



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 01:24 PM UTC

PDB ID : 8IA0 / pdb_00008ia0
EMDB ID : EMD-35290
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- State Puf6
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 2.70 Å(reported)
Based on initial model : .

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

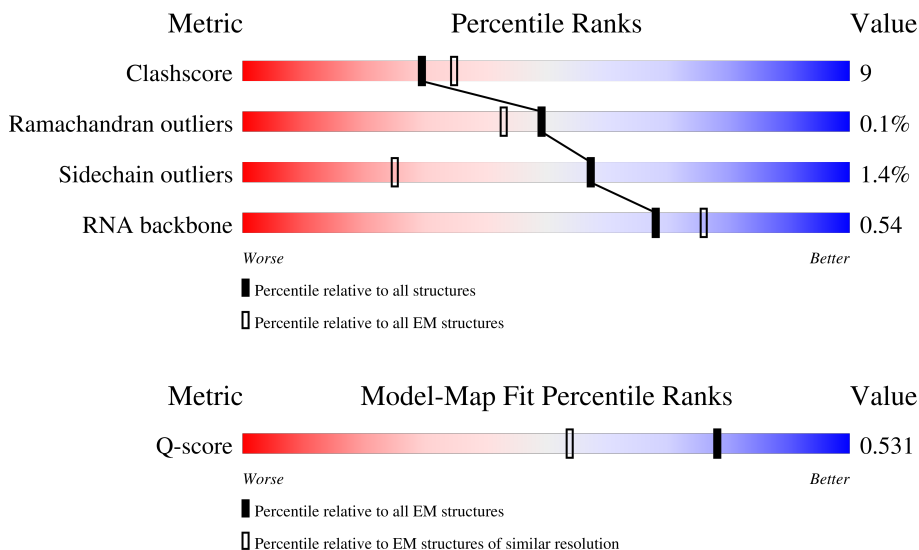
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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.



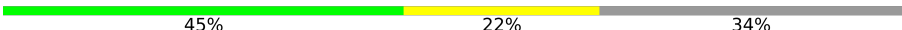
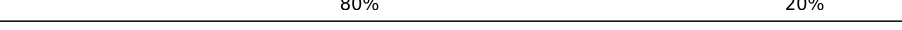
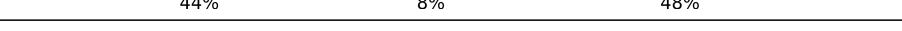
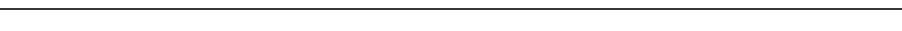
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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

Mol	Chain	Length	Quality of chain
1	C1	3341	
2	C2	319	
3	CA	316	

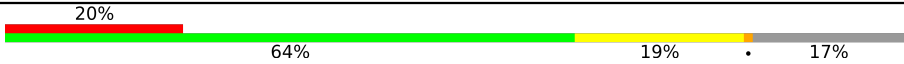
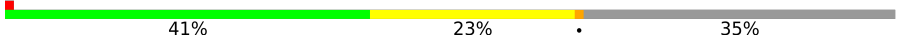
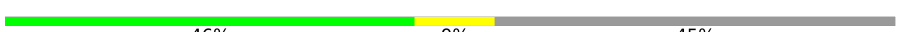
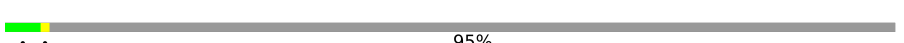
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Mol	Chain	Length	Quality of chain
4	CB	391	
5	CC	801	
6	CD	495	
7	CE	598	
8	CF	270	
9	CG	184	
10	CH	661	
11	CI	414	
12	CJ	679	
13	CK	261	
14	CL	558	
15	CM	249	
15	LF	249	
16	CN	246	
17	CO	120	
18	CP	751	
19	CQ	225	
20	CR	237	
21	CS	834	
22	CT	688	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

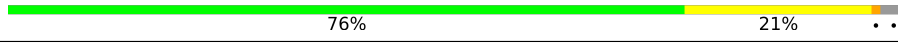
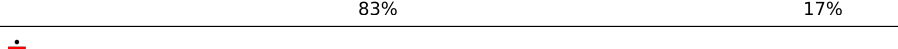
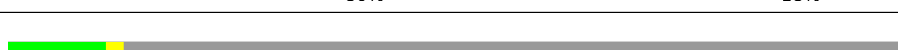
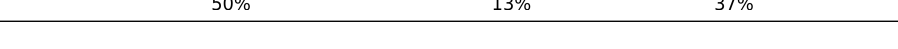
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Mol	Chain	Length	Quality of chain
28	CZ	697	
29	Ca	227	
30	Cz	123	
31	LA	254	
32	LB	392	
33	LC	365	
34	LE	200	
35	LG	262	
36	LH	192	
37	LK	165	
38	LL	213	
39	LM	142	
40	LN	203	
41	LO	204	
42	LP	187	
43	LQ	213	
44	LR	2898	
45	LS	174	
46	LT	160	
47	LU	127	
48	LV	139	
49	LX	156	
50	LY	138	
51	LZ	135	
52	Lc	108	

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Mol	Chain	Length	Quality of chain
53	Ld	120	
54	Le	131	
55	Lf	109	
56	Lg	119	
57	Lh	935	
58	Li	110	
59	Lj	95	
60	Lk	81	
61	Lp	92	
62	Ll	51	
63	Lq	217	

2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 177631 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	2928	Total	C	N	O	P	0	0
			62650	27959	11356	20407	2928		

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 7 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CE	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

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

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

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

There are 4 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

- Molecule 12 is a protein called Pescadillo homolog.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CK	229	Total	C	N	O	S	0	0
			1835	1149	362	320	4		

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

- Molecule 20 is a protein called Nucleolar protein 16.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CS	629	Total	C	N	O	S	0	0
			5082	3220	925	918	19		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	CW	540	Total	C	N	O	S		
			4310	2748	765	783	14	0	0

- Molecule 26 is a protein called 60S ribosomal subunit-like protein.

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

- Molecule 27 is a protein called Putative NOC2 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	CY	420	Total	C	N	O	S		
			3413	2191	619	591	12	0	0

- Molecule 28 is a protein called PUM-HD domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	CZ	576	Total	C	N	O	S		
			3975	2502	708	753	12	0	0

- Molecule 29 is a protein called Nucleolar protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ca	117	Total	C	N	O	S		
			982	609	199	173	1	0	0

- Molecule 30 is a protein called rRNA-processing protein.

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

- Molecule 31 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LA	166	Total	C	N	O	S	0	0
			1259	798	233	226	2		

- Molecule 32 is a protein called 60S ribosomal protein L3-like protein.

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

- Molecule 33 is a protein called 60S ribosomal protein L4-like protein.

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

- Molecule 34 is a protein called 60S ribosomal protein L6.

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

- Molecule 35 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LG	205	Total	C	N	O	S	0	0
			1651	1065	298	283	5		

- Molecule 36 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 37 is a protein called 60S ribosomal protein L12-like protein.

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

- Molecule 38 is a protein called 60S ribosomal protein L13.

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

- Molecule 39 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 40 is a protein called Ribosomal protein L15.

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

- Molecule 41 is a protein called 60S ribosomal protein L16-like protein.

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

- Molecule 42 is a protein called 60S ribosomal protein l17-like protein.

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

- Molecule 43 is a protein called Ribosomal protein L18-like protein.

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

- Molecule 44 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LR	148	Total	C	N	O	S	0	0
			1219	756	253	205	5		

- Molecule 45 is a protein called 60S ribosomal protein L20.

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

- Molecule 46 is a protein called 60S ribosomal protein l21-like protein.

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

- Molecule 47 is a protein called 60S ribosomal protein L22-like protein.

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

- Molecule 48 is a protein called 60S ribosomal protein l23-like protein.

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

- Molecule 49 is a protein called 60S ribosomal protein L25-like protein.

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

- Molecule 50 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 51 is a protein called 60S ribosomal protein L27.

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

- Molecule 52 is a protein called 60S ribosomal protein l30-like protein.

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

- Molecule 53 is a protein called Putative 60S ribosomal protein.

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

- Molecule 54 is a protein called 60S ribosomal protein L32-like protein.

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

- Molecule 55 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 56 is a protein called Ribosomal protein l34-like protein.

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

- Molecule 57 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 58 is a protein called 60S ribosomal protein L36.

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

- Molecule 59 is a protein called Ribosomal protein L37.

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

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

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

There are 13 discrepancies between the modelled and reference sequences:

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

- Molecule 61 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Lp	58	Total	C	N	O	S	0	0
			436	266	85	79	6		

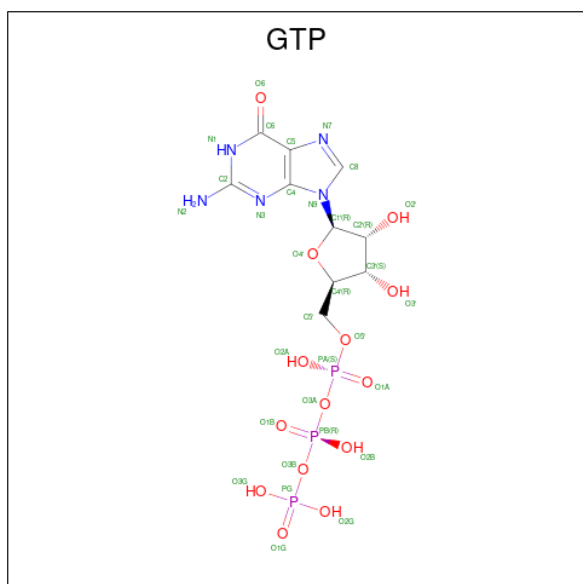
- Molecule 62 is a protein called 60S ribosomal protein L39.

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

- Molecule 63 is a protein called Ribosomal protein.

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

- Molecule 64 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

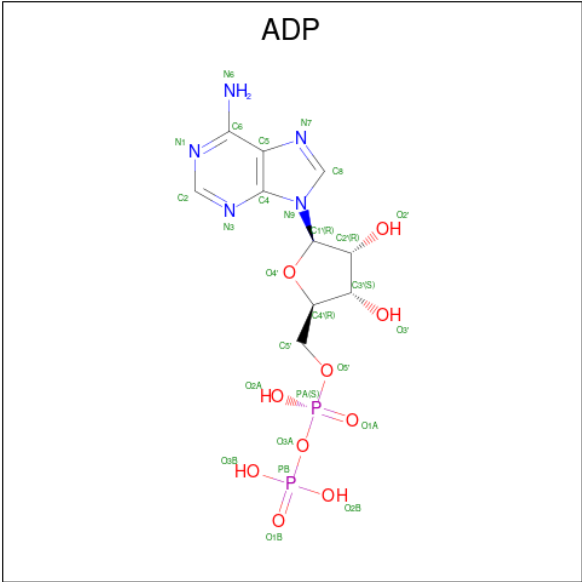


Mol	Chain	Residues	Atoms					AltConf
64	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
65	CQ	1	Total	Zn	0
			1	1	
65	Lj	1	Total	Zn	0
			1	1	
65	Lp	1	Total	Zn	0
			1	1	

- Molecule 66 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
66	CW	1	Total	C	N	O	P	0
			27	10	5	10	2	

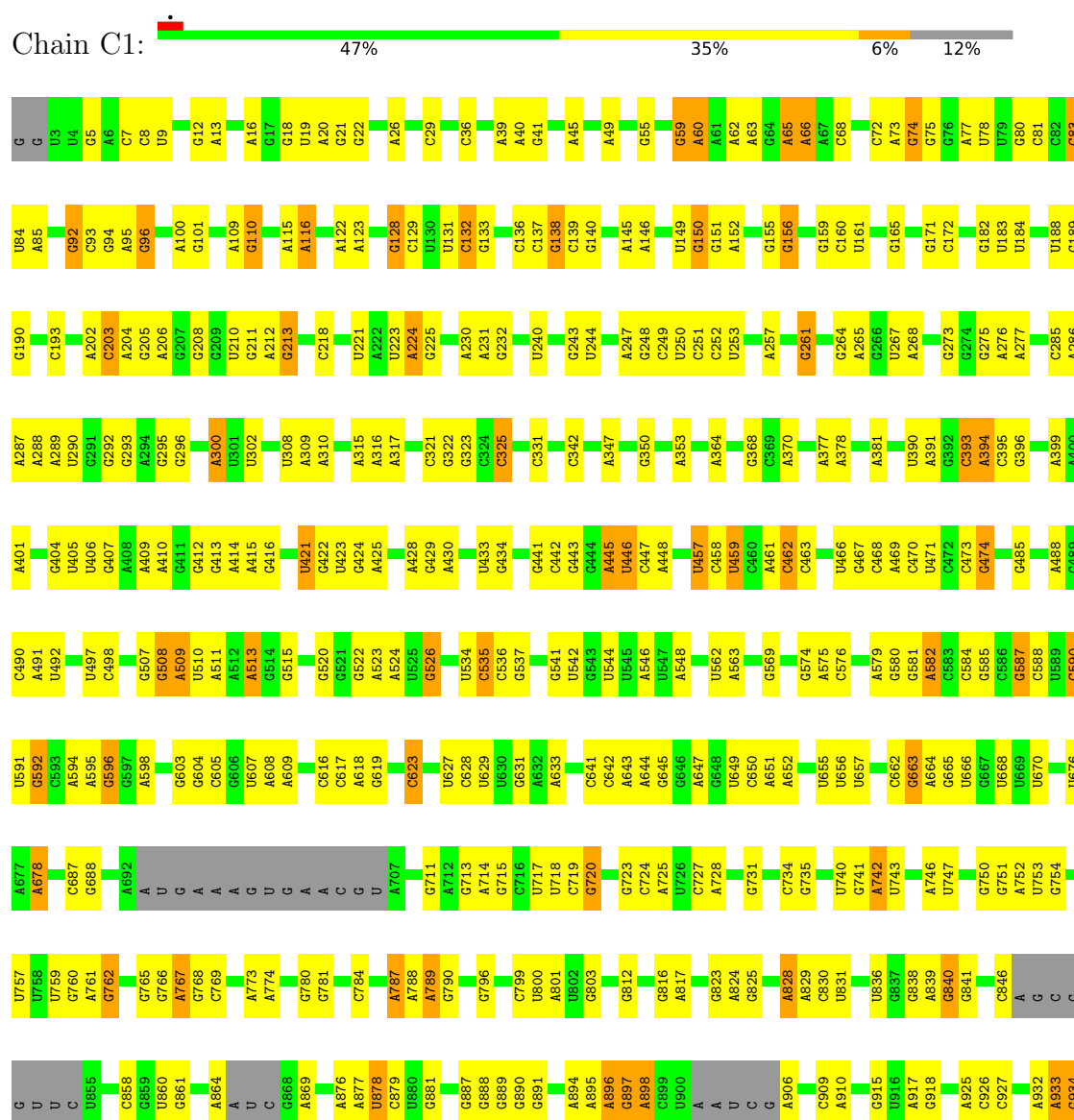
- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
67	CW	1	Total	Mg	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)

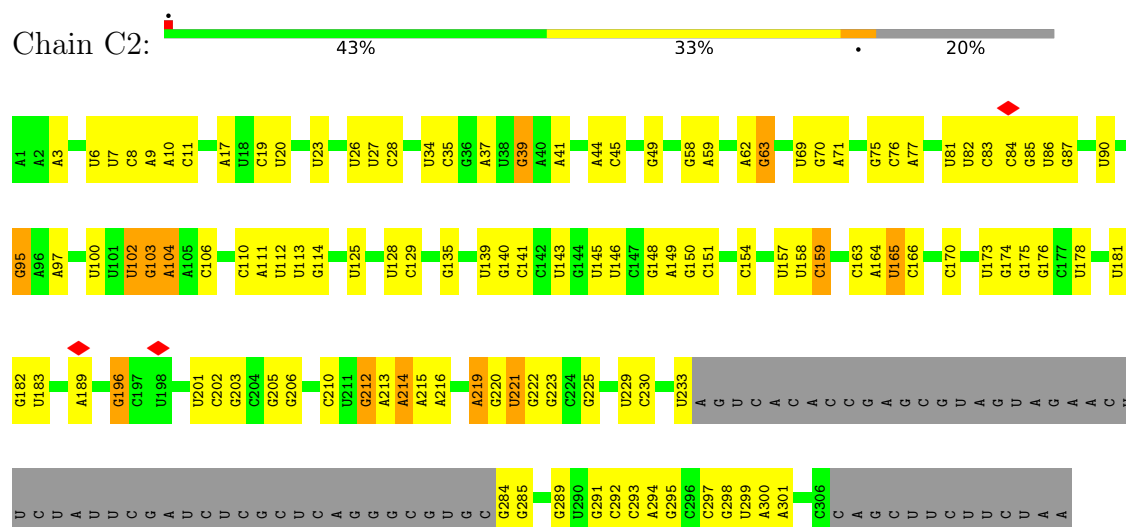




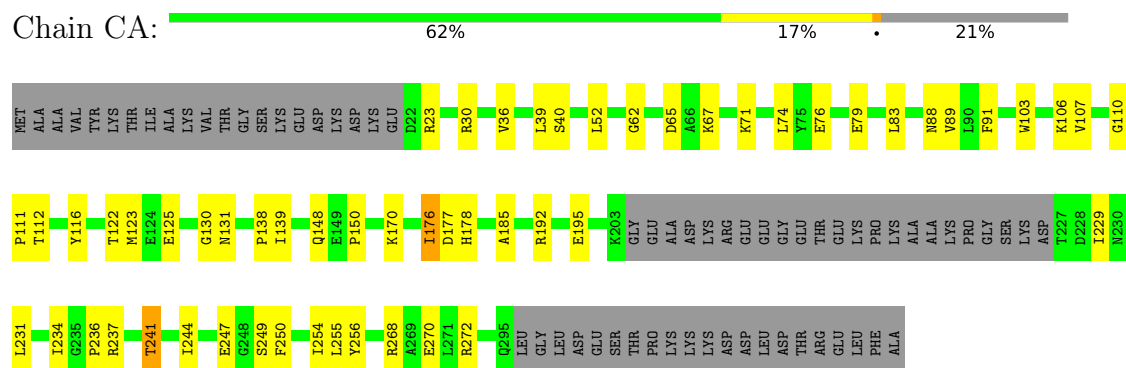
U3217	A3137	A3051	A2945	U2867	C2794	C	A	G	U2466	U2396	A2307	U	U2167
A3218	G3140	U3052	C2954	A2868	A2795	G	U	G	U2467	G2397	G	U	G2168
A3220	G3145	U3064	U2955	A2869	A2796	A	A	C	U2468	U2398	A	A	A2169
G3225	C3144	G3065	C2956	C2871	C2870	A	C	C	U2469	G2399	A	A	A2170
G3226	G3145	G3066	G2957	U2874	U2723	C	C	C	U2470	G2404	G	G	U2171
G3227	G3146	G3067	U2958	G2875	U2724	A	C	A	U2471	A2405	U	U	U2172
G3228	G3147	U3068	C2959	G2876	U2725	C	C	C	A2472	C2406	A	A	U2173
G3229	U3153	U3069	A2963	A2877	U2726	C	C	C	U2473	A2407	G	C	C2174
G3230	A3070	A3071	U2964	A2877	C2730	C	C	C	A2477	U2408	C	C	A2175
G3233	C3157	C3074	G2965	G2880	U2733	C	C	C	G2484	C2327	A	A	A2176
A3234	U3158	C3075	A2969	U2881	C2734	U	U	U	A	C2328	A	A	G2177
A3235	A3159	U3076	U2970	U2882	G2735	C	C	U	G2414	A2329	A	A	U2178
A3236	G3160	C3077	U2971	A2883	A2736	C	C	C	U2415	A2330	A	A	U2179
U3237	C3161	U3078	C2972	C2885	A2737	A	A	A	G2416	G2331	C	C	G2180
C3238	A3162	A3079	A2973	A2886	A2738	U	U	U	U2417	G2332	C	C	A2181
G3243	G3163	G3079	G2974	C2887	U2739	U	U	U	A2418	U2248	C	C	A2182
C3244	G3164	A3086	U2977	A2888	U2740	U	U	U	G2419	C2249	C	C	G2183
A3245	A3087	A3087	U2977	U2888	U2741	C	C	C	A2420	C2252	C	C	A2184
C3248	U3088	U3088	U2985	A2891	U2747	C	C	C	A2421	A2253	C	C	A2185
U3283	G3096	G3087	G2985	A2892	A2748	U	U	U	G2424	U2256	C	C	G2186
U3286	A3098	A3098	A2990	U2893	A2749	U	U	U	G2425	U2257	C	C	C2189
U3257	C3100	C3100	C2992	A2894	G2750	U	U	U	U2426	A2258	C	C	A2190
U3259	G3101	G3101	U2999	A2899	A2751	C	C	C	G2427	A2259	C	C	A2191
G3260	C3102	C3102	U3004	C	G2752	U	U	U	G2428	U2260	C	C	C2192
A3264	G3103	A3104	A3005	U	U	C	C	C	U2429	U2261	C	C	C2193
A3265	G3104	U3108	A3006	U	U	C	C	C	A2430	U2262	C	C	A2194
G3266	U3109	U3111	U3007	A2900	A2757	C	C	C	G2431	U2263	C	C	G2198
U3272	C3112	C3112	G3008	G2905	G2758	U	U	U	U2432	U2264	C	C	C2199
G3273	G3113	G3113	G3009	G2906	A2759	C	C	C	U2433	U2265	C	C	G2200
U3274	C3114	C3114	G3010	G2909	A2760	U	U	U	C2435	A2266	C	C	G2201
A3275	U3115	U3115	U3013	U2910	A2761	C	C	C	G2436	G2267	C	C	G2202
G3280	G3116	G3116	G3016	C	U2764	U	U	U	G2437	C2268	C	C	U2203
U3281	C3117	C3117	U3023	G2915	C2767	C	C	C	C2438	U2269	C	C	A2204
A3282	A3118	A3118	G3026	A2916	A2768	C	C	C	A	A	C	C	C
G3285	G3119	G3119	A3027	C2917	A2769	C	C	C	U2442	A2271	C	C	A2205
G3288	U3120	U3120	U3027	U2922	G2773	C	C	C	G2443	U2272	C	C	C
G3289	C3121	C3121	G3035	U2923	G2774	C	C	C	U2444	G	C	C	G
C3290	U3122	U3122	U3036	G2924	A2775	C	C	C	G2445	A	C	C	C
U3292	G3123	G3123	U3037	G2925	U2776	C	C	C	U2449	U	C	C	G
G3293	A3124	A3124	G3037	G2926	A2777	C	C	C	C2452	G2277	C	C	G
U3294	G3125	G3125	G3037	U2936	U2778	C	C	C	A2453	G2278	C	C	A
U3295	U3126	U3126	G3040	U	G2782	C	C	C	U2370	A2279	C	C	G
G3296	C3127	C3127	C3041	U2936	C2783	C	C	C	U2371	U2280	C	C	U
U3297	A3128	A3128	G3042	U	U2784	C	C	C	U2372	U	C	C	A
U3298	U3129	U3129	A3043	A	A2785	C	C	C	U2373	A2282	C	C	A
A3299	G3130	G3130	G3045	C2941	G2786	C	C	C	A2375	A2286	C	C	C
	C3131	C3131	C3049	C2942	U2787	C	C	C	G2376	A	C	C	C
	U3132	U3132	C3050	U2944	G2789	C	C	C		A2289	C	C	C
	A3133	A3133								C2295	C	C	C
	G3134	G3134								G2297	C	C	C
	C3135	C3135								C3301	C	C	C
	U3136	U3136								U2306	C	C	C



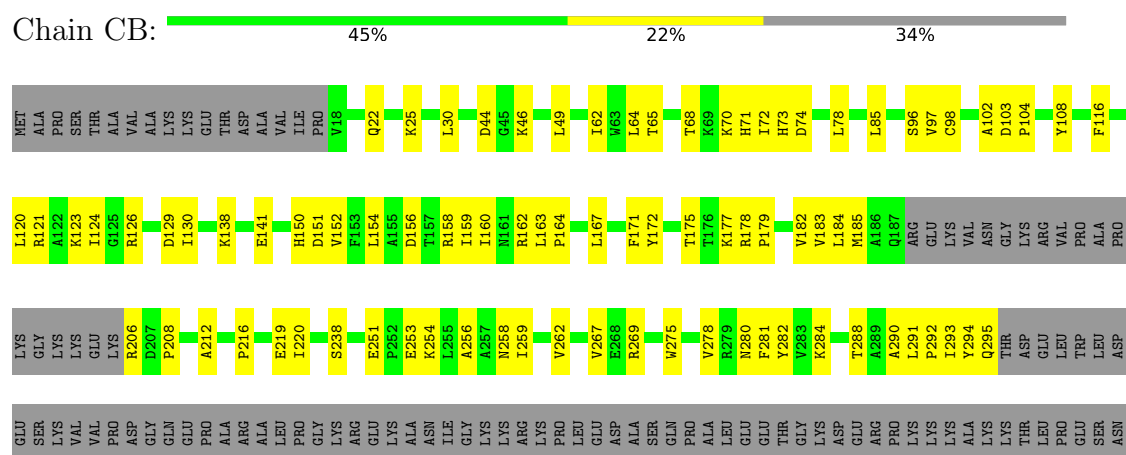
• Molecule 2: RNA (319-MER)



• Molecule 3: Brix domain-containing protein



• Molecule 4: Ribosome biogenesis protein C8F11.04



ASP
ASP
LYS
LEU
ASP
LYS
ALA
ILE
ALA
GLU
GLU
LYS
LYS
ARG
GLU
GLN
GLN
LEU
LYS
LYS
GLN
LYS
ALA
ALA
LYS
LYS
VAL
VAL
ALA
ALA
ASP
ASP
ILE

• Molecule 5: Ribosome biogenesis protein ERB1

Chain CC:

67%

14%

18%

MET
GLY
SER
LYS
ILE
VAL
GLU
LYS
LYS
ARG
LYS
SER
ARG
ASP
SER
ASP
SER
GLU
SER
ASP
ASN
LEU
LEU
SER
GLY
ASP
GLY
PHE
LEU
GLY
GLY
VAL
SER
GLU
SER
GLN
SER
GLU
ASP
GLU
GLY
TYR
PRO
SER
SER
GLU
VAL
ASP
GLU
ASP
ASP
ASP
ASP
PRO
ALA
ASP
GLU
SER
SER
SER

GLU
ASP
SER
ASP
ASP
SER
ASN
ASP
SER
SER
ASP
ASP
VAL
GLU
GLU
ASP
ASP
GLU
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ASP
ASP
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PRO
SER
GLU
GLY
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SER
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LYS
GLN
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GLN
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SER
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E119
F120
F121

V122
R126
L126
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GLU
GLU
GLU
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R135
N136
Y137
R138
E140
S160
T163
V167
L177
S178
F179
Y180
D181
I186
R197
A203
D222
T225
L229
W230
L231
S232
R233
D234
E237
L238
T239
L246
L247
V251
T258
E260
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W269
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Q445
Q446

R455
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GLY
LYS
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R571
R575
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G600
H642

R645
P646
F648
R654
L661
E665
L666
K668
L669
L689
D695
K696
L703
D704
L705
S706
N707
Y710
K711
T712
E718
R721
R724
F725
H726
L730
F733
A734
S737
D738
D739
G740
S741
L742
H746
V749
Q753
L765
K766

I779
D780
W781
A793
W801

• Molecule 6: Ribosome biogenesis protein YTM1

Chain CD:

61%

31%

7%

MET
ASP
ALA
PRO
MET
GLU
ASP
ALA
PRO
A10
P11
V12
A13
Q14
T20
T21
P24
ASP
LEU
E27
L28
P29
S31
K32
R33
L36
A39
R43
Y44
G45
L46
S47
R48
I49
N51
S52
E53
S54
M55
L56
D57
T58
I67
L72
R73
L76
E77
D78
Y79
L80

T81
S82
N83
Q84
Y85
V86
R87
P102
E105
F108
D112
W113
V114
D118
V119
L120
R128
A132
ALA
ASN
SER
SER
A137
Q140
P141
G142
Q143
E144
R145
V146
L147
S150
Y151
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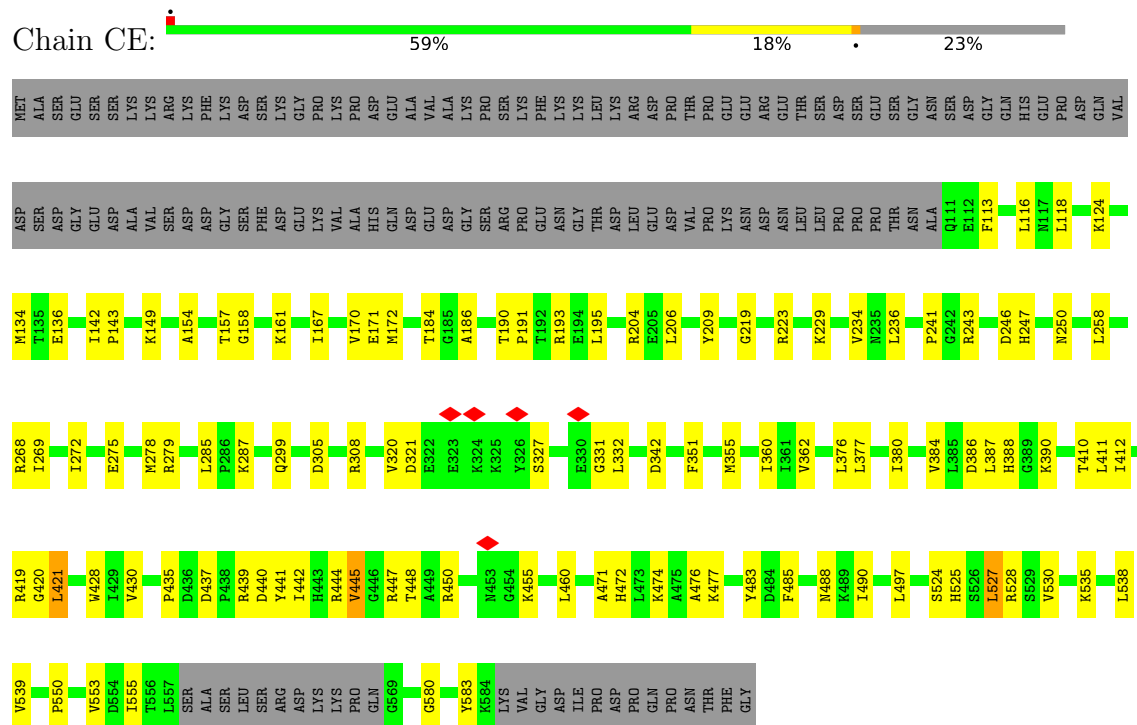
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Y222
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W230
V233
D234
L240
L241
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A248
W252
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K256
A270
H271
V272
SER
LYS
ARG
LYS

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T297
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T335
L336
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I367
T368
M369

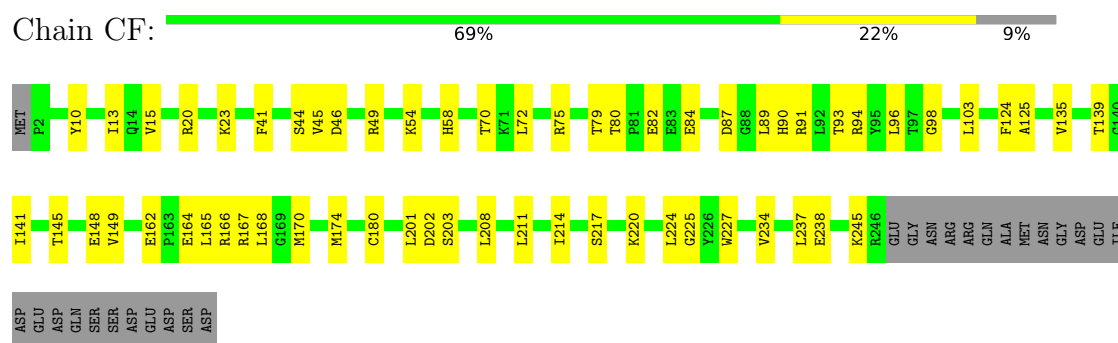
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S376
A377
T378
T379
M382
T383
L384
N389
K390
V391
S397
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M400
E401
L404
V405
S408
H409
D410
R414
S430
V440
R443
E444
A447
K462
V463
V467
W468
D469
K470
L471
G472
I473
F474
S475
E478
D479
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LYS

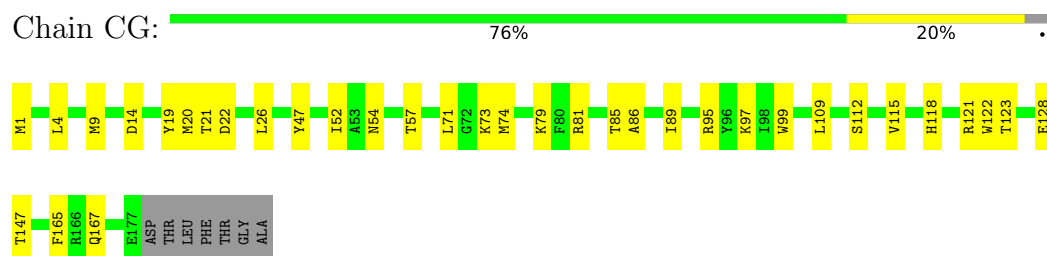
- Molecule 7: RNA helicase



- Molecule 8: Ribosome assembly factor mrt4

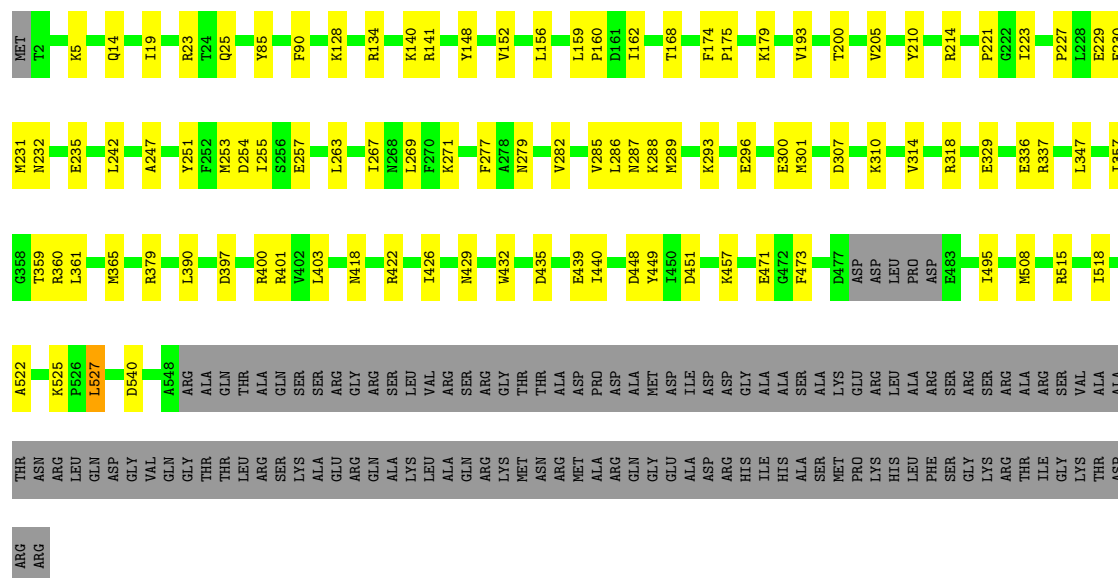


- Molecule 9: 60S ribosome subunit biogenesis protein NIP7

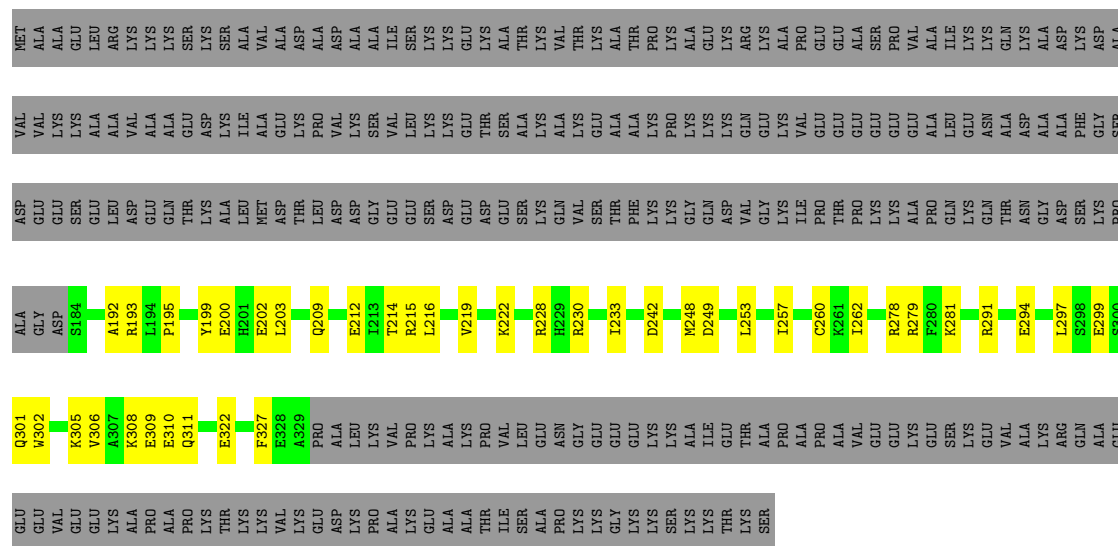


- Molecule 10: Nucleolar GTP-binding protein 1

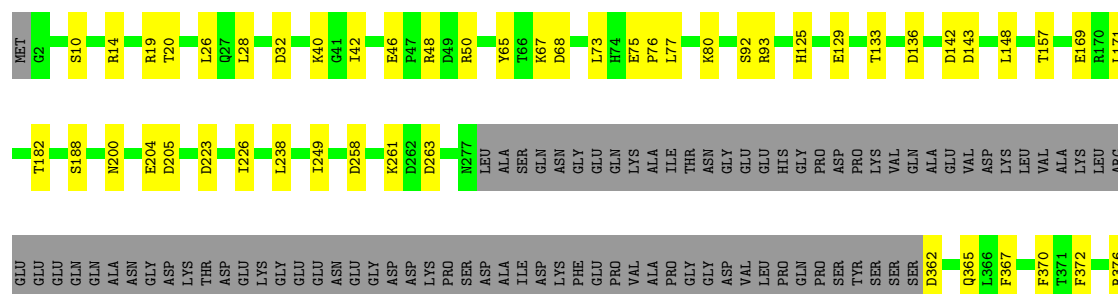


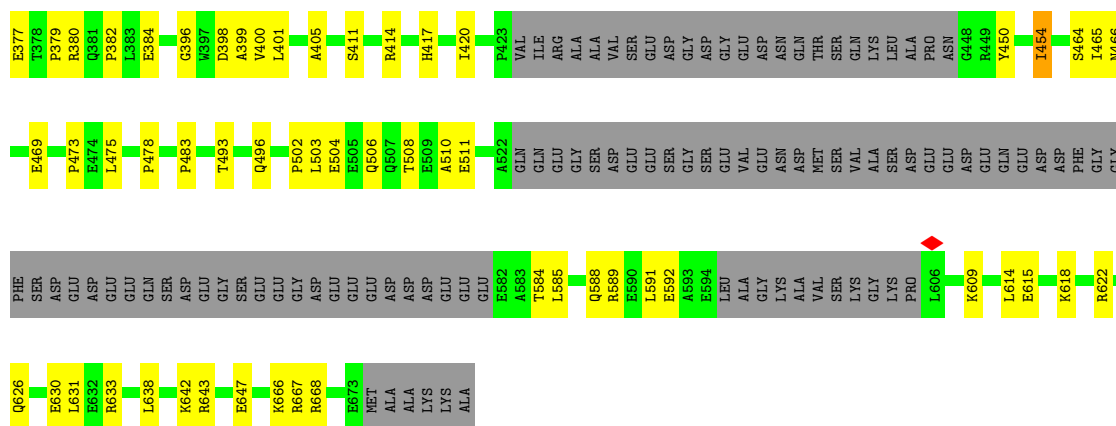


- Molecule 11: Putative RNA-binding protein



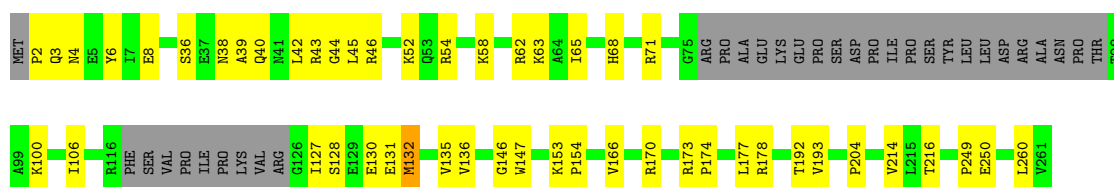
- Molecule 12: Pescadillo homolog





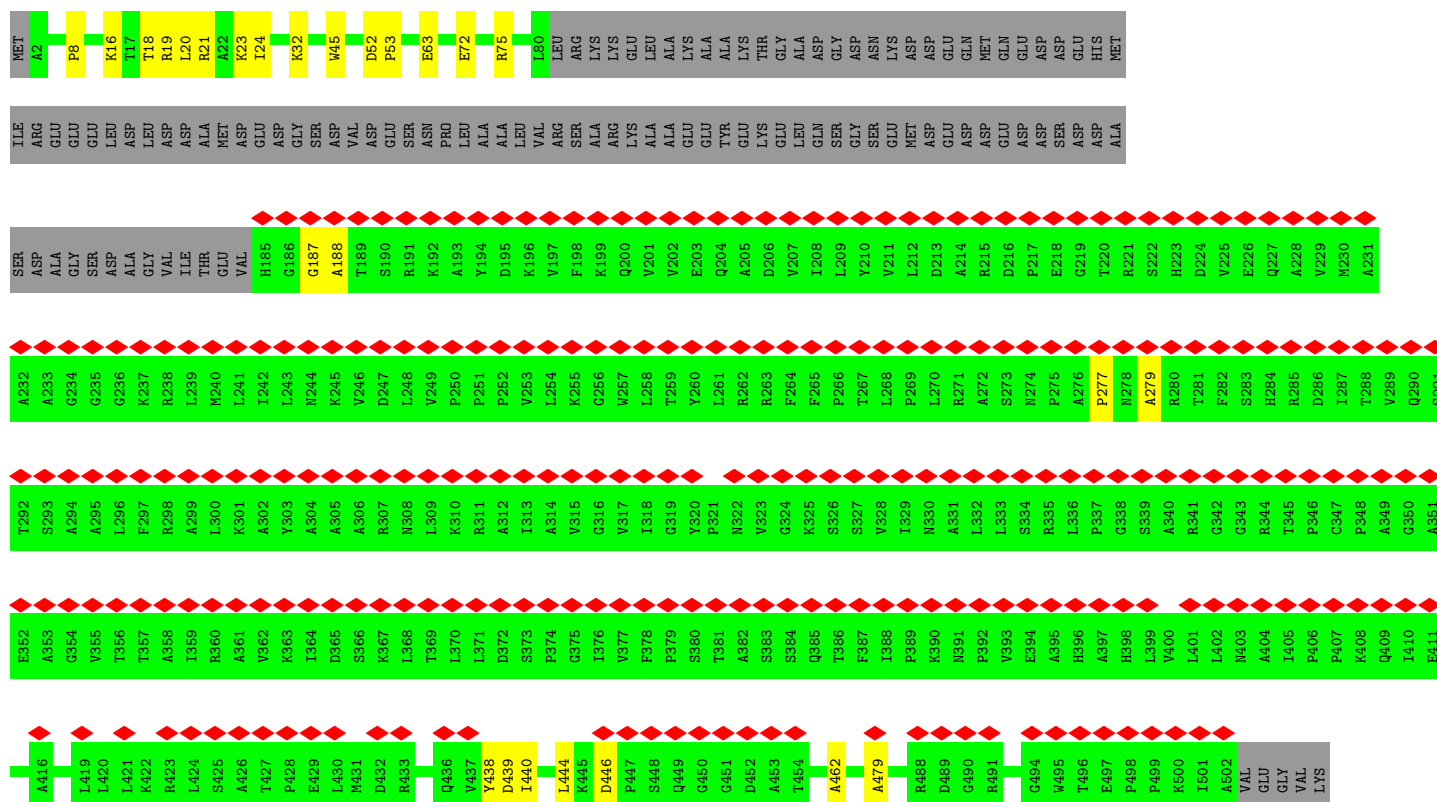
• Molecule 13: Ribosome biogenesis protein NSA2 homolog

Chain CK: 69% 18% 12%



• Molecule 14: Putative GTP binding protein

Chain CL: 47% 66% 5% 29%



GLY GLY ASN THR GLY LYS VAL ARG LYS ILE ASP ALA ASP GLN GLU VAL K20 ALA PRO ASP GLN LYS ILE THR VAL THR GLU TRP ALA LYS PHE LYS LEU GLY LEU TRP GLY ASP GLU GLN THR GLU GLY ASP LYS MET GLU ALA

- Molecule 15: 60S ribosomal protein 17-like protein

Chain CM: 72% 18% 10%

MET SER THR THR VAL PRO THR GLN ASP I12 T17 L18 L19 K20 A29 R29 A30 E31 K52 E55 K56 Y57 Q64 K68 I69 R73 S80 F81 H82 I83 P84 V90 F91 K100 I101 P102 P105 T108 V123 K124 T129 M132 I133 K134

P145 N146 R151 E152 L153 R166 T170 D171 E176 I184 I185 C186 I187 E188 D189 E193 V197 W209 L213 S214 G219 PHE ARG PRO ARG LYS PHE LYS HIS PHE ILE GLU GLY ASP LEU G235 T241 L244 M248 H249

- Molecule 15: 60S ribosomal protein 17-like protein

Chain LF: 87% 12%

MET SER S3 L18 E31 V49 R62 R66 R73 K76 Q77 I85 N99 K104 P105 L114 V121 T126 K127 A128 T129 A130 P138 I154 N178 Y182 I187 Q203 L213 N217 R221 K224 G232 D233 L234

R237 R240 R249

- Molecule 16: Eukaryotic translation initiation factor 6

Chain CN: 80% 20%

M1 N11 E12 S22 E32 E39 D44 R50 I53 T56 R67 L70 D78 Q79 R85 P89 D90 D91 I94 E98 E99 R100 L101 V107 I108 V109 D112 H113 L116 I117 L121 E122 G149 M152 M156 S166 I167

Q168 D169 Q170 E172 L177 V182 A183 M197 D201 G207 L208 D209 V221 T233 S236 W237 Y246

- Molecule 17: DUF2423 domain-containing protein

Chain CO: 44% 8% 48%

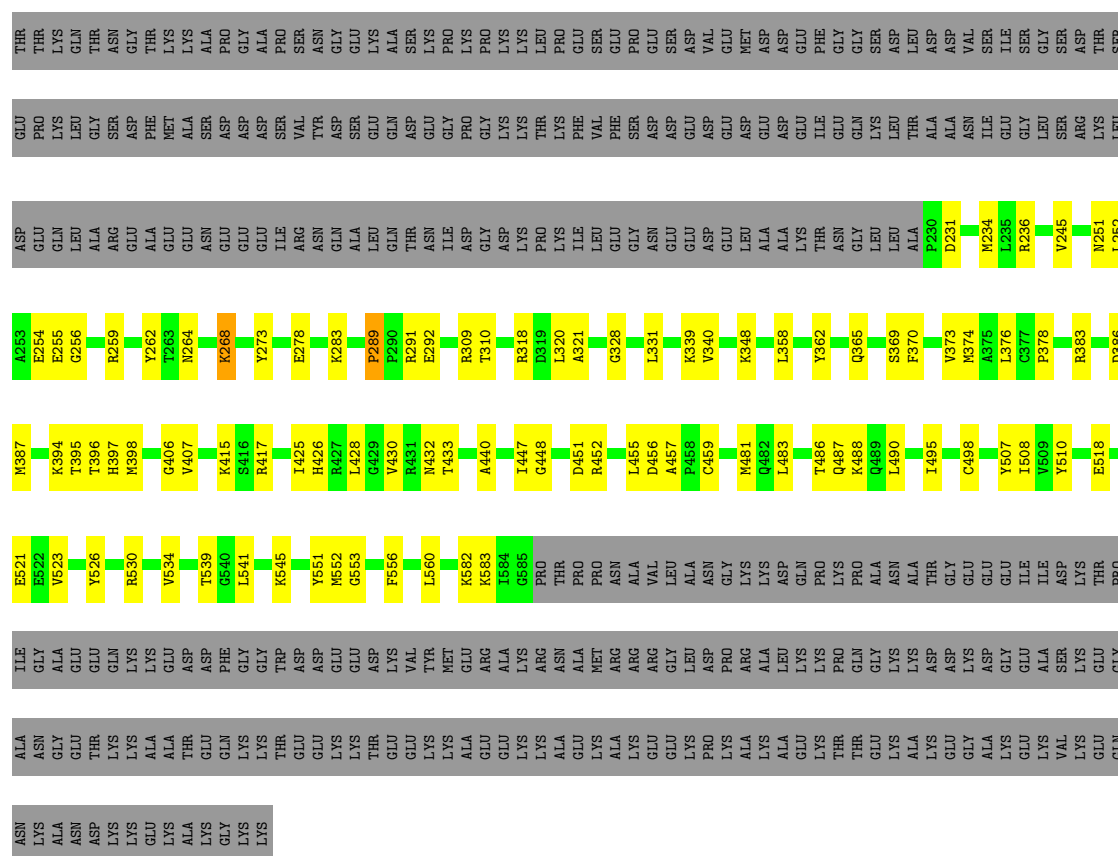
MET A2 R9 L30 L37 M38 A43 PRO LYS PRO ASP ILE GLU MET LYS GLU GLU GLU SER GLU ALA THR ALA GLN PRO LYS LEU GLU THR THR LYS ASP ASP THR ALA MET ASP VAL ASP GLY LYS LYS PRO THR LEU S83 G92 D95 SER ARG LYS ARG

GLY LYS LYS S104 S105 I106 V107 M110 LYS PRO PRO ARG ASN ASN LEU LYS LYS

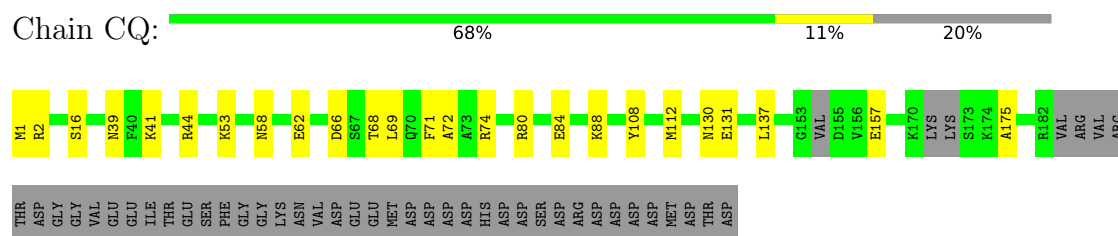
- Molecule 18: RNA methyltransferase nop2-like protein

Chain CP: 35% 12% 53%

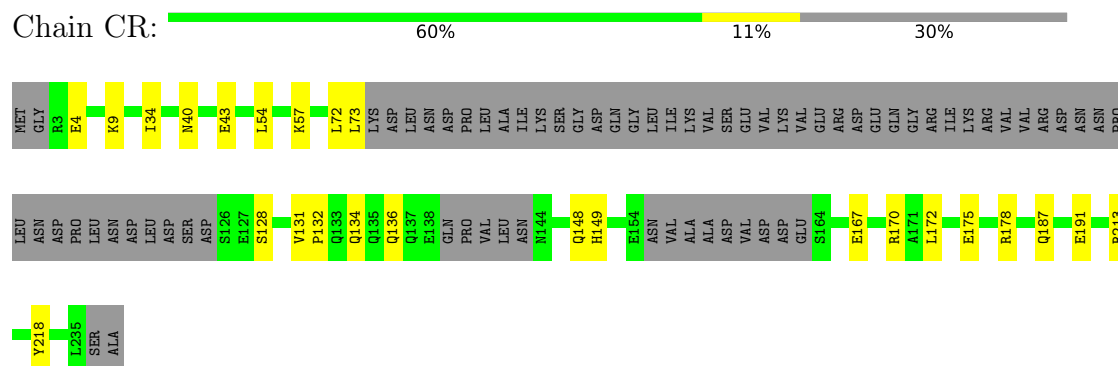
MET GLY THR LYS ARG ARG LEU LYS HIS GLN PRO PRO GLU PRO PRO LEU PRO GLU GLU HIS PHE LEU LYS LYS THR ARG LYS LYS GLY LEU PRO VAL GLU ASP THR THR PRO PRO ALA ALA PRO PRO ALA LYS ASP VAL ASP LYS ARG ARG THR SER THR LYS THR GLU LYS GLU THR LYS PRO HIS LYS ARG ALA



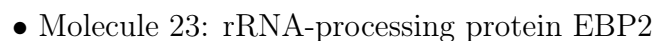
• Molecule 19: Ribosome biogenesis protein RLP24



• Molecule 20: Nucleolar protein 16



• Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1



Device Type	Percentage
Smartphone	61%
Tablet	33%
Feature phone	6%

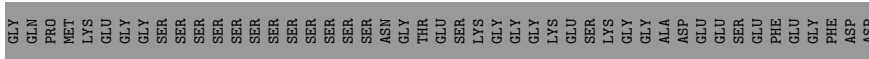


84% 10% 5%

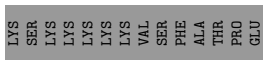
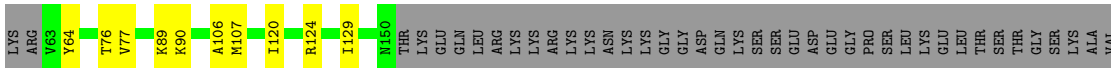
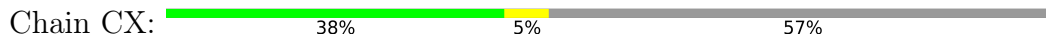


Response	Percentage
Yes	44%
No	34%
Don't know	20%

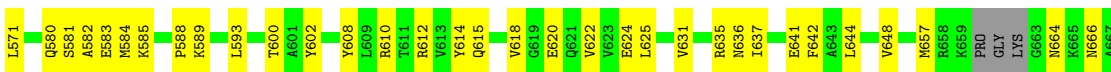
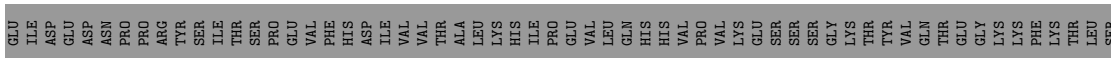
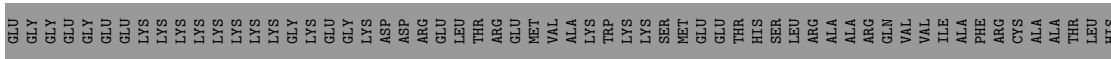
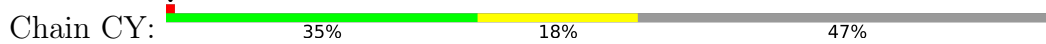




- Molecule 26: 60S ribosomal subunit-like protein

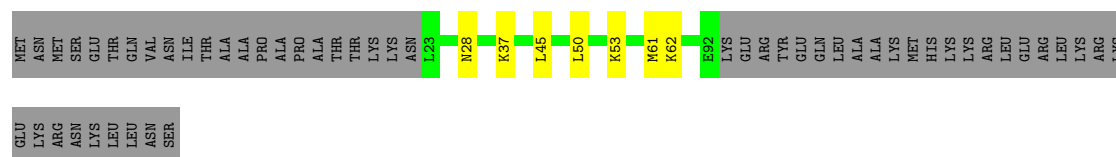


- Molecule 27: Putative NOC2 family protein



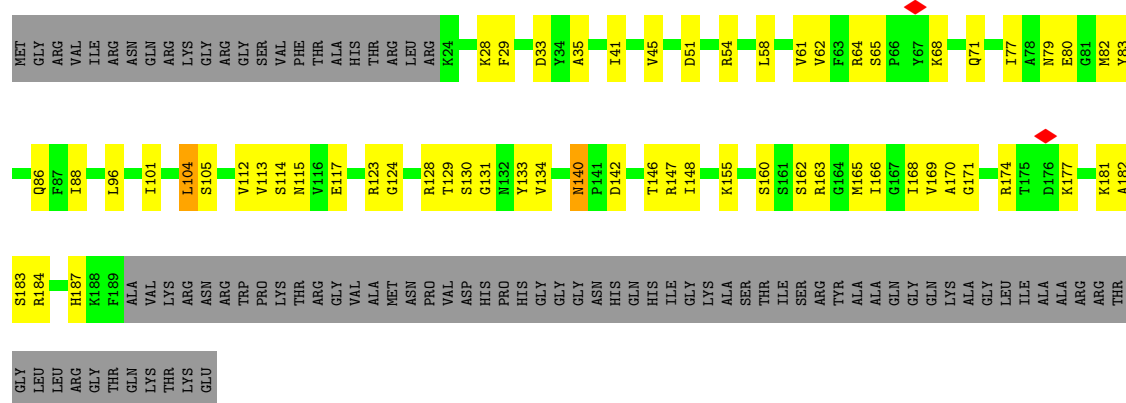
- Molecule 30: rRNA-processing protein

Chain Cz:  51% 6% 43%



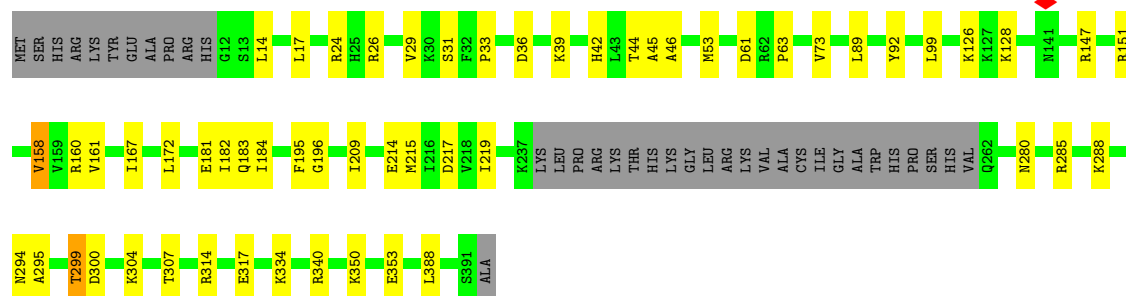
- Molecule 31: 60S ribosomal protein L2-like protein

Chain LA:  41% 23% 35%



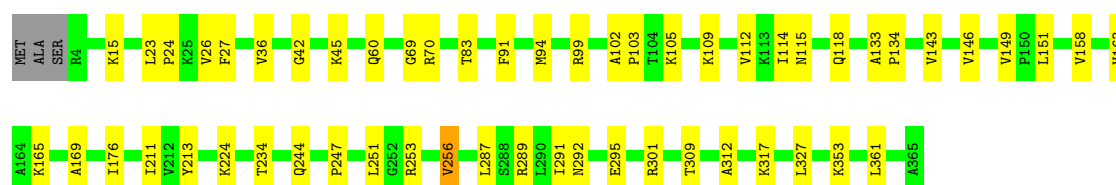
- Molecule 32: 60S ribosomal protein L3-like protein

Chain LB:  77% 14% 9%

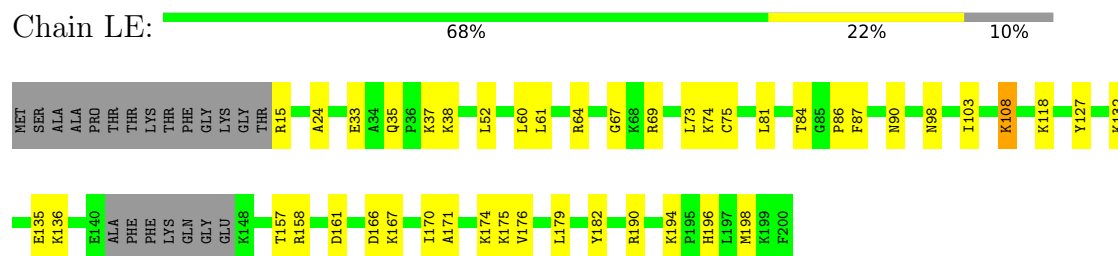


- Molecule 33: 60S ribosomal protein L4-like protein

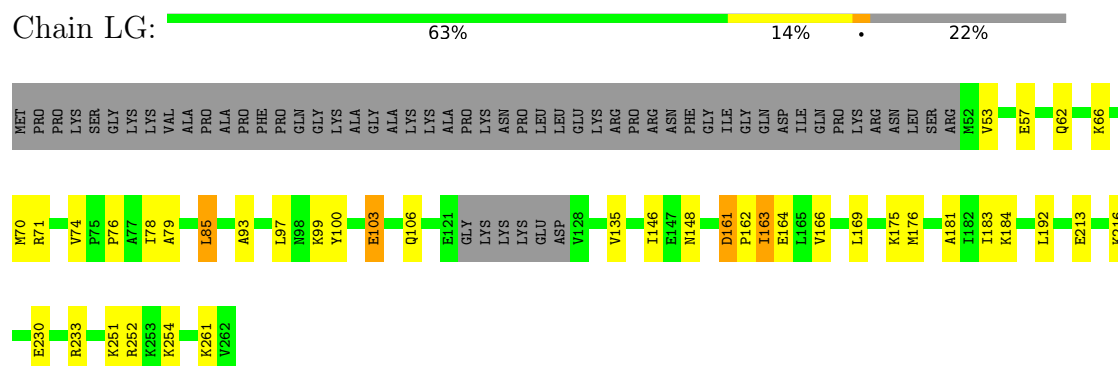
Chain LC:  84% 15% 1%



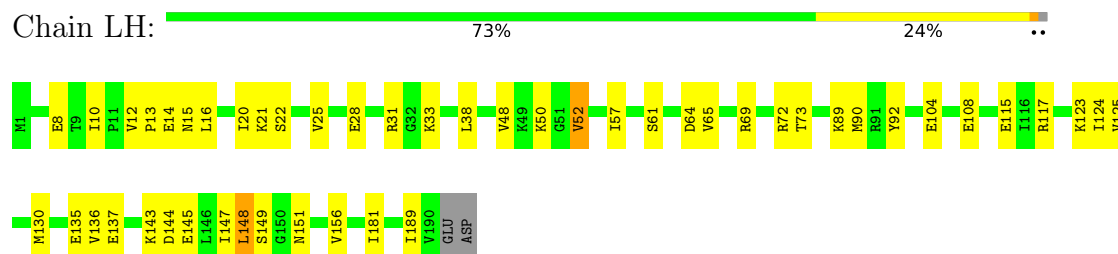
- Molecule 34: 60S ribosomal protein L6



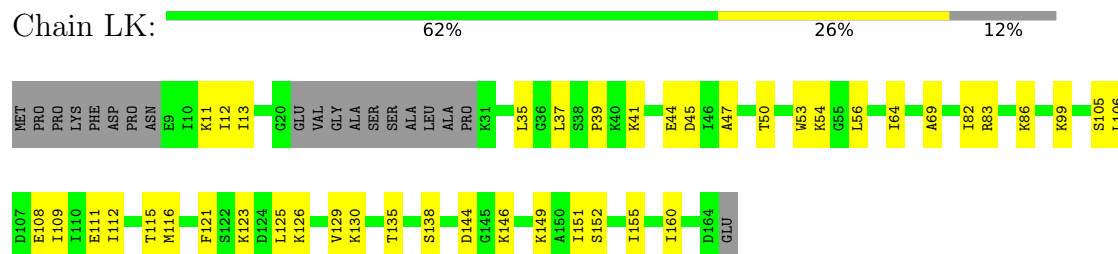
- Molecule 35: 60S ribosomal protein L8



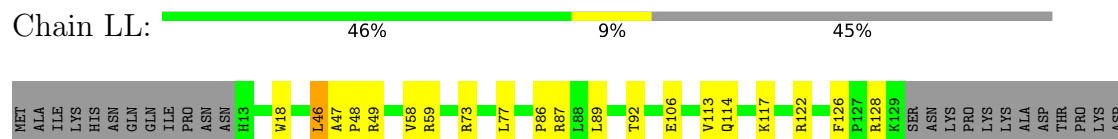
- Molecule 36: 60S ribosomal protein l9-like protein

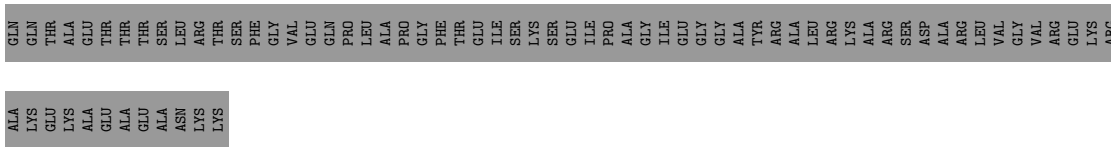


- Molecule 37: 60S ribosomal protein L12-like protein

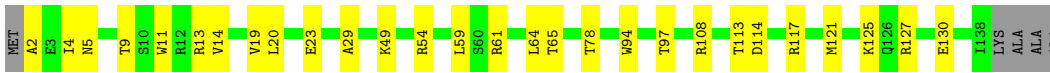
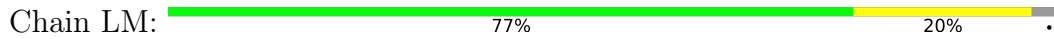


- Molecule 38: 60S ribosomal protein L13

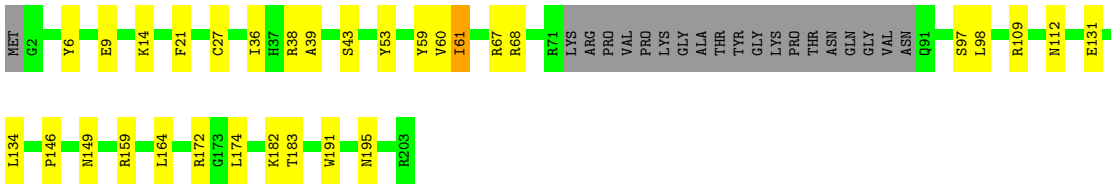
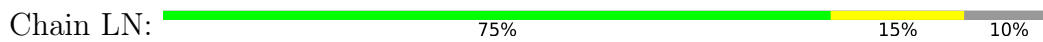




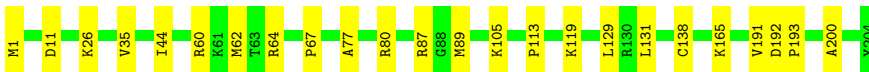
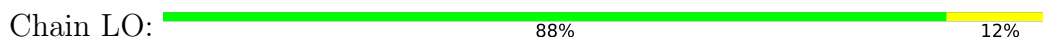
- Molecule 39: 60S ribosomal protein L14-like protein



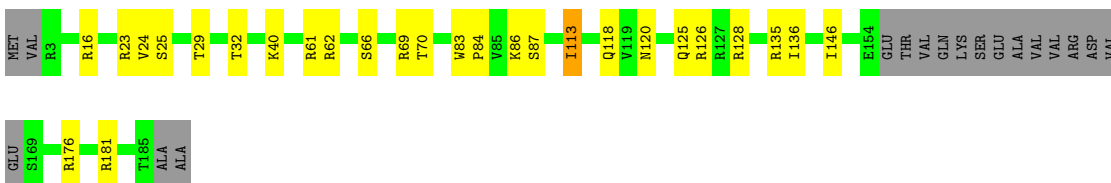
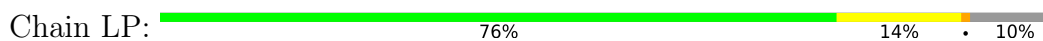
- Molecule 40: Ribosomal protein L15



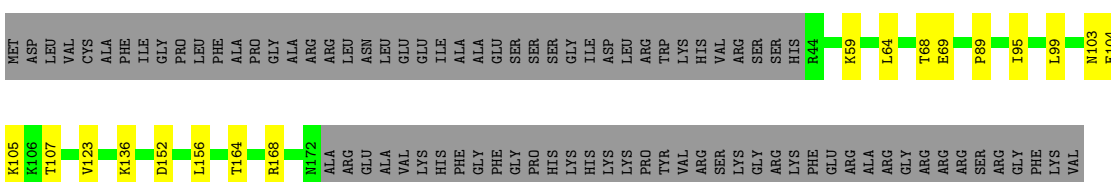
- Molecule 41: 60S ribosomal protein L16-like protein



- Molecule 42: 60S ribosomal protein l17-like protein



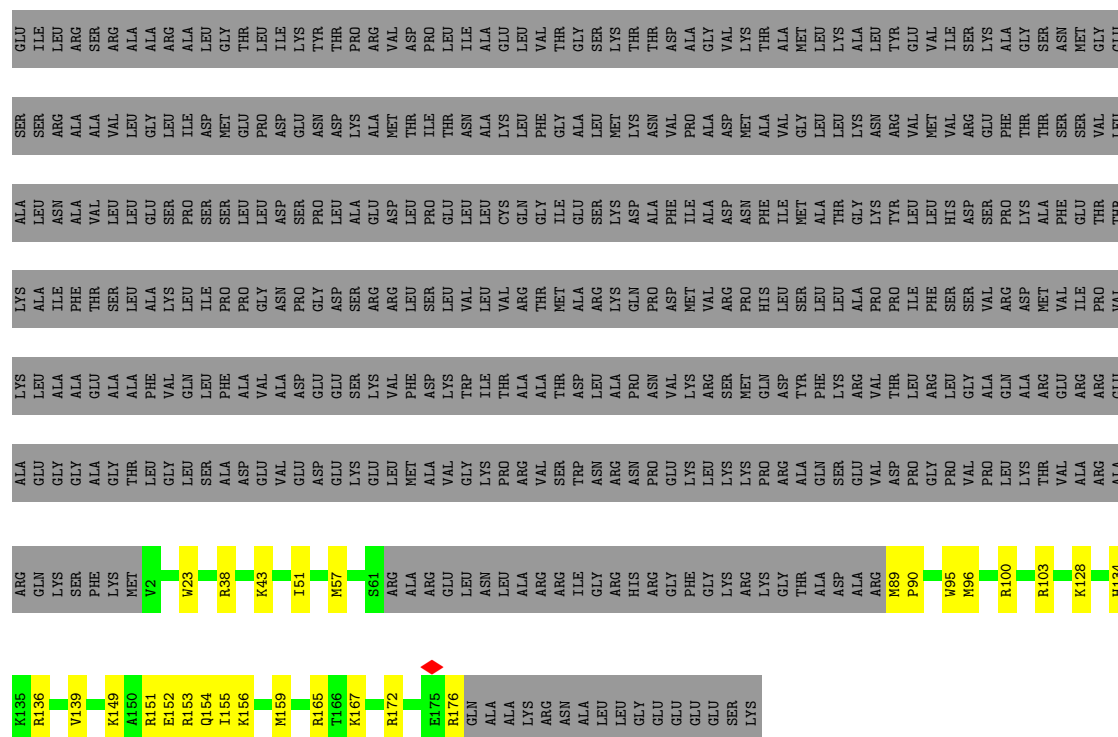
- Molecule 43: Ribosomal protein L18-like protein



Chain LR: 95%

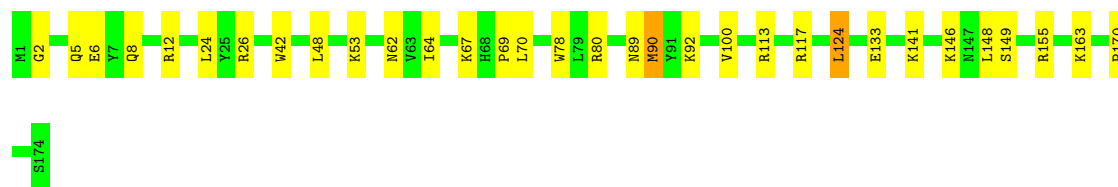






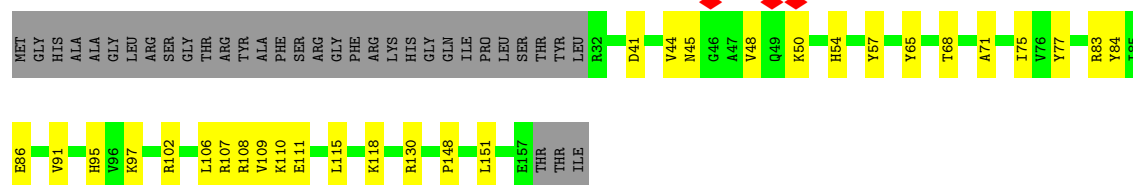
• Molecule 45: 60S ribosomal protein L20

Chain LS: 82% 17%



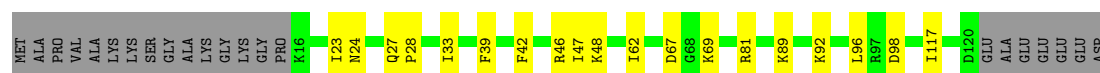
• Molecule 46: 60S ribosomal protein l21-like protein

Chain LT: 60% 19% 21%



• Molecule 47: 60S ribosomal protein L22-like protein

Chain LU: 68% 15% 17%



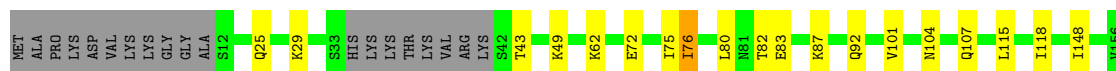
• Molecule 48: 60S ribosomal protein l23-like protein

Chain LV:  83% 14%



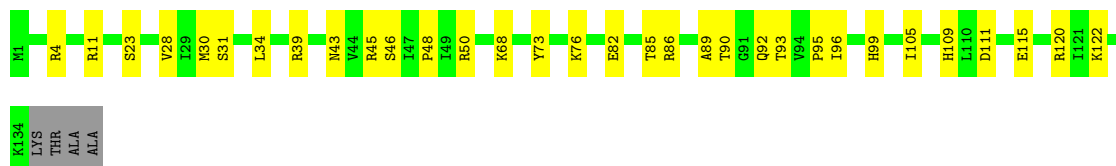
- Molecule 49: 60S ribosomal protein L25-like protein

Chain LX:  76% 12% 12%



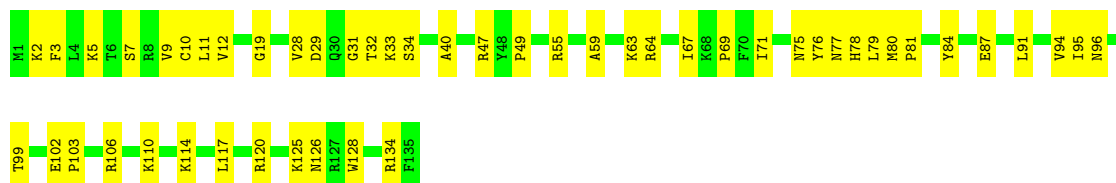
- Molecule 50: 60S ribosomal protein L26-like protein

Chain LY:  74% 23%



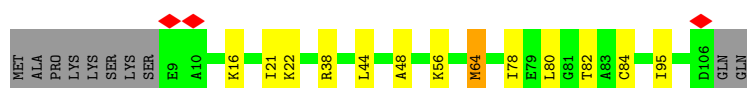
- Molecule 51: 60S ribosomal protein L27

Chain LZ:  63% 37%



- Molecule 52: 60S ribosomal protein l30-like protein

Chain Lc:  79% 11% 9%



- Molecule 53: Putative 60S ribosomal protein

Chain Ld:  78% 12% 9%



- Molecule 54: 60S ribosomal protein L32-like protein

M1	V2	A3	D24	K27	W33	R34	K35	P36	N41	R42	N61	K62	K63	T64	G65	H66	M67	V77	D82	V83	L87	M88	N100	V101	S102	S103	R106	L116	V120	T121	N122	A123	K126	V127	THR	THR	GLU	GLU
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| MET | P2 | R8 | L9 | Y10 | L16 | S17 | K33 | L47 | R50 | Y55 | R56 | K59 | G63 | R67 | W70 | G71 | K72 | P76 | P90 | L91 | S99 | I109 |
|-----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|

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|-----|-----|----|----|----|----|----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|-----|-----|--|-----|-----|--|-----|--|-----|--|-----|--|-----|--|-----|--|-----|-----|--|-----|--|------|--|------|------|
| MET | ALA | P3 | T4 | R5 | V6 | T7 | | T16 | T17 | S18 | N19 | R20 | T21 | R22 | V23 | I24 | K25 | | R32 | V33 | L34 | | C45 | G46 | | P53 | | L58 | | E62 | | K68 | | R75 | | S80 | R81 | | R92 | | V102 | | K118 | K119 |
|-----|-----|----|----|----|----|----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|-----|-----|--|-----|-----|--|-----|--|-----|--|-----|--|-----|--|-----|--|-----|-----|--|-----|--|------|--|------|------|

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| MET | SER | SER | SER | ASN | G5 | K6 | I36 | S42 | L46 | L52 | I56 | R68 | L71 | R72 | L73 | F74 | Y75 | Y80 | D84 | R91 | L106 | E107 | K110 | T114 | Q118 | A122 | A125 | ALA | THR | THR | SER | SER | GLU | GLY | PRO | ALA | LEU | SER | SER | ILE | TYR | HIS | HIS | SER | SER | HIS | HIS | GLN | ASP |
|-----|-----|-----|-----|-----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|

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

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

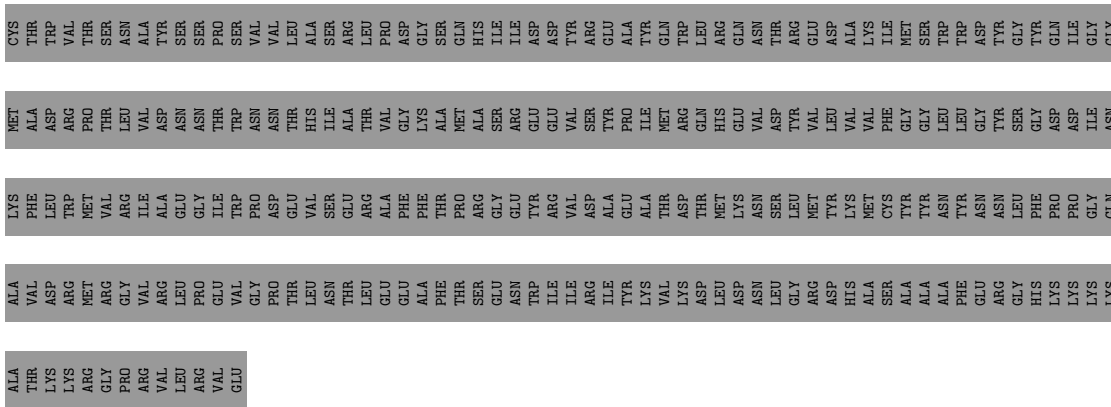
LEU LYS GLN GLY SER MET LEU TRP TRP GLY ALA LEU LEU CYS ALA LEU PHE TYR TYR GLY VAL MET SER SER TRP TRP GLY GLY TYR TYR ALA PHE PHE LE ILE THR CYS LEU LEU LEU PRO HIS SER SER PHE VAL LEU LEU CYS MET GLY ARG TYR TYR SER THR ARG LEU LEU TYR VAL ALA TYR THR THR TRP TYR TYR ALA LEU

GLY THR LEU LEU ALA SER MET GLN ILE PRO PHE VAL GLY PHE LEU PRO LYS THR SER GLU HIS MET PRO ALA LEU ILE GLY PHE GLY PHE LEU GLN LEU LEU ALA PHE LEU ASP TYR VAL ARG SER THR ILE SER SER SER ALN GLN PHE GLN THR PHE LEU TRP LEU PHE ALA GLY GLY

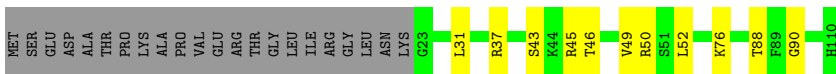
PHE GLY LEU LEU LEU LEU LEU VAL ILE ALA THR SER SER GLY ALA GLY LEU LEU ILE ILE ALA ALA PRO TRP TRP SER SER GLY ARG ARG PHE TYR SER SER LEU LEU TRP TRP THR THR GLY TYR ALA ALA LYS ILE HIS ILE ILE ILE ILE ILE ILE ILE SER SER VAL VAL SER SER GLU HIS HIS GLN GLN PRO PRO THR THR ALA ALA TRP TRP PRO PRO PHE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

LEU VAL TRP LEU PHE PRO VAL GLY VAL TYR LEU CYS PHE GLN GLY LEU ASP GLJ HIS VAL PHE PHE ILE ILE VAL TYR ALA ALA LEU PHE GLY SER TYR PHE ARG VAL MET LEU THR LEU THR PRO VAL VAL CYS VAL ALA ALA ALA ILE PHE ALA SER SER LEU LEU

ASP	THR	TYR	LEU	ASN	LYS	THR	PRO	ASN	GLY	GLN	ALA	ALA	THR	THR	GLU	ASP	ALA	ALA	LYS	LYS	LYS	SER	GLY	LEU	LYS	ALA	ALA	SER	LYS	PRO	ALA	VAL	GLY	VAL	TYR	ALA	LEU	TRP	GLY	LYS	THR	MET	MET	ILE	SER	GLY	LEU	THR	THR	VAL	VAL	LEU	LEU	LEU	PHE	VAL	VAL	LEU	LEU	HIS
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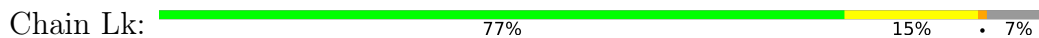
- Molecule 58: 60S ribosomal protein L36



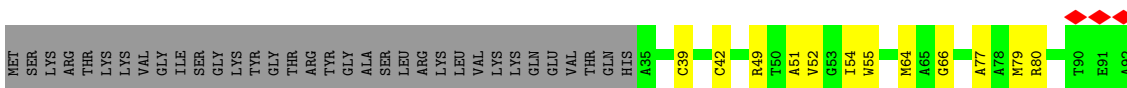
- Molecule 59: Ribosomal protein L37



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



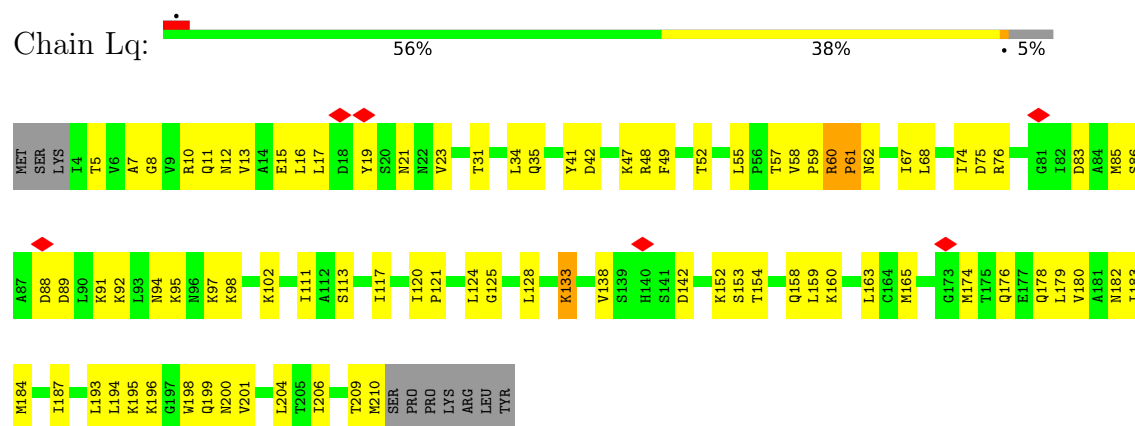
- Molecule 61: 60S ribosomal protein L43-like protein



- Molecule 62: 60S ribosomal protein L39



- Molecule 63: Ribosomal protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	170689	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	0.772	Depositor
Minimum map value	-0.289	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	508.32, 508.32, 508.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	C1	0.14	0/70087	0.27	0/109235
2	C2	0.12	0/6097	0.25	0/9499
3	CA	0.14	0/2115	0.33	0/2840
4	CB	0.15	0/2109	0.43	0/2866
5	CC	0.14	0/5423	0.33	0/7380
6	CD	0.15	0/3543	0.42	0/4824
7	CE	0.14	0/3743	0.36	0/5045
8	CF	0.13	0/1982	0.35	0/2671
9	CG	0.14	0/1422	0.29	0/1920
10	CH	0.13	0/4468	0.32	0/6029
11	CI	0.13	0/1225	0.34	0/1645
12	CJ	0.14	0/4125	0.33	0/5548
13	CK	0.13	0/1863	0.30	0/2494
14	CL	0.12	0/2247	0.35	0/3076
15	CM	0.13	0/1851	0.31	0/2481
15	LF	0.13	0/2055	0.30	0/2758
16	CN	0.14	0/1881	0.36	1/2560 (0.0%)
17	CO	0.11	0/470	0.25	0/619
18	CP	0.18	0/2859	0.45	1/3870 (0.0%)
19	CQ	0.14	0/1507	0.34	0/1996
20	CR	0.13	0/1369	0.24	0/1828
21	CS	0.17	0/5162	0.39	0/6904
22	CT	0.15	0/3974	0.38	1/5357 (0.0%)
23	CU	0.12	0/1428	0.30	0/1910
24	CV	0.12	0/1091	0.29	0/1468
25	CW	0.28	0/4397	0.63	9/5951 (0.2%)
26	CX	0.11	0/705	0.24	0/938
27	CY	0.22	0/3470	0.51	1/4659 (0.0%)
28	CZ	0.16	0/4025	0.44	0/5467
29	Ca	0.13	0/988	0.35	0/1302
30	Cz	0.10	0/598	0.24	0/785
31	LA	0.16	0/1286	0.42	0/1734

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
32	LB	0.15	0/2885	0.33	0/3872
33	LC	0.13	0/2809	0.32	0/3787
34	LE	0.13	0/1428	0.31	0/1921
35	LG	0.13	0/1674	0.28	0/2240
36	LH	0.13	0/1516	0.31	0/2038
37	LK	0.14	0/1124	0.39	0/1507
38	LL	0.14	0/983	0.29	0/1318
39	LM	0.13	0/1120	0.27	0/1507
40	LN	0.14	0/1595	0.29	0/2132
41	LO	0.15	0/1652	0.34	0/2215
42	LP	0.12	0/1367	0.27	0/1838
43	LQ	0.13	0/1033	0.29	0/1391
44	LR	0.12	0/1235	0.29	0/1644
45	LS	0.14	0/1468	0.31	0/1975
46	LT	0.13	0/1033	0.33	0/1389
47	LU	0.11	0/863	0.25	0/1155
48	LV	0.14	0/1013	0.31	0/1361
49	LX	0.12	0/1078	0.27	0/1451
50	LY	0.11	0/1079	0.26	0/1443
51	LZ	0.15	0/1135	0.32	0/1519
52	Lc	0.12	0/740	0.27	0/995
53	Ld	0.12	0/904	0.25	0/1209
54	Le	0.12	0/1043	0.28	0/1389
55	Lf	0.15	0/883	0.35	0/1187
56	Lg	0.12	0/943	0.29	0/1258
57	Lh	0.10	0/1006	0.24	0/1338
58	Li	0.11	0/738	0.22	0/971
59	Lj	0.13	0/606	0.30	0/803
60	Lk	0.14	0/628	0.35	0/835
61	Lp	0.10	0/441	0.32	0/590
62	Ll	0.10	0/329	0.27	0/440
63	Lq	0.19	0/1621	0.53	0/2180
All	All	0.15	0/187537	0.33	13/268557 (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	CC	0	1
63	Lq	0	1
All	All	0	2

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	CP	289	PRO	CA-N-CD	-12.47	94.54	112.00
22	CT	159	PRO	CA-N-CD	-11.68	95.64	112.00
27	CY	85	ILE	N-CA-C	-8.27	105.85	113.71
25	CW	429	PRO	CA-N-CD	-7.14	102.00	112.00
25	CW	168	GLY	CA-C-N	6.59	130.69	120.68
25	CW	168	GLY	C-N-CA	6.59	130.69	120.68
25	CW	38	PRO	N-CA-CB	-5.63	97.34	103.25
25	CW	163	PRO	CA-N-CD	-5.40	104.44	112.00
25	CW	277	PRO	CA-N-CD	-5.40	104.45	112.00
25	CW	590	ARG	CB-CG-CD	5.17	123.20	111.30
25	CW	38	PRO	CB-CA-C	-5.17	103.03	111.56
25	CW	40	PRO	CB-CA-C	-5.08	103.81	112.64
16	CN	237	MET	CB-CG-SD	5.04	127.84	112.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	CC	519	GLU	Peptide
63	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	62650	0	31592	939	0
2	C2	5456	0	2762	70	0
3	CA	2069	0	2109	44	0
4	CB	2063	0	2131	64	0
5	CC	5297	0	5220	89	0
6	CD	3468	0	3428	133	0
7	CE	3673	0	3778	79	0
8	CF	1945	0	1965	37	0
9	CG	1396	0	1420	24	0
10	CH	4388	0	4454	82	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	CI	1196	0	1202	31	0
12	CJ	4040	0	4087	78	0
13	CK	1835	0	1935	38	0
14	CL	2239	0	1495	20	0
15	CM	1820	0	1938	38	0
15	LF	2017	0	2130	24	0
16	CN	1856	0	1856	31	0
17	CO	468	0	503	10	0
18	CP	2798	0	2812	69	0
19	CQ	1485	0	1549	22	0
20	CR	1354	0	1400	24	0
21	CS	5082	0	5244	113	0
22	CT	3911	0	4023	47	0
23	CU	1415	0	1457	30	0
24	CV	1073	0	1130	14	0
25	CW	4310	0	4444	197	0
26	CX	701	0	742	9	0
27	CY	3413	0	3584	131	0
28	CZ	3975	0	3497	100	0
29	Ca	982	0	1044	27	0
30	Cz	592	0	640	8	0
31	LA	1259	0	1300	57	0
32	LB	2829	0	2933	42	0
33	LC	2752	0	2878	44	0
34	LE	1403	0	1503	34	0
35	LG	1651	0	1802	32	0
36	LH	1496	0	1575	35	0
37	LK	1112	0	1190	33	0
38	LL	964	0	1041	19	0
39	LM	1101	0	1170	27	0
40	LN	1563	0	1618	22	0
41	LO	1618	0	1714	22	0
42	LP	1345	0	1389	21	0
43	LQ	1021	0	1118	13	0
44	LR	1219	0	1291	29	0
45	LS	1433	0	1496	29	0
46	LT	1014	0	1073	20	0
47	LU	850	0	894	13	0
48	LV	995	0	1055	14	0
49	LX	1062	0	1145	16	0
50	LY	1065	0	1156	22	0
51	LZ	1112	0	1181	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	Lc	731	0	772	10	0
53	Ld	890	0	940	11	0
54	Le	1025	0	1104	23	0
55	Lf	862	0	891	15	0
56	Lg	930	0	1011	17	0
57	Lh	995	0	1110	14	0
58	Li	731	0	797	9	0
59	Lj	595	0	625	9	0
60	Lk	620	0	680	10	0
61	Lp	436	0	448	9	0
62	Ll	322	0	346	5	0
63	Lq	1600	0	1703	68	0
64	CH	32	0	12	4	0
65	CQ	1	0	0	0	0
65	Lj	1	0	0	0	0
65	Lp	1	0	0	0	0
66	CW	27	0	12	0	0
67	CW	1	0	0	0	0
All	All	177631	0	146544	2952	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 9.

All (2952) 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:C1:1886:C:H42	1:C1:2294:A:N6	1.34	1.23
1:C1:1886:C:N4	1:C1:2294:A:H61	1.36	1.23
1:C1:3118:A:N6	1:C1:3225:C:H42	1.40	1.18
1:C1:3118:A:H61	1:C1:3225:C:N4	1.41	1.18
27:CY:525:ARG:NH2	27:CY:565:THR:HG23	1.62	1.14
1:C1:407:G:H21	1:C1:1381:A:N6	1.49	1.09
1:C1:891:G:H1	1:C1:898:A:N6	1.51	1.07
1:C1:1954:C:N4	1:C1:2015:U:H3	1.57	1.02
1:C1:2848:A:N6	1:C1:2871:C:H42	1.60	1.00
1:C1:407:G:H21	1:C1:1381:A:H61	1.04	0.98
1:C1:1951:G:H21	1:C1:2018:A:H62	0.98	0.97
1:C1:2848:A:H61	1:C1:2871:C:N4	1.64	0.93
1:C1:974:G:H1	1:C1:1038:U:H3	0.95	0.93
1:C1:1954:C:N4	1:C1:2015:U:N3	2.15	0.93
1:C1:796:G:H1	1:C1:906:A:H61	0.93	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1901:A:N6	1:C1:2073:G:H1	1.66	0.92
1:C1:1955:G:H1	1:C1:2014:U:H3	1.09	0.91
1:C1:1901:A:H61	1:C1:2073:G:H1	0.99	0.91
1:C1:1953:A:N6	1:C1:2015:U:C2	2.40	0.89
1:C1:2414:G:H1	1:C1:2456:A:H2	1.11	0.89
1:C1:796:G:H1	1:C1:906:A:N6	1.69	0.89
6:CD:137:ALA:N	6:CD:188:SER:HG	1.71	0.88
1:C1:2112:G:H1	1:C1:2148:U:H3	1.19	0.88
6:CD:28:LEU:HD12	6:CD:33:ARG:HD3	1.54	0.87
1:C1:2849:U:HO2'	17:CO:2:ALA:N	1.72	0.87
1:C1:1938:U:N3	1:C1:2045:C:N4	2.23	0.87
5:CC:529:PRO:HG3	6:CD:196:MET:HE2	1.57	0.87
1:C1:1951:G:N2	1:C1:2018:A:H62	1.72	0.86
1:C1:66:A:N6	1:C1:75:G:N2	2.24	0.85
2:C2:219:A:OP1	11:CI:222:LYS:NZ	2.09	0.85
1:C1:891:G:H1	1:C1:898:A:H61	0.86	0.85
1:C1:1938:U:H3	1:C1:2045:C:N4	1.74	0.84
22:CT:236:GLU:N	22:CT:236:GLU:OE2	2.10	0.83
25:CW:499:PRO:HB2	25:CW:501:MET:HE1	1.61	0.83
1:C1:1953:A:N6	1:C1:2015:U:N3	2.27	0.83
27:CY:525:ARG:HH22	27:CY:565:THR:HG23	1.42	0.83
1:C1:2387:G:O6	1:C1:2563:G:C2	2.32	0.83
2:C2:298:G:H3'	11:CI:291:ARG:HH22	1.43	0.82
25:CW:300:ILE:HG23	25:CW:372:VAL:HG23	1.61	0.81
34:LE:118:LYS:NZ	34:LE:161:ASP:OD1	2.13	0.81
48:LV:12:LYS:HG3	48:LV:127:LEU:HD11	1.61	0.81
1:C1:2735:G:H1	1:C1:2741:U:H3	0.87	0.81
24:CV:34:ASN:HD21	24:CV:43:HIS:HB3	1.46	0.81
63:Lq:10:ARG:HH12	63:Lq:180:VAL:HG11	1.45	0.80
16:CN:109:VAL:HG13	16:CN:149:GLY:HA2	1.63	0.80
63:Lq:194:LEU:HD21	63:Lq:200:ASN:HD22	1.47	0.80
1:C1:3118:A:N1	1:C1:3225:C:N3	2.29	0.80
11:CI:214:THR:HG22	11:CI:215:ARG:HG3	1.63	0.79
1:C1:1217:U:H4'	1:C1:1218:G:H5'	1.64	0.79
1:C1:2877:A:N1	1:C1:2885:C:N3	2.31	0.79
1:C1:1877:G:N2	1:C1:1880:A:C6	2.50	0.78
2:C2:196:G:H1	2:C2:201:U:H3	1.28	0.78
1:C1:2297:G:N2	1:C1:2301:C:O2	2.15	0.78
1:C1:2848:A:H61	1:C1:2871:C:H42	0.82	0.78
25:CW:433:VAL:HG22	25:CW:435:ASP:H	1.49	0.78
7:CE:360:ILE:HD13	7:CE:428:TRP:HB2	1.64	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LA:140:ASN:C	31:LA:140:ASN:HD22	1.91	0.77
1:C1:934:G:H3'	1:C1:1098:G:H21	1.48	0.77
1:C1:2414:G:O6	1:C1:2456:A:N1	2.17	0.77
24:CV:96:SER:HB2	24:CV:100:LYS:HD2	1.66	0.77
3:CA:150:PRO:HG2	23:CU:193:LYS:HG2	1.66	0.77
5:CC:414:PRO:HG2	15:CM:20:LYS:HB3	1.67	0.77
10:CH:223:ILE:HG23	10:CH:231:MET:HE1	1.67	0.77
1:C1:2433:U:O2	1:C1:2436:G:C6	2.39	0.76
6:CD:28:LEU:HD22	6:CD:29:PRO:HD2	1.68	0.76
1:C1:3216:U:O2'	1:C1:3218:A:N6	2.16	0.76
1:C1:2433:U:O2	1:C1:2436:G:O6	2.02	0.76
1:C1:3108:U:O2	1:C1:3337:C:N3	2.19	0.76
1:C1:1641:G:H1	1:C1:1766:A:H61	1.34	0.76
2:C2:71:A:C6	2:C2:85:G:N2	2.54	0.76
3:CA:148:GLN:OE1	23:CU:225:ARG:NH1	2.19	0.75
21:CS:503:GLU:OE2	21:CS:503:GLU:N	2.18	0.75
20:CR:136:GLN:HE22	38:LL:114:GLN:HB2	1.52	0.75
27:CY:411:GLY:HA3	27:CY:416:ARG:HE	1.49	0.75
1:C1:2848:A:N1	1:C1:2871:C:N3	2.34	0.75
25:CW:46:LEU:HD12	25:CW:50:ARG:HH21	1.50	0.75
33:LC:301:ARG:HD3	43:LQ:69:GLU:HG2	1.67	0.75
25:CW:67:LEU:HA	25:CW:70:LEU:HB2	1.67	0.75
28:CZ:370:ALA:HB3	28:CZ:371:LYS:HZ2	1.51	0.74
1:C1:974:G:O6	1:C1:1038:U:O4	2.05	0.74
63:Lq:121:PRO:HA	63:Lq:125:GLY:HA3	1.69	0.74
25:CW:611:LYS:HA	25:CW:614:GLU:HG2	1.69	0.74
1:C1:1189:G:OP1	13:CK:54:ARG:NH1	2.20	0.74
25:CW:334:GLU:OE1	25:CW:334:GLU:N	2.21	0.74
6:CD:342:LEU:HA	6:CD:362:THR:HA	1.70	0.74
6:CD:462:LYS:HG2	6:CD:478:GLU:HG2	1.70	0.74
3:CA:106:LYS:HB2	3:CA:110:GLY:HA3	1.70	0.74
28:CZ:164:ARG:HA	28:CZ:167:GLN:HE22	1.53	0.74
27:CY:429:GLN:HB3	27:CY:432:ARG:HH21	1.53	0.74
16:CN:32:GLU:OE1	16:CN:50:ARG:NH1	2.20	0.73
27:CY:636:ASN:OD1	27:CY:637:ILE:N	2.20	0.73
21:CS:713:GLU:N	21:CS:713:GLU:OE2	2.21	0.73
61:Lp:39:CYS:CB	61:Lp:42:CYS:SG	2.76	0.73
1:C1:789:A:H2'	1:C1:790:G:C8	2.23	0.73
1:C1:1484:G:N2	1:C1:1495:G:O6	2.20	0.73
61:Lp:39:CYS:HB3	61:Lp:42:CYS:SG	2.27	0.73
1:C1:182:G:OP2	50:LY:45:ARG:NH2	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1547:A:OP2	12:CJ:19:ARG:NH2	2.20	0.73
1:C1:2881:U:OP1	21:CS:28:ARG:NH2	2.21	0.73
5:CC:669:ILE:O	5:CC:707:ASN:ND2	2.22	0.73
32:LB:128:LYS:HB2	32:LB:128:LYS:HZ3	1.53	0.73
1:C1:2404:G:H1	1:C1:2467:U:H3	1.35	0.73
1:C1:1394:G:OP1	54:Le:106:ARG:NH2	2.21	0.73
2:C2:297:C:H1'	2:C2:301:A:H61	1.54	0.73
6:CD:295:ILE:O	6:CD:323:ARG:NH2	2.21	0.73
25:CW:129:GLU:OE2	25:CW:129:GLU:N	2.21	0.73
6:CD:105:GLU:OE2	6:CD:486:ARG:NH1	2.21	0.73
27:CY:393:THR:N	27:CY:396:THR:HG1	1.87	0.73
1:C1:2248:U:O4	1:C1:2268:C:N3	2.22	0.72
1:C1:2759:A:H5'	26:CX:89:LYS:HG3	1.71	0.72
6:CD:120:LEU:HB3	6:CD:145:ARG:HB2	1.71	0.72
18:CP:396:THR:HG21	18:CP:428:LEU:HD13	1.70	0.72
2:C2:299:U:OP2	11:CI:291:ARG:NH2	2.22	0.72
10:CH:300:GLU:OE2	10:CH:300:GLU:N	2.20	0.72
25:CW:19:ASN:OD1	25:CW:20:PRO:HD3	1.89	0.72
1:C1:642:C:H2'	1:C1:643:A:H8	1.54	0.72
1:C1:2773:G:O3'	23:CU:309:LYS:NZ	2.22	0.72
1:C1:230:A:H2'	1:C1:231:A:C8	2.24	0.72
13:CK:173:ARG:HB2	13:CK:178:ARG:HH21	1.53	0.72
2:C2:219:A:H4'	2:C2:220:G:H5'	1.72	0.72
25:CW:503:GLU:OE2	25:CW:503:GLU:N	2.23	0.72
1:C1:2833:U:O4	1:C1:2909:G:O6	2.08	0.72
6:CD:444:GLU:OE1	6:CD:483:GLN:NE2	2.22	0.72
25:CW:594:GLU:OE1	25:CW:594:GLU:N	2.18	0.72
1:C1:1788:A:OP2	51:LZ:64:ARG:NH2	2.23	0.71
21:CS:504:TRP:HH2	22:CT:208:GLN:HE22	1.38	0.71
25:CW:333:LEU:HB2	25:CW:338:ARG:HG2	1.71	0.71
25:CW:454:GLU:HA	25:CW:457:GLN:HE22	1.54	0.71
2:C2:100:U:O4	59:Lj:65:ARG:NH2	2.19	0.71
32:LB:92:TYR:HB2	32:LB:158:VAL:HG13	1.71	0.71
6:CD:112:ASP:OD1	6:CD:113:TRP:N	2.23	0.71
6:CD:414:ARG:HD3	6:CD:440:VAL:HG22	1.72	0.71
18:CP:495:ILE:HD12	18:CP:534:VAL:HG11	1.71	0.71
27:CY:413:LYS:O	27:CY:413:LYS:NZ	2.19	0.71
13:CK:130:GLU:OE1	13:CK:130:GLU:N	2.17	0.71
25:CW:409:GLU:N	25:CW:409:GLU:OE2	2.21	0.71
25:CW:372:VAL:HG12	25:CW:400:SER:HA	1.71	0.71
1:C1:781:G:H22	33:LC:102:ALA:HA	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:663:G:O2'	1:C1:665:G:O2'	2.09	0.71
1:C1:812:G:H4'	1:C1:1845:C:H42	1.55	0.71
1:C1:2999:U:H5''	48:LV:47:ARG:HD2	1.73	0.71
12:CJ:588:GLN:HE22	12:CJ:589:ARG:HH22	1.39	0.71
19:CQ:131:GLU:OE1	19:CQ:131:GLU:N	2.21	0.71
16:CN:152:MET:HE1	16:CN:177:LEU:HD11	1.73	0.70
54:Le:64:THR:HA	54:Le:67:MET:HE2	1.73	0.70
25:CW:269:LEU:HD11	25:CW:392:GLY:HA3	1.73	0.70
25:CW:329:LEU:HA	25:CW:333:LEU:HD11	1.73	0.70
27:CY:565:THR:HG22	27:CY:566:ASP:H	1.57	0.70
1:C1:407:G:N2	1:C1:1381:A:N6	2.34	0.70
1:C1:3052:U:OP1	48:LV:88:LYS:NZ	2.24	0.70
25:CW:121:LEU:HD11	25:CW:140:VAL:HG22	1.72	0.70
6:CD:369:MET:HB2	6:CD:382:MET:HB3	1.72	0.70
1:C1:2156:G:N1	1:C1:2203:U:N3	2.38	0.70
31:LA:28:LYS:HB3	31:LA:123:ARG:HE	1.56	0.70
1:C1:789:A:H2'	1:C1:790:G:H8	1.57	0.70
10:CH:301:MET:HE2	10:CH:301:MET:HA	1.74	0.70
25:CW:289:LEU:HB3	25:CW:321:PRO:HG3	1.73	0.69
21:CS:206:ARG:O	21:CS:206:ARG:NH1	2.25	0.69
63:Lq:68:LEU:HA	63:Lq:85:MET:HG2	1.74	0.69
10:CH:307:ASP:HA	10:CH:310:LYS:HB3	1.74	0.69
1:C1:2387:G:O6	1:C1:2563:G:N2	2.26	0.69
1:C1:3076:U:OP2	30:Cz:28:ASN:ND2	2.26	0.69
6:CD:105:GLU:OE1	6:CD:105:GLU:N	2.26	0.69
7:CE:527:LEU:HD12	7:CE:530:VAL:HG22	1.75	0.69
1:C1:407:G:N2	1:C1:1381:A:H61	1.87	0.69
12:CJ:263:ASP:OD1	15:CM:146:ASN:ND2	2.26	0.69
31:LA:29:PHE:H	31:LA:123:ARG:HB3	1.58	0.69
1:C1:1948:G:H2'	1:C1:1949:G:C8	2.28	0.69
15:CM:91:PHE:HB2	15:CM:145:PRO:HG3	1.74	0.69
1:C1:934:G:H3'	1:C1:1098:G:N2	2.08	0.69
28:CZ:417:GLU:O	28:CZ:429:ASN:ND2	2.26	0.69
37:LK:108:GLU:OE2	37:LK:108:GLU:N	2.24	0.69
1:C1:2376:G:OP2	9:CG:73:LYS:NZ	2.23	0.68
1:C1:3162:A:OP1	42:LP:181:ARG:NH2	2.26	0.68
6:CD:191:LEU:HB2	6:CD:203:TRP:HB2	1.75	0.68
6:CD:321:THR:HG22	6:CD:337:THR:HG22	1.75	0.68
11:CI:219:VAL:HG23	11:CI:228:ARG:HB2	1.75	0.68
61:Lp:55:TRP:HB2	61:Lp:64:MET:HB2	1.75	0.68
18:CP:488:LYS:HG3	18:CP:523:VAL:HG12	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:LZ:33:LYS:HA	51:LZ:33:LYS:HE2	1.75	0.68
1:C1:1951:G:H21	1:C1:2018:A:N6	1.82	0.68
5:CC:576:LEU:HB3	5:CC:581:VAL:HB	1.75	0.68
3:CA:130:GLY:HA3	3:CA:234:ILE:HG22	1.75	0.68
7:CE:223:ARG:NH2	7:CE:246:ASP:OD1	2.24	0.68
16:CN:79:GLN:OE1	19:CQ:1:MET:N	2.26	0.68
1:C1:7:C:OP1	12:CJ:93:ARG:NH1	2.26	0.68
6:CD:373:ARG:H	6:CD:373:ARG:HD2	1.59	0.68
7:CE:136:GLU:HG3	7:CE:320:VAL:HG13	1.76	0.68
25:CW:447:GLU:HA	25:CW:450:LYS:HE2	1.75	0.68
27:CY:584:MET:O	27:CY:664:ASN:ND2	2.27	0.68
36:LH:115:GLU:OE1	36:LH:117:ARG:NH2	2.27	0.68
63:Lq:60:ARG:O	63:Lq:62:ASN:N	2.27	0.68
11:CI:203:LEU:HD22	11:CI:233:ILE:HD11	1.75	0.68
1:C1:526:G:OP1	45:LS:146:LYS:NZ	2.22	0.68
18:CP:264:ASN:OD1	18:CP:268:LYS:NZ	2.26	0.68
21:CS:499:VAL:O	22:CT:183:ARG:NH1	2.26	0.68
63:Lq:11:GLN:OE1	63:Lq:11:GLN:N	2.23	0.68
1:C1:812:G:OP1	27:CY:6:LYS:NZ	2.26	0.68
1:C1:1696:C:N4	21:CS:389:GLU:OE1	2.27	0.67
1:C1:891:G:N2	1:C1:898:A:N1	2.35	0.67
1:C1:2959:C:OP1	32:LB:26:ARG:NH1	2.26	0.67
28:CZ:167:GLN:N	28:CZ:167:GLN:OE1	2.26	0.67
1:C1:605:C:OP1	42:LP:176:ARG:NH2	2.27	0.67
1:C1:2053:U:H4'	1:C1:2054:A:H5'	1.76	0.67
8:CF:162:GLU:OE2	8:CF:166:ARG:NH1	2.27	0.67
12:CJ:400:VAL:O	15:CM:151:ARG:NH2	2.27	0.67
6:CD:470:LYS:H	6:CD:470:LYS:HE2	1.58	0.67
36:LH:92:TYR:HB3	36:LH:181:ILE:HG12	1.76	0.67
27:CY:15:GLU:HA	27:CY:19:LEU:HB2	1.76	0.67
28:CZ:388:CYS:O	28:CZ:438:THR:OG1	2.13	0.67
1:C1:63:A:H5''	40:LN:174:LEU:HD13	1.75	0.67
1:C1:66:A:N6	1:C1:75:G:C2	2.63	0.67
21:CS:96:THR:HG22	21:CS:98:LYS:H	1.58	0.67
25:CW:139:ILE:HA	25:CW:164:ASN:HD21	1.59	0.67
27:CY:489:ASN:O	27:CY:492:ASN:ND2	2.28	0.67
8:CF:93:THR:HA	8:CF:96:LEU:HD13	1.77	0.67
10:CH:522:ALA:HB1	44:LR:51:ILE:HD13	1.76	0.67
1:C1:1765:G:H2'	1:C1:1766:A:C8	2.29	0.66
1:C1:2725:U:H3	1:C1:2749:G:H1	1.43	0.66
10:CH:527:LEU:HD13	47:LU:117:ILE:HG21	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:83:C:N3	50:LY:50:ARG:NH2	2.42	0.66
25:CW:428:HIS:HB3	25:CW:429:PRO:HD2	1.77	0.66
39:LM:108:ARG:NH1	41:LO:200:ALA:O	2.28	0.66
1:C1:741:G:H1'	1:C1:752:A:H61	1.59	0.66
1:C1:796:G:N2	1:C1:906:A:N1	2.35	0.66
5:CC:528:HIS:CD2	5:CC:529:PRO:HD2	2.31	0.66
25:CW:98:ARG:NH1	25:CW:146:GLY:O	2.21	0.66
28:CZ:139:GLN:HA	28:CZ:142:ILE:HG12	1.78	0.66
1:C1:1743:C:OP2	44:LR:43:LYS:NZ	2.29	0.66
6:CD:140:GLN:NE2	6:CD:143:GLN:OE1	2.27	0.66
25:CW:243:TYR:HB2	52:Lc:22:LYS:HG2	1.78	0.66
55:Lf:59:LYS:O	55:Lf:67:ARG:NH2	2.29	0.66
1:C1:1877:G:N2	1:C1:1880:A:C5	2.64	0.66
1:C1:2833:U:H3	1:C1:2909:G:H1	0.76	0.66
17:CO:38:MET:HE2	17:CO:38:MET:HA	1.77	0.66
27:CY:80:LYS:H	27:CY:80:LYS:HE2	1.60	0.66
27:CY:556:ARG:NH2	27:CY:624:GLU:OE2	2.29	0.66
2:C2:71:A:N6	2:C2:85:G:N2	2.44	0.66
39:LM:19:VAL:O	39:LM:65:THR:OG1	2.13	0.66
19:CQ:53:LYS:NZ	19:CQ:62:GLU:OE2	2.24	0.65
1:C1:1694:A:H4'	1:C1:1695:A:H5'	1.76	0.65
1:C1:2021:C:OP1	6:CD:256:LYS:N	2.29	0.65
42:LP:118:GLN:NE2	42:LP:120:ASN:OD1	2.28	0.65
51:LZ:106:ARG:O	51:LZ:110:LYS:NZ	2.28	0.65
6:CD:44:TYR:HB2	12:CJ:592:GLU:HG2	1.77	0.65
1:C1:2056:C:H2'	1:C1:2057:A:H8	1.61	0.65
22:CT:123:GLN:H	22:CT:123:GLN:CD	2.05	0.65
31:LA:140:ASN:C	31:LA:140:ASN:ND2	2.55	0.65
1:C1:213:G:C6	1:C1:1371:G:C2	2.84	0.65
25:CW:160:ARG:HH21	25:CW:161:LEU:HD21	1.62	0.65
35:LG:161:ASP:HB2	35:LG:162:PRO:HD3	1.78	0.65
6:CD:362:THR:HG23	6:CD:364:ALA:H	1.61	0.65
27:CY:593:LEU:HD11	27:CY:608:TYR:HE1	1.62	0.65
1:C1:1475:G:OP2	1:C1:1475:G:N2	2.29	0.65
1:C1:1834:C:OP2	27:CY:17:LYS:NZ	2.29	0.65
1:C1:1988:C:H2'	1:C1:1989:G:C8	2.32	0.65
28:CZ:242:TYR:OH	28:CZ:316:ASP:OD2	2.11	0.65
32:LB:307:THR:HG21	32:LB:317:GLU:HG3	1.79	0.65
63:Lq:98:LYS:HA	63:Lq:98:LYS:HE3	1.78	0.65
26:CX:76:THR:HG22	26:CX:77:VAL:H	1.61	0.65
40:LN:172:ARG:O	40:LN:183:THR:OG1	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CW:81:ASP:OD1	25:CW:82:GLU:N	2.30	0.65
6:CD:204:LYS:HZ2	6:CD:206:THR:HG22	1.61	0.64
29:Ca:34:ILE:O	29:Ca:38:THR:OG1	2.12	0.64
21:CS:433:LYS:HZ3	21:CS:435:LYS:HD3	1.62	0.64
1:C1:663:G:HO2'	1:C1:665:G:HO2'	1.44	0.64
5:CC:246:LEU:HG	5:CC:247:ILE:HG13	1.78	0.64
6:CD:28:LEU:HD23	6:CD:55:MET:HE1	1.79	0.64
25:CW:495:LEU:HD21	25:CW:499:PRO:HD3	1.79	0.64
36:LH:21:LYS:HG3	36:LH:22:SER:H	1.62	0.64
21:CS:394:GLN:HA	21:CS:397:MET:HE2	1.79	0.64
32:LB:172:LEU:HD11	32:LB:334:LYS:HB2	1.78	0.64
36:LH:14:GLU:OE2	39:LM:2:ALA:N	2.31	0.64
1:C1:1614:G:N2	1:C1:1617:A:OP2	2.26	0.64
6:CD:43:ARG:HH12	6:CD:47:SER:HB2	1.62	0.64
25:CW:249:VAL:HG12	29:Ca:151:VAL:HG12	1.80	0.64
24:CV:34:ASN:ND2	24:CV:43:HIS:O	2.31	0.64
1:C1:1765:G:H2'	1:C1:1766:A:H8	1.61	0.64
9:CG:71:LEU:HA	9:CG:86:ALA:HB2	1.80	0.64
25:CW:309:VAL:HG23	25:CW:355:LEU:HB3	1.78	0.64
28:CZ:208:GLN:OE1	28:CZ:208:GLN:N	2.25	0.64
29:Ca:154:GLU:OE1	29:Ca:154:GLU:N	2.31	0.64
1:C1:890:G:H2'	1:C1:891:G:C8	2.33	0.64
8:CF:41:PHE:HB2	8:CF:103:LEU:HB3	1.80	0.64
31:LA:131:GLY:H	31:LA:169:VAL:HG23	1.62	0.64
3:CA:231:LEU:HB2	23:CU:244:MET:HE3	1.80	0.64
25:CW:298:ARG:HG2	25:CW:345:PHE:CE1	2.32	0.64
1:C1:1548:C:H5''	15:CM:29:ARG:HD2	1.79	0.64
12:CJ:133:THR:OG1	12:CJ:136:ASP:OD1	2.15	0.64
31:LA:79:ASN:HA	31:LA:169:VAL:HA	1.80	0.64
5:CC:263:THR:HG22	35:LG:175:LYS:HB2	1.79	0.63
1:C1:83:C:O2'	1:C1:687:C:O2'	2.16	0.63
1:C1:524:A:O2'	1:C1:526:G:OP2	2.16	0.63
1:C1:1071:G:H2'	1:C1:1072:G:C8	2.33	0.63
21:CS:744:GLN:OE1	21:CS:744:GLN:N	2.31	0.63
25:CW:358:ASP:OD1	25:CW:387:ARG:NH2	2.31	0.63
27:CY:588:PRO:HA	27:CY:610:ARG:HG2	1.78	0.63
5:CC:503:ARG:HG3	5:CC:594:ILE:HG23	1.81	0.63
10:CH:19:ILE:HG23	10:CH:23:ARG:HH21	1.63	0.63
21:CS:433:LYS:NZ	21:CS:435:LYS:HD3	2.13	0.63
31:LA:86:GLN:OE1	31:LA:86:GLN:N	2.32	0.63
21:CS:92:SER:HG	21:CS:99:CYS:HG	1.45	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CS:694:ASP:OD1	35:LG:252:ARG:NH2	2.30	0.63
22:CT:501:ALA:HB1	22:CT:505:LEU:HD13	1.81	0.63
63:Lq:8:GLY:O	63:Lq:12:ASN:ND2	2.28	0.63
62:Ll:21:ARG:NH1	62:Ll:22:PRO:O	2.28	0.63
1:C1:128:G:OP1	57:Lh:80:TYR:OH	2.13	0.63
1:C1:404:G:OP1	42:LP:62:ARG:NH1	2.32	0.63
1:C1:1901:A:N1	1:C1:2073:G:N2	2.43	0.63
1:C1:2461:U:H2'	1:C1:2462:A:C8	2.33	0.63
6:CD:155:LEU:HD12	6:CD:168:SER:HB2	1.81	0.63
28:CZ:471:GLU:HA	28:CZ:474:LYS:HG2	1.79	0.63
1:C1:562:U:H2'	1:C1:563:A:H8	1.64	0.63
28:CZ:258:TRP:NE1	28:CZ:313:MET:SD	2.71	0.63
36:LH:104:GLU:OE1	36:LH:104:GLU:N	2.31	0.63
1:C1:1950:C:H4'	6:CD:137:ALA:HA	1.81	0.63
1:C1:2116:U:OP2	31:LA:181:LYS:NZ	2.32	0.63
2:C2:141:C:O2	40:LN:112:ASN:ND2	2.32	0.63
42:LP:126:ARG:HH21	42:LP:128:ARG:HH11	1.46	0.63
60:Lk:7:ASP:N	60:Lk:7:ASP:OD1	2.32	0.63
30:Cz:37:LYS:O	36:LH:69:ARG:NH2	2.30	0.62
5:CC:138:ARG:NH2	5:CC:140:GLU:OE2	2.32	0.62
6:CD:323:ARG:HD2	6:CD:335:THR:HG23	1.79	0.62
44:LR:167:LYS:HA	44:LR:167:LYS:HE3	1.80	0.62
1:C1:3108:U:O2	1:C1:3337:C:C4	2.52	0.62
5:CC:494:ASN:HD22	5:CC:497:GLU:HG3	1.63	0.62
7:CE:157:THR:HB	7:CE:419:ARG:HH12	1.63	0.62
7:CE:331:GLY:O	7:CE:450:ARG:NH2	2.32	0.62
17:CO:92:GLY:O	32:LB:151:ARG:NH2	2.32	0.62
18:CP:425:ILE:HG23	18:CP:430:VAL:HB	1.81	0.62
18:CP:457:ALA:HB1	18:CP:487:GLN:HG2	1.81	0.62
25:CW:270:GLN:HE21	25:CW:399:LEU:HA	1.64	0.62
42:LP:70:THR:HG21	42:LP:83:TRP:HH2	1.65	0.62
1:C1:1218:G:N2	1:C1:1226:A:OP1	2.27	0.62
25:CW:488:ASP:OD1	25:CW:488:ASP:N	2.32	0.62
1:C1:445:A:H4'	1:C1:446:U:OP1	1.99	0.62
1:C1:2172:G:N1	1:C1:2186:A:C6	2.68	0.62
3:CA:139:ILE:HG13	3:CA:176:ILE:HD11	1.82	0.62
4:CB:206:ARG:HH22	4:CB:212:ALA:HA	1.64	0.62
9:CG:19:TYR:OH	9:CG:167:GLN:OE1	2.18	0.62
1:C1:662:C:O2'	1:C1:666:U:OP1	2.15	0.62
24:CV:34:ASN:ND2	24:CV:43:HIS:HB3	2.14	0.62
28:CZ:185:LEU:HD22	28:CZ:192:LEU:HD11	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:249:C:H4'	20:CR:148:GLN:HE22	1.65	0.62
1:C1:1171:C:N3	1:C1:1297:U:O2	2.33	0.62
1:C1:2769:A:OP1	13:CK:170:ARG:NH1	2.33	0.62
6:CD:331:GLN:NE2	6:CD:332:VAL:O	2.33	0.62
7:CE:419:ARG:HG2	7:CE:444:ARG:NH2	2.15	0.62
10:CH:230:GLU:OE2	10:CH:230:GLU:N	2.32	0.62
27:CY:657:MET:HA	27:CY:657:MET:HE2	1.82	0.62
38:LL:77:LEU:HD22	38:LL:87:ARG:HD2	1.81	0.62
45:LS:8:GLN:HB2	45:LS:64:ILE:HD11	1.81	0.62
1:C1:66:A:H61	1:C1:75:G:N2	1.95	0.62
1:C1:2816:U:O4	10:CH:141:ARG:NH2	2.33	0.62
10:CH:85:TYR:O	10:CH:148:TYR:OH	2.18	0.62
1:C1:1612:C:O2	5:CC:654:ARG:NH2	2.31	0.62
5:CC:270:PRO:HB3	35:LG:148:ASN:HA	1.82	0.62
15:LF:221:ARG:NH1	15:LF:232:GLY:O	2.32	0.62
1:C1:1976:U:H2'	1:C1:1977:A:H8	1.65	0.61
1:C1:2555:U:H2'	1:C1:2556:G:H8	1.64	0.61
1:C1:3211:G:N7	34:LE:136:LYS:NZ	2.47	0.61
14:CL:72:GLU:OE1	14:CL:75:ARG:NH2	2.29	0.61
15:CM:108:ILE:HD12	15:CM:132:MET:HG2	1.82	0.61
16:CN:117:ILE:HB	16:CN:121:LEU:HD22	1.82	0.61
18:CP:251:ASN:OD1	18:CP:252:LEU:N	2.33	0.61
18:CP:328:GLY:HA3	18:CP:348:LYS:HE2	1.80	0.61
33:LC:60:GLN:O	59:Lj:52:LYS:NZ	2.33	0.61
5:CC:180:TYR:O	5:CC:197:ARG:NH2	2.31	0.61
12:CJ:398:ASP:OD1	12:CJ:399:ALA:N	2.33	0.61
22:CT:415:ARG:HH22	22:CT:453:THR:HG22	1.64	0.61
27:CY:445:MET:O	27:CY:445:MET:HE3	2.00	0.61
31:LA:54:ARG:HH21	31:LA:58:LEU:HG	1.65	0.61
63:Lq:31:THR:O	63:Lq:209:THR:OG1	2.17	0.61
10:CH:448:ASP:OD1	19:CQ:2:ARG:NH2	2.33	0.61
25:CW:291:LYS:HB3	25:CW:431:ILE:HD13	1.82	0.61
25:CW:411:GLY:O	25:CW:414:GLN:NE2	2.33	0.61
27:CY:541:LEU:HG	27:CY:542:ILE:HG23	1.81	0.61
36:LH:13:PRO:HG2	36:LH:16:LEU:HG	1.81	0.61
1:C1:734:C:H2'	1:C1:735:G:H8	1.64	0.61
8:CF:165:LEU:HD22	8:CF:170:MET:HE2	1.81	0.61
25:CW:468:ARG:NH1	25:CW:471:MET:SD	2.73	0.61
1:C1:2203:U:H2'	1:C1:2204:A:H8	1.64	0.61
44:LR:159:MET:N	44:LR:159:MET:SD	2.73	0.61
1:C1:1640:G:H2'	1:C1:1641:G:C8	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1725:C:O2'	60:Lk:4:GLU:OE1	2.18	0.61
4:CB:104:PRO:HD3	4:CB:208:PRO:HB3	1.83	0.61
5:CC:529:PRO:HB2	6:CD:227:SER:HB2	1.81	0.61
6:CD:43:ARG:HH21	12:CJ:592:GLU:HB3	1.65	0.61
6:CD:46:LEU:HA	6:CD:49:ILE:HG12	1.82	0.61
10:CH:296:GLU:N	10:CH:296:GLU:OE2	2.34	0.61
25:CW:231:ASP:O	44:LR:153:ARG:NH2	2.34	0.61
25:CW:446:ARG:HH11	25:CW:446:ARG:HG3	1.65	0.61
1:C1:2904:A:H2'	1:C1:2905:G:C8	2.35	0.61
1:C1:3188:U:H2'	1:C1:3189:G:C8	2.35	0.61
25:CW:608:GLU:OE1	25:CW:608:GLU:N	2.30	0.61
31:LA:77:ILE:HD11	31:LA:115:ASN:HB2	1.82	0.61
12:CJ:200:ASN:ND2	12:CJ:205:ASP:OD1	2.32	0.61
21:CS:375:LYS:HA	21:CS:375:LYS:HE2	1.83	0.61
25:CW:460:GLN:H	25:CW:460:GLN:CD	2.09	0.61
1:C1:1700:U:O4	44:LR:128:LYS:NZ	2.33	0.61
5:CC:666:LEU:HD21	5:CC:669:ILE:HG13	1.82	0.61
22:CT:122:GLU:OE1	22:CT:123:GLN:NE2	2.30	0.61
32:LB:285:ARG:NH1	32:LB:294:ASN:O	2.34	0.61
4:CB:141:GLU:OE1	4:CB:141:GLU:N	2.33	0.61
18:CP:289:PRO:HD2	18:CP:289:PRO:O	2.01	0.61
27:CY:539:MET:O	27:CY:539:MET:HE3	2.01	0.61
8:CF:225:GLY:HA2	8:CF:237:LEU:HG	1.82	0.60
20:CR:73:LEU:HD21	38:LL:122:ARG:HH22	1.65	0.60
21:CS:146:THR:HG22	21:CS:201:PHE:HE2	1.66	0.60
25:CW:571:ALA:O	25:CW:573:SER:N	2.34	0.60
1:C1:741:G:H1'	1:C1:752:A:N6	2.17	0.60
27:CY:620:GLU:OE2	27:CY:668:LYS:NZ	2.32	0.60
28:CZ:257:GLU:HG3	28:CZ:264:ALA:HB2	1.83	0.60
33:LC:36:VAL:HG21	33:LC:251:LEU:HD21	1.83	0.60
1:C1:676:U:H3	33:LC:234:THR:HG23	1.66	0.60
2:C2:165:U:OP2	4:CB:162:ARG:NH2	2.33	0.60
3:CA:112:THR:OG1	3:CA:249:SER:O	2.13	0.60
5:CC:443:THR:HG22	5:CC:444:VAL:HG13	1.83	0.60
22:CT:575:LEU:HD22	22:CT:589:LEU:HD23	1.83	0.60
51:LZ:71:ILE:HD11	51:LZ:106:ARG:HB2	1.82	0.60
1:C1:1405:C:N4	1:C1:1406:C:N4	2.49	0.60
1:C1:1935:A:N6	1:C1:2048:G:O6	2.35	0.60
1:C1:2112:G:N2	1:C1:2148:U:O2	2.29	0.60
13:CK:130:GLU:OE2	13:CK:174:PRO:HA	2.01	0.60
18:CP:309:ARG:HH11	18:CP:365:GLN:HE22	1.48	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:CY:432:ARG:HB2	27:CY:494:GLN:HB3	1.82	0.60
46:LT:111:GLU:N	46:LT:111:GLU:OE1	2.34	0.60
54:Le:88:MET:HA	54:Le:88:MET:HE2	1.83	0.60
34:LE:69:ARG:O	34:LE:90:ASN:ND2	2.34	0.60
5:CC:231:LEU:HD11	21:CS:663:ALA:HB1	1.83	0.60
5:CC:446:GLN:HA	5:CC:446:GLN:HE21	1.66	0.60
5:CC:737:SER:OG	5:CC:739:ASP:OD1	2.19	0.60
21:CS:422:ILE:HD13	56:Lg:102:VAL:HG13	1.83	0.60
1:C1:2452:C:O2'	1:C1:2453:A:H8	1.84	0.60
4:CB:254:LYS:O	4:CB:258:ASN:ND2	2.35	0.60
25:CW:292:LEU:HD11	25:CW:429:PRO:HD3	1.82	0.60
28:CZ:142:ILE:HG13	28:CZ:143:GLU:OE1	2.02	0.60
1:C1:1886:C:N3	1:C1:2294:A:N1	2.48	0.60
6:CD:190:ARG:NH1	6:CD:203:TRP:O	2.35	0.60
6:CD:193:SER:OG	6:CD:203:TRP:NE1	2.33	0.60
7:CE:327:SER:O	7:CE:447:ARG:NH2	2.34	0.60
28:CZ:136:GLU:HA	28:CZ:139:GLN:HE22	1.66	0.60
1:C1:393:C:H5'	1:C1:394:A:H5''	1.83	0.60
1:C1:603:G:H2'	1:C1:604:G:C8	2.37	0.60
1:C1:2891:A:OP2	48:LV:6:ARG:NH1	2.35	0.60
1:C1:2973:A:H2'	1:C1:2974:G:H8	1.66	0.60
1:C1:3157:C:O2	34:LE:190:ARG:NH2	2.35	0.60
1:C1:3208:A:OP1	34:LE:64:ARG:NH2	2.21	0.60
32:LB:161:VAL:HG23	32:LB:184:ILE:HD11	1.82	0.60
40:LN:43:SER:OG	40:LN:131:GLU:OE2	2.17	0.60
51:LZ:77:ASN:OD1	52:Lc:38:ARG:NH2	2.35	0.60
1:C1:261:G:H5''	40:LN:14:LYS:HE3	1.83	0.60
1:C1:1403:G:H2'	1:C1:1404:G:H8	1.67	0.60
1:C1:3159:A:OP2	39:LM:125:LYS:NZ	2.35	0.60
3:CA:185:ALA:HA	23:CU:227:GLU:HB3	1.83	0.60
5:CC:229:LEU:HD13	21:CS:667:ALA:HB1	1.83	0.60
18:CP:321:ALA:HA	18:CP:331:LEU:HD13	1.84	0.60
25:CW:298:ARG:HG2	25:CW:345:PHE:HE1	1.65	0.60
27:CY:593:LEU:HD11	27:CY:608:TYR:CE1	2.36	0.60
6:CD:399:GLU:CD	6:CD:399:GLU:H	2.10	0.59
21:CS:356:GLU:CD	25:CW:408:ARG:HH12	2.10	0.59
25:CW:290:GLU:OE2	25:CW:290:GLU:N	2.32	0.59
1:C1:1372:A:N6	1:C1:1400:A:O2'	2.35	0.59
1:C1:2443:G:OP2	63:Lq:102:LYS:NZ	2.31	0.59
25:CW:48:ILE:HG23	25:CW:55:VAL:HG11	1.83	0.59
28:CZ:419:LEU:HA	28:CZ:430:ILE:HD11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:LV:24:ILE:HD11	48:LV:65:LYS:HD3	1.84	0.59
1:C1:2977:U:O2'	36:LH:123:LYS:NZ	2.36	0.59
28:CZ:334:GLU:OE2	31:LA:147:ARG:NH2	2.35	0.59
1:C1:1364:G:H2'	1:C1:1365:G:C8	2.37	0.59
27:CY:393:THR:OG1	27:CY:394:ASP:N	2.35	0.59
1:C1:3212:C:O2	34:LE:98:ASN:ND2	2.30	0.59
5:CC:741:SER:OG	5:CC:766:LYS:NZ	2.35	0.59
51:LZ:11:LEU:HD12	51:LZ:80:MET:HB3	1.84	0.59
63:Lq:76:ARG:NH1	63:Lq:142:ASP:O	2.36	0.59
1:C1:1582:A:OP1	44:LR:38:ARG:NH1	2.36	0.59
1:C1:2127:G:N2	1:C1:2130:A:OP2	2.34	0.59
28:CZ:154:LYS:H	28:CZ:154:LYS:HD2	1.68	0.59
36:LH:10:ILE:HG12	36:LH:72:ARG:HG2	1.84	0.59
39:LM:94:TRP:O	39:LM:97:THR:OG1	2.21	0.59
1:C1:897:G:H2'	1:C1:898:A:H8	1.68	0.59
1:C1:1179:A:H1'	14:CL:24:ILE:HD13	1.85	0.59
16:CN:166:SER:OG	16:CN:169:ASP:OD2	2.15	0.59
18:CP:425:ILE:HD13	18:CP:433:THR:HG21	1.83	0.59
33:LC:115:ASN:HB2	33:LC:118:GLN:HG3	1.84	0.59
39:LM:23:GLU:OE2	39:LM:61:ARG:NH1	2.36	0.59
41:LO:11:ASP:HB2	41:LO:119:LYS:HB3	1.85	0.59
1:C1:895:A:O2'	1:C1:896:A:H8	1.86	0.59
1:C1:1611:G:OP1	51:LZ:47:ARG:NH2	2.36	0.59
6:CD:369:MET:HA	6:CD:369:MET:HE3	1.85	0.59
21:CS:368:LYS:HE2	21:CS:368:LYS:HA	1.85	0.59
1:C1:231:A:H2'	1:C1:232:G:C8	2.38	0.59
27:CY:69:LYS:HE2	27:CY:73:MET:HE1	1.83	0.59
27:CY:473:ILE:O	27:CY:477:ASN:ND2	2.35	0.59
1:C1:2456:A:H2'	1:C1:2457:C:C6	2.37	0.58
1:C1:2737:A:H2'	1:C1:2738:A:O4'	2.03	0.58
2:C2:221:U:H3	11:CI:281:LYS:HE2	1.68	0.58
5:CC:505:ARG:NH1	5:CC:507:THR:OG1	2.35	0.58
10:CH:439:GLU:HB2	32:LB:299:THR:HG23	1.85	0.58
10:CH:525:LYS:NZ	47:LU:98:ASP:O	2.35	0.58
63:Lq:5:THR:HG23	63:Lq:8:GLY:H	1.68	0.58
1:C1:910:A:O2'	59:Lj:49:TRP:O	2.21	0.58
1:C1:1136:A:OP2	1:C1:2333:G:N1	2.35	0.58
1:C1:1921:U:O2	25:CW:199:ARG:NH2	2.37	0.58
1:C1:1940:G:H2'	1:C1:1941:G:C8	2.38	0.58
38:LL:86:PRO:HG2	38:LL:89:LEU:HB3	1.84	0.58
1:C1:1955:G:N2	1:C1:2014:U:O2	2.30	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:LM:127:ARG:HA	41:LO:191:VAL:HG21	1.86	0.58
7:CE:384:VAL:HG12	7:CE:410:THR:HB	1.85	0.58
15:CM:52:LYS:HD3	15:CM:57:TYR:CE1	2.39	0.58
36:LH:20:ILE:HD12	36:LH:25:VAL:HG22	1.86	0.58
46:LT:77:TYR:HB2	46:LT:84:TYR:HB3	1.85	0.58
1:C1:2788:G:H2'	1:C1:2789:G:C8	2.39	0.58
18:CP:556:PHE:HB3	18:CP:560:LEU:HD22	1.85	0.58
1:C1:2414:G:N1	1:C1:2456:A:C2	2.65	0.58
10:CH:200:THR:HG23	10:CH:221:PRO:HA	1.86	0.58
20:CR:148:GLN:HA	38:LL:86:PRO:HG3	1.84	0.58
63:Lq:180:VAL:O	63:Lq:184:MET:HG2	2.04	0.58
1:C1:2047:U:H2'	1:C1:2048:G:C8	2.39	0.58
2:C2:128:U:OP1	2:C2:129:C:N4	2.32	0.58
6:CD:150:SER:OG	6:CD:152:ASP:OD1	2.20	0.58
29:Ca:207:LYS:HD2	29:Ca:210:ARG:HH21	1.68	0.58
32:LB:24:ARG:HH11	32:LB:26:ARG:HB3	1.69	0.58
57:Lh:68:ARG:HH22	57:Lh:84:ASP:HB3	1.68	0.58
6:CD:204:LYS:NZ	6:CD:206:THR:HG22	2.19	0.58
10:CH:267:ILE:HG22	10:CH:271:LYS:HD2	1.86	0.58
25:CW:292:LEU:HD21	25:CW:429:PRO:HB3	1.85	0.58
2:C2:71:A:C5	2:C2:85:G:N2	2.72	0.58
15:CM:176:GLU:HB2	15:CM:185:ILE:HG22	1.86	0.58
25:CW:587:GLU:HG3	25:CW:590:ARG:HH21	1.69	0.58
27:CY:446:LYS:HE2	27:CY:501:PHE:HB2	1.86	0.58
54:Le:36:PRO:HB2	54:Le:41:ASN:ND2	2.19	0.58
1:C1:2183:G:H2'	1:C1:2184:A:C8	2.39	0.58
1:C1:2387:G:C6	1:C1:2563:G:N2	2.72	0.58
1:C1:3234:A:H5''	32:LB:128:LYS:NZ	2.19	0.58
7:CE:269:ILE:HG21	7:CE:278:MET:HE3	1.85	0.58
25:CW:57:VAL:HG22	25:CW:225:PHE:HA	1.84	0.58
27:CY:525:ARG:NH2	27:CY:565:THR:CG2	2.54	0.58
27:CY:635:ARG:HH21	27:CY:713:TRP:HB3	1.68	0.58
37:LK:126:LYS:HD2	37:LK:130:LYS:HZ2	1.69	0.58
1:C1:642:C:H2'	1:C1:643:A:C8	2.36	0.57
1:C1:1263:U:H2'	1:C1:1264:G:H8	1.69	0.57
1:C1:1938:U:O2	1:C1:2045:C:N3	2.37	0.57
1:C1:3319:C:O2'	32:LB:317:GLU:OE2	2.22	0.57
6:CD:102:PRO:HB2	6:CD:485:ASN:HB3	1.86	0.57
13:CK:174:PRO:HG2	13:CK:177:LEU:HD12	1.85	0.57
16:CN:11:ASN:ND2	16:CN:209:ASP:OD2	2.37	0.57
38:LL:46:LEU:HB3	38:LL:49:ARG:HD2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LO:77:ALA:HB3	41:LO:80:ARG:HG2	1.86	0.57
1:C1:2129:A:O2'	10:CH:360:ARG:NH1	2.37	0.57
13:CK:106:ILE:HD13	13:CK:193:VAL:HG21	1.86	0.57
14:CL:20:LEU:O	14:CL:24:ILE:N	2.36	0.57
15:LF:126:THR:HG22	15:LF:128:ALA:H	1.69	0.57
63:Lq:86:SER:OG	63:Lq:88:ASP:OD1	2.21	0.57
1:C1:580:G:H21	34:LE:37:LYS:HD3	1.67	0.57
1:C1:887:G:H2'	1:C1:888:G:C8	2.39	0.57
1:C1:1641:G:H1	1:C1:1766:A:N6	1.99	0.57
5:CC:455:ARG:HB2	5:CC:793:ALA:HA	1.85	0.57
12:CJ:609:LYS:H	12:CJ:609:LYS:HE2	1.68	0.57
28:CZ:370:ALA:HA	28:CZ:373:ARG:HE	1.69	0.57
36:LH:117:ARG:HG2	36:LH:125:VAL:HG22	1.85	0.57
1:C1:1778:A:H2'	1:C1:1779:A:C8	2.40	0.57
18:CP:417:ARG:HG2	18:CP:417:ARG:HH11	1.70	0.57
27:CY:488:ARG:HA	27:CY:491:TYR:HB2	1.86	0.57
28:CZ:256:ARG:HA	28:CZ:259:TYR:HD2	1.70	0.57
31:LA:96:LEU:HD23	31:LA:96:LEU:H	1.69	0.57
36:LH:149:SER:HB2	36:LH:189:ILE:HD11	1.84	0.57
1:C1:966:U:H2'	1:C1:967:U:H6	1.68	0.57
1:C1:1516:A:H2'	1:C1:1517:A:C8	2.39	0.57
1:C1:3184:G:OP1	41:LO:165:LYS:NZ	2.30	0.57
6:CD:151:TYR:HA	6:CD:179:SER:HB2	1.87	0.57
34:LE:52:LEU:HD22	34:LE:81:LEU:HD21	1.87	0.57
50:LY:39:ARG:HD3	50:LY:45:ARG:HA	1.86	0.57
1:C1:1935:A:H2'	1:C1:1936:C:C6	2.40	0.57
1:C1:2156:G:O6	1:C1:2203:U:O4	2.21	0.57
1:C1:2834:C:H2'	1:C1:2835:G:H8	1.68	0.57
10:CH:174:PHE:HD1	10:CH:175:PRO:HD2	1.69	0.57
21:CS:40:TYR:OH	21:CS:180:GLU:OE1	2.15	0.57
21:CS:63:CYS:O	21:CS:67:MET:HG2	2.04	0.57
28:CZ:370:ALA:HB3	28:CZ:371:LYS:NZ	2.18	0.57
29:Ca:203:ARG:HB2	29:Ca:210:ARG:HH11	1.70	0.57
31:LA:64:ARG:NH1	31:LA:68:LYS:O	2.34	0.57
62:Ll:5:LYS:HB2	62:Ll:9:ILE:HD11	1.85	0.57
63:Lq:52:THR:HB	63:Lq:154:THR:HB	1.85	0.57
1:C1:522:G:H2'	1:C1:523:A:C8	2.38	0.57
20:CR:57:LYS:HE3	20:CR:72:LEU:HD22	1.87	0.57
1:C1:1201:C:O2'	1:C1:1268:A:N1	2.35	0.57
1:C1:1236:C:H5''	37:LK:149:LYS:HD2	1.85	0.57
1:C1:2156:G:N2	1:C1:2203:U:O2	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:159:ASN:ND2	6:CD:163:SER:OG	2.37	0.57
7:CE:524:SER:O	7:CE:524:SER:OG	2.20	0.57
21:CS:436:MET:HG3	51:LZ:126:ASN:HD22	1.69	0.57
1:C1:1088:G:H2'	1:C1:1089:A:H8	1.70	0.57
10:CH:282:VAL:HB	10:CH:314:VAL:HG22	1.86	0.57
21:CS:367:ILE:HD11	44:LR:155:ILE:HG12	1.87	0.57
28:CZ:218:ILE:HD12	28:CZ:219:PRO:N	2.20	0.57
63:Lq:194:LEU:HD23	63:Lq:196:LYS:H	1.69	0.57
1:C1:724:C:N3	43:LQ:168:ARG:NH2	2.47	0.57
25:CW:488:ASP:O	25:CW:492:GLY:N	2.31	0.57
1:C1:2047:U:H2'	1:C1:2048:G:H8	1.68	0.56
1:C1:2329:A:H2'	1:C1:2330:A:C8	2.40	0.56
25:CW:75:GLU:O	25:CW:79:ARG:HG3	2.05	0.56
27:CY:417:GLU:OE1	27:CY:417:GLU:N	2.31	0.56
31:LA:155:LYS:HE2	31:LA:155:LYS:HA	1.86	0.56
63:Lq:59:PRO:C	63:Lq:61:PRO:HD3	2.29	0.56
1:C1:63:A:N3	1:C1:78:U:O2'	2.37	0.56
1:C1:780:G:O2'	38:LL:18:TRP:NE1	2.33	0.56
1:C1:909:C:H2'	1:C1:910:A:C8	2.40	0.56
1:C1:1171:C:N3	1:C1:1297:U:C2	2.73	0.56
1:C1:1933:G:N1	1:C1:2050:G:N7	2.53	0.56
4:CB:70:LYS:HZ2	11:CI:294:GLU:HB2	1.70	0.56
4:CB:116:PHE:O	4:CB:121:ARG:NH1	2.38	0.56
32:LB:295:ALA:HB3	32:LB:304:LYS:HG3	1.87	0.56
1:C1:1875:A:H61	1:C1:2301:C:H42	1.53	0.56
1:C1:1988:C:H2'	1:C1:1989:G:H8	1.68	0.56
1:C1:2046:G:H2'	1:C1:2047:U:C6	2.40	0.56
1:C1:2057:A:H2'	1:C1:2058:A:C8	2.40	0.56
1:C1:2433:U:O2'	1:C1:2436:G:N1	2.35	0.56
1:C1:2955:U:H2'	1:C1:2956:C:C6	2.40	0.56
1:C1:3265:A:H2'	1:C1:3266:G:H8	1.70	0.56
11:CI:195:PRO:HG2	11:CI:253:LEU:HD23	1.85	0.56
18:CP:539:THR:HG22	18:CP:541:LEU:HG	1.87	0.56
22:CT:605:GLU:OE2	22:CT:668:TYR:OH	2.22	0.56
30:Cz:45:LEU:HD23	45:LS:141:LYS:HB3	1.88	0.56
42:LP:40:LYS:HD2	42:LP:113:ILE:HG22	1.87	0.56
1:C1:895:A:O2'	1:C1:896:A:O5'	2.23	0.56
1:C1:2741:U:O2'	18:CP:481:MET:SD	2.61	0.56
6:CD:79:TYR:O	6:CD:83:ASN:ND2	2.38	0.56
8:CF:84:GLU:OE1	8:CF:90:HIS:ND1	2.30	0.56
21:CS:55:ALA:HB3	21:CS:56:PRO:HD3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CW:296:PRO:HB3	25:CW:370:ASP:HB2	1.86	0.56
28:CZ:139:GLN:H	28:CZ:139:GLN:CD	2.14	0.56
1:C1:149:U:O2	1:C1:150:G:N2	2.38	0.56
1:C1:488:A:O2'	1:C1:3213:A:N1	2.39	0.56
1:C1:2112:G:O6	1:C1:2148:U:O4	2.23	0.56
1:C1:3298:U:H2'	1:C1:3299:A:H8	1.71	0.56
5:CC:355:ASN:OD1	5:CC:386:LYS:NZ	2.33	0.56
12:CJ:42:ILE:HG12	12:CJ:68:ASP:HB3	1.87	0.56
21:CS:259:ILE:H	21:CS:259:ILE:HD12	1.71	0.56
27:CY:539:MET:HE1	27:CY:551:ARG:HG3	1.86	0.56
32:LB:29:VAL:HA	32:LB:219:ILE:HD13	1.86	0.56
34:LE:33:GLU:OE2	34:LE:35:GLN:NE2	2.38	0.56
37:LK:11:LYS:HG3	37:LK:64:ILE:HD11	1.87	0.56
1:C1:399:A:C2	2:C2:17:A:H1'	2.41	0.56
1:C1:510:U:OP2	15:LF:76:LYS:NZ	2.36	0.56
1:C1:2171:U:H2'	1:C1:2172:G:C8	2.41	0.56
1:C1:2841:U:H1'	41:LO:64:ARG:HH22	1.69	0.56
6:CD:120:LEU:HD11	6:CD:188:SER:HA	1.88	0.56
6:CD:157:ILE:HD13	6:CD:166:ALA:HB3	1.87	0.56
31:LA:124:GLY:O	31:LA:128:ARG:NH2	2.39	0.56
56:Lg:16:THR:O	56:Lg:20:ARG:NH1	2.38	0.56
1:C1:1825:C:OP1	1:C1:1828:C:N4	2.39	0.56
1:C1:2924:G:O4'	9:CG:81:ARG:NH2	2.39	0.56
32:LB:217:ASP:OD2	32:LB:340:ARG:NH1	2.39	0.56
1:C1:713:G:C6	1:C1:723:G:C2	2.93	0.56
3:CA:123:MET:HE3	3:CA:236:PRO:HD3	1.88	0.56
6:CD:348:LEU:HD11	6:CD:404:LEU:HD23	1.86	0.56
25:CW:231:ASP:HA	44:LR:153:ARG:HE	1.71	0.56
1:C1:325:C:OP2	20:CR:9:LYS:NZ	2.37	0.56
1:C1:401:A:OP1	54:Le:27:LYS:NZ	2.37	0.56
1:C1:1176:G:H2'	1:C1:1177:A:C8	2.40	0.56
1:C1:1697:A:H2'	1:C1:1698:G:C8	2.41	0.56
1:C1:2020:C:H4'	6:CD:255:SER:HA	1.88	0.56
5:CC:121:PHE:HE2	7:CE:442:ILE:HD13	1.70	0.56
25:CW:201:LEU:HD23	25:CW:232:ALA:HB1	1.88	0.56
25:CW:312:PHE:HA	25:CW:315:VAL:HG12	1.87	0.56
63:Lq:92:LYS:HA	63:Lq:95:LYS:HE2	1.86	0.56
1:C1:649:U:H2'	1:C1:650:C:C6	2.41	0.56
1:C1:1526:G:OP1	40:LN:67:ARG:NH1	2.39	0.56
1:C1:3265:A:H2'	1:C1:3266:G:C8	2.41	0.56
2:C2:219:A:H8	11:CI:278:ARG:HH21	1.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:51:ASN:OD1	6:CD:58:THR:OG1	2.17	0.56
9:CG:20:MET:HE1	9:CG:26:LEU:HD11	1.87	0.56
10:CH:242:LEU:HG	10:CH:277:PHE:HE1	1.70	0.56
15:CM:214:SER:O	15:CM:248:MET:HG3	2.06	0.56
22:CT:134:ILE:HG21	22:CT:152:LEU:HG	1.87	0.56
22:CT:269:LYS:HE2	22:CT:278:ASP:HB2	1.89	0.56
28:CZ:199:LYS:HA	28:CZ:202:ILE:HG22	1.88	0.56
28:CZ:253:GLN:HA	28:CZ:256:ARG:HG3	1.87	0.56
31:LA:112:VAL:HG13	31:LA:133:TYR:HB2	1.88	0.56
63:Lq:48:ARG:NH2	63:Lq:159:LEU:O	2.39	0.56
1:C1:353:A:O3'	59:Lj:45:ARG:NH2	2.39	0.55
1:C1:1371:G:H5''	54:Le:102:SER:HB3	1.88	0.55
6:CD:190:ARG:HH12	6:CD:204:LYS:HA	1.71	0.55
7:CE:388:HIS:CE1	7:CE:390:LYS:HB3	2.41	0.55
20:CR:136:GLN:O	38:LL:117:LYS:NZ	2.38	0.55
21:CS:232:VAL:HG23	21:CS:272:ALA:HB2	1.88	0.55
27:CY:429:GLN:CD	27:CY:429:GLN:H	2.14	0.55
37:LK:56:LEU:HD13	37:LK:82:ILE:HG21	1.88	0.55
56:Lg:24:ILE:HG21	56:Lg:34:LEU:HD12	1.88	0.55
1:C1:1336:G:N2	1:C1:1338:U:O2'	2.29	0.55
22:CT:521:LEU:O	22:CT:524:SER:OG	2.25	0.55
25:CW:93:ILE:HG22	25:CW:193:VAL:HB	1.87	0.55
25:CW:241:MET:HB2	25:CW:244:PRO:HG3	1.88	0.55
1:C1:115:A:H2'	1:C1:257:A:H2'	1.89	0.55
1:C1:1618:C:OP2	56:Lg:75:ARG:NH1	2.33	0.55
4:CB:64:LEU:HD22	4:CB:259:ILE:HG13	1.89	0.55
7:CE:376:LEU:HD21	7:CE:497:LEU:HD11	1.88	0.55
21:CS:231:ARG:NH2	21:CS:272:ALA:O	2.40	0.55
1:C1:1071:G:H2'	1:C1:1072:G:H8	1.70	0.55
1:C1:2056:C:H2'	1:C1:2057:A:C8	2.42	0.55
1:C1:2057:A:H2'	1:C1:2058:A:H8	1.69	0.55
12:CJ:668:ARG:HH11	12:CJ:668:ARG:HG3	1.71	0.55
31:LA:79:ASN:N	31:LA:82:MET:SD	2.79	0.55
1:C1:424:G:H2'	1:C1:425:A:C8	2.42	0.55
1:C1:1599:U:OP2	12:CJ:48:ARG:NH1	2.31	0.55
12:CJ:420:ILE:HD11	12:CJ:478:PRO:HB3	1.89	0.55
28:CZ:306:LYS:O	31:LA:184:ARG:HD3	2.06	0.55
1:C1:1181:C:C4	14:CL:24:ILE:HD11	2.42	0.55
12:CJ:609:LYS:HE2	12:CJ:609:LYS:N	2.21	0.55
21:CS:74:ILE:HG12	21:CS:88:ILE:HD12	1.89	0.55
37:LK:35:LEU:HD22	37:LK:37:LEU:HD23	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LO:129:LEU:HD11	45:LS:170:PRO:HG2	1.88	0.55
4:CB:154:LEU:HD12	4:CB:182:VAL:HG11	1.88	0.55
4:CB:175:THR:HG1	4:CB:178:ARG:HH21	1.53	0.55
13:CK:2:PRO:HB2	13:CK:6:TYR:CD2	2.42	0.55
20:CR:131:VAL:HG13	20:CR:134:GLN:HG2	1.89	0.55
22:CT:184:ILE:HD12	22:CT:207:GLU:HB3	1.89	0.55
35:LG:78:ILE:HG23	35:LG:163:ILE:HD12	1.87	0.55
63:Lq:113:SER:HA	63:Lq:138:VAL:HG22	1.89	0.55
1:C1:2404:G:O6	1:C1:2467:U:O4	2.24	0.55
4:CB:120:LEU:HD23	4:CB:123:LYS:HZ3	1.72	0.55
8:CF:23:LYS:HG2	8:CF:72:LEU:HD21	1.89	0.55
31:LA:105:SER:HB3	31:LA:160:SER:HB3	1.87	0.55
35:LG:97:LEU:HD12	35:LG:192:LEU:HD21	1.87	0.55
1:C1:1606:U:O2'	1:C1:1791:G:N2	2.30	0.55
1:C1:2180:G:N2	28:CZ:566:HIS:O	2.40	0.55
2:C2:135:G:H5''	49:LX:62:LYS:HD2	1.88	0.55
6:CD:30:GLU:HA	6:CD:33:ARG:HG2	1.87	0.55
13:CK:204:PRO:O	23:CU:327:LYS:HG3	2.06	0.55
18:CP:309:ARG:HD3	18:CP:365:GLN:HE22	1.72	0.55
28:CZ:205:LEU:HA	28:CZ:208:GLN:HE22	1.72	0.55
37:LK:45:ASP:OD1	37:LK:45:ASP:N	2.37	0.55
1:C1:40:A:O2'	1:C1:92:G:N2	2.40	0.55
1:C1:975:G:N2	1:C1:976:U:O4	2.39	0.55
1:C1:976:U:O2	1:C1:1036:A:N7	2.39	0.55
1:C1:979:A:H2'	1:C1:980:G:C8	2.42	0.55
1:C1:1080:A:OP2	46:LT:130:ARG:NH1	2.39	0.55
1:C1:2970:U:H2'	1:C1:2971:U:C6	2.42	0.55
2:C2:95:G:OP2	59:Lj:72:ARG:NH1	2.40	0.55
6:CD:56:LEU:HD12	6:CD:58:THR:HG23	1.88	0.55
6:CD:308:ARG:NH2	6:CD:353:THR:O	2.40	0.55
10:CH:310:LYS:NZ	28:CZ:328:GLU:O	2.36	0.55
27:CY:5:LYS:HD2	27:CY:8:LEU:HD13	1.88	0.55
1:C1:595:A:OP1	33:LC:317:LYS:NZ	2.36	0.54
1:C1:2569:U:H2'	1:C1:2570:U:C6	2.42	0.54
12:CJ:171:LEU:HB3	12:CJ:238:LEU:HD23	1.88	0.54
22:CT:184:ILE:HD11	22:CT:211:VAL:HG23	1.89	0.54
25:CW:237:ILE:HD11	29:Ca:159:ASP:O	2.07	0.54
28:CZ:214:ARG:HA	28:CZ:217:ILE:HG22	1.90	0.54
21:CS:814:MET:HB2	33:LC:69:GLY:HA3	1.88	0.54
46:LT:77:TYR:HB3	46:LT:86:GLU:HG3	1.89	0.54
49:LX:80:LEU:HD22	49:LX:82:THR:HG23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Lq:8:GLY:HA2	63:Lq:11:GLN:HE22	1.72	0.54
1:C1:409:A:H2'	1:C1:410:A:H8	1.72	0.54
1:C1:1331:G:H4'	1:C1:1332:A:H5''	1.89	0.54
1:C1:1835:C:N4	1:C1:1836:C:N4	2.55	0.54
21:CS:134:GLN:NE2	21:CS:158:LYS:O	2.34	0.54
30:Cz:53:LYS:HB2	30:Cz:53:LYS:NZ	2.22	0.54
35:LG:230:GLU:OE1	35:LG:233:ARG:NH1	2.40	0.54
39:LM:130:GLU:HG2	41:LO:191:VAL:HG23	1.89	0.54
40:LN:9:GLU:HG3	58:Li:49:VAL:HG12	1.89	0.54
63:Lq:152:LYS:HD2	63:Lq:153:SER:HB3	1.88	0.54
4:CB:158:ARG:HG3	4:CB:185:MET:HE1	1.89	0.54
4:CB:163:LEU:HD23	4:CB:179:PRO:HG2	1.89	0.54
6:CD:323:ARG:HG3	6:CD:335:THR:HA	1.90	0.54
19:CQ:16:SER:HB3	32:LB:73:VAL:HG11	1.89	0.54
21:CS:436:MET:HE2	51:LZ:84:TYR:HB3	1.88	0.54
35:LG:251:LYS:HG3	35:LG:254:LYS:HE2	1.89	0.54
63:Lq:57:THR:OG1	63:Lq:182:ASN:ND2	2.39	0.54
63:Lq:158:GLN:HE22	63:Lq:160:LYS:HD3	1.73	0.54
1:C1:2077:G:H2'	1:C1:2078:G:H8	1.71	0.54
1:C1:3243:G:O2'	1:C1:3245:A:N6	2.37	0.54
2:C2:205:G:H4'	4:CB:238:SER:HB3	1.88	0.54
11:CI:249:ASP:HA	11:CI:260:CYS:HB2	1.89	0.54
15:CM:64:GLN:NE2	15:CM:100:LYS:O	2.41	0.54
21:CS:206:ARG:HD3	21:CS:206:ARG:N	2.22	0.54
28:CZ:373:ARG:HH22	28:CZ:476:THR:HB	1.72	0.54
33:LC:353:LYS:O	15:LF:77:GLN:NE2	2.36	0.54
55:Lf:18:TYR:OH	55:Lf:91:LEU:O	2.24	0.54
1:C1:1952:G:H2'	1:C1:2016:G:H21	1.72	0.54
6:CD:176:HIS:CE1	6:CD:201:ARG:HD2	2.42	0.54
6:CD:190:ARG:HH22	6:CD:204:LYS:HA	1.72	0.54
25:CW:131:ARG:NH1	25:CW:140:VAL:HG21	2.23	0.54
27:CY:376:LEU:HD12	27:CY:377:LYS:HG3	1.89	0.54
51:LZ:120:ARG:HE	51:LZ:125:LYS:HG3	1.73	0.54
1:C1:513:A:O2'	45:LS:69:PRO:HD2	2.08	0.54
1:C1:1639:C:H2'	1:C1:1640:G:H8	1.73	0.54
1:C1:2797:G:C6	1:C1:2808:G:N2	2.75	0.54
13:CK:146:GLY:O	13:CK:170:ARG:NH2	2.40	0.54
18:CP:259:ARG:HA	18:CP:262:TYR:HB2	1.90	0.54
21:CS:679:GLU:O	21:CS:682:ASN:ND2	2.40	0.54
1:C1:249:C:C4'	20:CR:148:GLN:HE22	2.21	0.54
1:C1:1594:C:H2'	1:C1:1595:U:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1841:U:O2'	1:C1:3023:U:OP1	2.23	0.54
5:CC:726:HIS:CD2	5:CC:730:LEU:HB2	2.43	0.54
6:CD:234:ASP:OD2	6:CD:310:ARG:NH1	2.41	0.54
10:CH:397:ASP:O	10:CH:400:ARG:HG2	2.08	0.54
12:CJ:377:GLU:CD	12:CJ:377:GLU:H	2.15	0.54
25:CW:299:SER:HB2	25:CW:371:LEU:HD12	1.90	0.54
28:CZ:127:LEU:HG	28:CZ:141:LEU:HD13	1.89	0.54
37:LK:106:LEU:HD23	37:LK:151:ILE:HD11	1.90	0.54
54:Le:120:VAL:HB	54:Le:123:ALA:HB2	1.90	0.54
1:C1:466:U:H2'	1:C1:467:G:O4'	2.08	0.54
1:C1:663:G:O6	43:LQ:89:PRO:HB3	2.08	0.54
1:C1:897:G:H2'	1:C1:898:A:C8	2.43	0.54
1:C1:1965:C:H2'	1:C1:1966:A:C8	2.43	0.54
6:CD:20:THR:HA	6:CD:33:ARG:HH12	1.72	0.54
25:CW:22:LEU:HD21	25:CW:50:ARG:HH22	1.73	0.54
25:CW:277:PRO:O	25:CW:279:SER:N	2.40	0.54
38:LL:113:VAL:O	38:LL:117:LYS:HG2	2.07	0.54
1:C1:231:A:H2'	1:C1:232:G:H8	1.71	0.54
22:CT:530:GLU:OE2	22:CT:607:SER:OG	2.25	0.54
25:CW:272:SER:HA	25:CW:424:THR:O	2.08	0.54
28:CZ:229:ILE:HG13	28:CZ:238:LEU:HD23	1.89	0.54
1:C1:1094:A:H2'	1:C1:1095:G:C8	2.43	0.53
4:CB:103:ASP:HB2	4:CB:108:TYR:HE1	1.73	0.53
12:CJ:380:ARG:HB2	12:CJ:401:LEU:HD13	1.88	0.53
33:LC:158:VAL:HG23	33:LC:163:VAL:HG21	1.90	0.53
1:C1:424:G:H2'	1:C1:425:A:H8	1.74	0.53
1:C1:1171:C:H42	1:C1:1297:U:H1'	1.73	0.53
24:CV:31:ASP:HB3	24:CV:34:ASN:HB2	1.89	0.53
28:CZ:411:ALA:HA	28:CZ:415:PHE:HD2	1.72	0.53
5:CC:295:VAL:HG12	5:CC:299:ARG:HH21	1.74	0.53
31:LA:64:ARG:NH1	31:LA:65:SER:O	2.41	0.53
63:Lq:198:TRP:O	63:Lq:201:VAL:HG12	2.08	0.53
1:C1:370:A:H4'	50:LY:90:THR:HG22	1.91	0.53
1:C1:1878:G:O2'	1:C1:2296:U:O4	2.21	0.53
1:C1:2091:U:H2'	1:C1:2092:G:C8	2.42	0.53
5:CC:361:LEU:O	12:CJ:666:LYS:NZ	2.39	0.53
7:CE:191:PRO:HD2	7:CE:195:LEU:HD12	1.89	0.53
15:CM:129:THR:HA	15:CM:132:MET:HE3	1.91	0.53
20:CR:4:GLU:OE2	59:Lj:55:ARG:HB2	2.09	0.53
25:CW:108:LEU:HD13	25:CW:112:ILE:HG12	1.90	0.53
28:CZ:154:LYS:HD2	28:CZ:154:LYS:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1862:A:H2'	1:C1:1863:A:H8	1.73	0.53
5:CC:119:GLU:HB3	5:CC:122:VAL:HG22	1.90	0.53
27:CY:556:ARG:HA	27:CY:559:LEU:HD12	1.90	0.53
63:Lq:55:LEU:HD21	63:Lq:182:ASN:HB3	1.90	0.53
1:C1:966:U:H2'	1:C1:967:U:C6	2.44	0.53
1:C1:1048:G:H2'	1:C1:1049:C:C6	2.44	0.53
8:CF:70:THR:OG1	8:CF:98:GLY:O	2.26	0.53
9:CG:146:VAL:HG12	9:CG:165:PHE:HB2	1.90	0.53
20:CR:175:GLU:HG2	20:CR:178:ARG:HH21	1.73	0.53
22:CT:602:GLN:NE2	27:CY:642:PHE:O	2.41	0.53
25:CW:69:PHE:HB3	25:CW:225:PHE:CE2	2.43	0.53
25:CW:602:THR:HG23	25:CW:604:LYS:H	1.73	0.53
35:LG:85:LEU:HD11	35:LG:183:ILE:HD13	1.89	0.53
50:LY:28:VAL:O	50:LY:31:SER:OG	2.25	0.53
1:C1:39:A:H2'	1:C1:40:A:C8	2.44	0.53
1:C1:1575:C:H2'	1:C1:1576:C:C6	2.44	0.53
21:CS:551:ASP:OD1	21:CS:551:ASP:N	2.42	0.53
1:C1:223:U:H2'	1:C1:224:A:C8	2.43	0.53
10:CH:401:ARG:NH2	16:CN:39:GLU:OE1	2.42	0.53
21:CS:322:LYS:HB3	21:CS:322:LYS:NZ	2.23	0.53
35:LG:99:LYS:NZ	35:LG:213:GLU:OE1	2.37	0.53
43:LQ:99:LEU:HA	43:LQ:103:ASN:HB2	1.88	0.53
1:C1:580:G:N2	34:LE:37:LYS:HD3	2.24	0.53
1:C1:861:G:H1'	1:C1:869:A:N6	2.24	0.53
1:C1:1090:C:H2'	1:C1:1091:A:H8	1.74	0.53
1:C1:1199:A:OP2	30:Cz:62:LYS:NZ	2.29	0.53
16:CN:22:SER:HB3	16:CN:67:ARG:HB2	1.90	0.53
19:CQ:84:GLU:O	19:CQ:88:LYS:HG2	2.09	0.53
25:CW:273:TYR:HD2	25:CW:423:ILE:HG12	1.73	0.53
25:CW:292:LEU:O	25:CW:295:ARG:NH2	2.41	0.53
25:CW:373:ILE:O	25:CW:373:ILE:HD12	2.08	0.53
60:Lk:14:ILE:HG12	60:Lk:17:ARG:HH21	1.73	0.53
63:Lq:128:LEU:O	63:Lq:133:LYS:NZ	2.30	0.53
1:C1:3211:G:N1	34:LE:135:GLU:OE1	2.36	0.53
2:C2:102:U:O2'	2:C2:103:G:OP1	2.25	0.53
12:CJ:28:LEU:HD22	12:CJ:32:ASP:HB3	1.90	0.53
25:CW:70:LEU:HD22	25:CW:108:LEU:HD23	1.89	0.53
31:LA:80:GLU:N	31:LA:168:ILE:O	2.30	0.53
34:LE:171:ALA:O	34:LE:175:LYS:NZ	2.42	0.53
37:LK:108:GLU:O	37:LK:112:ILE:HG13	2.08	0.53
1:C1:116:A:OP1	58:Li:45:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1171:C:C4	1:C1:1297:U:O2	2.62	0.52
1:C1:1877:G:C2	1:C1:1880:A:N6	2.77	0.52
1:C1:1989:G:H2'	1:C1:1990:G:C8	2.44	0.52
1:C1:2257:A:OP2	27:CY:413:LYS:N	2.42	0.52
7:CE:441:TYR:O	7:CE:445:VAL:HG22	2.08	0.52
46:LT:54:HIS:HB2	46:LT:57:TYR:HD1	1.71	0.52
51:LZ:49:PRO:HD3	51:LZ:67:ILE:HG12	1.90	0.52
1:C1:1483:U:H2'	1:C1:1484:G:C8	2.44	0.52
1:C1:1489:G:O2'	1:C1:1490:C:OP1	2.25	0.52
4:CB:282:TYR:HB3	4:CB:290:ALA:HB1	1.90	0.52
21:CS:179:VAL:HG12	21:CS:198:CYS:HB3	1.91	0.52
27:CY:565:THR:HG22	27:CY:566:ASP:N	2.24	0.52
31:LA:134:VAL:HG11	31:LA:148:ILE:HB	1.91	0.52
52:Lc:78:ILE:O	52:Lc:82:THR:HG23	2.10	0.52
60:Lk:26:LYS:HD2	60:Lk:71:VAL:HG21	1.91	0.52
1:C1:295:G:H2'	1:C1:296:G:H8	1.73	0.52
5:CC:121:PHE:CE1	7:CE:472:HIS:HB3	2.44	0.52
7:CE:223:ARG:HH22	7:CE:250:ASN:HB2	1.75	0.52
8:CF:162:GLU:OE1	8:CF:174:MET:HE2	2.09	0.52
12:CJ:40:LYS:HD2	12:CJ:75:GLU:HG3	1.91	0.52
13:CK:127:ILE:HD11	13:CK:132:MET:HG2	1.92	0.52
27:CY:581:SER:HB3	27:CY:584:MET:HE1	1.90	0.52
1:C1:829:A:O2'	29:Ca:75:LYS:NZ	2.39	0.52
1:C1:2266:C:H2'	1:C1:2267:G:H8	1.73	0.52
1:C1:2768:C:H2'	1:C1:2769:A:H8	1.75	0.52
10:CH:156:LEU:HD23	10:CH:159:LEU:HD12	1.91	0.52
12:CJ:475:LEU:HG	12:CJ:483:PRO:HG3	1.90	0.52
12:CJ:614:LEU:HG	12:CJ:618:LYS:HE3	1.92	0.52
17:CO:106:ILE:HG23	17:CO:107:VAL:HG13	1.91	0.52
21:CS:38:LYS:HB3	21:CS:38:LYS:NZ	2.25	0.52
25:CW:14:SER:C	25:CW:16:THR:H	2.18	0.52
25:CW:373:ILE:HG22	25:CW:401:VAL:HG12	1.90	0.52
43:LQ:64:LEU:O	43:LQ:68:THR:OG1	2.20	0.52
1:C1:2457:C:H2'	1:C1:2458:U:H6	1.75	0.52
1:C1:2841:U:H2'	1:C1:2842:C:H6	1.73	0.52
7:CE:193:ARG:NH1	7:CE:219:GLY:O	2.41	0.52
8:CF:164:GLU:HG3	8:CF:211:LEU:HD21	1.90	0.52
11:CI:216:LEU:HG	11:CI:233:ILE:HG12	1.91	0.52
16:CN:100:ARG:NH1	16:CN:122:GLU:OE2	2.42	0.52
21:CS:416:PHE:HE1	56:Lg:92:ARG:HG3	1.75	0.52
22:CT:571:LEU:HD22	22:CT:596:LEU:HD11	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CW:96:PRO:HG3	25:CW:200:LEU:HG	1.92	0.52
27:CY:569:ILE:HG22	27:CY:571:LEU:HD22	1.91	0.52
49:LX:72:GLU:HG3	49:LX:115:LEU:HD11	1.92	0.52
52:Lc:48:ALA:O	52:Lc:56:LYS:NZ	2.35	0.52
61:Lp:77:ALA:HA	61:Lp:80:ARG:HH12	1.74	0.52
1:C1:1795:A:H2'	1:C1:1796:A:C8	2.44	0.52
1:C1:2329:A:H2'	1:C1:2330:A:H8	1.73	0.52
1:C1:2427:G:H2'	1:C1:2428:G:C8	2.44	0.52
1:C1:2736:A:H5''	18:CP:526:TYR:CE1	2.45	0.52
1:C1:3118:A:H2'	1:C1:3119:C:C6	2.44	0.52
6:CD:467:VAL:HG23	6:CD:474:PHE:HB2	1.90	0.52
7:CE:538:LEU:HD21	7:CE:555:ILE:HD11	1.91	0.52
15:CM:90:VAL:HG13	15:CM:123:VAL:HG23	1.91	0.52
25:CW:222:THR:HG21	25:CW:241:MET:HG2	1.91	0.52
25:CW:470:TYR:CE1	25:CW:479:PHE:HB3	2.44	0.52
27:CY:475:LEU:HD23	27:CY:490:VAL:HG11	1.92	0.52
1:C1:308:U:O4	58:Li:37:ARG:NH2	2.43	0.52
1:C1:881:G:H1'	1:C1:1568:A:N6	2.25	0.52
1:C1:894:A:C8	21:CS:728:ARG:HG2	2.45	0.52
1:C1:2319:A:H2'	1:C1:2320:A:H8	1.75	0.52
25:CW:92:ILE:HG12	25:CW:166:LEU:HB3	1.90	0.52
33:LC:211:ILE:HG13	33:LC:256:VAL:HG13	1.91	0.52
49:LX:49:LYS:N	49:LX:49:LYS:HE2	2.25	0.52
61:Lp:79:MET:SD	61:Lp:80:ARG:N	2.83	0.52
1:C1:110:G:OP2	38:LL:73:ARG:NH2	2.41	0.52
1:C1:1188:G:N2	13:CK:39:ALA:O	2.38	0.52
12:CJ:204:GLU:N	12:CJ:204:GLU:OE2	2.42	0.52
28:CZ:267:LYS:HD2	28:CZ:268:PRO:HD2	1.91	0.52
47:LU:42:PHE:O	47:LU:46:ARG:HG2	2.10	0.52
63:Lq:86:SER:H	63:Lq:89:ASP:HB3	1.75	0.52
8:CF:167:ARG:HG2	8:CF:167:ARG:HH11	1.75	0.52
12:CJ:504:GLU:N	12:CJ:504:GLU:OE2	2.42	0.52
27:CY:393:THR:O	27:CY:396:THR:OG1	2.27	0.52
28:CZ:310:GLY:H	31:LA:187:HIS:CE1	2.28	0.52
1:C1:213:G:C6	1:C1:1371:G:N2	2.77	0.52
1:C1:409:A:H2'	1:C1:410:A:C8	2.45	0.52
1:C1:742:A:H2'	1:C1:743:U:C6	2.45	0.52
1:C1:1989:G:H2'	1:C1:1990:G:H8	1.75	0.52
4:CB:156:ASP:OD1	4:CB:156:ASP:N	2.43	0.52
7:CE:435:PRO:O	7:CE:525:HIS:NE2	2.39	0.52
18:CP:291:ARG:HD3	18:CP:291:ARG:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:320:LEU:HD11	18:CP:362:TYR:HD1	1.75	0.52
27:CY:552:PHE:CZ	27:CY:618:VAL:HG23	2.45	0.52
1:C1:1178:C:H41	1:C1:1302:C:H5''	1.75	0.51
1:C1:1587:C:O3'	49:LX:92:GLN:NE2	2.43	0.51
1:C1:1622:A:H5'	1:C1:1801:C:H5'	1.92	0.51
2:C2:76:C:H2'	2:C2:77:A:H8	1.76	0.51
3:CA:229:ILE:HD11	23:CU:255:ARG:HD3	1.92	0.51
7:CE:539:VAL:HA	7:CE:550:PRO:HG3	1.92	0.51
21:CS:731:LYS:O	21:CS:735:GLU:HG2	2.10	0.51
1:C1:2020:C:H5'	1:C1:2021:C:OP2	2.09	0.51
1:C1:2841:U:H2'	1:C1:2842:C:C6	2.45	0.51
2:C2:219:A:H5''	11:CI:222:LYS:NZ	2.25	0.51
3:CA:39:LEU:HD13	3:CA:65:ASP:HB3	1.91	0.51
14:CL:52:ASP:OD1	45:LS:80:ARG:NH2	2.43	0.51
21:CS:26:ARG:HH12	21:CS:82:LYS:HD2	1.75	0.51
25:CW:447:GLU:OE2	25:CW:447:GLU:N	2.42	0.51
31:LA:29:PHE:HB2	31:LA:123:ARG:HA	1.92	0.51
31:LA:77:ILE:HD13	31:LA:128:ARG:HG3	1.91	0.51
33:LC:361:LEU:HD11	46:LT:148:PRO:HG2	1.91	0.51
39:LM:59:LEU:O	45:LS:155:ARG:NH1	2.34	0.51
48:LV:47:ARG:HG3	48:LV:50:ARG:HB3	1.91	0.51
62:L1:27:ILE:O	62:L1:33:ASN:ND2	2.42	0.51
63:Lq:17:LEU:HD23	63:Lq:176:GLN:HE22	1.75	0.51
63:Lq:55:LEU:O	63:Lq:60:ARG:NH2	2.42	0.51
1:C1:1697:A:H2'	1:C1:1698:G:H8	1.75	0.51
1:C1:1778:A:H2'	1:C1:1779:A:H8	1.75	0.51
1:C1:2455:U:O2'	1:C1:2456:A:H5'	2.10	0.51
1:C1:2973:A:H2'	1:C1:2974:G:C8	2.45	0.51
5:CC:724:ARG:HG2	5:CC:781:TRP:HD1	1.74	0.51
21:CS:100:ARG:HH11	21:CS:100:ARG:HG3	1.76	0.51
25:CW:287:GLN:NE2	25:CW:431:ILE:O	2.43	0.51
1:C1:155:G:H2'	1:C1:156:G:C8	2.45	0.51
1:C1:1960:G:H2'	1:C1:1961:G:H8	1.76	0.51
27:CY:429:GLN:HB3	27:CY:432:ARG:NH2	2.24	0.51
31:LA:35:ALA:HB1	31:LA:41:ILE:HD11	1.91	0.51
1:C1:132:C:O2	1:C1:133:G:N1	2.43	0.51
1:C1:3332:G:O2'	1:C1:3333:A:H8	1.93	0.51
6:CD:50:LEU:HA	6:CD:55:MET:HG2	1.91	0.51
13:CK:44:GLY:C	13:CK:46:ARG:H	2.19	0.51
16:CN:107:VAL:HG23	16:CN:108:ILE:HG13	1.92	0.51
20:CR:167:GLU:OE2	20:CR:170:ARG:NH2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:CY:373:ARG:HG2	27:CY:374:LYS:HD2	1.93	0.51
29:Ca:44:LYS:O	29:Ca:48:ILE:HG13	2.10	0.51
35:LG:106:GLN:N	35:LG:106:GLN:OE1	2.43	0.51
47:LU:47:ILE:HD12	47:LU:62:ILE:HD11	1.92	0.51
54:Le:100:ASN:OD1	54:Le:100:ASN:N	2.40	0.51
1:C1:20:A:H2'	1:C1:21:G:C8	2.46	0.51
1:C1:1070:U:H2'	1:C1:1071:G:C8	2.46	0.51
1:C1:1275:U:H2'	1:C1:1276:A:H8	1.74	0.51
1:C1:1405:C:C4	1:C1:1406:C:N4	2.78	0.51
1:C1:1954:C:N4	1:C1:2015:U:C4	2.78	0.51
2:C2:70:G:OP1	50:LY:120:ARG:NH2	2.43	0.51
7:CE:124:LYS:HD2	7:CE:209:TYR:CE2	2.46	0.51
9:CG:109:LEU:HD13	18:CP:358:LEU:HD12	1.93	0.51
12:CJ:362:ASP:N	12:CJ:365:GLN:OE1	2.44	0.51
46:LT:109:VAL:HG23	46:LT:110:LYS:HE2	1.93	0.51
63:Lq:74:ILE:H	63:Lq:74:ILE:HD12	1.73	0.51
1:C1:2163:G:H1'	28:CZ:128:ARG:HA	1.93	0.51
5:CC:232:SER:OG	5:CC:234:ASP:OD1	2.25	0.51
11:CI:242:ASP:HA	11:CI:262:ILE:HD11	1.93	0.51
21:CS:62:VAL:O	21:CS:66:THR:HG22	2.10	0.51
23:CU:210:LYS:H	23:CU:210:LYS:HD2	1.76	0.51
25:CW:117:GLU:OE2	25:CW:117:GLU:N	2.27	0.51
25:CW:264:LYS:HB2	25:CW:421:THR:HG22	1.92	0.51
27:CY:471:LEU:HD22	27:CY:495:TYR:CE1	2.46	0.51
31:LA:130:SER:HB3	31:LA:171:GLY:HA3	1.91	0.51
31:LA:131:GLY:H	31:LA:169:VAL:CG2	2.24	0.51
1:C1:508:G:OP2	15:LF:73:ARG:NH2	2.39	0.51
1:C1:1227:A:H2'	1:C1:1254:C:OP1	2.11	0.51
1:C1:2418:A:H2'	1:C1:2419:G:O4'	2.10	0.51
3:CA:138:PRO:HB3	3:CA:178:HIS:NE2	2.26	0.51
10:CH:495:ILE:HD13	19:CQ:130:ASN:HB2	1.92	0.51
18:CP:318:ARG:NE	22:CT:633:GLU:OE2	2.44	0.51
36:LH:48:VAL:HG23	36:LH:52:VAL:HG13	1.93	0.51
44:LR:89:MET:HE3	44:LR:89:MET:HA	1.92	0.51
51:LZ:28:VAL:HG12	51:LZ:31:GLY:H	1.74	0.51
1:C1:1600:G:H2'	1:C1:1601:U:C6	2.45	0.51
1:C1:1784:C:H2'	1:C1:1785:G:H8	1.76	0.51
1:C1:2370:U:H2'	1:C1:2371:G:H8	1.74	0.51
10:CH:361:LEU:O	10:CH:365:MET:HG2	2.10	0.51
22:CT:291:GLN:HA	22:CT:329:ARG:HB2	1.92	0.51
27:CY:379:LEU:HD23	27:CY:379:LEU:H	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:CY:552:PHE:HZ	27:CY:618:VAL:HG23	1.76	0.51
31:LA:113:VAL:HG23	31:LA:166:ILE:HD13	1.93	0.51
1:C1:2458:U:H2'	1:C1:2459:C:H6	1.76	0.51
9:CG:52:ILE:HG12	18:CP:407:VAL:HG22	1.92	0.51
25:CW:573:SER:HA	25:CW:576:HIS:HB2	1.92	0.51
63:Lq:83:ASP:N	63:Lq:83:ASP:OD1	2.44	0.51
1:C1:1936:C:H2'	1:C1:1937:G:C8	2.47	0.50
5:CC:343:PRO:HD3	15:CM:17:THR:HG22	1.93	0.50
6:CD:391:VAL:HG12	6:CD:408:SER:HB2	1.93	0.50
18:CP:521:GLU:HB3	18:CP:560:LEU:HD23	1.93	0.50
25:CW:264:LYS:HE2	25:CW:264:LYS:N	2.26	0.50
25:CW:416:LEU:HD13	25:CW:419:ARG:HG3	1.93	0.50
27:CY:384:VAL:HA	27:CY:387:TRP:HD1	1.76	0.50
33:LC:295:GLU:OE2	33:LC:295:GLU:N	2.42	0.50
39:LM:49:LYS:NZ	39:LM:49:LYS:HB3	2.26	0.50
1:C1:66:A:N6	1:C1:75:G:H22	2.05	0.50
1:C1:377:A:H2'	1:C1:378:A:C8	2.46	0.50
1:C1:2458:U:H2'	1:C1:2459:C:C6	2.46	0.50
11:CI:322:GLU:H	11:CI:322:GLU:CD	2.20	0.50
18:CP:530:ARG:HH11	18:CP:530:ARG:HG3	1.76	0.50
25:CW:292:LEU:H	25:CW:295:ARG:HH22	1.60	0.50
27:CY:394:ASP:N	27:CY:394:ASP:OD1	2.41	0.50
27:CY:451:GLU:OE1	27:CY:451:GLU:N	2.29	0.50
28:CZ:466:LEU:O	28:CZ:470:HIS:NE2	2.44	0.50
1:C1:19:U:H2'	1:C1:20:A:C8	2.47	0.50
1:C1:137:C:H2'	1:C1:138:G:O4'	2.11	0.50
1:C1:740:U:H2'	1:C1:741:G:O4'	2.10	0.50
1:C1:1842:G:N2	1:C1:1845:C:OP2	2.41	0.50
2:C2:44:A:H2'	2:C2:45:C:C6	2.46	0.50
3:CA:131:ASN:HB2	23:CU:282:MET:HE2	1.93	0.50
9:CG:21:THR:HG22	9:CG:95:ARG:HG3	1.92	0.50
20:CR:148:GLN:OE1	38:LL:86:PRO:HB3	2.12	0.50
22:CT:208:GLN:NE2	22:CT:208:GLN:HA	2.25	0.50
39:LM:19:VAL:HA	39:LM:29:ALA:HA	1.93	0.50
46:LT:68:THR:OG1	46:LT:71:ALA:O	2.22	0.50
1:C1:864:A:H61	9:CG:122:TRP:CD1	2.30	0.50
1:C1:1134:G:N2	14:CL:18:THR:OG1	2.44	0.50
1:C1:2816:U:O2'	10:CH:134:ARG:NH2	2.44	0.50
4:CB:22:GLN:HG2	4:CB:25:LYS:HD3	1.93	0.50
5:CC:233:ARG:NH2	5:CC:237:GLU:OE2	2.44	0.50
5:CC:575:ARG:HB3	5:CC:575:ARG:NH1	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CG:26:LEU:O	9:CG:47:TYR:OH	2.29	0.50
12:CJ:379:PRO:HB2	12:CJ:382:PRO:HD2	1.93	0.50
27:CY:381:LYS:HA	27:CY:384:VAL:HG22	1.93	0.50
27:CY:727:LYS:HB2	27:CY:727:LYS:NZ	2.26	0.50
1:C1:36:C:O2'	1:C1:915:G:N3	2.43	0.50
1:C1:643:A:H2'	1:C1:644:A:C8	2.47	0.50
1:C1:1657:G:O6	47:LU:81:ARG:NH2	2.44	0.50
1:C1:2320:A:H5'	42:LP:135:ARG:HH12	1.76	0.50
1:C1:2331:G:N1	1:C1:2341:U:C4	2.80	0.50
1:C1:3078:U:H1'	1:C1:3079:A:H5''	1.92	0.50
1:C1:3119:C:H2'	1:C1:3120:G:H8	1.77	0.50
6:CD:200:VAL:HB	6:CD:221:LEU:HD12	1.93	0.50
8:CF:145:THR:HG21	8:CF:149:VAL:HG23	1.93	0.50
12:CJ:26:LEU:HD23	12:CJ:73:LEU:HD12	1.93	0.50
25:CW:486:TRP:CZ2	25:CW:503:GLU:HG2	2.47	0.50
36:LH:61:SER:O	36:LH:65:VAL:HG23	2.11	0.50
1:C1:115:A:N6	1:C1:149:U:C2	2.79	0.50
1:C1:1452:U:OP1	1:C1:1491:G:N2	2.40	0.50
1:C1:1924:A:H5''	25:CW:171:GLY:HA3	1.94	0.50
7:CE:580:GLY:O	7:CE:583:TYR:OH	2.24	0.50
12:CJ:585:LEU:HA	12:CJ:588:GLN:HE21	1.77	0.50
21:CS:749:GLU:HA	21:CS:749:GLU:OE2	2.11	0.50
27:CY:417:GLU:O	27:CY:421:LYS:HG3	2.11	0.50
1:C1:2404:G:H2'	1:C1:2405:A:C8	2.46	0.50
1:C1:2414:G:H3'	1:C1:2415:U:H5'	1.93	0.50
7:CE:154:ALA:HB2	7:CE:299:GLN:HE22	1.77	0.50
10:CH:288:LYS:HG2	64:CH:1001:GTP:C5	2.45	0.50
27:CY:708:LEU:HD13	27:CY:711:LEU:HD23	1.92	0.50
53:Ld:59:LEU:HB3	53:Ld:63:LEU:HD23	1.94	0.50
60:Lk:14:ILE:HG12	60:Lk:17:ARG:NH2	2.26	0.50
1:C1:742:A:C2	1:C1:752:A:H1'	2.47	0.50
1:C1:1049:C:H2'	1:C1:1050:C:C6	2.47	0.50
1:C1:1429:G:N7	42:LP:25:SER:OG	2.45	0.50
1:C1:1877:G:N2	1:C1:1880:A:N6	2.58	0.50
1:C1:2001:U:H2'	1:C1:2002:C:C6	2.47	0.50
1:C1:2043:G:H8	1:C1:2044:G:H5'	1.76	0.50
1:C1:2373:U:H2'	1:C1:2374:G:H8	1.77	0.50
1:C1:2453:A:N3	63:Lq:35:GLN:NE2	2.60	0.50
6:CD:43:ARG:HA	6:CD:46:LEU:HD23	1.93	0.50
21:CS:504:TRP:CD2	22:CT:186:PRO:HG3	2.47	0.50
22:CT:514:THR:O	22:CT:518:ARG:HG3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:978:A:H2'	1:C1:979:A:C8	2.47	0.50
3:CA:170:LYS:HE2	5:CC:167:VAL:HG23	1.94	0.50
4:CB:175:THR:OG1	4:CB:178:ARG:NH2	2.38	0.50
8:CF:167:ARG:HG2	8:CF:167:ARG:NH1	2.26	0.50
10:CH:223:ILE:HG22	10:CH:269:LEU:HD11	1.93	0.50
10:CH:347:LEU:HD23	10:CH:361:LEU:HD11	1.92	0.50
27:CY:711:LEU:HD11	27:CY:715:LYS:HB2	1.94	0.50
42:LP:70:THR:HG21	42:LP:83:TRP:CH2	2.44	0.50
42:LP:84:PRO:HB2	42:LP:87:SER:HB2	1.94	0.50
1:C1:596:G:OP2	33:LC:317:LYS:NZ	2.35	0.49
1:C1:1066:A:H2'	1:C1:1067:A:C8	2.47	0.49
1:C1:1126:U:H6	1:C1:1142:C:H41	1.58	0.49
1:C1:1305:C:H4'	45:LS:2:GLY:H	1.77	0.49
1:C1:2432:C:H2'	1:C1:2433:U:O4'	2.12	0.49
7:CE:116:LEU:HB3	7:CE:118:LEU:HD13	1.93	0.49
13:CK:250:GLU:H	13:CK:250:GLU:CD	2.19	0.49
18:CP:383:ARG:NH2	18:CP:448:GLY:O	2.42	0.49
31:LA:114:SER:N	31:LA:165:MET:O	2.35	0.49
1:C1:202:A:H4'	1:C1:204:A:N7	2.27	0.49
1:C1:652:A:OP1	33:LC:109:LYS:NZ	2.39	0.49
1:C1:2200:G:H2'	1:C1:2201:G:H8	1.77	0.49
1:C1:3069:G:O6	1:C1:3077:C:H5''	2.12	0.49
1:C1:3288:G:N1	1:C1:3298:U:C2	2.80	0.49
2:C2:69:U:H2'	2:C2:70:G:O4'	2.12	0.49
5:CC:721:ARG:NH1	51:LZ:102:GLU:OE1	2.43	0.49
6:CD:256:LYS:HD3	6:CD:287:ARG:HH21	1.77	0.49
15:CM:69:ILE:O	15:CM:73:ARG:HG2	2.12	0.49
21:CS:330:ILE:O	25:CW:620:ARG:NH1	2.44	0.49
25:CW:271:MET:HG2	25:CW:423:ILE:HA	1.93	0.49
27:CY:398:ILE:HD12	27:CY:399:THR:N	2.27	0.49
47:LU:23:ILE:HG21	47:LU:39:PHE:HE2	1.77	0.49
1:C1:816:G:H22	1:C1:838:G:H1'	1.77	0.49
1:C1:2414:G:C6	1:C1:2456:A:N1	2.81	0.49
13:CK:147:TRP:O	13:CK:170:ARG:NE	2.30	0.49
20:CR:54:LEU:HD22	57:Lh:122:ALA:HB1	1.94	0.49
23:CU:210:LYS:HD2	23:CU:210:LYS:N	2.28	0.49
28:CZ:431:ILE:O	28:CZ:435:ASN:ND2	2.45	0.49
29:Ca:207:LYS:HD2	29:Ca:210:ARG:NH2	2.26	0.49
44:LR:134:HIS:HD2	44:LR:136:ARG:HB3	1.76	0.49
1:C1:575:A:H2'	1:C1:576:C:C6	2.48	0.49
1:C1:713:G:N1	1:C1:724:C:OP2	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:781:G:H1	33:LC:103:PRO:HD2	1.76	0.49
2:C2:83:C:O2	50:LY:109:HIS:NE2	2.43	0.49
8:CF:45:VAL:HG23	8:CF:45:VAL:O	2.13	0.49
21:CS:54:ALA:HB1	21:CS:57:GLY:HA2	1.94	0.49
21:CS:81:ILE:HD12	21:CS:89:THR:HG23	1.93	0.49
25:CW:375:HIS:HD1	25:CW:375:HIS:C	2.20	0.49
27:CY:542:ILE:HD11	27:CY:547:TYR:HD2	1.78	0.49
27:CY:589:LYS:HB3	27:CY:610:ARG:HD2	1.94	0.49
28:CZ:262:GLU:H	28:CZ:262:GLU:CD	2.17	0.49
15:LF:182:TYR:CZ	15:LF:203:GLN:HG2	2.47	0.49
37:LK:35:LEU:HD11	37:LK:64:ILE:HD13	1.93	0.49
1:C1:687:C:H2'	1:C1:688:G:H8	1.77	0.49
1:C1:977:A:C2	1:C1:1036:A:H1'	2.46	0.49
1:C1:1675:A:H2'	1:C1:1676:A:C8	2.48	0.49
5:CC:689:LEU:HD12	5:CC:703:LEU:HD21	1.95	0.49
7:CE:437:ASP:HB3	7:CE:440:ASP:HB3	1.93	0.49
14:CL:53:PRO:HB2	45:LS:89:ASN:HD22	1.76	0.49
21:CS:655:ILE:HD13	35:LG:261:LYS:HD2	1.94	0.49
21:CS:822:GLU:O	21:CS:826:LEU:HD22	2.12	0.49
31:LA:83:TYR:C	31:LA:86:GLN:HE22	2.19	0.49
1:C1:8:C:H2'	1:C1:9:U:C6	2.47	0.49
1:C1:623:C:OP1	54:Le:42:ARG:NH1	2.45	0.49
1:C1:909:C:H2'	1:C1:910:A:H8	1.75	0.49
1:C1:1210:A:H5''	8:CF:203:SER:HB3	1.95	0.49
1:C1:1835:C:C4	1:C1:1836:C:N4	2.81	0.49
2:C2:178:U:P	4:CB:269:ARG:HH21	2.36	0.49
2:C2:297:C:O2'	2:C2:301:A:N1	2.42	0.49
6:CD:233:VAL:HG12	6:CD:240:ILE:HG12	1.94	0.49
7:CE:441:TYR:OH	7:CE:460:LEU:HB2	2.13	0.49
21:CS:425:THR:HG22	21:CS:427:ALA:H	1.78	0.49
25:CW:80:LEU:HD21	25:CW:190:GLU:OE1	2.13	0.49
27:CY:393:THR:N	27:CY:396:THR:OG1	2.45	0.49
28:CZ:384:PHE:HA	28:CZ:387:MET:SD	2.53	0.49
15:LF:104:LYS:HB3	15:LF:105:PRO:HD3	1.93	0.49
15:LF:178:ASN:HD22	15:LF:178:ASN:N	2.10	0.49
1:C1:590:C:O2	1:C1:592:G:N2	2.46	0.49
1:C1:3069:G:O3'	36:LH:73:THR:HG21	2.12	0.49
1:C1:3108:U:C2	1:C1:3337:C:N3	2.80	0.49
5:CC:494:ASN:ND2	5:CC:497:GLU:HG3	2.27	0.49
15:CM:153:LEU:HD11	15:CM:213:LEU:HD21	1.93	0.49
18:CP:386:ASP:OD2	18:CP:395:THR:OG1	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CT:201:LYS:HD3	22:CT:201:LYS:N	2.26	0.49
27:CY:413:LYS:HE2	27:CY:459:LEU:HD22	1.95	0.49
31:LA:45:VAL:HG12	31:LA:61:VAL:HG22	1.94	0.49
34:LE:182:TYR:OH	39:LM:114:ASP:OD2	2.27	0.49
37:LK:54:LYS:HD2	37:LK:54:LYS:N	2.27	0.49
43:LQ:104:GLU:O	43:LQ:105:LYS:HG3	2.13	0.49
46:LT:45:ASN:H	46:LT:95:HIS:CE1	2.31	0.49
59:Lj:64:MET:HE2	59:Lj:67:LEU:HB3	1.93	0.49
63:Lq:15:GLU:OE1	63:Lq:15:GLU:HA	2.12	0.49
63:Lq:117:ILE:HA	63:Lq:120:ILE:HG22	1.93	0.49
1:C1:2069:A:N6	25:CW:570:GLU:O	2.46	0.49
1:C1:2833:U:O2	1:C1:2909:G:N2	2.34	0.49
1:C1:3026:G:C2	1:C1:3027:A:C8	3.01	0.49
1:C1:3045:G:OP1	32:LB:314:ARG:NH1	2.46	0.49
1:C1:3285:G:OP1	25:CW:586:LYS:HE3	2.13	0.49
3:CA:116:TYR:HB3	3:CA:241:THR:HG23	1.95	0.49
4:CB:253:GLU:OE1	4:CB:253:GLU:N	2.25	0.49
19:CQ:66:ASP:OD2	19:CQ:68:THR:OG1	2.28	0.49
27:CY:417:GLU:HB3	27:CY:459:LEU:HD21	1.94	0.49
28:CZ:191:GLN:O	28:CZ:194:GLU:HG3	2.13	0.49
28:CZ:309:THR:HG23	28:CZ:350:ASN:HD21	1.77	0.49
1:C1:784:C:O2'	33:LC:94:MET:HE1	2.12	0.49
1:C1:1479:C:H2'	1:C1:1480:A:H8	1.78	0.49
1:C1:1655:C:H2'	1:C1:1656:A:C8	2.47	0.49
1:C1:1696:C:H2'	1:C1:1697:A:C8	2.47	0.49
1:C1:2078:G:H2'	1:C1:2079:A:H8	1.77	0.49
1:C1:2963:A:H2'	1:C1:2964:U:O4'	2.13	0.49
4:CB:129:ASP:OD1	4:CB:129:ASP:N	2.37	0.49
5:CC:135:ARG:NH1	5:CC:137:TYR:OH	2.40	0.49
10:CH:162:ILE:HG12	10:CH:205:VAL:HG21	1.95	0.49
21:CS:729:PRO:HD2	21:CS:732:LYS:HB2	1.95	0.49
28:CZ:183:LYS:HD2	28:CZ:183:LYS:N	2.28	0.49
31:LA:142:ASP:OD1	31:LA:142:ASP:N	2.45	0.49
31:LA:181:LYS:HG3	31:LA:183:SER:H	1.78	0.49
46:LT:48:VAL:HG12	46:LT:50:LYS:H	1.77	0.49
1:C1:404:G:H2'	1:C1:405:U:C6	2.48	0.49
1:C1:773:A:H2'	1:C1:774:A:C8	2.48	0.49
1:C1:836:U:H4'	44:LR:95:TRP:NE1	2.28	0.49
1:C1:1446:G:N2	1:C1:1449:A:OP2	2.43	0.49
1:C1:1974:U:H2'	1:C1:1975:C:C6	2.48	0.49
1:C1:3120:G:H4'	1:C1:3121:U:OP2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CF:20:ARG:HH21	8:CF:23:LYS:HD3	1.78	0.49
11:CI:199:TYR:HB3	11:CI:200:GLU:OE1	2.12	0.49
21:CS:60:CYS:HB3	21:CS:87:VAL:HG11	1.94	0.49
25:CW:246:LYS:NZ	29:Ca:156:VAL:HG12	2.28	0.49
27:CY:453:TRP:CZ3	27:CY:501:PHE:HZ	2.31	0.49
28:CZ:322:PHE:HD2	28:CZ:335:PHE:HD2	1.60	0.49
38:LL:128:ARG:NH2	57:Lh:114:THR:O	2.37	0.49
1:C1:1140:A:H62	15:LF:99:ASN:ND2	2.10	0.48
1:C1:2858:A:OP1	13:CK:6:TYR:OH	2.29	0.48
1:C1:2885:C:H1'	1:C1:2886:C:C6	2.48	0.48
2:C2:175:G:H2'	2:C2:176:G:C8	2.48	0.48
11:CI:297:LEU:HD22	11:CI:301:GLN:HE22	1.78	0.48
25:CW:454:GLU:H	25:CW:454:GLU:CD	2.21	0.48
25:CW:616:ILE:O	25:CW:620:ARG:HG3	2.12	0.48
27:CY:711:LEU:HD12	27:CY:712:GLU:H	1.78	0.48
44:LR:134:HIS:CD2	44:LR:136:ARG:HB3	2.48	0.48
1:C1:350:G:N2	1:C1:353:A:OP2	2.37	0.48
1:C1:422:G:H2'	1:C1:423:U:C6	2.48	0.48
1:C1:917:A:O2'	1:C1:918:G:H2'	2.13	0.48
1:C1:1297:U:H4'	1:C1:1299:A:O4'	2.13	0.48
1:C1:1674:U:O2'	1:C1:1728:A:N1	2.40	0.48
1:C1:2835:G:H2'	1:C1:2836:G:H8	1.78	0.48
3:CA:36:VAL:HG22	3:CA:88:ASN:HB2	1.94	0.48
12:CJ:469:GLU:N	12:CJ:469:GLU:OE2	2.46	0.48
15:CM:124:LYS:HD3	15:CM:197:VAL:HG21	1.94	0.48
25:CW:158:PHE:CE2	25:CW:182:VAL:HG22	2.48	0.48
28:CZ:214:ARG:HH21	28:CZ:250:GLN:NE2	2.11	0.48
28:CZ:401:TYR:CE1	28:CZ:414:ILE:HD12	2.48	0.48
31:LA:86:GLN:HB2	31:LA:88:ILE:HG23	1.95	0.48
36:LH:57:ILE:HD13	36:LH:64:ASP:HB3	1.95	0.48
57:Lh:42:SER:HB2	57:Lh:46:LEU:HD11	1.94	0.48
63:Lq:210:MET:N	63:Lq:210:MET:HE2	2.27	0.48
1:C1:423:U:H2'	1:C1:424:G:C8	2.47	0.48
1:C1:1748:G:N7	60:Lk:74:ARG:NH2	2.60	0.48
1:C1:2374:G:H2'	1:C1:2375:A:C8	2.48	0.48
1:C1:3070:A:H2'	1:C1:3071:A:O4'	2.13	0.48
1:C1:3235:A:H2'	1:C1:3236:A:C8	2.47	0.48
4:CB:44:ASP:OD1	4:CB:46:LYS:HG2	2.13	0.48
4:CB:62:ILE:HD12	4:CB:62:ILE:O	2.14	0.48
10:CH:254:ASP:OD1	10:CH:288:LYS:HD3	2.13	0.48
10:CH:289:MET:HE1	10:CH:318:ARG:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:615:GLU:HA	12:CJ:618:LYS:HD2	1.94	0.48
21:CS:574:VAL:O	21:CS:578:ILE:HG22	2.13	0.48
25:CW:594:GLU:HA	25:CW:597:LYS:HE2	1.94	0.48
27:CY:608:TYR:HB3	27:CY:614:TYR:HB2	1.95	0.48
28:CZ:326:LYS:HG3	28:CZ:329:SER:HB3	1.95	0.48
48:LV:68:LYS:HE2	48:LV:68:LYS:HB3	1.62	0.48
1:C1:750:G:H2'	1:C1:751:G:C8	2.48	0.48
1:C1:1954:C:H2'	1:C1:1955:G:O4'	2.14	0.48
1:C1:3189:G:H2'	1:C1:3190:G:H8	1.78	0.48
2:C2:159:C:C5	15:CM:55:GLU:HG2	2.48	0.48
5:CC:177:LEU:HD22	5:CC:186:ILE:HD11	1.95	0.48
5:CC:203:ALA:HB2	26:CX:124:ARG:HH22	1.77	0.48
5:CC:258:THR:HG23	35:LG:76:PRO:HG2	1.94	0.48
6:CD:193:SER:HG	6:CD:203:TRP:NE1	2.11	0.48
6:CD:369:MET:N	6:CD:382:MET:O	2.41	0.48
6:CD:470:LYS:H	6:CD:470:LYS:CE	2.26	0.48
12:CJ:380:ARG:NH1	12:CJ:384:GLU:OE2	2.46	0.48
12:CJ:622:ARG:O	12:CJ:626:GLN:HG2	2.12	0.48
21:CS:789:VAL:HG22	21:CS:811:ARG:HE	1.77	0.48
22:CT:131:LEU:HD21	22:CT:155:ILE:HD11	1.94	0.48
23:CU:194:GLU:H	23:CU:194:GLU:CD	2.19	0.48
25:CW:460:GLN:O	25:CW:464:VAL:HG22	2.13	0.48
42:LP:29:THR:HG21	42:LP:146:ILE:HD11	1.96	0.48
45:LS:6:GLU:HB3	45:LS:64:ILE:HB	1.95	0.48
1:C1:267:U:H2'	1:C1:268:A:C8	2.49	0.48
1:C1:1116:G:H4'	23:CU:317:VAL:HG21	1.95	0.48
1:C1:1758:C:H2'	27:CY:4:ALA:HB2	1.95	0.48
4:CB:65:THR:OG1	4:CB:282:TYR:HB2	2.14	0.48
6:CD:55:MET:O	6:CD:55:MET:HE3	2.14	0.48
21:CS:105:SER:O	21:CS:108:LYS:NZ	2.34	0.48
21:CS:356:GLU:O	21:CS:359:LYS:HG3	2.14	0.48
25:CW:426:LEU:HD11	25:CW:429:PRO:HG2	1.95	0.48
31:LA:117:GLU:HB2	31:LA:162:SER:HB3	1.95	0.48
36:LH:12:VAL:HG21	39:LM:4:ILE:HD11	1.95	0.48
37:LK:151:ILE:HG13	37:LK:160:ILE:HD12	1.95	0.48
47:LU:42:PHE:HZ	47:LU:89:LYS:HG2	1.79	0.48
1:C1:68:C:OP2	1:C1:293:G:N2	2.46	0.48
1:C1:1526:G:H5'	40:LN:67:ARG:HD2	1.95	0.48
3:CA:195:GLU:HB2	3:CA:234:ILE:HG21	1.95	0.48
5:CC:725:PHE:CD1	5:CC:733:PHE:HB3	2.47	0.48
10:CH:193:VAL:HG13	64:CH:1001:GTP:H5''	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CL:63:GLU:HG2	30:Cz:61:MET:HE1	1.95	0.48
14:CL:277:PRO:O	14:CL:279:ALA:N	2.44	0.48
16:CN:67:ARG:HD3	16:CN:112:ASP:OD2	2.14	0.48
18:CP:394:LYS:HE2	18:CP:456:ASP:OD2	2.13	0.48
22:CT:129:GLU:HA	22:CT:129:GLU:OE2	2.13	0.48
25:CW:617:ASN:N	25:CW:617:ASN:OD1	2.45	0.48
41:LO:35:VAL:HG22	41:LO:105:LYS:HB2	1.94	0.48
46:LT:65:TYR:HB3	46:LT:75:ILE:HD11	1.95	0.48
51:LZ:7:SER:OG	51:LZ:87:GLU:OE1	2.27	0.48
1:C1:713:G:C5	1:C1:723:G:C2	3.01	0.48
1:C1:727:C:H2'	1:C1:728:A:H8	1.77	0.48
1:C1:1054:G:H2'	1:C1:1055:U:C6	2.49	0.48
1:C1:1156:G:N2	41:LO:89:MET:HE2	2.28	0.48
1:C1:1595:U:H2'	1:C1:1596:G:H8	1.78	0.48
1:C1:2991:C:H5''	17:CO:9:ARG:HH12	1.77	0.48
1:C1:3119:C:H2'	1:C1:3120:G:C8	2.49	0.48
1:C1:3131:A:O2'	1:C1:3132:U:OP1	2.28	0.48
1:C1:3314:U:OP1	53:Ld:23:HIS:NE2	2.40	0.48
2:C2:9:A:H2'	2:C2:10:A:C8	2.49	0.48
5:CC:359:GLU:HG2	12:CJ:667:ARG:HB2	1.95	0.48
6:CD:203:TRP:HB3	6:CD:215:LEU:HD12	1.94	0.48
11:CI:212:GLU:OE1	11:CI:212:GLU:N	2.42	0.48
12:CJ:400:VAL:HG13	12:CJ:401:LEU:HD23	1.95	0.48
22:CT:174:VAL:O	22:CT:178:VAL:HG22	2.13	0.48
27:CY:615:GLN:CD	27:CY:666:ASN:HD21	2.22	0.48
37:LK:41:LYS:O	37:LK:44:GLU:HG3	2.14	0.48
51:LZ:10:CYS:HB3	51:LZ:79:LEU:HD22	1.96	0.48
51:LZ:91:LEU:HD11	51:LZ:117:LEU:HD11	1.95	0.48
63:Lq:180:VAL:O	63:Lq:183:ILE:HG13	2.14	0.48
63:Lq:198:TRP:CD1	63:Lq:198:TRP:C	2.92	0.48
4:CB:126:ARG:HD3	4:CB:150:HIS:HE1	1.77	0.48
6:CD:349:THR:OG1	6:CD:401:GLU:OE2	2.26	0.48
18:CP:551:TYR:O	18:CP:553:GLY:N	2.46	0.48
40:LN:39:ALA:HB3	40:LN:61:ILE:HG22	1.96	0.48
54:Le:1:MET:HG2	54:Le:3:ALA:H	1.78	0.48
61:Lp:49:ARG:HH21	61:Lp:52:VAL:HA	1.78	0.48
63:Lq:58:VAL:HA	63:Lq:60:ARG:HD3	1.96	0.48
1:C1:579:A:H1'	1:C1:1319:G:H5''	1.95	0.48
1:C1:753:U:H2'	1:C1:754:G:C8	2.49	0.48
1:C1:1842:G:H1	1:C1:1845:C:P	2.37	0.48
1:C1:1953:A:H2'	1:C1:1954:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2059:C:H2'	1:C1:2060:C:C6	2.49	0.48
1:C1:3180:C:H2'	1:C1:3181:C:O4'	2.13	0.48
20:CR:172:LEU:HD22	38:LL:126:PHE:HZ	1.79	0.48
33:LC:289:ARG:HH11	33:LC:289:ARG:HG3	1.79	0.48
33:LC:301:ARG:NH1	43:LQ:69:GLU:OE2	2.47	0.48
40:LN:191:TRP:CE2	40:LN:195:ASN:ND2	2.82	0.48
45:LS:80:ARG:HG3	45:LS:124:LEU:HD22	1.96	0.48
48:LV:73:LYS:HB2	48:LV:73:LYS:HE3	1.66	0.48
1:C1:264:G:H2'	1:C1:265:A:H8	1.78	0.48
1:C1:768:G:H2'	1:C1:769:C:C6	2.49	0.48
1:C1:1321:C:H2'	1:C1:1322:C:C6	2.48	0.48
1:C1:1467:G:N2	56:Lg:5:ARG:HD2	2.29	0.48
1:C1:3295:U:O2	25:CW:592:LYS:NZ	2.47	0.48
6:CD:221:LEU:HB3	6:CD:252:TRP:CZ3	2.49	0.48
18:CP:394:LYS:O	18:CP:398:MET:HG3	2.14	0.48
21:CS:259:ILE:HD12	21:CS:259:ILE:N	2.29	0.48
25:CW:194:MET:HB2	25:CW:224:LEU:HD23	1.96	0.48
25:CW:354:LEU:HD13	25:CW:356:THR:HG21	1.95	0.48
25:CW:460:GLN:O	25:CW:463:PHE:N	2.47	0.48
28:CZ:394:HIS:HA	28:CZ:397:ILE:HG12	1.95	0.48
36:LH:28:GLU:HG3	36:LH:33:LYS:HG3	1.95	0.48
51:LZ:2:LYS:O	51:LZ:5:LYS:NZ	2.43	0.48
53:Ld:89:ASP:OD1	53:Ld:89:ASP:N	2.44	0.48
55:Lf:50:ARG:HB3	55:Lf:70:TRP:HZ3	1.77	0.48
61:Lp:77:ALA:HA	61:Lp:80:ARG:NH1	2.29	0.48
1:C1:416:G:O2'	54:Le:24:ASP:OD2	2.21	0.47
1:C1:773:A:H2'	1:C1:774:A:H8	1.77	0.47
1:C1:817:A:C2	1:C1:839:A:H1'	2.49	0.47
1:C1:1963:A:H2'	1:C1:1964:G:H8	1.79	0.47
1:C1:2797:G:C6	1:C1:2808:G:C2	3.01	0.47
1:C1:2959:C:O2'	32:LB:181:GLU:OE2	2.31	0.47
25:CW:327:VAL:HG13	25:CW:354:LEU:HD23	1.96	0.47
28:CZ:436:ASP:O	28:CZ:440:ARG:NH1	2.47	0.47
37:LK:99:LYS:HB2	37:LK:99:LYS:NZ	2.28	0.47
39:LM:5:ASN:OD1	39:LM:5:ASN:N	2.46	0.47
1:C1:2380:G:H5''	1:C1:2381:A:H5'	1.95	0.47
1:C1:2774:G:H2'	1:C1:2775:A:H8	1.78	0.47
8:CF:145:THR:HG22	8:CF:148:GLU:HB2	1.96	0.47
12:CJ:258:ASP:HB3	12:CJ:261:LYS:HB2	1.96	0.47
17:CO:92:GLY:H	32:LB:147:ARG:HD2	1.79	0.47
21:CS:803:GLY:O	33:LC:70:ARG:NH2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CW:298:ARG:HB2	25:CW:368:GLN:O	2.14	0.47
27:CY:378:MET:HA	27:CY:381:LYS:NZ	2.29	0.47
29:Ca:71:ARG:HH21	29:Ca:74:ARG:HH12	1.62	0.47
45:LS:12:ARG:HB3	45:LS:24:LEU:HD12	1.94	0.47
1:C1:188:U:H2'	1:C1:189:G:O4'	2.15	0.47
1:C1:247:A:H2'	1:C1:248:G:H8	1.80	0.47
1:C1:1615:C:O2'	51:LZ:78:HIS:ND1	2.44	0.47
1:C1:2199:C:H2'	1:C1:2200:G:C8	2.50	0.47
1:C1:3115:C:H2'	1:C1:3116:G:H8	1.78	0.47
3:CA:111:PRO:HD2	23:CU:203:ILE:HD13	1.96	0.47
27:CY:581:SER:OG	27:CY:582:ALA:N	2.46	0.47
29:Ca:57:ARG:HG2	29:Ca:60:ARG:HH12	1.79	0.47
31:LA:51:ASP:O	31:LA:54:ARG:NH1	2.47	0.47
39:LM:13:ARG:NH2	45:LS:149:SER:O	2.48	0.47
46:LT:118:LYS:C	46:LT:118:LYS:HD3	2.39	0.47
54:Le:77:VAL:HG13	54:Le:82:ASP:HB2	1.95	0.47
55:Lf:55:TYR:CZ	55:Lf:67:ARG:HB2	2.49	0.47
63:Lq:165:MET:N	63:Lq:165:MET:SD	2.87	0.47
1:C1:448:A:H61	1:C1:467:G:H1'	1.79	0.47
1:C1:1777:A:H2'	1:C1:1778:A:C8	2.49	0.47
1:C1:2076:C:H2'	1:C1:2077:G:C8	2.49	0.47
1:C1:3298:U:H2'	1:C1:3299:A:C8	2.50	0.47
2:C2:75:G:OP2	50:LY:73:TYR:OH	2.28	0.47
7:CE:172:MET:HE1	7:CE:186:ALA:HB2	1.97	0.47
7:CE:186:ALA:HB3	7:CE:236:LEU:HD12	1.96	0.47
16:CN:109:VAL:HG23	16:CN:116:LEU:HB2	1.94	0.47
20:CR:34:ILE:HD12	20:CR:172:LEU:HD23	1.96	0.47
25:CW:173:LEU:HD23	25:CW:212:ILE:HD13	1.96	0.47
25:CW:277:PRO:HD2	25:CW:280:HIS:ND1	2.29	0.47
28:CZ:347:LEU:HD23	28:CZ:347:LEU:H	1.78	0.47
29:Ca:60:ARG:NH1	29:Ca:60:ARG:HB3	2.29	0.47
31:LA:51:ASP:H	31:LA:54:ARG:NH1	2.13	0.47
31:LA:83:TYR:H	31:LA:86:GLN:NE2	2.12	0.47
42:LP:24:VAL:HG12	42:LP:86:LYS:HG2	1.96	0.47
1:C1:753:U:H2'	1:C1:754:G:H8	1.80	0.47
1:C1:926:C:H2'	1:C1:927:C:C6	2.49	0.47
1:C1:1263:U:H2'	1:C1:1264:G:C8	2.47	0.47
1:C1:1283:A:N1	13:CK:45:LEU:HD22	2.29	0.47
1:C1:1285:A:H2'	1:C1:1286:A:C4	2.50	0.47
1:C1:1288:G:O6	1:C1:2328:C:O2'	2.33	0.47
1:C1:1448:G:N2	1:C1:1492:G:H5''	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2078:G:H2'	1:C1:2079:A:C8	2.49	0.47
1:C1:2867:U:H2'	1:C1:2868:A:O4'	2.15	0.47
3:CA:39:LEU:HD12	3:CA:40:SER:H	1.79	0.47
6:CD:24:PRO:HA	6:CD:27:GLU:HG2	1.97	0.47
6:CD:230:TRP:HB3	6:CD:243:ALA:HB3	1.96	0.47
9:CG:54:ASN:O	9:CG:57:THR:OG1	2.29	0.47
13:CK:42:LEU:HD13	13:CK:46:ARG:HG2	1.96	0.47
14:CL:45:TRP:N	14:CL:45:TRP:CD1	2.83	0.47
15:CM:184:ILE:HD13	15:CM:189:ASP:HB3	1.95	0.47
18:CP:339:LYS:HE2	18:CP:339:LYS:HB3	1.58	0.47
20:CR:213:ARG:HH11	20:CR:213:ARG:HG3	1.79	0.47
27:CY:413:LYS:NZ	27:CY:416:ARG:HB2	2.29	0.47
34:LE:132:LYS:HE2	34:LE:136:LYS:HE2	1.96	0.47
45:LS:133:GLU:O	45:LS:133:GLU:HG2	2.14	0.47
46:LT:83:ARG:NH1	46:LT:84:TYR:O	2.46	0.47
1:C1:651:A:H2'	1:C1:652:A:H8	1.78	0.47
1:C1:983:A:N1	1:C1:1032:U:O2'	2.47	0.47
1:C1:1655:C:H2'	1:C1:1656:A:H8	1.80	0.47
1:C1:1784:C:OP2	56:Lg:68:LYS:NZ	2.48	0.47
1:C1:2555:U:H2'	1:C1:2556:G:C8	2.47	0.47
1:C1:3297:U:O2'	1:C1:3298:U:OP1	2.27	0.47
6:CD:20:THR:HA	6:CD:33:ARG:NH1	2.30	0.47
6:CD:189:ASP:OD1	6:CD:190:ARG:NE	2.47	0.47
7:CE:184:THR:HA	7:CE:234:VAL:O	2.15	0.47
11:CI:202:GLU:OE2	11:CI:202:GLU:N	2.43	0.47
21:CS:77:ASP:HB3	21:CS:81:ILE:HD11	1.97	0.47
21:CS:206:ARG:NH1	29:Ca:25:GLU:HA	2.29	0.47
25:CW:56:VAL:HG23	25:CW:224:LEU:HB3	1.95	0.47
28:CZ:199:LYS:HG3	28:CZ:200:PHE:N	2.29	0.47
15:LF:237:ARG:HB3	15:LF:240:HIS:HB2	1.97	0.47
53:Ld:18:ARG:HG2	53:Ld:116:VAL:HG22	1.95	0.47
63:Lq:7:ALA:HA	63:Lq:10:ARG:HG2	1.96	0.47
1:C1:662:C:H2'	1:C1:663:G:O4'	2.14	0.47
1:C1:1281:U:OP1	13:CK:43:ARG:NH2	2.47	0.47
1:C1:1303:G:H2'	1:C1:1304:U:C6	2.50	0.47
1:C1:1575:C:H2'	1:C1:1576:C:H6	1.80	0.47
4:CB:167:LEU:HD23	4:CB:171:PHE:CG	2.49	0.47
4:CB:282:TYR:CD1	4:CB:292:PRO:HA	2.49	0.47
6:CD:73:ARG:HA	6:CD:73:ARG:NE	2.28	0.47
6:CD:94:GLN:HE22	6:CD:96:VAL:HG22	1.79	0.47
7:CE:268:ARG:HH21	7:CE:272:ILE:HD11	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CE:485:PHE:CE1	7:CE:490:ILE:HD12	2.48	0.47
8:CF:79:THR:HG23	8:CF:80:THR:HG23	1.97	0.47
9:CG:74:MET:HE3	9:CG:74:MET:HB3	1.84	0.47
10:CH:360:ARG:HH11	10:CH:360:ARG:HG3	1.79	0.47
11:CI:248:MET:HE3	11:CI:248:MET:HB3	1.78	0.47
16:CN:53:ILE:O	16:CN:56:THR:OG1	2.32	0.47
21:CS:112:ALA:O	21:CS:150:ILE:HG22	2.14	0.47
21:CS:282:PRO:HD3	21:CS:289:LEU:HD23	1.96	0.47
21:CS:357:GLU:HA	21:CS:360:ILE:HG13	1.95	0.47
25:CW:403:MET:HE1	25:CW:405:GLN:HG3	1.96	0.47
27:CY:404:ILE:HD12	27:CY:405:ARG:N	2.30	0.47
27:CY:711:LEU:HD12	27:CY:712:GLU:N	2.30	0.47
28:CZ:237:ILE:O	28:CZ:241:ILE:HG22	2.15	0.47
28:CZ:297:PHE:HB2	28:CZ:321:TYR:HE2	1.80	0.47
36:LH:8:GLU:OE2	36:LH:69:ARG:HD2	2.14	0.47
45:LS:5:GLN:HA	45:LS:100:VAL:HG11	1.95	0.47
46:LT:102:ARG:O	46:LT:106:LEU:HD22	2.15	0.47
48:LV:81:VAL:HG12	48:LV:82:ARG:HG3	1.96	0.47
50:LY:31:SER:HA	50:LY:48:PRO:HA	1.96	0.47
54:Le:62:LYS:HB2	54:Le:62:LYS:HE3	1.74	0.47
1:C1:491:A:H2'	1:C1:492:U:C6	2.49	0.47
1:C1:1595:U:H2'	1:C1:1596:G:C8	2.50	0.47
1:C1:2314:A:H5''	42:LP:83:TRP:O	2.15	0.47
1:C1:2319:A:H2'	1:C1:2320:A:C8	2.49	0.47
1:C1:2341:U:C2'	1:C1:2342:U:H5'	2.45	0.47
1:C1:2944:U:H2'	1:C1:2945:A:H8	1.79	0.47
3:CA:192:ARG:CZ	3:CA:237:ARG:HG3	2.45	0.47
6:CD:14:GLN:HB3	6:CD:36:LEU:HD11	1.97	0.47
10:CH:457:LYS:HB3	19:CQ:71:PHE:CE1	2.50	0.47
25:CW:15:TRP:HA	25:CW:15:TRP:CE3	2.50	0.47
28:CZ:275:THR:OG1	28:CZ:276:ALA:N	2.48	0.47
28:CZ:395:MET:O	28:CZ:398:LEU:HB3	2.14	0.47
30:Cz:50:LEU:HG	45:LS:133:GLU:HG3	1.95	0.47
40:LN:191:TRP:NE1	40:LN:195:ASN:ND2	2.62	0.47
51:LZ:59:ALA:O	51:LZ:63:LYS:HG3	2.15	0.47
1:C1:441:G:H2'	1:C1:442:C:O4'	2.14	0.47
1:C1:631:G:H5''	1:C1:1098:G:C8	2.50	0.47
1:C1:651:A:H2'	1:C1:652:A:C8	2.50	0.47
1:C1:1607:U:H5'	1:C1:1608:U:H5'	1.97	0.47
1:C1:1967:G:H2'	1:C1:1968:A:H8	1.78	0.47
1:C1:2408:U:H2'	1:C1:2409:A:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2751:G:H2'	1:C1:2752:G:C8	2.50	0.47
3:CA:111:PRO:HG3	23:CU:199:ALA:HB1	1.97	0.47
6:CD:73:ARG:HH11	12:CJ:589:ARG:HE	1.63	0.47
21:CS:369:GLU:OE1	21:CS:372:ARG:NH2	2.46	0.47
25:CW:245:HIS:ND1	29:Ca:155:ALA:HA	2.30	0.47
28:CZ:315:HIS:CG	28:CZ:354:THR:HG21	2.50	0.47
34:LE:176:VAL:HG12	34:LE:179:LEU:HB2	1.96	0.47
35:LG:74:VAL:HG23	35:LG:79:ALA:HB2	1.97	0.47
40:LN:68:ARG:HA	40:LN:98:LEU:HD21	1.97	0.47
63:Lq:94:ASN:O	63:Lq:97:LYS:NZ	2.38	0.47
1:C1:447:C:N3	34:LE:15:ARG:NH1	2.63	0.47
1:C1:523:A:H2'	1:C1:524:A:C8	2.49	0.47
1:C1:643:A:H2'	1:C1:644:A:H8	1.80	0.47
1:C1:1077:U:O2'	1:C1:1078:C:O5'	2.28	0.47
1:C1:1843:A:C8	1:C1:1894:A:H5''	2.50	0.47
1:C1:2011:G:H2'	1:C1:2012:G:C8	2.50	0.47
1:C1:2157:C:H2'	1:C1:2158:C:C6	2.50	0.47
1:C1:2849:U:O2'	17:CO:2:ALA:N	2.44	0.47
2:C2:71:A:N6	2:C2:85:G:C2	2.83	0.47
2:C2:76:C:H2'	2:C2:77:A:C8	2.50	0.47
5:CC:239:ILE:HD11	21:CS:666:LEU:HD12	1.96	0.47
5:CC:455:ARG:HG2	5:CC:473:ASP:OD2	2.15	0.47
7:CE:190:THR:OG1	7:CE:195:LEU:HB2	2.15	0.47
10:CH:401:ARG:NH1	16:CN:44:ASP:OD2	2.47	0.47
21:CS:23:LYS:HD2	21:CS:23:LYS:O	2.14	0.47
23:CU:217:HIS:CD2	23:CU:217:HIS:H	2.33	0.47
27:CY:398:ILE:O	27:CY:402:LEU:HD23	2.14	0.47
36:LH:135:GLU:OE1	36:LH:135:GLU:N	2.47	0.47
41:LO:191:VAL:HG13	41:LO:192:ASP:N	2.30	0.47
45:LS:67:LYS:HE3	45:LS:67:LYS:HB3	1.57	0.47
57:Lh:71:LEU:HD22	57:Lh:75:TYR:HE2	1.79	0.47
1:C1:243:G:N2	20:CR:191:GLU:OE1	2.45	0.46
1:C1:535:C:O2	36:LH:50:LYS:NZ	2.33	0.46
1:C1:1054:G:H2'	1:C1:1055:U:H6	1.80	0.46
1:C1:1151:A:H2'	1:C1:1152:A:C8	2.50	0.46
1:C1:1995:C:N4	1:C1:1996:G:O6	2.48	0.46
1:C1:2407:A:H2'	1:C1:2408:U:C6	2.50	0.46
6:CD:39:ALA:O	6:CD:77:GLU:N	2.44	0.46
8:CF:135:VAL:HG11	8:CF:214:ILE:HD13	1.97	0.46
27:CY:539:MET:HE3	27:CY:539:MET:C	2.40	0.46
28:CZ:371:LYS:HA	28:CZ:374:LYS:HE2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:LM:14:VAL:HG13	39:LM:64:LEU:HD11	1.97	0.46
50:LY:85:THR:HG22	50:LY:95:PRO:HA	1.97	0.46
1:C1:1090:C:H2'	1:C1:1091:A:C8	2.49	0.46
1:C1:1696:C:H2'	1:C1:1697:A:H8	1.80	0.46
1:C1:3299:A:H2'	1:C1:3300:C:H6	1.80	0.46
5:CC:571:ARG:HE	5:CC:571:ARG:HB3	1.59	0.46
10:CH:310:LYS:HE2	28:CZ:327:PRO:O	2.16	0.46
16:CN:101:LEU:HD12	16:CN:121:LEU:HD12	1.97	0.46
18:CP:283:LYS:HE3	18:CP:518:GLU:OE2	2.15	0.46
19:CQ:175:ALA:HA	53:Ld:104:VAL:HA	1.96	0.46
21:CS:660:MET:HE3	21:CS:663:ALA:HB3	1.97	0.46
25:CW:152:ALA:HA	25:CW:155:LEU:HD23	1.98	0.46
34:LE:194:LYS:HB3	34:LE:196:HIS:CE1	2.50	0.46
37:LK:108:GLU:HA	37:LK:111:GLU:HG2	1.96	0.46
48:LV:81:VAL:HG13	48:LV:120:VAL:HA	1.96	0.46
63:Lq:34:LEU:HD12	63:Lq:204:LEU:HD21	1.96	0.46
1:C1:101:G:OP2	1:C1:101:G:N2	2.46	0.46
1:C1:1436:A:N6	1:C1:1858:A:O2'	2.48	0.46
1:C1:2735:G:O6	1:C1:2741:U:O4	2.32	0.46
2:C2:26:U:H2'	2:C2:27:U:C6	2.51	0.46
6:CD:49:ILE:O	6:CD:55:MET:HG2	2.15	0.46
6:CD:319:ASP:OD1	6:CD:321:THR:OG1	2.26	0.46
7:CE:321:ASP:OD1	7:CE:321:ASP:N	2.48	0.46
7:CE:342:ASP:OD1	7:CE:342:ASP:N	2.37	0.46
8:CF:44:SER:HB2	8:CF:224:LEU:HD11	1.98	0.46
10:CH:429:ASN:HB3	10:CH:432:TRP:CD2	2.51	0.46
13:CK:132:MET:HE3	13:CK:132:MET:HB3	1.76	0.46
25:CW:283:PRO:O	25:CW:287:GLN:N	2.48	0.46
28:CZ:297:PHE:HB2	28:CZ:321:TYR:CE2	2.50	0.46
32:LB:160:ARG:HG2	32:LB:183:GLN:HA	1.96	0.46
1:C1:1055:U:H2'	1:C1:1056:U:C6	2.50	0.46
1:C1:1259:C:H2'	1:C1:1260:A:H8	1.80	0.46
6:CD:443:ARG:NH1	6:CD:475:SER:OG	2.49	0.46
7:CE:113:PHE:CZ	7:CE:134:MET:HG3	2.50	0.46
12:CJ:77:LEU:HA	12:CJ:80:LYS:HB2	1.98	0.46
22:CT:624:ARG:H	22:CT:624:ARG:HG2	1.53	0.46
25:CW:58:GLU:HB2	25:CW:248:THR:HG22	1.98	0.46
27:CY:387:TRP:HA	27:CY:397:ARG:HH12	1.81	0.46
54:Le:77:VAL:HG11	54:Le:83:VAL:HG13	1.97	0.46
1:C1:817:A:O5'	1:C1:817:A:H8	1.97	0.46
1:C1:1701:U:O4'	44:LR:96:MET:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1949:G:H2'	1:C1:1950:C:C6	2.51	0.46
1:C1:2433:U:C2	1:C1:2436:G:O6	2.68	0.46
1:C1:3164:G:C6	1:C1:3206:G:C2	3.04	0.46
3:CA:39:LEU:HD12	3:CA:40:SER:N	2.30	0.46
6:CD:120:LEU:HB2	6:CD:185:PHE:CE2	2.50	0.46
9:CG:128:GLU:O	9:CG:147:THR:OG1	2.19	0.46
10:CH:440:ILE:HB	32:LB:300:ASP:HB2	1.97	0.46
24:CV:88:ARG:NH1	34:LE:24:ALA:O	2.45	0.46
24:CV:106:ASP:OD1	24:CV:106:ASP:N	2.47	0.46
29:Ca:161:GLU:OE1	29:Ca:164:HIS:NE2	2.48	0.46
32:LB:45:ALA:H	32:LB:182:ILE:HG23	1.79	0.46
34:LE:73:LEU:HD11	34:LE:84:THR:HB	1.98	0.46
50:LY:111:ASP:N	50:LY:111:ASP:OD1	2.47	0.46
51:LZ:3:PHE:HE2	51:LZ:81:PRO:HG3	1.79	0.46
1:C1:224:A:H2'	1:C1:225:G:O4'	2.14	0.46
1:C1:1514:C:H2'	1:C1:1515:U:C6	2.50	0.46
1:C1:1576:C:H2'	1:C1:1577:G:C8	2.50	0.46
1:C1:2000:C:H2'	1:C1:2001:U:C6	2.51	0.46
1:C1:2747:U:O4	1:C1:2748:A:N6	2.48	0.46
1:C1:3008:U:H2'	1:C1:3009:G:H8	1.81	0.46
1:C1:3162:A:H5''	1:C1:3163:G:C5	2.50	0.46
4:CB:120:LEU:HD23	4:CB:123:LYS:NZ	2.31	0.46
4:CB:256:ALA:HA	4:CB:259:ILE:HG22	1.98	0.46
5:CC:234:ASP:OD1	5:CC:234:ASP:N	2.47	0.46
5:CC:704:ASP:OD2	5:CC:753:GLN:NE2	2.48	0.46
7:CE:362:VAL:HB	7:CE:412:ILE:HG22	1.98	0.46
7:CE:386:ASP:N	7:CE:386:ASP:OD1	2.47	0.46
7:CE:387:LEU:HD13	7:CE:411:LEU:HD11	1.97	0.46
9:CG:47:TYR:CD2	9:CG:89:ILE:HD11	2.51	0.46
16:CN:197:MET:HE3	16:CN:197:MET:HB2	1.83	0.46
19:CQ:66:ASP:HB3	19:CQ:69:LEU:HG	1.97	0.46
22:CT:322:LEU:HD12	22:CT:419:LEU:HD22	1.97	0.46
25:CW:43:LYS:HG3	25:CW:44:SER:H	1.81	0.46
27:CY:580:GLN:O	27:CY:585:LYS:NZ	2.48	0.46
27:CY:584:MET:H	27:CY:584:MET:HE2	1.80	0.46
28:CZ:218:ILE:HD12	28:CZ:219:PRO:CD	2.46	0.46
28:CZ:256:ARG:HA	28:CZ:259:TYR:CD2	2.48	0.46
35:LG:53:VAL:HG11	49:LX:43:THR:HB	1.98	0.46
1:C1:2370:U:H2'	1:C1:2371:G:C8	2.51	0.46
5:CC:119:GLU:OE2	7:CE:439:ARG:NH2	2.49	0.46
15:CM:166:ARG:HD2	15:CM:209:TRP:CD1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CN:156:ASN:ND2	16:CN:201:ASP:OD2	2.47	0.46
21:CS:176:PHE:CE2	21:CS:201:PHE:HB2	2.50	0.46
25:CW:426:LEU:HD21	25:CW:429:PRO:HG2	1.97	0.46
25:CW:446:ARG:HG3	25:CW:446:ARG:NH1	2.28	0.46
34:LE:170:ILE:O	34:LE:174:LYS:HG2	2.16	0.46
15:LF:114:LEU:HD21	15:LF:121:VAL:HG22	1.98	0.46
49:LX:118:ILE:HG12	49:LX:148:ILE:HD13	1.98	0.46
53:Ld:34:LYS:HE2	53:Ld:34:LYS:HB2	1.62	0.46
1:C1:663:G:H2'	1:C1:767:A:H61	1.81	0.46
1:C1:2342:U:O2'	1:C1:2343:G:O5'	2.30	0.46
1:C1:2453:A:H2'	1:C1:2454:C:C6	2.51	0.46
1:C1:3130:U:O2'	1:C1:3131:A:OP1	2.30	0.46
1:C1:3172:U:H2'	1:C1:3173:C:C6	2.51	0.46
1:C1:3328:C:O2'	1:C1:3329:C:H5'	2.16	0.46
7:CE:419:ARG:HG2	7:CE:444:ARG:HH22	1.79	0.46
11:CI:305:LYS:O	11:CI:309:GLU:N	2.42	0.46
18:CP:406:GLY:O	18:CP:432:ASN:HB2	2.16	0.46
23:CU:340:LYS:NZ	23:CU:369:ASP:OD1	2.48	0.46
28:CZ:167:GLN:HA	28:CZ:170:ILE:HG12	1.98	0.46
28:CZ:282:LEU:HD13	28:CZ:289:ARG:HG2	1.98	0.46
28:CZ:369:ASN:OD1	28:CZ:370:ALA:N	2.49	0.46
32:LB:33:PRO:HD2	32:LB:44:THR:HG21	1.96	0.46
37:LK:53:TRP:C	37:LK:54:LYS:HD2	2.41	0.46
44:LR:149:LYS:O	44:LR:151:ARG:NH1	2.49	0.46
1:C1:95:A:C5	1:C1:96:G:H1'	2.51	0.46
1:C1:218:C:OP1	50:LY:46:SER:OG	2.34	0.46
1:C1:316:A:H2'	1:C1:317:A:C8	2.51	0.46
1:C1:509:A:OP1	45:LS:62:ASN:ND2	2.48	0.46
1:C1:717:U:O2'	1:C1:720:G:O6	2.27	0.46
1:C1:823:G:OP1	21:CS:381:LYS:NZ	2.47	0.46
1:C1:1203:U:O4'	8:CF:75:ARG:NH1	2.49	0.46
1:C1:1789:G:OP1	51:LZ:55:ARG:NH2	2.49	0.46
3:CA:30:ARG:HG2	23:CU:216:PHE:CE1	2.51	0.46
3:CA:74:LEU:HB3	3:CA:250:PHE:HB3	1.97	0.46
3:CA:76:GLU:HA	3:CA:79:GLU:OE1	2.16	0.46
4:CB:120:LEU:O	4:CB:124:ILE:HD13	2.16	0.46
5:CC:269:MET:HE2	7:CE:553:VAL:H	1.80	0.46
6:CD:181:LYS:HB3	6:CD:181:LYS:HE3	1.71	0.46
6:CD:362:THR:HG22	6:CD:366:HIS:O	2.16	0.46
6:CD:405:VAL:HG21	6:CD:468:TRP:HB2	1.98	0.46
7:CE:149:LYS:NZ	7:CE:149:LYS:HB3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CG:4:LEU:HB2	9:CG:9:MET:HE2	1.98	0.46
12:CJ:136:ASP:OD1	12:CJ:136:ASP:N	2.49	0.46
33:LC:42:GLY:HA3	33:LC:114:ILE:HD11	1.97	0.46
49:LX:25:GLN:HG2	49:LX:29:LYS:HD3	1.98	0.46
1:C1:75:G:H5''	38:LL:58:VAL:HB	1.98	0.46
1:C1:292:G:OP2	3:CA:71:LYS:NZ	2.48	0.46
1:C1:407:G:N2	1:C1:1381:A:C6	2.82	0.46
1:C1:582:A:H5'	34:LE:35:GLN:O	2.15	0.46
1:C1:1576:C:P	56:Lg:32:ARG:HH21	2.39	0.46
1:C1:2119:G:H4'	1:C1:2120:A:H5'	1.97	0.46
1:C1:2774:G:H2'	1:C1:2775:A:C8	2.50	0.46
1:C1:2785:U:H1'	10:CH:25:GLN:HE22	1.81	0.46
1:C1:2955:U:O2	1:C1:3337:C:N4	2.49	0.46
3:CA:244:ILE:HG12	3:CA:254:ILE:HD12	1.96	0.46
5:CC:178:SER:O	5:CC:181:ASP:HB2	2.16	0.46
12:CJ:182:THR:OG1	12:CJ:249:ILE:HD11	2.16	0.46
14:CL:72:GLU:CD	14:CL:75:ARG:HH22	2.23	0.46
15:CM:184:ILE:HD11	15:CM:193:GLU:HG3	1.98	0.46
18:CP:545:LYS:HB2	18:CP:545:LYS:NZ	2.31	0.46
24:CV:13:SER:O	24:CV:17:ASN:ND2	2.49	0.46
25:CW:483:ASP:OD1	25:CW:483:ASP:N	2.43	0.46
27:CY:614:TYR:O	27:CY:618:VAL:HG12	2.16	0.46
1:C1:29:C:H4'	1:C1:62:A:H4'	1.98	0.45
1:C1:3004:U:O2'	1:C1:3005:A:H5'	2.15	0.45
1:C1:3164:G:C6	1:C1:3206:G:N1	2.84	0.45
4:CB:49:LEU:HB2	7:CE:483:TYR:HB3	1.97	0.45
6:CD:108:PHE:HB2	6:CD:482:VAL:HB	1.99	0.45
6:CD:443:ARG:HH21	6:CD:479:ASP:CG	2.23	0.45
21:CS:433:LYS:NZ	21:CS:433:LYS:HB3	2.30	0.45
23:CU:340:LYS:HE2	23:CU:340:LYS:HB2	1.67	0.45
25:CW:41:VAL:HG12	25:CW:249:VAL:HG11	1.97	0.45
25:CW:407:GLY:N	25:CW:410:GLU:OE2	2.50	0.45
25:CW:410:GLU:O	25:CW:413:VAL:HG12	2.15	0.45
25:CW:437:GLN:OE1	25:CW:437:GLN:N	2.48	0.45
37:LK:12:ILE:C	37:LK:13:ILE:HD13	2.41	0.45
37:LK:152:SER:O	37:LK:155:ILE:HG22	2.16	0.45
53:Ld:66:LYS:HA	53:Ld:69:GLU:HG3	1.98	0.45
54:Le:103:SER:HB3	54:Le:126:LYS:HD3	1.98	0.45
61:Lp:51:ALA:HB3	61:Lp:54:ILE:HB	1.97	0.45
1:C1:139:C:H2'	1:C1:140:G:O4'	2.16	0.45
1:C1:1077:U:HO2'	1:C1:1078:C:P	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1976:U:H2'	1:C1:1977:A:C8	2.47	0.45
1:C1:2313:U:H2'	1:C1:2314:A:H8	1.81	0.45
1:C1:2738:A:H4'	1:C1:2739:U:OP1	2.15	0.45
1:C1:2874:U:H2'	1:C1:2875:G:H8	1.81	0.45
1:C1:3272:U:H2'	1:C1:3273:G:O4'	2.16	0.45
4:CB:70:LYS:HD3	4:CB:71:HIS:H	1.81	0.45
4:CB:150:HIS:O	4:CB:177:LYS:NZ	2.36	0.45
5:CC:359:GLU:OE2	5:CC:359:GLU:N	2.25	0.45
6:CD:256:LYS:HG2	6:CD:287:ARG:HE	1.81	0.45
6:CD:341:PRO:O	6:CD:362:THR:OG1	2.26	0.45
6:CD:389:ASN:HB2	6:CD:410:ASP:HB3	1.98	0.45
7:CE:116:LEU:HD23	7:CE:116:LEU:HA	1.84	0.45
9:CG:21:THR:OG1	9:CG:22:ASP:N	2.50	0.45
13:CK:58:LYS:O	13:CK:62:ARG:HG3	2.16	0.45
18:CP:376:LEU:HD11	18:CP:452:ARG:HB3	1.97	0.45
23:CU:294:THR:HG23	26:CX:64:TYR:HE2	1.81	0.45
24:CV:36:THR:HA	54:Le:88:MET:HG3	1.98	0.45
25:CW:440:ASP:HA	25:CW:443:ASN:HB2	1.98	0.45
27:CY:545:ALA:HB2	27:CY:583:GLU:OE2	2.16	0.45
28:CZ:343:GLU:CD	28:CZ:345:GLY:H	2.25	0.45
29:Ca:203:ARG:HB2	29:Ca:210:ARG:NH1	2.31	0.45
15:LF:62:ARG:O	15:LF:66:ARG:HG2	2.16	0.45
63:Lq:88:ASP:HA	63:Lq:91:LYS:HE2	1.99	0.45
1:C1:975:G:H4'	1:C1:976:U:H5'	1.99	0.45
1:C1:1757:G:O2'	1:C1:1759:G:OP2	2.23	0.45
1:C1:2167:U:H2'	1:C1:2168:G:H8	1.81	0.45
1:C1:2992:C:H5'	36:LH:124:ILE:HD12	1.98	0.45
1:C1:3116:G:H2'	1:C1:3117:C:C6	2.51	0.45
4:CB:22:GLN:O	4:CB:25:LYS:HG2	2.17	0.45
16:CN:170:GLN:HE22	16:CN:183:ALA:HB2	1.81	0.45
18:CP:231:ASP:HB3	18:CP:234:MET:HB3	1.98	0.45
18:CP:415:LYS:HB3	18:CP:415:LYS:HE3	1.47	0.45
18:CP:498:CYS:CB	18:CP:508:ILE:HD11	2.46	0.45
21:CS:282:PRO:HD2	21:CS:286:ASP:H	1.81	0.45
27:CY:502:TRP:O	27:CY:506:LEU:HB2	2.15	0.45
27:CY:641:GLU:OE1	27:CY:691:ARG:NH2	2.49	0.45
34:LE:194:LYS:O	34:LE:198:MET:HG2	2.16	0.45
40:LN:159:ARG:HB3	40:LN:164:LEU:HB2	1.98	0.45
42:LP:128:ARG:NH2	42:LP:136:ILE:O	2.42	0.45
58:Li:88:THR:HG22	58:Li:90:GLY:H	1.82	0.45
1:C1:221:U:OP1	50:LY:4:ARG:NH2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:603:G:H2'	1:C1:604:G:H8	1.80	0.45
1:C1:713:G:H1'	1:C1:725:A:H61	1.81	0.45
1:C1:1661:U:C5	47:LU:92:LYS:HD3	2.52	0.45
1:C1:1967:G:H2'	1:C1:1968:A:C8	2.51	0.45
1:C1:2110:U:H2'	1:C1:2111:A:C8	2.51	0.45
1:C1:3086:A:H2'	1:C1:3087:A:H5''	1.99	0.45
3:CA:247:GLU:HB3	3:CA:255:LEU:HD11	1.97	0.45
5:CC:734:ALA:HB3	5:CC:779:ILE:HD12	1.99	0.45
7:CE:158:GLY:HA3	7:CE:420:GLY:HA2	1.99	0.45
10:CH:288:LYS:HE3	64:CH:1001:GTP:N3	2.32	0.45
10:CH:293:LYS:HE2	10:CH:293:LYS:HB2	1.81	0.45
12:CJ:10:SER:HA	12:CJ:14:ARG:HG3	1.99	0.45
21:CS:62:VAL:O	21:CS:65:GLU:HG3	2.16	0.45
27:CY:373:ARG:H	27:CY:373:ARG:HD2	1.82	0.45
29:Ca:67:ARG:HG2	29:Ca:67:ARG:HH11	1.81	0.45
37:LK:35:LEU:HD21	37:LK:64:ILE:HD13	1.97	0.45
63:Lq:113:SER:O	63:Lq:117:ILE:HG13	2.17	0.45
1:C1:5:G:H5''	12:CJ:92:SER:HB3	1.99	0.45
1:C1:100:A:H2'	1:C1:101:G:N3	2.32	0.45
1:C1:1053:U:HO2'	1:C1:1054:G:H8	1.63	0.45
1:C1:1280:C:O2'	13:CK:40:GLN:O	2.33	0.45
1:C1:1332:A:H5'	33:LC:292:ASN:ND2	2.32	0.45
1:C1:1949:G:O2'	1:C1:1950:C:OP1	2.27	0.45
12:CJ:75:GLU:OE2	12:CJ:77:LEU:HB2	2.16	0.45
12:CJ:414:ARG:HG2	12:CJ:414:ARG:HH11	1.82	0.45
12:CJ:465:ILE:HG13	12:CJ:466:ASN:N	2.31	0.45
20:CR:132:PRO:HG2	38:LL:106:GLU:HB3	1.98	0.45
35:LG:74:VAL:HG12	40:LN:21:PHE:CZ	2.51	0.45
45:LS:48:LEU:HD13	46:LT:151:LEU:HD23	1.99	0.45
51:LZ:96:ASN:O	51:LZ:99:THR:HG22	2.16	0.45
1:C1:1216:G:H2'	1:C1:1217:U:C5	2.52	0.45
1:C1:1569:G:OP1	56:Lg:18:SER:OG	2.27	0.45
1:C1:2146:U:H2'	1:C1:2147:G:C8	2.52	0.45
1:C1:2419:G:H2'	1:C1:2421:A:H62	1.81	0.45
1:C1:2887:C:H2'	1:C1:2888:A:O4'	2.16	0.45
1:C1:3067:C:H2'	1:C1:3068:U:C6	2.51	0.45
1:C1:3140:G:H5'	36:LH:22:SER:HB2	1.97	0.45
5:CC:668:LYS:HE2	5:CC:703:LEU:O	2.17	0.45
6:CD:345:LEU:HA	6:CD:359:ALA:O	2.17	0.45
7:CE:305:ASP:HA	7:CE:308:ARG:NH1	2.31	0.45
7:CE:351:PHE:CE1	7:CE:360:ILE:HD12	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CK:154:PRO:HG3	13:CK:249:PRO:HB2	1.99	0.45
18:CP:447:ILE:HG23	18:CP:448:GLY:H	1.81	0.45
20:CR:40:ASN:HB3	20:CR:43:GLU:HG3	1.98	0.45
32:LB:288:LYS:HA	32:LB:288:LYS:HD2	1.71	0.45
37:LK:144:ASP:O	37:LK:146:LYS:NZ	2.48	0.45
1:C1:1185:A:H62	1:C1:1282:G:H21	1.65	0.45
1:C1:2123:G:H2'	1:C1:2124:C:C6	2.51	0.45
1:C1:2796:A:H2'	1:C1:2797:G:O4'	2.17	0.45
1:C1:3219:G:H2'	1:C1:3220:A:C8	2.51	0.45
1:C1:3233:C:H4'	1:C1:3234:A:H5'	1.99	0.45
14:CL:19:ARG:NH1	14:CL:23:LYS:HD3	2.32	0.45
25:CW:460:GLN:HB3	25:CW:499:PRO:HG2	1.98	0.45
27:CY:493:TRP:NE1	27:CY:602:TYR:HB3	2.32	0.45
28:CZ:183:LYS:NZ	28:CZ:216:MET:SD	2.90	0.45
34:LE:60:LEU:O	34:LE:67:GLY:N	2.42	0.45
36:LH:90:MET:HE2	36:LH:181:ILE:HG22	1.99	0.45
48:LV:15:MET:HE1	48:LV:56:VAL:HB	1.98	0.45
1:C1:288:A:H2'	1:C1:289:A:C8	2.51	0.45
1:C1:585:G:H1	1:C1:596:G:H5''	1.82	0.45
1:C1:645:G:N2	33:LC:94:MET:HB2	2.30	0.45
1:C1:1537:U:O2'	1:C1:1539:A:OP2	2.24	0.45
1:C1:1879:A:H4'	1:C1:1880:A:O5'	2.17	0.45
3:CA:91:PHE:HB3	3:CA:103:TRP:HB2	1.98	0.45
4:CB:282:TYR:HD1	4:CB:292:PRO:HA	1.82	0.45
6:CD:140:GLN:NE2	6:CD:142:GLY:H	2.15	0.45
9:CG:115:VAL:HG22	9:CG:118:HIS:CE1	2.52	0.45
16:CN:12:GLU:N	16:CN:12:GLU:OE2	2.50	0.45
23:CU:194:GLU:OE1	23:CU:194:GLU:N	2.26	0.45
25:CW:235:ARG:HE	25:CW:235:ARG:HB3	1.70	0.45
27:CY:506:LEU:HD12	27:CY:531:LEU:HD23	1.99	0.45
28:CZ:465:LEU:O	28:CZ:468:GLU:HG3	2.16	0.45
37:LK:135:THR:O	37:LK:138:SER:OG	2.30	0.45
55:Lf:50:ARG:CZ	55:Lf:72:LYS:HG2	2.47	0.45
1:C1:457:U:H5	24:CV:97:GLN:O	2.00	0.45
1:C1:656:U:H2'	1:C1:657:U:C6	2.51	0.45
1:C1:735:G:H1	1:C1:759:U:H3	1.65	0.45
1:C1:890:G:H2'	1:C1:891:G:H8	1.80	0.45
1:C1:1548:C:C2	5:CC:408:MET:HE1	2.52	0.45
2:C2:151:C:O2'	35:LG:66:LYS:NZ	2.49	0.45
7:CE:377:LEU:HD23	7:CE:380:ILE:HD11	1.99	0.45
8:CF:49:ARG:NE	8:CF:124:PHE:HB2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CG:99:TRP:HB2	9:CG:121:ARG:HB3	1.97	0.45
14:CL:32:LYS:HB2	14:CL:32:LYS:NZ	2.31	0.45
15:CM:124:LYS:HE2	15:CM:124:LYS:HB3	1.72	0.45
16:CN:98:GLU:OE2	19:CQ:74:ARG:NH1	2.47	0.45
18:CP:373:VAL:HG21	18:CP:397:HIS:ND1	2.32	0.45
25:CW:144:LEU:HD11	25:CW:176:LEU:HD22	1.98	0.45
25:CW:458:LEU:HD23	25:CW:458:LEU:HA	1.83	0.45
27:CY:542:ILE:HD11	27:CY:547:TYR:CD2	2.52	0.45
33:LC:244:GLN:O	33:LC:253:ARG:HD3	2.17	0.45
15:LF:126:THR:O	15:LF:130:ALA:N	2.39	0.45
36:LH:143:LYS:HE3	36:LH:143:LYS:HB2	1.84	0.45
38:LL:92:THR:HG23	57:Lh:118:GLN:HA	1.98	0.45
43:LQ:107:THR:HB	43:LQ:164:THR:HG22	1.98	0.45
1:C1:190:G:N2	1:C1:364:A:C5	2.85	0.45
1:C1:1455:A:H5'	44:LR:23:TRP:CD1	2.52	0.45
1:C1:1576:C:H2'	1:C1:1577:G:H8	1.82	0.45
1:C1:2091:U:H2'	1:C1:2092:G:H8	1.81	0.45
1:C1:2404:G:H2'	1:C1:2405:A:H8	1.80	0.45
1:C1:2722:C:H2'	1:C1:2723:C:C6	2.52	0.45
1:C1:2807:C:H2'	1:C1:2808:G:O4'	2.17	0.45
2:C2:145:U:H2'	2:C2:146:U:C6	2.52	0.45
4:CB:85:LEU:HD21	4:CB:262:VAL:HG23	1.98	0.45
5:CC:135:ARG:HD3	5:CC:137:TYR:CZ	2.52	0.45
5:CC:642:HIS:HB3	5:CC:645:ARG:O	2.17	0.45
6:CD:77:GLU:O	6:CD:81:THR:HG23	2.18	0.45
6:CD:137:ALA:N	6:CD:188:SER:OG	2.42	0.45
7:CE:299:GLN:OE1	7:CE:299:GLN:N	2.49	0.45
8:CF:58:HIS:CD2	37:LK:121:PHE:HA	2.52	0.45
10:CH:255:ILE:HD11	10:CH:286:LEU:HD22	1.99	0.45
17:CO:106:ILE:HD13	41:LO:113:PRO:HG2	1.99	0.45
18:CP:309:ARG:HD3	18:CP:365:GLN:NE2	2.32	0.45
21:CS:570:PHE:HZ	22:CT:131:LEU:HB2	1.81	0.45
25:CW:121:LEU:HG	25:CW:138:VAL:HG11	1.99	0.45
27:CY:384:VAL:HA	27:CY:387:TRP:CD1	2.52	0.45
27:CY:404:ILE:O	27:CY:408:VAL:HG13	2.17	0.45
37:LK:111:GLU:O	37:LK:115:THR:HG22	2.17	0.45
40:LN:60:VAL:HG22	40:LN:134:LEU:HB2	1.98	0.45
62:LI:21:ARG:HG2	62:LI:22:PRO:HD2	1.99	0.45
1:C1:72:C:N3	1:C1:74:G:C5	2.85	0.44
1:C1:1205:A:N7	1:C1:1268:A:C6	2.85	0.44
1:C1:2395:U:H2'	1:C1:2396:U:H2'	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2856:G:O6	13:CK:8:GLU:HG3	2.17	0.44
1:C1:2965:G:O6	1:C1:3096:A:N6	2.51	0.44
2:C2:8:C:H2'	2:C2:9:A:C8	2.52	0.44
4:CB:164:PRO:HA	4:CB:172:TYR:CE2	2.52	0.44
4:CB:281:PHE:HB2	4:CB:293:ILE:O	2.17	0.44
11:CI:192:ALA:HA	11:CI:230:ARG:HA	1.99	0.44
21:CS:656:THR:HG22	21:CS:658:GLU:OE2	2.16	0.44
27:CY:6:LYS:HD2	27:CY:6:LYS:HA	1.72	0.44
27:CY:451:GLU:H	27:CY:451:GLU:CD	2.18	0.44
28:CZ:304:ILE:HD11	28:CZ:318:MET:HE2	1.99	0.44
31:LA:79:ASN:OD1	31:LA:169:VAL:HG12	2.16	0.44
31:LA:101:ILE:HG22	31:LA:165:MET:HA	1.99	0.44
33:LC:94:MET:HE3	33:LC:94:MET:HB3	1.79	0.44
38:LL:47:ALA:HB3	38:LL:48:PRO:HD3	1.98	0.44
63:Lq:42:ASP:OD1	63:Lq:42:ASP:N	2.49	0.44
1:C1:171:G:H2'	1:C1:172:C:C6	2.52	0.44
1:C1:370:A:H1'	50:LY:89:ALA:O	2.16	0.44
1:C1:618:A:H2'	1:C1:619:G:C8	2.52	0.44
1:C1:1318:C:H2'	1:C1:1319:G:H8	1.82	0.44
1:C1:1702:G:P	44:LR:103:ARG:HH22	2.40	0.44
1:C1:1817:C:H5''	1:C1:1818:A:H5'	1.98	0.44
1:C1:2077:G:H2'	1:C1:2078:G:C8	2.51	0.44
2:C2:58:G:O6	59:Lj:63:ARG:NH1	2.45	0.44
6:CD:189:ASP:OD1	6:CD:189:ASP:C	2.60	0.44
7:CE:275:GLU:OE1	7:CE:279:ARG:NH1	2.50	0.44
21:CS:96:THR:HG22	21:CS:98:LYS:N	2.30	0.44
21:CS:438:MET:HE2	21:CS:438:MET:HB3	1.90	0.44
25:CW:329:LEU:HB3	25:CW:356:THR:HG22	1.98	0.44
25:CW:368:GLN:CD	25:CW:396:ARG:HH12	2.25	0.44
27:CY:615:GLN:OE1	27:CY:666:ASN:ND2	2.45	0.44
27:CY:708:LEU:HD23	27:CY:708:LEU:HA	1.85	0.44
35:LG:93:ALA:O	35:LG:97:LEU:HD23	2.16	0.44
36:LH:31:ARG:NH1	36:LH:151:ASN:OD1	2.44	0.44
51:LZ:69:PRO:HG3	51:LZ:114:LYS:HB2	1.98	0.44
1:C1:473:C:H2'	1:C1:474:G:C8	2.53	0.44
1:C1:497:U:H2'	1:C1:498:C:C6	2.52	0.44
1:C1:1470:G:H5''	1:C1:1817:C:H42	1.82	0.44
1:C1:2881:U:H4'	21:CS:27:ALA:HB1	1.98	0.44
3:CA:83:LEU:HD12	58:Li:76:LYS:HG2	2.00	0.44
3:CA:177:ASP:OD1	3:CA:177:ASP:N	2.50	0.44
5:CC:645:ARG:HG2	5:CC:646:PRO:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:56:LEU:O	6:CD:56:LEU:HD13	2.17	0.44
6:CD:112:ASP:OD1	6:CD:151:TYR:HB2	2.18	0.44
7:CE:485:PHE:HE1	7:CE:490:ILE:HD12	1.83	0.44
25:CW:85:LYS:O	25:CW:88:HIS:ND1	2.50	0.44
25:CW:126:LYS:HD3	25:CW:126:LYS:HA	1.60	0.44
29:Ca:57:ARG:HG2	29:Ca:60:ARG:HH22	1.81	0.44
37:LK:123:LYS:HB3	37:LK:123:LYS:HE3	1.68	0.44
40:LN:6:TYR:HE2	58:Li:52:LEU:HD23	1.82	0.44
45:LS:78:TRP:CZ2	45:LS:124:LEU:HD23	2.52	0.44
50:LY:34:LEU:HD23	50:LY:105:ILE:HB	1.99	0.44
50:LY:68:LYS:H	50:LY:82:GLU:HG2	1.83	0.44
63:Lq:41:TYR:OH	63:Lq:47:LYS:O	2.36	0.44
1:C1:1151:A:H4'	15:LF:224:LYS:HD3	1.98	0.44
1:C1:1322:C:H2'	1:C1:1323:U:C6	2.52	0.44
1:C1:1862:A:H2'	1:C1:1863:A:C8	2.50	0.44
1:C1:1922:C:H5''	25:CW:359:ILE:HG12	1.98	0.44
1:C1:2306:U:H2'	1:C1:2307:A:C8	2.52	0.44
1:C1:2337:G:OP2	1:C1:2337:G:N2	2.41	0.44
1:C1:2371:G:H2'	1:C1:2372:U:C6	2.53	0.44
1:C1:2562:U:H2'	1:C1:2563:G:O4'	2.17	0.44
4:CB:267:VAL:HG21	4:CB:275:TRP:CH2	2.53	0.44
4:CB:275:TRP:O	4:CB:278:VAL:HG12	2.18	0.44
6:CD:118:ASP:O	6:CD:147:LEU:N	2.38	0.44
10:CH:418:ASN:ND2	32:LB:61:ASP:OD2	2.51	0.44
10:CH:439:GLU:OE1	19:CQ:1:MET:N	2.51	0.44
10:CH:471:GLU:OE2	10:CH:473:PHE:HB2	2.17	0.44
10:CH:508:MET:HE1	53:Ld:65:LYS:HB3	1.98	0.44
12:CJ:588:GLN:HA	12:CJ:591:LEU:HG	2.00	0.44
21:CS:106:HIS:ND1	21:CS:106:HIS:N	2.65	0.44
21:CS:144:LEU:HD12	21:CS:144:LEU:HA	1.84	0.44
23:CU:245:ASN:O	23:CU:249:GLU:HG2	2.17	0.44
27:CY:444:LEU:O	27:CY:448:SER:OG	2.18	0.44
35:LG:176:MET:HA	35:LG:176:MET:HE2	1.98	0.44
39:LM:9:THR:HG21	39:LM:11:TRP:CE2	2.51	0.44
39:LM:130:GLU:HG3	41:LO:191:VAL:HA	1.99	0.44
44:LR:172:ARG:HB3	44:LR:176:ARG:HH11	1.83	0.44
46:LT:107:ARG:HG2	46:LT:107:ARG:HH11	1.82	0.44
1:C1:1480:A:H2'	1:C1:1481:U:C6	2.53	0.44
1:C1:2051:G:O2'	1:C1:2052:U:O4'	2.30	0.44
1:C1:2413:G:H2'	1:C1:2414:G:C8	2.53	0.44
1:C1:2768:C:H2'	1:C1:2769:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2990:A:H2'	1:C1:2991:C:H6	1.83	0.44
5:CC:403:ARG:NH1	12:CJ:143:ASP:OD1	2.45	0.44
8:CF:82:GLU:OE1	8:CF:82:GLU:N	2.50	0.44
10:CH:232:ASN:OD1	10:CH:235:GLU:HG2	2.18	0.44
21:CS:740:ARG:HD3	21:CS:743:ARG:NH2	2.32	0.44
25:CW:368:GLN:OE1	25:CW:396:ARG:NH2	2.48	0.44
27:CY:688:GLU:OE1	27:CY:688:GLU:HA	2.18	0.44
28:CZ:136:GLU:O	28:CZ:139:GLN:NE2	2.51	0.44
31:LA:117:GLU:OE2	31:LA:163:ARG:NH2	2.49	0.44
33:LC:165:LYS:HA	33:LC:165:LYS:HD2	1.72	0.44
34:LE:108:LYS:HB3	34:LE:108:LYS:HE3	1.76	0.44
1:C1:508:G:H3'	1:C1:509:A:H3'	1.99	0.44
1:C1:1171:C:N4	1:C1:1297:U:H1'	2.32	0.44
1:C1:2017:A:C2	1:C1:2018:A:C8	3.06	0.44
5:CC:260:GLU:HG2	5:CC:263:THR:OG1	2.18	0.44
5:CC:343:PRO:HD2	15:CM:19:LEU:HD13	1.99	0.44
5:CC:695:ASP:OD1	5:CC:695:ASP:N	2.51	0.44
6:CD:73:ARG:NH1	12:CJ:589:ARG:HE	2.16	0.44
6:CD:175:GLY:HA2	6:CD:203:TRP:HH2	1.83	0.44
7:CE:497:LEU:HD12	7:CE:497:LEU:HA	1.79	0.44
10:CH:160:PRO:HB3	13:CK:3:GLN:HB2	2.00	0.44
10:CH:287:ASN:OD1	10:CH:288:LYS:N	2.47	0.44
11:CI:200:GLU:OE1	11:CI:200:GLU:N	2.29	0.44
11:CI:202:GLU:HA	15:CM:57:TYR:CD2	2.53	0.44
13:CK:63:LYS:HE2	13:CK:63:LYS:HB3	1.53	0.44
17:CO:37:LEU:HG	32:LB:195:PHE:HZ	1.83	0.44
18:CP:309:ARG:HG2	18:CP:340:VAL:HG12	1.99	0.44
18:CP:451:ASP:N	18:CP:451:ASP:OD1	2.49	0.44
21:CS:256:THR:HG23	21:CS:274:TYR:CE2	2.52	0.44
24:CV:9:ILE:HG22	24:CV:47:VAL:HG22	1.99	0.44
27:CY:728:LEU:O	27:CY:731:GLU:HG3	2.18	0.44
28:CZ:353:PHE:HE1	28:CZ:387:MET:HB3	1.83	0.44
36:LH:15:ASN:OD1	36:LH:15:ASN:N	2.49	0.44
37:LK:116:MET:HE3	37:LK:116:MET:HB3	1.77	0.44
44:LR:57:MET:HE2	44:LR:57:MET:HB3	1.78	0.44
1:C1:628:C:H2'	1:C1:629:U:C6	2.53	0.44
1:C1:655:U:H2'	1:C1:656:U:C6	2.52	0.44
1:C1:933:A:H4'	1:C1:949:G:N2	2.32	0.44
1:C1:1960:G:H2'	1:C1:1961:G:C8	2.52	0.44
1:C1:2120:A:C8	1:C1:2122:G:C4	3.06	0.44
1:C1:2306:U:H2'	1:C1:2307:A:H8	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:229:U:H2'	2:C2:230:C:H6	1.82	0.44
4:CB:68:THR:OG1	4:CB:70:LYS:O	2.35	0.44
5:CC:718:GLU:OE1	5:CC:718:GLU:HA	2.18	0.44
6:CD:367:ILE:HB	6:CD:384:LEU:HB2	1.99	0.44
12:CJ:65:TYR:CE2	12:CJ:67:LYS:HB2	2.53	0.44
25:CW:246:LYS:HZ2	29:Ca:156:VAL:HG12	1.83	0.44
25:CW:608:GLU:HA	25:CW:611:LYS:NZ	2.32	0.44
36:LH:148:LEU:HD23	36:LH:156:VAL:HG13	2.00	0.44
41:LO:1:MET:H1	45:LS:163:LYS:HG3	1.83	0.44
45:LS:141:LYS:HA	45:LS:141:LYS:HD2	1.81	0.44
63:Lq:160:LYS:HD3	63:Lq:160:LYS:HA	1.81	0.44
1:C1:627:U:H2'	1:C1:628:C:C6	2.53	0.44
1:C1:1333:A:C4	15:LF:18:LEU:HD13	2.53	0.44
1:C1:2063:C:H2'	1:C1:2064:U:C2	2.53	0.44
1:C1:2133:G:H2'	1:C1:2134:G:C8	2.53	0.44
1:C1:2764:U:O2'	1:C1:2765:U:H5'	2.18	0.44
1:C1:3248:C:O2'	42:LP:69:ARG:O	2.24	0.44
3:CA:89:VAL:HG23	3:CA:107:VAL:HG22	2.00	0.44
4:CB:102:ALA:HB2	4:CB:159:ILE:HG12	2.00	0.44
10:CH:227:PRO:HB2	10:CH:229:GLU:OE1	2.18	0.44
10:CH:426:ILE:O	19:CQ:80:ARG:NH1	2.51	0.44
12:CJ:376:ARG:HH21	15:CM:189:ASP:HA	1.83	0.44
16:CN:78:ASP:OD1	16:CN:78:ASP:N	2.49	0.44
21:CS:431:ILE:HG22	52:Lc:64:MET:HE1	2.00	0.44
22:CT:561:GLN:OE1	22:CT:561:GLN:HA	2.18	0.44
22:CT:593:CYS:O	22:CT:597:MET:HG2	2.18	0.44
25:CW:53:LYS:HD3	25:CW:53:LYS:HA	1.83	0.44
25:CW:577:GLU:HA	25:CW:580:GLU:HG2	2.00	0.44
27:CY:85:ILE:HG23	27:CY:86:LEU:HG	1.98	0.44
27:CY:447:ASN:N	27:CY:447:ASN:OD1	2.50	0.44
27:CY:685:LYS:O	27:CY:689:GLU:HG3	2.18	0.44
28:CZ:249:GLN:OE1	28:CZ:249:GLN:N	2.48	0.44
31:LA:80:GLU:HG3	61:Lp:66:GLY:HA2	2.00	0.44
31:LA:80:GLU:HB2	31:LA:170:ALA:HA	2.00	0.44
32:LB:53:MET:HE2	32:LB:53:MET:HB3	1.74	0.44
47:LU:33:ILE:HG22	47:LU:96:LEU:HD21	2.00	0.44
56:Lg:20:ARG:HA	56:Lg:20:ARG:HD3	1.81	0.44
63:Lq:49:PHE:HD2	63:Lq:193:LEU:HD23	1.83	0.44
1:C1:146:A:H5''	57:Lh:107:GLU:HG3	2.00	0.44
1:C1:787:A:H2'	1:C1:788:A:N3	2.33	0.44
1:C1:1667:U:H2'	1:C1:1668:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2812:U:H2'	1:C1:2813:C:C6	2.53	0.44
1:C1:2840:U:H2'	1:C1:2841:U:C6	2.53	0.44
4:CB:294:TYR:H	11:CI:327:PHE:HZ	1.66	0.44
5:CC:438:LEU:HD13	5:CC:746:HIS:CG	2.53	0.44
21:CS:364:LEU:HD11	44:LR:159:MET:HE1	2.00	0.44
21:CS:436:MET:SD	51:LZ:128:TRP:HB3	2.58	0.44
22:CT:160:ILE:HG22	22:CT:162:ALA:H	1.82	0.44
25:CW:306:CYS:HB2	25:CW:330:HIS:CD2	2.53	0.44
25:CW:354:LEU:HB3	25:CW:356:THR:HG23	2.00	0.44
25:CW:598:MET:HE2	25:CW:598:MET:N	2.32	0.44
27:CY:453:TRP:HD1	27:CY:460:GLY:CA	2.30	0.44
28:CZ:411:ALA:HA	28:CZ:415:PHE:CD2	2.52	0.44
31:LA:104:LEU:HB3	31:LA:146:THR:HG21	1.99	0.44
37:LK:125:LEU:O	37:LK:129:VAL:HG23	2.18	0.44
40:LN:36:ILE:O	40:LN:109:ARG:NH1	2.51	0.44
43:LQ:59:LYS:HE2	43:LQ:59:LYS:HB2	1.78	0.44
52:Lc:16:LYS:H	52:Lc:16:LYS:HG2	1.64	0.44
63:Lq:17:LEU:O	63:Lq:21:ASN:HB3	2.18	0.44
1:C1:65:A:H1'	1:C1:77:A:H1'	2.00	0.43
1:C1:584:C:H2'	1:C1:596:G:O6	2.18	0.43
1:C1:616:C:H2'	1:C1:617:C:C6	2.52	0.43
1:C1:953:U:H2'	1:C1:954:G:H8	1.83	0.43
1:C1:3035:G:OP1	1:C1:3037:G:H5'	2.18	0.43
4:CB:97:VAL:HG12	4:CB:123:LYS:O	2.18	0.43
4:CB:138:LYS:HB2	4:CB:138:LYS:NZ	2.33	0.43
4:CB:284:LYS:NZ	4:CB:288:THR:O	2.29	0.43
5:CC:394:PRO:HB3	15:CM:171:ASP:HB3	2.00	0.43
5:CC:710:TYR:CD2	5:CC:711:LYS:HG2	2.53	0.43
6:CD:443:ARG:NH2	6:CD:479:ASP:OD2	2.42	0.43
10:CH:360:ARG:HE	16:CN:246:TYR:C	2.26	0.43
11:CI:306:VAL:O	11:CI:310:GLU:HG2	2.17	0.43
33:LC:24:PRO:O	33:LC:26:VAL:N	2.51	0.43
34:LE:127:TYR:CE2	34:LE:158:ARG:HD3	2.53	0.43
36:LH:130:MET:HG3	36:LH:136:VAL:HG21	2.00	0.43
44:LR:152:GLU:H	44:LR:152:GLU:CD	2.26	0.43
49:LX:104:ASN:OD1	49:LX:107:GLN:NE2	2.40	0.43
1:C1:247:A:H2'	1:C1:248:G:C8	2.52	0.43
1:C1:497:U:H2'	1:C1:498:C:H6	1.83	0.43
1:C1:645:G:H21	33:LC:94:MET:HB2	1.83	0.43
1:C1:895:A:HO2'	1:C1:896:A:C5'	2.29	0.43
1:C1:2053:U:OP1	1:C1:2055:A:N6	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2278:G:H2'	1:C1:2279:A:C8	2.53	0.43
2:C2:39:G:H1'	2:C2:104:A:N6	2.33	0.43
6:CD:44:TYR:O	6:CD:48:ARG:HG2	2.18	0.43
6:CD:304:ILE:HD12	6:CD:314:TYR:HB2	2.00	0.43
6:CD:444:GLU:OE1	6:CD:444:GLU:N	2.51	0.43
14:CL:21:ARG:O	14:CL:24:ILE:HG22	2.17	0.43
15:CM:68:LYS:HB2	15:CM:68:LYS:NZ	2.33	0.43
25:CW:474:GLN:CD	44:LR:151:ARG:HH22	2.26	0.43
31:LA:62:VAL:HG13	31:LA:71:GLN:HB3	2.00	0.43
33:LC:133:ALA:HB3	33:LC:134:PRO:HD3	2.00	0.43
40:LN:53:TYR:CE1	40:LN:59:TYR:HB3	2.53	0.43
44:LR:89:MET:HE3	44:LR:90:PRO:HD2	2.00	0.43
47:LU:48:LYS:HB3	47:LU:48:LYS:HE2	1.75	0.43
1:C1:84:U:OP2	1:C1:85:A:O2'	2.24	0.43
1:C1:190:G:N2	1:C1:364:A:C8	2.86	0.43
1:C1:381:A:H5''	42:LP:16:ARG:HG3	2.00	0.43
1:C1:976:U:C2	1:C1:1036:A:N7	2.87	0.43
1:C1:1692:G:N2	1:C1:1709:G:H1'	2.33	0.43
1:C1:3043:A:H3'	1:C1:3044:A:H8	1.84	0.43
1:C1:3237:U:H2'	1:C1:3238:C:H6	1.83	0.43
8:CF:168:LEU:HD12	8:CF:208:LEU:HG	2.00	0.43
11:CI:193:ARG:HD3	11:CI:257:ILE:O	2.18	0.43
13:CK:128:SER:N	13:CK:131:GLU:OE1	2.45	0.43
16:CN:11:ASN:HB3	16:CN:207:GLY:HA3	2.01	0.43
19:CQ:58:ASN:OD1	19:CQ:58:ASN:C	2.61	0.43
20:CR:187:GLN:HB3	20:CR:191:GLU:CD	2.44	0.43
25:CW:98:ARG:HB2	25:CW:145:VAL:HG23	2.01	0.43
25:CW:300:ILE:O	25:CW:372:VAL:HA	2.19	0.43
28:CZ:560:HIS:O	28:CZ:564:THR:N	2.51	0.43
32:LB:14:LEU:HA	32:LB:17:LEU:HD13	2.00	0.43
33:LC:133:ALA:HB2	33:LC:149:VAL:HG21	2.00	0.43
37:LK:11:LYS:HE3	37:LK:11:LYS:HB3	1.78	0.43
37:LK:83:ARG:O	37:LK:86:LYS:HG2	2.18	0.43
46:LT:83:ARG:HH11	46:LT:84:TYR:H	1.66	0.43
47:LU:24:ASN:HA	47:LU:69:LYS:HG2	2.01	0.43
56:Lg:58:LEU:HB3	56:Lg:62:GLU:OE1	2.17	0.43
63:Lq:174:MET:SD	63:Lq:178:GLN:NE2	2.91	0.43
1:C1:249:C:H2'	1:C1:250:U:H6	1.84	0.43
1:C1:421:U:O2'	55:Lf:90:PRO:O	2.27	0.43
1:C1:1978:G:H2'	1:C1:1979:C:H6	1.83	0.43
1:C1:2942:C:H2'	1:C1:2943:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2957:G:H2'	1:C1:2958:U:H6	1.83	0.43
1:C1:3208:A:H5''	34:LE:64:ARG:NH1	2.33	0.43
2:C2:10:A:H2'	2:C2:11:C:C6	2.54	0.43
3:CA:268:ARG:O	3:CA:272:ARG:HG3	2.18	0.43
12:CJ:370:PHE:HE2	12:CJ:417:HIS:CD2	2.36	0.43
12:CJ:643:ARG:O	12:CJ:647:GLU:HG3	2.18	0.43
18:CP:370:PHE:HB3	18:CP:374:MET:HE2	2.00	0.43
21:CS:30:ALA:HB2	21:CS:58:SER:HB3	2.00	0.43
21:CS:150:ILE:HD12	21:CS:151:GLU:H	1.81	0.43
21:CS:573:ASP:OD1	21:CS:574:VAL:N	2.52	0.43
22:CT:651:SER:O	22:CT:653:PRO:HD3	2.18	0.43
25:CW:271:MET:N	25:CW:271:MET:HE3	2.32	0.43
27:CY:536:LEU:O	27:CY:539:MET:HB3	2.18	0.43
31:LA:83:TYR:H	31:LA:86:GLN:HE22	1.66	0.43
32:LB:89:LEU:HD13	32:LB:196:GLY:HA3	2.00	0.43
47:LU:67:ASP:HB3	47:LU:69:LYS:HE2	2.00	0.43
58:Li:31:LEU:HD13	58:Li:31:LEU:HA	1.91	0.43
63:Lq:183:ILE:O	63:Lq:187:ILE:HG22	2.19	0.43
1:C1:347:A:N1	33:LC:83:THR:HG22	2.33	0.43
1:C1:461:A:H2'	1:C1:462:C:C6	2.53	0.43
1:C1:490:C:H2'	1:C1:491:A:H8	1.84	0.43
1:C1:581:G:H1'	34:LE:37:LYS:HG3	1.99	0.43
1:C1:981:C:H5''	1:C1:982:G:H5'	2.00	0.43
1:C1:1576:C:H5'	1:C1:1675:A:H1'	2.01	0.43
1:C1:1768:G:H2'	1:C1:1769:U:H6	1.83	0.43
1:C1:2263:U:H2'	1:C1:2264:G:C8	2.54	0.43
1:C1:2279:A:H2'	1:C1:2280:U:O4'	2.19	0.43
1:C1:2394:A:C6	1:C1:2556:G:C6	3.06	0.43
1:C1:2794:C:H2'	1:C1:2795:A:O4'	2.18	0.43
1:C1:3169:U:H2'	1:C1:3170:C:C6	2.53	0.43
1:C1:3234:A:H5''	32:LB:128:LYS:HZ2	1.82	0.43
2:C2:219:A:H5''	11:CI:222:LYS:HZ2	1.82	0.43
2:C2:223:G:H21	2:C2:301:A:N6	2.16	0.43
7:CE:157:THR:HA	7:CE:161:LYS:HE2	2.00	0.43
8:CF:84:GLU:OE2	8:CF:87:ASP:HA	2.18	0.43
36:LH:108:GLU:OE1	36:LH:108:GLU:N	2.50	0.43
37:LK:64:ILE:HG22	37:LK:69:ALA:HB2	2.00	0.43
44:LR:96:MET:SD	44:LR:100:ARG:NH2	2.92	0.43
49:LX:75:ILE:HG22	49:LX:76:ILE:HD12	2.01	0.43
1:C1:12:G:H2'	1:C1:13:A:C8	2.54	0.43
1:C1:100:A:H3'	1:C1:101:G:H21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:404:G:H2'	1:C1:405:U:H6	1.83	0.43
1:C1:575:A:H5''	55:Lf:72:LYS:HE2	2.01	0.43
1:C1:878:U:H2'	1:C1:879:C:C6	2.53	0.43
2:C2:159:C:C4	15:CM:55:GLU:HG2	2.53	0.43
3:CA:30:ARG:NH2	23:CU:212:THR:OG1	2.51	0.43
6:CD:10:ALA:HA	6:CD:11:PRO:HD3	1.86	0.43
8:CF:44:SER:OG	8:CF:46:ASP:OD1	2.35	0.43
10:CH:310:LYS:HG3	10:CH:310:LYS:O	2.19	0.43
12:CJ:125:HIS:O	12:CJ:129:GLU:HG2	2.19	0.43
15:CM:185:ILE:HD12	15:CM:186:CYS:N	2.34	0.43
22:CT:208:GLN:HA	22:CT:208:GLN:HE21	1.84	0.43
22:CT:601:LEU:HD23	22:CT:601:LEU:HA	1.84	0.43
28:CZ:372:ASP:O	28:CZ:376:ILE:HG13	2.18	0.43
28:CZ:401:TYR:HE1	28:CZ:414:ILE:HD12	1.84	0.43
32:LB:61:ASP:O	32:LB:63:PRO:HD3	2.18	0.43
33:LC:163:VAL:HG13	33:LC:169:ALA:HB2	2.00	0.43
63:Lq:13:VAL:HG11	63:Lq:180:VAL:HG12	2.00	0.43
1:C1:423:U:H2'	1:C1:424:G:H8	1.81	0.43
1:C1:1179:A:C4	14:CL:16:LYS:HD3	2.53	0.43
1:C1:1260:A:H4'	8:CF:13:ILE:HD13	2.01	0.43
1:C1:2097:U:H5'	29:Ca:58:LYS:NZ	2.34	0.43
4:CB:73:HIS:ND1	4:CB:74:ASP:OD1	2.51	0.43
6:CD:48:ARG:CZ	6:CD:48:ARG:HA	2.48	0.43
7:CE:167:ILE:O	7:CE:171:GLU:HG2	2.19	0.43
7:CE:243:ARG:HG3	7:CE:247:HIS:HD2	1.82	0.43
15:CM:151:ARG:NH1	15:CM:188:GLU:OE1	2.47	0.43
25:CW:56:VAL:HG12	25:CW:246:LYS:HA	2.00	0.43
25:CW:176:LEU:HD12	25:CW:176:LEU:HA	1.78	0.43
25:CW:453:ARG:HG2	25:CW:453:ARG:HH11	1.83	0.43
39:LM:121:MET:HE2	39:LM:121:MET:HB3	1.81	0.43
1:C1:155:G:H2'	1:C1:156:G:H8	1.82	0.43
1:C1:248:G:H2'	1:C1:249:C:O4'	2.18	0.43
1:C1:429:G:C4	1:C1:430:A:C8	3.07	0.43
1:C1:1548:C:N3	5:CC:408:MET:HE1	2.32	0.43
1:C1:1584:A:O2'	1:C1:1585:U:H5''	2.18	0.43
1:C1:1698:G:H2'	1:C1:1699:U:O4'	2.19	0.43
1:C1:2345:C:OP2	41:LO:87:ARG:NH2	2.50	0.43
1:C1:2469:U:H2'	1:C1:2470:U:C6	2.53	0.43
1:C1:2557:U:H2'	1:C1:2558:C:C6	2.53	0.43
1:C1:2858:A:N7	10:CH:5:LYS:NZ	2.67	0.43
2:C2:139:U:H2'	2:C2:140:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:143:U:P	40:LN:38:ARG:HH12	2.41	0.43
4:CB:158:ARG:C	4:CB:159:ILE:HD13	2.43	0.43
5:CC:417:ARG:NH1	5:CC:417:ARG:HG2	2.33	0.43
5:CC:489:TRP:CE3	5:CC:526:PRO:HB3	2.53	0.43
6:CD:128:ARG:NH1	6:CD:128:ARG:HG3	2.34	0.43
6:CD:295:ILE:HD12	6:CD:323:ARG:NH2	2.33	0.43
6:CD:444:GLU:HA	6:CD:447:ALA:HB3	2.00	0.43
7:CE:455:LYS:HA	7:CE:455:LYS:HD3	1.66	0.43
10:CH:403:LEU:HA	16:CN:39:GLU:OE2	2.19	0.43
16:CN:233:ILE:HA	16:CN:236:SER:HB3	2.00	0.43
21:CS:250:TYR:C	21:CS:252:GLN:H	2.25	0.43
25:CW:376:ASP:OD2	25:CW:466:TRP:NE1	2.51	0.43
26:CX:106:ALA:HB1	26:CX:129:ILE:HG12	2.00	0.43
29:Ca:30:LYS:O	29:Ca:34:ILE:HG13	2.19	0.43
31:LA:131:GLY:N	31:LA:169:VAL:HG23	2.30	0.43
36:LH:38:LEU:HD12	36:LH:38:LEU:O	2.19	0.43
49:LX:101:VAL:HG21	62:LI:7:PHE:CZ	2.54	0.43
58:Li:46:THR:O	58:Li:50:ARG:HG3	2.18	0.43
1:C1:66:A:C2	1:C1:77:A:H5'	2.53	0.43
1:C1:213:G:O6	1:C1:1371:G:C2	2.71	0.43
1:C1:760:G:H2'	1:C1:762:G:H8	1.84	0.43
1:C1:864:A:H61	9:CG:122:TRP:HD1	1.66	0.43
1:C1:1468:G:H21	56:Lg:7:THR:HG22	1.83	0.43
1:C1:1549:U:O2'	12:CJ:223:ASP:OD2	2.36	0.43
1:C1:1673:U:O2'	1:C1:1674:U:H5'	2.19	0.43
1:C1:1978:G:H2'	1:C1:1979:C:C6	2.53	0.43
1:C1:1980:C:H2'	1:C1:1981:G:C8	2.53	0.43
1:C1:2167:U:H2'	1:C1:2168:G:C8	2.53	0.43
1:C1:2248:U:O4	1:C1:2268:C:C4	2.72	0.43
1:C1:2760:A:H5'	26:CX:90:LYS:HG2	2.00	0.43
2:C2:210:C:P	7:CE:488:ASN:HD21	2.42	0.43
6:CD:165:ILE:N	6:CD:165:ILE:HD12	2.34	0.43
6:CD:397:SER:HB2	6:CD:468:TRP:CZ3	2.54	0.43
7:CE:243:ARG:HG3	7:CE:247:HIS:CD2	2.54	0.43
7:CE:440:ASP:OD1	7:CE:444:ARG:NH2	2.51	0.43
10:CH:179:LYS:HB2	10:CH:179:LYS:HE2	1.89	0.43
10:CH:263:LEU:O	10:CH:267:ILE:HG12	2.19	0.43
10:CH:379:ARG:HD2	16:CN:113:HIS:CD2	2.53	0.43
15:CM:171:ASP:N	15:CM:171:ASP:OD1	2.49	0.43
16:CN:70:LEU:HD23	16:CN:94:ILE:HD13	2.01	0.43
18:CP:255:GLU:HG2	18:CP:256:GLY:N	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:320:LEU:HD21	18:CP:362:TYR:HB3	2.00	0.43
21:CS:14:ASP:H	21:CS:17:TYR:HB3	1.84	0.43
21:CS:206:ARG:HH12	29:Ca:25:GLU:HA	1.84	0.43
25:CW:457:GLN:HA	25:CW:460:GLN:OE1	2.19	0.43
25:CW:602:THR:HG22	25:CW:605:GLU:HG3	2.01	0.43
27:CY:637:ILE:HD11	27:CY:691:ARG:HB2	2.01	0.43
28:CZ:357:GLY:HA2	28:CZ:360:LEU:HB3	2.00	0.43
28:CZ:465:LEU:O	28:CZ:469:ILE:HG12	2.19	0.43
35:LG:71:ARG:HD3	35:LG:71:ARG:HA	1.87	0.43
39:LM:113:THR:O	39:LM:117:ARG:HG3	2.18	0.43
54:Le:122:ASN:OD1	54:Le:122:ASN:N	2.51	0.43
1:C1:115:A:N6	1:C1:149:U:N3	2.67	0.43
1:C1:300:A:H2'	1:C1:300:A:N3	2.34	0.43
1:C1:541:G:H2'	1:C1:542:U:H6	1.84	0.43
1:C1:1158:C:H5''	1:C1:1159:G:H2'	2.01	0.43
1:C1:1193:U:O2'	45:LS:113:ARG:NH1	2.52	0.43
1:C1:2050:G:C6	1:C1:2051:G:C2	3.07	0.43
1:C1:2180:G:H21	28:CZ:566:HIS:HA	1.84	0.43
1:C1:2874:U:H2'	1:C1:2875:G:C8	2.54	0.43
1:C1:3176:C:H2'	1:C1:3177:C:C6	2.54	0.43
3:CA:244:ILE:HG13	3:CA:256:TYR:O	2.19	0.43
4:CB:96:SER:N	4:CB:151:ASP:OD2	2.35	0.43
4:CB:216:PRO:O	4:CB:219:GLU:HG3	2.19	0.43
4:CB:294:TYR:HD1	4:CB:295:GLN:N	2.17	0.43
6:CD:128:ARG:HG3	6:CD:128:ARG:HH11	1.82	0.43
10:CH:422:ARG:NH1	10:CH:435:ASP:O	2.40	0.43
18:CP:255:GLU:HG2	18:CP:256:GLY:H	1.83	0.43
18:CP:510:TYR:OH	18:CP:523:VAL:HG21	2.19	0.43
21:CS:661:THR:O	21:CS:665:GLN:HG3	2.18	0.43
23:CU:309:LYS:HD2	23:CU:309:LYS:HA	1.86	0.43
27:CY:588:PRO:HG2	27:CY:612:ARG:HH21	1.84	0.43
28:CZ:623:MET:HA	28:CZ:626:ALA:HB2	2.01	0.43
29:Ca:60:ARG:HB3	29:Ca:60:ARG:HH11	1.84	0.43
51:LZ:75:ASN:OD1	51:LZ:76:TYR:N	2.52	0.43
63:Lq:16:LEU:HD12	63:Lq:17:LEU:HD22	1.99	0.43
63:Lq:41:TYR:O	63:Lq:163:LEU:HD21	2.18	0.43
63:Lq:58:VAL:HA	63:Lq:60:ARG:HH11	1.83	0.43
63:Lq:124:LEU:HD23	63:Lq:124:LEU:H	1.84	0.43
1:C1:159:G:H2'	1:C1:160:C:C6	2.54	0.42
1:C1:1044:A:HO2'	46:LT:108:ARG:HH22	1.62	0.42
1:C1:1304:U:OP1	45:LS:117:ARG:NH1	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1908:G:C6	44:LR:139:VAL:HG11	2.54	0.42
1:C1:1938:U:C2	1:C1:2045:C:N4	2.86	0.42
1:C1:2468:U:H2'	1:C1:2469:U:C6	2.54	0.42
1:C1:3264:A:OP1	53:Ld:27:ARG:NH2	2.52	0.42
2:C2:174:G:H1'	2:C2:175:G:C8	2.54	0.42
3:CA:23:ARG:HH12	5:CC:160:SEP:HB2	1.84	0.42
4:CB:280:ASN:HB3	4:CB:282:TYR:CE1	2.54	0.42
10:CH:518:ILE:HD11	44:LR:23:TRP:CD2	2.54	0.42
21:CS:372:ARG:HB3	21:CS:372:ARG:CZ	2.49	0.42
25:CW:262:GLU:HG2	25:CW:264:LYS:NZ	2.33	0.42
25:CW:305:THR:HG21	25:CW:465:SER:C	2.43	0.42
27:CY:398:ILE:HD12	27:CY:399:THR:H	1.83	0.42
34:LE:166:ASP:OD1	34:LE:167:LYS:N	2.52	0.42
15:LF:95:ILE:HD11	15:LF:234:LEU:HD23	2.00	0.42
15:LF:138:PRO:HA	15:LF:234:LEU:HD13	2.00	0.42
48:LV:20:PRO:HA	48:LV:53:ALA:HA	2.00	0.42
48:LV:106:ASN:HB2	48:LV:107:PRO:HD2	2.01	0.42
51:LZ:32:THR:OG1	51:LZ:34:SER:O	2.27	0.42
52:Lc:21:ILE:HD13	52:Lc:84:CYS:SG	2.59	0.42
63:Lq:196:LYS:HZ1	63:Lq:199:GLN:HB3	1.84	0.42
1:C1:161:U:O2'	20:CR:149:HIS:ND1	2.46	0.42
1:C1:322:G:C2	1:C1:323:G:C8	3.07	0.42
1:C1:507:G:OP1	15:LF:73:ARG:NH2	2.45	0.42
1:C1:1618:C:OP1	56:Lg:53:PRO:HG2	2.19	0.42
1:C1:1865:A:H2'	1:C1:1866:A:H8	1.84	0.42
1:C1:2011:G:H2'	1:C1:2012:G:H8	1.84	0.42
1:C1:3075:C:H5''	30:Cz:28:ASN:OD1	2.20	0.42
1:C1:3297:U:H2'	1:C1:3298:U:C6	2.54	0.42
1:C1:3299:A:H2'	1:C1:3300:C:C6	2.53	0.42
4:CB:30:LEU:HB2	4:CB:291:LEU:HD11	2.00	0.42
5:CC:282:ILE:HD12	20:CR:218:TYR:HD1	1.84	0.42
6:CD:97:ARG:HE	6:CD:97:ARG:HB3	1.70	0.42
8:CF:89:LEU:HD23	8:CF:89:LEU:HA	1.84	0.42
8:CF:94:ARG:HD3	8:CF:245:LYS:HG2	2.02	0.42
15:CM:102:PRO:HB2	15:CM:105:PRO:HD2	2.02	0.42
24:CV:25:THR:HG22	54:Le:66:HIS:HB3	2.01	0.42
25:CW:281:LYS:HD3	25:CW:375:HIS:CE1	2.54	0.42
25:CW:297:GLN:HE22	25:CW:350:SER:C	2.27	0.42
27:CY:374:LYS:HE3	27:CY:377:LYS:HZ1	1.84	0.42
27:CY:377:LYS:O	27:CY:381:LYS:HG3	2.19	0.42
27:CY:569:ILE:HD13	27:CY:569:ILE:HA	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:CZ:323:LEU:HD12	28:CZ:323:LEU:HA	1.86	0.42
46:LT:41:ASP:HB2	46:LT:97:LYS:HG3	2.01	0.42
1:C1:953:U:H2'	1:C1:954:G:C8	2.54	0.42
1:C1:1239:C:H2'	1:C1:1240:U:O4'	2.19	0.42
1:C1:1322:C:H2'	1:C1:1323:U:H6	1.84	0.42
1:C1:2328:C:H2'	1:C1:2329:A:C8	2.54	0.42
1:C1:3136:A:H2'	1:C1:3137:A:H8	1.84	0.42
1:C1:3158:U:C5	39:LM:121:MET:HG3	2.53	0.42
2:C2:71:A:O2'	2:C2:83:C:N4	2.42	0.42
3:CA:67:LYS:HE3	3:CA:67:LYS:HB3	1.77	0.42
5:CC:380:LYS:HZ2	5:CC:380:LYS:HB3	1.84	0.42
5:CC:429:LEU:HD12	12:CJ:638:LEU:HD11	2.01	0.42
6:CD:20:THR:O	6:CD:94:GLN:HA	2.20	0.42
9:CG:112:SER:HB3	13:CK:136:VAL:HA	2.01	0.42
21:CS:369:GLU:HA	21:CS:372:ARG:HH22	1.84	0.42
22:CT:597:MET:HE3	22:CT:597:MET:HB3	1.84	0.42
25:CW:243:TYR:HD1	52:Lc:22:LYS:HZ3	1.68	0.42
25:CW:314:ARG:HD2	25:CW:458:LEU:HD12	2.02	0.42
27:CY:618:VAL:O	27:CY:622:VAL:HG12	2.19	0.42
31:LA:181:LYS:CB	31:LA:184:ARG:HG3	2.50	0.42
34:LE:38:LYS:HA	34:LE:38:LYS:HD3	1.76	0.42
35:LG:97:LEU:HB3	35:LG:192:LEU:HD11	2.01	0.42
51:LZ:40:ALA:HB2	51:LZ:76:TYR:HE1	1.84	0.42
51:LZ:134:ARG:HD2	51:LZ:134:ARG:HA	1.91	0.42
63:Lq:120:ILE:N	63:Lq:121:PRO:HD3	2.34	0.42
1:C1:7:C:H2'	1:C1:8:C:H6	1.84	0.42
1:C1:18:G:N2	40:LN:112:ASN:HD22	2.16	0.42
1:C1:405:U:H2'	1:C1:406:U:C6	2.54	0.42
1:C1:1333:A:C5	15:LF:18:LEU:HD13	2.54	0.42
1:C1:1464:A:N7	27:CY:12:LYS:HG2	2.35	0.42
1:C1:1979:C:H2'	1:C1:1980:C:C6	2.54	0.42
1:C1:2051:G:H2'	1:C1:2052:U:C6	2.55	0.42
1:C1:2200:G:H2'	1:C1:2201:G:C8	2.54	0.42
6:CD:143:GLN:OE1	6:CD:143:GLN:N	2.52	0.42
6:CD:181:LYS:H	6:CD:195:GLY:HA2	1.84	0.42
6:CD:479:ASP:O	6:CD:481:LYS:HD3	2.19	0.42
7:CE:332:LEU:HA	7:CE:450:ARG:HH21	1.84	0.42
7:CE:444:ARG:O	7:CE:448:THR:HG23	2.19	0.42
11:CI:308:LYS:O	11:CI:311:GLN:HG2	2.20	0.42
18:CP:455:LEU:HD11	18:CP:490:LEU:HB3	2.00	0.42
21:CS:45:LYS:HA	21:CS:68:PRO:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CU:224:LYS:HA	23:CU:224:LYS:HD3	1.59	0.42
25:CW:177:LEU:HB3	25:CW:215:TYR:HD2	1.84	0.42
25:CW:617:ASN:HA	25:CW:620:ARG:HD3	2.01	0.42
34:LE:86:PRO:HB3	34:LE:166:ASP:HB2	2.00	0.42
37:LK:12:ILE:N	37:LK:12:ILE:HD12	2.34	0.42
56:Lg:45:CYS:SG	56:Lg:46:GLY:N	2.92	0.42
63:Lq:128:LEU:HD23	63:Lq:128:LEU:HA	1.89	0.42
1:C1:753:U:C2	1:C1:754:G:C8	3.07	0.42
1:C1:1639:C:H2'	1:C1:1640:G:C8	2.53	0.42
1:C1:1874:A:O2'	1:C1:3010:G:H4'	2.19	0.42
1:C1:2444:U:H2'	1:C1:2445:G:O4'	2.18	0.42
2:C2:63:G:H22	2:C2:97:A:H2	1.67	0.42
4:CB:251:GLU:HG3	4:CB:253:GLU:OE1	2.18	0.42
6:CD:241:LEU:HD23	6:CD:305:PHE:CZ	2.55	0.42
7:CE:355:MET:HE2	7:CE:355:MET:HB2	1.85	0.42
7:CE:471:ALA:HA	7:CE:474:LYS:HE3	2.02	0.42
12:CJ:142:ASP:OD1	12:CJ:142:ASP:N	2.53	0.42
14:CL:462:ALA:HB2	14:CL:479:ALA:HB2	2.02	0.42
25:CW:185:PRO:HD2	25:CW:188:SER:HB3	2.01	0.42
27:CY:413:LYS:HZ3	27:CY:416:ARG:HB2	1.85	0.42
28:CZ:210:ASP:O	28:CZ:214:ARG:HG3	2.20	0.42
32:LB:350:LYS:O	32:LB:353:GLU:HG2	2.19	0.42
53:Ld:28:LEU:HD11	53:Ld:40:ALA:HB2	2.00	0.42
1:C1:74:G:O2'	38:LL:59:ARG:O	2.37	0.42
1:C1:588:C:H4'	33:LC:327:LEU:HD13	2.01	0.42
1:C1:1599:U:H2'	1:C1:1600:G:C8	2.54	0.42
1:C1:1672:C:HO2'	1:C1:1751:U:HO2'	1.66	0.42
1:C1:1722:G:C2	1:C1:1723:G:C8	3.08	0.42
1:C1:2123:G:H2'	1:C1:2124:C:H6	1.84	0.42
1:C1:3217:U:N3	55:Lf:63:GLY:O	2.47	0.42
2:C2:3:A:H4'	42:LP:61:ARG:HH11	1.85	0.42
2:C2:149:A:H2'	2:C2:150:G:C8	2.54	0.42
3:CA:40:SER:HB2	3:CA:52:LEU:HD13	2.02	0.42
7:CE:528:ARG:HH11	7:CE:528:ARG:HG2	1.85	0.42
10:CH:90:PHE:CE1	10:CH:152:VAL:HG11	2.54	0.42
21:CS:99:CYS:HA	21:CS:102:THR:HG22	2.02	0.42
22:CT:229:ILE:N	22:CT:230:PRO:HD2	2.35	0.42
22:CT:318:ASP:OD1	22:CT:318:ASP:O	2.37	0.42
25:CW:143:LEU:HD11	25:CW:145:VAL:HB	2.02	0.42
25:CW:612:LEU:O	25:CW:616:ILE:HG13	2.20	0.42
27:CY:540:ARG:NH1	27:CY:543:PRO:HG3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:CZ:321:TYR:O	28:CZ:325:LEU:HD13	2.20	0.42
28:CZ:359:ARG:O	28:CZ:363:LEU:HG	2.20	0.42
28:CZ:466:LEU:HA	28:CZ:469:ILE:HD11	2.01	0.42
31:LA:33:ASP:N	31:LA:33:ASP:OD1	2.50	0.42
31:LA:181:LYS:CG	31:LA:184:ARG:HG3	2.49	0.42
36:LH:137:GLU:HG3	36:LH:147:ILE:HB	2.02	0.42
39:LM:23:GLU:H	39:LM:23:GLU:HG2	1.65	0.42
60:Lk:57:LYS:HB3	60:Lk:57:LYS:HE2	1.84	0.42
1:C1:515:G:H5''	39:LM:78:THR:HB	2.00	0.42
1:C1:1599:U:H2'	1:C1:1600:G:H8	1.83	0.42
1:C1:2985:G:O3'	10:CH:214:ARG:NH2	2.50	0.42
1:C1:3103:G:H2'	1:C1:3104:A:H8	1.84	0.42
1:C1:3207:U:H2'	34:LE:87:PHE:CZ	2.54	0.42
3:CA:270:GLU:OE1	3:CA:270:GLU:HA	2.20	0.42
4:CB:160:ILE:HD12	4:CB:160:ILE:HA	1.84	0.42
5:CC:439:LYS:HD2	5:CC:439:LYS:HA	1.75	0.42
6:CD:220:GLU:OE1	6:CD:222:TYR:OH	2.31	0.42
7:CE:485:PHE:O	7:CE:485:PHE:CG	2.73	0.42
13:CK:260:LEU:HD23	23:CU:337:LEU:HD23	2.01	0.42
16:CN:85:ARG:NH2	16:CN:89:PRO:O	2.53	0.42
21:CS:250:TYR:H	21:CS:250:TYR:HD1	1.63	0.42
25:CW:616:ILE:HD12	25:CW:617:ASN:N	2.35	0.42
27:CY:465:PHE:CE1	27:CY:469:ARG:HD2	2.55	0.42
27:CY:471:LEU:HD22	27:CY:495:TYR:CZ	2.55	0.42
28:CZ:178:ARG:H	28:CZ:178:ARG:HD3	1.84	0.42
28:CZ:191:GLN:OE1	28:CZ:191:GLN:N	2.45	0.42
31:LA:174:ARG:NH1	31:LA:177:LYS:HB2	2.35	0.42
31:LA:181:LYS:HB3	31:LA:184:ARG:HG3	2.02	0.42
31:LA:181:LYS:HG2	31:LA:184:ARG:HG3	2.01	0.42
35:LG:76:PRO:HA	35:LG:79:ALA:HB3	2.02	0.42
35:LG:146:ILE:HG22	35:LG:176:MET:HG3	2.01	0.42
55:Lf:72:LYS:HB2	55:Lf:72:LYS:NZ	2.35	0.42
1:C1:860:U:H2'	1:C1:861:G:O4'	2.20	0.42
1:C1:1156:G:H2'	1:C1:1157:C:C6	2.55	0.42
1:C1:2248:U:H2'	1:C1:2249:C:O4'	2.19	0.42
1:C1:2364:A:H3'	1:C1:2365:G:H8	1.85	0.42
1:C1:2427:G:O6	1:C1:2453:A:N6	2.52	0.42
1:C1:3118:A:H2'	1:C1:3119:C:H6	1.83	0.42
1:C1:3290:C:C4	1:C1:3291:U:N3	2.88	0.42
2:C2:37:A:OP2	57:Lh:91:ARG:HD2	2.20	0.42
2:C2:212:G:OP1	2:C2:214:A:H8	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CE:142:ILE:HB	7:CE:143:PRO:HD3	2.01	0.42
10:CH:357:ILE:HG23	10:CH:361:LEU:HD23	2.02	0.42
12:CJ:508:THR:HG22	12:CJ:511:GLU:OE2	2.19	0.42
14:CL:187:GLY:HA2	14:CL:188:ALA:HA	1.55	0.42
15:CM:241:ILE:HD12	15:CM:241:ILE:HA	1.93	0.42
16:CN:182:VAL:HG22	16:CN:221:VAL:HG21	2.02	0.42
21:CS:282:PRO:HG2	21:CS:286:ASP:HB2	2.01	0.42
25:CW:434:THR:HB	25:CW:437:GLN:HB2	2.01	0.42
25:CW:460:GLN:HG3	25:CW:495:LEU:HD11	2.02	0.42
27:CY:542:ILE:HD12	27:CY:542:ILE:O	2.20	0.42
28:CZ:267:LYS:HD2	28:CZ:268:PRO:CD	2.50	0.42
28:CZ:347:LEU:HG	28:CZ:348:LEU:HD22	2.01	0.42
32:LB:29:VAL:HG12	32:LB:31:SER:H	1.85	0.42
39:LM:54:ARG:HD3	45:LS:70:LEU:HD13	2.02	0.42
42:LP:23:ARG:NE	42:LP:125:GLN:OE1	2.53	0.42
1:C1:759:U:H2'	1:C1:760:G:C8	2.54	0.42
1:C1:824:A:N6	1:C1:825:G:O6	2.52	0.42
1:C1:1207:A:H2'	1:C1:1208:G:O4'	2.20	0.42
1:C1:1275:U:H2'	1:C1:1276:A:C8	2.53	0.42
1:C1:1479:C:H2'	1:C1:1480:A:C8	2.54	0.42
1:C1:1600:G:H2'	1:C1:1601:U:H6	1.85	0.42
1:C1:1835:C:C4	1:C1:1836:C:C4	3.08	0.42
1:C1:2795:A:H1'	1:C1:2809:A:N6	2.35	0.42
1:C1:3294:U:OP2	25:CW:591:ARG:HD2	2.20	0.42
4:CB:72:ILE:N	4:CB:72:ILE:HD13	2.35	0.42
6:CD:118:ASP:OD2	6:CD:185:PHE:N	2.53	0.42
7:CE:243:ARG:HD3	7:CE:243:ARG:HA	1.86	0.42
8:CF:220:LYS:HB2	8:CF:220:LYS:HE2	1.84	0.42
10:CH:168:THR:HB	10:CH:247:ALA:HB2	2.02	0.42
13:CK:4:ASN:O	13:CK:6:TYR:N	2.53	0.42
14:CL:438:TYR:O	14:CL:440:ILE:N	2.53	0.42
15:CM:31:GLU:H	15:CM:31:GLU:HG2	1.66	0.42
15:CM:134:LYS:HD3	15:CM:134:LYS:HA	1.79	0.42
19:CQ:108:TYR:O	19:CQ:112:MET:HG2	2.20	0.42
25:CW:42:GLN:O	25:CW:46:LEU:HD23	2.20	0.42
25:CW:385:ILE:H	25:CW:385:ILE:HD12	1.85	0.42
25:CW:498:LEU:HA	25:CW:499:PRO:HD3	1.91	0.42
27:CY:471:LEU:HD23	27:CY:471:LEU:HA	1.81	0.42
33:LC:23:LEU:HD22	33:LC:27:PHE:CD2	2.55	0.42
34:LE:61:LEU:HD11	34:LE:103:ILE:HG13	2.01	0.42
35:LG:100:TYR:O	35:LG:135:VAL:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:LH:90:MET:HE2	36:LH:90:MET:HB3	1.89	0.42
41:LO:62:MET:HE3	41:LO:67:PRO:HB3	2.02	0.42
45:LS:42:TRP:CD1	45:LS:53:LYS:HZ3	2.38	0.42
54:Le:41:ASN:OD1	54:Le:41:ASN:N	2.53	0.42
55:Lf:47:LEU:HD11	55:Lf:76:PRO:HD3	2.02	0.42
56:Lg:25:LYS:HD2	56:Lg:25:LYS:HA	1.85	0.42
63:Lq:163:LEU:HD23	63:Lq:163:LEU:HA	1.75	0.42
1:C1:203:C:O2	33:LC:224:LYS:HD2	2.20	0.42
1:C1:830:C:H2'	1:C1:831:U:H6	1.84	0.42
1:C1:836:U:H4'	44:LR:95:TRP:CE2	2.54	0.42
1:C1:1315:C:O2'	15:LF:213:LEU:O	2.38	0.42
1:C1:1954:C:H2'	1:C1:1955:G:C8	2.55	0.42
1:C1:2045:C:H2'	1:C1:2046:G:C8	2.55	0.42
1:C1:2252:C:H2'	1:C1:2253:A:C8	2.55	0.42
1:C1:2418:A:H2	1:C1:2445:G:H1'	1.85	0.42
1:C1:2922:G:C2	1:C1:2926:G:C5	3.08	0.42
1:C1:3327:G:H2'	1:C1:3328:C:C6	2.55	0.42
5:CC:408:MET:O	5:CC:412:LEU:HB2	2.20	0.42
5:CC:697:ARG:HH11	5:CC:712:THR:HG22	1.85	0.42
6:CD:114:VAL:HA	6:CD:150:SER:HA	2.01	0.42
13:CK:38:ASN:O	13:CK:42:LEU:HG	2.20	0.42
13:CK:52:LYS:HB3	13:CK:52:LYS:NZ	2.35	0.42
18:CP:309:ARG:HH22	18:CP:396:THR:HG22	1.84	0.42
18:CP:459:CYS:HA	18:CP:483:LEU:HD22	2.01	0.42
21:CS:26:ARG:HE	21:CS:84:ILE:HD11	1.84	0.42
21:CS:676:LEU:HD23	21:CS:676:LEU:HA	1.86	0.42
22:CT:375:LYS:HE2	22:CT:375:LYS:HB3	1.56	0.42
25:CW:99:GLU:OE1	25:CW:99:GLU:HA	2.20	0.42
25:CW:457:GLN:H	25:CW:457:GLN:CD	2.26	0.42
27:CY:435:ASN:O	27:CY:600:THR:HB	2.20	0.42
29:Ca:157:SER:OG	29:Ca:166:PRO:HG3	2.20	0.42
32:LB:29:VAL:HG13	32:LB:340:ARG:HD3	2.02	0.42
33:LC:91:PHE:O	33:LC:99:ARG:NH2	2.53	0.42
60:Lk:11:PHE:CZ	60:Lk:36:PHE:HB3	2.55	0.42
1:C1:1545:G:H2'	1:C1:1546:C:C6	2.54	0.41
1:C1:2199:C:H2'	1:C1:2200:G:H8	1.84	0.41
2:C2:233:U:H3	2:C2:284:G:H1	1.68	0.41
7:CE:258:LEU:HD22	7:CE:285:LEU:HD22	2.02	0.41
9:CG:79:LYS:HB2	9:CG:79:LYS:HE2	1.88	0.41
10:CH:140:LYS:HB3	10:CH:140:LYS:HE3	1.66	0.41
10:CH:253:MET:HE3	10:CH:253:MET:HB3	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:257:GLU:HB2	37:LK:39:PRO:HG2	2.02	0.41
12:CJ:223:ASP:HB3	12:CJ:226:ILE:HD12	2.01	0.41
12:CJ:420:ILE:HD12	12:CJ:420:ILE:O	2.21	0.41
12:CJ:584:THR:O	12:CJ:588:GLN:HG3	2.20	0.41
15:CM:20:LYS:NZ	15:CM:20:LYS:HB2	2.34	0.41
15:CM:244:LEU:HG	15:CM:248:MET:HE2	2.02	0.41
17:CO:30:LEU:HD11	32:LB:42:HIS:CG	2.55	0.41
18:CP:310:THR:HG23	18:CP:340:VAL:O	2.20	0.41
18:CP:320:LEU:HD11	18:CP:362:TYR:CD1	2.53	0.41
21:CS:367:ILE:HG13	21:CS:368:LYS:HD2	2.01	0.41
22:CT:131:LEU:HD13	22:CT:170:THR:HG21	2.02	0.41
25:CW:105:TYR:CD1	25:CW:143:LEU:HB2	2.55	0.41
25:CW:291:LYS:O	25:CW:292:LEU:HD13	2.20	0.41
25:CW:453:ARG:HG2	25:CW:453:ARG:NH1	2.35	0.41
27:CY:415:VAL:O	27:CY:419:VAL:HG12	2.20	0.41
27:CY:731:GLU:HB2	27:CY:734:ARG:HH21	1.85	0.41
28:CZ:326:LYS:H	28:CZ:326:LYS:HG2	1.63	0.41
29:Ca:214:SER:OG	29:Ca:218:LYS:NZ	2.53	0.41
32:LB:46:ALA:HB2	32:LB:209:ILE:HD12	2.02	0.41
35:LG:85:LEU:HD23	35:LG:181:ALA:HB1	2.02	0.41
41:LO:192:ASP:OD1	41:LO:193:PRO:HD2	2.19	0.41
50:LY:43:ASN:HB3	50:LY:122:LYS:HG3	2.02	0.41
53:Ld:60:ASP:OD1	53:Ld:100:TYR:OH	2.30	0.41
63:Lq:19:TYR:O	63:Lq:23:VAL:HG22	2.20	0.41
1:C1:273:G:N7	40:LN:182:LYS:NZ	2.61	0.41
1:C1:498:C:OP1	15:LF:217:ASN:ND2	2.53	0.41
1:C1:1453:U:H2'	1:C1:1454:G:H8	1.85	0.41
1:C1:1938:U:O2	1:C1:2045:C:C4	2.73	0.41
1:C1:2461:U:H2'	1:C1:2462:A:H8	1.82	0.41
1:C1:2733:U:H2'	1:C1:2734:C:C6	2.55	0.41
3:CA:122:THR:O	3:CA:125:GLU:HG3	2.20	0.41
5:CC:390:LEU:HD23	5:CC:390:LEU:HA	1.89	0.41
9:CG:85:THR:HG22	18:CP:426:HIS:HB3	2.02	0.41
10:CH:235:GLU:HG2	10:CH:235:GLU:H	1.65	0.41
12:CJ:493:THR:OG1	12:CJ:496:GLN:OE1	2.35	0.41
14:CL:444:LEU:HA	15:LF:49:VAL:HG21	2.01	0.41
21:CS:241:LYS:HG3	21:CS:243:GLU:OE1	2.19	0.41
21:CS:371:GLU:C	21:CS:371:GLU:CD	2.88	0.41
22:CT:671:LYS:HD2	22:CT:671:LYS:HA	1.90	0.41
25:CW:269:LEU:CD1	25:CW:392:GLY:HA3	2.47	0.41
28:CZ:233:GLU:O	28:CZ:237:ILE:HG12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LA:88:ILE:HD12	31:LA:88:ILE:O	2.20	0.41
51:LZ:103:PRO:HA	51:LZ:106:ARG:HD3	2.02	0.41
1:C1:45:A:O2'	1:C1:95:A:N1	2.50	0.41
1:C1:665:G:OP1	43:LQ:136:LYS:NZ	2.53	0.41
1:C1:828:A:H8	1:C1:828:A:OP2	2.03	0.41
1:C1:962:U:H2'	1:C1:963:C:C6	2.56	0.41
1:C1:1191:G:OP1	13:CK:36:SER:OG	2.27	0.41
1:C1:1315:C:C2	1:C1:1316:C:C5	3.08	0.41
1:C1:1594:C:H2'	1:C1:1595:U:H6	1.81	0.41
1:C1:1692:G:H22	1:C1:1709:G:H1'	1.85	0.41
1:C1:2394:A:H2'	1:C1:2395:U:C6	2.55	0.41
1:C1:2797:G:O6	1:C1:2808:G:C2	2.73	0.41
2:C2:182:G:C6	4:CB:78:LEU:HG	2.55	0.41
3:CA:74:LEU:HD23	3:CA:74:LEU:HA	1.81	0.41
6:CD:72:LEU:HD21	6:CD:76:LEU:HD12	2.03	0.41
6:CD:479:ASP:OD1	6:CD:479:ASP:N	2.47	0.41
10:CH:90:PHE:HE1	10:CH:152:VAL:HG11	1.85	0.41
12:CJ:46:GLU:OE2	12:CJ:50:ARG:NH2	2.53	0.41
12:CJ:148:LEU:HD23	12:CJ:148:LEU:HA	1.88	0.41
18:CP:291:ARG:HD3	18:CP:291:ARG:N	2.35	0.41
22:CT:662:GLU:OE1	22:CT:662:GLU:HA	2.20	0.41
25:CW:72:PRO:O	25:CW:76:ARG:HG3	2.20	0.41
25:CW:308:ALA:HA	25:CW:462:ALA:HB1	2.02	0.41
28:CZ:218:ILE:O	28:CZ:222:PHE:HD1	2.04	0.41
33:LC:151:LEU:HD21	33:LC:176:ILE:HD12	2.01	0.41
34:LE:52:LEU:O	34:LE:52:LEU:HD12	2.20	0.41
35:LG:166:VAL:HG12	35:LG:169:LEU:HD12	2.02	0.41
54:Le:61:ASN:HB3	54:Le:64:THR:OG1	2.21	0.41
1:C1:208:G:H5''	50:LY:11:ARG:HG3	2.02	0.41
1:C1:587:G:H2'	1:C1:588:C:C6	2.55	0.41
1:C1:967:U:OP1	15:LF:104:LYS:NZ	2.49	0.41
1:C1:1116:G:H5''	23:CU:313:LYS:HZ1	1.84	0.41
1:C1:1968:A:H2'	1:C1:1969:G:H8	1.86	0.41
1:C1:2201:G:H2'	1:C1:2202:G:C8	2.56	0.41
1:C1:2374:G:H2'	1:C1:2375:A:H8	1.84	0.41
1:C1:2396:U:OP1	1:C1:2477:A:O2'	2.30	0.41
1:C1:2813:C:H2'	1:C1:2814:G:H8	1.84	0.41
1:C1:3162:A:H4'	1:C1:3163:G:O5'	2.19	0.41
2:C2:3:A:H4'	42:LP:61:ARG:NH1	2.36	0.41
6:CD:270:ALA:O	6:CD:271:HIS:ND1	2.49	0.41
7:CE:421:LEU:HD12	7:CE:421:LEU:HA	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:360:ARG:NH1	10:CH:360:ARG:HG3	2.36	0.41
12:CJ:396:GLY:HA2	12:CJ:405:ALA:HB1	2.02	0.41
12:CJ:508:THR:HG23	12:CJ:510:ALA:H	1.85	0.41
15:CM:73:ARG:HG2	15:CM:73:ARG:H	1.72	0.41
18:CP:254:GLU:HG2	18:CP:262:TYR:OH	2.20	0.41
19:CQ:157:GLU:H	19:CQ:157:GLU:CD	2.28	0.41
21:CS:45:LYS:HD3	21:CS:45:LYS:H	1.86	0.41
22:CT:441:ASP:HB3	26:CX:120:ILE:HD12	2.02	0.41
23:CU:249:GLU:O	23:CU:253:LEU:HD13	2.20	0.41
23:CU:343:GLU:OE1	23:CU:343:GLU:HA	2.19	0.41
25:CW:325:SER:OG	25:CW:352:THR:HG22	2.20	0.41
27:CY:465:PHE:HE1	27:CY:469:ARG:HD2	1.85	0.41
27:CY:631:VAL:HG21	27:CY:722:VAL:HG11	2.01	0.41
28:CZ:121:LYS:O	28:CZ:125:GLU:HG2	2.20	0.41
41:LO:44:ILE:HB	41:LO:138:CYS:SG	2.60	0.41
43:LQ:152:ASP:OD1	43:LQ:152:ASP:N	2.45	0.41
47:LU:27:GLN:HB3	47:LU:28:PRO:HD3	2.03	0.41
49:LX:104:ASN:H	49:LX:107:GLN:HE21	1.67	0.41
56:Lg:21:THR:OG1	56:Lg:22:ARG:N	2.53	0.41
1:C1:55:G:OP1	59:Lj:43:LYS:HE3	2.21	0.41
1:C1:541:G:H2'	1:C1:542:U:C6	2.56	0.41
1:C1:676:U:O4	33:LC:213:TYR:OH	2.36	0.41
1:C1:978:A:H2'	1:C1:979:A:H8	1.85	0.41
1:C1:1502:G:H5''	49:LX:82:THR:HG22	2.01	0.41
1:C1:1822:C:H2'	1:C1:1823:C:C6	2.56	0.41
1:C1:2112:G:N1	1:C1:2148:U:N3	2.38	0.41
1:C1:2146:U:H2'	1:C1:2147:G:H8	1.84	0.41
1:C1:2416:G:N1	18:CP:552:MET:HE1	2.36	0.41
1:C1:2436:G:HO2'	1:C1:2437:G:P	2.43	0.41
1:C1:3086:A:C6	1:C1:3088:U:H1'	2.56	0.41
10:CH:210:TYR:OH	10:CH:336:GLU:OE1	2.21	0.41
10:CH:329:GLU:H	10:CH:329:GLU:CD	2.25	0.41
10:CH:449:TYR:CZ	19:CQ:72:ALA:HB2	2.54	0.41
12:CJ:75:GLU:HA	12:CJ:76:PRO:HD3	1.97	0.41
12:CJ:398:ASP:OD1	12:CJ:398:ASP:C	2.62	0.41
13:CK:100:LYS:HE3	13:CK:100:LYS:HB3	1.87	0.41
15:CM:166:ARG:HD2	15:CM:209:TRP:NE1	2.35	0.41
18:CP:376:LEU:O	18:CP:378:PRO:HD3	2.20	0.41
18:CP:507:TYR:CE1	18:CP:582:LYS:HG2	2.56	0.41
21:CS:100:ARG:O	21:CS:103:ILE:HG22	2.20	0.41
25:CW:70:LEU:HD23	25:CW:70:LEU:HA	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:CZ:430:ILE:HD13	28:CZ:430:ILE:N	2.36	0.41
35:LG:216:LYS:HE2	35:LG:216:LYS:HB2	1.77	0.41
36:LH:89:LYS:HE2	36:LH:145:GLU:OE2	2.21	0.41
46:LT:115:LEU:HA	46:LT:118:LYS:HB3	2.02	0.41
52:Lc:44:LEU:HD23	52:Lc:95:ILE:HD12	2.03	0.41
55:Lf:50:ARG:NH1	55:Lf:72:LYS:HG2	2.36	0.41
56:Lg:80:SER:OG	56:Lg:81:ARG:NH1	2.53	0.41
1:C1:7:C:H2'	1:C1:8:C:C6	2.55	0.41
1:C1:171:G:H2'	1:C1:172:C:H6	1.85	0.41
1:C1:1213:A:H5''	1:C1:1214:C:H5'	2.03	0.41
1:C1:1986:A:N7	1:C1:1987:C:H1'	2.36	0.41
1:C1:2058:A:H2'	1:C1:2059:C:C6	2.55	0.41
1:C1:2328:C:H2'	1:C1:2329:A:H8	1.85	0.41
1:C1:2373:U:H2'	1:C1:2374:G:C8	2.55	0.41
2:C2:6:U:H2'	2:C2:7:U:C6	2.55	0.41
2:C2:150:G:H21	35:LG:62:GLN:HE22	1.68	0.41
2:C2:293:C:H5''	11:CI:279:ARG:HD2	2.02	0.41
4:CB:97:VAL:HG23	4:CB:152:VAL:HG23	2.03	0.41
5:CC:742:LEU:HB3	5:CC:765:LEU:HB2	2.02	0.41
6:CD:21:THR:HB	6:CD:95:TYR:CZ	2.55	0.41
6:CD:248:ALA:HB1	6:CD:292:LEU:HD11	2.02	0.41
6:CD:472:GLY:HA3	6:CD:486:ARG:HB3	2.02	0.41
8:CF:227:TRP:HD1	8:CF:234:VAL:HG12	1.84	0.41
12:CJ:588:GLN:HG3	12:CJ:588:GLN:H	1.74	0.41
20:CR:73:LEU:HD21	38:LL:122:ARG:NH2	2.35	0.41
25:CW:268:SER:O	25:CW:269:LEU:HD13	2.20	0.41
25:CW:280:HIS:HD2	25:CW:438:ALA:HB3	1.85	0.41
25:CW:282:ILE:N	25:CW:283:PRO:HD2	2.36	0.41
25:CW:411:GLY:HA3	44:LR:165:ARG:HH22	1.86	0.41
27:CY:453:TRP:HD1	27:CY:460:GLY:HA2	1.84	0.41
27:CY:644:LEU:O	27:CY:648:VAL:HG23	2.20	0.41
35:LG:103:GLU:H	35:LG:103:GLU:HG2	1.60	0.41
39:LM:130:GLU:CG	41:LO:191:VAL:HG23	2.49	0.41
51:LZ:12:VAL:O	51:LZ:19:GLY:N	2.39	0.41
52:Lc:16:LYS:HB3	52:Lc:16:LYS:HE2	1.73	0.41
55:Lf:56:ARG:HE	55:Lf:56:ARG:HB3	1.75	0.41
1:C1:72:C:N3	1:C1:74:G:C6	2.89	0.41
1:C1:250:U:H2'	1:C1:251:C:C6	2.55	0.41
1:C1:1321:C:H2'	1:C1:1322:C:H6	1.85	0.41
1:C1:1488:A:H1'	1:C1:1827:G:C6	2.56	0.41
1:C1:1546:C:OP2	12:CJ:20:THR:OG1	2.30	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1768:G:H2'	1:C1:1769:U:C6	2.56	0.41
1:C1:1810:U:O2'	2:C2:114:G:OP1	2.38	0.41
1:C1:1975:C:H2'	1:C1:1976:U:C6	2.56	0.41
1:C1:1985:A:H2'	1:C1:1986:A:H8	1.86	0.41
1:C1:2089:U:H2'	1:C1:2090:C:C6	2.56	0.41
7:CE:535:LYS:NZ	7:CE:535:LYS:HB3	2.35	0.41
10:CH:540:ASP:OD1	10:CH:540:ASP:N	2.54	0.41
13:CK:214:VAL:HG12	13:CK:216:THR:HG23	2.02	0.41
18:CP:278:GLU:CD	18:CP:278:GLU:H	2.29	0.41
21:CS:175:LEU:HD12	21:CS:175:LEU:HA	1.84	0.41
21:CS:250:TYR:O	21:CS:251:THR:OG1	2.30	0.41
22:CT:492:LEU:HD23	22:CT:492:LEU:HA	1.92	0.41
25:CW:90:GLN:HE21	25:CW:164:ASN:HB2	1.85	0.41
27:CY:378:MET:O	27:CY:382:THR:HG23	2.21	0.41
31:LA:184:ARG:HA	31:LA:187:HIS:HB2	2.02	0.41
32:LB:99:LEU:HD23	32:LB:99:LEU:HA	1.94	0.41
32:LB:388:LEU:HA	32:LB:388:LEU:HD23	1.79	0.41
41:LO:191:VAL:CG1	41:LO:192:ASP:N	2.84	0.41
1:C1:458:C:H4'	1:C1:459:U:O4'	2.21	0.41
1:C1:1288:G:O2'	1:C1:1289:G:H5''	2.21	0.41
1:C1:2473:A:H2'	1:C1:2474:C:H6	1.86	0.41
2:C2:284:G:H2'	2:C2:285:G:C8	2.55	0.41
4:CB:130:ILE:HD12	4:CB:159:ILE:HG23	2.02	0.41
6:CD:358:LEU:HD12	6:CD:358:LEU:HA	1.80	0.41
7:CE:476:ALA:C	7:CE:477:LYS:HG3	2.46	0.41
10:CH:14:GLN:OE1	10:CH:14:GLN:HA	2.21	0.41
12:CJ:642:LYS:HD3	12:CJ:642:LYS:HA	1.83	0.41
21:CS:236:GLU:CD	21:CS:236:GLU:H	2.29	0.41
25:CW:157:ILE:O	25:CW:161:LEU:HG	2.21	0.41
27:CY:397:ARG:HA	27:CY:397:ARG:HD3	1.71	0.41
32:LB:215:MET:HE3	32:LB:280:ASN:HA	2.03	0.41
37:LK:47:ALA:HA	37:LK:50:THR:HG22	2.03	0.41
42:LP:32:THR:HG21	42:LP:87:SER:HB3	2.03	0.41
43:LQ:95:ILE:O	43:LQ:99:LEU:HG	2.21	0.41
50:LY:86:ARG:HB3	50:LY:96:ILE:HD11	2.03	0.41
55:Lf:8:ARG:HG3	55:Lf:10:TYR:CE1	2.55	0.41
57:Lh:52:LEU:O	57:Lh:56:ILE:HG13	2.20	0.41
63:Lq:179:LEU:O	63:Lq:183:ILE:HG23	2.21	0.41
1:C1:378:A:H8	1:C1:378:A:O5'	2.03	0.41
1:C1:828:A:H2'	1:C1:829:A:C8	2.56	0.41
1:C1:840:G:C8	1:C1:841:G:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1116:G:H5''	23:CU:313:LYS:NZ	2.36	0.41
1:C1:1360:U:H2'	1:C1:1361:G:H8	1.86	0.41
1:C1:1581:A:N6	49:LX:83:GLU:OE2	2.47	0.41
1:C1:1659:G:H2'	1:C1:1660:U:H6	1.85	0.41
1:C1:1700:U:O2'	1:C1:1702:G:N7	2.45	0.41
1:C1:1952:G:OP1	1:C1:1953:A:H5'	2.21	0.41
1:C1:1979:C:H2'	1:C1:1980:C:H6	1.85	0.41
1:C1:2356:G:H2'	1:C1:2357:G:H8	1.86	0.41
1:C1:2566:G:OP2	26:CX:89:LYS:NZ	2.52	0.41
1:C1:3040:G:H2'	1:C1:3041:C:C6	2.55	0.41
5:CC:461:ILE:HG12	5:CC:468:LEU:HD12	2.02	0.41
5:CC:697:ARG:NH1	5:CC:712:THR:HG22	2.36	0.41
7:CE:287:LYS:HB2	7:CE:287:LYS:HE2	1.83	0.41
7:CE:476:ALA:O	7:CE:477:LYS:HG3	2.21	0.41
8:CF:10:TYR:CD2	13:CK:65:ILE:HG12	2.56	0.41
8:CF:202:ASP:OD1	8:CF:202:ASP:N	2.39	0.41
10:CH:128:LYS:HE3	10:CH:128:LYS:HB3	1.95	0.41
10:CH:251:TYR:OH	10:CH:269:LEU:HD23	2.21	0.41
12:CJ:188:SER:HB3	12:CJ:465:ILE:HD11	2.02	0.41
12:CJ:411:SER:HA	12:CJ:450:TYR:CE2	2.56	0.41
12:CJ:502:PRO:HB2	12:CJ:504:GLU:OE2	2.20	0.41
18:CP:245:VAL:HG11	18:CP:262:TYR:CZ	2.56	0.41
18:CP:289:PRO:CD	18:CP:292:GLU:HB3	2.51	0.41
19:CQ:39:ASN:O	19:CQ:44:ARG:HG2	2.21	0.41
19:CQ:41:LYS:HE2	19:CQ:41:LYS:HB2	1.90	0.41
21:CS:469:GLU:OE1	35:LG:71:ARG:NE	2.53	0.41
22:CT:229:ILE:HG23	22:CT:237:PRO:HG2	2.02	0.41
24:CV:13:SER:HB2	24:CV:17:ASN:OD1	2.21	0.41
25:CW:131:ARG:HH11	25:CW:140:VAL:HG21	1.84	0.41
25:CW:611:LYS:O	25:CW:615:LEU:HB2	2.21	0.41
27:CY:506:LEU:HD23	27:CY:506:LEU:HA	1.79	0.41
28:CZ:191:GLN:N	28:CZ:191:GLN:CD	2.79	0.41
28:CZ:235:SER:HB2	28:CZ:311:PHE:CZ	2.55	0.41
28:CZ:238:LEU:HD12	28:CZ:238:LEU:HA	1.88	0.41
34:LE:74:LYS:HG3	34:LE:75:CYS:N	2.36	0.41
43:LQ:156:LEU:HD23	43:LQ:156:LEU:HA	1.86	0.41
49:LX:76:ILE:HG22	57:Lh:36:ILE:HD11	2.03	0.41
51:LZ:94:VAL:HG13	51:LZ:95:ILE:HG23	2.02	0.41
1:C1:59:G:H4'	1:C1:60:A:H4'	2.03	0.41
1:C1:711:G:O6	1:C1:728:A:N6	2.55	0.41
1:C1:1077:U:H4'	1:C1:1078:C:H5''	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1186:A:N6	1:C1:2809:A:N7	2.69	0.41
1:C1:1239:C:O2	8:CF:54:LYS:NZ	2.51	0.41
1:C1:2020:C:H3'	1:C1:2021:C:C6	2.56	0.41
1:C1:2371:G:H2'	1:C1:2372:U:H6	1.85	0.41
1:C1:3234:A:H5''	32:LB:128:LYS:HZ1	1.84	0.41
2:C2:102:U:HO2'	2:C2:103:G:P	2.44	0.41
4:CB:184:LEU:C	4:CB:185:MET:HE2	2.46	0.41
5:CC:380:LYS:HB3	5:CC:380:LYS:NZ	2.36	0.41
5:CC:417:ARG:HG2	5:CC:417:ARG:HH11	1.85	0.41
5:CC:505:ARG:NH2	5:CC:600:GLY:O	2.54	0.41
6:CD:155:LEU:CD1	6:CD:168:SER:HB2	2.50	0.41
6:CD:400:ASN:OD1	6:CD:401:GLU:N	2.54	0.41
7:CE:190:THR:O	7:CE:241:PRO:HD3	2.21	0.41
12:CJ:367:PHE:HD2	12:CJ:372:PHE:HZ	1.68	0.41
21:CS:660:MET:HE2	21:CS:664:HIS:CD2	2.56	0.41
25:CW:620:ARG:HH11	25:CW:620:ARG:HG2	1.86	0.41
33:LC:103:PRO:HB2	33:LC:105:LYS:NZ	2.36	0.41
33:LC:143:VAL:HG13	33:LC:146:VAL:HG12	2.02	0.41
39:LM:130:GLU:OE2	39:LM:130:GLU:HA	2.20	0.41
40:LN:146:PRO:HA	40:LN:149:ASN:OD1	2.21	0.41
45:LS:8:GLN:HG3	45:LS:26:ARG:HE	1.85	0.41
49:LX:87:LYS:HE2	49:LX:87:LYS:HB2	1.84	0.41
50:LY:30:MET:HE2	50:LY:30:MET:HB3	1.83	0.41
63:Lq:67:ILE:HG22	63:Lq:111:ILE:HD11	2.03	0.41
1:C1:210:U:H4'	50:LY:99:HIS:CD2	2.56	0.40
1:C1:678:A:N1	2:C2:28:C:O2'	2.51	0.40
1:C1:714:A:H2'	1:C1:715:G:O4'	2.20	0.40
1:C1:1374:G:H1'	1:C1:1400:A:N6	2.36	0.40
1:C1:3041:C:H2'	1:C1:3042:G:O4'	2.20	0.40
1:C1:3205:C:N4	1:C1:3206:G:O6	2.53	0.40
1:C1:3288:G:C6	1:C1:3298:U:N3	2.90	0.40
1:C1:3331:A:N3	1:C1:3331:A:H2'	2.35	0.40
2:C2:154:C:H5''	35:LG:184:LYS:HG2	2.03	0.40
3:CA:247:GLU:O	3:CA:247:GLU:HG3	2.22	0.40
4:CB:216:PRO:O	4:CB:220:ILE:HG13	2.21	0.40
7:CE:204:ARG:HG2	7:CE:204:ARG:HH11	1.86	0.40
11:CI:299:GLU:HB3	11:CI:302:TRP:HB3	2.03	0.40
12:CJ:454:ILE:HD11	12:CJ:473:PRO:HB3	2.04	0.40
18:CP:387:MET:HE2	18:CP:440:ALA:HB1	2.03	0.40
19:CQ:44:ARG:HH11	19:CQ:44:ARG:HG3	1.85	0.40
24:CV:63:VAL:HG21	24:CV:94:ILE:HG12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LF:154:ILE:HG22	15:LF:187:ILE:HD11	2.02	0.40
36:LH:143:LYS:HE2	36:LH:144:ASP:OD2	2.22	0.40
54:Le:77:VAL:HG22	54:Le:82:ASP:HB3	2.03	0.40
63:Lq:194:LEU:HD23	63:Lq:195:LYS:N	2.36	0.40
1:C1:442:C:H2'	1:C1:443:G:C8	2.56	0.40
1:C1:1172:A:H2'	1:C1:1172:A:N3	2.36	0.40
1:C1:1365:G:H4'	33:LC:247:PRO:HB2	2.02	0.40
1:C1:1452:U:H2'	1:C1:1453:U:C6	2.56	0.40
1:C1:1457:G:H3'	10:CH:515:ARG:NH1	2.36	0.40
1:C1:1815:C:H2'	1:C1:1816:U:H6	1.86	0.40
1:C1:2468:U:H2'	1:C1:2469:U:H6	1.87	0.40
1:C1:2471:U:H2'	1:C1:2472:U:C6	2.56	0.40
1:C1:3333:A:H2'	1:C1:3334:U:C6	2.57	0.40
2:C2:19:C:C4	2:C2:20:U:C4	3.09	0.40
2:C2:41:A:H61	2:C2:103:G:C2'	2.35	0.40
2:C2:201:U:H2'	2:C2:202:C:C6	2.56	0.40
5:CC:356:PRO:HG2	5:CC:361:LEU:HD21	2.04	0.40
6:CD:67:ILE:HD11	6:CD:72:LEU:HB2	2.03	0.40
8:CF:141:ILE:HG12	8:CF:180:CYS:SG	2.60	0.40
10:CH:288:LYS:HE3	64:CH:1001:GTP:C4	2.56	0.40
12:CJ:630:GLU:OE1	12:CJ:633:ARG:NH1	2.54	0.40
13:CK:153:LYS:HB3	13:CK:214:VAL:HG13	2.02	0.40
18:CP:245:VAL:HG22	18:CP:252:LEU:HD12	2.03	0.40
19:CQ:137:LEU:HD12	19:CQ:137:LEU:HA	1.92	0.40
21:CS:221:LEU:HD23	21:CS:221:LEU:HA	1.85	0.40
22:CT:676:LEU:HD12	22:CT:676:LEU:O	2.21	0.40
25:CW:373:ILE:HD12	25:CW:373:ILE:C	2.47	0.40
27:CY:492:ASN:CG	27:CY:494:GLN:HE22	2.29	0.40
27:CY:556:ARG:HG2	27:CY:625:LEU:HD11	2.02	0.40
28:CZ:247:THR:HG22	28:CZ:249:GLN:OE1	2.22	0.40
28:CZ:260:GLY:HA2	28:CZ:295:TYR:CD2	2.56	0.40
48:LV:111:MET:HE2	48:LV:111:MET:HB3	1.93	0.40
57:Lh:110:LYS:HB2	57:Lh:110:LYS:HE3	1.83	0.40
60:Lk:63:PRO:HA	60:Lk:64:PRO:HD3	1.90	0.40
1:C1:123:A:C6	1:C1:145:A:C5	3.09	0.40
1:C1:596:G:H1'	33:LC:312:ALA:O	2.21	0.40
1:C1:787:A:H2'	1:C1:788:A:C2	2.56	0.40
1:C1:2091:U:OP2	29:Ca:203:ARG:NH2	2.55	0.40
1:C1:2269:G:H2'	1:C1:2270:C:C6	2.56	0.40
1:C1:3294:U:OP1	25:CW:591:ARG:NH1	2.54	0.40
5:CC:648:PHE:HB2	5:CC:661:LEU:HD13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:337:ARG:HE	10:CH:337:ARG:HB3	1.72	0.40
12:CJ:169:GLU:OE1	12:CJ:169:GLU:HA	2.22	0.40
18:CP:236:ARG:NH2	18:CP:273:TYR:OH	2.54	0.40
18:CP:291:ARG:NH1	18:CP:292:GLU:HB2	2.35	0.40
18:CP:582:LYS:HD3	18:CP:583:LYS:N	2.37	0.40
25:CW:312:PHE:HZ	25:CW:493:TYR:CD1	2.39	0.40
27:CY:376:LEU:HD12	27:CY:377:LYS:N	2.36	0.40
27:CY:473:ILE:HD13	27:CY:473:ILE:HA	1.89	0.40
33:LC:353:LYS:HA	33:LC:353:LYS:HD3	1.76	0.40
37:LK:105:SER:OG	37:LK:108:GLU:OE2	2.37	0.40
41:LO:26:LYS:HA	41:LO:26:LYS:HD2	1.90	0.40
44:LR:154:GLN:HG3	44:LR:155:ILE:HD12	2.02	0.40
51:LZ:9:VAL:HG11	51:LZ:128:TRP:HZ3	1.85	0.40
51:LZ:10:CYS:CB	51:LZ:79:LEU:HD22	2.51	0.40
54:Le:33:TRP:O	54:Le:34:ARG:NH1	2.47	0.40
54:Le:87:LEU:HD12	54:Le:116:LEU:HG	2.03	0.40
57:Lh:107:GLU:H	57:Lh:107:GLU:CD	2.27	0.40
63:Lq:62:ASN:N	63:Lq:62:ASN:OD1	2.54	0.40
1:C1:80:G:H2'	1:C1:81:C:H6	1.86	0.40
1:C1:264:G:H2'	1:C1:265:A:C8	2.56	0.40
1:C1:285:C:H2'	1:C1:286:A:O4'	2.21	0.40
1:C1:641:C:H2'	1:C1:642:C:C6	2.56	0.40
1:C1:1048:G:H2'	1:C1:1049:C:C5	2.56	0.40
1:C1:1197:A:H2'	1:C1:1198:C:C6	2.57	0.40
1:C1:1208:G:H2'	1:C1:1209:C:C6	2.57	0.40
1:C1:1822:C:H2'	1:C1:1823:C:H6	1.86	0.40
1:C1:3064:U:H2'	1:C1:3065:G:H8	1.86	0.40
1:C1:3127:A:OP1	55:Lf:99:SER:OG	2.33	0.40
3:CA:36:VAL:O	3:CA:62:GLY:HA2	2.21	0.40
3:CA:107:VAL:O	3:CA:249:SER:OG	2.32	0.40
4:CB:163:LEU:N	4:CB:164:PRO:HD2	2.35	0.40
5:CC:222:ASP:HB3	5:CC:225:THR:O	2.21	0.40
5:CC:267:GLU:OE2	35:LG:176:MET:HE1	2.22	0.40
7:CE:170:VAL:HG21	7:CE:206:LEU:HG	2.02	0.40
8:CF:125:ALA:HA	8:CF:217:SER:HB2	2.04	0.40
9:CG:97:LYS:O	9:CG:123:THR:OG1	2.29	0.40
13:CK:68:HIS:HA	13:CK:71:ARG:HG2	2.03	0.40
18:CP:386:ASP:OD1	18:CP:386:ASP:C	2.65	0.40
22:CT:167:CYS:O	22:CT:171:GLN:HG3	2.22	0.40
25:CW:58:GLU:O	25:CW:249:VAL:HG22	2.21	0.40
25:CW:403:MET:SD	25:CW:403:MET:C	3.05	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LA:181:LYS:HD3	31:LA:182:ALA:H	1.85	0.40
33:LC:45:LYS:HD2	33:LC:112:VAL:HG21	2.02	0.40
39:LM:13:ARG:NH2	45:LS:149:SER:OG	2.45	0.40
45:LS:90:MET:HE3	45:LS:92:LYS:HD2	2.03	0.40
55:Lf:16:LEU:HD11	55:Lf:33:LYS:HB2	2.02	0.40
58:Li:43:SER:OG	58:Li:46:THR:OG1	2.31	0.40
63:Lq:49:PHE:HB2	63:Lq:193:LEU:HG	2.03	0.40
1:C1:252:C:P	7:CE:229:LYS:HG2	2.60	0.40
1:C1:2557:U:H2'	1:C1:2558:C:H6	1.87	0.40
1:C1:2957:G:H2'	1:C1:2958:U:C6	2.56	0.40
1:C1:3297:U:HO2'	1:C1:3298:U:P	2.42	0.40
4:CB:98:CYS:HB2	4:CB:150:HIS:ND1	2.37	0.40
14:CL:8:PRO:O	41:LO:60:ARG:HD2	2.21	0.40
16:CN:168:GLN:O	16:CN:172:GLU:HG3	2.21	0.40
23:CU:272:PHE:HB3	26:CX:77:VAL:HG12	2.03	0.40
25:CW:334:GLU:O	25:CW:338:ARG:HG3	2.21	0.40
25:CW:408:ARG:H	25:CW:408:ARG:HG2	1.74	0.40
27:CY:474:HIS:HA	27:CY:477:ASN:HD21	1.86	0.40
27:CY:551:ARG:O	27:CY:555:ILE:HG13	2.21	0.40
28:CZ:390:ASP:O	28:CZ:394:HIS:HD2	2.04	0.40
32:LB:24:ARG:HD2	32:LB:26:ARG:HB3	2.04	0.40
32:LB:36:ASP:OD1	32:LB:39:LYS:HE3	2.22	0.40
50:LY:92:GLN:NE2	50:LY:93:THR:O	2.54	0.40
57:Lh:106:LEU:HD23	57:Lh:106:LEU:HA	1.96	0.40
60:Lk:54:LYS:HA	60:Lk:57:LYS:HB2	2.04	0.40
63:Lq:75:ASP:OD1	63:Lq:75:ASP:N	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	
3	CA	247/316 (78%)	232 (94%)	15 (6%)	0	100	100
4	CB	256/391 (66%)	239 (93%)	17 (7%)	0	100	100
5	CC	648/801 (81%)	623 (96%)	24 (4%)	1 (0%)	43	68
6	CD	450/495 (91%)	425 (94%)	25 (6%)	0	100	100
7	CE	459/598 (77%)	449 (98%)	10 (2%)	0	100	100
8	CF	243/270 (90%)	234 (96%)	9 (4%)	0	100	100
9	CG	175/184 (95%)	165 (94%)	10 (6%)	0	100	100
10	CH	538/661 (81%)	522 (97%)	16 (3%)	0	100	100
11	CI	144/414 (35%)	140 (97%)	4 (3%)	0	100	100
12	CJ	484/679 (71%)	473 (98%)	11 (2%)	0	100	100
13	CK	223/261 (85%)	214 (96%)	9 (4%)	0	100	100
14	CL	393/558 (70%)	368 (94%)	23 (6%)	2 (0%)	24	48
15	CM	219/249 (88%)	212 (97%)	7 (3%)	0	100	100
15	LF	245/249 (98%)	237 (97%)	8 (3%)	0	100	100
16	CN	244/246 (99%)	233 (96%)	11 (4%)	0	100	100
17	CO	56/120 (47%)	56 (100%)	0	0	100	100
18	CP	354/751 (47%)	336 (95%)	18 (5%)	0	100	100
19	CQ	173/225 (77%)	167 (96%)	6 (4%)	0	100	100
20	CR	159/237 (67%)	158 (99%)	1 (1%)	0	100	100
21	CS	609/834 (73%)	584 (96%)	25 (4%)	0	100	100
22	CT	478/688 (70%)	461 (96%)	17 (4%)	0	100	100
23	CU	174/451 (39%)	170 (98%)	4 (2%)	0	100	100
24	CV	137/147 (93%)	135 (98%)	2 (2%)	0	100	100
25	CW	534/679 (79%)	479 (90%)	54 (10%)	1 (0%)	43	68
26	CX	86/203 (42%)	85 (99%)	1 (1%)	0	100	100
27	CY	406/788 (52%)	380 (94%)	25 (6%)	1 (0%)	43	68
28	CZ	572/697 (82%)	552 (96%)	20 (4%)	0	100	100
29	Ca	111/227 (49%)	109 (98%)	2 (2%)	0	100	100
30	Cz	68/123 (55%)	66 (97%)	2 (3%)	0	100	100
31	LA	164/254 (65%)	155 (94%)	9 (6%)	0	100	100
32	LB	352/392 (90%)	335 (95%)	17 (5%)	0	100	100
33	LC	360/365 (99%)	346 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	LE	175/200 (88%)	169 (97%)	6 (3%)	0	100	100
35	LG	201/262 (77%)	197 (98%)	4 (2%)	0	100	100
36	LH	188/192 (98%)	180 (96%)	8 (4%)	0	100	100
37	LK	142/165 (86%)	136 (96%)	6 (4%)	0	100	100
38	LL	115/213 (54%)	112 (97%)	3 (3%)	0	100	100
39	LM	135/142 (95%)	129 (96%)	6 (4%)	0	100	100
40	LN	179/203 (88%)	170 (95%)	9 (5%)	0	100	100
41	LO	202/204 (99%)	195 (96%)	7 (4%)	0	100	100
42	LP	165/187 (88%)	160 (97%)	5 (3%)	0	100	100
43	LQ	127/213 (60%)	121 (95%)	6 (5%)	0	100	100
44	LR	144/2898 (5%)	143 (99%)	1 (1%)	0	100	100
45	LS	172/174 (99%)	165 (96%)	7 (4%)	0	100	100
46	LT	124/160 (78%)	117 (94%)	6 (5%)	1 (1%)	16	37
47	LU	103/127 (81%)	100 (97%)	3 (3%)	0	100	100
48	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
49	LX	133/156 (85%)	131 (98%)	2 (2%)	0	100	100
50	LY	132/138 (96%)	127 (96%)	5 (4%)	0	100	100
51	LZ	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
52	Lc	96/108 (89%)	96 (100%)	0	0	100	100
53	Ld	107/120 (89%)	105 (98%)	2 (2%)	0	100	100
54	Le	125/131 (95%)	123 (98%)	2 (2%)	0	100	100
55	Lf	106/109 (97%)	104 (98%)	2 (2%)	0	100	100
56	Lg	115/119 (97%)	114 (99%)	1 (1%)	0	100	100
57	Lh	119/935 (13%)	116 (98%)	3 (2%)	0	100	100
58	Li	86/110 (78%)	86 (100%)	0	0	100	100
59	Lj	72/95 (76%)	71 (99%)	1 (1%)	0	100	100
60	Lk	73/81 (90%)	68 (93%)	5 (7%)	0	100	100
61	Lp	56/92 (61%)	52 (93%)	4 (7%)	0	100	100
62	Ll	36/51 (71%)	35 (97%)	1 (3%)	0	100	100
63	Lq	205/217 (94%)	183 (89%)	21 (10%)	1 (0%)	24	48
All	All	13660/21629 (63%)	13103 (96%)	550 (4%)	7 (0%)	49	73

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	CW	393	ARG
27	CY	457	GLN
14	CL	439	ASP
14	CL	446	ASP
46	LT	44	VAL
5	CC	251	VAL
63	Lq	61	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CA	223/276 (81%)	221 (99%)	2 (1%)	70	87
4	CB	222/329 (68%)	221 (100%)	1 (0%)	81	92
5	CC	578/708 (82%)	568 (98%)	10 (2%)	53	79
6	CD	381/410 (93%)	375 (98%)	6 (2%)	55	80
7	CE	398/517 (77%)	394 (99%)	4 (1%)	68	86
8	CF	214/236 (91%)	209 (98%)	5 (2%)	44	73
9	CG	150/155 (97%)	147 (98%)	3 (2%)	48	76
10	CH	481/575 (84%)	475 (99%)	6 (1%)	63	84
11	CI	121/336 (36%)	120 (99%)	1 (1%)	73	88
12	CJ	428/579 (74%)	422 (99%)	6 (1%)	59	82
13	CK	195/225 (87%)	191 (98%)	4 (2%)	47	75
14	CL	72/458 (16%)	72 (100%)	0	100	100
15	CM	191/215 (89%)	190 (100%)	1 (0%)	81	92
15	LF	213/215 (99%)	211 (99%)	2 (1%)	70	87
16	CN	206/206 (100%)	204 (99%)	2 (1%)	68	86
17	CO	48/99 (48%)	47 (98%)	1 (2%)	47	75
18	CP	302/632 (48%)	299 (99%)	3 (1%)	68	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	CQ	150/192 (78%)	150 (100%)	0	100	100
20	CR	144/206 (70%)	143 (99%)	1 (1%)	76	90
21	CS	532/716 (74%)	522 (98%)	10 (2%)	50	77
22	CT	427/600 (71%)	425 (100%)	2 (0%)	81	92
23	CU	149/376 (40%)	149 (100%)	0	100	100
24	CV	109/112 (97%)	108 (99%)	1 (1%)	70	87
25	CW	476/577 (82%)	459 (96%)	17 (4%)	31	60
26	CX	76/172 (44%)	75 (99%)	1 (1%)	61	83
27	CY	369/686 (54%)	363 (98%)	6 (2%)	55	80
28	CZ	310/581 (53%)	301 (97%)	9 (3%)	37	67
29	Ca	101/195 (52%)	101 (100%)	0	100	100
30	Cz	60/107 (56%)	60 (100%)	0	100	100
31	LA	131/198 (66%)	128 (98%)	3 (2%)	44	73
32	LB	301/331 (91%)	296 (98%)	5 (2%)	53	79
33	LC	283/285 (99%)	278 (98%)	5 (2%)	51	78
34	LE	151/166 (91%)	149 (99%)	2 (1%)	61	83
35	LG	176/222 (79%)	169 (96%)	7 (4%)	28	56
36	LH	167/169 (99%)	165 (99%)	2 (1%)	63	84
37	LK	121/136 (89%)	120 (99%)	1 (1%)	73	88
38	LL	99/176 (56%)	98 (99%)	1 (1%)	68	86
39	LM	115/117 (98%)	114 (99%)	1 (1%)	70	87
40	LN	164/180 (91%)	161 (98%)	3 (2%)	51	78
41	LO	163/163 (100%)	162 (99%)	1 (1%)	78	91
42	LP	137/152 (90%)	135 (98%)	2 (2%)	57	81
43	LQ	110/178 (62%)	109 (99%)	1 (1%)	70	87
44	LR	128/2396 (5%)	127 (99%)	1 (1%)	73	88
45	LS	154/154 (100%)	151 (98%)	3 (2%)	50	77
46	LT	109/135 (81%)	108 (99%)	1 (1%)	70	87
47	LU	93/108 (86%)	93 (100%)	0	100	100
48	LV	99/102 (97%)	99 (100%)	0	100	100
49	LX	114/129 (88%)	113 (99%)	1 (1%)	70	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	LY	117/119 (98%)	114 (97%)	3 (3%)	40	70
51	LZ	121/121 (100%)	120 (99%)	1 (1%)	73	88
52	Lc	79/88 (90%)	77 (98%)	2 (2%)	42	71
53	Ld	95/105 (90%)	94 (99%)	1 (1%)	65	85
54	Le	110/114 (96%)	109 (99%)	1 (1%)	70	87
55	Lf	89/90 (99%)	89 (100%)	0	100	100
56	Lg	101/102 (99%)	100 (99%)	1 (1%)	68	86
57	Lh	108/781 (14%)	105 (97%)	3 (3%)	38	68
58	Li	75/93 (81%)	75 (100%)	0	100	100
59	Lj	61/78 (78%)	61 (100%)	0	100	100
60	Lk	71/76 (93%)	70 (99%)	1 (1%)	59	82
61	Lp	45/74 (61%)	45 (100%)	0	100	100
62	Ll	34/46 (74%)	34 (100%)	0	100	100
63	Lq	179/189 (95%)	177 (99%)	2 (1%)	65	85
All	All	11426/18264 (63%)	11267 (99%)	159 (1%)	57	82

All (159) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	CA	176	ILE
3	CA	241	THR
4	CB	183	VAL
5	CC	229	LEU
5	CC	239	ILE
5	CC	351	ASP
5	CC	439	LYS
5	CC	590	THR
5	CC	665	GLU
5	CC	695	ASP
5	CC	706	SER
5	CC	742	LEU
5	CC	749	VAL
6	CD	55	MET
6	CD	196	MET
6	CD	218	THR
6	CD	297	THR
6	CD	358	LEU

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Mol	Chain	Res	Type
6	CD	463	VAL
7	CE	421	LEU
7	CE	430	VAL
7	CE	445	VAL
7	CE	527	LEU
8	CF	15	VAL
8	CF	91	ARG
8	CF	139	THR
8	CF	201	LEU
8	CF	238	GLU
9	CG	1	MET
9	CG	14	ASP
9	CG	130	SER
10	CH	279	ASN
10	CH	285	VAL
10	CH	359	THR
10	CH	390	LEU
10	CH	451	ASP
10	CH	527	LEU
11	CI	209	GLN
12	CJ	157	THR
12	CJ	454	ILE
12	CJ	464	SER
12	CJ	503	LEU
12	CJ	506	GLN
12	CJ	631	LEU
13	CK	132	MET
13	CK	135	VAL
13	CK	166	VAL
13	CK	192	THR
15	CM	170	THR
16	CN	91	ASP
16	CN	109	VAL
17	CO	110	MET
18	CP	268	LYS
18	CP	369	SER
18	CP	486	THR
20	CR	128	SER
21	CS	62	VAL
21	CS	103	ILE
21	CS	106	HIS
21	CS	175	LEU

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Mol	Chain	Res	Type
21	CS	186	SER
21	CS	280	GLU
21	CS	289	LEU
21	CS	365	GLU
21	CS	367	ILE
21	CS	823	MET
22	CT	376	GLU
22	CT	437	ASP
24	CV	96	SER
25	CW	36	GLU
25	CW	38	PRO
25	CW	61	THR
25	CW	94	ILE
25	CW	121	LEU
25	CW	198	ASP
25	CW	219	GLN
25	CW	274	ILE
25	CW	314	ARG
25	CW	364	LEU
25	CW	366	ILE
25	CW	415	LEU
25	CW	458	LEU
25	CW	488	ASP
25	CW	616	ILE
25	CW	617	ASN
25	CW	618	GLU
26	CX	107	MET
27	CY	407	LEU
27	CY	433	VAL
27	CY	473	ILE
27	CY	488	ARG
27	CY	496	VAL
27	CY	504	CYS
28	CZ	128	ARG
28	CZ	164	ARG
28	CZ	231	HIS
28	CZ	313	MET
28	CZ	324	ASN
28	CZ	331	GLU
28	CZ	380	TYR
28	CZ	438	THR
28	CZ	442	THR

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Mol	Chain	Res	Type
31	LA	104	LEU
31	LA	129	THR
31	LA	140	ASN
32	LB	126	LYS
32	LB	158	VAL
32	LB	167	ILE
32	LB	214	GLU
32	LB	299	THR
33	LC	15	LYS
33	LC	256	VAL
33	LC	287	LEU
33	LC	291	ILE
33	LC	309	THR
34	LE	108	LYS
34	LE	157	THR
15	LF	31	GLU
15	LF	178	ASN
35	LG	57	GLU
35	LG	70	MET
35	LG	85	LEU
35	LG	103	GLU
35	LG	161	ASP
35	LG	163	ILE
35	LG	164	GLU
36	LH	52	VAL
36	LH	148	LEU
37	LK	109	ILE
38	LL	46	LEU
39	LM	20	LEU
40	LN	27	CYS
40	LN	61	ILE
40	LN	97	SER
41	LO	131	LEU
42	LP	66	SER
42	LP	113	ILE
43	LQ	123	VAL
44	LR	156	LYS
45	LS	90	MET
45	LS	124	LEU
45	LS	148	LEU
46	LT	91	VAL
49	LX	76	ILE

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Mol	Chain	Res	Type
50	LY	23	SER
50	LY	76	LYS
50	LY	115	GLU
51	LZ	29	ASP
52	Lc	64	MET
52	Lc	80	LEU
53	Ld	104	VAL
54	Le	100	ASN
56	Lg	21	THR
57	Lh	6	LYS
57	Lh	52	LEU
57	Lh	73	LEU
60	Lk	7	ASP
63	Lq	133	LYS
63	Lq	206	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (115) such sidechains are listed below:

Mol	Chain	Res	Type
3	CA	32	ASN
3	CA	34	GLN
3	CA	88	ASN
3	CA	193	ASN
4	CB	90	ASN
4	CB	150	HIS
5	CC	206	ASN
5	CC	286	ASN
5	CC	446	GLN
5	CC	494	ASN
5	CC	528	HIS
5	CC	544	ASN
5	CC	671	GLN
5	CC	707	ASN
6	CD	94	GLN
6	CD	176	HIS
7	CE	235	ASN
7	CE	250	ASN
7	CE	319	ASN
7	CE	388	HIS
7	CE	394	GLN
7	CE	398	ASN
7	CE	425	GLN

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Mol	Chain	Res	Type
7	CE	431	GLN
7	CE	488	ASN
8	CF	50	ASN
8	CF	159	HIS
9	CG	18	ASN
9	CG	118	HIS
10	CH	25	GLN
10	CH	77	HIS
10	CH	96	GLN
10	CH	163	ASN
10	CH	429	ASN
11	CI	277	ASN
11	CI	286	ASN
12	CJ	198	GLN
12	CJ	216	GLN
12	CJ	457	GLN
12	CJ	507	GLN
13	CK	41	ASN
13	CK	248	ASN
14	CL	68	GLN
15	CM	192	HIS
18	CP	265	GLN
18	CP	322	GLN
18	CP	365	GLN
18	CP	381	ASN
18	CP	426	HIS
18	CP	520	ASN
19	CQ	130	ASN
20	CR	6	GLN
20	CR	21	ASN
20	CR	133	GLN
20	CR	148	GLN
21	CS	263	ASN
21	CS	281	GLN
21	CS	383	ASN
21	CS	394	GLN
21	CS	396	HIS
21	CS	682	ASN
22	CT	208	GLN
22	CT	251	ASN
22	CT	323	ASN
22	CT	397	GLN

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Mol	Chain	Res	Type
23	CU	232	GLN
24	CV	34	ASN
24	CV	43	HIS
24	CV	101	HIS
24	CV	109	GLN
25	CW	90	GLN
25	CW	287	GLN
25	CW	297	GLN
25	CW	578	GLN
25	CW	623	ASN
27	CY	435	ASN
27	CY	477	ASN
27	CY	494	GLN
27	CY	497	HIS
27	CY	533	GLN
27	CY	580	GLN
28	CZ	139	GLN
28	CZ	394	HIS
28	CZ	450	GLN
30	Cz	58	GLN
31	LA	71	GLN
32	LB	141	ASN
33	LC	244	GLN
33	LC	284	GLN
33	LC	315	GLN
33	LC	330	ASN
34	LE	25	GLN
34	LE	53	GLN
15	LF	99	ASN
35	LG	62	GLN
35	LG	80	GLN
35	LG	158	ASN
36	LH	96	HIS
36	LH	164	GLN
36	LH	171	ASN
37	LK	65	GLN
40	LN	138	ASN
40	LN	153	ASN
41	LO	27	GLN
42	LP	121	GLN
44	LR	99	GLN
48	LV	26	ASN

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Mol	Chain	Res	Type
49	LX	32	HIS
49	LX	73	HIS
54	Le	72	HIS
56	Lg	15	ASN
57	Lh	50	HIS
57	Lh	115	HIS
63	Lq	188	ASN
63	Lq	200	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2903/3341 (86%)	554 (19%)	22 (0%)
2	C2	254/319 (79%)	54 (21%)	1 (0%)
All	All	3157/3660 (86%)	608 (19%)	23 (0%)

All (608) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	16	A
1	C1	22	G
1	C1	26	A
1	C1	41	G
1	C1	49	A
1	C1	59	G
1	C1	60	A
1	C1	65	A
1	C1	66	A
1	C1	73	A
1	C1	74	G
1	C1	83	C
1	C1	92	G
1	C1	93	C
1	C1	94	G
1	C1	96	G
1	C1	109	A
1	C1	110	G
1	C1	116	A
1	C1	122	A
1	C1	128	G
1	C1	129	C

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Mol	Chain	Res	Type
1	C1	131	U
1	C1	132	C
1	C1	136	C
1	C1	138	G
1	C1	150	G
1	C1	151	G
1	C1	152	A
1	C1	156	G
1	C1	165	G
1	C1	183	U
1	C1	184	U
1	C1	193	C
1	C1	203	C
1	C1	205	G
1	C1	206	A
1	C1	211	G
1	C1	212	A
1	C1	213	G
1	C1	224	A
1	C1	240	U
1	C1	244	U
1	C1	253	U
1	C1	261	G
1	C1	275	G
1	C1	276	A
1	C1	277	A
1	C1	287	A
1	C1	290	U
1	C1	300	A
1	C1	302	U
1	C1	309	A
1	C1	310	A
1	C1	315	A
1	C1	321	C
1	C1	325	C
1	C1	331	C
1	C1	342	C
1	C1	368	G
1	C1	390	U
1	C1	391	A
1	C1	393	C
1	C1	394	A

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Mol	Chain	Res	Type
1	C1	395	C
1	C1	396	G
1	C1	412	G
1	C1	413	G
1	C1	414	A
1	C1	415	A
1	C1	421	U
1	C1	428	A
1	C1	433	U
1	C1	434	G
1	C1	446	U
1	C1	457	U
1	C1	459	U
1	C1	462	C
1	C1	463	C
1	C1	468	C
1	C1	469	A
1	C1	470	C
1	C1	471	U
1	C1	474	G
1	C1	485	G
1	C1	508	G
1	C1	509	A
1	C1	511	A
1	C1	513	A
1	C1	520	G
1	C1	526	G
1	C1	534	U
1	C1	535	C
1	C1	536	C
1	C1	537	G
1	C1	544	U
1	C1	546	A
1	C1	548	A
1	C1	569	G
1	C1	574	G
1	C1	582	A
1	C1	587	G
1	C1	590	C
1	C1	591	U
1	C1	592	G
1	C1	594	A

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Mol	Chain	Res	Type
1	C1	596	G
1	C1	598	A
1	C1	607	U
1	C1	608	A
1	C1	609	A
1	C1	623	C
1	C1	633	A
1	C1	647	A
1	C1	663	G
1	C1	664	A
1	C1	668	U
1	C1	670	U
1	C1	678	A
1	C1	718	U
1	C1	719	C
1	C1	720	G
1	C1	731	G
1	C1	742	A
1	C1	746	A
1	C1	747	U
1	C1	757	U
1	C1	761	A
1	C1	762	G
1	C1	765	G
1	C1	766	G
1	C1	767	A
1	C1	787	A
1	C1	789	A
1	C1	800	U
1	C1	801	A
1	C1	803	G
1	C1	828	A
1	C1	840	G
1	C1	846	C
1	C1	858	C
1	C1	876	A
1	C1	877	A
1	C1	878	U
1	C1	889	G
1	C1	896	A
1	C1	898	A
1	C1	925	A

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Mol	Chain	Res	Type
1	C1	932	A
1	C1	933	A
1	C1	934	G
1	C1	941	U
1	C1	942	C
1	C1	943	A
1	C1	944	G
1	C1	959	C
1	C1	960	C
1	C1	974	G
1	C1	975	G
1	C1	976	U
1	C1	982	G
1	C1	983	A
1	C1	1031	C
1	C1	1033	U
1	C1	1039	A
1	C1	1046	A
1	C1	1047	A
1	C1	1049	C
1	C1	1053	U
1	C1	1054	G
1	C1	1058	C
1	C1	1063	C
1	C1	1064	U
1	C1	1078	C
1	C1	1079	G
1	C1	1080	A
1	C1	1085	A
1	C1	1086	U
1	C1	1095	G
1	C1	1097	G
1	C1	1098	G
1	C1	1114	C
1	C1	1124	G
1	C1	1126	U
1	C1	1135	A
1	C1	1141	A
1	C1	1159	G
1	C1	1160	G
1	C1	1163	U
1	C1	1164	G

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Mol	Chain	Res	Type
1	C1	1174	C
1	C1	1175	A
1	C1	1178	C
1	C1	1179	A
1	C1	1180	C
1	C1	1186	A
1	C1	1187	A
1	C1	1189	G
1	C1	1190	C
1	C1	1191	G
1	C1	1203	U
1	C1	1204	G
1	C1	1218	G
1	C1	1227	A
1	C1	1228	G
1	C1	1234	A
1	C1	1240	U
1	C1	1245	A
1	C1	1247	U
1	C1	1254	C
1	C1	1268	A
1	C1	1269	A
1	C1	1286	A
1	C1	1287	U
1	C1	1289	G
1	C1	1291	U
1	C1	1295	G
1	C1	1298	C
1	C1	1312	A
1	C1	1314	A
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	1368	A
1	C1	1369	G
1	C1	1374	G
1	C1	1381	A

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Mol	Chain	Res	Type
1	C1	1401	A
1	C1	1416	G
1	C1	1419	C
1	C1	1434	A
1	C1	1437	U
1	C1	1438	A
1	C1	1463	A
1	C1	1464	A
1	C1	1465	G
1	C1	1466	U
1	C1	1470	G
1	C1	1478	C
1	C1	1489	G
1	C1	1490	C
1	C1	1535	U
1	C1	1537	U
1	C1	1538	C
1	C1	1541	A
1	C1	1548	C
1	C1	1549	U
1	C1	1551	G
1	C1	1552	U
1	C1	1553	G
1	C1	1556	C
1	C1	1557	C
1	C1	1559	U
1	C1	1560	G
1	C1	1561	U
1	C1	1562	G
1	C1	1566	A
1	C1	1568	A
1	C1	1575	C
1	C1	1584	A
1	C1	1607	U
1	C1	1608	U
1	C1	1609	G
1	C1	1610	C
1	C1	1618	C
1	C1	1621	A
1	C1	1622	A
1	C1	1623	C
1	C1	1624	U

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Mol	Chain	Res	Type
1	C1	1637	G
1	C1	1662	C
1	C1	1695	A
1	C1	1709	G
1	C1	1715	G
1	C1	1720	A
1	C1	1722	G
1	C1	1729	A
1	C1	1730	G
1	C1	1739	A
1	C1	1741	U
1	C1	1744	U
1	C1	1752	C
1	C1	1759	G
1	C1	1774	U
1	C1	1775	G
1	C1	1776	A
1	C1	1787	G
1	C1	1794	U
1	C1	1795	A
1	C1	1798	U
1	C1	1800	U
1	C1	1818	A
1	C1	1819	U
1	C1	1821	A
1	C1	1825	C
1	C1	1828	C
1	C1	1829	A
1	C1	1837	A
1	C1	1842	G
1	C1	1843	A
1	C1	1845	C
1	C1	1846	A
1	C1	1857	G
1	C1	1858	A
1	C1	1859	U
1	C1	1865	A
1	C1	1868	G
1	C1	1875	A
1	C1	1881	G
1	C1	1885	G
1	C1	1895	U

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Mol	Chain	Res	Type
1	C1	1897	C
1	C1	1900	A
1	C1	1901	A
1	C1	1904	U
1	C1	1909	A
1	C1	1911	A
1	C1	1925	A
1	C1	1927	G
1	C1	1932	G
1	C1	1938	U
1	C1	1942	G
1	C1	1950	C
1	C1	1952	G
1	C1	1961	G
1	C1	1971	G
1	C1	1981	G
1	C1	1987	C
1	C1	1994	G
1	C1	1997	G
1	C1	2004	G
1	C1	2006	A
1	C1	2020	C
1	C1	2021	C
1	C1	2024	U
1	C1	2043	G
1	C1	2044	G
1	C1	2048	G
1	C1	2049	C
1	C1	2052	U
1	C1	2054	A
1	C1	2055	A
1	C1	2064	U
1	C1	2065	U
1	C1	2066	A
1	C1	2075	A
1	C1	2099	U
1	C1	2114	A
1	C1	2119	G
1	C1	2120	A
1	C1	2126	A
1	C1	2131	G
1	C1	2132	U

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Mol	Chain	Res	Type
1	C1	2133	G
1	C1	2142	G
1	C1	2144	A
1	C1	2146	U
1	C1	2160	A
1	C1	2161	G
1	C1	2164	C
1	C1	2174	C
1	C1	2177	A
1	C1	2178	G
1	C1	2179	U
1	C1	2180	G
1	C1	2182	A
1	C1	2183	G
1	C1	2189	C
1	C1	2191	A
1	C1	2198	G
1	C1	2199	C
1	C1	2247	C
1	C1	2248	U
1	C1	2256	U
1	C1	2260	U
1	C1	2286	A
1	C1	2325	A
1	C1	2327	C
1	C1	2328	C
1	C1	2335	A
1	C1	2336	C
1	C1	2338	G
1	C1	2339	G
1	C1	2342	U
1	C1	2343	G
1	C1	2347	A
1	C1	2350	U
1	C1	2356	G
1	C1	2396	U
1	C1	2397	G
1	C1	2399	G
1	C1	2407	A
1	C1	2409	A
1	C1	2414	G
1	C1	2415	U

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Mol	Chain	Res	Type
1	C1	2424	G
1	C1	2425	G
1	C1	2430	A
1	C1	2434	U
1	C1	2436	G
1	C1	2437	G
1	C1	2438	C
1	C1	2439	G
1	C1	2442	A
1	C1	2443	G
1	C1	2444	U
1	C1	2449	U
1	C1	2453	A
1	C1	2456	A
1	C1	2464	U
1	C1	2465	G
1	C1	2467	U
1	C1	2484	G
1	C1	2551	A
1	C1	2558	C
1	C1	2560	G
1	C1	2564	G
1	C1	2730	C
1	C1	2739	U
1	C1	2740	U
1	C1	2749	G
1	C1	2759	A
1	C1	2760	A
1	C1	2761	A
1	C1	2767	C
1	C1	2775	A
1	C1	2777	A
1	C1	2778	A
1	C1	2782	G
1	C1	2784	U
1	C1	2786	G
1	C1	2806	G
1	C1	2816	U
1	C1	2838	U
1	C1	2839	C
1	C1	2845	A
1	C1	2847	C

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Mol	Chain	Res	Type
1	C1	2856	G
1	C1	2857	C
1	C1	2858	A
1	C1	2862	U
1	C1	2869	A
1	C1	2880	G
1	C1	2881	U
1	C1	2883	C
1	C1	2884	A
1	C1	2885	C
1	C1	2888	A
1	C1	2893	U
1	C1	2894	A
1	C1	2899	A
1	C1	2905	G
1	C1	2906	C
1	C1	2917	C
1	C1	2922	G
1	C1	2936	U
1	C1	2942	C
1	C1	2954	C
1	C1	2955	U
1	C1	2956	C
1	C1	2969	A
1	C1	3006	A
1	C1	3013	U
1	C1	3016	G
1	C1	3035	G
1	C1	3043	A
1	C1	3049	C
1	C1	3050	C
1	C1	3074	C
1	C1	3075	C
1	C1	3079	A
1	C1	3086	A
1	C1	3087	A
1	C1	3088	U
1	C1	3098	A
1	C1	3099	A
1	C1	3100	C
1	C1	3101	G
1	C1	3108	U

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Mol	Chain	Res	Type
1	C1	3111	U
1	C1	3112	A
1	C1	3113	C
1	C1	3118	A
1	C1	3119	C
1	C1	3121	U
1	C1	3122	U
1	C1	3123	G
1	C1	3124	U
1	C1	3125	A
1	C1	3126	G
1	C1	3127	A
1	C1	3130	U
1	C1	3131	A
1	C1	3132	U
1	C1	3134	A
1	C1	3140	G
1	C1	3144	C
1	C1	3145	C
1	C1	3146	G
1	C1	3147	G
1	C1	3153	U
1	C1	3154	A
1	C1	3161	C
1	C1	3162	A
1	C1	3163	G
1	C1	3167	A
1	C1	3170	C
1	C1	3171	C
1	C1	3178	G
1	C1	3181	C
1	C1	3183	C
1	C1	3185	A
1	C1	3187	G
1	C1	3188	U
1	C1	3199	A
1	C1	3203	C
1	C1	3210	U
1	C1	3217	U
1	C1	3227	C
1	C1	3228	G
1	C1	3229	G

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Mol	Chain	Res	Type
1	C1	3230	G
1	C1	3244	C
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	3275	A
1	C1	3280	G
1	C1	3281	U
1	C1	3282	A
1	C1	3291	U
1	C1	3293	G
1	C1	3294	U
1	C1	3295	U
1	C1	3296	G
1	C1	3298	U
1	C1	3309	G
1	C1	3318	C
1	C1	3322	C
1	C1	3323	C
1	C1	3324	U
1	C1	3325	U
1	C1	3330	U
1	C1	3331	A
1	C1	3332	G
1	C1	3333	A
2	C2	23	U
2	C2	34	U
2	C2	35	C
2	C2	39	G
2	C2	49	G
2	C2	59	A
2	C2	62	A
2	C2	63	G
2	C2	81	U
2	C2	82	U
2	C2	84	C
2	C2	86	U
2	C2	87	G
2	C2	90	U

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Mol	Chain	Res	Type
2	C2	95	G
2	C2	103	G
2	C2	104	A
2	C2	106	C
2	C2	110	C
2	C2	111	A
2	C2	112	U
2	C2	113	U
2	C2	125	U
2	C2	148	G
2	C2	157	U
2	C2	158	U
2	C2	159	C
2	C2	163	C
2	C2	164	A
2	C2	165	U
2	C2	166	C
2	C2	170	C
2	C2	173	U
2	C2	181	U
2	C2	183	U
2	C2	189	A
2	C2	196	G
2	C2	203	G
2	C2	206	G
2	C2	212	G
2	C2	213	A
2	C2	214	A
2	C2	215	A
2	C2	216	A
2	C2	219	A
2	C2	221	U
2	C2	222	G
2	C2	225	G
2	C2	289	G
2	C2	291	G
2	C2	292	C
2	C2	294	A
2	C2	295	G
2	C2	300	A

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	150	G
1	C1	445	A
1	C1	799	C
1	C1	897	G
1	C1	1046	A
1	C1	1063	C
1	C1	1077	U
1	C1	1489	G
1	C1	1949	G
1	C1	2173	U
1	C1	2176	A
1	C1	2327	C
1	C1	3078	U
1	C1	3131	A
1	C1	3162	A
1	C1	3209	U
1	C1	3216	U
1	C1	3229	G
1	C1	3257	U
1	C1	3281	U
1	C1	3297	U
1	C1	3321	U
2	C2	102	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SEP	CC	160	5	8,9,10	1.58	1 (12%)	7,12,14	1.22	1 (14%)
5	TPO	CC	163	5	8,10,11	1.71	1 (12%)	10,14,16	1.23	1 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	SEP	CC	160	5	-	0/6/8/10	-
5	TPO	CC	163	5	-	6/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	CC	163	TPO	P-O1P	3.55	1.61	1.50
5	CC	160	SEP	P-O1P	3.47	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CC	163	TPO	P-OG1-CB	-2.77	115.79	123.33
5	CC	160	SEP	OG-CB-CA	2.53	110.61	108.14

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	CC	163	TPO	N-CA-CB-CG2
5	CC	163	TPO	N-CA-CB-OG1
5	CC	163	TPO	C-CA-CB-CG2
5	CC	163	TPO	O-C-CA-CB
5	CC	163	TPO	CG2-CB-OG1-P
5	CC	163	TPO	CB-OG1-P-O3P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	CC	160	SEP	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
66	ADP	CW	1001	67	28,29,29	0.44	0	43,45,45	0.56	0
64	GTP	CH	1001	-	33,34,34	0.97	1 (3%)	50,54,54	1.61	8 (16%)

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
66	ADP	CW	1001	67	-	5/16/32/32	0/3/3/3
64	GTP	CH	1001	-	-	5/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	CH	1001	GTP	C2-N3	2.03	1.38	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	CH	1001	GTP	C5-C4-N3	-4.92	120.56	128.39
64	CH	1001	GTP	C2-N3-C4	4.68	120.36	112.30
64	CH	1001	GTP	N9-C4-N3	3.05	132.05	125.95
64	CH	1001	GTP	C2-N1-C6	-2.88	119.88	125.11
64	CH	1001	GTP	N9-C8-N7	-2.74	108.31	113.40
64	CH	1001	GTP	C8-N7-C5	2.54	108.78	104.26
64	CH	1001	GTP	C5-C6-N1	2.53	119.70	113.25
64	CH	1001	GTP	O6-C6-C5	-2.39	120.23	126.53

There are no chirality outliers.

All (10) torsion outliers are listed below:

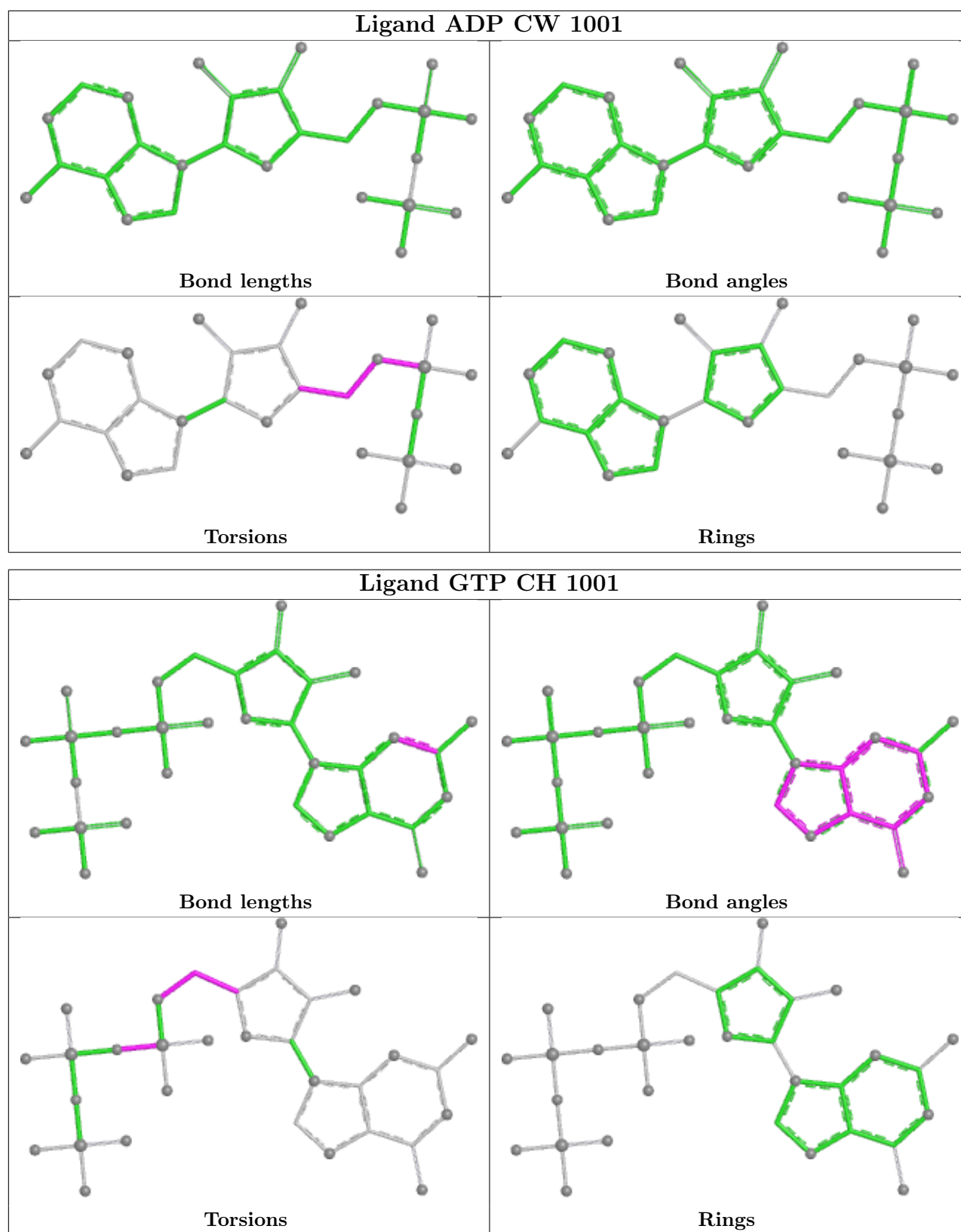
Mol	Chain	Res	Type	Atoms
66	CW	1001	ADP	C5'-O5'-PA-O2A
66	CW	1001	ADP	C5'-O5'-PA-O3A
66	CW	1001	ADP	C4'-C5'-O5'-PA
66	CW	1001	ADP	O4'-C4'-C5'-O5'
66	CW	1001	ADP	C3'-C4'-C5'-O5'
64	CH	1001	GTP	C3'-C4'-C5'-O5'
64	CH	1001	GTP	PB-O3A-PA-O1A
64	CH	1001	GTP	O4'-C4'-C5'-O5'
64	CH	1001	GTP	C4'-C5'-O5'-PA
64	CH	1001	GTP	PB-O3A-PA-O2A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
64	CH	1001	GTP	4	0

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

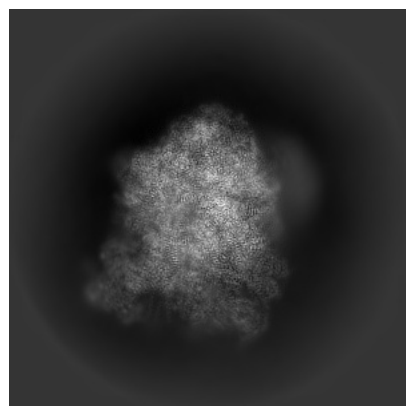
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35290. These allow visual inspection of the internal detail of the map and identification of artifacts.

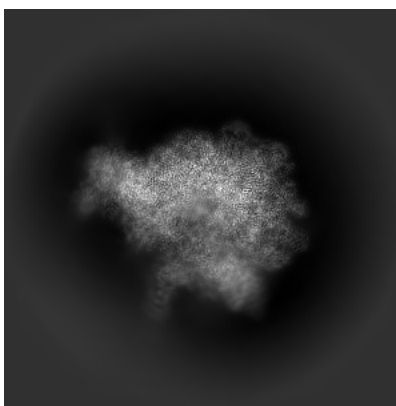
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

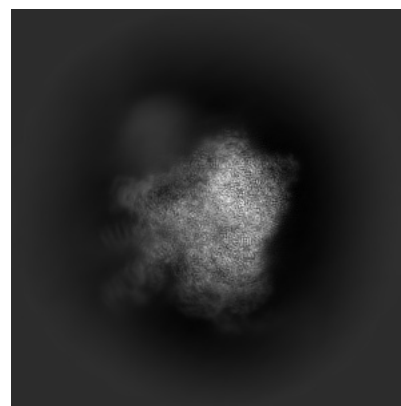
6.1.1 Primary map



X

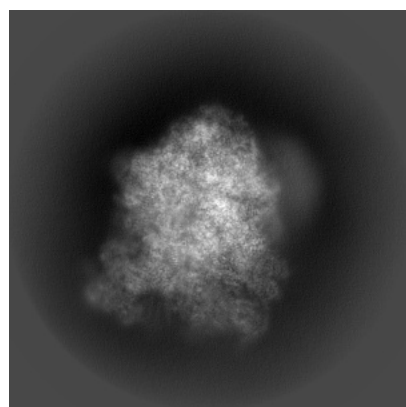


Y

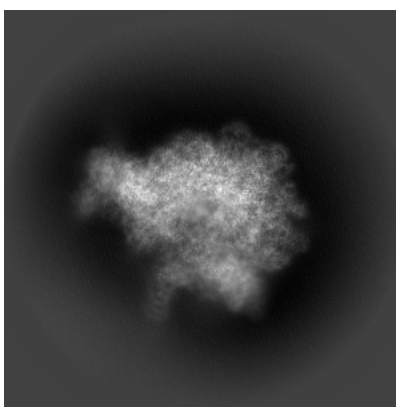


Z

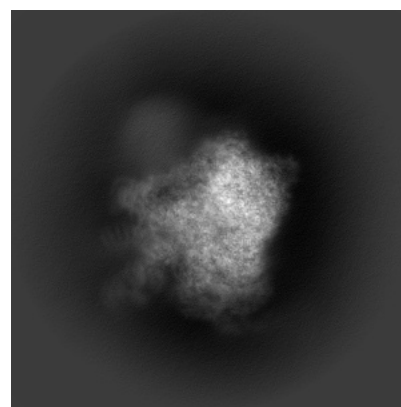
6.1.2 Raw map



X



Y

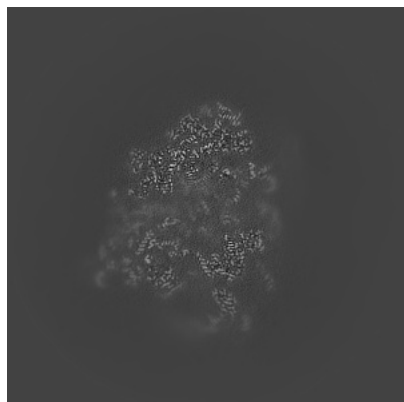


Z

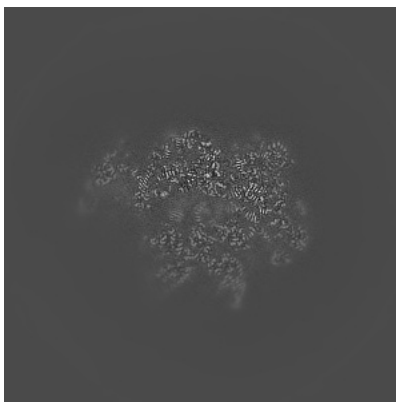
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

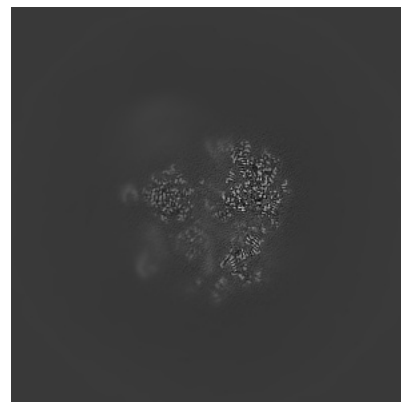
6.2.1 Primary map



X Index: 240

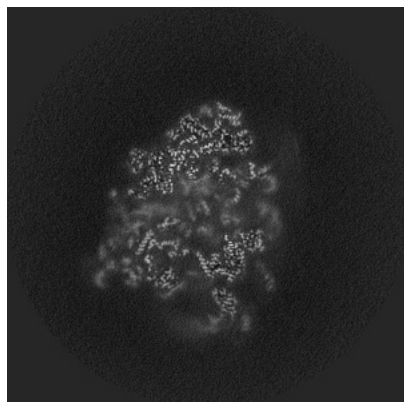


Y Index: 240

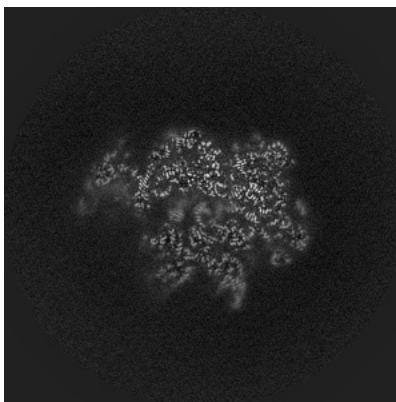


Z Index: 240

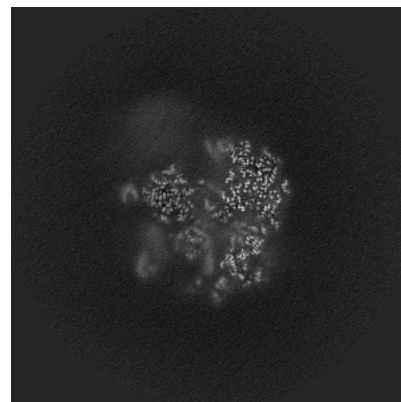
6.2.2 Raw map



X Index: 240



Y Index: 240

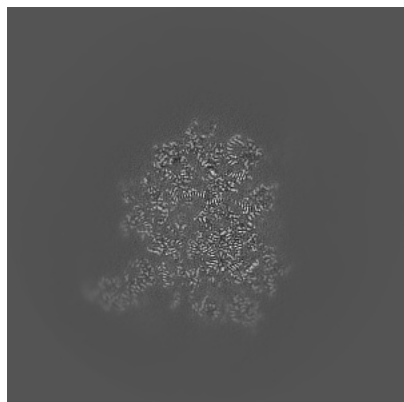


Z Index: 240

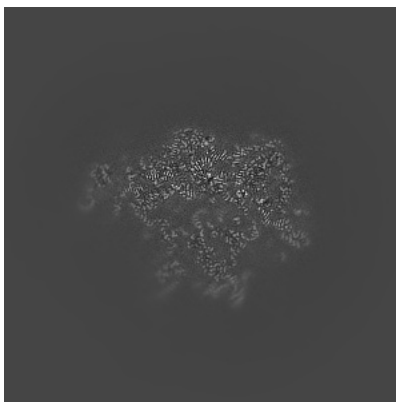
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

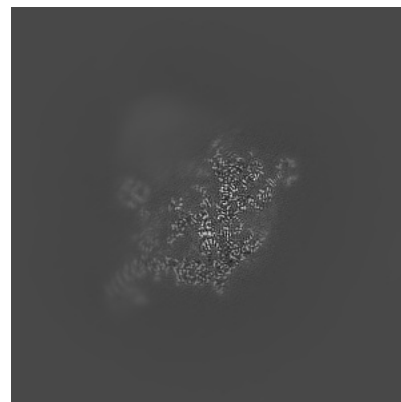
6.3.1 Primary map



X Index: 276

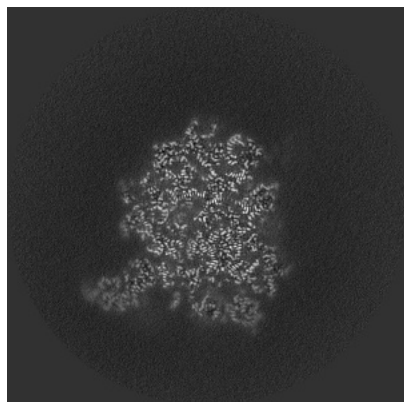


Y Index: 247

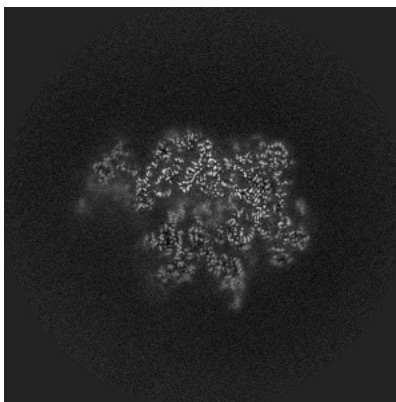


Z Index: 289

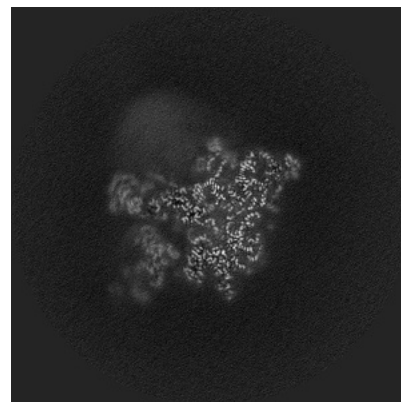
6.3.2 Raw map



X Index: 276



Y Index: 238

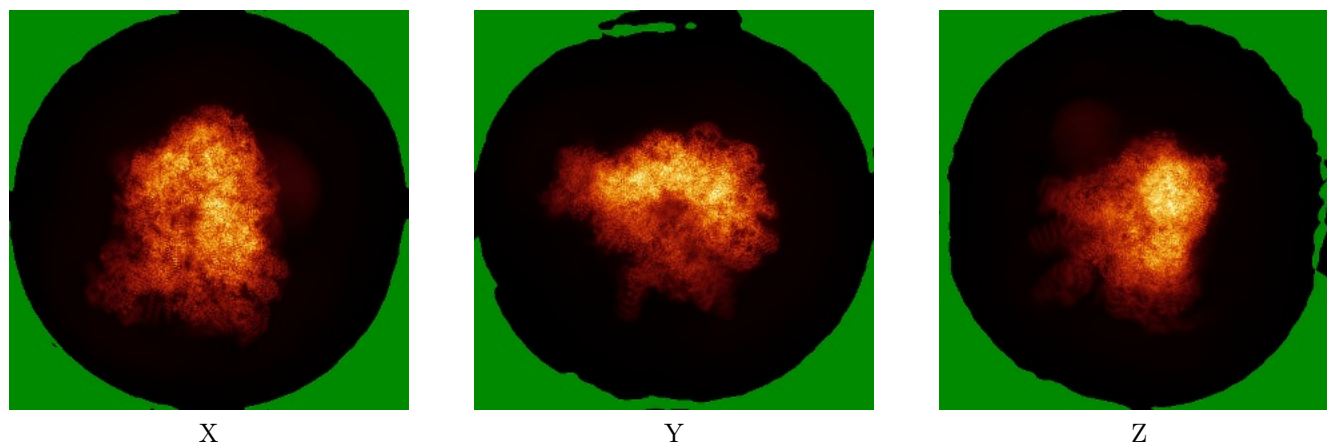


Z Index: 276

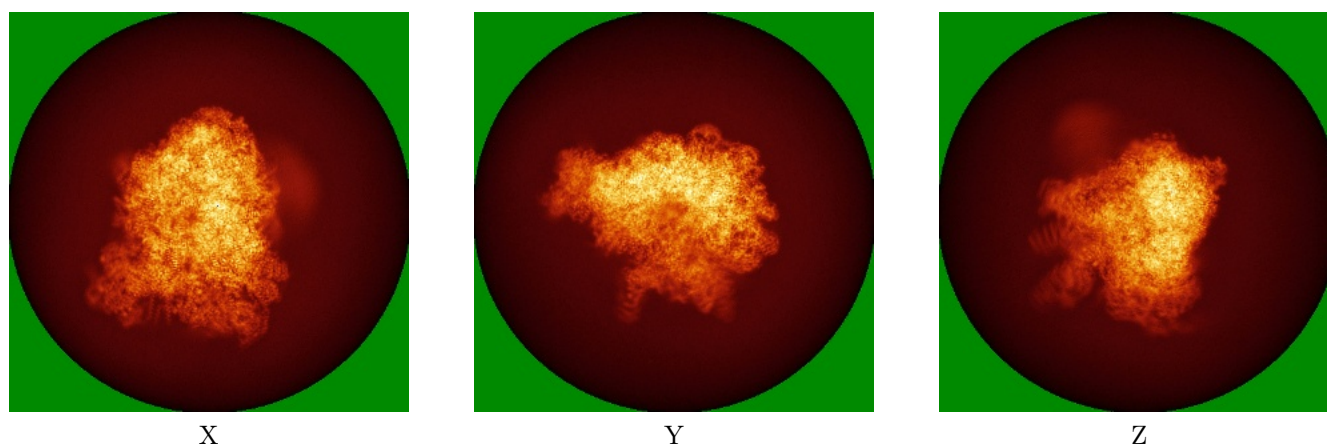
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

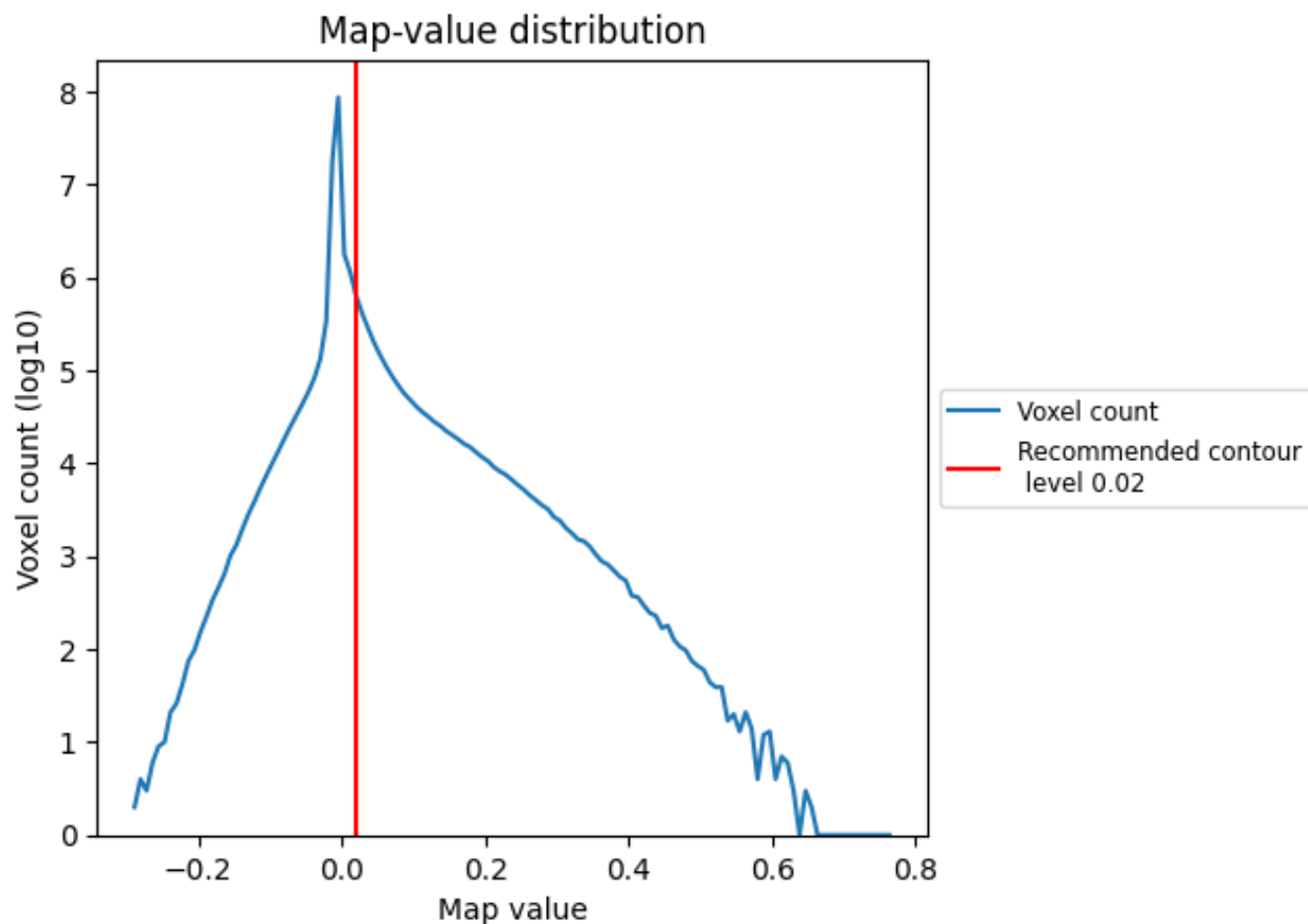
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

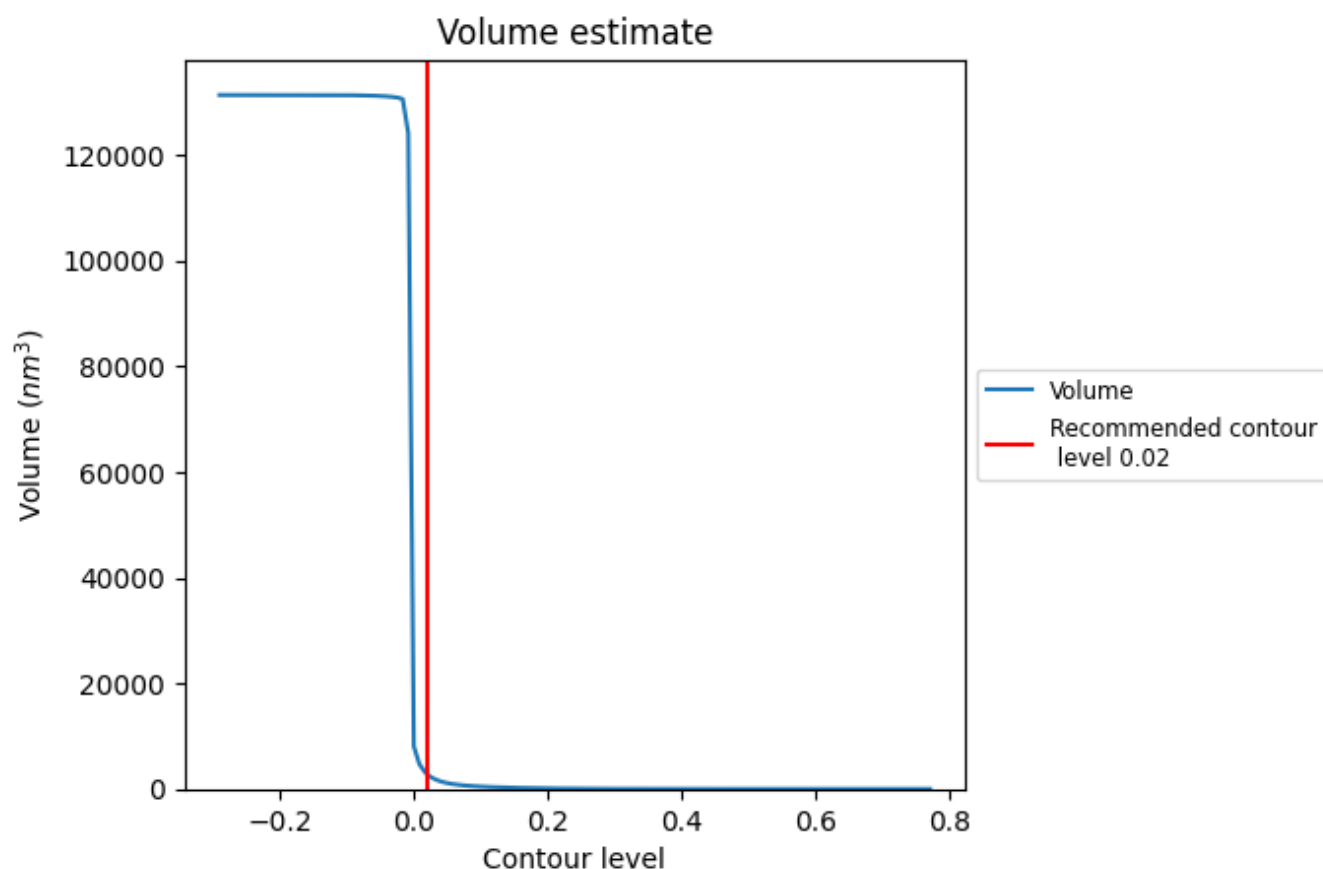
This section contains the results of statistical analysis of the map.

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.

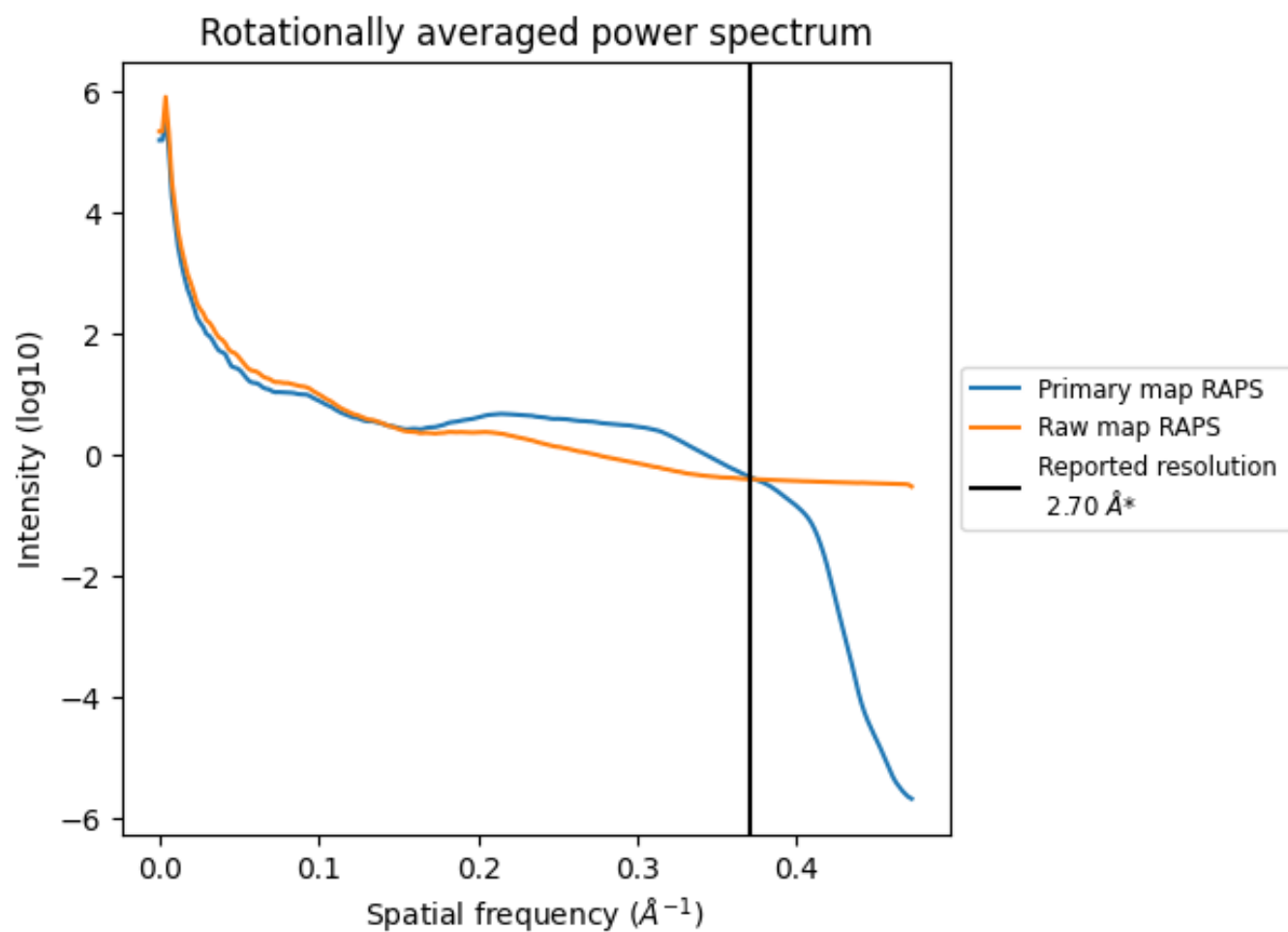
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2911 nm^3 ; this corresponds to an approximate mass of 2630 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 ⓘ

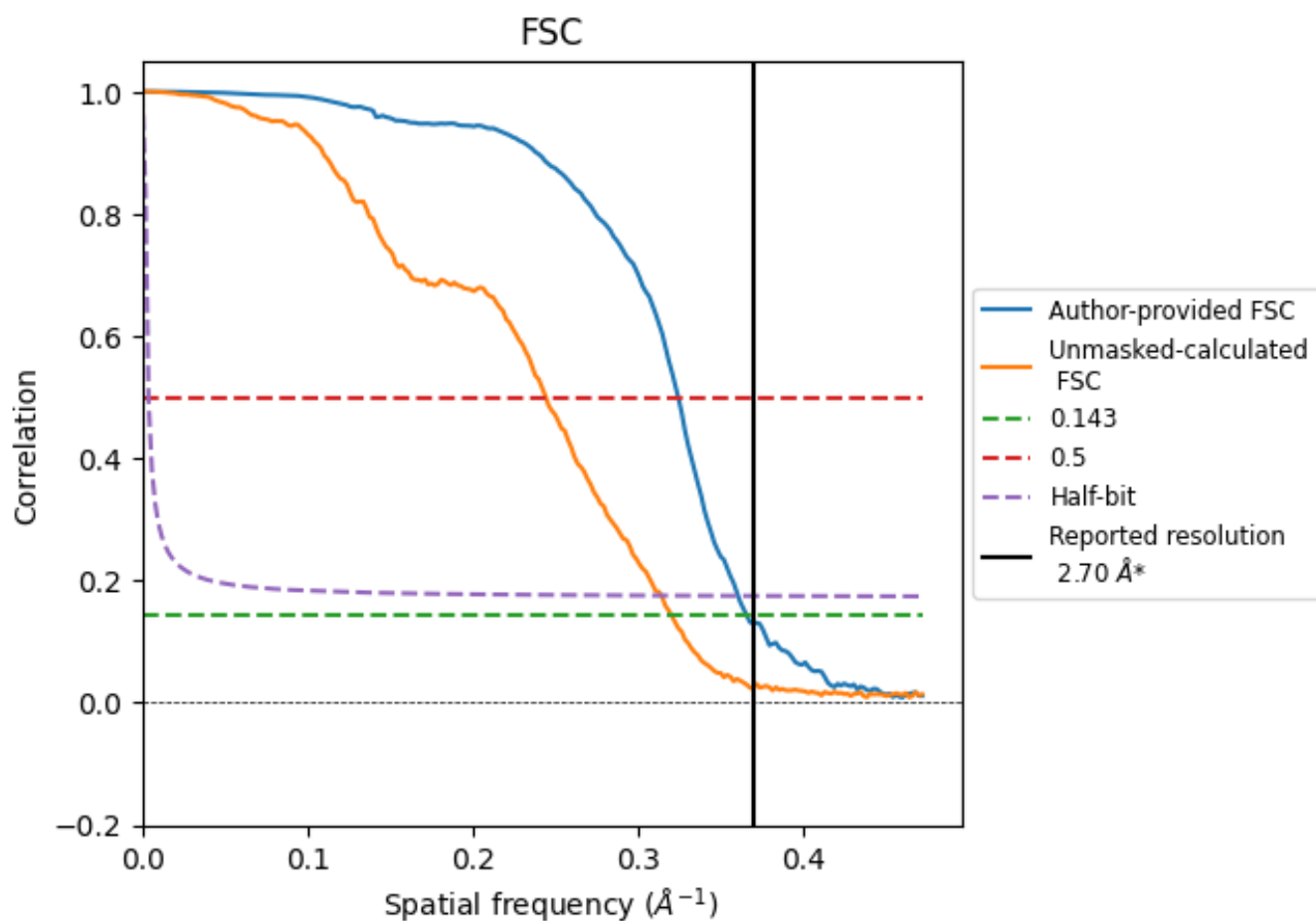


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 $0.370 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

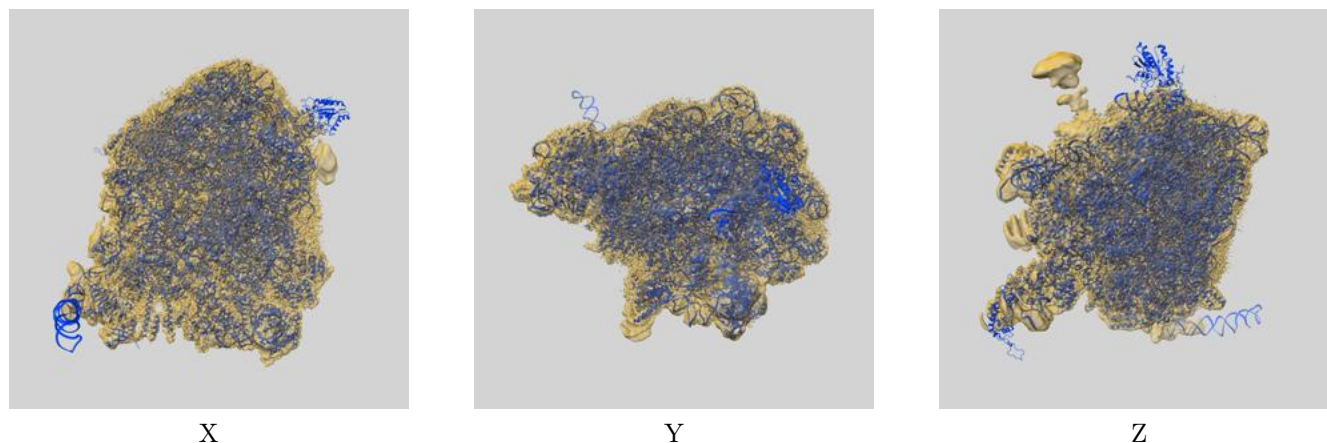
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.73	3.08	2.77
Unmasked-calculated*	3.12	4.09	3.18

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.12 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

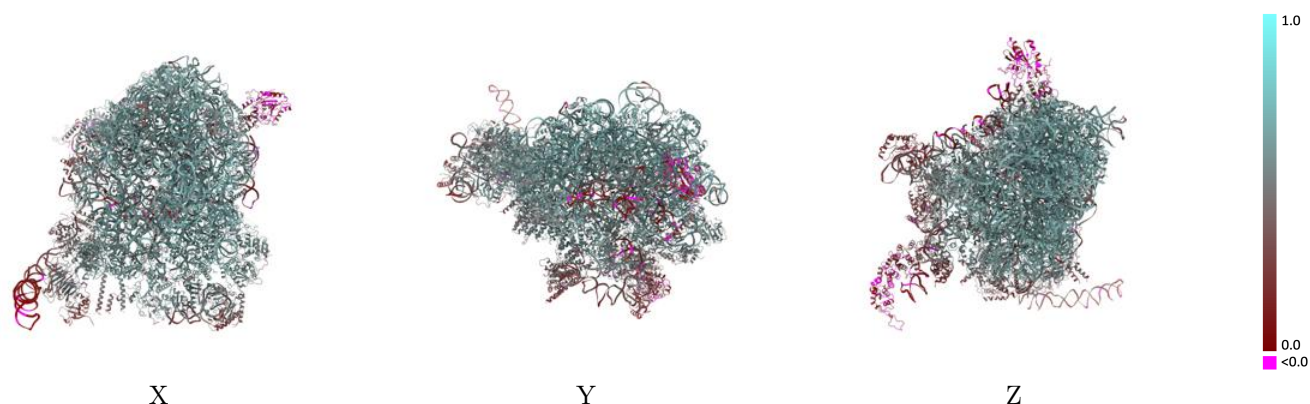
This section contains information regarding the fit between EMDB map EMD-35290 and PDB model 8IA0. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



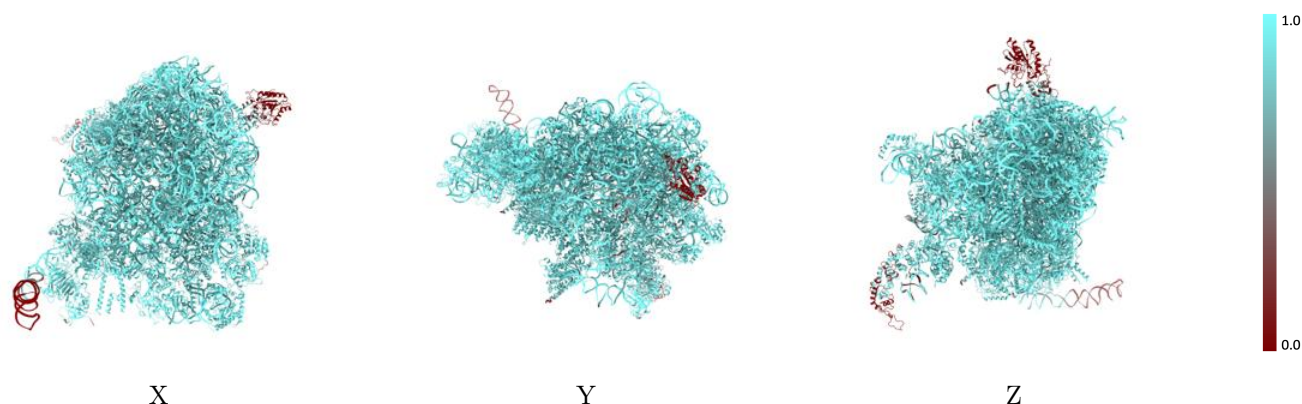
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



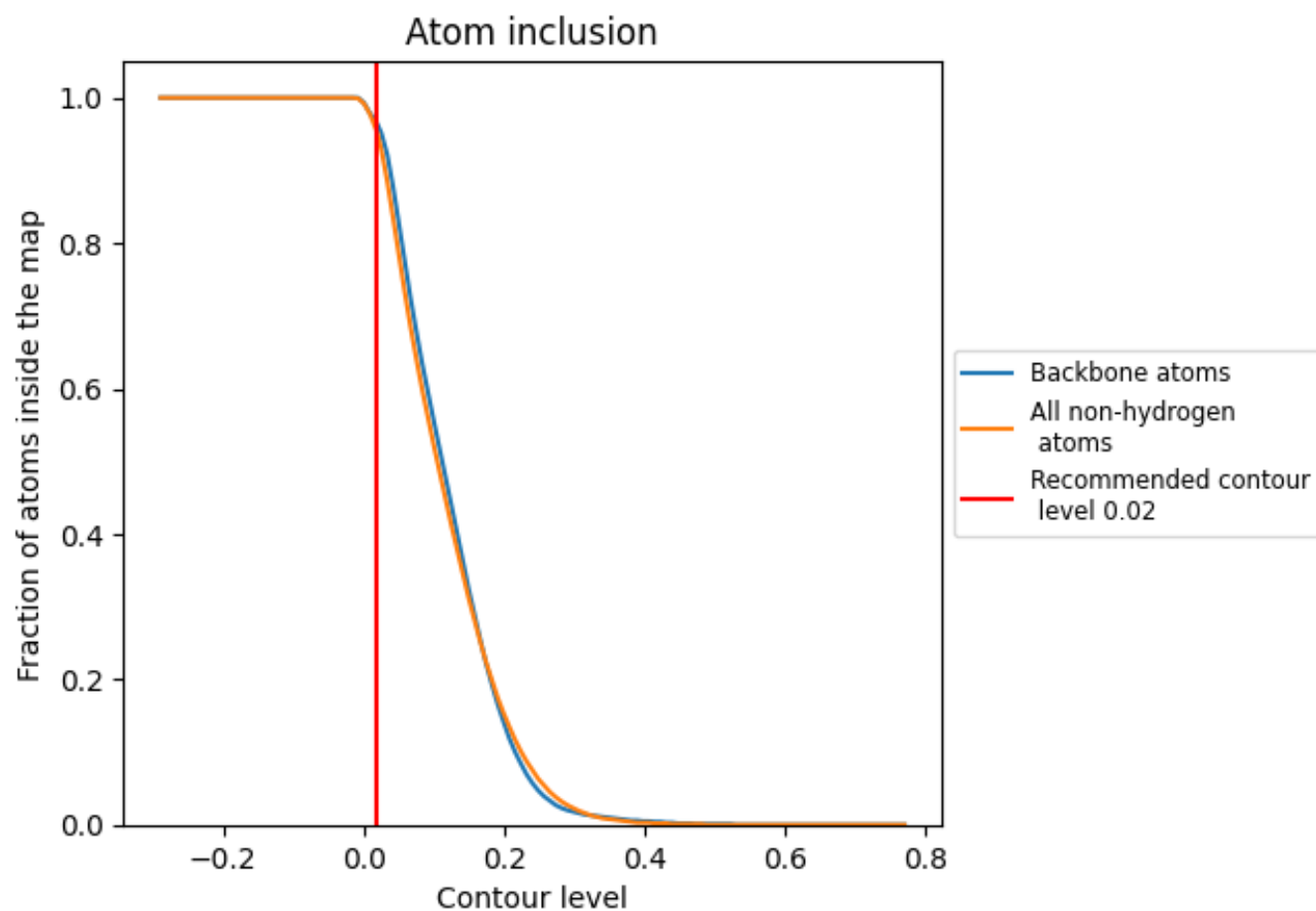
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 96% of all backbone atoms, 95% 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	 0.9520	 0.5310
C1	 0.9590	 0.5350
C2	 0.9740	 0.5430
CA	 0.9820	 0.6050
CB	 0.9430	 0.4610
CC	 0.9730	 0.5670
CD	 0.9330	 0.4020
CE	 0.9580	 0.5390
CF	 0.9740	 0.5520
CG	 0.9770	 0.5990
CH	 0.9740	 0.5750
CI	 0.9470	 0.4850
CJ	 0.9690	 0.5480
CK	 0.9720	 0.5790
CL	 0.4030	 0.2400
CM	 0.9540	 0.5100
CN	 0.9730	 0.5890
CO	 0.9890	 0.6280
CP	 0.9750	 0.5550
CQ	 0.9610	 0.5570
CR	 0.9790	 0.6090
CS	 0.9670	 0.5170
CT	 0.9770	 0.5510
CU	 0.9750	 0.5740
CV	 0.9880	 0.6470
CW	 0.9410	 0.3990
CX	 0.9550	 0.5450
CY	 0.9270	 0.4090
CZ	 0.7470	 0.2500
Ca	 0.9210	 0.4000
Cz	 0.9090	 0.3960
LA	 0.9200	 0.3540
LB	 0.9820	 0.6200
LC	 0.9830	 0.6380
LE	 0.9800	 0.6080



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Chain	Atom inclusion	Q-score
LF	 0.9830	 0.6290
LG	 0.9800	 0.6220
LH	 0.9790	 0.6120
LK	 0.9520	 0.4670
LL	 0.9950	 0.6520
LM	 0.9870	 0.6290
LN	 0.9950	 0.6680
LO	 0.9900	 0.6470
LP	 0.9820	 0.6060
LQ	 0.9830	 0.6010
LR	 0.9510	 0.5120
LS	 0.9810	 0.6200
LT	 0.9230	 0.3850
LU	 0.9750	 0.5490
LV	 0.9910	 0.6280
LX	 0.9710	 0.5840
LY	 0.9780	 0.6210
LZ	 0.9770	 0.5890
Lc	 0.9570	 0.5300
Ld	 0.9720	 0.6140
Le	 0.9840	 0.6450
Lf	 0.9900	 0.6620
Lg	 0.9620	 0.5960
Lh	 0.9800	 0.5850
Li	 0.9780	 0.6070
Lj	 0.9950	 0.6710
Lk	 0.9740	 0.5390
Ll	 0.9810	 0.5580
Lp	 0.8500	 0.2560
Lq	 0.8990	 0.2370