



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 12:28 AM UTC

PDB ID : 8I9Z / pdb_00008i9z
EMDB ID : EMD-35289
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- State Spb4
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

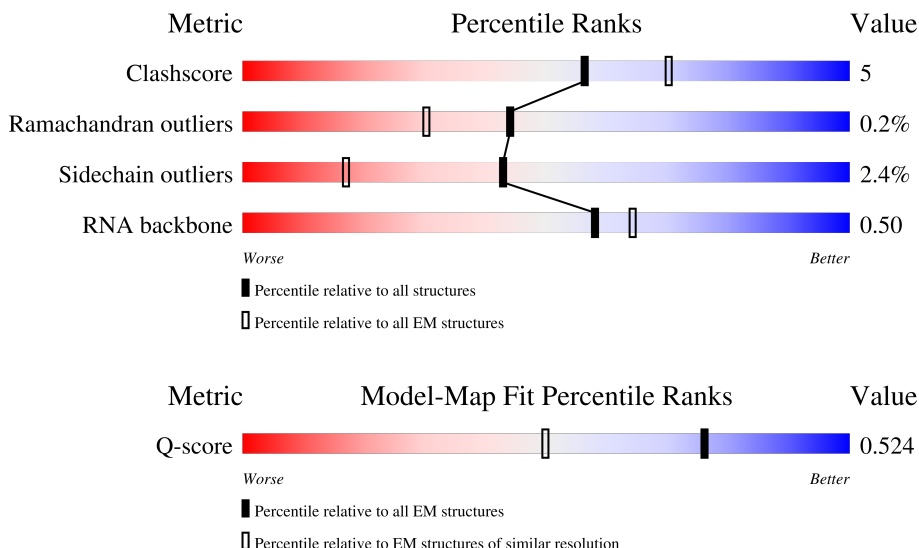
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 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	

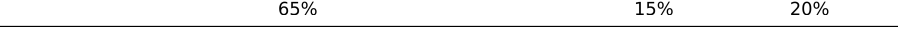
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Mol	Chain	Length	Quality of chain
28	Cz	123	
29	LB	392	
30	LC	365	
31	LE	200	
32	LG	262	
33	LH	192	
34	LK	165	
35	LL	213	
36	LM	142	
37	LN	203	
38	LO	204	
39	LP	187	
40	LQ	213	
41	LR	2898	
42	LS	174	
43	LT	160	
44	LU	127	
45	LV	139	
46	LX	156	
47	LY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

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

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 167255 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	2787	Total	C	N	O	P	0	0
			59633	26611	10807	19428	2787		

- 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	S	0	0
			5289	3368	931	977	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	465	Total	C	N	O	S	0	0
			3689	2362	646	670	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	390	Total	C	N	O		0	0
			2173	1307	446	420			

There is a discrepancy between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CM	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	324	Total	C	N	O	S	0	0
			2535	1618	445	457	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CQ	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	625	Total	C	N	O	S	0	0
			5036	3190	917	910	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	0	0
			1073	672	213	188		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	CW	537	Total	C	N	O	S	0	0
			4284	2733	760	777	14		

- 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	0	0
			701	435	128	135	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	CY	382	Total	C	N	O	S	0	0
			3035	1943	558	523	11		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LE	189	Total	C	N	O	S	0	0
			1475	944	267	261	3		

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

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

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

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

There are 37 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

- Molecule 37 is a protein called Ribosomal protein L15.

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

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

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

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

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

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

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

- Molecule 41 is a protein called Ribosomal protein L19.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 56 is a protein called Ribosomal protein L37.

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

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

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

There are 13 discrepancies between the modelled and reference sequences:

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

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

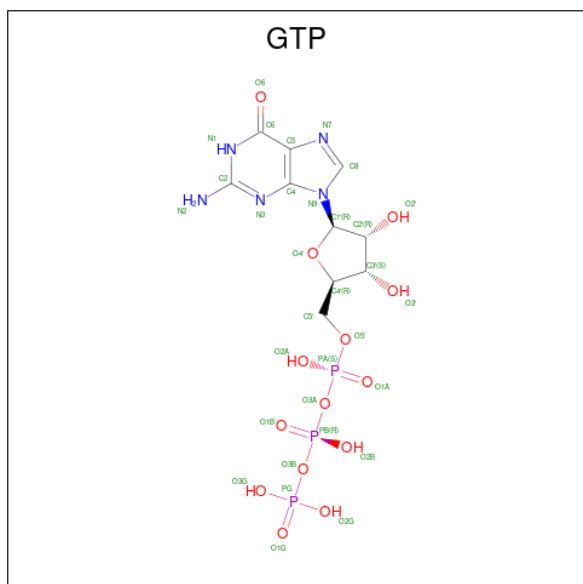
- Molecule 58 is a protein called 60S ribosomal protein L39.

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

- Molecule 59 is a protein called Ribosomal protein.

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

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

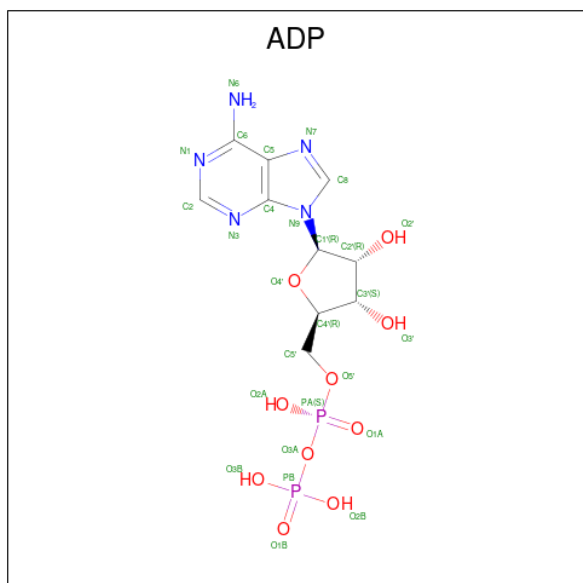


Mol	Chain	Residues	Atoms					AltConf
60	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	

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

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

- Molecule 62 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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

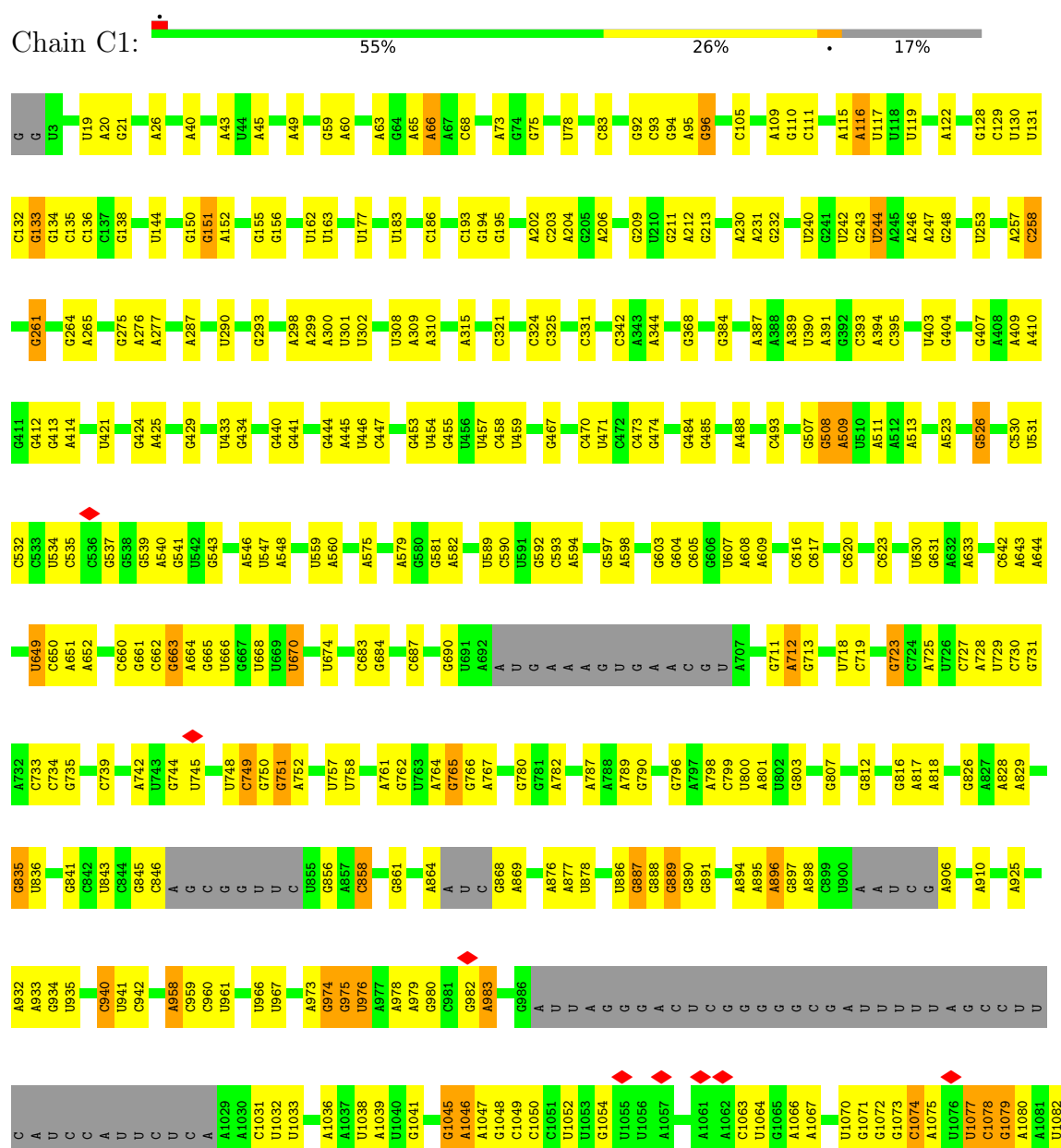
- Molecule 63 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
63	CW	1	Total	Mg	0
			1	1	

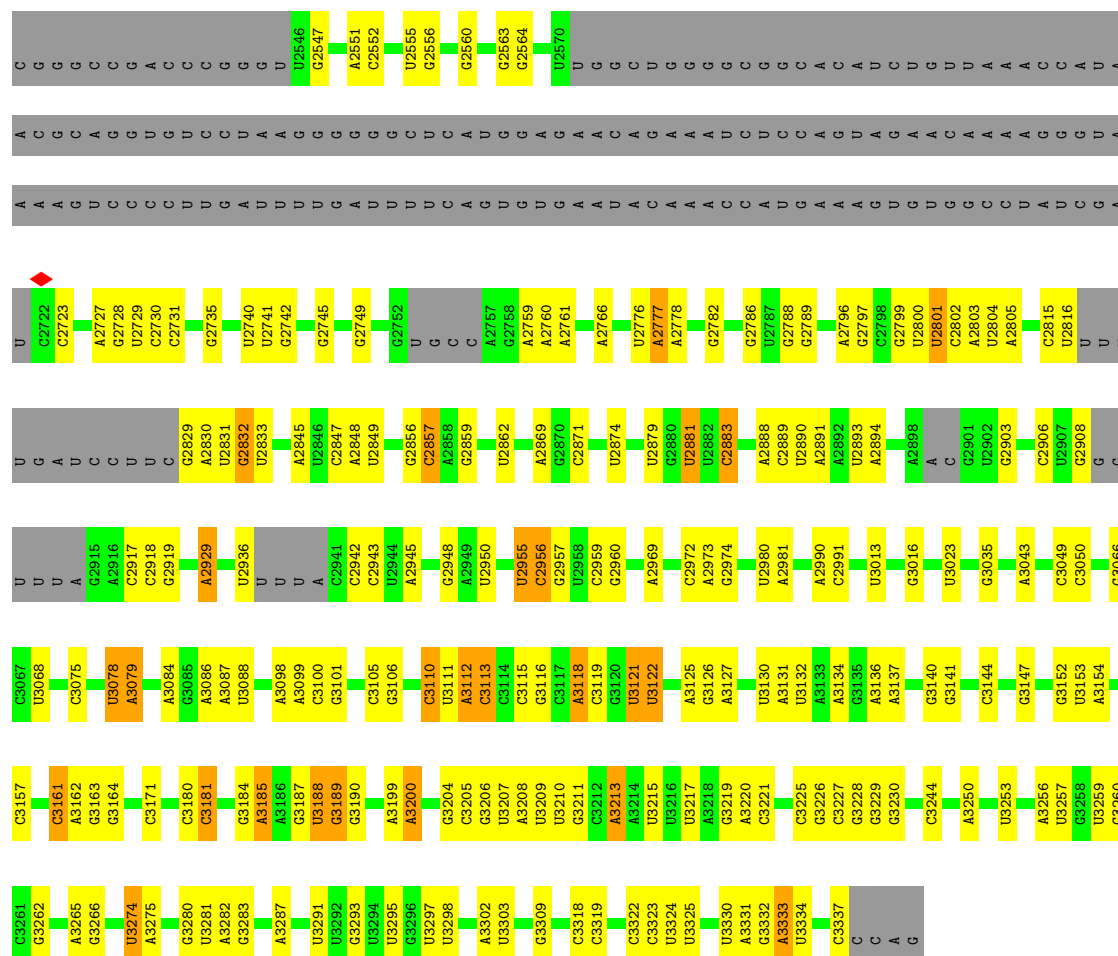
3 Residue-property plots

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)

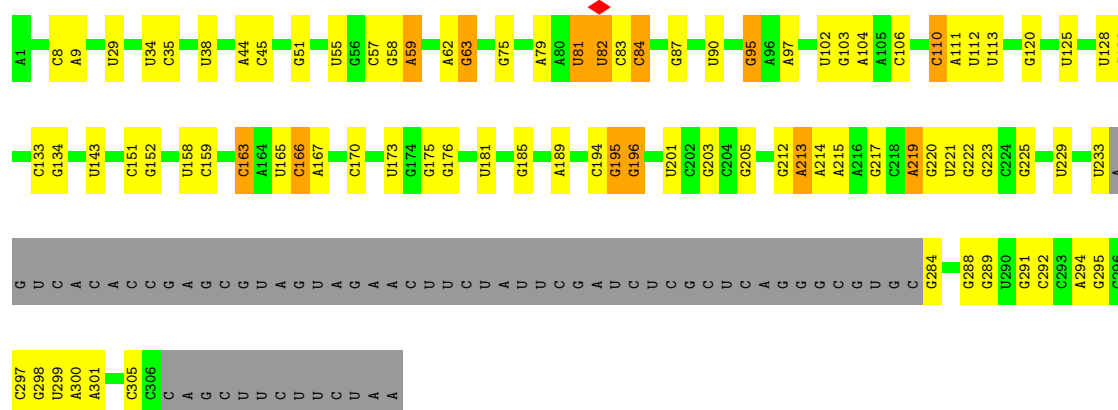






• Molecule 2: RNA (319-MER)

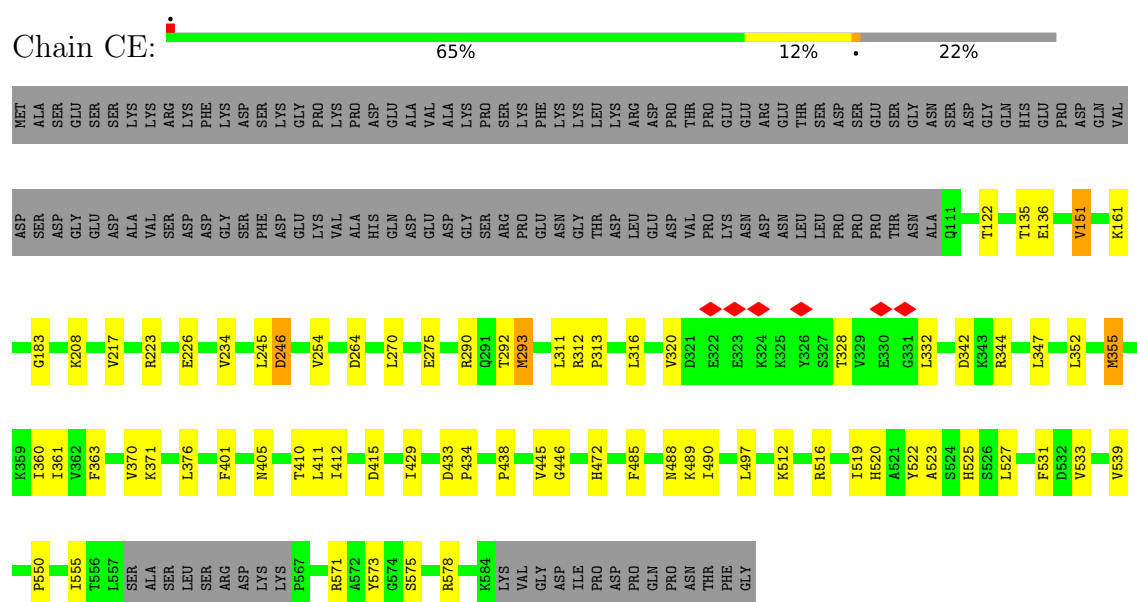
Chain C2: 53% 23% 20%



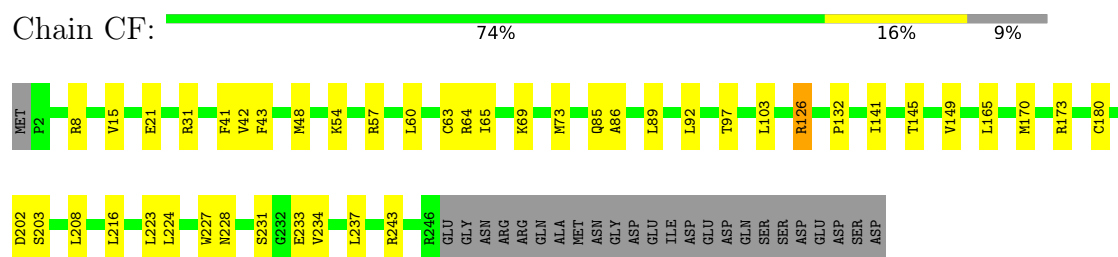
• Molecule 3: Brix domain-containing protein

Chain CA: 68% 11% 21%

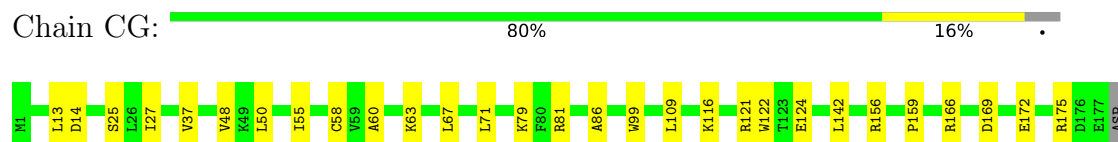
- Molecule 7: RNA helicase

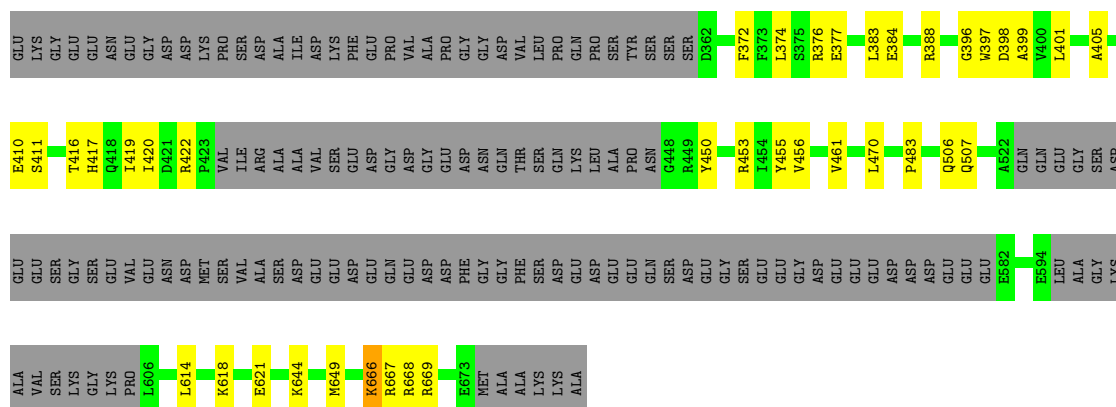


- Molecule 8: Ribosome assembly factor *mrt4*



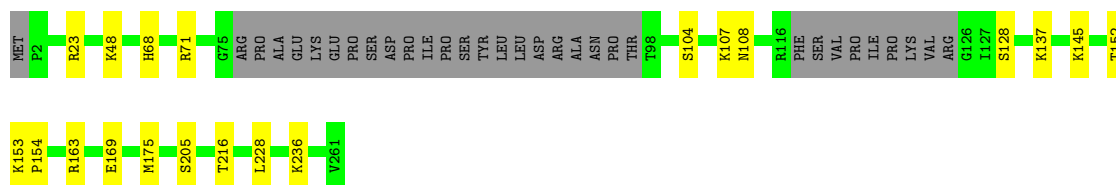
- Molecule 9: 60S ribosome subunit biogenesis protein NIP7





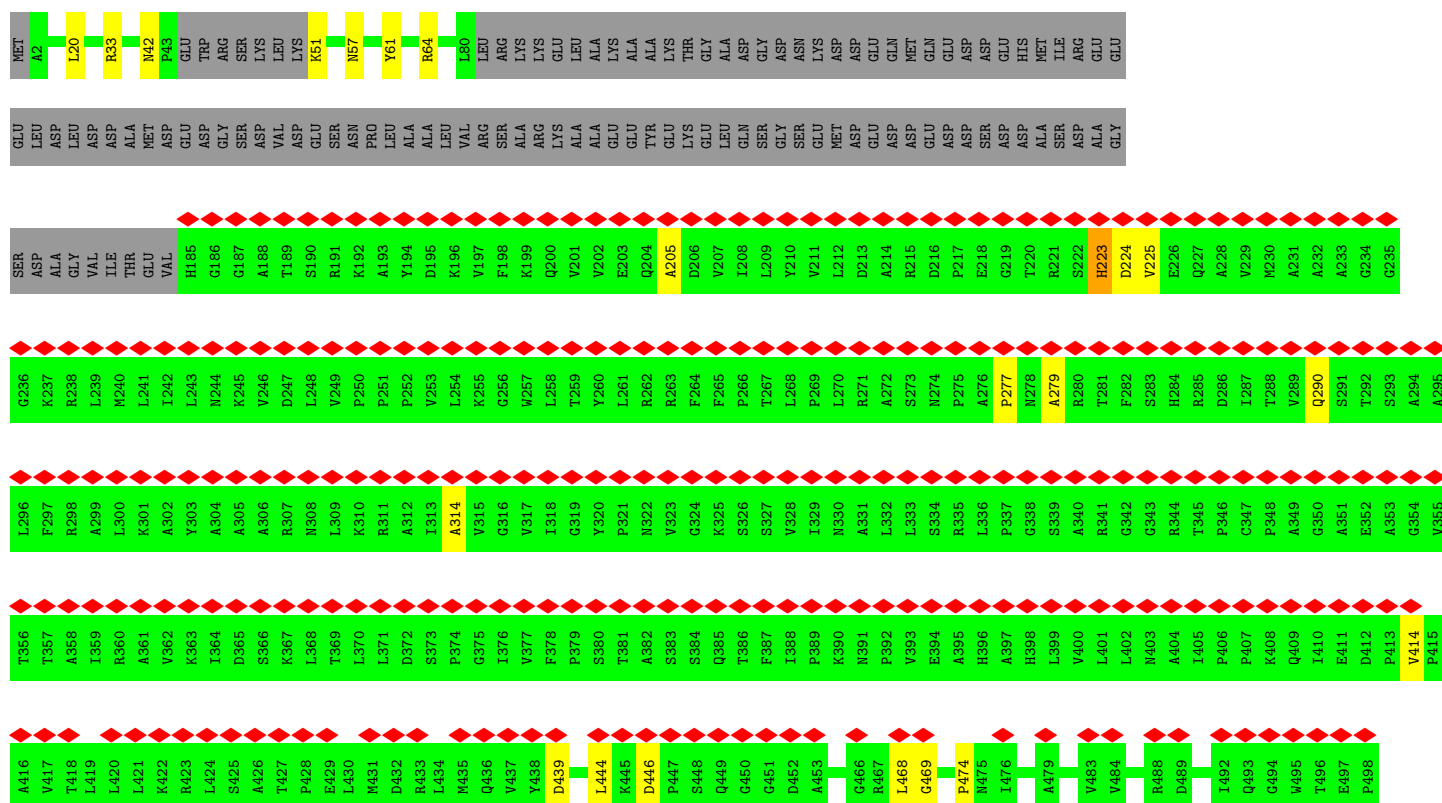
• Molecule 13: Ribosome biogenesis protein NSA2 homolog

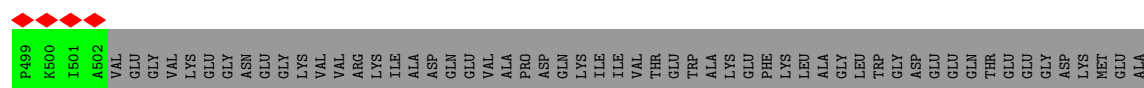
Chain CK: 80% 8% 12%



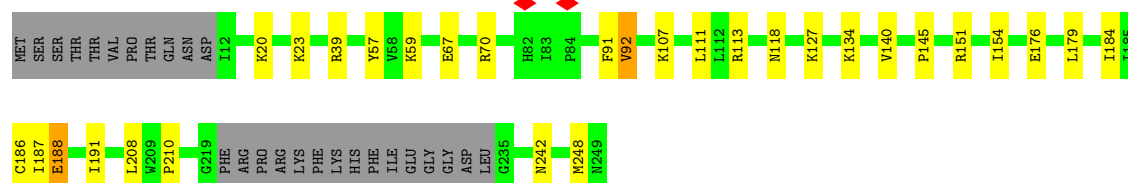
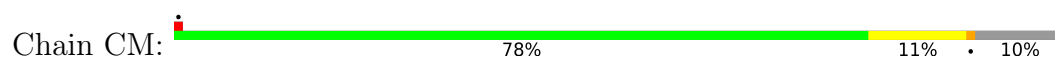
• Molecule 14: Putative GTP binding protein

Chain CL: 50% 66% 30%





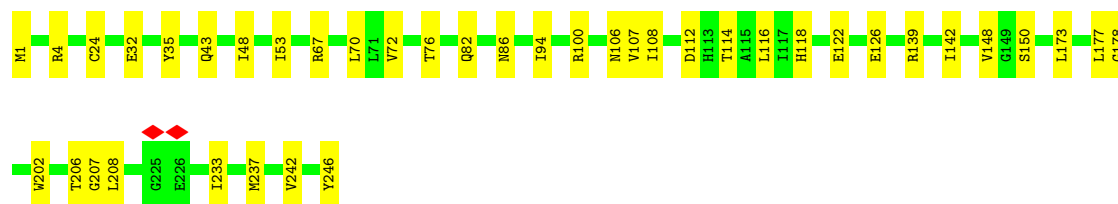
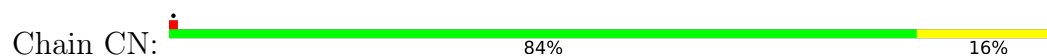
- Molecule 15: 60S ribosomal protein l7-like protein



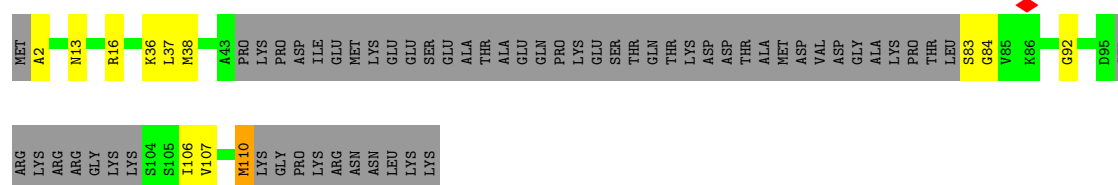
- Molecule 15: 60S ribosomal protein l7-like protein



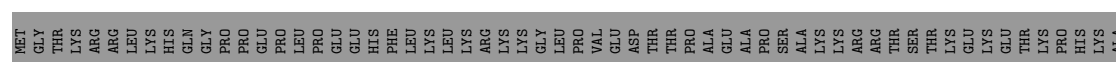
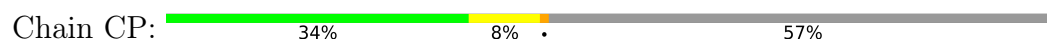
- Molecule 16: Eukaryotic translation initiation factor 6

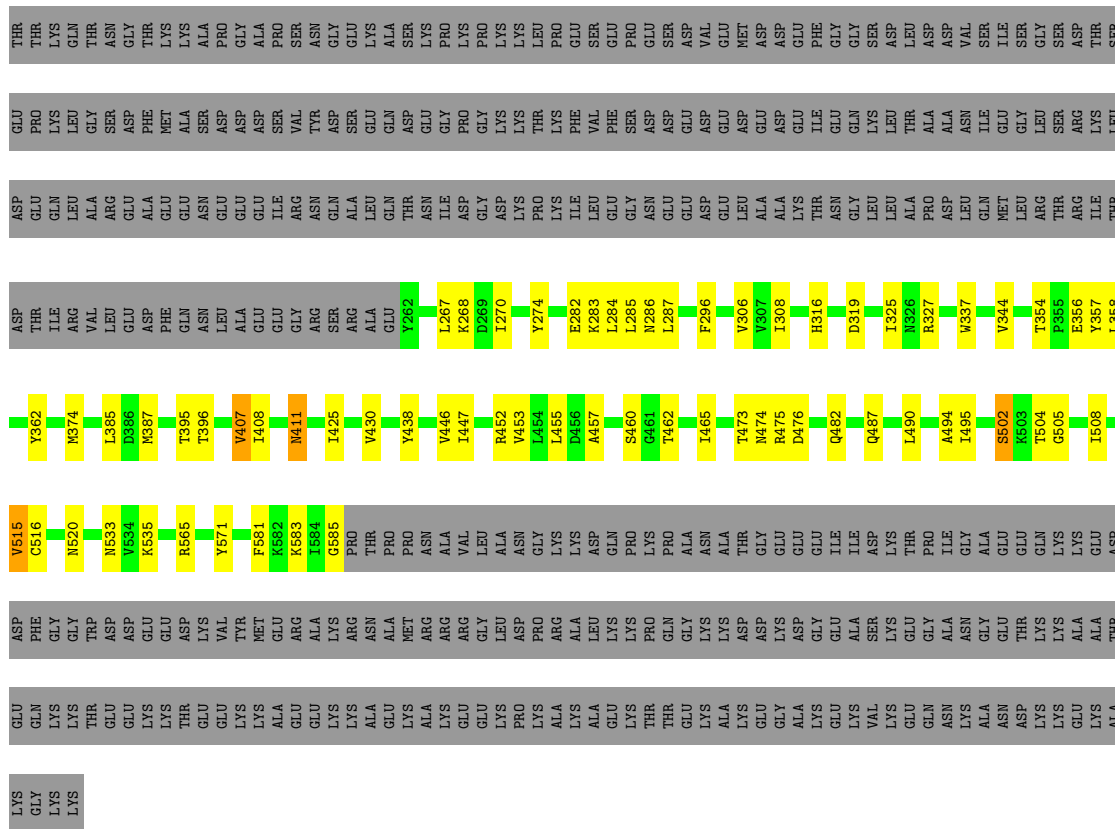


- Molecule 17: DUF2423 domain-containing protein

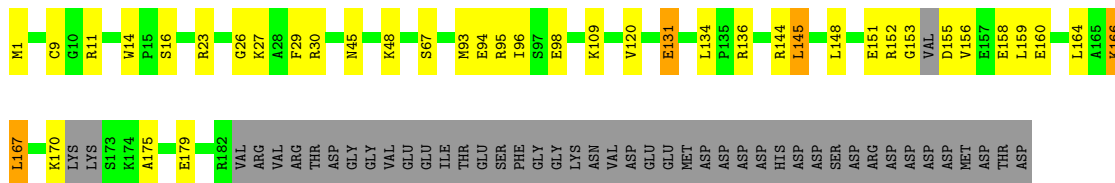


- Molecule 18: RNA methyltransferase nop2-like protein

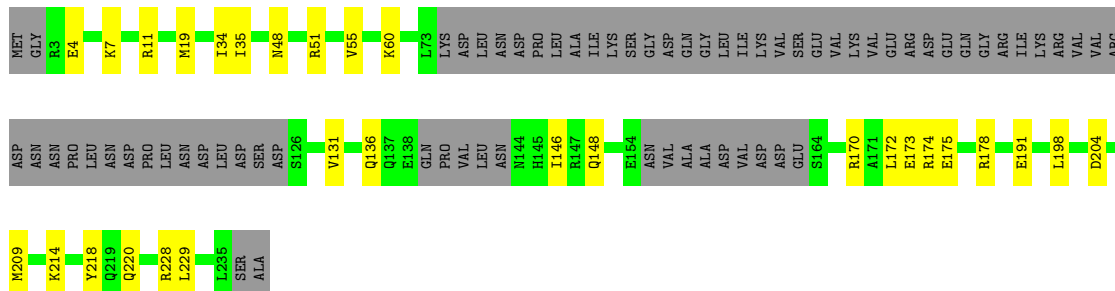




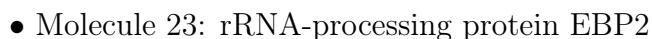
- Molecule 19: Ribosome biogenesis protein RLP24

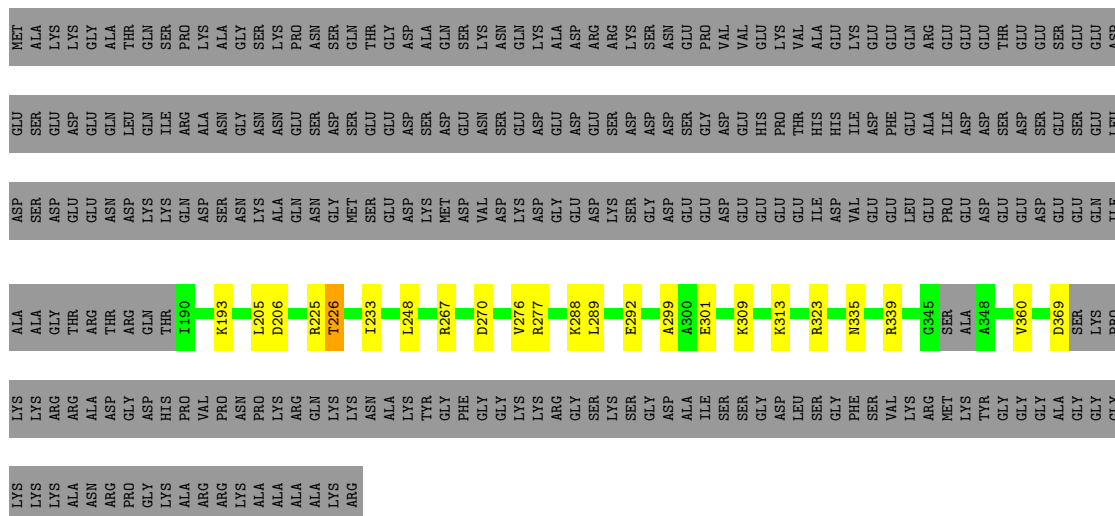


- Molecule 20: Nucleolar protein 16

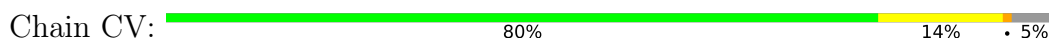


- Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1

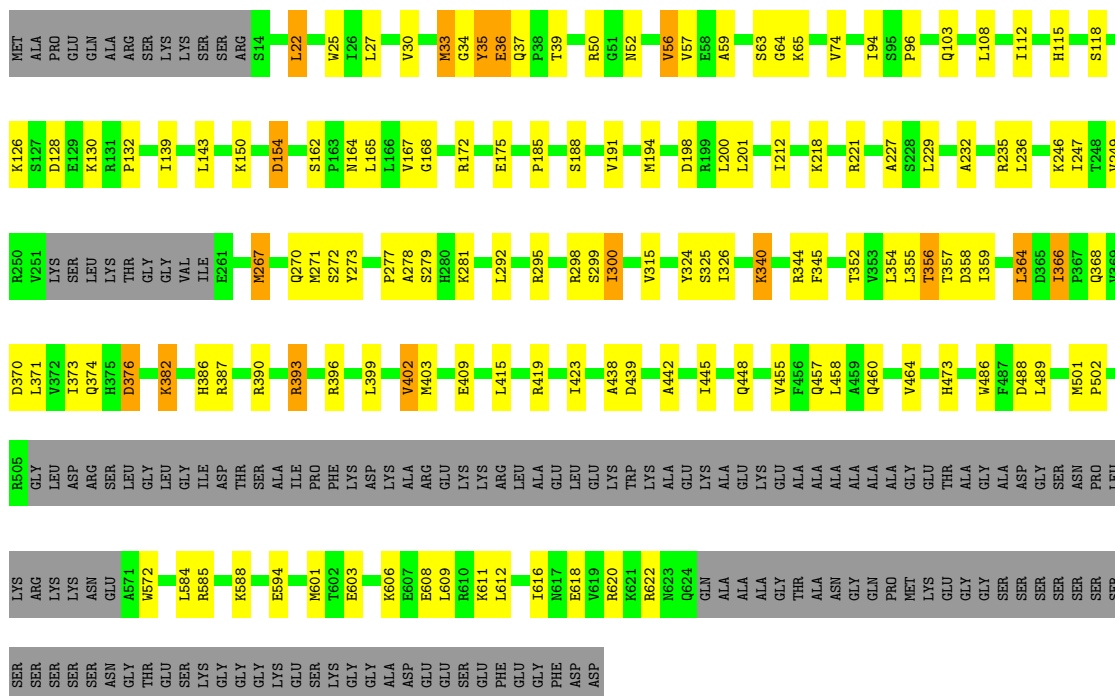




- Molecule 24: Putative 60S ribosomal protein

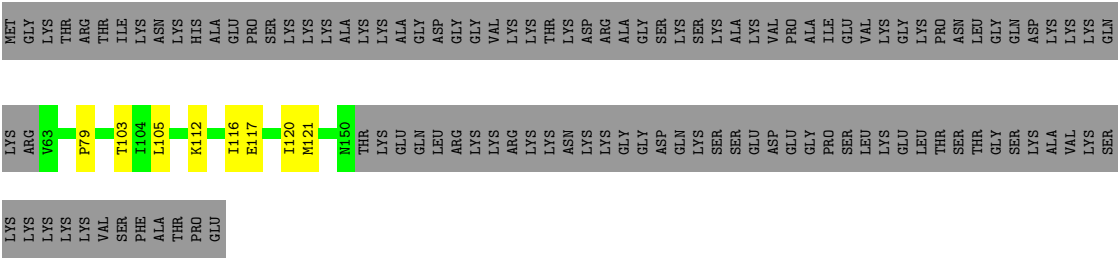


- Molecule 25: ATP-dependent RNA helicase

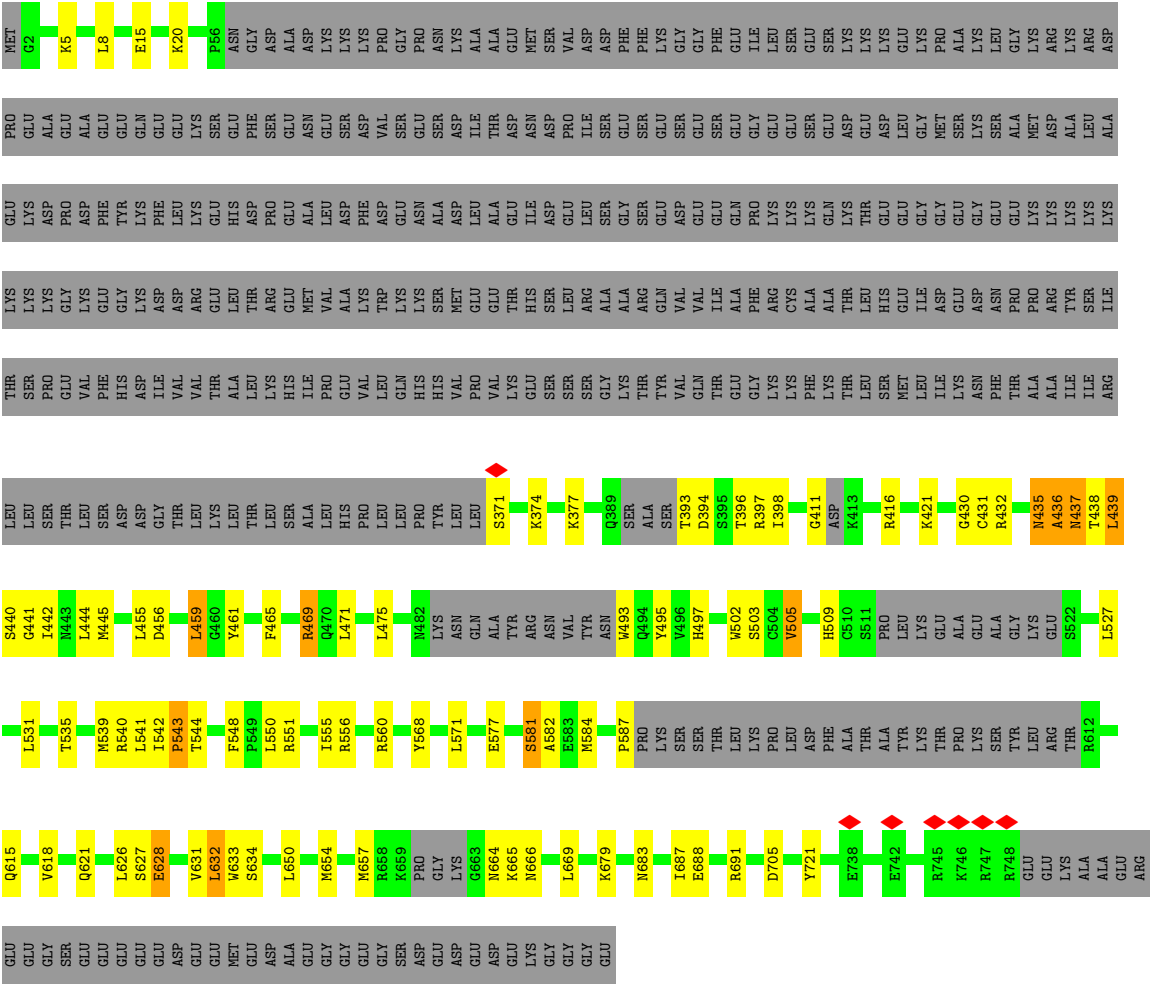
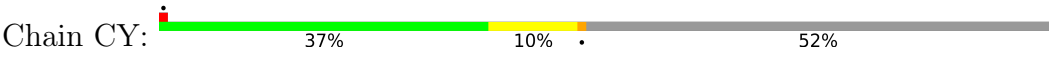


- Molecule 26: 60S ribosomal subunit-like protein

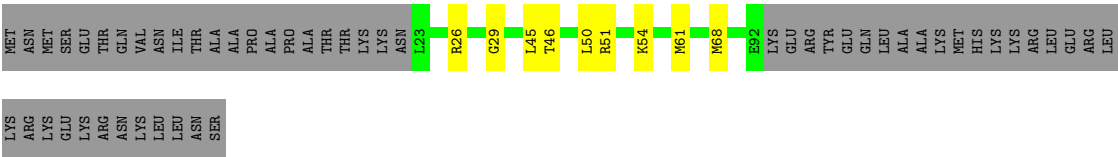




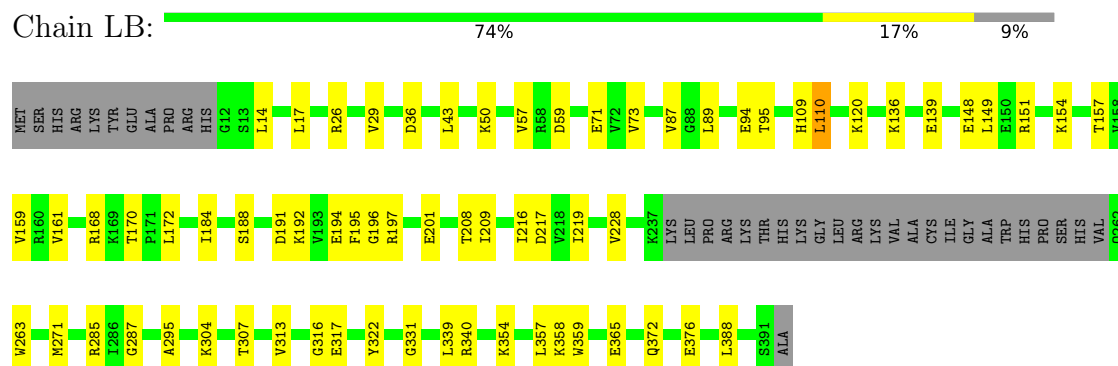
• Molecule 27: Putative NOC2 family protein



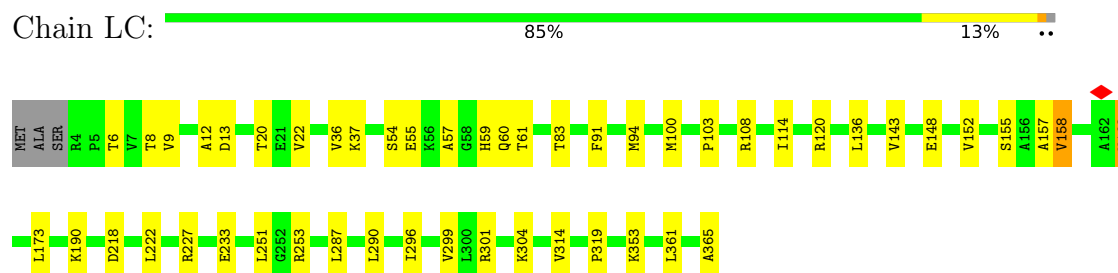
• Molecule 28: rRNA-processing protein



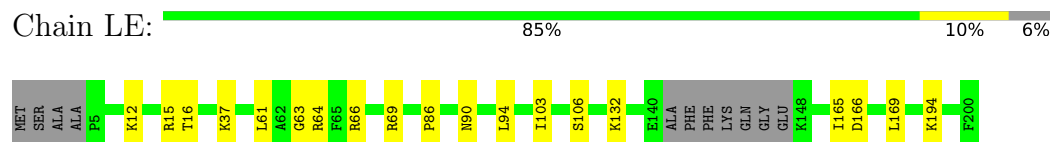
- Molecule 29: 60S ribosomal protein L3-like protein



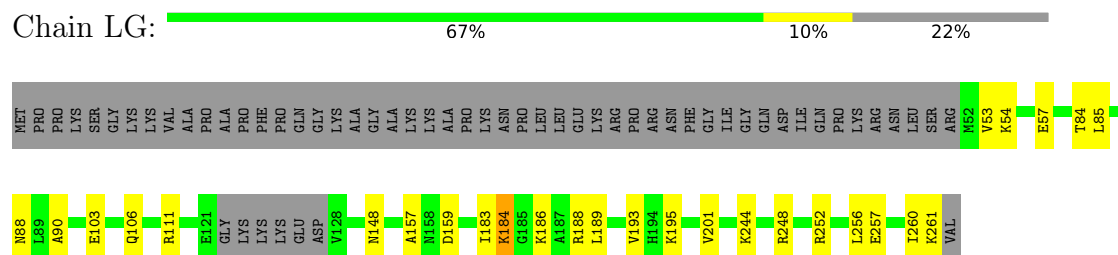
- Molecule 30: 60S ribosomal protein L4-like protein



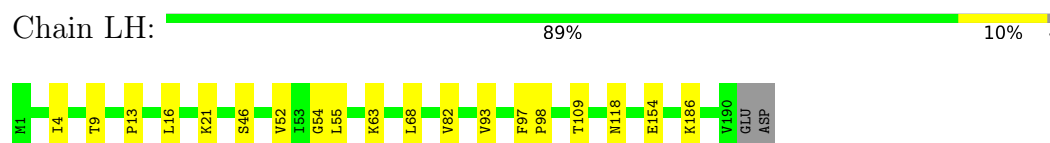
- Molecule 31: 60S ribosomal protein L6



- Molecule 32: 60S ribosomal protein L8

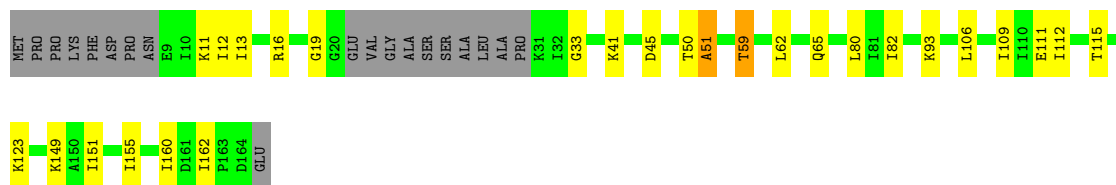


- Molecule 33: 60S ribosomal protein L9-like protein

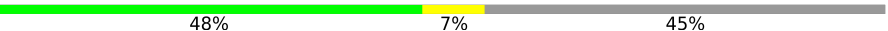


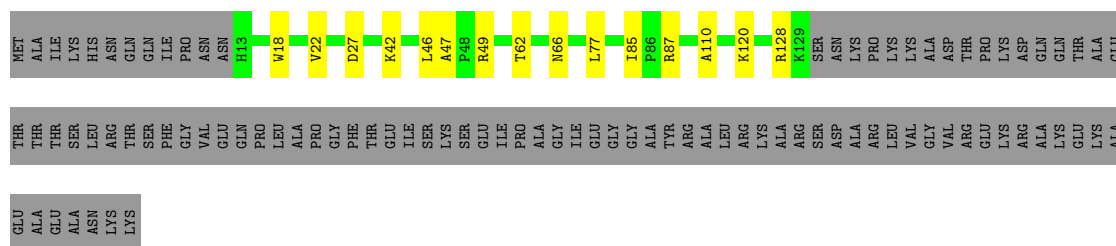
- Molecule 34: 60S ribosomal protein L12-like protein

Chain LK:  72% 15% 12%



- Molecule 35: 60S ribosomal protein L13

Chain LL:  48% 7% 45%



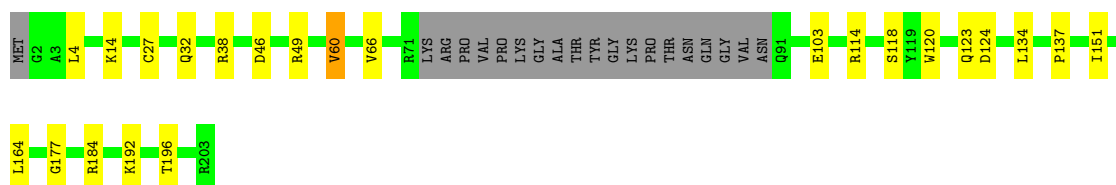
- Molecule 36: 60S ribosomal protein L14-like protein

Chain LM:  88% 8% 4%



- Molecule 37: Ribosomal protein L15

Chain LN:  79% 11% 10%



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

Chain LO:  88% 12%

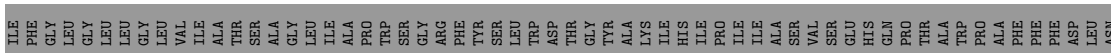


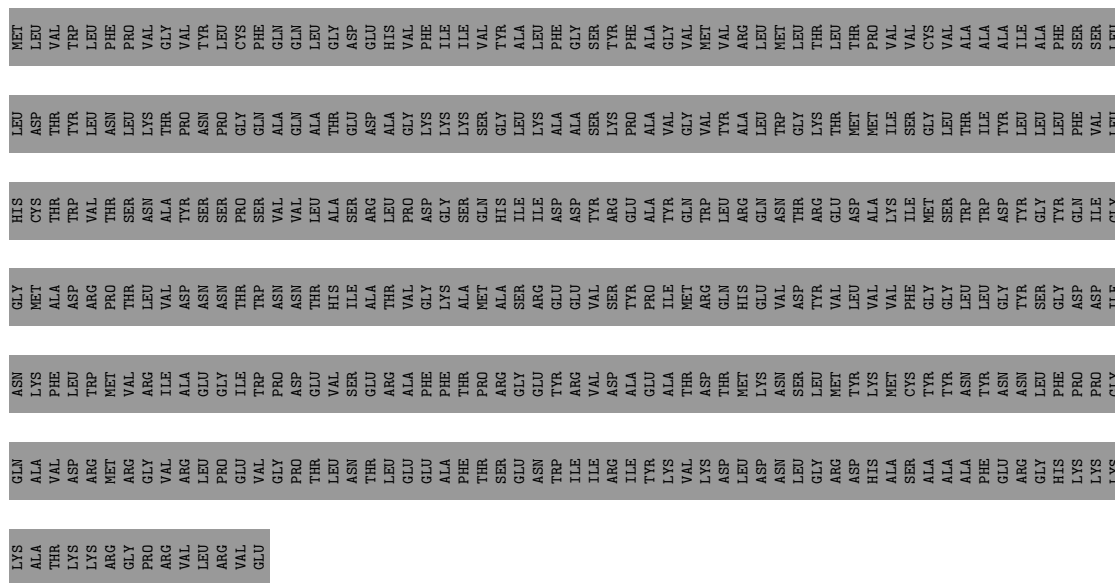
- Molecule 39: 60S ribosomal protein l17-like protein

Chain LP:  82% 9% 10%

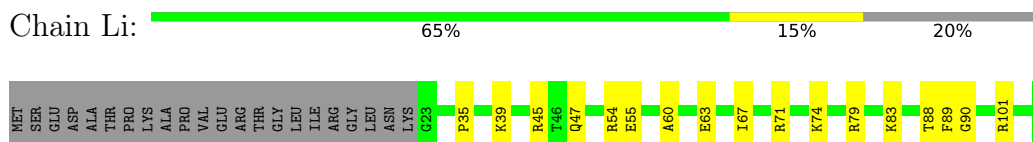




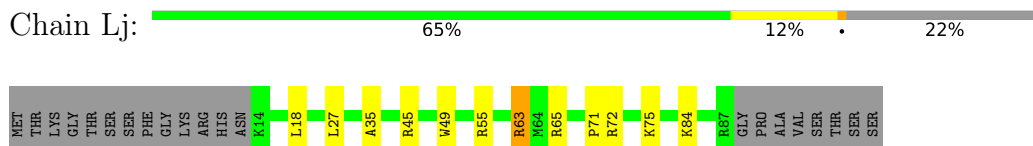




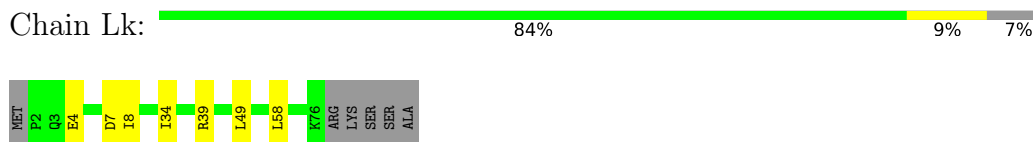
- Molecule 55: 60S ribosomal protein L36



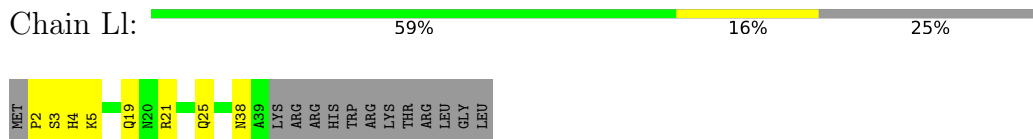
- Molecule 56: Ribosomal protein L37



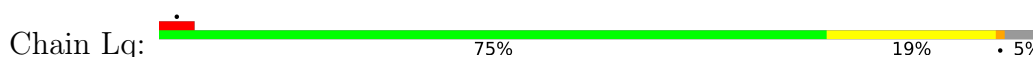
- Molecule 57: 60S ribosomal protein L38-like protein

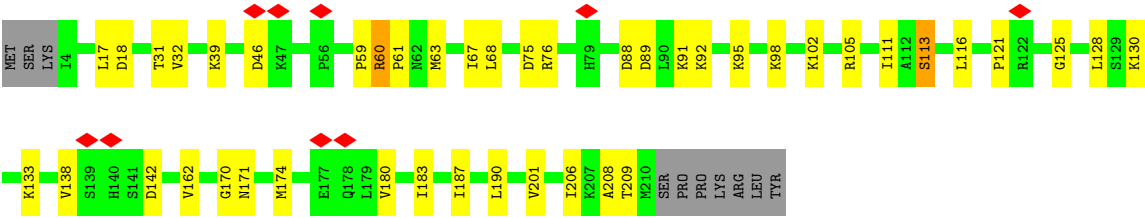


- Molecule 58: 60S ribosomal protein L39



- Molecule 59: Ribosomal protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	173028	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	0.758	Depositor
Minimum map value	-0.259	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	444.78, 444.78, 444.78	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	C1	0.24	0/66718	0.36	1/104004 (0.0%)
2	C2	0.21	0/6097	0.32	0/9499
3	CA	0.23	0/2115	0.43	0/2840
4	CB	0.26	0/2109	0.64	4/2866 (0.1%)
5	CC	0.23	0/5438	0.46	0/7404
6	CD	0.22	0/3543	0.57	2/4824 (0.0%)
7	CE	0.21	0/3760	0.49	2/5068 (0.0%)
8	CF	0.23	0/1982	0.50	0/2671
9	CG	0.24	0/1422	0.44	0/1920
10	CH	0.26	0/4468	0.54	1/6029 (0.0%)
11	CI	0.19	0/1225	0.44	0/1645
12	CJ	0.24	0/4125	0.51	0/5548
13	CK	0.25	1/1863 (0.1%)	0.43	0/2494
14	CL	0.20	0/2178	0.52	0/2983
15	CM	0.21	0/1851	0.49	0/2481
15	LF	0.25	0/2055	0.44	0/2758
16	CN	0.23	0/1881	0.52	0/2560
17	CO	0.20	0/470	0.46	1/619 (0.2%)
18	CP	0.23	0/2594	0.50	1/3514 (0.0%)
19	CQ	0.43	0/1507	0.75	0/1996
20	CR	0.20	0/1369	0.39	0/1828
21	CS	0.19	0/5115	0.48	0/6841
22	CT	0.26	0/3974	0.57	4/5357 (0.1%)
23	CU	0.19	0/1428	0.46	3/1910 (0.2%)
24	CV	0.22	0/1091	0.45	2/1468 (0.1%)
25	CW	0.34	0/4371	0.81	9/5917 (0.2%)
26	CX	0.20	0/705	0.48	0/938
27	CY	0.34	0/3079	0.74	3/4136 (0.1%)
28	Cz	0.15	0/598	0.29	0/785
29	LB	0.24	0/2885	0.48	0/3872
30	LC	0.23	0/2809	0.43	0/3787
31	LE	0.22	0/1502	0.44	0/2020

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LG	0.28	0/1667	0.56	1/2230 (0.0%)
33	LH	0.22	0/1516	0.43	0/2038
34	LK	0.20	0/1124	0.55	0/1507
35	LL	0.22	0/983	0.43	0/1318
36	LM	0.21	0/1120	0.38	0/1507
37	LN	0.24	0/1595	0.41	0/2132
38	LO	0.22	0/1652	0.43	0/2215
39	LP	0.19	0/1367	0.36	0/1838
40	LQ	0.21	0/1033	0.42	0/1391
41	LR	0.25	0/1235	0.49	0/1644
42	LS	0.23	0/1468	0.46	0/1975
43	LT	0.18	0/1033	0.44	0/1389
44	LU	0.17	0/863	0.32	0/1155
45	LV	0.20	0/1013	0.41	0/1361
46	LX	0.18	0/1078	0.34	0/1451
47	LY	0.19	0/1079	0.41	0/1443
48	LZ	0.22	0/1135	0.42	0/1519
49	Lc	0.21	0/740	0.48	0/995
50	Ld	0.21	0/904	0.40	0/1209
51	Le	0.20	0/1043	0.38	0/1389
52	Lf	0.25	0/883	0.41	0/1187
53	Lg	0.24	0/943	0.45	0/1258
54	Lh	0.17	0/1006	0.36	0/1338
55	Li	0.23	0/738	0.43	0/971
56	Lj	0.25	0/606	0.45	0/803
57	Lk	0.28	0/628	0.54	0/835
58	Ll	0.19	0/329	0.47	0/440
59	Lq	0.20	0/1621	0.59	0/2180
All	All	0.24	1/176729 (0.0%)	0.45	34/253300 (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
14	CL	0	1
22	CT	0	1
59	Lq	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	CK	152	THR	C-N	-6.27	1.23	1.33

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	CW	277	PRO	CA-N-CD	-11.12	96.43	112.00
22	CT	146	PRO	CA-N-CD	-10.08	97.88	112.00
7	CE	320	VAL	N-CA-C	-7.55	106.13	113.53
4	CB	103	ASP	CB-CA-C	6.99	123.93	110.17
4	CB	104	PRO	CA-N-CD	-6.31	103.17	112.00
25	CW	168	GLY	CA-C-N	6.12	129.98	120.68
25	CW	168	GLY	C-N-CA	6.12	129.98	120.68
27	CY	632	LEU	CA-CB-CG	6.09	137.63	116.30
25	CW	132	PRO	CA-N-CD	-6.08	103.50	112.00
1	C1	835	G	P-O3'-C3'	6.00	129.21	120.20
25	CW	33	MET	N-CA-C	-5.96	104.86	111.71
7	CE	355	MET	CB-CG-SD	5.79	130.06	112.70
22	CT	146	PRO	N-CD-CG	-5.77	94.54	103.20
18	CP	515	VAL	N-CA-C	-5.76	107.20	112.96
23	CU	360	VAL	N-CA-C	-5.76	107.07	111.62
6	CD	369	MET	CB-CG-SD	5.68	129.74	112.70
23	CU	225	ARG	CA-C-N	5.61	132.25	121.54
23	CU	225	ARG	C-N-CA	5.61	132.25	121.54
25	CW	366	ILE	CB-CA-C	5.58	117.20	110.78
27	CY	539	MET	CB-CG-SD	5.58	129.43	112.70
17	CO	38	MET	CB-CG-SD	5.53	129.30	112.70
10	CH	72	ASP	CB-CA-C	5.50	118.78	111.14
27	CY	543	PRO	CA-N-CD	-5.42	104.42	112.00
6	CD	204	LYS	CA-CB-CG	5.39	124.88	114.10
4	CB	104	PRO	N-CA-CB	-5.38	97.60	103.25
32	LG	193	VAL	N-CA-C	-5.32	104.25	110.05
25	CW	300	ILE	CA-CB-CG1	5.29	119.40	110.40
25	CW	126	LYS	CB-CG-CD	5.21	123.28	111.30
22	CT	318	ASP	CA-C-N	5.12	130.60	122.61
22	CT	318	ASP	C-N-CA	5.12	130.60	122.61
4	CB	129	ASP	CB-CA-C	5.11	118.77	109.83
24	CV	35	LEU	CA-C-N	5.08	131.25	121.54
24	CV	35	LEU	C-N-CA	5.08	131.25	121.54
25	CW	267	MET	CB-CG-SD	5.00	127.71	112.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	CL	223	HIS	Peptide
22	CT	253	VAL	Peptide
59	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	59633	0	30064	410	0
2	C2	5456	0	2762	38	0
3	CA	2069	0	2109	22	0
4	CB	2063	0	2131	36	0
5	CC	5289	0	5222	68	0
6	CD	3468	0	3428	59	0
7	CE	3689	0	3794	43	0
8	CF	1945	0	1965	29	0
9	CG	1396	0	1420	18	0
10	CH	4388	0	4454	66	0
11	CI	1196	0	1202	19	0
12	CJ	4040	0	4087	44	0
13	CK	1835	0	1935	12	0
14	CL	2173	0	1423	11	0
15	CM	1820	0	1938	20	0
15	LF	2017	0	2130	15	0
16	CN	1856	0	1856	28	0
17	CO	468	0	503	10	0
18	CP	2535	0	2549	45	0
19	CQ	1485	0	1549	30	0
20	CR	1354	0	1400	20	0
21	CS	5036	0	5202	64	0
22	CT	3911	0	4023	37	0
23	CU	1415	0	1457	15	0
24	CV	1073	0	1130	10	0
25	CW	4284	0	4419	85	0
26	CX	701	0	742	8	0
27	CY	3035	0	3134	50	0
28	Cz	592	0	640	8	0
29	LB	2829	0	2933	42	0
30	LC	2752	0	2878	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	LE	1475	0	1580	11	0
32	LG	1644	0	1793	19	0
33	LH	1496	0	1575	13	0
34	LK	1112	0	1190	15	0
35	LL	964	0	1041	10	0
36	LM	1101	0	1170	8	0
37	LN	1563	0	1618	14	0
38	LO	1618	0	1714	16	0
39	LP	1345	0	1389	11	0
40	LQ	1021	0	1118	12	0
41	LR	1219	0	1291	8	0
42	LS	1433	0	1496	25	0
43	LT	1014	0	1073	8	0
44	LU	850	0	894	7	0
45	LV	995	0	1055	13	0
46	LX	1062	0	1145	9	0
47	LY	1065	0	1156	8	0
48	LZ	1112	0	1181	18	0
49	Lc	731	0	772	8	0
50	Ld	890	0	940	9	0
51	Le	1025	0	1104	7	0
52	Lf	862	0	891	9	0
53	Lg	930	0	1011	12	0
54	Lh	995	0	1110	14	0
55	Li	731	0	797	13	0
56	Lj	595	0	625	9	0
57	Lk	620	0	680	5	0
58	Ll	322	0	346	5	0
59	Lq	1600	0	1703	29	0
60	CH	32	0	12	0	0
61	CQ	1	0	0	0	0
61	Lj	1	0	0	0	0
62	CW	27	0	12	1	0
63	CW	1	0	0	0	0
All	All	167255	0	137961	1469	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 5.

All (1469) 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)
19:CQ:153:GLY:O	19:CQ:155:ASP:CB	1.66	1.39
10:CH:544:ILE:HD11	10:CH:546:LEU:CG	1.75	1.15
19:CQ:153:GLY:O	19:CQ:155:ASP:HB3	1.48	1.09
10:CH:544:ILE:CD1	10:CH:546:LEU:HG	1.83	1.08
10:CH:544:ILE:CG1	10:CH:546:LEU:HG	1.84	1.08
10:CH:544:ILE:HD11	10:CH:546:LEU:CD1	1.83	1.08
1:C1:3118:A:N6	1:C1:3225:C:H42	1.52	1.07
1:C1:1205:A:N6	1:C1:1267:G:H21	1.51	1.05
1:C1:3118:A:H61	1:C1:3225:C:N4	1.55	1.04
19:CQ:153:GLY:O	19:CQ:155:ASP:HB2	1.57	1.03
27:CY:435:ASN:O	27:CY:437:ASN:N	1.92	1.02
1:C1:407:G:H21	1:C1:1381:A:N6	1.59	1.00
19:CQ:153:GLY:O	19:CQ:155:ASP:CG	2.03	1.00
1:C1:2429:G:H21	1:C1:2450:A:H62	1.12	0.96
1:C1:1955:G:H1	1:C1:2014:U:H3	1.14	0.95
1:C1:407:G:H21	1:C1:1381:A:H61	1.03	0.94
10:CH:544:ILE:HG13	10:CH:546:LEU:HG	1.46	0.94
1:C1:2848:A:H61	1:C1:2871:C:H42	0.95	0.93
10:CH:544:ILE:HD11	10:CH:546:LEU:HD11	1.46	0.93
1:C1:1205:A:H62	1:C1:1267:G:H21	1.05	0.93
1:C1:1205:A:H62	1:C1:1267:G:N2	1.67	0.91
10:CH:544:ILE:HD11	10:CH:546:LEU:HG	1.45	0.90
2:C2:196:G:H1	2:C2:201:U:H3	1.21	0.89
1:C1:2848:A:N6	1:C1:2871:C:H42	1.68	0.89
1:C1:2735:G:H1	1:C1:2741:U:H3	1.21	0.87
10:CH:531:GLU:OE1	10:CH:546:LEU:HD13	1.75	0.86
1:C1:974:G:H1	1:C1:1038:U:H3	0.89	0.86
4:CB:103:ASP:HB3	4:CB:104:PRO:HD2	1.55	0.85
1:C1:2848:A:H61	1:C1:2871:C:N4	1.75	0.84
1:C1:1954:C:N4	1:C1:2015:U:H3	1.75	0.83
1:C1:1877:G:N2	1:C1:1880:A:C6	2.47	0.82
10:CH:544:ILE:CD1	10:CH:546:LEU:CG	2.46	0.82
27:CY:435:ASN:O	27:CY:437:ASN:OD1	1.95	0.82
1:C1:1938:U:H3	1:C1:2045:C:N4	1.80	0.80
1:C1:1954:C:N4	1:C1:2015:U:N3	2.29	0.78
2:C2:185:G:N7	4:CB:169:LYS:NZ	2.32	0.78
6:CD:145:ARG:HB3	6:CD:157:ILE:HD11	1.65	0.78
1:C1:539:G:C6	1:C1:540:A:N6	2.52	0.77
1:C1:2849:U:HO2'	17:CO:2:ALA:N	1.83	0.76
1:C1:1953:A:N6	1:C1:2015:U:C2	2.53	0.76
1:C1:1938:U:N3	1:C1:2045:C:N4	2.35	0.74
1:C1:2387:G:O6	1:C1:2563:G:C2	2.42	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1953:A:N6	1:C1:2015:U:N3	2.37	0.73
55:Li:60:ALA:HB3	55:Li:63:GLU:HG3	1.70	0.72
30:LC:100:MET:HE3	30:LC:103:PRO:HA	1.69	0.72
1:C1:2429:G:N2	1:C1:2450:A:H62	1.87	0.72
5:CC:287:GLU:OE1	32:LG:111:ARG:NH2	2.23	0.72
52:Lf:61:VAL:HG12	52:Lf:62:ARG:HG2	1.71	0.71
10:CH:19:ILE:HG23	10:CH:23:ARG:HH21	1.54	0.71
22:CT:379:LYS:O	22:CT:383:GLN:NE2	2.22	0.71
1:C1:1411:G:OP2	30:LC:108:ARG:NH2	2.25	0.70
1:C1:3118:A:N1	1:C1:3225:C:N3	2.40	0.69
3:CA:150:PRO:HG2	23:CU:193:LYS:HG2	1.73	0.69
1:C1:1205:A:N6	1:C1:1267:G:N2	2.31	0.69
19:CQ:153:GLY:C	19:CQ:155:ASP:CB	2.63	0.69
27:CY:550:LEU:HD12	27:CY:551:ARG:HH21	1.56	0.69
1:C1:796:G:H1	1:C1:906:A:H61	1.39	0.69
1:C1:2429:G:H21	1:C1:2450:A:N6	1.88	0.69
1:C1:66:A:N6	1:C1:75:G:N2	2.40	0.68
1:C1:2848:A:N1	1:C1:2871:C:N3	2.41	0.68
12:CJ:58:THR:HG22	12:CJ:60:SER:H	1.59	0.68
7:CE:525:HIS:CE1	7:CE:527:LEU:HB2	2.29	0.68
14:CL:444:LEU:HA	15:LF:49:VAL:HG21	1.75	0.67
1:C1:2799:G:N2	1:C1:2805:A:C8	2.58	0.67
2:C2:297:C:H1'	2:C2:301:A:H61	1.60	0.67
1:C1:670:U:O4	1:C1:684:G:O6	2.12	0.67
5:CC:519:GLU:OE2	48:LZ:33:LYS:NZ	2.28	0.67
10:CH:170:LEU:HD13	10:CH:242:LEU:HD23	1.77	0.67
34:LK:13:ILE:HD11	34:LK:62:LEU:HD12	1.77	0.67
6:CD:238:LYS:HB3	6:CD:254:ALA:HB3	1.76	0.67
21:CS:499:VAL:HG22	22:CT:183:ARG:HD3	1.77	0.66
32:LG:84:THR:HG21	32:LG:184:LYS:HB2	1.77	0.66
21:CS:119:GLY:H	21:CS:158:LYS:HB3	1.60	0.66
12:CJ:377:GLU:OE2	12:CJ:422:ARG:NH2	2.29	0.66
1:C1:1537:U:O2'	1:C1:1539:A:OP2	2.14	0.66
25:CW:386:HIS:O	25:CW:390:ARG:NH1	2.30	0.65
25:CW:584:LEU:O	25:CW:588:LYS:NZ	2.29	0.65
5:CC:591:ILE:HG22	5:CC:607:SER:HB2	1.79	0.65
1:C1:1850:U:OP1	10:CH:513:LYS:NZ	2.30	0.65
12:CJ:102:ASN:OD1	32:LG:106:GLN:NE2	2.30	0.65
29:LB:228:VAL:HG21	29:LB:271:MET:HE2	1.78	0.65
31:LE:194:LYS:HE2	38:LO:1:MET:HG2	1.77	0.65
1:C1:1536:U:H4'	1:C1:1537:U:H5'	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2729:U:O4	1:C1:2745:G:O6	2.14	0.65
18:CP:446:VAL:HG13	18:CP:447:ILE:HG13	1.78	0.65
25:CW:201:LEU:HD21	25:CW:235:ARG:HB2	1.79	0.65
1:C1:532:C:H42	1:C1:540:A:H61	1.44	0.64
1:C1:532:C:N4	1:C1:540:A:H61	1.95	0.64
1:C1:2416:G:N2	18:CP:286:ASN:O	2.29	0.64
1:C1:1599:U:H5''	12:CJ:48:ARG:HD3	1.79	0.64
10:CH:442:ASP:OD1	10:CH:444:LYS:NZ	2.31	0.64
12:CJ:160:VAL:HG13	12:CJ:164:MET:HE2	1.80	0.64
1:C1:2435:C:C2	1:C1:2437:G:C2	2.85	0.64
10:CH:379:ARG:HH21	16:CN:178:GLY:HA3	1.62	0.64
17:CO:106:ILE:HG23	17:CO:107:VAL:HG23	1.80	0.64
1:C1:308:U:O2'	55:LI:39:LYS:NZ	2.30	0.64
8:CF:57:ARG:HG2	8:CF:65:ILE:HG21	1.79	0.64
24:CV:92:LYS:HG3	15:LF:11:ASP:HB3	1.80	0.64
34:LK:16:ARG:HE	34:LK:59:THR:HG22	1.61	0.64
10:CH:520:ARG:NH1	44:LU:98:ASP:OD1	2.30	0.63
25:CW:74:VAL:HG23	25:CW:139:ILE:HD13	1.81	0.63
29:LB:307:THR:HG21	29:LB:317:GLU:HG2	1.79	0.63
16:CN:106:ASN:ND2	16:CN:150:SER:OG	2.32	0.63
7:CE:161:LYS:NZ	7:CE:264:ASP:OD1	2.32	0.63
18:CP:455:LEU:HD11	18:CP:490:LEU:HD23	1.80	0.63
6:CD:191:LEU:HB2	6:CD:203:TRP:HB2	1.81	0.63
15:CM:67:GLU:OE2	15:CM:70:ARG:NH1	2.32	0.63
25:CW:139:ILE:HA	25:CW:164:ASN:HD21	1.64	0.63
4:CB:105:GLN:HB2	4:CB:129:ASP:HB3	1.81	0.63
6:CD:159:ASN:HB3	6:CD:165:ILE:HD11	1.79	0.63
1:C1:2959:C:OP1	29:LB:26:ARG:NH2	2.31	0.63
1:C1:1271:G:H5''	8:CF:8:ARG:HH21	1.63	0.62
10:CH:230:GLU:HG3	34:LK:93:LYS:HE3	1.81	0.62
18:CP:508:ILE:HB	18:CP:581:PHE:HB2	1.80	0.62
1:C1:690:G:O6	3:CA:282:ARG:NH1	2.31	0.62
1:C1:384:G:H22	1:C1:389:A:H62	1.48	0.62
1:C1:864:A:H61	9:CG:122:TRP:HD1	1.45	0.62
13:CK:153:LYS:NZ	13:CK:216:THR:OG1	2.31	0.62
1:C1:974:G:O6	1:C1:1038:U:O4	2.17	0.62
2:C2:217:G:O2'	11:CI:217:ARG:NH2	2.33	0.62
10:CH:439:GLU:OE1	19:CQ:1:MET:N	2.32	0.62
12:CJ:252:LYS:NZ	12:CJ:274:GLU:OE1	2.30	0.62
1:C1:2387:G:O6	1:C1:2563:G:N2	2.32	0.62
10:CH:544:ILE:HD11	10:CH:546:LEU:CD2	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:425:ILE:HG23	18:CP:430:VAL:HB	1.81	0.62
19:CQ:153:GLY:C	19:CQ:155:ASP:HB3	2.24	0.62
2:C2:219:A:OP1	11:CI:222:LYS:NZ	2.24	0.62
48:LZ:94:VAL:HG13	48:LZ:95:ILE:HG23	1.80	0.62
1:C1:1437:U:O2	50:Ld:34:LYS:NZ	2.32	0.62
10:CH:531:GLU:OE1	10:CH:546:LEU:CD1	2.48	0.61
1:C1:3262:G:O2'	50:Ld:50:LYS:NZ	2.28	0.61
2:C2:229:U:H3	2:C2:288:G:H1	1.46	0.61
5:CC:229:LEU:HD21	21:CS:667:ALA:HB1	1.80	0.61
1:C1:642:C:H2'	1:C1:643:A:H8	1.66	0.61
6:CD:51:ASN:ND2	6:CD:58:THR:O	2.32	0.61
49:Lc:12:SER:O	49:Lc:16:LYS:NZ	2.33	0.61
6:CD:240:ILE:HB	6:CD:252:TRP:HB2	1.83	0.61
2:C2:58:G:O6	56:Lj:63:ARG:NH2	2.34	0.61
29:LB:71:GLU:OE2	29:LB:358:LYS:NZ	2.33	0.61
29:LB:217:ASP:OD2	29:LB:340:ARG:NH1	2.34	0.61
7:CE:525:HIS:HE1	7:CE:527:LEU:HB2	1.64	0.61
16:CN:233:ILE:HG22	16:CN:237:MET:HG2	1.83	0.61
1:C1:407:G:N2	1:C1:1381:A:N6	2.41	0.60
1:C1:68:C:OP2	1:C1:293:G:N2	2.34	0.60
1:C1:1243:G:O6	8:CF:54:LYS:NZ	2.34	0.60
16:CN:53:ILE:HG23	16:CN:76:THR:HG22	1.83	0.60
22:CT:444:GLU:HG3	26:CX:121:MET:HG2	1.82	0.60
1:C1:1206:C:O2'	8:CF:8:ARG:NH2	2.35	0.60
20:CR:173:GLU:OE2	54:Lh:124:LYS:NZ	2.34	0.60
25:CW:601:MET:HE1	25:CW:606:LYS:HG2	1.84	0.60
15:CM:118:ASN:ND2	15:CM:248:MET:SD	2.73	0.60
2:C2:95:G:OP2	56:Lj:72:ARG:NH1	2.34	0.60
42:LS:6:GLU:HG2	42:LS:64:ILE:HD12	1.83	0.60
1:C1:204:A:OP1	30:LC:227:ARG:NH1	2.35	0.60
25:CW:300:ILE:HG22	25:CW:354:LEU:HB3	1.84	0.60
1:C1:745:U:O2	1:C1:749:C:N3	2.34	0.60
5:CC:801:MET:HE1	6:CD:363:SER:HB2	1.84	0.60
1:C1:2056:C:H2'	1:C1:2057:A:H8	1.67	0.60
5:CC:416:VAL:HG11	15:CM:20:LYS:HE2	1.84	0.60
18:CP:267:LEU:HD11	18:CP:282:GLU:HG2	1.83	0.60
19:CQ:179:GLU:OE2	50:Ld:86:ARG:NH1	2.35	0.60
21:CS:53:CYS:HB2	21:CS:118:ASP:H	1.67	0.60
6:CD:43:ARG:HB2	6:CD:72:LEU:HD12	1.84	0.59
1:C1:2433:U:H2'	1:C1:2436:G:H22	1.67	0.59
1:C1:2801:U:H4'	14:CL:51:LYS:HG3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:299:U:OP2	11:CI:291:ARG:NH1	2.35	0.59
5:CC:697:ARG:HE	5:CC:712:THR:HG22	1.66	0.59
19:CQ:109:LYS:HZ3	29:LB:388:LEU:HD11	1.68	0.59
1:C1:539:G:O6	1:C1:540:A:N6	2.35	0.59
1:C1:1239:C:OP1	34:LK:123:LYS:NZ	2.35	0.59
1:C1:1547:A:OP1	15:CM:23:LYS:NZ	2.36	0.59
1:C1:933:A:N3	1:C1:1096:U:O2'	2.35	0.59
12:CJ:36:LEU:HD23	12:CJ:72:LEU:HD13	1.82	0.59
27:CY:540:ARG:NH1	27:CY:577:GLU:OE1	2.36	0.59
48:LZ:8:ARG:NH1	48:LZ:82:THR:O	2.35	0.59
25:CW:370:ASP:OD1	25:CW:396:ARG:NH2	2.31	0.59
59:Lq:121:PRO:HA	59:Lq:125:GLY:HA3	1.84	0.59
1:C1:1622:A:H5'	1:C1:1801:C:H5'	1.84	0.59
5:CC:414:PRO:HG2	15:CM:20:LYS:HB2	1.85	0.59
25:CW:57:VAL:HG22	25:CW:247:ILE:HD11	1.84	0.59
1:C1:1205:A:C5	1:C1:1267:G:N2	2.71	0.59
27:CY:584:MET:O	27:CY:664:ASN:ND2	2.35	0.59
4:CB:106:ARG:HA	4:CB:109:LYS:HE2	1.84	0.59
5:CC:459:VAL:HG12	5:CC:470:THR:HG22	1.85	0.59
5:CC:510:THR:O	5:CC:539:SER:OG	2.17	0.59
5:CC:594:ILE:HG12	5:CC:605:THR:HG22	1.85	0.59
1:C1:3122:U:OP1	52:Lf:65:LYS:NZ	2.36	0.58
6:CD:17:VAL:HG12	6:CD:91:LEU:HB2	1.85	0.58
10:CH:544:ILE:CD1	10:CH:546:LEU:CD2	2.81	0.58
13:CK:104:SER:O	13:CK:108:ASN:ND2	2.33	0.58
1:C1:858:C:H5'	9:CG:156:ARG:HH22	1.68	0.58
1:C1:1386:G:OP2	51:Le:12:LYS:NZ	2.37	0.58
5:CC:142:ASP:HB3	5:CC:148:ARG:HB2	1.86	0.58
9:CG:166:ARG:NH1	9:CG:169:ASP:OD1	2.36	0.58
32:LG:103:GLU:OE2	32:LG:111:ARG:NH1	2.37	0.58
48:LZ:26:GLN:HB3	48:LZ:41:LEU:HD12	1.83	0.58
7:CE:135:THR:OG1	7:CE:136:GLU:N	2.37	0.58
21:CS:661:THR:HG23	21:CS:711:THR:HG23	1.84	0.58
1:C1:1371:G:H5''	51:Le:102:SER:HB3	1.85	0.58
19:CQ:153:GLY:C	19:CQ:155:ASP:HB2	2.27	0.58
25:CW:52:ASN:O	25:CW:221:ARG:NH1	2.36	0.58
1:C1:1903:U:C2	1:C1:2072:G:C2	2.92	0.58
34:LK:11:LYS:NZ	34:LK:12:ILE:O	2.37	0.58
52:Lf:34:ILE:HG12	52:Lf:102:ILE:HD13	1.85	0.58
1:C1:663:G:O2'	1:C1:665:G:O2'	2.22	0.58
46:LX:79:PRO:HD2	54:Lh:39:ILE:HG21	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:404:G:N3	39:LP:118:GLN:NE2	2.51	0.58
3:CA:91:PHE:HB3	3:CA:103:TRP:HB2	1.84	0.58
11:CI:191:ILE:HG13	11:CI:260:CYS:HB3	1.85	0.58
10:CH:177:VAL:HG23	10:CH:254:ASP:HB2	1.85	0.58
1:C1:1634:G:N7	22:CT:365:LYS:NZ	2.51	0.57
2:C2:59:A:N7	46:LX:69:ARG:NH2	2.51	0.57
7:CE:539:VAL:HA	7:CE:550:PRO:HG3	1.86	0.57
48:LZ:50:SER:HB2	48:LZ:64:ARG:HB3	1.85	0.57
19:CQ:45:ASN:HB3	19:CQ:48:LYS:HG3	1.85	0.57
27:CY:531:LEU:O	27:CY:535:THR:OG1	2.21	0.57
38:LO:11:ASP:HB2	38:LO:119:LYS:HB3	1.86	0.57
59:Lq:67:ILE:HG22	59:Lq:111:ILE:HB	1.86	0.57
1:C1:1694:A:OP2	25:CW:218:LYS:NZ	2.32	0.57
18:CP:385:LEU:HB3	18:CP:453:VAL:HG12	1.86	0.57
8:CF:42:VAL:HG13	8:CF:224:LEU:HB2	1.87	0.57
38:LO:35:VAL:HG22	38:LO:105:LYS:HB2	1.86	0.57
1:C1:1045:G:O2'	1:C1:1079:G:N2	2.37	0.57
2:C2:55:U:OP1	20:CR:11:ARG:NH1	2.38	0.57
5:CC:270:PRO:HB3	32:LG:148:ASN:HA	1.86	0.57
8:CF:41:PHE:HB2	8:CF:103:LEU:HB3	1.86	0.57
18:CP:387:MET:HE3	18:CP:455:LEU:HD13	1.86	0.57
1:C1:213:G:C6	1:C1:1371:G:C2	2.92	0.57
1:C1:826:G:N2	1:C1:829:A:OP2	2.36	0.57
1:C1:1903:U:C2	1:C1:2072:G:N1	2.72	0.57
25:CW:96:PRO:HG3	25:CW:200:LEU:HG	1.86	0.57
27:CY:503:SER:OG	27:CY:560:ARG:NH1	2.38	0.57
37:LN:177:GLY:O	37:LN:184:ARG:NH1	2.37	0.57
57:Lk:7:ASP:OD1	57:Lk:7:ASP:N	2.36	0.57
1:C1:3144:C:OP1	38:LO:178:ARG:NH1	2.37	0.57
44:LU:40:GLU:OE1	44:LU:64:GLN:NE2	2.35	0.57
7:CE:523:ALA:HA	7:CE:533:VAL:HG21	1.87	0.57
25:CW:185:PRO:HD2	25:CW:188:SER:HB3	1.87	0.57
1:C1:429:G:O6	24:CV:134:ARG:NH2	2.38	0.57
5:CC:233:ARG:NH2	21:CS:650:PRO:O	2.37	0.57
14:CL:61:TYR:OH	42:LS:130:GLU:OE1	2.23	0.57
21:CS:128:VAL:HG11	45:LV:65:LYS:HA	1.85	0.57
21:CS:134:GLN:NE2	21:CS:158:LYS:O	2.38	0.57
1:C1:868:G:H2'	1:C1:869:A:H8	1.70	0.57
1:C1:1925:A:OP1	25:CW:172:ARG:NH2	2.36	0.57
1:C1:3152:G:O2'	42:LS:163:LYS:NZ	2.36	0.57
27:CY:581:SER:OG	27:CY:582:ALA:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:693:SER:OG	5:CC:695:ASP:OD1	2.23	0.56
8:CF:202:ASP:OD1	8:CF:203:SER:N	2.38	0.56
31:LE:86:PRO:HB3	31:LE:166:ASP:HB2	1.86	0.56
15:LF:221:ARG:NH1	15:LF:232:GLY:O	2.37	0.56
9:CG:169:ASP:OD2	13:CK:163:ARG:NH2	2.38	0.56
11:CI:204:ARG:NH2	11:CI:277:ASN:OD1	2.38	0.56
5:CC:524:MET:HB3	5:CC:581:VAL:HG12	1.88	0.56
10:CH:392:LYS:HE3	16:CN:1:MET:HE1	1.86	0.56
59:Lq:171:ASN:H	59:Lq:174:MET:HE2	1.70	0.56
15:CM:145:PRO:HA	15:CM:242:ASN:HD21	1.70	0.56
25:CW:618:GLU:OE2	25:CW:618:GLU:N	2.37	0.56
8:CF:227:TRP:HB2	8:CF:234:VAL:HG12	1.86	0.56
19:CQ:153:GLY:O	19:CQ:155:ASP:OD1	2.23	0.56
21:CS:261:PHE:O	21:CS:324:ARG:NH1	2.38	0.56
21:CS:364:LEU:HG	41:LR:159:MET:HE1	1.88	0.56
59:Lq:76:ARG:NH1	59:Lq:142:ASP:O	2.38	0.56
1:C1:66:A:H61	1:C1:75:G:N2	2.02	0.56
10:CH:232:ASN:HB3	10:CH:235:GLU:H	1.69	0.56
11:CI:298:SER:HB2	11:CI:301:GLN:HG3	1.88	0.56
21:CS:146:THR:HA	21:CS:201:PHE:HE2	1.70	0.56
6:CD:367:ILE:HB	6:CD:384:LEU:HB2	1.87	0.56
1:C1:1877:G:C2	1:C1:1880:A:N6	2.74	0.56
7:CE:290:ARG:O	7:CE:312:ARG:NH1	2.38	0.56
15:CM:113:ARG:NH2	15:CM:208:LEU:O	2.38	0.56
1:C1:1940:G:H2'	1:C1:1941:G:C8	2.40	0.56
22:CT:632:THR:OG1	22:CT:635:ARG:NH2	2.39	0.56
56:Lj:63:ARG:HD3	56:Lj:65:ARG:HG3	1.88	0.56
21:CS:208:ASP:OD2	21:CS:210:ARG:NH1	2.39	0.56
25:CW:115:HIS:HB3	25:CW:118:SER:HB2	1.87	0.56
25:CW:344:ARG:HH22	25:CW:352:THR:HG21	1.70	0.56
1:C1:2306:U:H2'	1:C1:2307:A:H8	1.71	0.55
14:CL:223:HIS:O	14:CL:225:VAL:N	2.32	0.55
35:LL:62:THR:O	35:LL:66:ASN:ND2	2.39	0.55
1:C1:3283:G:H21	1:C1:3302:A:H2	1.55	0.55
15:CM:186:CYS:SG	15:CM:187:ILE:N	2.79	0.55
25:CW:299:SER:HB3	25:CW:371:LEU:HB3	1.88	0.55
29:LB:94:GLU:HG3	29:LB:157:THR:HG21	1.87	0.55
1:C1:2766:A:N6	13:CK:205:SER:O	2.40	0.55
42:LS:80:ARG:HH11	42:LS:89:ASN:HD21	1.53	0.55
1:C1:1577:G:OP2	53:Lg:32:ARG:NH2	2.39	0.55
5:CC:784:ARG:NH1	6:CD:297:THR:O	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:295:ILE:O	6:CD:323:ARG:NH1	2.39	0.55
10:CH:379:ARG:NH2	16:CN:177:LEU:O	2.40	0.55
36:LM:54:ARG:HD3	42:LS:70:LEU:HD23	1.88	0.55
48:LZ:69:PRO:HD3	48:LZ:114:LYS:HG3	1.88	0.55
27:CY:666:ASN:HB3	27:CY:669:LEU:HB3	1.88	0.55
38:LO:129:LEU:HD11	42:LS:170:PRO:HG2	1.89	0.55
54:Lh:68:ARG:HH22	54:Lh:84:ASP:HB3	1.71	0.55
45:LV:85:LYS:HD2	45:LV:86:PRO:HD2	1.89	0.55
1:C1:978:A:N6	1:C1:1032:U:O4	2.39	0.55
1:C1:1052:U:O4	1:C1:1071:G:O6	2.24	0.55
1:C1:1116:G:OP1	23:CU:313:LYS:NZ	2.40	0.55
1:C1:1217:U:H4'	1:C1:1218:G:H5'	1.89	0.55
11:CI:198:PHE:HA	11:CI:202:GLU:HG3	1.88	0.55
23:CU:288:LYS:NZ	23:CU:292:GLU:OE2	2.40	0.55
30:LC:36:VAL:HG21	30:LC:251:LEU:HD21	1.87	0.55
1:C1:1938:U:O2	1:C1:2045:C:N3	2.40	0.55
12:CJ:376:ARG:HA	12:CJ:401:LEU:HD21	1.89	0.55
6:CD:342:LEU:HA	6:CD:362:THR:HA	1.89	0.55
22:CT:497:ASP:N	22:CT:497:ASP:OD1	2.39	0.55
25:CW:616:ILE:HG22	25:CW:620:ARG:HD3	1.89	0.55
1:C1:243:G:N2	20:CR:191:GLU:OE2	2.41	0.54
4:CB:42:ARG:NH2	4:CB:46:LYS:O	2.40	0.54
31:LE:63:GLY:O	31:LE:66:ARG:NH1	2.40	0.54
4:CB:281:PHE:HB2	4:CB:293:ILE:HB	1.89	0.54
25:CW:22:LEU:HD13	25:CW:27:LEU:HD21	1.87	0.54
25:CW:139:ILE:HD11	25:CW:165:LEU:HD22	1.89	0.54
25:CW:603:GLU:HA	25:CW:606:LYS:HG3	1.90	0.54
1:C1:144:U:OP2	37:LN:49:ARG:NH2	2.40	0.54
1:C1:3066:G:OP1	13:CK:23:ARG:NE	2.37	0.54
29:LB:285:ARG:HH11	29:LB:357:LEU:HD12	1.73	0.54
59:Lq:187:ILE:HD13	59:Lq:190:LEU:HD21	1.89	0.54
5:CC:697:ARG:HD2	5:CC:714:ARG:HG3	1.88	0.54
12:CJ:411:SER:HA	12:CJ:450:TYR:HE2	1.72	0.54
25:CW:298:ARG:NH1	25:CW:345:PHE:O	2.39	0.54
42:LS:66:GLU:HG3	42:LS:98:SER:HB2	1.89	0.54
17:CO:92:GLY:O	29:LB:151:ARG:NH2	2.39	0.54
1:C1:1283:A:OP2	13:CK:48:LYS:NZ	2.41	0.54
1:C1:1784:C:H2'	1:C1:1785:G:H8	1.72	0.54
1:C1:1947:G:H2'	1:C1:1948:G:C8	2.42	0.54
6:CD:317:SER:OG	6:CD:318:GLN:N	2.40	0.54
10:CH:401:ARG:HD2	16:CN:43:GLN:HG3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:410:GLU:O	12:CJ:453:ARG:NH1	2.40	0.54
17:CO:13:ASN:OD1	17:CO:16:ARG:NH2	2.41	0.54
4:CB:282:TYR:HB3	4:CB:290:ALA:HB1	1.88	0.54
5:CC:171:THR:OG1	5:CC:188:TYR:O	2.24	0.54
8:CF:21:GLU:N	8:CF:21:GLU:OE1	2.38	0.54
1:C1:1620:C:O2	5:CC:654:ARG:NH1	2.40	0.54
1:C1:2394:A:C6	1:C1:2556:G:C6	2.96	0.54
5:CC:336:ASN:OD1	5:CC:336:ASN:N	2.41	0.54
6:CD:24:PRO:HA	6:CD:27:GLU:HG2	1.89	0.54
19:CQ:175:ALA:HA	50:Ld:104:VAL:HA	1.90	0.54
36:LM:121:MET:HE2	36:LM:125:LYS:HE3	1.89	0.54
41:LR:32:ILE:HD13	41:LR:44:LEU:HD13	1.90	0.54
1:C1:3161:C:O2'	39:LP:181:ARG:NH2	2.41	0.54
7:CE:223:ARG:NH2	7:CE:246:ASP:OD1	2.38	0.54
25:CW:358:ASP:OD1	25:CW:387:ARG:NH2	2.41	0.54
37:LN:60:VAL:HG22	37:LN:134:LEU:HB2	1.90	0.54
2:C2:110:C:H42	56:Lj:27:LEU:HD22	1.73	0.54
4:CB:62:ILE:HG21	4:CB:255:LEU:HD11	1.90	0.54
5:CC:391:ARG:NH2	15:CM:176:GLU:OE2	2.41	0.54
5:CC:449:PHE:HB2	5:CC:797:ALA:HB3	1.90	0.54
7:CE:376:LEU:HD21	7:CE:497:LEU:HD11	1.90	0.54
10:CH:539:VAL:HG11	44:LU:33:ILE:HG22	1.88	0.54
12:CJ:383:LEU:HD21	12:CJ:461:VAL:HG11	1.90	0.54
16:CN:107:VAL:HG23	16:CN:108:ILE:HG13	1.90	0.54
1:C1:1698:G:OP1	41:LR:110:ARG:NH1	2.41	0.53
1:C1:1924:A:H1'	1:C1:1925:A:H5'	1.90	0.53
5:CC:487:GLN:OE1	5:CC:490:SER:OG	2.23	0.53
10:CH:365:MET:HA	10:CH:368:ILE:HG22	1.88	0.53
25:CW:128:ASP:OD1	25:CW:128:ASP:N	2.40	0.53
27:CY:435:ASN:O	27:CY:436:ALA:C	2.51	0.53
53:Lg:24:ILE:HD13	53:Lg:34:LEU:HG	1.90	0.53
1:C1:642:C:H2'	1:C1:643:A:C8	2.44	0.53
8:CF:43:PHE:HB3	8:CF:223:LEU:HD23	1.89	0.53
21:CS:140:HIS:HA	21:CS:143:LYS:HD2	1.90	0.53
5:CC:411:TYR:HE2	12:CJ:34:ARG:HD2	1.73	0.53
33:LH:98:PRO:O	33:LH:118:ASN:ND2	2.41	0.53
46:LX:149:ALA:HA	46:LX:153:LEU:HB2	1.88	0.53
1:C1:1103:U:OP1	14:CL:33:ARG:NH2	2.40	0.53
18:CP:520:ASN:OD1	18:CP:520:ASN:N	2.41	0.53
20:CR:209:MET:HE1	20:CR:229:LEU:HD11	1.90	0.53
29:LB:29:VAL:HA	29:LB:219:ILE:HD13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:532:C:H42	1:C1:540:A:N6	2.05	0.53
1:C1:958:A:H61	1:C1:1086:U:H3	1.56	0.53
1:C1:1757:G:O2'	1:C1:1759:G:OP2	2.22	0.53
27:CY:587:PRO:HB3	27:CY:664:ASN:HA	1.91	0.53
37:LN:114:ARG:HG2	37:LN:137:PRO:HG3	1.91	0.53
1:C1:447:C:O2	31:LE:15:ARG:NH1	2.41	0.53
4:CB:67:THR:HG23	4:CB:279:ARG:HB3	1.89	0.53
18:CP:337:TRP:HE3	18:CP:374:MET:HE1	1.73	0.53
25:CW:191:VAL:HG12	25:CW:221:ARG:HB2	1.90	0.53
30:LC:60:GLN:OE1	56:Lj:55:ARG:NH2	2.41	0.53
40:LQ:90:VAL:HG13	40:LQ:94:ARG:HD2	1.90	0.53
9:CG:55:ILE:HD11	18:CP:407:VAL:HG11	1.90	0.53
24:CV:31:ASP:HB3	24:CV:34:ASN:HB2	1.90	0.53
1:C1:662:C:O2'	1:C1:666:U:OP1	2.25	0.53
5:CC:589:SER:OG	5:CC:607:SER:OG	2.25	0.53
6:CD:246:ASP:OD1	6:CD:246:ASP:N	2.42	0.53
6:CD:369:MET:HB2	6:CD:382:MET:HB3	1.90	0.53
10:CH:541:THR:HB	10:CH:546:LEU:HD12	1.90	0.53
21:CS:257:SER:HB3	21:CS:259:ILE:HD12	1.91	0.53
42:LS:162:LYS:HG3	52:Lf:38:ASP:HB2	1.91	0.53
1:C1:1903:U:N3	1:C1:2072:G:C6	2.77	0.53
37:LN:46:ASP:OD1	37:LN:46:ASP:N	2.41	0.53
48:LZ:71:ILE:HD11	48:LZ:106:ARG:HB2	1.91	0.53
2:C2:143:U:OP1	37:LN:38:ARG:NH2	2.36	0.53
2:C2:194:C:OP2	11:CI:316:ARG:NH2	2.41	0.52
1:C1:1903:U:N3	1:C1:2072:G:N1	2.57	0.52
1:C1:2057:A:H2'	1:C1:2058:A:C8	2.45	0.52
1:C1:2891:A:OP2	45:LV:6:ARG:NH1	2.42	0.52
25:CW:143:LEU:HA	25:CW:167:VAL:HG23	1.91	0.52
25:CW:354:LEU:HG	25:CW:356:THR:HG22	1.90	0.52
33:LH:9:THR:HG23	33:LH:52:VAL:HG13	1.91	0.52
1:C1:727:C:H2'	1:C1:728:A:H8	1.74	0.52
1:C1:796:G:H1	1:C1:906:A:N6	2.06	0.52
1:C1:1046:A:H61	1:C1:1074:C:H2'	1.74	0.52
1:C1:3110:C:N4	1:C1:3337:C:OP2	2.42	0.52
10:CH:544:ILE:CD1	10:CH:546:LEU:HD21	2.39	0.52
30:LC:361:LEU:HD11	43:LT:148:PRO:HG2	1.90	0.52
1:C1:1592:A:OP2	57:Lk:39:ARG:NH1	2.41	0.52
44:LU:28:PRO:HG2	44:LU:112:LEU:HB3	1.91	0.52
57:Lk:34:ILE:HG23	57:Lk:49:LEU:HB2	1.91	0.52
3:CA:30:ARG:NH2	23:CU:206:ASP:OD1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:240:ARG:HH11	32:LG:260:ILE:HG21	1.75	0.52
16:CN:126:GLU:OE1	16:CN:139:ARG:NH1	2.42	0.52
8:CF:233:GLU:OE1	8:CF:233:GLU:N	2.43	0.52
12:CJ:396:GLY:HA2	12:CJ:405:ALA:HB1	1.91	0.52
35:LL:77:LEU:HD22	35:LL:87:ARG:HD2	1.90	0.52
1:C1:1817:C:H5'	1:C1:1818:A:H5'	1.90	0.52
1:C1:1942:G:OP1	6:CD:256:LYS:NZ	2.43	0.52
2:C2:166:C:OP2	4:CB:158:ARG:NH1	2.43	0.52
9:CG:172:GLU:OE1	9:CG:175:ARG:NH1	2.43	0.52
21:CS:425:THR:HG1	53:Lg:109:GLN:HE22	1.56	0.52
27:CY:634:SER:OG	27:CY:683:ASN:OD1	2.28	0.52
1:C1:2408:U:H2'	1:C1:2409:A:C8	2.45	0.52
1:C1:2788:G:H2'	1:C1:2789:G:C8	2.45	0.52
1:C1:2799:G:N2	1:C1:2805:A:OP1	2.42	0.52
23:CU:270:ASP:OD2	23:CU:270:ASP:N	2.36	0.52
27:CY:5:LYS:HD2	27:CY:8:LEU:HD22	1.91	0.52
51:Le:24:ASP:N	51:Le:24:ASP:OD1	2.42	0.52
1:C1:1236:C:H4'	34:LK:149:LYS:HD3	1.91	0.52
1:C1:2435:C:C2	1:C1:2437:G:N2	2.77	0.52
10:CH:6:ASP:OD1	10:CH:6:ASP:N	2.39	0.52
21:CS:121:PRO:HG3	21:CS:134:GLN:HB2	1.91	0.52
21:CS:154:THR:HG22	21:CS:199:ARG:HG2	1.91	0.52
49:Lc:46:LEU:HB2	49:Lc:93:MET:HG3	1.92	0.52
59:Lq:92:LYS:HA	59:Lq:95:LYS:HB2	1.91	0.52
6:CD:230:TRP:HB3	6:CD:243:ALA:HB3	1.92	0.52
6:CD:236:HIS:HB3	6:CD:310:ARG:HH12	1.74	0.52
8:CF:31:ARG:HD2	8:CF:85:GLN:HE21	1.75	0.52
21:CS:161:ARG:H	21:CS:192:ALA:HB1	1.74	0.52
25:CW:292:LEU:HD13	25:CW:371:LEU:HD12	1.92	0.52
38:LO:79:SER:OG	38:LO:108:GLU:OE2	2.24	0.52
1:C1:1841:U:O2'	1:C1:3023:U:OP1	2.20	0.51
1:C1:3208:A:OP1	31:LE:64:ARG:NH2	2.41	0.51
5:CC:660:ASP:OD2	5:CC:663:LYS:NZ	2.41	0.51
13:CK:128:SER:HB2	13:CK:175:MET:HE3	1.91	0.51
29:LB:170:THR:HG22	29:LB:172:LEU:HG	1.92	0.51
5:CC:532:THR:HG22	5:CC:534:ALA:H	1.76	0.51
6:CD:357:LEU:HG	6:CD:369:MET:HE2	1.92	0.51
7:CE:352:LEU:HD13	7:CE:410:THR:HG21	1.91	0.51
30:LC:158:VAL:HA	30:LC:163:VAL:HG21	1.90	0.51
30:LC:365:ALA:HB3	42:LS:28:ARG:HD2	1.91	0.51
34:LK:41:LYS:NZ	34:LK:45:ASP:OD2	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:LZ:103:PRO:HA	48:LZ:106:ARG:HG2	1.91	0.51
1:C1:683:C:OP2	30:LC:120:ARG:NH2	2.41	0.51
5:CC:742:LEU:HB3	5:CC:765:LEU:HB2	1.92	0.51
10:CH:488:ILE:HA	10:CH:491:LYS:HB2	1.92	0.51
49:Lc:77:ASN:OD1	49:Lc:77:ASN:N	2.41	0.51
1:C1:1976:U:H2'	1:C1:1977:A:H8	1.75	0.51
18:CP:452:ARG:NH1	18:CP:505:GLY:O	2.43	0.51
21:CS:725:LEU:HD23	22:CT:401:LEU:HB3	1.93	0.51
29:LB:372:GLN:N	29:LB:376:GLU:OE2	2.39	0.51
32:LG:183:ILE:HG21	32:LG:189:LEU:HG	1.92	0.51
47:LY:30:MET:HB3	47:LY:100:PRO:HG2	1.91	0.51
50:Ld:28:LEU:HD11	50:Ld:40:ALA:HB2	1.93	0.51
12:CJ:6:LYS:HB2	12:CJ:9:LYS:HG2	1.92	0.51
13:CK:236:LYS:HG2	18:CP:474:ASN:HB3	1.91	0.51
18:CP:325:ILE:O	21:CS:69:LYS:NZ	2.43	0.51
39:LP:40:LYS:HD2	39:LP:113:ILE:HG22	1.92	0.51
1:C1:66:A:N6	1:C1:75:G:C2	2.79	0.51
1:C1:1430:U:OP1	39:LP:82:ARG:NH2	2.44	0.51
1:C1:1936:C:H2'	1:C1:1937:G:C8	2.46	0.51
3:CA:112:THR:OG1	3:CA:249:SER:O	2.26	0.51
30:LC:290:LEU:HD21	40:LQ:152:ASP:HB2	1.93	0.51
6:CD:264:ALA:HA	6:CD:267:LEU:HD23	1.91	0.51
21:CS:369:GLU:HB3	21:CS:372:ARG:HH22	1.76	0.51
1:C1:1205:A:C6	1:C1:1267:G:N2	2.78	0.51
16:CN:107:VAL:HB	16:CN:118:HIS:HB2	1.92	0.51
4:CB:103:ASP:HB3	4:CB:104:PRO:CD	2.34	0.51
8:CF:173:ARG:HH12	33:LH:93:VAL:HG12	1.76	0.51
12:CJ:374:LEU:HD23	12:CJ:419:ILE:HD13	1.91	0.51
1:C1:1171:C:N3	1:C1:1297:U:O2	2.44	0.51
6:CD:48:ARG:NH2	6:CD:51:ASN:OD1	2.44	0.51
21:CS:161:ARG:NH2	21:CS:162:SER:O	2.42	0.51
25:CW:438:ALA:O	25:CW:442:ALA:N	2.44	0.51
40:LQ:120:LEU:HD23	40:LQ:123:VAL:HG22	1.92	0.51
1:C1:3188:U:H2'	1:C1:3189:G:C8	2.46	0.50
2:C2:213:A:OP2	4:CB:144:ARG:NH2	2.43	0.50
4:CB:273:GLN:HB3	4:CB:276:GLN:HB2	1.93	0.50
5:CC:177:LEU:HD11	5:CC:223:PRO:HA	1.92	0.50
8:CF:48:MET:O	8:CF:126:ARG:NH1	2.44	0.50
12:CJ:384:GLU:HG3	12:CJ:388:ARG:HH22	1.76	0.50
22:CT:236:GLU:OE2	22:CT:236:GLU:N	2.43	0.50
30:LC:54:SER:HB3	30:LC:57:ALA:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LE:94:LEU:HD11	31:LE:165:ILE:HD12	1.93	0.50
39:LP:64:ALA:O	39:LP:80:ARG:NH1	2.44	0.50
1:C1:3079:A:O2'	33:LH:63:LYS:NZ	2.43	0.50
10:CH:544:ILE:O	10:CH:545:GLY:C	2.52	0.50
27:CY:435:ASN:C	27:CY:437:ASN:H	2.18	0.50
29:LB:216:ILE:HD12	29:LB:339:LEU:HB3	1.93	0.50
40:LQ:68:THR:HG22	40:LQ:70:ALA:H	1.76	0.50
42:LS:1:MET:SD	42:LS:1:MET:N	2.85	0.50
59:Lq:18:ASP:OD1	59:Lq:18:ASP:N	2.43	0.50
1:C1:1372:A:N6	1:C1:1400:A:O2'	2.45	0.50
1:C1:2395:U:H3'	1:C1:2396:U:H2'	1.93	0.50
4:CB:158:ARG:HG3	4:CB:185:MET:HE1	1.92	0.50
6:CD:348:LEU:HB2	6:CD:357:LEU:HB3	1.92	0.50
10:CH:464:GLU:OE2	19:CQ:67:SER:OG	2.27	0.50
24:CV:54:ILE:HG12	24:CV:63:VAL:HG22	1.94	0.50
25:CW:64:GLY:HA2	62:CW:1001:ADP:H5'2	1.93	0.50
25:CW:292:LEU:O	25:CW:295:ARG:NH2	2.44	0.50
25:CW:325:SER:HB3	25:CW:352:THR:HG22	1.92	0.50
27:CY:393:THR:O	27:CY:396:THR:OG1	2.28	0.50
27:CY:421:LYS:O	27:CY:421:LYS:NZ	2.35	0.50
28:Cz:45:LEU:HD13	42:LS:141:LYS:HB3	1.94	0.50
30:LC:59:HIS:HA	30:LC:91:PHE:HE1	1.76	0.50
1:C1:605:C:OP1	39:LP:176:ARG:NH2	2.44	0.50
1:C1:780:G:O2'	35:LL:18:TRP:NE1	2.43	0.50
1:C1:1706:G:O6	21:CS:392:ARG:NH2	2.44	0.50
6:CD:39:ALA:HB1	6:CD:77:GLU:HB3	1.94	0.50
17:CO:36:LYS:HB3	29:LB:208:THR:HG22	1.93	0.50
21:CS:431:ILE:HG22	49:Lc:64:MET:HE1	1.94	0.50
25:CW:112:ILE:HG23	25:CW:118:SER:HB3	1.92	0.50
42:LS:1:MET:HE2	42:LS:107:TYR:HB3	1.93	0.50
1:C1:1955:G:N2	1:C1:2014:U:O2	2.38	0.50
5:CC:501:THR:H	5:CC:516:ALA:HB3	1.76	0.50
15:CM:179:LEU:HB2	15:CM:184:ILE:HD11	1.93	0.50
29:LB:295:ALA:HB3	29:LB:304:LYS:HG3	1.93	0.50
2:C2:219:A:H4'	2:C2:220:G:H5'	1.93	0.50
5:CC:120:PRO:O	7:CE:472:HIS:ND1	2.44	0.50
5:CC:695:ASP:OD1	5:CC:695:ASP:N	2.44	0.50
13:CK:68:HIS:HA	13:CK:71:ARG:HG2	1.94	0.50
27:CY:493:TRP:HE3	27:CY:497:HIS:HE1	1.58	0.50
29:LB:50:LYS:NZ	29:LB:331:GLY:O	2.32	0.50
1:C1:975:G:H4'	1:C1:976:U:H5'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1475:G:OP2	1:C1:1475:G:N2	2.36	0.50
1:C1:2072:G:H2'	1:C1:2073:G:C8	2.47	0.50
10:CH:77:HIS:HB3	10:CH:81:MET:HE3	1.94	0.50
12:CJ:28:LEU:HB3	12:CJ:32:ASP:HB3	1.94	0.50
14:CL:61:TYR:HB3	14:CL:64:ARG:HG2	1.94	0.50
25:CW:34:GLY:O	25:CW:35:TYR:C	2.53	0.50
27:CY:411:GLY:O	27:CY:416:ARG:NH1	2.44	0.50
50:Ld:89:ASP:OD1	50:Ld:89:ASP:N	2.39	0.50
21:CS:690:GLU:O	32:LG:252:ARG:NH1	2.43	0.50
46:LX:83:GLU:HA	46:LX:86:LEU:HD12	1.94	0.50
1:C1:684:G:O2'	20:CR:60:LYS:NZ	2.40	0.50
1:C1:1573:A:OP1	53:Lg:37:LYS:NZ	2.44	0.50
1:C1:3078:U:H1'	1:C1:3079:A:H5''	1.93	0.50
3:CA:106:LYS:HB2	3:CA:110:GLY:HA3	1.94	0.50
6:CD:417:ASP:HB3	6:CD:438:VAL:HG21	1.92	0.50
20:CR:34:ILE:HD12	20:CR:172:LEU:HD23	1.94	0.50
22:CT:527:PRO:HG3	27:CY:577:GLU:HB2	1.94	0.50
38:LO:55:TYR:OH	38:LO:75:PHE:O	2.30	0.50
18:CP:457:ALA:HB1	18:CP:487:GLN:HG2	1.94	0.49
43:LT:104:ASP:OD1	43:LT:107:ARG:NH2	2.45	0.49
1:C1:3075:C:OP2	28:Cz:26:ARG:NH1	2.45	0.49
1:C1:3250:A:OP1	39:LP:74:LYS:NZ	2.35	0.49
18:CP:316:HIS:NE2	18:CP:319:ASP:OD2	2.45	0.49
19:CQ:95:ARG:NH1	19:CQ:98:GLU:OE2	2.45	0.49
33:LH:13:PRO:HD2	33:LH:16:LEU:HD12	1.94	0.49
1:C1:1880:A:H1'	45:LV:22:GLY:HA3	1.94	0.49
1:C1:1922:C:H5''	25:CW:359:ILE:HG12	1.94	0.49
12:CJ:372:PHE:HD1	12:CJ:419:ILE:HD11	1.77	0.49
17:CO:37:LEU:HB3	29:LB:195:PHE:HZ	1.76	0.49
5:CC:373:MET:HE1	5:CC:377:ASP:HB3	1.93	0.49
38:LO:28:LEU:O	38:LO:103:ARG:NH1	2.44	0.49
1:C1:1316:C:H5''	15:LF:212:LYS:HB3	1.93	0.49
1:C1:2057:A:H2'	1:C1:2058:A:H8	1.76	0.49
1:C1:2404:G:H2'	1:C1:2405:A:C8	2.47	0.49
6:CD:54:SER:HB2	6:CD:55:MET:HE3	1.94	0.49
6:CD:120:LEU:HG	6:CD:145:ARG:HB2	1.94	0.49
8:CF:64:ARG:NH1	8:CF:65:ILE:O	2.45	0.49
21:CS:469:GLU:OE2	32:LG:248:ARG:NH2	2.39	0.49
9:CG:27:ILE:HD12	26:CX:105:LEU:HD22	1.93	0.49
16:CN:142:ILE:HG12	16:CN:148:VAL:HG12	1.95	0.49
21:CS:699:ASP:OD1	37:LN:32:GLN:NE2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CW:390:ARG:HH21	25:CW:393:ARG:HH22	1.59	0.49
28:Cz:45:LEU:HB3	42:LS:141:LYS:HG2	1.93	0.49
4:CB:160:ILE:HA	4:CB:163:LEU:HD12	1.95	0.49
6:CD:23:GLU:HG2	6:CD:97:ARG:HD2	1.95	0.49
7:CE:183:GLY:HA2	7:CE:254:VAL:HB	1.95	0.49
21:CS:245:TYR:OH	45:LV:82:ARG:NH2	2.45	0.49
29:LB:194:GLU:OE1	29:LB:197:ARG:NH2	2.45	0.49
41:LR:105:LEU:HD23	41:LR:138:LEU:HD13	1.94	0.49
59:Lq:128:LEU:HB2	59:Lq:133:LYS:HE2	1.95	0.49
1:C1:935:U:OP1	1:C1:1098:G:N2	2.44	0.49
1:C1:1504:U:OP2	46:LX:134:LYS:NZ	2.42	0.49
1:C1:3118:A:H2'	1:C1:3119:C:C6	2.48	0.49
4:CB:19:ASP:OD1	4:CB:19:ASP:N	2.40	0.49
7:CE:525:HIS:CE1	7:CE:531:PHE:HD2	2.30	0.49
7:CE:525:HIS:CE1	7:CE:531:PHE:CD2	3.00	0.49
25:CW:271:MET:HE1	25:CW:423:ILE:HG13	1.94	0.49
48:LZ:49:PRO:HD3	48:LZ:67:ILE:HG12	1.93	0.49
59:Lq:39:LYS:NZ	59:Lq:201:VAL:O	2.46	0.49
1:C1:812:G:H4'	1:C1:1845:C:H42	1.78	0.49
1:C1:3136:A:H2'	1:C1:3137:A:H8	1.78	0.49
3:CA:35:ARG:NH2	3:CA:84:TYR:O	2.46	0.49
8:CF:145:THR:HG21	8:CF:149:VAL:H	1.76	0.49
19:CQ:145:LEU:HD13	19:CQ:159:LEU:HB3	1.95	0.49
27:CY:502:TRP:HA	27:CY:505:VAL:HG12	1.94	0.49
54:Lh:51:ASP:O	54:Lh:55:SER:OG	2.28	0.49
1:C1:713:G:C5	1:C1:723:G:C2	3.01	0.49
19:CQ:1:MET:HE1	29:LB:358:LYS:HB3	1.95	0.49
22:CT:134:ILE:HG23	22:CT:148:HIS:HB3	1.95	0.49
27:CY:493:TRP:O	27:CY:497:HIS:ND1	2.40	0.49
29:LB:57:VAL:HG22	29:LB:73:VAL:HG22	1.95	0.49
1:C1:230:A:H2'	1:C1:231:A:C8	2.48	0.48
12:CJ:116:THR:HG22	12:CJ:118:LYS:HD3	1.95	0.48
29:LB:57:VAL:HB	29:LB:359:TRP:HD1	1.78	0.48
30:LC:301:ARG:HH12	30:LC:304:LYS:HE2	1.78	0.48
37:LN:114:ARG:NH1	37:LN:151:ILE:O	2.46	0.48
1:C1:1158:C:H4'	38:LO:91:PRO:HD3	1.95	0.48
1:C1:1263:U:H2'	1:C1:1264:G:H8	1.78	0.48
1:C1:2387:G:C6	1:C1:2563:G:N2	2.81	0.48
2:C2:219:A:N6	11:CI:218:VAL:O	2.33	0.48
18:CP:515:VAL:O	18:CP:565:ARG:NH2	2.42	0.48
25:CW:201:LEU:HD22	25:CW:232:ALA:HB1	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:910:A:O2'	56:Lj:49:TRP:O	2.31	0.48
1:C1:1924:A:H62	25:CW:175:GLU:HG2	1.78	0.48
5:CC:355:ASN:ND2	12:CJ:483:PRO:O	2.47	0.48
58:Ll:2:PRO:O	58:Ll:5:LYS:NZ	2.46	0.48
1:C1:2857:C:O2'	1:C1:2859:G:OP2	2.28	0.48
1:C1:3115:C:H2'	1:C1:3116:G:H8	1.78	0.48
12:CJ:398:ASP:OD2	12:CJ:399:ALA:N	2.46	0.48
18:CP:473:THR:OG1	18:CP:474:ASN:OD1	2.31	0.48
19:CQ:23:ARG:HH21	19:CQ:29:PHE:HZ	1.60	0.48
21:CS:93:ASP:OD1	21:CS:93:ASP:N	2.41	0.48
21:CS:220:ASP:OD1	21:CS:220:ASP:N	2.47	0.48
54:Lh:46:LEU:HA	54:Lh:49:ILE:HD12	1.94	0.48
4:CB:233:VAL:HG21	4:CB:266:LEU:HD13	1.94	0.48
6:CD:123:THR:HG21	6:CD:470:LYS:HB2	1.95	0.48
6:CD:446:TRP:NE1	6:CD:453:LYS:O	2.43	0.48
15:CM:154:ILE:HD12	15:CM:191:ILE:HG12	1.95	0.48
17:CO:83:SER:OG	17:CO:84:GLY:N	2.47	0.48
27:CY:650:LEU:HB3	27:CY:654:MET:HE2	1.95	0.48
30:LC:12:ALA:HB2	30:LC:157:ALA:HB1	1.94	0.48
1:C1:845:G:N2	27:CY:15:GLU:OE2	2.47	0.48
1:C1:2742:G:H5'	18:CP:482:GLN:HE22	1.77	0.48
5:CC:591:ILE:HA	5:CC:607:SER:HA	1.95	0.48
18:CP:396:THR:HG22	18:CP:430:VAL:HG21	1.94	0.48
29:LB:136:LYS:HA	29:LB:139:GLU:HB2	1.96	0.48
40:LQ:94:ARG:HE	40:LQ:170:PRO:HD3	1.78	0.48
43:LT:35:ARG:NH1	43:LT:36:VAL:O	2.47	0.48
1:C1:651:A:H2'	1:C1:652:A:H8	1.78	0.48
1:C1:890:G:H2'	1:C1:891:G:C8	2.49	0.48
1:C1:1826:A:O2'	1:C1:1828:C:OP2	2.31	0.48
1:C1:1988:C:H2'	1:C1:1989:G:C8	2.49	0.48
5:CC:459:VAL:HG13	5:CC:791:ALA:HB2	1.96	0.48
5:CC:530:SER:O	5:CC:530:SER:OG	2.31	0.48
10:CH:223:ILE:HA	10:CH:235:GLU:HG2	1.95	0.48
55:Li:88:THR:HG22	55:Li:90:GLY:H	1.77	0.48
57:Lk:8:ILE:HG23	57:Lk:58:LEU:HD13	1.96	0.48
1:C1:247:A:H2'	1:C1:248:G:C8	2.49	0.48
1:C1:764:A:H5''	1:C1:765:G:H5'	1.96	0.48
16:CN:116:LEU:HD11	16:CN:177:LEU:HD11	1.95	0.48
22:CT:253:VAL:O	22:CT:255:HIS:N	2.47	0.48
45:LV:82:ARG:NH1	45:LV:119:PRO:O	2.41	0.48
48:LZ:96:ASN:OD1	48:LZ:96:ASN:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:Lh:22:LYS:NZ	54:Lh:26:GLU:OE2	2.43	0.48
1:C1:324:C:H4'	56:Lj:71:PRO:HB3	1.95	0.48
1:C1:973:A:O2'	43:LT:58:HIS:NE2	2.46	0.48
1:C1:1939:U:H2'	1:C1:1940:G:C8	2.49	0.48
1:C1:2918:C:H2'	1:C1:2919:G:H8	1.79	0.48
2:C2:63:G:H22	2:C2:97:A:H2	1.62	0.48
10:CH:85:TYR:O	10:CH:148:TYR:OH	2.30	0.48
22:CT:157:GLU:N	22:CT:157:GLU:OE2	2.46	0.48
27:CY:555:ILE:HD12	27:CY:571:LEU:HD23	1.96	0.48
15:LF:95:ILE:HD11	15:LF:234:LEU:HD23	1.94	0.48
33:LH:55:LEU:HD12	33:LH:68:LEU:HD22	1.94	0.48
1:C1:2051:G:O2'	1:C1:2052:U:O4'	2.28	0.48
1:C1:2980:U:H2'	1:C1:2981:A:H8	1.79	0.48
5:CC:496:ASP:OD1	5:CC:496:ASP:N	2.39	0.48
7:CE:332:LEU:HD21	7:CE:446:GLY:HA3	1.95	0.48
18:CP:460:SER:HG	18:CP:462:THR:HG1	1.56	0.48
1:C1:2380:G:H5''	1:C1:2381:A:H5'	1.95	0.47
13:CK:153:LYS:HE2	13:CK:154:PRO:HD2	1.96	0.47
21:CS:250:TYR:HD2	21:CS:251:THR:HG23	1.78	0.47
25:CW:439:ASP:HA	25:CW:442:ALA:HB3	1.96	0.47
34:LK:13:ILE:HG12	34:LK:62:LEU:HB2	1.96	0.47
38:LO:4:PHE:N	52:Lf:35:GLU:OE2	2.44	0.47
42:LS:158:LYS:HD2	42:LS:158:LYS:HA	1.61	0.47
1:C1:887:G:H2'	1:C1:888:G:C8	2.49	0.47
1:C1:976:U:N3	1:C1:1036:A:C8	2.78	0.47
5:CC:520:ASP:OD1	5:CC:520:ASP:N	2.43	0.47
9:CG:58:CYS:SG	18:CP:447:ILE:HG12	2.54	0.47
18:CP:453:VAL:HG23	18:CP:508:ILE:HG23	1.95	0.47
29:LB:14:LEU:HA	29:LB:17:LEU:HG	1.95	0.47
30:LC:218:ASP:HB3	30:LC:222:LEU:HD11	1.96	0.47
47:LY:86:ARG:HB3	47:LY:96:ILE:HD11	1.95	0.47
58:Ll:21:ARG:O	58:Ll:38:ASN:ND2	2.47	0.47
1:C1:298:A:O2'	3:CA:114:LYS:NZ	2.47	0.47
1:C1:861:G:H1'	1:C1:869:A:N6	2.28	0.47
1:C1:2973:A:H2'	1:C1:2974:G:H8	1.78	0.47
2:C2:81:U:O2	2:C2:82:U:O2'	2.32	0.47
3:CA:39:LEU:HD11	3:CA:68:PHE:HB2	1.96	0.47
10:CH:491:LYS:HG2	19:CQ:134:LEU:HD11	1.96	0.47
18:CP:395:THR:HG23	18:CP:408:ILE:HG21	1.95	0.47
27:CY:441:GLY:O	27:CY:444:LEU:HD12	2.14	0.47
1:C1:712:A:H3'	1:C1:713:G:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2053:U:H4'	1:C1:2054:A:H5'	1.96	0.47
10:CH:397:ASP:O	10:CH:400:ARG:NH1	2.47	0.47
11:CI:295:ARG:HD3	11:CI:296:PRO:HD2	1.95	0.47
22:CT:127:ALA:O	22:CT:131:LEU:N	2.39	0.47
30:LC:287:LEU:HD11	40:LQ:60:LEU:HB2	1.95	0.47
51:Le:1:MET:HE3	51:Le:3:ALA:HB3	1.96	0.47
1:C1:83:C:O2'	1:C1:687:C:O2'	2.20	0.47
12:CJ:178:TYR:O	12:CJ:182:THR:OG1	2.29	0.47
1:C1:1260:A:O2'	8:CF:15:VAL:O	2.33	0.47
1:C1:2766:A:C6	23:CU:323:ARG:HD3	2.49	0.47
1:C1:2945:A:H5''	38:LO:69:ARG:HH22	1.78	0.47
22:CT:124:ILE:HG22	22:CT:163:ILE:HD11	1.97	0.47
23:CU:309:LYS:HB2	23:CU:309:LYS:HE3	1.63	0.47
32:LG:157:ALA:HA	32:LG:183:ILE:HG22	1.96	0.47
36:LM:123:LEU:HD22	38:LO:195:VAL:HG13	1.97	0.47
48:LZ:101:LYS:HA	48:LZ:101:LYS:HD3	1.64	0.47
1:C1:424:G:H2'	1:C1:425:A:C8	2.50	0.47
1:C1:531:U:O4	1:C1:541:G:O6	2.32	0.47
1:C1:1640:G:H2'	1:C1:1641:G:C8	2.48	0.47
1:C1:2046:G:H2'	1:C1:2047:U:C6	2.50	0.47
1:C1:2300:C:H3'	1:C1:2301:C:H2'	1.97	0.47
2:C2:194:C:H2'	2:C2:195:G:H8	1.79	0.47
4:CB:44:ASP:OD1	4:CB:44:ASP:N	2.48	0.47
4:CB:206:ARG:HE	4:CB:212:ALA:HA	1.80	0.47
5:CC:152:ASP:O	7:CE:573:TYR:OH	2.28	0.47
9:CG:109:LEU:HD13	18:CP:358:LEU:HD12	1.97	0.47
10:CH:203:LEU:HD13	10:CH:237:GLN:HG2	1.97	0.47
21:CS:431:ILE:HD11	53:Lg:105:VAL:HG21	1.96	0.47
27:CY:371:SER:HA	27:CY:374:LYS:HB2	1.97	0.47
27:CY:436:ALA:O	27:CY:439:LEU:HB2	2.15	0.47
30:LC:155:SER:HA	30:LC:158:VAL:HG12	1.96	0.47
45:LV:110:GLU:HG2	45:LV:130:ARG:HG3	1.97	0.47
1:C1:1041:G:H4'	43:LT:60:LYS:HE3	1.96	0.47
6:CD:130:SER:OG	6:CD:188:SER:N	2.48	0.47
15:CM:186:CYS:SG	15:CM:188:GLU:N	2.87	0.47
32:LG:90:ALA:HB1	32:LG:188:ARG:HH22	1.80	0.47
1:C1:631:G:H5''	1:C1:1098:G:C8	2.50	0.47
1:C1:2990:A:H2'	1:C1:2991:C:H6	1.80	0.47
6:CD:56:LEU:HB3	6:CD:58:THR:HG23	1.97	0.47
12:CJ:666:LYS:HG3	12:CJ:669:ARG:HH22	1.80	0.47
15:CM:113:ARG:HG3	15:CM:210:PRO:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CT:619:VAL:HG11	22:CT:683:LEU:HD12	1.96	0.47
32:LG:85:LEU:HD11	32:LG:183:ILE:HD12	1.97	0.47
1:C1:1448:G:N2	1:C1:1492:G:H5''	2.30	0.47
19:CQ:9:CYS:SG	19:CQ:11:ARG:HG3	2.55	0.47
19:CQ:16:SER:HB3	29:LB:73:VAL:HG11	1.96	0.47
1:C1:620:C:O2'	52:Lf:23:ARG:O	2.27	0.46
4:CB:22:GLN:NE2	11:CI:328:GLU:OE2	2.48	0.46
5:CC:381:ASP:OD1	5:CC:381:ASP:N	2.43	0.46
7:CE:151:VAL:HG13	7:CE:293:MET:HG3	1.97	0.46
10:CH:242:LEU:O	10:CH:280:LYS:NZ	2.47	0.46
23:CU:369:ASP:N	23:CU:369:ASP:OD1	2.48	0.46
25:CW:295:ARG:NH1	25:CW:324:TYR:OH	2.48	0.46
42:LS:27:MET:HE1	42:LS:44:PHE:HD2	1.80	0.46
46:LX:92:GLN:HB2	46:LX:94:THR:HG22	1.97	0.46
1:C1:2329:A:H2'	1:C1:2330:A:C8	2.50	0.46
4:CB:100:ILE:HG21	4:CB:163:LEU:HD21	1.97	0.46
6:CD:102:PRO:HA	6:CD:487:GLY:HA2	1.97	0.46
11:CI:202:GLU:HB2	15:CM:57:TYR:HB3	1.98	0.46
16:CN:32:GLU:HB3	16:CN:35:TYR:HB3	1.98	0.46
37:LN:120:TRP:HE1	37:LN:123:GLN:HB2	1.80	0.46
40:LQ:161:GLY:O	40:LQ:164:THR:OG1	2.31	0.46
1:C1:1213:A:H5''	1:C1:1214:C:H5'	1.98	0.46
1:C1:1538:C:O2'	32:LG:57:GLU:OE2	2.31	0.46
1:C1:2056:C:H2'	1:C1:2057:A:C8	2.49	0.46
1:C1:2306:U:H2'	1:C1:2307:A:C8	2.51	0.46
1:C1:2832:G:N2	1:C1:2881:U:O4	2.49	0.46
12:CJ:397:TRP:CE2	12:CJ:405:ALA:HB2	2.50	0.46
16:CN:67:ARG:NH1	16:CN:112:ASP:OD2	2.37	0.46
21:CS:503:GLU:HG2	22:CT:186:PRO:HG2	1.97	0.46
21:CS:823:MET:HE3	21:CS:823:MET:HB2	1.80	0.46
25:CW:618:GLU:HB2	25:CW:622:ARG:HH12	1.81	0.46
27:CY:584:MET:HE2	27:CY:584:MET:H	1.79	0.46
1:C1:532:C:N3	1:C1:540:A:C6	2.83	0.46
1:C1:1951:G:H21	1:C1:2018:A:H62	1.63	0.46
1:C1:3121:U:H3	52:Lf:59:LYS:HG3	1.80	0.46
6:CD:55:MET:HG2	6:CD:56:LEU:HD22	1.97	0.46
7:CE:516:ARG:O	7:CE:520:HIS:ND1	2.48	0.46
9:CG:116:LYS:HB3	9:CG:159:PRO:HA	1.97	0.46
12:CJ:85:LYS:HA	12:CJ:85:LYS:HD3	1.65	0.46
22:CT:666:LYS:HE3	27:CY:568:TYR:HB2	1.97	0.46
36:LM:39:VAL:HG23	36:LM:57:VAL:HG13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:725:A:OP1	40:LQ:94:ARG:NH1	2.48	0.46
1:C1:2344:G:OP1	38:LO:87:ARG:NH2	2.49	0.46
1:C1:2555:U:H2'	1:C1:2556:G:H8	1.80	0.46
1:C1:2849:U:O2'	17:CO:2:ALA:N	2.47	0.46
18:CP:533:ASN:HB2	18:CP:585:GLY:H	1.81	0.46
19:CQ:166:LYS:O	19:CQ:170:LYS:N	2.46	0.46
21:CS:369:GLU:HB3	21:CS:372:ARG:NH2	2.31	0.46
25:CW:326:ILE:HD11	25:CW:355:LEU:HD11	1.97	0.46
46:LX:88:LYS:HB3	46:LX:94:THR:HG23	1.97	0.46
48:LZ:11:LEU:HB2	48:LZ:80:MET:HB3	1.98	0.46
1:C1:384:G:H22	1:C1:389:A:N6	2.12	0.46
1:C1:1046:A:C6	1:C1:1078:C:N3	2.84	0.46
1:C1:1765:G:H2'	1:C1:1766:A:C8	2.51	0.46
5:CC:468:LEU:HD13	5:CC:789:VAL:HG11	1.97	0.46
6:CD:151:TYR:OH	6:CD:181:LYS:NZ	2.44	0.46
27:CY:542:ILE:O	27:CY:551:ARG:NH1	2.49	0.46
28:Cz:50:LEU:HD22	42:LS:133:GLU:HG2	1.97	0.46
1:C1:244:U:O2'	20:CR:228:ARG:NH1	2.47	0.46
1:C1:1077:U:O2	43:LT:129:LYS:NZ	2.41	0.46
1:C1:1288:G:O6	1:C1:2328:C:O2'	2.34	0.46
1:C1:1885:G:C2	1:C1:2296:U:O2	2.68	0.46
1:C1:2423:A:O2'	1:C1:2425:G:OP2	2.32	0.46
1:C1:2889:C:H5''	45:LV:42:LYS:HD3	1.97	0.46
2:C2:128:U:OP1	2:C2:129:C:N4	2.40	0.46
5:CC:403:ARG:NH1	12:CJ:143:ASP:OD2	2.49	0.46
32:LG:159:ASP:O	32:LG:186:LYS:NZ	2.42	0.46
33:LH:97:PHE:HB3	33:LH:118:ASN:HD21	1.80	0.46
41:LR:102:LEU:HD22	41:LR:138:LEU:HD12	1.96	0.46
1:C1:3157:C:OP1	36:LM:132:ARG:NH2	2.47	0.46
2:C2:8:C:H2'	2:C2:9:A:H8	1.80	0.46
3:CA:231:LEU:HG	23:CU:248:LEU:HD13	1.98	0.46
6:CD:369:MET:HE3	6:CD:369:MET:HA	1.98	0.46
7:CE:270:LEU:HD12	7:CE:275:GLU:HB3	1.97	0.46
21:CS:703:HIS:HB3	37:LN:124:ASP:OD2	2.16	0.46
25:CW:356:THR:OG1	25:CW:357:THR:O	2.33	0.46
29:LB:148:GLU:OE2	29:LB:151:ARG:NH1	2.49	0.46
39:LP:60:MET:HE3	39:LP:60:MET:HB3	1.85	0.46
1:C1:526:G:O2'	1:C1:543:G:N1	2.39	0.46
1:C1:895:A:O2'	1:C1:896:A:O5'	2.32	0.46
1:C1:966:U:H2'	1:C1:967:U:H6	1.81	0.46
1:C1:979:A:H2'	1:C1:980:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:308:ILE:HG23	18:CP:362:TYR:HB2	1.98	0.46
31:LE:61:LEU:HD21	31:LE:103:ILE:HD12	1.98	0.46
44:LU:20:LYS:HE3	44:LU:20:LYS:HB3	1.62	0.46
59:Lq:75:ASP:OD1	59:Lq:75:ASP:N	2.46	0.46
1:C1:750:G:H2'	1:C1:751:G:C4	2.50	0.46
1:C1:1072:G:H2'	1:C1:1073:G:C8	2.51	0.46
1:C1:1903:U:O2	1:C1:2072:G:C2	2.69	0.46
1:C1:2307:A:H5''	50:Ld:32:THR:HG23	1.98	0.46
10:CH:250:LEU:HD11	10:CH:334:VAL:HG21	1.97	0.46
18:CP:354:THR:HG22	18:CP:356:GLU:H	1.80	0.46
27:CY:628:GLU:HA	27:CY:631:VAL:HG22	1.97	0.46
59:Lq:102:LYS:HA	59:Lq:105:ARG:HG2	1.98	0.46
1:C1:575:A:H4'	52:Lf:74:THR:HG23	1.97	0.45
1:C1:789:A:H2'	1:C1:790:G:C8	2.50	0.45
1:C1:1360:U:H2'	1:C1:1361:G:H8	1.80	0.45
5:CC:266:GLU:OE2	5:CC:268:LYS:NZ	2.42	0.45
7:CE:488:ASN:HB3	7:CE:489:LYS:HE2	1.98	0.45
15:CM:151:ARG:NH2	15:CM:188:GLU:OE1	2.49	0.45
16:CN:242:VAL:O	16:CN:246:TYR:HB2	2.16	0.45
21:CS:657:ALA:HA	21:CS:718:ILE:HG13	1.98	0.45
24:CV:23:GLN:O	24:CV:25:THR:N	2.49	0.45
34:LK:111:GLU:O	34:LK:115:THR:OG1	2.27	0.45
36:LM:44:PRO:HG3	36:LM:81:VAL:HG12	1.98	0.45
59:Lq:59:PRO:HB2	59:Lq:170:GLY:H	1.81	0.45
1:C1:115:A:H2'	1:C1:257:A:H2'	1.98	0.45
1:C1:1777:A:OP1	22:CT:369:LYS:NZ	2.49	0.45
3:CA:85:ASN:ND2	5:CC:157:VAL:O	2.49	0.45
7:CE:208:LYS:HE3	7:CE:208:LYS:HB2	1.70	0.45
14:CL:277:PRO:O	14:CL:279:ALA:N	2.49	0.45
22:CT:605:GLU:H	22:CT:605:GLU:HG2	1.57	0.45
24:CV:33:LEU:HB3	24:CV:45:GLY:HA3	1.98	0.45
34:LK:19:GLY:HA2	34:LK:50:THR:HG21	1.96	0.45
59:Lq:128:LEU:O	59:Lq:133:LYS:NZ	2.32	0.45
1:C1:2425:G:H21	59:Lq:162:VAL:HG21	1.81	0.45
7:CE:355:MET:HE3	7:CE:355:MET:HA	1.99	0.45
21:CS:470:ARG:HA	32:LG:244:LYS:HE2	1.97	0.45
25:CW:409:GLU:H	25:CW:409:GLU:CD	2.24	0.45
29:LB:354:LYS:HE3	29:LB:354:LYS:HB2	1.65	0.45
1:C1:63:A:N3	1:C1:78:U:O2'	2.46	0.45
1:C1:247:A:H2'	1:C1:248:G:H8	1.80	0.45
1:C1:2439:G:OP1	1:C1:2449:U:O2'	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:618:LYS:HA	12:CJ:621:GLU:HB2	1.99	0.45
16:CN:24:CYS:HB3	16:CN:48:ILE:HG13	1.98	0.45
23:CU:267:ARG:HD3	26:CX:79:PRO:HB3	1.99	0.45
25:CW:267:MET:HA	25:CW:267:MET:HE3	1.98	0.45
38:LO:87:ARG:HG3	38:LO:101:LEU:HD11	1.99	0.45
1:C1:488:A:O2'	1:C1:3213:A:N1	2.43	0.45
1:C1:651:A:H2'	1:C1:652:A:C8	2.51	0.45
1:C1:1077:U:H5''	14:CL:469:GLY:HA2	1.99	0.45
1:C1:1272:U:H2'	1:C1:1273:A:C8	2.51	0.45
1:C1:1575:C:H2'	1:C1:1576:C:C6	2.52	0.45
1:C1:1812:G:O2'	58:LI:3:SER:O	2.34	0.45
1:C1:1935:A:H2'	1:C1:1936:C:C6	2.52	0.45
25:CW:130:LYS:HE3	25:CW:130:LYS:HB2	1.70	0.45
25:CW:445:ILE:HA	25:CW:448:GLN:NE2	2.32	0.45
30:LC:319:PRO:HG2	15:LF:155:TYR:HB3	1.99	0.45
1:C1:2435:C:O2	1:C1:2437:G:N2	2.49	0.45
1:C1:2859:G:O2'	1:C1:2981:A:N1	2.47	0.45
1:C1:3112:A:H1'	1:C1:3113:C:H5	1.81	0.45
5:CC:445:GLN:OE1	5:CC:798:ARG:NH1	2.38	0.45
6:CD:222:TYR:HE2	6:CD:268:PRO:HD3	1.81	0.45
10:CH:387:VAL:HG21	16:CN:202:TRP:CD1	2.52	0.45
18:CP:460:SER:HA	18:CP:475:ARG:HH21	1.82	0.45
20:CR:214:LYS:HB3	20:CR:214:LYS:HE2	1.59	0.45
25:CW:364:LEU:HA	25:CW:364:LEU:HD23	1.74	0.45
27:CY:543:PRO:O	27:CY:544:THR:OG1	2.33	0.45
35:LL:46:LEU:HB3	35:LL:49:ARG:HD2	1.98	0.45
37:LN:4:LEU:HD13	37:LN:46:ASP:HA	1.98	0.45
48:LZ:53:THR:HG23	48:LZ:55:ARG:H	1.81	0.45
59:Lq:31:THR:O	59:Lq:209:THR:OG1	2.30	0.45
59:Lq:88:ASP:HA	59:Lq:91:LYS:HE2	1.98	0.45
1:C1:2729:U:C4	1:C1:2731:C:N4	2.84	0.45
1:C1:2829:G:H2'	1:C1:2830:A:C8	2.52	0.45
7:CE:342:ASP:OD2	7:CE:342:ASP:N	2.38	0.45
7:CE:370:VAL:HG13	7:CE:412:ILE:HG22	1.99	0.45
29:LB:313:VAL:HG23	29:LB:365:GLU:HB3	1.98	0.45
40:LQ:93:SER:OG	40:LQ:117:ASP:OD2	2.34	0.45
1:C1:130:U:O2	1:C1:133:G:N2	2.50	0.45
1:C1:258:C:C2	55:LI:39:LYS:HE2	2.51	0.45
1:C1:1697:A:H2'	1:C1:1698:G:C8	2.51	0.45
1:C1:3332:G:HO2'	1:C1:3333:A:H8	1.64	0.45
2:C2:29:U:H5''	35:LL:27:ASP:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CE:363:PHE:HB3	7:CE:415:ASP:OD2	2.17	0.45
10:CH:236:MET:HE3	10:CH:236:MET:HB3	1.85	0.45
12:CJ:453:ARG:HE	12:CJ:455:TYR:HE2	1.64	0.45
1:C1:116:A:OP1	55:Li:45:ARG:NH1	2.50	0.45
1:C1:630:U:OP1	21:CS:832:LYS:NZ	2.49	0.45
1:C1:2047:U:H2'	1:C1:2048:G:C8	2.52	0.45
4:CB:49:LEU:HA	4:CB:49:LEU:HD12	1.81	0.45
5:CC:231:LEU:HD11	21:CS:663:ALA:HB1	1.97	0.45
6:CD:186:LEU:HD11	6:CD:240:ILE:HD11	1.99	0.45
7:CE:401:PHE:O	7:CE:405:ASN:ND2	2.50	0.45
27:CY:394:ASP:O	27:CY:398:ILE:HD12	2.17	0.45
30:LC:6:THR:HB	30:LC:20:THR:HG22	1.99	0.45
15:LF:83:ILE:HD11	42:LS:59:VAL:HG13	1.99	0.45
59:Lq:89:ASP:HA	59:Lq:92:LYS:HE3	1.99	0.45
1:C1:202:A:H4'	1:C1:204:A:N7	2.32	0.45
1:C1:507:G:OP1	15:LF:73:ARG:NH2	2.40	0.45
1:C1:3118:A:H61	1:C1:3225:C:H42	0.71	0.45
2:C2:84:C:O2	47:LY:112:LYS:NZ	2.49	0.45
4:CB:49:LEU:HD23	7:CE:347:LEU:HD11	1.98	0.45
7:CE:522:TYR:HD2	7:CE:533:VAL:HG22	1.82	0.45
20:CR:55:VAL:HG22	54:Lh:123:VAL:HB	1.98	0.45
25:CW:345:PHE:CE2	25:CW:354:LEU:HB2	2.52	0.45
42:LS:141:LYS:HB2	42:LS:141:LYS:HE3	1.82	0.45
1:C1:261:G:H5''	37:LN:14:LYS:HE3	1.98	0.44
1:C1:2776:U:H2'	1:C1:2777:A:H4'	1.99	0.44
1:C1:3115:C:H2'	1:C1:3116:G:C8	2.53	0.44
3:CA:105:SER:HB2	3:CA:112:THR:HG23	1.99	0.44
4:CB:284:LYS:HD3	4:CB:290:ALA:HB2	1.98	0.44
29:LB:154:LYS:HB2	29:LB:154:LYS:HE3	1.73	0.44
15:LF:155:TYR:CE1	15:LF:187:ILE:HG21	2.52	0.44
59:Lq:113:SER:HA	59:Lq:138:VAL:HG22	1.99	0.44
1:C1:966:U:H2'	1:C1:967:U:C6	2.52	0.44
1:C1:2929:A:H62	21:CS:752:LYS:HD3	1.82	0.44
1:C1:3185:A:H4'	29:LB:95:THR:HG23	1.99	0.44
2:C2:196:G:O6	2:C2:201:U:O4	2.34	0.44
5:CC:261:TRP:N	55:Li:55:GLU:OE2	2.51	0.44
7:CE:344:ARG:NH2	7:CE:433:ASP:OD1	2.50	0.44
21:CS:210:ARG:HA	21:CS:213:ASP:HB2	1.99	0.44
21:CS:282:PRO:HD3	21:CS:289:LEU:HD13	1.99	0.44
21:CS:578:ILE:HD12	21:CS:579:PRO:HD2	1.99	0.44
24:CV:132:LYS:HB2	24:CV:132:LYS:HE2	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CW:56:VAL:HG13	25:CW:246:LYS:HA	1.98	0.44
27:CY:374:LYS:HA	27:CY:377:LYS:HE2	1.99	0.44
1:C1:45:A:O2'	1:C1:95:A:N1	2.48	0.44
1:C1:1158:C:H2'	1:C1:1159:G:N2	2.32	0.44
2:C2:75:G:OP2	47:LY:73:TYR:OH	2.33	0.44
3:CA:83:LEU:HD11	55:Li:79:ARG:HB2	1.98	0.44
10:CH:263:LEU:HD23	10:CH:263:LEU:HA	1.87	0.44
12:CJ:170:ARG:HH11	12:CJ:170:ARG:HB2	1.82	0.44
12:CJ:186:ARG:HD3	12:CJ:186:ARG:HA	1.69	0.44
18:CP:387:MET:HE1	18:CP:494:ALA:HB2	1.98	0.44
18:CP:411:ASN:ND2	18:CP:438:TYR:O	2.51	0.44
19:CQ:167:LEU:HD23	19:CQ:167:LEU:HA	1.79	0.44
27:CY:394:ASP:HA	27:CY:397:ARG:HG2	1.99	0.44
32:LG:53:VAL:HG11	46:LX:43:THR:HB	1.99	0.44
34:LK:80:LEU:HD12	34:LK:112:ILE:HG23	1.98	0.44
1:C1:424:G:H2'	1:C1:425:A:H8	1.82	0.44
1:C1:745:U:H3	1:C1:749:C:N4	2.16	0.44
16:CN:4:ARG:HB3	16:CN:208:LEU:HA	1.99	0.44
18:CP:270:ILE:HD12	18:CP:285:LEU:HD21	1.99	0.44
19:CQ:95:ARG:HD2	19:CQ:95:ARG:HA	1.75	0.44
22:CT:236:GLU:HG3	22:CT:240:SER:HB2	1.99	0.44
29:LB:59:ASP:HB2	29:LB:358:LYS:HD3	1.98	0.44
15:LF:189:ASP:OD1	15:LF:189:ASP:N	2.48	0.44
52:Lf:16:LEU:HD11	52:Lf:33:LYS:HB2	1.99	0.44
54:Lh:76:LYS:HB3	54:Lh:76:LYS:HE2	1.68	0.44
1:C1:246:A:OP1	5:CC:289:LYS:NZ	2.50	0.44
1:C1:643:A:H2'	1:C1:644:A:C8	2.53	0.44
1:C1:1877:G:N2	1:C1:1880:A:N6	2.64	0.44
5:CC:423:ILE:HD11	12:CJ:649:MET:HE1	1.99	0.44
6:CD:29:PRO:HG2	6:CD:32:LYS:HE3	1.99	0.44
8:CF:86:ALA:HB3	8:CF:89:LEU:HD13	1.99	0.44
10:CH:544:ILE:HD11	10:CH:546:LEU:HD21	2.00	0.44
16:CN:72:VAL:HB	16:CN:76:THR:HG21	2.00	0.44
16:CN:82:GLN:HG3	16:CN:86:ASN:HD21	1.82	0.44
21:CS:125:THR:HB	21:CS:129:GLN:HB3	2.00	0.44
30:LC:6:THR:HG22	30:LC:22:VAL:HA	1.98	0.44
45:LV:99:ASP:N	45:LV:99:ASP:OD1	2.50	0.44
55:Li:54:ARG:HA	55:Li:54:ARG:HD3	1.92	0.44
1:C1:1691:G:N2	1:C1:1711:U:O4	2.46	0.44
7:CE:361:ILE:HG23	7:CE:411:LEU:HD23	2.00	0.44
11:CI:273:PHE:HB3	11:CI:276:ALA:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CJ:507:GLN:HG2	12:CJ:668:ARG:NH2	2.33	0.44
18:CP:337:TRP:CD1	18:CP:337:TRP:H	2.35	0.44
21:CS:167:LYS:HD3	21:CS:218:PHE:HA	2.00	0.44
21:CS:169:LEU:O	21:CS:173:ASN:ND2	2.43	0.44
22:CT:670:PRO:HA	22:CT:673:ARG:HG3	1.99	0.44
33:LH:118:ASN:ND2	33:LH:118:ASN:O	2.51	0.44
55:Li:83:LYS:HD2	55:Li:89:PHE:CE1	2.53	0.44
1:C1:1614:G:N2	1:C1:1617:A:OP2	2.40	0.44
2:C2:57:C:H4'	2:C2:63:G:N7	2.33	0.44
22:CT:241:ILE:HD12	22:CT:241:ILE:H	1.82	0.44
25:CW:373:ILE:HD11	25:CW:403:MET:HG3	2.00	0.44
25:CW:415:LEU:O	25:CW:419:ARG:HG3	2.18	0.44
1:C1:3265:A:H2'	1:C1:3266:G:C8	2.53	0.44
6:CD:259:ALA:HA	6:CD:260:PRO:HD3	1.88	0.44
8:CF:228:ASN:HB3	8:CF:231:SER:HB3	2.00	0.44
15:CM:92:VAL:HG23	15:CM:140:VAL:HB	2.00	0.44
22:CT:319:GLU:HB3	22:CT:419:LEU:HD23	1.99	0.44
27:CY:465:PHE:CZ	27:CY:469:ARG:NH2	2.85	0.44
59:Lq:130:LYS:HE2	59:Lq:130:LYS:HB3	1.84	0.44
1:C1:20:A:H2'	1:C1:21:G:C8	2.52	0.44
3:CA:235:GLY:HA3	3:CA:236:PRO:HD3	1.81	0.44
4:CB:72:ILE:HD11	4:CB:271:VAL:HG22	1.99	0.44
5:CC:334:PRO:HA	5:CC:335:PRO:HD3	1.92	0.44
5:CC:510:THR:HB	5:CC:512:ILE:HG13	2.00	0.44
5:CC:617:ILE:HD12	5:CC:628:PRO:HG3	2.00	0.44
6:CD:444:GLU:OE2	6:CD:448:SER:OG	2.35	0.44
7:CE:217:VAL:HG12	7:CE:226:GLU:HG2	2.00	0.44
8:CF:31:ARG:HD2	8:CF:85:GLN:NE2	2.31	0.44
10:CH:544:ILE:HD12	10:CH:546:LEU:HD21	1.99	0.44
36:LM:29:ALA:HB2	36:LM:85:TRP:HZ3	1.82	0.44
1:C1:603:G:H2'	1:C1:604:G:C8	2.53	0.43
1:C1:749:C:H2'	1:C1:750:G:C8	2.53	0.43
1:C1:1160:G:N3	1:C1:1310:C:O2'	2.47	0.43
1:C1:1468:G:H21	53:Lg:7:THR:HG22	1.83	0.43
1:C1:1743:C:H3'	1:C1:1744:U:H4'	2.00	0.43
1:C1:2955:U:H2'	1:C1:2956:C:C6	2.53	0.43
5:CC:768:HIS:NE2	5:CC:790:SER:OG	2.49	0.43
7:CE:361:ILE:HB	7:CE:429:ILE:HD13	2.00	0.43
16:CN:150:SER:OG	45:LV:133:SER:O	2.29	0.43
19:CQ:131:GLU:HA	19:CQ:134:LEU:HD23	1.99	0.43
23:CU:335:ASN:HB3	23:CU:339:ARG:HH12	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CW:162:SER:OG	25:CW:162:SER:O	2.32	0.43
1:C1:1090:C:H2'	1:C1:1091:A:C8	2.52	0.43
1:C1:1206:C:H41	1:C1:1267:G:N2	2.15	0.43
1:C1:1567:A:C6	58:LI:4:HIS:HB3	2.54	0.43
6:CD:366:HIS:C	6:CD:366:HIS:HD1	2.25	0.43
8:CF:170:MET:HE2	8:CF:208:LEU:HD22	2.00	0.43
10:CH:60:PHE:HE2	10:CH:104:ILE:HD12	1.83	0.43
10:CH:375:ASP:OD1	10:CH:377:THR:OG1	2.35	0.43
11:CI:248:MET:HE3	11:CI:248:MET:HB3	1.88	0.43
14:CL:205:ALA:HA	14:CL:314:ALA:HB3	1.99	0.43
16:CN:206:THR:OG1	16:CN:207:GLY:N	2.51	0.43
25:CW:585:ARG:HD3	25:CW:585:ARG:HA	1.65	0.43
27:CY:459:LEU:C	27:CY:461:TYR:N	2.75	0.43
29:LB:43:LEU:HB2	29:LB:209:ILE:HD12	2.00	0.43
31:LE:69:ARG:O	31:LE:90:ASN:ND2	2.51	0.43
49:Lc:54:LEU:HD21	53:Lg:91:ILE:HG22	2.00	0.43
1:C1:95:A:C5	1:C1:96:G:H1'	2.54	0.43
1:C1:3105:C:H2'	1:C1:3106:G:H8	1.83	0.43
6:CD:10:ALA:HA	6:CD:11:PRO:HD3	1.89	0.43
6:CD:175:GLY:HA2	6:CD:203:TRP:HH2	1.83	0.43
25:CW:94:ILE:HG13	25:CW:194:MET:HB3	1.99	0.43
25:CW:457:GLN:CD	25:CW:457:GLN:H	2.25	0.43
38:LO:77:ALA:HB3	38:LO:80:ARG:HG3	2.00	0.43
1:C1:1330:A:OP2	40:LQ:66:ARG:NH2	2.47	0.43
1:C1:3189:G:H2'	1:C1:3190:G:H8	1.84	0.43
2:C2:133:C:H2'	2:C2:134:G:H8	1.83	0.43
3:CA:129:GLN:NE2	23:CU:289:LEU:HD21	2.33	0.43
7:CE:355:MET:HE2	7:CE:358:LYS:HD2	2.00	0.43
55:LI:101:ARG:HE	55:LI:101:ARG:HB2	1.48	0.43
59:Lq:68:LEU:HB3	59:Lq:116:LEU:HD11	1.99	0.43
1:C1:745:U:N3	1:C1:749:C:N4	2.67	0.43
1:C1:2973:A:H2'	1:C1:2974:G:C8	2.53	0.43
18:CP:535:LYS:HB3	18:CP:535:LYS:HE3	1.85	0.43
26:CX:112:LYS:HE3	26:CX:112:LYS:HB3	1.79	0.43
30:LC:9:VAL:HG13	30:LC:152:VAL:HG12	1.99	0.43
1:C1:117:U:O2'	1:C1:119:U:OP2	2.28	0.43
1:C1:231:A:H2'	1:C1:232:G:C8	2.53	0.43
1:C1:1675:A:H4'	53:Lg:24:ILE:HD12	2.01	0.43
1:C1:1954:C:N3	1:C1:2015:U:O2	2.52	0.43
1:C1:1989:G:H2'	1:C1:1990:G:C8	2.54	0.43
1:C1:3265:A:H2'	1:C1:3266:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CC:457:ARG:NE	5:CC:473:ASP:OD1	2.52	0.43
7:CE:438:PRO:HG2	7:CE:527:LEU:HD12	2.00	0.43
9:CG:109:LEU:HD21	9:CG:142:LEU:HD22	2.00	0.43
15:CM:127:LYS:HD2	15:CM:127:LYS:HA	1.86	0.43
18:CP:268:LYS:HA	18:CP:268:LYS:HD2	1.89	0.43
18:CP:476:ASP:OD1	18:CP:476:ASP:N	2.51	0.43
30:LC:37:LYS:HB3	30:LC:37:LYS:HE2	1.76	0.43
39:LP:140:MET:HE3	39:LP:140:MET:HB2	1.79	0.43
58:Ll:25:GLN:CD	58:Ll:25:GLN:H	2.26	0.43
1:C1:194:G:H2'	1:C1:195:G:C8	2.53	0.43
1:C1:1933:G:N1	1:C1:2050:G:N7	2.66	0.43
1:C1:3274:U:H4'	1:C1:3275:A:H5'	2.01	0.43
2:C2:159:C:N4	32:LG:88:ASN:OD1	2.47	0.43
4:CB:103:ASP:O	4:CB:104:PRO:C	2.62	0.43
6:CD:410:ASP:OD1	6:CD:410:ASP:N	2.51	0.43
6:CD:443:ARG:HA	6:CD:443:ARG:HD2	1.77	0.43
15:CM:39:ARG:HA	15:CM:39:ARG:HD3	1.86	0.43
25:CW:374:GLN:HB2	25:CW:402:VAL:HA	2.01	0.43
29:LB:109:HIS:HB2	29:LB:201:GLU:OE2	2.19	0.43
59:Lq:60:ARG:HB3	59:Lq:63:MET:HE2	2.01	0.43
1:C1:616:C:H2'	1:C1:617:C:C6	2.54	0.43
1:C1:1171:C:N3	1:C1:1297:U:C2	2.87	0.43
1:C1:1176:G:H2'	1:C1:1177:A:C8	2.53	0.43
1:C1:1479:C:H2'	1:C1:1480:A:H8	1.84	0.43
1:C1:2394:A:N1	1:C1:2556:G:C6	2.87	0.43
3:CA:138:PRO:HB3	3:CA:178:HIS:NE2	2.33	0.43
7:CE:352:LEU:HD22	7:CE:360:ILE:HG21	2.00	0.43
7:CE:512:LYS:HB3	7:CE:512:LYS:HE3	1.79	0.43
9:CG:48:VAL:HG11	9:CG:67:LEU:HD23	2.01	0.43
9:CG:99:TRP:CE3	9:CG:121:ARG:HB3	2.54	0.43
10:CH:42:ARG:NH2	10:CH:118:ALA:O	2.46	0.43
19:CQ:14:TRP:O	19:CQ:30:ARG:NH2	2.49	0.43
20:CR:35:ILE:HG21	35:LL:47:ALA:HB1	2.01	0.43
25:CW:279:SER:N	25:CW:488:ASP:OD2	2.47	0.43
25:CW:326:ILE:HD12	25:CW:326:ILE:HA	1.82	0.43
27:CY:440:SER:O	27:CY:444:LEU:HG	2.19	0.43
37:LN:192:LYS:O	37:LN:196:THR:HG23	2.19	0.43
45:LV:68:LYS:HE3	45:LV:68:LYS:HB2	1.83	0.43
50:Ld:80:ARG:HG3	50:Ld:104:VAL:HG22	2.00	0.43
54:Lh:88:LYS:O	54:Lh:94:ARG:NH1	2.44	0.43
2:C2:305:C:OP1	15:CM:107:LYS:NZ	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CB:68:THR:OG1	4:CB:70:LYS:O	2.31	0.43
6:CD:255:SER:HB2	6:CD:258:SER:HB3	2.00	0.43
16:CN:100:ARG:NH2	16:CN:122:GLU:OE2	2.52	0.43
18:CP:284:LEU:HD22	18:CP:296:PHE:HE2	1.84	0.43
25:CW:409:GLU:OE1	25:CW:409:GLU:N	2.49	0.43
27:CY:679:LYS:HD2	27:CY:721:TYR:CD2	2.54	0.43
46:LX:63:SER:HB3	54:Lh:71:LEU:HD13	2.00	0.43
59:Lq:17:LEU:HA	59:Lq:18:ASP:HA	1.57	0.43
1:C1:2000:C:H2'	1:C1:2001:U:C6	2.54	0.43
1:C1:2076:C:H2'	1:C1:2077:G:H8	1.84	0.43
1:C1:2786:G:O6	10:CH:22:SER:OG	2.37	0.43
3:CA:265:ASN:OD1	3:CA:268:ARG:NH1	2.52	0.43
5:CC:268:LYS:HB3	5:CC:268:LYS:HE3	1.89	0.43
5:CC:359:GLU:HG2	12:CJ:667:ARG:HB2	2.01	0.43
10:CH:65:SER:O	10:CH:65:SER:OG	2.28	0.43
14:CL:468:LEU:HA	14:CL:474:PRO:HA	2.01	0.43
16:CN:70:LEU:HD23	16:CN:94:ILE:HG12	2.00	0.43
22:CT:163:ILE:HD12	22:CT:163:ILE:H	1.84	0.43
22:CT:259:ARG:HH22	22:CT:297:ASN:HB3	1.83	0.43
47:LY:1:MET:HE2	47:LY:1:MET:HB3	1.85	0.43
1:C1:3211:G:C4	31:LE:132:LYS:HD2	2.54	0.42
10:CH:281:MET:H	10:CH:281:MET:HG2	1.61	0.42
21:CS:164:ASP:HA	21:CS:167:LYS:HD2	2.00	0.42
25:CW:22:LEU:HB3	25:CW:50:ARG:HH12	1.84	0.42
1:C1:248:G:O2'	20:CR:148:GLN:OE1	2.21	0.42
1:C1:1877:G:N2	1:C1:1880:A:C5	2.87	0.42
1:C1:1967:G:H2'	1:C1:1968:A:H8	1.83	0.42
1:C1:2385:U:H2'	1:C1:2386:A:H8	1.85	0.42
1:C1:2890:U:H3'	45:LV:6:ARG:HH12	1.83	0.42
2:C2:298:G:H3'	11:CI:291:ARG:HH12	1.84	0.42
4:CB:62:ILE:HD11	4:CB:283:VAL:HG12	2.01	0.42
4:CB:83:ILE:HG21	4:CB:262:VAL:HG22	2.01	0.42
10:CH:258:GLN:HG3	34:LK:33:GLY:HA3	2.00	0.42
24:CV:17:ASN:HD21	24:CV:19:PHE:HD2	1.67	0.42
27:CY:705:ASP:OD1	27:CY:705:ASP:N	2.50	0.42
48:LZ:3:PHE:O	48:LZ:8:ARG:NE	2.51	0.42
1:C1:508:G:H3'	1:C1:509:A:H3'	2.02	0.42
1:C1:540:A:H2'	1:C1:541:G:H8	1.84	0.42
1:C1:1070:U:H2'	1:C1:1071:G:H8	1.83	0.42
1:C1:1386:G:N2	1:C1:1389:A:OP2	2.39	0.42
6:CD:131:SER:OG	6:CD:138:ALA:O	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CG:71:LEU:HA	9:CG:86:ALA:HB2	2.00	0.42
10:CH:471:GLU:OE1	10:CH:471:GLU:N	2.53	0.42
12:CJ:119:PRO:HB3	12:CJ:232:GLU:HG2	2.00	0.42
16:CN:114:THR:HG21	16:CN:177:LEU:HG	2.01	0.42
20:CR:204:ASP:OD1	20:CR:204:ASP:N	2.52	0.42
21:CS:48:VAL:HG13	21:CS:72:LEU:HB3	2.01	0.42
25:CW:59:ALA:HA	25:CW:249:VAL:HG22	2.01	0.42
25:CW:609:LEU:HA	25:CW:612:LEU:HG	2.01	0.42
30:LC:299:VAL:HG21	40:LQ:159:PRO:HG2	2.01	0.42
31:LE:12:LYS:HD3	31:LE:15:ARG:NH1	2.34	0.42
37:LN:103:GLU:OE2	37:LN:118:SER:OG	2.36	0.42
42:LS:106:MET:HE3	42:LS:106:MET:HB3	1.75	0.42
44:LU:42:PHE:HZ	44:LU:89:LYS:HG2	1.84	0.42
1:C1:403:U:H2'	1:C1:404:G:H8	1.85	0.42
3:CA:58:MET:HE1	3:CA:193:ASN:ND2	2.34	0.42
8:CF:165:LEU:HD22	8:CF:170:MET:HE3	2.02	0.42
13:CK:104:SER:HA	13:CK:107:LYS:HG3	2.02	0.42
18:CP:502:SER:OG	18:CP:504:THR:O	2.35	0.42
20:CR:170:ARG:HB3	20:CR:174:ARG:HH21	1.84	0.42
21:CS:292:LEU:HD12	21:CS:295:LEU:HD12	2.01	0.42
22:CT:381:MET:HE2	22:CT:381:MET:HA	2.01	0.42
27:CY:430:GLY:O	27:CY:431:CYS:C	2.62	0.42
29:LB:17:LEU:HD22	29:LB:263:TRP:HE3	1.84	0.42
32:LG:54:LYS:HB3	32:LG:54:LYS:HE2	1.89	0.42
35:LL:42:LYS:HE2	35:LL:42:LYS:HB2	1.85	0.42
35:LL:128:ARG:HD2	35:LL:128:ARG:HA	1.80	0.42
49:Lc:27:VAL:HB	49:Lc:32:SER:HB3	2.02	0.42
1:C1:19:U:H2'	1:C1:20:A:C8	2.55	0.42
1:C1:66:A:N6	1:C1:75:G:H22	2.16	0.42
1:C1:3200:A:H1'	36:LM:129:PHE:CD2	2.55	0.42
3:CA:272:ARG:HE	3:CA:272:ARG:HB3	1.65	0.42
10:CH:466:GLU:OE2	10:CH:470:LYS:NZ	2.52	0.42
22:CT:286:LEU:HD23	22:CT:286:LEU:HA	1.82	0.42
27:CY:556:ARG:NH2	27:CY:621:GLN:OE1	2.49	0.42
42:LS:81:TYR:CE1	42:LS:90:MET:HE3	2.54	0.42
1:C1:155:G:H2'	1:C1:156:G:C8	2.54	0.42
1:C1:1241:A:H2'	1:C1:1242:A:C8	2.55	0.42
1:C1:1948:G:H2'	1:C1:1949:G:C8	2.55	0.42
1:C1:1995:C:N4	1:C1:1996:G:O6	2.53	0.42
1:C1:2374:G:H4'	9:CG:81:ARG:HH12	1.85	0.42
20:CR:4:GLU:HA	20:CR:7:LYS:HE3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CR:136:GLN:NE2	35:LL:110:ALA:O	2.46	0.42
29:LB:188:SER:OG	29:LB:191:ASP:OD1	2.34	0.42
41:LR:117:LYS:HB2	41:LR:117:LYS:HE2	1.91	0.42
42:LS:78:TRP:CE2	42:LS:124:LEU:HD13	2.54	0.42
42:LS:169:ARG:HA	42:LS:170:PRO:HD3	1.93	0.42
59:Lq:46:ASP:OD1	59:Lq:46:ASP:N	2.53	0.42
1:C1:473:C:H2'	1:C1:474:G:H8	1.85	0.42
1:C1:733:C:H2'	1:C1:734:C:H6	1.84	0.42
1:C1:2317:G:OP1	39:LP:141:SER:OG	2.31	0.42
10:CH:329:GLU:OE1	10:CH:329:GLU:N	2.51	0.42
25:CW:59:ALA:HB3	25:CW:65:LYS:HD3	2.01	0.42
27:CY:657:MET:SD	27:CY:657:MET:N	2.93	0.42
27:CY:665:LYS:HD3	27:CY:665:LYS:HA	1.95	0.42
29:LB:87:VAL:HB	29:LB:110:LEU:HD11	2.02	0.42
30:LC:55:GLU:H	30:LC:55:GLU:CD	2.28	0.42
48:LZ:60:ARG:O	48:LZ:64:ARG:HG3	2.19	0.42
1:C1:581:G:H1'	31:LE:37:LYS:HG3	2.02	0.42
1:C1:1201:C:O2	28:Cz:51:ARG:NH2	2.52	0.42
1:C1:1516:A:H2'	1:C1:1517:A:C8	2.55	0.42
2:C2:219:A:H5''	11:CI:222:LYS:NZ	2.34	0.42
4:CB:87:HIS:CE1	4:CB:254:LYS:HG3	2.55	0.42
5:CC:588:ARG:HD3	5:CC:613:SER:HB2	2.01	0.42
12:CJ:141:LEU:HD23	12:CJ:141:LEU:HA	1.90	0.42
22:CT:137:GLN:H	22:CT:137:GLN:HG2	1.61	0.42
22:CT:162:ALA:O	22:CT:166:LEU:HD12	2.20	0.42
24:CV:9:ILE:HG22	24:CV:47:VAL:HG22	2.02	0.42
25:CW:212:ILE:HD13	25:CW:212:ILE:HA	1.87	0.42
27:CY:687:ILE:O	27:CY:691:ARG:HB2	2.20	0.42
28:Cz:29:GLY:HA3	33:LH:186:LYS:HE3	2.00	0.42
29:LB:36:ASP:N	29:LB:36:ASP:OD1	2.53	0.42
29:LB:161:VAL:HG23	29:LB:184:ILE:HD11	2.01	0.42
30:LC:136:LEU:HD23	30:LC:143:VAL:HG21	2.02	0.42
34:LK:50:THR:OG1	34:LK:51:ALA:N	2.53	0.42
42:LS:1:MET:HG3	42:LS:118:PHE:CD1	2.54	0.42
43:LT:85:ILE:H	43:LT:85:ILE:HG13	1.60	0.42
53:Lg:80:SER:HB3	53:Lg:81:ARG:HH11	1.84	0.42
56:Lj:35:ALA:O	56:Lj:45:ARG:NH2	2.40	0.42
1:C1:209:G:OP1	47:LY:15:ARG:NH1	2.48	0.42
1:C1:409:A:H2'	1:C1:410:A:C8	2.54	0.42
1:C1:616:C:H2'	1:C1:617:C:H6	1.85	0.42
6:CD:174:GLY:O	6:CD:201:ARG:NH1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CD:451:LYS:HE3	6:CD:451:LYS:HB3	1.83	0.42
7:CE:434:PRO:HB3	7:CE:531:PHE:CE1	2.55	0.42
18:CP:357:TYR:HB2	18:CP:362:TYR:CZ	2.55	0.42
22:CT:318:ASP:O	22:CT:319:GLU:HG3	2.20	0.42
25:CW:273:TYR:HB3	25:CW:423:ILE:HD11	2.01	0.42
29:LB:89:LEU:HD13	29:LB:196:GLY:HA3	2.02	0.42
30:LC:94:MET:HE3	30:LC:94:MET:HB3	1.89	0.42
15:LF:96:LYS:HD3	15:LF:225:PHE:CE1	2.54	0.42
55:Li:74:LYS:H	55:Li:74:LYS:HG2	1.72	0.42
1:C1:1210:A:H5'	8:CF:203:SER:HB2	2.01	0.42
1:C1:1725:C:O2'	57:Lk:4:GLU:OE1	2.30	0.42
7:CE:485:PHE:HE1	7:CE:490:ILE:HD11	1.84	0.42
18:CP:306:VAL:HG23	18:CP:344:VAL:HB	2.01	0.42
23:CU:276:VAL:HG23	23:CU:277:ARG:HG3	2.02	0.42
25:CW:22:LEU:HA	25:CW:50:ARG:HH22	1.85	0.42
25:CW:30:VAL:HG23	25:CW:35:TYR:HD2	1.85	0.42
28:Cz:68:MET:HE2	28:Cz:68:MET:HB3	1.82	0.42
48:LZ:82:THR:HG23	53:Lg:94:PHE:CZ	2.55	0.42
1:C1:649:U:H2'	1:C1:650:C:C6	2.55	0.41
1:C1:1576:C:H2'	1:C1:1577:G:C8	2.54	0.41
1:C1:1594:C:H2'	1:C1:1595:U:C6	2.55	0.41
5:CC:403:ARG:HD2	12:CJ:147:MET:HG2	2.01	0.41
6:CD:131:SER:HA	6:CD:137:ALA:HB3	2.02	0.41
6:CD:153:GLY:HA2	6:CD:180:ILE:HG13	2.02	0.41
10:CH:395:LYS:H	10:CH:395:LYS:HG2	1.55	0.41
12:CJ:97:ARG:NH2	32:LG:195:LYS:O	2.53	0.41
20:CR:218:TYR:HB2	20:CR:220:GLN:HE21	1.85	0.41
24:CV:64:ILE:HD12	24:CV:78:LEU:HD13	2.02	0.41
26:CX:116:ILE:HG21	26:CX:121:MET:HE2	2.02	0.41
51:Le:81:LYS:HB3	51:Le:81:LYS:HE3	1.90	0.41
1:C1:745:U:O2	1:C1:749:C:C4	2.73	0.41
1:C1:894:A:C6	21:CS:727:ALA:HB1	2.56	0.41
1:C1:1082:U:H2'	1:C1:1083:G:O4'	2.21	0.41
1:C1:1120:U:H2'	1:C1:1121:G:H8	1.85	0.41
1:C1:1227:A:H2'	1:C1:1254:C:OP1	2.20	0.41
10:CH:385:GLU:OE1	10:CH:385:GLU:N	2.53	0.41
25:CW:227:ALA:HB3	25:CW:386:HIS:CE1	2.55	0.41
25:CW:278:ALA:HA	25:CW:281:LYS:HE2	2.01	0.41
25:CW:393:ARG:HE	25:CW:393:ARG:HB2	1.58	0.41
29:LB:287:GLY:HA3	29:LB:322:TYR:CE1	2.55	0.41
15:LF:148:LYS:O	15:LF:152:GLU:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LR:146:LYS:HE3	41:LR:146:LYS:HB3	1.89	0.41
51:Le:48:LYS:HB2	51:Le:48:LYS:HE2	1.82	0.41
1:C1:729:U:H2'	1:C1:730:C:C6	2.55	0.41
1:C1:1066:A:H2'	1:C1:1067:A:C8	2.55	0.41
1:C1:1237:C:H2'	1:C1:1238:G:H8	1.86	0.41
1:C1:1697:A:H2'	1:C1:1698:G:H8	1.86	0.41
8:CF:141:ILE:HA	8:CF:180:CYS:HB3	2.02	0.41
9:CG:13:LEU:HD13	26:CX:105:LEU:HD13	2.03	0.41
10:CH:221:PRO:HD2	10:CH:238:SER:HB2	2.01	0.41
25:CW:376:ASP:OD1	25:CW:376:ASP:N	2.53	0.41
25:CW:460:GLN:O	25:CW:464:VAL:HG12	2.20	0.41
43:LT:75:ILE:HG12	43:LT:88:ARG:HG2	2.02	0.41
54:Lh:42:SER:HB3	54:Lh:46:LEU:HD11	2.02	0.41
1:C1:539:G:H2'	1:C1:540:A:H8	1.85	0.41
1:C1:2727:A:H2'	1:C1:2728:G:C8	2.54	0.41
1:C1:2796:A:H2'	1:C1:2797:G:O4'	2.20	0.41
1:C1:3220:A:H2'	1:C1:3221:C:C6	2.55	0.41
3:CA:124:GLU:N	3:CA:124:GLU:OE1	2.54	0.41
4:CB:104:PRO:HD2	4:CB:206:ARG:HH22	1.85	0.41
7:CE:519:ILE:H	7:CE:519:ILE:HG12	1.72	0.41
8:CF:69:LYS:O	8:CF:73:MET:HG3	2.21	0.41
8:CF:92:LEU:HD12	8:CF:92:LEU:HA	1.94	0.41
18:CP:495:ILE:O	18:CP:583:LYS:NZ	2.42	0.41
21:CS:75:GLY:N	21:CS:88:ILE:O	2.52	0.41
21:CS:238:LYS:HA	21:CS:238:LYS:HD2	1.83	0.41
21:CS:371:GLU:HA	21:CS:374:LYS:HB3	2.01	0.41
25:CW:340:LYS:HE2	25:CW:340:LYS:HB3	1.85	0.41
25:CW:382:LYS:HB2	25:CW:382:LYS:HE3	1.62	0.41
29:LB:168:ARG:H	29:LB:168:ARG:HG3	1.71	0.41
30:LC:173:LEU:HD23	30:LC:173:LEU:HA	1.92	0.41
34:LK:151:ILE:O	34:LK:155:ILE:HG13	2.20	0.41
51:Le:62:LYS:HB2	51:Le:62:LYS:HE2	1.77	0.41
59:Lq:102:LYS:H	59:Lq:102:LYS:HD2	1.84	0.41
1:C1:151:G:OP2	55:Li:35:PRO:HG2	2.19	0.41
2:C2:163:C:H42	4:CB:165:LYS:HG3	1.86	0.41
4:CB:215:ARG:NH2	4:CB:219:GLU:OE1	2.53	0.41
7:CE:328:THR:HG22	7:CE:332:LEU:HD22	2.01	0.41
12:CJ:256:LYS:HE3	12:CJ:256:LYS:HB3	1.81	0.41
23:CU:226:THR:O	23:CU:226:THR:OG1	2.38	0.41
25:CW:150:LYS:O	25:CW:154:ASP:HB2	2.21	0.41
30:LC:13:ASP:N	30:LC:13:ASP:OD1	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:LS:27:MET:HE1	42:LS:44:PHE:CD2	2.55	0.41
1:C1:889:G:H2'	1:C1:890:G:C8	2.56	0.41
1:C1:1595:U:H2'	1:C1:1596:G:H8	1.85	0.41
1:C1:2477:A:N1	1:C1:2552:C:N4	2.62	0.41
1:C1:2972:C:OP2	17:CO:2:ALA:N	2.53	0.41
14:CL:57:ASN:HA	28:Cz:61:MET:HE1	2.02	0.41
18:CP:283:LYS:HD3	18:CP:516:CYS:SG	2.60	0.41
19:CQ:26:GLY:HA2	45:LV:139:MET:HE2	2.03	0.41
21:CS:15:LYS:HA	21:CS:18:LYS:HE3	2.02	0.41
21:CS:728:ARG:NH2	26:CX:117:GLU:OE1	2.54	0.41
22:CT:441:ASP:HB3	26:CX:120:ILE:HD12	2.01	0.41
27:CY:632:LEU:HB2	27:CY:633:TRP:CD1	2.55	0.41
59:Lq:32:VAL:HG23	59:Lq:208:ALA:HA	2.01	0.41
59:Lq:59:PRO:C	59:Lq:61:PRO:HD3	2.46	0.41
1:C1:508:G:OP2	15:LF:73:ARG:NH2	2.39	0.41
1:C1:711:G:O6	1:C1:728:A:N6	2.54	0.41
1:C1:1046:A:N7	1:C1:1079:G:N2	2.62	0.41
1:C1:1954:C:N4	1:C1:2015:U:C4	2.86	0.41
1:C1:1960:G:H2'	1:C1:1961:G:H8	1.86	0.41
1:C1:3180:C:H2'	1:C1:3181:C:O4'	2.20	0.41
3:CA:89:VAL:HG23	3:CA:107:VAL:HG22	2.01	0.41
5:CC:672:PRO:HG2	5:CC:677:ILE:HD11	2.02	0.41
7:CE:292:THR:HG21	7:CE:311:LEU:HA	2.03	0.41
8:CF:97:THR:OG1	8:CF:243:ARG:NH2	2.53	0.41
9:CG:60:ALA:HB3	9:CG:63:LYS:HB2	2.02	0.41
16:CN:142:ILE:HD12	16:CN:173:LEU:HD11	2.02	0.41
18:CP:270:ILE:HG23	18:CP:274:TYR:HD2	1.84	0.41
22:CT:601:LEU:HD23	22:CT:601:LEU:HA	1.90	0.41
25:CW:270:GLN:NE2	25:CW:272:SER:OG	2.54	0.41
29:LB:159:VAL:HG12	29:LB:192:LYS:HD3	2.03	0.41
1:C1:889:G:H2'	1:C1:890:G:H8	1.86	0.41
1:C1:1452:U:OP1	1:C1:1491:G:N2	2.44	0.41
1:C1:2735:G:N2	1:C1:2741:U:O2	2.41	0.41
2:C2:8:C:H2'	2:C2:9:A:C8	2.56	0.41
4:CB:185:MET:N	4:CB:215:ARG:HD2	2.36	0.41
5:CC:794:ASP:N	5:CC:794:ASP:OD1	2.47	0.41
6:CD:116:ALA:HB3	6:CD:149:ALA:HB3	2.02	0.41
12:CJ:266:ALA:HB3	12:CJ:270:ALA:HB2	2.02	0.41
12:CJ:416:THR:OG1	12:CJ:417:HIS:ND1	2.50	0.41
21:CS:357:GLU:OE1	21:CS:357:GLU:N	2.47	0.41
27:CY:627:SER:O	27:CY:631:VAL:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:LL:85:ILE:HD11	35:LL:120:LYS:HD2	2.03	0.41
48:LZ:2:LYS:NZ	48:LZ:29:ASP:OD2	2.50	0.41
59:Lq:59:PRO:HB3	59:Lq:174:MET:HE1	2.03	0.41
1:C1:264:G:H2'	1:C1:265:A:H8	1.86	0.41
1:C1:940:C:C4	23:CU:299:ALA:HB2	2.56	0.41
1:C1:1171:C:C4	1:C1:1297:U:O2	2.73	0.41
1:C1:1556:C:H2'	1:C1:1557:C:C6	2.56	0.41
1:C1:1967:G:H2'	1:C1:1968:A:C8	2.56	0.41
1:C1:2047:U:H2'	1:C1:2048:G:H8	1.84	0.41
1:C1:2076:C:H2'	1:C1:2077:G:C8	2.56	0.41
1:C1:2830:A:N6	1:C1:2883:C:N3	2.68	0.41
1:C1:3220:A:O2'	17:CO:110:MET:O	2.35	0.41
2:C2:233:U:H3	2:C2:284:G:H1	1.69	0.41
5:CC:241:LYS:NZ	5:CC:248:PRO:O	2.51	0.41
6:CD:319:ASP:OD1	6:CD:319:ASP:N	2.47	0.41
10:CH:178:GLY:HA3	10:CH:287:ASN:ND2	2.36	0.41
12:CJ:136:ASP:OD2	12:CJ:136:ASP:N	2.53	0.41
18:CP:325:ILE:HG23	21:CS:69:LYS:HD2	2.02	0.41
18:CP:465:ILE:HD13	18:CP:465:ILE:HA	1.91	0.41
20:CR:19:MET:HE1	56:Lj:75:LYS:HB2	2.02	0.41
20:CR:48:ASN:OD1	20:CR:51:ARG:NH2	2.53	0.41
21:CS:716:GLN:HA	21:CS:719:LYS:NZ	2.36	0.41
22:CT:274:LYS:HB3	22:CT:274:LYS:HE3	1.73	0.41
22:CT:296:GLY:HA3	22:CT:330:LEU:HD21	2.02	0.41
25:CW:455:VAL:HA	25:CW:458:LEU:HB2	2.01	0.41
25:CW:486:TRP:HA	25:CW:489:LEU:HD12	2.03	0.41
30:LC:8:THR:HB	30:LC:148:GLU:HG3	2.03	0.41
44:LU:43:LEU:HD23	44:LU:43:LEU:HA	1.93	0.41
48:LZ:13:THR:HA	53:Lg:90:ILE:HD12	2.02	0.41
59:Lq:180:VAL:HA	59:Lq:183:ILE:HG12	2.03	0.41
1:C1:1595:U:H2'	1:C1:1596:G:C8	2.56	0.41
1:C1:2050:G:C6	1:C1:2051:G:C2	3.10	0.41
10:CH:390:LEU:HD21	16:CN:43:GLN:HB2	2.03	0.41
11:CI:203:LEU:HD23	11:CI:203:LEU:HA	1.88	0.41
21:CS:49:VAL:HG13	21:CS:73:ILE:HA	2.03	0.41
22:CT:403:MET:HE3	22:CT:403:MET:HB2	1.92	0.41
27:CY:471:LEU:HD22	27:CY:495:TYR:HE1	1.86	0.41
50:Ld:28:LEU:O	50:Ld:36:ARG:NH2	2.54	0.41
54:Lh:6:LYS:H	54:Lh:6:LYS:HG2	1.68	0.41
59:Lq:98:LYS:HE2	59:Lq:98:LYS:N	2.36	0.41
1:C1:868:G:H2'	1:C1:869:A:C8	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1576:C:H2'	1:C1:1577:G:H8	1.86	0.40
1:C1:1935:A:N6	1:C1:2048:G:O6	2.54	0.40
4:CB:272:PRO:HB2	4:CB:273:GLN:OE1	2.21	0.40
5:CC:364:LYS:H	5:CC:364:LYS:HG2	1.57	0.40
5:CC:750:PRO:HG2	5:CC:755:GLU:HB3	2.03	0.40
6:CD:21:THR:OG1	6:CD:22:THR:N	2.54	0.40
6:CD:362:THR:HG21	6:CD:366:HIS:HE1	1.86	0.40
8:CF:60:LEU:HB3	8:CF:63:CYS:SG	2.61	0.40
12:CJ:125:HIS:O	12:CJ:129:GLU:HG2	2.21	0.40
19:CQ:27:LYS:HA	19:CQ:27:LYS:HD3	1.88	0.40
19:CQ:93:MET:HA	19:CQ:96:ILE:HB	2.02	0.40
25:CW:608:GLU:HA	25:CW:611:LYS:HD3	2.02	0.40
30:LC:233:GLU:HG3	30:LC:253:ARG:HH22	1.86	0.40
33:LH:46:SER:N	33:LH:54:GLY:O	2.55	0.40
49:Lc:56:LYS:HZ3	49:Lc:56:LYS:HB2	1.85	0.40
54:Lh:8:LYS:HB2	54:Lh:11:GLN:HG2	2.03	0.40
1:C1:734:C:H2'	1:C1:735:G:H8	1.84	0.40
1:C1:1224:G:H1	10:CH:201:LYS:HE3	1.86	0.40
1:C1:1548:C:C2	5:CC:408:MET:HE1	2.57	0.40
1:C1:1988:C:H2'	1:C1:1989:G:H8	1.85	0.40
3:CA:29:GLU:OE1	3:CA:29:GLU:N	2.54	0.40
5:CC:528:HIS:O	5:CC:531:VAL:HG22	2.21	0.40
11:CI:242:ASP:HA	11:CI:262:ILE:HD11	2.03	0.40
12:CJ:470:LEU:HD23	12:CJ:470:LEU:HA	1.91	0.40
15:CM:91:PHE:HB2	15:CM:145:PRO:HG3	2.03	0.40
20:CR:175:GLU:HG2	20:CR:178:ARG:HH21	1.87	0.40
21:CS:491:ARG:NH1	22:CT:381:MET:HE3	2.37	0.40
21:CS:729:PRO:HG2	21:CS:732:LYS:HG3	2.02	0.40
21:CS:806:LYS:HA	21:CS:806:LYS:HE2	2.03	0.40
22:CT:667:HIS:HA	27:CY:568:TYR:HB3	2.02	0.40
25:CW:198:ASP:HB2	25:CW:229:LEU:HD12	2.03	0.40
30:LC:353:LYS:HB2	30:LC:353:LYS:HE2	1.86	0.40
1:C1:301:U:H5''	7:CE:578:ARG:HD2	2.02	0.40
1:C1:660:C:H2'	1:C1:661:G:C8	2.56	0.40
1:C1:983:A:N1	1:C1:1032:U:O2'	2.55	0.40
1:C1:2045:C:H2'	1:C1:2046:G:C8	2.56	0.40
1:C1:3334:U:H4'	39:LP:43:ARG:HH21	1.86	0.40
2:C2:44:A:H2'	2:C2:45:C:C6	2.56	0.40
7:CE:571:ARG:NH1	7:CE:575:SER:OG	2.54	0.40
8:CF:132:PRO:HD2	8:CF:216:LEU:HD23	2.03	0.40
9:CG:37:VAL:HG11	9:CG:50:LEU:HD13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CH:281:MET:HE1	10:CH:341:GLU:HG2	2.02	0.40
15:LF:155:TYR:OH	15:LF:188:GLU:OE1	2.40	0.40
38:LO:111:PRO:HA	38:LO:112:PRO:HD3	1.87	0.40
41:LR:96:MET:HE3	41:LR:96:MET:HB2	1.82	0.40
49:Lc:9:GLU:HG3	49:Lc:12:SER:HB3	2.03	0.40
53:Lg:86:VAL:O	53:Lg:90:ILE:HG13	2.20	0.40
1:C1:2043:G:H8	1:C1:2044:G:H5'	1.87	0.40
1:C1:3068:U:O2'	33:LH:154:GLU:OE2	2.30	0.40
1:C1:3319:C:H4'	29:LB:316:GLY:HA2	2.02	0.40
11:CI:219:VAL:HG23	11:CI:228:ARG:HB2	2.03	0.40
13:CK:228:LEU:HD23	13:CK:228:LEU:HA	1.91	0.40
20:CR:198:LEU:HG	20:CR:209:MET:HB3	2.03	0.40
21:CS:238:LYS:HE3	21:CS:240:ARG:HH21	1.86	0.40
25:CW:501:MET:HA	25:CW:502:PRO:HD3	1.99	0.40
27:CY:615:GLN:HA	27:CY:618:VAL:HG12	2.03	0.40
15:LF:25:GLN:OE1	15:LF:29:ARG:NH1	2.41	0.40
33:LH:4:ILE:HD12	42:LS:142:GLN:HG3	2.03	0.40
34:LK:82:ILE:HD12	34:LK:82:ILE:H	1.86	0.40
47:LY:57:ILE:HD11	47:LY:81:VAL:HG11	2.03	0.40
2:C2:175:G:H2'	2:C2:176:G:C8	2.55	0.40
4:CB:22:GLN:HA	4:CB:25:LYS:HG2	2.04	0.40
6:CD:179:SER:OG	6:CD:180:ILE:N	2.55	0.40
6:CD:357:LEU:HD12	6:CD:357:LEU:HA	1.94	0.40
10:CH:348:LYS:HE2	10:CH:348:LYS:HB2	1.93	0.40
10:CH:390:LEU:HD11	16:CN:43:GLN:HB2	2.04	0.40
10:CH:485:GLU:HB2	19:CQ:120:VAL:HG21	2.02	0.40
12:CJ:52:LYS:HB3	12:CJ:52:LYS:HE3	1.82	0.40
25:CW:368:GLN:HA	25:CW:396:ARG:HH21	1.87	0.40
30:LC:296:ILE:HD13	40:LQ:159:PRO:HB3	2.03	0.40
33:LH:21:LYS:HD3	33:LH:21:LYS:HA	1.83	0.40
47:LY:62:HIS:HB3	47:LY:65:LYS:HE3	2.03	0.40
54:Lh:34:LEU:HD21	54:Lh:49:ILE:HG13	2.02	0.40
55:Li:67:ILE:HG23	55:Li:71:ARG:HE	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	235 (95%)	12 (5%)	0	100	100
4	CB	256/391 (66%)	242 (94%)	12 (5%)	2 (1%)	16	37
5	CC	650/801 (81%)	625 (96%)	24 (4%)	1 (0%)	43	68
6	CD	450/495 (91%)	429 (95%)	21 (5%)	0	100	100
7	CE	461/598 (77%)	440 (95%)	20 (4%)	1 (0%)	43	68
8	CF	243/270 (90%)	232 (96%)	10 (4%)	1 (0%)	30	54
9	CG	175/184 (95%)	169 (97%)	6 (3%)	0	100	100
10	CH	538/661 (81%)	517 (96%)	21 (4%)	0	100	100
11	CI	144/414 (35%)	139 (96%)	5 (4%)	0	100	100
12	CJ	484/679 (71%)	468 (97%)	16 (3%)	0	100	100
13	CK	223/261 (85%)	216 (97%)	7 (3%)	0	100	100
14	CL	384/558 (69%)	353 (92%)	25 (6%)	6 (2%)	7	20
15	CM	219/249 (88%)	208 (95%)	11 (5%)	0	100	100
15	LF	245/249 (98%)	236 (96%)	9 (4%)	0	100	100
16	CN	244/246 (99%)	229 (94%)	15 (6%)	0	100	100
17	CO	56/120 (47%)	55 (98%)	1 (2%)	0	100	100
18	CP	322/751 (43%)	309 (96%)	13 (4%)	0	100	100
19	CQ	173/225 (77%)	169 (98%)	4 (2%)	0	100	100
20	CR	159/237 (67%)	154 (97%)	5 (3%)	0	100	100
21	CS	607/834 (73%)	577 (95%)	29 (5%)	1 (0%)	43	68
22	CT	478/688 (70%)	454 (95%)	23 (5%)	1 (0%)	43	68
23	CU	174/451 (39%)	169 (97%)	4 (2%)	1 (1%)	21	44
24	CV	137/147 (93%)	131 (96%)	5 (4%)	1 (1%)	18	41
25	CW	531/679 (78%)	495 (93%)	34 (6%)	2 (0%)	30	54
26	CX	86/203 (42%)	85 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	CY	366/788 (46%)	346 (94%)	19 (5%)	1 (0%)	36	60
28	Cz	68/123 (55%)	65 (96%)	3 (4%)	0	100	100
29	LB	352/392 (90%)	338 (96%)	14 (4%)	0	100	100
30	LC	360/365 (99%)	345 (96%)	15 (4%)	0	100	100
31	LE	185/200 (92%)	172 (93%)	13 (7%)	0	100	100
32	LG	200/262 (76%)	189 (94%)	11 (6%)	0	100	100
33	LH	188/192 (98%)	174 (93%)	14 (7%)	0	100	100
34	LK	142/165 (86%)	132 (93%)	8 (6%)	2 (1%)	9	23
35	LL	115/213 (54%)	109 (95%)	6 (5%)	0	100	100
36	LM	135/142 (95%)	129 (96%)	6 (4%)	0	100	100
37	LN	179/203 (88%)	173 (97%)	6 (3%)	0	100	100
38	LO	202/204 (99%)	200 (99%)	2 (1%)	0	100	100
39	LP	165/187 (88%)	162 (98%)	3 (2%)	0	100	100
40	LQ	127/213 (60%)	122 (96%)	5 (4%)	0	100	100
41	LR	144/2898 (5%)	143 (99%)	1 (1%)	0	100	100
42	LS	172/174 (99%)	164 (95%)	8 (5%)	0	100	100
43	LT	124/160 (78%)	118 (95%)	5 (4%)	1 (1%)	16	37
44	LU	103/127 (81%)	101 (98%)	2 (2%)	0	100	100
45	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
46	LX	133/156 (85%)	130 (98%)	3 (2%)	0	100	100
47	LY	132/138 (96%)	126 (96%)	6 (4%)	0	100	100
48	LZ	133/135 (98%)	125 (94%)	8 (6%)	0	100	100
49	Lc	96/108 (89%)	95 (99%)	1 (1%)	0	100	100
50	Ld	107/120 (89%)	104 (97%)	3 (3%)	0	100	100
51	Le	125/131 (95%)	123 (98%)	2 (2%)	0	100	100
52	Lf	106/109 (97%)	103 (97%)	3 (3%)	0	100	100
53	Lg	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
54	Lh	119/935 (13%)	117 (98%)	2 (2%)	0	100	100
55	Li	86/110 (78%)	84 (98%)	2 (2%)	0	100	100
56	Lj	72/95 (76%)	70 (97%)	2 (3%)	0	100	100
57	Lk	73/81 (90%)	70 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	Ll	36/51 (71%)	36 (100%)	0	0	100	100
59	Lq	205/217 (94%)	184 (90%)	21 (10%)	0	100	100
All	All	12684/20359 (62%)	12128 (96%)	535 (4%)	21 (0%)	44	68

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CB	103	ASP
4	CB	104	PRO
7	CE	313	PRO
14	CL	224	ASP
14	CL	414	VAL
27	CY	436	ALA
34	LK	51	ALA
14	CL	439	ASP
21	CS	14	ASP
22	CT	237	PRO
25	CW	36	GLU
14	CL	42	ASN
25	CW	63	SER
34	LK	160	ILE
8	CF	126	ARG
23	CU	226	THR
24	CV	24	ARG
14	CL	290	GLN
14	CL	446	ASP
43	LT	44	VAL
5	CC	251	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CA	223/276 (81%)	219 (98%)	4 (2%)	51	78
4	CB	222/329 (68%)	212 (96%)	10 (4%)	24	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	CC	580/710 (82%)	569 (98%)	11 (2%)	50	77
6	CD	381/410 (93%)	374 (98%)	7 (2%)	51	78
7	CE	400/517 (77%)	390 (98%)	10 (2%)	42	71
8	CF	214/236 (91%)	213 (100%)	1 (0%)	81	92
9	CG	150/155 (97%)	146 (97%)	4 (3%)	39	69
10	CH	481/575 (84%)	467 (97%)	14 (3%)	37	67
11	CI	121/336 (36%)	118 (98%)	3 (2%)	42	71
12	CJ	428/579 (74%)	420 (98%)	8 (2%)	50	77
13	CK	195/225 (87%)	192 (98%)	3 (2%)	57	81
14	CL	65/458 (14%)	64 (98%)	1 (2%)	57	81
15	CM	191/215 (89%)	186 (97%)	5 (3%)	40	70
15	LF	213/215 (99%)	211 (99%)	2 (1%)	70	87
16	CN	206/206 (100%)	206 (100%)	0	100	100
17	CO	48/99 (48%)	47 (98%)	1 (2%)	47	75
18	CP	273/632 (43%)	267 (98%)	6 (2%)	45	74
19	CQ	150/192 (78%)	136 (91%)	14 (9%)	8	21
20	CR	144/206 (70%)	142 (99%)	2 (1%)	59	82
21	CS	527/716 (74%)	522 (99%)	5 (1%)	70	87
22	CT	427/600 (71%)	411 (96%)	16 (4%)	30	59
23	CU	149/376 (40%)	146 (98%)	3 (2%)	48	76
24	CV	109/112 (97%)	105 (96%)	4 (4%)	30	59
25	CW	473/577 (82%)	448 (95%)	25 (5%)	20	46
26	CX	76/172 (44%)	75 (99%)	1 (1%)	61	83
27	CY	315/686 (46%)	293 (93%)	22 (7%)	14	34
28	Cz	60/107 (56%)	58 (97%)	2 (3%)	33	63
29	LB	301/331 (91%)	298 (99%)	3 (1%)	68	86
30	LC	283/285 (99%)	276 (98%)	7 (2%)	42	71
31	LE	159/166 (96%)	156 (98%)	3 (2%)	50	77
32	LG	175/222 (79%)	170 (97%)	5 (3%)	37	67
33	LH	167/169 (99%)	165 (99%)	2 (1%)	63	84
34	LK	121/136 (89%)	116 (96%)	5 (4%)	27	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	LL	99/176 (56%)	98 (99%)	1 (1%)	68	86
36	LM	115/117 (98%)	114 (99%)	1 (1%)	70	87
37	LN	164/180 (91%)	160 (98%)	4 (2%)	43	72
38	LO	163/163 (100%)	162 (99%)	1 (1%)	78	91
39	LP	137/152 (90%)	134 (98%)	3 (2%)	45	74
40	LQ	110/178 (62%)	109 (99%)	1 (1%)	70	87
41	LR	128/2396 (5%)	123 (96%)	5 (4%)	28	57
42	LS	154/154 (100%)	146 (95%)	8 (5%)	21	47
43	LT	109/135 (81%)	102 (94%)	7 (6%)	16	38
44	LU	93/108 (86%)	93 (100%)	0	100	100
45	LV	99/102 (97%)	99 (100%)	0	100	100
46	LX	114/129 (88%)	112 (98%)	2 (2%)	51	78
47	LY	117/119 (98%)	115 (98%)	2 (2%)	53	79
48	LZ	121/121 (100%)	121 (100%)	0	100	100
49	Lc	79/88 (90%)	77 (98%)	2 (2%)	42	71
50	Ld	95/105 (90%)	93 (98%)	2 (2%)	47	75
51	Le	110/114 (96%)	108 (98%)	2 (2%)	51	78
52	Lf	89/90 (99%)	87 (98%)	2 (2%)	45	74
53	Lg	101/102 (99%)	101 (100%)	0	100	100
54	Lh	108/781 (14%)	107 (99%)	1 (1%)	70	87
55	Li	75/93 (81%)	74 (99%)	1 (1%)	61	83
56	Lj	61/78 (78%)	58 (95%)	3 (5%)	22	49
57	Lk	71/76 (93%)	71 (100%)	0	100	100
58	Ll	34/46 (74%)	33 (97%)	1 (3%)	37	67
59	Lq	179/189 (95%)	177 (99%)	2 (1%)	65	85
All	All	10752/17218 (62%)	10492 (98%)	260 (2%)	43	72

All (260) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	CA	78	CYS
3	CA	179	VAL
3	CA	233	GLU

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Mol	Chain	Res	Type
3	CA	266	LYS
4	CB	34	ILE
4	CB	60	THR
4	CB	71	HIS
4	CB	91	THR
4	CB	104	PRO
4	CB	129	ASP
4	CB	159	ILE
4	CB	209	LEU
4	CB	266	LEU
4	CB	287	GLU
5	CC	152	ASP
5	CC	229	LEU
5	CC	285	LYS
5	CC	390	LEU
5	CC	392	LYS
5	CC	477	VAL
5	CC	591	ILE
5	CC	695	ASP
5	CC	699	LEU
5	CC	705	LEU
5	CC	764	MET
6	CD	18	ILE
6	CD	67	ILE
6	CD	249	ILE
6	CD	322	VAL
6	CD	366	HIS
6	CD	435	SER
6	CD	482	VAL
7	CE	122	THR
7	CE	151	VAL
7	CE	234	VAL
7	CE	245	LEU
7	CE	246	ASP
7	CE	293	MET
7	CE	316	LEU
7	CE	371	LYS
7	CE	445	VAL
7	CE	555	ILE
8	CF	237	LEU
9	CG	14	ASP
9	CG	25	SER

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Mol	Chain	Res	Type
9	CG	79	LYS
9	CG	124	GLU
10	CH	10	VAL
10	CH	26	ARG
10	CH	27	ARG
10	CH	54	GLU
10	CH	65	SER
10	CH	69	VAL
10	CH	223	ILE
10	CH	297	LEU
10	CH	323	THR
10	CH	359	THR
10	CH	361	LEU
10	CH	523	VAL
10	CH	540	ASP
10	CH	547	ARG
11	CI	224	THR
11	CI	282	VAL
11	CI	311	GLN
12	CJ	147	MET
12	CJ	232	GLU
12	CJ	420	ILE
12	CJ	456	VAL
12	CJ	506	GLN
12	CJ	614	LEU
12	CJ	644	LYS
12	CJ	666	LYS
13	CK	137	LYS
13	CK	145	LYS
13	CK	169	GLU
14	CL	20	LEU
15	CM	59	LYS
15	CM	92	VAL
15	CM	111	LEU
15	CM	134	LYS
15	CM	188	GLU
17	CO	110	MET
18	CP	287	LEU
18	CP	327	ARG
18	CP	407	VAL
18	CP	411	ASN
18	CP	502	SER

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Mol	Chain	Res	Type
18	CP	571	TYR
19	CQ	94	GLU
19	CQ	131	GLU
19	CQ	136	ARG
19	CQ	144	ARG
19	CQ	145	LEU
19	CQ	148	LEU
19	CQ	151	GLU
19	CQ	152	ARG
19	CQ	156	VAL
19	CQ	158	GLU
19	CQ	160	GLU
19	CQ	164	LEU
19	CQ	166	LYS
19	CQ	167	LEU
20	CR	131	VAL
20	CR	146	ILE
21	CS	130	ASP
21	CS	563	SER
21	CS	668	THR
21	CS	676	LEU
21	CS	688	GLN
22	CT	133	LYS
22	CT	143	GLU
22	CT	152	LEU
22	CT	184	ILE
22	CT	208	GLN
22	CT	257	ASN
22	CT	427	LEU
22	CT	503	SER
22	CT	529	LEU
22	CT	562	THR
22	CT	587	ILE
22	CT	599	LEU
22	CT	602	GLN
22	CT	603	VAL
22	CT	611	ILE
22	CT	647	THR
23	CU	205	LEU
23	CU	233	ILE
23	CU	301	GLU
24	CV	21	VAL

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Mol	Chain	Res	Type
24	CV	33	LEU
24	CV	76	SER
24	CV	120	ARG
25	CW	22	LEU
25	CW	25	TRP
25	CW	33	MET
25	CW	35	TYR
25	CW	36	GLU
25	CW	37	GLN
25	CW	39	THR
25	CW	56	VAL
25	CW	103	GLN
25	CW	108	LEU
25	CW	154	ASP
25	CW	236	LEU
25	CW	315	VAL
25	CW	340	LYS
25	CW	356	THR
25	CW	364	LEU
25	CW	366	ILE
25	CW	376	ASP
25	CW	382	LYS
25	CW	393	ARG
25	CW	399	LEU
25	CW	402	VAL
25	CW	473	HIS
25	CW	572	TRP
25	CW	594	GLU
26	CX	103	THR
27	CY	20	LYS
27	CY	432	ARG
27	CY	435	ASN
27	CY	437	ASN
27	CY	438	THR
27	CY	439	LEU
27	CY	442	ILE
27	CY	445	MET
27	CY	455	LEU
27	CY	456	ASP
27	CY	459	LEU
27	CY	469	ARG
27	CY	475	LEU

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Mol	Chain	Res	Type
27	CY	505	VAL
27	CY	509	HIS
27	CY	527	LEU
27	CY	541	LEU
27	CY	548	PHE
27	CY	581	SER
27	CY	626	LEU
27	CY	628	GLU
27	CY	688	GLU
28	Cz	46	THR
28	Cz	54	LYS
29	LB	110	LEU
29	LB	120	LYS
29	LB	149	LEU
30	LC	61	THR
30	LC	83	THR
30	LC	114	ILE
30	LC	158	VAL
30	LC	163	VAL
30	LC	190	LYS
30	LC	314	VAL
31	LE	16	THR
31	LE	106	SER
31	LE	169	LEU
15	LF	88	LYS
15	LF	230	GLU
32	LG	184	LYS
32	LG	201	VAL
32	LG	256	LEU
32	LG	257	GLU
32	LG	261	LYS
33	LH	82	VAL
33	LH	109	THR
34	LK	59	THR
34	LK	65	GLN
34	LK	106	LEU
34	LK	109	ILE
34	LK	162	ILE
35	LL	22	VAL
36	LM	57	VAL
37	LN	27	CYS
37	LN	60	VAL

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Mol	Chain	Res	Type
37	LN	66	VAL
37	LN	164	LEU
38	LO	190	LYS
39	LP	8	GLU
39	LP	24	VAL
39	LP	79	SER
40	LQ	148	THR
41	LR	89	MET
41	LR	91	GLN
41	LR	93	VAL
41	LR	154	GLN
41	LR	159	MET
42	LS	38	LYS
42	LS	45	LEU
42	LS	119	ARG
42	LS	124	LEU
42	LS	133	GLU
42	LS	160	SER
42	LS	163	LYS
42	LS	172	THR
43	LT	52	MET
43	LT	80	VAL
43	LT	81	LYS
43	LT	85	ILE
43	LT	145	ASP
43	LT	146	ASN
43	LT	147	LYS
46	LX	43	THR
46	LX	94	THR
47	LY	66	GLU
47	LY	118	LEU
49	Lc	54	LEU
49	Lc	78	ILE
50	Ld	104	VAL
50	Ld	114	THR
51	Le	110	ILE
51	Le	114	LYS
52	Lf	59	LYS
52	Lf	67	ARG
54	Lh	34	LEU
55	Li	47	GLN
56	Lj	18	LEU

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Mol	Chain	Res	Type
56	Lj	63	ARG
56	Lj	84	LYS
58	Ll	19	GLN
59	Lq	113	SER
59	Lq	206	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
3	CA	61	HIS
3	CA	279	HIS
4	CB	90	ASN
4	CB	161	ASN
4	CB	240	ASN
5	CC	446	GLN
5	CC	537	GLN
7	CE	235	ASN
7	CE	431	GLN
7	CE	525	HIS
7	CE	534	HIS
7	CE	576	GLN
8	CF	61	ASN
9	CG	92	GLN
10	CH	73	GLN
10	CH	102	ASN
10	CH	119	GLN
10	CH	123	GLN
10	CH	244	HIS
10	CH	332	ASN
10	CH	369	HIS
10	CH	498	GLN
10	CH	499	HIS
12	CJ	200	ASN
12	CJ	264	GLN
12	CJ	506	GLN
13	CK	40	GLN
13	CK	68	HIS
13	CK	72	ASN
13	CK	224	ASN
13	CK	244	GLN
13	CK	248	ASN
14	CL	42	ASN

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Mol	Chain	Res	Type
15	CM	178	ASN
15	CM	242	ASN
16	CN	79	GLN
16	CN	86	ASN
16	CN	106	ASN
16	CN	145	HIS
17	CO	14	HIS
17	CO	15	GLN
18	CP	432	ASN
19	CQ	5	ASN
20	CR	196	GLN
20	CR	220	GLN
21	CS	117	HIS
21	CS	237	GLN
21	CS	275	ASN
21	CS	788	GLN
22	CT	323	ASN
22	CT	390	HIS
23	CU	232	GLN
23	CU	336	GLN
24	CV	15	ASN
25	CW	19	ASN
25	CW	287	GLN
25	CW	368	GLN
25	CW	414	GLN
25	CW	430	GLN
25	CW	623	ASN
27	CY	458	ASN
30	LC	142	GLN
30	LC	292	ASN
15	LF	192	HIS
15	LF	236	ASN
32	LG	92	GLN
32	LG	194	HIS
33	LH	96	HIS
33	LH	118	ASN
34	LK	65	GLN
35	LL	66	ASN
37	LN	95	GLN
37	LN	138	ASN
37	LN	153	ASN
37	LN	195	ASN

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Mol	Chain	Res	Type
38	LO	27	GLN
38	LO	132	GLN
39	LP	97	ASN
39	LP	116	HIS
39	LP	175	GLN
41	LR	91	GLN
41	LR	99	GLN
42	LS	21	ASN
42	LS	89	ASN
47	LY	62	HIS
48	LZ	77	ASN
50	Ld	102	GLN
51	Le	21	HIS
52	Lf	7	HIS
54	Lh	47	ASN
54	Lh	50	HIS
56	Lj	76	ASN
58	Ll	4	HIS
59	Lq	71	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2770/3341 (82%)	564 (20%)	21 (0%)
2	C2	254/319 (79%)	54 (21%)	1 (0%)
All	All	3024/3660 (82%)	618 (20%)	22 (0%)

All (618) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	26	A
1	C1	40	A
1	C1	43	A
1	C1	49	A
1	C1	59	G
1	C1	60	A
1	C1	65	A
1	C1	66	A
1	C1	73	A
1	C1	92	G
1	C1	93	C

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Mol	Chain	Res	Type
1	C1	94	G
1	C1	96	G
1	C1	105	C
1	C1	109	A
1	C1	110	G
1	C1	111	C
1	C1	116	A
1	C1	122	A
1	C1	128	G
1	C1	129	C
1	C1	131	U
1	C1	132	C
1	C1	133	G
1	C1	134	G
1	C1	135	C
1	C1	136	C
1	C1	138	G
1	C1	150	G
1	C1	151	G
1	C1	152	A
1	C1	162	U
1	C1	163	U
1	C1	177	U
1	C1	183	U
1	C1	186	C
1	C1	193	C
1	C1	203	C
1	C1	206	A
1	C1	211	G
1	C1	212	A
1	C1	240	U
1	C1	242	U
1	C1	244	U
1	C1	253	U
1	C1	258	C
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	299	A

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Mol	Chain	Res	Type
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	344	A
1	C1	368	G
1	C1	387	A
1	C1	390	U
1	C1	391	A
1	C1	393	C
1	C1	394	A
1	C1	395	C
1	C1	412	G
1	C1	413	G
1	C1	414	A
1	C1	421	U
1	C1	433	U
1	C1	434	G
1	C1	440	G
1	C1	441	G
1	C1	444	G
1	C1	445	A
1	C1	446	U
1	C1	453	G
1	C1	454	U
1	C1	455	G
1	C1	457	U
1	C1	458	C
1	C1	459	U
1	C1	467	G
1	C1	470	C
1	C1	471	U
1	C1	484	G
1	C1	485	G
1	C1	493	C
1	C1	508	G
1	C1	509	A

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Mol	Chain	Res	Type
1	C1	511	A
1	C1	513	A
1	C1	523	A
1	C1	526	G
1	C1	530	C
1	C1	534	U
1	C1	535	C
1	C1	537	G
1	C1	546	A
1	C1	547	U
1	C1	548	A
1	C1	559	U
1	C1	560	A
1	C1	579	A
1	C1	582	A
1	C1	589	U
1	C1	590	C
1	C1	592	G
1	C1	593	C
1	C1	594	A
1	C1	597	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	649	U
1	C1	663	G
1	C1	664	A
1	C1	668	U
1	C1	670	U
1	C1	674	U
1	C1	712	A
1	C1	718	U
1	C1	719	C
1	C1	723	G
1	C1	731	G
1	C1	739	C
1	C1	742	A
1	C1	744	G
1	C1	748	U

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Mol	Chain	Res	Type
1	C1	749	C
1	C1	751	G
1	C1	752	A
1	C1	757	U
1	C1	758	U
1	C1	761	A
1	C1	762	G
1	C1	765	G
1	C1	766	G
1	C1	767	A
1	C1	782	A
1	C1	787	A
1	C1	798	A
1	C1	799	C
1	C1	800	U
1	C1	801	A
1	C1	803	G
1	C1	807	G
1	C1	816	G
1	C1	817	A
1	C1	818	A
1	C1	828	A
1	C1	835	G
1	C1	836	U
1	C1	841	G
1	C1	843	U
1	C1	846	C
1	C1	856	G
1	C1	858	C
1	C1	876	A
1	C1	877	A
1	C1	878	U
1	C1	887	G
1	C1	889	G
1	C1	896	A
1	C1	898	A
1	C1	925	A
1	C1	932	A
1	C1	934	G
1	C1	940	C
1	C1	941	U
1	C1	942	C

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Mol	Chain	Res	Type
1	C1	958	A
1	C1	959	C
1	C1	960	C
1	C1	961	U
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	1045	G
1	C1	1046	A
1	C1	1047	A
1	C1	1048	G
1	C1	1049	C
1	C1	1050	C
1	C1	1054	G
1	C1	1063	C
1	C1	1064	U
1	C1	1074	C
1	C1	1075	A
1	C1	1077	U
1	C1	1078	C
1	C1	1079	G
1	C1	1080	A
1	C1	1085	A
1	C1	1086	U
1	C1	1095	G
1	C1	1097	G
1	C1	1098	G
1	C1	1114	C
1	C1	1126	U
1	C1	1134	G
1	C1	1135	A
1	C1	1141	A
1	C1	1157	C
1	C1	1158	C
1	C1	1160	G
1	C1	1164	G
1	C1	1174	C

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Mol	Chain	Res	Type
1	C1	1175	A
1	C1	1178	C
1	C1	1180	C
1	C1	1181	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	1208	G
1	C1	1218	G
1	C1	1227	A
1	C1	1228	G
1	C1	1240	U
1	C1	1245	A
1	C1	1247	U
1	C1	1254	C
1	C1	1268	A
1	C1	1271	G
1	C1	1272	U
1	C1	1277	G
1	C1	1286	A
1	C1	1287	U
1	C1	1289	G
1	C1	1291	U
1	C1	1295	G
1	C1	1312	A
1	C1	1313	U
1	C1	1327	G
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	1338	U
1	C1	1368	A
1	C1	1374	G

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Mol	Chain	Res	Type
1	C1	1381	A
1	C1	1400	A
1	C1	1401	A
1	C1	1416	G
1	C1	1419	C
1	C1	1434	A
1	C1	1437	U
1	C1	1438	A
1	C1	1463	A
1	C1	1465	G
1	C1	1470	G
1	C1	1478	C
1	C1	1490	C
1	C1	1510	G
1	C1	1521	A
1	C1	1535	U
1	C1	1537	U
1	C1	1539	A
1	C1	1541	A
1	C1	1542	G
1	C1	1543	G
1	C1	1548	C
1	C1	1549	U
1	C1	1550	C
1	C1	1553	G
1	C1	1555	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	1572	A
1	C1	1584	A
1	C1	1598	A
1	C1	1599	U
1	C1	1607	U
1	C1	1608	U
1	C1	1609	G
1	C1	1610	C
1	C1	1618	C
1	C1	1621	A

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Mol	Chain	Res	Type
1	C1	1622	A
1	C1	1623	C
1	C1	1624	U
1	C1	1637	G
1	C1	1662	C
1	C1	1693	A
1	C1	1695	A
1	C1	1696	C
1	C1	1722	G
1	C1	1729	A
1	C1	1730	G
1	C1	1739	A
1	C1	1741	U
1	C1	1744	U
1	C1	1745	G
1	C1	1746	U
1	C1	1750	G
1	C1	1759	G
1	C1	1774	U
1	C1	1775	G
1	C1	1776	A
1	C1	1794	U
1	C1	1795	A
1	C1	1796	A
1	C1	1797	U
1	C1	1798	U
1	C1	1799	C
1	C1	1800	U
1	C1	1819	U
1	C1	1820	A
1	C1	1821	A
1	C1	1825	C
1	C1	1828	C
1	C1	1829	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	1881	G

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Mol	Chain	Res	Type
1	C1	1885	G
1	C1	1886	C
1	C1	1897	C
1	C1	1900	A
1	C1	1901	A
1	C1	1904	U
1	C1	1911	A
1	C1	1920	C
1	C1	1924	A
1	C1	1925	A
1	C1	1927	G
1	C1	1928	G
1	C1	1932	G
1	C1	1942	G
1	C1	1944	U
1	C1	1950	C
1	C1	1952	G
1	C1	1961	G
1	C1	1970	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	2010	G
1	C1	2020	C
1	C1	2021	C
1	C1	2023	U
1	C1	2024	U
1	C1	2043	G
1	C1	2044	G
1	C1	2048	G
1	C1	2049	C
1	C1	2054	A
1	C1	2064	U
1	C1	2065	U
1	C1	2066	A
1	C1	2075	A
1	C1	2297	G
1	C1	2298	U

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Mol	Chain	Res	Type
1	C1	2325	A
1	C1	2335	A
1	C1	2336	C
1	C1	2338	G
1	C1	2339	G
1	C1	2342	U
1	C1	2347	A
1	C1	2350	U
1	C1	2356	G
1	C1	2359	A
1	C1	2361	A
1	C1	2362	G
1	C1	2364	A
1	C1	2384	C
1	C1	2396	U
1	C1	2397	G
1	C1	2407	A
1	C1	2409	A
1	C1	2414	G
1	C1	2421	A
1	C1	2422	U
1	C1	2423	A
1	C1	2424	G
1	C1	2425	G
1	C1	2429	G
1	C1	2430	A
1	C1	2431	G
1	C1	2434	U
1	C1	2435	C
1	C1	2436	G
1	C1	2441	C
1	C1	2449	U
1	C1	2453	A
1	C1	2455	U
1	C1	2456	A
1	C1	2464	U
1	C1	2465	G
1	C1	2467	U
1	C1	2484	G
1	C1	2547	G
1	C1	2551	A
1	C1	2560	G

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Mol	Chain	Res	Type
1	C1	2564	G
1	C1	2723	C
1	C1	2730	C
1	C1	2740	U
1	C1	2749	G
1	C1	2759	A
1	C1	2760	A
1	C1	2761	A
1	C1	2777	A
1	C1	2778	A
1	C1	2782	G
1	C1	2800	U
1	C1	2801	U
1	C1	2802	C
1	C1	2803	A
1	C1	2804	U
1	C1	2815	C
1	C1	2816	U
1	C1	2832	G
1	C1	2833	U
1	C1	2845	A
1	C1	2847	C
1	C1	2856	G
1	C1	2857	C
1	C1	2862	U
1	C1	2869	A
1	C1	2874	U
1	C1	2879	U
1	C1	2881	U
1	C1	2883	C
1	C1	2888	A
1	C1	2893	U
1	C1	2894	A
1	C1	2903	G
1	C1	2906	C
1	C1	2908	G
1	C1	2917	C
1	C1	2929	A
1	C1	2936	U
1	C1	2942	C
1	C1	2943	C
1	C1	2948	G

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Mol	Chain	Res	Type
1	C1	2950	U
1	C1	2955	U
1	C1	2956	C
1	C1	2957	G
1	C1	2960	G
1	C1	2969	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	3079	A
1	C1	3084	A
1	C1	3086	A
1	C1	3087	A
1	C1	3088	U
1	C1	3098	A
1	C1	3099	A
1	C1	3100	C
1	C1	3101	G
1	C1	3110	C
1	C1	3111	U
1	C1	3112	A
1	C1	3113	C
1	C1	3118	A
1	C1	3121	U
1	C1	3122	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	3141	G
1	C1	3147	G
1	C1	3153	U
1	C1	3154	A
1	C1	3161	C
1	C1	3162	A

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Mol	Chain	Res	Type
1	C1	3163	G
1	C1	3164	G
1	C1	3171	C
1	C1	3181	C
1	C1	3184	G
1	C1	3185	A
1	C1	3187	G
1	C1	3188	U
1	C1	3189	G
1	C1	3199	A
1	C1	3200	A
1	C1	3205	C
1	C1	3206	G
1	C1	3207	U
1	C1	3210	U
1	C1	3213	A
1	C1	3215	U
1	C1	3217	U
1	C1	3219	G
1	C1	3226	G
1	C1	3227	C
1	C1	3228	G
1	C1	3229	G
1	C1	3230	G
1	C1	3244	C
1	C1	3253	U
1	C1	3256	A
1	C1	3257	U
1	C1	3259	U
1	C1	3260	G
1	C1	3274	U
1	C1	3280	G
1	C1	3281	U
1	C1	3282	A
1	C1	3287	A
1	C1	3291	U
1	C1	3293	G
1	C1	3295	U
1	C1	3298	U
1	C1	3303	U
1	C1	3309	G
1	C1	3318	C

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Mol	Chain	Res	Type
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	3333	A
2	C2	34	U
2	C2	35	C
2	C2	38	U
2	C2	51	G
2	C2	59	A
2	C2	62	A
2	C2	63	G
2	C2	79	A
2	C2	81	U
2	C2	82	U
2	C2	83	C
2	C2	84	C
2	C2	87	G
2	C2	90	U
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	120	G
2	C2	125	U
2	C2	151	C
2	C2	152	G
2	C2	158	U
2	C2	163	C
2	C2	165	U
2	C2	166	C
2	C2	167	A
2	C2	170	C
2	C2	173	U
2	C2	181	U
2	C2	189	A

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Mol	Chain	Res	Type
2	C2	195	G
2	C2	196	G
2	C2	203	G
2	C2	205	G
2	C2	212	G
2	C2	213	A
2	C2	214	A
2	C2	215	A
2	C2	219	A
2	C2	221	U
2	C2	222	G
2	C2	223	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 (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	150	G
1	C1	835	G
1	C1	886	U
1	C1	897	G
1	C1	940	C
1	C1	960	C
1	C1	1046	A
1	C1	1063	C
1	C1	1134	G
1	C1	1185	A
1	C1	1924	A
1	C1	1949	G
1	C1	2355	G
1	C1	2831	U
1	C1	3078	U
1	C1	3131	A
1	C1	3162	A
1	C1	3204	G
1	C1	3209	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	3229	G
1	C1	3297	U
2	C2	102	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 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	$\# Z > 2$
62	ADP	CW	1001	63	28,29,29	0.45	0	43,45,45	0.50	0
60	GTP	CH	701	-	33,34,34	0.90	0	50,54,54	1.60	9 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	ADP	CW	1001	63	-	4/16/32/32	0/3/3/3
60	GTP	CH	701	-	-	4/22/38/38	0/3/3/3

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	CH	701	GTP	C5-C4-N3	-4.91	120.57	128.39
60	CH	701	GTP	C2-N3-C4	4.58	120.19	112.30
60	CH	701	GTP	N9-C4-N3	3.10	132.14	125.95
60	CH	701	GTP	C2-N1-C6	-2.90	119.85	125.11
60	CH	701	GTP	N9-C8-N7	-2.70	108.39	113.40
60	CH	701	GTP	C5-C6-N1	2.50	119.61	113.25
60	CH	701	GTP	C8-N7-C5	2.47	108.66	104.26
60	CH	701	GTP	O6-C6-C5	-2.41	120.18	126.53
60	CH	701	GTP	C3'-C2'-C1'	2.13	105.49	101.46

There are no chirality outliers.

All (8) torsion outliers are listed below:

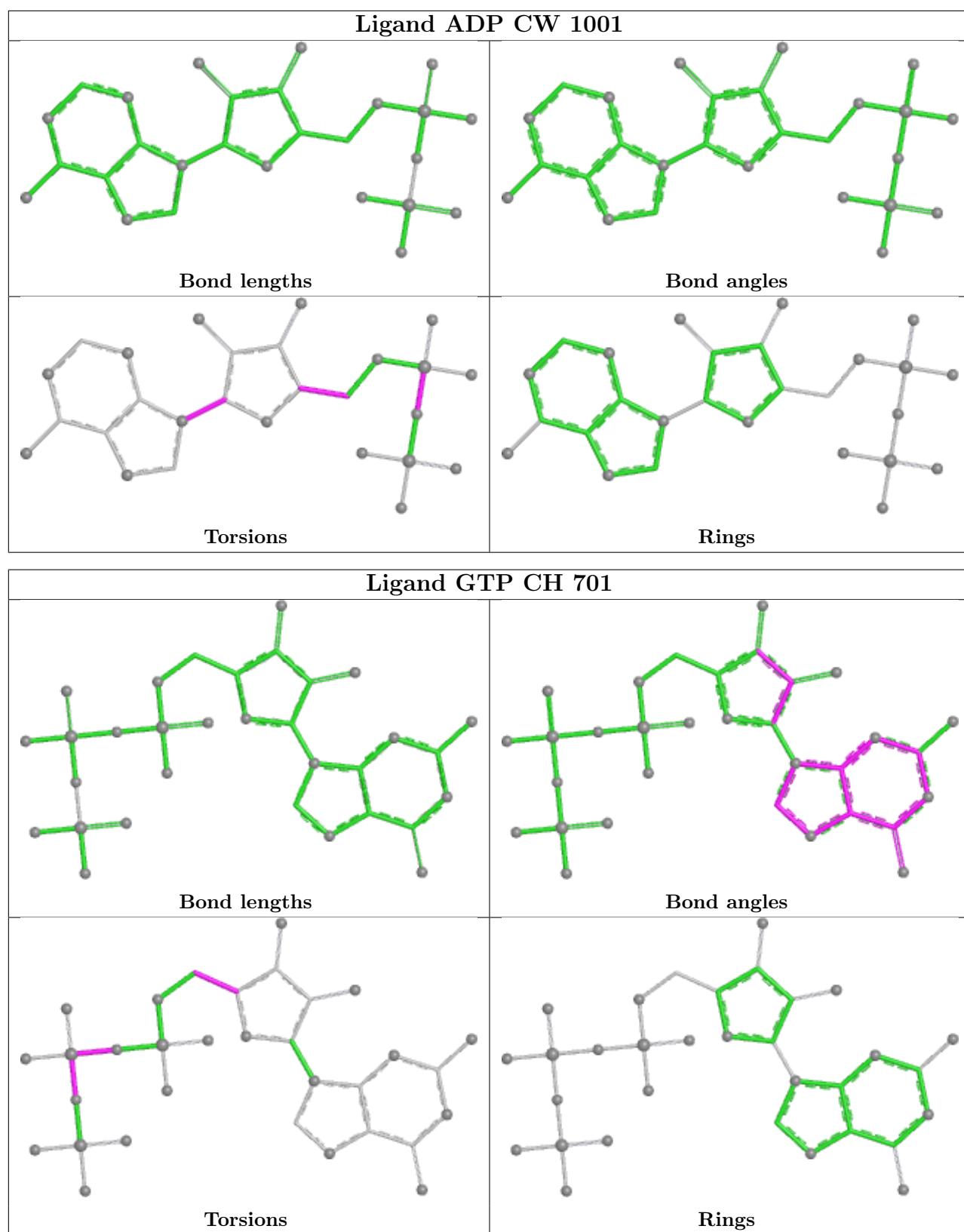
Mol	Chain	Res	Type	Atoms
62	CW	1001	ADP	C3'-C4'-C5'-O5'
62	CW	1001	ADP	O4'-C4'-C5'-O5'
60	CH	701	GTP	PG-O3B-PB-O2B
62	CW	1001	ADP	PB-O3A-PA-O1A
60	CH	701	GTP	PA-O3A-PB-O3B
60	CH	701	GTP	PA-O3A-PB-O1B
62	CW	1001	ADP	C2'-C1'-N9-C8
60	CH	701	GTP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	CW	1001	ADP	1	0

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

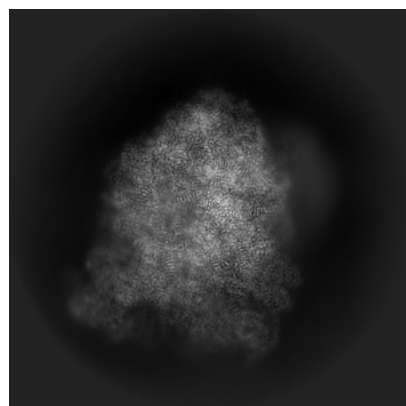
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35289. These allow visual inspection of the internal detail of the map and identification of artifacts.

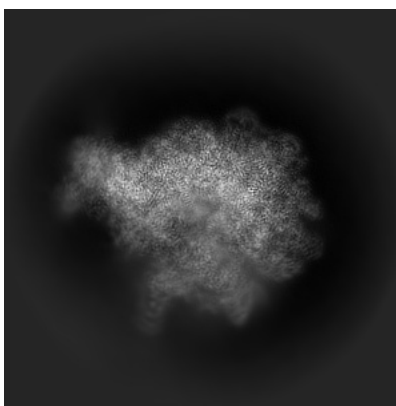
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

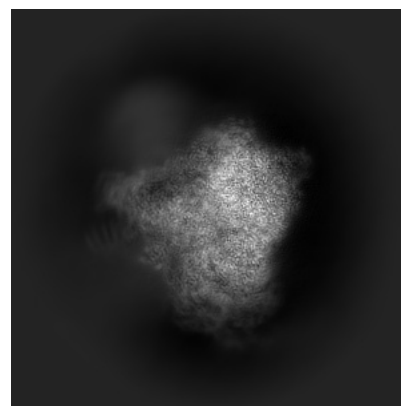
6.1.1 Primary map



X

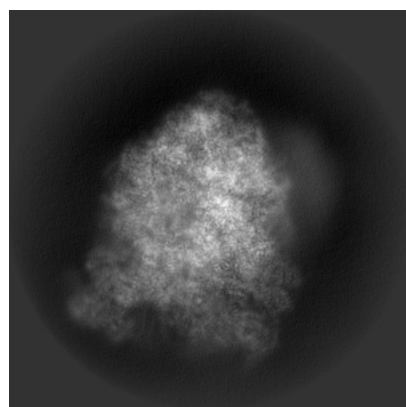


Y

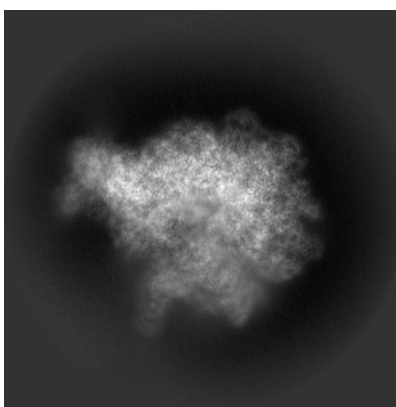


Z

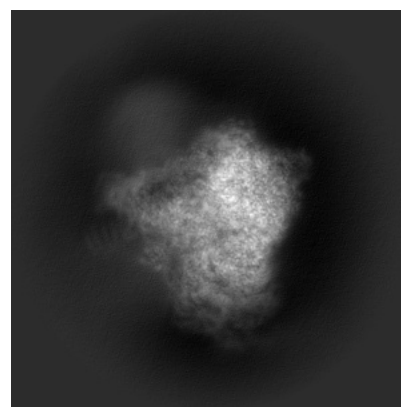
6.1.2 Raw map



X



Y

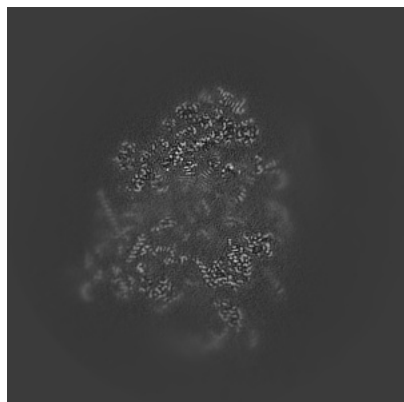


Z

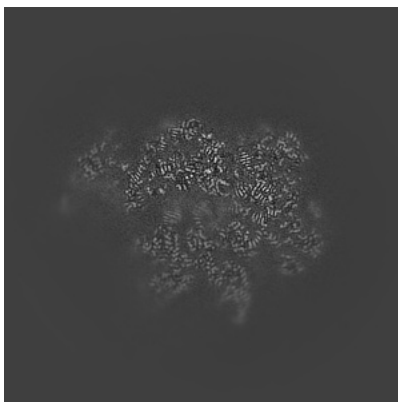
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

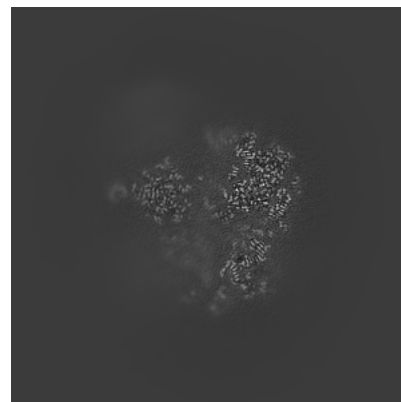
6.2.1 Primary map



X Index: 210

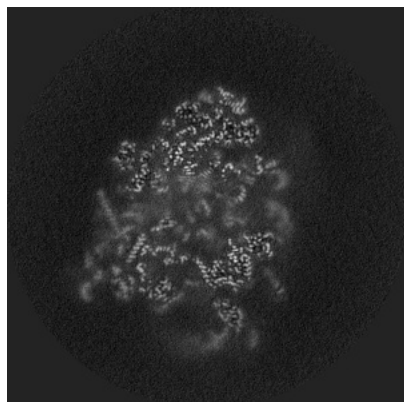


Y Index: 210

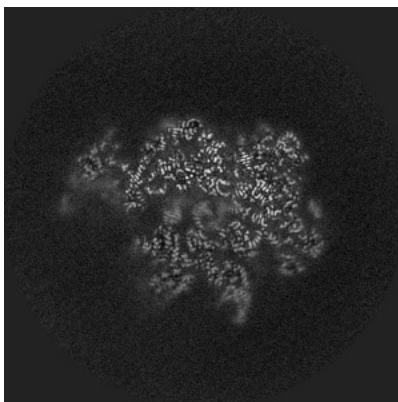


Z Index: 210

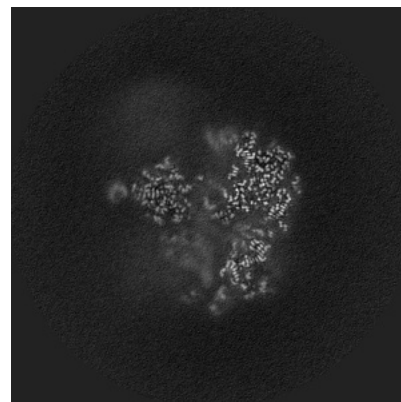
6.2.2 Raw map



X Index: 210



Y Index: 210

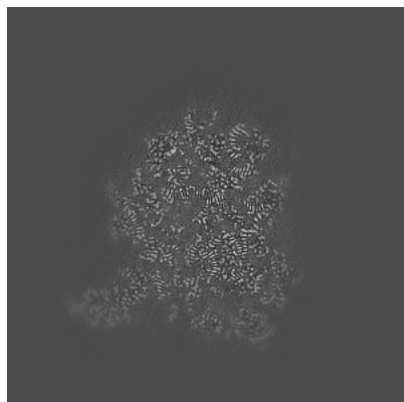


Z Index: 210

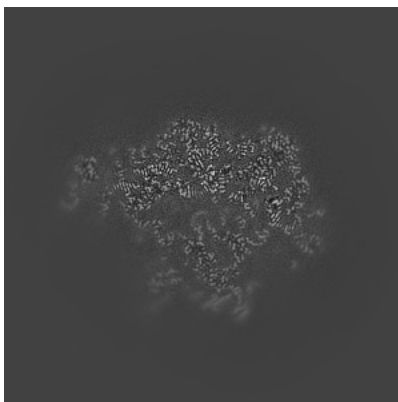
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

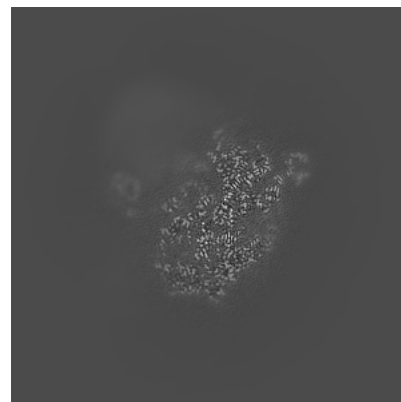
6.3.1 Primary map



X Index: 246

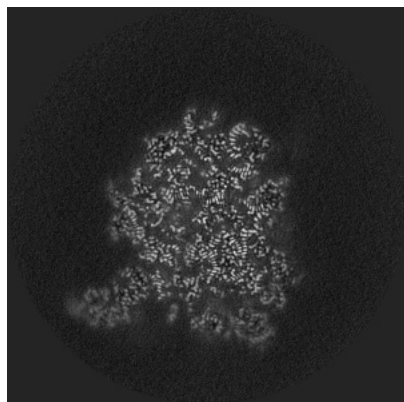


Y Index: 219

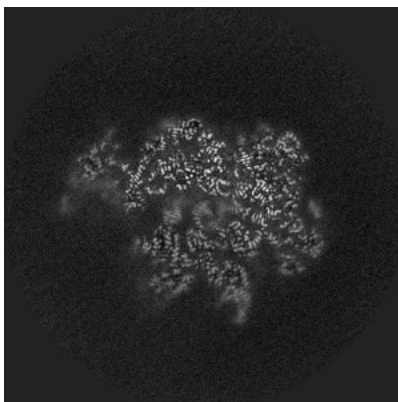


Z Index: 261

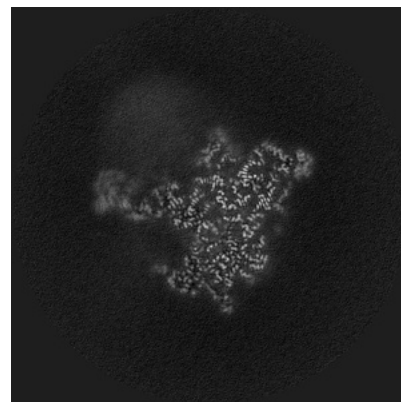
6.3.2 Raw map



X Index: 246



Y Index: 210

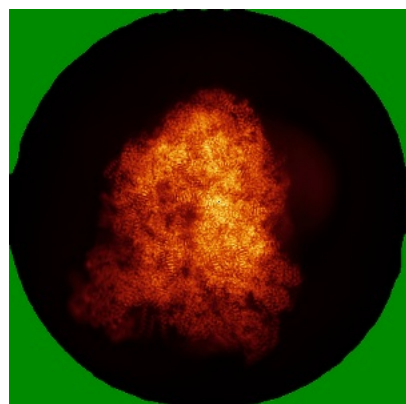


Z Index: 249

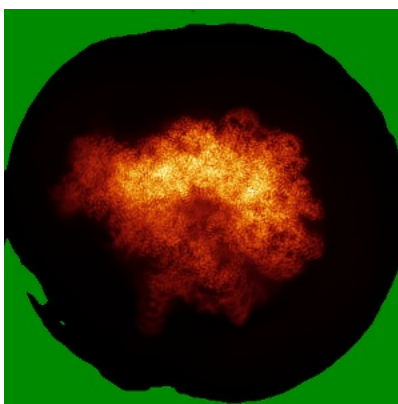
The images above show the largest variance slices of the map in three orthogonal directions.

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

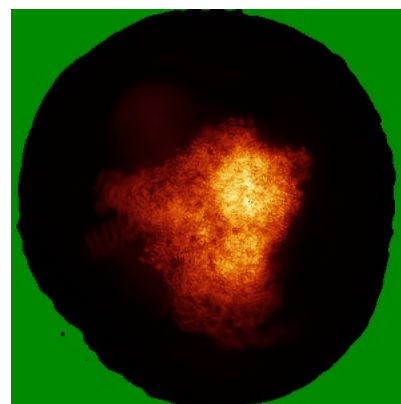
6.4.1 Primary map



X

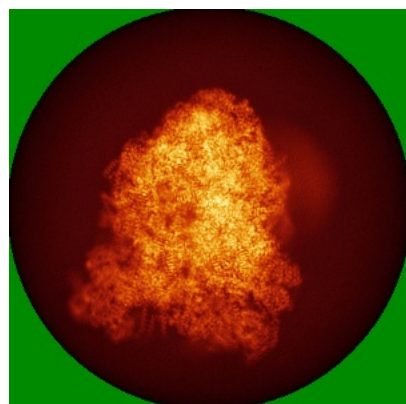


Y

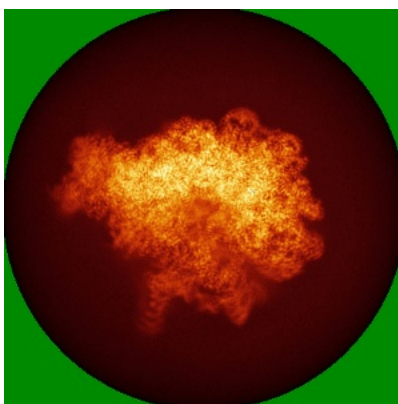


Z

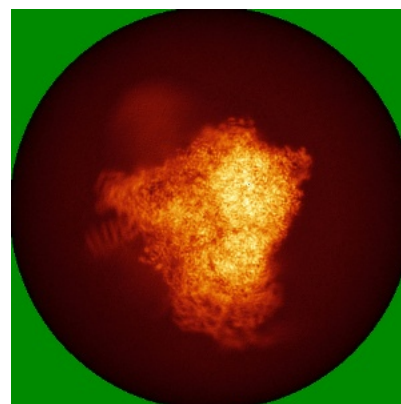
6.4.2 Raw map



X



Y



Z

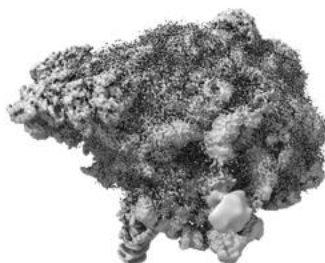
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

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

6.5.2 Raw map



X



Y



Z

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

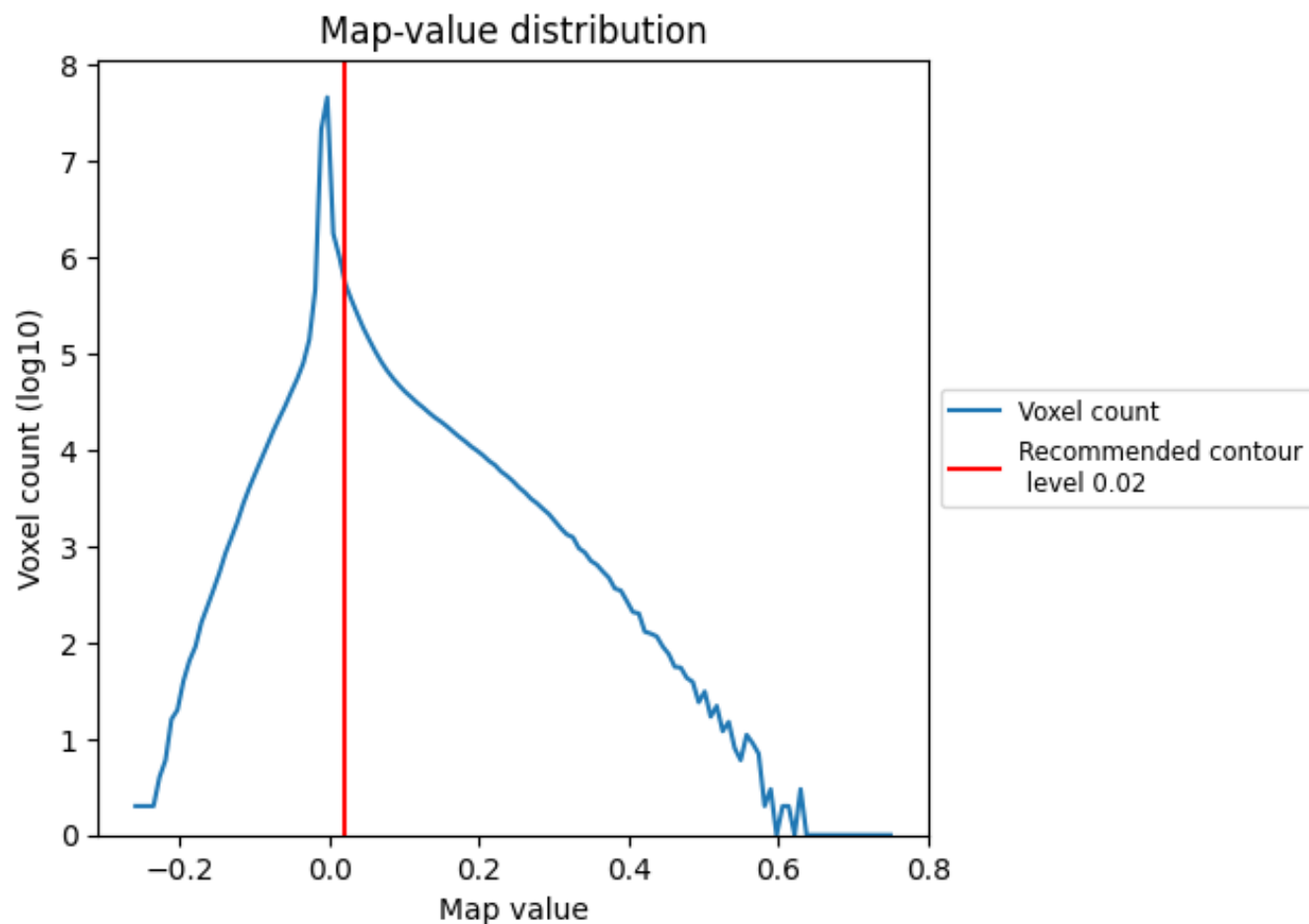
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

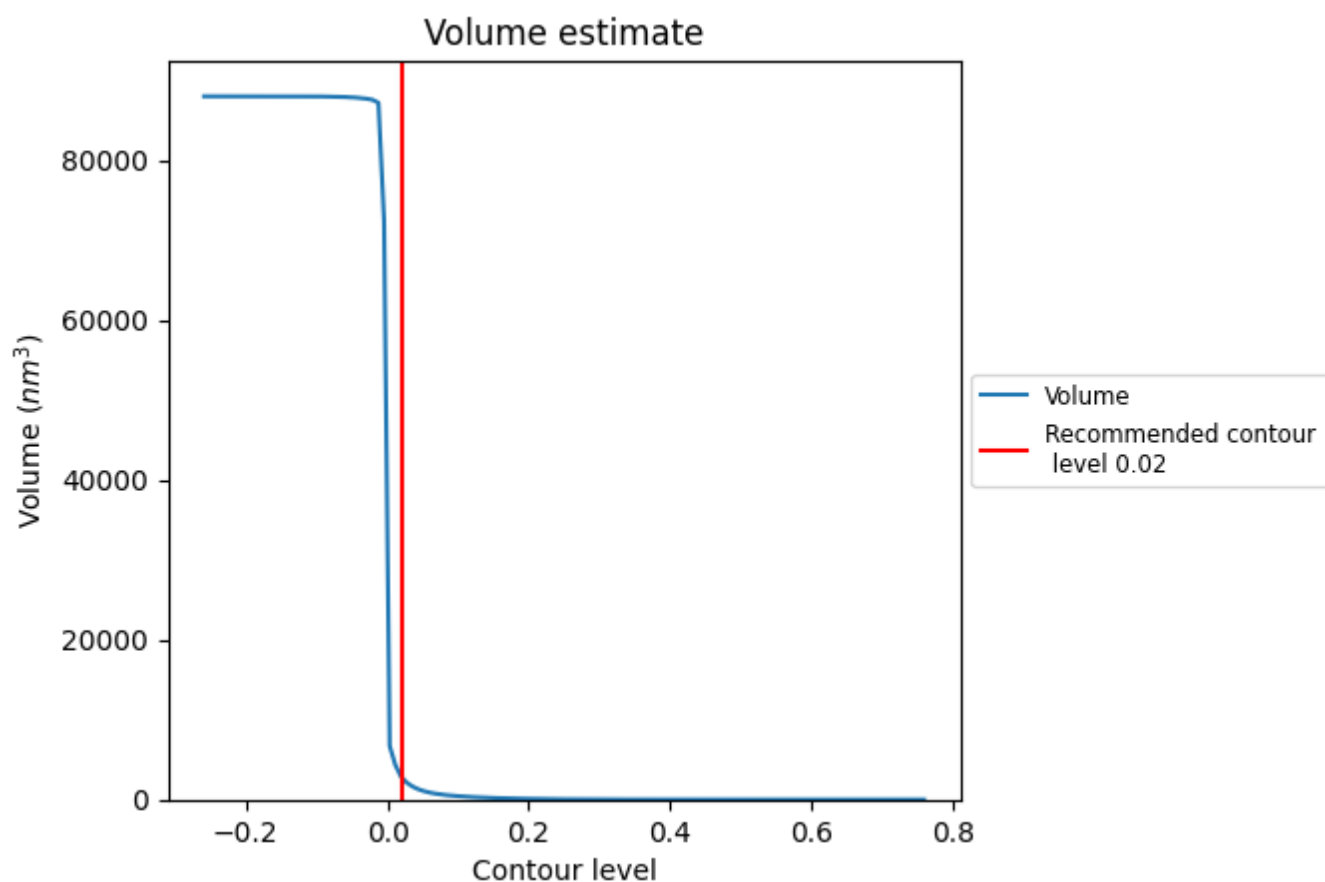
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

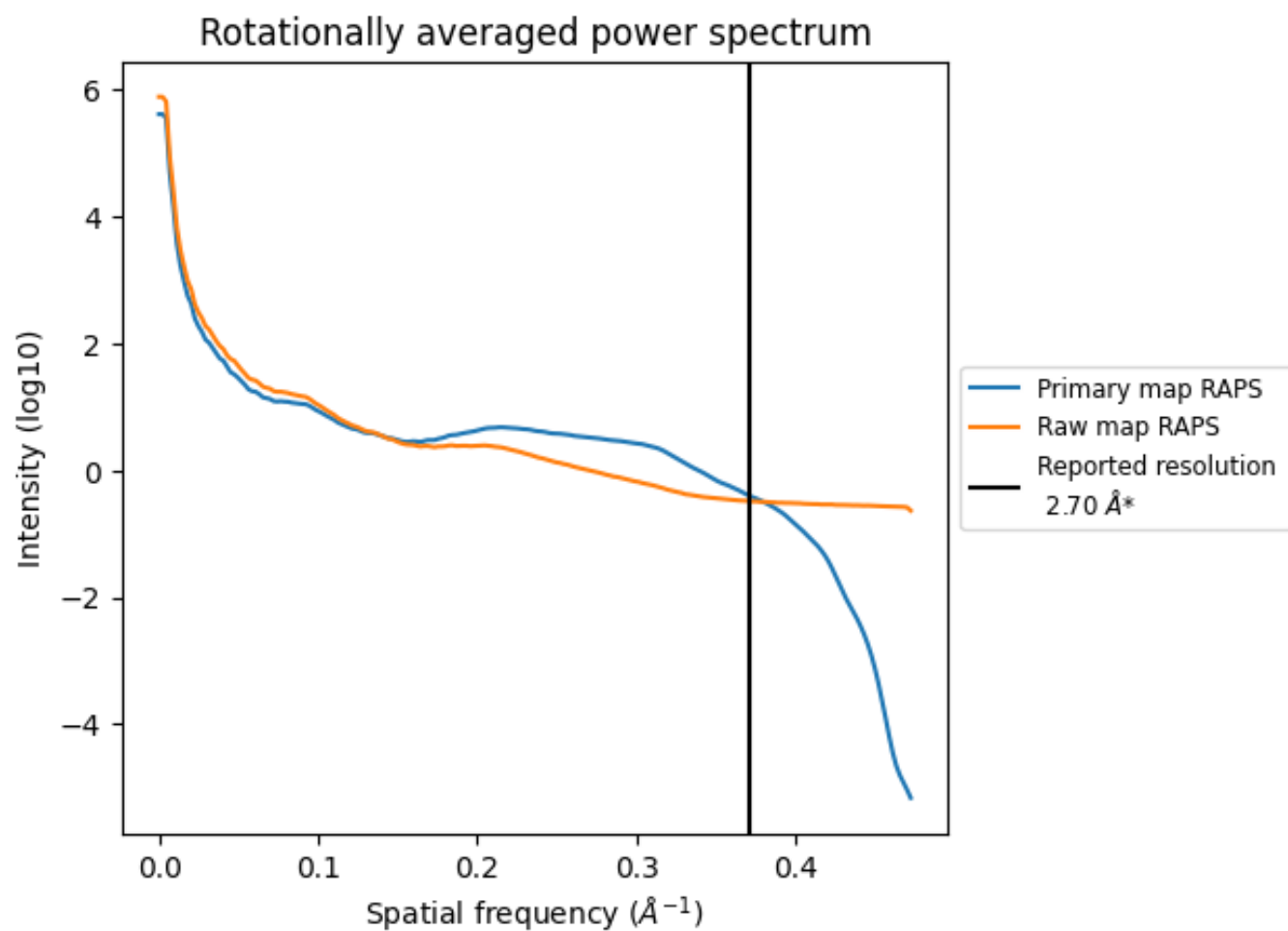
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2816 nm^3 ; this corresponds to an approximate mass of 2544 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 ⓘ

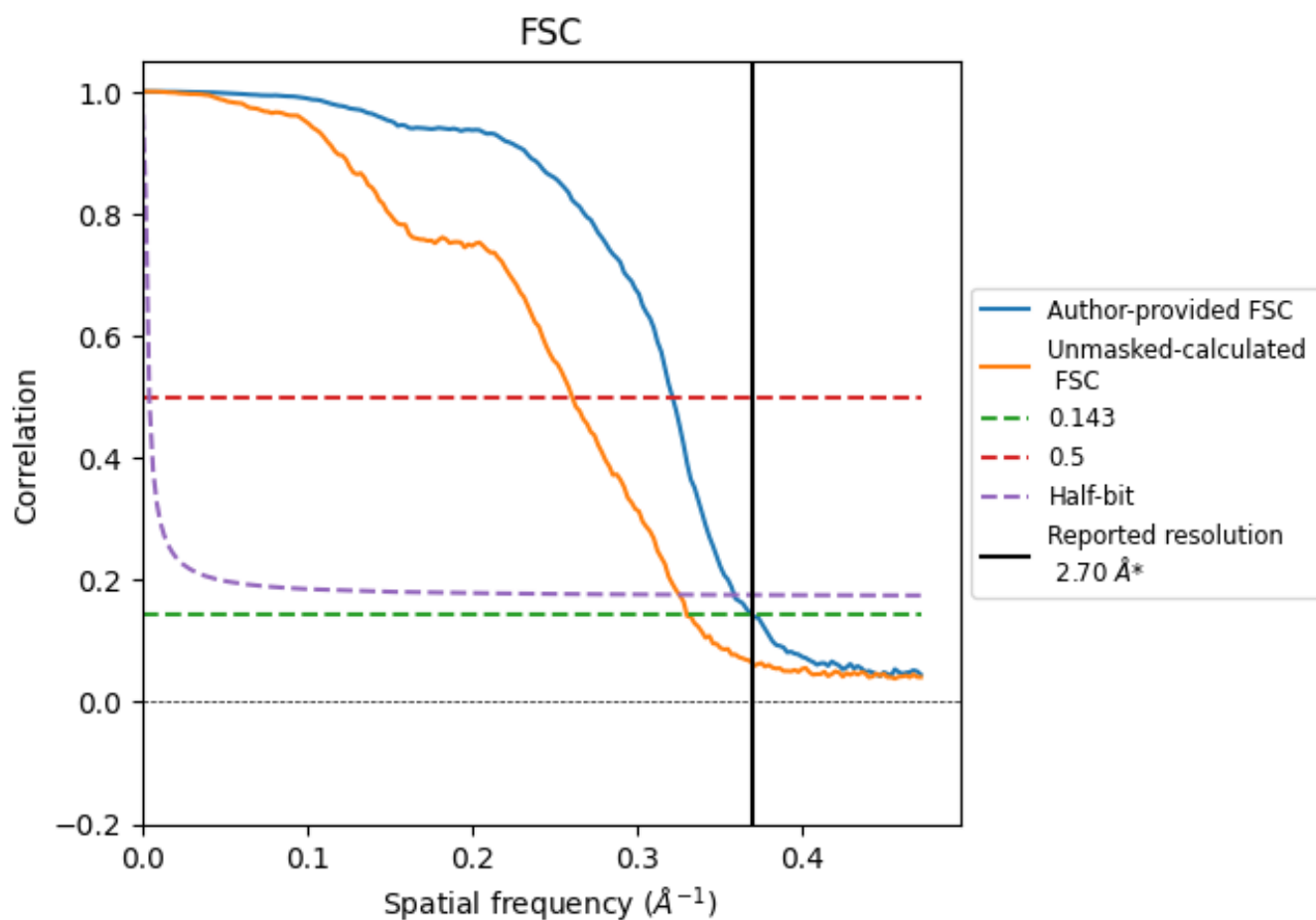


*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

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

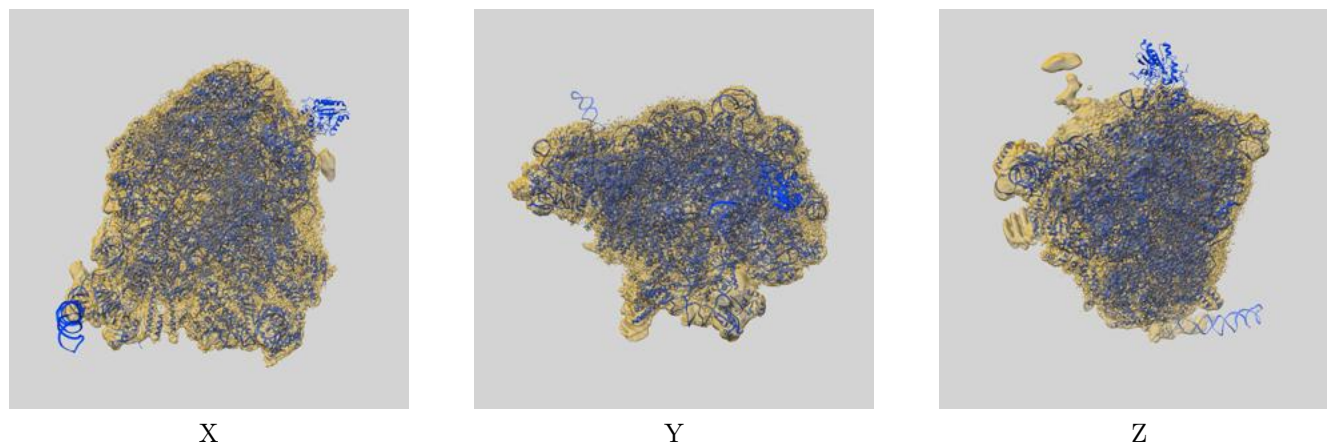
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.71	3.11	2.79
Unmasked-calculated*	3.03	3.84	3.07

*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 3.03 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

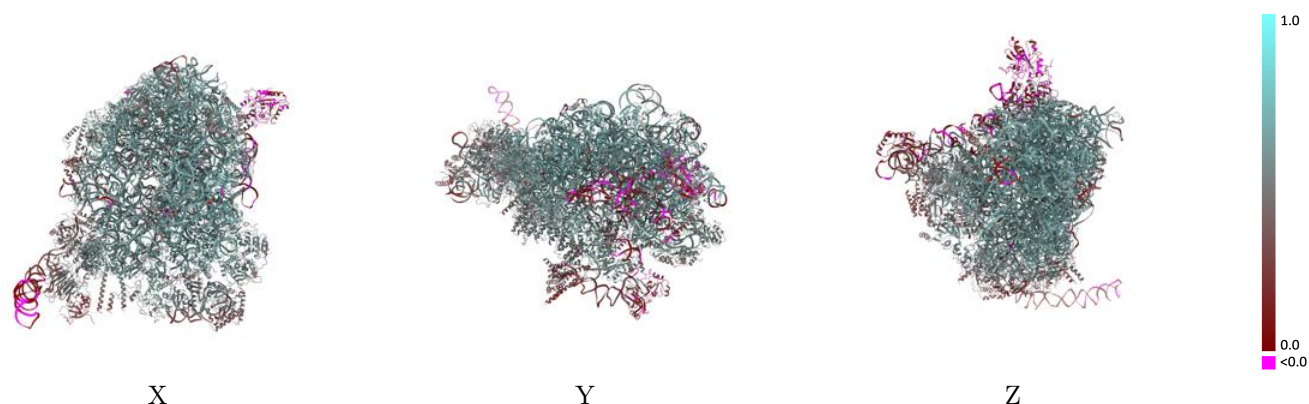
This section contains information regarding the fit between EMDB map EMD-35289 and PDB model 8I9Z. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



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

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

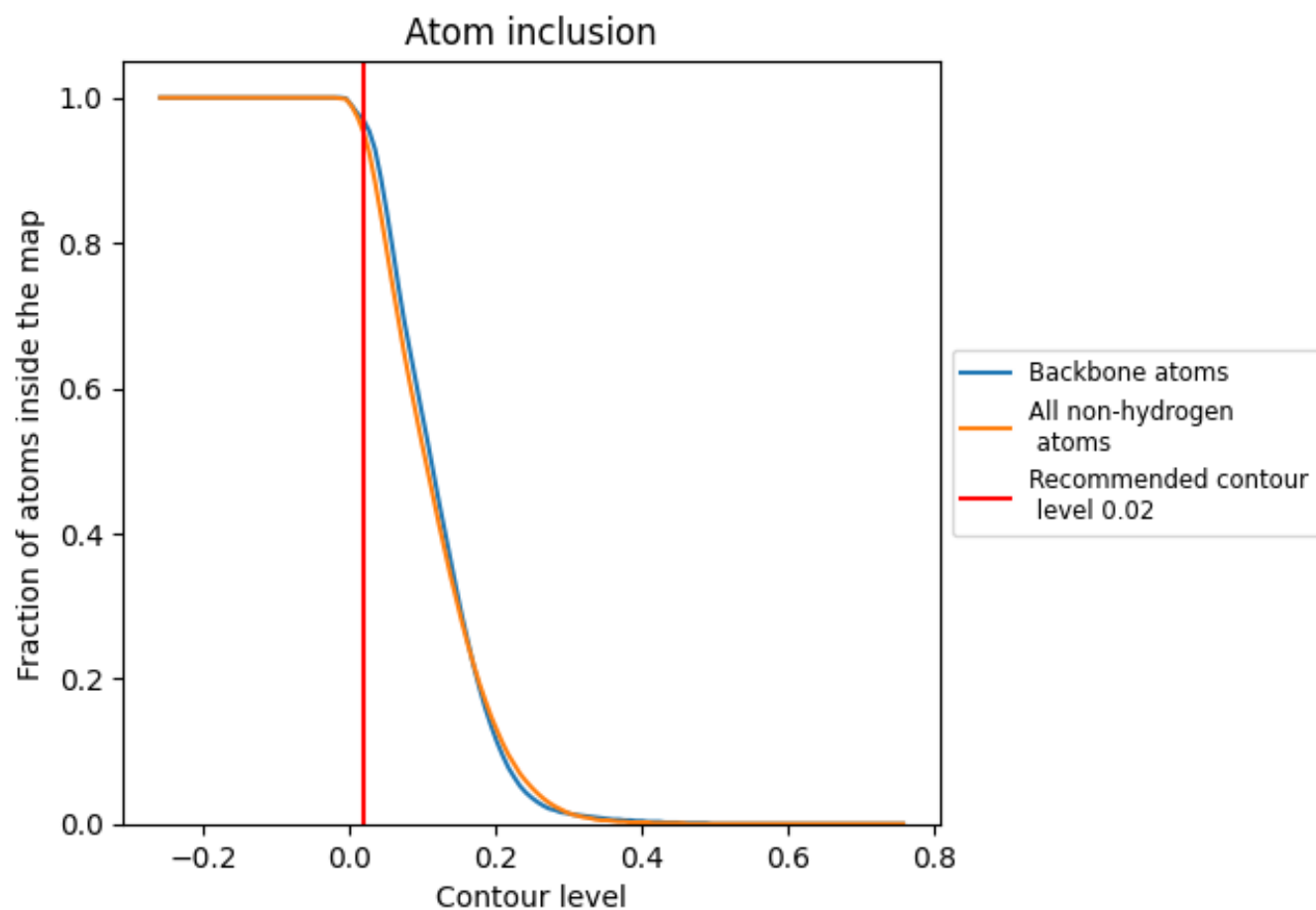


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% 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	 0.9510	 0.5240
C1	 0.9610	 0.5300
C2	 0.9790	 0.5420
CA	 0.9810	 0.5940
CB	 0.9340	 0.4530
CC	 0.9670	 0.5520
CD	 0.9330	 0.3950
CE	 0.9450	 0.5220
CF	 0.9540	 0.5110
CG	 0.9690	 0.5750
CH	 0.9640	 0.5440
CI	 0.9280	 0.4660
CJ	 0.9510	 0.5260
CK	 0.9660	 0.5600
CL	 0.3380	 0.2040
CM	 0.9450	 0.4760
CN	 0.9630	 0.5610
CO	 0.9540	 0.5600
CP	 0.9720	 0.5530
CQ	 0.9490	 0.5230
CR	 0.9650	 0.5790
CS	 0.9240	 0.4080
CT	 0.9660	 0.5230
CU	 0.9650	 0.5490
CV	 0.9790	 0.6210
CW	 0.9330	 0.3830
CX	 0.9240	 0.4990
CY	 0.9060	 0.3620
Cz	 0.9060	 0.3840
LB	 0.9800	 0.6080
LC	 0.9790	 0.6320
LE	 0.9670	 0.5790
LF	 0.9710	 0.6050
LG	 0.9760	 0.6100
LH	 0.9730	 0.5960



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Chain	Atom inclusion	Q-score
LK	 0.9390	 0.4380
LL	 0.9850	 0.6300
LM	 0.9760	 0.6110
LN	 0.9980	 0.6700
LO	 0.9860	 0.6440
LP	 0.9730	 0.5830
LQ	 0.9800	 0.5950
LR	 0.9520	 0.5090
LS	 0.9830	 0.6110
LT	 0.9320	 0.3910
LU	 0.9610	 0.5410
LV	 0.9820	 0.5820
LX	 0.9670	 0.5730
LY	 0.9720	 0.6020
LZ	 0.9750	 0.5790
Lc	 0.9620	 0.5250
Ld	 0.9620	 0.6020
Le	 0.9830	 0.6420
Lf	 0.9870	 0.6500
Lg	 0.9610	 0.5850
Lh	 0.9580	 0.5680
Li	 0.9570	 0.5740
Lj	 0.9880	 0.6440
Lk	 0.9420	 0.5120
Ll	 0.9810	 0.5260
Lq	 0.8570	 0.1750