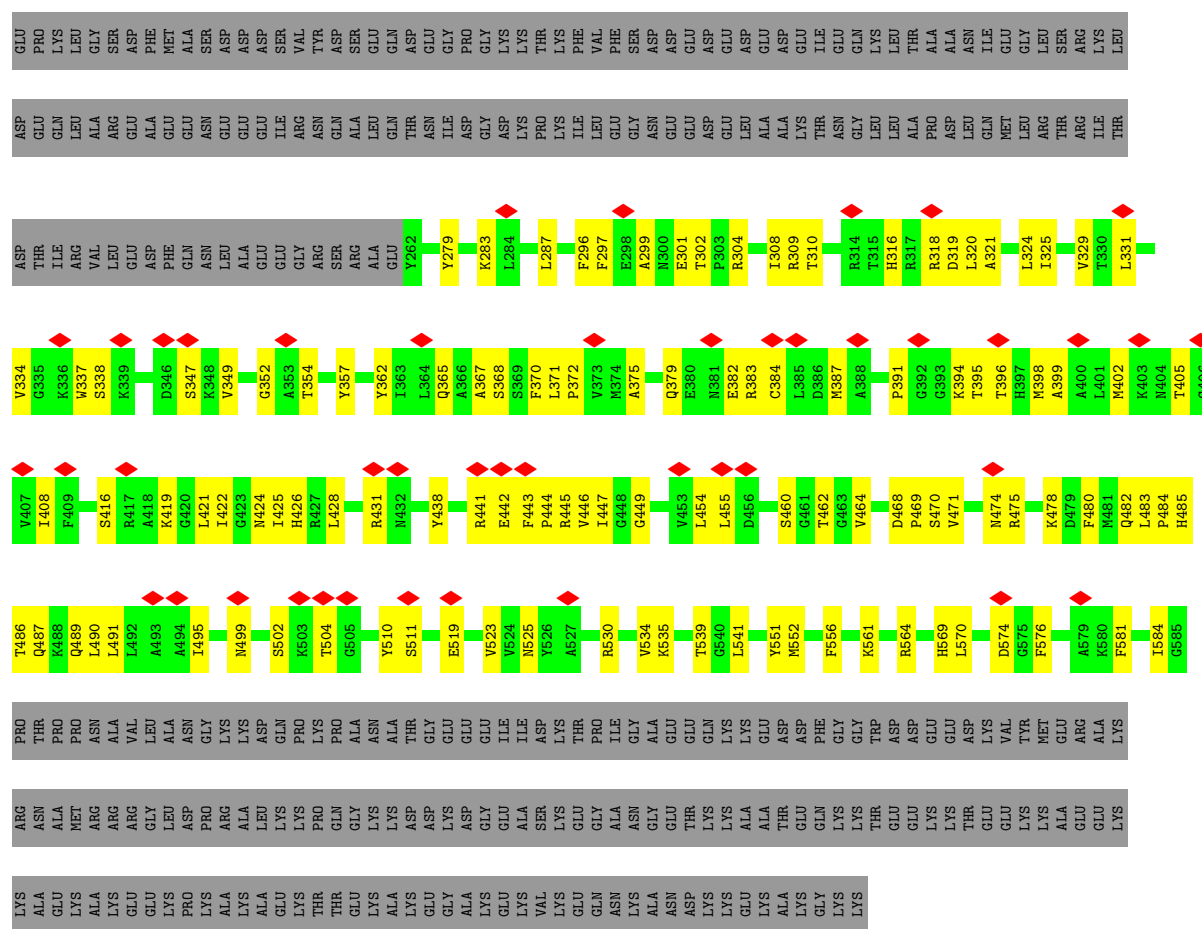
Chain CO: 37% 15% 48%



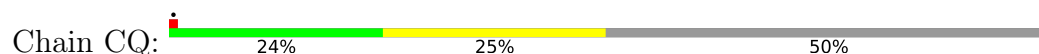
- Molecule 18: RNA methyltransferase nop2-like protein

Chain CP: 6% 28% 15% 57%



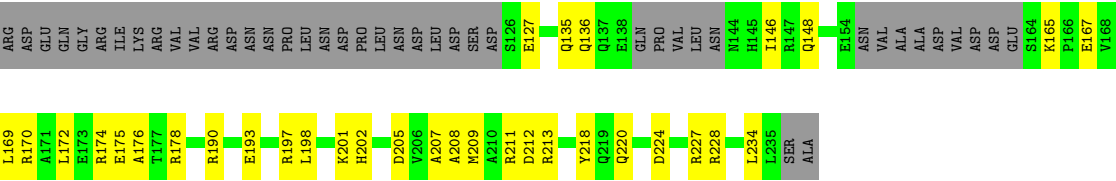


• Molecule 19: Ribosome biogenesis protein RLP24

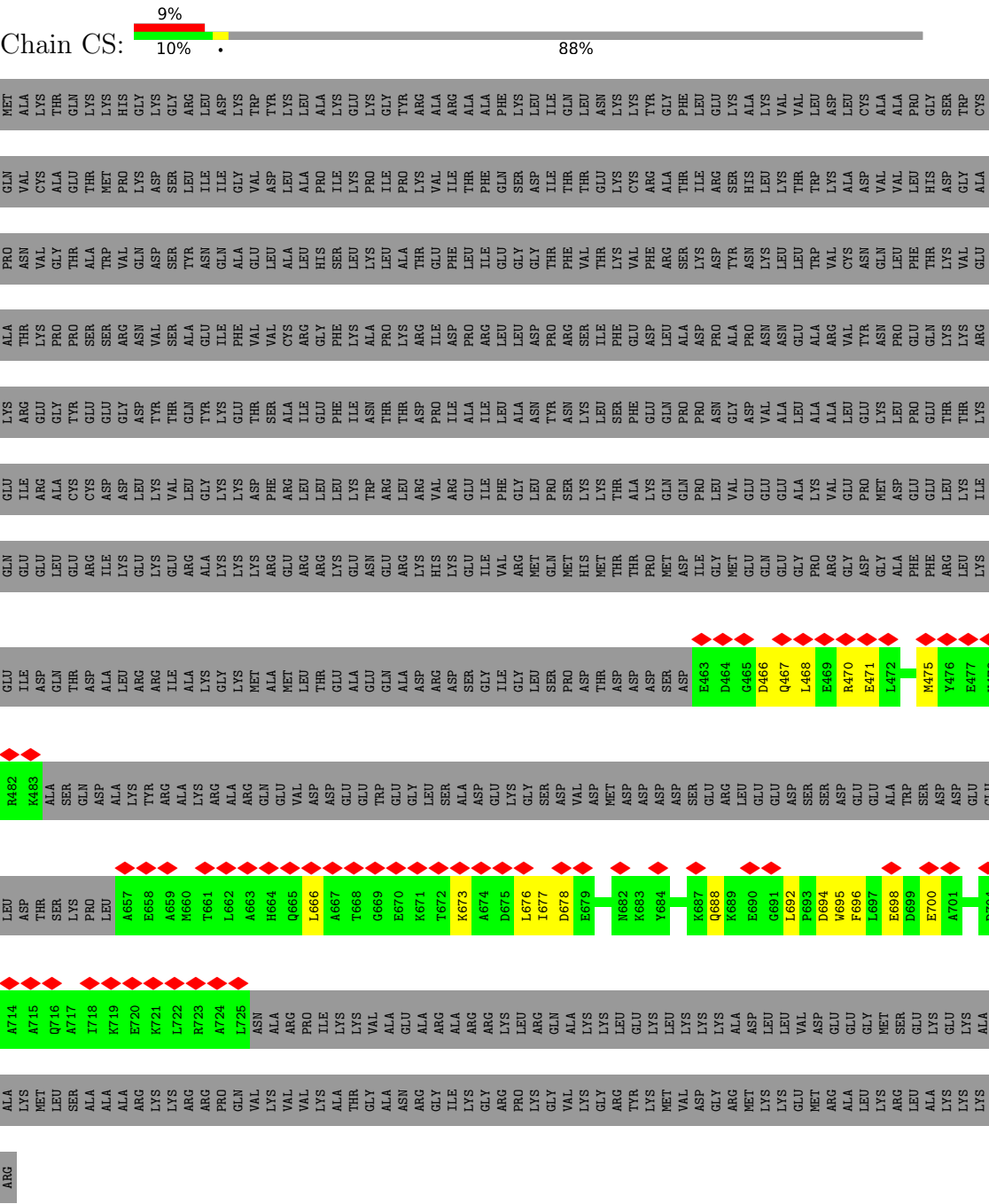


• Molecule 20: Nucleolar protein 16



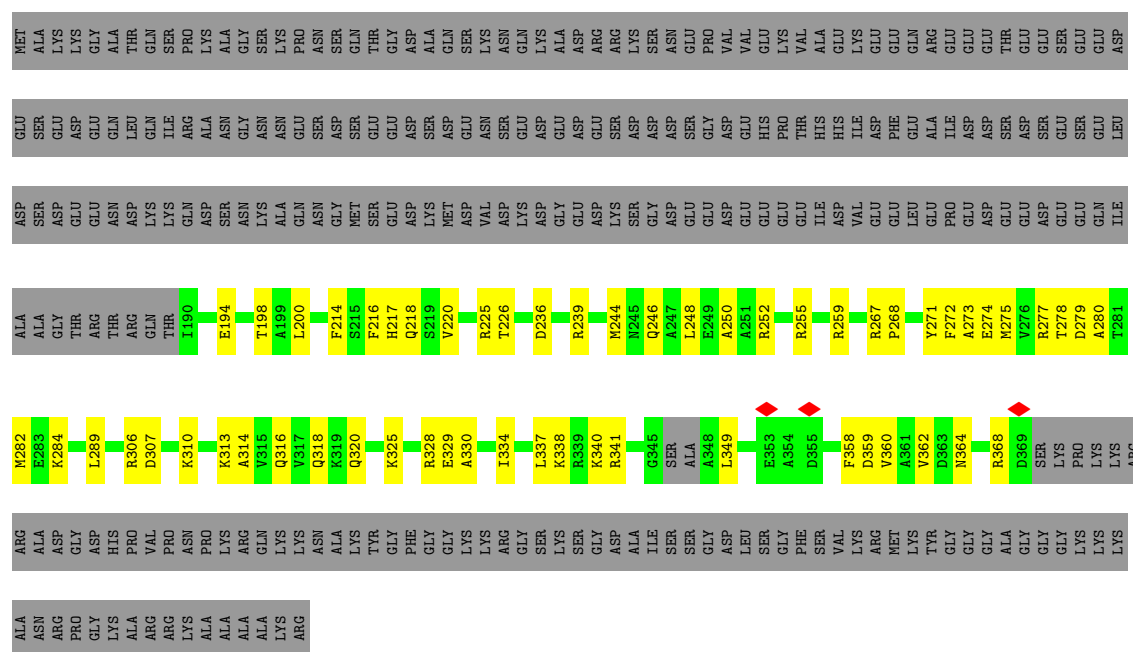


• Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1

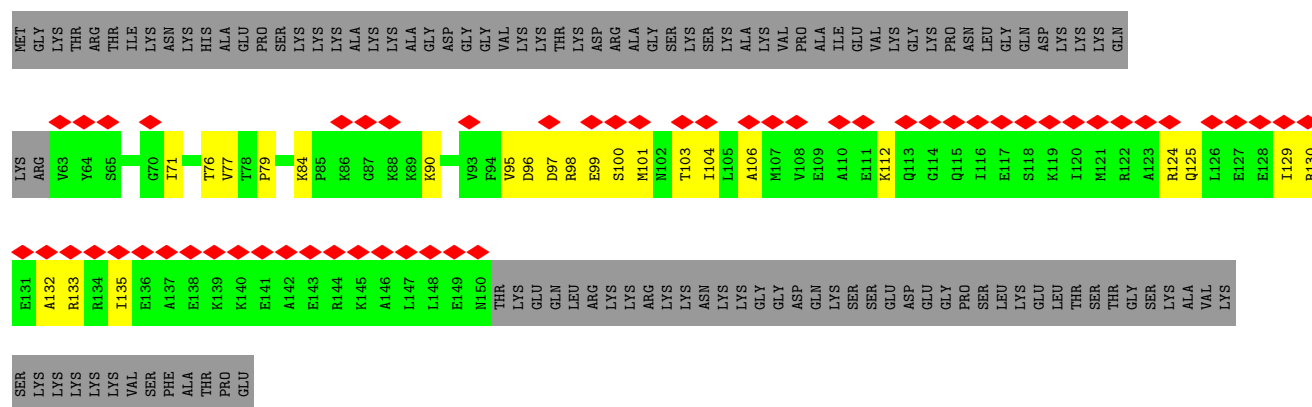
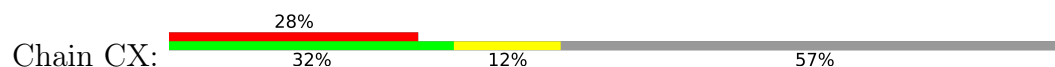


• Molecule 22: rRNA-processing protein EBP2

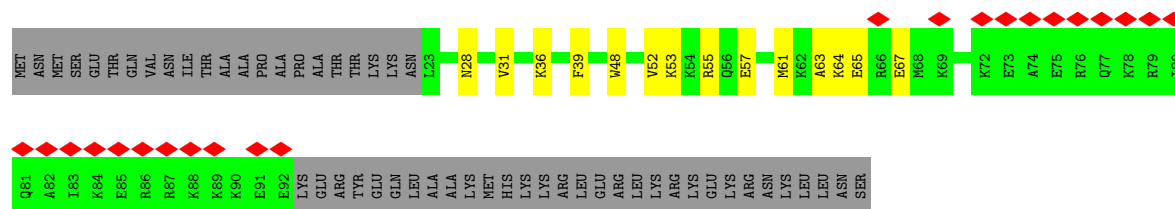




- Molecule 23: 60S ribosomal subunit-like protein



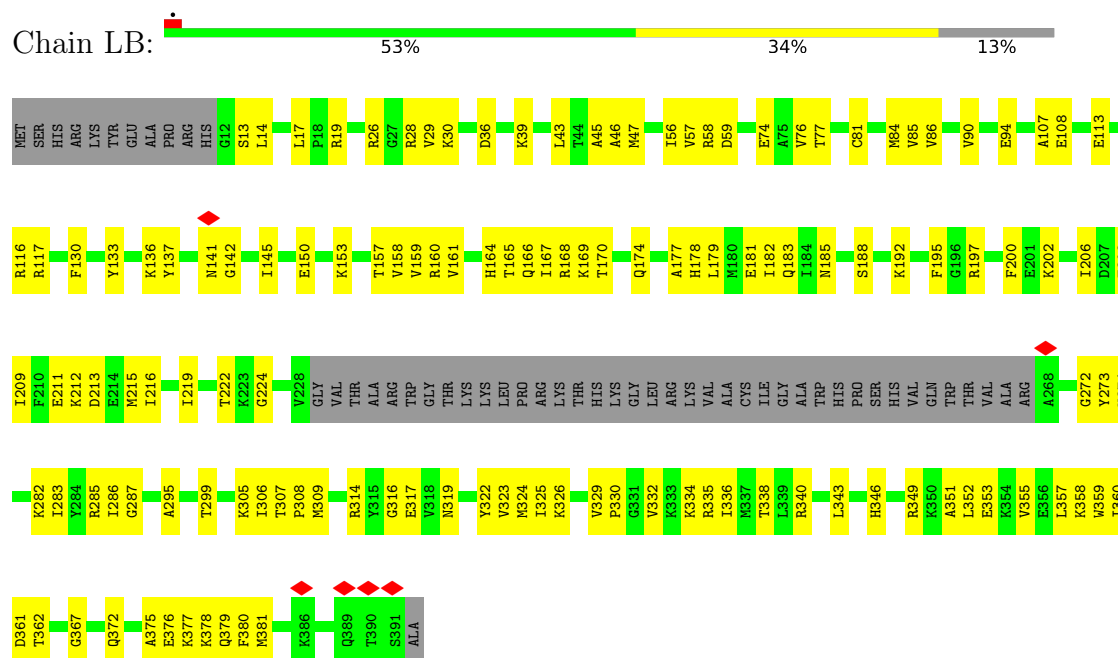
- Molecule 24: rRNA-processing protein



- Molecule 25: ATP-dependent RNA helicase DBP10



- Molecule 27: 60S ribosomal protein L3-like protein

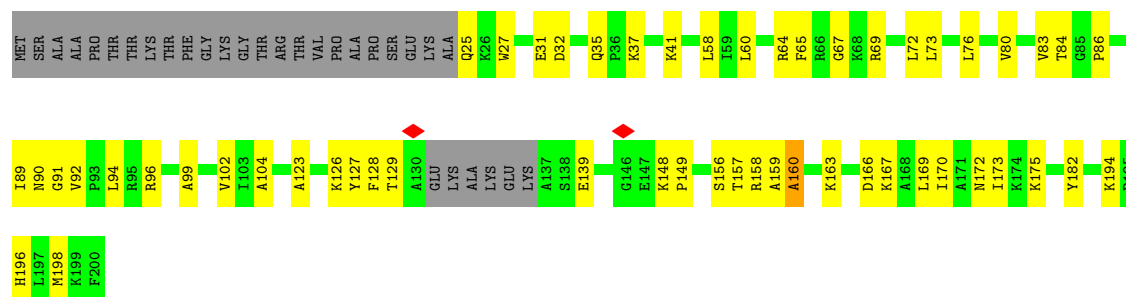


- Molecule 28: 60S ribosomal protein L4-like protein

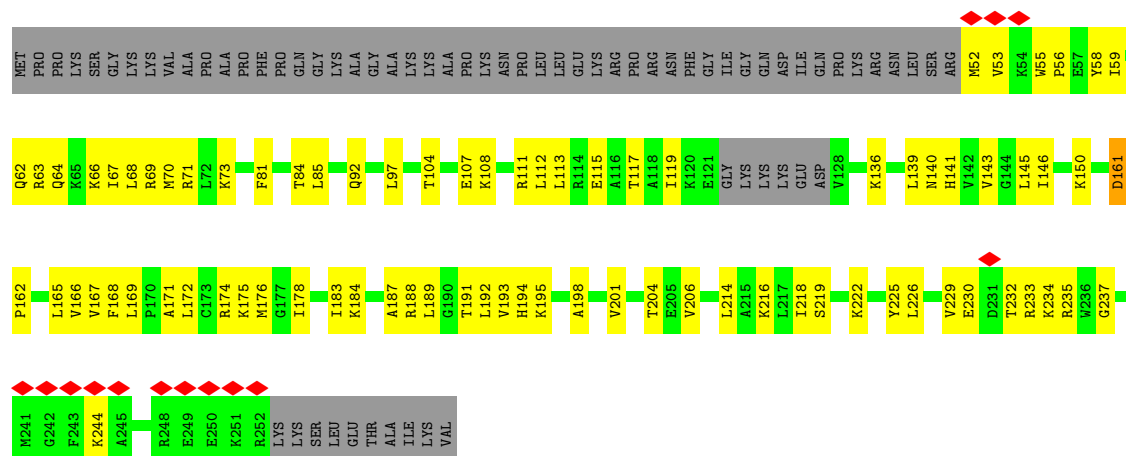


- Molecule 29: 60S ribosomal protein L6

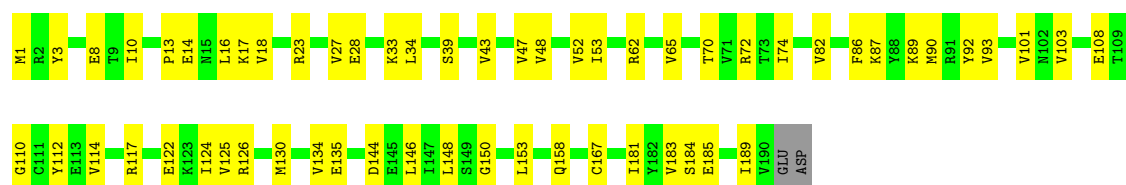




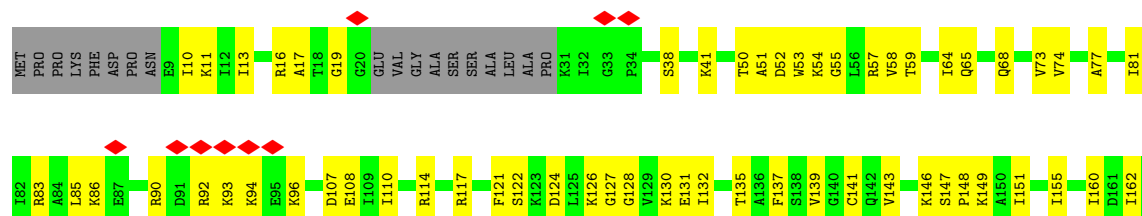
- Molecule 30: 60S ribosomal protein L8



- Molecule 31: 60S ribosomal protein l9-like protein

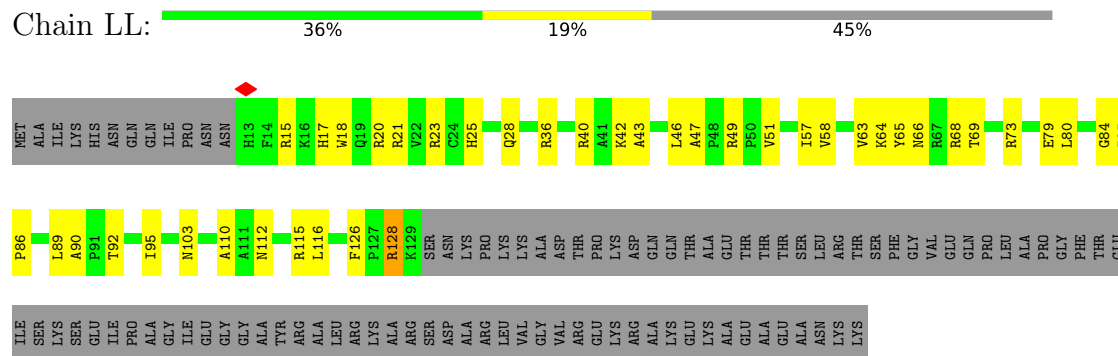


- Molecule 32: 60S ribosomal protein L12-like protein

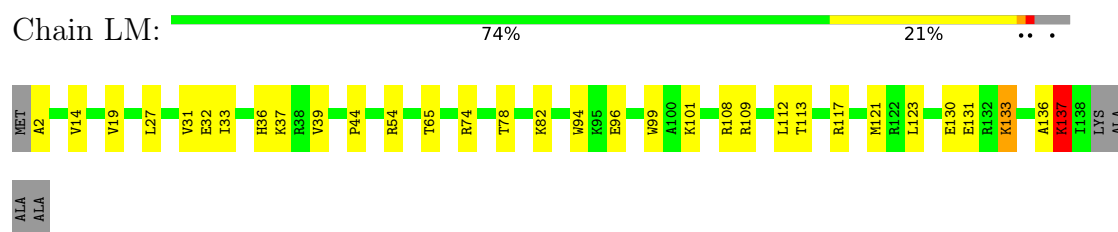




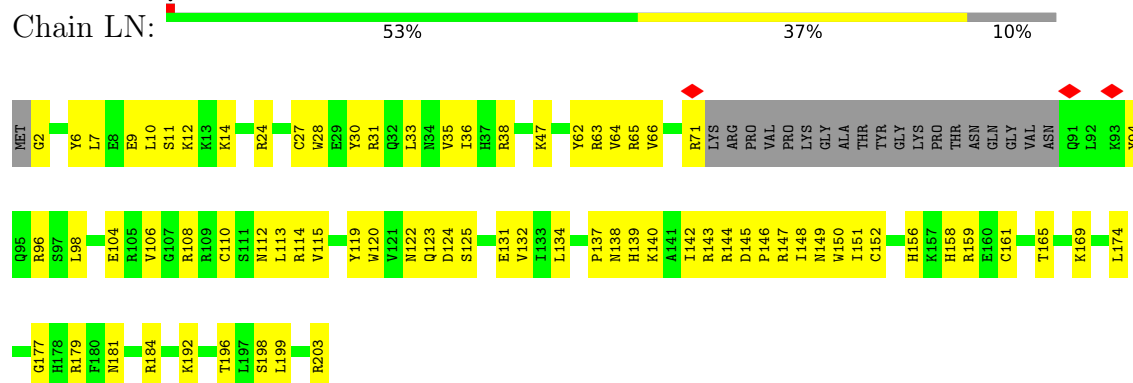
• Molecule 33: 60S ribosomal protein L13



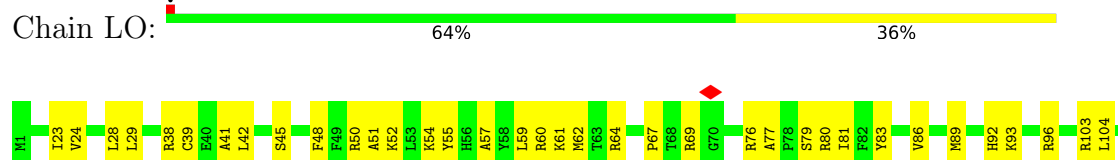
• Molecule 34: 60S ribosomal protein L14-like protein



• Molecule 35: Ribosomal protein L15



• Molecule 36: 60S ribosomal protein L16-like protein

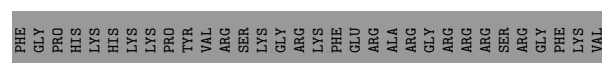
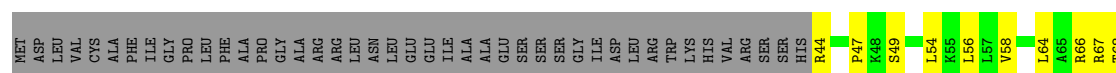




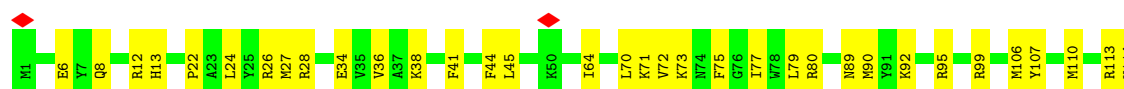
- Molecule 37: 60S ribosomal protein l17-like protein



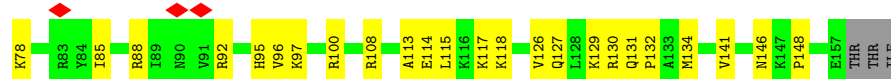
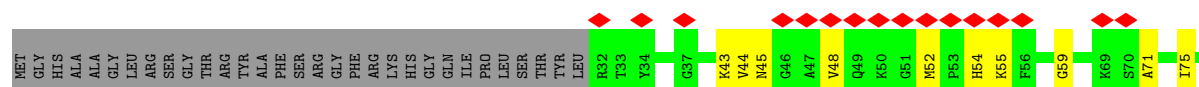
- Molecule 38: Ribosomal protein L18-like protein



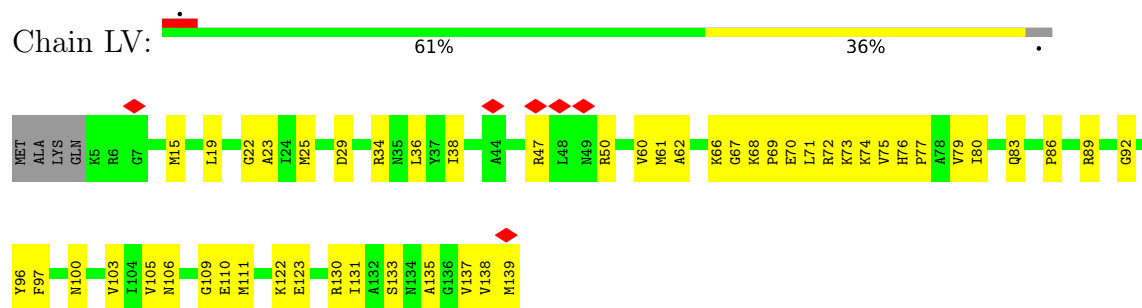
- Molecule 39: 60S ribosomal protein L20



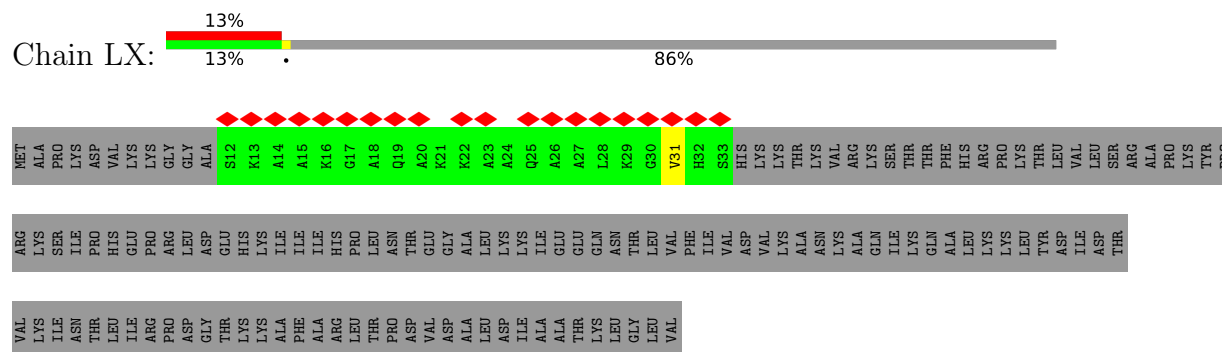
- Molecule 40: 60S ribosomal protein l21-like protein



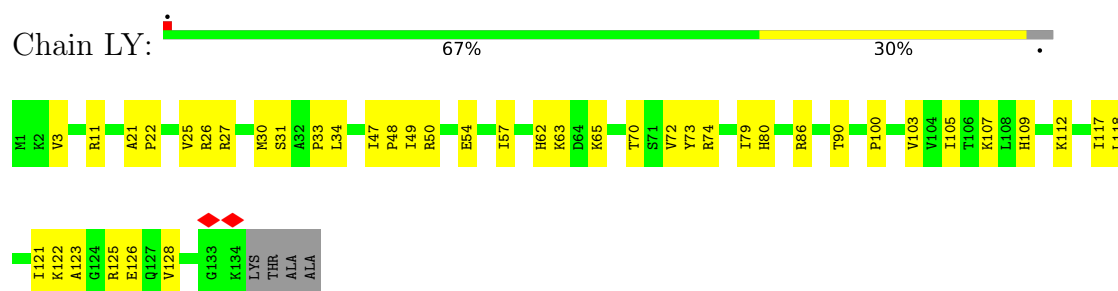
- Molecule 41: 60S ribosomal protein l23-like protein



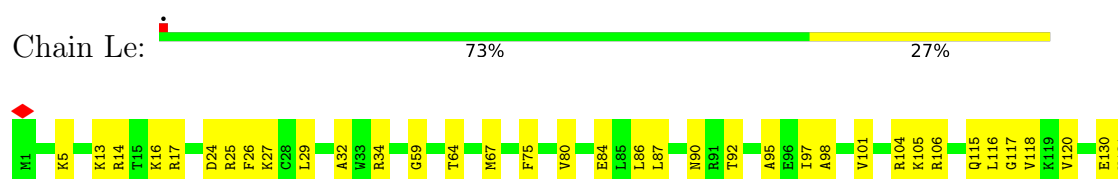
- Molecule 42: 60S ribosomal protein L25-like protein



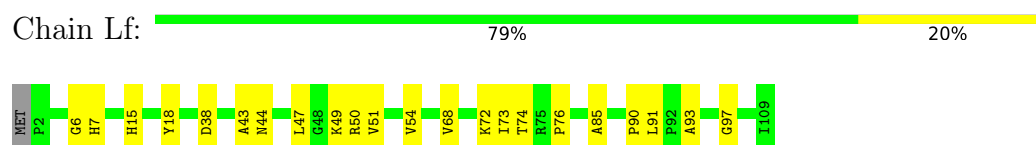
- Molecule 43: 60S ribosomal protein L26-like protein



- Molecule 44: 60S ribosomal protein L32-like protein

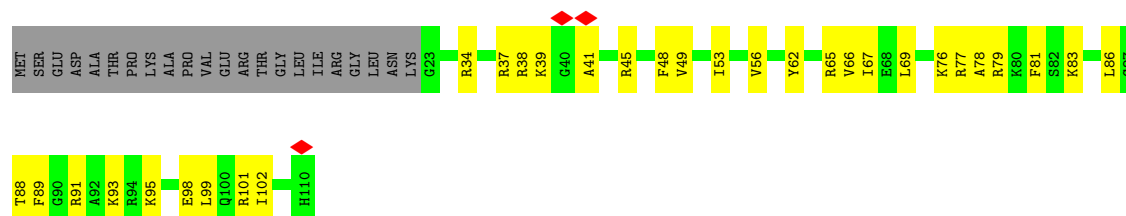
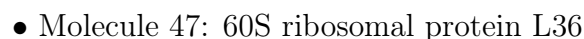


- Molecule 45: 60S ribosomal protein l33-like protein

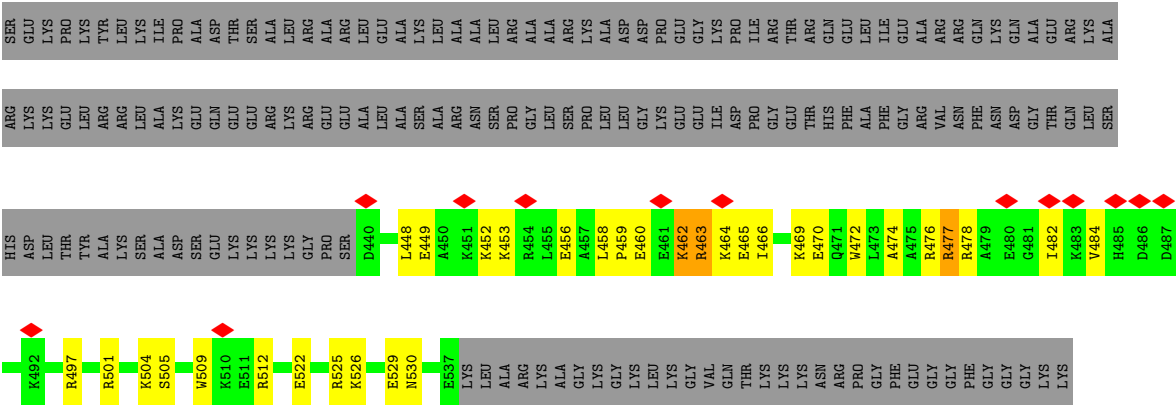


- Molecule 46: dolichyl-diphosphooligosaccharide--protein glycotransferase

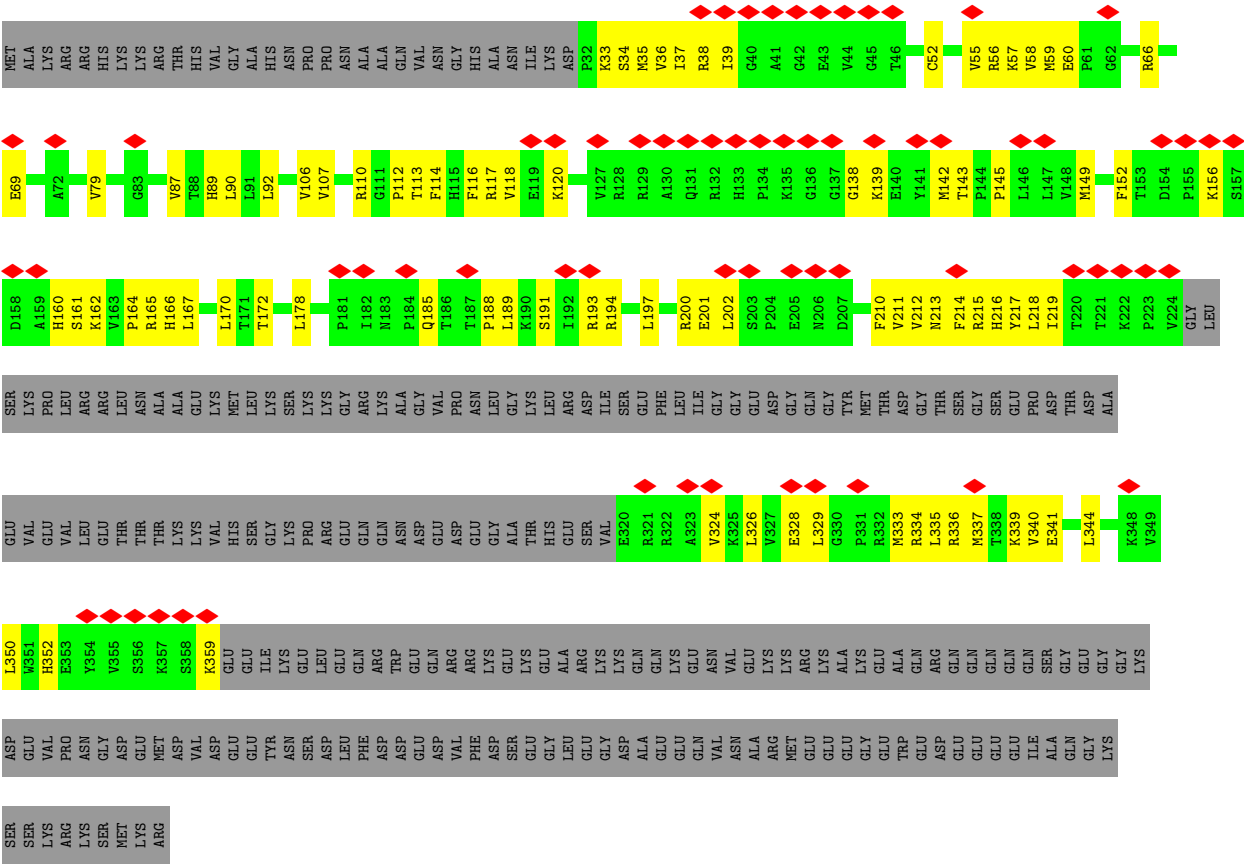
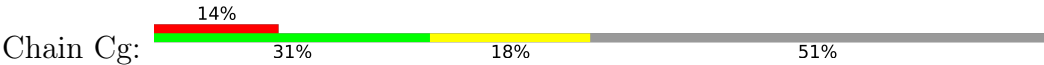








• Molecule 54: Brix domain-containing protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52677	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	0.369	Depositor
Minimum map value	-0.177	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.007	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: ZN, GTP

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	0.12	0/51017	0.29	3/79513 (0.0%)
2	C2	0.10	0/3754	0.26	0/5846
3	C3	0.11	0/2342	0.29	0/3649
4	CA	0.20	0/2190	0.53	0/2940
5	CB	0.20	0/2109	0.54	0/2866
6	CC	0.15	0/2459	0.37	0/3350
7	CE	0.17	0/3743	0.49	0/5045
8	CF	0.16	0/1982	0.42	0/2671
9	CG	0.19	0/1422	0.47	0/1920
10	CH	0.23	0/3927	0.56	0/5307
11	CI	0.18	0/1225	0.56	0/1645
12	CJ	0.15	0/3189	0.40	0/4309
13	CK	0.18	0/1804	0.45	0/2417
14	CL	0.18	0/2178	0.46	0/2983
15	CM	0.16	0/1555	0.45	0/2091
15	LF	0.15	0/2004	0.39	0/2686
16	CN	0.16	0/1881	0.46	0/2560
17	CO	0.13	0/470	0.36	0/619
18	CP	0.18	0/2594	0.47	0/3514
19	CQ	0.20	0/981	0.59	0/1301
20	CR	0.15	0/1369	0.38	0/1828
21	CS	0.12	0/746	0.33	0/997
22	CU	0.18	0/1428	0.53	0/1910
23	CX	0.16	0/705	0.41	0/938
24	Cz	0.16	0/598	0.53	1/785 (0.1%)
25	Cb	0.16	0/4474	0.44	1/6037 (0.0%)
26	Ch	0.23	0/563	0.64	1/746 (0.1%)
27	LB	0.18	0/2760	0.51	0/3701
28	LC	0.15	0/2809	0.40	0/3787
29	LE	0.18	0/1363	0.43	0/1833
30	LG	0.18	0/1597	0.53	0/2138
31	LH	0.15	0/1516	0.42	0/2038

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LK	0.18	0/1124	0.49	0/1507
33	LL	0.15	0/983	0.44	1/1318 (0.1%)
34	LM	0.26	0/1120	0.57	3/1507 (0.2%)
35	LN	0.14	0/1595	0.37	0/2132
36	LO	0.17	0/1652	0.42	0/2215
37	LP	0.17	0/1231	0.45	0/1658
38	LQ	0.14	0/1033	0.39	0/1391
39	LS	0.16	0/1468	0.44	1/1975 (0.1%)
40	LT	0.15	0/1033	0.44	0/1389
41	LV	0.16	0/1013	0.42	0/1361
42	LX	0.09	0/148	0.40	0/194
43	LY	0.16	0/1079	0.43	0/1443
44	Le	0.13	0/1073	0.32	0/1431
45	Lf	0.14	0/883	0.39	0/1187
46	Lh	0.15	0/1006	0.42	0/1338
47	Li	0.15	0/738	0.42	0/971
48	Lj	0.13	0/606	0.34	0/803
49	Lq	0.17	0/1621	0.52	0/2180
50	Cc	0.17	0/1934	0.50	0/2614
51	Cd	0.32	0/2818	0.63	2/3786 (0.1%)
52	Ce	0.18	0/1638	0.51	0/2196
53	Cf	0.27	0/851	0.71	3/1118 (0.3%)
54	Cg	0.17	0/1887	0.48	2/2544 (0.1%)
All	All	0.16	0/141288	0.40	18/202228 (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
5	CB	0	1
14	CL	0	1
30	LG	0	1
49	Lq	0	1
51	Cd	0	1
53	Cf	0	1
All	All	0	6

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1084	U	OP1-P-O3'	-8.87	81.39	108.00
1	C1	1084	U	OP2-P-O3'	-7.84	84.49	108.00
39	LS	170	PRO	CA-N-CD	-6.29	103.20	112.00
53	Cf	463	ARG	CA-CB-CG	6.20	126.50	114.10
26	Ch	331	ARG	CB-CG-CD	6.12	125.38	111.30
24	Cz	31	VAL	N-CA-C	-6.02	107.63	113.53
51	Cd	280	PRO	N-CA-C	5.94	116.17	110.47
33	LL	128	ARG	CB-CA-C	-5.88	109.78	116.54
54	Cg	142	MET	CA-C-N	-5.65	111.52	122.70
54	Cg	142	MET	C-N-CA	-5.65	111.52	122.70
51	Cd	280	PRO	CB-CA-C	-5.44	106.27	111.39
25	Cb	447	PRO	CA-N-CD	-5.24	104.66	112.00
53	Cf	477	ARG	CA-CB-CG	5.22	124.54	114.10
53	Cf	463	ARG	CB-CG-CD	5.10	123.02	111.30
34	LM	133	LYS	N-CA-C	-5.08	105.66	111.14
34	LM	137	LYS	CA-C-N	-5.03	112.64	121.70
34	LM	137	LYS	C-N-CA	-5.03	112.64	121.70
1	C1	436	G	C4'-C3'-O3'	-5.01	105.48	113.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	CB	103	ASP	Peptide
14	CL	223	HIS	Peptide
51	Cd	360	TYR	Peptide
53	Cf	462	LYS	Peptide
30	LG	161	ASP	Peptide
49	Lq	60	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C1	45600	0	22990	1043	0
2	C2	3359	0	1698	87	0
3	C3	2097	0	1065	58	0
4	CA	2144	0	2178	109	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	CB	2063	0	2131	82	0
6	CC	2388	0	2301	87	0
7	CE	3673	0	3778	127	0
8	CF	1945	0	1965	64	0
9	CG	1396	0	1420	72	0
10	CH	3851	0	3894	171	0
11	CI	1196	0	1202	57	0
12	CJ	3109	0	3122	121	0
13	CK	1778	0	1865	65	0
14	CL	2173	0	1423	23	0
15	CM	1525	0	1604	57	0
15	LF	1967	0	2080	50	0
16	CN	1856	0	1856	89	0
17	CO	468	0	503	20	0
18	CP	2535	0	2549	100	0
19	CQ	960	0	1000	73	0
20	CR	1354	0	1400	46	0
21	CS	734	0	721	15	0
22	CU	1415	0	1457	62	0
23	CX	701	0	742	24	0
24	Cz	592	0	640	14	0
25	Cb	4397	0	4541	146	0
26	Ch	562	0	611	34	0
27	LB	2708	0	2811	118	0
28	LC	2752	0	2878	87	0
29	LE	1338	0	1423	42	0
30	LG	1574	0	1709	74	0
31	LH	1496	0	1575	42	0
32	LK	1112	0	1190	49	0
33	LL	964	0	1041	44	0
34	LM	1101	0	1170	21	0
35	LN	1563	0	1618	65	0
36	LO	1618	0	1714	69	0
37	LP	1212	0	1250	44	0
38	LQ	1021	0	1118	27	0
39	LS	1433	0	1496	40	0
40	LT	1014	0	1073	30	0
41	LV	995	0	1055	51	0
42	LX	148	0	163	1	0
43	LY	1065	0	1156	36	0
44	Le	1055	0	1133	32	0
45	Lf	862	0	891	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	Lh	995	0	1110	41	0
47	Li	731	0	797	33	0
48	Lj	595	0	625	25	0
49	Lq	1600	0	1703	61	0
50	Cc	1898	0	1931	61	0
51	Cd	2763	0	2859	108	0
52	Ce	1609	0	1682	67	0
53	Cf	845	0	900	52	0
54	Cg	1850	0	1937	82	0
55	CH	32	0	12	0	0
56	CQ	1	0	0	0	0
56	Ce	1	0	0	0	0
56	Lj	1	0	0	0	0
All	All	133790	0	110756	3671	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 15.

All (3671) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1055:U:C4	1:C1:1063:C:N4	2.08	1.20
1:C1:788:A:N6	1:C1:915:G:H1	1.36	1.20
1:C1:1055:U:O4	1:C1:1063:C:C4	1.96	1.16
1:C1:2848:A:H61	1:C1:2871:C:N4	1.48	1.09
1:C1:2848:A:N6	1:C1:2871:C:H42	1.62	0.98
1:C1:2848:A:H61	1:C1:2871:C:H42	0.97	0.97
1:C1:1055:U:C4	1:C1:1063:C:C4	2.48	0.96
1:C1:2404:G:H1	1:C1:2467:U:H3	1.03	0.95
3:C3:38:G:H1	3:C3:43:U:H3	1.09	0.95
49:Lq:53:VAL:O	49:Lq:154:THR:HA	1.70	0.92
1:C1:2388:U:H3	1:C1:2561:G:H1	1.16	0.91
36:LO:153:ASP:HB3	36:LO:157:ARG:HH12	1.35	0.91
19:CQ:99:ILE:HD12	19:CQ:102:ARG:HH21	1.38	0.89
5:CB:117:PRO:HA	5:CB:121:ARG:HG3	1.52	0.89
1:C1:934:G:H3'	1:C1:1098:G:H21	1.37	0.89
16:CN:81:LEU:HD22	16:CN:96:ARG:HE	1.36	0.88
32:LK:59:THR:HG23	32:LK:74:VAL:HB	1.55	0.88
1:C1:974:G:H1	1:C1:1038:U:H3	0.87	0.87
18:CP:371:LEU:HD12	18:CP:541:LEU:HD23	1.55	0.87
25:Cb:513:GLU:O	25:Cb:517:ASN:ND2	2.09	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2785:U:OP2	10:CH:125:LYS:NZ	2.08	0.85
10:CH:474:TYR:OH	19:CQ:102:ARG:NH1	2.09	0.85
1:C1:213:G:C6	1:C1:1371:G:C2	2.63	0.85
29:LE:86:PRO:HG3	29:LE:169:LEU:HD22	1.58	0.85
28:LC:148:GLU:HG3	28:LC:150:PRO:HD2	1.57	0.85
1:C1:2389:U:H5'	9:CG:54:ASN:HB3	1.59	0.84
1:C1:6:A:OP1	12:CJ:93:ARG:NH1	2.11	0.84
15:CM:141:ALA:HB1	15:CM:237:ARG:HH12	1.42	0.84
13:CK:245:ILE:HD13	13:CK:257:ALA:HB2	1.59	0.83
26:Ch:276:ILE:HG22	26:Ch:280:ARG:HH11	1.41	0.83
1:C1:115:A:N6	1:C1:149:U:C2	2.47	0.83
1:C1:1263:U:H5''	8:CF:69:LYS:HZ3	1.44	0.83
1:C1:1263:U:H2'	1:C1:1264:G:H8	1.44	0.83
4:CA:227:THR:HG23	22:CU:255:ARG:HH22	1.44	0.82
1:C1:2390:U:C4	1:C1:2560:G:O6	2.31	0.82
7:CE:239:ALA:HB3	7:CE:244:LEU:HD12	1.62	0.82
6:CC:403:ARG:HG3	12:CJ:150:LEU:HD22	1.60	0.82
29:LE:160:ALA:HA	29:LE:163:LYS:HE2	1.61	0.82
4:CA:100:LEU:HB3	4:CA:117:ALA:HB3	1.60	0.82
53:Cf:460:GLU:HA	53:Cf:463:ARG:HD3	1.62	0.81
1:C1:2416:G:O6	1:C1:2446:A:N1	2.13	0.81
46:Lh:15:LYS:HG2	46:Lh:19:GLU:HG2	1.60	0.81
13:CK:19:ASP:OD1	13:CK:23:ARG:NH1	2.12	0.81
29:LE:156:SER:O	29:LE:159:ALA:O	1.98	0.80
8:CF:32:GLU:O	8:CF:36:LYS:NZ	2.13	0.80
27:LB:314:ARG:O	27:LB:334:LYS:NZ	2.13	0.80
1:C1:108:C:OP1	33:LL:42:LYS:NZ	2.13	0.80
1:C1:3135:G:H4'	36:LO:163:LYS:HE3	1.61	0.80
6:CC:197:ARG:HH12	23:CX:130:ARG:HD3	1.46	0.80
10:CH:425:TRP:HH2	16:CN:83:HIS:HA	1.46	0.79
16:CN:117:ILE:HD11	16:CN:139:ARG:HH21	1.48	0.79
54:Cg:118:VAL:HG13	54:Cg:333:MET:HE1	1.63	0.79
10:CH:53:GLN:HE21	10:CH:105:GLU:HG3	1.47	0.78
25:Cb:493:ARG:HH11	25:Cb:581:ALA:HB2	1.48	0.78
22:CU:316:GLN:HG2	22:CU:320:GLN:HE22	1.47	0.78
13:CK:149:ARG:HH22	13:CK:170:ARG:HH21	1.28	0.78
4:CA:139:ILE:HB	4:CA:179:VAL:HG22	1.64	0.78
51:Cd:310:GLU:OE2	51:Cd:360:TYR:OH	2.01	0.78
39:LS:80:ARG:HH21	39:LS:89:ASN:HD21	1.31	0.78
1:C1:2380:G:H5''	1:C1:2381:A:H5'	1.66	0.78
1:C1:2848:A:N1	1:C1:2871:C:N3	2.32	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LH:8:GLU:OE1	31:LH:72:ARG:NH1	2.17	0.78
3:C3:71:U:H3	3:C3:130:G:H1	1.29	0.77
22:CU:278:THR:HG22	22:CU:280:ALA:H	1.49	0.77
1:C1:788:A:N6	1:C1:915:G:N1	2.20	0.77
4:CA:102:MET:HE2	4:CA:117:ALA:HB2	1.67	0.77
1:C1:361:A:OP2	51:Cd:21:LYS:NZ	2.17	0.77
28:LC:210:LEU:HB3	28:LC:255:ILE:HG12	1.66	0.77
1:C1:1055:U:O4	1:C1:1063:C:N3	2.18	0.77
4:CA:113:VAL:HG12	4:CA:245:ILE:HG12	1.66	0.77
25:Cb:369:THR:O	25:Cb:419:ILE:HA	1.84	0.77
25:Cb:242:GLU:HG2	25:Cb:245:ARG:HH21	1.50	0.77
31:LH:23:ARG:HD2	31:LH:39:SER:HA	1.67	0.77
41:LV:15:MET:HE1	41:LV:123:GLU:HG2	1.67	0.77
6:CC:260:GLU:OE2	30:LG:233:ARG:NH1	2.18	0.76
1:C1:2936:U:C2	53:Cf:526:LYS:HE2	2.20	0.76
21:CS:688:GLN:HE21	30:LG:73:LYS:HB3	1.49	0.76
36:LO:77:ALA:HB3	36:LO:80:ARG:HG2	1.68	0.76
41:LV:68:LYS:HE2	41:LV:70:GLU:HB3	1.68	0.76
1:C1:974:G:O6	1:C1:1038:U:O4	2.04	0.76
34:LM:108:ARG:NH1	36:LO:200:ALA:O	2.18	0.76
1:C1:713:G:C6	1:C1:723:G:C2	2.73	0.76
52:Ce:34:VAL:O	52:Ce:112:ARG:NH1	2.19	0.76
54:Cg:210:PHE:HB2	54:Cg:336:ARG:HH12	1.50	0.76
1:C1:213:G:C6	1:C1:1371:G:N2	2.53	0.76
10:CH:316:ILE:HB	10:CH:318:ARG:HH22	1.50	0.76
10:CH:422:ARG:HA	10:CH:425:TRP:CD1	2.20	0.76
54:Cg:120:LYS:HB2	54:Cg:334:ARG:HG3	1.68	0.76
4:CA:36:VAL:HG21	4:CA:59:LEU:HD13	1.67	0.76
7:CE:391:GLN:HB3	7:CE:395:LYS:HE3	1.66	0.76
8:CF:134:THR:HG23	8:CF:197:GLU:HG3	1.68	0.75
12:CJ:376:ARG:NH2	15:CM:189:ASP:OD1	2.19	0.75
16:CN:40:ALA:O	16:CN:43:GLN:NE2	2.20	0.75
10:CH:228:LEU:HD23	25:Cb:590:LEU:HD12	1.68	0.75
34:LM:123:LEU:HD22	36:LO:195:VAL:HG23	1.67	0.75
51:Cd:373:VAL:O	52:Ce:168:ARG:NH1	2.19	0.75
51:Cd:374:GLY:HA2	52:Ce:168:ARG:HH12	1.50	0.75
13:CK:236:LYS:HD2	13:CK:237:ILE:H	1.51	0.75
1:C1:3117:C:H2'	51:Cd:303:ARG:HH12	1.50	0.75
9:CG:71:LEU:HA	9:CG:86:ALA:HB2	1.69	0.75
28:LC:298:SER:HB3	50:Cc:244:ARG:HH21	1.51	0.75
15:CM:94:ARG:HG2	15:CM:114:LEU:HB3	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LK:90:ARG:HH22	32:LK:94:LYS:HB2	1.52	0.75
15:LF:14:VAL:HG11	15:LF:22:ARG:HH12	1.50	0.75
49:Lq:143:ASP:O	49:Lq:147:LYS:HB2	1.86	0.75
18:CP:478:LYS:O	18:CP:482:GLN:NE2	2.19	0.75
49:Lq:59:PRO:HB2	49:Lq:170:GLY:H	1.52	0.74
54:Cg:212:VAL:HB	54:Cg:335:LEU:HB2	1.67	0.74
17:CO:9:ARG:O	17:CO:13:ASN:ND2	2.18	0.74
51:Cd:55:GLU:OE1	51:Cd:59:LYS:NZ	2.20	0.74
35:LN:36:ILE:HG12	35:LN:64:VAL:HG22	1.69	0.74
1:C1:2389:U:O2	1:C1:2560:G:O6	2.05	0.74
1:C1:2735:G:H1	1:C1:2741:U:H3	1.34	0.74
2:C2:152:G:H5'	30:LG:66:LYS:HD2	1.68	0.74
52:Ce:121:ILE:HD13	52:Ce:124:ARG:HH22	1.51	0.74
1:C1:705:G:OP2	1:C1:705:G:N2	2.21	0.74
2:C2:127:U:O2	12:CJ:15:ASN:ND2	2.21	0.74
11:CI:291:ARG:HA	11:CI:294:GLU:HG2	1.68	0.74
25:Cb:396:VAL:HG12	25:Cb:426:ALA:HB1	1.68	0.74
22:CU:314:ALA:O	22:CU:318:GLN:NE2	2.21	0.74
32:LK:38:SER:H	32:LK:41:LYS:HE3	1.52	0.74
53:Cf:458:LEU:O	53:Cf:463:ARG:NH1	2.21	0.74
4:CA:35:ARG:HH22	6:CC:158:TYR:HD2	1.35	0.74
7:CE:377:LEU:HB3	7:CE:382:LEU:HB2	1.69	0.74
12:CJ:161:PRO:HD2	12:CJ:164:MET:HE2	1.68	0.74
17:CO:36:LYS:NZ	27:LB:208:THR:OG1	2.21	0.74
6:CC:182:SER:O	23:CX:133:ARG:NH2	2.20	0.74
1:C1:223:U:H2'	1:C1:224:A:C8	2.23	0.74
21:CS:470:ARG:HG2	30:LG:244:LYS:HD2	1.69	0.74
1:C1:230:A:H2'	1:C1:231:A:C8	2.23	0.73
10:CH:416:VAL:HG22	27:LB:349:ARG:HH12	1.52	0.73
10:CH:267:ILE:HG22	10:CH:271:LYS:HZ2	1.53	0.73
1:C1:2764:U:O4	9:CG:76:LYS:NZ	2.22	0.73
20:CR:148:GLN:HA	33:LL:86:PRO:HG3	1.68	0.73
27:LB:36:ASP:OD1	27:LB:39:LYS:NZ	2.17	0.73
26:Ch:320:LYS:HA	26:Ch:323:GLU:HG3	1.70	0.73
36:LO:127:ARG:HG3	36:LO:131:LEU:HD12	1.70	0.73
21:CS:700:GLU:OE2	35:LN:31:ARG:NH2	2.22	0.73
1:C1:1181:C:O2'	14:CL:27:ARG:NH2	2.21	0.73
10:CH:126:GLN:HG2	13:CK:251:ASN:HB3	1.70	0.73
41:LV:109:GLY:O	41:LV:130:ARG:NH1	2.21	0.73
48:Lj:54:LYS:O	48:Lj:58:VAL:HB	1.88	0.73
10:CH:361:LEU:HG	10:CH:365:MET:HE1	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:LS:8:GLN:HG3	39:LS:26:ARG:HE	1.53	0.73
49:Lq:34:LEU:HA	49:Lq:205:THR:O	1.89	0.73
1:C1:2432:C:H4'	49:Lq:27:ASN:HD21	1.54	0.72
21:CS:688:GLN:OE1	35:LN:24:ARG:NH1	2.21	0.72
9:CG:114:ILE:HD12	9:CG:164:CYS:HB3	1.71	0.72
12:CJ:101:SER:HB2	12:CJ:105:ARG:HH12	1.54	0.72
41:LV:105:VAL:HG22	41:LV:111:MET:HG2	1.71	0.72
1:C1:2944:U:H2'	1:C1:2945:A:H8	1.53	0.72
30:LG:84:THR:HG21	30:LG:184:LYS:HG3	1.72	0.72
1:C1:345:G:OP2	20:CR:7:LYS:NZ	2.23	0.72
20:CR:224:ASP:OD1	20:CR:227:ARG:NH1	2.22	0.72
13:CK:232:THR:N	13:CK:236:LYS:O	2.19	0.72
28:LC:115:ASN:HB2	28:LC:118:GLN:HG3	1.71	0.72
22:CU:316:GLN:O	22:CU:320:GLN:NE2	2.22	0.72
1:C1:21:G:H3'	1:C1:22:G:H8	1.55	0.71
1:C1:2390:U:N3	1:C1:2560:G:C6	2.58	0.71
46:Lh:83:LEU:HA	46:Lh:86:ARG:HD2	1.72	0.71
50:Cc:199:ASP:OD2	50:Cc:244:ARG:NH1	2.23	0.71
27:LB:26:ARG:HG3	27:LB:336:ILE:HD13	1.71	0.71
1:C1:350:G:N2	1:C1:353:A:OP2	2.19	0.71
1:C1:507:G:OP1	15:LF:73:ARG:NH2	2.21	0.71
18:CP:491:LEU:HD12	18:CP:523:VAL:HG12	1.72	0.71
25:Cb:444:PRO:HB3	25:Cb:453:ARG:HH21	1.54	0.71
37:LP:119:VAL:HG22	37:LP:146:ILE:HG12	1.71	0.71
5:CB:67:THR:O	5:CB:279:ARG:HB3	1.90	0.71
10:CH:105:GLU:HB3	10:CH:109:ARG:NH1	2.05	0.71
12:CJ:180:ILE:HA	12:CJ:389:ALA:HA	1.72	0.71
10:CH:277:PHE:HB3	10:CH:282:VAL:HG11	1.72	0.71
18:CP:474:ASN:O	18:CP:475:ARG:NE	2.22	0.71
27:LB:84:MET:HG2	27:LB:165:THR:HG22	1.72	0.71
10:CH:183:VAL:HG11	10:CH:219:ASP:HB2	1.73	0.71
15:CM:67:GLU:OE2	15:CM:70:ARG:NH2	2.23	0.71
43:LY:31:SER:HA	43:LY:48:PRO:HA	1.72	0.71
1:C1:2390:U:C4	1:C1:2560:G:C6	2.79	0.71
14:CL:223:HIS:O	14:CL:225:VAL:N	2.21	0.71
47:Li:37:ARG:HH11	47:Li:38:ARG:HG3	1.56	0.71
50:Cc:206:GLU:OE1	50:Cc:253:ARG:NH1	2.24	0.71
53:Cf:462:LYS:O	53:Cf:466:ILE:HG12	1.91	0.71
1:C1:3001:A:H4'	27:LB:13:SER:HB2	1.73	0.70
1:C1:3283:G:H21	1:C1:3302:A:H2	1.39	0.70
4:CA:171:LYS:NZ	6:CC:164:ASP:OD2	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Le:90:ASN:HD21	52:Ce:115:ARG:HH22	1.39	0.70
46:Lh:11:GLN:HB3	46:Lh:15:LYS:NZ	2.05	0.70
50:Cc:94:TRP:CZ3	50:Cc:166:PRO:HG3	2.26	0.70
54:Cg:113:THR:HB	54:Cg:341:GLU:HB2	1.72	0.70
1:C1:642:C:H2'	1:C1:643:A:H8	1.56	0.70
10:CH:474:TYR:HH	19:CQ:102:ARG:HH11	1.39	0.70
4:CA:114:LYS:HB3	4:CA:244:ILE:HG12	1.71	0.70
44:Le:131:VAL:HG12	52:Ce:135:GLU:HG2	1.74	0.70
5:CB:69:LYS:NZ	5:CB:278:VAL:O	2.25	0.70
5:CB:261:THR:HA	5:CB:264:ARG:HE	1.57	0.70
14:CL:55:ILE:HB	14:CL:62:LYS:HE3	1.72	0.70
32:LK:17:ALA:O	32:LK:57:ARG:HA	1.92	0.70
50:Cc:30:HIS:O	50:Cc:80:GLN:NE2	2.23	0.70
1:C1:123:A:OP1	30:LG:108:LYS:NZ	2.25	0.70
53:Cf:478:ARG:HH12	54:Cg:110:ARG:C	2.00	0.70
4:CA:107:VAL:O	4:CA:249:SER:OG	2.10	0.70
44:Le:115:GLN:HB3	52:Ce:123:MET:HG2	1.73	0.70
1:C1:208:G:OP1	43:LY:11:ARG:NH1	2.25	0.70
1:C1:1371:G:OP2	44:Le:105:LYS:NZ	2.25	0.70
1:C1:3298:U:H2'	1:C1:3299:A:H8	1.55	0.70
8:CF:77:LEU:HD11	8:CF:102:LEU:HD21	1.72	0.70
51:Cd:200:LYS:H	51:Cd:254:THR:HG22	1.56	0.70
5:CB:97:VAL:HG23	5:CB:152:VAL:HG13	1.74	0.70
10:CH:75:PRO:HA	10:CH:78:ARG:HG2	1.74	0.70
16:CN:61:ARG:HD3	41:LV:133:SER:HA	1.74	0.70
25:Cb:446:GLN:HB2	25:Cb:449:ILE:HG13	1.72	0.70
25:Cb:471:ARG:NH1	25:Cb:542:GLU:OE2	2.25	0.70
1:C1:202:A:N3	28:LC:228:ASN:ND2	2.40	0.69
10:CH:425:TRP:CZ3	16:CN:86:ASN:HB3	2.26	0.69
30:LG:189:LEU:HB3	30:LG:198:ALA:HB3	1.73	0.69
6:CC:362:PRO:HD3	6:CC:384:PRO:HG2	1.72	0.69
15:CM:70:ARG:HH12	15:CM:138:PRO:HD3	1.58	0.69
18:CP:399:ALA:HA	18:CP:402:MET:HE2	1.74	0.69
31:LH:134:VAL:HG12	31:LH:150:GLY:HA3	1.72	0.69
4:CA:243:ILE:HG22	4:CA:244:ILE:HG23	1.73	0.69
9:CG:145:GLY:HA2	9:CG:167:GLN:HG2	1.72	0.69
12:CJ:398:ASP:HB3	12:CJ:401:LEU:HD23	1.74	0.69
31:LH:87:LYS:HB2	31:LH:189:ILE:HD13	1.75	0.69
1:C1:2406:C:H2'	1:C1:2407:A:H5''	1.74	0.69
27:LB:349:ARG:O	27:LB:353:GLU:HB2	1.93	0.69
41:LV:22:GLY:N	41:LV:38:ILE:O	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:941:U:OP2	22:CU:306:ARG:NH2	2.26	0.69
2:C2:39:G:C2	2:C2:105:A:C2	2.81	0.69
7:CE:151:VAL:HG12	7:CE:316:LEU:HB3	1.75	0.69
47:Li:88:THR:HB	47:Li:91:ARG:HG3	1.73	0.69
4:CA:112:THR:OG1	4:CA:249:SER:O	2.11	0.69
16:CN:214:GLU:HA	16:CN:217:VAL:HG22	1.74	0.69
15:LF:56:LYS:NZ	15:LF:60:GLU:OE2	2.26	0.69
41:LV:122:LYS:HE3	41:LV:139:MET:HA	1.75	0.69
50:Cc:174:ARG:NH1	50:Cc:175:ILE:O	2.26	0.69
1:C1:1071:G:H2'	1:C1:1072:G:C8	2.27	0.69
1:C1:1364:G:OP2	28:LC:204:ARG:NH1	2.25	0.69
9:CG:149:ARG:NH1	9:CG:162:ILE:O	2.26	0.69
1:C1:1049:C:H2'	1:C1:1050:C:C6	2.27	0.69
1:C1:2768:C:H2'	1:C1:2769:A:C8	2.27	0.69
12:CJ:116:THR:HG22	12:CJ:118:LYS:H	1.57	0.68
1:C1:694:U:O2'	1:C1:735:G:N3	2.26	0.68
4:CA:99:ASP:HB3	4:CA:116:TYR:HE1	1.58	0.68
5:CB:275:TRP:HE3	5:CB:278:VAL:HG11	1.58	0.68
12:CJ:113:PRO:HA	12:CJ:116:THR:HB	1.74	0.68
22:CU:255:ARG:HE	22:CU:259:ARG:HH22	1.40	0.68
25:Cb:513:GLU:HA	25:Cb:516:ASN:HD22	1.58	0.68
54:Cg:214:PHE:HB3	54:Cg:333:MET:HB3	1.74	0.68
1:C1:1217:U:H4'	1:C1:1218:G:H5'	1.75	0.68
6:CC:367:ARG:HH22	6:CC:385:THR:HA	1.59	0.68
12:CJ:141:LEU:HD11	12:CJ:241:VAL:HG11	1.73	0.68
33:LL:86:PRO:HG2	33:LL:89:LEU:HB3	1.74	0.68
54:Cg:167:LEU:HD11	54:Cg:337:MET:HE2	1.76	0.68
1:C1:954:G:H2'	1:C1:955:U:C6	2.29	0.68
10:CH:421:LEU:HD13	16:CN:83:HIS:CE1	2.29	0.68
16:CN:99:GLU:HG3	16:CN:101:LEU:H	1.58	0.68
25:Cb:4:ARG:NH2	25:Cb:537:VAL:O	2.26	0.68
31:LH:89:LYS:HB2	31:LH:185:GLU:HB3	1.73	0.68
49:Lq:148:VAL:O	49:Lq:152:LYS:HG3	1.92	0.68
51:Cd:221:ILE:HD11	51:Cd:395:PRO:HG2	1.74	0.68
1:C1:127:G:P	35:LN:140:LYS:HE2	2.33	0.68
15:CM:143:GLY:HA3	15:CM:241:ILE:HD13	1.75	0.68
1:C1:100:A:H3'	1:C1:101:G:H21	1.59	0.68
10:CH:13:ALA:HB2	10:CH:143:LYS:HA	1.73	0.68
18:CP:525:ASN:HD22	18:CP:556:PHE:HD1	1.42	0.68
19:CQ:87:GLN:OE1	19:CQ:91:LYS:NZ	2.27	0.68
1:C1:713:G:C5	1:C1:723:G:C2	2.81	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CM:182:TYR:O	15:CM:200:ASN:ND2	2.26	0.68
10:CH:249:VAL:HB	10:CH:282:VAL:HG12	1.76	0.68
1:C1:975:G:H4'	1:C1:976:U:H5'	1.75	0.68
1:C1:3108:U:O2	1:C1:3337:C:N3	2.27	0.68
50:Cc:47:VAL:HG21	50:Cc:89:TRP:HA	1.76	0.68
7:CE:370:VAL:HG13	7:CE:412:ILE:HG22	1.75	0.67
35:LN:115:VAL:HA	35:LN:134:LEU:HD23	1.77	0.67
4:CA:36:VAL:O	4:CA:62:GLY:HA2	1.95	0.67
50:Cc:129:LYS:HD2	50:Cc:149:ALA:HA	1.77	0.67
52:Ce:163:GLU:HA	52:Ce:166:ILE:HD12	1.76	0.67
53:Cf:476:ARG:HH22	54:Cg:165:ARG:C	2.02	0.67
1:C1:342:C:OP1	20:CR:10:ARG:NH2	2.28	0.67
1:C1:920:U:O2	28:LC:74:ARG:NH2	2.27	0.67
1:C1:3253:U:H4'	27:LB:174:GLN:HE22	1.58	0.67
34:LM:108:ARG:HD3	36:LO:201:ALA:O	1.95	0.67
1:C1:386:U:OP2	51:Cd:431:ARG:NH1	2.27	0.67
1:C1:2780:U:H4'	10:CH:34:PRO:HB2	1.76	0.67
2:C2:66:A:H5''	48:Lj:87:ARG:HG3	1.77	0.67
4:CA:134:LYS:O	4:CA:173:LYS:NZ	2.27	0.67
10:CH:123:GLN:HE22	13:CK:250:GLU:HB2	1.60	0.67
16:CN:96:ARG:NH2	19:CQ:75:ARG:O	2.27	0.67
53:Cf:477:ARG:HB2	53:Cf:482:ILE:HD12	1.76	0.67
1:C1:36:C:O2'	1:C1:915:G:N3	2.27	0.67
1:C1:116:A:OP1	47:Li:45:ARG:NH1	2.27	0.67
1:C1:3323:C:N4	1:C1:3326:C:OP2	2.27	0.67
4:CA:73:ARG:NH1	4:CA:75:TYR:OH	2.28	0.67
36:LO:38:ARG:HB3	36:LO:41:ALA:HB3	1.77	0.67
43:LY:34:LEU:HD11	43:LY:47:ILE:HG12	1.77	0.67
13:CK:236:LYS:NZ	18:CP:474:ASN:HA	2.10	0.67
22:CU:267:ARG:HH12	23:CX:79:PRO:HB3	1.60	0.67
1:C1:983:A:N1	1:C1:1032:U:O2'	2.28	0.67
15:CM:244:LEU:HG	15:CM:248:MET:HE2	1.77	0.67
16:CN:187:ASN:H	16:CN:210:THR:HG22	1.59	0.67
44:Le:87:LEU:HD13	44:Le:116:LEU:HD11	1.76	0.67
52:Ce:64:TYR:HA	52:Ce:79:GLU:O	1.94	0.67
4:CA:116:TYR:CE2	4:CA:118:GLN:HG2	2.30	0.67
8:CF:205:GLN:O	8:CF:209:LEU:HD12	1.94	0.67
26:Ch:327:THR:HB	26:Ch:331:ARG:NH1	2.09	0.67
28:LC:30:PRO:HG3	28:LC:280:ASN:HB2	1.76	0.67
45:Lf:73:ILE:HD13	45:Lf:85:ALA:HB2	1.76	0.67
1:C1:2351:C:O2'	1:C1:3247:A:N1	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2975:C:OP1	16:CN:9:ASN:ND2	2.28	0.67
4:CA:59:LEU:HD21	4:CA:163:PHE:HA	1.77	0.67
30:LG:226:LEU:O	30:LG:230:GLU:HB2	1.95	0.67
51:Cd:217:GLU:O	51:Cd:221:ILE:HD12	1.94	0.67
8:CF:43:PHE:HB3	8:CF:223:LEU:HD13	1.77	0.66
9:CG:45:VAL:HG13	9:CG:71:LEU:HB2	1.76	0.66
7:CE:537:ASP:OD2	7:CE:540:LYS:NZ	2.28	0.66
6:CC:142:ASP:OD1	6:CC:146:GLY:N	2.24	0.66
53:Cf:501:ARG:HE	53:Cf:504:LYS:HE3	1.60	0.66
1:C1:390:U:N3	2:C2:12:A:OP1	2.27	0.66
18:CP:309:ARG:HH12	18:CP:396:THR:HG22	1.60	0.66
28:LC:287:LEU:HD12	38:LQ:56:LEU:HG	1.76	0.66
16:CN:163:PRO:HD3	16:CN:193:ILE:HD11	1.78	0.66
1:C1:3021:U:H2'	1:C1:3022:G:C8	2.31	0.66
32:LK:53:TRP:HE1	32:LK:73:VAL:HG11	1.60	0.66
1:C1:2564:G:N7	9:CG:1:MET:N	2.43	0.66
25:Cb:510:LYS:HZ2	25:Cb:512:VAL:H	1.42	0.66
28:LC:83:THR:HG22	28:LC:85:ARG:H	1.59	0.66
1:C1:281:U:H2'	1:C1:282:G:H8	1.60	0.66
1:C1:607:U:OP2	51:Cd:229:ARG:NH2	2.29	0.66
1:C1:1202:U:H2'	24:Cz:48:TRP:CH2	2.30	0.66
5:CB:158:ARG:HH21	5:CB:185:MET:HE1	1.61	0.66
9:CG:17:ALA:O	9:CG:95:ARG:NH2	2.29	0.66
29:LE:194:LYS:HB3	29:LE:196:HIS:CE1	2.31	0.66
34:LM:109:ARG:HA	34:LM:112:LEU:HD12	1.77	0.66
4:CA:34:GLN:HA	4:CA:87:ASN:HD21	1.60	0.66
6:CC:326:LEU:HD13	12:CJ:124:ASN:HD21	1.61	0.66
10:CH:401:ARG:NH2	16:CN:44:ASP:OD2	2.28	0.66
32:LK:38:SER:HB2	32:LK:41:LYS:HG2	1.78	0.66
1:C1:603:G:H2'	1:C1:604:G:H8	1.61	0.66
10:CH:420:ASP:HB3	10:CH:423:LYS:NZ	2.11	0.66
12:CJ:164:MET:HE3	12:CJ:231:VAL:HG11	1.78	0.66
16:CN:26:VAL:HG21	16:CN:35:TYR:HD2	1.60	0.66
1:C1:2334:A:OP2	1:C1:2336:C:N4	2.29	0.65
9:CG:1:MET:HA	9:CG:39:ARG:NH2	2.11	0.65
10:CH:425:TRP:CH2	16:CN:83:HIS:HA	2.30	0.65
10:CH:432:TRP:HD1	19:CQ:83:ARG:CZ	2.08	0.65
16:CN:142:ILE:HG12	16:CN:148:VAL:HG12	1.79	0.65
53:Cf:501:ARG:HE	53:Cf:504:LYS:CE	2.08	0.65
1:C1:289:A:O2'	47:Li:41:ALA:O	2.12	0.65
1:C1:2813:C:H2'	1:C1:2814:G:H8	1.59	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Cb:318:GLU:OE2	25:Cb:535:LYS:NZ	2.29	0.65
29:LE:172:ASN:HA	29:LE:175:LYS:NZ	2.11	0.65
1:C1:934:G:H3'	1:C1:1098:G:N2	2.09	0.65
7:CE:213:THR:H	7:CE:235:ASN:HD22	1.43	0.65
18:CP:561:LYS:O	18:CP:564:ARG:NH2	2.29	0.65
26:Ch:294:PHE:HE1	54:Cg:189:LEU:HD21	1.61	0.65
31:LH:130:MET:HE1	31:LH:148:LEU:HD23	1.78	0.65
1:C1:115:A:N6	1:C1:149:U:N3	2.45	0.65
1:C1:695:G:H5'	1:C1:735:G:H21	1.62	0.65
1:C1:781:G:H22	28:LC:102:ALA:HA	1.61	0.65
6:CC:186:ILE:HD11	6:CC:197:ARG:HD2	1.76	0.65
19:CQ:22:MET:HE2	41:LV:97:PHE:HE1	1.61	0.65
15:LF:93:ILE:HA	15:LF:119:ASN:O	1.97	0.65
50:Cc:33:LEU:HD13	50:Cc:81:LEU:HD11	1.77	0.65
1:C1:1194:A:O2'	39:LS:92:LYS:NZ	2.29	0.65
1:C1:3144:C:O4'	36:LO:178:ARG:NH1	2.28	0.65
6:CC:282:ILE:HD12	6:CC:285:LYS:NZ	2.11	0.65
26:Ch:283:ARG:NH2	54:Cg:326:LEU:O	2.29	0.65
32:LK:162:ILE:HG22	32:LK:164:ASP:H	1.62	0.65
1:C1:2334:A:H5'	1:C1:2335:A:H5''	1.79	0.65
1:C1:3188:U:H2'	1:C1:3189:G:C8	2.32	0.65
27:LB:150:GLU:HA	27:LB:153:LYS:HZ3	1.62	0.65
53:Cf:474:ALA:HA	53:Cf:477:ARG:NH1	2.12	0.65
1:C1:288:A:N3	1:C1:291:G:O2'	2.28	0.65
4:CA:231:LEU:H	22:CU:244:MET:HE1	1.61	0.65
22:CU:360:VAL:O	22:CU:364:ASN:ND2	2.30	0.65
30:LG:136:LYS:HD2	30:LG:141:HIS:HE1	1.61	0.65
31:LH:17:LYS:HB2	31:LH:28:GLU:HB2	1.78	0.65
49:Lq:68:LEU:HB3	49:Lq:116:LEU:HD23	1.77	0.65
2:C2:75:G:OP2	43:LY:73:TYR:OH	2.14	0.65
9:CG:39:ARG:NH1	9:CG:40:MET:O	2.30	0.65
30:LG:232:THR:OG1	30:LG:235:ARG:NH2	2.26	0.65
4:CA:106:LYS:HB3	4:CA:110:GLY:HA3	1.79	0.65
10:CH:359:THR:HG23	10:CH:360:ARG:HE	1.60	0.65
22:CU:337:LEU:HA	22:CU:340:LYS:HE2	1.79	0.65
25:Cb:587:ARG:HH21	25:Cb:590:LEU:HB2	1.62	0.65
35:LN:104:GLU:HB3	35:LN:108:ARG:NH1	2.11	0.65
1:C1:213:G:O6	1:C1:1371:G:C2	2.50	0.65
10:CH:258:GLN:OE1	10:CH:288:LYS:NZ	2.29	0.65
52:Ce:71:SER:O	52:Ce:77:TRP:NE1	2.30	0.65
1:C1:734:C:H2'	1:C1:735:G:H8	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CI:207:PHE:HA	11:CI:210:PHE:HD2	1.62	0.64
12:CJ:410:GLU:O	12:CJ:453:ARG:NH1	2.31	0.64
33:LL:46:LEU:HD22	33:LL:49:ARG:HD2	1.80	0.64
54:Cg:213:ASN:OD1	54:Cg:334:ARG:NH2	2.29	0.64
1:C1:2414:G:C2	1:C1:2424:G:H1'	2.32	0.64
26:Ch:272:THR:O	26:Ch:276:ILE:HD12	1.97	0.64
13:CK:218:GLY:N	13:CK:245:ILE:O	2.31	0.64
1:C1:3125:A:O2'	36:LO:103:ARG:NH1	2.30	0.64
25:Cb:17:ILE:HG23	25:Cb:448:LYS:HZ3	1.61	0.64
25:Cb:151:ARG:NH1	25:Cb:267:GLN:OE1	2.31	0.64
1:C1:162:U:O2	46:Lh:115:HIS:NE2	2.31	0.64
2:C2:103:G:OP2	2:C2:105:A:O2'	2.15	0.64
8:CF:96:LEU:HD21	8:CF:102:LEU:HD11	1.78	0.64
13:CK:154:PRO:HG3	13:CK:249:PRO:HB2	1.79	0.64
16:CN:95:GLN:NE2	19:CQ:76:ASN:OD1	2.30	0.64
1:C1:385:U:O2'	43:LY:86:ARG:NH2	2.31	0.64
2:C2:8:C:H2'	2:C2:9:A:H8	1.62	0.64
10:CH:430:PRO:O	10:CH:433:LYS:HG2	1.97	0.64
41:LV:74:LYS:HB3	41:LV:76:HIS:HE1	1.60	0.64
41:LV:111:MET:H	41:LV:130:ARG:HH22	1.44	0.64
1:C1:2788:G:N2	13:CK:254:CYS:SG	2.71	0.64
1:C1:3119:C:H2'	1:C1:3120:G:H8	1.62	0.64
1:C1:3134:A:OP2	36:LO:173:LYS:NZ	2.30	0.64
3:C3:71:U:C2	3:C3:131:G:N1	2.65	0.64
1:C1:386:U:H5'	43:LY:86:ARG:HH22	1.63	0.64
1:C1:401:A:OP1	44:Le:27:LYS:NZ	2.31	0.64
1:C1:1269:A:H2'	1:C1:1270:U:O4'	1.98	0.64
3:C3:66:C:O2'	3:C3:144:A:N7	2.31	0.64
6:CC:142:ASP:HB3	6:CC:148:ARG:HB2	1.80	0.64
11:CI:200:GLU:HG2	11:CI:201:HIS:H	1.62	0.64
12:CJ:376:ARG:HH21	15:CM:189:ASP:HA	1.62	0.64
20:CR:46:SER:O	20:CR:50:THR:HG23	1.98	0.64
35:LN:104:GLU:HB3	35:LN:108:ARG:HH12	1.62	0.64
19:CQ:37:HIS:NE2	41:LV:96:TYR:OH	2.26	0.64
43:LY:72:VAL:HG23	43:LY:79:ILE:HG22	1.80	0.64
45:Lf:44:ASN:HA	45:Lf:47:LEU:HG	1.78	0.64
48:Lj:60:GLY:HA2	48:Lj:64:MET:HE3	1.80	0.64
1:C1:243:G:OP1	6:CC:296:ARG:NH1	2.31	0.64
28:LC:209:PRO:HD2	28:LC:232:VAL:HG12	1.79	0.64
18:CP:419:LYS:HA	18:CP:422:ILE:HG12	1.79	0.63
25:Cb:309:PHE:CE2	25:Cb:504:ILE:HG23	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:LO:39:CYS:HA	36:LO:42:LEU:HG	1.79	0.63
18:CP:475:ARG:HB3	18:CP:480:PHE:HE1	1.63	0.63
37:LP:92:ILE:HG22	37:LP:96:LYS:HE2	1.79	0.63
49:Lq:98:LYS:HG3	49:Lq:102:LYS:HZ2	1.62	0.63
1:C1:3143:U:OP1	36:LO:174:LYS:NZ	2.30	0.63
1:C1:3180:C:OP1	17:CO:83:SER:OG	2.16	0.63
50:Cc:249:LEU:O	50:Cc:257:ASN:ND2	2.31	0.63
1:C1:75:G:H5''	33:LL:58:VAL:HB	1.80	0.63
5:CB:90:ASN:HD21	5:CB:95:ILE:HD11	1.64	0.63
6:CC:255:TYR:CD2	30:LG:73:LYS:HG2	2.34	0.63
8:CF:73:MET:HE2	8:CF:102:LEU:HD13	1.79	0.63
18:CP:446:VAL:HG12	18:CP:447:ILE:HG13	1.80	0.63
37:LP:115:LYS:NZ	37:LP:151:THR:HG23	2.14	0.63
1:C1:1170:U:OP1	1:C1:1192:U:O2'	2.12	0.63
1:C1:3189:G:H2'	1:C1:3190:G:H8	1.64	0.63
16:CN:72:VAL:HG23	16:CN:96:ARG:HG2	1.80	0.63
19:CQ:102:ARG:HH22	19:CQ:103:ARG:HH21	1.47	0.63
20:CR:5:LEU:HG	48:Lj:64:MET:HE1	1.80	0.63
31:LH:14:GLU:HA	34:LM:2:ALA:HB2	1.81	0.63
50:Cc:74:LEU:HA	50:Cc:77:LEU:HD12	1.80	0.63
50:Cc:213:GLU:OE2	50:Cc:258:ARG:NH1	2.31	0.63
1:C1:2972:C:OP2	17:CO:2:ALA:N	2.32	0.63
2:C2:50:C:OP2	2:C2:51:G:N2	2.31	0.63
20:CR:136:GLN:NE2	33:LL:110:ALA:O	2.29	0.63
29:LE:172:ASN:HA	29:LE:175:LYS:HZ3	1.62	0.63
4:CA:196:ILE:HG23	4:CA:229:ILE:HG23	1.81	0.63
7:CE:377:LEU:HD22	7:CE:382:LEU:HG	1.79	0.63
11:CI:301:GLN:O	11:CI:305:LYS:HG2	1.98	0.63
25:Cb:297:ALA:HB1	25:Cb:300:LYS:HB2	1.81	0.63
1:C1:947:U:H2'	1:C1:948:A:H8	1.63	0.63
1:C1:3269:U:H5''	27:LB:309:MET:HG2	1.81	0.63
15:CM:242:ASN:HB3	15:CM:246:ARG:HH12	1.64	0.63
31:LH:28:GLU:HG2	31:LH:33:LYS:HG2	1.80	0.63
39:LS:6:GLU:OE2	39:LS:99:ARG:NH2	2.31	0.63
50:Cc:106:VAL:HA	50:Cc:109:MET:HB2	1.81	0.63
1:C1:1202:U:H2'	24:Cz:48:TRP:HH2	1.64	0.62
3:C3:23:U:H3	5:CB:75:SER:HG	1.47	0.62
12:CJ:183:HIS:ND1	12:CJ:389:ALA:O	2.31	0.62
18:CP:535:LYS:NZ	18:CP:584:ILE:HD11	2.14	0.62
39:LS:8:GLN:HB2	39:LS:64:ILE:HD11	1.80	0.62
51:Cd:374:GLY:HA2	52:Cc:168:ARG:NH1	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CA:121:HIS:HB2	4:CA:237:ARG:HB3	1.80	0.62
7:CE:190:THR:HG21	7:CE:196:ALA:HB2	1.81	0.62
7:CE:441:TYR:O	7:CE:445:VAL:HG12	1.99	0.62
27:LB:45:ALA:HB3	27:LB:182:ILE:HG12	1.81	0.62
52:Ce:104:PHE:O	52:Ce:108:LYS:HG2	1.99	0.62
1:C1:766:G:H1	38:LQ:117:ASP:HA	1.64	0.62
1:C1:1220:C:H5''	32:LK:139:VAL:HG12	1.80	0.62
1:C1:1257:C:OP1	8:CF:210:LYS:NZ	2.32	0.62
10:CH:268:ASN:HA	10:CH:271:LYS:HZ3	1.64	0.62
12:CJ:113:PRO:HD3	12:CJ:120:ARG:HE	1.63	0.62
27:LB:166:GLN:NE2	27:LB:169:LYS:HD2	2.13	0.62
31:LH:92:TYR:HB3	31:LH:181:ILE:HG12	1.80	0.62
54:Cg:143:THR:O	54:Cg:194:ARG:NH2	2.32	0.62
1:C1:92:G:H5'	1:C1:93:C:H5''	1.81	0.62
1:C1:3264:A:H8	1:C1:3264:A:OP1	1.82	0.62
18:CP:422:ILE:O	18:CP:426:HIS:ND1	2.16	0.62
1:C1:1272:U:H2'	1:C1:1273:A:C8	2.33	0.62
8:CF:187:GLU:HG2	8:CF:188:ALA:H	1.64	0.62
20:CR:167:GLU:HA	20:CR:170:ARG:NH1	2.15	0.62
46:Lh:90:THR:HG23	48:Lj:78:PHE:HE2	1.64	0.62
1:C1:2435:C:OP2	1:C1:2436:G:N2	2.33	0.62
1:C1:3243:G:O2'	1:C1:3245:A:N6	2.32	0.62
7:CE:437:ASP:O	7:CE:441:TYR:HB3	1.99	0.62
9:CG:166:ARG:HH12	9:CG:168:ALA:C	2.07	0.62
15:CM:87:ALA:HA	15:CM:125:VAL:O	1.99	0.62
19:CQ:6:CYS:O	19:CQ:10:GLY:HA2	1.98	0.62
27:LB:26:ARG:NH1	27:LB:179:LEU:O	2.33	0.62
29:LE:170:ILE:HG13	29:LE:173:ILE:HD12	1.82	0.62
30:LG:140:ASN:OD1	35:LN:2:GLY:N	2.32	0.62
53:Cf:476:ARG:NH2	54:Cg:165:ARG:O	2.26	0.62
1:C1:2931:G:H2'	1:C1:2932:U:C6	2.34	0.62
10:CH:149:LEU:HA	10:CH:152:VAL:HG12	1.82	0.62
4:CA:252:GLY:O	7:CE:579:GLN:NE2	2.33	0.62
7:CE:116:LEU:HD12	7:CE:134:MET:HE1	1.80	0.62
10:CH:228:LEU:H	10:CH:231:MET:HE2	1.64	0.62
12:CJ:88:GLU:HA	12:CJ:91:ILE:HG22	1.81	0.62
25:Cb:372:PHE:HA	25:Cb:422:VAL:O	2.00	0.62
33:LL:126:PHE:HD2	46:Lh:120:LYS:HZ2	1.48	0.62
41:LV:106:ASN:OD1	41:LV:110:GLU:N	2.33	0.62
1:C1:2385:U:H2'	1:C1:2386:A:H8	1.65	0.62
4:CA:119:ASN:O	4:CA:238:PHE:HA	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CC:326:LEU:HD11	12:CJ:128:ARG:HB2	1.81	0.62
54:Cg:120:LYS:H	54:Cg:334:ARG:HB2	1.64	0.62
3:C3:65:G:H21	3:C3:143:A:H61	1.47	0.62
8:CF:26:LEU:HD22	8:CF:72:LEU:HG	1.81	0.62
27:LB:299:THR:HG21	27:LB:358:LYS:HD3	1.81	0.62
31:LH:90:MET:HE3	31:LH:181:ILE:HG22	1.82	0.62
1:C1:559:U:N3	28:LC:348:GLU:OE1	2.30	0.61
6:CC:300:GLU:OE1	6:CC:302:ARG:NH1	2.30	0.61
7:CE:140:ARG:HH22	7:CE:318:ILE:HG23	1.65	0.61
25:Cb:588:ASP:O	25:Cb:592:SER:N	2.28	0.61
31:LH:89:LYS:O	31:LH:184:SER:OG	2.18	0.61
1:C1:1134:G:OP2	1:C1:1134:G:N2	2.24	0.61
7:CE:157:THR:HA	7:CE:161:LYS:HZ1	1.65	0.61
10:CH:180:SER:O	10:CH:184:ARG:HG3	2.00	0.61
18:CP:396:THR:HG21	18:CP:428:LEU:HG	1.80	0.61
37:LP:95:LEU:HD21	37:LP:114:ILE:HD11	1.82	0.61
51:Cd:371:ASN:ND2	51:Cd:379:GLU:OE2	2.34	0.61
1:C1:773:A:H2'	1:C1:774:A:H8	1.65	0.61
3:C3:71:U:O4	3:C3:130:G:O6	2.18	0.61
5:CB:129:ASP:OD1	5:CB:130:ILE:N	2.33	0.61
7:CE:538:LEU:HA	7:CE:541:VAL:HG12	1.81	0.61
51:Cd:201:ILE:HG13	51:Cd:255:ALA:HB3	1.82	0.61
1:C1:375:G:H1'	1:C1:377:A:N6	2.15	0.61
1:C1:2404:G:O6	1:C1:2467:U:O4	2.19	0.61
1:C1:3138:U:HO2'	39:LS:172:THR:HG1	1.36	0.61
2:C2:155:A:H4'	30:LG:188:ARG:HH22	1.65	0.61
8:CF:37:TYR:HA	8:CF:106:ASN:HD21	1.64	0.61
13:CK:236:LYS:HD2	13:CK:237:ILE:N	2.15	0.61
26:Ch:331:ARG:HB3	54:Cg:185:GLN:NE2	2.16	0.61
40:LT:52:MET:HA	40:LT:92:ARG:HH12	1.64	0.61
51:Cd:243:GLU:O	51:Cd:247:PHE:HD1	1.81	0.61
54:Cg:56:ARG:NH2	54:Cg:69:GLU:OE2	2.33	0.61
1:C1:1360:U:H2'	1:C1:1361:G:H8	1.65	0.61
10:CH:105:GLU:O	10:CH:108:SER:OG	2.15	0.61
14:CL:223:HIS:C	14:CL:225:VAL:H	2.06	0.61
22:CU:267:ARG:NH1	23:CX:79:PRO:HB3	2.14	0.61
26:Ch:285:ILE:HG12	26:Ch:288:ARG:HH21	1.62	0.61
27:LB:157:THR:HG23	27:LB:158:VAL:HG23	1.81	0.61
44:Le:90:ASN:HB3	44:Le:118:VAL:HG22	1.83	0.61
1:C1:307:C:OP2	47:Li:34:ARG:NH1	2.34	0.61
1:C1:3270:C:H4'	27:LB:367:GLY:HA3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3314:U:H2'	1:C1:3318:C:H41	1.65	0.61
6:CC:211:ILE:HG22	6:CC:212:GLU:HG3	1.82	0.61
12:CJ:366:LEU:HD11	12:CJ:468:GLU:HA	1.83	0.61
1:C1:1186:A:N6	1:C1:2809:A:N7	2.48	0.61
3:C3:58:A:N1	11:CI:261:LYS:NZ	2.42	0.61
4:CA:118:GLN:OE1	4:CA:241:THR:OG1	2.16	0.61
6:CC:408:MET:O	6:CC:412:LEU:HB2	2.00	0.61
12:CJ:136:ASP:OD1	12:CJ:139:ARG:NH1	2.34	0.61
19:CQ:71:PHE:O	19:CQ:75:ARG:NH2	2.34	0.61
27:LB:295:ALA:HB2	27:LB:306:ILE:HA	1.82	0.61
1:C1:231:A:H2'	1:C1:232:G:C8	2.34	0.61
7:CE:265:GLU:OE1	7:CE:268:ARG:HD2	2.00	0.61
14:CL:29:ALA:O	14:CL:33:ARG:NH1	2.34	0.61
22:CU:364:ASN:HB3	22:CU:368:ARG:HH12	1.64	0.61
27:LB:14:LEU:HD23	27:LB:17:LEU:HD21	1.80	0.61
41:LV:89:ARG:HH22	41:LV:122:LYS:H	1.47	0.61
1:C1:642:C:H2'	1:C1:643:A:C8	2.36	0.61
10:CH:109:ARG:HB3	10:CH:113:ARG:HH12	1.64	0.61
25:Cb:400:LEU:O	25:Cb:405:ARG:NH2	2.33	0.61
27:LB:117:ARG:NE	27:LB:177:ALA:O	2.28	0.61
27:LB:216:ILE:HD13	27:LB:283:ILE:HD11	1.83	0.61
31:LH:101:VAL:HG21	31:LH:146:LEU:HD11	1.80	0.61
50:Cc:93:PHE:CE2	50:Cc:119:VAL:HG11	2.36	0.61
1:C1:694:U:H1'	1:C1:735:G:H1'	1.83	0.61
1:C1:2294:A:H2'	1:C1:2295:C:C6	2.35	0.61
4:CA:291:ALA:O	4:CA:295:GLN:NE2	2.33	0.61
8:CF:120:SER:OG	8:CF:218:GLU:OE2	2.11	0.61
1:C1:2388:U:O4	1:C1:2561:G:O6	2.19	0.60
13:CK:220:ILE:HD12	22:CU:334:ILE:HD12	1.82	0.60
25:Cb:15:VAL:HG22	25:Cb:274:THR:HB	1.83	0.60
49:Lq:26:ARG:HH22	49:Lq:208:ALA:HB1	1.65	0.60
1:C1:258:C:O2	47:Li:39:LYS:NZ	2.34	0.60
1:C1:1372:A:N6	1:C1:1400:A:O2'	2.34	0.60
4:CA:195:GLU:HB2	4:CA:234:ILE:HD11	1.83	0.60
6:CC:304:LEU:HD12	6:CC:305:PRO:HD2	1.83	0.60
7:CE:439:ARG:O	7:CE:443:HIS:ND1	2.31	0.60
17:CO:33:LEU:HD21	27:LB:211:GLU:HB3	1.83	0.60
25:Cb:259:LEU:HD21	25:Cb:286:GLY:HA3	1.82	0.60
27:LB:107:ALA:HB2	27:LB:200:PHE:HD2	1.65	0.60
5:CB:109:LYS:NZ	5:CB:127:VAL:O	2.18	0.60
6:CC:177:LEU:HD22	6:CC:221:THR:HB	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:174:GLU:O	12:CJ:246:TYR:OH	2.18	0.60
39:LS:73:LYS:HG3	39:LS:75:PHE:HE1	1.66	0.60
1:C1:687:C:H2'	1:C1:688:G:H8	1.65	0.60
1:C1:2769:A:P	13:CK:170:ARG:HH22	2.24	0.60
4:CA:39:LEU:HD23	4:CA:65:ASP:HB3	1.82	0.60
12:CJ:119:PRO:HD3	12:CJ:235:MET:HE3	1.83	0.60
22:CU:289:LEU:HB3	23:CX:71:ILE:HD12	1.83	0.60
32:LK:16:ARG:HE	32:LK:57:ARG:HB3	1.65	0.60
47:Li:66:VAL:HG13	47:Li:78:ALA:HB1	1.82	0.60
54:Cg:37:ILE:HG22	54:Cg:39:ILE:H	1.66	0.60
1:C1:3002:G:OP1	27:LB:19:ARG:NH2	2.33	0.60
51:Cd:350:ARG:HH11	52:Ce:156:ALA:HA	1.65	0.60
5:CB:215:ARG:NH2	5:CB:219:GLU:HB3	2.16	0.60
25:Cb:444:PRO:HB3	25:Cb:453:ARG:NH2	2.17	0.60
37:LP:163:VAL:O	51:Cd:306:ASN:ND2	2.34	0.60
41:LV:74:LYS:HB3	41:LV:76:HIS:CE1	2.36	0.60
1:C1:419:C:OP2	44:Le:16:LYS:NZ	2.33	0.60
1:C1:574:G:H2'	1:C1:575:A:H8	1.67	0.60
1:C1:1087:C:H2'	1:C1:1088:G:H8	1.67	0.60
3:C3:36:C:OP2	11:CI:316:ARG:NH2	2.35	0.60
4:CA:116:TYR:HB2	4:CA:243:ILE:HD11	1.84	0.60
7:CE:157:THR:HA	7:CE:161:LYS:NZ	2.16	0.60
9:CG:41:GLN:HB3	9:CG:46:TYR:HE1	1.66	0.60
11:CI:220:ARG:HD2	11:CI:280:PHE:HB3	1.83	0.60
38:LQ:92:LEU:HD13	38:LQ:116:ASP:HA	1.82	0.60
1:C1:1120:U:H2'	1:C1:1121:G:H8	1.67	0.60
5:CB:31:LEU:HB3	5:CB:35:LYS:NZ	2.16	0.60
6:CC:135:ARG:NH2	7:CE:569:GLY:O	2.35	0.60
10:CH:86:ASP:CG	10:CH:89:HIS:HD2	2.09	0.60
10:CH:267:ILE:HG22	10:CH:271:LYS:NZ	2.16	0.60
11:CI:237:ASP:HB2	11:CI:240:VAL:HG22	1.84	0.60
20:CR:23:ARG:HD2	20:CR:27:LEU:HD21	1.83	0.60
26:Ch:277:GLU:HG3	26:Ch:280:ARG:NH2	2.17	0.60
33:LL:85:ILE:HD12	33:LL:116:LEU:HD22	1.84	0.60
51:Cd:308:TYR:HB2	51:Cd:337:GLU:HG3	1.84	0.60
51:Cd:355:PHE:HD2	51:Cd:397:MET:HG2	1.66	0.60
1:C1:493:C:O2	29:LE:41:LYS:NZ	2.35	0.60
1:C1:979:A:H2'	1:C1:980:G:C8	2.37	0.60
7:CE:223:ARG:NH2	7:CE:246:ASP:OD2	2.35	0.60
15:CM:94:ARG:NH2	15:CM:115:ARG:O	2.33	0.60
27:LB:46:ALA:HB2	27:LB:209:ILE:HG21	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LH:103:VAL:HG12	31:LH:114:VAL:HG22	1.84	0.60
36:LO:188:ALA:HA	36:LO:191:VAL:HB	1.82	0.60
53:Cf:464:LYS:HD2	54:Cg:359:LYS:HA	1.83	0.60
1:C1:231:A:H2'	1:C1:232:G:H8	1.65	0.60
8:CF:16:ASN:ND2	13:CK:72:ASN:OD1	2.35	0.60
19:CQ:100:ARG:NH1	27:LB:379:GLN:HE22	2.00	0.60
36:LO:180:LEU:O	36:LO:184:LYS:HG2	2.01	0.60
5:CB:143:GLN:NE2	5:CB:170:THR:OG1	2.33	0.59
16:CN:119:PRO:HA	16:CN:139:ARG:HD3	1.84	0.59
27:LB:222:THR:O	27:LB:273:TYR:HA	2.02	0.59
28:LC:137:MET:HE2	52:Ce:45:LEU:HD22	1.83	0.59
1:C1:3139:A:O2'	31:LH:43:VAL:O	2.19	0.59
5:CB:22:GLN:NE2	11:CI:328:GLU:OE1	2.35	0.59
7:CE:391:GLN:O	7:CE:396:ARG:NH1	2.35	0.59
19:CQ:95:ARG:O	19:CQ:99:ILE:HG12	2.02	0.59
20:CR:224:ASP:O	20:CR:228:ARG:HG2	2.03	0.59
21:CS:692:LEU:HD13	21:CS:696:PHE:HE2	1.67	0.59
40:LT:114:GLU:HB3	40:LT:118:LYS:NZ	2.17	0.59
51:Cd:423:TRP:HE1	51:Cd:428:GLU:HG3	1.67	0.59
1:C1:158:U:H2'	1:C1:159:G:C8	2.38	0.59
1:C1:613:U:O2	1:C1:1381:A:O2'	2.20	0.59
6:CC:175:ILE:HD11	22:CU:274:GLU:N	2.18	0.59
12:CJ:70:GLN:O	12:CJ:74:HIS:ND1	2.35	0.59
54:Cg:35:MET:HE2	54:Cg:87:VAL:HG21	1.84	0.59
1:C1:247:A:H2'	1:C1:248:G:H8	1.67	0.59
5:CB:257:ALA:O	5:CB:261:THR:HG23	2.03	0.59
28:LC:332:TYR:CE1	15:LF:55:GLU:HG2	2.37	0.59
34:LM:54:ARG:HG2	39:LS:70:LEU:HD12	1.84	0.59
1:C1:562:U:H2'	1:C1:563:A:H8	1.67	0.59
1:C1:1087:C:H2'	1:C1:1088:G:C8	2.38	0.59
1:C1:1202:U:OP2	24:Cz:55:ARG:NH1	2.34	0.59
1:C1:1397:U:OP1	52:Ce:147:LYS:NZ	2.23	0.59
4:CA:170:LYS:HB3	6:CC:190:ILE:HD11	1.85	0.59
10:CH:255:ILE:HG23	10:CH:297:LEU:HD13	1.84	0.59
12:CJ:131:TYR:OH	12:CJ:140:ASP:OD2	2.16	0.59
22:CU:255:ARG:HG2	22:CU:259:ARG:HH12	1.67	0.59
26:Ch:320:LYS:HA	26:Ch:323:GLU:CG	2.32	0.59
27:LB:108:GLU:HB3	27:LB:137:TYR:HD2	1.67	0.59
36:LO:132:GLN:HB3	36:LO:135:ARG:HG2	1.85	0.59
1:C1:134:G:OP1	6:CC:302:ARG:NE	2.35	0.59
1:C1:713:G:C5	1:C1:723:G:N2	2.71	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1090:C:H2'	1:C1:1091:A:H8	1.68	0.59
1:C1:1272:U:H2'	1:C1:1273:A:H8	1.68	0.59
13:CK:68:HIS:HA	13:CK:71:ARG:HG2	1.85	0.59
15:LF:126:THR:HB	40:LT:132:PRO:HB2	1.84	0.59
1:C1:155:G:H2'	1:C1:156:G:C8	2.37	0.59
1:C1:2302:U:H2'	1:C1:2303:A:H8	1.66	0.59
7:CE:335:GLY:O	7:CE:459:LEU:HA	2.02	0.59
9:CG:70:CYS:HB3	9:CG:85:THR:HG21	1.84	0.59
13:CK:149:ARG:NH2	13:CK:170:ARG:HH21	1.99	0.59
30:LG:97:LEU:HD22	30:LG:192:LEU:HD21	1.85	0.59
1:C1:1104:U:OP2	14:CL:33:ARG:NH2	2.36	0.59
1:C1:1884:G:N2	1:C1:2293:C:OP1	2.36	0.59
18:CP:375:ALA:HB2	18:CP:541:LEU:HD11	1.85	0.59
25:Cb:142:ALA:HA	25:Cb:145:VAL:HG12	1.83	0.59
25:Cb:624:PHE:CE2	25:Cb:628:ILE:HD11	2.37	0.59
31:LH:70:THR:O	31:LH:74:ILE:HG13	2.02	0.59
43:LY:30:MET:HE1	43:LY:74:ARG:HA	1.83	0.59
54:Cg:117:ARG:HB3	54:Cg:336:ARG:HB3	1.85	0.59
28:LC:37:LYS:O	28:LC:41:THR:HG23	2.01	0.59
28:LC:149:VAL:HG13	28:LC:150:PRO:HD3	1.84	0.59
46:Lh:34:LEU:O	46:Lh:38:LYS:HB2	2.02	0.59
49:Lq:34:LEU:HD13	49:Lq:183:ILE:HD11	1.85	0.59
1:C1:222:A:H5''	43:LY:3:VAL:HG12	1.84	0.59
1:C1:1156:G:N2	36:LO:89:MET:SD	2.75	0.59
1:C1:1322:C:H2'	1:C1:1323:U:C6	2.38	0.59
1:C1:3041:C:O2'	1:C1:3272:U:OP1	2.20	0.59
4:CA:58:MET:SD	4:CA:193:ASN:ND2	2.76	0.59
9:CG:48:VAL:HG12	9:CG:68:GLY:HA3	1.84	0.59
11:CI:255:GLY:O	30:LG:216:LYS:NZ	2.33	0.59
26:Ch:276:ILE:HG22	26:Ch:280:ARG:NH1	2.15	0.59
35:LN:6:TYR:HD2	47:Li:53:ILE:HD11	1.68	0.59
40:LT:78:LYS:NZ	40:LT:85:ILE:HD11	2.17	0.59
1:C1:2829:G:H2'	1:C1:2830:A:C8	2.38	0.58
2:C2:141:C:O2	35:LN:112:ASN:ND2	2.36	0.58
16:CN:107:VAL:HG23	16:CN:108:ILE:HG13	1.84	0.58
22:CU:364:ASN:HB3	22:CU:368:ARG:NH1	2.17	0.58
1:C1:159:G:OP2	20:CR:227:ARG:NH2	2.36	0.58
1:C1:295:G:OP1	35:LN:179:ARG:NH2	2.36	0.58
1:C1:3074:C:N3	8:CF:6:ARG:NH1	2.51	0.58
9:CG:174:LEU:HB3	13:CK:163:ARG:HE	1.68	0.58
52:Ce:74:PRO:HA	52:Ce:77:TRP:CD2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:20:A:H2'	1:C1:21:G:C8	2.38	0.58
1:C1:68:C:N4	1:C1:306:U:O2'	2.35	0.58
1:C1:612:G:H2'	1:C1:613:U:C6	2.39	0.58
1:C1:1403:G:H2'	1:C1:1404:G:H8	1.68	0.58
4:CA:74:LEU:HB3	4:CA:250:PHE:HB3	1.85	0.58
5:CB:172:TYR:O	5:CB:178:ARG:NE	2.33	0.58
10:CH:439:GLU:HG2	10:CH:447:TYR:HE1	1.67	0.58
19:CQ:57:LYS:NZ	19:CQ:64:VAL:HG13	2.18	0.58
22:CU:194:GLU:O	22:CU:198:THR:HG23	2.03	0.58
31:LH:90:MET:CE	31:LH:181:ILE:HG22	2.33	0.58
32:LK:92:ARG:HG3	32:LK:93:LYS:H	1.68	0.58
49:Lq:141:SER:OG	49:Lq:147:LYS:NZ	2.36	0.58
1:C1:324:C:OP1	20:CR:9:LYS:NZ	2.36	0.58
1:C1:399:A:H4'	1:C1:1379:C:H5'	1.84	0.58
1:C1:399:A:C2	2:C2:17:A:H1'	2.38	0.58
1:C1:3066:G:N2	31:LH:158:GLN:OE1	2.36	0.58
1:C1:3332:G:HO2'	1:C1:3333:A:H8	1.50	0.58
19:CQ:89:THR:O	19:CQ:93:MET:HG2	2.03	0.58
25:Cb:402:GLN:O	25:Cb:406:LYS:HG2	2.04	0.58
52:Ce:121:ILE:HD13	52:Ce:124:ARG:NH2	2.19	0.58
1:C1:583:C:OP2	29:LE:37:LYS:NZ	2.36	0.58
13:CK:198:LEU:HD12	13:CK:222:GLU:HG2	1.84	0.58
16:CN:50:ARG:O	16:CN:83:HIS:NE2	2.36	0.58
19:CQ:47:ARG:HH21	19:CQ:54:ALA:HB3	1.68	0.58
22:CU:248:LEU:O	22:CU:252:ARG:HG3	2.03	0.58
25:Cb:323:HIS:HD2	25:Cb:509:LEU:HD22	1.68	0.58
31:LH:117:ARG:HG2	31:LH:125:VAL:HG22	1.86	0.58
35:LN:33:LEU:O	35:LN:65:ARG:NH2	2.32	0.58
35:LN:62:TYR:HE2	35:LN:110:CYS:HG	1.51	0.58
35:LN:192:LYS:O	35:LN:196:THR:HG23	2.04	0.58
39:LS:79:LEU:HD21	39:LS:106:MET:HE2	1.85	0.58
49:Lq:101:LYS:HZ3	49:Lq:105:ARG:CZ	2.16	0.58
50:Cc:174:ARG:HH12	50:Cc:184:GLU:HA	1.67	0.58
51:Cd:214:GLU:O	51:Cd:218:ILE:HG12	2.03	0.58
52:Ce:70:ARG:NH2	52:Ce:79:GLU:OE2	2.35	0.58
1:C1:1055:U:C5	1:C1:1063:C:N4	2.70	0.58
1:C1:1386:G:O6	44:Le:17:ARG:NH2	2.37	0.58
3:C3:38:G:O6	3:C3:43:U:O4	2.21	0.58
7:CE:276:ASP:OD1	7:CE:280:GLN:NE2	2.37	0.58
9:CG:39:ARG:O	9:CG:46:TYR:N	2.23	0.58
18:CP:470:SER:HB2	18:CP:474:ASN:HD22	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LC:139:ARG:HD2	28:LC:247:PRO:HD2	1.85	0.58
1:C1:581:G:O2'	29:LE:35:GLN:O	2.21	0.58
5:CB:46:LYS:HE2	7:CE:482:GLU:HG2	1.86	0.58
7:CE:504:ASN:HD22	7:CE:507:LEU:HG	1.67	0.58
25:Cb:479:LEU:HD13	25:Cb:559:ARG:HG2	1.84	0.58
35:LN:143:ARG:HE	46:Lh:97:LEU:HD23	1.67	0.58
36:LO:159:GLU:O	36:LO:163:LYS:HG2	2.04	0.58
44:Le:24:ASP:OD1	44:Le:25:ARG:N	2.37	0.58
54:Cg:217:TYR:HB3	54:Cg:326:LEU:HD12	1.86	0.58
2:C2:155:A:O2'	30:LG:188:ARG:NH2	2.36	0.58
3:C3:16:G:H4'	3:C3:17:G:OP1	2.02	0.58
4:CA:130:GLY:O	22:CU:277:ARG:NH1	2.36	0.58
10:CH:93:ALA:C	10:CH:95:GLY:N	2.62	0.58
20:CR:175:GLU:OE2	20:CR:178:ARG:NH2	2.26	0.58
40:LT:78:LYS:HZ2	40:LT:85:ILE:HD11	1.68	0.58
46:Lh:38:LYS:HD3	46:Lh:49:ILE:HG13	1.85	0.58
49:Lq:143:ASP:O	49:Lq:147:LYS:CB	2.51	0.58
50:Cc:109:MET:O	50:Cc:113:LEU:HD23	2.02	0.58
1:C1:2569:U:H2'	1:C1:2570:U:C6	2.39	0.58
1:C1:2725:U:H3	1:C1:2749:G:H1	1.52	0.58
1:C1:2788:G:H2'	1:C1:2789:G:C8	2.39	0.58
3:C3:17:G:H2'	3:C3:18:G:O4'	2.02	0.58
3:C3:23:U:N3	5:CB:75:SER:OG	2.35	0.58
12:CJ:151:PHE:CE2	12:CJ:231:VAL:HG22	2.38	0.58
18:CP:308:ILE:C	18:CP:365:GLN:HE22	2.12	0.58
27:LB:47:MET:HB2	27:LB:165:THR:HG21	1.85	0.58
36:LO:159:GLU:OE1	36:LO:162:ARG:NH1	2.37	0.58
43:LY:49:ILE:HG22	43:LY:105:ILE:HD11	1.86	0.58
1:C1:506:G:H5''	28:LC:346:ALA:HB2	1.85	0.58
1:C1:643:A:H2'	1:C1:644:A:C8	2.38	0.58
1:C1:1109:G:OP2	22:CU:328:ARG:NH2	2.36	0.58
1:C1:3326:C:H2'	1:C1:3327:G:C8	2.39	0.58
2:C2:141:C:H4'	35:LN:110:CYS:SG	2.44	0.58
4:CA:133:LEU:HB3	4:CA:173:LYS:HE2	1.86	0.58
4:CA:182:PHE:HE1	4:CA:191:VAL:HG23	1.68	0.58
10:CH:168:THR:HG23	10:CH:216:GLN:HG3	1.86	0.58
10:CH:461:LEU:HD21	19:CQ:99:ILE:HG13	1.86	0.58
19:CQ:14:TRP:HE3	19:CQ:15:PRO:HD2	1.69	0.58
25:Cb:440:ASN:OD1	25:Cb:468:ALA:HA	2.04	0.58
28:LC:151:LEU:HD23	28:LC:256:VAL:HG22	1.85	0.58
35:LN:181:ASN:OD1	35:LN:184:ARG:NH2	2.30	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LV:89:ARG:O	41:LV:92:GLY:N	2.37	0.58
43:LY:70:THR:N	43:LY:80:HIS:O	2.35	0.58
1:C1:2947:U:H2'	1:C1:2948:G:H8	1.69	0.57
1:C1:3001:A:H2'	1:C1:3002:G:C8	2.39	0.57
4:CA:99:ASP:HB3	4:CA:116:TYR:CE1	2.39	0.57
6:CC:358:PRO:HA	6:CC:361:LEU:HD23	1.85	0.57
10:CH:444:LYS:HD2	10:CH:449:TYR:HE2	1.68	0.57
26:Ch:270:VAL:N	26:Ch:273:GLU:OE1	2.37	0.57
54:Cg:152:PHE:HA	54:Cg:200:ARG:CZ	2.34	0.57
2:C2:55:U:OP1	20:CR:11:ARG:NH1	2.36	0.57
4:CA:141:SER:OG	22:CU:246:GLN:OE1	2.21	0.57
7:CE:394:GLN:O	7:CE:397:THR:OG1	2.17	0.57
8:CF:69:LYS:HB2	8:CF:72:LEU:HB3	1.86	0.57
9:CG:87:LEU:HD21	9:CG:141:PRO:HB2	1.86	0.57
15:CM:242:ASN:HB3	15:CM:246:ARG:HH22	1.69	0.57
17:CO:29:ARG:O	17:CO:33:LEU:HD23	2.05	0.57
51:Cd:318:THR:HG23	51:Cd:321:GLY:H	1.68	0.57
1:C1:2452:C:HO2'	1:C1:2453:A:H8	1.53	0.57
3:C3:23:U:OP2	15:CM:73:ARG:NH2	2.37	0.57
25:Cb:313:LYS:O	25:Cb:317:LYS:HB2	2.04	0.57
50:Cc:63:ARG:HB2	50:Cc:66:PRO:HG2	1.86	0.57
1:C1:338:C:N4	1:C1:341:A:OP2	2.30	0.57
1:C1:376:A:H8	51:Cd:37:ARG:HH12	1.53	0.57
1:C1:1042:U:H2'	1:C1:1043:A:H8	1.69	0.57
1:C1:1377:G:O2'	2:C2:18:U:O2	2.22	0.57
1:C1:2936:U:H5'	53:Cf:526:LYS:HG3	1.86	0.57
4:CA:91:PHE:HB3	4:CA:103:TRP:HB2	1.85	0.57
4:CA:137:ARG:HH22	4:CA:167:GLN:HA	1.68	0.57
10:CH:446:VAL:O	10:CH:450:ILE:HG12	2.05	0.57
25:Cb:376:LYS:O	25:Cb:380:GLU:HG3	2.05	0.57
41:LV:22:GLY:CA	41:LV:38:ILE:O	2.52	0.57
49:Lq:49:PHE:H	49:Lq:159:LEU:HD12	1.69	0.57
1:C1:3184:G:H5'	1:C1:3187:G:H21	1.68	0.57
2:C2:77:A:H2'	2:C2:78:G:H5'	1.87	0.57
7:CE:504:ASN:ND2	7:CE:507:LEU:HG	2.19	0.57
8:CF:227:TRP:HB2	8:CF:234:VAL:HG22	1.86	0.57
12:CJ:173:HIS:O	12:CJ:177:HIS:ND1	2.33	0.57
14:CL:277:PRO:O	14:CL:279:ALA:N	2.36	0.57
16:CN:85:ARG:NH2	16:CN:92:ILE:O	2.35	0.57
18:CP:551:TYR:O	18:CP:552:MET:HE2	2.04	0.57
22:CU:325:LYS:NZ	22:CU:329:GLU:OE2	2.29	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Lh:68:ARG:O	46:Lh:72:ARG:HG3	2.05	0.57
1:C1:978:A:H2'	1:C1:979:A:C8	2.39	0.57
2:C2:95:G:O2'	48:Lj:81:GLY:O	2.14	0.57
7:CE:112:GLU:HA	7:CE:134:MET:HG3	1.85	0.57
23:CX:99:GLU:O	23:CX:103:THR:HG23	2.05	0.57
27:LB:74:GLU:OE1	27:LB:326:LYS:NZ	2.37	0.57
28:LC:137:MET:HB3	52:Ce:17:PHE:HE2	1.68	0.57
41:LV:38:ILE:HG23	41:LV:60:VAL:HG11	1.87	0.57
47:Li:62:TYR:HB2	47:Li:81:PHE:HE2	1.69	0.57
49:Lq:93:LEU:HB3	49:Lq:100:ILE:HD12	1.86	0.57
1:C1:2973:A:H2'	1:C1:2974:G:H8	1.70	0.57
6:CC:180:TYR:OH	22:CU:272:PHE:O	2.21	0.57
7:CE:533:VAL:HB	7:CE:555:ILE:HD11	1.86	0.57
10:CH:85:TYR:CD2	10:CH:152:VAL:HG23	2.40	0.57
16:CN:54:ALA:N	16:CN:80:GLU:OE1	2.36	0.57
18:CP:442:GLU:OE1	18:CP:445:ARG:NH2	2.38	0.57
25:Cb:190:LYS:HB2	25:Cb:211:PRO:HA	1.86	0.57
30:LG:165:LEU:HD23	35:LN:7:LEU:HD11	1.87	0.57
6:CC:354:TYR:OH	12:CJ:459:GLN:OE1	2.21	0.57
27:LB:167:ILE:HA	27:LB:170:THR:OG1	2.05	0.57
43:LY:100:PRO:HA	43:LY:103:VAL:HG22	1.87	0.57
1:C1:1083:G:H5''	15:LF:113:ARG:HH11	1.69	0.57
3:C3:71:U:C2	3:C3:131:G:C2	2.92	0.57
10:CH:130:ALA:O	10:CH:134:ARG:HG2	2.05	0.57
18:CP:569:HIS:CE1	18:CP:570:LEU:HG	2.40	0.57
28:LC:43:MET:HE2	28:LC:243:LEU:HG	1.87	0.57
32:LK:85:LEU:HD11	32:LK:141:CYS:SG	2.45	0.57
50:Ce:108:ARG:HH21	52:Ce:68:ILE:HG12	1.70	0.57
53:Cf:472:TRP:CE2	54:Cg:166:HIS:HB3	2.39	0.57
1:C1:955:U:OP1	38:LQ:44:ARG:NH2	2.37	0.57
1:C1:1173:U:OP2	36:LO:50:ARG:NH1	2.36	0.57
10:CH:89:HIS:HB3	25:Cb:625:ARG:NH2	2.20	0.57
51:Cd:76:ASP:OD1	51:Cd:433:ARG:NH1	2.38	0.57
53:Cf:478:ARG:NH1	54:Cg:110:ARG:HD2	2.19	0.57
1:C1:916:U:H2'	1:C1:917:A:C8	2.40	0.56
1:C1:3119:C:H2'	1:C1:3120:G:C8	2.39	0.56
8:CF:80:THR:OG1	8:CF:82:GLU:OE1	2.21	0.56
13:CK:236:LYS:HZ3	18:CP:474:ASN:HA	1.70	0.56
19:CQ:68:THR:HG21	19:CQ:100:ARG:HG2	1.87	0.56
1:C1:1343:U:H2'	1:C1:1344:G:C8	2.41	0.56
1:C1:3097:G:O6	27:LB:30:LYS:NZ	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:309:ARG:N	18:CP:365:GLN:HE22	2.03	0.56
51:Cd:190:LEU:HD11	51:Cd:283:PRO:HG3	1.86	0.56
1:C1:966:U:H2'	1:C1:967:U:H6	1.69	0.56
3:C3:6:A:N1	5:CB:161:ASN:ND2	2.53	0.56
5:CB:226:LYS:O	5:CB:230:ALA:HB2	2.05	0.56
7:CE:494:GLN:NE2	7:CE:543:LYS:O	2.38	0.56
10:CH:432:TRP:CD1	19:CQ:83:ARG:CZ	2.88	0.56
10:CH:457:LYS:HE2	19:CQ:71:PHE:CE2	2.40	0.56
11:CI:200:GLU:HG2	11:CI:201:HIS:N	2.20	0.56
12:CJ:224:PHE:O	12:CJ:228:GLY:N	2.33	0.56
13:CK:61:MET:O	13:CK:65:ILE:HG12	2.06	0.56
14:CL:22:ALA:O	14:CL:26:LYS:HG3	2.05	0.56
19:CQ:103:ARG:HA	19:CQ:106:VAL:HG22	1.87	0.56
27:LB:76:VAL:HG12	27:LB:326:LYS:HA	1.88	0.56
28:LC:141:HIS:CD2	28:LC:254:PHE:H	2.23	0.56
29:LE:156:SER:O	29:LE:159:ALA:C	2.47	0.56
32:LK:107:ASP:OD1	32:LK:108:GLU:N	2.38	0.56
36:LO:76:ARG:HH11	36:LO:76:ARG:HG3	1.70	0.56
49:Lq:66:CYS:HB3	49:Lq:107:TYR:HD2	1.70	0.56
49:Lq:174:MET:SD	49:Lq:179:LEU:HB3	2.45	0.56
1:C1:643:A:H2'	1:C1:644:A:H8	1.70	0.56
10:CH:379:ARG:NH1	16:CN:177:LEU:O	2.39	0.56
18:CP:535:LYS:HZ3	18:CP:584:ILE:HD11	1.70	0.56
26:Ch:327:THR:HB	26:Ch:331:ARG:CZ	2.34	0.56
50:Cc:174:ARG:NH1	50:Cc:185:ILE:H	2.03	0.56
53:Cf:462:LYS:HA	53:Cf:465:GLU:HB2	1.86	0.56
1:C1:1295:G:O2'	1:C1:1300:A:N1	2.39	0.56
9:CG:40:MET:HA	9:CG:45:VAL:HA	1.86	0.56
12:CJ:387:LEU:HD13	12:CJ:395:ILE:HG12	1.87	0.56
13:CK:184:VAL:HG21	13:CK:223:VAL:HG11	1.87	0.56
16:CN:96:ARG:O	19:CQ:76:ASN:ND2	2.31	0.56
17:CO:41:ALA:O	27:LB:202:LYS:NZ	2.38	0.56
26:Ch:286:ALA:HB2	54:Cg:197:LEU:HD22	1.86	0.56
28:LC:133:ALA:HA	28:LC:149:VAL:HG21	1.88	0.56
29:LE:31:GLU:HG3	29:LE:32:ASP:H	1.69	0.56
44:Le:90:ASN:ND2	52:Ce:115:ARG:HH22	2.04	0.56
47:Li:53:ILE:HA	47:Li:56:VAL:HG22	1.87	0.56
1:C1:954:G:H2'	1:C1:955:U:H6	1.70	0.56
1:C1:2463:U:O2'	1:C1:2465:G:OP2	2.23	0.56
8:CF:123:ASP:OD1	8:CF:124:PHE:N	2.39	0.56
32:LK:137:PHE:HB2	32:LK:148:PRO:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Lq:104:ALA:HA	49:Lq:110:PHE:HZ	1.70	0.56
1:C1:457:U:O3'	50:Cc:63:ARG:NH1	2.38	0.56
1:C1:2292:C:OP1	41:LV:66:LYS:NZ	2.39	0.56
2:C2:8:C:H2'	2:C2:9:A:C8	2.40	0.56
4:CA:146:PHE:HA	4:CA:152:LEU:HB3	1.87	0.56
5:CB:273:GLN:NE2	5:CB:276:GLN:OE1	2.39	0.56
9:CG:23:LEU:HD23	9:CG:26:LEU:HD12	1.87	0.56
10:CH:422:ARG:HA	10:CH:425:TRP:HD1	1.69	0.56
15:CM:53:ARG:HD2	15:CM:55:GLU:OE2	2.05	0.56
16:CN:109:VAL:HB	16:CN:149:GLY:HA2	1.87	0.56
27:LB:81:CYS:HB3	27:LB:206:ILE:HG21	1.86	0.56
28:LC:296:ILE:O	28:LC:300:LEU:HG	2.05	0.56
32:LK:110:ILE:O	32:LK:114:ARG:HG3	2.06	0.56
37:LP:115:LYS:HZ1	37:LP:151:THR:HG23	1.71	0.56
51:Cd:217:GLU:O	51:Cd:220:SER:OG	2.15	0.56
1:C1:50:U:H2'	1:C1:51:A:H8	1.71	0.56
1:C1:1289:G:N3	36:LO:61:LYS:NZ	2.42	0.56
1:C1:1434:A:H2'	53:Cf:509:TRP:CE2	2.41	0.56
1:C1:2548:A:H2'	1:C1:2549:A:C8	2.40	0.56
1:C1:2558:C:H2'	1:C1:2559:A:C8	2.41	0.56
10:CH:92:VAL:O	10:CH:96:GLN:HG3	2.06	0.56
12:CJ:147:MET:HE3	12:CJ:151:PHE:CZ	2.40	0.56
25:Cb:512:VAL:O	25:Cb:516:ASN:ND2	2.38	0.56
37:LP:115:LYS:NZ	37:LP:149:ILE:HG22	2.21	0.56
40:LT:108:ARG:HE	40:LT:130:ARG:HD2	1.70	0.56
46:Lh:89:LEU:HA	48:Lj:78:PHE:HD2	1.70	0.56
49:Lq:60:ARG:O	49:Lq:62:ASN:N	2.39	0.56
1:C1:603:G:H2'	1:C1:604:G:C8	2.40	0.56
1:C1:2965:G:H4'	36:LO:67:PRO:HB2	1.88	0.56
3:C3:71:U:N3	3:C3:131:G:C6	2.74	0.56
5:CB:251:GLU:OE2	5:CB:254:LYS:HG3	2.06	0.56
7:CE:336:TYR:CZ	7:CE:470:LEU:HD11	2.41	0.56
9:CG:24:LYS:O	9:CG:28:ALA:HB2	2.06	0.56
12:CJ:101:SER:HB2	12:CJ:105:ARG:NH1	2.19	0.56
15:CM:242:ASN:HB3	15:CM:246:ARG:NH1	2.21	0.56
18:CP:316:HIS:CD2	18:CP:318:ARG:HG2	2.41	0.56
44:Le:13:LYS:NZ	44:Le:59:GLY:O	2.35	0.56
1:C1:322:G:C2	1:C1:323:G:C8	2.93	0.56
1:C1:413:G:O6	36:LO:69:ARG:NH1	2.38	0.56
1:C1:584:C:OP2	1:C1:596:G:N1	2.34	0.56
1:C1:796:G:H1	1:C1:906:A:H61	1.51	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2729:U:H2'	1:C1:2731:C:C6	2.41	0.56
1:C1:3073:G:OP1	1:C1:3073:G:N2	2.37	0.56
5:CB:217:ILE:H	5:CB:217:ILE:HD12	1.70	0.56
10:CH:60:PHE:HD2	10:CH:101:LYS:HB3	1.71	0.56
12:CJ:374:LEU:HD22	12:CJ:383:LEU:HD13	1.87	0.56
13:CK:4:ASN:O	13:CK:6:TYR:N	2.39	0.56
16:CN:36:SER:HA	16:CN:39:GLU:HG2	1.87	0.56
26:Ch:282:LEU:HD11	54:Cg:215:ARG:CZ	2.35	0.56
35:LN:106:VAL:HG21	35:LN:132:VAL:HG21	1.88	0.56
1:C1:749:C:H2'	1:C1:750:G:C8	2.41	0.55
1:C1:788:A:H61	1:C1:915:G:H22	1.54	0.55
10:CH:11:PRO:HG2	10:CH:16:PHE:HB2	1.89	0.55
15:CM:216:PRO:HD3	15:CM:248:MET:HG2	1.88	0.55
28:LC:139:ARG:HH21	28:LC:141:HIS:CE1	2.24	0.55
51:Cd:354:PHE:HD1	52:Ce:162:LEU:HD21	1.70	0.55
52:Ce:102:PRO:HG2	52:Ce:105:LEU:HD13	1.87	0.55
1:C1:2836:G:H2'	1:C1:2837:C:C6	2.41	0.55
5:CB:116:PHE:CD2	5:CB:120:LEU:HD23	2.40	0.55
51:Cd:398:THR:HG21	52:Ce:153:GLU:OE2	2.05	0.55
1:C1:788:A:H62	1:C1:915:G:H1	0.66	0.55
1:C1:1083:G:H1'	15:LF:111:LEU:HD23	1.89	0.55
6:CC:306:TYR:H	30:LG:117:THR:HG21	1.72	0.55
10:CH:21:LEU:HA	10:CH:24:THR:HG22	1.88	0.55
25:Cb:17:ILE:H	25:Cb:448:LYS:NZ	2.04	0.55
43:LY:57:ILE:HG22	43:LY:63:LYS:HA	1.88	0.55
1:C1:21:G:H3'	1:C1:22:G:C8	2.37	0.55
1:C1:1089:A:H2'	1:C1:1090:C:C6	2.40	0.55
18:CP:491:LEU:HD21	18:CP:510:TYR:CD1	2.41	0.55
35:LN:165:THR:O	35:LN:169:LYS:HG3	2.06	0.55
37:LP:9:ILE:HG21	37:LP:151:THR:HG21	1.87	0.55
50:Cc:165:TRP:HB2	50:Cc:166:PRO:HD3	1.89	0.55
1:C1:1176:G:H2'	1:C1:1177:A:C8	2.42	0.55
1:C1:1321:C:H2'	1:C1:1322:C:C6	2.41	0.55
1:C1:2480:C:H2'	1:C1:2481:A:H8	1.71	0.55
9:CG:171:GLY:HA2	13:CK:163:ARG:CZ	2.35	0.55
11:CI:245:ALA:O	11:CI:249:ASP:HB2	2.06	0.55
25:Cb:624:PHE:HE2	25:Cb:628:ILE:HD11	1.72	0.55
27:LB:159:VAL:HG22	27:LB:192:LYS:HD3	1.88	0.55
32:LK:83:ARG:O	32:LK:86:LYS:HG3	2.06	0.55
37:LP:82:ARG:HG2	37:LP:83:TRP:H	1.70	0.55
43:LY:21:ALA:HB1	43:LY:25:VAL:HB	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2561:G:H21	9:CG:58:CYS:HA	1.72	0.55
3:C3:28:G:OP1	11:CI:221:ASN:ND2	2.27	0.55
4:CA:227:THR:HG23	22:CU:255:ARG:NH2	2.19	0.55
12:CJ:119:PRO:HB3	12:CJ:232:GLU:HG3	1.87	0.55
15:LF:17:THR:HG23	15:LF:18:LEU:HD12	1.88	0.55
32:LK:146:LYS:HG3	32:LK:151:ILE:HD11	1.89	0.55
44:Le:5:LYS:NZ	44:Le:92:THR:HG22	2.22	0.55
49:Lq:48:ARG:NH2	49:Lq:159:LEU:O	2.39	0.55
54:Cg:213:ASN:HA	54:Cg:334:ARG:HH21	1.72	0.55
1:C1:671:G:OP2	33:LL:28:GLN:NE2	2.37	0.55
1:C1:683:C:OP1	28:LC:273:LYS:HG3	2.06	0.55
1:C1:2947:U:H2'	1:C1:2948:G:C8	2.42	0.55
3:C3:4:C:H2'	15:CM:66:ARG:HH22	1.71	0.55
3:C3:52:C:OP1	7:CE:488:ASN:ND2	2.34	0.55
4:CA:32:ASN:HB2	22:CU:216:PHE:CE1	2.42	0.55
7:CE:290:ARG:O	7:CE:312:ARG:NH2	2.39	0.55
18:CP:484:PRO:HA	18:CP:487:GLN:HG2	1.87	0.55
27:LB:351:ALA:O	27:LB:352:LEU:HG	2.06	0.55
35:LN:9:GLU:HB2	47:Li:53:ILE:HG13	1.88	0.55
54:Cg:200:ARG:HG2	54:Cg:202:LEU:HB3	1.88	0.55
1:C1:68:C:OP2	1:C1:293:G:N2	2.32	0.55
1:C1:191:A:N3	1:C1:211:G:O2'	2.35	0.55
1:C1:773:A:H2'	1:C1:774:A:C8	2.41	0.55
1:C1:2399:G:H1	1:C1:2472:U:H3	1.55	0.55
1:C1:3189:G:H2'	1:C1:3190:G:C8	2.42	0.55
2:C2:152:G:H1'	30:LG:62:GLN:HE21	1.72	0.55
5:CB:275:TRP:CE3	5:CB:278:VAL:HG11	2.41	0.55
26:Ch:283:ARG:NH1	26:Ch:287:GLN:HB2	2.22	0.55
50:Cc:175:ILE:HB	50:Cc:185:ILE:HB	1.89	0.55
1:C1:2480:C:H2'	1:C1:2481:A:C8	2.42	0.55
1:C1:2841:U:H2'	1:C1:2842:C:H6	1.72	0.55
25:Cb:493:ARG:NH2	25:Cb:573:HIS:O	2.39	0.55
32:LK:128:GLY:O	32:LK:132:ILE:HD12	2.07	0.55
46:Lh:34:LEU:O	46:Lh:38:LYS:CB	2.55	0.55
1:C1:1415:A:C6	44:Le:29:LEU:HD11	2.42	0.55
1:C1:1429:G:N7	37:LP:25:SER:OG	2.36	0.55
4:CA:267:ILE:O	4:CA:270:GLU:HG3	2.07	0.55
5:CB:263:ILE:HG23	5:CB:281:PHE:HE2	1.72	0.55
7:CE:473:LEU:HD22	7:CE:478:VAL:HG11	1.89	0.55
22:CU:236:ASP:OD1	22:CU:239:ARG:NH2	2.39	0.55
25:Cb:171:GLU:HG2	25:Cb:402:GLN:HG2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LB:222:THR:HG22	27:LB:330:PRO:HB3	1.89	0.55
30:LG:171:ALA:HA	30:LG:174:ARG:NH1	2.22	0.55
30:LG:171:ALA:HA	30:LG:174:ARG:HH12	1.72	0.55
50:Cc:196:HIS:O	50:Cc:200:ILE:HG12	2.07	0.55
52:Ce:182:GLN:H	52:Ce:191:TRP:HH2	1.54	0.55
54:Cg:339:LYS:HG3	54:Cg:352:HIS:HD2	1.72	0.55
1:C1:1363:A:H2'	1:C1:1364:G:H8	1.73	0.54
2:C2:133:C:H2'	2:C2:134:G:H8	1.72	0.54
7:CE:515:TYR:HE1	7:CE:541:VAL:HG13	1.72	0.54
12:CJ:39:TRP:HA	12:CJ:233:PHE:CZ	2.41	0.54
22:CU:282:MET:HA	22:CU:282:MET:HE3	1.89	0.54
25:Cb:105:ILE:HG23	25:Cb:110:PHE:HB2	1.87	0.54
25:Cb:309:PHE:HE2	25:Cb:504:ILE:HG23	1.72	0.54
41:LV:111:MET:HB2	41:LV:130:ARG:HH22	1.72	0.54
50:Cc:33:LEU:HD12	50:Cc:77:LEU:HD22	1.90	0.54
1:C1:529:G:O6	1:C1:543:G:N2	2.41	0.54
1:C1:2408:U:H2'	1:C1:2409:A:C8	2.42	0.54
10:CH:93:ALA:C	10:CH:95:GLY:H	2.14	0.54
10:CH:174:PHE:O	10:CH:179:LYS:NZ	2.40	0.54
13:CK:17:ARG:HG3	13:CK:17:ARG:HH11	1.72	0.54
15:LF:62:ARG:O	15:LF:66:ARG:HG2	2.08	0.54
41:LV:110:GLU:HA	41:LV:130:ARG:NH1	2.23	0.54
43:LY:50:ARG:HD3	43:LY:109:HIS:HB3	1.88	0.54
50:Cc:54:LEU:HD23	50:Cc:74:LEU:HG	1.89	0.54
51:Cd:371:ASN:HD21	51:Cd:384:LYS:HA	1.72	0.54
1:C1:403:U:H2'	1:C1:404:G:H8	1.72	0.54
1:C1:2796:A:H2'	1:C1:2797:G:O4'	2.06	0.54
1:C1:3309:G:N3	19:CQ:56:ARG:NH1	2.55	0.54
6:CC:327:TRP:HB3	6:CC:330:GLU:HB2	1.89	0.54
9:CG:149:ARG:HH21	9:CG:154:ALA:HA	1.71	0.54
12:CJ:406:PHE:HZ	12:CJ:414:ARG:HD2	1.71	0.54
19:CQ:2:ARG:HH11	19:CQ:4:GLU:HA	1.73	0.54
51:Cd:341:ARG:HB3	51:Cd:360:TYR:HB2	1.90	0.54
1:C1:2959:C:O2'	27:LB:181:GLU:OE2	2.22	0.54
1:C1:3115:C:H4'	37:LP:158:GLN:OE1	2.07	0.54
5:CB:104:PRO:HB2	5:CB:107:PHE:HB3	1.89	0.54
8:CF:37:TYR:HA	8:CF:106:ASN:ND2	2.22	0.54
10:CH:187:THR:HG21	10:CH:206:GLY:HA3	1.88	0.54
10:CH:349:ALA:O	16:CN:246:TYR:OH	2.22	0.54
18:CP:485:HIS:CE1	18:CP:489:GLN:HE21	2.26	0.54
25:Cb:324:ILE:HG12	25:Cb:328:ILE:HD12	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LG:230:GLU:HG2	30:LG:233:ARG:HH21	1.73	0.54
35:LN:156:HIS:HB3	35:LN:159:ARG:HD2	1.88	0.54
49:Lq:94:ASN:OD1	49:Lq:97:LYS:NZ	2.36	0.54
1:C1:117:U:OP2	30:LG:140:ASN:ND2	2.40	0.54
1:C1:121:A:N1	30:LG:111:ARG:NH1	2.56	0.54
1:C1:616:C:H2'	1:C1:617:C:C6	2.43	0.54
16:CN:59:ILE:O	16:CN:63:THR:HG22	2.07	0.54
16:CN:85:ARG:HD2	19:CQ:78:PRO:HG2	1.88	0.54
18:CP:357:TYR:HB2	18:CP:362:TYR:CZ	2.42	0.54
39:LS:75:PHE:HE2	39:LS:99:ARG:HG2	1.72	0.54
43:LY:49:ILE:HD11	43:LY:79:ILE:HG21	1.90	0.54
43:LY:62:HIS:HB3	43:LY:65:LYS:HD2	1.89	0.54
44:Le:5:LYS:HZ3	44:Le:92:THR:HG22	1.72	0.54
49:Lq:48:ARG:HA	49:Lq:159:LEU:HD12	1.89	0.54
53:Cf:459:PRO:HD2	53:Cf:462:LYS:NZ	2.22	0.54
1:C1:1297:U:OP2	36:LO:45:SER:OG	2.22	0.54
1:C1:2315:G:H5''	37:LP:86:LYS:HD3	1.89	0.54
1:C1:2779:C:H2'	1:C1:2780:U:C6	2.43	0.54
13:CK:245:ILE:HD12	13:CK:255:VAL:HG22	1.89	0.54
16:CN:102:SER:HG	41:LV:138:VAL:H	1.56	0.54
41:LV:111:MET:H	41:LV:130:ARG:NH2	2.05	0.54
46:Lh:90:THR:HG23	48:Lj:78:PHE:CE2	2.43	0.54
49:Lq:59:PRO:C	49:Lq:61:PRO:HD3	2.33	0.54
1:C1:462:C:O3'	52:Ce:58:LYS:NZ	2.41	0.54
1:C1:712:A:H3'	1:C1:713:G:H8	1.72	0.54
1:C1:927:C:H2'	1:C1:928:G:H8	1.72	0.54
1:C1:2917:C:H2'	1:C1:2918:C:C6	2.42	0.54
1:C1:3224:G:H2'	1:C1:3225:C:C6	2.43	0.54
7:CE:213:THR:H	7:CE:235:ASN:ND2	2.05	0.54
18:CP:511:SER:HB2	18:CP:576:PHE:CZ	2.42	0.54
29:LE:170:ILE:HA	29:LE:173:ILE:HD12	1.90	0.54
46:Lh:34:LEU:HD13	46:Lh:37:GLN:NE2	2.23	0.54
1:C1:2949:A:H2	37:LP:69:ARG:HH22	1.55	0.54
2:C2:84:C:H1'	43:LY:112:LYS:HE3	1.90	0.54
4:CA:238:PHE:CD2	4:CA:240:LEU:HD21	2.43	0.54
4:CA:238:PHE:HD2	4:CA:240:LEU:HD21	1.72	0.54
27:LB:299:THR:OG1	27:LB:358:LYS:O	2.24	0.54
29:LE:58:LEU:HD13	29:LE:104:ALA:HA	1.90	0.54
30:LG:81:PHE:HZ	30:LG:167:VAL:HA	1.73	0.54
30:LG:115:GLU:O	30:LG:119:ILE:HG12	2.08	0.54
32:LK:81:ILE:HD11	32:LK:132:ILE:HG23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Cc:113:LEU:HD12	50:Cc:196:HIS:CG	2.43	0.54
1:C1:222:A:H2'	1:C1:223:U:C6	2.42	0.54
2:C2:86:U:H3	48:Lj:87:ARG:HD3	1.72	0.54
4:CA:150:PRO:O	4:CA:153:LYS:HB2	2.08	0.54
6:CC:214:PRO:HD2	6:CC:217:TRP:HB2	1.90	0.54
13:CK:44:GLY:C	13:CK:46:ARG:H	2.16	0.54
13:CK:164:ARG:HG3	13:CK:165:PRO:HD2	1.89	0.54
41:LV:83:GLN:H	41:LV:97:PHE:HD2	1.56	0.54
43:LY:22:PRO:O	43:LY:26:ARG:HG3	2.08	0.54
51:Cd:374:GLY:H	51:Cd:379:GLU:H	1.56	0.54
1:C1:698:A:H4'	4:CA:262:ILE:HG21	1.88	0.54
1:C1:3297:U:H2'	1:C1:3298:U:C6	2.43	0.54
7:CE:419:ARG:HD2	7:CE:444:ARG:NH1	2.21	0.54
20:CR:201:LYS:HG3	20:CR:202:HIS:CE1	2.43	0.54
26:Ch:327:THR:HB	26:Ch:331:ARG:HH12	1.72	0.54
27:LB:197:ARG:HA	27:LB:200:PHE:HD1	1.73	0.54
30:LG:169:LEU:HD12	30:LG:172:LEU:HD11	1.88	0.54
35:LN:71:ARG:HB2	35:LN:94:TYR:HB2	1.89	0.54
36:LO:28:LEU:HD11	36:LO:104:LEU:HD22	1.89	0.54
41:LV:73:LYS:HD2	41:LV:73:LYS:O	2.08	0.54
1:C1:247:A:H1'	46:Lh:115:HIS:CD2	2.43	0.53
1:C1:2329:A:H2'	1:C1:2330:A:C8	2.44	0.53
1:C1:3192:C:H2'	1:C1:3193:G:H8	1.72	0.53
10:CH:284:ILE:HD11	10:CH:316:ILE:HG22	1.91	0.53
11:CI:189:MET:HE3	11:CI:191:ILE:HD11	1.89	0.53
11:CI:207:PHE:HB3	11:CI:235:PHE:CZ	2.43	0.53
18:CP:470:SER:HB2	18:CP:474:ASN:ND2	2.23	0.53
20:CR:69:ASN:OD1	20:CR:70:LYS:N	2.41	0.53
25:Cb:114:THR:H	25:Cb:117:GLN:NE2	2.06	0.53
25:Cb:320:ALA:O	25:Cb:324:ILE:HG13	2.08	0.53
28:LC:75:ILE:HD12	28:LC:76:PRO:HD2	1.90	0.53
28:LC:213:TYR:HB3	28:LC:222:LEU:HD11	1.90	0.53
30:LG:66:LYS:O	30:LG:69:ARG:HG2	2.08	0.53
39:LS:27:MET:HE1	39:LS:44:PHE:HB2	1.89	0.53
1:C1:1237:C:H2'	1:C1:1238:G:H8	1.73	0.53
1:C1:2849:U:O2'	1:C1:2971:U:OP1	2.23	0.53
1:C1:2999:U:OP2	1:C1:3049:C:N4	2.41	0.53
1:C1:3139:A:H2'	31:LH:23:ARG:HH21	1.73	0.53
3:C3:13:C:H2'	3:C3:14:C:H2'	1.89	0.53
10:CH:105:GLU:HB3	10:CH:109:ARG:HH12	1.73	0.53
10:CH:148:TYR:HD1	10:CH:149:LEU:HD22	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:242:LEU:HD13	10:CH:277:PHE:HZ	1.72	0.53
16:CN:14:GLY:O	16:CN:61:ARG:NH1	2.41	0.53
24:Cz:52:VAL:O	24:Cz:55:ARG:HB3	2.08	0.53
27:LB:56:ILE:HG22	27:LB:360:ILE:HG13	1.89	0.53
15:LF:53:ARG:NH1	15:LF:189:ASP:OD2	2.37	0.53
32:LK:143:VAL:HB	32:LK:151:ILE:HD13	1.89	0.53
49:Lq:98:LYS:HE3	49:Lq:102:LYS:NZ	2.23	0.53
51:Cd:290:ARG:HB2	51:Cd:398:THR:HG23	1.89	0.53
1:C1:508:G:H3'	1:C1:509:A:H3'	1.91	0.53
1:C1:2566:G:H2'	1:C1:2567:A:H8	1.73	0.53
1:C1:2724:U:C4	1:C1:2751:G:C6	2.96	0.53
1:C1:2775:A:H2'	1:C1:2776:U:C6	2.43	0.53
1:C1:3246:G:O2'	1:C1:3249:G:N1	2.38	0.53
2:C2:123:G:H2'	2:C2:124:G:C8	2.44	0.53
6:CC:139:ILE:HG23	6:CC:147:ILE:HG23	1.90	0.53
7:CE:213:THR:HG23	7:CE:234:VAL:HA	1.90	0.53
18:CP:384:CYS:HB2	18:CP:408:ILE:HD13	1.89	0.53
21:CS:695:TRP:HZ3	35:LN:28:TRP:HE1	1.55	0.53
28:LC:258:THR:HG23	28:LC:261:ALA:H	1.73	0.53
31:LH:122:GLU:OE1	31:LH:126:ARG:NH2	2.39	0.53
50:Cc:162:LEU:HA	50:Cc:166:PRO:HD2	1.90	0.53
1:C1:400:A:N3	1:C1:642:C:O2'	2.39	0.53
1:C1:1386:G:N2	1:C1:1389:A:OP2	2.20	0.53
1:C1:2788:G:H2'	1:C1:2789:G:H8	1.73	0.53
1:C1:2924:G:C4	9:CG:167:GLN:NE2	2.76	0.53
5:CB:282:TYR:HB3	5:CB:290:ALA:HB1	1.89	0.53
6:CC:180:TYR:HE2	22:CU:272:PHE:HD2	1.56	0.53
6:CC:198:PRO:HG3	6:CC:225:THR:HB	1.91	0.53
10:CH:38:ILE:O	10:CH:42:ARG:HG2	2.08	0.53
10:CH:46:THR:OG1	10:CH:50:LYS:NZ	2.42	0.53
16:CN:126:GLU:OE1	16:CN:139:ARG:NH2	2.41	0.53
21:CS:466:ASP:OD2	21:CS:470:ARG:NH1	2.42	0.53
25:Cb:170:ARG:HG3	25:Cb:195:VAL:HG21	1.90	0.53
29:LE:60:LEU:O	29:LE:67:GLY:N	2.41	0.53
33:LL:63:VAL:HA	33:LL:66:ASN:ND2	2.24	0.53
35:LN:38:ARG:HD3	35:LN:62:TYR:HE1	1.73	0.53
1:C1:628:C:H2'	1:C1:629:U:C6	2.43	0.53
1:C1:1434:A:H1'	53:Cf:505:SER:HB2	1.90	0.53
1:C1:2089:U:O3'	19:CQ:23:ARG:NH2	2.42	0.53
1:C1:2328:C:H2'	1:C1:2329:A:H8	1.73	0.53
1:C1:3010:G:H2'	1:C1:3011:U:C6	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:129:C:O5'	12:CJ:10:SER:OG	2.25	0.53
3:C3:18:G:H2'	3:C3:19:C:C6	2.43	0.53
5:CB:115:GLU:HG2	5:CB:221:VAL:HG21	1.90	0.53
7:CE:140:ARG:NH2	7:CE:318:ILE:HG23	2.23	0.53
19:CQ:2:ARG:NH1	19:CQ:4:GLU:HA	2.24	0.53
25:Cb:493:ARG:NH1	25:Cb:581:ALA:HB2	2.22	0.53
27:LB:375:ALA:HA	27:LB:378:LYS:HE3	1.91	0.53
31:LH:92:TYR:CZ	31:LH:144:ASP:HA	2.44	0.53
1:C1:421:U:O2'	45:Lf:90:PRO:O	2.25	0.53
1:C1:966:U:H2'	1:C1:967:U:C6	2.44	0.53
1:C1:2300:C:H2'	1:C1:2301:C:C6	2.43	0.53
1:C1:3117:C:HO2'	1:C1:3118:A:H8	1.56	0.53
2:C2:57:C:OP2	20:CR:14:ARG:NH2	2.38	0.53
3:C3:140:G:H3'	11:CI:291:ARG:NH1	2.23	0.53
7:CE:336:TYR:CZ	7:CE:482:GLU:HB2	2.43	0.53
10:CH:174:PHE:HE2	10:CH:266:GLN:HA	1.73	0.53
12:CJ:84:GLN:HG3	12:CJ:121:TYR:HE1	1.73	0.53
19:CQ:106:VAL:HB	19:CQ:110:LYS:NZ	2.23	0.53
25:Cb:17:ILE:H	25:Cb:448:LYS:HZ1	1.55	0.53
27:LB:285:ARG:HB3	27:LB:324:MET:HE3	1.91	0.53
32:LK:143:VAL:HG23	32:LK:148:PRO:HG3	1.91	0.53
54:Cg:116:PHE:HB3	54:Cg:335:LEU:HD22	1.89	0.53
1:C1:218:C:H5'	43:LY:33:PRO:HD3	1.91	0.53
1:C1:2366:A:H62	1:C1:2775:A:H2	1.55	0.53
1:C1:3195:C:H2'	1:C1:3196:G:H8	1.74	0.53
4:CA:85:ASN:ND2	6:CC:159:ASP:OD2	2.42	0.53
6:CC:282:ILE:HD12	6:CC:285:LYS:HZ3	1.74	0.53
7:CE:522:TYR:CE1	7:CE:531:PHE:HB3	2.44	0.53
9:CG:149:ARG:NH1	9:CG:163:VAL:HA	2.24	0.53
18:CP:309:ARG:HB2	18:CP:365:GLN:NE2	2.23	0.53
18:CP:324:LEU:HB2	18:CP:331:LEU:HD11	1.91	0.53
25:Cb:528:ASN:HB3	25:Cb:531:ILE:HD13	1.89	0.53
30:LG:63:ARG:O	30:LG:66:LYS:HG2	2.07	0.53
32:LK:147:SER:O	32:LK:151:ILE:HD12	2.09	0.53
51:Cd:374:GLY:H	51:Cd:379:GLU:N	2.07	0.53
52:Ce:166:ILE:O	52:Ce:170:LEU:HG	2.08	0.53
1:C1:683:C:OP2	28:LC:120:ARG:NH2	2.42	0.53
1:C1:3108:U:O2	1:C1:3337:C:C4	2.61	0.53
1:C1:3328:C:H2'	1:C1:3329:C:C6	2.44	0.53
3:C3:7:U:O2'	5:CB:206:ARG:NH2	2.41	0.53
5:CB:31:LEU:HA	5:CB:34:ILE:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CB:184:LEU:O	5:CB:185:MET:HE2	2.07	0.53
16:CN:206:THR:HB	16:CN:210:THR:HG21	1.91	0.53
19:CQ:84:GLU:C	19:CQ:88:LYS:HZ2	2.17	0.53
20:CR:193:GLU:O	20:CR:197:ARG:HG3	2.09	0.53
26:Ch:289:GLY:O	26:Ch:292:LYS:HG3	2.09	0.53
36:LO:55:TYR:CE1	36:LO:147:VAL:HG21	2.44	0.53
1:C1:398:G:OP1	1:C1:1397:U:O2'	2.26	0.53
1:C1:1860:A:H2'	1:C1:1861:G:H8	1.73	0.53
1:C1:2561:G:O2'	9:CG:58:CYS:O	2.24	0.53
5:CB:42:ARG:HH12	5:CB:46:LYS:HG3	1.74	0.53
6:CC:269:MET:HE1	7:CE:553:VAL:H	1.74	0.53
10:CH:131:ALA:O	10:CH:135:MET:HE3	2.09	0.53
10:CH:174:PHE:CD2	10:CH:266:GLN:HG3	2.43	0.53
16:CN:84:LEU:HB3	16:CN:94:ILE:HD13	1.91	0.53
16:CN:88:LEU:HG	16:CN:94:ILE:HD11	1.91	0.53
25:Cb:238:VAL:HG21	25:Cb:266:ARG:HD2	1.90	0.53
25:Cb:378:HIS:HE1	25:Cb:542:GLU:HB2	1.74	0.53
29:LE:84:THR:HB	29:LE:94:LEU:HD23	1.90	0.53
50:Cc:39:ALA:HA	50:Cc:42:LEU:HG	1.90	0.53
1:C1:3235:A:H2'	1:C1:3236:A:C8	2.44	0.53
5:CB:216:PRO:HG2	5:CB:219:GLU:OE1	2.08	0.53
6:CC:399:PHE:O	6:CC:403:ARG:HG2	2.08	0.53
7:CE:204:ARG:NH1	7:CE:205:GLU:OE2	2.42	0.53
27:LB:213:ASP:HA	27:LB:283:ILE:O	2.09	0.53
40:LT:127:GLN:NE2	40:LT:131:GLN:HE21	2.07	0.53
41:LV:122:LYS:HD3	41:LV:138:VAL:HG22	1.91	0.53
2:C2:22:U:OP2	28:LC:198:MET:HG2	2.09	0.52
4:CA:63:ARG:HH12	6:CC:163:THR:HB	1.72	0.52
6:CC:370:TRP:CD1	6:CC:378:ARG:HG2	2.44	0.52
7:CE:500:LEU:HA	7:CE:503:THR:HG22	1.90	0.52
18:CP:337:TRP:CD1	18:CP:337:TRP:H	2.25	0.52
18:CP:530:ARG:NE	18:CP:530:ARG:HA	2.24	0.52
19:CQ:82:ASN:O	19:CQ:86:TRP:HD1	1.92	0.52
28:LC:289:ARG:HE	50:Cc:109:MET:HG3	1.73	0.52
46:Lh:89:LEU:O	48:Lj:73:ARG:NH2	2.42	0.52
54:Cg:33:LYS:HB2	54:Cg:87:VAL:HA	1.90	0.52
54:Cg:201:GLU:HB2	54:Cg:211:VAL:HB	1.90	0.52
1:C1:977:A:C2	1:C1:978:A:H1'	2.44	0.52
1:C1:2865:G:H2'	1:C1:2866:G:C8	2.44	0.52
15:CM:92:VAL:HG23	15:CM:142:TYR:HB3	1.91	0.52
25:Cb:329:ILE:HD11	25:Cb:439:ILE:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:213:G:N1	1:C1:1371:G:N2	2.57	0.52
1:C1:713:G:C4	1:C1:723:G:N2	2.77	0.52
1:C1:1090:C:H2'	1:C1:1091:A:C8	2.43	0.52
1:C1:1343:U:H2'	1:C1:1344:G:H8	1.73	0.52
1:C1:1385:C:N4	44:Le:17:ARG:HH22	2.07	0.52
1:C1:3058:G:H2'	1:C1:3059:G:C8	2.45	0.52
9:CG:72:GLY:HA3	9:CG:81:ARG:O	2.10	0.52
10:CH:109:ARG:HB3	10:CH:113:ARG:NH1	2.24	0.52
11:CI:218:VAL:HG23	11:CI:231:ALA:HB2	1.89	0.52
15:CM:242:ASN:HB3	15:CM:246:ARG:NH2	2.24	0.52
25:Cb:625:ARG:HH21	25:Cb:628:ILE:HD12	1.73	0.52
30:LG:70:MET:HE2	30:LG:71:ARG:HH12	1.74	0.52
35:LN:124:ASP:OD1	35:LN:125:SER:N	2.38	0.52
51:Cd:46:ARG:HA	51:Cd:49:GLU:HG2	1.90	0.52
53:Cf:478:ARG:NH2	54:Cg:110:ARG:HB3	2.25	0.52
1:C1:3093:G:H4'	27:LB:343:LEU:HD12	1.91	0.52
1:C1:3136:A:H2'	1:C1:3137:A:C8	2.44	0.52
1:C1:3272:U:H2'	1:C1:3273:G:O4'	2.09	0.52
2:C2:91:C:H2'	2:C2:92:A:C8	2.44	0.52
2:C2:104:A:OP1	48:Lj:21:ARG:NH1	2.43	0.52
10:CH:283:PHE:HE1	10:CH:337:ARG:HH21	1.58	0.52
11:CI:208:SER:HA	11:CI:211:GLY:O	2.10	0.52
18:CP:487:GLN:OE1	18:CP:510:TYR:OH	2.28	0.52
29:LE:65:PHE:CD2	29:LE:92:VAL:HG22	2.44	0.52
1:C1:1185:A:H2'	1:C1:1187:A:H5'	1.92	0.52
1:C1:2769:A:H5'	13:CK:170:ARG:HH12	1.74	0.52
5:CB:261:THR:HA	5:CB:264:ARG:NE	2.24	0.52
8:CF:162:GLU:HG3	8:CF:174:MET:HB2	1.92	0.52
10:CH:151:GLN:HB3	25:Cb:604:PHE:CE2	2.43	0.52
22:CU:279:ASP:OD1	23:CX:76:THR:OG1	2.27	0.52
1:C1:247:A:H2'	1:C1:248:G:C8	2.44	0.52
1:C1:2387:G:N2	9:CG:57:THR:OG1	2.42	0.52
1:C1:3144:C:O2'	1:C1:3146:G:N7	2.43	0.52
3:C3:65:G:O6	11:CI:281:LYS:NZ	2.41	0.52
4:CA:309:LEU:O	50:Cc:52:LYS:NZ	2.42	0.52
12:CJ:177:HIS:HB3	12:CJ:273:LEU:HD21	1.91	0.52
15:CM:51:PHE:HB3	42:LX:31:VAL:HG21	1.90	0.52
18:CP:379:GLN:N	18:CP:382:GLU:OE1	2.35	0.52
22:CU:255:ARG:HG2	22:CU:259:ARG:NH1	2.24	0.52
28:LC:341:LEU:HD23	15:LF:62:ARG:HH22	1.74	0.52
31:LH:92:TYR:CB	31:LH:181:ILE:HG12	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LL:23:ARG:HH12	33:LL:25:HIS:CE1	2.28	0.52
50:Cc:75:ALA:HB1	50:Cc:122:ALA:HB2	1.91	0.52
51:Cd:344:VAL:HG13	51:Cd:355:PHE:HE1	1.74	0.52
52:Ce:165:THR:O	52:Ce:168:ARG:HB2	2.09	0.52
1:C1:2469:U:H2'	1:C1:2470:U:C6	2.45	0.52
1:C1:2569:U:O2'	1:C1:2570:U:OP1	2.26	0.52
1:C1:2933:U:H2'	1:C1:2934:A:H8	1.74	0.52
10:CH:179:LYS:O	10:CH:183:VAL:HG13	2.10	0.52
12:CJ:371:THR:HB	12:CJ:416:THR:HG23	1.92	0.52
16:CN:182:VAL:HG12	16:CN:221:VAL:HG21	1.91	0.52
25:Cb:1:MET:HB3	25:Cb:2:PRO:HD3	1.92	0.52
25:Cb:100:ASN:OD1	25:Cb:103:ARG:NH2	2.43	0.52
1:C1:2726:U:H2'	1:C1:2727:A:C8	2.45	0.52
3:C3:8:C:OP2	5:CB:206:ARG:NH2	2.33	0.52
6:CC:338:MET:O	12:CJ:45:ARG:NH1	2.37	0.52
7:CE:419:ARG:HD2	7:CE:444:ARG:HH11	1.75	0.52
8:CF:69:LYS:HB2	8:CF:72:LEU:CB	2.39	0.52
16:CN:162:HIS:NE2	16:CN:191:ASN:OD1	2.42	0.52
27:LB:113:GLU:HG3	27:LB:177:ALA:HB2	1.90	0.52
15:LF:16:GLU:O	15:LF:20:LYS:HG3	2.10	0.52
49:Lq:17:LEU:HD13	49:Lq:172:VAL:HB	1.92	0.52
54:Cg:219:ILE:HG23	54:Cg:324:VAL:HG13	1.91	0.52
1:C1:378:A:O3'	51:Cd:32:LYS:NZ	2.42	0.52
1:C1:692:A:H61	1:C1:701:G:H2'	1.74	0.52
1:C1:1085:A:H3'	1:C1:1086:U:H5'	1.92	0.52
1:C1:1234:A:H2'	1:C1:1235:U:O4'	2.10	0.52
1:C1:1422:G:OP1	28:LC:84:HIS:NE2	2.42	0.52
1:C1:2845:A:H4'	10:CH:26:ARG:HD3	1.91	0.52
3:C3:25:U:O2'	5:CB:164:PRO:O	2.23	0.52
5:CB:128:ILE:HG22	5:CB:129:ASP:O	2.10	0.52
7:CE:331:GLY:O	7:CE:450:ARG:NH1	2.43	0.52
7:CE:457:ARG:NH2	7:CE:483:TYR:OH	2.43	0.52
17:CO:33:LEU:HD21	27:LB:211:GLU:HG2	1.92	0.52
29:LE:25:GLN:HE22	29:LE:27:TRP:HB2	1.74	0.52
15:LF:229:ILE:HA	39:LS:36:VAL:HG22	1.92	0.52
32:LK:11:LYS:HG2	32:LK:64:ILE:HB	1.92	0.52
37:LP:108:ASP:OD2	51:Cd:366:ARG:NH2	2.42	0.52
41:LV:36:LEU:HB3	41:LV:62:ALA:HB1	1.91	0.52
51:Cd:298:ILE:HD11	51:Cd:396:ARG:HG3	1.92	0.52
1:C1:910:A:O2'	48:Lj:49:TRP:O	2.28	0.52
1:C1:1318:C:H2'	1:C1:1319:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1860:A:H2'	1:C1:1861:G:C8	2.45	0.52
1:C1:3116:G:H5''	37:LP:159:LYS:NZ	2.25	0.52
5:CB:279:ARG:HG2	5:CB:280:ASN:H	1.75	0.52
10:CH:170:LEU:HD21	10:CH:245:LEU:HD12	1.91	0.52
14:CL:188:ALA:HB3	14:CL:377:VAL:H	1.75	0.52
16:CN:19:LEU:HG	16:CN:200:ASN:HB3	1.92	0.52
19:CQ:11:ARG:NH2	19:CQ:32:CYS:SG	2.83	0.52
25:Cb:242:GLU:CG	25:Cb:245:ARG:HH21	2.19	0.52
32:LK:126:LYS:NZ	32:LK:155:ILE:HG22	2.25	0.52
41:LV:29:ASP:HB3	41:LV:103:VAL:HG23	1.91	0.52
1:C1:2291:C:H2'	1:C1:2292:C:H6	1.75	0.51
1:C1:2876:G:H2'	1:C1:2877:A:N3	2.25	0.51
1:C1:2973:A:H2'	1:C1:2974:G:C8	2.45	0.51
2:C2:7:U:H2'	2:C2:8:C:H6	1.75	0.51
2:C2:57:C:H4'	2:C2:63:G:C8	2.45	0.51
9:CG:10:LYS:HG2	23:CX:104:ILE:HG21	1.92	0.51
10:CH:108:SER:O	10:CH:112:VAL:HG23	2.10	0.51
25:Cb:422:VAL:HG13	25:Cb:426:ALA:HB3	1.92	0.51
25:Cb:426:ALA:O	25:Cb:430:ILE:HG12	2.10	0.51
29:LE:25:GLN:NE2	29:LE:27:TRP:O	2.43	0.51
54:Cg:217:TYR:CE1	54:Cg:328:GLU:HG2	2.44	0.51
1:C1:1303:G:H2'	1:C1:1304:U:C6	2.46	0.51
1:C1:1331:G:C4	28:LC:297:GLN:HG3	2.45	0.51
1:C1:2433:U:H4'	1:C1:2434:U:H5	1.76	0.51
1:C1:2435:C:H2'	1:C1:2436:G:H21	1.74	0.51
1:C1:3066:G:OP2	13:CK:30:ARG:NH1	2.40	0.51
6:CC:135:ARG:HE	6:CC:136:ASN:H	1.57	0.51
6:CC:241:LYS:NZ	6:CC:250:ASP:OD1	2.43	0.51
7:CE:278:MET:HG2	7:CE:306:LEU:HD11	1.92	0.51
7:CE:527:LEU:HD23	7:CE:531:PHE:HE2	1.74	0.51
14:CL:262:ARG:HA	14:CL:265:PHE:O	2.10	0.51
19:CQ:44:ARG:NE	25:Cb:860:ASP:OD2	2.44	0.51
28:LC:149:VAL:CG1	28:LC:150:PRO:HD3	2.40	0.51
30:LG:161:ASP:OD1	30:LG:162:PRO:HD3	2.10	0.51
32:LK:90:ARG:NH2	32:LK:94:LYS:HB2	2.24	0.51
47:Li:98:GLU:HG3	47:Li:101:ARG:NH1	2.25	0.51
52:Ce:98:LEU:O	52:Ce:101:PHE:HB2	2.11	0.51
53:Cf:449:GLU:HG3	53:Cf:453:LYS:NZ	2.25	0.51
54:Cg:160:HIS:O	54:Cg:164:PRO:HD2	2.09	0.51
1:C1:27:C:O2'	1:C1:319:A:N3	2.33	0.51
1:C1:308:U:H2'	47:Li:39:LYS:HD3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:680:A:H5''	28:LC:43:MET:HE3	1.91	0.51
1:C1:1398:C:H2'	1:C1:1399:G:C4	2.45	0.51
1:C1:2432:C:H4'	49:Lq:27:ASN:ND2	2.23	0.51
1:C1:2841:U:H2'	1:C1:2842:C:C6	2.45	0.51
1:C1:2971:U:H2'	1:C1:2972:C:C6	2.46	0.51
6:CC:152:ASP:O	7:CE:573:TYR:OH	2.27	0.51
7:CE:360:ILE:HB	7:CE:410:THR:HG22	1.93	0.51
7:CE:388:HIS:CE1	7:CE:390:LYS:HB2	2.45	0.51
18:CP:383:ARG:NH1	18:CP:449:GLY:O	2.44	0.51
18:CP:421:LEU:O	18:CP:425:ILE:HG12	2.10	0.51
25:Cb:383:SER:O	25:Cb:387:ARG:HG3	2.10	0.51
27:LB:323:VAL:HG12	27:LB:325:ILE:HG13	1.93	0.51
29:LE:64:ARG:HG3	29:LE:65:PHE:CD1	2.45	0.51
15:LF:92:VAL:HG13	15:LF:142:TYR:HB3	1.91	0.51
15:LF:197:VAL:HG12	15:LF:201:PHE:CD1	2.45	0.51
35:LN:142:ILE:HG22	35:LN:152:CYS:SG	2.51	0.51
35:LN:146:PRO:HG2	46:Lh:106:LEU:HD23	1.93	0.51
49:Lq:26:ARG:NH2	49:Lq:210:MET:H	2.09	0.51
1:C1:288:A:H2'	1:C1:289:A:C8	2.45	0.51
1:C1:2091:U:N3	1:C1:2287:G:N1	2.58	0.51
3:C3:35:G:H2'	3:C3:36:C:C6	2.46	0.51
44:Le:14:ARG:NH1	44:Le:16:LYS:O	2.42	0.51
49:Lq:63:MET:HE2	49:Lq:152:LYS:HE2	1.93	0.51
50:Cc:10:PHE:HE1	50:Cc:29:LEU:HD12	1.75	0.51
53:Cf:460:GLU:O	53:Cf:463:ARG:HB2	2.10	0.51
1:C1:397:U:H4'	1:C1:1398:C:H4'	1.91	0.51
1:C1:1080:A:O2'	40:LT:130:ARG:O	2.26	0.51
1:C1:1435:A:C8	53:Cf:509:TRP:HZ2	2.28	0.51
1:C1:2391:G:H2'	1:C1:2392:A:C8	2.45	0.51
1:C1:2881:U:H2'	1:C1:2882:U:C6	2.45	0.51
5:CB:90:ASN:HD22	5:CB:228:ILE:HG23	1.74	0.51
5:CB:291:LEU:HD23	11:CI:320:LEU:HD13	1.92	0.51
7:CE:136:GLU:OE2	7:CE:140:ARG:NE	2.44	0.51
7:CE:340:GLU:HB2	7:CE:343:LYS:HE2	1.93	0.51
19:CQ:44:ARG:HG3	25:Cb:862:TRP:HB2	1.92	0.51
26:Ch:320:LYS:O	26:Ch:324:GLU:HG3	2.10	0.51
27:LB:142:GLY:HA2	27:LB:145:ILE:HD12	1.92	0.51
31:LH:48:VAL:HG23	31:LH:52:VAL:HG23	1.92	0.51
34:LM:32:GLU:HG3	34:LM:74:ARG:HD2	1.91	0.51
51:Cd:304:ALA:HA	51:Cd:393:ILE:HD12	1.93	0.51
1:C1:1193:U:H2'	1:C1:1194:A:H8	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2724:U:N3	1:C1:2751:G:C6	2.79	0.51
1:C1:2979:G:O2'	1:C1:2988:G:O6	2.25	0.51
2:C2:119:C:OP1	12:CJ:25:LYS:NZ	2.36	0.51
3:C3:54:G:N2	30:LG:219:SER:HG	2.09	0.51
4:CA:200:GLU:OE2	23:CX:84:LYS:HA	2.10	0.51
13:CK:209:TYR:HB3	13:CK:214:VAL:HB	1.92	0.51
18:CP:354:THR:HG23	18:CP:357:TYR:H	1.75	0.51
27:LB:136:LYS:HG3	27:LB:141:ASN:HD22	1.76	0.51
39:LS:12:ARG:HB3	39:LS:24:LEU:HD23	1.91	0.51
1:C1:224:A:H2'	1:C1:225:G:O4'	2.10	0.51
1:C1:369:C:O2'	1:C1:383:G:N2	2.43	0.51
1:C1:404:G:H2'	1:C1:405:U:C6	2.46	0.51
1:C1:772:U:H2'	1:C1:773:A:H8	1.74	0.51
1:C1:949:G:H2'	1:C1:950:C:C6	2.46	0.51
1:C1:1416:G:OP1	1:C1:1419:C:N4	2.37	0.51
4:CA:45:THR:HB	4:CA:48:HIS:CD2	2.46	0.51
4:CA:247:GLU:OE2	6:CC:148:ARG:NE	2.44	0.51
7:CE:216:VAL:O	7:CE:229:LYS:NZ	2.42	0.51
10:CH:286:LEU:HD12	10:CH:318:ARG:NE	2.24	0.51
12:CJ:108:ARG:HH12	12:CJ:115:LYS:HE2	1.76	0.51
12:CJ:136:ASP:HA	12:CJ:139:ARG:HD2	1.92	0.51
14:CL:63:GLU:O	14:CL:67:GLN:HG3	2.10	0.51
17:CO:29:ARG:HA	17:CO:32:ARG:HH11	1.75	0.51
22:CU:330:ALA:O	22:CU:334:ILE:HG12	2.11	0.51
25:Cb:159:PHE:HA	25:Cb:210:ASN:HD21	1.75	0.51
30:LG:194:HIS:C	30:LG:195:LYS:HD3	2.36	0.51
35:LN:94:TYR:CE2	35:LN:96:ARG:HB2	2.46	0.51
45:Lf:47:LEU:HD11	45:Lf:76:PRO:HD3	1.91	0.51
51:Cd:341:ARG:HB3	51:Cd:360:TYR:CD2	2.45	0.51
53:Cf:456:GLU:O	53:Cf:463:ARG:NH2	2.43	0.51
54:Cg:37:ILE:HD12	54:Cg:90:LEU:HD11	1.91	0.51
1:C1:633:A:HO2'	1:C1:2334:A:N6	2.08	0.51
1:C1:745:U:O2	1:C1:749:C:N3	2.44	0.51
1:C1:1236:C:H2'	1:C1:1237:C:H6	1.76	0.51
1:C1:1434:A:N3	53:Cf:509:TRP:NE1	2.57	0.51
1:C1:2381:A:OP1	1:C1:2759:A:N6	2.44	0.51
2:C2:122:C:H2'	2:C2:123:G:C8	2.46	0.51
4:CA:153:LYS:HB3	22:CU:200:LEU:CD1	2.41	0.51
7:CE:213:THR:HG22	7:CE:235:ASN:ND2	2.26	0.51
8:CF:125:ALA:HA	8:CF:217:SER:HB3	1.93	0.51
11:CI:198:PHE:HB2	15:CM:58:VAL:HG22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CN:33:ASN:O	16:CN:37:VAL:HG23	2.10	0.51
18:CP:551:TYR:CZ	18:CP:552:MET:HE3	2.46	0.51
45:Lf:18:TYR:OH	45:Lf:91:LEU:O	2.22	0.51
50:Cc:208:VAL:HG13	50:Cc:210:LEU:HD23	1.92	0.51
51:Cd:68:SER:OG	51:Cd:71:LYS:HE2	2.11	0.51
1:C1:37:U:O2	33:LL:15:ARG:NH2	2.44	0.51
1:C1:246:A:O3'	46:Lh:111:LYS:NZ	2.42	0.51
1:C1:768:G:H2'	1:C1:769:C:C6	2.46	0.51
1:C1:2472:U:H2'	1:C1:2473:A:C8	2.46	0.51
1:C1:2727:A:H2'	1:C1:2728:G:C8	2.45	0.51
1:C1:3078:U:H1'	1:C1:3079:A:H5''	1.91	0.51
1:C1:3331:A:H3'	1:C1:3332:G:H8	1.76	0.51
3:C3:19:C:H2'	3:C3:20:U:H6	1.75	0.51
3:C3:56:A:H4'	11:CI:193:ARG:HH21	1.75	0.51
4:CA:26:ILE:HB	4:CA:31:LYS:HD3	1.93	0.51
6:CC:137:TYR:CD2	6:CC:149:TYR:HD1	2.28	0.51
8:CF:68:GLY:N	8:CF:73:MET:SD	2.80	0.51
8:CF:89:LEU:O	8:CF:93:THR:HG23	2.10	0.51
25:Cb:276:PRO:HG2	25:Cb:279:LEU:HB2	1.93	0.51
27:LB:86:VAL:HG13	27:LB:161:VAL:HG13	1.92	0.51
27:LB:219:ILE:HB	27:LB:338:THR:HB	1.93	0.51
15:LF:15:PRO:HB2	15:LF:18:LEU:HD13	1.91	0.51
15:LF:102:PRO:HB2	15:LF:105:PRO:HD2	1.92	0.51
54:Cg:149:MET:SD	54:Cg:172:THR:HG22	2.51	0.51
1:C1:155:G:H2'	1:C1:156:G:H8	1.75	0.51
1:C1:397:U:O2'	1:C1:1377:G:N2	2.43	0.51
1:C1:491:A:H2'	1:C1:492:U:C6	2.45	0.51
1:C1:1124:G:OP2	1:C1:1124:G:N2	2.36	0.51
1:C1:1224:G:N2	10:CH:232:ASN:HD21	2.09	0.51
1:C1:1869:U:H2'	1:C1:1870:A:C8	2.46	0.51
1:C1:2799:G:H1'	1:C1:2805:A:N6	2.26	0.51
1:C1:3309:G:H2'	19:CQ:56:ARG:HH12	1.76	0.51
1:C1:3333:A:H2'	1:C1:3334:U:C6	2.46	0.51
2:C2:95:G:OP1	48:Lj:76:ASN:ND2	2.43	0.51
6:CC:306:TYR:HB2	30:LG:113:LEU:HG	1.93	0.51
8:CF:77:LEU:HD22	8:CF:89:LEU:HD11	1.92	0.51
16:CN:7:PHE:HE2	16:CN:57:ARG:HD3	1.75	0.51
17:CO:42:GLN:OE1	17:CO:42:GLN:N	2.44	0.51
21:CS:673:LYS:O	21:CS:677:ILE:HD12	2.11	0.51
29:LE:73:LEU:HD21	29:LE:84:THR:HG22	1.93	0.51
15:LF:42:ALA:O	15:LF:46:LYS:HG2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:LN:35:VAL:HA	35:LN:65:ARG:HG2	1.93	0.51
53:Cf:449:GLU:HA	53:Cf:452:LYS:NZ	2.26	0.51
54:Cg:114:PHE:HD2	54:Cg:337:MET:HE1	1.75	0.51
4:CA:182:PHE:CE1	4:CA:191:VAL:HG23	2.45	0.50
6:CC:414:PRO:HB2	12:CJ:46:GLU:HG2	1.94	0.50
9:CG:109:LEU:HD21	9:CG:142:LEU:HD22	1.92	0.50
9:CG:128:GLU:HG3	9:CG:149:ARG:HA	1.93	0.50
11:CI:316:ARG:HA	11:CI:319:LYS:HE3	1.93	0.50
15:CM:207:PHE:HD2	15:CM:208:LEU:HD12	1.76	0.50
28:LC:170:TYR:HE1	28:LC:182:VAL:HG11	1.75	0.50
30:LG:56:PRO:HG2	30:LG:59:ILE:HD12	1.93	0.50
32:LK:126:LYS:HZ2	32:LK:155:ILE:HG22	1.75	0.50
54:Cg:34:SER:HA	54:Cg:89:HIS:O	2.10	0.50
1:C1:540:A:H2'	1:C1:541:G:C8	2.46	0.50
1:C1:3188:U:H2'	1:C1:3189:G:H8	1.75	0.50
15:CM:241:ILE:H	15:CM:241:ILE:HD12	1.76	0.50
20:CR:136:GLN:HE22	33:LL:110:ALA:C	2.19	0.50
24:Cz:64:LYS:HA	24:Cz:67:GLU:CD	2.36	0.50
35:LN:120:TRP:HE1	35:LN:123:GLN:HB3	1.75	0.50
36:LO:144:SER:HA	36:LO:147:VAL:HG12	1.93	0.50
1:C1:126:U:H4'	35:LN:139:HIS:CE1	2.47	0.50
1:C1:729:U:H2'	1:C1:730:C:C6	2.46	0.50
1:C1:1055:U:O4	1:C1:1063:C:N4	2.19	0.50
6:CC:283:PRO:HB2	20:CR:218:TYR:HE1	1.76	0.50
7:CE:188:VAL:HB	7:CE:238:ILE:HA	1.92	0.50
7:CE:362:VAL:HG22	7:CE:430:VAL:HB	1.92	0.50
7:CE:419:ARG:NH1	7:CE:444:ARG:HD3	2.27	0.50
8:CF:77:LEU:HB3	8:CF:89:LEU:HG	1.93	0.50
10:CH:159:LEU:HD12	10:CH:160:PRO:HD2	1.93	0.50
10:CH:420:ASP:HB3	10:CH:423:LYS:HZ1	1.75	0.50
12:CJ:104:ALA:O	12:CJ:107:GLU:HG2	2.11	0.50
16:CN:101:LEU:HB3	16:CN:107:VAL:HG11	1.93	0.50
16:CN:117:ILE:HD11	16:CN:139:ARG:NH2	2.22	0.50
22:CU:255:ARG:CG	22:CU:259:ARG:HH12	2.23	0.50
31:LH:62:ARG:HA	31:LH:65:VAL:HG22	1.93	0.50
35:LN:66:VAL:HG21	35:LN:98:LEU:HB3	1.94	0.50
36:LO:51:ALA:HA	36:LO:54:LYS:NZ	2.27	0.50
44:Le:87:LEU:HA	44:Le:116:LEU:HD21	1.92	0.50
46:Lh:11:GLN:HB3	46:Lh:15:LYS:HZ1	1.75	0.50
51:Cd:341:ARG:HB3	51:Cd:360:TYR:HD2	1.77	0.50
1:C1:258:C:N4	47:Li:39:LYS:HA	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:933:A:N3	1:C1:1096:U:O2'	2.40	0.50
1:C1:1430:U:H2'	1:C1:1431:A:H8	1.76	0.50
3:C3:6:A:N6	3:C3:23:U:OP1	2.42	0.50
10:CH:135:MET:O	10:CH:139:ILE:HG12	2.11	0.50
11:CI:252:LEU:HD23	30:LG:92:GLN:HG3	1.94	0.50
16:CN:17:ALA:HB2	16:CN:34:PHE:HZ	1.76	0.50
1:C1:671:G:H2'	1:C1:672:G:H8	1.76	0.50
1:C1:1322:C:H2'	1:C1:1323:U:H6	1.74	0.50
1:C1:1363:A:H2'	1:C1:1364:G:C8	2.46	0.50
1:C1:2813:C:H2'	1:C1:2814:G:C8	2.43	0.50
1:C1:2838:U:H2'	1:C1:2839:C:H6	1.76	0.50
1:C1:3248:C:O2'	37:LP:69:ARG:O	2.27	0.50
7:CE:437:ASP:O	7:CE:441:TYR:CB	2.60	0.50
8:CF:47:ASN:C	8:CF:126:ARG:HD3	2.37	0.50
10:CH:87:ALA:O	10:CH:91:LYS:HG3	2.12	0.50
13:CK:42:LEU:HD21	13:CK:46:ARG:HH21	1.77	0.50
25:Cb:452:HIS:CE1	25:Cb:456:ARG:HE	2.30	0.50
29:LE:139:GLU:HG2	51:Cd:247:PHE:CD2	2.46	0.50
34:LM:31:VAL:HG11	34:LM:54:ARG:NH2	2.27	0.50
1:C1:975:G:H22	1:C1:1035:A:H2'	1.77	0.50
1:C1:1042:U:H2'	1:C1:1043:A:C8	2.46	0.50
1:C1:1190:C:H4'	8:CF:4:SER:H	1.76	0.50
7:CE:120:GLU:HG2	7:CE:121:LYS:HD3	1.92	0.50
10:CH:98:SER:HA	10:CH:101:LYS:HG2	1.93	0.50
18:CP:279:TYR:CE2	18:CP:283:LYS:HE2	2.46	0.50
19:CQ:88:LYS:HA	19:CQ:91:LYS:HZ2	1.77	0.50
22:CU:214:PHE:HD1	22:CU:217:HIS:CE1	2.30	0.50
24:Cz:53:LYS:O	24:Cz:57:GLU:HG3	2.12	0.50
25:Cb:375:THR:OG1	25:Cb:378:HIS:ND1	2.41	0.50
28:LC:295:GLU:HG2	28:LC:296:ILE:N	2.26	0.50
40:LT:48:VAL:O	40:LT:92:ARG:NH2	2.45	0.50
49:Lq:13:VAL:HG11	49:Lq:180:VAL:HG12	1.93	0.50
52:Ce:65:ILE:HB	52:Ce:79:GLU:HB2	1.94	0.50
1:C1:425:A:H2'	1:C1:426:C:C6	2.46	0.50
1:C1:1046:A:H4'	1:C1:1047:A:O5'	2.11	0.50
1:C1:2836:G:H2'	1:C1:2837:C:H6	1.76	0.50
1:C1:2965:G:O6	1:C1:3096:A:N6	2.45	0.50
4:CA:258:ASN:OD1	4:CA:260:ARG:HG2	2.12	0.50
5:CB:273:GLN:HB2	5:CB:277:ASN:HB2	1.94	0.50
7:CE:572:ALA:HB3	7:CE:575:SER:HB3	1.94	0.50
9:CG:27:ILE:HG13	23:CX:98:ARG:HG3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:457:LYS:HE2	19:CQ:71:PHE:HE2	1.77	0.50
12:CJ:166:ALA:O	12:CJ:170:ARG:HD2	2.10	0.50
13:CK:19:ASP:CG	13:CK:23:ARG:HD3	2.36	0.50
27:LB:197:ARG:HA	27:LB:200:PHE:CD1	2.46	0.50
15:LF:151:ARG:HG2	15:LF:191:ILE:HD13	1.92	0.50
35:LN:147:ARG:O	35:LN:150:TRP:NE1	2.45	0.50
35:LN:158:HIS:HB3	35:LN:161:CYS:HB2	1.94	0.50
51:Cd:69:ILE:HB	51:Cd:350:ARG:HH21	1.76	0.50
52:Ce:15:CYS:HB3	52:Ce:18:LYS:HE2	1.93	0.50
1:C1:745:U:H3	1:C1:748:U:H3	1.60	0.50
1:C1:1120:U:H2'	1:C1:1121:G:C8	2.46	0.50
1:C1:2768:C:O3'	13:CK:170:ARG:NH2	2.42	0.50
7:CE:280:GLN:HA	7:CE:283:LYS:HG2	1.94	0.50
10:CH:89:HIS:HA	10:CH:92:VAL:HG12	1.94	0.50
47:Li:49:VAL:O	47:Li:53:ILE:HG12	2.11	0.50
51:Cd:360:TYR:OH	52:Ce:170:LEU:HD22	2.11	0.50
1:C1:57:A:H2'	1:C1:58:G:C8	2.47	0.50
1:C1:978:A:H2'	1:C1:979:A:H8	1.77	0.50
1:C1:2398:U:C2	1:C1:2399:G:C8	2.99	0.50
10:CH:315:GLU:HG2	10:CH:337:ARG:HH22	1.77	0.50
15:CM:138:PRO:HG2	15:CM:139:TRP:CE3	2.47	0.50
16:CN:22:SER:HB3	16:CN:67:ARG:HG3	1.93	0.50
17:CO:106:ILE:HG23	17:CO:107:VAL:HG13	1.93	0.50
18:CP:316:HIS:CE1	18:CP:319:ASP:HB2	2.47	0.50
25:Cb:192:VAL:HG23	25:Cb:206:LEU:HD13	1.94	0.50
29:LE:127:TYR:OH	29:LE:158:ARG:HA	2.12	0.50
15:LF:157:ARG:HG2	15:LF:157:ARG:HH11	1.77	0.50
31:LH:1:MET:HE2	39:LS:138:PRO:HB2	1.93	0.50
50:Cc:166:PRO:HB3	50:Cc:197:VAL:HG21	1.94	0.50
1:C1:297:U:H2'	4:CA:95:ARG:HH12	1.77	0.49
1:C1:370:A:H4'	43:LY:90:THR:HG22	1.94	0.49
1:C1:1241:A:H2'	1:C1:1242:A:C8	2.47	0.49
1:C1:2316:C:H2'	1:C1:2317:G:O4'	2.12	0.49
16:CN:17:ALA:HB2	16:CN:34:PHE:CZ	2.47	0.49
27:LB:287:GLY:HA3	27:LB:322:TYR:CE2	2.47	0.49
28:LC:141:HIS:NE2	28:LC:253:ARG:HD2	2.26	0.49
29:LE:90:ASN:OD1	29:LE:91:GLY:N	2.45	0.49
44:Le:130:GLU:OE2	51:Cd:403:ARG:NH1	2.40	0.49
48:Lj:14:LYS:O	48:Lj:29:ASN:ND2	2.45	0.49
51:Cd:386:ILE:HG21	52:Ce:190:ILE:HG23	1.93	0.49
1:C1:1344:G:H2'	1:C1:1345:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2818:U:OP2	13:CK:107:LYS:NZ	2.37	0.49
2:C2:128:U:H3'	2:C2:129:C:C6	2.47	0.49
8:CF:53:LEU:HA	8:CF:56:VAL:HG12	1.92	0.49
10:CH:244:HIS:HE1	25:Cb:591:LEU:HD22	1.77	0.49
19:CQ:46:PRO:HB2	19:CQ:47:ARG:NH2	2.27	0.49
20:CR:44:THR:HA	33:LL:40:ARG:HH21	1.77	0.49
25:Cb:182:GLU:O	25:Cb:185:LYS:NZ	2.34	0.49
50:Cc:45:LEU:HD21	50:Cc:49:LYS:HE3	1.94	0.49
1:C1:36:C:H4'	1:C1:789:A:H2	1.78	0.49
1:C1:1181:C:H2'	1:C1:1182:A:H8	1.77	0.49
1:C1:2388:U:H3'	1:C1:2389:U:H6	1.77	0.49
1:C1:2992:C:H5'	31:LH:124:ILE:HD12	1.94	0.49
10:CH:444:LYS:HD2	10:CH:449:TYR:CE2	2.45	0.49
10:CH:466:GLU:HB3	10:CH:467:ARG:HH12	1.77	0.49
15:CM:104:LYS:HB3	15:CM:105:PRO:HD3	1.94	0.49
18:CP:468:ASP:OD1	18:CP:470:SER:OG	2.27	0.49
25:Cb:392:SER:HB2	25:Cb:417:THR:HA	1.93	0.49
25:Cb:393:VAL:HG22	25:Cb:419:ILE:HB	1.94	0.49
25:Cb:498:PRO:HG2	25:Cb:500:PHE:HE1	1.77	0.49
32:LK:10:ILE:HD11	32:LK:65:GLN:HE22	1.76	0.49
38:LQ:161:GLY:O	38:LQ:164:THR:OG1	2.24	0.49
54:Cg:162:LYS:O	54:Cg:166:HIS:HB2	2.11	0.49
1:C1:68:C:H41	1:C1:306:U:HO2'	1.60	0.49
1:C1:260:A:C5	35:LN:12:LYS:HG2	2.46	0.49
1:C1:686:A:H5'	33:LL:68:ARG:NH2	2.27	0.49
1:C1:736:A:H2'	1:C1:737:U:H6	1.77	0.49
1:C1:2404:G:H2'	1:C1:2405:A:C8	2.47	0.49
1:C1:2722:C:H2'	1:C1:2723:C:C6	2.47	0.49
1:C1:2837:C:H2'	1:C1:2838:U:C6	2.47	0.49
1:C1:2839:C:H2'	1:C1:2840:U:H6	1.77	0.49
1:C1:3150:U:P	34:LM:99:TRP:HE1	2.35	0.49
2:C2:91:C:H2'	2:C2:92:A:H8	1.76	0.49
5:CB:105:GLN:HB2	5:CB:129:ASP:HB2	1.95	0.49
9:CG:41:GLN:HB3	9:CG:46:TYR:CE1	2.46	0.49
10:CH:50:LYS:O	10:CH:54:GLU:HG3	2.13	0.49
10:CH:183:VAL:HA	10:CH:186:VAL:HG12	1.94	0.49
21:CS:467:GLN:O	21:CS:471:GLU:HG3	2.11	0.49
28:LC:365:ALA:HB3	39:LS:28:ARG:HD2	1.94	0.49
38:LQ:82:MET:O	38:LQ:87:ARG:NH1	2.46	0.49
44:Le:95:ALA:HB3	44:Le:120:VAL:HG22	1.94	0.49
48:Lj:28:HIS:HE1	48:Lj:30:GLN:HB3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Cd:202:LEU:HD11	51:Cd:228:ILE:HG12	1.95	0.49
51:Cd:240:SER:O	51:Cd:244:ILE:HD12	2.12	0.49
1:C1:386:U:H5'	43:LY:86:ARG:NH2	2.25	0.49
1:C1:457:U:O2'	50:Cc:63:ARG:NH2	2.45	0.49
1:C1:599:U:H2'	1:C1:600:G:H8	1.77	0.49
1:C1:972:G:OP1	40:LT:100:ARG:NH1	2.45	0.49
1:C1:1289:G:O4'	36:LO:61:LYS:NZ	2.43	0.49
1:C1:2419:G:H2'	1:C1:2421:A:H62	1.78	0.49
1:C1:2468:U:H2'	1:C1:2469:U:C6	2.48	0.49
1:C1:2567:A:H2'	1:C1:2568:G:H8	1.78	0.49
1:C1:2807:C:H2'	1:C1:2808:G:O4'	2.12	0.49
1:C1:2837:C:H2'	1:C1:2838:U:H6	1.78	0.49
1:C1:2963:A:H2'	1:C1:2964:U:O4'	2.11	0.49
3:C3:48:G:C2	3:C3:49:G:C8	3.00	0.49
7:CE:512:LYS:O	7:CE:516:ARG:HG2	2.13	0.49
10:CH:413:GLY:H	10:CH:416:VAL:HB	1.77	0.49
19:CQ:106:VAL:HB	19:CQ:110:LYS:HZ1	1.75	0.49
27:LB:164:HIS:HB3	27:LB:179:LEU:HD23	1.94	0.49
15:LF:242:ASN:O	15:LF:246:ARG:HG2	2.12	0.49
30:LG:52:MET:HE2	30:LG:53:VAL:HG22	1.95	0.49
30:LG:81:PHE:CZ	30:LG:167:VAL:HA	2.47	0.49
30:LG:174:ARG:HE	30:LG:233:ARG:CZ	2.26	0.49
35:LN:30:TYR:O	35:LN:65:ARG:NH2	2.38	0.49
41:LV:106:ASN:ND2	41:LV:110:GLU:HB3	2.27	0.49
1:C1:3117:C:H5''	51:Cd:301:HIS:O	2.13	0.49
7:CE:268:ARG:NH2	7:CE:437:ASP:HB2	2.28	0.49
8:CF:24:GLU:HA	8:CF:27:PHE:HD2	1.78	0.49
8:CF:42:VAL:HG13	8:CF:224:LEU:HB2	1.94	0.49
12:CJ:246:TYR:HA	12:CJ:249:ILE:HG12	1.95	0.49
16:CN:22:SER:O	16:CN:47:PRO:HD2	2.12	0.49
18:CP:487:GLN:HE22	18:CP:519:GLU:HA	1.77	0.49
19:CQ:68:THR:HA	19:CQ:71:PHE:HD1	1.76	0.49
22:CU:364:ASN:HB3	22:CU:368:ARG:NH2	2.28	0.49
25:Cb:16:ASP:N	25:Cb:275:LEU:O	2.45	0.49
52:Ce:89:LYS:O	52:Ce:93:GLN:HG3	2.13	0.49
53:Cf:474:ALA:O	53:Cf:478:ARG:HG2	2.12	0.49
1:C1:3232:U:H2'	1:C1:3233:C:C6	2.47	0.49
4:CA:60:PRO:HD2	4:CA:61:HIS:H	1.77	0.49
6:CC:175:ILE:HD12	6:CC:175:ILE:H	1.77	0.49
7:CE:320:VAL:O	7:CE:320:VAL:HG12	2.13	0.49
11:CI:291:ARG:HB3	11:CI:295:ARG:NH1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:400:VAL:O	15:CM:151:ARG:NH1	2.46	0.49
22:CU:255:ARG:HE	22:CU:259:ARG:NH2	2.10	0.49
23:CX:95:VAL:O	23:CX:100:SER:OG	2.30	0.49
1:C1:351:U:O2'	48:Lj:16:HIS:ND1	2.45	0.49
1:C1:374:U:H3'	1:C1:375:G:H8	1.78	0.49
1:C1:1211:G:C1'	8:CF:126:ARG:HH12	2.26	0.49
1:C1:1434:A:H2'	53:Cf:509:TRP:CZ2	2.48	0.49
1:C1:2558:C:H2'	1:C1:2559:A:H8	1.78	0.49
1:C1:2942:C:H2'	1:C1:2943:C:C6	2.48	0.49
9:CG:136:ASN:HB3	9:CG:142:LEU:HD11	1.95	0.49
16:CN:152:MET:HG3	16:CN:161:VAL:HA	1.93	0.49
27:LB:113:GLU:CG	27:LB:177:ALA:HB2	2.42	0.49
45:Lf:49:LYS:O	45:Lf:72:LYS:HA	2.13	0.49
51:Cd:298:ILE:O	51:Cd:301:HIS:ND1	2.42	0.49
52:Ce:15:CYS:HB3	52:Ce:18:LYS:HB2	1.94	0.49
1:C1:446:U:C5	52:Ce:82:LYS:HD3	2.47	0.49
1:C1:579:A:H1'	1:C1:1319:G:H5''	1.94	0.49
1:C1:584:C:P	1:C1:596:G:H1	2.36	0.49
1:C1:3296:G:H2'	1:C1:3297:U:C6	2.48	0.49
3:C3:65:G:H21	3:C3:143:A:N6	2.10	0.49
13:CK:218:GLY:CA	13:CK:245:ILE:O	2.61	0.49
15:CM:169:LEU:HD22	15:CM:175:ILE:HD11	1.93	0.49
18:CP:321:ALA:O	18:CP:325:ILE:HG12	2.12	0.49
27:LB:308:PRO:HG3	27:LB:362:THR:HA	1.95	0.49
15:LF:94:ARG:HA	15:LF:140:VAL:HG12	1.95	0.49
31:LH:112:TYR:OH	31:LH:135:GLU:HG3	2.13	0.49
38:LQ:64:LEU:O	38:LQ:68:THR:HB	2.12	0.49
46:Lh:100:GLU:OE1	46:Lh:104:ARG:NH2	2.45	0.49
48:Lj:66:TYR:O	48:Lj:70:VAL:HG23	2.12	0.49
1:C1:298:A:OP2	4:CA:265:ASN:ND2	2.41	0.49
1:C1:649:U:H2'	1:C1:650:C:C6	2.48	0.49
1:C1:694:U:OP1	1:C1:761:A:O2'	2.31	0.49
1:C1:742:A:H2'	1:C1:743:U:C6	2.47	0.49
1:C1:786:G:H1'	28:LC:74:ARG:HE	1.78	0.49
1:C1:972:G:N2	40:LT:59:GLY:O	2.46	0.49
1:C1:2371:G:H2'	1:C1:2372:U:H6	1.78	0.49
1:C1:3263:A:H5''	54:Cg:66:ARG:NE	2.27	0.49
2:C2:63:G:H22	2:C2:97:A:H2	1.59	0.49
6:CC:162:ASP:OD1	6:CC:163:THR:N	2.46	0.49
7:CE:527:LEU:HD23	7:CE:531:PHE:CE2	2.48	0.49
9:CG:116:LYS:HB3	9:CG:159:PRO:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:155:HIS:HA	10:CH:158:ARG:HG2	1.95	0.49
14:CL:361:ALA:HA	14:CL:370:LEU:O	2.12	0.49
18:CP:347:SER:OG	18:CP:349:VAL:O	2.30	0.49
20:CR:146:ILE:HD13	33:LL:84:GLY:HA2	1.94	0.49
27:LB:113:GLU:HA	27:LB:116:ARG:HG3	1.94	0.49
27:LB:381:MET:HA	27:LB:381:MET:HE3	1.94	0.49
34:LM:44:PRO:HB2	34:LM:82:LYS:HG3	1.94	0.49
36:LO:24:VAL:O	36:LO:28:LEU:HG	2.13	0.49
36:LO:121:VAL:HG11	39:LS:169:ARG:HG2	1.94	0.49
1:C1:671:G:H2'	1:C1:672:G:C8	2.48	0.48
1:C1:2459:C:H2'	1:C1:2460:C:O4'	2.12	0.48
1:C1:2724:U:O4	1:C1:2751:G:O6	2.31	0.48
1:C1:3116:G:C2'	1:C1:3117:C:H5'	2.43	0.48
1:C1:3296:G:O2'	1:C1:3297:U:OP1	2.24	0.48
5:CB:226:LYS:O	5:CB:229:GLY:O	2.31	0.48
12:CJ:3:LYS:HB3	12:CJ:5:LYS:HE3	1.94	0.48
16:CN:201:ASP:HB3	16:CN:202:TRP:CE3	2.48	0.48
20:CR:198:LEU:HD21	20:CR:209:MET:HB3	1.95	0.48
25:Cb:587:ARG:NH2	25:Cb:590:LEU:HB2	2.26	0.48
41:LV:131:ILE:O	41:LV:135:ALA:HB2	2.13	0.48
52:Ce:189:GLN:O	52:Ce:190:ILE:HB	2.12	0.48
53:Cf:458:LEU:HD12	53:Cf:466:ILE:HD13	1.95	0.48
1:C1:8:C:H2'	1:C1:9:U:C6	2.48	0.48
1:C1:2772:G:H2'	1:C1:2773:G:H8	1.78	0.48
1:C1:2832:G:N3	1:C1:2833:U:O2'	2.46	0.48
1:C1:3067:C:H2'	1:C1:3068:U:C6	2.48	0.48
1:C1:3136:A:H2'	1:C1:3137:A:H8	1.76	0.48
1:C1:3139:A:C2'	31:LH:23:ARG:HH21	2.25	0.48
1:C1:3235:A:H2'	1:C1:3236:A:H8	1.78	0.48
4:CA:105:SER:HB2	4:CA:112:THR:HG23	1.95	0.48
4:CA:231:LEU:HB2	22:CU:244:MET:HE1	1.95	0.48
7:CE:245:LEU:HD13	7:CE:281:ILE:HG13	1.96	0.48
7:CE:528:ARG:O	7:CE:532:ASP:HB2	2.13	0.48
10:CH:255:ILE:HA	10:CH:263:LEU:HD21	1.94	0.48
10:CH:421:LEU:HD13	16:CN:83:HIS:HE1	1.78	0.48
16:CN:111:ASN:OD1	16:CN:114:THR:N	2.27	0.48
25:Cb:263:PRO:O	25:Cb:266:ARG:NH1	2.39	0.48
26:Ch:279:GLU:HG3	54:Cg:215:ARG:HH12	1.78	0.48
28:LC:295:GLU:OE2	38:LQ:156:LEU:HD12	2.13	0.48
33:LL:43:ALA:O	33:LL:47:ALA:HA	2.12	0.48
39:LS:110:MET:HA	39:LS:110:MET:HE3	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LV:79:VAL:HG11	41:LV:131:ILE:HD11	1.94	0.48
49:Lq:113:SER:HA	49:Lq:138:VAL:HG22	1.95	0.48
51:Cd:14:LEU:HB3	51:Cd:24:ARG:HG3	1.95	0.48
1:C1:538:G:H2'	1:C1:539:G:H8	1.78	0.48
1:C1:1289:G:O2'	1:C1:1290:A:N7	2.45	0.48
1:C1:2389:U:O2	1:C1:2560:G:C6	2.66	0.48
1:C1:2848:A:H2'	1:C1:2849:U:C6	2.48	0.48
1:C1:3315:A:C2	1:C1:3318:C:H5''	2.48	0.48
6:CC:186:ILE:CD1	6:CC:197:ARG:HD2	2.43	0.48
7:CE:393:GLN:HA	7:CE:396:ARG:HE	1.77	0.48
8:CF:166:ARG:HD3	13:CK:18:LEU:HD22	1.93	0.48
25:Cb:559:ARG:O	25:Cb:563:VAL:HG23	2.13	0.48
27:LB:136:LYS:HG2	27:LB:141:ASN:HB2	1.95	0.48
28:LC:236:PRO:HG2	28:LC:239:ALA:HB3	1.95	0.48
28:LC:338:LYS:O	28:LC:340:LYS:NZ	2.33	0.48
37:LP:115:LYS:HZ2	37:LP:149:ILE:HG22	1.77	0.48
49:Lq:98:LYS:HG3	49:Lq:102:LYS:NZ	2.29	0.48
1:C1:422:G:H2'	1:C1:423:U:C6	2.48	0.48
4:CA:75:TYR:O	4:CA:78:CYS:HB2	2.14	0.48
4:CA:191:VAL:HG11	4:CA:238:PHE:CZ	2.48	0.48
6:CC:135:ARG:NE	6:CC:135:ARG:HA	2.27	0.48
7:CE:143:PRO:HB2	7:CE:144:PRO:HD3	1.95	0.48
11:CI:288:MET:O	11:CI:291:ARG:N	2.45	0.48
16:CN:101:LEU:HA	41:LV:137:VAL:HG22	1.96	0.48
25:Cb:493:ARG:HE	25:Cb:574:ALA:HA	1.78	0.48
26:Ch:283:ARG:HD3	54:Cg:217:TYR:CZ	2.48	0.48
27:LB:164:HIS:HA	27:LB:178:HIS:O	2.13	0.48
35:LN:10:LEU:HD22	47:Li:53:ILE:HG23	1.96	0.48
35:LN:177:GLY:O	35:LN:184:ARG:NH2	2.37	0.48
37:LP:70:THR:HG23	37:LP:72:GLN:H	1.78	0.48
38:LQ:106:LYS:HG2	38:LQ:163:ASN:OD1	2.14	0.48
49:Lq:39:LYS:HD2	49:Lq:40:ASN:N	2.29	0.48
49:Lq:116:LEU:HD12	49:Lq:119:GLN:HB3	1.96	0.48
53:Cf:478:ARG:NH1	54:Cg:110:ARG:O	2.33	0.48
1:C1:115:A:H2'	1:C1:257:A:H2'	1.95	0.48
1:C1:180:G:H2'	1:C1:181:A:C8	2.47	0.48
1:C1:2090:C:C2	1:C1:2288:A:C2	3.02	0.48
2:C2:67:U:H2'	2:C2:68:G:H8	1.78	0.48
6:CC:262:PHE:CZ	30:LG:175:LYS:HE2	2.49	0.48
6:CC:282:ILE:HD12	6:CC:285:LYS:HZ2	1.78	0.48
7:CE:512:LYS:HG2	7:CE:516:ARG:HH12	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CG:8:GLU:HB3	9:CG:74:MET:HE1	1.96	0.48
10:CH:145:PRO:O	10:CH:149:LEU:HD23	2.13	0.48
18:CP:402:MET:HE1	18:CP:408:ILE:HG12	1.96	0.48
23:CX:129:ILE:HG22	23:CX:133:ARG:NH1	2.28	0.48
15:LF:80:SER:HB2	40:LT:141:VAL:O	2.14	0.48
38:LQ:92:LEU:HA	38:LQ:95:ILE:HG12	1.95	0.48
1:C1:694:U:H2'	1:C1:695:G:C8	2.49	0.48
1:C1:1263:U:H5''	8:CF:69:LYS:NZ	2.24	0.48
1:C1:1332:A:O2'	1:C1:1333:A:O5'	2.31	0.48
1:C1:2555:U:H2'	1:C1:2556:G:C8	2.48	0.48
1:C1:3001:A:H2'	1:C1:3002:G:H8	1.77	0.48
7:CE:429:ILE:HG21	7:CE:445:VAL:HG22	1.96	0.48
10:CH:429:ASN:HD21	19:CQ:83:ARG:HH22	1.61	0.48
11:CI:251:TYR:O	11:CI:258:LEU:HD12	2.14	0.48
16:CN:24:CYS:SG	16:CN:48:ILE:HG23	2.53	0.48
22:CU:220:VAL:HG11	22:CU:250:ALA:HA	1.96	0.48
26:Ch:313:ARG:NH2	51:Cd:368:THR:O	2.47	0.48
15:LF:190:LEU:HD21	15:LF:208:LEU:HD21	1.96	0.48
31:LH:13:PRO:HG2	31:LH:16:LEU:HG	1.96	0.48
36:LO:77:ALA:HB1	36:LO:108:GLU:OE2	2.12	0.48
39:LS:131:LYS:HG2	39:LS:132:THR:O	2.13	0.48
1:C1:495:G:O4'	28:LC:315:GLN:NE2	2.47	0.48
1:C1:1373:C:C2	44:Le:104:ARG:NH1	2.82	0.48
1:C1:3058:G:H2'	1:C1:3059:G:H8	1.79	0.48
1:C1:3116:G:H5''	37:LP:159:LYS:HZ3	1.79	0.48
10:CH:361:LEU:HA	10:CH:364:VAL:HG22	1.94	0.48
12:CJ:229:THR:HG22	12:CJ:233:PHE:CE2	2.49	0.48
30:LG:145:LEU:HD13	30:LG:204:THR:HG21	1.95	0.48
44:Le:90:ASN:ND2	44:Le:117:GLY:O	2.46	0.48
51:Cd:256:LEU:HB3	51:Cd:272:VAL:HB	1.95	0.48
1:C1:11:G:H2'	1:C1:12:G:H8	1.78	0.48
1:C1:2291:C:H2'	1:C1:2292:C:C6	2.49	0.48
1:C1:3118:A:H2'	1:C1:3119:C:C6	2.49	0.48
2:C2:26:U:H2'	2:C2:27:U:C6	2.48	0.48
2:C2:148:G:H2'	2:C2:149:A:C8	2.49	0.48
5:CB:291:LEU:HD22	11:CI:325:TYR:HD2	1.79	0.48
10:CH:246:ARG:HH12	10:CH:342:ARG:HH21	1.61	0.48
11:CI:312:ARG:HD2	11:CI:316:ARG:HH22	1.78	0.48
16:CN:34:PHE:CZ	16:CN:38:PHE:HE2	2.31	0.48
18:CP:391:PRO:O	18:CP:424:ASN:ND2	2.47	0.48
20:CR:205:ASP:O	20:CR:209:MET:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CU:364:ASN:HB3	22:CU:368:ARG:HH22	1.78	0.48
26:Ch:317:ILE:HG22	26:Ch:319:SER:H	1.79	0.48
15:LF:15:PRO:HB3	50:Cc:110:GLU:HG2	1.96	0.48
36:LO:51:ALA:HA	36:LO:54:LYS:HZ3	1.79	0.48
51:Cd:357:ARG:HB3	51:Cd:394:GLY:HA3	1.95	0.48
1:C1:36:C:O3'	1:C1:915:G:N2	2.46	0.48
1:C1:934:G:O2'	1:C1:1097:G:H4'	2.13	0.48
1:C1:2838:U:H2'	1:C1:2839:C:C6	2.49	0.48
2:C2:69:U:H2'	2:C2:70:G:O4'	2.14	0.48
8:CF:90:HIS:HD2	8:CF:94:ARG:HH22	1.62	0.48
8:CF:145:THR:HG21	8:CF:149:VAL:HG22	1.96	0.48
10:CH:53:GLN:NE2	10:CH:105:GLU:HG3	2.25	0.48
18:CP:365:GLN:HE21	18:CP:370:PHE:HE1	1.58	0.48
25:Cb:114:THR:OG1	25:Cb:117:GLN:OE1	2.31	0.48
25:Cb:312:VAL:HG11	25:Cb:317:LYS:HA	1.95	0.48
25:Cb:479:LEU:HA	25:Cb:482:GLN:HG2	1.96	0.48
26:Ch:279:GLU:HG3	54:Cg:215:ARG:HH22	1.77	0.48
30:LG:218:ILE:O	30:LG:222:LYS:HG2	2.14	0.48
32:LK:68:GLN:H	32:LK:68:GLN:CD	2.22	0.48
35:LN:11:SER:O	35:LN:14:LYS:HD2	2.14	0.48
40:LT:127:GLN:HE22	40:LT:129:LYS:C	2.21	0.48
41:LV:71:LEU:HA	41:LV:74:LYS:HD2	1.95	0.48
49:Lq:133:LYS:HD2	49:Lq:133:LYS:O	2.13	0.48
1:C1:1157:C:O2	36:LO:89:MET:HG2	2.13	0.48
1:C1:3069:G:O6	1:C1:3077:C:H5''	2.13	0.48
2:C2:142:C:H2'	2:C2:143:U:C6	2.49	0.48
6:CC:353:SER:HB2	12:CJ:485:HIS:CE1	2.49	0.48
6:CC:411:TYR:OH	12:CJ:130:ARG:NH2	2.47	0.48
7:CE:113:PHE:CD1	7:CE:134:MET:HE3	2.48	0.48
7:CE:438:PRO:O	7:CE:442:ILE:HG12	2.13	0.48
7:CE:512:LYS:HG2	7:CE:516:ARG:NH1	2.29	0.48
15:CM:213:LEU:HB3	15:CM:248:MET:HB3	1.96	0.48
20:CR:43:GLU:O	33:LL:40:ARG:NH2	2.47	0.48
29:LE:157:THR:O	29:LE:159:ALA:O	2.32	0.48
15:LF:94:ARG:HD2	15:LF:109:LEU:HD23	1.96	0.48
15:LF:104:LYS:HB3	15:LF:105:PRO:HD3	1.95	0.48
45:Lf:54:VAL:HG22	45:Lf:68:VAL:HG22	1.96	0.48
53:Cf:459:PRO:O	53:Cf:463:ARG:N	2.39	0.48
1:C1:727:C:H2'	1:C1:728:A:C8	2.49	0.47
1:C1:2770:C:H2'	1:C1:2771:A:C8	2.49	0.47
1:C1:3334:U:H2'	1:C1:3335:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CC:121:PHE:HD2	7:CE:438:PRO:HB2	1.79	0.47
6:CC:400:VAL:HG22	12:CJ:150:LEU:HD11	1.95	0.47
7:CE:217:VAL:HG23	7:CE:237:LEU:HD11	1.95	0.47
7:CE:220:GLY:HA2	7:CE:557:LEU:HB3	1.96	0.47
10:CH:144:ASP:HB3	25:Cb:624:PHE:HD1	1.77	0.47
12:CJ:171:LEU:HB3	12:CJ:238:LEU:HD23	1.94	0.47
13:CK:9:ARG:NH2	13:CK:13:LEU:HD11	2.29	0.47
18:CP:475:ARG:NH1	18:CP:483:LEU:HD11	2.30	0.47
25:Cb:9:ALA:HB3	25:Cb:10:PRO:HD3	1.95	0.47
25:Cb:603:ILE:HA	25:Cb:606:ILE:HD12	1.95	0.47
30:LG:73:LYS:HD3	30:LG:237:GLY:O	2.13	0.47
47:Li:69:LEU:HD13	47:Li:77:ARG:HG3	1.96	0.47
52:Ce:74:PRO:HA	52:Ce:77:TRP:CE2	2.49	0.47
54:Cg:167:LEU:HD21	54:Cg:337:MET:HG2	1.97	0.47
1:C1:404:G:N3	37:LP:118:GLN:NE2	2.61	0.47
1:C1:631:G:H5'	1:C1:1098:G:C8	2.49	0.47
1:C1:655:U:H2'	1:C1:656:U:C6	2.49	0.47
1:C1:772:U:H2'	1:C1:773:A:C8	2.49	0.47
1:C1:985:U:O2	1:C1:1031:C:O2'	2.32	0.47
1:C1:3319:C:H4'	27:LB:316:GLY:HA2	1.96	0.47
7:CE:170:VAL:HG22	7:CE:207:MET:HE3	1.96	0.47
9:CG:28:ALA:HA	23:CX:98:ARG:HE	1.79	0.47
12:CJ:66:THR:O	12:CJ:70:GLN:HG2	2.14	0.47
16:CN:121:LEU:HD11	16:CN:125:THR:HG21	1.95	0.47
18:CP:324:LEU:HB3	18:CP:329:VAL:HB	1.95	0.47
18:CP:487:GLN:HA	18:CP:490:LEU:HD12	1.95	0.47
19:CQ:47:ARG:NH2	19:CQ:54:ALA:HB3	2.29	0.47
23:CX:125:GLN:O	23:CX:129:ILE:HG13	2.14	0.47
25:Cb:509:LEU:HD23	25:Cb:576:PHE:HZ	1.79	0.47
27:LB:332:VAL:HG22	27:LB:335:ARG:CZ	2.44	0.47
27:LB:359:TRP:CZ3	27:LB:361:ASP:HA	2.49	0.47
53:Cf:472:TRP:CH2	54:Cg:350:LEU:HB3	2.48	0.47
1:C1:466:U:C2	1:C1:467:G:C8	3.03	0.47
1:C1:1261:C:H2'	1:C1:1262:C:C6	2.49	0.47
1:C1:2968:A:N1	1:C1:3000:C:O2'	2.45	0.47
7:CE:336:TYR:HB2	7:CE:462:LEU:HD23	1.95	0.47
8:CF:45:VAL:HG13	8:CF:45:VAL:O	2.14	0.47
10:CH:420:ASP:HB3	10:CH:423:LYS:HZ2	1.77	0.47
12:CJ:108:ARG:HH22	12:CJ:115:LYS:NZ	2.11	0.47
18:CP:551:TYR:CD2	18:CP:552:MET:HG2	2.50	0.47
20:CR:8:ARG:HH21	48:Lj:63:ARG:HA	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Cb:283:THR:HA	25:Cb:287:LEU:HD13	1.97	0.47
26:Ch:323:GLU:O	26:Ch:327:THR:HG23	2.15	0.47
28:LC:155:SER:HA	28:LC:158:VAL:HG22	1.95	0.47
29:LE:157:THR:C	29:LE:159:ALA:O	2.57	0.47
53:Cf:466:ILE:O	53:Cf:470:GLU:OE1	2.31	0.47
54:Cg:161:SER:HB2	54:Cg:165:ARG:HB3	1.95	0.47
1:C1:80:G:O6	1:C1:106:A:N6	2.48	0.47
1:C1:455:G:H2'	1:C1:456:U:O4'	2.14	0.47
1:C1:946:A:H2'	1:C1:947:U:C6	2.49	0.47
1:C1:3071:A:OP1	24:Cz:39:PHE:HB2	2.14	0.47
1:C1:3095:C:H2'	1:C1:3096:A:H8	1.80	0.47
2:C2:126:A:O2'	2:C2:128:U:OP1	2.26	0.47
3:C3:15:U:H5'	3:C3:16:G:C2	2.49	0.47
6:CC:203:ALA:HB2	23:CX:124:ARG:NH2	2.29	0.47
10:CH:466:GLU:HB3	10:CH:467:ARG:NH1	2.28	0.47
17:CO:37:LEU:HD12	27:LB:195:PHE:HZ	1.79	0.47
20:CR:201:LYS:HG3	20:CR:202:HIS:ND1	2.29	0.47
31:LH:86:PHE:CD2	31:LH:153:LEU:HD13	2.49	0.47
31:LH:167:CYS:SG	31:LH:181:ILE:HD12	2.54	0.47
38:LQ:79:ARG:HA	38:LQ:82:MET:SD	2.55	0.47
38:LQ:90:VAL:HG11	38:LQ:110:VAL:HG11	1.96	0.47
1:C1:713:G:N1	1:C1:724:C:OP2	2.42	0.47
1:C1:1875:A:H2'	1:C1:1876:G:C8	2.48	0.47
1:C1:2405:A:H2'	1:C1:2406:C:H6	1.80	0.47
8:CF:80:THR:HG23	8:CF:83:GLU:H	1.79	0.47
12:CJ:84:GLN:HG3	12:CJ:121:TYR:CE1	2.50	0.47
12:CJ:189:PHE:HE1	12:CJ:485:HIS:HE1	1.60	0.47
19:CQ:57:LYS:HZ3	19:CQ:64:VAL:HG13	1.79	0.47
20:CR:167:GLU:HA	20:CR:170:ARG:HH12	1.79	0.47
30:LG:194:HIS:O	30:LG:195:LYS:HD3	2.14	0.47
41:LV:25:MET:HB2	41:LV:100:ASN:O	2.14	0.47
51:Cd:342:GLN:HG2	51:Cd:393:ILE:HD11	1.96	0.47
54:Cg:90:LEU:HB3	54:Cg:106:VAL:CG2	2.45	0.47
1:C1:434:G:H2'	1:C1:435:C:C6	2.49	0.47
1:C1:648:G:H4'	1:C1:649:U:H6	1.80	0.47
1:C1:926:C:H2'	1:C1:927:C:C6	2.50	0.47
1:C1:2370:U:H2'	1:C1:2371:G:C8	2.49	0.47
1:C1:2426:U:H2'	1:C1:2427:G:C8	2.49	0.47
1:C1:2476:U:O2'	1:C1:2551:A:N6	2.48	0.47
1:C1:3160:G:O4'	1:C1:3199:A:N6	2.48	0.47
3:C3:41:G:H2'	3:C3:42:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CE:113:PHE:CD1	7:CE:126:ILE:HD13	2.49	0.47
7:CE:361:ILE:HB	7:CE:429:ILE:HD13	1.96	0.47
8:CF:91:ARG:HG2	8:CF:95:TYR:HE1	1.80	0.47
11:CI:321:LYS:HG2	11:CI:326:GLU:HG3	1.97	0.47
12:CJ:227:MET:O	12:CJ:231:VAL:HG23	2.14	0.47
13:CK:127:ILE:HD11	13:CK:132:MET:HE3	1.96	0.47
13:CK:166:VAL:HA	13:CK:169:GLU:HB2	1.97	0.47
13:CK:260:LEU:HD22	22:CU:338:LYS:HG2	1.96	0.47
16:CN:161:VAL:HG21	16:CN:181:LEU:HD13	1.95	0.47
18:CP:316:HIS:HD2	18:CP:318:ARG:HG2	1.80	0.47
25:Cb:323:HIS:CD2	25:Cb:509:LEU:HD22	2.49	0.47
46:Lh:33:GLN:O	46:Lh:37:GLN:HG3	2.14	0.47
54:Cg:58:VAL:HG13	54:Cg:216:HIS:HD2	1.80	0.47
1:C1:6:A:H5'	12:CJ:93:ARG:NH1	2.29	0.47
1:C1:1263:U:H2'	1:C1:1264:G:C8	2.36	0.47
1:C1:1401:A:N7	28:LC:191:LEU:HD23	2.29	0.47
1:C1:2894:A:H2'	1:C1:2895:G:C8	2.49	0.47
1:C1:3195:C:H2'	1:C1:3196:G:C8	2.50	0.47
3:C3:26:U:OP1	5:CB:169:LYS:N	2.44	0.47
3:C3:147:C:H5''	15:CM:107:LYS:HE2	1.96	0.47
4:CA:48:HIS:CE1	4:CA:100:LEU:HB2	2.50	0.47
5:CB:159:ILE:O	5:CB:163:LEU:HG	2.15	0.47
5:CB:260:GLU:HG2	5:CB:264:ARG:NH2	2.30	0.47
8:CF:58:HIS:CE1	32:LK:121:PHE:HA	2.50	0.47
8:CF:107:ARG:HH22	8:CF:111:ASP:HB3	1.80	0.47
9:CG:84:ILE:O	9:CG:173:TYR:OH	2.32	0.47
9:CG:85:THR:HG23	18:CP:426:HIS:CD2	2.50	0.47
12:CJ:460:TRP:HA	12:CJ:476:TYR:CD2	2.50	0.47
15:CM:104:LYS:O	15:CM:108:ILE:HG12	2.15	0.47
16:CN:162:HIS:HB3	16:CN:165:THR:HG23	1.97	0.47
17:CO:30:LEU:HD13	27:LB:39:LYS:HD2	1.97	0.47
18:CP:287:LEU:HD12	18:CP:551:TYR:OH	2.14	0.47
18:CP:297:PHE:O	18:CP:301:GLU:HG3	2.15	0.47
18:CP:402:MET:O	18:CP:405:THR:OG1	2.28	0.47
18:CP:422:ILE:HB	18:CP:426:HIS:HE1	1.78	0.47
25:Cb:525:LEU:HD23	25:Cb:531:ILE:HG22	1.97	0.47
27:LB:58:ARG:HD2	27:LB:355:VAL:HG23	1.96	0.47
27:LB:372:GLN:N	27:LB:376:GLU:OE2	2.47	0.47
28:LC:341:LEU:HB3	15:LF:62:ARG:HH22	1.78	0.47
29:LE:58:LEU:HD23	29:LE:72:LEU:HB2	1.95	0.47
30:LG:176:MET:HA	30:LG:176:MET:HE3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LG:206:VAL:HG22	30:LG:214:LEU:HD22	1.95	0.47
44:Le:64:THR:HA	44:Le:67:MET:SD	2.55	0.47
49:Lq:39:LYS:HD2	49:Lq:40:ASN:HB2	1.96	0.47
50:Cc:93:PHE:HD2	50:Cc:94:TRP:CD1	2.33	0.47
50:Cc:127:MET:HE3	50:Cc:155:VAL:HA	1.96	0.47
1:C1:126:U:P	35:LN:144:ARG:HH21	2.38	0.47
1:C1:778:U:H2'	1:C1:779:U:C6	2.50	0.47
1:C1:927:C:H2'	1:C1:928:G:C8	2.50	0.47
1:C1:1259:C:C2	1:C1:1260:A:C8	3.03	0.47
1:C1:2799:G:O6	1:C1:2802:C:H3'	2.14	0.47
4:CA:152:LEU:HD23	4:CA:155:ILE:HD12	1.97	0.47
7:CE:313:PRO:O	7:CE:315:PRO:HD3	2.15	0.47
12:CJ:42:ILE:HD12	12:CJ:68:ASP:HB3	1.95	0.47
12:CJ:148:LEU:HD11	12:CJ:234:TYR:O	2.15	0.47
12:CJ:421:ASP:OD1	12:CJ:421:ASP:N	2.48	0.47
13:CK:133:PHE:CD2	13:CK:172:ILE:HD11	2.50	0.47
18:CP:475:ARG:HB3	18:CP:480:PHE:CE1	2.47	0.47
25:Cb:165:VAL:HG22	25:Cb:239:VAL:HB	1.97	0.47
25:Cb:479:LEU:O	25:Cb:482:GLN:HG2	2.15	0.47
27:LB:224:GLY:HA2	27:LB:272:GLY:HA3	1.95	0.47
27:LB:285:ARG:HE	27:LB:357:LEU:HD12	1.80	0.47
28:LC:266:ASP:O	28:LC:270:GLU:HG2	2.15	0.47
41:LV:122:LYS:HE3	41:LV:139:MET:CA	2.44	0.47
49:Lq:120:ILE:HG13	49:Lq:121:PRO:HD3	1.96	0.47
52:Ce:112:ARG:O	52:Ce:116:LEU:HD23	2.15	0.47
1:C1:490:C:H2'	1:C1:491:A:C8	2.50	0.47
1:C1:1332:A:O2'	1:C1:1333:A:O4'	2.31	0.47
1:C1:1429:G:O2'	1:C1:2317:G:O6	2.31	0.47
1:C1:2295:C:H2'	1:C1:2296:U:C6	2.50	0.47
1:C1:3225:C:H2'	1:C1:3226:G:O4'	2.15	0.47
7:CE:162:THR:HG23	7:CE:199:ILE:HG12	1.97	0.47
10:CH:155:HIS:HA	10:CH:158:ARG:CG	2.45	0.47
10:CH:250:LEU:HG	10:CH:283:PHE:HB2	1.97	0.47
10:CH:361:LEU:O	10:CH:364:VAL:HG22	2.15	0.47
11:CI:300:SER:O	11:CI:303:GLN:HG3	2.15	0.47
12:CJ:246:TYR:CD1	12:CJ:251:LEU:HD22	2.50	0.47
13:CK:174:PRO:HG2	13:CK:177:LEU:HD13	1.96	0.47
21:CS:694:ASP:O	21:CS:698:GLU:HG3	2.14	0.47
22:CU:225:ARG:O	22:CU:226:THR:OG1	2.27	0.47
23:CX:103:THR:HG22	23:CX:132:ALA:HB1	1.95	0.47
30:LG:63:ARG:O	30:LG:67:ILE:HG12	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Lq:59:PRO:HB2	49:Lq:170:GLY:N	2.26	0.47
50:Cc:113:LEU:HD12	50:Cc:196:HIS:ND1	2.30	0.47
51:Cd:217:GLU:CD	51:Cd:395:PRO:HG3	2.39	0.47
1:C1:130:U:O2	1:C1:133:G:N2	2.32	0.47
1:C1:2378:U:H2'	1:C1:2379:U:H6	1.80	0.47
1:C1:2441:C:C2	1:C1:2442:A:C8	3.03	0.47
1:C1:2469:U:H2'	1:C1:2470:U:H6	1.80	0.47
1:C1:3003:A:H4'	27:LB:222:THR:HG21	1.96	0.47
1:C1:3331:A:H2'	1:C1:3331:A:N3	2.30	0.47
5:CB:44:ASP:OD1	5:CB:46:LYS:HB3	2.15	0.47
15:CM:102:PRO:HB2	15:CM:105:PRO:HD2	1.97	0.47
26:Ch:279:GLU:HG3	54:Cg:215:ARG:NH2	2.30	0.47
26:Ch:294:PHE:HD1	54:Cg:189:LEU:HD11	1.79	0.47
27:LB:14:LEU:HA	27:LB:17:LEU:HG	1.97	0.47
28:LC:36:VAL:HG21	28:LC:251:LEU:HD21	1.97	0.47
36:LO:116:LYS:HB3	36:LO:116:LYS:HE3	1.65	0.47
39:LS:107:TYR:HE2	39:LS:118:PHE:HA	1.79	0.47
40:LT:71:ALA:HA	40:LT:92:ARG:HA	1.97	0.47
40:LT:113:ALA:O	40:LT:117:LYS:HG2	2.14	0.47
46:Lh:38:LYS:HD2	46:Lh:46:LEU:HD23	1.96	0.47
51:Cd:184:THR:HG22	51:Cd:191:PHE:HD2	1.80	0.47
1:C1:446:U:H6	52:Ce:82:LYS:HZ3	1.62	0.46
1:C1:2344:G:OP2	36:LO:92:HIS:NE2	2.48	0.46
1:C1:2812:U:H2'	1:C1:2813:C:C6	2.50	0.46
1:C1:3298:U:H2'	1:C1:3299:A:C8	2.44	0.46
4:CA:138:PRO:HB3	4:CA:178:HIS:CE1	2.51	0.46
22:CU:359:ASP:HA	22:CU:362:VAL:HG22	1.97	0.46
25:Cb:372:PHE:HB2	25:Cb:453:ARG:HD3	1.96	0.46
25:Cb:394:SER:OG	25:Cb:408:GLN:HB3	2.15	0.46
29:LE:76:LEU:HD21	29:LE:123:ALA:HB1	1.96	0.46
31:LH:10:ILE:HG12	31:LH:72:ARG:HG3	1.96	0.46
51:Cd:374:GLY:N	51:Cd:378:LYS:HA	2.30	0.46
1:C1:213:G:C6	1:C1:1371:G:N1	2.83	0.46
1:C1:378:A:C4	51:Cd:29:ILE:HD11	2.50	0.46
1:C1:1364:G:OP2	28:LC:192:ARG:NH1	2.32	0.46
1:C1:2316:C:P	37:LP:86:LYS:HE3	2.55	0.46
1:C1:2413:G:H2'	1:C1:2414:G:C8	2.51	0.46
1:C1:2970:U:H2'	1:C1:2971:U:C6	2.50	0.46
1:C1:3296:G:HO2'	1:C1:3297:U:P	2.36	0.46
2:C2:9:A:H2'	2:C2:10:A:C8	2.50	0.46
2:C2:152:G:C1'	30:LG:62:GLN:HE21	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CC:292:MET:O	6:CC:296:ARG:HG3	2.15	0.46
10:CH:90:PHE:HE1	10:CH:152:VAL:HG11	1.79	0.46
16:CN:188:ARG:HG3	16:CN:188:ARG:O	2.16	0.46
38:LQ:79:ARG:HB3	38:LQ:111:VAL:HG21	1.96	0.46
50:Cc:51:TRP:CD2	50:Cc:93:PHE:HD1	2.33	0.46
1:C1:137:C:H2'	1:C1:138:G:O4'	2.15	0.46
1:C1:188:U:O4'	1:C1:1373:C:N4	2.48	0.46
1:C1:613:U:H2'	1:C1:614:C:C6	2.50	0.46
1:C1:1221:C:C2	1:C1:1222:A:C8	3.04	0.46
1:C1:1435:A:C8	53:Cf:509:TRP:CZ2	3.03	0.46
1:C1:2390:U:C2	1:C1:2560:G:N1	2.83	0.46
1:C1:3315:A:O2'	1:C1:3318:C:OP2	2.25	0.46
5:CB:98:CYS:HB2	5:CB:150:HIS:ND1	2.31	0.46
6:CC:399:PHE:CE2	12:CJ:150:LEU:HD13	2.50	0.46
7:CE:443:HIS:HD1	7:CE:443:HIS:H	1.63	0.46
10:CH:168:THR:HB	10:CH:247:ALA:HB2	1.97	0.46
14:CL:10:LYS:NZ	36:LO:60:ARG:HH22	2.13	0.46
15:CM:153:LEU:HD13	15:CM:245:ILE:HD11	1.96	0.46
25:Cb:365:THR:HG23	25:Cb:368:SER:H	1.79	0.46
28:LC:32:ARG:HG3	28:LC:121:PHE:CE2	2.50	0.46
47:Li:83:LYS:HE3	47:Li:89:PHE:CE1	2.51	0.46
51:Cd:194:GLU:HB3	51:Cd:195:PRO:HD3	1.98	0.46
51:Cd:293:ALA:HB3	51:Cd:396:ARG:HB2	1.96	0.46
54:Cg:57:LYS:HA	54:Cg:60:GLU:HG3	1.98	0.46
1:C1:114:A:H2'	1:C1:115:A:O4'	2.15	0.46
1:C1:1237:C:O3'	32:LK:130:LYS:NZ	2.44	0.46
1:C1:2924:G:C2	9:CG:167:GLN:HB3	2.50	0.46
1:C1:2944:U:H2'	1:C1:2945:A:C8	2.42	0.46
1:C1:3190:G:H2'	1:C1:3191:C:C6	2.51	0.46
2:C2:7:U:H2'	2:C2:8:C:C6	2.50	0.46
3:C3:7:U:O3'	5:CB:158:ARG:NH1	2.49	0.46
10:CH:283:PHE:HD1	10:CH:315:GLU:HB3	1.80	0.46
10:CH:473:PHE:CE2	19:CQ:106:VAL:HG21	2.50	0.46
12:CJ:151:PHE:CD2	12:CJ:231:VAL:HG22	2.50	0.46
12:CJ:254:PRO:O	12:CJ:256:LYS:NZ	2.48	0.46
35:LN:27:CYS:SG	35:LN:31:ARG:NH1	2.88	0.46
1:C1:510:U:C4	28:LC:351:PRO:HB3	2.50	0.46
1:C1:514:G:H2'	1:C1:515:G:H8	1.80	0.46
1:C1:1135:A:N1	1:C1:2333:G:O2'	2.38	0.46
1:C1:1156:G:H2'	1:C1:1157:C:C6	2.50	0.46
1:C1:2470:U:H2'	1:C1:2471:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2567:A:H2'	1:C1:2568:G:C8	2.51	0.46
1:C1:2858:A:N7	13:CK:2:PRO:HG3	2.30	0.46
1:C1:2860:A:H2'	1:C1:2861:A:O4'	2.16	0.46
2:C2:52:A:H2'	2:C2:52:A:N3	2.29	0.46
10:CH:174:PHE:HD2	10:CH:266:GLN:HG3	1.80	0.46
18:CP:534:VAL:HG13	18:CP:581:PHE:HB3	1.98	0.46
28:LC:27:PHE:CD1	28:LC:131:ALA:HB2	2.51	0.46
30:LG:108:LYS:O	30:LG:112:LEU:HD23	2.15	0.46
32:LK:53:TRP:NE1	32:LK:73:VAL:HG11	2.27	0.46
35:LN:149:ASN:HB2	46:Lh:97:LEU:HD11	1.98	0.46
38:LQ:47:PRO:HG3	38:LQ:58:VAL:HG11	1.96	0.46
41:LV:86:PRO:HA	41:LV:96:TYR:HB3	1.96	0.46
51:Cd:383:VAL:HG23	51:Cd:383:VAL:O	2.15	0.46
1:C1:127:G:OP1	35:LN:140:LYS:HE2	2.14	0.46
1:C1:1158:C:H2'	1:C1:1159:G:N2	2.31	0.46
1:C1:2299:C:H2'	1:C1:2300:C:C6	2.51	0.46
1:C1:2329:A:H2'	1:C1:2330:A:H8	1.79	0.46
1:C1:2389:U:C2	1:C1:2560:G:O6	2.68	0.46
1:C1:2548:A:H2'	1:C1:2549:A:H8	1.81	0.46
1:C1:3183:C:H42	17:CO:93:ARG:HD3	1.81	0.46
2:C2:49:G:O4'	46:Lh:46:LEU:HD13	2.16	0.46
4:CA:45:THR:HG22	4:CA:47:ARG:H	1.80	0.46
7:CE:418:ALA:HA	7:CE:421:LEU:HB2	1.98	0.46
8:CF:183:ASP:OD1	8:CF:184:GLU:N	2.48	0.46
10:CH:359:THR:O	10:CH:363:GLU:HG3	2.15	0.46
19:CQ:8:PHE:HB3	19:CQ:36:CYS:HB2	1.97	0.46
27:LB:28:ARG:HH21	27:LB:30:LYS:HG2	1.80	0.46
27:LB:94:GLU:OE2	36:LO:157:ARG:NH2	2.40	0.46
30:LG:81:PHE:CZ	30:LG:166:VAL:HG12	2.51	0.46
30:LG:225:TYR:O	30:LG:229:VAL:HG22	2.15	0.46
35:LN:145:ASP:HB3	35:LN:148:ILE:HG22	1.97	0.46
35:LN:148:ILE:O	35:LN:151:ILE:HG22	2.16	0.46
36:LO:57:ALA:O	36:LO:61:LYS:HG2	2.15	0.46
51:Cd:324:ALA:O	51:Cd:328:MET:HG2	2.15	0.46
52:Ce:87:TYR:CZ	52:Ce:91:LEU:HD11	2.50	0.46
1:C1:23:A:OP2	48:Lj:43:LYS:NZ	2.39	0.46
1:C1:979:A:H2'	1:C1:980:G:H8	1.80	0.46
1:C1:1336:G:OP1	52:Ce:39:ASN:HB2	2.15	0.46
1:C1:2870:G:H2'	1:C1:2871:C:O4'	2.16	0.46
3:C3:71:U:O2	3:C3:131:G:C2	2.69	0.46
4:CA:59:LEU:HD22	4:CA:61:HIS:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:365:MET:HA	10:CH:368:ILE:HG12	1.97	0.46
13:CK:149:ARG:HH22	13:CK:170:ARG:NH2	2.06	0.46
15:CM:88:LYS:HB2	15:CM:125:VAL:HB	1.96	0.46
18:CP:502:SER:OG	18:CP:504:THR:O	2.26	0.46
24:Cz:63:ALA:O	24:Cz:67:GLU:OE1	2.34	0.46
25:Cb:325:LEU:HA	25:Cb:329:ILE:HD12	1.98	0.46
15:LF:179:LEU:HB3	15:LF:184:ILE:HB	1.97	0.46
35:LN:114:ARG:HG2	35:LN:137:PRO:HG3	1.97	0.46
36:LO:112:PRO:HA	36:LO:115:ASP:CG	2.41	0.46
40:LT:75:ILE:HG12	40:LT:88:ARG:HG2	1.98	0.46
51:Cd:203:VAL:HG12	51:Cd:227:TYR:HD1	1.80	0.46
1:C1:333:G:O2'	2:C2:22:U:O4	2.33	0.46
1:C1:1228:G:N2	1:C1:1246:C:O2'	2.48	0.46
1:C1:1332:A:H2'	1:C1:1333:A:C8	2.51	0.46
1:C1:2424:G:O6	1:C1:2455:U:O2	2.33	0.46
1:C1:2840:U:H2'	1:C1:2841:U:C6	2.51	0.46
1:C1:2950:U:OP1	1:C1:3250:A:O2'	2.28	0.46
2:C2:18:U:C2	2:C2:19:C:C5	3.03	0.46
5:CB:105:GLN:HE21	5:CB:109:LYS:CE	2.29	0.46
9:CG:106:GLN:HB3	9:CG:107:PRO:HD3	1.98	0.46
9:CG:115:VAL:HB	9:CG:118:HIS:CD2	2.50	0.46
15:CM:101:ILE:CG2	15:CM:105:PRO:HB2	2.46	0.46
18:CP:387:MET:SD	18:CP:455:LEU:HD13	2.55	0.46
25:Cb:425:VAL:HG13	25:Cb:428:ARG:NH2	2.30	0.46
32:LK:114:ARG:HA	32:LK:117:ARG:HG2	1.98	0.46
49:Lq:17:LEU:HA	49:Lq:18:ASP:HA	1.56	0.46
49:Lq:101:LYS:HZ3	49:Lq:105:ARG:NH2	2.14	0.46
1:C1:1337:A:OP2	52:Ce:7:TRP:NE1	2.29	0.46
1:C1:2371:G:H2'	1:C1:2372:U:C6	2.51	0.46
1:C1:2556:G:H2'	1:C1:2557:U:C6	2.50	0.46
1:C1:2924:G:N1	9:CG:167:GLN:HB3	2.31	0.46
1:C1:3058:G:N7	17:CO:11:LYS:NZ	2.63	0.46
1:C1:3250:A:OP1	37:LP:74:LYS:HD2	2.16	0.46
5:CB:70:LYS:HG2	5:CB:277:ASN:ND2	2.31	0.46
6:CC:307:LYS:NZ	6:CC:315:GLU:OE2	2.45	0.46
22:CU:271:TYR:CZ	22:CU:273:ALA:HB2	2.51	0.46
22:CU:334:ILE:HG22	22:CU:338:LYS:NZ	2.30	0.46
25:Cb:134:ALA:HB3	25:Cb:140:LYS:HD3	1.97	0.46
31:LH:27:VAL:HG13	31:LH:82:VAL:HG11	1.98	0.46
36:LO:59:LEU:O	36:LO:62:MET:HE2	2.16	0.46
50:Cc:43:THR:HG23	50:Cc:46:ASP:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Cd:360:TYR:CZ	52:Ce:170:LEU:HD22	2.51	0.46
51:Cd:382:GLY:H	51:Cd:384:LYS:HD3	1.81	0.46
1:C1:497:U:H2'	1:C1:498:C:C6	2.51	0.46
1:C1:650:C:H2'	1:C1:651:A:H8	1.79	0.46
1:C1:1286:A:O2'	1:C1:2842:C:O2'	2.34	0.46
1:C1:2856:G:C5	13:CK:7:ILE:HG12	2.50	0.46
1:C1:3179:G:H2'	1:C1:3180:C:C6	2.51	0.46
1:C1:3278:C:H2'	1:C1:3279:A:H8	1.81	0.46
1:C1:3333:A:H2'	1:C1:3334:U:H6	1.81	0.46
4:CA:147:GLU:O	4:CA:153:LYS:NZ	2.45	0.46
5:CB:22:GLN:HA	5:CB:25:LYS:HG2	1.98	0.46
5:CB:85:LEU:HD12	5:CB:86:PRO:HD2	1.97	0.46
14:CL:62:LYS:HD3	24:Cz:61:MET:SD	2.56	0.46
16:CN:18:THR:OG1	16:CN:60:GLY:HA2	2.16	0.46
25:Cb:370:ILE:HG21	25:Cb:435:LEU:HD13	1.97	0.46
30:LG:219:SER:HA	30:LG:222:LYS:HG2	1.98	0.46
37:LP:84:PRO:HB2	37:LP:87:SER:HB2	1.98	0.46
43:LY:63:LYS:HB3	43:LY:63:LYS:HE2	1.85	0.46
46:Lh:35:ARG:O	46:Lh:39:ILE:HG23	2.16	0.46
1:C1:9:U:H2'	1:C1:10:C:C6	2.51	0.45
1:C1:423:U:H2'	1:C1:424:G:H8	1.79	0.45
1:C1:523:A:H2'	1:C1:524:A:C8	2.51	0.45
1:C1:2395:U:H3'	1:C1:2396:U:H2'	1.98	0.45
1:C1:2400:A:H2'	1:C1:2401:A:C8	2.51	0.45
1:C1:2405:A:H2'	1:C1:2406:C:C6	2.51	0.45
1:C1:2452:C:O2'	1:C1:2453:A:H8	1.98	0.45
1:C1:2847:C:OP1	10:CH:27:ARG:NH1	2.49	0.45
1:C1:3274:U:H3	1:C1:3309:G:H5''	1.82	0.45
2:C2:155:A:H4'	30:LG:188:ARG:HH12	1.81	0.45
7:CE:165:PHE:CG	7:CE:262:ILE:HG12	2.51	0.45
10:CH:402:VAL:O	10:CH:406:ASP:HB2	2.16	0.45
11:CI:222:LYS:HA	11:CI:280:PHE:HZ	1.82	0.45
16:CN:162:HIS:CE1	16:CN:164:LYS:HB2	2.51	0.45
25:Cb:15:VAL:C	25:Cb:448:LYS:HZ2	2.25	0.45
32:LK:50:THR:HA	32:LK:53:TRP:HD1	1.82	0.45
35:LN:63:ARG:NH2	35:LN:131:GLU:OE2	2.49	0.45
37:LP:122:ALA:HB3	37:LP:143:PRO:HB2	1.98	0.45
1:C1:404:G:H2'	1:C1:405:U:H6	1.81	0.45
1:C1:493:C:H2'	1:C1:494:G:H8	1.81	0.45
1:C1:1875:A:H2'	1:C1:1876:G:H8	1.81	0.45
1:C1:2425:G:H2'	1:C1:2426:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2455:U:O2'	1:C1:2456:A:H5''	2.16	0.45
1:C1:2768:C:H2'	1:C1:2769:A:H8	1.78	0.45
1:C1:2805:A:C4	1:C1:2806:G:H1'	2.51	0.45
5:CB:86:PRO:HG2	5:CB:261:THR:HG21	1.97	0.45
9:CG:59:VAL:HG21	18:CP:438:TYR:OH	2.16	0.45
10:CH:123:GLN:NE2	13:CK:250:GLU:HB2	2.29	0.45
12:CJ:12:ALA:HB1	12:CJ:53:VAL:HG22	1.97	0.45
12:CJ:251:LEU:HD11	12:CJ:273:LEU:HB3	1.97	0.45
13:CK:175:MET:O	13:CK:178:ARG:NH1	2.48	0.45
16:CN:72:VAL:O	16:CN:96:ARG:HA	2.16	0.45
19:CQ:65:VAL:HG22	19:CQ:66:ASP:N	2.32	0.45
27:LB:215:MET:HB2	27:LB:346:HIS:NE2	2.31	0.45
28:LC:146:VAL:HG23	28:LC:151:LEU:HD13	1.98	0.45
36:LO:83:TYR:HA	36:LO:86:VAL:HG22	1.99	0.45
43:LY:121:ILE:O	43:LY:125:ARG:HG3	2.16	0.45
49:Lq:61:PRO:O	49:Lq:63:MET:N	2.50	0.45
49:Lq:142:ASP:N	49:Lq:147:LYS:HZ1	2.15	0.45
51:Cd:423:TRP:NE1	51:Cd:428:GLU:HG3	2.31	0.45
54:Cg:39:ILE:HG22	54:Cg:92:LEU:HD22	1.98	0.45
54:Cg:170:LEU:HD23	54:Cg:170:LEU:HA	1.81	0.45
1:C1:316:A:H2'	1:C1:317:A:C8	2.51	0.45
1:C1:522:G:H2'	1:C1:523:A:C8	2.51	0.45
1:C1:1053:U:N3	1:C1:1054:G:N7	2.64	0.45
1:C1:1109:G:H2'	1:C1:1110:U:C6	2.51	0.45
1:C1:3192:C:H2'	1:C1:3193:G:C8	2.51	0.45
1:C1:3245:A:H2'	1:C1:3246:G:C8	2.51	0.45
12:CJ:38:ILE:HG22	12:CJ:233:PHE:CZ	2.52	0.45
19:CQ:66:ASP:OD2	19:CQ:103:ARG:NH1	2.49	0.45
20:CR:167:GLU:HA	20:CR:170:ARG:CZ	2.46	0.45
25:Cb:559:ARG:HA	25:Cb:562:GLU:OE1	2.17	0.45
25:Cb:588:ASP:HA	25:Cb:591:LEU:HB2	1.97	0.45
27:LB:160:ARG:HG2	27:LB:183:GLN:HA	1.98	0.45
27:LB:317:GLU:OE1	27:LB:319:ASN:ND2	2.49	0.45
33:LL:36:ARG:HG2	33:LL:36:ARG:HH11	1.82	0.45
35:LN:47:LYS:HG2	35:LN:119:TYR:CD2	2.51	0.45
35:LN:112:ASN:OD1	35:LN:113:LEU:N	2.49	0.45
39:LS:72:VAL:HG22	39:LS:95:ARG:HD2	1.98	0.45
54:Cg:36:VAL:HG21	54:Cg:55:VAL:HG12	1.97	0.45
1:C1:340:C:O2	1:C1:344:A:O2'	2.31	0.45
1:C1:564:C:H2'	1:C1:565:C:C6	2.52	0.45
1:C1:1200:U:H2'	1:C1:1201:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3010:G:H2'	1:C1:3011:U:H6	1.81	0.45
1:C1:3158:U:C2	34:LM:121:MET:HE1	2.51	0.45
1:C1:3169:U:H2'	1:C1:3170:C:C6	2.50	0.45
7:CE:497:LEU:O	7:CE:501:ILE:HG12	2.16	0.45
10:CH:277:PHE:HB3	10:CH:282:VAL:CG1	2.45	0.45
12:CJ:196:TYR:CZ	12:CJ:209:LEU:HD22	2.52	0.45
12:CJ:373:PHE:HD1	12:CJ:418:GLN:HG3	1.81	0.45
15:CM:69:ILE:O	15:CM:73:ARG:HG3	2.16	0.45
25:Cb:228:MET:HB2	25:Cb:230:LEU:HG	1.98	0.45
28:LC:259:SER:HB2	28:LC:263:LYS:HZ1	1.80	0.45
15:LF:148:LYS:HZ2	15:LF:246:ARG:HE	1.65	0.45
39:LS:77:ILE:HG12	39:LS:126:VAL:HG23	1.97	0.45
41:LV:22:GLY:HA2	41:LV:38:ILE:O	2.14	0.45
51:Cd:307:HIS:CG	51:Cd:340:GLY:HA3	2.52	0.45
1:C1:618:A:H2'	1:C1:619:G:C8	2.51	0.45
1:C1:2840:U:H2'	1:C1:2841:U:H6	1.82	0.45
7:CE:515:TYR:O	7:CE:519:ILE:HG12	2.17	0.45
9:CG:41:GLN:N	9:CG:44:ARG:O	2.47	0.45
10:CH:473:PHE:HE2	19:CQ:106:VAL:HG21	1.82	0.45
15:CM:207:PHE:CD2	15:CM:208:LEU:HD12	2.51	0.45
18:CP:449:GLY:HA2	18:CP:499:ASN:HD21	1.80	0.45
19:CQ:22:MET:HE1	41:LV:139:MET:HB2	1.97	0.45
21:CS:666:LEU:HD13	21:CS:676:LEU:HD11	1.97	0.45
25:Cb:875:GLU:HG2	25:Cb:879:LYS:HE3	1.97	0.45
27:LB:178:HIS:ND1	27:LB:336:ILE:HD12	2.32	0.45
32:LK:52:ASP:OD1	32:LK:53:TRP:N	2.49	0.45
40:LT:114:GLU:HB3	40:LT:118:LYS:HZ1	1.80	0.45
46:Lh:18:GLU:HA	46:Lh:21:THR:HG22	1.98	0.45
50:Cc:113:LEU:HD12	50:Cc:196:HIS:CE1	2.51	0.45
52:Ce:49:ARG:HA	52:Ce:66:LYS:O	2.16	0.45
53:Cf:448:LEU:HD12	53:Cf:452:LYS:NZ	2.31	0.45
1:C1:1248:G:N2	1:C1:1258:U:H1'	2.31	0.45
1:C1:2287:G:H2'	1:C1:2288:A:H8	1.81	0.45
1:C1:2305:C:H2'	1:C1:2306:U:C6	2.51	0.45
1:C1:2460:C:H2'	1:C1:2461:U:C6	2.51	0.45
3:C3:69:G:H2'	3:C3:70:C:C6	2.52	0.45
5:CB:44:ASP:CG	5:CB:46:LYS:HB3	2.41	0.45
7:CE:449:ALA:O	7:CE:456:GLY:HA3	2.16	0.45
10:CH:429:ASN:ND2	19:CQ:83:ARG:HH22	2.14	0.45
10:CH:445:ASN:HB2	10:CH:448:ASP:HB2	1.98	0.45
26:Ch:279:GLU:HG3	54:Cg:215:ARG:NH1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LF:94:ARG:HH22	15:LF:98:ILE:HG12	1.81	0.45
32:LK:77:ALA:O	32:LK:81:ILE:HD12	2.16	0.45
36:LO:174:LYS:O	36:LO:178:ARG:HG2	2.17	0.45
45:Lf:15:HIS:O	45:Lf:97:GLY:N	2.39	0.45
49:Lq:26:ARG:NH2	49:Lq:208:ALA:HB1	2.31	0.45
49:Lq:116:LEU:HD12	49:Lq:116:LEU:HA	1.81	0.45
51:Cd:239:TYR:HB3	51:Cd:244:ILE:HD11	1.99	0.45
52:Ce:95:ASP:OD1	52:Ce:110:LYS:NZ	2.38	0.45
54:Cg:339:LYS:HD3	54:Cg:340:VAL:N	2.32	0.45
1:C1:59:G:H4'	1:C1:60:A:H4'	1.97	0.45
1:C1:418:G:H2'	1:C1:419:C:C6	2.52	0.45
1:C1:2306:U:H2'	1:C1:2307:A:C8	2.51	0.45
1:C1:2424:G:O6	1:C1:2455:U:C2	2.69	0.45
1:C1:2877:A:H2'	1:C1:2878:U:O4'	2.17	0.45
1:C1:3162:A:H4'	1:C1:3163:G:O5'	2.16	0.45
2:C2:66:A:H2'	2:C2:67:U:C6	2.52	0.45
3:C3:54:G:H3'	3:C3:55:A:H5''	1.98	0.45
3:C3:143:A:H2'	3:C3:144:A:O4'	2.16	0.45
4:CA:82:GLU:OE2	47:Li:76:LYS:NZ	2.48	0.45
7:CE:372:TYR:CZ	7:CE:376:LEU:HD22	2.52	0.45
7:CE:391:GLN:HB3	7:CE:395:LYS:CE	2.43	0.45
8:CF:66:PHE:HB3	8:CF:73:MET:HE3	1.99	0.45
9:CG:79:LYS:C	9:CG:79:LYS:HD3	2.42	0.45
9:CG:84:ILE:HD11	9:CG:87:LEU:HD22	1.99	0.45
9:CG:153:GLU:O	9:CG:157:LEU:HB2	2.17	0.45
11:CI:289:ALA:O	11:CI:293:LEU:HD23	2.16	0.45
12:CJ:113:PRO:O	12:CJ:161:PRO:HG3	2.16	0.45
16:CN:4:ARG:HB3	16:CN:208:LEU:HA	1.99	0.45
18:CP:539:THR:HG23	18:CP:541:LEU:HD13	1.99	0.45
20:CR:148:GLN:HG2	33:LL:86:PRO:HB3	1.98	0.45
25:Cb:404:ALA:HB2	41:LV:69:PRO:HB3	1.99	0.45
26:Ch:331:ARG:HG2	54:Cg:185:GLN:HB3	1.98	0.45
27:LB:19:ARG:HB3	27:LB:274:HIS:HE1	1.81	0.45
15:LF:36:LEU:O	15:LF:40:LYS:HG2	2.17	0.45
30:LG:104:THR:HG22	30:LG:107:GLU:HG2	1.99	0.45
30:LG:169:LEU:HA	30:LG:172:LEU:HG	1.97	0.45
46:Lh:38:LYS:O	46:Lh:42:SER:HB3	2.16	0.45
50:Cc:78:ILE:HD12	50:Cc:90:LEU:HD21	1.99	0.45
1:C1:1181:C:H2'	1:C1:1182:A:C8	2.51	0.45
1:C1:1217:U:O4	32:LK:135:THR:HG22	2.17	0.45
1:C1:2292:C:H2'	1:C1:2293:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CB:74:ASP:HB3	5:CB:77:ARG:HG2	1.99	0.45
7:CE:504:ASN:HB3	7:CE:507:LEU:HD12	1.98	0.45
8:CF:53:LEU:O	8:CF:57:ARG:HG3	2.16	0.45
9:CG:113:ASN:HA	9:CG:166:ARG:HB2	1.98	0.45
11:CI:242:ASP:HA	11:CI:262:ILE:HD11	1.99	0.45
12:CJ:104:ALA:O	12:CJ:108:ARG:HG2	2.16	0.45
16:CN:99:GLU:HG3	16:CN:101:LEU:N	2.29	0.45
18:CP:334:VAL:HG21	18:CP:370:PHE:HE2	1.82	0.45
21:CS:468:LEU:HD22	30:LG:67:ILE:HD11	1.99	0.45
28:LC:108:ARG:HG2	28:LC:109:LYS:N	2.32	0.45
30:LG:193:VAL:HG12	30:LG:195:LYS:HG2	1.99	0.45
33:LL:36:ARG:HG2	33:LL:36:ARG:NH1	2.32	0.45
50:Cc:33:LEU:HD13	50:Cc:81:LEU:CD1	2.46	0.45
53:Cf:474:ALA:CA	53:Cf:477:ARG:NH1	2.80	0.45
54:Cg:89:HIS:CD2	54:Cg:178:LEU:HA	2.51	0.45
54:Cg:145:PRO:HB3	54:Cg:194:ARG:HB3	1.98	0.45
1:C1:787:A:H2'	1:C1:788:A:O4'	2.17	0.45
1:C1:2481:A:C6	1:C1:2547:G:N1	2.85	0.45
1:C1:2781:G:H3'	14:CL:19:ARG:HH12	1.81	0.45
2:C2:130:C:H2'	2:C2:131:G:C8	2.52	0.45
10:CH:89:HIS:HB3	25:Cb:625:ARG:HH22	1.81	0.45
13:CK:229:GLY:HA2	13:CK:237:ILE:HD11	1.98	0.45
16:CN:62:LEU:HD23	16:CN:62:LEU:HA	1.75	0.45
16:CN:115:ALA:HB3	16:CN:137:VAL:HG22	1.99	0.45
19:CQ:12:PRO:HD3	27:LB:380:PHE:CE2	2.51	0.45
19:CQ:22:MET:HE2	41:LV:97:PHE:CE1	2.46	0.45
19:CQ:63:MET:HB3	19:CQ:107:PHE:CG	2.52	0.45
30:LG:85:LEU:HD21	30:LG:183:ILE:HG22	1.97	0.45
33:LL:17:HIS:HB2	33:LL:20:ARG:HD2	1.99	0.45
40:LT:127:GLN:NE2	40:LT:129:LYS:O	2.46	0.45
51:Cd:211:ILE:HD13	51:Cd:261:GLU:HB3	1.98	0.45
1:C1:540:A:H2'	1:C1:541:G:H8	1.82	0.45
1:C1:728:A:H2'	1:C1:729:U:C6	2.52	0.45
1:C1:975:G:N2	1:C1:976:U:O4	2.50	0.45
1:C1:2477:A:H2	1:C1:2553:A:N6	2.14	0.45
1:C1:2946:C:OP1	36:LO:69:ARG:HD3	2.17	0.45
1:C1:3332:G:O2'	1:C1:3333:A:H8	1.98	0.45
2:C2:112:U:C2	2:C2:114:G:H1'	2.52	0.45
4:CA:184:VAL:HA	4:CA:188:LYS:O	2.17	0.45
6:CC:367:ARG:NH2	6:CC:384:PRO:O	2.49	0.45
7:CE:135:THR:O	7:CE:139:ARG:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CE:151:VAL:HG22	7:CE:293:MET:HG2	1.99	0.45
8:CF:203:SER:O	8:CF:207:ARG:HG3	2.17	0.45
11:CI:207:PHE:HB3	11:CI:235:PHE:HZ	1.82	0.45
12:CJ:177:HIS:HA	12:CJ:180:ILE:HG12	1.98	0.45
16:CN:2:ALA:HA	16:CN:204:ALA:O	2.17	0.45
25:Cb:378:HIS:CE1	25:Cb:542:GLU:HB2	2.50	0.45
28:LC:143:VAL:HG13	28:LC:143:VAL:O	2.17	0.45
29:LE:156:SER:O	29:LE:160:ALA:HB3	2.17	0.45
32:LK:90:ARG:NH1	32:LK:92:ARG:HB3	2.32	0.45
37:LP:114:ILE:HA	37:LP:150:LEU:HD22	1.99	0.45
38:LQ:97:ARG:HA	38:LQ:100:LYS:HE2	1.99	0.45
43:LY:117:ILE:O	43:LY:121:ILE:HG13	2.17	0.45
49:Lq:59:PRO:O	49:Lq:61:PRO:HD3	2.17	0.45
49:Lq:146:ALA:HA	49:Lq:149:ASN:HB2	1.98	0.45
52:Ce:182:GLN:HA	52:Ce:191:TRP:CZ3	2.52	0.45
1:C1:101:G:N2	1:C1:101:G:OP2	2.50	0.44
1:C1:375:G:O6	51:Cd:43:ARG:HD3	2.16	0.44
1:C1:1303:G:H2'	1:C1:1304:U:H6	1.82	0.44
1:C1:1316:C:C2	1:C1:1317:C:C5	3.05	0.44
1:C1:1877:G:H2'	1:C1:1878:G:H8	1.83	0.44
1:C1:2091:U:C2	1:C1:2287:G:N1	2.85	0.44
2:C2:61:A:H4'	2:C2:63:G:H1'	1.99	0.44
4:CA:147:GLU:HA	4:CA:153:LYS:NZ	2.32	0.44
5:CB:156:ASP:O	5:CB:160:ILE:HG12	2.18	0.44
6:CC:271:LEU:HD11	47:Li:48:PHE:CD2	2.52	0.44
12:CJ:380:ARG:HD2	12:CJ:401:LEU:HB3	2.00	0.44
17:CO:106:ILE:O	36:LO:114:TYR:OH	2.22	0.44
19:CQ:102:ARG:HH22	19:CQ:103:ARG:NH2	2.12	0.44
25:Cb:554:SER:O	25:Cb:558:LYS:HG3	2.18	0.44
28:LC:332:TYR:HE1	15:LF:55:GLU:HG2	1.82	0.44
32:LK:92:ARG:HG3	32:LK:93:LYS:N	2.32	0.44
36:LO:76:ARG:HD3	36:LO:148:GLY:HA3	1.99	0.44
37:LP:47:PHE:HE1	37:LP:56:GLU:HB3	1.81	0.44
51:Cd:294:PRO:HD2	51:Cd:297:ALA:HB3	1.99	0.44
1:C1:265:A:H5''	4:CA:67:LYS:HD3	1.99	0.44
1:C1:342:C:N3	1:C1:359:A:H2'	2.32	0.44
1:C1:398:G:H1'	2:C2:17:A:N6	2.32	0.44
1:C1:403:U:H2'	1:C1:404:G:C8	2.52	0.44
1:C1:553:U:H2'	1:C1:554:G:H8	1.82	0.44
1:C1:763:U:H2'	1:C1:764:A:O4'	2.17	0.44
1:C1:1067:A:H2'	1:C1:1068:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1292:G:H2'	1:C1:1293:G:C8	2.53	0.44
1:C1:2336:C:H2'	1:C1:2337:G:C2	2.52	0.44
1:C1:2472:U:H2'	1:C1:2473:A:H8	1.82	0.44
1:C1:2971:U:H2'	1:C1:2972:C:H6	1.82	0.44
2:C2:39:G:N2	2:C2:105:A:C4	2.85	0.44
10:CH:368:ILE:HD12	16:CN:238:LYS:HE3	1.98	0.44
12:CJ:419:ILE:HD13	12:CJ:456:VAL:HG23	1.98	0.44
13:CK:186:HIS:HD2	13:CK:187:PRO:HD2	1.81	0.44
15:CM:242:ASN:O	15:CM:245:ILE:HG22	2.16	0.44
21:CS:692:LEU:HD13	21:CS:696:PHE:CE2	2.51	0.44
15:LF:124:LYS:HD2	40:LT:134:MET:HE1	2.00	0.44
38:LQ:99:LEU:HD11	38:LQ:104:GLU:HA	2.00	0.44
40:LT:43:LYS:HB3	40:LT:97:LYS:HZ1	1.83	0.44
44:Le:34:ARG:HA	44:Le:34:ARG:HD3	1.73	0.44
46:Lh:89:LEU:HA	48:Lj:78:PHE:CD2	2.51	0.44
48:Lj:35:ALA:O	48:Lj:45:ARG:NH1	2.50	0.44
50:Cc:14:LEU:HG	50:Cc:25:ALA:HB1	2.00	0.44
50:Cc:108:ARG:HB3	50:Cc:111:LYS:HE2	1.99	0.44
51:Cd:311:LEU:HD23	51:Cd:311:LEU:H	1.82	0.44
53:Cf:478:ARG:HH22	54:Cg:110:ARG:C	2.24	0.44
54:Cg:333:MET:HE3	54:Cg:334:ARG:H	1.81	0.44
1:C1:139:C:H2'	1:C1:140:G:O4'	2.17	0.44
1:C1:459:U:O2'	1:C1:460:C:H5''	2.17	0.44
1:C1:1055:U:N3	1:C1:1063:C:N4	2.58	0.44
1:C1:1434:A:H2'	53:Cf:509:TRP:NE1	2.32	0.44
1:C1:2764:U:H2'	1:C1:2765:U:C6	2.52	0.44
1:C1:2875:G:H2'	1:C1:2876:G:H8	1.82	0.44
2:C2:155:A:C4'	30:LG:188:ARG:HH22	2.31	0.44
9:CG:100:VAL:HA	9:CG:119:VAL:HA	1.98	0.44
10:CH:168:THR:O	10:CH:247:ALA:HB1	2.18	0.44
10:CH:465:GLU:OE1	19:CQ:102:ARG:NH1	2.50	0.44
21:CS:678:ASP:CG	47:Li:77:ARG:HH22	2.26	0.44
27:LB:107:ALA:HB2	27:LB:200:PHE:CD2	2.49	0.44
27:LB:215:MET:SD	27:LB:282:LYS:HB2	2.57	0.44
29:LE:86:PRO:HD2	29:LE:89:ILE:HB	1.98	0.44
36:LO:192:ASP:HB3	36:LO:195:VAL:HG12	2.00	0.44
43:LY:123:ALA:HA	43:LY:126:GLU:CD	2.42	0.44
44:Le:75:PHE:CG	44:Le:86:LEU:HD21	2.53	0.44
50:Cc:32:PHE:HE1	50:Cc:42:LEU:HD21	1.83	0.44
50:Cc:44:THR:HA	50:Cc:47:VAL:HG12	1.98	0.44
50:Cc:123:SER:O	50:Cc:127:MET:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Cc:205:VAL:HA	50:Cc:208:VAL:HG12	1.98	0.44
51:Cd:221:ILE:HA	51:Cd:357:ARG:NH1	2.31	0.44
51:Cd:365:ALA:N	51:Cd:385:GLY:O	2.39	0.44
1:C1:8:C:H2'	1:C1:9:U:H6	1.83	0.44
1:C1:72:C:N3	1:C1:74:G:C6	2.85	0.44
1:C1:497:U:H2'	1:C1:498:C:H6	1.83	0.44
1:C1:1098:G:H2'	1:C1:1099:G:O4'	2.18	0.44
1:C1:1315:C:O2'	15:LF:213:LEU:O	2.34	0.44
1:C1:1426:G:H2'	1:C1:1427:U:O4'	2.17	0.44
1:C1:2894:A:H2'	1:C1:2895:G:H8	1.82	0.44
1:C1:2918:C:C4	1:C1:2919:G:C8	3.06	0.44
2:C2:30:G:H2'	2:C2:31:G:H8	1.82	0.44
10:CH:60:PHE:CD2	10:CH:101:LYS:HB3	2.51	0.44
15:CM:141:ALA:HB1	15:CM:237:ARG:NH1	2.23	0.44
25:Cb:14:GLU:HG2	25:Cb:276:PRO:HB3	2.00	0.44
27:LB:305:LYS:HZ3	27:LB:319:ASN:HA	1.82	0.44
28:LC:300:LEU:HD22	38:LQ:67:ARG:HB3	1.99	0.44
15:LF:89:LEU:HD22	15:LF:194:ILE:O	2.18	0.44
39:LS:132:THR:HG22	39:LS:133:GLU:N	2.31	0.44
50:Cc:11:ILE:HA	50:Cc:14:LEU:HD12	2.00	0.44
51:Cd:410:ARG:HG2	51:Cd:410:ARG:HH11	1.82	0.44
1:C1:179:U:O2	43:LY:128:VAL:HG21	2.17	0.44
1:C1:1200:U:O2	1:C1:1205:A:O2'	2.29	0.44
1:C1:1233:A:H2'	1:C1:1234:A:C8	2.53	0.44
1:C1:1236:C:H5''	32:LK:149:LYS:HE3	2.00	0.44
1:C1:1238:G:H2'	1:C1:1239:C:C6	2.52	0.44
1:C1:1420:U:H2'	1:C1:1421:U:C6	2.53	0.44
1:C1:2566:G:H2'	1:C1:2567:A:C8	2.52	0.44
1:C1:3165:C:H2'	1:C1:3166:G:C8	2.53	0.44
2:C2:6:U:C2	2:C2:7:U:C5	3.06	0.44
7:CE:222:ASN:O	7:CE:226:GLU:HG3	2.18	0.44
10:CH:172:ALA:HA	10:CH:220:THR:HG22	2.00	0.44
10:CH:275:PRO:HB2	25:Cb:587:ARG:NH1	2.33	0.44
13:CK:167:LYS:HE3	13:CK:168:TYR:CE2	2.53	0.44
18:CP:372:PRO:HG3	18:CP:576:PHE:CZ	2.53	0.44
25:Cb:244:ASP:N	25:Cb:244:ASP:OD1	2.49	0.44
34:LM:27:LEU:HD11	34:LM:94:TRP:CG	2.53	0.44
51:Cd:371:ASN:ND2	51:Cd:384:LYS:HA	2.32	0.44
54:Cg:35:MET:O	54:Cg:90:LEU:HD12	2.17	0.44
1:C1:258:C:N3	47:Li:39:LYS:HG3	2.33	0.44
1:C1:1206:C:C2	1:C1:1207:A:C8	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1855:U:H2'	1:C1:1856:U:C6	2.52	0.44
1:C1:3241:U:C2	1:C1:3254:A:C2	3.06	0.44
1:C1:3265:A:H2'	1:C1:3266:G:H8	1.82	0.44
1:C1:3326:C:H2'	1:C1:3327:G:H8	1.81	0.44
4:CA:32:ASN:HB2	22:CU:216:PHE:HE1	1.81	0.44
9:CG:29:PRO:HD3	23:CX:98:ARG:NE	2.33	0.44
10:CH:101:LYS:O	10:CH:105:GLU:OE1	2.35	0.44
12:CJ:49:ASP:HB3	12:CJ:52:LYS:HB2	2.00	0.44
12:CJ:380:ARG:HG3	12:CJ:384:GLU:CD	2.43	0.44
12:CJ:381:GLN:HB3	12:CJ:382:PRO:HD3	2.00	0.44
13:CK:203:ASN:OD1	13:CK:216:THR:OG1	2.36	0.44
16:CN:104:LEU:O	16:CN:108:ILE:HB	2.18	0.44
20:CR:127:GLU:OE2	20:CR:135:GLN:HG3	2.18	0.44
20:CR:218:TYR:O	20:CR:220:GLN:N	2.45	0.44
22:CU:364:ASN:HB3	22:CU:368:ARG:CZ	2.48	0.44
25:Cb:396:VAL:HG11	25:Cb:430:ILE:HG21	2.00	0.44
27:LB:167:ILE:HG21	27:LB:174:GLN:HB2	2.00	0.44
27:LB:183:GLN:NE2	27:LB:185:ASN:HD21	2.15	0.44
29:LE:99:ALA:HA	29:LE:102:VAL:HG12	1.98	0.44
36:LO:23:ILE:HD13	36:LO:122:VAL:HG11	1.98	0.44
37:LP:139:TYR:O	37:LP:140:MET:HE2	2.18	0.44
1:C1:1086:U:H2'	1:C1:1087:C:H6	1.83	0.44
1:C1:2285:G:C6	1:C1:2287:G:C5	3.05	0.44
1:C1:2984:A:H2'	1:C1:2985:G:C8	2.53	0.44
1:C1:3258:G:C8	1:C1:3260:G:C8	3.05	0.44
2:C2:143:U:OP1	35:LN:38:ARG:NH2	2.45	0.44
3:C3:1:C:H4'	15:CM:59:LYS:HD2	1.99	0.44
3:C3:7:U:H1'	5:CB:158:ARG:HH11	1.83	0.44
8:CF:187:GLU:O	8:CF:189:SER:N	2.51	0.44
11:CI:300:SER:O	11:CI:304:VAL:HG23	2.18	0.44
15:CM:197:VAL:HG23	15:CM:201:PHE:HB2	2.00	0.44
16:CN:11:ASN:HB3	16:CN:207:GLY:HA3	1.98	0.44
17:CO:37:LEU:HD11	27:LB:43:LEU:HD13	2.00	0.44
20:CR:212:ASP:OD1	20:CR:213:ARG:N	2.51	0.44
25:Cb:628:ILE:HG22	25:Cb:628:ILE:O	2.18	0.44
28:LC:32:ARG:HG3	28:LC:121:PHE:HE2	1.83	0.44
40:LT:115:LEU:HG	40:LT:126:VAL:HG11	2.00	0.44
43:LY:27:ARG:NH1	43:LY:48:PRO:HB2	2.33	0.44
53:Cf:509:TRP:HD1	53:Cf:512:ARG:HH21	1.66	0.44
54:Cg:139:LYS:HB2	54:Cg:193:ARG:HH12	1.83	0.44
1:C1:47:C:OP2	1:C1:48:A:O2'	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:110:G:OP2	33:LL:73:ARG:NH1	2.50	0.44
1:C1:128:G:OP1	46:Lh:80:TYR:OH	2.26	0.44
1:C1:386:U:H5	51:Cd:431:ARG:HH12	1.65	0.44
1:C1:551:C:O3'	39:LS:71:LYS:NZ	2.50	0.44
1:C1:727:C:H2'	1:C1:728:A:H8	1.83	0.44
1:C1:2419:G:C2	1:C1:2421:A:C5	3.05	0.44
1:C1:2957:G:H2'	1:C1:2958:U:C6	2.53	0.44
2:C2:71:A:H4'	2:C2:72:A:O5'	2.18	0.44
3:C3:135:C:H3'	11:CI:279:ARG:HH21	1.83	0.44
4:CA:74:LEU:HB3	4:CA:250:PHE:CB	2.47	0.44
8:CF:204:ARG:O	8:CF:208:LEU:HD23	2.18	0.44
9:CG:5:THR:O	9:CG:9:MET:HG3	2.18	0.44
9:CG:45:VAL:HG12	9:CG:72:GLY:O	2.17	0.44
10:CH:387:VAL:HG21	16:CN:202:TRP:NE1	2.32	0.44
10:CH:440:ILE:HD12	19:CQ:1:MET:HE3	1.99	0.44
12:CJ:376:ARG:HA	12:CJ:401:LEU:HD21	1.99	0.44
12:CJ:406:PHE:CG	12:CJ:407:THR:N	2.86	0.44
15:CM:143:GLY:HA3	15:CM:241:ILE:CD1	2.45	0.44
20:CR:56:ALA:O	33:LL:51:VAL:HG12	2.18	0.44
25:Cb:2:PRO:HD2	41:LV:75:VAL:HG11	1.99	0.44
25:Cb:159:PHE:HA	25:Cb:210:ASN:ND2	2.33	0.44
25:Cb:367:HIS:O	25:Cb:436:ALA:HB3	2.18	0.44
15:LF:138:PRO:HA	15:LF:234:LEU:HD13	2.00	0.44
34:LM:96:GLU:O	34:LM:101:LYS:NZ	2.51	0.44
40:LT:54:HIS:CE1	40:LT:55:LYS:HG2	2.53	0.44
41:LV:105:VAL:HG12	41:LV:106:ASN:O	2.18	0.44
43:LY:27:ARG:HB2	43:LY:74:ARG:NH1	2.33	0.44
47:Li:98:GLU:HG3	47:Li:101:ARG:HH12	1.83	0.44
51:Cd:37:ARG:NH2	51:Cd:40:HIS:HD2	2.15	0.44
52:Ce:76:LYS:HA	52:Ce:76:LYS:HD2	1.88	0.44
53:Cf:466:ILE:O	53:Cf:469:LYS:HB2	2.17	0.44
1:C1:305:U:H2'	1:C1:306:U:C6	2.53	0.44
1:C1:2344:G:H22	36:LO:69:ARG:HH22	1.65	0.44
1:C1:2468:U:H2'	1:C1:2469:U:H6	1.82	0.44
1:C1:2839:C:H2'	1:C1:2840:U:C6	2.53	0.44
1:C1:3264:A:OP1	1:C1:3264:A:C8	2.68	0.44
7:CE:234:VAL:HG11	7:CE:237:LEU:HD13	2.00	0.44
12:CJ:397:TRP:CZ2	12:CJ:405:ALA:HB2	2.52	0.44
15:CM:138:PRO:HG2	15:CM:139:TRP:CZ3	2.53	0.44
27:LB:85:VAL:HB	27:LB:164:HIS:NE2	2.33	0.44
27:LB:94:GLU:OE2	36:LO:154:VAL:HG22	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LC:241:ASN:O	28:LC:245:LEU:HG	2.18	0.44
36:LO:192:ASP:O	36:LO:195:VAL:HG12	2.18	0.44
37:LP:91:LEU:O	37:LP:95:LEU:HD12	2.18	0.44
39:LS:107:TYR:HE1	39:LS:123:ILE:HD11	1.83	0.44
39:LS:131:LYS:NZ	39:LS:133:GLU:OE1	2.44	0.44
40:LT:96:VAL:C	40:LT:97:LYS:HD3	2.43	0.44
43:LY:47:ILE:HD13	43:LY:118:LEU:HD11	1.98	0.44
49:Lq:50:SER:HA	49:Lq:157:PHE:O	2.17	0.44
51:Cd:374:GLY:H	51:Cd:378:LYS:HA	1.83	0.44
1:C1:489:G:O4'	1:C1:3213:A:N6	2.51	0.43
1:C1:684:G:H2'	1:C1:685:C:C6	2.53	0.43
1:C1:1221:C:C4	1:C1:1222:A:N7	2.86	0.43
1:C1:2378:U:H2'	1:C1:2379:U:C6	2.53	0.43
1:C1:2397:G:H2'	1:C1:2398:U:C6	2.54	0.43
1:C1:2852:C:H1'	1:C1:3063:A:H2	1.82	0.43
1:C1:3229:G:C2	1:C1:3230:G:C8	3.06	0.43
2:C2:6:U:H2'	2:C2:7:U:H6	1.83	0.43
2:C2:25:G:H5''	20:CR:3:ARG:HH21	1.83	0.43
4:CA:26:ILE:HG23	4:CA:168:GLY:H	1.83	0.43
4:CA:59:LEU:HD23	4:CA:59:LEU:HA	1.92	0.43
6:CC:198:PRO:HG2	6:CC:227:LYS:HG3	1.99	0.43
8:CF:227:TRP:CH2	8:CF:229:SER:HA	2.53	0.43
11:CI:190:TYR:CZ	11:CI:192:ALA:HB2	2.53	0.43
18:CP:365:GLN:OE1	18:CP:365:GLN:N	2.51	0.43
18:CP:464:VAL:HG22	18:CP:574:ASP:HB3	2.00	0.43
19:CQ:27:LYS:HG3	19:CQ:29:PHE:CZ	2.53	0.43
20:CR:170:ARG:HB3	20:CR:174:ARG:NH1	2.33	0.43
22:CU:341:ARG:HH12	22:CU:349:LEU:HD11	1.82	0.43
22:CU:358:PHE:C	22:CU:360:VAL:H	2.25	0.43
28:LC:153:VAL:HG22	28:LC:257:TRP:O	2.17	0.43
33:LL:18:TRP:CD1	33:LL:18:TRP:H	2.36	0.43
33:LL:89:LEU:HD12	33:LL:92:THR:OG1	2.18	0.43
35:LN:146:PRO:HA	35:LN:149:ASN:ND2	2.33	0.43
39:LS:75:PHE:CE2	39:LS:99:ARG:HG2	2.52	0.43
40:LT:92:ARG:HD3	40:LT:92:ARG:H	1.83	0.43
46:Lh:11:GLN:HB3	46:Lh:15:LYS:HZ3	1.78	0.43
48:Lj:74:PHE:HA	48:Lj:78:PHE:CE1	2.52	0.43
49:Lq:111:ILE:HD12	49:Lq:151:VAL:HG11	2.00	0.43
51:Cd:326:LYS:O	51:Cd:330:ILE:HG12	2.18	0.43
52:Ce:104:PHE:CE2	52:Ce:108:LYS:HD3	2.53	0.43
1:C1:31:C:H4'	35:LN:96:ARG:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:538:G:H2'	1:C1:539:G:C8	2.52	0.43
1:C1:1038:U:H2'	1:C1:1039:A:C8	2.53	0.43
1:C1:1134:G:O2'	1:C1:2333:G:N2	2.51	0.43
1:C1:2385:U:H2'	1:C1:2386:A:C8	2.49	0.43
1:C1:2943:C:H2'	1:C1:2944:U:C6	2.53	0.43
1:C1:3108:U:C2	1:C1:3337:C:N3	2.86	0.43
1:C1:3283:G:O2'	1:C1:3302:A:N6	2.41	0.43
2:C2:66:A:H2'	2:C2:67:U:H6	1.82	0.43
5:CB:251:GLU:OE2	5:CB:254:LYS:N	2.50	0.43
8:CF:18:LYS:HB3	8:CF:22:ALA:HB2	2.00	0.43
10:CH:196:TYR:CZ	10:CH:199:THR:HA	2.53	0.43
10:CH:247:ALA:H	10:CH:280:LYS:HE2	1.82	0.43
10:CH:330:VAL:O	10:CH:334:VAL:HG22	2.18	0.43
12:CJ:144:CYS:HA	12:CJ:234:TYR:CG	2.53	0.43
12:CJ:218:ILE:HG22	12:CJ:218:ILE:O	2.18	0.43
16:CN:143:ALA:HB2	16:CN:165:THR:HG22	1.99	0.43
18:CP:308:ILE:HG23	18:CP:362:TYR:HB2	2.00	0.43
18:CP:431:ARG:HG2	18:CP:431:ARG:O	2.18	0.43
19:CQ:100:ARG:HH11	27:LB:379:GLN:HE22	1.67	0.43
25:Cb:2:PRO:HA	25:Cb:5:ALA:HB2	2.00	0.43
28:LC:146:VAL:HG22	28:LC:148:GLU:H	1.83	0.43
33:LL:90:ALA:HB1	33:LL:95:ILE:HB	1.99	0.43
41:LV:34:ARG:HG2	41:LV:67:GLY:HA2	2.00	0.43
49:Lq:39:LYS:HD2	49:Lq:40:ASN:CB	2.49	0.43
1:C1:202:A:H4'	1:C1:204:A:N7	2.33	0.43
1:C1:698:A:H5'	4:CA:267:ILE:CD1	2.48	0.43
1:C1:1118:A:H2'	1:C1:1119:C:C6	2.53	0.43
1:C1:1196:U:H2'	1:C1:1197:A:C8	2.53	0.43
1:C1:2432:C:H42	1:C1:2451:C:H5'	1.83	0.43
1:C1:2549:A:H2'	1:C1:2550:G:O4'	2.17	0.43
1:C1:2760:A:H4'	23:CX:90:LYS:HD2	1.98	0.43
1:C1:2946:C:H2'	1:C1:2947:U:H6	1.82	0.43
3:C3:6:A:O2'	3:C3:7:U:O5'	2.30	0.43
4:CA:37:LEU:HB2	4:CA:86:CYS:SG	2.59	0.43
4:CA:134:LYS:HD3	22:CU:274:GLU:CD	2.43	0.43
4:CA:229:ILE:HD11	22:CU:255:ARG:HD2	2.00	0.43
5:CB:156:ASP:OD2	5:CB:185:MET:HE3	2.19	0.43
7:CE:244:LEU:O	7:CE:248:LEU:HD23	2.17	0.43
11:CI:316:ARG:O	11:CI:320:LEU:HG	2.18	0.43
12:CJ:125:HIS:CD2	12:CJ:126:ILE:HG13	2.52	0.43
15:CM:113:ARG:HG3	15:CM:210:PRO:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CM:122:PHE:CZ	15:CM:150:VAL:HG23	2.53	0.43
18:CP:394:LYS:HD3	18:CP:454:LEU:HD21	2.00	0.43
19:CQ:6:CYS:HB3	19:CQ:10:GLY:C	2.43	0.43
19:CQ:56:ARG:HE	19:CQ:61:LYS:HB3	1.84	0.43
28:LC:301:ARG:HE	28:LC:304:LYS:HZ2	1.67	0.43
32:LK:54:LYS:HG2	32:LK:55:GLY:H	1.83	0.43
39:LS:80:ARG:HB2	39:LS:124:LEU:HD11	1.99	0.43
44:Le:101:VAL:O	44:Le:106:ARG:NH1	2.52	0.43
51:Cd:328:MET:HE2	51:Cd:346:LEU:HD11	1.99	0.43
1:C1:134:G:H5'	6:CC:302:ARG:HB3	2.00	0.43
1:C1:568:C:P	15:LF:148:LYS:HD2	2.58	0.43
1:C1:572:G:H2'	1:C1:573:G:H8	1.82	0.43
1:C1:1126:U:H6	1:C1:1142:C:H41	1.66	0.43
1:C1:1236:C:H2'	1:C1:1237:C:C6	2.53	0.43
1:C1:1336:G:OP1	52:Ce:41:GLN:HG2	2.18	0.43
1:C1:2090:C:N3	1:C1:2288:A:N1	2.66	0.43
1:C1:2315:G:P	37:LP:86:LYS:HZ2	2.40	0.43
1:C1:2955:U:H2'	1:C1:2956:C:C6	2.53	0.43
1:C1:3134:A:C5	36:LO:170:TYR:CE1	3.06	0.43
1:C1:3276:A:H2'	1:C1:3277:G:O4'	2.18	0.43
4:CA:104:PHE:HB2	4:CA:113:VAL:CG2	2.48	0.43
4:CA:200:GLU:HA	4:CA:227:THR:HA	2.00	0.43
9:CG:47:TYR:HB2	9:CG:71:LEU:HD21	2.00	0.43
10:CH:270:PHE:CE2	10:CH:308:LEU:HD11	2.52	0.43
15:CM:126:THR:OG1	15:CM:127:LYS:N	2.51	0.43
15:CM:146:ASN:OD1	15:CM:148:LYS:N	2.48	0.43
16:CN:186:VAL:O	16:CN:190:SER:N	2.50	0.43
18:CP:367:ALA:O	18:CP:371:LEU:HD23	2.17	0.43
23:CX:76:THR:OG1	23:CX:77:VAL:N	2.52	0.43
27:LB:285:ARG:CB	27:LB:324:MET:HE3	2.48	0.43
33:LL:17:HIS:H	33:LL:21:ARG:HH22	1.66	0.43
33:LL:79:GLU:OE2	33:LL:103:ASN:ND2	2.47	0.43
33:LL:115:ARG:HH11	33:LL:115:ARG:HG3	1.83	0.43
41:LV:23:ALA:HB3	41:LV:38:ILE:HD12	2.00	0.43
51:Cd:311:LEU:HA	51:Cd:344:VAL:O	2.19	0.43
1:C1:67:A:N1	1:C1:292:G:O2'	2.45	0.43
1:C1:278:U:H2'	1:C1:279:G:C8	2.53	0.43
1:C1:527:U:C2	1:C1:528:G:C8	3.06	0.43
1:C1:961:U:H5	1:C1:962:U:H1'	1.83	0.43
1:C1:1119:C:H2'	1:C1:1120:U:C6	2.53	0.43
1:C1:2724:U:C4	1:C1:2751:G:N1	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3116:G:H5'	37:LP:157:VAL:O	2.19	0.43
9:CG:174:LEU:HB3	13:CK:163:ARG:HH21	1.82	0.43
10:CH:227:PRO:C	10:CH:229:GLU:H	2.27	0.43
10:CH:236:MET:HA	10:CH:239:VAL:HG22	2.00	0.43
12:CJ:198:GLN:HA	12:CJ:206:ILE:O	2.18	0.43
18:CP:372:PRO:HB3	18:CP:511:SER:HB3	2.00	0.43
25:Cb:368:SER:HB2	25:Cb:436:ALA:H	1.82	0.43
29:LE:166:ASP:OD1	29:LE:167:LYS:N	2.52	0.43
15:LF:57:TYR:CE1	15:LF:192:HIS:CG	3.07	0.43
32:LK:53:TRP:CE3	32:LK:83:ARG:HD2	2.53	0.43
38:LQ:136:LYS:O	38:LQ:140:ARG:HG3	2.17	0.43
40:LT:43:LYS:HB3	40:LT:97:LYS:NZ	2.33	0.43
45:Lf:51:VAL:CG2	45:Lf:73:ILE:HG12	2.47	0.43
48:Lj:28:HIS:CE1	48:Lj:30:GLN:HB3	2.53	0.43
1:C1:271:U:H2'	1:C1:272:U:C6	2.54	0.43
1:C1:434:G:O2'	1:C1:435:C:O4'	2.23	0.43
1:C1:515:G:H5''	34:LM:78:THR:HB	2.00	0.43
1:C1:1056:U:O2'	1:C1:1057:A:H2'	2.18	0.43
1:C1:1094:A:H2'	1:C1:1095:G:C8	2.54	0.43
4:CA:73:ARG:HD3	4:CA:75:TYR:CZ	2.53	0.43
5:CB:261:THR:O	5:CB:264:ARG:HG2	2.18	0.43
6:CC:271:LEU:HD21	47:Li:48:PHE:CD2	2.53	0.43
7:CE:419:ARG:CZ	7:CE:444:ARG:HD3	2.48	0.43
9:CG:84:ILE:HG13	9:CG:173:TYR:OH	2.19	0.43
9:CG:166:ARG:HH22	9:CG:168:ALA:HA	1.82	0.43
11:CI:213:ILE:HD13	11:CI:233:ILE:HD11	2.01	0.43
18:CP:309:ARG:HH22	18:CP:396:THR:HB	1.84	0.43
18:CP:416:SER:O	18:CP:419:LYS:HG2	2.18	0.43
25:Cb:371:ILE:HA	25:Cb:439:ILE:O	2.18	0.43
28:LC:257:TRP:CZ3	28:LC:265:LEU:HD11	2.54	0.43
33:LL:80:LEU:HD23	33:LL:80:LEU:HA	1.89	0.43
37:LP:39:TRP:HH2	37:LP:76:TRP:HH2	1.67	0.43
38:LQ:111:VAL:HG12	38:LQ:151:LEU:HD11	2.00	0.43
45:Lf:43:ALA:HB1	45:Lf:76:PRO:HB3	2.00	0.43
46:Lh:101:ASP:OD1	46:Lh:104:ARG:NH1	2.51	0.43
1:C1:18:G:H2'	1:C1:19:U:C6	2.54	0.43
1:C1:362:U:OP1	51:Cd:16:ARG:NH2	2.52	0.43
1:C1:374:U:OP1	26:Ch:317:ILE:HG23	2.19	0.43
1:C1:548:A:H2'	1:C1:549:G:O4'	2.19	0.43
1:C1:1374:G:O6	52:Ce:144:LYS:HB2	2.18	0.43
1:C1:2464:U:H5''	1:C1:2465:G:OP1	2.19	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:C8	2.54	0.43
1:C1:3086:A:C6	1:C1:3088:U:H1'	2.54	0.43
5:CB:74:ASP:OD2	5:CB:77:ARG:NH1	2.52	0.43
9:CG:36:TYR:HB3	9:CG:47:TYR:CZ	2.54	0.43
10:CH:427:LEU:HD13	10:CH:432:TRP:HB3	1.99	0.43
12:CJ:77:LEU:HD23	12:CJ:80:LYS:HD2	2.01	0.43
12:CJ:178:TYR:HB2	12:CJ:246:TYR:CZ	2.54	0.43
13:CK:38:ASN:HA	13:CK:42:LEU:HD13	2.00	0.43
23:CX:106:ALA:HB3	23:CX:129:ILE:HG23	2.01	0.43
24:Cz:64:LYS:HA	24:Cz:67:GLU:OE2	2.18	0.43
27:LB:178:HIS:CE1	27:LB:336:ILE:HB	2.54	0.43
28:LC:100:MET:HE3	28:LC:100:MET:HB2	1.87	0.43
32:LK:90:ARG:HH12	32:LK:92:ARG:HB3	1.84	0.43
39:LS:13:HIS:O	39:LS:22:PRO:HG2	2.19	0.43
47:Li:86:LEU:HD11	47:Li:95:LYS:HG3	1.99	0.43
50:Cc:97:MET:HE3	50:Cc:97:MET:HA	2.01	0.43
50:Cc:225:ILE:O	50:Cc:229:VAL:HG22	2.18	0.43
51:Cd:59:LYS:HA	51:Cd:62:GLU:HG3	2.00	0.43
1:C1:120:G:O3'	6:CC:284:SER:OG	2.36	0.43
1:C1:391:A:O2'	1:C1:395:C:O2'	2.26	0.43
1:C1:441:G:H2'	1:C1:442:C:C6	2.53	0.43
1:C1:636:A:O3'	53:Cf:530:ASN:ND2	2.52	0.43
1:C1:676:U:N3	28:LC:234:THR:O	2.50	0.43
1:C1:678:A:N1	2:C2:28:C:O2'	2.48	0.43
1:C1:698:A:H5'	4:CA:267:ILE:HD13	2.00	0.43
1:C1:748:U:C2	1:C1:749:C:C5	3.06	0.43
1:C1:796:G:H1	1:C1:906:A:N6	2.17	0.43
1:C1:2380:G:H2'	1:C1:2759:A:C2	2.53	0.43
1:C1:2400:A:H2'	1:C1:2401:A:H8	1.84	0.43
1:C1:2451:C:O2'	1:C1:2452:C:H5'	2.19	0.43
1:C1:2803:A:O2'	1:C1:2806:G:O6	2.36	0.43
1:C1:2936:U:O4'	53:Cf:522:GLU:HB3	2.19	0.43
1:C1:3273:G:H1'	1:C1:3310:A:N6	2.34	0.43
2:C2:39:G:C2	2:C2:105:A:N1	2.86	0.43
6:CC:311:GLU:HG3	6:CC:314:ARG:NH2	2.34	0.43
7:CE:230:LEU:HD23	7:CE:253:PHE:CD1	2.54	0.43
7:CE:379:TYR:CD2	7:CE:507:LEU:HD11	2.53	0.43
7:CE:532:ASP:HB3	7:CE:535:LYS:NZ	2.33	0.43
7:CE:571:ARG:NH2	7:CE:575:SER:O	2.51	0.43
16:CN:239:ASN:OD1	16:CN:240:THR:N	2.51	0.43
20:CR:19:MET:HE3	20:CR:19:MET:HB3	1.88	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CR:169:LEU:HD11	46:Lh:124:LYS:HD2	2.00	0.43
21:CS:475:MET:HE1	30:LG:55:TRP:CE2	2.52	0.43
30:LG:189:LEU:HD23	30:LG:201:VAL:HG23	2.00	0.43
30:LG:222:LYS:HB2	30:LG:222:LYS:HE3	1.77	0.43
37:LP:42:GLN:OE1	37:LP:42:GLN:HA	2.19	0.43
41:LV:19:LEU:HD12	41:LV:80:ILE:HD13	1.99	0.43
46:Lh:34:LEU:HA	46:Lh:37:GLN:HE21	1.83	0.43
1:C1:63:A:N3	1:C1:78:U:O2'	2.50	0.43
1:C1:572:G:H2'	1:C1:573:G:C8	2.54	0.43
1:C1:1290:A:H5''	14:CL:13:SER:HA	2.01	0.43
1:C1:2975:C:C4	1:C1:2976:U:C4	3.06	0.43
4:CA:75:TYR:O	4:CA:79:GLU:OE1	2.37	0.43
7:CE:441:TYR:HA	7:CE:444:ARG:HH21	1.84	0.43
7:CE:460:LEU:HG	7:CE:462:LEU:HD22	2.00	0.43
8:CF:145:THR:HG23	8:CF:148:GLU:H	1.84	0.43
12:CJ:65:TYR:O	12:CJ:69:ILE:HG12	2.17	0.43
12:CJ:90:LYS:O	12:CJ:93:ARG:HB2	2.18	0.43
12:CJ:189:PHE:C	12:CJ:462:TRP:HZ2	2.27	0.43
18:CP:460:SER:O	18:CP:475:ARG:HD2	2.19	0.43
18:CP:462:THR:HA	18:CP:471:VAL:HG11	2.00	0.43
19:CQ:102:ARG:NH1	19:CQ:103:ARG:HE	2.17	0.43
23:CX:97:ASP:O	23:CX:101:MET:HG2	2.19	0.43
25:Cb:438:VAL:O	25:Cb:466:ALA:HA	2.19	0.43
27:LB:377:LYS:O	27:LB:381:MET:HG2	2.18	0.43
29:LE:69:ARG:HD2	29:LE:182:TYR:O	2.19	0.43
15:LF:157:ARG:HG2	15:LF:157:ARG:NH1	2.34	0.43
15:LF:237:ARG:HD2	15:LF:241:ILE:HD12	2.00	0.43
34:LM:33:ILE:HG23	34:LM:39:VAL:HG12	2.00	0.43
36:LO:175:LEU:HA	36:LO:178:ARG:HG2	2.00	0.43
40:LT:92:ARG:CZ	40:LT:95:HIS:CD2	3.02	0.43
46:Lh:105:VAL:HG22	46:Lh:109:THR:OG1	2.18	0.43
49:Lq:117:ILE:HA	49:Lq:120:ILE:HG12	2.01	0.43
1:C1:92:G:C5	1:C1:94:G:C2	3.07	0.43
1:C1:298:A:H5''	4:CA:95:ARG:NH1	2.34	0.43
1:C1:332:C:H2'	1:C1:333:G:O4'	2.19	0.43
1:C1:369:C:H1'	1:C1:384:G:N2	2.33	0.43
1:C1:579:A:N6	1:C1:597:G:H1'	2.34	0.43
1:C1:602:U:H2'	1:C1:603:G:H8	1.84	0.43
1:C1:767:A:O3'	1:C1:768:G:H8	2.01	0.43
1:C1:1193:U:O2'	39:LS:113:ARG:NH1	2.52	0.43
1:C1:1277:G:H1'	39:LS:113:ARG:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2374:G:H2'	1:C1:2375:A:H8	1.83	0.43
1:C1:2564:G:C4	9:CG:2:ARG:HD3	2.54	0.43
2:C2:4:C:H2'	2:C2:5:U:H6	1.83	0.43
2:C2:14:C:C4	2:C2:15:G:C6	3.07	0.43
7:CE:305:ASP:HA	7:CE:308:ARG:HG2	2.01	0.43
7:CE:380:ILE:O	7:CE:380:ILE:HG22	2.19	0.43
7:CE:433:ASP:HB3	7:CE:434:PRO:HD2	2.01	0.43
8:CF:143:TYR:HA	8:CF:156:PRO:HA	2.01	0.43
8:CF:157:VAL:HG22	8:CF:158:SER:H	1.84	0.43
16:CN:13:VAL:HG23	16:CN:34:PHE:HE1	1.84	0.43
16:CN:124:GLU:O	16:CN:127:GLU:HG3	2.19	0.43
25:Cb:124:ILE:HA	25:Cb:267:GLN:HE22	1.84	0.43
25:Cb:542:GLU:O	25:Cb:546:MET:HG2	2.19	0.43
27:LB:77:THR:HG21	27:LB:329:VAL:HB	2.00	0.43
31:LH:1:MET:HE3	31:LH:3:TYR:CE1	2.54	0.43
33:LL:58:VAL:O	33:LL:69:THR:OG1	2.21	0.43
39:LS:41:PHE:O	39:LS:45:LEU:HD23	2.19	0.43
51:Cd:207:ILE:HD13	51:Cd:238:LYS:HG2	2.00	0.43
52:Ce:94:ILE:HD11	52:Ce:113:LEU:HD22	2.01	0.43
1:C1:302:U:OP1	7:CE:583:TYR:OH	2.36	0.42
1:C1:702:A:N1	1:C1:762:G:O2'	2.49	0.42
1:C1:1086:U:H2'	1:C1:1087:C:C6	2.54	0.42
1:C1:1288:G:OP1	36:LO:64:ARG:NH1	2.52	0.42
1:C1:2312:C:H2'	1:C1:2313:U:C6	2.54	0.42
1:C1:2777:A:C2	1:C1:2778:A:C8	3.07	0.42
1:C1:2841:U:O2'	36:LO:64:ARG:NH2	2.52	0.42
1:C1:2986:A:O5'	1:C1:2986:A:H8	2.02	0.42
1:C1:3008:U:C2	1:C1:3009:G:C8	3.07	0.42
1:C1:3070:A:H2'	1:C1:3071:A:O4'	2.19	0.42
3:C3:61:A:H4'	3:C3:62:G:H5'	2.00	0.42
4:CA:79:GLU:OE2	7:CE:573:TYR:N	2.47	0.42
5:CB:291:LEU:HD22	11:CI:325:TYR:CD2	2.53	0.42
18:CP:302:THR:O	18:CP:304:ARG:NH2	2.52	0.42
18:CP:304:ARG:HA	18:CP:304:ARG:NE	2.34	0.42
29:LE:128:PHE:HA	29:LE:158:ARG:HH21	1.83	0.42
30:LG:222:LYS:HA	30:LG:226:LEU:HB2	2.01	0.42
50:Cc:174:ARG:NH1	50:Cc:184:GLU:HA	2.31	0.42
52:Ce:190:ILE:O	52:Ce:194:VAL:HG23	2.19	0.42
53:Cf:472:TRP:CZ2	54:Cg:350:LEU:HB3	2.54	0.42
1:C1:337:G:O2'	2:C2:25:G:N3	2.52	0.42
1:C1:423:U:H2'	1:C1:424:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1333:A:OP1	52:Ce:103:LYS:NZ	2.43	0.42
1:C1:3070:A:OP2	24:Cz:36:LYS:NZ	2.51	0.42
1:C1:3226:G:N3	1:C1:3226:G:H2'	2.34	0.42
1:C1:3327:G:H5'	54:Cg:138:GLY:HA2	2.01	0.42
5:CB:243:ILE:HG13	5:CB:266:LEU:HD11	2.00	0.42
10:CH:295:GLU:N	10:CH:295:GLU:OE1	2.53	0.42
10:CH:422:ARG:O	10:CH:433:LYS:HE2	2.19	0.42
10:CH:429:ASN:O	10:CH:432:TRP:HB2	2.19	0.42
11:CI:269:HIS:HB3	11:CI:272:LEU:HG	2.01	0.42
12:CJ:177:HIS:NE2	12:CJ:268:LEU:O	2.52	0.42
19:CQ:95:ARG:O	19:CQ:98:GLU:HG2	2.19	0.42
25:Cb:192:VAL:HG11	25:Cb:207:MET:HE1	2.00	0.42
25:Cb:196:GLY:HA2	25:Cb:220:ARG:HH21	1.84	0.42
27:LB:57:VAL:HG13	27:LB:358:LYS:HB2	2.01	0.42
47:Li:95:LYS:HA	47:Li:98:GLU:OE1	2.19	0.42
49:Lq:68:LEU:HD12	49:Lq:90:LEU:HD12	2.02	0.42
49:Lq:76:ARG:NH1	49:Lq:142:ASP:O	2.51	0.42
53:Cf:459:PRO:HD2	53:Cf:462:LYS:HZ1	1.84	0.42
1:C1:283:C:C2	1:C1:284:U:C5	3.07	0.42
1:C1:633:A:O2'	1:C1:2334:A:N6	2.53	0.42
1:C1:2391:G:N1	1:C1:2559:A:C6	2.88	0.42
1:C1:2863:U:H2'	1:C1:2864:C:H6	1.84	0.42
1:C1:3076:U:OP2	24:Cz:28:ASN:ND2	2.53	0.42
2:C2:27:U:H2'	2:C2:28:C:C6	2.54	0.42
3:C3:55:A:OP2	5:CB:144:ARG:NH2	2.52	0.42
4:CA:92:PHE:CE1	4:CA:102:MET:HG2	2.54	0.42
10:CH:55:THR:HA	10:CH:58:GLU:HG2	2.01	0.42
12:CJ:251:LEU:HD23	12:CJ:252:LYS:O	2.18	0.42
12:CJ:376:ARG:NH2	15:CM:192:HIS:HB3	2.34	0.42
18:CP:296:PHE:HD1	18:CP:569:HIS:HD2	1.66	0.42
20:CR:165:LYS:HE3	20:CR:170:ARG:HG2	2.01	0.42
25:Cb:2:PRO:HG2	41:LV:75:VAL:HG21	2.00	0.42
25:Cb:196:GLY:HA2	25:Cb:220:ARG:HE	1.83	0.42
25:Cb:306:GLU:OE2	25:Cb:500:PHE:HB2	2.18	0.42
25:Cb:309:PHE:HB2	25:Cb:506:VAL:HG22	2.01	0.42
27:LB:47:MET:SD	27:LB:336:ILE:HD11	2.59	0.42
29:LE:194:LYS:HB3	29:LE:196:HIS:HE1	1.81	0.42
36:LO:55:TYR:HE1	36:LO:147:VAL:HG11	1.83	0.42
37:LP:157:VAL:HB	51:Cd:361:VAL:CG2	2.50	0.42
43:LY:123:ALA:HA	43:LY:126:GLU:OE2	2.19	0.42
52:Ce:148:ARG:O	52:Ce:152:ARG:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:Cg:106:VAL:HA	54:Cg:112:PRO:O	2.19	0.42
1:C1:550:C:H2'	1:C1:551:C:H6	1.85	0.42
1:C1:581:G:H1'	29:LE:37:LYS:HG3	2.00	0.42
1:C1:746:A:H3'	1:C1:747:U:H6	1.83	0.42
1:C1:937:U:H2'	1:C1:938:C:H6	1.84	0.42
1:C1:947:U:H2'	1:C1:948:A:C8	2.51	0.42
1:C1:1193:U:H2'	1:C1:1194:A:C8	2.53	0.42
1:C1:2562:U:O2'	9:CG:57:THR:O	2.27	0.42
1:C1:2848:A:N6	1:C1:2871:C:N4	2.30	0.42
1:C1:2869:A:H4'	1:C1:2870:G:C8	2.54	0.42
1:C1:3176:C:H2'	1:C1:3177:C:C6	2.55	0.42
1:C1:3269:U:H5''	27:LB:309:MET:CG	2.49	0.42
4:CA:263:SER:H	4:CA:266:LYS:HD3	1.84	0.42
5:CB:215:ARG:HH22	5:CB:219:GLU:HB3	1.82	0.42
6:CC:292:MET:SD	20:CR:190:ARG:NH2	2.83	0.42
6:CC:355:ASN:HB3	12:CJ:485:HIS:HD2	1.84	0.42
7:CE:493:VAL:O	7:CE:497:LEU:HD23	2.19	0.42
8:CF:32:GLU:O	8:CF:35:PRO:HD2	2.18	0.42
10:CH:192:PRO:HD2	10:CH:204:PHE:CE2	2.54	0.42
11:CI:309:GLU:HA	11:CI:312:ARG:HG2	2.02	0.42
13:CK:157:VAL:HG23	13:CK:178:ARG:HD3	2.00	0.42
14:CL:62:LYS:NZ	24:Cz:65:GLU:OE2	2.51	0.42
15:CM:113:ARG:NH2	15:CM:205:ALA:O	2.52	0.42
23:CX:112:LYS:HE3	23:CX:112:LYS:HB3	1.82	0.42
30:LG:229:VAL:O	30:LG:233:ARG:HB3	2.20	0.42
33:LL:128:ARG:NH2	46:Lh:117:PRO:HG3	2.33	0.42
36:LO:29:LEU:HD12	36:LO:96:ARG:NH1	2.34	0.42
36:LO:48:PHE:HE2	36:LO:52:LYS:HE2	1.84	0.42
40:LT:45:ASN:HB2	40:LT:95:HIS:CE1	2.54	0.42
41:LV:131:ILE:O	41:LV:135:ALA:CB	2.68	0.42
44:Le:80:VAL:O	44:Le:84:GLU:HG3	2.19	0.42
1:C1:489:G:H2'	1:C1:490:C:C6	2.55	0.42
1:C1:1151:A:H2'	1:C1:1152:A:C8	2.55	0.42
1:C1:1389:A:H5''	44:Le:32:ALA:HB1	2.02	0.42
1:C1:2442:A:H2'	1:C1:2443:G:N3	2.34	0.42
1:C1:2442:A:H61	1:C1:2449:U:H5	1.67	0.42
1:C1:2565:G:C2	1:C1:2566:G:C8	3.08	0.42
1:C1:3078:U:H4'	1:C1:3079:A:OP1	2.18	0.42
1:C1:3257:U:H1'	1:C1:3258:G:OP2	2.20	0.42
2:C2:146:U:H2'	2:C2:147:C:C6	2.54	0.42
4:CA:131:ASN:HD21	22:CU:275:MET:HB3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CF:149:VAL:HB	8:CF:150:PRO:HD2	2.02	0.42
9:CG:11:ILE:HG22	9:CG:80:PHE:HB3	2.01	0.42
10:CH:466:GLU:O	10:CH:470:LYS:HG2	2.20	0.42
11:CI:292:GLN:HG3	11:CI:295:ARG:NH2	2.34	0.42
12:CJ:26:LEU:HD23	12:CJ:33:PHE:HD1	1.84	0.42
12:CJ:251:LEU:HG	12:CJ:274:GLU:O	2.19	0.42
12:CJ:258:ASP:OD1	12:CJ:261:LYS:HB2	2.20	0.42
13:CK:17:ARG:HG3	13:CK:17:ARG:NH1	2.34	0.42
16:CN:73:PRO:O	16:CN:76:THR:HG22	2.19	0.42
19:CQ:92:ALA:O	19:CQ:96:ILE:HG12	2.19	0.42
26:Ch:327:THR:HB	26:Ch:331:ARG:NH2	2.35	0.42
27:LB:213:ASP:HB3	27:LB:355:VAL:HG12	2.00	0.42
28:LC:341:LEU:HB3	15:LF:62:ARG:NH2	2.35	0.42
28:LC:361:LEU:HD12	28:LC:361:LEU:HA	1.94	0.42
33:LL:23:ARG:NH1	33:LL:25:HIS:CE1	2.87	0.42
37:LP:12:THR:HG21	52:Ce:161:LYS:HG2	2.01	0.42
41:LV:61:MET:HE1	41:LV:77:PRO:HG3	2.00	0.42
43:LY:30:MET:HB3	43:LY:100:PRO:HG2	2.01	0.42
47:Li:98:GLU:O	47:Li:102:ILE:HG13	2.20	0.42
50:Cc:10:PHE:CE1	50:Cc:29:LEU:HD12	2.54	0.42
51:Cd:358:HIS:NE2	51:Cd:392:GLU:HG3	2.34	0.42
1:C1:70:A:O5'	1:C1:101:G:O2'	2.38	0.42
1:C1:84:U:OP2	1:C1:85:A:O2'	2.30	0.42
1:C1:415:A:H3'	1:C1:416:G:H8	1.85	0.42
1:C1:602:U:H2'	1:C1:603:G:C8	2.55	0.42
1:C1:631:G:H5''	1:C1:1098:G:H8	1.84	0.42
1:C1:768:G:H2'	1:C1:769:C:H6	1.85	0.42
1:C1:958:A:H3'	1:C1:959:C:C6	2.54	0.42
1:C1:1174:C:P	13:CK:43:ARG:HH12	2.42	0.42
1:C1:2875:G:C6	1:C1:2888:A:N6	2.88	0.42
1:C1:3176:C:H2'	1:C1:3177:C:H6	1.84	0.42
2:C2:148:G:H2'	2:C2:149:A:H8	1.84	0.42
5:CB:63:TRP:HB2	5:CB:243:ILE:O	2.19	0.42
5:CB:105:GLN:HE21	5:CB:109:LYS:HE2	1.84	0.42
6:CC:403:ARG:HD2	6:CC:406:ARG:NH1	2.35	0.42
7:CE:152:LEU:HD13	7:CE:294:LEU:HD22	2.01	0.42
10:CH:15:GLU:O	10:CH:19:ILE:HD12	2.20	0.42
10:CH:288:LYS:HE2	10:CH:291:ILE:HD11	2.00	0.42
16:CN:156:ASN:OD1	16:CN:157:GLN:HG2	2.19	0.42
18:CP:551:TYR:CE2	18:CP:552:MET:HE3	2.55	0.42
22:CU:307:ASP:HA	22:CU:310:LYS:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Cb:553:SER:O	25:Cb:556:SER:OG	2.30	0.42
28:LC:361:LEU:HD11	40:LT:148:PRO:HG2	2.02	0.42
29:LE:139:GLU:HA	51:Cd:247:PHE:CE2	2.54	0.42
38:LQ:96:ALA:O	38:LQ:100:LYS:HG3	2.20	0.42
47:Li:67:ILE:HD11	47:Li:99:LEU:HD22	2.01	0.42
54:Cg:90:LEU:HB3	54:Cg:106:VAL:HG23	2.00	0.42
1:C1:92:G:C6	1:C1:94:G:N2	2.87	0.42
1:C1:702:A:O2'	1:C1:703:A:OP1	2.36	0.42
1:C1:745:U:O2	1:C1:749:C:C4	2.73	0.42
1:C1:977:A:N1	1:C1:1036:A:H1'	2.35	0.42
1:C1:1121:G:H2'	1:C1:1122:G:H8	1.84	0.42
1:C1:1417:A:H5''	1:C1:1418:U:H5''	2.01	0.42
1:C1:2373:U:H3	1:C1:2768:C:H42	1.68	0.42
1:C1:2389:U:H2'	1:C1:2390:U:C6	2.55	0.42
1:C1:2957:G:H2'	1:C1:2958:U:H6	1.85	0.42
1:C1:3064:U:H2'	1:C1:3065:G:H8	1.85	0.42
4:CA:38:VAL:HG23	4:CA:64:LYS:HA	2.02	0.42
5:CB:175:THR:HG22	5:CB:177:LYS:H	1.85	0.42
9:CG:165:PHE:O	9:CG:167:GLN:OE1	2.37	0.42
11:CI:284:PRO:HB2	11:CI:287:LYS:HB3	2.01	0.42
16:CN:219:GLU:OE1	16:CN:224:LEU:HB2	2.20	0.42
17:CO:14:HIS:O	17:CO:18:LYS:HG3	2.19	0.42
18:CP:438:TYR:HD2	18:CP:443:PHE:CD1	2.38	0.42
18:CP:491:LEU:O	18:CP:495:ILE:HG12	2.20	0.42
25:Cb:15:VAL:HB	25:Cb:448:LYS:HD2	2.00	0.42
28:LC:167:ALA:O	28:LC:171:LYS:HG3	2.20	0.42
15:LF:142:TYR:CZ	15:LF:236:ASN:HB2	2.55	0.42
34:LM:136:ALA:O	34:LM:137:LYS:C	2.63	0.42
37:LP:12:THR:OG1	52:Ce:163:GLU:OE2	2.34	0.42
38:LQ:49:SER:HB2	38:LQ:54:LEU:HD22	2.02	0.42
49:Lq:26:ARG:HG2	49:Lq:28:PHE:H	1.83	0.42
51:Cd:285:LEU:HG	51:Cd:404:VAL:HG23	2.00	0.42
53:Cf:474:ALA:HA	53:Cf:477:ARG:HH11	1.82	0.42
1:C1:18:G:OP1	46:Lh:86:ARG:NH2	2.52	0.42
1:C1:190:G:H8	1:C1:190:G:OP1	2.03	0.42
1:C1:564:C:H2'	1:C1:565:C:H6	1.84	0.42
1:C1:1395:G:H2'	1:C1:1396:G:H8	1.84	0.42
1:C1:2795:A:P	1:C1:2803:A:H61	2.43	0.42
1:C1:3007:U:C2	1:C1:3008:U:C5	3.07	0.42
2:C2:71:A:H2'	43:LY:50:ARG:NH1	2.35	0.42
2:C2:123:G:H2'	2:C2:124:G:H8	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CA:73:ARG:HD3	4:CA:75:TYR:CE2	2.55	0.42
8:CF:173:ARG:NH2	31:LH:93:VAL:HG12	2.34	0.42
9:CG:149:ARG:HE	9:CG:154:ALA:HA	1.84	0.42
15:CM:74:ILE:HG12	15:CM:134:LYS:HE3	2.02	0.42
16:CN:81:LEU:HD22	16:CN:96:ARG:NE	2.18	0.42
20:CR:170:ARG:NH1	20:CR:170:ARG:HB2	2.34	0.42
27:LB:59:ASP:HB2	27:LB:358:LYS:HE2	2.02	0.42
30:LG:187:ALA:O	30:LG:191:THR:HG23	2.19	0.42
34:LM:109:ARG:HD2	36:LO:204:TYR:CE2	2.54	0.42
38:LQ:147:ARG:NH2	38:LQ:149:LEU:HD21	2.35	0.42
51:Cd:16:ARG:HA	51:Cd:16:ARG:HD3	1.91	0.42
51:Cd:305:THR:OG1	51:Cd:342:GLN:OE1	2.17	0.42
51:Cd:356:ARG:CZ	51:Cd:396:ARG:HD3	2.50	0.42
1:C1:264:G:H2'	1:C1:265:A:H8	1.83	0.42
1:C1:293:G:H2'	1:C1:294:A:C8	2.55	0.42
1:C1:1394:G:C2	1:C1:1395:G:C8	3.08	0.42
1:C1:1869:U:H2'	1:C1:1870:A:H8	1.84	0.42
1:C1:2805:A:C2	1:C1:2806:G:H1'	2.54	0.42
1:C1:3007:U:H5''	19:CQ:17:LYS:NZ	2.34	0.42
1:C1:3022:G:H2'	1:C1:3023:U:C6	2.55	0.42
1:C1:3190:G:H2'	1:C1:3191:C:H6	1.85	0.42
1:C1:3253:U:H4'	27:LB:174:GLN:NE2	2.30	0.42
1:C1:3335:U:H2'	1:C1:3336:U:C6	2.54	0.42
4:CA:35:ARG:HD2	4:CA:86:CYS:HA	2.02	0.42
8:CF:108:ASP:OD2	8:CF:110:ALA:HB3	2.19	0.42
9:CG:48:VAL:HG11	9:CG:67:LEU:HG	2.01	0.42
10:CH:205:VAL:N	13:CK:3:GLN:OE1	2.32	0.42
10:CH:236:MET:HG3	25:Cb:597:TYR:CE2	2.55	0.42
12:CJ:58:THR:HB	12:CJ:61:THR:HG23	2.01	0.42
12:CJ:362:ASP:HB2	12:CJ:363:PRO:HD3	2.02	0.42
15:CM:59:LYS:O	15:CM:63:GLU:HG3	2.20	0.42
25:Cb:510:LYS:HA	25:Cb:510:LYS:HD2	1.87	0.42
27:LB:133:TYR:HE1	27:LB:137:TYR:OH	2.03	0.42
34:LM:19:VAL:O	34:LM:65:THR:OG1	2.31	0.42
35:LN:119:TYR:OH	35:LN:131:GLU:OE1	2.22	0.42
36:LO:129:LEU:HD11	39:LS:170:PRO:HB2	2.01	0.42
37:LP:155:GLU:OE2	51:Cd:363:ARG:NH1	2.39	0.42
39:LS:28:ARG:NH2	39:LS:64:ILE:HG21	2.34	0.42
51:Cd:410:ARG:HG2	51:Cd:410:ARG:NH1	2.34	0.42
1:C1:66:A:N6	1:C1:76:G:H1'	2.34	0.42
1:C1:448:A:H8	1:C1:448:A:OP2	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:471:U:H2'	1:C1:472:C:H6	1.85	0.42
1:C1:766:G:N1	38:LQ:117:ASP:HA	2.32	0.42
1:C1:1199:A:H2'	1:C1:1200:U:C6	2.54	0.42
1:C1:1261:C:H2'	1:C1:1262:C:H6	1.85	0.42
1:C1:2848:A:N3	1:C1:2891:A:H2	2.18	0.42
3:C3:61:A:N6	11:CI:218:VAL:O	2.47	0.42
4:CA:92:PHE:CD1	4:CA:102:MET:HG2	2.55	0.42
8:CF:91:ARG:O	8:CF:95:TYR:HD1	2.03	0.42
10:CH:100:ALA:O	10:CH:104:ILE:HG13	2.20	0.42
10:CH:210:TYR:OH	10:CH:336:GLU:HB2	2.19	0.42
12:CJ:116:THR:HG22	12:CJ:118:LYS:HB2	2.02	0.42
14:CL:187:GLY:HA2	14:CL:188:ALA:HA	1.68	0.42
18:CP:422:ILE:HB	18:CP:426:HIS:CE1	2.54	0.42
25:Cb:251:PHE:HD1	25:Cb:254:GLN:NE2	2.18	0.42
25:Cb:493:ARG:NE	25:Cb:574:ALA:HA	2.34	0.42
30:LG:146:ILE:HG23	30:LG:178:ILE:HD13	2.01	0.42
37:LP:121:GLN:OE1	37:LP:124:LYS:NZ	2.52	0.42
43:LY:122:LYS:O	43:LY:126:GLU:OE1	2.37	0.42
1:C1:471:U:H2'	1:C1:472:C:C6	2.55	0.41
1:C1:577:C:O2'	1:C1:578:G:H5'	2.20	0.41
1:C1:1223:U:OP1	32:LK:96:LYS:HD3	2.20	0.41
1:C1:1260:A:H4'	8:CF:13:ILE:HG21	2.01	0.41
1:C1:2326:G:H8	1:C1:2326:G:OP2	2.03	0.41
1:C1:2408:U:H2'	1:C1:2409:A:H8	1.85	0.41
1:C1:2439:G:OP1	1:C1:2449:U:O2'	2.26	0.41
2:C2:130:C:H5''	12:CJ:5:LYS:NZ	2.35	0.41
4:CA:80:LEU:HD12	4:CA:80:LEU:HA	1.92	0.41
6:CC:370:TRP:O	6:CC:378:ARG:NH1	2.53	0.41
8:CF:60:LEU:HB3	8:CF:63:CYS:SG	2.60	0.41
10:CH:300:GLU:CD	10:CH:300:GLU:H	2.26	0.41
12:CJ:124:ASN:HD22	12:CJ:124:ASN:C	2.27	0.41
13:CK:133:PHE:HE2	13:CK:148:LYS:HG2	1.84	0.41
15:CM:154:ILE:HD12	15:CM:191:ILE:HG12	2.02	0.41
16:CN:107:VAL:HB	16:CN:118:HIS:HB2	2.02	0.41
22:CU:337:LEU:HD23	22:CU:340:LYS:HE2	2.01	0.41
26:Ch:282:LEU:HA	26:Ch:285:ILE:HD12	2.02	0.41
27:LB:29:VAL:HG23	27:LB:340:ARG:HD3	2.02	0.41
27:LB:90:VAL:HG11	27:LB:181:GLU:OE1	2.20	0.41
27:LB:285:ARG:HH21	27:LB:357:LEU:HD12	1.84	0.41
28:LC:223:VAL:HA	28:LC:234:THR:HG21	2.01	0.41
15:LF:244:LEU:HD11	15:LF:248:MET:HE3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LH:10:ILE:HD11	31:LH:72:ARG:HA	2.02	0.41
44:Le:97:ILE:HG21	44:Le:106:ARG:HG2	2.02	0.41
1:C1:118:U:O2	1:C1:121:A:H5''	2.19	0.41
1:C1:909:C:H2'	1:C1:910:A:C8	2.55	0.41
1:C1:1066:A:H2'	1:C1:1067:A:C8	2.55	0.41
1:C1:1200:U:H2'	1:C1:1201:C:C6	2.55	0.41
1:C1:2724:U:C2	1:C1:2751:G:C2	3.08	0.41
1:C1:2800:U:H2'	1:C1:2801:U:H5	1.84	0.41
1:C1:2947:U:C2	1:C1:2948:G:C8	3.08	0.41
1:C1:2984:A:H5''	10:CH:188:ARG:NH2	2.35	0.41
3:C3:136:A:OP2	11:CI:279:ARG:NH2	2.53	0.41
4:CA:40:SER:HB3	4:CA:52:LEU:HD22	2.02	0.41
6:CC:369:GLU:O	6:CC:373:MET:HG3	2.19	0.41
8:CF:30:ILE:O	8:CF:34:ILE:HG12	2.20	0.41
10:CH:463:GLU:O	10:CH:467:ARG:HG2	2.20	0.41
12:CJ:19:ARG:O	12:CJ:23:VAL:HG13	2.20	0.41
27:LB:285:ARG:HB3	27:LB:324:MET:HB3	2.01	0.41
28:LC:181:ASP:OD2	28:LC:208:GLY:HA2	2.19	0.41
15:LF:53:ARG:HG2	15:LF:57:TYR:CE2	2.55	0.41
15:LF:159:TYR:HB3	15:LF:166:ARG:HG3	2.01	0.41
34:LM:14:VAL:HG22	39:LS:150:PHE:O	2.20	0.41
35:LN:104:GLU:HB3	35:LN:108:ARG:CZ	2.49	0.41
39:LS:34:GLU:O	39:LS:38:LYS:HG3	2.20	0.41
49:Lq:55:LEU:HD11	49:Lq:182:ASN:HB3	2.02	0.41
1:C1:159:G:H2'	1:C1:160:C:H6	1.85	0.41
1:C1:495:G:OP1	28:LC:322:ASN:HB2	2.20	0.41
1:C1:780:G:O2'	33:LL:18:TRP:NE1	2.53	0.41
1:C1:1242:A:H2'	1:C1:1243:G:C4	2.55	0.41
1:C1:2374:G:H2'	1:C1:2375:A:C8	2.56	0.41
1:C1:2388:U:H3'	1:C1:2389:U:C6	2.54	0.41
1:C1:2800:U:H2'	1:C1:2801:U:C5	2.55	0.41
1:C1:2869:A:H4'	1:C1:2870:G:H8	1.85	0.41
1:C1:2875:G:H2'	1:C1:2876:G:C8	2.55	0.41
1:C1:2978:A:OP1	1:C1:2980:U:H1'	2.20	0.41
3:C3:21:U:OP1	5:CB:76:HIS:HB2	2.20	0.41
4:CA:126:LEU:HD21	22:CU:284:LYS:HB3	2.02	0.41
4:CA:247:GLU:HB2	4:CA:255:LEU:CD1	2.49	0.41
5:CB:222:ALA:HA	5:CB:225:ARG:NH1	2.35	0.41
5:CB:226:LYS:O	5:CB:229:GLY:C	2.62	0.41
6:CC:184:PRO:O	6:CC:197:ARG:HD3	2.21	0.41
6:CC:306:TYR:HD1	30:LG:113:LEU:HD23	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CE:268:ARG:O	7:CE:272:ILE:HG12	2.20	0.41
7:CE:305:ASP:O	7:CE:308:ARG:HG2	2.21	0.41
10:CH:192:PRO:HD2	10:CH:204:PHE:HE2	1.86	0.41
10:CH:402:VAL:O	10:CH:403:LEU:HB2	2.20	0.41
15:CM:182:TYR:CE1	15:CM:203:GLN:HG3	2.55	0.41
16:CN:106:ASN:ND2	41:LV:135:ALA:O	2.49	0.41
18:CP:486:THR:O	18:CP:490:LEU:HG	2.19	0.41
28:LC:286:ASP:HB3	28:LC:289:ARG:HB3	2.02	0.41
29:LE:194:LYS:O	29:LE:198:MET:HG3	2.20	0.41
33:LL:49:ARG:HG3	33:LL:49:ARG:HH11	1.84	0.41
37:LP:39:TRP:HH2	37:LP:76:TRP:CH2	2.39	0.41
49:Lq:67:ILE:HA	49:Lq:111:ILE:O	2.21	0.41
51:Cd:186:GLN:OE1	51:Cd:186:GLN:HA	2.19	0.41
1:C1:948:A:C2	1:C1:949:G:C8	3.09	0.41
1:C1:2547:G:H2'	1:C1:2548:A:H8	1.84	0.41
1:C1:2936:U:OP1	53:Cf:525:ARG:HB3	2.20	0.41
1:C1:3156:C:H2'	1:C1:3157:C:O4'	2.21	0.41
1:C1:3253:U:OP1	27:LB:117:ARG:NH1	2.54	0.41
5:CB:31:LEU:HB3	5:CB:35:LYS:HZ3	1.84	0.41
6:CC:363:THR:HB	6:CC:366:GLU:HG3	2.00	0.41
6:CC:411:TYR:CE2	12:CJ:38:ILE:HG23	2.55	0.41
7:CE:384:VAL:HG22	7:CE:410:THR:OG1	2.21	0.41
7:CE:512:LYS:HE3	7:CE:512:LYS:HB2	1.83	0.41
10:CH:339:LEU:O	10:CH:343:VAL:HG23	2.20	0.41
11:CI:244:ALA:HA	11:CI:247:THR:HG22	2.02	0.41
11:CI:278:ARG:NH1	11:CI:279:ARG:O	2.54	0.41
12:CJ:84:GLN:O	12:CJ:88:GLU:OE1	2.39	0.41
13:CK:220:ILE:CD1	22:CU:334:ILE:HD12	2.47	0.41
16:CN:74:THR:HG23	19:CQ:74:ARG:HH22	1.85	0.41
18:CP:310:THR:HG23	18:CP:320:LEU:HD22	2.01	0.41
19:CQ:88:LYS:HA	19:CQ:91:LYS:NZ	2.35	0.41
22:CU:316:GLN:HG2	22:CU:320:GLN:NE2	2.26	0.41
25:Cb:11:SER:O	25:Cb:12:GLU:HG3	2.19	0.41
25:Cb:451:VAL:HG21	25:Cb:484:PHE:HE2	1.84	0.41
29:LE:72:LEU:HA	29:LE:83:VAL:HG12	2.02	0.41
31:LH:47:VAL:HG13	31:LH:47:VAL:O	2.20	0.41
32:LK:11:LYS:HE2	32:LK:13:ILE:HD11	2.01	0.41
35:LN:10:LEU:CD2	47:Li:53:ILE:HD12	2.49	0.41
37:LP:29:THR:HG21	37:LP:144:CYS:SG	2.60	0.41
39:LS:73:LYS:HG3	39:LS:75:PHE:CE1	2.52	0.41
49:Lq:16:LEU:O	49:Lq:20:SER:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Lq:91:LYS:O	49:Lq:95:LYS:HG2	2.21	0.41
49:Lq:101:LYS:HD2	49:Lq:101:LYS:C	2.45	0.41
52:Ce:94:ILE:HG23	52:Ce:98:LEU:HD12	2.02	0.41
53:Cf:497:ARG:O	53:Cf:501:ARG:HG2	2.19	0.41
1:C1:127:G:O2'	1:C1:128:G:H5'	2.20	0.41
1:C1:597:G:N7	28:LC:311:ARG:NH2	2.68	0.41
1:C1:664:A:N1	1:C1:690:G:O2'	2.51	0.41
1:C1:767:A:H1'	1:C1:768:G:C8	2.55	0.41
1:C1:1050:C:H2'	1:C1:1051:C:C6	2.55	0.41
1:C1:1360:U:H2'	1:C1:1361:G:C8	2.50	0.41
1:C1:2363:A:H2'	1:C1:2364:A:C8	2.55	0.41
1:C1:2980:U:H2'	1:C1:2981:A:H8	1.86	0.41
1:C1:3009:G:H21	1:C1:3050:C:N4	2.18	0.41
1:C1:3022:G:H2'	1:C1:3023:U:H6	1.85	0.41
2:C2:95:G:C4	48:Lj:79:ARG:HD2	2.56	0.41
4:CA:247:GLU:HB2	4:CA:255:LEU:HD11	2.03	0.41
7:CE:166:LEU:HD23	7:CE:166:LEU:HA	1.95	0.41
7:CE:242:GLY:HA2	7:CE:277:GLU:OE1	2.20	0.41
10:CH:390:LEU:HD23	16:CN:43:GLN:HB2	2.03	0.41
11:CI:219:VAL:HG23	11:CI:228:ARG:HG2	2.02	0.41
14:CL:64:ARG:O	14:CL:68:GLN:HG2	2.20	0.41
15:CM:245:ILE:O	15:CM:249:ASN:HB2	2.19	0.41
17:CO:37:LEU:HB3	27:LB:195:PHE:HZ	1.85	0.41
18:CP:299:ALA:O	18:CP:304:ARG:NH2	2.50	0.41
18:CP:352:GLY:HA2	18:CP:357:TYR:CD2	2.55	0.41
18:CP:368:SER:OG	18:CP:574:ASP:HB2	2.20	0.41
19:CQ:18:GLY:HA3	19:CQ:31:PHE:O	2.21	0.41
22:CU:218:GLN:HG3	22:CU:218:GLN:O	2.21	0.41
28:LC:317:LYS:HD2	28:LC:322:ASN:HD22	1.85	0.41
35:LN:62:TYR:HE2	35:LN:110:CYS:SG	2.41	0.41
37:LP:75:GLN:HG3	37:LP:76:TRP:CE2	2.56	0.41
41:LV:47:ARG:HD2	41:LV:50:ARG:HB2	2.02	0.41
46:Lh:30:GLU:O	46:Lh:34:LEU:HD23	2.21	0.41
46:Lh:42:SER:HB2	46:Lh:46:LEU:HG	2.03	0.41
50:Cc:78:ILE:HG23	50:Cc:79:TRP:CD1	2.56	0.41
51:Cd:191:PHE:HA	51:Cd:326:LYS:NZ	2.36	0.41
51:Cd:326:LYS:HE2	51:Cd:330:ILE:HD11	2.01	0.41
52:Ce:114:THR:HA	52:Ce:117:VAL:HG22	2.02	0.41
52:Ce:115:ARG:HD2	52:Ce:115:ARG:HA	1.91	0.41
1:C1:227:U:H2'	1:C1:228:G:C8	2.54	0.41
1:C1:248:G:H2'	1:C1:249:C:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1199:A:H2'	1:C1:1200:U:H6	1.85	0.41
1:C1:2390:U:C2	1:C1:2560:G:C6	3.09	0.41
3:C3:71:U:N3	3:C3:131:G:N1	2.68	0.41
4:CA:173:LYS:HG2	6:CC:171:THR:HG22	2.02	0.41
4:CA:191:VAL:HG11	4:CA:238:PHE:CE1	2.55	0.41
9:CG:6:ASP:O	9:CG:10:LYS:HG3	2.20	0.41
10:CH:45:TYR:HD1	10:CH:128:LYS:HD3	1.86	0.41
10:CH:101:LYS:HA	10:CH:104:ILE:HD12	2.02	0.41
10:CH:173:GLY:HA2	10:CH:251:TYR:CE1	2.56	0.41
10:CH:328:GLN:O	10:CH:331:LYS:HG3	2.20	0.41
10:CH:450:ILE:HD13	19:CQ:89:THR:HG21	2.02	0.41
11:CI:217:ARG:CZ	11:CI:219:VAL:HG12	2.51	0.41
12:CJ:160:VAL:HG22	12:CJ:165:ILE:HG13	2.03	0.41
13:CK:239:TRP:CH2	18:CP:469:PRO:HB2	2.55	0.41
15:CM:93:ILE:HG21	15:CM:248:MET:HE1	2.03	0.41
15:CM:158:GLY:C	15:CM:169:LEU:HG	2.45	0.41
20:CR:202:HIS:HD2	20:CR:208:ALA:HB1	1.84	0.41
25:Cb:298:GLU:HG2	25:Cb:299:THR:HG23	2.03	0.41
28:LC:35:ILE:HG22	28:LC:122:ALA:HB2	2.01	0.41
30:LG:145:LEU:HD22	30:LG:150:LYS:HB2	2.02	0.41
30:LG:234:LYS:HE2	30:LG:234:LYS:HB2	1.91	0.41
32:LK:19:GLY:HA2	32:LK:50:THR:HG21	2.03	0.41
32:LK:58:VAL:HG12	32:LK:74:VAL:O	2.20	0.41
32:LK:127:GLY:O	32:LK:131:GLU:HG3	2.19	0.41
32:LK:146:LYS:HG3	32:LK:151:ILE:CD1	2.50	0.41
33:LL:79:GLU:CD	33:LL:112:ASN:HD22	2.27	0.41
35:LN:27:CYS:HB2	35:LN:122:ASN:HD21	1.84	0.41
35:LN:199:LEU:HB3	35:LN:203:ARG:NH1	2.35	0.41
39:LS:90:MET:HE1	39:LS:114:HIS:CE1	2.55	0.41
50:Cc:104:ILE:HB	50:Cc:109:MET:SD	2.61	0.41
51:Cd:354:PHE:HE1	52:Ce:157:LEU:HA	1.86	0.41
53:Cf:458:LEU:HD22	53:Cf:462:LYS:NZ	2.35	0.41
54:Cg:107:VAL:HB	54:Cg:112:PRO:HD2	2.01	0.41
1:C1:287:A:H1'	47:Li:91:ARG:HH11	1.85	0.41
1:C1:366:A:O2'	1:C1:368:G:H5'	2.20	0.41
1:C1:627:U:H2'	1:C1:628:C:C6	2.55	0.41
1:C1:700:U:H2'	1:C1:701:G:O4'	2.21	0.41
1:C1:933:A:H4'	1:C1:949:G:N2	2.35	0.41
1:C1:2426:U:H2'	1:C1:2427:G:H8	1.85	0.41
1:C1:2959:C:H5''	27:LB:26:ARG:HH12	1.85	0.41
1:C1:2975:C:H5''	16:CN:8:GLU:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3265:A:H2'	1:C1:3266:G:C8	2.55	0.41
6:CC:278:LYS:O	6:CC:282:ILE:HG12	2.19	0.41
6:CC:370:TRP:HD1	6:CC:378:ARG:HG2	1.83	0.41
8:CF:28:SER:O	8:CF:32:GLU:HG2	2.21	0.41
12:CJ:398:ASP:HA	12:CJ:408:THR:HG23	2.03	0.41
14:CL:42:ASN:HB3	14:CL:43:PRO:CD	2.50	0.41
15:CM:100:LYS:HD3	15:CM:100:LYS:C	2.45	0.41
18:CP:372:PRO:HG2	18:CP:394:LYS:HE3	2.03	0.41
18:CP:441:ARG:O	18:CP:444:PRO:HD2	2.21	0.41
19:CQ:96:ILE:O	19:CQ:100:ARG:HG3	2.20	0.41
25:Cb:478:LEU:HD21	25:Cb:506:VAL:HG21	2.03	0.41
32:LK:122:SER:OG	32:LK:124:ASP:O	2.31	0.41
36:LO:28:LEU:HD11	36:LO:104:LEU:HB2	2.02	0.41
36:LO:190:LYS:HD2	36:LO:190:LYS:O	2.20	0.41
37:LP:13:LYS:O	37:LP:151:THR:HG22	2.19	0.41
37:LP:90:PHE:HD1	37:LP:90:PHE:HA	1.76	0.41
44:Le:98:ALA:HB3	44:Le:101:VAL:HG23	2.02	0.41
45:Lf:6:GLY:C	45:Lf:7:HIS:HD2	2.28	0.41
46:Lh:36:ILE:O	46:Lh:39:ILE:HG12	2.21	0.41
47:Li:65:ARG:O	47:Li:69:LEU:HG	2.21	0.41
50:Cc:109:MET:HE3	50:Cc:113:LEU:HD21	2.03	0.41
52:Ce:92:GLU:O	52:Ce:95:ASP:HB2	2.20	0.41
53:Cf:472:TRP:HE3	54:Cg:170:LEU:HD12	1.85	0.41
54:Cg:58:VAL:HG12	54:Cg:59:MET:HE2	2.02	0.41
1:C1:65:A:H1'	1:C1:77:A:H1'	2.01	0.41
1:C1:247:A:H1'	46:Lh:115:HIS:NE2	2.36	0.41
1:C1:462:C:H2'	1:C1:463:C:H6	1.86	0.41
1:C1:1220:C:HO2'	1:C1:1221:C:P	2.44	0.41
1:C1:1242:A:O2'	1:C1:1243:G:O4'	2.34	0.41
1:C1:2364:A:C5	1:C1:2365:G:H1'	2.55	0.41
1:C1:2404:G:H2'	1:C1:2405:A:H8	1.85	0.41
1:C1:2421:A:OP2	1:C1:2421:A:H8	2.04	0.41
1:C1:3051:A:H2'	1:C1:3052:U:C6	2.56	0.41
1:C1:3191:C:H2'	1:C1:3192:C:C6	2.56	0.41
2:C2:26:U:H2'	2:C2:27:U:H6	1.85	0.41
6:CC:137:TYR:CD2	6:CC:149:TYR:CD1	3.08	0.41
10:CH:86:ASP:OD1	25:Cb:599:PRO:HD2	2.21	0.41
10:CH:128:LYS:O	10:CH:132:LEU:HG	2.21	0.41
10:CH:154:GLN:O	10:CH:158:ARG:HG2	2.21	0.41
10:CH:439:GLU:OE1	19:CQ:1:MET:HG2	2.21	0.41
12:CJ:97:ARG:NH2	30:LG:195:LYS:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:183:HIS:O	12:CJ:186:ARG:NH1	2.54	0.41
13:CK:236:LYS:NZ	13:CK:237:ILE:HG22	2.35	0.41
25:Cb:370:ILE:HG13	25:Cb:420:LEU:O	2.20	0.41
30:LG:139:LEU:O	30:LG:143:VAL:HG13	2.21	0.41
33:LL:25:HIS:NE2	35:LN:198:SER:OG	2.31	0.41
33:LL:64:LYS:HD3	33:LL:65:TYR:CZ	2.56	0.41
35:LN:106:VAL:HG11	35:LN:132:VAL:HG21	2.02	0.41
35:LN:138:ASN:HA	35:LN:143:ARG:NH1	2.35	0.41
35:LN:199:LEU:HB3	35:LN:203:ARG:HH11	1.85	0.41
39:LS:162:LYS:HG3	45:Lf:38:ASP:HB3	2.02	0.41
43:LY:54:GLU:HB3	43:LY:107:LYS:HB3	2.03	0.41
48:Lj:52:LYS:HA	48:Lj:55:ARG:HG2	2.02	0.41
49:Lq:176:GLN:O	49:Lq:180:VAL:HG13	2.20	0.41
49:Lq:180:VAL:O	49:Lq:183:ILE:HG22	2.21	0.41
51:Cd:91:GLU:O	51:Cd:95:ARG:HD3	2.20	0.41
51:Cd:404:VAL:HG13	51:Cd:420:LYS:HB2	2.03	0.41
1:C1:66:A:H61	1:C1:76:G:H1'	1.86	0.41
1:C1:434:G:C2	1:C1:483:A:C2	3.08	0.41
1:C1:790:G:H2'	1:C1:791:A:C8	2.55	0.41
1:C1:1435:A:C5	1:C1:1436:A:C5	3.09	0.41
1:C1:2409:A:C6	1:C1:2462:A:N1	2.88	0.41
1:C1:2569:U:O2'	1:C1:2570:U:P	2.79	0.41
1:C1:2727:A:H2'	1:C1:2728:G:H8	1.84	0.41
1:C1:2883:C:H2'	1:C1:2884:A:H8	1.86	0.41
1:C1:3053:C:H2'	1:C1:3054:U:C6	2.55	0.41
1:C1:3107:A:H5'	27:LB:130:PHE:H	1.85	0.41
2:C2:44:A:H2'	2:C2:45:C:C6	2.55	0.41
2:C2:133:C:H2'	2:C2:134:G:C8	2.54	0.41
4:CA:192:ARG:HH12	4:CA:237:ARG:NE	2.19	0.41
4:CA:314:LEU:HD21	50:Cc:11:ILE:HG21	2.03	0.41
5:CB:31:LEU:HD23	5:CB:34:ILE:HD12	2.03	0.41
5:CB:85:LEU:HD11	5:CB:258:ASN:HB3	2.02	0.41
6:CC:326:LEU:HD13	12:CJ:124:ASN:ND2	2.32	0.41
7:CE:162:THR:HA	7:CE:165:PHE:CE2	2.56	0.41
7:CE:385:LEU:O	7:CE:411:LEU:HA	2.21	0.41
7:CE:395:LYS:O	7:CE:399:THR:HG23	2.21	0.41
8:CF:91:ARG:HA	8:CF:94:ARG:HG2	2.02	0.41
10:CH:238:SER:O	10:CH:242:LEU:HG	2.21	0.41
10:CH:401:ARG:NH1	16:CN:43:GLN:HB3	2.36	0.41
12:CJ:176:GLN:O	12:CJ:180:ILE:HG23	2.21	0.41
12:CJ:362:ASP:O	12:CJ:365:GLN:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:366:LEU:HD23	12:CJ:366:LEU:HA	1.94	0.41
16:CN:84:LEU:O	16:CN:88:LEU:HD23	2.21	0.41
18:CP:304:ARG:HG3	18:CP:574:ASP:OD1	2.21	0.41
25:Cb:141:THR:HA	25:Cb:144:PHE:CZ	2.56	0.41
25:Cb:245:ARG:HH12	25:Cb:273:ALA:H	1.69	0.41
25:Cb:396:VAL:O	25:Cb:422:VAL:HG22	2.21	0.41
25:Cb:493:ARG:HH22	25:Cb:577:GLY:N	2.19	0.41
15:LF:197:VAL:HG12	15:LF:201:PHE:CE1	2.56	0.41
30:LG:64:GLN:O	30:LG:68:LEU:HG	2.21	0.41
31:LH:34:LEU:HD12	31:LH:82:VAL:HG13	2.03	0.41
33:LL:42:LYS:HD2	33:LL:51:VAL:HG23	2.02	0.41
36:LO:154:VAL:O	36:LO:158:LEU:HD23	2.21	0.41
40:LT:134:MET:H	40:LT:134:MET:HG2	1.66	0.41
43:LY:72:VAL:O	43:LY:72:VAL:HG13	2.20	0.41
45:Lf:50:ARG:HE	45:Lf:50:ARG:HB3	1.67	0.41
49:Lq:26:ARG:HD2	49:Lq:30:GLU:HG3	2.03	0.41
51:Cd:73:ARG:HD2	51:Cd:434:PHE:HD2	1.85	0.41
51:Cd:309:PRO:HB2	51:Cd:344:VAL:HG23	2.03	0.41
52:Ce:180:GLY:O	52:Ce:183:PRO:HG3	2.20	0.41
53:Cf:449:GLU:HA	53:Cf:452:LYS:HZ2	1.85	0.41
54:Cg:38:ARG:HG2	54:Cg:52:CYS:SG	2.61	0.41
54:Cg:79:VAL:HG11	54:Cg:344:LEU:HD13	2.02	0.41
54:Cg:218:LEU:HB2	54:Cg:329:LEU:HD11	2.03	0.41
1:C1:169:A:H3'	1:C1:170:G:H8	1.86	0.41
1:C1:206:A:N6	1:C1:221:U:O4'	2.54	0.41
1:C1:233:C:H2'	1:C1:234:C:C6	2.56	0.41
1:C1:519:A:H2'	1:C1:520:G:H8	1.86	0.41
1:C1:587:G:H2'	1:C1:588:C:C6	2.56	0.41
1:C1:614:C:H2'	1:C1:615:A:C8	2.56	0.41
1:C1:700:U:O2	1:C1:735:G:H4'	2.21	0.41
1:C1:1103:U:OP1	14:CL:33:ARG:NH2	2.54	0.41
1:C1:1436:A:H2'	1:C1:1437:U:O4'	2.21	0.41
1:C1:2290:U:C2	1:C1:2291:C:C5	3.09	0.41
1:C1:3023:U:H2'	1:C1:3024:C:C6	2.56	0.41
1:C1:3105:C:H2'	1:C1:3106:G:H8	1.86	0.41
2:C2:93:U:H2'	2:C2:94:C:O4'	2.21	0.41
2:C2:107:G:C2	2:C2:116:G:C5	3.09	0.41
4:CA:89:VAL:CG1	4:CA:105:SER:HB3	2.51	0.41
5:CB:53:GLU:O	5:CB:57:VAL:HG23	2.20	0.41
6:CC:307:LYS:HA	6:CC:308:PRO:HD3	1.92	0.41
18:CP:334:VAL:HG23	18:CP:338:SER:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CQ:88:LYS:HA	19:CQ:91:LYS:HG2	2.01	0.41
20:CR:176:ALA:HB2	33:LL:126:PHE:CE1	2.56	0.41
25:Cb:456:ARG:HA	25:Cb:459:ARG:NH2	2.35	0.41
29:LE:126:LYS:HA	29:LE:129:THR:HB	2.04	0.41
15:LF:182:TYR:CZ	15:LF:203:GLN:HG2	2.56	0.41
31:LH:18:VAL:HG11	31:LH:53:ILE:HD11	2.02	0.41
32:LK:16:ARG:HA	32:LK:59:THR:HA	2.02	0.41
38:LQ:95:ILE:HG22	38:LQ:167:LEU:HD12	2.03	0.41
49:Lq:53:VAL:HG21	49:Lq:157:PHE:HE2	1.85	0.41
53:Cf:484:VAL:O	54:Cg:110:ARG:NH2	2.54	0.41
1:C1:508:G:H5'	1:C1:510:U:OP2	2.20	0.40
1:C1:575:A:H4'	45:Lf:74:THR:HB	2.04	0.40
1:C1:1344:G:H2'	1:C1:1345:A:C8	2.55	0.40
1:C1:1877:G:H2'	1:C1:1878:G:C8	2.56	0.40
1:C1:2413:G:H2'	1:C1:2414:G:N7	2.37	0.40
1:C1:2775:A:H5''	22:CU:313:LYS:HZ2	1.86	0.40
1:C1:3089:C:H2'	1:C1:3090:C:C6	2.57	0.40
1:C1:3194:U:H2'	1:C1:3195:C:C6	2.55	0.40
2:C2:14:C:H2'	2:C2:15:G:C8	2.56	0.40
2:C2:68:G:H2'	2:C2:69:U:H6	1.86	0.40
3:C3:126:G:H2'	3:C3:127:G:C8	2.56	0.40
6:CC:120:PRO:HB2	6:CC:121:PHE:CD1	2.56	0.40
7:CE:435:PRO:O	7:CE:525:HIS:NE2	2.54	0.40
7:CE:495:SER:O	7:CE:499:LYS:HG2	2.21	0.40
9:CG:116:LYS:HB3	9:CG:159:PRO:O	2.21	0.40
11:CI:269:HIS:HE2	11:CI:271:ASP:HB2	1.86	0.40
12:CJ:112:LEU:HD13	12:CJ:114:GLU:HB2	2.03	0.40
13:CK:59:ILE:HD13	13:CK:62:ARG:HH21	1.87	0.40
14:CL:53:PRO:HD2	39:LS:80:ARG:CZ	2.51	0.40
25:Cb:248:GLU:OE1	25:Cb:428:ARG:NH2	2.51	0.40
25:Cb:373:THR:OG1	25:Cb:423:THR:HG22	2.21	0.40
28:LC:147:PRO:O	52:Ce:73:MET:HG2	2.21	0.40
29:LE:80:VAL:HG11	29:LE:96:ARG:HD2	2.03	0.40
33:LL:64:LYS:HD3	33:LL:65:TYR:CE1	2.56	0.40
37:LP:116:HIS:HB3	37:LP:149:ILE:HB	2.02	0.40
41:LV:19:LEU:HD21	41:LV:100:ASN:CG	2.47	0.40
41:LV:72:ARG:O	41:LV:73:LYS:HG3	2.20	0.40
51:Cd:56:LEU:HA	51:Cd:59:LYS:NZ	2.36	0.40
54:Cg:156:LYS:NZ	54:Cg:165:ARG:HH11	2.19	0.40
54:Cg:188:PRO:HG2	54:Cg:191:SER:OG	2.21	0.40
1:C1:82:C:N3	1:C1:104:G:N1	2.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:115:A:C6	1:C1:149:U:C2	3.09	0.40
1:C1:464:G:C2	1:C1:465:G:C8	3.09	0.40
1:C1:537:G:H2'	1:C1:538:G:O4'	2.21	0.40
1:C1:662:C:H41	38:LQ:84:ARG:HH12	1.68	0.40
1:C1:724:C:O2	38:LQ:168:ARG:HD3	2.20	0.40
1:C1:735:G:C4	1:C1:736:A:C8	3.09	0.40
1:C1:1368:A:O5'	1:C1:1369:G:H5'	2.21	0.40
1:C1:1433:C:O5'	1:C1:1434:A:H8	2.04	0.40
1:C1:1862:A:C5	1:C1:1863:A:C8	3.09	0.40
1:C1:2724:U:N3	1:C1:2751:G:N1	2.69	0.40
1:C1:2729:U:N3	1:C1:2731:C:N4	2.69	0.40
1:C1:3008:U:H2'	1:C1:3009:G:H8	1.87	0.40
3:C3:18:G:H2'	3:C3:19:C:H6	1.87	0.40
3:C3:59:G:O2'	11:CI:217:ARG:NH1	2.50	0.40
5:CB:63:TRP:HA	5:CB:245:VAL:HG12	2.03	0.40
5:CB:104:PRO:HB2	5:CB:107:PHE:CB	2.51	0.40
6:CC:340:ILE:N	12:CJ:43:TYR:OH	2.37	0.40
10:CH:94:LEU:HD12	10:CH:94:LEU:HA	1.89	0.40
10:CH:169:LEU:HG	10:CH:250:LEU:HD13	2.03	0.40
11:CI:307:ALA:O	11:CI:310:GLU:HG3	2.21	0.40
14:CL:285:ARG:C	14:CL:287:ILE:H	2.29	0.40
19:CQ:23:ARG:HB3	19:CQ:27:LYS:NZ	2.36	0.40
20:CR:234:LEU:HD23	20:CR:234:LEU:H	1.86	0.40
22:CU:314:ALA:HB1	22:CU:318:GLN:HE22	1.86	0.40
23:CX:99:GLU:HG2	23:CX:135:ILE:HG22	2.03	0.40
27:LB:57:VAL:HG12	27:LB:359:TRP:CD1	2.56	0.40
27:LB:168:ARG:HH22	27:LB:169:LYS:HE2	1.86	0.40
27:LB:211:GLU:OE1	27:LB:212:LYS:N	2.55	0.40
28:LC:4:ARG:NH1	28:LC:148:GLU:OE2	2.49	0.40
28:LC:308:ARG:NH1	28:LC:308:ARG:HB2	2.36	0.40
29:LE:148:LYS:HD3	29:LE:149:PRO:O	2.21	0.40
15:LF:41:GLN:O	15:LF:45:GLU:OE1	2.39	0.40
33:LL:46:LEU:HB3	33:LL:49:ARG:HB2	2.04	0.40
33:LL:57:ILE:HG13	33:LL:115:ARG:HD2	2.03	0.40
34:LM:113:THR:O	34:LM:117:ARG:HG3	2.21	0.40
36:LO:77:ALA:O	36:LO:81:ILE:HG13	2.20	0.40
36:LO:79:SER:HB3	36:LO:108:GLU:HG3	2.04	0.40
53:Cf:526:LYS:HA	53:Cf:529:GLU:HB2	2.03	0.40
1:C1:61:A:C4	1:C1:62:A:C8	3.10	0.40
1:C1:63:A:H5''	35:LN:174:LEU:HD13	2.03	0.40
1:C1:574:G:N3	1:C1:575:A:C8	2.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1329:U:H3'	38:LQ:66:ARG:HH12	1.87	0.40
1:C1:2445:G:N2	1:C1:2447:A:H3'	2.36	0.40
1:C1:3127:A:H4'	1:C1:3130:U:C2	2.56	0.40
1:C1:3269:U:C5'	27:LB:309:MET:HG2	2.49	0.40
2:C2:97:A:P	46:Lh:68:ARG:HH22	2.45	0.40
3:C3:57:A:O2'	11:CI:190:TYR:OH	2.38	0.40
3:C3:126:G:H2'	3:C3:127:G:H8	1.87	0.40
8:CF:141:ILE:HD12	8:CF:141:ILE:H	1.86	0.40
9:CG:19:TYR:HB3	9:CG:90:LEU:HD13	2.03	0.40
11:CI:283:VAL:HA	11:CI:284:PRO:HD3	1.93	0.40
16:CN:15:VAL:HA	16:CN:61:ARG:HG2	2.03	0.40
18:CP:395:THR:HA	18:CP:398:MET:HE3	2.03	0.40
20:CR:207:ALA:O	20:CR:211:ARG:HG3	2.22	0.40
25:Cb:439:ILE:HA	25:Cb:467:TYR:O	2.21	0.40
26:Ch:294:PHE:CE1	54:Cg:189:LEU:HD21	2.48	0.40
27:LB:136:LYS:O	27:LB:141:ASN:HB2	2.21	0.40
27:LB:285:ARG:HG3	27:LB:286:ILE:N	2.36	0.40
31:LH:108:GLU:C	31:LH:110:GLY:H	2.29	0.40
36:LO:92:HIS:CE1	36:LO:93:LYS:HG3	2.57	0.40
39:LS:24:LEU:HD12	40:LT:146:ASN:HB3	2.03	0.40
44:Le:25:ARG:HG3	44:Le:26:PHE:CD2	2.56	0.40
44:Le:75:PHE:HE2	52:Ce:21:THR:HG21	1.87	0.40
47:Li:79:ARG:HD2	47:Li:93:LYS:HD2	2.03	0.40
1:C1:519:A:H2'	1:C1:520:G:C8	2.57	0.40
1:C1:584:C:H2'	1:C1:596:G:O6	2.21	0.40
1:C1:704:C:OP1	1:C1:732:A:O2'	2.28	0.40
1:C1:771:U:H2'	1:C1:772:U:C6	2.56	0.40
1:C1:1121:G:H2'	1:C1:1122:G:C8	2.56	0.40
1:C1:2344:G:N2	36:LO:69:ARG:HH22	2.20	0.40
1:C1:2367:C:H2'	1:C1:2368:C:H6	1.86	0.40
1:C1:2839:C:C2	1:C1:2840:U:C5	3.09	0.40
1:C1:3227:C:O2	1:C1:3227:C:H2'	2.22	0.40
1:C1:3230:G:H2'	1:C1:3231:A:C8	2.57	0.40
1:C1:3327:G:H5'	54:Cg:138:GLY:CA	2.51	0.40
2:C2:49:G:H2'	2:C2:50:C:C6	2.56	0.40
2:C2:76:C:H2'	2:C2:77:A:H8	1.86	0.40
4:CA:132:CYS:HB2	4:CA:177:ASP:OD1	2.21	0.40
7:CE:380:ILE:HD12	7:CE:380:ILE:HG23	1.77	0.40
7:CE:439:ARG:HG2	7:CE:443:HIS:CE1	2.56	0.40
9:CG:174:LEU:CB	13:CK:163:ARG:HH21	2.33	0.40
10:CH:98:SER:O	10:CH:99:THR:C	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:128:LYS:HE3	10:CH:128:LYS:HB3	1.86	0.40
12:CJ:367:PHE:HA	12:CJ:370:PHE:CD1	2.57	0.40
12:CJ:396:GLY:HA3	12:CJ:406:PHE:HB3	2.02	0.40
16:CN:4:ARG:HD2	16:CN:215:LEU:HD12	2.03	0.40
18:CP:525:ASN:ND2	18:CP:556:PHE:HA	2.36	0.40
25:Cb:531:ILE:HD12	25:Cb:531:ILE:H	1.86	0.40
27:LB:307:THR:HG21	27:LB:317:GLU:HG2	2.03	0.40
30:LG:58:TYR:CE2	30:LG:59:ILE:HG13	2.56	0.40
31:LH:90:MET:SD	31:LH:183:VAL:HA	2.62	0.40
35:LN:6:TYR:CD2	47:Li:53:ILE:HD11	2.52	0.40
36:LO:153:ASP:HB3	36:LO:157:ARG:NH1	2.17	0.40
50:Cc:224:ARG:O	50:Cc:228:MET:HG3	2.21	0.40
51:Cd:373:VAL:C	52:Ce:168:ARG:HH12	2.28	0.40
1:C1:133:G:O2'	1:C1:134:G:O4'	2.31	0.40
1:C1:280:C:H2'	1:C1:281:U:C6	2.56	0.40
1:C1:682:C:OP1	28:LC:272:LYS:NZ	2.39	0.40
1:C1:1271:G:C4	1:C1:1272:U:C5	3.10	0.40
1:C1:1284:A:C2	1:C1:2845:A:C2	3.09	0.40
1:C1:1396:G:H2'	1:C1:1397:U:C6	2.56	0.40
1:C1:1401:A:H5''	28:LC:197:LYS:HE3	2.04	0.40
1:C1:1402:C:C5	28:LC:193:ALA:HB2	2.56	0.40
1:C1:2458:U:H2'	1:C1:2459:C:C6	2.56	0.40
1:C1:2821:G:H1	10:CH:69:VAL:HA	1.86	0.40
4:CA:137:ARG:HH12	4:CA:167:GLN:HA	1.86	0.40
5:CB:120:LEU:HD12	5:CB:124:ILE:HD11	2.04	0.40
9:CG:54:ASN:O	9:CG:57:THR:HG22	2.21	0.40
9:CG:94:ALA:HB3	9:CG:97:LYS:NZ	2.37	0.40
9:CG:158:ASP:OD1	9:CG:159:PRO:HD2	2.20	0.40
11:CI:312:ARG:HD2	11:CI:316:ARG:NH2	2.36	0.40
13:CK:248:ASN:HD22	13:CK:251:ASN:ND2	2.20	0.40
17:CO:37:LEU:HB3	27:LB:195:PHE:CZ	2.55	0.40
20:CR:35:ILE:HD11	20:CR:172:LEU:HD11	2.03	0.40
22:CU:267:ARG:HA	22:CU:268:PRO:HD3	1.94	0.40
23:CX:96:ASP:HA	23:CX:101:MET:HE2	2.03	0.40
24:Cz:48:TRP:CD1	24:Cz:48:TRP:O	2.74	0.40
25:Cb:868:VAL:O	25:Cb:872:ARG:HG3	2.22	0.40
26:Ch:322:LYS:HE2	51:Cd:47:ARG:HD3	2.04	0.40
27:LB:188:SER:O	27:LB:192:LYS:HG2	2.22	0.40
30:LG:168:PHE:HD2	30:LG:172:LEU:HD23	1.86	0.40
34:LM:36:HIS:CD2	34:LM:37:LYS:HG3	2.57	0.40
37:LP:87:SER:O	37:LP:91:LEU:HD13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Cd:208:ASN:ND2	51:Cd:231:THR:HG21	2.37	0.40
52:Ce:107:HIS:NE2	52:Ce:111:GLN:OE1	2.54	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	
4	CA	254/316 (80%)	230 (91%)	24 (9%)	0	100	100
5	CB	256/391 (66%)	237 (93%)	18 (7%)	1 (0%)	30	61
6	CC	283/801 (35%)	271 (96%)	12 (4%)	0	100	100
7	CE	459/598 (77%)	435 (95%)	24 (5%)	0	100	100
8	CF	243/270 (90%)	230 (95%)	12 (5%)	1 (0%)	30	61
9	CG	175/184 (95%)	167 (95%)	8 (5%)	0	100	100
10	CH	474/661 (72%)	446 (94%)	26 (6%)	2 (0%)	30	61
11	CI	144/414 (35%)	133 (92%)	10 (7%)	1 (1%)	18	51
12	CJ	374/679 (55%)	363 (97%)	11 (3%)	0	100	100
13	CK	214/261 (82%)	208 (97%)	6 (3%)	0	100	100
14	CL	384/558 (69%)	347 (90%)	31 (8%)	6 (2%)	7	36
15	CM	183/249 (74%)	175 (96%)	8 (4%)	0	100	100
15	LF	238/249 (96%)	232 (98%)	5 (2%)	1 (0%)	30	61
16	CN	244/246 (99%)	234 (96%)	10 (4%)	0	100	100
17	CO	56/120 (47%)	56 (100%)	0	0	100	100
18	CP	322/751 (43%)	308 (96%)	14 (4%)	0	100	100
19	CQ	110/225 (49%)	103 (94%)	6 (6%)	1 (1%)	14	46
20	CR	159/237 (67%)	155 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	CS	86/726 (12%)	84 (98%)	2 (2%)	0	100	100
22	CU	174/451 (39%)	168 (97%)	6 (3%)	0	100	100
23	CX	86/203 (42%)	83 (96%)	3 (4%)	0	100	100
24	Cz	68/123 (55%)	68 (100%)	0	0	100	100
25	Cb	550/732 (75%)	527 (96%)	23 (4%)	0	100	100
26	Ch	69/354 (20%)	65 (94%)	4 (6%)	0	100	100
27	LB	337/392 (86%)	322 (96%)	15 (4%)	0	100	100
28	LC	360/365 (99%)	346 (96%)	14 (4%)	0	100	100
29	LE	166/200 (83%)	159 (96%)	6 (4%)	1 (1%)	21	54
30	LG	191/262 (73%)	179 (94%)	12 (6%)	0	100	100
31	LH	188/192 (98%)	180 (96%)	8 (4%)	0	100	100
32	LK	142/165 (86%)	131 (92%)	9 (6%)	2 (1%)	9	38
33	LL	115/213 (54%)	110 (96%)	5 (4%)	0	100	100
34	LM	135/142 (95%)	130 (96%)	5 (4%)	0	100	100
35	LN	179/203 (88%)	173 (97%)	6 (3%)	0	100	100
36	LO	202/204 (99%)	194 (96%)	8 (4%)	0	100	100
37	LP	150/187 (80%)	143 (95%)	7 (5%)	0	100	100
38	LQ	127/213 (60%)	121 (95%)	6 (5%)	0	100	100
39	LS	172/174 (99%)	164 (95%)	8 (5%)	0	100	100
40	LT	124/160 (78%)	116 (94%)	7 (6%)	1 (1%)	16	49
41	LV	133/139 (96%)	128 (96%)	5 (4%)	0	100	100
42	LX	20/156 (13%)	20 (100%)	0	0	100	100
43	LY	132/138 (96%)	125 (95%)	7 (5%)	0	100	100
44	Le	129/131 (98%)	126 (98%)	3 (2%)	0	100	100
45	Lf	106/109 (97%)	103 (97%)	2 (2%)	1 (1%)	14	46
46	Lh	119/935 (13%)	113 (95%)	6 (5%)	0	100	100
47	Li	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
48	Lj	72/95 (76%)	69 (96%)	3 (4%)	0	100	100
49	Lq	205/217 (94%)	181 (88%)	23 (11%)	1 (0%)	24	57
50	Cc	232/282 (82%)	223 (96%)	9 (4%)	0	100	100
51	Cd	334/436 (77%)	314 (94%)	20 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	Ce	192/336 (57%)	187 (97%)	4 (2%)	1 (0%)	24	57
53	Cf	96/570 (17%)	93 (97%)	3 (3%)	0	100	100
54	Cg	229/478 (48%)	218 (95%)	11 (5%)	0	100	100
All	All	10278/17003 (60%)	9776 (95%)	482 (5%)	20 (0%)	44	72

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	CB	104	PRO
11	CI	268	VAL
14	CL	224	ASP
14	CL	414	VAL
8	CF	238	GLU
10	CH	354	ASN
14	CL	42	ASN
14	CL	396	HIS
19	CQ	66	ASP
45	Lf	93	ALA
14	CL	439	ASP
32	LK	160	ILE
49	Lq	61	PRO
10	CH	403	LEU
14	CL	446	ASP
29	LE	160	ALA
32	LK	51	ALA
15	LF	12	ILE
40	LT	44	VAL
52	Ce	190	ILE

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	
4	CA	231/276 (84%)	231 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	CB	222/329 (68%)	222 (100%)	0	100	100
6	CC	266/710 (38%)	266 (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%)	150 (100%)	0	100	100
10	CH	424/575 (74%)	422 (100%)	2 (0%)	81	80
11	CI	121/336 (36%)	121 (100%)	0	100	100
12	CJ	332/579 (57%)	332 (100%)	0	100	100
13	CK	189/225 (84%)	189 (100%)	0	100	100
14	CL	65/458 (14%)	65 (100%)	0	100	100
15	CM	161/215 (75%)	161 (100%)	0	100	100
15	LF	206/215 (96%)	206 (100%)	0	100	100
16	CN	206/206 (100%)	206 (100%)	0	100	100
17	CO	48/99 (48%)	48 (100%)	0	100	100
18	CP	273/632 (43%)	273 (100%)	0	100	100
19	CQ	100/192 (52%)	100 (100%)	0	100	100
20	CR	144/206 (70%)	144 (100%)	0	100	100
21	CS	74/618 (12%)	74 (100%)	0	100	100
22	CU	149/376 (40%)	149 (100%)	0	100	100
23	CX	76/172 (44%)	76 (100%)	0	100	100
24	Cz	60/107 (56%)	60 (100%)	0	100	100
25	Cb	470/619 (76%)	470 (100%)	0	100	100
26	Ch	58/291 (20%)	58 (100%)	0	100	100
27	LB	290/331 (88%)	290 (100%)	0	100	100
28	LC	283/285 (99%)	283 (100%)	0	100	100
29	LE	143/166 (86%)	143 (100%)	0	100	100
30	LG	167/222 (75%)	167 (100%)	0	100	100
31	LH	167/169 (99%)	167 (100%)	0	100	100
32	LK	121/136 (89%)	121 (100%)	0	100	100
33	LL	99/176 (56%)	99 (100%)	0	100	100
34	LM	115/117 (98%)	111 (96%)	4 (4%)	32	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	LN	164/180 (91%)	164 (100%)	0	100	100
36	LO	163/163 (100%)	163 (100%)	0	100	100
37	LP	125/152 (82%)	125 (100%)	0	100	100
38	LQ	110/178 (62%)	110 (100%)	0	100	100
39	LS	154/154 (100%)	154 (100%)	0	100	100
40	LT	109/135 (81%)	109 (100%)	0	100	100
41	LV	99/102 (97%)	99 (100%)	0	100	100
42	LX	12/129 (9%)	12 (100%)	0	100	100
43	LY	117/119 (98%)	117 (100%)	0	100	100
44	Le	114/114 (100%)	114 (100%)	0	100	100
45	Lf	89/90 (99%)	89 (100%)	0	100	100
46	Lh	108/781 (14%)	108 (100%)	0	100	100
47	Li	75/93 (81%)	75 (100%)	0	100	100
48	Lj	61/78 (78%)	61 (100%)	0	100	100
49	Lq	179/189 (95%)	179 (100%)	0	100	100
50	Cc	204/244 (84%)	204 (100%)	0	100	100
51	Cd	291/367 (79%)	282 (97%)	9 (3%)	35	59
52	Ce	173/297 (58%)	173 (100%)	0	100	100
53	Cf	88/482 (18%)	88 (100%)	0	100	100
54	Cg	210/417 (50%)	210 (100%)	0	100	100
All	All	8667/14410 (60%)	8652 (100%)	15 (0%)	85	85

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	CH	69	VAL
10	CH	70	LEU
34	LM	130	GLU
34	LM	131	GLU
34	LM	133	LYS
34	LM	137	LYS
51	Cd	260	GLN
51	Cd	267	SER
51	Cd	269	LEU
51	Cd	284	THR

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Mol	Chain	Res	Type
51	Cd	285	LEU
51	Cd	288	THR
51	Cd	290	ARG
51	Cd	398	THR
51	Cd	406	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (96) such sidechains are listed below:

Mol	Chain	Res	Type
4	CA	48	HIS
4	CA	167	GLN
4	CA	230	ASN
4	CA	285	GLN
4	CA	295	GLN
5	CB	105	GLN
5	CB	161	ASN
5	CB	211	ASN
5	CB	273	GLN
5	CB	277	ASN
6	CC	339	HIS
7	CE	111	GLN
7	CE	138	GLN
7	CE	235	ASN
7	CE	250	ASN
7	CE	405	ASN
7	CE	504	ASN
9	CG	92	GLN
9	CG	106	GLN
9	CG	118	HIS
9	CG	167	GLN
10	CH	53	GLN
10	CH	123	GLN
10	CH	244	HIS
10	CH	268	ASN
10	CH	411	ASN
10	CH	429	ASN
11	CI	256	HIS
12	CJ	15	ASN
12	CJ	84	GLN
12	CJ	124	ASN
12	CJ	135	GLN
12	CJ	485	HIS

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Mol	Chain	Res	Type
13	CK	10	HIS
13	CK	35	ASN
13	CK	38	ASN
13	CK	55	HIS
13	CK	248	ASN
14	CL	42	ASN
14	CL	68	GLN
16	CN	95	GLN
18	CP	316	HIS
18	CP	365	GLN
18	CP	482	GLN
18	CP	525	ASN
18	CP	569	HIS
20	CR	6	GLN
20	CR	187	GLN
20	CR	196	GLN
21	CS	682	ASN
22	CU	318	GLN
22	CU	320	GLN
22	CU	364	ASN
23	CX	73	GLN
25	Cb	402	GLN
25	Cb	446	GLN
25	Cb	516	ASN
25	Cb	585	GLN
27	LB	183	GLN
27	LB	319	ASN
27	LB	368	HIS
27	LB	379	GLN
28	LC	60	GLN
28	LC	118	GLN
28	LC	217	HIS
28	LC	228	ASN
28	LC	315	GLN
28	LC	322	ASN
15	LF	119	ASN
15	LF	203	GLN
30	LG	62	GLN
30	LG	92	GLN
30	LG	140	ASN
31	LH	44	ASN
31	LH	76	ASN

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Mol	Chain	Res	Type
33	LL	66	ASN
33	LL	114	GLN
34	LM	5	ASN
34	LM	36	HIS
35	LN	15	GLN
37	LP	72	GLN
37	LP	118	GLN
39	LS	89	ASN
40	LT	131	GLN
41	LV	134	ASN
46	Lh	50	HIS
49	Lq	27	ASN
50	Cc	37	GLN
50	Cc	72	ASN
50	Cc	80	GLN
50	Cc	257	ASN
51	Cd	250	ASN
51	Cd	260	GLN
51	Cd	347	HIS
52	Ce	88	GLN
54	Cg	89	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2116/3341 (63%)	485 (22%)	20 (0%)
2	C2	157/256 (61%)	36 (22%)	1 (0%)
3	C3	96/161 (59%)	32 (33%)	2 (2%)
All	All	2369/3758 (63%)	553 (23%)	23 (0%)

All (553) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	6	A
1	C1	20	A
1	C1	26	A
1	C1	40	A
1	C1	43	A
1	C1	49	A
1	C1	60	A
1	C1	65	A

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Mol	Chain	Res	Type
1	C1	66	A
1	C1	67	A
1	C1	92	G
1	C1	96	G
1	C1	105	C
1	C1	108	C
1	C1	110	G
1	C1	113	C
1	C1	116	A
1	C1	122	A
1	C1	127	G
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	141	U
1	C1	143	G
1	C1	150	G
1	C1	151	G
1	C1	152	A
1	C1	163	U
1	C1	176	U
1	C1	179	U
1	C1	183	U
1	C1	189	G
1	C1	193	C
1	C1	203	C
1	C1	206	A
1	C1	211	G
1	C1	212	A
1	C1	224	A
1	C1	232	G
1	C1	241	G
1	C1	242	U
1	C1	244	U
1	C1	249	C
1	C1	253	U
1	C1	258	C
1	C1	261	G

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Mol	Chain	Res	Type
1	C1	262	U
1	C1	275	G
1	C1	276	A
1	C1	277	A
1	C1	287	A
1	C1	299	A
1	C1	300	A
1	C1	302	U
1	C1	308	U
1	C1	309	A
1	C1	310	A
1	C1	315	A
1	C1	321	C
1	C1	325	C
1	C1	331	C
1	C1	342	C
1	C1	343	A
1	C1	368	G
1	C1	376	A
1	C1	377	A
1	C1	378	A
1	C1	390	U
1	C1	391	A
1	C1	393	C
1	C1	394	A
1	C1	395	C
1	C1	413	G
1	C1	414	A
1	C1	432	U
1	C1	434	G
1	C1	437	C
1	C1	445	A
1	C1	447	C
1	C1	448	A
1	C1	450	C
1	C1	457	U
1	C1	458	C
1	C1	460	C
1	C1	462	C
1	C1	467	G
1	C1	468	C
1	C1	474	G

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Mol	Chain	Res	Type
1	C1	478	G
1	C1	484	G
1	C1	485	G
1	C1	493	C
1	C1	504	G
1	C1	508	G
1	C1	509	A
1	C1	511	A
1	C1	513	A
1	C1	517	C
1	C1	520	G
1	C1	526	G
1	C1	534	U
1	C1	535	C
1	C1	539	G
1	C1	546	A
1	C1	548	A
1	C1	569	G
1	C1	587	G
1	C1	590	C
1	C1	592	G
1	C1	593	C
1	C1	596	G
1	C1	598	A
1	C1	623	C
1	C1	633	A
1	C1	635	C
1	C1	664	A
1	C1	668	U
1	C1	678	A
1	C1	684	G
1	C1	692	A
1	C1	693	A
1	C1	698	A
1	C1	699	G
1	C1	703	A
1	C1	706	U
1	C1	708	G
1	C1	718	U
1	C1	719	C
1	C1	721	G
1	C1	731	G

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Mol	Chain	Res	Type
1	C1	739	C
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	762	G
1	C1	765	G
1	C1	766	G
1	C1	767	A
1	C1	798	A
1	C1	799	C
1	C1	918	G
1	C1	925	A
1	C1	931	G
1	C1	932	A
1	C1	934	G
1	C1	935	U
1	C1	940	C
1	C1	941	U
1	C1	942	C
1	C1	943	A
1	C1	944	G
1	C1	958	A
1	C1	959	C
1	C1	960	C
1	C1	963	C
1	C1	972	G
1	C1	973	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	1039	A
1	C1	1045	G
1	C1	1046	A
1	C1	1047	A

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Mol	Chain	Res	Type
1	C1	1048	G
1	C1	1054	G
1	C1	1057	A
1	C1	1063	C
1	C1	1069	G
1	C1	1075	A
1	C1	1076	U
1	C1	1077	U
1	C1	1078	C
1	C1	1079	G
1	C1	1080	A
1	C1	1085	A
1	C1	1086	U
1	C1	1097	G
1	C1	1098	G
1	C1	1114	C
1	C1	1126	U
1	C1	1135	A
1	C1	1141	A
1	C1	1142	C
1	C1	1160	G
1	C1	1164	G
1	C1	1174	C
1	C1	1175	A
1	C1	1178	C
1	C1	1179	A
1	C1	1180	C
1	C1	1185	A
1	C1	1186	A
1	C1	1189	G
1	C1	1202	U
1	C1	1204	G
1	C1	1211	G
1	C1	1217	U
1	C1	1218	G
1	C1	1220	C
1	C1	1221	C
1	C1	1223	U
1	C1	1224	G
1	C1	1225	G
1	C1	1227	A
1	C1	1228	G

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Mol	Chain	Res	Type
1	C1	1240	U
1	C1	1241	A
1	C1	1245	A
1	C1	1247	U
1	C1	1253	A
1	C1	1254	C
1	C1	1263	U
1	C1	1268	A
1	C1	1269	A
1	C1	1271	G
1	C1	1272	U
1	C1	1277	G
1	C1	1286	A
1	C1	1287	U
1	C1	1289	G
1	C1	1312	A
1	C1	1313	U
1	C1	1330	A
1	C1	1331	G
1	C1	1332	A
1	C1	1333	A
1	C1	1334	A
1	C1	1335	C
1	C1	1336	G
1	C1	1337	A
1	C1	1369	G
1	C1	1374	G
1	C1	1381	A
1	C1	1382	G
1	C1	1384	G
1	C1	1399	G
1	C1	1400	A
1	C1	1401	A
1	C1	1416	G
1	C1	1418	U
1	C1	1419	C
1	C1	1433	C
1	C1	1435	A
1	C1	1856	U
1	C1	1857	G
1	C1	1859	U
1	C1	1860	A

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Mol	Chain	Res	Type
1	C1	1865	A
1	C1	1866	A
1	C1	1868	G
1	C1	1875	A
1	C1	1883	C
1	C1	1885	G
1	C1	1886	C
1	C1	2088	A
1	C1	2285	G
1	C1	2287	G
1	C1	2288	A
1	C1	2294	A
1	C1	2297	G
1	C1	2302	U
1	C1	2309	U
1	C1	2310	A
1	C1	2324	C
1	C1	2334	A
1	C1	2338	G
1	C1	2347	A
1	C1	2356	G
1	C1	2365	G
1	C1	2388	U
1	C1	2393	C
1	C1	2396	U
1	C1	2397	G
1	C1	2399	G
1	C1	2402	A
1	C1	2407	A
1	C1	2410	G
1	C1	2413	G
1	C1	2414	G
1	C1	2415	U
1	C1	2421	A
1	C1	2422	U
1	C1	2423	A
1	C1	2424	G
1	C1	2428	G
1	C1	2429	G
1	C1	2430	A
1	C1	2431	G
1	C1	2432	C

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Mol	Chain	Res	Type
1	C1	2433	U
1	C1	2434	U
1	C1	2435	C
1	C1	2436	G
1	C1	2438	C
1	C1	2439	G
1	C1	2443	G
1	C1	2449	U
1	C1	2452	C
1	C1	2455	U
1	C1	2456	A
1	C1	2457	C
1	C1	2458	U
1	C1	2459	C
1	C1	2460	C
1	C1	2464	U
1	C1	2465	G
1	C1	2466	U
1	C1	2467	U
1	C1	2484	G
1	C1	2551	A
1	C1	2558	C
1	C1	2560	G
1	C1	2564	G
1	C1	2565	G
1	C1	2570	U
1	C1	2729	U
1	C1	2730	C
1	C1	2735	G
1	C1	2739	U
1	C1	2749	G
1	C1	2759	A
1	C1	2761	A
1	C1	2766	A
1	C1	2776	U
1	C1	2777	A
1	C1	2778	A
1	C1	2782	G
1	C1	2783	C
1	C1	2784	U
1	C1	2800	U
1	C1	2802	C

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Mol	Chain	Res	Type
1	C1	2803	A
1	C1	2804	U
1	C1	2805	A
1	C1	2818	U
1	C1	2819	U
1	C1	2820	U
1	C1	2832	G
1	C1	2833	U
1	C1	2834	C
1	C1	2835	G
1	C1	2845	A
1	C1	2847	C
1	C1	2852	C
1	C1	2856	G
1	C1	2857	C
1	C1	2862	U
1	C1	2869	A
1	C1	2872	G
1	C1	2879	U
1	C1	2882	U
1	C1	2887	C
1	C1	2888	A
1	C1	2889	C
1	C1	2893	U
1	C1	2894	A
1	C1	2899	A
1	C1	2900	C
1	C1	2901	G
1	C1	2902	U
1	C1	2916	A
1	C1	2917	C
1	C1	2919	G
1	C1	2922	G
1	C1	2924	G
1	C1	2925	A
1	C1	2929	A
1	C1	2930	G
1	C1	2933	U
1	C1	2936	U
1	C1	2942	C
1	C1	2950	U
1	C1	2955	U

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Mol	Chain	Res	Type
1	C1	2956	C
1	C1	2968	A
1	C1	2987	G
1	C1	3013	U
1	C1	3014	U
1	C1	3015	U
1	C1	3032	G
1	C1	3033	C
1	C1	3034	A
1	C1	3035	G
1	C1	3037	G
1	C1	3048	A
1	C1	3049	C
1	C1	3050	C
1	C1	3058	G
1	C1	3066	G
1	C1	3079	A
1	C1	3086	A
1	C1	3087	A
1	C1	3088	U
1	C1	3099	A
1	C1	3100	C
1	C1	3101	G
1	C1	3109	A
1	C1	3117	C
1	C1	3118	A
1	C1	3125	A
1	C1	3126	G
1	C1	3130	U
1	C1	3134	A
1	C1	3139	A
1	C1	3140	G
1	C1	3144	C
1	C1	3145	C
1	C1	3146	G
1	C1	3147	G
1	C1	3151	C
1	C1	3154	A
1	C1	3161	C
1	C1	3162	A
1	C1	3163	G
1	C1	3167	A

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Mol	Chain	Res	Type
1	C1	3170	C
1	C1	3171	C
1	C1	3173	C
1	C1	3181	C
1	C1	3183	C
1	C1	3185	A
1	C1	3187	G
1	C1	3199	A
1	C1	3200	A
1	C1	3205	C
1	C1	3206	G
1	C1	3209	U
1	C1	3212	C
1	C1	3213	A
1	C1	3214	A
1	C1	3225	C
1	C1	3227	C
1	C1	3228	G
1	C1	3232	U
1	C1	3233	C
1	C1	3244	C
1	C1	3248	C
1	C1	3249	G
1	C1	3253	U
1	C1	3256	A
1	C1	3257	U
1	C1	3258	G
1	C1	3259	U
1	C1	3260	G
1	C1	3262	G
1	C1	3263	A
1	C1	3264	A
1	C1	3274	U
1	C1	3281	U
1	C1	3282	A
1	C1	3285	G
1	C1	3291	U
1	C1	3292	U
1	C1	3295	U
1	C1	3296	G
1	C1	3297	U
1	C1	3298	U

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Mol	Chain	Res	Type
1	C1	3302	A
1	C1	3304	C
1	C1	3308	U
1	C1	3309	G
1	C1	3318	C
1	C1	3320	C
1	C1	3322	C
1	C1	3323	C
1	C1	3324	U
1	C1	3328	C
1	C1	3330	U
1	C1	3331	A
1	C1	3332	G
1	C1	3333	A
1	C1	3337	C
2	C2	16	G
2	C2	34	U
2	C2	35	C
2	C2	39	G
2	C2	53	A
2	C2	59	A
2	C2	62	A
2	C2	63	G
2	C2	71	A
2	C2	72	A
2	C2	77	A
2	C2	78	G
2	C2	80	A
2	C2	81	U
2	C2	84	C
2	C2	86	U
2	C2	87	G
2	C2	90	U
2	C2	91	C
2	C2	95	G
2	C2	100	U
2	C2	104	A
2	C2	106	C
2	C2	107	G
2	C2	111	A
2	C2	113	U
2	C2	116	G

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Mol	Chain	Res	Type
2	C2	124	G
2	C2	126	A
2	C2	127	U
2	C2	129	C
2	C2	136	G
2	C2	152	G
2	C2	155	A
2	C2	156	U
2	C2	158	U
3	C3	5	C
3	C3	6	A
3	C3	7	U
3	C3	8	C
3	C3	13	C
3	C3	16	G
3	C3	17	G
3	C3	18	G
3	C3	21	U
3	C3	22	G
3	C3	26	U
3	C3	31	A
3	C3	32	C
3	C3	38	G
3	C3	53	U
3	C3	54	G
3	C3	55	A
3	C3	56	A
3	C3	57	A
3	C3	58	A
3	C3	61	A
3	C3	64	G
3	C3	66	C
3	C3	67	G
3	C3	71	U
3	C3	72	C
3	C3	73	G
3	C3	75	U
3	C3	133	G
3	C3	136	A
3	C3	137	G
3	C3	142	A

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	150	G
1	C1	519	A
1	C1	702	A
1	C1	1044	A
1	C1	1046	A
1	C1	1220	C
1	C1	1223	U
1	C1	1332	A
1	C1	2301	C
1	C1	2569	U
1	C1	2888	A
1	C1	2929	A
1	C1	3078	U
1	C1	3162	A
1	C1	3204	G
1	C1	3213	A
1	C1	3257	U
1	C1	3281	U
1	C1	3296	G
1	C1	3297	U
2	C2	123	G
3	C3	6	A
3	C3	16	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 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	$\# Z > 2$
55	GTP	CH	701	-	33,34,34	1.00	3 (9%)	50,54,54	1.58	9 (18%)

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
55	GTP	CH	701	-	-	5/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	CH	701	GTP	C2-N3	2.19	1.38	1.33
55	CH	701	GTP	PB-O3B	2.15	1.61	1.59
55	CH	701	GTP	PB-O3A	2.15	1.61	1.59

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	CH	701	GTP	C5-C4-N3	-5.06	120.34	128.39
55	CH	701	GTP	C2-N3-C4	4.64	120.30	112.30
55	CH	701	GTP	N9-C4-N3	3.24	132.42	125.95
55	CH	701	GTP	C2-N1-C6	-2.87	119.91	125.11
55	CH	701	GTP	N9-C8-N7	-2.57	108.64	113.40
55	CH	701	GTP	C5-C6-N1	2.47	119.55	113.25
55	CH	701	GTP	C8-N7-C5	2.45	108.62	104.26
55	CH	701	GTP	O6-C6-C5	-2.39	120.24	126.53
55	CH	701	GTP	C3'-C2'-C1'	2.06	105.36	101.46

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	CH	701	GTP	C5'-O5'-PA-O3A
55	CH	701	GTP	C5'-O5'-PA-O2A
55	CH	701	GTP	PB-O3A-PA-O2A
55	CH	701	GTP	C4'-C5'-O5'-PA

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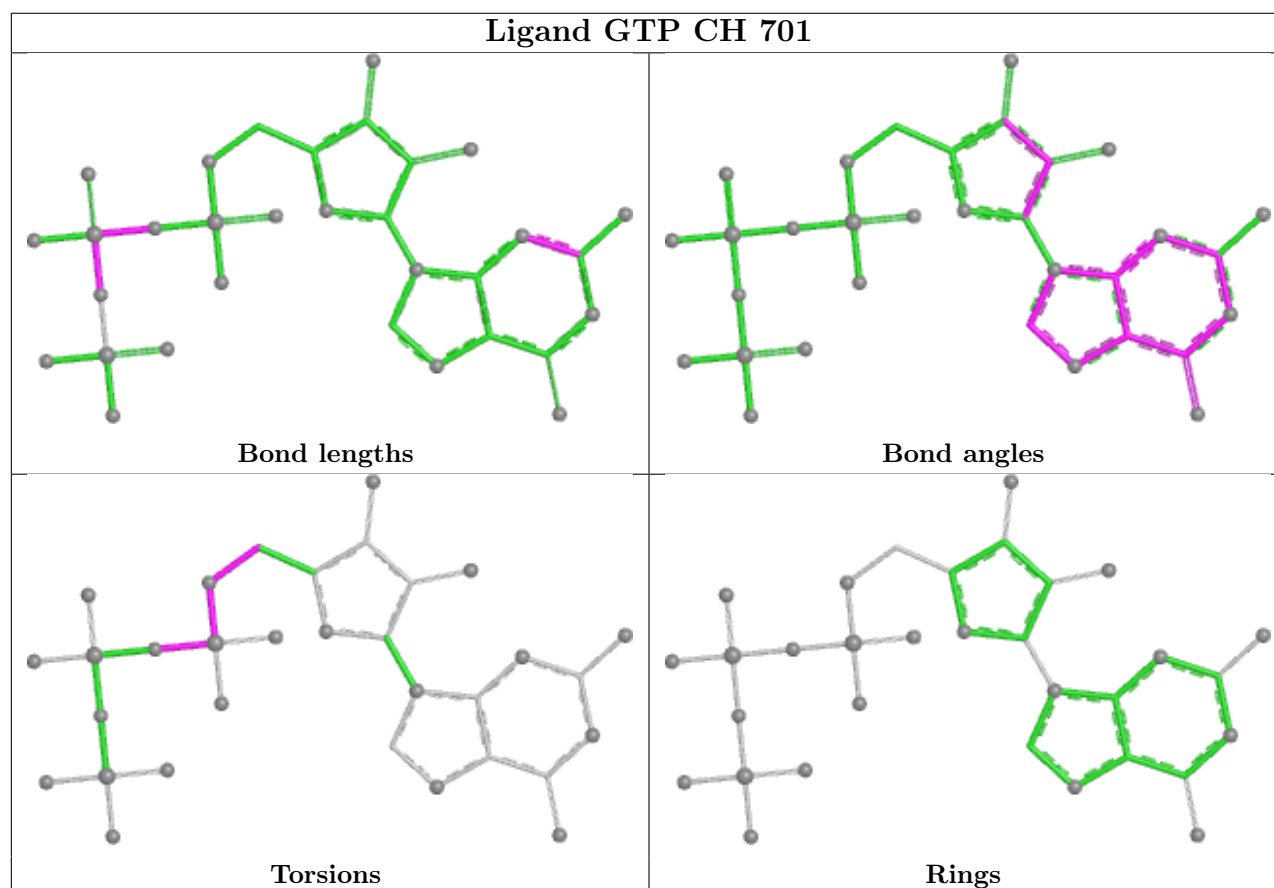
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Mol	Chain	Res	Type	Atoms
55	CH	701	GTP	PB-O3A-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

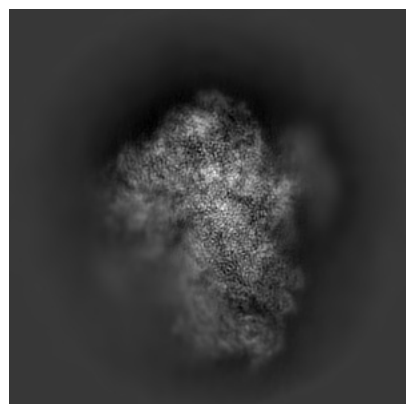
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35283. These allow visual inspection of the internal detail of the map and identification of artifacts.

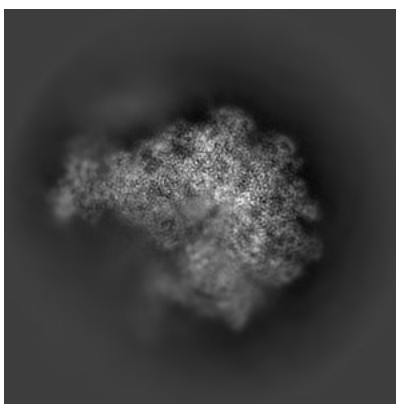
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

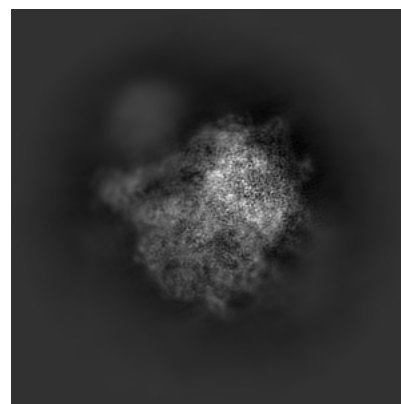
6.1.1 Primary map



X

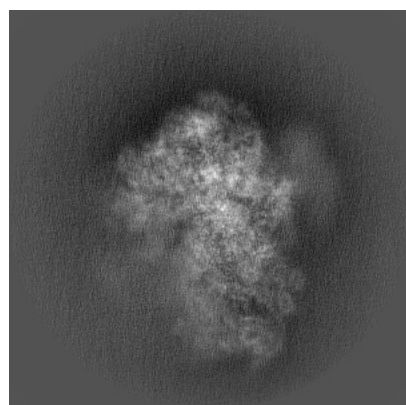


Y

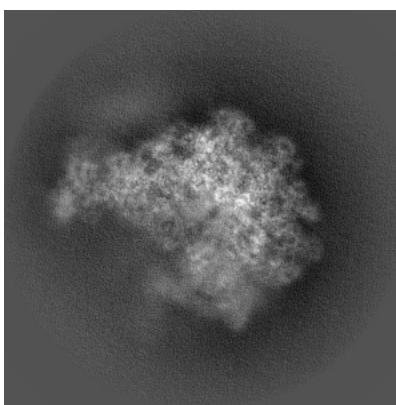


Z

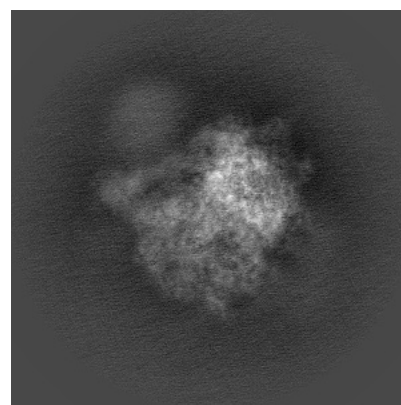
6.1.2 Raw map



X



Y

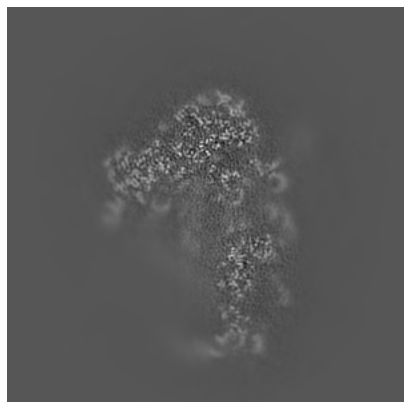


Z

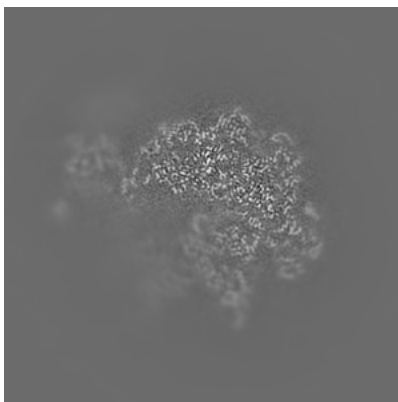
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

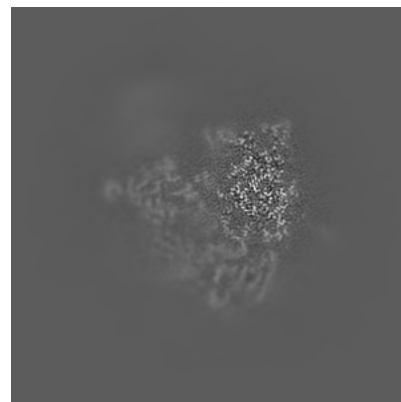
6.2.1 Primary map



X Index: 210

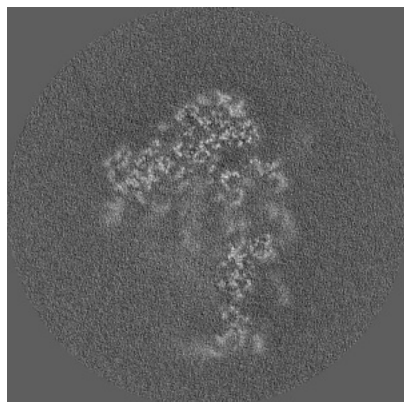


Y Index: 210

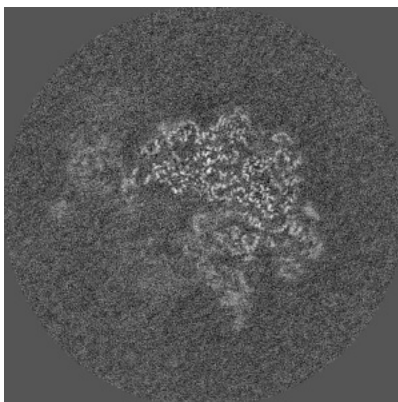


Z Index: 210

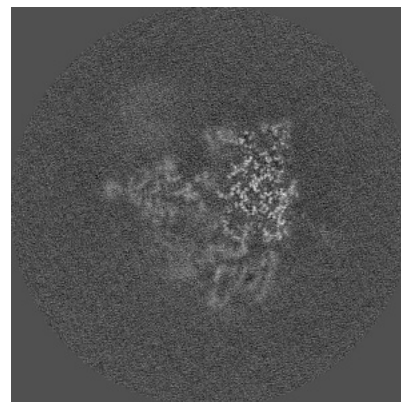
6.2.2 Raw map



X Index: 210



Y Index: 210

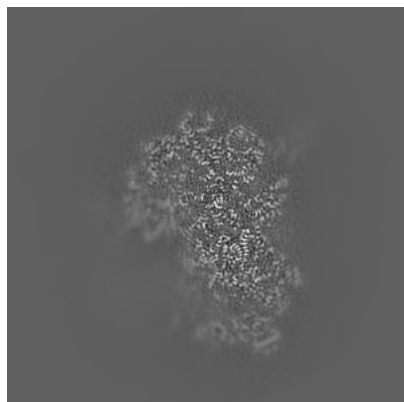


Z Index: 210

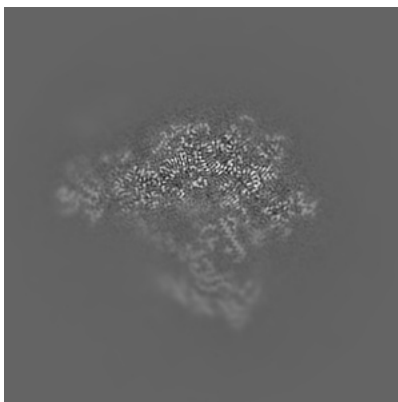
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

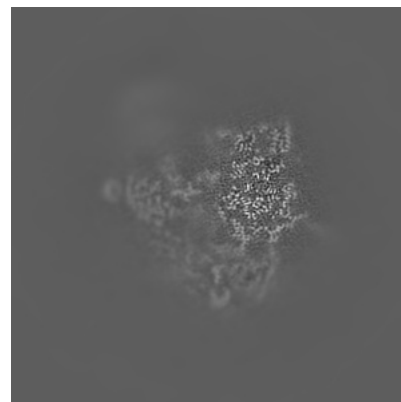
6.3.1 Primary map



X Index: 242

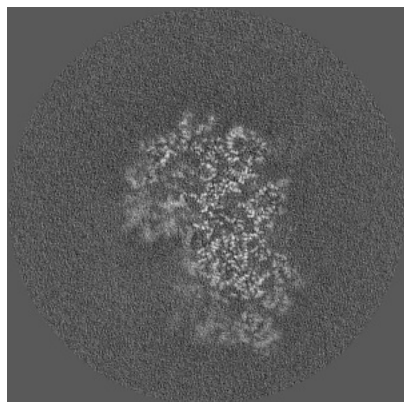


Y Index: 232

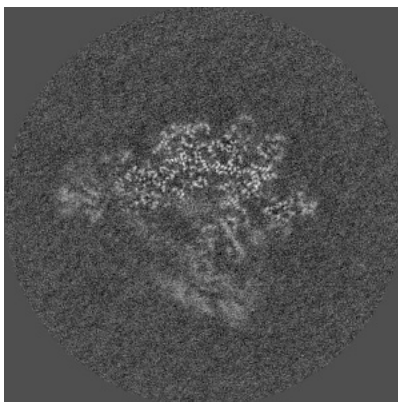


Z Index: 213

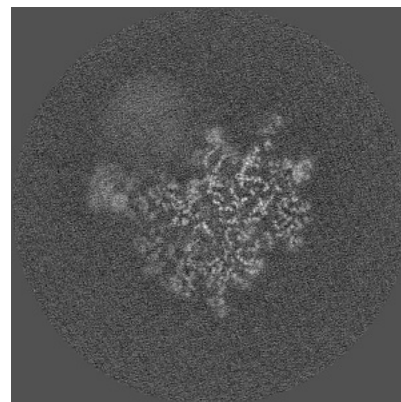
6.3.2 Raw map



X Index: 244



Y Index: 232

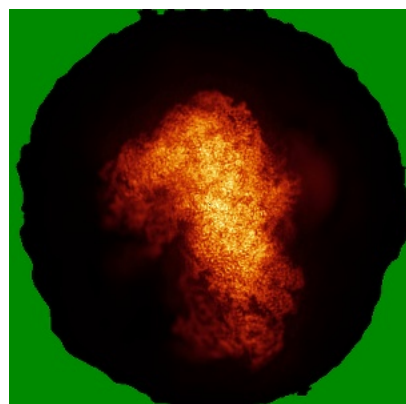


Z Index: 244

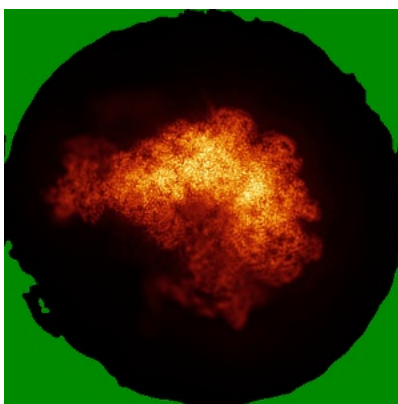
The images above show the largest variance slices of the map in three orthogonal directions.

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

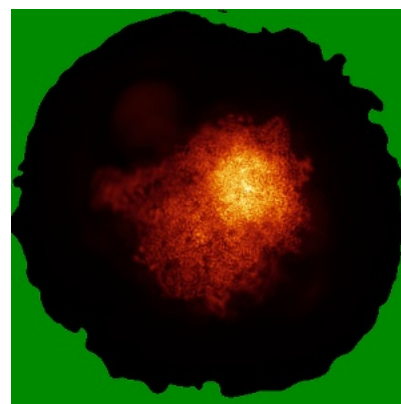
6.4.1 Primary map



X

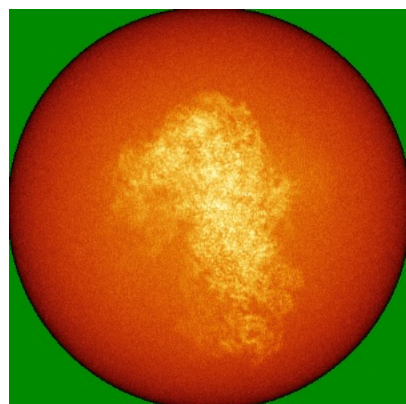


Y

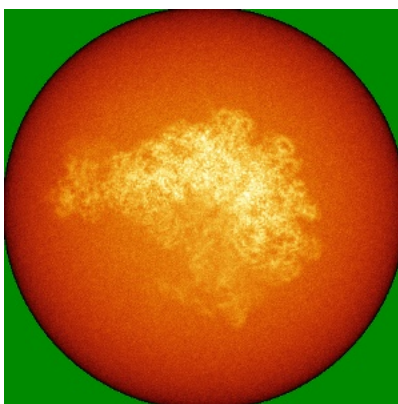


Z

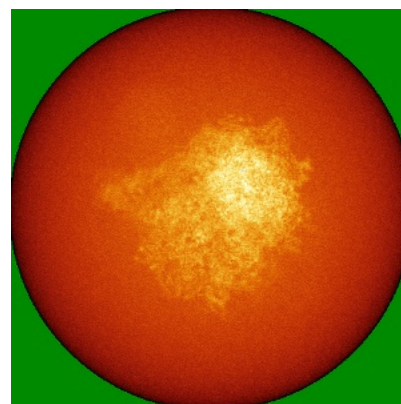
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

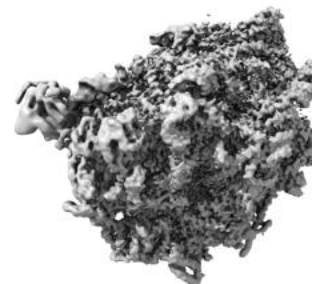
6.5.1 Primary map



X



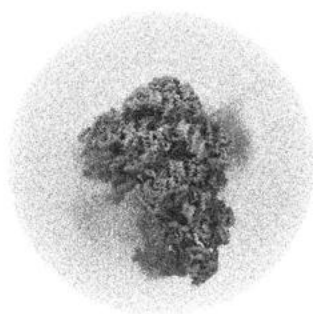
Y



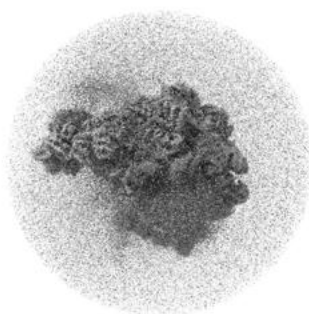
Z

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.

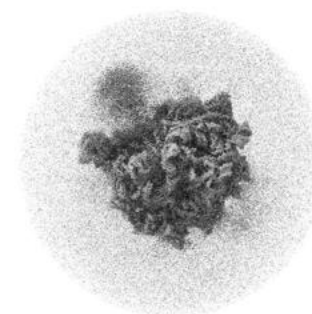
6.5.2 Raw map



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.

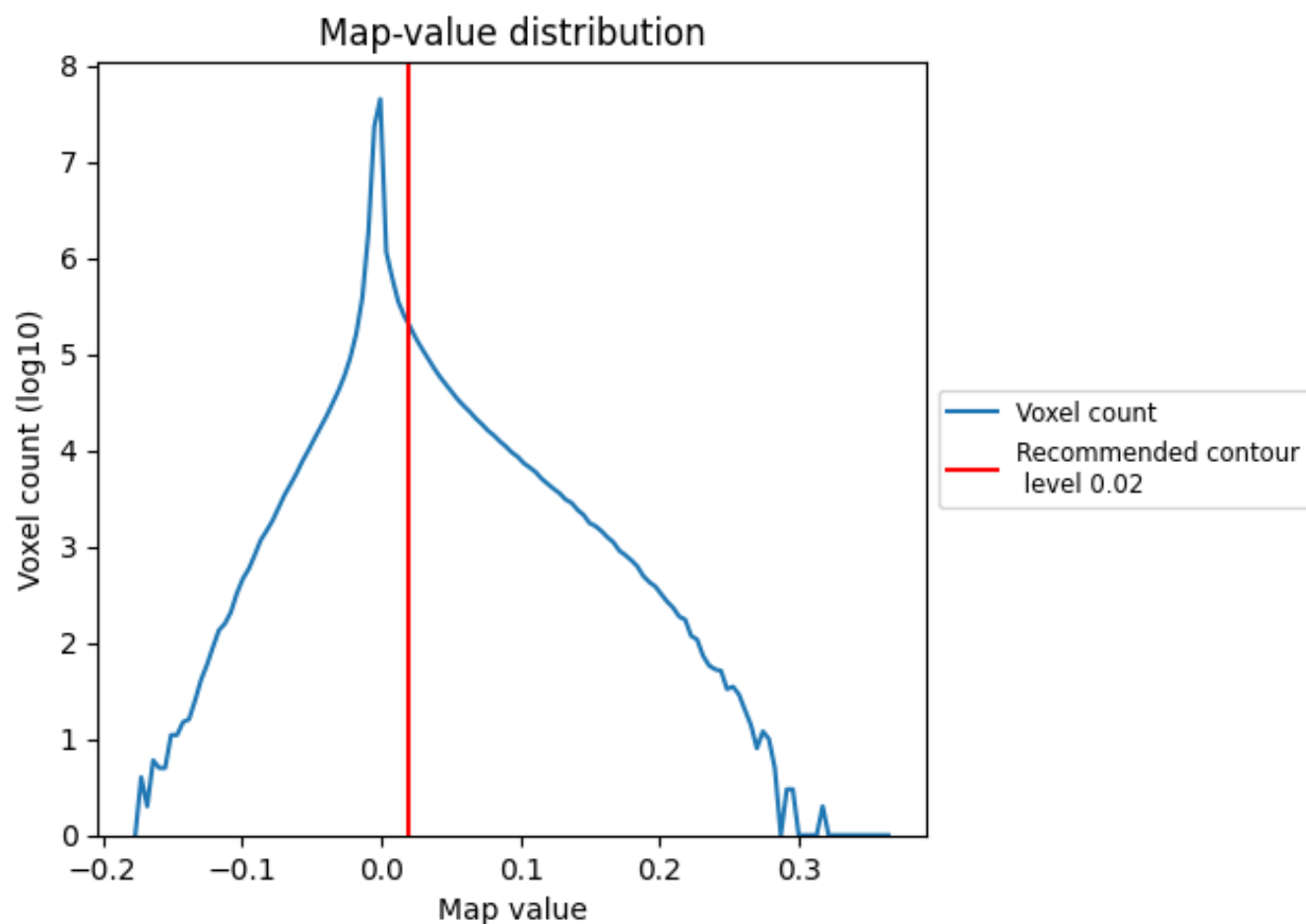
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

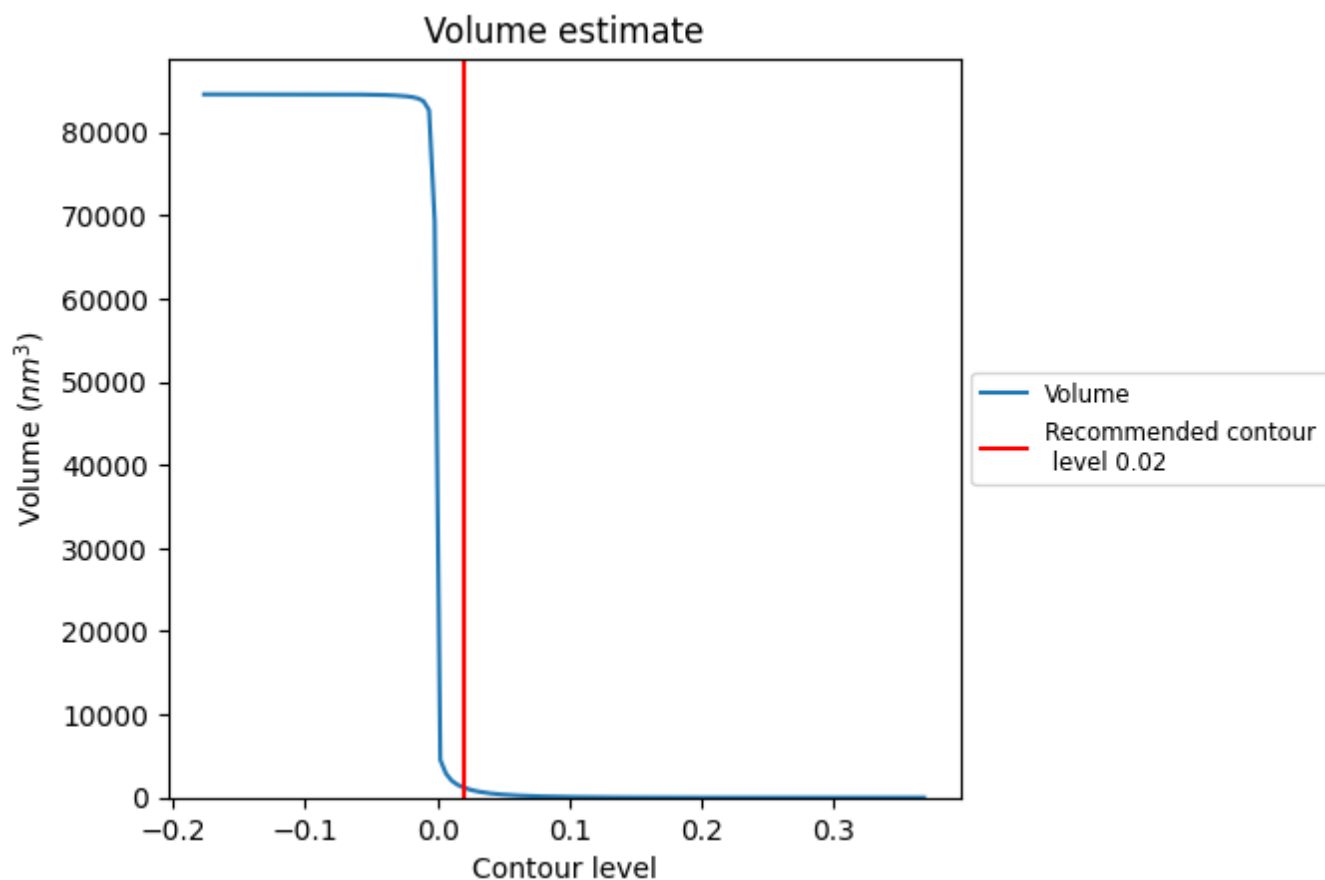
This section contains the results of statistical analysis of the map.

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.

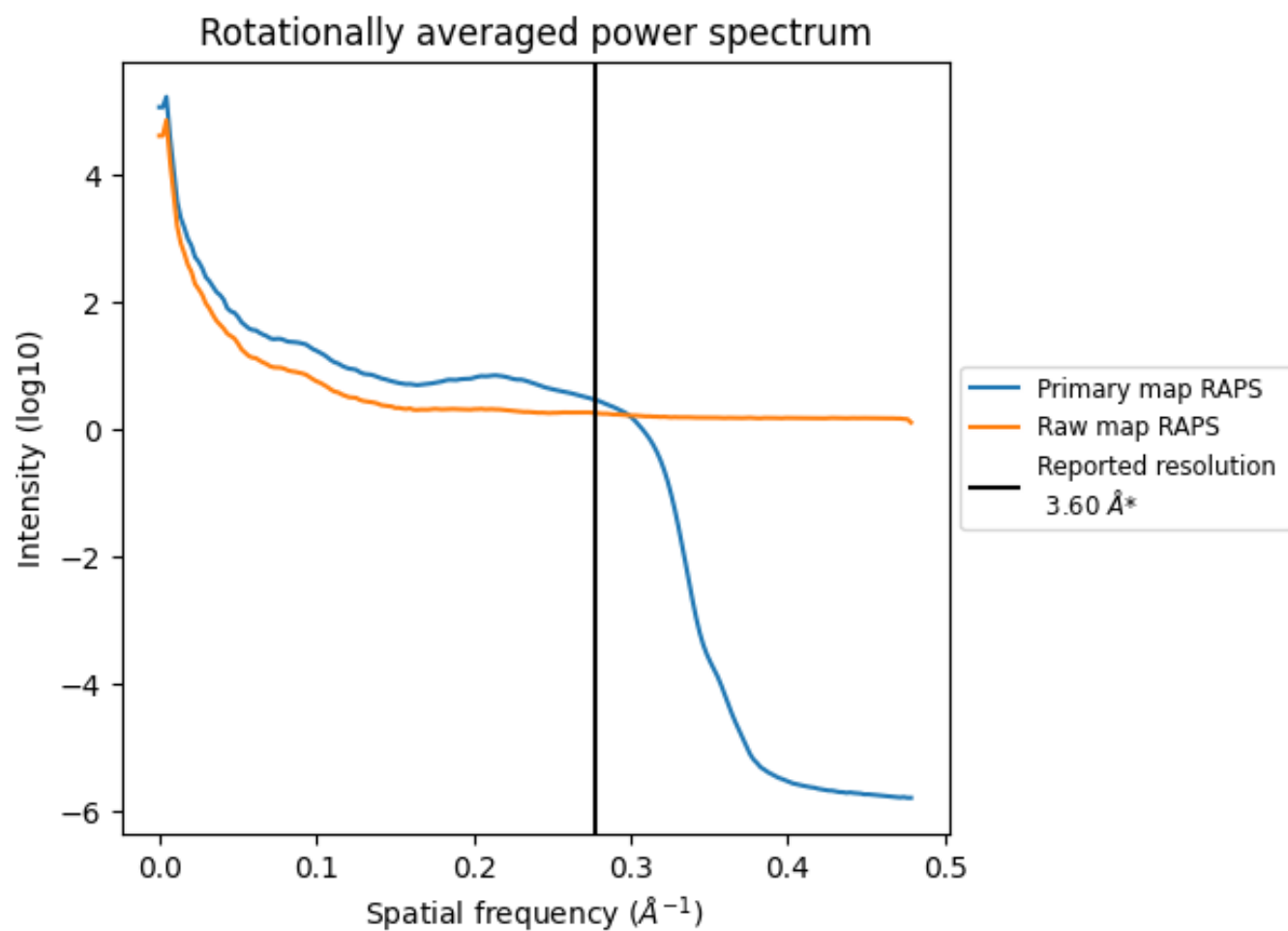
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1215 nm^3 ; this corresponds to an approximate mass of 1097 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 ⓘ

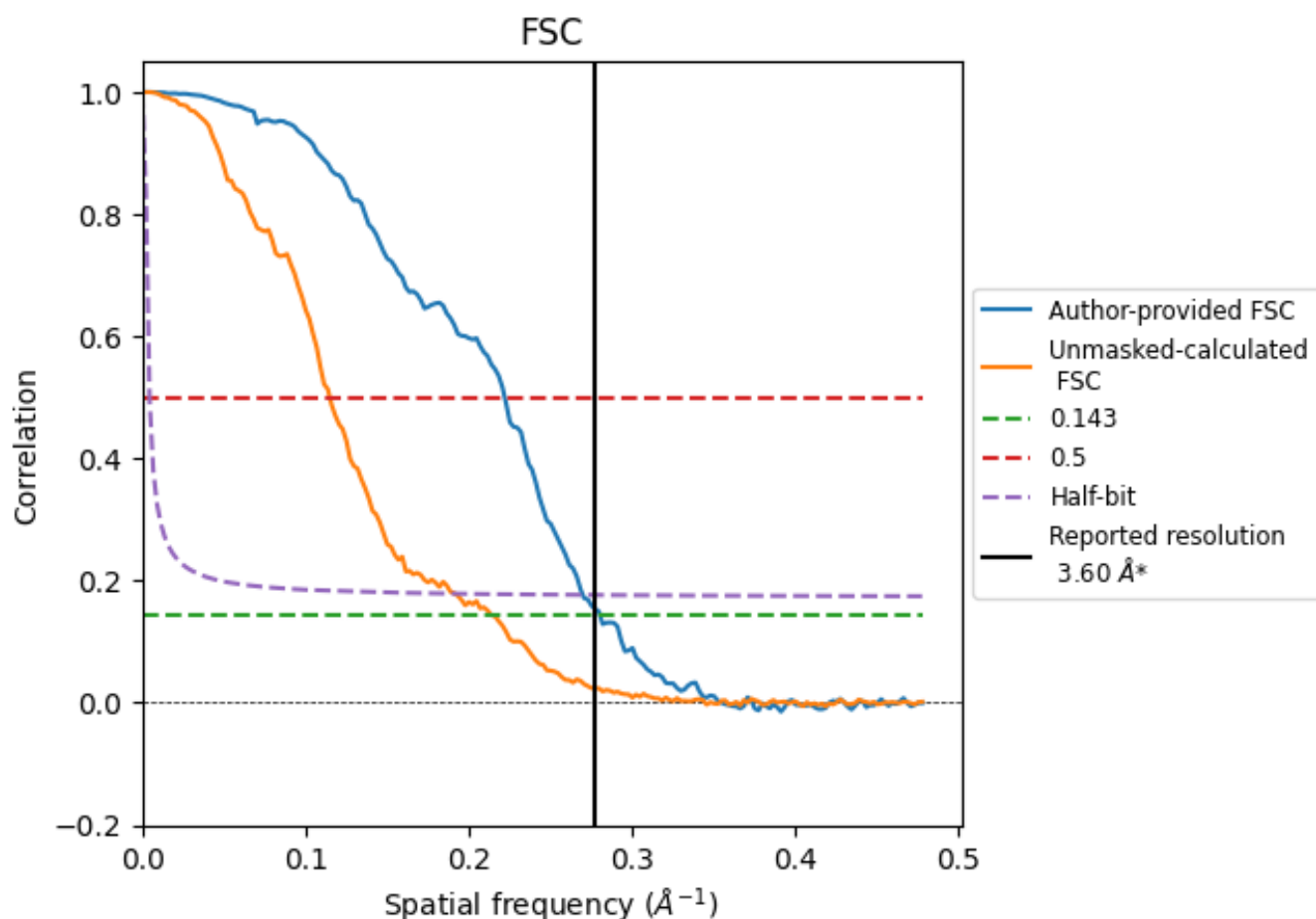


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

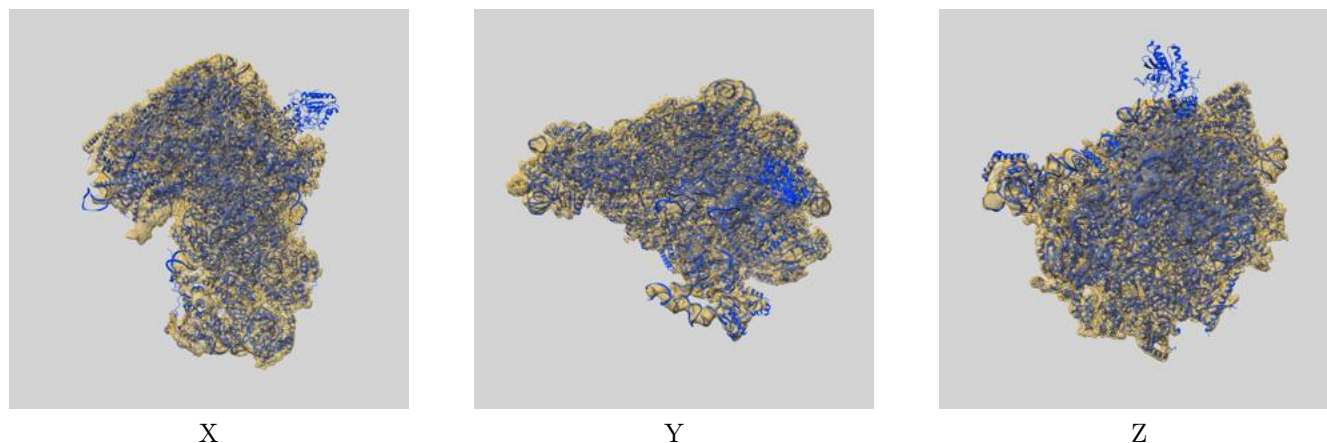
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.56	4.50	3.70
Unmasked-calculated*	4.66	8.69	5.21

*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 4.66 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

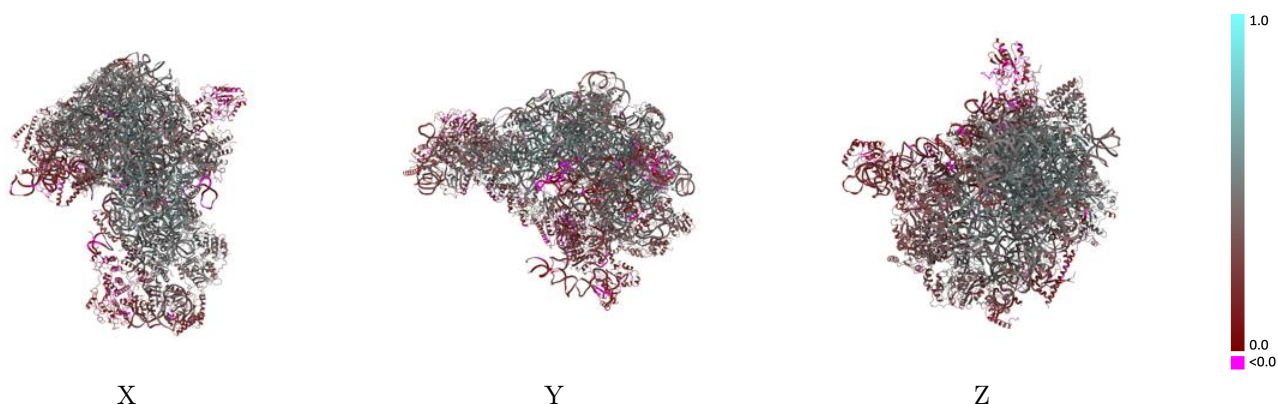
This section contains information regarding the fit between EMDB map EMD-35283 and PDB model 8I9T. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



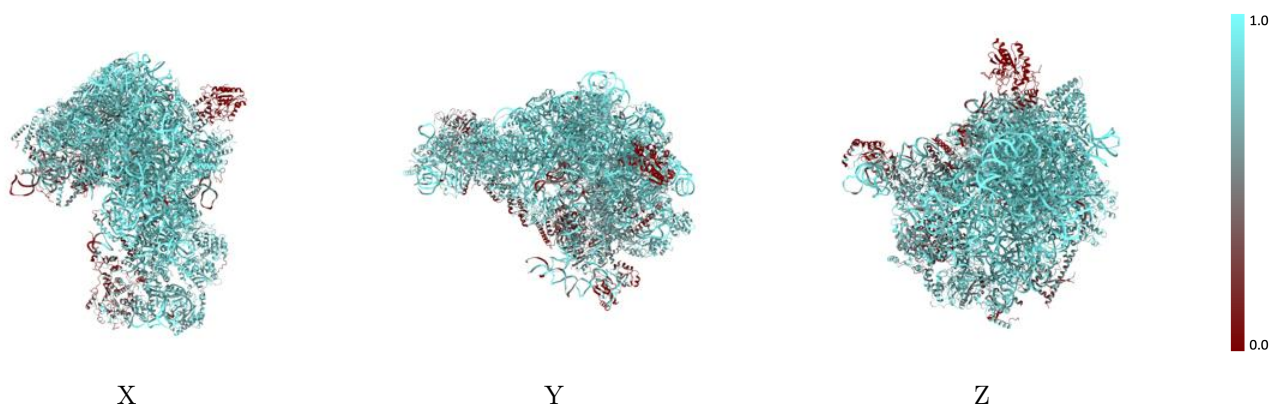
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



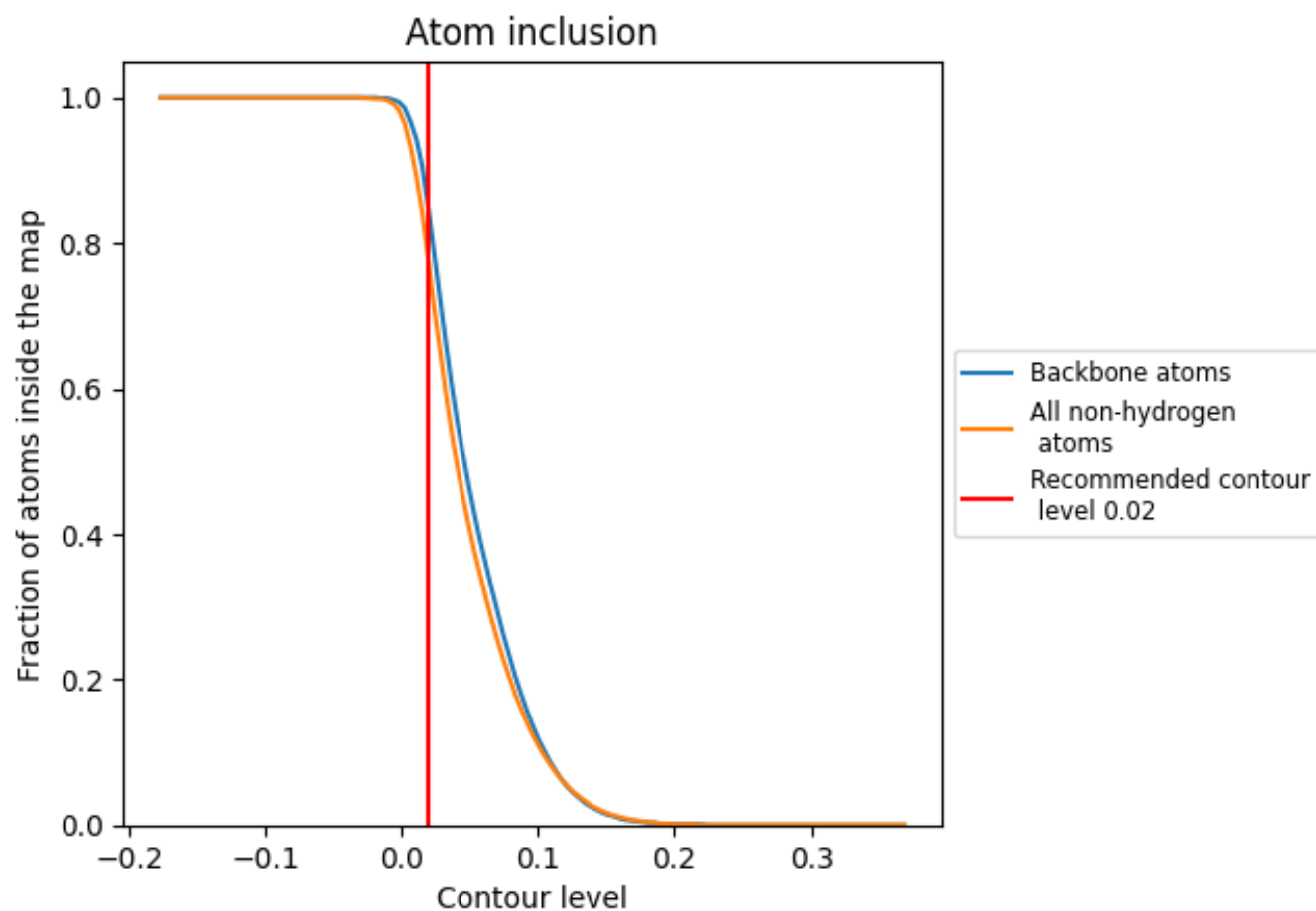
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 ⓘ



At the recommended contour level, 84% of all backbone atoms, 77% 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	 0.7710	 0.3750
C1	 0.8860	 0.4120
C2	 0.8660	 0.4100
C3	 0.8870	 0.3110
CA	 0.8320	 0.4290
CB	 0.7210	 0.2920
CC	 0.5080	 0.2730
CE	 0.7810	 0.4020
CF	 0.7680	 0.3480
CG	 0.4980	 0.1520
CH	 0.7500	 0.3580
CI	 0.7680	 0.3200
CJ	 0.4140	 0.1510
CK	 0.7620	 0.3940
CL	 0.2490	 0.1870
CM	 0.5960	 0.2100
CN	 0.7580	 0.3560
CO	 0.8400	 0.4510
CP	 0.6230	 0.2460
CQ	 0.7690	 0.3300
CR	 0.8640	 0.4410
CS	 0.2770	 0.2040
CU	 0.7450	 0.3580
CX	 0.2990	 0.1810
Cb	 0.2540	 0.2280
Cc	 0.7800	 0.4090
Cd	 0.8460	 0.4460
Ce	 0.8800	 0.4780
Cf	 0.6630	 0.2310
Cg	 0.5090	 0.1830
Ch	 0.5000	 0.1270
Cz	 0.5370	 0.3050
LB	 0.8450	 0.4430
LC	 0.8980	 0.4990
LE	 0.8530	 0.4590



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Chain	Atom inclusion	Q-score
LF	 0.8750	 0.4740
LG	 0.7730	 0.4010
LH	 0.8640	 0.4640
LK	 0.6810	 0.2650
LL	 0.9130	 0.5060
LM	 0.8740	 0.4700
LN	 0.8910	 0.4970
LO	 0.8700	 0.4780
LP	 0.8100	 0.4370
LQ	 0.8580	 0.4800
LS	 0.8750	 0.4820
LT	 0.6560	 0.3130
LV	 0.7450	 0.3920
LX	 0.1760	 0.2040
LY	 0.8640	 0.4710
Le	 0.8850	 0.5080
Lf	 0.9050	 0.5060
Lh	 0.8100	 0.4000
Li	 0.8080	 0.4200
Lj	 0.9310	 0.5150
Lq	 0.3240	 0.1390