



Full wwPDB EM Validation Report ⓘ

Jun 17, 2026 – 04:48 PM EDT

PDB ID : 9YXB / pdb_00009yxb
EMDB ID : EMD-73602
Title : Babesia divergens ribosome structure by single-particle cryo-EM (3D class1, A-, P-, and E-site tRNAs and mRNA)
Authors : Gutierrez-Vargas, C.; Izhaki-Tavor, L.S.; Leger-Abraham, M.
Deposited on : 2025-10-27
Resolution : 3.10 Å (reported)
Based on initial models : 9YGM, .

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:

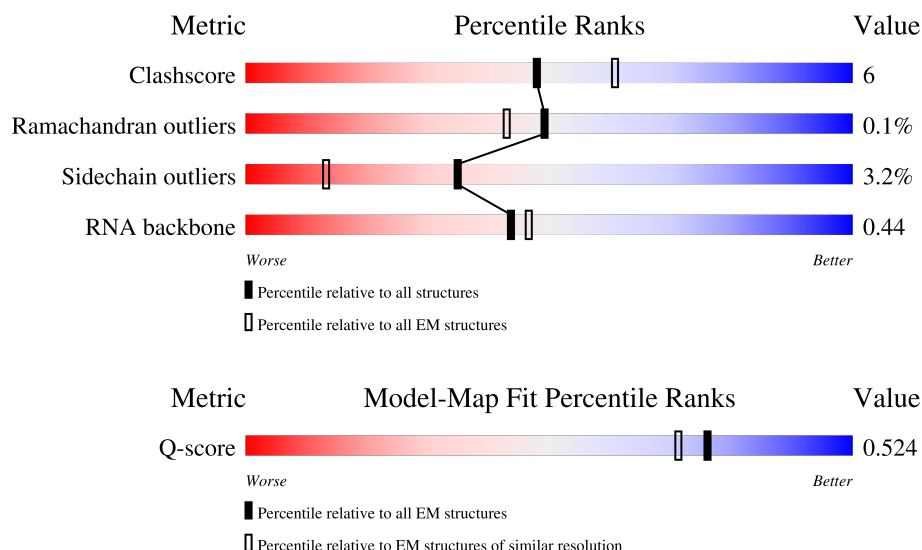
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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.




















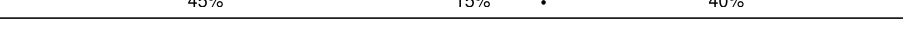







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	SP	145	
2	SX	174	
3	SU	156	



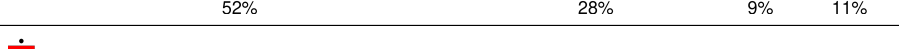
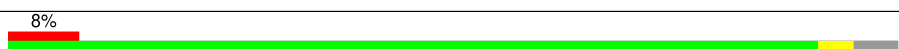



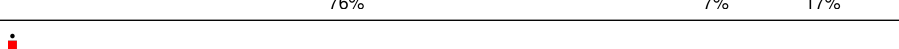



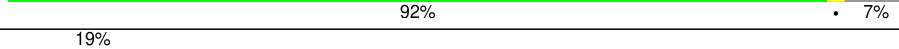

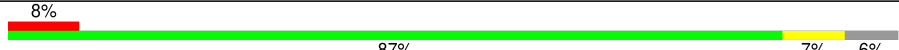


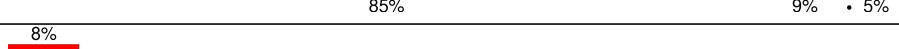







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Mol	Chain	Length	Quality of chain
4	SL	149	
5	SR	154	
6	SH	192	
7	ST	151	
8	SA	264	
9	SN	113	
10	SJ	130	
11	SI	194	
12	SK	192	
13	SG	239	
14	SM	120	
15	Se	61	
16	SS	66	
17	Sd	67	
18	SC	223	
19	SW	149	
20	SB	274	
21	SF	196	
22	Sb	115	
23	SV	134	
24	SO	157	
25	SZ	135	
26	Sa	104	
27	SQ	135	
28	SD	184	

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Mol	Chain	Length	Quality of chain
29	Sf	77	
30	Sc	82	
31	S1	1728	
32	LM	147	
33	LS	188	
34	Le	117	
35	Lf	132	
36	Lj	98	
37	LQ	222	
38	LB	257	
39	LI	202	
40	LJ	203	
41	LX	137	
42	La	123	
43	LD	360	
44	LP	306	
45	LZ	146	
46	LU	194	
47	LH	285	
48	LC	395	
49	LL	133	
50	LK	139	
51	LW	153	
52	Li	116	
53	Lm	55	

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Mol	Chain	Length	Quality of chain
54	LT	160	
55	Lo	105	
56	Ll	59	
57	LR	194	
58	LE	171	
59	LO	227	
60	LN	204	
61	Lg	115	
62	Lc	259	
63	LV	122	
64	Ld	108	
65	Lp	94	
66	Lb	59	
67	Lh	150	
68	LY	156	
69	LG	212	
70	Ln	39	
71	L3	122	
72	L4	159	
73	L5	3326	
74	S7	74	
75	S8	76	
76	S9	76	
77	S6	11	
78	SY	79	

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Mol	Chain	Length	Quality of chain
79	SE	266	<div><div></div><div>79%</div><div>14%</div><div></div><div></div></div>
80	Sg	323	<div><div></div><div>79%</div><div>17%</div><div></div><div></div></div>
81	LF	190	<div><div>6%</div><div></div><div>87%</div><div>10%</div><div></div><div></div></div>
82	Lk	70	<div><div>6%</div><div></div><div>80%</div><div>13%</div><div>7%</div><div></div></div>

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 186450 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 protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	SP	123	Total	C	N	O	S	0	0
			959	605	194	158	2		

- Molecule 2 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SX	167	Total	C	N	O	S	0	0
			1365	860	262	237	6		

- Molecule 3 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SU	151	Total	C	N	O	S	0	0
			1237	794	230	203	10		

- Molecule 4 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SL	139	Total	C	N	O	S	0	0
			1090	686	215	186	3		

- Molecule 5 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SR	141	Total	C	N	O	S	0	0
			1128	699	221	201	7		

- Molecule 6 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SH	187	Total	C	N	O	S	0	0
			1466	918	278	261	9		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SH	?	-	LYS	deletion	UNP A0AAD9GEF4
SH	?	-	TYR	deletion	UNP A0AAD9GEF4
SH	?	-	ASP	deletion	UNP A0AAD9GEF4
SH	?	-	ASP	deletion	UNP A0AAD9GEF4
SH	?	-	ILE	deletion	UNP A0AAD9GEF4
SH	?	-	ASN	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	ASN	deletion	UNP A0AAD9GEF4
SH	?	-	GLU	deletion	UNP A0AAD9GEF4
SH	?	-	LEU	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	GLU	deletion	UNP A0AAD9GEF4
SH	?	-	LEU	deletion	UNP A0AAD9GEF4
SH	?	-	CYS	deletion	UNP A0AAD9GEF4
SH	?	-	ASN	deletion	UNP A0AAD9GEF4
SH	?	-	LYS	deletion	UNP A0AAD9GEF4
SH	?	-	PHE	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	PRO	deletion	UNP A0AAD9GEF4
SH	?	-	LEU	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	ASP	deletion	UNP A0AAD9GEF4
SH	?	-	PHE	deletion	UNP A0AAD9GEF4
SH	?	-	ARG	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	ASN	deletion	UNP A0AAD9GEF4
SH	?	-	ALA	deletion	UNP A0AAD9GEF4

- Molecule 7 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	ST	145	Total	C	N	O	S	0	0
			1182	757	221	199	5		

- Molecule 8 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SA	208	Total	C	N	O	S	0	0
			1687	1073	304	297	13		

- Molecule 9 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SN	96	Total	C	N	O	S	0	0
			802	528	135	134	5		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SN	?	-	GLY	deletion	UNP A0AAD9G6F1
SN	?	-	GLU	deletion	UNP A0AAD9G6F1
SN	?	-	LEU	deletion	UNP A0AAD9G6F1
SN	?	-	ARG	deletion	UNP A0AAD9G6F1
SN	?	-	PHE	deletion	UNP A0AAD9G6F1
SN	?	-	MET	deletion	UNP A0AAD9G6F1
SN	?	-	THR	deletion	UNP A0AAD9G6F1
SN	?	-	VAL	deletion	UNP A0AAD9G6F1
SN	?	-	LEU	deletion	UNP A0AAD9G6F1
SN	?	-	THR	deletion	UNP A0AAD9G6F1
SN	?	-	TYR	deletion	UNP A0AAD9G6F1
SN	?	-	TYR	deletion	UNP A0AAD9G6F1
SN	?	-	PHE	deletion	UNP A0AAD9G6F1
SN	?	-	VAL	deletion	UNP A0AAD9G6F1
SN	?	-	GLY	deletion	UNP A0AAD9G6F1
SN	?	-	SER	deletion	UNP A0AAD9G6F1
SN	?	-	LEU	deletion	UNP A0AAD9G6F1
SN	?	-	HIS	deletion	UNP A0AAD9G6F1
SN	?	-	GLY	deletion	UNP A0AAD9G6F1
SN	?	-	ARG	deletion	UNP A0AAD9G6F1
SN	?	-	ALA	deletion	UNP A0AAD9G6F1

- Molecule 10 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SJ	126	Total	C	N	O	S	0	0
			1004	641	184	173	6		

- Molecule 11 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SI	126	Total	C	N	O	S	0	0
			1038	670	193	174	1		

- Molecule 12 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SK	175	Total	C	N	O	S	0	0
			1412	882	277	246	7		

- Molecule 13 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SG	186	Total	C	N	O	S	0	0
			1517	955	298	254	10		

- Molecule 14 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SM	96	Total	C	N	O	S	0	0
			761	474	139	142	6		

- Molecule 15 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	Se	38	Total	C	N	O	0	0
			313	193	71	49		

- Molecule 16 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SS	50	Total	C	N	O	S	0	0
			411	258	84	65	4		

- Molecule 17 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Sd	54	Total	C	N	O	0	0
			421	261	86	74		

- Molecule 18 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SC	187	Total	C	N	O	S	0	0
			1459	922	273	258	6		

- Molecule 19 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SW	108	Total	C	N	O	S	0	0
			875	564	158	148	5		

- Molecule 20 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SB	165	Total	C	N	O	S	0	0
			1289	825	223	231	10		

- Molecule 21 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SF	152	Total	C	N	O	S	0	0
			1141	730	204	200	7		

- Molecule 22 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Sb	82	Total	C	N	O	S	0	0
			661	407	145	103	6		

- Molecule 23 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SV	75	Total	C	N	O	S	0	0
			616	392	121	101	2		

- Molecule 24 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SO	98	Total	C	N	O	S	0	0
			739	462	142	131	4		

- Molecule 25 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SZ	69	Total	C	N	O	S	0	0
			582	367	120	94	1		

- Molecule 26 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Sa	71	Total	C	N	O	S	0	0
			569	361	100	104	4		

- Molecule 27 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SQ	87	Total	C	N	O	S	0	0
			660	418	114	123	5		

- Molecule 28 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SD	108	Total	C	N	O	S	0	0
			935	594	184	153	4		

- Molecule 29 is a protein called 40S ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Sf	52	Total	C	N	O	S	0	0
			407	261	73	68	5		

- Molecule 30 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Sc	60	Total	C	N	O	S	0	0
			474	299	89	81	5		

- Molecule 31 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	S1	1535	Total	C	N	O	P	0	0
			32741	14634	5836	10736	1535		

- Molecule 32 is a protein called 60S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LM	144	Total	C	N	O	S	0	0
			1146	730	228	182	6		

- Molecule 33 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LS	179	Total	C	N	O	S	0	0
			1445	919	274	244	8		

- Molecule 34 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Le	98	Total	C	N	O	S	0	0
			818	520	161	134	3		

- Molecule 35 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lf	125	Total	C	N	O	S	0	0
			1026	647	212	165	2		

- Molecule 36 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	87	Total	C	N	O	S	0	0
			689	419	152	111	7		

- Molecule 37 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LQ	184	Total	C	N	O	S	0	0
			1432	900	282	245	5		

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LQ	?	-	VAL	deletion	UNP A0AAD9G7R0
LQ	?	-	ASP	deletion	UNP A0AAD9G7R0
LQ	?	-	PHE	deletion	UNP A0AAD9G7R0
LQ	?	-	HIS	deletion	UNP A0AAD9G7R0
LQ	?	-	GLU	deletion	UNP A0AAD9G7R0
LQ	?	-	LYS	deletion	UNP A0AAD9G7R0
LQ	?	-	ASP	deletion	UNP A0AAD9G7R0
LQ	?	-	MET	deletion	UNP A0AAD9G7R0
LQ	?	-	MET	deletion	UNP A0AAD9G7R0
LQ	?	-	MET	deletion	UNP A0AAD9G7R0
LQ	?	-	HIS	deletion	UNP A0AAD9G7R0
LQ	?	-	VAL	deletion	UNP A0AAD9G7R0

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Chain	Residue	Modelled	Actual	Comment	Reference
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	THR	deletion	UNP A0AAD9G7R0
LQ	?	-	GLU	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	ARG	deletion	UNP A0AAD9G7R0
LQ	?	-	ARG	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	ASP	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	ALA	deletion	UNP A0AAD9G7R0
LQ	?	-	GLY	deletion	UNP A0AAD9G7R0
LQ	?	-	GLU	deletion	UNP A0AAD9G7R0

- Molecule 38 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LB	245	Total	C	N	O	S	0	0
			1868	1165	375	323	5		

- Molecule 39 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LI	198	Total	C	N	O	S	0	0
			1610	1027	314	260	9		

- Molecule 40 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LJ	193	Total	C	N	O	S	0	0
			1522	956	303	253	10		

- Molecule 41 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LX	121	Total	C	N	O	S	0	0
			1003	623	203	173	4		

- Molecule 42 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	La	115	Total	C	N	O	S	0	0
			957	606	190	158	3		

- Molecule 43 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LD	327	Total	C	N	O	S	0	0
			2521	1587	490	433	11		

- Molecule 44 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LP	281	Total	C	N	O	S	0	0
			2293	1447	424	413	9		

- Molecule 45 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LZ	137	Total	C	N	O	S	0	0
			1114	703	216	189	6		

- Molecule 46 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LU	172	Total	C	N	O	S	0	0
			1392	875	281	231	5		

- Molecule 47 is a protein called 60S ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LH	224	Total	C	N	O	S	0	0
			1816	1164	336	308	8		

- Molecule 48 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LC	377	Total	C	N	O	S	0	0
			3009	1918	561	515	15		

- Molecule 49 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LL	128	Total	C	N	O	S	0	0
			1016	655	183	175	3		

- Molecule 50 is a protein called 60S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LK	128	Total	C	N	O	S	0	0
			964	616	177	165	6		

- Molecule 51 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LW	116	Total	C	N	O	S	0	0
			946	600	178	165	3		

- Molecule 52 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Li	105	Total	C	N	O	S	0	0
			827	518	162	142	5		

- Molecule 53 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Lm	50	Total	C	N	O	S	0	0
			407	252	85	63	7		

- Molecule 54 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LT	148	Total	C	N	O	S	0	0
			1196	757	235	199	5		

- Molecule 55 is a protein called 60S ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Lo	96	Total	C	N	O	S	0	0
			776	489	154	127	6		

- Molecule 56 is a protein called 60S ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	Ll	49	Total	C	N	O	0	0
			435	279	93	63		

- Molecule 57 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LR	170	Total	C	N	O	S	0	0
			1387	865	287	224	11		

- Molecule 58 is a protein called 60S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LE	155	Total	C	N	O	S	0	0
			1259	794	238	221	6		

- Molecule 59 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LO	205	Total	C	N	O	S	0	0
			1648	1061	308	272	7		

- Molecule 60 is a protein called 60S ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LN	197	Total	C	N	O	S	0	0
			1656	1040	349	258	9		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LN	1	MET	-	insertion	UNP A0AAD9LIN3
LN	2	GLY	-	insertion	UNP A0AAD9LIN3
LN	3	ALA	-	insertion	UNP A0AAD9LIN3
LN	4	TYR	-	insertion	UNP A0AAD9LIN3
LN	5	ARG	-	insertion	UNP A0AAD9LIN3
LN	6	TYR	-	insertion	UNP A0AAD9LIN3

- Molecule 61 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Lg	108	Total	C	N	O	S	0	0
			879	563	167	144	5		

- Molecule 62 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Lc	214	Total	C	N	O	S	0	0
			1751	1128	331	286	6		

- Molecule 63 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LV	97	Total	C	N	O	S	0	0
			799	513	141	144	1		

- Molecule 64 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Ld	93	Total	C	N	O	S	0	0
			706	444	126	127	9		

- Molecule 65 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Lp	88	Total	C	N	O	S	0	0
			695	434	139	117	5		

- Molecule 66 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Lb	51	Total	C	N	O	S	0	0
			417	258	92	64	3		

- Molecule 67 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Lh	100	Total	C	N	O	S	0	0
			816	501	181	129	5		

- Molecule 68 is a protein called 60S ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	LY	61	Total	C	N	O	S	0	0
			509	331	95	82	1		

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	CYS	deletion	UNP A0AAD9LE14
LY	?	-	PRO	deletion	UNP A0AAD9LE14
LY	?	-	LYS	deletion	UNP A0AAD9LE14
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	CYS	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	GLN	deletion	UNP A0AAD9LE14
LY	?	-	TRP	deletion	UNP A0AAD9LE14
LY	?	-	PRO	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	HIS	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	CYS	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	ALA	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	THR	deletion	UNP A0AAD9LE14
LY	?	-	MET	deletion	UNP A0AAD9LE14
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	THR	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	THR	deletion	UNP A0AAD9LE14
LY	?	-	LYS	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	ASP	deletion	UNP A0AAD9LE14
LY	?	-	ILE	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	ILE	deletion	UNP A0AAD9LE14
LY	?	-	ILE	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	ALA	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14

- Molecule 69 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	LG	155	Total	C	N	O	S	0	0
			1223	791	212	215	5		

- Molecule 70 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ln	38	Total	C	N	O	S	0	0
			349	213	89	45	2		

- Molecule 71 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	L3	122	Total	C	N	O	P	0	0
			2610	1163	476	849	122		

- Molecule 72 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	L4	145	Total	C	N	O	P	0	0
			3082	1380	552	1005	145		

- Molecule 73 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	L5	2875	Total	C	N	O	P	0	0
			61352	27401	10974	20102	2875		

- Molecule 74 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	S7	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

- Molecule 75 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	S8	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		

- Molecule 76 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	S9	72	Total	C	N	O	P	0	0
			1532	684	273	504	71		

- Molecule 77 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	S6	11	Total	C	N	O	P	0	0
			227	102	31	83	11		

- Molecule 78 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	78	Total	C	N	O	S	0	0
			600	368	107	121	4		

- Molecule 79 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SE	255	Total	C	N	O	S	0	0
			2034	1291	375	360	8		

- Molecule 80 is a protein called Receptor for activated C kinase 1, RACK1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sg	315	Total	C	N	O	S	0	0
			2429	1534	418	463	14		

- Molecule 81 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	LF	186	Total	C	N	O	S	0	0
			1469	934	263	266	6		

- Molecule 82 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Lk	65	Total	C	N	O	S	0	0
			525	333	99	92	1		

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	S1	1	Total 1	Mg 1	0
83	L3	1	Total 1	Mg 1	0
83	L5	122	Total 122	Mg 122	0

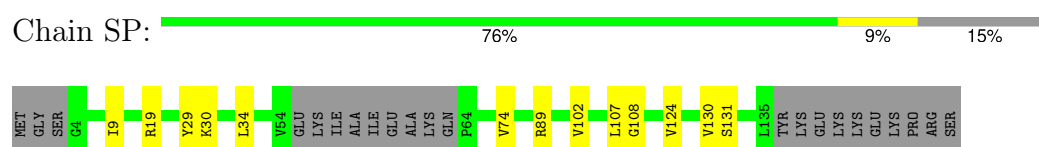
- Molecule 84 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
84	L5	12	Total 12	K 12	0

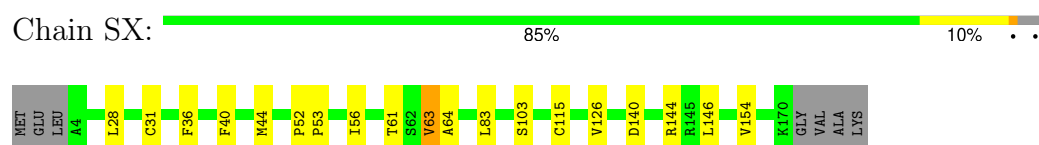
3 Residue-property plots [i](#)

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.

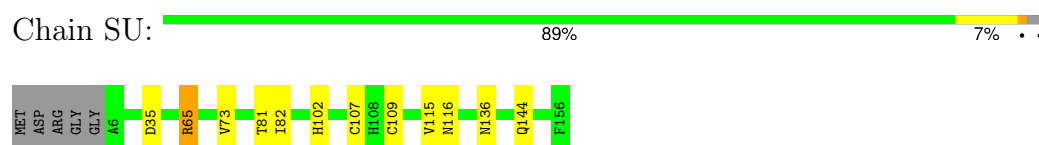
- Molecule 1: 40S ribosomal protein uS12



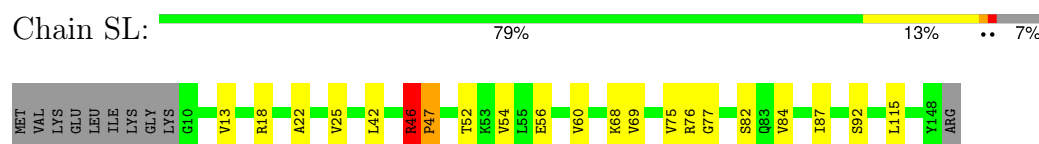
- Molecule 2: 40S ribosomal protein eS19



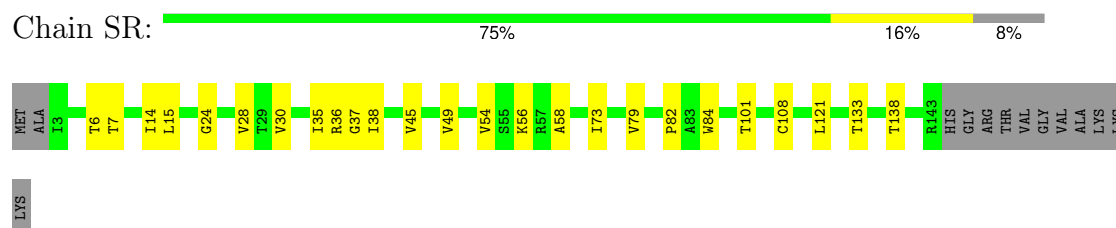
- Molecule 3: 40S ribosomal protein uS17



- Molecule 4: 40S ribosomal protein uS9

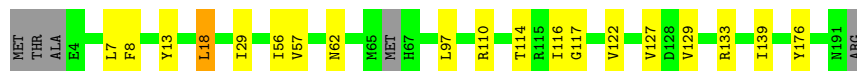


- Molecule 5: 40S ribosomal protein uS13




- Molecule 6: 40S ribosomal protein uS7

Chain SH:  88% 9% ..



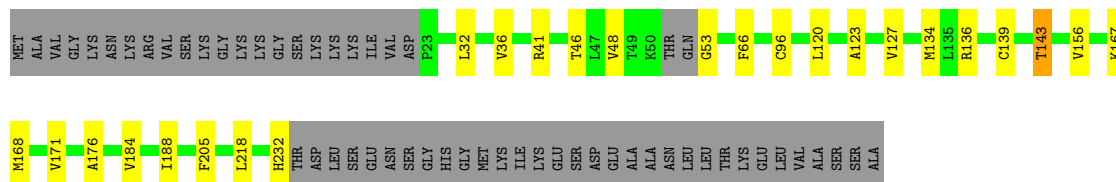
- Molecule 7: 40S ribosomal protein uS15

Chain ST:  85% 11% ..



- Molecule 8: 40S ribosomal protein eS1

Chain SA:  69% 9% 21%




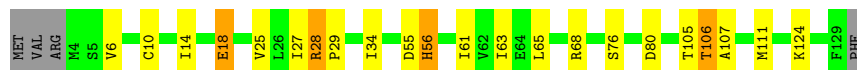
- Molecule 9: 40S ribosomal protein eS10

Chain SN:  73% 12% 15%



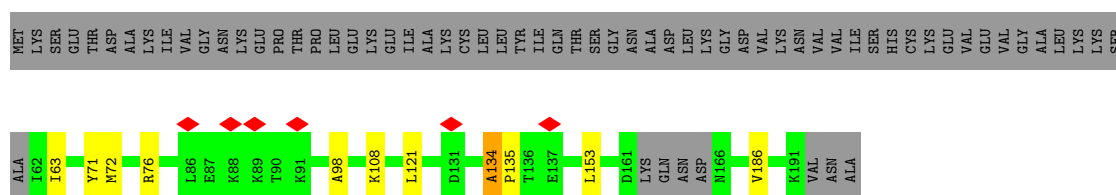
- Molecule 10: 40S ribosomal protein uS8

Chain SJ:  80% 14% ..




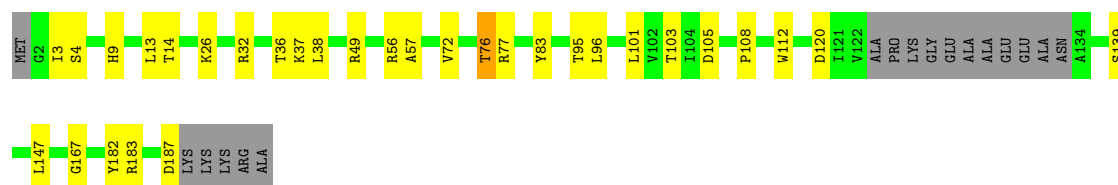
- Molecule 11: 40S ribosomal protein eS7

Chain SI:  59% 5% 35%



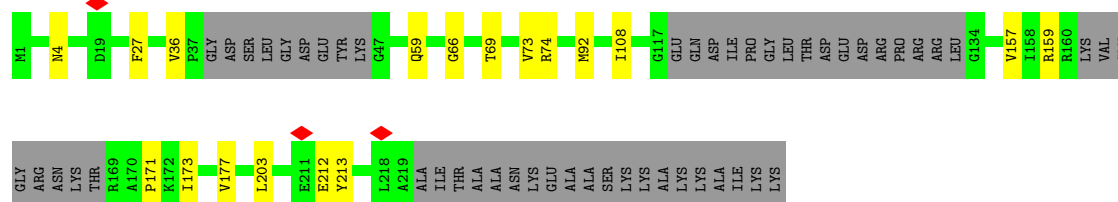
- Molecule 12: 40S ribosomal protein eS8

Chain SK: 



- Molecule 13: 40S ribosomal protein eS6

Chain SG: 



- Molecule 14: 40S ribosomal protein uS10

Chain SM: 



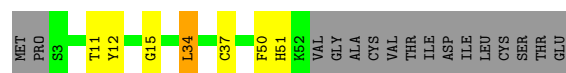
- Molecule 15: 40S ribosomal protein eS30

Chain Se: 



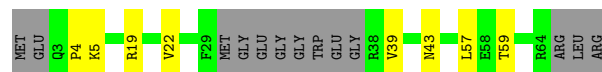
- Molecule 16: 40S ribosomal protein uS14

Chain SS: 



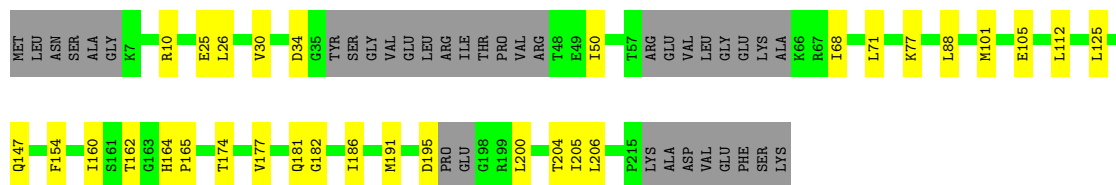
- Molecule 17: 40S ribosomal protein eS28

Chain Sd: 



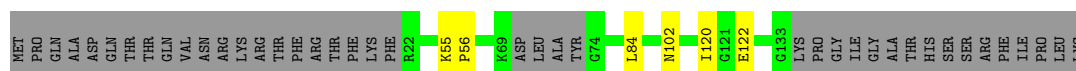
- Molecule 18: 40S ribosomal protein uS3

Chain SC:  70% 14% 16%



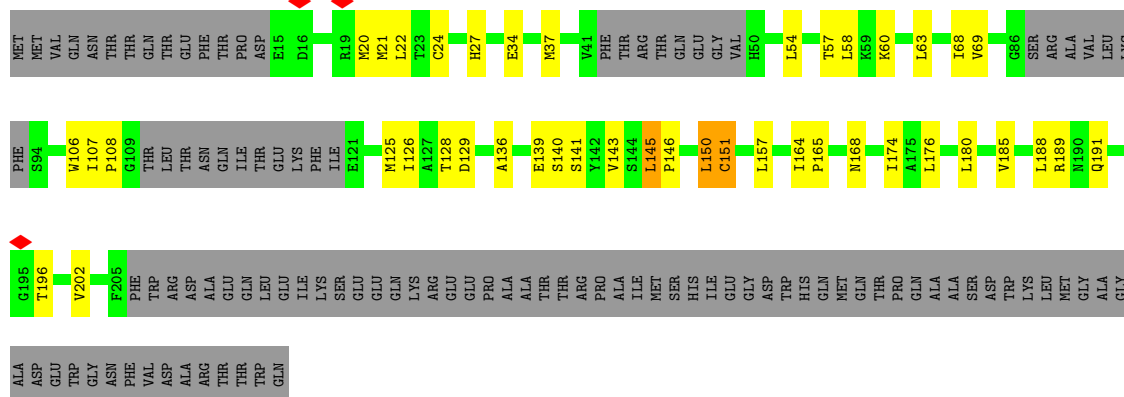
- Molecule 19: 40S ribosomal protein uS19

Chain SW:  68% 0% 28%



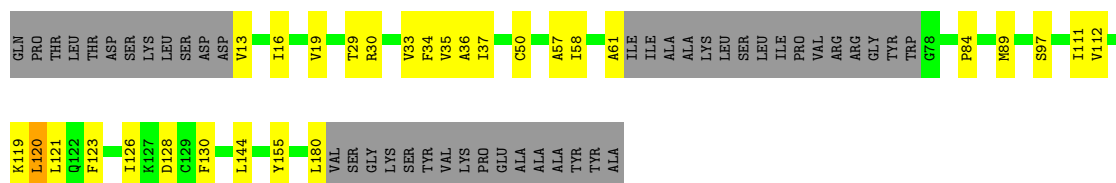
- Molecule 20: 40S ribosomal protein uS2

Chain SB:  45% 15% 40%



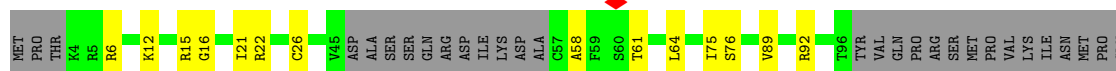
- Molecule 21: 40S ribosomal protein uS5

Chain SF:  63% 14% 22%



- Molecule 22: 40S ribosomal protein eS26

Chain Sb:  59% 12% 29%



ASN
LYS
ASP
ASN

• Molecule 23: 40S ribosomal protein eS17

Chain SV:  51% 44%

MET GLY V4 Y21 K32 K33 V34 V38 A51 M58 R78 GLU ARG ARG MET MET ASP PHE VAL PRO GLU ARG SER SER VAL ASP VAL PRO LEU ILE ILE ASP GLN ASP THR ALA ASP MET LEU SER PHE LEU LYS MET ASN ILE PRO VAL LYS VAL ILE THR SER ASN THR ARG TYR

• Molecule 24: 40S ribosomal protein uS11

Chain SO:  52% 10% 38%

MET ALA SER THR GLU ALA LYS PRO THR THR THR LYS GLU SER ALA PRO VAL VAL VAL ALA ALA LEU ARG SER ALA ARG LEU SER GLY PRO GLN ASN GLY ASP Q32 V33 F34 A37 F43 E57 T58 L59 K67 VAL LYS ALA SER ASP ARG ASP GLU SER S76 M82 ALA ALA ASP V87

I96 T97 A98 V99 T106 R110 G115 PRO GLY ALA GLN SER ALA LEU ARG SER ALA ARG SER GLY G129 L130 K131 I135 V138 D144 C150 G154 ARG ARG LEU

• Molecule 25: 40S ribosomal protein eS24

Chain SZ:  40% 10% 49%

MET ALA SER THR ASP GLN PHE SER ILE ARG VAL LYS LYS PHE MET ASN PRO LEU LEU ALA ARG ALA LYS GLN PHE CYS LEU ASP VAL LEU HIS PRO GLY ARG ALA LYS V37 D41 L42 R43 L52 K53 D54 P55 L58 V59 L60 F61 GLY PHE LYS THR PHE TYR PHE GLY GLY

ARG SER SER GLY TYR C76 V77 I78 Y92 R93 Q94 Y95 R96 L99 GLU ALA PRO ALA LYS MET MET MET GLY R108 R122 A127 CYS SER GLY GLY LYS LYS

• Molecule 26: 40S ribosomal protein eS25

Chain Sa:  62% 6% 32%

MET ALA VAL GLU LYS LYS SER LYS GLU ALA VAL MET LYS ALA ALA MET GLU ALA ALA SER ARG GLY LYS ARG LYS LYS TRP VAL VAL LYS LYS THR LYS P33 I39 F40 V61 L74 A75 R76 K103 VAL

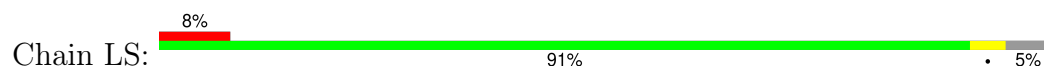
• Molecule 27: 40S ribosomal protein eS12

Chain SQ:  48% 15% 36%

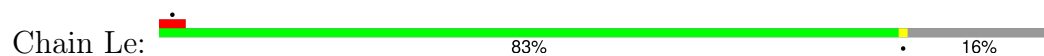
MET ALA GLU GLY VAL PRO GLU ALA VAL GLU THR VAL VAL GLN THR PRO GLU ASP ASP L20 Q21 K22 A27 I34 R35 G36 I37 H38 Q39 V40 Y63 I67 R68 V69 L70 C71 K72 L78 T81 T87 W91 L94 C95 R96 TYR ASP ILE GLU VAL VAL ALA

ARG ASN V112 A113 V114 T115 ILE ASP GLU ASN SER SER GLU ALA LEU LEU MET VAL ALA LYS

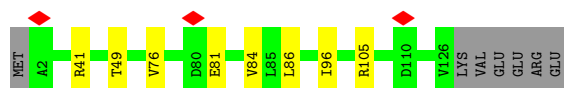
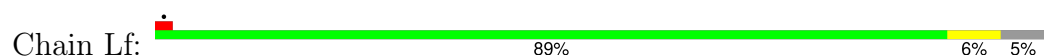
• Molecule 33: 60S ribosomal protein eL20



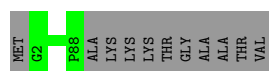
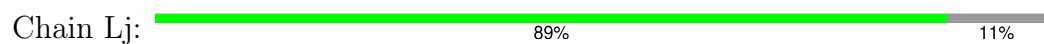
• Molecule 34: 60S ribosomal protein eL31



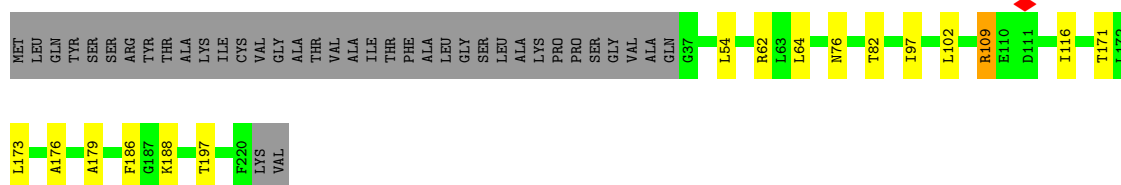
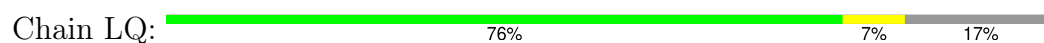
• Molecule 35: 60S ribosomal protein eL32



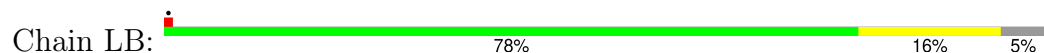
• Molecule 36: 60S ribosomal protein eL37



• Molecule 37: 60S ribosomal protein eL18

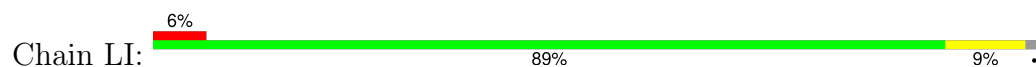


• Molecule 38: 60S ribosomal protein uL2

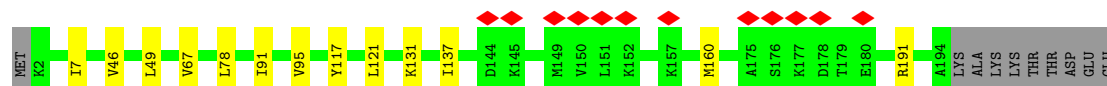
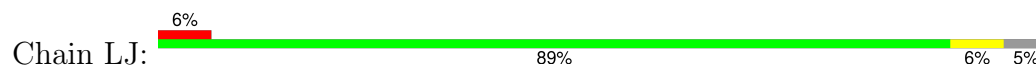




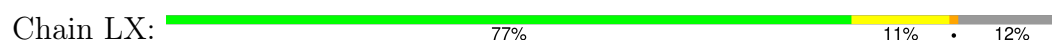
- Molecule 39: 60S ribosomal protein uL13



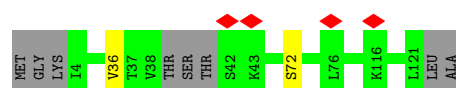
- Molecule 40: 60S ribosomal protein eL13



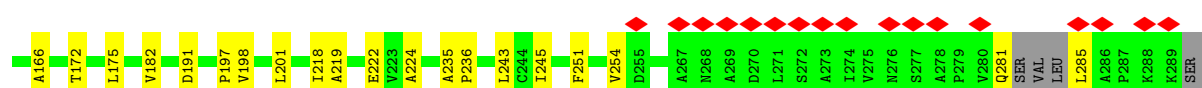
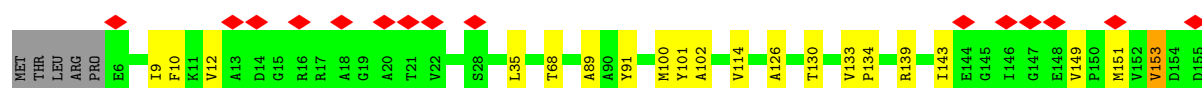
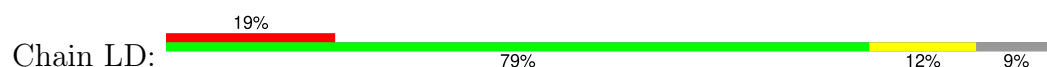
- Molecule 41: 60S ribosomal protein uL24

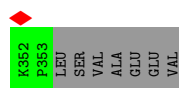


- Molecule 42: 60S ribosomal protein uL29

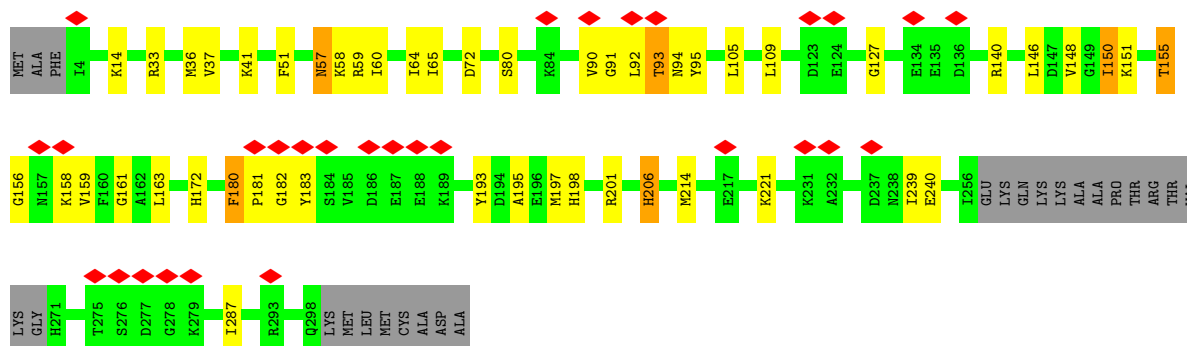
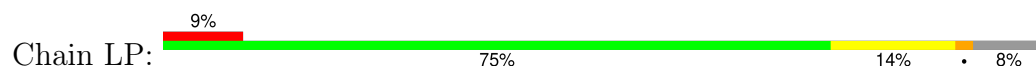


- Molecule 43: 60S ribosomal protein uL4

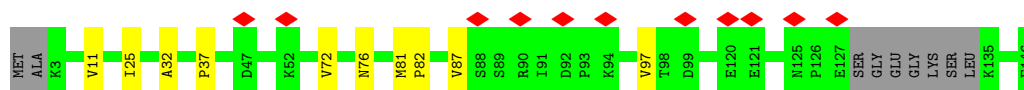
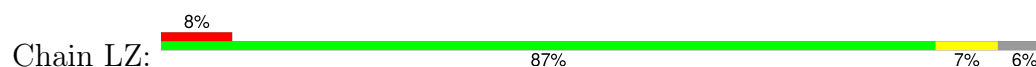




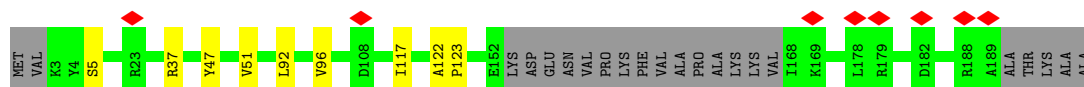
- Molecule 44: 60S ribosomal protein uL18



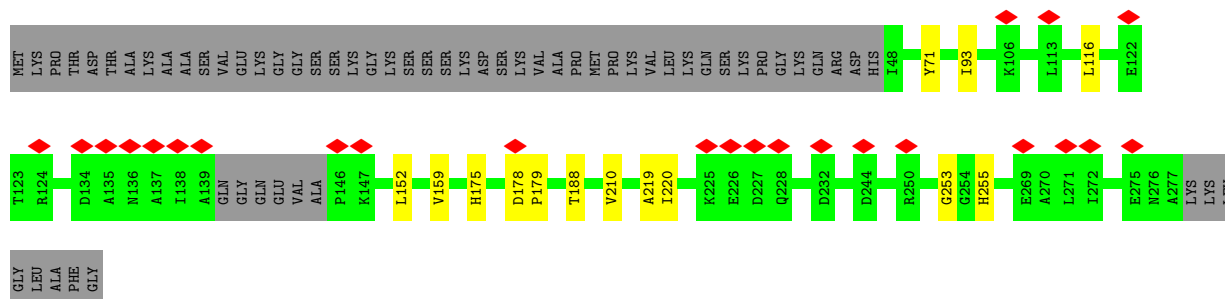
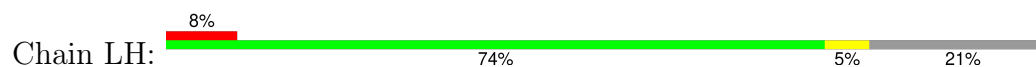
- Molecule 45: 60S ribosomal protein eL27



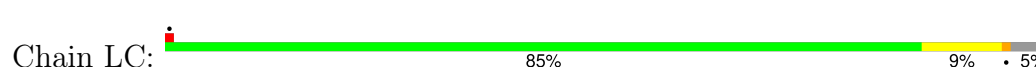
- Molecule 46: 60S ribosomal protein uL22

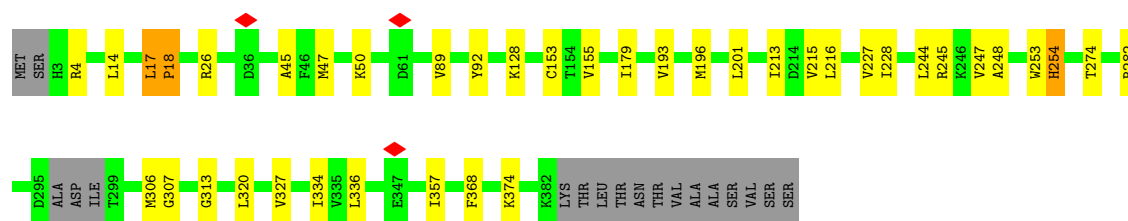


- Molecule 47: 60S ribosomal protein eL8

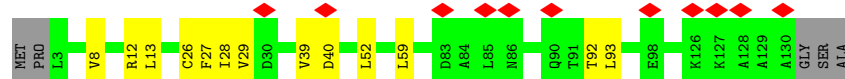
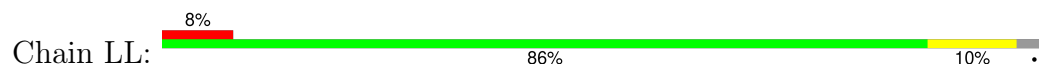


- Molecule 48: 60S ribosomal protein uL3





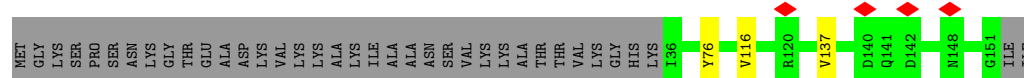
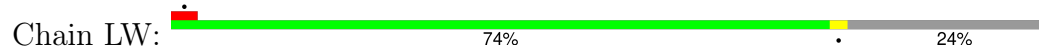
- Molecule 49: 60S ribosomal protein eL14



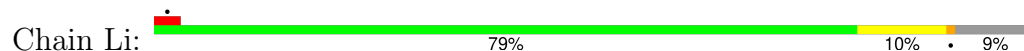
- Molecule 50: 60S ribosomal protein uL14



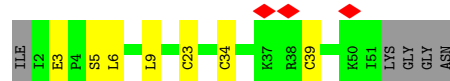
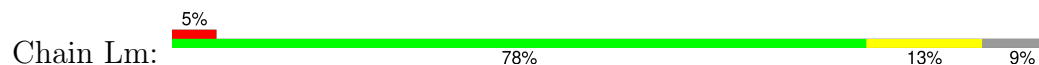
- Molecule 51: 60S ribosomal protein uL23



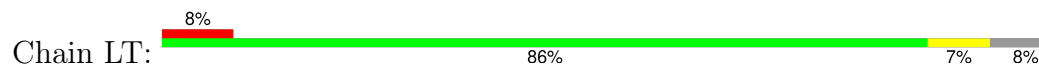
- Molecule 52: 60S ribosomal protein eL36

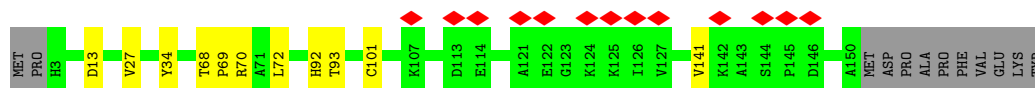


- Molecule 53: 60S ribosomal protein eL40



- Molecule 54: 60S ribosomal protein eL21





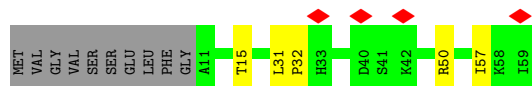
- Molecule 55: 60S ribosomal protein eL42

Chain Lo: 86% 6% 9%



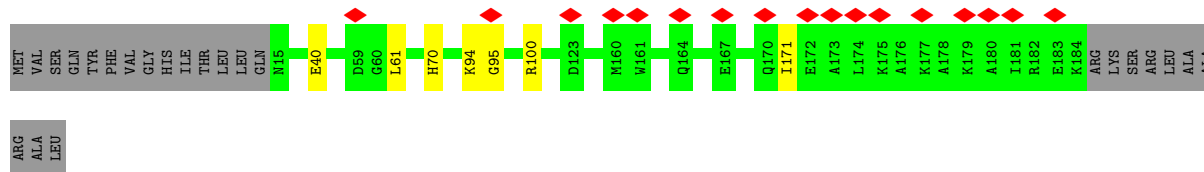
- Molecule 56: 60S ribosomal protein eL39

Chain L1: 7% 75% 8% 17%



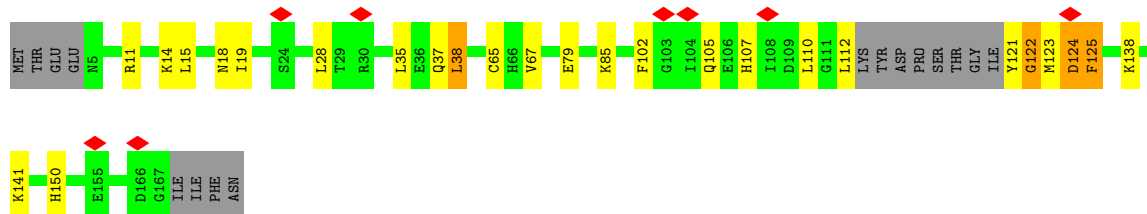
- Molecule 57: 60S ribosomal protein eL19

Chain LR: 9% 84% 12%



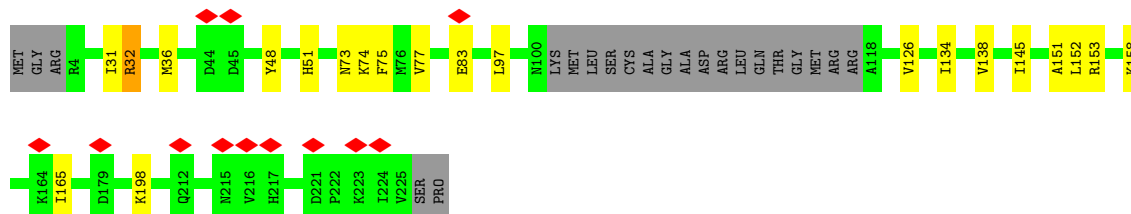
- Molecule 58: 60S ribosomal protein uL5

Chain LE: 5% 75% 13% 9%



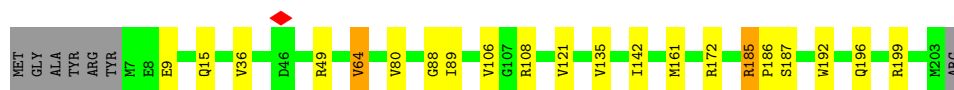
- Molecule 59: 60S ribosomal protein uL16

Chain LO: 5% 81% 9% 10%




- Molecule 60: 60S ribosomal protein eL15

Chain LN:  86% 9% ..




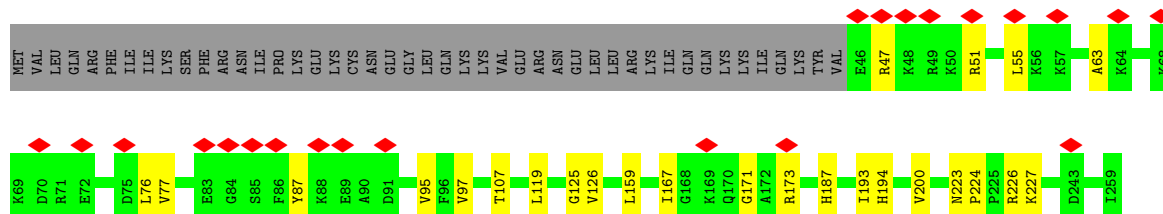
- Molecule 61: 60S ribosomal protein eL33

Chain Lg:  83% 9% • 6%




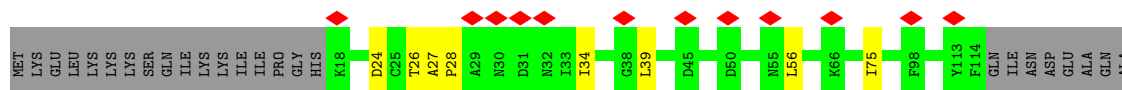
- Molecule 62: 60S ribosomal protein uL30

Chain Lc:  8% 73% 10% 17%




- Molecule 63: 60S ribosomal protein eL22

Chain LV:  10% 73% 7% 20%



- Molecule 64: 60S ribosomal protein eL30

Chain Ld:  76% 10% 14%



- Molecule 65: 60S ribosomal protein eL43

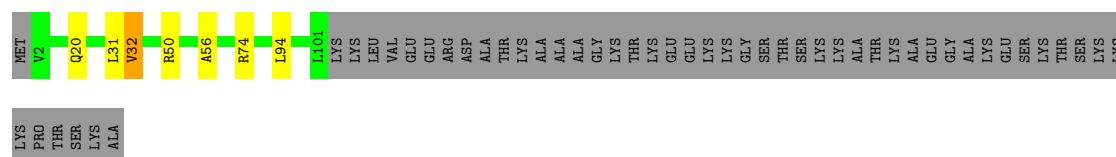
Chain Lp:  89% • 6%



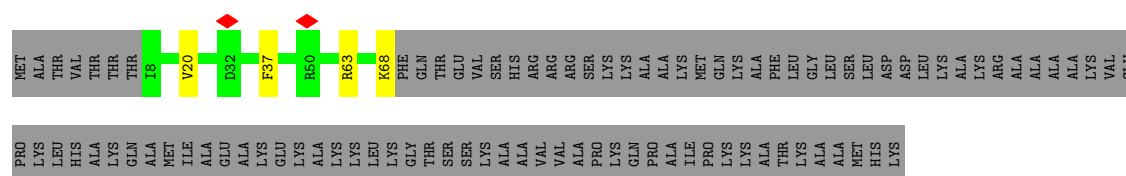
- Molecule 66: 60S ribosomal protein eL29

MET
ALA
LYS
S4
K28
C46
G53
R54
GLY
ASP
SER
ASP
GLU

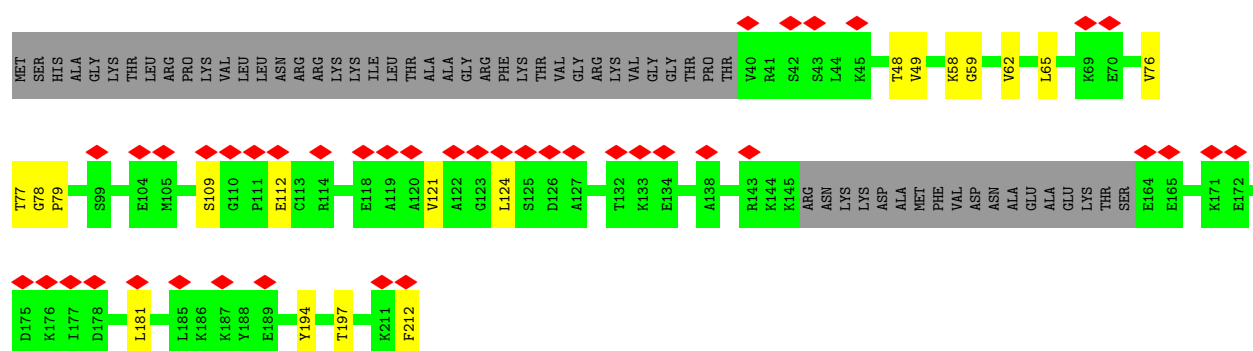
- Chain Lh: 62% 3% 33%



- Chain LY: 



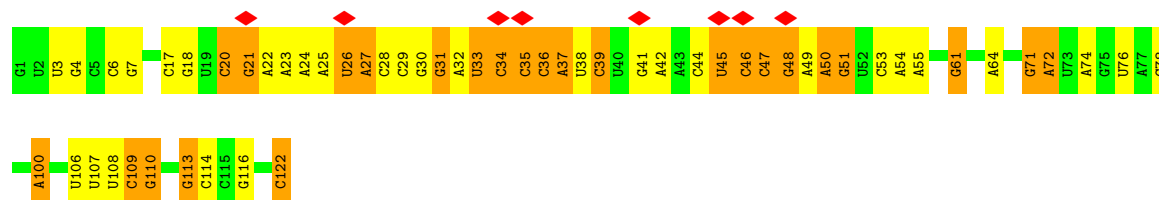
- Chain LG: 



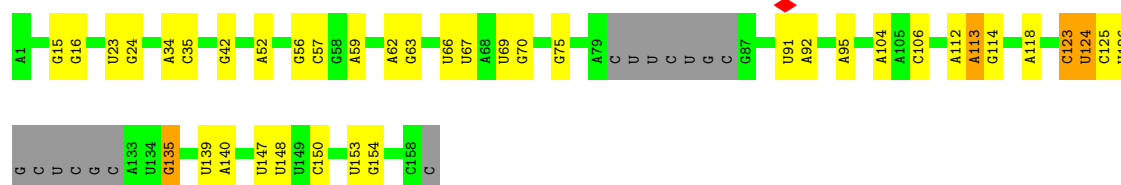
- Chain Ln: 95%



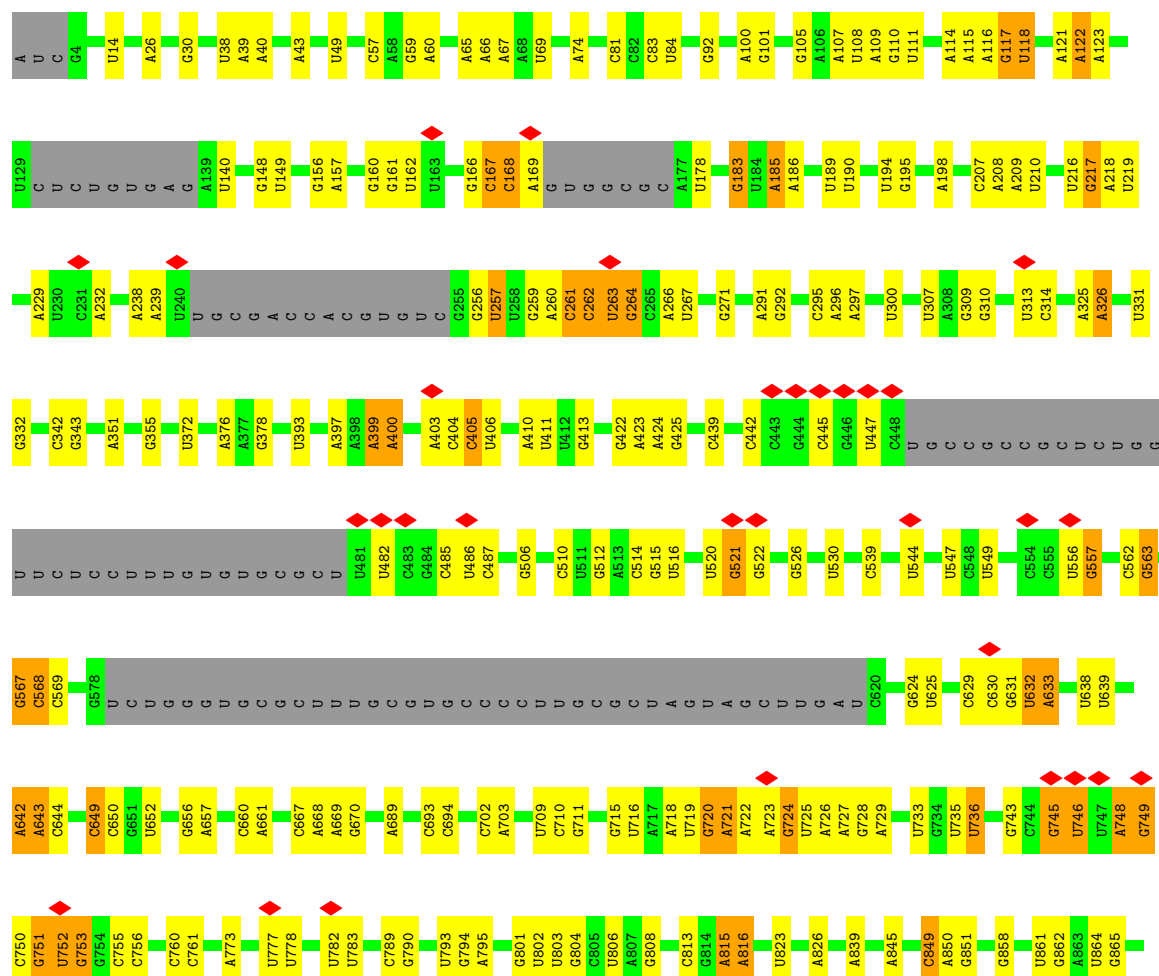
- Chain L3: 



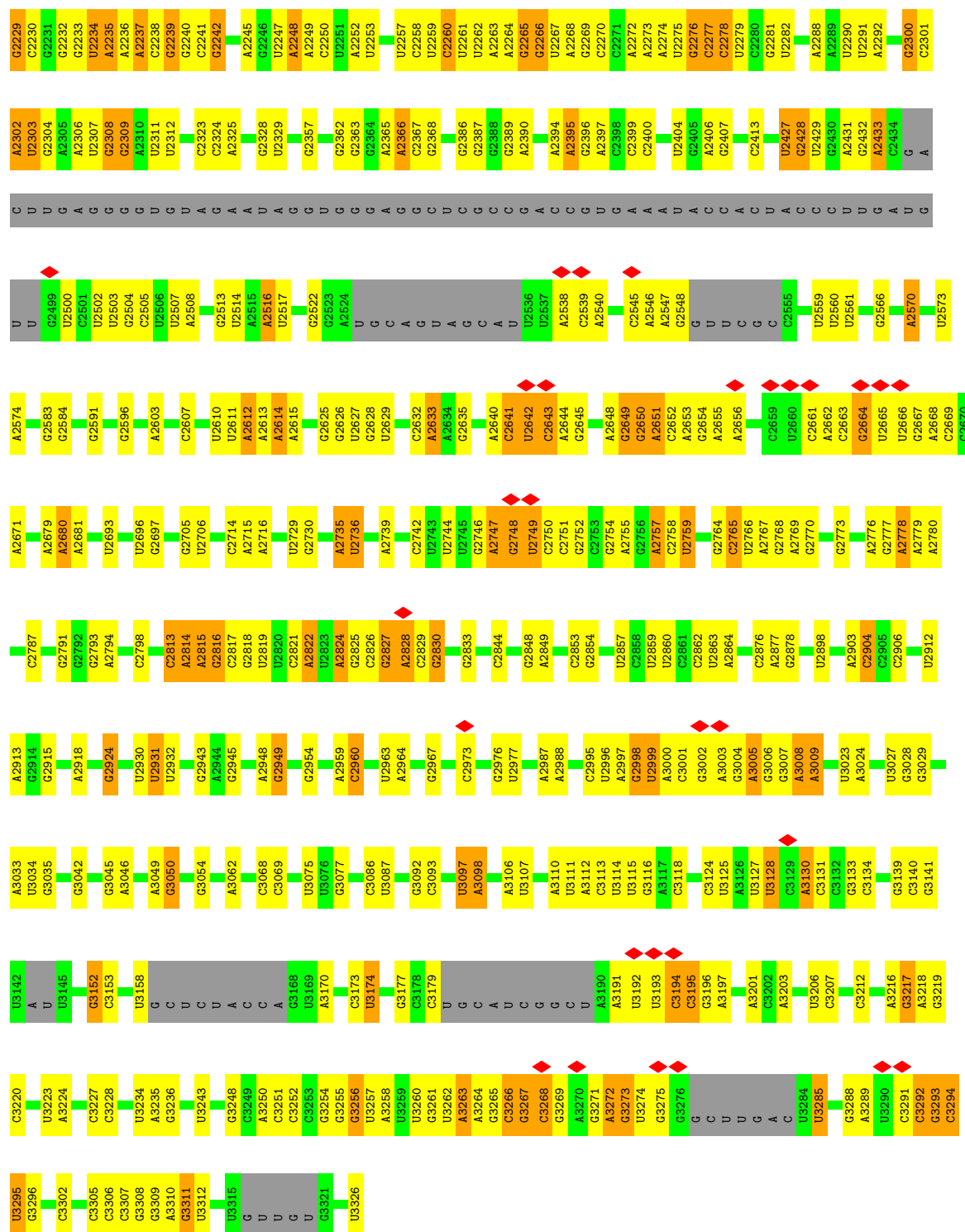
• Molecule 72: 5.8S ribosomal RNA



• Molecule 73: 28S ribosomal RNA



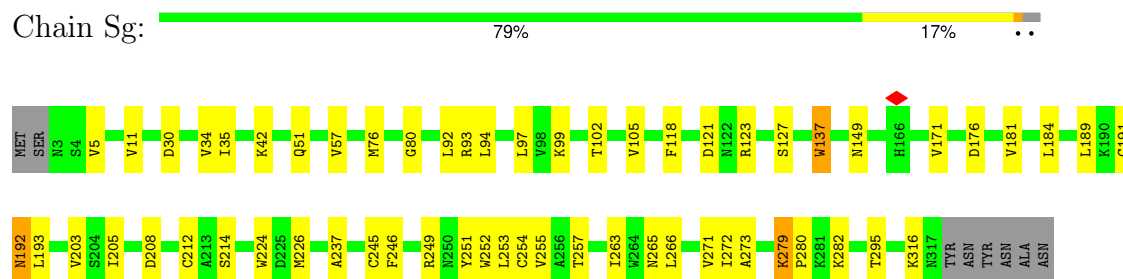




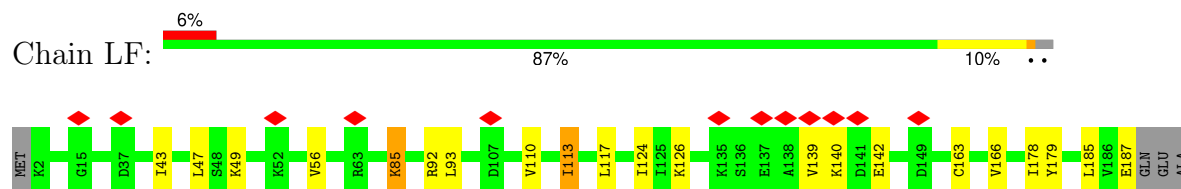
• Molecule 74: E-site tRNA



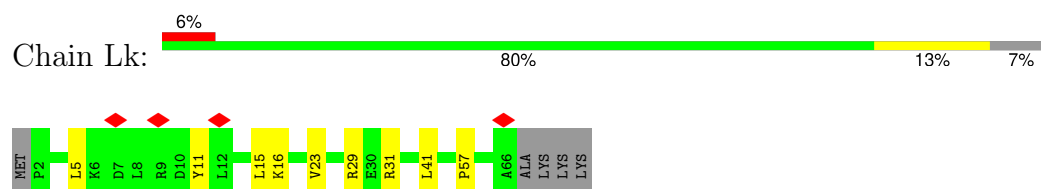
- Molecule 80: Receptor for activated C kinase 1, RACK1 protein



- Molecule 81: 60S ribosomal protein uL6



- Molecule 82: 60S ribosomal protein eL38



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26467	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	30.107	Depositor
Minimum map value	-2.428	Depositor
Average map value	0.586	Depositor
Map value standard deviation	1.329	Depositor
Recommended contour level	4	Depositor
Map size (Å)	369.6, 369.6, 369.6	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor

5 Model quality

5.1 Standard geometry

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

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	SP	0.25	0/975	0.30	0/1304
2	SX	0.38	0/1393	0.34	0/1871
3	SU	0.27	0/1263	0.30	0/1689
4	SL	0.41	0/1106	0.38	0/1480
5	SR	0.35	0/1142	0.36	0/1535
6	SH	0.37	0/1486	0.33	0/1997
7	ST	0.25	0/1208	0.29	0/1621
8	SA	0.23	0/1711	0.28	0/2289
9	SN	0.30	0/828	0.32	0/1128
10	SJ	0.28	0/1023	0.36	0/1374
11	SI	0.20	0/1053	0.28	0/1413
12	SK	0.25	0/1436	0.31	0/1919
13	SG	0.20	0/1535	0.28	0/2037
14	SM	0.34	0/772	0.29	0/1040
15	Se	0.22	0/318	0.43	0/422
16	SS	0.41	0/422	0.36	0/564
17	Sd	0.33	0/422	0.32	0/563
18	SC	0.31	0/1475	0.31	0/1973
19	SW	0.33	0/890	0.33	0/1191
20	SB	0.20	0/1313	0.36	0/1780
21	SF	0.28	0/1164	0.34	0/1570
22	Sb	0.25	0/669	0.33	0/889
23	SV	0.35	0/624	0.36	0/829
24	SO	0.25	0/747	0.33	0/999
25	SZ	0.20	0/585	0.40	0/769
26	Sa	0.35	0/576	0.31	0/773
27	SQ	0.20	0/666	0.32	0/898
28	SD	0.22	0/947	0.32	0/1253
29	Sf	0.20	0/413	0.28	0/548
30	Sc	0.24	0/479	0.30	0/634
31	S1	0.36	0/36610	0.38	11/57011 (0.0%)
32	LM	0.23	0/1176	0.28	0/1569

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LS	0.19	0/1477	0.24	0/1987
34	Le	0.21	0/833	0.25	0/1119
35	Lf	0.21	0/1043	0.27	0/1389
36	Lj	0.24	0/704	0.29	0/933
37	LQ	0.20	0/1453	0.29	0/1941
38	LB	0.22	0/1906	0.29	0/2559
39	LI	0.21	0/1643	0.27	0/2196
40	LJ	0.20	0/1545	0.27	0/2064
41	LX	0.19	0/1018	0.28	0/1353
42	La	0.18	0/964	0.23	0/1278
43	LD	0.19	0/2556	0.28	0/3426
44	LP	0.20	0/2335	0.36	0/3126
45	LZ	0.18	0/1128	0.23	0/1504
46	LU	0.20	0/1416	0.27	0/1895
47	LH	0.18	0/1850	0.25	0/2486
48	LC	0.22	0/3082	0.31	0/4143
49	LL	0.17	0/1030	0.25	0/1381
50	LK	0.21	0/980	0.31	0/1322
51	LW	0.20	0/960	0.26	0/1289
52	Li	0.19	0/836	0.27	0/1112
53	Lm	0.18	0/412	0.35	0/547
54	LT	0.21	0/1221	0.25	0/1637
55	Lo	0.21	0/786	0.25	0/1034
56	Ll	0.21	0/445	0.23	0/591
57	LR	0.20	0/1405	0.27	0/1859
58	LE	0.17	0/1276	0.30	0/1698
59	LO	0.18	0/1691	0.25	0/2276
60	LN	0.24	0/1690	0.29	0/2252
61	Lg	0.23	0/901	0.31	0/1203
62	Lc	0.20	0/1785	0.28	0/2385
63	LV	0.15	0/813	0.26	0/1090
64	Ld	0.20	0/716	0.34	0/961
65	Lp	0.22	0/706	0.32	0/941
66	Lb	0.20	0/424	0.25	0/557
67	Lh	0.22	0/826	0.27	0/1100
68	LY	0.20	0/523	0.29	0/698
69	LG	0.16	0/1243	0.25	0/1665
70	Ln	0.29	0/354	0.34	0/458
71	L3	0.24	0/2918	0.35	0/4549
72	L4	0.25	0/3444	0.36	2/5357 (0.0%)
73	L5	0.25	0/68607	0.35	20/106896 (0.0%)
74	S7	0.16	0/1754	0.29	0/2732
75	S8	0.25	0/1810	0.44	2/2821 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	S9	0.20	0/1708	0.35	0/2654
77	S6	0.26	0/251	0.39	0/387
78	SY	0.22	0/607	0.29	0/818
79	SE	0.23	0/2074	0.35	0/2794
80	Sg	0.29	0/2484	0.33	0/3377
81	LF	0.16	0/1488	0.27	0/2005
82	Lk	0.18	0/532	0.27	0/716
All	All	0.27	0/200080	0.34	35/293493 (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
4	SL	0	1
10	SJ	0	1
20	SB	0	1
38	LB	0	1
48	LC	0	2
58	LE	0	1
60	LN	0	1
61	Lg	0	1
All	All	0	9

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	S1	1506	G	OP2-P-O3'	-11.66	73.02	108.00
73	L5	916	G	OP2-P-O3'	-11.40	73.79	108.00
73	L5	660	C	OP2-P-O3'	-11.28	74.17	108.00
31	S1	1195	G	OP1-P-O3'	-11.07	74.79	108.00
72	L4	42	G	OP1-P-O3'	-11.07	74.80	108.00
73	L5	2413	C	OP1-P-O3'	-11.06	74.83	108.00
73	L5	813	C	OP1-P-O3'	-11.02	74.95	108.00
73	L5	657	A	OP2-P-O3'	-11.00	75.00	108.00
31	S1	1360	A	OP1-P-O3'	-10.74	75.76	108.00
73	L5	2791	G	OP1-P-O3'	-10.67	76.00	108.00
73	L5	2930	U	OP1-P-O3'	-10.62	76.13	108.00
31	S1	1506	G	OP1-P-O3'	-10.62	76.15	108.00
73	L5	2898	U	OP1-P-O3'	-10.61	76.16	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	S1	411	A	OP1-P-O3'	-10.57	76.30	108.00
73	L5	1908	A	OP2-P-O3'	-10.31	77.07	108.00
73	L5	1908	A	OP1-P-O3'	-10.30	77.11	108.00
73	L5	2930	U	OP2-P-O3'	-10.29	77.12	108.00
73	L5	2898	U	OP2-P-O3'	-10.26	77.21	108.00
73	L5	657	A	OP1-P-O3'	-10.18	77.45	108.00
31	S1	1360	A	OP2-P-O3'	-10.15	77.55	108.00
31	S1	411	A	OP2-P-O3'	-10.08	77.75	108.00
73	L5	2791	G	OP2-P-O3'	-10.08	77.76	108.00
73	L5	2413	C	OP2-P-O3'	-9.84	78.48	108.00
72	L4	42	G	OP2-P-O3'	-9.60	79.19	108.00
73	L5	660	C	OP1-P-O3'	-9.59	79.22	108.00
31	S1	1195	G	OP2-P-O3'	-9.39	79.82	108.00
73	L5	813	C	OP2-P-O3'	-9.28	80.15	108.00
73	L5	916	G	OP1-P-O3'	-9.18	80.46	108.00
73	L5	1811	G	OP1-P-O3'	-8.87	81.39	108.00
75	S8	33	U	OP1-P-O3'	-8.86	81.42	108.00
31	S1	1504	G	OP2-P-O3'	-8.77	81.70	108.00
31	S1	1504	G	OP1-P-O3'	-7.97	84.10	108.00
75	S8	33	U	OP2-P-O3'	-7.75	84.74	108.00
73	L5	1811	G	OP2-P-O3'	-7.74	84.79	108.00
31	S1	1361	G	OP1-P-OP2	5.06	134.79	119.60

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
38	LB	196	TRP	Peptide
48	LC	17	LEU	Peptide
48	LC	254	HIS	Peptide
58	LE	122	GLY	Peptide
60	LN	185	ARG	Peptide
61	Lg	111	TYR	Peptide
20	SB	150	LEU	Peptide
10	SJ	28	ARG	Peptide
4	SL	46	ARG	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	SP	959	0	1019	5	0
2	SX	1365	0	1393	15	0
3	SU	1237	0	1306	5	0
4	SL	1090	0	1158	11	0
5	SR	1128	0	1173	15	0
6	SH	1466	0	1522	14	0
7	ST	1182	0	1250	9	0
8	SA	1687	0	1791	16	0
9	SN	802	0	812	12	0
10	SJ	1004	0	1039	15	0
11	SI	1038	0	1123	6	0
12	SK	1412	0	1448	16	0
13	SG	1517	0	1647	11	0
14	SM	761	0	784	15	0
15	Se	313	0	340	6	0
16	SS	411	0	405	5	0
17	Sd	421	0	456	5	0
18	SC	1459	0	1548	21	0
19	SW	875	0	945	3	0
20	SB	1289	0	1333	31	0
21	SF	1141	0	1184	18	0
22	Sb	661	0	707	8	0
23	SV	616	0	668	3	0
24	SO	739	0	771	7	0
25	SZ	582	0	636	10	0
26	Sa	569	0	596	4	0
27	SQ	660	0	697	10	0
28	SD	935	0	987	12	0
29	Sf	407	0	427	3	0
30	Sc	474	0	499	2	0
31	S1	32741	0	16498	399	0
32	LM	1146	0	1180	8	0
33	LS	1445	0	1510	6	0
34	Le	818	0	867	1	0
35	Lf	1026	0	1108	6	0
36	Lj	689	0	702	0	0
37	LQ	1432	0	1554	9	0
38	LB	1868	0	1922	39	0
39	LI	1610	0	1717	13	0
40	LJ	1522	0	1638	9	0
41	LX	1003	0	1066	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	La	957	0	1079	1	0
43	LD	2521	0	2686	26	0
44	LP	2293	0	2323	89	0
45	LZ	1114	0	1206	6	0
46	LU	1392	0	1457	4	0
47	LH	1816	0	1926	10	0
48	LC	3009	0	3120	29	0
49	LL	1016	0	1099	8	0
50	LK	964	0	1024	3	0
51	LW	946	0	1009	2	0
52	Li	827	0	902	9	0
53	Lm	407	0	445	2	0
54	LT	1196	0	1257	9	0
55	Lo	776	0	852	2	0
56	Ll	435	0	479	4	0
57	LR	1387	0	1494	4	0
58	LE	1259	0	1307	30	0
59	LO	1648	0	1689	15	0
60	LN	1656	0	1754	15	0
61	Lg	879	0	915	8	0
62	Lc	1751	0	1867	14	0
63	LV	799	0	836	5	0
64	Ld	706	0	726	12	0
65	Lp	695	0	730	3	0
66	Lb	417	0	451	2	0
67	Lh	816	0	875	4	0
68	LY	509	0	531	2	0
69	LG	1223	0	1311	10	0
70	Ln	349	0	393	0	0
71	L3	2610	0	1323	93	0
72	L4	3082	0	1565	10	0
73	L5	61352	0	30940	685	0
74	S7	1571	0	797	38	0
75	S8	1620	0	827	34	0
76	S9	1532	0	782	44	0
77	S6	227	0	114	1	0
78	SY	600	0	590	12	0
79	SE	2034	0	2114	24	0
80	Sg	2429	0	2400	30	0
81	LF	1469	0	1561	9	0
82	Lk	525	0	568	7	0
83	L3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	L5	122	0	0	0	0
83	S1	1	0	0	0	0
84	L5	12	0	0	0	0
All	All	186450	0	138750	1897	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 6.

All (1897) 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)
31:S1:518:G:N2	31:S1:559:C:C2	2.21	1.07
73:L5:1104:U:O2	73:L5:1106:A:N7	1.92	1.02
73:L5:3000:A:N6	73:L5:3007:G:H21	1.57	1.01
73:L5:1960:G:O6	73:L5:2103:U:O2	1.77	1.00
73:L5:2999:U:O4	73:L5:3008:A:N7	1.93	1.00
73:L5:3275:G:O6	73:L5:3285:U:O2	1.84	0.95
73:L5:1733:G:N2	73:L5:1751:A:H62	1.66	0.93
74:S7:16:U:O2	74:S7:57:C:N3	2.01	0.93
73:L5:2764:G:N2	73:L5:2765:C:H41	1.65	0.92
73:L5:3000:A:H62	73:L5:3007:G:N2	1.68	0.92
73:L5:2429:U:O2	73:L5:2504:G:O6	1.88	0.91
31:S1:518:G:N2	31:S1:559:C:O2	2.05	0.89
73:L5:3000:A:H62	73:L5:3007:G:H21	1.18	0.87
73:L5:1733:G:H21	73:L5:1751:A:N6	1.71	0.86
73:L5:1935:G:O6	73:L5:1959:U:O2	1.94	0.85
31:S1:823:A:N6	31:S1:839:G:N2	2.24	0.85
73:L5:990:G:O6	73:L5:1001:U:O2	1.97	0.82
15:Se:15:VAL:O	15:Se:19:THR:HG23	1.79	0.81
21:SF:13:VAL:HG22	21:SF:35:VAL:HG13	1.64	0.80
76:S9:27:G:H21	76:S9:43:C:H41	1.27	0.79
73:L5:1733:G:N2	73:L5:1751:A:N6	2.27	0.79
44:LP:201:ARG:HD2	71:L3:35:C:H41	1.48	0.79
73:L5:2814:A:C6	73:L5:2827:G:N1	2.50	0.78
71:L3:25:A:H3'	71:L3:26:U:H4'	1.64	0.78
73:L5:520:U:O4	73:L5:557:G:O6	2.02	0.78
9:SN:24:ILE:HD12	9:SN:88:LEU:HD12	1.65	0.78
71:L3:27:A:H61	71:L3:53:C:H42	1.30	0.77
73:L5:1080:A:H61	73:L5:2614:A:H5''	1.50	0.76
76:S9:54:U:O2	76:S9:58:A:N7	2.20	0.75
21:SF:16:ILE:HG23	21:SF:33:VAL:HG12	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:SB:37:MET:HE2	20:SB:157:LEU:HD21	1.67	0.74
31:S1:701:A:N6	31:S1:713:U:C2	2.56	0.73
31:S1:823:A:N6	31:S1:839:G:H21	1.84	0.73
17:Sd:5:LYS:HD2	17:Sd:59:THR:HG21	1.72	0.72
44:LP:92:LEU:HD12	71:L3:48:G:O6	1.88	0.72
31:S1:823:A:H62	31:S1:839:G:N2	1.84	0.72
37:LQ:97:ILE:HG21	37:LQ:116:ILE:HD13	1.71	0.72
44:LP:64:ILE:HD13	44:LP:109:LEU:HD22	1.70	0.72
31:S1:701:A:N1	31:S1:713:U:C4	2.59	0.71
82:Lk:5:LEU:HD13	82:Lk:11:TYR:HA	1.72	0.71
31:S1:418:A:H62	31:S1:494:A:N6	1.89	0.71
73:L5:2262:U:O2	73:L5:2264:A:N7	2.24	0.71
54:LT:101:CYS:CB	73:L5:1084:G:H21	2.04	0.71
25:SZ:43:ARG:HG3	25:SZ:58:LEU:HD11	1.73	0.71
25:SZ:58:LEU:HB2	25:SZ:78:ILE:HG22	1.73	0.70
31:S1:481:A:H61	31:S1:507:A:H62	1.40	0.70
2:SX:28:LEU:HD22	2:SX:154:VAL:CG1	2.21	0.70
22:Sb:58:ALA:HB2	24:SO:131:LYS:HB3	1.73	0.70
44:LP:60:ILE:HG13	44:LP:92:LEU:HD13	1.74	0.70
19:SW:84:LEU:O	19:SW:120:ILE:HD11	1.92	0.70
73:L5:1733:G:H22	73:L5:1750:G:N2	1.89	0.69
8:SA:139:CYS:SG	8:SA:168:MET:HE3	2.32	0.69
64:Ld:87:TYR:H	73:L5:1735:A:H62	1.40	0.69
64:Ld:88:PHE:HD1	73:L5:1735:A:H61	1.38	0.69
73:L5:1114:C:H2'	73:L5:1115:U:C2	2.27	0.69
73:L5:3257:U:H2'	73:L5:3258:A:O4'	1.92	0.69
48:LC:196:MET:HE1	48:LC:201:LEU:HD13	1.74	0.68
48:LC:14:LEU:HD22	48:LC:17:LEU:HD11	1.74	0.68
41:LX:49:ILE:HD12	41:LX:100:PRO:HB3	1.73	0.68
64:Ld:73:PHE:HZ	64:Ld:83:VAL:HG21	1.57	0.68
44:LP:64:ILE:CD1	44:LP:109:LEU:HD22	2.22	0.68
75:S8:33:U:N3	75:S8:35:A:H5''	2.08	0.68
10:SJ:25:VAL:HG21	10:SJ:65:LEU:HD11	1.76	0.68
43:LD:126:ALA:O	43:LD:130:THR:HG23	1.94	0.68
79:SE:214:ILE:HG13	79:SE:231:VAL:HG21	1.75	0.68
73:L5:2814:A:C6	73:L5:2827:G:C6	2.81	0.67
54:LT:34:TYR:CD2	54:LT:72:LEU:HD11	2.29	0.67
6:SH:110:ARG:HD2	17:Sd:57:LEU:HD21	1.76	0.67
2:SX:28:LEU:HD22	2:SX:154:VAL:HG11	1.75	0.67
21:SF:34:PHE:HB3	21:SF:144:LEU:HD12	1.76	0.67
21:SF:33:VAL:HG22	21:SF:57:ALA:HB1	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Lf:41:ARG:HG2	35:Lf:49:THR:HG21	1.77	0.67
39:LI:53:TYR:CD1	39:LI:144:VAL:HG11	2.30	0.67
9:SN:24:ILE:CD1	9:SN:88:LEU:HD12	2.24	0.67
58:LE:35:LEU:HD13	58:LE:67:VAL:HG23	1.76	0.67
58:LE:37:GLN:HB3	58:LE:112:LEU:HD22	1.75	0.67
80:Sg:171:VAL:HG23	80:Sg:205:ILE:HD11	1.77	0.67
38:LB:132:THR:HG21	73:L5:2171:A:H5'	1.77	0.67
10:SJ:10:CYS:SG	10:SJ:27:ILE:HD13	2.35	0.66
14:SM:24:ILE:HG13	14:SM:102:VAL:HG21	1.78	0.66
74:S7:16:U:O2	74:S7:57:C:C4	2.47	0.66
14:SM:43:MET:HE2	14:SM:106:THR:HG22	1.77	0.66
32:LM:58:MET:HE1	73:L5:2752:G:H1'	1.77	0.66
73:L5:2814:A:N6	73:L5:2827:G:C6	2.64	0.66
74:S7:26:C:H42	74:S7:41:C:N4	1.93	0.66
76:S9:13:C:H42	76:S9:46:G:H22	1.42	0.66
64:Ld:87:TYR:N	73:L5:1735:A:H62	1.92	0.66
73:L5:1796:G:H2'	73:L5:1797:G:O4'	1.96	0.66
76:S9:54:U:C2	76:S9:58:A:N7	2.63	0.66
73:L5:2997:A:H61	73:L5:3008:A:H3'	1.60	0.66
31:S1:1116:U:C2	75:S8:35:A:OP1	2.49	0.65
4:SL:54:VAL:HG23	4:SL:84:VAL:HG13	1.78	0.65
73:L5:520:U:C4	73:L5:557:G:O6	2.49	0.65
44:LP:93:THR:HA	71:L3:46:C:H2'	1.76	0.65
52:Li:91:LEU:HD11	52:Li:100:LYS:HG3	1.79	0.65
4:SL:56:GLU:O	4:SL:60:VAL:HG23	1.97	0.65
59:LO:48:TYR:CG	59:LO:145:ILE:HD11	2.32	0.65
8:SA:123:ALA:HB3	8:SA:168:MET:HE2	1.79	0.65
44:LP:180:PHE:HB3	71:L3:35:C:C2'	2.27	0.65
73:L5:2643:C:H1'	73:L5:2681:A:H62	1.62	0.65
24:SO:37:ALA:HB2	24:SO:99:VAL:HG11	1.78	0.64
32:LM:90:THR:HG21	32:LM:98:PRO:HD3	1.79	0.64
48:LC:216:LEU:CD2	48:LC:274:THR:HG23	2.27	0.64
71:L3:34:C:P	71:L3:36:C:H42	2.19	0.64
73:L5:520:U:N3	73:L5:557:G:C6	2.64	0.64
56:Ll:31:LEU:HD12	56:Ll:32:PRO:HD2	1.80	0.64
44:LP:33:ARG:O	44:LP:37:VAL:HG22	1.98	0.64
10:SJ:14:ILE:HG13	10:SJ:27:ILE:HD11	1.78	0.64
44:LP:148:VAL:HG12	44:LP:159:VAL:HG21	1.80	0.64
76:S9:27:G:N2	76:S9:43:C:H41	1.95	0.64
52:Li:70:GLU:O	52:Li:74:THR:HG23	1.98	0.64
58:LE:35:LEU:HD12	58:LE:65:CYS:SG	2.37	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:S9:54:U:N3	76:S9:58:A:C8	2.65	0.64
80:Sg:93:ARG:NH1	80:Sg:102:THR:HG21	2.13	0.63
14:SM:54:VAL:HG22	14:SM:95:LEU:CD2	2.28	0.63
18:SC:10:ARG:NH2	31:S1:1449:A:H62	1.97	0.63
10:SJ:18:GLU:OE1	10:SJ:65:LEU:HD13	1.97	0.63
5:SR:30:VAL:HG21	31:S1:1471:G:C5	2.34	0.63
12:SK:13:LEU:HD12	12:SK:14:THR:HG23	1.81	0.63
73:L5:3257:U:C2	73:L5:3258:A:C8	2.87	0.63
73:L5:262:C:H2'	73:L5:263:U:C2	2.33	0.63
48:LC:45:ALA:HB3	48:LC:179:ILE:HG23	1.81	0.63
31:S1:693:U:O4	31:S1:697:A:N7	2.32	0.62
5:SR:15:LEU:HD11	5:SR:58:ALA:O	1.98	0.62
38:LB:94:ALA:O	38:LB:102:LEU:HD21	1.99	0.62
31:S1:922:G:N2	31:S1:923:A:H62	1.97	0.62
44:LP:181:PRO:HA	71:L3:36:C:O4'	1.98	0.62
18:SC:30:VAL:HG11	18:SC:71:LEU:HD21	1.82	0.62
73:L5:2213:U:H2'	73:L5:2214:G:C4	2.35	0.62
20:SB:20:MET:SD	20:SB:202:VAL:HG21	2.39	0.62
73:L5:2215:A:H2'	73:L5:2216:A:C4	2.35	0.61
10:SJ:25:VAL:CG2	10:SJ:65:LEU:HD11	2.30	0.61
44:LP:91:GLY:O	44:LP:92:LEU:HD23	1.99	0.61
39:LI:144:VAL:O	39:LI:144:VAL:HG12	2.00	0.61
62:Lc:119:LEU:HD21	62:Lc:126:VAL:HG22	1.81	0.61
44:LP:181:PRO:HD2	71:L3:35:C:C2	2.36	0.61
58:LE:19:ILE:HG23	58:LE:122:GLY:CA	2.30	0.61
2:SX:63:VAL:HG13	2:SX:115:CYS:SG	2.41	0.61
20:SB:128:THR:HG23	20:SB:150:LEU:HD12	1.83	0.61
48:LC:320:LEU:HD12	48:LC:336:LEU:HD13	1.83	0.61
56:Ll:15:THR:HG21	72:L4:113:A:H5'	1.82	0.61
65:Lp:10:LEU:HD23	65:Lp:10:LEU:O	2.01	0.61
73:L5:2277:C:C4	73:L5:2278:C:C4	2.89	0.61
76:S9:22:G:N7	76:S9:46:G:O6	2.34	0.61
73:L5:310:G:H21	73:L5:2215:A:H2	1.47	0.61
73:L5:1724:A:H2'	73:L5:1725:G:O4'	2.01	0.61
73:L5:723:A:C5	73:L5:724:G:H1'	2.36	0.60
47:LH:210:VAL:O	47:LH:210:VAL:HG12	2.00	0.60
73:L5:1062:C:H2'	73:L5:1063:C:C1'	2.31	0.60
47:LH:116:LEU:HD21	47:LH:220:ILE:HD11	1.83	0.60
48:LC:14:LEU:CD2	48:LC:17:LEU:HD11	2.31	0.60
76:S9:13:C:N4	76:S9:46:G:N2	2.49	0.60
73:L5:1037:G:N1	73:L5:1064:U:C4	2.69	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:1725:G:H2'	73:L5:1726:U:O4'	2.00	0.60
73:L5:1935:G:O6	73:L5:1959:U:C2	2.53	0.60
14:SM:98:SER:OG	14:SM:101:VAL:HG23	2.02	0.60
18:SC:125:LEU:HD11	18:SC:154:PHE:CB	2.32	0.60
27:SQ:35:ARG:HD2	27:SQ:94:LEU:HD21	1.84	0.60
73:L5:1795:C:H3'	73:L5:1796:G:O4'	2.01	0.60
21:SF:13:VAL:N	21:SF:119:LYS:HZ1	1.98	0.60
31:S1:524:A:N1	31:S1:560:A:H4'	2.17	0.60
38:LB:240:ALA:HB1	38:LB:243:THR:HG23	1.83	0.60
73:L5:1104:U:C2	73:L5:1106:A:N7	2.69	0.60
80:Sg:92:LEU:HD21	80:Sg:127:SER:HB3	1.84	0.60
60:LN:80:VAL:HG23	60:LN:89:ILE:HD11	1.83	0.59
72:L4:125:C:H41	72:L4:135:G:H1'	1.67	0.59
14:SM:102:VAL:O	14:SM:106:THR:HG23	2.02	0.59
38:LB:126:LEU:HD13	38:LB:150:LEU:HD21	1.84	0.59
37:LQ:102:LEU:HD13	37:LQ:116:ILE:HD11	1.84	0.59
44:LP:150:ILE:HD13	58:LE:141:LYS:HG3	1.84	0.59
79:SE:227:ARG:O	79:SE:231:VAL:HG23	2.01	0.59
73:L5:1022:A:H2'	73:L5:1023:A:O4'	2.03	0.59
45:LZ:11:VAL:HG11	45:LZ:25:ILE:HD11	1.82	0.59
71:L3:35:C:H5''	71:L3:36:C:OP2	2.03	0.59
35:Lf:96:ILE:HG21	35:Lf:105:ARG:HG2	1.85	0.59
40:LJ:191:ARG:HG2	52:Li:18:VAL:HG11	1.83	0.59
33:LS:41:ASN:OD1	43:LD:349:ILE:HD12	2.03	0.58
43:LD:151:MET:HE3	43:LD:243:LEU:HD11	1.85	0.58
81:LF:43:ILE:HD11	81:LF:56:VAL:CG1	2.32	0.58
47:LH:188:THR:HG21	52:Li:58:VAL:HG22	1.84	0.58
73:L5:2429:U:C2	73:L5:2504:G:O6	2.56	0.58
8:SA:32:LEU:HD23	8:SA:96:CYS:HB2	1.85	0.58
31:S1:810:G:H2'	31:S1:811:U:C6	2.38	0.58
31:S1:1116:U:N3	75:S8:35:A:OP1	2.36	0.58
22:Sb:89:VAL:HG22	22:Sb:92:ARG:HH12	1.68	0.58
73:L5:2277:C:C5	73:L5:2301:C:C2	2.91	0.58
73:L5:2999:U:H3	73:L5:3008:A:N6	2.02	0.58
7:ST:99:ARG:HG2	7:ST:115:LEU:HD11	1.85	0.58
14:SM:47:ALA:N	14:SM:105:LEU:HD21	2.19	0.58
71:L3:27:A:N6	71:L3:53:C:H42	2.02	0.58
12:SK:101:LEU:HD11	12:SK:182:TYR:CD1	2.39	0.58
31:S1:825:A:C8	31:S1:826:G:N2	2.72	0.58
73:L5:1114:C:H2'	73:L5:1115:U:N1	2.19	0.58
73:L5:2995:C:H2'	73:L5:2996:U:O4'	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:LE:124:ASP:HA	73:L5:2651:A:H5'	1.86	0.57
8:SA:127:VAL:HG11	8:SA:176:ALA:HB3	1.86	0.57
44:LP:180:PHE:HB3	71:L3:35:C:H2'	1.86	0.57
54:LT:70:ARG:O	54:LT:93:THR:HG23	2.04	0.57
82:Lk:11:TYR:HB2	82:Lk:41:LEU:HD22	1.85	0.57
73:L5:720:G:C6	73:L5:722:A:OP2	2.57	0.57
53:Lm:5:SER:O	53:Lm:9:LEU:HD13	2.04	0.57
69:LG:197:THR:HG22	73:L5:3173:C:H5'	1.86	0.57
73:L5:2241:C:H2'	73:L5:2266:G:H5'	1.85	0.57
74:S7:19:G:H1	74:S7:57:C:H41	1.52	0.57
14:SM:52:LEU:O	14:SM:54:VAL:HG23	2.04	0.57
20:SB:151:CYS:SG	20:SB:164:ILE:O	2.61	0.57
31:S1:232:A:H2	79:SE:137:LEU:HD23	1.69	0.57
48:LC:227:VAL:HG11	48:LC:247:VAL:HG23	1.87	0.57
31:S1:28:A:H2'	31:S1:29:U:O4'	2.03	0.57
73:L5:2190:C:H42	73:L5:2234:U:H2'	1.69	0.57
42:La:36:VAL:HG21	51:LW:76:TYR:CD1	2.39	0.57
44:LP:95:TYR:CZ	44:LP:161:GLY:HA2	2.39	0.57
60:LN:88:GLY:C	60:LN:89:ILE:HD12	2.30	0.57
64:Ld:88:PHE:CZ	73:L5:1748:G:C2	2.93	0.57
73:L5:2828:A:N3	73:L5:2829:C:C5	2.72	0.57
41:LX:47:MET:HE1	41:LX:117:ILE:CG2	2.35	0.57
20:SB:21:MET:HE1	20:SB:57:THR:HG21	1.87	0.57
31:S1:526:G:H1'	31:S1:527:U:OP1	2.04	0.57
73:L5:2814:A:C5	73:L5:2827:G:N1	2.72	0.57
76:S9:13:C:H42	76:S9:46:G:N2	2.03	0.57
25:SZ:58:LEU:CB	25:SZ:78:ILE:HG22	2.34	0.56
31:S1:701:A:C6	31:S1:713:U:N3	2.73	0.56
5:SR:37:GLY:C	5:SR:38:ILE:HD12	2.30	0.56
9:SN:9:SER:O	9:SN:52:MET:HE1	2.03	0.56
12:SK:83:TYR:HB3	12:SK:101:LEU:HD12	1.85	0.56
14:SM:60:MET:HE3	31:S1:1272:U:C4	2.40	0.56
44:LP:180:PHE:O	71:L3:36:C:O5'	2.23	0.56
73:L5:1963:U:H3'	73:L5:1964:C:H5''	1.87	0.56
73:L5:3000:A:N6	73:L5:3007:G:N2	2.31	0.56
9:SN:26:GLU:HB3	18:SC:77:LYS:HZ1	1.70	0.56
14:SM:43:MET:CE	14:SM:106:THR:HG22	2.35	0.56
31:S1:720:U:H5''	31:S1:721:U:O4'	2.05	0.56
48:LC:313:GLY:HA2	73:L5:3306:C:H4'	1.86	0.56
73:L5:2276:G:P	73:L5:2949:G:H21	2.28	0.56
44:LP:182:GLY:N	71:L3:36:C:O4'	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:LP:183:TYR:OH	44:LP:193:TYR:HA	2.05	0.56
76:S9:13:C:N4	76:S9:46:G:H22	2.02	0.56
31:S1:150:A:H2'	31:S1:151:A:O4'	2.06	0.56
38:LB:112:VAL:HG13	38:LB:133:TYR:CD2	2.40	0.56
5:SR:49:VAL:HG11	5:SR:79:VAL:HG11	1.87	0.56
73:L5:2213:U:O3'	73:L5:2214:G:O4'	2.24	0.56
48:LC:248:ALA:HB1	73:L5:2924:G:C2	2.41	0.56
73:L5:2642:U:C4	73:L5:2680:A:H4'	2.41	0.56
73:L5:2997:A:O3'	73:L5:2998:G:O4'	2.24	0.56
18:SC:112:LEU:HD23	18:SC:112:LEU:O	2.06	0.56
31:S1:796:G:H2'	31:S1:797:G:C8	2.41	0.56
73:L5:1018:G:C4	73:L5:2614:A:C2	2.94	0.56
73:L5:1025:C:O2	73:L5:1071:A:N6	2.37	0.56
73:L5:2778:A:O2'	73:L5:2779:A:H2'	2.06	0.56
73:L5:2814:A:C2	73:L5:2827:G:N2	2.74	0.56
73:L5:2996:U:C6	73:L5:2997:A:C8	2.93	0.56
54:LT:101:CYS:HB2	73:L5:1084:G:H21	1.71	0.55
31:S1:713:U:O2	31:S1:714:G:N1	2.40	0.55
31:S1:1158:G:H2'	31:S1:1159:A:O4'	2.06	0.55
31:S1:1216:G:H22	31:S1:1249:G:N2	2.03	0.55
73:L5:1062:C:C4	73:L5:1063:C:N4	2.74	0.55
75:S8:34:C:C2'	75:S8:35:A:OP1	2.53	0.55
46:LU:37:ARG:HE	46:LU:117:ILE:HG22	1.72	0.55
73:L5:990:G:O6	73:L5:1001:U:C2	2.60	0.55
12:SK:76:THR:HG23	12:SK:108:PRO:HG2	1.89	0.55
31:S1:699:G:H2'	31:S1:700:C:O4'	2.05	0.55
73:L5:1964:C:H3'	73:L5:1965:U:C6	2.41	0.55
38:LB:237:LEU:HD13	38:LB:243:THR:HG22	1.87	0.55
58:LE:124:ASP:C	73:L5:2651:A:C8	2.85	0.55
73:L5:1019:G:C4	73:L5:1078:A:N6	2.74	0.55
7:ST:4:MET:HE3	7:ST:124:ARG:NH2	2.22	0.55
18:SC:177:VAL:CG2	18:SC:186:ILE:HD11	2.37	0.55
44:LP:93:THR:HB	71:L3:47:C:C4	2.42	0.55
76:S9:27:G:H21	76:S9:43:C:N4	2.02	0.55
9:SN:73:TYR:CE2	18:SC:26:LEU:HD13	2.42	0.55
24:SO:106:THR:HG22	24:SO:110:ARG:HD2	1.88	0.55
31:S1:811:U:C2	31:S1:812:A:C8	2.95	0.55
58:LE:19:ILE:HG23	58:LE:122:GLY:N	2.22	0.55
38:LB:203:THR:HG21	73:L5:2140:C:H5''	1.89	0.55
80:Sg:265:ASN:HB2	80:Sg:272:ILE:HD13	1.88	0.55
35:Lf:41:ARG:CD	35:Lf:49:THR:HG21	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:2276:G:H4'	73:L5:2301:C:H41	1.72	0.55
73:L5:2828:A:H2	73:L5:2829:C:H41	1.55	0.55
80:Sg:189:LEU:HD21	80:Sg:192:ASN:OD1	2.07	0.55
62:Lc:159:LEU:HD12	62:Lc:200:VAL:HG22	1.89	0.55
7:ST:112:LYS:O	7:ST:116:ILE:HG23	2.07	0.54
7:ST:144:GLU:HG2	7:ST:145:THR:HG23	1.88	0.54
11:SI:121:LEU:HD21	31:S1:609:U:C2	2.43	0.54
44:LP:41:LYS:HE3	54:LT:93:THR:HG21	1.88	0.54
53:Lm:6:LEU:HD21	81:LF:92:ARG:HH11	1.71	0.54
63:LV:56:LEU:HD12	63:LV:56:LEU:O	2.07	0.54
5:SR:35:ILE:O	5:SR:37:GLY:N	2.40	0.54
22:Sb:89:VAL:HG23	31:S1:1560:U:OP1	2.07	0.54
23:SV:34:VAL:O	23:SV:38:VAL:HG22	2.08	0.54
31:S1:251:C:H42	31:S1:261:C:H42	1.53	0.54
31:S1:966:G:H2'	31:S1:967:G:C8	2.43	0.54
39:LI:72:LEU:HD13	39:LI:77:LYS:HB3	1.88	0.54
44:LP:51:PHE:CE1	44:LP:105:LEU:HD23	2.43	0.54
73:L5:399:A:H4'	73:L5:400:A:OP1	2.05	0.54
73:L5:1025:C:N3	73:L5:1071:A:N7	2.55	0.54
73:L5:3307:C:H2'	73:L5:3308:G:H8	1.73	0.54
38:LB:112:VAL:HG11	38:LB:168:ILE:HG13	1.89	0.54
44:LP:60:ILE:HD12	44:LP:92:LEU:HD22	1.89	0.54
73:L5:100:A:H3'	73:L5:101:G:H21	1.73	0.54
73:L5:114:A:H2'	73:L5:115:A:O4'	2.07	0.54
11:SI:134:ALA:HB3	11:SI:135:PRO:CD	2.38	0.54
12:SK:76:THR:HG21	12:SK:105:ASP:O	2.08	0.54
31:S1:197:G:H8	31:S1:232:A:H62	1.55	0.54
73:L5:185:A:C2	73:L5:229:A:C2	2.96	0.54
76:S9:27:G:H2'	76:S9:28:G:C8	2.43	0.54
44:LP:57:ASN:HB3	71:L3:29:C:H41	1.72	0.54
73:L5:2997:A:C2	73:L5:2999:U:O4	2.61	0.54
73:L5:3255:G:C4	73:L5:3256:G:C8	2.96	0.54
80:Sg:189:LEU:HD11	80:Sg:191:CYS:O	2.07	0.54
74:S7:24:C:C2	74:S7:25:G:C8	2.95	0.54
38:LB:104:VAL:HG12	38:LB:146:THR:HG21	1.90	0.54
63:LV:24:ASP:OD1	63:LV:26:THR:HG23	2.08	0.54
73:L5:1020:U:H1'	73:L5:2614:A:O4'	2.08	0.54
75:S8:51:C:C2	75:S8:64:G:N2	2.76	0.54
13:SG:73:VAL:HG12	13:SG:74:ARG:H	1.73	0.54
44:LP:150:ILE:H	44:LP:150:ILE:HD12	1.73	0.54
56:Ll:50:ARG:NH2	56:Ll:57:ILE:HD11	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:SH:117:GLY:CA	6:SH:122:VAL:HG22	2.38	0.54
25:SZ:52:LEU:O	25:SZ:53:LYS:CB	2.55	0.54
28:SD:52:ILE:HD12	28:SD:104:MET:HE1	1.90	0.54
73:L5:3255:G:C6	73:L5:3256:G:C5	2.96	0.54
76:S9:65:G:C2	76:S9:66:U:C4	2.96	0.54
23:SV:21:TYR:CE1	23:SV:58:MET:HE1	2.43	0.54
73:L5:2196:U:C2	73:L5:2233:G:N1	2.76	0.54
31:S1:1269:A:H2'	31:S1:1270:A:C8	2.43	0.53
2:SX:40:PHE:CE2	2:SX:44:MET:HE3	2.43	0.53
12:SK:101:LEU:HD11	12:SK:182:TYR:CG	2.42	0.53
31:S1:133:C:H1'	31:S1:134:C:OP2	2.08	0.53
49:LL:13:LEU:HD12	49:LL:26:CYS:O	2.08	0.53
73:L5:2260:C:H2'	73:L5:2261:U:O4'	2.08	0.53
73:L5:3256:G:C4	73:L5:3257:U:C6	2.97	0.53
75:S8:50:U:O4	75:S8:64:G:O6	2.26	0.53
31:S1:823:A:N6	31:S1:839:G:C2	2.76	0.53
31:S1:1095:G:C2	31:S1:1096:A:C8	2.96	0.53
31:S1:1225:A:OP2	31:S1:1226:U:C5	2.60	0.53
73:L5:2996:U:H3'	73:L5:2997:A:H8	1.73	0.53
21:SF:36:ALA:HB2	21:SF:120:LEU:HD12	1.91	0.53
73:L5:2198:U:H2'	73:L5:2199:G:O4'	2.08	0.53
74:S7:58:G:H3'	74:S7:59:A:N7	2.23	0.53
75:S8:26:G:O6	75:S8:44:A:N1	2.42	0.53
31:S1:418:A:N7	31:S1:494:A:C5	2.76	0.53
31:S1:492:C:H2'	31:S1:493:U:O4'	2.09	0.53
44:LP:183:TYR:CE2	71:L3:35:C:H4'	2.44	0.53
58:LE:123:MET:HB3	73:L5:2651:A:H2'	1.89	0.53
8:SA:167:LYS:O	8:SA:171:VAL:HG23	2.09	0.53
21:SF:112:VAL:O	21:SF:112:VAL:HG12	2.08	0.53
64:Ld:28:LEU:HD22	64:Ld:90:VAL:HG11	1.91	0.53
71:L3:44:C:H3'	71:L3:45:U:H5''	1.89	0.53
31:S1:173:G:O2'	31:S1:174:A:O5'	2.25	0.53
31:S1:1220:G:C6	31:S1:1221:A:N7	2.77	0.53
48:LC:248:ALA:HB1	73:L5:2924:G:N3	2.23	0.53
73:L5:2513:G:H2'	73:L5:2514:U:O2	2.09	0.53
79:SE:254:ILE:HD12	79:SE:255:ILE:H	1.74	0.53
11:SI:134:ALA:CB	11:SI:135:PRO:CD	2.87	0.53
20:SB:106:TRP:CD1	20:SB:136:ALA:HA	2.44	0.53
64:Ld:90:VAL:HG22	73:L5:1748:G:C2	2.44	0.53
73:L5:2827:G:H1'	73:L5:2828:A:N7	2.24	0.53
74:S7:8:U:O4	74:S7:14:A:N7	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:SM:69:THR:HG22	31:S1:1124:G:O6	2.09	0.53
31:S1:679:A:O2'	31:S1:680:G:P	2.67	0.53
44:LP:148:VAL:CG1	44:LP:159:VAL:HG21	2.39	0.53
62:Lc:47:ARG:HH21	73:L5:994:A:H62	1.57	0.53
73:L5:2818:G:H2'	73:L5:2818:G:N3	2.23	0.53
4:SL:92:SER:HB3	4:SL:115:LEU:HD13	1.91	0.53
73:L5:1017:A:H2	73:L5:1082:G:H22	1.57	0.53
73:L5:1726:U:H3'	73:L5:1727:U:C5'	2.38	0.53
73:L5:1963:U:H2'	73:L5:1964:C:H4'	1.91	0.53
73:L5:2642:U:C5	73:L5:2680:A:H4'	2.43	0.53
21:SF:35:VAL:HG21	21:SF:61:ALA:HB3	1.89	0.52
35:Lf:81:GLU:O	35:Lf:84:VAL:HG22	2.09	0.52
44:LP:158:LYS:HA	71:L3:46:C:O5'	2.09	0.52
73:L5:1097:G:H2'	73:L5:1098:C:O4'	2.10	0.52
73:L5:1961:G:N2	73:L5:3289:A:C8	2.77	0.52
41:LX:30:MET:HE1	41:LX:74:ARG:HG2	1.91	0.52
59:LO:32:ARG:CZ	76:S9:58:A:H61	2.22	0.52
60:LN:108:ARG:HG2	60:LN:161:MET:HE2	1.90	0.52
73:L5:2189:C:N4	73:L5:2235:A:H2'	2.23	0.52
69:LG:121:VAL:O	69:LG:121:VAL:HG12	2.09	0.52
73:L5:2814:A:N1	73:L5:2828:A:C6	2.77	0.52
73:L5:2815:A:H62	73:L5:2827:G:H21	1.56	0.52
73:L5:2815:A:N1	73:L5:2828:A:H1'	2.25	0.52
79:SE:179:LEU:N	79:SE:179:LEU:HD12	2.24	0.52
80:Sg:263:ILE:HB	80:Sg:273:ALA:HB3	1.91	0.52
15:Se:19:THR:HB	15:Se:20:PRO:HD3	1.91	0.52
31:S1:828:U:H2'	31:S1:829:G:H3'	1.90	0.52
31:S1:1269:A:O2'	31:S1:1270:A:P	2.68	0.52
73:L5:709:U:H2'	73:L5:710:C:C5	2.45	0.52
73:L5:1098:C:H2'	73:L5:1099:U:C6	2.45	0.52
80:Sg:245:CYS:O	80:Sg:253:LEU:HD12	2.09	0.52
9:SN:30:VAL:HG22	9:SN:73:TYR:HD1	1.75	0.52
31:S1:550:U:O2	31:S1:550:U:H2'	2.10	0.52
44:LP:181:PRO:HG2	71:L3:35:C:C4	2.45	0.52
73:L5:2357:G:H22	73:L5:2389:G:H1'	1.74	0.52
7:ST:4:MET:HE3	7:ST:124:ARG:HH21	1.75	0.52
31:S1:489:G:H2'	31:S1:490:A:O4'	2.09	0.52
31:S1:1532:A:C2'	31:S1:1532:A:N3	2.72	0.52
37:LQ:188:LYS:O	37:LQ:197:THR:HG21	2.10	0.52
38:LB:196:TRP:HA	38:LB:196:TRP:CE3	2.45	0.52
73:L5:259:G:C4	73:L5:260:A:C8	2.98	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:Lk:15:LEU:HD21	82:Lk:57:PRO:CD	2.40	0.52
35:Lf:41:ARG:CG	35:Lf:49:THR:HG21	2.40	0.52
73:L5:2204:U:C4	73:L5:2205:C:H1'	2.44	0.52
11:SI:71:TYR:CD2	11:SI:98:ALA:HB2	2.44	0.52
26:Sa:39:ILE:C	26:Sa:74:LEU:HD11	2.35	0.52
31:S1:607:U:O2	31:S1:607:U:H2'	2.10	0.52
31:S1:824:G:H2'	31:S1:825:A:O4'	2.09	0.52
31:S1:834:U:H2'	31:S1:835:C:C6	2.45	0.52
71:L3:36:C:H2'	71:L3:37:A:O5'	2.10	0.52
2:SX:83:LEU:CD1	2:SX:146:LEU:HD21	2.40	0.52
8:SA:136:ARG:HB2	8:SA:218:LEU:HD11	1.92	0.52
9:SN:48:LEU:HG	9:SN:52:MET:HE2	1.91	0.52
38:LB:104:VAL:CG1	38:LB:146:THR:HG21	2.39	0.52
44:LP:150:ILE:HG23	73:L5:2680:A:C6	2.44	0.52
51:LW:116:VAL:HG13	51:LW:137:VAL:HG13	1.92	0.52
73:L5:521:G:H22	73:L5:556:U:H2'	1.73	0.52
31:S1:418:A:H1'	31:S1:494:A:OP1	2.09	0.51
31:S1:1448:U:O2	31:S1:1448:U:H2'	2.10	0.51
69:LG:78:GLY:O	69:LG:79:PRO:C	2.53	0.51
73:L5:262:C:H2'	73:L5:263:U:N1	2.25	0.51
73:L5:1008:A:H61	73:L5:1125:A:H61	1.57	0.51
73:L5:2266:G:H1'	73:L5:2304:G:C6	2.45	0.51
78:SY:54:LEU:HD13	78:SY:68:MET:HE2	1.93	0.51
3:SU:81:THR:HG23	3:SU:107:CYS:O	2.10	0.51
31:S1:1216:G:N2	31:S1:1249:G:N2	2.59	0.51
73:L5:117:G:H4'	73:L5:118:U:OP1	2.08	0.51
58:LE:19:ILE:HD11	73:L5:2651:A:H61	1.74	0.51
60:LN:185:ARG:O	60:LN:187:SER:N	2.43	0.51
67:Lh:31:LEU:HD12	73:L5:1615:G:OP1	2.09	0.51
20:SB:125:MET:HB2	20:SB:145:LEU:HD11	1.92	0.51
28:SD:24:LEU:HD23	31:S1:524:A:H62	1.76	0.51
31:S1:37:U:O2	31:S1:37:U:O5'	2.29	0.51
31:S1:415:C:O2'	31:S1:495:A:C2	2.60	0.51
44:LP:37:VAL:HG21	54:LT:27:VAL:CG1	2.41	0.51
44:LP:93:THR:HG23	71:L3:48:G:H21	1.75	0.51
49:LL:8:VAL:HG22	49:LL:59:LEU:HD21	1.93	0.51
58:LE:19:ILE:HG23	58:LE:122:GLY:H	1.75	0.51
73:L5:2240:G:H2'	73:L5:2241:C:O4'	2.10	0.51
79:SE:139:PRO:O	79:SE:142:VAL:HG12	2.11	0.51
2:SX:53:PRO:HG2	2:SX:56:ILE:HG23	1.92	0.51
12:SK:72:VAL:HG21	12:SK:112:TRP:CE2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:1733:G:N2	73:L5:1750:G:N2	2.57	0.51
12:SK:76:THR:HG22	12:SK:77:ARG:H	1.75	0.51
55:Lo:8:ARG:O	55:Lo:21:LEU:HD12	2.11	0.51
73:L5:723:A:C8	73:L5:724:G:H1'	2.46	0.51
12:SK:13:LEU:HD12	12:SK:14:THR:N	2.26	0.51
21:SF:111:ILE:HD11	21:SF:126:ILE:O	2.10	0.51
39:LI:47:TYR:HE2	39:LI:51:LEU:HD11	1.76	0.51
43:LD:101:TYR:O	43:LD:102:ALA:C	2.52	0.51
58:LE:105:GLN:HA	58:LE:123:MET:SD	2.51	0.51
62:Lc:55:LEU:HD21	62:Lc:194:HIS:HB2	1.92	0.51
69:LG:121:VAL:HG13	69:LG:124:LEU:HD12	1.93	0.51
73:L5:1808:A:C6	73:L5:1809:C:H1'	2.46	0.51
76:S9:49:C:H2'	76:S9:50:U:C6	2.45	0.51
3:SU:65:ARG:HH22	31:S1:113:G:H21	1.58	0.51
31:S1:926:A:H2'	31:S1:927:G:C8	2.46	0.51
73:L5:1726:U:C2	73:L5:1727:U:C6	2.99	0.51
73:L5:2218:U:HO2'	73:L5:2219:U:P	2.34	0.51
73:L5:2666:U:H4'	73:L5:2667:G:O4'	2.10	0.51
31:S1:269:C:O2	31:S1:269:C:O4'	2.29	0.51
31:S1:518:G:C2	31:S1:559:C:O2	2.62	0.51
47:LH:178:ASP:CB	47:LH:179:PRO:HD3	2.41	0.51
40:LJ:191:ARG:CG	52:Li:18:VAL:HG11	2.40	0.50
61:Lg:26:ARG:HG2	61:Lg:27:SER:O	2.11	0.50
73:L5:643:A:H2'	73:L5:644:C:C6	2.46	0.50
73:L5:1884:U:C2	73:L5:1886:G:O5'	2.64	0.50
73:L5:2199:G:H21	73:L5:2202:U:H3	1.59	0.50
74:S7:71:C:H2'	74:S7:72:C:O4'	2.11	0.50
75:S8:33:U:H1'	75:S8:35:A:C8	2.46	0.50
31:S1:524:A:H2'	31:S1:524:A:N3	2.25	0.50
43:LD:133:VAL:HA	43:LD:149:VAL:HG21	1.92	0.50
73:L5:1885:A:H4'	73:L5:1886:G:OP1	2.09	0.50
24:SO:138:VAL:O	24:SO:138:VAL:HG12	2.10	0.50
44:LP:59:ARG:HA	44:LP:92:LEU:HD11	1.94	0.50
73:L5:1744:C:H2'	73:L5:1744:C:O2	2.10	0.50
73:L5:2262:U:C2	73:L5:2264:A:N7	2.79	0.50
73:L5:3256:G:C5	73:L5:3257:U:C5	2.99	0.50
74:S7:23:G:C2	74:S7:24:C:C6	2.99	0.50
1:SP:102:VAL:CG1	1:SP:124:VAL:HG13	2.41	0.50
18:SC:50:ILE:HB	18:SC:88:LEU:HD23	1.93	0.50
73:L5:1747:G:C2'	73:L5:1748:G:H5''	2.41	0.50
74:S7:31:G:H21	74:S7:36:A:N6	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:SC:125:LEU:HD11	18:SC:154:PHE:HB3	1.93	0.50
31:S1:69:A:H61	31:S1:80:U:H3	1.60	0.50
31:S1:173:G:H2'	31:S1:173:G:N3	2.26	0.50
31:S1:828:U:O2'	31:S1:829:G:C8	2.63	0.50
31:S1:1569:C:C2'	31:S1:1570:G:H5'	2.41	0.50
31:S1:1578:C:C2	31:S1:1579:U:C5	3.00	0.50
32:LM:112:GLY:N	32:LM:132:ALA:HB2	2.26	0.50
73:L5:520:U:N3	73:L5:557:G:N1	2.59	0.50
73:L5:567:G:O2'	73:L5:568:C:H5'	2.10	0.50
73:L5:2241:C:H3'	73:L5:2266:G:C8	2.46	0.50
73:L5:2826:C:C4	73:L5:2827:G:C6	2.99	0.50
73:L5:3006:G:H2'	73:L5:3007:G:C8	2.46	0.50
20:SB:146:PRO:HB2	78:SY:34:ILE:HD11	1.93	0.50
25:SZ:43:ARG:CG	25:SZ:58:LEU:HD11	2.39	0.50
31:S1:1266:G:C2	31:S1:1267:C:C6	3.00	0.50
59:LO:153:ARG:HA	59:LO:165:ILE:HD11	1.94	0.50
73:L5:2101:A:HO2'	73:L5:3272:A:H8	1.57	0.50
73:L5:2262:U:H2'	73:L5:2263:A:H8	1.76	0.50
73:L5:2650:G:H4'	73:L5:2651:A:OP1	2.11	0.50
73:L5:2108:C:O2	73:L5:2110:G:O6	2.30	0.50
5:SR:45:VAL:O	5:SR:49:VAL:HG23	2.12	0.50
10:SJ:27:ILE:HD12	10:SJ:63:ILE:HD12	1.94	0.50
26:Sa:61:VAL:HG13	26:Sa:75:ALA:HB3	1.94	0.50
31:S1:701:A:H62	31:S1:714:G:H1	1.60	0.50
38:LB:196:TRP:HA	38:LB:196:TRP:HE3	1.77	0.50
73:L5:2827:G:O2'	73:L5:2828:A:N7	2.40	0.50
73:L5:3256:G:H2'	73:L5:3257:U:O4'	2.11	0.50
76:S9:2:C:H2'	76:S9:3:C:C5	2.47	0.50
18:SC:160:ILE:HD11	18:SC:206:LEU:HD21	1.94	0.50
21:SF:112:VAL:HG21	21:SF:130:PHE:CD1	2.47	0.50
22:Sb:75:ILE:N	22:Sb:75:ILE:HD12	2.27	0.50
31:S1:820:G:H2'	31:S1:821:U:C6	2.46	0.50
31:S1:820:G:H3'	31:S1:821:U:C5	2.47	0.50
31:S1:1173:C:O2	31:S1:1173:C:O5'	2.29	0.50
31:S1:1569:C:N1	75:S8:34:C:N4	2.60	0.50
49:LL:13:LEU:HD13	49:LL:27:PHE:CZ	2.47	0.50
73:L5:260:A:H2'	73:L5:261:C:C6	2.46	0.50
73:L5:1751:A:C2	73:L5:1752:U:C6	3.00	0.50
73:L5:3291:C:C2	73:L5:3292:C:C5	3.00	0.50
31:S1:416:C:O2'	31:S1:494:A:N9	2.45	0.49
44:LP:183:TYR:CG	71:L3:36:C:OP2	2.65	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:LO:138:VAL:HG23	59:LO:152:LEU:HD21	1.93	0.49
73:L5:642:A:O2'	73:L5:643:A:H8	1.95	0.49
73:L5:670:G:H22	73:L5:1460:C:H5	1.59	0.49
73:L5:1037:G:O6	73:L5:1064:U:O4	2.29	0.49
73:L5:2278:C:OP2	73:L5:2279:U:H3'	2.11	0.49
73:L5:2612:A:H4'	73:L5:2613:A:O5'	2.12	0.49
17:Sd:4:PRO:HB3	17:Sd:57:LEU:HD23	1.94	0.49
31:S1:819:U:H2'	31:S1:820:G:C8	2.47	0.49
38:LB:196:TRP:CG	38:LB:197:PRO:HD3	2.47	0.49
44:LP:214:MET:HE1	44:LP:221:LYS:HG2	1.94	0.49
73:L5:1022:A:H2'	73:L5:1023:A:C8	2.47	0.49
73:L5:1764:U:C2	73:L5:1765:G:N7	2.80	0.49
73:L5:2211:G:O2'	73:L5:2212:G:H5'	2.12	0.49
80:Sg:271:VAL:HG23	80:Sg:271:VAL:O	2.11	0.49
37:LQ:109:ARG:HD2	37:LQ:171:THR:HG21	1.93	0.49
73:L5:2108:C:O4'	73:L5:2110:G:C5	2.65	0.49
73:L5:2272:A:H2'	73:L5:2281:G:N7	2.27	0.49
81:LF:117:LEU:HD11	81:LF:166:VAL:HG12	1.94	0.49
4:SL:22:ALA:HA	4:SL:77:GLY:HA3	1.93	0.49
5:SR:121:LEU:HD11	19:SW:122:GLU:OE1	2.12	0.49
31:S1:524:A:H2'	31:S1:525:A:C8	2.47	0.49
31:S1:1489:U:H2'	31:S1:1491:C:O2'	2.12	0.49
38:LB:179:LEU:O	73:L5:2143:A:H4'	2.12	0.49
48:LC:50:LYS:HB2	48:LC:334:ILE:HD12	1.93	0.49
52:Li:88:LYS:HA	52:Li:97:ALA:HB2	1.94	0.49
73:L5:862:G:H2'	73:L5:862:G:N3	2.28	0.49
31:S1:1474:G:N2	31:S1:1501:A:OP2	2.46	0.49
38:LB:96:LEU:HD11	38:LB:111:THR:HG21	1.94	0.49
43:LD:281:GLN:HG2	43:LD:285:LEU:HD12	1.93	0.49
65:Lp:10:LEU:HD23	65:Lp:10:LEU:C	2.37	0.49
73:L5:1074:C:H2'	73:L5:1075:U:O5'	2.13	0.49
73:L5:1744:C:O2'	73:L5:1745:G:P	2.70	0.49
73:L5:2142:A:H2'	73:L5:2143:A:C8	2.48	0.49
73:L5:2262:U:O2	73:L5:2264:A:C5	2.65	0.49
74:S7:36:A:C2'	74:S7:37:U:O5'	2.59	0.49
7:ST:25:TRP:HZ3	7:ST:59:ALA:HB1	1.78	0.49
73:L5:1934:G:H21	73:L5:2115:G:H5''	1.78	0.49
73:L5:2240:G:C5	73:L5:2241:C:C4	3.01	0.49
9:SN:76:LEU:HD21	9:SN:84:LEU:HD12	1.95	0.49
18:SC:125:LEU:HD11	18:SC:154:PHE:HB2	1.95	0.49
31:S1:1420:A:H2'	31:S1:1421:G:O4'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:2213:U:C5	73:L5:2214:G:C6	3.01	0.49
73:L5:3308:G:H2'	73:L5:3309:G:O4'	2.13	0.49
79:SE:61:ALA:HB1	79:SE:66:GLU:HB3	1.95	0.49
8:SA:36:VAL:HG23	8:SA:232:HIS:HA	1.95	0.49
25:SZ:92:TYR:CG	31:S1:494:A:OP2	2.66	0.49
31:S1:1296:G:H4'	31:S1:1297:U:OP2	2.13	0.49
44:LP:90:VAL:O	71:L3:48:G:H5''	2.12	0.49
78:SY:2:ILE:HD12	78:SY:2:ILE:N	2.28	0.49
81:LF:43:ILE:CG1	81:LF:56:VAL:HG13	2.42	0.49
10:SJ:55:ASP:O	10:SJ:56:HIS:HB2	2.13	0.49
31:S1:719:C:C2'	31:S1:720:U:H5'	2.43	0.49
63:LV:39:LEU:O	63:LV:39:LEU:HD23	2.13	0.49
73:L5:168:C:H2'	73:L5:169:A:O4'	2.13	0.49
73:L5:1613:U:H1'	73:L5:1614:A:C8	2.47	0.49
73:L5:1776:U:H3	73:L5:1777:C:H41	1.60	0.49
73:L5:1797:G:H2'	73:L5:1798:U:C1'	2.43	0.49
73:L5:2429:U:O2	73:L5:2504:G:C6	2.65	0.49
73:L5:3307:C:C2	73:L5:3308:G:N7	2.81	0.49
76:S9:54:U:O2	76:S9:55:U:C5	2.65	0.49
22:Sb:89:VAL:HG22	22:Sb:92:ARG:NH1	2.28	0.49
45:LZ:32:ALA:HB1	45:LZ:37:PRO:C	2.38	0.49
48:LC:228:ILE:HD12	48:LC:245:ARG:HD3	1.94	0.49
56:Ll:50:ARG:CZ	56:Ll:57:ILE:HD11	2.43	0.49
73:L5:1805:G:N3	73:L5:1805:G:H2'	2.27	0.49
80:Sg:265:ASN:HB2	80:Sg:272:ILE:HG21	1.95	0.49
31:S1:491:C:H2'	31:S1:492:C:O4'	2.13	0.48
62:Lc:77:VAL:HG22	62:Lc:87:TYR:CD2	2.48	0.48
62:Lc:107:THR:HG22	73:L5:1163:U:O2'	2.13	0.48
73:L5:118:U:O2	73:L5:118:U:O4'	2.31	0.48
73:L5:2300:G:O2'	73:L5:2302:A:H3'	2.13	0.48
48:LC:248:ALA:HB3	73:L5:2857:U:H1'	1.95	0.48
67:Lh:20:GLN:HB3	67:Lh:32:VAL:HG22	1.95	0.48
73:L5:925:G:H5'	73:L5:926:A:OP1	2.13	0.48
73:L5:2214:G:C2	73:L5:2216:A:C8	3.01	0.48
75:S8:49:G:H2'	75:S8:50:U:C6	2.47	0.48
76:S9:68:C:H2'	76:S9:69:G:C1'	2.43	0.48
31:S1:303:G:H1	31:S1:311:C:H5	1.62	0.48
31:S1:715:A:OP1	79:SE:112:LYS:CB	2.62	0.48
31:S1:1269:A:H2'	31:S1:1270:A:H8	1.77	0.48
44:LP:94:ASN:O	71:L3:47:C:P	2.72	0.48
44:LP:182:GLY:HA2	71:L3:36:C:C2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:LG:49:VAL:HG11	69:LG:194:TYR:HE2	1.78	0.48
73:L5:723:A:N7	73:L5:724:G:H1'	2.27	0.48
73:L5:1030:G:H3'	73:L5:1031:A:C8	2.49	0.48
78:SY:38:LEU:HD12	78:SY:48:GLN:O	2.12	0.48
12:SK:13:LEU:CD1	12:SK:14:THR:HG23	2.43	0.48
31:S1:30:G:C6	31:S1:566:G:C6	3.01	0.48
31:S1:715:A:N7	79:SE:114:ARG:HA	2.28	0.48
61:Lg:15:LEU:HD12	69:LG:58:LYS:HB3	1.95	0.48
12:SK:3:ILE:HG22	12:SK:4:SER:N	2.29	0.48
20:SB:21:MET:HE2	20:SB:54:LEU:HD22	1.96	0.48
28:SD:38:ASN:HB2	31:S1:562:U:OP2	2.14	0.48
31:S1:717:U:H2'	31:S1:718:A:O4'	2.13	0.48
58:LE:122:GLY:C	58:LE:123:MET:HG2	2.38	0.48
71:L3:25:A:O3'	71:L3:27:A:OP1	2.31	0.48
73:L5:1114:C:H2'	73:L5:1115:U:C6	2.48	0.48
73:L5:2262:U:H2'	73:L5:2263:A:C8	2.49	0.48
73:L5:2995:C:H2'	73:L5:2996:U:C4'	2.44	0.48
73:L5:3267:G:H3'	73:L5:3268:C:O3'	2.14	0.48
78:SY:53:ALA:O	78:SY:54:LEU:HD12	2.13	0.48
80:Sg:171:VAL:HG22	80:Sg:181:VAL:HG22	1.95	0.48
27:SQ:27:ALA:HB1	27:SQ:114:VAL:HG13	1.95	0.48
28:SD:36:LEU:HD21	28:SD:108:ARG:CZ	2.44	0.48
31:S1:473:U:O2	31:S1:473:U:H2'	2.13	0.48
31:S1:487:G:H3'	31:S1:488:U:H5''	1.95	0.48
31:S1:797:G:H2'	31:S1:798:U:O4'	2.13	0.48
61:Lg:40:LEU:HD22	61:Lg:108:VAL:HG21	1.96	0.48
73:L5:2196:U:O2	73:L5:2232:G:N2	2.44	0.48
73:L5:2997:A:N1	73:L5:3008:A:C8	2.82	0.48
75:S8:51:C:O2	75:S8:52:G:C8	2.66	0.48
79:SE:242:ILE:HD13	79:SE:242:ILE:O	2.13	0.48
5:SR:24:GLY:HA2	5:SR:58:ALA:HB3	1.96	0.48
13:SG:4:ASN:HB2	13:SG:108:ILE:HD11	1.95	0.48
31:S1:698:A:C2	31:S1:699:G:H1'	2.49	0.48
73:L5:721:A:N7	73:L5:2765:C:H1'	2.29	0.48
75:S8:3:C:O2	75:S8:3:C:H2'	2.13	0.48
31:S1:38:U:O2'	31:S1:39:A:P	2.72	0.48
58:LE:125:PHE:CG	73:L5:2651:A:C8	3.02	0.48
73:L5:624:G:H2'	73:L5:625:U:C6	2.48	0.48
73:L5:649:C:O2	73:L5:649:C:H2'	2.13	0.48
73:L5:849:C:O2	73:L5:849:C:H2'	2.14	0.48
73:L5:1460:C:O4'	73:L5:1460:C:O2	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:1721:A:N6	73:L5:1762:G:N1	2.62	0.48
73:L5:2814:A:N1	73:L5:2828:A:N6	2.62	0.48
5:SR:79:VAL:O	5:SR:79:VAL:HG12	2.14	0.48
15:Se:19:THR:CB	15:Se:20:PRO:HD3	2.44	0.48
20:SB:106:TRP:CD1	20:SB:139:GLU:HB2	2.48	0.48
20:SB:128:THR:HG22	20:SB:129:ASP:H	1.78	0.48
31:S1:1350:A:H2'	31:S1:1351:G:O4'	2.14	0.48
39:LI:47:TYR:CE2	39:LI:51:LEU:HD11	2.49	0.48
73:L5:238:A:H2'	73:L5:239:A:C8	2.49	0.48
73:L5:719:U:H2'	73:L5:720:G:C8	2.48	0.48
73:L5:1088:G:H5''	73:L5:1089:A:OP2	2.14	0.48
80:Sg:92:LEU:N	80:Sg:92:LEU:HD12	2.28	0.48
82:Lk:15:LEU:HD21	82:Lk:57:PRO:HD2	1.95	0.48
5:SR:54:VAL:O	5:SR:54:VAL:HG12	2.13	0.48
10:SJ:61:ILE:HG22	10:SJ:63:ILE:HG13	1.96	0.48
18:SC:160:ILE:HD12	18:SC:191:MET:HE3	1.95	0.48
31:S1:121:G:H22	31:S1:269:C:H5	1.62	0.48
31:S1:715:A:OP2	79:SE:114:ARG:HD2	2.13	0.48
31:S1:1116:U:O2	31:S1:1117:C:C2	2.67	0.48
58:LE:38:LEU:HA	58:LE:112:LEU:HD21	1.95	0.48
73:L5:1019:G:N3	73:L5:1078:A:C6	2.82	0.48
73:L5:1739:C:H1'	73:L5:1752:U:H4'	1.96	0.48
73:L5:1881:G:H2'	73:L5:1881:G:N3	2.28	0.48
73:L5:2261:U:H2'	73:L5:2262:U:C6	2.48	0.48
73:L5:2308:G:C2	73:L5:2309:G:N7	2.82	0.48
24:SO:59:LEU:HD13	24:SO:96:ILE:CD1	2.44	0.47
31:S1:683:A:C8	31:S1:684:A:C8	3.02	0.47
31:S1:701:A:N6	31:S1:713:U:N3	2.61	0.47
31:S1:1170:G:O6	31:S1:1175:U:O4	2.31	0.47
31:S1:1269:A:O2'	31:S1:1270:A:O5'	2.30	0.47
73:L5:803:U:C5	73:L5:804:G:N7	2.82	0.47
80:Sg:246:PHE:CE2	80:Sg:253:LEU:HD13	2.49	0.47
10:SJ:6:VAL:HG12	10:SJ:34:ILE:HD11	1.95	0.47
13:SG:92:MET:HE3	31:S1:367:C:H4'	1.97	0.47
21:SF:35:VAL:HG12	21:SF:36:ALA:N	2.28	0.47
31:S1:494:A:N3	31:S1:495:A:N7	2.61	0.47
33:LS:41:ASN:CG	43:LD:349:ILE:HD12	2.38	0.47
73:L5:1127:G:C2'	73:L5:1128:U:H4'	2.44	0.47
73:L5:2212:G:O2'	73:L5:2213:U:H5'	2.13	0.47
73:L5:2859:U:H2'	73:L5:2860:U:C6	2.50	0.47
73:L5:3308:G:H2'	73:L5:3309:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:S7:62:C:H2'	74:S7:63:U:C6	2.49	0.47
5:SR:28:VAL:HG23	5:SR:56:LYS:O	2.14	0.47
6:SH:56:ILE:HD11	6:SH:139:ILE:HD11	1.96	0.47
44:LP:93:THR:HB	71:L3:47:C:C2	2.49	0.47
59:LO:153:ARG:CA	59:LO:165:ILE:HD11	2.44	0.47
72:L4:123:C:H1'	72:L4:124:U:OP2	2.15	0.47
73:L5:1063:C:C4	73:L5:1064:U:O4	2.68	0.47
73:L5:2270:C:O2	73:L5:2270:C:O5'	2.32	0.47
80:Sg:76:MET:HE2	80:Sg:97:LEU:HD11	1.96	0.47
14:SM:84:PHE:HA	16:SS:51:HIS:O	2.14	0.47
31:S1:1577:G:C2	31:S1:1578:C:C6	3.02	0.47
71:L3:27:A:C6	71:L3:28:C:C5	3.02	0.47
73:L5:1031:A:H2	73:L5:1070:C:N3	2.13	0.47
73:L5:1807:G:C2	73:L5:1808:A:N7	2.83	0.47
79:SE:98:LEU:HD12	79:SE:105:PHE:HE2	1.79	0.47
31:S1:15:U:H2'	31:S1:16:G:O4'	2.14	0.47
31:S1:517:G:N1	31:S1:560:A:C6	2.83	0.47
31:S1:1497:C:C2	31:S1:1498:A:C8	3.02	0.47
73:L5:1087:A:O5'	73:L5:1088:G:O5'	2.33	0.47
73:L5:1732:G:O3'	73:L5:1733:G:O4'	2.33	0.47
73:L5:2239:G:N1	73:L5:2240:G:C6	2.83	0.47
73:L5:2432:G:H2'	73:L5:2433:A:C8	2.49	0.47
75:S8:32:C:H2'	75:S8:33:U:O2	2.14	0.47
76:S9:74:C:O2'	76:S9:75:C:P	2.72	0.47
80:Sg:57:VAL:HG22	80:Sg:57:VAL:O	2.14	0.47
12:SK:139:SER:HA	12:SK:147:LEU:HD11	1.95	0.47
31:S1:32:U:O2'	31:S1:563:A:N1	2.44	0.47
38:LB:116:LEU:HD21	38:LB:158:ILE:HD13	1.95	0.47
47:LH:116:LEU:HD22	47:LH:152:LEU:HD21	1.96	0.47
57:LR:100:ARG:HE	73:L5:1884:U:H5''	1.80	0.47
73:L5:1173:G:O4'	73:L5:1195:A:H2	1.98	0.47
73:L5:1738:A:H2	73:L5:1751:A:HO2'	1.63	0.47
73:L5:2220:C:H2'	73:L5:2221:A:C8	2.50	0.47
80:Sg:203:VAL:HG12	80:Sg:214:SER:CB	2.45	0.47
81:LF:110:VAL:HG22	81:LF:126:LYS:HD2	1.96	0.47
27:SQ:36:GLY:O	27:SQ:40:VAL:HG23	2.15	0.47
30:Sc:65:THR:HG23	30:Sc:68:LYS:O	2.15	0.47
31:S1:1216:G:C2	31:S1:1217:G:N7	2.83	0.47
31:S1:1368:G:H4'	31:S1:1369:A:H5'	1.96	0.47
38:LB:182:ALA:HB2	73:L5:2142:A:O2'	2.15	0.47
44:LP:93:THR:N	71:L3:47:C:O5'	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:LC:306:MET:HE2	48:LC:368:PHE:O	2.14	0.47
50:LK:63:THR:HG22	50:LK:74:LYS:O	2.15	0.47
71:L3:39:C:O2	71:L3:39:C:H2'	2.15	0.47
73:L5:1004:C:H2'	73:L5:1123:G:OP2	2.15	0.47
73:L5:1062:C:H2'	73:L5:1063:C:N1	2.30	0.47
73:L5:1097:G:N2	73:L5:1115:U:H3	2.12	0.47
73:L5:1733:G:H4'	73:L5:1734:A:OP1	2.15	0.47
73:L5:2170:G:H4'	73:L5:2173:G:H1'	1.97	0.47
73:L5:2278:C:H2'	73:L5:2279:U:C5	2.49	0.47
73:L5:2648:A:H3'	73:L5:2649:G:C8	2.49	0.47
73:L5:2663:C:H2'	73:L5:2664:G:O4'	2.14	0.47
73:L5:3023:U:O2'	73:L5:3024:A:H5'	2.15	0.47
73:L5:3257:U:C4	73:L5:3258:A:N7	2.83	0.47
80:Sg:203:VAL:HG12	80:Sg:214:SER:HB3	1.96	0.47
2:SX:28:LEU:HD12	2:SX:31:CYS:SG	2.54	0.47
8:SA:184:VAL:HG12	8:SA:188:ILE:CD1	2.44	0.47
28:SD:36:LEU:HD21	28:SD:108:ARG:NH2	2.30	0.47
31:S1:517:G:C2	31:S1:560:A:C2	3.02	0.47
31:S1:838:A:C2	73:L5:2201:A:N6	2.83	0.47
31:S1:1149:G:H2'	31:S1:1150:U:C6	2.50	0.47
59:LO:97:LEU:HD11	59:LO:126:VAL:CG1	2.45	0.47
73:L5:1938:C:N3	73:L5:1939:C:C5	2.82	0.47
73:L5:2242:G:C8	73:L5:2265:G:C5	3.02	0.47
73:L5:3255:G:C5	73:L5:3256:G:N7	2.82	0.47
74:S7:56:U:H1'	74:S7:58:G:H2'	1.97	0.47
74:S7:66:C:H2'	74:S7:67:A:H8	1.80	0.47
75:S8:3:C:O2'	75:S8:4:G:H5'	2.14	0.47
8:SA:32:LEU:HD22	8:SA:66:PHE:CZ	2.49	0.47
18:SC:68:ILE:HD11	18:SC:88:LEU:HB3	1.96	0.47
21:SF:35:VAL:HG12	21:SF:36:ALA:H	1.80	0.47
31:S1:679:A:C2'	31:S1:680:G:O5'	2.63	0.47
31:S1:715:A:C8	79:SE:23:HIS:HA	2.50	0.47
31:S1:981:A:C2	31:S1:989:G:C6	3.02	0.47
31:S1:1184:C:N3	31:S1:1185:U:C5	2.83	0.47
38:LB:114:SER:O	38:LB:127:ALA:O	2.33	0.47
38:LB:196:TRP:CG	38:LB:197:PRO:CD	2.98	0.47
73:L5:1218:A:C2'	73:L5:1219:G:O5'	2.63	0.47
73:L5:2228:C:H2'	73:L5:2229:G:H5'	1.97	0.47
73:L5:3218:A:H3'	73:L5:3219:G:H21	1.80	0.47
74:S7:35:C:H3'	74:S7:36:A:C8	2.50	0.47
14:SM:84:PHE:HB3	16:SS:50:PHE:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:SQ:20:LEU:N	27:SQ:22:LYS:HZ1	2.13	0.47
31:S1:1690:A:C2'	31:S1:1691:A:O5'	2.63	0.47
43:LD:101:TYR:CG	43:LD:102:ALA:N	2.83	0.47
44:LP:198:HIS:CG	71:L3:35:C:H1'	2.50	0.47
71:L3:23:A:H2'	71:L3:24:A:O4'	2.15	0.47
73:L5:194:U:H2'	73:L5:195:G:O4'	2.15	0.47
74:S7:33:C:HO2'	74:S7:34:U:P	2.37	0.47
6:SH:18:LEU:HD12	6:SH:18:LEU:H	1.79	0.46
21:SF:111:ILE:HD13	21:SF:121:LEU:HB2	1.96	0.46
31:S1:418:A:C4	31:S1:419:A:H8	2.33	0.46
31:S1:1096:A:H2'	31:S1:1097:G:C8	2.50	0.46
31:S1:1212:A:H4'	31:S1:1213:G:OP1	2.15	0.46
44:LP:95:TYR:CE2	44:LP:161:GLY:HA2	2.50	0.46
48:LC:374:LYS:HB2	73:L5:3257:U:OP1	2.14	0.46
73:L5:118:U:H3	73:L5:123:A:H62	1.62	0.46
73:L5:256:G:C2'	73:L5:257:U:O5'	2.63	0.46
73:L5:262:C:H2'	73:L5:263:U:C6	2.50	0.46
20:SB:151:CYS:SG	20:SB:164:ILE:C	2.99	0.46
31:S1:147:G:H2'	31:S1:148:C:C6	2.50	0.46
31:S1:311:C:O2	31:S1:311:C:O4'	2.31	0.46
31:S1:382:C:N4	31:S1:383:A:H62	2.13	0.46
57:LR:40:GLU:HG3	57:LR:61:LEU:HD22	1.97	0.46
63:LV:27:ALA:HB3	63:LV:28:PRO:HD3	1.96	0.46
73:L5:1103:U:H2'	73:L5:1104:U:O4'	2.16	0.46
73:L5:1744:C:O2'	73:L5:1745:G:OP2	2.32	0.46
31:S1:505:A:H3'	31:S1:506:G:H5''	1.98	0.46
31:S1:721:U:H5''	31:S1:722:C:OP2	2.14	0.46
31:S1:923:A:H2'	31:S1:924:U:H5'	1.96	0.46
31:S1:1132:C:H42	31:S1:1389:C:H5	1.63	0.46
73:L5:291:A:H2'	73:L5:292:G:H8	1.80	0.46
73:L5:406:U:H4'	73:L5:1439:G:H4'	1.98	0.46
73:L5:755:C:H2'	73:L5:756:C:C6	2.51	0.46
73:L5:1387:A:H2'	73:L5:1388:U:O4'	2.14	0.46
73:L5:2853:C:H2'	73:L5:2854:G:O4'	2.16	0.46
75:S8:59:A:H3'	75:S8:60:U:C6	2.50	0.46
76:S9:56:C:O2	76:S9:56:C:O4'	2.32	0.46
11:SI:72:MET:HE1	11:SI:76:ARG:NH1	2.30	0.46
20:SB:63:LEU:HD11	78:SY:78:LEU:CD1	2.45	0.46
31:S1:495:A:H3'	31:S1:496:A:H8	1.80	0.46
31:S1:524:A:N3	31:S1:524:A:C2'	2.79	0.46
31:S1:1538:U:H2'	31:S1:1539:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:LI:185:LEU:HD23	39:LI:188:LEU:HD12	1.97	0.46
46:LU:92:LEU:O	46:LU:96:VAL:HG23	2.16	0.46
58:LE:123:MET:HA	73:L5:2651:A:C4	2.51	0.46
66:Lb:46:CYS:SG	73:L5:1100:U:O2	2.73	0.46
73:L5:424:A:H2'	73:L5:425:G:O4'	2.16	0.46
73:L5:667:C:H2'	73:L5:668:A:H8	1.80	0.46
73:L5:801:G:H2'	73:L5:802:U:H6	1.79	0.46
73:L5:961:A:H4'	73:L5:977:G:N2	2.30	0.46
73:L5:2241:C:C2'	73:L5:2266:G:H5'	2.46	0.46
73:L5:2248:A:H62	73:L5:2253:U:H3	1.62	0.46
73:L5:2751:C:C2	73:L5:2764:G:N2	2.83	0.46
73:L5:3254:G:C4	73:L5:3255:G:C8	3.03	0.46
76:S9:43:C:C2'	76:S9:44:G:OP1	2.63	0.46
1:SP:131:SER:HB3	31:S1:30:G:H4'	1.97	0.46
9:SN:68:ASN:O	9:SN:69:TRP:C	2.58	0.46
31:S1:530:G:O6	31:S1:554:A:N7	2.49	0.46
31:S1:924:U:O3'	31:S1:925:C:O4'	2.34	0.46
32:LM:33:GLY:HA2	73:L5:806:U:O3'	2.15	0.46
66:Lb:46:CYS:HA	73:L5:1100:U:O2'	2.15	0.46
67:Lh:50:ARG:NH2	67:Lh:56:ALA:HB2	2.31	0.46
73:L5:1935:G:H2'	73:L5:1936:A:O5'	2.16	0.46
73:L5:2311:U:H2'	73:L5:2312:U:O4'	2.16	0.46
73:L5:3130:A:H62	73:L5:3223:U:H3	1.62	0.46
80:Sg:102:THR:HG23	80:Sg:102:THR:O	2.14	0.46
2:SX:52:PRO:HB2	2:SX:56:ILE:HD11	1.97	0.46
20:SB:164:ILE:O	20:SB:165:PRO:C	2.59	0.46
31:S1:36:C:O2	31:S1:36:C:O5'	2.34	0.46
31:S1:683:A:H8	31:S1:684:A:C8	2.34	0.46
31:S1:789:U:O2	31:S1:789:U:O4'	2.33	0.46
40:LJ:91:ILE:HD11	40:LJ:137:ILE:HG23	1.97	0.46
60:LN:185:ARG:HB3	60:LN:186:PRO:CD	2.46	0.46
73:L5:1241:C:C2	73:L5:1242:A:C8	3.03	0.46
73:L5:1881:G:N2	73:L5:3042:G:H5''	2.30	0.46
5:SR:6:THR:HG22	5:SR:7:THR:N	2.31	0.46
8:SA:36:VAL:HG22	8:SA:41:ARG:NH1	2.31	0.46
31:S1:34:G:O2'	31:S1:35:U:P	2.73	0.46
31:S1:1226:U:C2	31:S1:1227:U:C6	3.03	0.46
44:LP:93:THR:OG1	71:L3:48:G:N3	2.49	0.46
64:Ld:90:VAL:HG13	73:L5:1748:G:O2'	2.15	0.46
73:L5:263:U:C2	73:L5:264:G:N7	2.84	0.46
73:L5:1074:C:H2'	73:L5:1075:U:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:1750:G:H4'	73:L5:1751:A:H5'	1.97	0.46
73:L5:2300:G:N1	73:L5:2303:U:C2	2.84	0.46
73:L5:2735:A:C2'	73:L5:2736:U:O5'	2.64	0.46
73:L5:3256:G:C6	73:L5:3257:U:N3	2.84	0.46
75:S8:67:C:H2'	75:S8:68:C:C5	2.50	0.46
76:S9:27:G:H2'	76:S9:28:G:H8	1.80	0.46
31:S1:30:G:H2'	31:S1:31:C:C6	2.51	0.46
31:S1:1094:G:N1	31:S1:1507:G:OP2	2.49	0.46
40:LJ:91:ILE:HG23	40:LJ:121:LEU:HD21	1.97	0.46
61:Lg:15:LEU:HD11	69:LG:59:GLY:N	2.30	0.46
73:L5:1557:A:H2'	73:L5:1558:A:C8	2.51	0.46
73:L5:1733:G:C2	73:L5:1751:A:N6	2.80	0.46
73:L5:1761:U:C4	73:L5:1762:G:C5	3.04	0.46
73:L5:2222:A:H2'	73:L5:2223:C:C6	2.50	0.46
73:L5:2573:U:C2	73:L5:2574:A:C8	3.04	0.46
73:L5:2633:A:C5	73:L5:2635:G:C8	3.04	0.46
2:SX:40:PHE:CD2	2:SX:44:MET:HE3	2.51	0.46
13:SG:73:VAL:HG12	13:SG:74:ARG:N	2.30	0.46
20:SB:22:LEU:HD23	20:SB:27:HIS:HD2	1.81	0.46
31:S1:526:G:O2'	31:S1:528:C:O4'	2.34	0.46
32:LM:72:THR:HB	32:LM:111:LEU:HD22	1.98	0.46
38:LB:244:GLY:O	73:L5:2147:U:H4'	2.16	0.46
44:LP:183:TYR:N	71:L3:36:C:OP2	2.49	0.46
61:Lg:53:MET:HE1	61:Lg:80:ARG:O	2.16	0.46
71:L3:3:U:H2'	71:L3:4:G:H8	1.81	0.46
73:L5:1965:U:H2'	73:L5:1966:G:O4'	2.16	0.46
73:L5:3257:U:O2'	73:L5:3258:A:H5'	2.15	0.46
73:L5:3293:G:C5'	73:L5:3294:C:OP2	2.64	0.46
75:S8:34:C:O2'	75:S8:35:A:OP1	2.31	0.46
18:SC:164:HIS:N	18:SC:165:PRO:CD	2.79	0.46
31:S1:194:U:O2	31:S1:194:U:O4'	2.34	0.46
31:S1:1116:U:C2	75:S8:35:A:P	3.09	0.46
31:S1:1221:A:N1	31:S1:1227:U:C2	2.84	0.46
33:LS:72:LEU:HD22	54:LT:141:VAL:HG21	1.98	0.46
49:LL:8:VAL:HG13	49:LL:28:ILE:HD13	1.97	0.46
73:L5:632:U:H4'	73:L5:633:A:O5'	2.16	0.46
73:L5:668:A:H2'	73:L5:669:A:C8	2.50	0.46
18:SC:204:THR:HG22	18:SC:205:ILE:H	1.82	0.45
20:SB:185:VAL:HG12	20:SB:189:ARG:HD2	1.97	0.45
26:Sa:40:PHE:N	26:Sa:74:LEU:HD11	2.31	0.45
28:SD:142:ASP:O	28:SD:142:ASP:CG	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:S1:124:A:O2'	31:S1:125:U:P	2.75	0.45
31:S1:1248:C:H2'	31:S1:1249:G:O4'	2.15	0.45
31:S1:1406:U:O2	31:S1:1406:U:H2'	2.17	0.45
71:L3:31:G:OP2	71:L3:31:G:C8	2.69	0.45
73:L5:750:C:O2'	73:L5:751:G:H5'	2.16	0.45
73:L5:1002:A:C8	73:L5:1003:A:C4	3.05	0.45
73:L5:2221:A:H2'	73:L5:2222:A:C8	2.51	0.45
73:L5:2714:C:C2	73:L5:2715:A:C8	3.04	0.45
73:L5:3256:G:C6	73:L5:3257:U:C2	3.04	0.45
19:SW:55:LYS:N	19:SW:56:PRO:CD	2.79	0.45
21:SF:13:VAL:HG21	21:SF:58:ILE:HG12	1.98	0.45
31:S1:921:C:H2'	31:S1:922:G:H5'	1.99	0.45
31:S1:1504:G:H2'	31:S1:1504:G:N3	2.31	0.45
32:LM:21:ARG:NH2	73:L5:652:U:OP1	2.50	0.45
32:LM:111:LEU:HD23	32:LM:111:LEU:H	1.81	0.45
40:LJ:117:TYR:HA	40:LJ:160:MET:HE3	1.98	0.45
44:LP:156:GLY:O	71:L3:45:U:H5'	2.16	0.45
44:LP:183:TYR:CD1	71:L3:36:C:OP2	2.69	0.45
47:LH:116:LEU:HD21	47:LH:220:ILE:CD1	2.45	0.45
60:LN:36:VAL:HG22	60:LN:64:VAL:HG13	1.98	0.45
64:Ld:73:PHE:CZ	64:Ld:83:VAL:HG21	2.46	0.45
73:L5:512:G:H22	73:L5:563:G:N2	2.14	0.45
73:L5:801:G:H2'	73:L5:802:U:C6	2.51	0.45
73:L5:1734:A:O4'	73:L5:1751:A:N1	2.49	0.45
73:L5:2877:A:C2	73:L5:2878:G:C8	3.04	0.45
75:S8:3:C:O2'	75:S8:4:G:OP1	2.30	0.45
31:S1:517:G:N2	31:S1:560:A:C4	2.84	0.45
31:S1:1505:A:H4'	31:S1:1506:G:OP2	2.16	0.45
37:LQ:171:THR:HG22	37:LQ:173:LEU:CD1	2.46	0.45
73:L5:1731:U:H2'	73:L5:1732:G:O5'	2.16	0.45
73:L5:1798:U:H2'	73:L5:1799:G:H5'	1.97	0.45
73:L5:1933:U:O2	73:L5:1933:U:H2'	2.15	0.45
73:L5:2560:U:O2	73:L5:2560:U:O4'	2.32	0.45
73:L5:2903:A:H2'	73:L5:2904:C:C6	2.50	0.45
76:S9:68:C:H2'	76:S9:69:G:O4'	2.17	0.45
6:SH:116:ILE:HD11	6:SH:127:VAL:HG11	1.98	0.45
6:SH:129:VAL:HG13	6:SH:133:ARG:HG2	1.99	0.45
20:SB:63:LEU:HD13	78:SY:72:PHE:CD2	2.51	0.45
31:S1:495:A:H3'	31:S1:496:A:C8	2.52	0.45
31:S1:1171:C:O2	31:S1:1171:C:O4'	2.32	0.45
47:LH:93:ILE:HB	47:LH:253:GLY:HA3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:L3:113:G:H2'	71:L3:114:C:C6	2.51	0.45
73:L5:1023:A:H2'	73:L5:1024:G:H8	1.81	0.45
73:L5:1097:G:H22	73:L5:1115:U:H3	1.64	0.45
73:L5:1106:A:O3'	73:L5:1107:G:H2'	2.17	0.45
73:L5:1885:A:H2'	73:L5:1886:G:C5	2.51	0.45
73:L5:2221:A:C6	73:L5:2222:A:N6	2.85	0.45
73:L5:2431:A:H2'	73:L5:2432:G:O4'	2.16	0.45
73:L5:3194:C:O2'	73:L5:3195:C:C6	2.70	0.45
73:L5:3216:A:C5	73:L5:3217:G:N2	2.84	0.45
31:S1:1662:C:C2	31:S1:1663:U:C5	3.05	0.45
39:LI:53:TYR:CE1	39:LI:144:VAL:HG11	2.51	0.45
43:LD:312:LEU:HD11	62:Lc:63:ALA:HB1	1.98	0.45
44:LP:146:LEU:HD22	44:LP:163:LEU:CD1	2.47	0.45
44:LP:181:PRO:O	71:L3:35:C:O5'	2.33	0.45
48:LC:253:TRP:C	48:LC:253:TRP:CD1	2.95	0.45
59:LO:31:ILE:HG23	59:LO:31:ILE:O	2.16	0.45
71:L3:36:C:C2'	71:L3:37:A:O5'	2.65	0.45
71:L3:78:C:HO2'	73:L5:1022:A:C2'	2.25	0.45
73:L5:968:C:H41	73:L5:2778:A:H5''	1.81	0.45
73:L5:1963:U:H2'	73:L5:1964:C:C4'	2.47	0.45
73:L5:2094:G:H2'	73:L5:2095:C:C6	2.52	0.45
73:L5:2399:C:H2'	73:L5:2400:C:C6	2.51	0.45
75:S8:19:G:H4'	75:S8:20:U:OP2	2.16	0.45
75:S8:32:C:H2'	75:S8:33:U:C2	2.52	0.45
76:S9:5:G:H2'	76:S9:6:G:O4'	2.17	0.45
78:SY:1:MET:O	78:SY:9:VAL:HG12	2.16	0.45
80:Sg:5:VAL:HG11	80:Sg:252:TRP:CH2	2.51	0.45
4:SL:52:THR:O	4:SL:56:GLU:HG3	2.16	0.45
31:S1:531:G:H2'	31:S1:531:G:N3	2.30	0.45
31:S1:534:C:H4'	31:S1:535:C:C6	2.51	0.45
31:S1:1183:U:C6	31:S1:1184:C:C6	3.04	0.45
38:LB:112:VAL:HG11	38:LB:168:ILE:CG1	2.47	0.45
44:LP:93:THR:C	71:L3:46:C:O2'	2.59	0.45
60:LN:135:VAL:HG12	60:LN:142:ILE:HD13	1.99	0.45
68:LY:20:VAL:HG11	68:LY:37:PHE:HE2	1.81	0.45
73:L5:1095:A:H2'	73:L5:1096:U:O4'	2.15	0.45
73:L5:1242:A:H2'	73:L5:1242:A:N3	2.32	0.45
73:L5:2138:A:H1'	73:L5:2274:A:N6	2.32	0.45
73:L5:2291:U:O2'	73:L5:2292:A:H5'	2.16	0.45
73:L5:3289:A:O5'	73:L5:3289:A:N3	2.49	0.45
73:L5:3294:C:O2	73:L5:3294:C:H2'	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:SB:128:THR:O	20:SB:129:ASP:C	2.59	0.45
21:SF:29:THR:HG22	21:SF:30:ARG:N	2.31	0.45
31:S1:1116:U:C6	75:S8:35:A:H4'	2.51	0.45
43:LD:89:ALA:CB	73:L5:1461:U:H4'	2.47	0.45
57:LR:94:LYS:C	73:L5:2109:G:H21	2.23	0.45
71:L3:44:C:H4'	71:L3:45:U:OP2	2.17	0.45
73:L5:1037:G:C6	73:L5:1064:U:C4	3.04	0.45
73:L5:2213:U:H3'	73:L5:2214:G:C8	2.52	0.45
73:L5:2234:U:C2'	73:L5:2235:A:O5'	2.65	0.45
31:S1:823:A:C6	31:S1:839:G:N2	2.85	0.45
44:LP:92:LEU:HB2	71:L3:48:G:C6	2.51	0.45
63:LV:34:ILE:HD11	63:LV:39:LEU:HD12	1.99	0.45
73:L5:2227:G:H2'	73:L5:2228:C:O4'	2.15	0.45
73:L5:2963:U:C2	73:L5:2964:A:C8	3.04	0.45
4:SL:75:VAL:HG21	4:SL:87:ILE:HD11	1.99	0.45
5:SR:73:ILE:HG22	5:SR:101:THR:HG21	1.99	0.45
31:S1:692:G:H21	31:S1:695:U:H4'	1.82	0.45
38:LB:96:LEU:HD22	38:LB:108:PRO:CD	2.46	0.45
43:LD:166:ALA:HB3	43:LD:218:ILE:HD11	1.99	0.45
44:LP:90:VAL:O	71:L3:48:G:OP2	2.35	0.45
54:LT:13:ASP:HB2	73:L5:1019:G:H5'	1.98	0.45
72:L4:15:G:H2'	72:L4:16:G:O4'	2.17	0.45
73:L5:752:U:H4'	73:L5:753:G:OP2	2.17	0.45
73:L5:1727:U:H2'	73:L5:1728:C:O4'	2.16	0.45
73:L5:2362:G:H2'	73:L5:2363:G:C8	2.52	0.45
73:L5:2826:C:H2'	73:L5:2827:G:O4'	2.17	0.45
15:Se:19:THR:HG22	31:S1:532:U:H1'	1.97	0.45
15:Se:31:PRO:HB2	15:Se:35:ALA:HB3	1.99	0.45
20:SB:57:THR:HG23	20:SB:165:PRO:O	2.17	0.45
22:Sb:64:LEU:CD1	24:SO:135:ILE:HD12	2.47	0.45
31:S1:922:G:HO2'	31:S1:923:A:H8	1.64	0.45
31:S1:1532:A:N3	31:S1:1532:A:H2'	2.32	0.45
31:S1:1534:C:H2'	31:S1:1535:U:C6	2.51	0.45
31:S1:1690:A:O2'	31:S1:1691:A:H5'	2.17	0.45
58:LE:122:GLY:C	58:LE:123:MET:CG	2.89	0.45
73:L5:1031:A:C2	73:L5:1070:C:N3	2.85	0.45
73:L5:1062:C:C4	73:L5:1063:C:C4	3.05	0.45
73:L5:1663:U:O2'	73:L5:1664:G:H5'	2.17	0.45
73:L5:1826:A:H2'	73:L5:1827:G:H8	1.82	0.45
73:L5:2813:C:OP1	73:L5:2813:C:H4'	2.17	0.45
6:SH:114:THR:HG21	17:Sd:22:VAL:CG2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:SC:177:VAL:HG21	18:SC:186:ILE:HD11	1.99	0.44
31:S1:1085:A:H2'	31:S1:1086:C:C6	2.52	0.44
58:LE:37:GLN:CB	58:LE:112:LEU:HD22	2.43	0.44
61:Lg:111:TYR:HB3	61:Lg:112:PRO:CD	2.47	0.44
72:L4:69:U:H2'	72:L4:70:G:O4'	2.17	0.44
73:L5:2131:U:C6	73:L5:2135:U:C4	3.05	0.44
73:L5:2239:G:C6	73:L5:2240:G:C6	3.06	0.44
73:L5:3275:G:O6	73:L5:3285:U:C2	2.66	0.44
74:S7:29:G:N1	74:S7:38:A:C2	2.81	0.44
74:S7:57:C:H3'	74:S7:58:G:H8	1.81	0.44
24:SO:34:PHE:CE1	24:SO:98:ALA:HB1	2.53	0.44
31:S1:89:G:H2'	31:S1:90:A:O4'	2.18	0.44
31:S1:121:G:H1	31:S1:269:C:H41	1.65	0.44
31:S1:330:G:H2'	31:S1:331:U:O4'	2.18	0.44
31:S1:490:A:H2	31:S1:499:C:H42	1.64	0.44
38:LB:196:TRP:CD1	38:LB:197:PRO:HD3	2.53	0.44
71:L3:33:U:O2'	71:L3:34:C:H5	2.00	0.44
73:L5:803:U:O2	73:L5:803:U:O4'	2.35	0.44
73:L5:2104:G:N1	73:L5:2107:G:H2'	2.32	0.44
73:L5:2748:G:H3'	73:L5:2749:U:H5''	1.99	0.44
74:S7:33:C:O2	74:S7:33:C:O4'	2.35	0.44
13:SG:203:LEU:HD21	79:SE:154:ARG:CZ	2.48	0.44
16:SS:12:TYR:CD1	31:S1:1529:A:C8	3.05	0.44
31:S1:825:A:H5''	31:S1:826:G:H21	1.81	0.44
31:S1:1183:U:O2	31:S1:1183:U:O4'	2.35	0.44
31:S1:1569:C:O2'	31:S1:1570:G:H5'	2.17	0.44
38:LB:179:LEU:HD22	38:LB:184:THR:HG21	1.98	0.44
38:LB:224:THR:CG2	38:LB:243:THR:HG21	2.48	0.44
44:LP:64:ILE:HG13	44:LP:105:LEU:HD21	1.99	0.44
58:LE:38:LEU:HD21	58:LE:110:LEU:HD13	1.99	0.44
58:LE:121:TYR:O	58:LE:123:MET:CG	2.65	0.44
58:LE:150:HIS:HB2	71:L3:55:A:H4'	1.99	0.44
73:L5:122:A:C2	73:L5:149:U:C2	3.05	0.44
73:L5:1126:U:H2'	73:L5:1127:G:O4'	2.16	0.44
73:L5:1626:C:C2	73:L5:1627:C:C5	3.06	0.44
73:L5:3291:C:H2'	73:L5:3292:C:C6	2.52	0.44
79:SE:53:LEU:C	79:SE:53:LEU:HD23	2.42	0.44
81:LF:85:LYS:HG3	81:LF:185:LEU:HD13	1.98	0.44
1:SP:29:TYR:CD1	1:SP:29:TYR:C	2.95	0.44
2:SX:83:LEU:HD11	2:SX:146:LEU:HD21	1.99	0.44
31:S1:535:C:H2'	31:S1:536:A:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:S1:1183:U:C5	31:S1:1184:C:C5	3.06	0.44
38:LB:238:ILE:O	73:L5:2149:G:H5'	2.17	0.44
44:LP:93:THR:HB	71:L3:47:C:C5	2.52	0.44
58:LE:19:ILE:HG23	58:LE:122:GLY:HA3	1.99	0.44
62:Lc:167:ILE:HG23	62:Lc:187:HIS:NE2	2.32	0.44
71:L3:45:U:C2'	71:L3:46:C:OP1	2.65	0.44
71:L3:50:A:H4'	71:L3:51:G:OP1	2.16	0.44
73:L5:185:A:H2'	73:L5:186:A:H5'	1.99	0.44
73:L5:2277:C:O2'	73:L5:2278:C:OP1	2.30	0.44
73:L5:2279:U:O4'	73:L5:2281:G:H5'	2.18	0.44
73:L5:2300:G:H4'	73:L5:2301:C:OP2	2.18	0.44
74:S7:9:G:H2'	74:S7:11:C:H41	1.82	0.44
75:S8:33:U:H2'	75:S8:34:C:H3'	2.00	0.44
6:SH:7:LEU:HD13	6:SH:13:TYR:OH	2.17	0.44
31:S1:418:A:C8	31:S1:494:A:O5'	2.70	0.44
31:S1:418:A:O4'	31:S1:494:A:O5'	2.36	0.44
38:LB:54:ARG:HH22	38:LB:77:VAL:HG22	1.82	0.44
44:LP:51:PHE:HE1	44:LP:105:LEU:HD23	1.82	0.44
44:LP:287:ILE:HD12	71:L3:61:G:H5'	2.00	0.44
48:LC:89:VAL:HG22	48:LC:193:VAL:HG11	2.00	0.44
59:LO:48:TYR:CD1	59:LO:145:ILE:HD11	2.52	0.44
73:L5:83:C:H2'	73:L5:84:U:O4'	2.17	0.44
73:L5:718:A:H2'	73:L5:719:U:C6	2.53	0.44
73:L5:3115:U:H2'	73:L5:3116:G:O4'	2.17	0.44
74:S7:64:C:H2'	74:S7:65:A:H5'	1.99	0.44
76:S9:57:G:H2'	76:S9:58:A:H5'	1.99	0.44
76:S9:61:C:H3'	76:S9:62:C:H5''	2.00	0.44
20:SB:150:LEU:C	20:SB:151:CYS:SG	3.01	0.44
31:S1:24:U:O2	31:S1:24:U:O5'	2.35	0.44
31:S1:435:G:C6	31:S1:436:U:C4	3.06	0.44
31:S1:534:C:H2'	31:S1:546:G:C8	2.53	0.44
31:S1:1032:G:O2'	31:S1:1033:G:H5'	2.17	0.44
31:S1:1069:U:O4'	31:S1:1225:A:C2	2.71	0.44
31:S1:1455:U:O2	31:S1:1455:U:O4'	2.36	0.44
44:LP:92:LEU:HD12	71:L3:48:G:C6	2.52	0.44
44:LP:182:GLY:HA3	71:L3:35:C:O5'	2.17	0.44
73:L5:38:U:H2'	73:L5:39:A:O4'	2.18	0.44
73:L5:1021:A:H2'	73:L5:1022:A:O4'	2.17	0.44
73:L5:1341:C:H3'	73:L5:1342:A:H5''	1.99	0.44
73:L5:1734:A:N6	73:L5:1748:G:C4	2.85	0.44
73:L5:2106:A:C4'	73:L5:2107:G:OP2	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:2747:A:O2'	73:L5:2748:G:H5'	2.16	0.44
21:SF:84:PRO:HD3	78:SY:9:VAL:HG21	1.99	0.44
31:S1:697:A:H2'	31:S1:698:A:O5'	2.18	0.44
31:S1:701:A:C6	31:S1:702:G:H1'	2.53	0.44
31:S1:1244:U:H2'	31:S1:1245:U:O4'	2.18	0.44
31:S1:1336:C:O2	31:S1:1336:C:O5'	2.36	0.44
31:S1:1368:G:C4'	31:S1:1369:A:H5'	2.47	0.44
31:S1:1724:C:O2	31:S1:1724:C:O4'	2.36	0.44
39:LI:6:ILE:HD12	39:LI:30:GLN:HG2	1.99	0.44
44:LP:180:PHE:HB3	71:L3:35:C:O3'	2.18	0.44
60:LN:199:ARG:HE	73:L5:81:C:H5''	1.83	0.44
61:Lg:66:ILE:HG22	61:Lg:67:LYS:O	2.18	0.44
72:L4:24:G:H1'	73:L5:351:A:C4	2.53	0.44
73:L5:1023:A:H2'	73:L5:1024:G:O4'	2.18	0.44
73:L5:1725:G:C2	73:L5:1726:U:O2	2.71	0.44
73:L5:1958:U:H2'	73:L5:1959:U:C6	2.53	0.44
73:L5:2258:C:C4	73:L5:2259:U:C4	3.06	0.44
73:L5:2643:C:C2	73:L5:2679:A:N1	2.85	0.44
73:L5:2824:A:H2'	73:L5:2825:G:H5'	1.99	0.44
74:S7:17:U:O2'	74:S7:18:G:H5''	2.17	0.44
81:LF:93:LEU:HD12	81:LF:93:LEU:N	2.32	0.44
13:SG:27:PHE:CD2	13:SG:36:VAL:HG21	2.53	0.44
28:SD:36:LEU:HD11	28:SD:105:MET:CE	2.48	0.44
31:S1:426:C:O2	31:S1:426:C:H2'	2.17	0.44
31:S1:1081:C:H5	31:S1:1554:G:H1	1.65	0.44
44:LP:94:ASN:O	71:L3:47:C:OP1	2.35	0.44
44:LP:198:HIS:CD2	71:L3:35:C:C2	3.06	0.44
73:L5:1062:C:H2'	73:L5:1063:C:C6	2.52	0.44
73:L5:1115:U:O4	73:L5:1116:U:C5	2.71	0.44
73:L5:1349:U:HO2'	73:L5:1350:U:H6	1.66	0.44
73:L5:1683:C:O2	73:L5:1683:C:O4'	2.36	0.44
73:L5:1964:C:H3'	73:L5:1965:U:H6	1.81	0.44
73:L5:2233:G:C2	73:L5:2234:U:C5	3.06	0.44
73:L5:2997:A:N6	73:L5:3009:A:C6	2.86	0.44
73:L5:3001:C:H2'	73:L5:3002:G:C1'	2.48	0.44
4:SL:46:ARG:O	4:SL:47:PRO:O	2.36	0.44
31:S1:37:U:O2	31:S1:37:U:O4'	2.35	0.44
31:S1:490:A:O2'	31:S1:491:C:H5'	2.18	0.44
31:S1:524:A:O2'	31:S1:525:A:O4'	2.33	0.44
31:S1:701:A:C6	31:S1:713:U:C4	3.06	0.44
31:S1:704:C:O2	31:S1:710:U:N3	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:S1:1407:G:H2'	31:S1:1408:A:H8	1.83	0.44
50:LK:24:ILE:HD11	50:LK:37:TYR:HB2	2.00	0.44
60:LN:172:ARG:HD3	73:L5:30:G:H5''	2.00	0.44
69:LG:48:THR:HG22	69:LG:49:VAL:N	2.33	0.44
73:L5:638:U:H2'	73:L5:639:U:C6	2.53	0.44
73:L5:1081:U:C4	73:L5:2614:A:C8	3.06	0.44
73:L5:1792:G:H2'	73:L5:1793:U:C2	2.53	0.44
73:L5:1861:C:O2	73:L5:1861:C:O4'	2.36	0.44
73:L5:2240:G:H2'	73:L5:2241:C:C6	2.53	0.44
73:L5:2257:U:H2'	73:L5:2258:C:C6	2.52	0.44
73:L5:2261:U:C2	73:L5:2262:U:H5	2.36	0.44
73:L5:3111:U:C4	73:L5:3112:A:N7	2.86	0.44
73:L5:3292:C:H5''	73:L5:3293:G:OP2	2.18	0.44
80:Sg:80:GLY:O	80:Sg:97:LEU:HD12	2.18	0.44
80:Sg:237:ALA:HB1	80:Sg:257:THR:HG21	2.00	0.44
31:S1:34:G:HO2'	31:S1:35:U:C5'	2.31	0.43
31:S1:925:C:C2	31:S1:927:G:OP2	2.71	0.43
31:S1:1389:C:O2	31:S1:1389:C:O4'	2.36	0.43
31:S1:1528:C:O2	31:S1:1528:C:O5'	2.35	0.43
35:Lf:76:VAL:HG13	35:Lf:81:GLU:HB2	1.99	0.43
37:LQ:54:LEU:HD23	37:LQ:62:ARG:HG2	2.00	0.43
39:LI:185:LEU:HD22	39:LI:193:LYS:HG3	2.00	0.43
41:LX:81:ILE:HG22	41:LX:82:GLU:N	2.32	0.43
73:L5:1949:G:H2'	73:L5:1950:G:O4'	2.18	0.43
73:L5:2228:C:C5	73:L5:2230:C:N4	2.86	0.43
73:L5:2607:C:H4'	73:L5:2735:A:C5'	2.48	0.43
73:L5:3112:A:C5	73:L5:3113:C:C5	3.06	0.43
73:L5:3254:G:H2'	73:L5:3255:G:O4'	2.18	0.43
79:SE:246:LYS:HD2	79:SE:247:ASP:N	2.32	0.43
10:SJ:28:ARG:O	10:SJ:29:PRO:C	2.61	0.43
25:SZ:58:LEU:HD23	25:SZ:58:LEU:H	1.83	0.43
25:SZ:92:TYR:CZ	31:S1:494:A:OP1	2.70	0.43
28:SD:19:PHE:CE1	31:S1:525:A:N6	2.86	0.43
28:SD:24:LEU:HB2	31:S1:524:A:N7	2.32	0.43
30:Sc:17:HIS:HB2	31:S1:997:C:H5'	2.00	0.43
31:S1:1005:U:H2'	31:S1:1006:G:O4'	2.19	0.43
31:S1:1236:U:C2	31:S1:1238:A:OP2	2.72	0.43
31:S1:1492:U:O2	31:S1:1492:U:O4'	2.36	0.43
37:LQ:82:THR:HG21	73:L5:736:U:O2'	2.18	0.43
58:LE:18:ASN:HB3	58:LE:124:ASP:HB3	2.00	0.43
60:LN:64:VAL:HG22	60:LN:106:VAL:CG1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:Lc:223:ASN:OD1	62:Lc:224:PRO:HD2	2.18	0.43
73:L5:735:U:O2'	73:L5:986:C:H5''	2.18	0.43
73:L5:755:C:H2'	73:L5:756:C:O4'	2.18	0.43
73:L5:1103:U:C4	73:L5:1104:U:C5	3.07	0.43
73:L5:1548:G:C8	73:L5:1850:G:C4	3.06	0.43
73:L5:3292:C:H2'	73:L5:3293:G:C8	2.53	0.43
5:SR:82:PRO:HB2	5:SR:84:TRP:CE3	2.53	0.43
8:SA:134:MET:HG3	8:SA:218:LEU:HD12	2.00	0.43
25:SZ:92:TYR:CE1	31:S1:494:A:OP1	2.71	0.43
31:S1:495:A:H2'	31:S1:496:A:C1'	2.47	0.43
31:S1:1216:G:C2	31:S1:1217:G:C8	3.06	0.43
44:LP:91:GLY:O	71:L3:47:C:H5''	2.17	0.43
73:L5:1002:A:C8	73:L5:1003:A:N3	2.87	0.43
73:L5:1018:G:H3'	73:L5:1019:G:O4'	2.18	0.43
73:L5:2656:A:H3'	73:L5:2656:A:N3	2.33	0.43
73:L5:3227:C:C2	73:L5:3228:C:C6	3.06	0.43
79:SE:25:LEU:HD12	79:SE:114:ARG:HH21	1.83	0.43
10:SJ:106:THR:HG23	10:SJ:111:MET:HE2	2.00	0.43
20:SB:68:ILE:CD1	20:SB:126:ILE:HD11	2.48	0.43
27:SQ:69:VAL:HG21	29:Sf:32:VAL:CG1	2.48	0.43
28:SD:19:PHE:CZ	31:S1:525:A:N6	2.87	0.43
31:S1:19:A:H2'	31:S1:20:G:O4'	2.18	0.43
31:S1:173:G:N3	31:S1:173:G:C2'	2.80	0.43
31:S1:420:U:H2'	31:S1:421:C:O4'	2.19	0.43
31:S1:689:A:H2'	31:S1:689:A:N3	2.34	0.43
31:S1:849:A:H2'	31:S1:850:G:C8	2.53	0.43
31:S1:1569:C:HO2'	31:S1:1570:G:P	2.42	0.43
44:LP:127:GLY:C	44:LP:195:ALA:HB1	2.43	0.43
58:LE:102:PHE:C	73:L5:2651:A:H4'	2.43	0.43
64:Ld:89:ARG:O	73:L5:1748:G:H5'	2.18	0.43
73:L5:976:A:C4	73:L5:977:G:C8	3.07	0.43
73:L5:2191:A:C5	73:L5:2192:G:N7	2.86	0.43
73:L5:2270:C:O2	73:L5:2270:C:O4'	2.33	0.43
5:SR:84:TRP:CD1	5:SR:84:TRP:C	2.97	0.43
6:SH:127:VAL:HG12	17:Sd:43:ASN:HB2	2.00	0.43
14:SM:52:LEU:HD22	14:SM:97:SER:HB3	2.00	0.43
31:S1:122:G:H1	31:S1:268:C:H5	1.66	0.43
31:S1:802:G:H22	31:S1:876:A:H2	1.67	0.43
31:S1:1500:G:H1'	31:S1:1501:A:OP2	2.18	0.43
31:S1:1706:G:N2	31:S1:1712:C:C2	2.86	0.43
39:LI:88:PRO:O	39:LI:94:GLY:HA3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:LD:143:ILE:HG21	43:LD:243:LEU:HD13	2.01	0.43
44:LP:80:SER:CB	44:LP:92:LEU:HD21	2.48	0.43
54:LT:68:THR:HB	54:LT:69:PRO:HD2	2.00	0.43
73:L5:521:G:N1	73:L5:556:U:C2	2.87	0.43
73:L5:649:C:C6	73:L5:650:C:C5	3.06	0.43
73:L5:1038:G:H2'	73:L5:1039:U:O5'	2.19	0.43
73:L5:1739:C:H1'	73:L5:1752:U:H5''	2.01	0.43
73:L5:1748:G:OP1	73:L5:1749:C:H2'	2.18	0.43
73:L5:1748:G:O4'	73:L5:1750:G:N2	2.52	0.43
73:L5:1825:A:H2'	73:L5:1826:A:O4'	2.19	0.43
79:SE:73:GLN:HB2	79:SE:75:VAL:HG13	2.01	0.43
80:Sg:137:TRP:CD1	80:Sg:137:TRP:N	2.87	0.43
18:SC:101:MET:O	18:SC:105:GLU:HG2	2.19	0.43
31:S1:268:C:O2	31:S1:268:C:O4'	2.36	0.43
31:S1:446:A:H2'	31:S1:447:A:O4'	2.19	0.43
31:S1:833:U:O2	31:S1:833:U:H2'	2.18	0.43
31:S1:1484:U:O2	31:S1:1529:A:H2	2.01	0.43
32:LM:34:LYS:HD2	40:LJ:7:ILE:HG23	2.00	0.43
43:LD:182:VAL:HA	43:LD:197:PRO:HG2	2.00	0.43
44:LP:94:ASN:N	71:L3:47:C:O4'	2.51	0.43
44:LP:158:LYS:O	71:L3:46:C:O5'	2.36	0.43
73:L5:1071:A:N6	73:L5:1074:C:O2	2.51	0.43
73:L5:1493:U:H2'	73:L5:1494:U:H6	1.84	0.43
73:L5:1732:G:H2'	73:L5:1733:G:C4	2.53	0.43
73:L5:1961:G:H2'	73:L5:1962:C:O5'	2.18	0.43
73:L5:2228:C:H2'	73:L5:2229:G:C5'	2.47	0.43
73:L5:2281:G:C4	73:L5:2282:U:C5	3.07	0.43
73:L5:3124:C:H2'	73:L5:3125:U:O4'	2.19	0.43
73:L5:3235:A:H2'	73:L5:3236:G:O4'	2.18	0.43
73:L5:3256:G:O2'	73:L5:3257:U:H5'	2.19	0.43
73:L5:3292:C:H2'	73:L5:3293:G:C1'	2.49	0.43
74:S7:42:C:H2'	74:S7:43:C:O4'	2.19	0.43
79:SE:90:ILE:HG22	79:SE:107:LEU:HD22	2.00	0.43
2:SX:126:VAL:HG11	2:SX:144:ARG:NH1	2.34	0.43
20:SB:24:CYS:SG	20:SB:176:LEU:HD22	2.58	0.43
21:SF:37:ILE:HG21	21:SF:61:ALA:O	2.19	0.43
27:SQ:69:VAL:HG21	29:Sf:32:VAL:HG13	2.00	0.43
31:S1:81:G:HO2'	31:S1:82:A:H8	1.63	0.43
31:S1:1694:A:H4'	31:S1:1695:G:OP2	2.18	0.43
48:LC:17:LEU:HB3	48:LC:18:PRO:CD	2.49	0.43
59:LO:97:LEU:HD11	59:LO:126:VAL:HG11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:LN:135:VAL:CG1	60:LN:142:ILE:HD13	2.49	0.43
73:L5:670:G:H1	73:L5:1460:C:H5	1.67	0.43
73:L5:1127:G:C8	73:L5:1128:U:H1'	2.53	0.43
73:L5:1160:A:C2	73:L5:1161:A:C8	3.07	0.43
73:L5:1742:U:C2'	73:L5:1743:G:O5'	2.67	0.43
73:L5:2200:A:C4'	73:L5:2201:A:OP2	2.65	0.43
73:L5:2209:G:N1	73:L5:2222:A:C2	2.83	0.43
73:L5:2234:U:O2'	73:L5:2235:A:P	2.77	0.43
73:L5:2561:U:O2	73:L5:2561:U:O4'	2.37	0.43
73:L5:2815:A:H3'	73:L5:2816:G:H5''	2.01	0.43
75:S8:59:A:H3'	75:S8:60:U:C5	2.54	0.43
3:SU:65:ARG:NH2	31:S1:113:G:H21	2.17	0.43
16:SS:15:GLY:HA3	31:S1:1130:C:O2	2.18	0.43
31:S1:1183:U:C5	31:S1:1184:C:C6	3.07	0.43
31:S1:1220:G:C5	31:S1:1221:A:N7	2.86	0.43
31:S1:1326:G:C6	31:S1:1337:G:C6	3.07	0.43
40:LJ:191:ARG:CZ	73:L5:724:G:H4'	2.49	0.43
58:LE:28:LEU:HD11	58:LE:65:CYS:HB2	1.99	0.43
58:LE:125:PHE:HB2	73:L5:2651:A:O4'	2.19	0.43
73:L5:1668:U:H2'	73:L5:1669:U:C6	2.53	0.43
73:L5:1731:U:C2'	73:L5:1732:G:O5'	2.67	0.43
73:L5:2265:G:C4'	73:L5:2266:G:OP1	2.66	0.43
73:L5:2522:G:N2	73:L5:2559:U:O2	2.51	0.43
73:L5:2747:A:H62	73:L5:2750:C:N4	2.17	0.43
76:S9:28:G:H2'	76:S9:29:G:O4'	2.19	0.43
4:SL:68:LYS:O	4:SL:69:VAL:HG23	2.19	0.43
14:SM:54:VAL:HG22	14:SM:95:LEU:HD21	1.99	0.43
31:S1:426:C:O2	31:S1:426:C:C2'	2.67	0.43
31:S1:1117:C:O2	31:S1:1117:C:O5'	2.37	0.43
31:S1:1498:A:C5	31:S1:1499:U:C5	3.07	0.43
31:S1:1546:A:H2'	31:S1:1547:C:H5'	2.00	0.43
44:LP:155:THR:HB	71:L3:36:C:O2'	2.18	0.43
59:LO:74:LYS:HB3	73:L5:2816:G:OP1	2.19	0.43
64:Ld:81:GLY:HA3	64:Ld:88:PHE:O	2.18	0.43
73:L5:720:G:N1	73:L5:722:A:OP2	2.51	0.43
73:L5:1098:C:H3'	73:L5:1099:U:C6	2.54	0.43
73:L5:2232:G:H2'	73:L5:2232:G:N3	2.34	0.43
73:L5:2276:G:C2	73:L5:2301:C:OP2	2.72	0.43
73:L5:2748:G:H3'	73:L5:2749:U:C5'	2.48	0.43
73:L5:3097:U:H4'	73:L5:3098:A:OP1	2.18	0.43
73:L5:3133:G:H2'	73:L5:3134:C:O2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:SN:73:TYR:CZ	18:SC:26:LEU:HD22	2.54	0.43
31:S1:28:A:O2'	31:S1:29:U:H5'	2.19	0.43
31:S1:494:A:H2'	31:S1:495:A:C8	2.54	0.43
31:S1:1232:U:O2	31:S1:1232:U:O4'	2.35	0.43
31:S1:1407:G:H2'	31:S1:1408:A:C8	2.54	0.43
62:Lc:76:LEU:HD23	62:Lc:87:TYR:CE1	2.53	0.43
71:L3:33:U:O2	71:L3:33:U:O4'	2.37	0.43
73:L5:815:A:C2'	73:L5:816:A:O5'	2.67	0.43
73:L5:2179:U:H2'	73:L5:2180:G:O4'	2.19	0.43
73:L5:2998:G:C2	73:L5:3007:G:C4	3.07	0.43
73:L5:3049:A:H2'	73:L5:3050:G:O4'	2.19	0.43
73:L5:3130:A:OP1	73:L5:3130:A:C4	2.72	0.43
73:L5:3273:G:H2'	73:L5:3274:U:C6	2.54	0.43
80:Sg:251:TYR:CE1	80:Sg:266:LEU:HD12	2.54	0.43
7:ST:98:MET:CE	7:ST:118:LEU:HD22	2.49	0.42
13:SG:157:VAL:HG21	13:SG:173:ILE:HD11	2.01	0.42
13:SG:171:PRO:HB3	31:S1:66:C:C6	2.54	0.42
18:SC:181:GLN:HG2	18:SC:182:GLY:N	2.34	0.42
27:SQ:37:ILE:HG23	27:SQ:63:TYR:CE1	2.54	0.42
31:S1:110:A:O2'	31:S1:111:U:H5'	2.19	0.42
31:S1:301:A:H2'	31:S1:302:G:O4'	2.19	0.42
31:S1:475:A:H2'	31:S1:476:U:O4'	2.19	0.42
31:S1:689:A:H3'	31:S1:690:G:H8	1.83	0.42
31:S1:1422:U:O2	31:S1:1422:U:O5'	2.37	0.42
45:LZ:81:MET:HE1	67:Lh:94:LEU:HD21	2.02	0.42
49:LL:39:VAL:HG21	49:LL:52:LEU:HD12	2.00	0.42
52:Li:43:LEU:O	52:Li:43:LEU:HD23	2.18	0.42
71:L3:100:A:N1	73:L5:1023:A:O2'	2.51	0.42
73:L5:1365:A:H2'	73:L5:1366:U:C6	2.54	0.42
73:L5:2931:U:O2	73:L5:2931:U:O4'	2.36	0.42
76:S9:48:C:H2'	76:S9:59:U:H4'	2.00	0.42
2:SX:61:THR:HG22	2:SX:61:THR:O	2.18	0.42
31:S1:5:U:H2'	31:S1:6:G:H8	1.83	0.42
31:S1:138:G:O2'	31:S1:139:A:P	2.76	0.42
31:S1:715:A:O5'	79:SE:114:ARG:HG3	2.20	0.42
31:S1:720:U:OP1	31:S1:721:U:H5'	2.18	0.42
31:S1:1166:G:H2'	31:S1:1167:A:O4'	2.19	0.42
33:LS:51:LYS:HG2	33:LS:71:ILE:HD13	2.01	0.42
72:L4:118:A:N1	72:L4:139:U:H5	2.17	0.42
73:L5:1030:G:H3'	73:L5:1031:A:H8	1.83	0.42
73:L5:1690:C:C2	73:L5:1797:G:N2	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:1747:G:H2'	73:L5:1748:G:H5''	2.01	0.42
73:L5:2365:A:H3'	73:L5:2366:A:C5'	2.49	0.42
73:L5:2644:A:H62	73:L5:2664:G:H21	1.66	0.42
73:L5:2815:A:C6	73:L5:2828:A:H1'	2.55	0.42
73:L5:2816:G:C2'	73:L5:2817:C:H5'	2.49	0.42
73:L5:2827:G:H1'	73:L5:2828:A:C8	2.54	0.42
76:S9:5:G:C6	76:S9:69:G:N1	2.88	0.42
4:SL:46:ARG:HG2	31:S1:1460:U:O2'	2.18	0.42
8:SA:143:THR:HG23	8:SA:205:PHE:HE2	1.84	0.42
13:SG:212:GLU:OE1	13:SG:213:TYR:N	2.52	0.42
20:SB:168:ASN:O	20:SB:174:ILE:HD11	2.19	0.42
31:S1:520:G:O4'	31:S1:550:U:N3	2.53	0.42
31:S1:522:G:H2'	31:S1:522:G:N3	2.34	0.42
31:S1:546:G:H4'	31:S1:547:U:OP2	2.19	0.42
31:S1:925:C:O2	31:S1:925:C:P	2.78	0.42
31:S1:1244:U:C2'	31:S1:1245:U:O5'	2.67	0.42
31:S1:1532:A:H4'	31:S1:1533:G:OP1	2.18	0.42
31:S1:1709:A:H2'	31:S1:1710:A:O4'	2.19	0.42
44:LP:140:ARG:NH2	73:L5:1104:U:H5'	2.35	0.42
44:LP:150:ILE:HG13	73:L5:2680:A:H61	1.84	0.42
48:LC:282:ARG:HH11	48:LC:357:ILE:HD11	1.85	0.42
49:LL:29:VAL:HG21	49:LL:40:ASP:HB3	2.01	0.42
50:LK:21:VAL:HG23	50:LK:52:PRO:O	2.19	0.42
59:LO:158:LYS:HE3	73:L5:2829:C:H42	1.85	0.42
60:LN:80:VAL:CG2	60:LN:89:ILE:HD11	2.49	0.42
71:L3:100:A:C2	73:L5:1023:A:O2'	2.69	0.42
72:L4:147:U:H2'	72:L4:148:U:C6	2.54	0.42
73:L5:1826:A:C5	73:L5:1827:G:N7	2.87	0.42
73:L5:1916:A:O2'	73:L5:3029:G:H4'	2.19	0.42
73:L5:2239:G:H2'	73:L5:2240:G:C8	2.53	0.42
75:S8:7:G:C6	75:S8:49:G:C6	3.07	0.42
76:S9:35:U:H2'	76:S9:36:U:O4'	2.19	0.42
12:SK:38:LEU:HD23	12:SK:96:LEU:HD11	2.00	0.42
20:SB:60:LYS:HG3	20:SB:165:PRO:HD2	2.00	0.42
31:S1:722:C:C2	31:S1:723:A:C8	3.07	0.42
31:S1:962:C:O2'	31:S1:963:U:H5'	2.19	0.42
31:S1:1116:U:C4	75:S8:35:A:OP1	2.73	0.42
31:S1:1267:C:N3	31:S1:1268:U:C5	2.88	0.42
44:LP:91:GLY:HA3	71:L3:48:G:C5'	2.49	0.42
48:LC:254:HIS:HB2	73:L5:2918:A:OP2	2.20	0.42
71:L3:44:C:H2'	71:L3:45:U:C5	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:L3:46:C:OP1	71:L3:46:C:H4'	2.19	0.42
73:L5:629:C:O4'	73:L5:631:G:C6	2.72	0.42
73:L5:1682:G:H2'	73:L5:1683:C:O2	2.20	0.42
73:L5:2204:U:H2'	73:L5:2205:C:H5'	2.01	0.42
73:L5:2643:C:N3	73:L5:2679:A:N1	2.68	0.42
31:S1:699:G:N2	31:S1:701:A:H1'	2.35	0.42
31:S1:1150:U:C2'	31:S1:1151:U:O5'	2.67	0.42
38:LB:59:ALA:HB2	38:LB:78:ALA:HB2	2.01	0.42
41:LX:55:VAL:HG13	41:LX:103:VAL:HB	2.01	0.42
43:LD:235:ALA:O	43:LD:236:PRO:C	2.62	0.42
44:LP:65:ILE:HD13	71:L3:6:C:O2'	2.20	0.42
44:LP:197:MET:HB3	71:L3:35:C:OP2	2.20	0.42
60:LN:192:TRP:O	60:LN:196:GLN:HG2	2.19	0.42
71:L3:24:A:O2'	71:L3:25:A:H5'	2.19	0.42
73:L5:216:U:H2'	73:L5:217:G:OP1	2.19	0.42
73:L5:749:G:H2'	73:L5:750:C:C6	2.53	0.42
73:L5:1029:U:C2	73:L5:1030:G:C8	3.07	0.42
73:L5:1619:C:C2	73:L5:1621:A:OP2	2.73	0.42
73:L5:2288:A:O2'	73:L5:2906:C:H4'	2.19	0.42
73:L5:3256:G:N7	73:L5:3257:U:C5	2.87	0.42
76:S9:64:A:H8	76:S9:64:A:O5'	2.03	0.42
6:SH:18:LEU:HD11	6:SH:29:ILE:HD11	2.00	0.42
18:SC:10:ARG:NH2	31:S1:1449:A:N7	2.67	0.42
20:SB:63:LEU:HD11	78:SY:78:LEU:HD13	2.02	0.42
27:SQ:35:ARG:CD	27:SQ:94:LEU:HD21	2.48	0.42
31:S1:18:C:H5'	31:S1:1062:A:H61	1.84	0.42
31:S1:139:A:HO2'	31:S1:140:U:H5	1.65	0.42
31:S1:196:A:O2'	31:S1:197:G:P	2.78	0.42
31:S1:245:G:H3'	31:S1:246:A:C5'	2.49	0.42
31:S1:488:U:C2	31:S1:489:G:C8	3.08	0.42
31:S1:721:U:C5	31:S1:722:C:C6	3.08	0.42
31:S1:880:A:H2'	31:S1:881:C:O4'	2.19	0.42
31:S1:925:C:O3'	31:S1:926:A:H8	2.02	0.42
31:S1:989:G:HO2'	31:S1:990:A:P	2.42	0.42
31:S1:1097:G:H2'	31:S1:1098:C:O4'	2.19	0.42
31:S1:1207:U:O2'	31:S1:1208:U:H5'	2.19	0.42
31:S1:1465:C:H4'	31:S1:1471:G:C6	2.55	0.42
44:LP:239:ILE:HG23	44:LP:240:GLU:N	2.35	0.42
47:LH:159:VAL:HG13	47:LH:219:ALA:HB2	2.00	0.42
69:LG:65:LEU:HD21	69:LG:181:LEU:HD11	2.02	0.42
73:L5:722:A:N1	73:L5:723:A:C5	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:1199:G:H2'	73:L5:1200:C:C6	2.55	0.42
73:L5:1580:G:C6	73:L5:1582:A:C6	3.06	0.42
74:S7:8:U:H3	74:S7:14:A:H62	1.67	0.42
74:S7:9:G:H2'	74:S7:11:C:N4	2.34	0.42
74:S7:26:C:H42	74:S7:41:C:H41	1.67	0.42
75:S8:68:C:H2'	75:S8:69:C:C6	2.54	0.42
80:Sg:11:VAL:O	80:Sg:11:VAL:HG13	2.18	0.42
12:SK:57:ALA:HB2	12:SK:167:GLY:HA2	2.01	0.42
31:S1:80:U:O2'	31:S1:81:G:C8	2.71	0.42
31:S1:139:A:O2'	31:S1:140:U:P	2.77	0.42
31:S1:517:G:N1	31:S1:518:G:C2	2.88	0.42
31:S1:647:U:H2'	31:S1:648:U:C6	2.55	0.42
31:S1:864:A:H2'	31:S1:865:A:C8	2.54	0.42
47:LH:71:TYR:O	73:L5:2516:A:H2'	2.20	0.42
73:L5:530:U:O2	73:L5:530:U:O5'	2.38	0.42
73:L5:954:C:O2'	73:L5:1429:A:H1'	2.20	0.42
73:L5:1022:A:H2'	73:L5:1023:A:H8	1.85	0.42
73:L5:1795:C:C3'	73:L5:1796:G:O4'	2.68	0.42
73:L5:2307:U:O2	73:L5:2307:U:O4'	2.37	0.42
73:L5:2324:C:C2	73:L5:2325:A:C8	3.07	0.42
73:L5:2817:C:H41	73:L5:2822:A:H1'	1.84	0.42
74:S7:9:G:C2'	74:S7:11:C:H41	2.33	0.42
75:S8:64:G:C2	75:S8:65:C:H1'	2.54	0.42
81:LF:113:ILE:HD13	81:LF:178:ILE:CD1	2.49	0.42
3:SU:109:CYS:SG	3:SU:115:VAL:HG21	2.59	0.42
8:SA:120:LEU:C	8:SA:120:LEU:HD23	2.44	0.42
9:SN:67:TYR:HD2	9:SN:72:LEU:HD23	1.85	0.42
31:S1:418:A:O5'	31:S1:494:A:H5'	2.19	0.42
43:LD:100:MET:HG2	43:LD:101:TYR:N	2.34	0.42
44:LP:58:LYS:CA	71:L3:48:G:O6	2.68	0.42
48:LC:374:LYS:CB	73:L5:3257:U:OP1	2.68	0.42
62:Lc:171:GLY:HA2	73:L5:1129:G:OP2	2.19	0.42
62:Lc:173:ARG:HD3	73:L5:1128:U:O5'	2.19	0.42
73:L5:295:C:H2'	73:L5:296:A:O4'	2.19	0.42
73:L5:642:A:C4	73:L5:643:A:C8	3.07	0.42
73:L5:1037:G:N1	73:L5:1064:U:N3	2.68	0.42
73:L5:1079:A:P	73:L5:2614:A:H61	2.43	0.42
73:L5:1726:U:C6	73:L5:1727:U:O4'	2.73	0.42
73:L5:2214:G:N7	73:L5:2216:A:OP2	2.52	0.42
73:L5:2216:A:H2'	73:L5:2217:A:C8	2.54	0.42
73:L5:2264:A:N6	73:L5:2265:G:N7	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:2279:U:O4'	73:L5:2281:G:C5'	2.68	0.42
73:L5:2427:U:O2	73:L5:2427:U:O4'	2.38	0.42
73:L5:3260:U:H2'	73:L5:3261:G:O4'	2.20	0.42
80:Sg:279:LYS:O	80:Sg:280:PRO:C	2.63	0.42
2:SX:28:LEU:HD13	2:SX:36:PHE:CE2	2.55	0.42
26:Sa:76:ARG:NH2	31:S1:1465:C:OP2	2.53	0.42
31:S1:29:U:O5'	31:S1:29:U:O2	2.38	0.42
31:S1:251:C:H42	31:S1:261:C:N4	2.18	0.42
31:S1:928:A:H1'	31:S1:930:A:N7	2.35	0.42
31:S1:1506:G:OP2	31:S1:1506:G:C8	2.73	0.42
43:LD:9:ILE:HG22	43:LD:10:PHE:N	2.35	0.42
43:LD:201:LEU:HD11	43:LD:224:ALA:HB2	2.01	0.42
43:LD:251:PHE:O	43:LD:254:VAL:HG12	2.19	0.42
48:LC:128:LYS:HG3	73:L5:3224:A:H5''	2.02	0.42
59:LO:73:ASN:O	59:LO:77:VAL:HG23	2.20	0.42
73:L5:1063:C:C2	73:L5:1064:U:C5	3.08	0.42
73:L5:1719:U:C4	73:L5:1765:G:O6	2.73	0.42
73:L5:2190:C:H5	73:L5:2237:A:N6	2.18	0.42
73:L5:2813:C:N3	73:L5:2830:G:N2	2.67	0.42
12:SK:36:THR:O	12:SK:95:THR:HA	2.19	0.42
31:S1:100:U:O2	31:S1:103:A:H2	2.03	0.42
31:S1:989:G:O2'	31:S1:990:A:P	2.77	0.42
41:LX:31:SER:HA	41:LX:48:PRO:HA	2.02	0.42
44:LP:14:LYS:HD3	73:L5:1027:A:H4'	2.02	0.42
44:LP:58:LYS:HA	71:L3:48:G:O6	2.20	0.42
48:LC:92:TYR:HB2	48:LC:155:VAL:HB	2.01	0.42
73:L5:1037:G:C6	73:L5:1064:U:N3	2.87	0.42
73:L5:1088:G:OP2	73:L5:1123:G:H2'	2.20	0.42
73:L5:1735:A:C5	73:L5:1737:C:H1'	2.55	0.42
73:L5:1739:C:C1'	73:L5:1752:U:H4'	2.50	0.42
73:L5:2828:A:H3'	73:L5:2828:A:OP2	2.19	0.42
8:SA:53:GLY:C	73:L5:2432:G:O2'	2.63	0.41
21:SF:97:SER:HB3	31:S1:14:C:H4'	2.00	0.41
29:Sf:17:HIS:HB3	31:S1:1172:U:OP1	2.20	0.41
31:S1:34:G:O2'	31:S1:35:U:O5'	2.35	0.41
31:S1:515:U:H2'	31:S1:516:U:C6	2.55	0.41
31:S1:840:A:C6	31:S1:841:U:H1'	2.55	0.41
31:S1:978:G:HO2'	31:S1:979:U:P	2.43	0.41
31:S1:1083:C:N4	31:S1:1514:U:C4	2.88	0.41
31:S1:1242:C:H2'	31:S1:1243:G:O4'	2.20	0.41
33:LS:55:TRP:HE1	33:LS:71:ILE:HD11	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:LB:231:PRO:HA	73:L5:2157:C:OP1	2.20	0.41
41:LX:49:ILE:HD12	41:LX:100:PRO:CB	2.44	0.41
46:LU:122:ALA:HB1	46:LU:123:PRO:HD2	2.02	0.41
48:LC:327:VAL:O	48:LC:334:ILE:HD11	2.20	0.41
57:LR:95:GLY:CA	73:L5:1885:A:OP1	2.68	0.41
73:L5:753:G:OP1	73:L5:753:G:C8	2.73	0.41
73:L5:1083:G:H2'	73:L5:1084:G:C8	2.55	0.41
73:L5:2191:A:C5	73:L5:2192:G:C8	3.08	0.41
73:L5:2241:C:C5	73:L5:2266:G:C6	3.08	0.41
73:L5:2259:U:H2'	73:L5:2260:C:C5	2.54	0.41
73:L5:2696:U:H2'	73:L5:2697:G:O4'	2.20	0.41
73:L5:2903:A:O2'	73:L5:2904:C:H5'	2.20	0.41
73:L5:3294:C:H2'	73:L5:3295:U:OP1	2.19	0.41
76:S9:43:C:O2	76:S9:43:C:H2'	2.20	0.41
76:S9:58:A:C8	76:S9:61:C:C4	3.08	0.41
28:SD:143:ILE:HD13	31:S1:695:U:N3	2.35	0.41
31:S1:541:C:O5'	31:S1:541:C:H6	2.03	0.41
31:S1:700:C:OP1	79:SE:27:ASP:HA	2.20	0.41
31:S1:1225:A:N7	31:S1:1226:U:H1'	2.35	0.41
31:S1:1498:A:O2'	31:S1:1499:U:H5'	2.20	0.41
31:S1:1695:G:H4'	31:S1:1696:G:O4'	2.20	0.41
34:Le:63:ARG:HD3	73:L5:1497:A:O2'	2.20	0.41
46:LU:47:TYR:O	46:LU:51:VAL:HG23	2.20	0.41
52:Li:68:MET:SD	52:Li:87:ALA:HB2	2.59	0.41
71:L3:25:A:C4	71:L3:27:A:C8	3.07	0.41
73:L5:888:U:H3'	73:L5:889:G:H5'	2.02	0.41
73:L5:1097:G:H2'	73:L5:1098:C:C1'	2.50	0.41
73:L5:1106:A:O2'	73:L5:1107:G:H3'	2.19	0.41
73:L5:2149:G:O2'	73:L5:2150:C:H5'	2.20	0.41
73:L5:2815:A:H3'	73:L5:2816:G:C5'	2.51	0.41
73:L5:3086:C:H2'	73:L5:3087:U:C6	2.55	0.41
76:S9:43:C:H2'	76:S9:44:G:OP1	2.19	0.41
1:SP:30:LYS:HD3	31:S1:1057:A:OP1	2.19	0.41
7:ST:98:MET:HE2	7:ST:118:LEU:HD22	2.02	0.41
11:SI:153:LEU:HB3	11:SI:186:VAL:HG22	2.01	0.41
14:SM:52:LEU:HD13	14:SM:97:SER:HB3	2.01	0.41
31:S1:60:U:C6	31:S1:62:A:OP2	2.73	0.41
31:S1:195:U:H5	31:S1:234:A:H61	1.68	0.41
31:S1:276:G:H2'	31:S1:277:U:O4'	2.20	0.41
31:S1:579:G:H2'	31:S1:583:C:C5	2.55	0.41
31:S1:1074:G:H1'	31:S1:1693:A:C4	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:S1:1267:C:C2	31:S1:1268:U:C5	3.09	0.41
31:S1:1690:A:H2'	31:S1:1691:A:O5'	2.19	0.41
37:LQ:176:ALA:HB1	37:LQ:179:ALA:HB2	2.01	0.41
38:LB:116:LEU:HD21	38:LB:148:VAL:HG21	2.03	0.41
44:LP:58:LYS:HA	71:L3:48:G:C6	2.55	0.41
44:LP:92:LEU:HA	71:L3:47:C:O5'	2.20	0.41
44:LP:181:PRO:HD2	71:L3:35:C:N1	2.35	0.41
48:LC:26:ARG:HD2	48:LC:47:MET:HE1	2.02	0.41
55:Lo:38:GLY:HA3	73:L5:2742:C:O3'	2.20	0.41
62:Lc:97:VAL:O	62:Lc:125:GLY:HA2	2.20	0.41
73:L5:562:C:H2'	73:L5:563:G:O4'	2.20	0.41
73:L5:1007:C:C2'	73:L5:1008:A:O5'	2.69	0.41
73:L5:1020:U:O2'	73:L5:2614:A:P	2.78	0.41
73:L5:1770:A:P	82:Lk:29:ARG:NH2	2.94	0.41
73:L5:2146:A:H2'	73:L5:2147:U:H6	1.85	0.41
73:L5:2242:G:C5	73:L5:2265:G:N1	2.88	0.41
73:L5:2502:U:H2'	73:L5:2503:U:O4'	2.20	0.41
73:L5:2959:A:O3'	73:L5:2960:C:O2	2.39	0.41
73:L5:3140:C:C2	73:L5:3141:G:C8	3.08	0.41
73:L5:3257:U:N3	73:L5:3258:A:C8	2.89	0.41
74:S7:15:G:N1	74:S7:46:G:C2	2.88	0.41
6:SH:7:LEU:HG	6:SH:8:PHE:CD2	2.55	0.41
15:Se:41:TYR:CG	28:SD:32:GLY:HA3	2.56	0.41
31:S1:365:G:O2'	31:S1:366:C:H5'	2.20	0.41
31:S1:694:U:H4'	31:S1:695:U:OP1	2.19	0.41
31:S1:996:U:H2'	31:S1:997:C:C6	2.55	0.41
31:S1:1368:G:C3'	31:S1:1369:A:H5'	2.50	0.41
31:S1:1422:U:O2	31:S1:1422:U:O4'	2.37	0.41
38:LB:238:ILE:O	38:LB:239:ALA:C	2.63	0.41
48:LC:213:ILE:HD12	48:LC:336:LEU:HB3	2.02	0.41
58:LE:102:PHE:O	73:L5:2651:A:H4'	2.20	0.41
59:LO:32:ARG:NE	76:S9:58:A:H61	2.19	0.41
61:Lg:111:TYR:O	61:Lg:112:PRO:C	2.64	0.41
71:L3:71:G:HO2'	71:L3:72:A:P	2.43	0.41
73:L5:325:A:C2'	73:L5:326:A:O5'	2.68	0.41
73:L5:510:C:O2	73:L5:510:C:O5'	2.38	0.41
73:L5:1003:A:H3'	73:L5:1004:C:H6	1.85	0.41
73:L5:1024:G:H2'	73:L5:1025:C:O4'	2.20	0.41
73:L5:2504:G:C5	73:L5:2505:C:C5	3.09	0.41
73:L5:2757:A:H4'	73:L5:2757:A:OP1	2.20	0.41
73:L5:3262:U:H4'	73:L5:3263:A:C5'	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:S7:36:A:H2'	74:S7:37:U:O5'	2.20	0.41
75:S8:64:G:H2'	75:S8:65:C:O4'	2.20	0.41
75:S8:67:C:H2'	75:S8:68:C:C6	2.55	0.41
4:SL:77:GLY:C	31:S1:1416:A:H4'	2.45	0.41
25:SZ:53:LYS:C	25:SZ:55:PRO:HD3	2.46	0.41
31:S1:361:G:C2'	31:S1:362:G:O5'	2.68	0.41
31:S1:368:U:H2'	31:S1:369:G:O4'	2.20	0.41
31:S1:483:G:N3	31:S1:483:G:C2'	2.84	0.41
31:S1:506:G:H22	31:S1:512:C:N4	2.18	0.41
31:S1:513:A:H3'	31:S1:514:A:C5'	2.50	0.41
31:S1:527:U:O2	31:S1:527:U:H2'	2.20	0.41
31:S1:905:G:H4'	31:S1:1704:A:H4'	2.03	0.41
31:S1:1215:U:H2'	31:S1:1216:G:O4'	2.20	0.41
37:LQ:186:PHE:O	37:LQ:197:THR:HG22	2.20	0.41
38:LB:5:ILE:HG22	38:LB:208:ASP:O	2.20	0.41
41:LX:120:ARG:HD2	73:L5:183:G:H4'	2.02	0.41
43:LD:12:VAL:HG23	43:LD:153:VAL:HG12	2.02	0.41
43:LD:151:MET:HE1	43:LD:175:LEU:HD21	2.03	0.41
44:LP:72:ASP:H	71:L3:116:G:H21	1.68	0.41
44:LP:150:ILE:HG13	73:L5:2680:A:N6	2.36	0.41
73:L5:167:C:H2'	73:L5:168:C:O4'	2.21	0.41
73:L5:745:G:O2'	73:L5:746:U:H2'	2.21	0.41
73:L5:1358:C:C2	73:L5:1359:C:C5	3.09	0.41
73:L5:1742:U:H2'	73:L5:1743:G:O5'	2.20	0.41
73:L5:2173:G:H2'	73:L5:2174:C:C6	2.55	0.41
73:L5:2277:C:H41	73:L5:2301:C:C1'	2.33	0.41
74:S7:12:G:N1	74:S7:23:G:C6	2.89	0.41
80:Sg:193:LEU:HD13	80:Sg:224:TRP:CG	2.56	0.41
81:LF:124:ILE:HD12	81:LF:124:ILE:N	2.35	0.41
8:SA:127:VAL:HG11	8:SA:176:ALA:CB	2.49	0.41
13:SG:59:GLN:N	13:SG:59:GLN:OE1	2.54	0.41
20:SB:143:VAL:O	20:SB:143:VAL:HG12	2.21	0.41
31:S1:35:U:H2'	31:S1:36:C:O2	2.20	0.41
31:S1:395:G:C2'	31:S1:396:G:O5'	2.68	0.41
31:S1:720:U:C5'	31:S1:721:U:O2	2.69	0.41
31:S1:1006:G:H2'	31:S1:1008:G:N7	2.36	0.41
31:S1:1319:A:C2	31:S1:1345:G:C4	3.09	0.41
31:S1:1406:U:O2	31:S1:1406:U:C2'	2.68	0.41
31:S1:1496:U:H2'	31:S1:1497:C:C6	2.56	0.41
38:LB:179:LEU:HD21	73:L5:1814:C:C4	2.55	0.41
43:LD:68:THR:HG21	73:L5:2395:A:H2'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:LD:201:LEU:HD12	43:LD:222:GLU:O	2.20	0.41
44:LP:91:GLY:HA3	71:L3:48:G:O5'	2.20	0.41
48:LC:215:VAL:HG13	48:LC:334:ILE:CG2	2.50	0.41
49:LL:92:THR:HG23	49:LL:93:LEU:N	2.36	0.41
73:L5:1023:A:H2'	73:L5:1024:G:C8	2.55	0.41
73:L5:1242:A:H2'	73:L5:1243:U:H5''	2.03	0.41
73:L5:2239:G:C2	73:L5:2240:G:C5	3.09	0.41
73:L5:2257:U:H2'	73:L5:2258:C:H6	1.85	0.41
73:L5:2633:A:C5	73:L5:2635:G:N7	2.88	0.41
73:L5:2642:U:H4'	73:L5:2643:C:OP1	2.20	0.41
73:L5:2736:U:O5'	73:L5:2736:U:O2	2.39	0.41
73:L5:2996:U:C5	73:L5:2997:A:C8	3.08	0.41
73:L5:3267:G:C3'	73:L5:3268:C:H5''	2.50	0.41
80:Sg:265:ASN:OD1	80:Sg:265:ASN:C	2.63	0.41
31:S1:1475:A:C2	31:S1:1501:A:C8	3.09	0.41
38:LB:116:LEU:CD2	38:LB:148:VAL:HG21	2.50	0.41
44:LP:180:PHE:CB	71:L3:35:C:H2'	2.51	0.41
73:L5:405:C:C2	73:L5:406:U:C6	3.09	0.41
73:L5:1348:G:O2'	73:L5:1349:U:H5'	2.20	0.41
73:L5:1723:A:O2'	73:L5:1724:A:H5'	2.20	0.41
73:L5:2269:G:C2	73:L5:2304:G:H1'	2.55	0.41
73:L5:2323:C:N3	73:L5:2324:C:C5	2.89	0.41
73:L5:2747:A:N1	73:L5:2766:U:O2	2.53	0.41
73:L5:3134:C:O2	73:L5:3134:C:O4'	2.39	0.41
73:L5:3254:G:C6	73:L5:3308:G:O6	2.74	0.41
4:SL:42:LEU:HD22	4:SL:54:VAL:HG11	2.01	0.41
10:SJ:105:THR:HG23	10:SJ:124:LYS:HB2	2.01	0.41
22:Sb:15:ARG:O	22:Sb:16:GLY:C	2.64	0.41
27:SQ:34:ILE:HG23	27:SQ:39:GLN:HB3	2.02	0.41
31:S1:249:C:O2'	31:S1:250:G:P	2.79	0.41
31:S1:1146:A:H2'	31:S1:1147:A:O4'	2.21	0.41
31:S1:1498:A:C6	31:S1:1499:U:C4	3.08	0.41
40:LJ:78:LEU:HD11	40:LJ:95:VAL:HG22	2.03	0.41
62:Lc:193:ILE:N	62:Lc:193:ILE:HD12	2.35	0.41
68:LY:63:ARG:HB3	68:LY:68:LYS:HB2	2.02	0.41
71:L3:31:G:OP2	71:L3:31:G:O4'	2.38	0.41
71:L3:74:A:O4'	71:L3:76:U:C6	2.73	0.41
71:L3:109:C:O2'	71:L3:110:G:P	2.79	0.41
72:L4:66:U:C2	72:L4:67:U:C5	3.08	0.41
73:L5:117:G:HO2'	73:L5:118:U:C5'	2.32	0.41
73:L5:1113:G:H2'	73:L5:1114:C:C2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:1135:C:H2'	73:L5:1136:A:O4'	2.21	0.41
73:L5:1827:G:H2'	73:L5:1828:G:O5'	2.21	0.41
73:L5:1934:G:H4'	73:L5:1935:G:OP2	2.20	0.41
73:L5:2219:U:H2'	73:L5:2220:C:C2	2.56	0.41
73:L5:2662:A:H2'	73:L5:2663:C:O4'	2.21	0.41
73:L5:2815:A:P	73:L5:2816:G:OP2	2.78	0.41
74:S7:56:U:C5	74:S7:59:A:N7	2.89	0.41
76:S9:67:C:C2	76:S9:68:C:C5	3.09	0.41
76:S9:74:C:O2'	76:S9:75:C:O2	2.39	0.41
79:SE:187:VAL:HG11	79:SE:201:ILE:HD11	2.02	0.41
80:Sg:93:ARG:HH12	80:Sg:102:THR:HG21	1.82	0.41
2:SX:64:ALA:HB2	2:SX:115:CYS:HB3	2.01	0.41
3:SU:73:VAL:HG22	3:SU:82:ILE:HD12	2.03	0.41
6:SH:176:TYR:CD1	6:SH:176:TYR:C	2.99	0.41
13:SG:66:GLY:HA2	31:S1:1613:A:H1'	2.03	0.41
16:SS:34:LEU:CD1	16:SS:34:LEU:O	2.69	0.41
18:SC:162:THR:HG23	31:S1:1253:G:H5''	2.03	0.41
20:SB:69:VAL:HG21	20:SB:188:LEU:CB	2.51	0.41
20:SB:69:VAL:HG11	78:SY:45:TYR:HB2	2.03	0.41
20:SB:107:ILE:O	20:SB:108:PRO:C	2.64	0.41
31:S1:50:C:H2'	31:S1:397:C:H41	1.86	0.41
31:S1:520:G:O4'	31:S1:550:U:C2	2.74	0.41
31:S1:524:A:C6	31:S1:560:A:H4'	2.55	0.41
31:S1:591:A:O2'	31:S1:957:G:H5'	2.21	0.41
31:S1:680:G:C5	31:S1:681:A:N6	2.89	0.41
31:S1:978:G:O2'	31:S1:979:U:P	2.78	0.41
31:S1:1116:U:O2	75:S8:35:A:OP2	2.39	0.41
31:S1:1226:U:O2'	31:S1:1227:U:H5'	2.21	0.41
31:S1:1360:A:C2'	31:S1:1361:G:OP2	2.69	0.41
31:S1:1545:U:C4	31:S1:1546:A:H2	2.39	0.41
31:S1:1579:U:H2'	31:S1:1580:C:C6	2.56	0.41
31:S1:1661:C:N3	31:S1:1662:C:C5	2.89	0.41
31:S1:1704:A:C6	31:S1:1714:G:O6	2.74	0.41
38:LB:103:PRO:HA	38:LB:162:SER:O	2.21	0.41
38:LB:177:LYS:HB2	65:Lp:29:ILE:HG21	2.03	0.41
39:LI:46:LEU:HD12	39:LI:140:VAL:HG22	2.02	0.41
44:LP:92:LEU:HA	71:L3:47:C:H5''	2.03	0.41
44:LP:95:TYR:HA	71:L3:46:C:OP1	2.20	0.41
44:LP:180:PHE:O	71:L3:36:C:C4'	2.69	0.41
59:LO:75:PHE:CD1	59:LO:151:ALA:HB2	2.56	0.41
71:L3:122:C:O2	71:L3:122:C:O4'	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:107:A:H2'	73:L5:108:U:O4'	2.21	0.41
73:L5:207:C:H2'	73:L5:208:A:O4'	2.21	0.41
73:L5:485:C:H2'	73:L5:486:U:O4'	2.21	0.41
73:L5:1065:A:H3'	73:L5:1066:U:H5''	2.01	0.41
73:L5:1565:G:C2	73:L5:1566:C:C5	3.09	0.41
73:L5:2102:C:C2	73:L5:3272:A:C6	3.08	0.41
73:L5:2270:C:H5	73:L5:2300:G:H1	1.67	0.41
73:L5:2275:U:H4'	73:L5:2949:G:N2	2.36	0.41
73:L5:2406:A:H2'	73:L5:2407:G:H8	1.86	0.41
73:L5:2514:U:O2	73:L5:2514:U:O4'	2.37	0.41
73:L5:2643:C:C4	73:L5:2679:A:N1	2.89	0.41
73:L5:3113:C:C2	73:L5:3114:U:C5	3.09	0.41
73:L5:3128:U:O5'	73:L5:3130:A:OP1	2.39	0.41
73:L5:3130:A:H2'	73:L5:3130:A:N3	2.36	0.41
73:L5:3311:G:P	73:L5:3311:G:H8	2.43	0.41
74:S7:34:U:C4	74:S7:35:C:H5	2.39	0.41
75:S8:4:G:O2'	75:S8:5:G:P	2.79	0.41
75:S8:33:U:C4	75:S8:35:A:H5''	2.55	0.41
75:S8:53:G:O2'	75:S8:54:U:H5'	2.21	0.41
76:S9:25:C:C4	76:S9:26:A:C8	3.09	0.41
76:S9:28:G:C2	76:S9:29:G:C4	3.08	0.41
76:S9:58:A:H1'	76:S9:60:U:OP2	2.21	0.41
76:S9:65:G:H2'	76:S9:65:G:N3	2.36	0.41
1:SP:108:GLY:HA2	31:S1:568:A:OP1	2.20	0.41
6:SH:56:ILE:HG23	6:SH:57:VAL:N	2.36	0.41
8:SA:32:LEU:HD21	8:SA:46:THR:HG22	2.03	0.41
9:SN:24:ILE:HD11	9:SN:84:LEU:HB3	2.02	0.41
23:SV:32:LYS:HA	23:SV:51:ALA:HB2	2.03	0.41
31:S1:195:U:C6	31:S1:235:A:C2	3.09	0.41
31:S1:427:A:H2'	31:S1:428:C:C5	2.56	0.41
31:S1:989:G:C2	31:S1:990:A:C5	3.09	0.41
31:S1:1327:G:N1	31:S1:1336:C:C5	2.89	0.41
38:LB:116:LEU:HA	38:LB:164:ALA:HB2	2.02	0.41
44:LP:150:ILE:HD12	44:LP:150:ILE:N	2.36	0.41
45:LZ:11:VAL:HG12	45:LZ:82:PRO:HA	2.03	0.41
48:LC:307:GLY:HA3	73:L5:3256:G:N2	2.36	0.41
64:Ld:29:GLY:N	73:L5:1748:G:O2'	2.54	0.41
73:L5:1064:U:O5'	73:L5:1065:A:P	2.79	0.41
73:L5:1087:A:OP1	73:L5:1088:G:H4'	2.21	0.41
73:L5:1349:U:C2	73:L5:1350:U:C5	3.09	0.41
73:L5:1690:C:O2'	73:L5:1691:G:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:1770:A:C4	73:L5:1772:A:C8	3.09	0.41
73:L5:2262:U:N3	73:L5:2264:A:OP2	2.54	0.41
73:L5:2268:A:N6	73:L5:2304:G:H1'	2.36	0.41
73:L5:2610:U:O2'	73:L5:2611:U:H5'	2.21	0.41
73:L5:2626:G:O2'	73:L5:2627:U:H5'	2.21	0.41
73:L5:3271:G:H2'	73:L5:3288:G:H2'	2.02	0.41
74:S7:52:G:O6	74:S7:53:A:C4	2.74	0.41
6:SH:62:ASN:HB3	31:S1:1543:A:O2'	2.20	0.40
10:SJ:105:THR:HG23	10:SJ:105:THR:O	2.20	0.40
12:SK:38:LEU:CD2	12:SK:96:LEU:HD11	2.51	0.40
31:S1:418:A:C4	31:S1:419:A:C8	3.09	0.40
31:S1:436:U:H2'	31:S1:437:A:O4'	2.21	0.40
31:S1:975:G:H2'	31:S1:976:U:O4'	2.21	0.40
31:S1:1402:A:H2'	31:S1:1403:C:C6	2.55	0.40
31:S1:1698:U:H2'	31:S1:1699:U:C6	2.56	0.40
43:LD:218:ILE:O	43:LD:219:ALA:C	2.63	0.40
44:LP:182:GLY:CA	71:L3:35:C:H5''	2.51	0.40
44:LP:206:HIS:HB2	71:L3:34:C:C2	2.56	0.40
58:LE:19:ILE:HA	58:LE:122:GLY:C	2.46	0.40
58:LE:125:PHE:N	73:L5:2651:A:O4'	2.54	0.40
71:L3:20:C:N3	71:L3:21:G:O6	2.54	0.40
71:L3:71:G:C2'	71:L3:72:A:O5'	2.69	0.40
73:L5:410:A:C8	73:L5:411:U:C5	3.09	0.40
73:L5:631:G:O2'	73:L5:632:U:H5'	2.21	0.40
73:L5:1520:C:O2'	73:L5:1620:A:H1'	2.21	0.40
73:L5:2238:C:H2'	73:L5:2239:G:O4'	2.22	0.40
73:L5:2266:G:H1'	73:L5:2304:G:O6	2.20	0.40
73:L5:2272:A:C4	73:L5:2281:G:C5	3.09	0.40
73:L5:2276:G:H4'	73:L5:2301:C:N4	2.35	0.40
73:L5:2862:C:O2'	73:L5:2863:U:H5'	2.21	0.40
73:L5:2976:G:H2'	73:L5:2977:U:C6	2.56	0.40
74:S7:29:G:N1	74:S7:39:A:C6	2.89	0.40
76:S9:26:A:C2'	76:S9:27:G:O5'	2.69	0.40
77:S6:47:U:O2'	77:S6:48:U:H5'	2.21	0.40
80:Sg:212:CYS:HB2	80:Sg:226:MET:SD	2.61	0.40
7:ST:120:SER:O	7:ST:124:ARG:HG3	2.21	0.40
10:SJ:106:THR:O	10:SJ:107:ALA:C	2.63	0.40
20:SB:63:LEU:HD13	78:SY:72:PHE:HD2	1.86	0.40
20:SB:196:THR:O	20:SB:196:THR:HG23	2.21	0.40
31:S1:188:C:C4	31:S1:189:G:N2	2.89	0.40
31:S1:406:C:H2'	31:S1:407:G:O4'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:S1:418:A:C1'	31:S1:494:A:O5'	2.69	0.40
31:S1:656:G:N2	31:S1:668:U:H1'	2.36	0.40
31:S1:946:C:C4	31:S1:947:C:C5	3.08	0.40
31:S1:1081:C:O2	31:S1:1081:C:O4'	2.36	0.40
31:S1:1694:A:C4	31:S1:1722:A:C2	3.09	0.40
39:LI:107:VAL:HB	39:LI:159:ARG:CD	2.51	0.40
47:LH:210:VAL:O	47:LH:210:VAL:CG1	2.69	0.40
48:LC:374:LYS:HG3	73:L5:3257:U:P	2.61	0.40
73:L5:291:A:C2	73:L5:292:G:C5	3.10	0.40
73:L5:342:C:O2'	73:L5:343:G:H5'	2.21	0.40
73:L5:642:A:O2'	73:L5:643:A:C5'	2.69	0.40
73:L5:643:A:H2'	73:L5:644:C:C5	2.57	0.40
73:L5:720:G:H2'	73:L5:721:A:H8	1.86	0.40
73:L5:803:U:C6	73:L5:804:G:C8	3.09	0.40
73:L5:1764:U:H2'	73:L5:1765:G:C8	2.55	0.40
73:L5:2113:A:H2'	73:L5:2114:A:O4'	2.21	0.40
73:L5:2205:C:H4'	73:L5:2206:A:H5'	2.03	0.40
73:L5:3152:G:H2'	73:L5:3153:C:O4'	2.21	0.40
73:L5:3174:U:O2	73:L5:3174:U:O4'	2.37	0.40
73:L5:3219:G:H2'	73:L5:3220:C:O4'	2.20	0.40
76:S9:26:A:H2'	76:S9:27:G:O5'	2.21	0.40
79:SE:51:ILE:HG23	79:SE:52:LEU:N	2.36	0.40
10:SJ:28:ARG:HB3	10:SJ:29:PRO:CD	2.50	0.40
22:Sb:21:ILE:HD12	22:Sb:21:ILE:C	2.46	0.40
31:S1:117:C:H1'	31:S1:370:A:C5	2.56	0.40
31:S1:613:G:H2'	31:S1:614:U:O4'	2.21	0.40
31:S1:656:G:H2'	31:S1:657:G:C1'	2.51	0.40
31:S1:1206:G:O2'	31:S1:1207:U:H5'	2.21	0.40
31:S1:1505:A:H4'	31:S1:1506:G:H5'	2.03	0.40
31:S1:1545:U:C4	31:S1:1546:A:C2	3.09	0.40
39:LI:88:PRO:HD3	73:L5:1201:C:H4'	2.01	0.40
40:LJ:46:VAL:O	40:LJ:46:VAL:HG12	2.21	0.40
43:LD:175:LEU:HD11	43:LD:245:ILE:HD11	2.02	0.40
43:LD:198:VAL:O	43:LD:198:VAL:HG23	2.21	0.40
49:LL:12:ARG:HD3	49:LL:59:LEU:HD22	2.03	0.40
60:LN:64:VAL:HG22	60:LN:106:VAL:HG11	2.03	0.40
71:L3:28:C:C4	71:L3:29:C:C2	3.10	0.40
72:L4:56:G:H2'	72:L4:57:C:O4'	2.21	0.40
73:L5:760:C:C2	73:L5:761:C:C5	3.10	0.40
73:L5:911:G:H2'	73:L5:912:U:O4'	2.21	0.40
73:L5:1128:U:O3'	73:L5:1129:G:H4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:L5:1134:C:H2'	73:L5:1135:C:C6	2.57	0.40
73:L5:1614:A:H2'	73:L5:1615:G:C8	2.57	0.40
73:L5:3027:U:C2	73:L5:3028:G:C8	3.09	0.40
73:L5:3256:G:C5	73:L5:3257:U:C4	3.09	0.40
73:L5:3256:G:H2'	73:L5:3257:U:C5'	2.51	0.40
74:S7:17:U:P	74:S7:58:G:H21	2.44	0.40
76:S9:67:C:H2'	76:S9:68:C:H6	1.87	0.40
31:S1:12:U:H2'	31:S1:13:C:C6	2.57	0.40
31:S1:418:A:O2'	31:S1:419:A:H5'	2.22	0.40
31:S1:522:G:OP2	31:S1:524:A:OP1	2.39	0.40
31:S1:524:A:H3'	31:S1:524:A:OP2	2.21	0.40
31:S1:610:U:H2'	31:S1:611:G:O4'	2.21	0.40
31:S1:715:A:N1	79:SE:57:ARG:CZ	2.85	0.40
31:S1:720:U:O5'	31:S1:721:U:H5'	2.21	0.40
31:S1:964:A:O2'	31:S1:965:G:O5'	2.37	0.40
31:S1:1005:U:H2'	31:S1:1006:G:C8	2.56	0.40
31:S1:1322:U:C2	31:S1:1323:U:C5	3.10	0.40
33:LS:23:VAL:HG22	33:LS:39:ARG:HB2	2.03	0.40
38:LB:196:TRP:O	38:LB:197:PRO:C	2.64	0.40
38:LB:240:ALA:CB	38:LB:243:THR:HG23	2.50	0.40
43:LD:133:VAL:HB	43:LD:134:PRO:HD3	2.03	0.40
44:LP:156:GLY:O	44:LP:181:PRO:HG3	2.21	0.40
44:LP:183:TYR:CD1	44:LP:183:TYR:O	2.74	0.40
52:Li:55:ILE:HG21	60:LN:9:GLU:HG3	2.03	0.40
69:LG:62:VAL:HG21	69:LG:76:VAL:HG21	2.04	0.40
73:L5:208:A:H4'	73:L5:210:U:C5	2.57	0.40
73:L5:309:G:H2'	73:L5:310:G:C8	2.57	0.40
73:L5:520:U:C4	73:L5:521:G:C6	3.09	0.40
73:L5:656:G:H1'	73:L5:1178:C:N4	2.37	0.40
73:L5:1194:A:C6	73:L5:1195:A:C6	3.09	0.40
73:L5:1386:A:H2'	73:L5:1387:A:C8	2.56	0.40
73:L5:1798:U:C3'	73:L5:1799:G:H5'	2.52	0.40
73:L5:2204:U:OP2	73:L5:2205:C:C5	2.74	0.40
73:L5:2301:C:P	73:L5:2302:A:HO2'	2.45	0.40
73:L5:2640:A:C2'	73:L5:2641:C:H5'	2.52	0.40
73:L5:2715:A:C2	73:L5:2716:A:C5	3.10	0.40
73:L5:2765:C:P	73:L5:2766:U:OP2	2.79	0.40
73:L5:3005:A:H3'	73:L5:3006:G:C8	2.57	0.40
73:L5:3308:G:H2'	73:L5:3309:G:C1'	2.52	0.40
74:S7:16:U:O2	74:S7:58:G:H1'	2.21	0.40
74:S7:33:C:O2'	74:S7:34:U:OP1	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:Lk:11:TYR:CB	82:Lk:41:LEU:HD22	2.50	0.40
2:SX:126:VAL:CG1	2:SX:144:ARG:HD2	2.52	0.40
27:SQ:87:THR:HG22	27:SQ:91:TRP:HD1	1.87	0.40
31:S1:418:A:H2'	31:S1:419:A:C5'	2.52	0.40
31:S1:720:U:H5''	31:S1:721:U:O5'	2.22	0.40
31:S1:972:G:O2'	31:S1:973:A:H5'	2.21	0.40
41:LX:51:LYS:O	41:LX:69:VAL:O	2.39	0.40
45:LZ:72:VAL:HG11	45:LZ:97:VAL:HG11	2.04	0.40
45:LZ:76:ASN:HB2	73:L5:1654:C:H1'	2.04	0.40
58:LE:15:LEU:HD21	58:LE:125:PHE:CE1	2.57	0.40
59:LO:51:HIS:HB3	59:LO:134:ILE:HG23	2.04	0.40
73:L5:748:A:C4'	73:L5:749:G:OP1	2.69	0.40
73:L5:1038:G:C2'	73:L5:1039:U:O5'	2.70	0.40
73:L5:1769:C:O4'	73:L5:1770:A:C4	2.74	0.40
73:L5:1939:C:N4	73:L5:1940:G:C6	2.90	0.40
73:L5:2428:G:N7	73:L5:2570:A:H2'	2.37	0.40
73:L5:2757:A:C8	73:L5:2758:C:C6	3.10	0.40
73:L5:2758:C:H2'	73:L5:2759:U:H5	1.87	0.40
73:L5:3266:C:H2'	73:L5:3267:G:O5'	2.21	0.40
74:S7:32:U:H2'	74:S7:33:C:OP1	2.21	0.40
80:Sg:34:VAL:HG12	80:Sg:35:ILE:N	2.36	0.40
82:Lk:23:VAL:HA	82:Lk:31:ARG:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	SP	119/145 (82%)	110 (92%)	9 (8%)	0	100	100
2	SX	165/174 (95%)	152 (92%)	13 (8%)	0	100	100
3	SU	149/156 (96%)	135 (91%)	14 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SL	137/149 (92%)	125 (91%)	10 (7%)	2 (2%)	8	32
5	SR	139/154 (90%)	129 (93%)	9 (6%)	1 (1%)	18	49
6	SH	183/192 (95%)	169 (92%)	14 (8%)	0	100	100
7	ST	143/151 (95%)	142 (99%)	1 (1%)	0	100	100
8	SA	204/264 (77%)	195 (96%)	9 (4%)	0	100	100
9	SN	94/113 (83%)	87 (93%)	7 (7%)	0	100	100
10	SJ	124/130 (95%)	110 (89%)	14 (11%)	0	100	100
11	SI	122/194 (63%)	115 (94%)	6 (5%)	1 (1%)	16	47
12	SK	171/192 (89%)	160 (94%)	11 (6%)	0	100	100
13	SG	178/239 (74%)	170 (96%)	8 (4%)	0	100	100
14	SM	94/120 (78%)	85 (90%)	9 (10%)	0	100	100
15	Se	36/61 (59%)	31 (86%)	4 (11%)	1 (3%)	4	20
16	SS	48/66 (73%)	44 (92%)	4 (8%)	0	100	100
17	Sd	50/67 (75%)	46 (92%)	4 (8%)	0	100	100
18	SC	179/223 (80%)	164 (92%)	15 (8%)	0	100	100
19	SW	104/149 (70%)	95 (91%)	9 (9%)	0	100	100
20	SB	157/274 (57%)	139 (88%)	18 (12%)	0	100	100
21	SF	148/196 (76%)	141 (95%)	7 (5%)	0	100	100
22	Sb	78/115 (68%)	71 (91%)	7 (9%)	0	100	100
23	SV	73/134 (54%)	71 (97%)	2 (3%)	0	100	100
24	SO	90/157 (57%)	78 (87%)	10 (11%)	2 (2%)	5	24
25	SZ	63/135 (47%)	56 (89%)	6 (10%)	1 (2%)	7	30
26	Sa	69/104 (66%)	65 (94%)	4 (6%)	0	100	100
27	SQ	83/135 (62%)	80 (96%)	3 (4%)	0	100	100
28	SD	98/184 (53%)	92 (94%)	6 (6%)	0	100	100
29	Sf	48/77 (62%)	42 (88%)	6 (12%)	0	100	100
30	Sc	54/82 (66%)	48 (89%)	6 (11%)	0	100	100
32	LM	142/147 (97%)	136 (96%)	6 (4%)	0	100	100
33	LS	177/188 (94%)	170 (96%)	7 (4%)	0	100	100
34	Le	94/117 (80%)	93 (99%)	1 (1%)	0	100	100
35	Lf	123/132 (93%)	117 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Lj	85/98 (87%)	79 (93%)	6 (7%)	0	100	100
37	LQ	182/222 (82%)	168 (92%)	14 (8%)	0	100	100
38	LB	243/257 (95%)	223 (92%)	20 (8%)	0	100	100
39	LI	196/202 (97%)	190 (97%)	6 (3%)	0	100	100
40	LJ	191/203 (94%)	184 (96%)	7 (4%)	0	100	100
41	LX	119/137 (87%)	116 (98%)	3 (2%)	0	100	100
42	La	111/123 (90%)	107 (96%)	4 (4%)	0	100	100
43	LD	319/360 (89%)	295 (92%)	24 (8%)	0	100	100
44	LP	277/306 (90%)	257 (93%)	20 (7%)	0	100	100
45	LZ	133/146 (91%)	127 (96%)	6 (4%)	0	100	100
46	LU	168/194 (87%)	159 (95%)	9 (5%)	0	100	100
47	LH	220/285 (77%)	214 (97%)	6 (3%)	0	100	100
48	LC	373/395 (94%)	349 (94%)	23 (6%)	1 (0%)	36	67
49	LL	126/133 (95%)	119 (94%)	7 (6%)	0	100	100
50	LK	126/139 (91%)	115 (91%)	11 (9%)	0	100	100
51	LW	114/153 (74%)	111 (97%)	3 (3%)	0	100	100
52	Li	101/116 (87%)	98 (97%)	3 (3%)	0	100	100
53	Lm	48/55 (87%)	44 (92%)	4 (8%)	0	100	100
54	LT	146/160 (91%)	135 (92%)	11 (8%)	0	100	100
55	Lo	94/105 (90%)	89 (95%)	5 (5%)	0	100	100
56	Ll	47/59 (80%)	46 (98%)	1 (2%)	0	100	100
57	LR	168/194 (87%)	161 (96%)	7 (4%)	0	100	100
58	LE	151/171 (88%)	137 (91%)	14 (9%)	0	100	100
59	LO	201/227 (88%)	190 (94%)	11 (6%)	0	100	100
60	LN	195/204 (96%)	187 (96%)	8 (4%)	0	100	100
61	Lg	106/115 (92%)	97 (92%)	7 (7%)	2 (2%)	6	27
62	Lc	212/259 (82%)	206 (97%)	6 (3%)	0	100	100
63	LV	95/122 (78%)	90 (95%)	5 (5%)	0	100	100
64	Ld	91/108 (84%)	86 (94%)	5 (6%)	0	100	100
65	Lp	86/94 (92%)	77 (90%)	9 (10%)	0	100	100
66	Lb	49/59 (83%)	47 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	Lh	98/150 (65%)	92 (94%)	6 (6%)	0	100	100
68	LY	59/156 (38%)	58 (98%)	1 (2%)	0	100	100
69	LG	151/212 (71%)	143 (95%)	8 (5%)	0	100	100
70	Ln	36/39 (92%)	34 (94%)	2 (6%)	0	100	100
78	SY	76/79 (96%)	70 (92%)	6 (8%)	0	100	100
79	SE	253/266 (95%)	236 (93%)	17 (7%)	0	100	100
80	Sg	313/323 (97%)	289 (92%)	24 (8%)	0	100	100
81	LF	184/190 (97%)	178 (97%)	6 (3%)	0	100	100
82	Lk	63/70 (90%)	61 (97%)	2 (3%)	0	100	100
All	All	9942/12002 (83%)	9327 (94%)	604 (6%)	11 (0%)	49	78

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	SR	36	ARG
11	SI	134	ALA
15	Se	20	PRO
25	SZ	53	LYS
48	LC	18	PRO
4	SL	46	ARG
4	SL	47	PRO
61	Lg	68	ASN
24	SO	43	PHE
24	SO	150	CYS
61	Lg	112	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	SP	99/118 (84%)	92 (93%)	7 (7%)	13	41
2	SX	146/151 (97%)	143 (98%)	3 (2%)	47	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	SU	137/140 (98%)	131 (96%)	6 (4%)	25	56
4	SL	113/122 (93%)	108 (96%)	5 (4%)	25	56
5	SR	122/131 (93%)	118 (97%)	4 (3%)	33	63
6	SH	158/162 (98%)	156 (99%)	2 (1%)	61	77
7	ST	128/132 (97%)	123 (96%)	5 (4%)	28	60
8	SA	191/237 (81%)	188 (98%)	3 (2%)	55	75
9	SN	92/105 (88%)	92 (100%)	0	100	100
10	SJ	110/114 (96%)	104 (94%)	6 (6%)	19	50
11	SI	115/173 (66%)	113 (98%)	2 (2%)	53	74
12	SK	153/164 (93%)	142 (93%)	11 (7%)	13	40
13	SG	166/208 (80%)	163 (98%)	3 (2%)	51	73
14	SM	89/108 (82%)	85 (96%)	4 (4%)	24	56
15	Se	32/48 (67%)	31 (97%)	1 (3%)	35	64
16	SS	44/58 (76%)	41 (93%)	3 (7%)	14	42
17	Sd	45/54 (83%)	43 (96%)	2 (4%)	25	56
18	SC	156/186 (84%)	150 (96%)	6 (4%)	29	60
19	SW	96/132 (73%)	95 (99%)	1 (1%)	68	79
20	SB	144/238 (60%)	136 (94%)	8 (6%)	19	49
21	SF	121/157 (77%)	113 (93%)	8 (7%)	15	43
22	Sb	73/104 (70%)	67 (92%)	6 (8%)	10	36
23	SV	65/118 (55%)	65 (100%)	0	100	100
24	SO	78/123 (63%)	74 (95%)	4 (5%)	21	52
25	SZ	61/115 (53%)	52 (85%)	9 (15%)	3	13
26	Sa	63/90 (70%)	63 (100%)	0	100	100
27	SQ	76/116 (66%)	67 (88%)	9 (12%)	5	21
28	SD	101/163 (62%)	94 (93%)	7 (7%)	14	41
29	Sf	45/68 (66%)	45 (100%)	0	100	100
30	Sc	54/73 (74%)	51 (94%)	3 (6%)	19	49
32	LM	119/121 (98%)	115 (97%)	4 (3%)	32	63
33	LS	155/164 (94%)	155 (100%)	0	100	100
34	Le	91/105 (87%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	Lf	110/117 (94%)	109 (99%)	1 (1%)	70	80
36	Lj	71/78 (91%)	71 (100%)	0	100	100
37	LQ	155/184 (84%)	152 (98%)	3 (2%)	50	73
38	LB	187/198 (94%)	183 (98%)	4 (2%)	47	71
39	LI	170/172 (99%)	169 (99%)	1 (1%)	78	83
40	LJ	161/170 (95%)	158 (98%)	3 (2%)	50	73
41	LX	113/128 (88%)	111 (98%)	2 (2%)	51	73
42	La	105/111 (95%)	104 (99%)	1 (1%)	68	79
43	LD	259/288 (90%)	251 (97%)	8 (3%)	35	64
44	LP	242/261 (93%)	233 (96%)	9 (4%)	30	61
45	LZ	123/129 (95%)	122 (99%)	1 (1%)	73	81
46	LU	146/163 (90%)	145 (99%)	1 (1%)	76	82
47	LH	195/243 (80%)	193 (99%)	2 (1%)	68	79
48	LC	330/345 (96%)	327 (99%)	3 (1%)	70	80
49	LL	107/110 (97%)	107 (100%)	0	100	100
50	LK	99/104 (95%)	97 (98%)	2 (2%)	48	72
51	LW	106/135 (78%)	106 (100%)	0	100	100
52	Li	91/100 (91%)	89 (98%)	2 (2%)	45	71
53	Lm	46/49 (94%)	42 (91%)	4 (9%)	9	34
54	LT	128/139 (92%)	127 (99%)	1 (1%)	73	81
55	Lo	85/90 (94%)	82 (96%)	3 (4%)	32	62
56	Ll	46/54 (85%)	46 (100%)	0	100	100
57	LR	144/164 (88%)	142 (99%)	2 (1%)	59	76
58	LE	136/151 (90%)	127 (93%)	9 (7%)	15	43
59	LO	171/188 (91%)	167 (98%)	4 (2%)	44	70
60	LN	171/176 (97%)	167 (98%)	4 (2%)	44	70
61	Lg	93/99 (94%)	91 (98%)	2 (2%)	45	71
62	Lc	184/228 (81%)	180 (98%)	4 (2%)	45	71
63	LV	89/111 (80%)	88 (99%)	1 (1%)	65	78
64	Ld	79/94 (84%)	77 (98%)	2 (2%)	42	69
65	Lp	70/76 (92%)	68 (97%)	2 (3%)	37	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	Lb	46/52 (88%)	46 (100%)	0	100	100
67	Lh	86/125 (69%)	84 (98%)	2 (2%)	44	70
68	LY	54/126 (43%)	54 (100%)	0	100	100
69	LG	135/181 (75%)	131 (97%)	4 (3%)	36	65
70	Ln	34/35 (97%)	33 (97%)	1 (3%)	37	66
78	SY	67/68 (98%)	60 (90%)	7 (10%)	7	27
79	SE	226/235 (96%)	205 (91%)	21 (9%)	8	31
80	Sg	274/281 (98%)	252 (92%)	22 (8%)	11	37
81	LF	167/170 (98%)	157 (94%)	10 (6%)	17	47
82	Lk	58/62 (94%)	57 (98%)	1 (2%)	53	74
All	All	8797/10288 (86%)	8516 (97%)	281 (3%)	35	64

All (281) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	SP	9	ILE
1	SP	19	ARG
1	SP	34	LEU
1	SP	74	VAL
1	SP	89	ARG
1	SP	107	LEU
1	SP	130	VAL
2	SX	63	VAL
2	SX	103	SER
2	SX	140	ASP
3	SU	35	ASP
3	SU	65	ARG
3	SU	102	HIS
3	SU	116	ASN
3	SU	136	ASN
3	SU	144	GLN
4	SL	13	VAL
4	SL	18	ARG
4	SL	25	VAL
4	SL	76	ARG
4	SL	82	SER
5	SR	14	ILE
5	SR	108	CYS

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Mol	Chain	Res	Type
5	SR	133	THR
5	SR	138	THR
6	SH	18	LEU
6	SH	97	LEU
7	ST	14	SER
7	ST	66	ILE
7	ST	76	ARG
7	ST	87	ASP
7	ST	115	LEU
8	SA	48	VAL
8	SA	143	THR
8	SA	156	VAL
10	SJ	18	GLU
10	SJ	56	HIS
10	SJ	68	ARG
10	SJ	76	SER
10	SJ	80	ASP
10	SJ	106	THR
11	SI	63	ILE
11	SI	108	LYS
12	SK	9	HIS
12	SK	26	LYS
12	SK	32	ARG
12	SK	37	LYS
12	SK	49	ARG
12	SK	56	ARG
12	SK	76	THR
12	SK	103	THR
12	SK	120	ASP
12	SK	183	ARG
12	SK	187	ASP
13	SG	69	THR
13	SG	159	ARG
13	SG	177	VAL
14	SM	24	ILE
14	SM	29	THR
14	SM	67	ILE
14	SM	78	THR
15	Se	24	THR
16	SS	11	THR
16	SS	34	LEU
16	SS	37	CYS

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Mol	Chain	Res	Type
17	Sd	19	ARG
17	Sd	39	VAL
18	SC	25	GLU
18	SC	34	ASP
18	SC	147	GLN
18	SC	174	THR
18	SC	195	ASP
18	SC	200	LEU
19	SW	102	ASN
20	SB	34	GLU
20	SB	58	LEU
20	SB	140	SER
20	SB	141	SER
20	SB	145	LEU
20	SB	151	CYS
20	SB	180	LEU
20	SB	191	GLN
21	SF	19	VAL
21	SF	50	CYS
21	SF	89	MET
21	SF	120	LEU
21	SF	123	PHE
21	SF	128	ASP
21	SF	155	TYR
21	SF	180	LEU
22	Sb	6	ARG
22	Sb	12	LYS
22	Sb	22	ARG
22	Sb	26	CYS
22	Sb	61	THR
22	Sb	76	SER
24	SO	57	GLU
24	SO	97	THR
24	SO	135	ILE
24	SO	144	ASP
25	SZ	41	ASP
25	SZ	43	ARG
25	SZ	59	VAL
25	SZ	60	LEU
25	SZ	93	ARG
25	SZ	94	GLN
25	SZ	96	ARG

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Mol	Chain	Res	Type
25	SZ	99	LEU
25	SZ	122	ARG
27	SQ	21	GLN
27	SQ	22	LYS
27	SQ	37	ILE
27	SQ	67	ILE
27	SQ	71	CYS
27	SQ	72	LYS
27	SQ	78	LEU
27	SQ	81	THR
27	SQ	112	VAL
28	SD	24	LEU
28	SD	38	ASN
28	SD	39	LYS
28	SD	78	ARG
28	SD	99	LEU
28	SD	143	ILE
28	SD	154	LYS
30	Sc	35	CYS
30	Sc	42	THR
30	Sc	65	THR
32	LM	65	LYS
32	LM	75	VAL
32	LM	102	VAL
32	LM	111	LEU
35	Lf	86	LEU
37	LQ	64	LEU
37	LQ	76	ASN
37	LQ	109	ARG
38	LB	139	HIS
38	LB	168	ILE
38	LB	196	TRP
38	LB	235	VAL
39	LI	35	VAL
40	LJ	49	LEU
40	LJ	67	VAL
40	LJ	131	LYS
41	LX	2	LYS
41	LX	103	VAL
42	La	72	SER
43	LD	35	LEU
43	LD	91	TYR

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Mol	Chain	Res	Type
43	LD	114	VAL
43	LD	139	ARG
43	LD	153	VAL
43	LD	172	THR
43	LD	191	ASP
43	LD	342	ILE
44	LP	36	MET
44	LP	57	ASN
44	LP	93	THR
44	LP	150	ILE
44	LP	151	LYS
44	LP	155	THR
44	LP	172	HIS
44	LP	180	PHE
44	LP	206	HIS
45	LZ	87	VAL
46	LU	5	SER
47	LH	175	HIS
47	LH	255	HIS
48	LC	4	ARG
48	LC	153	CYS
48	LC	244	LEU
50	LK	24	ILE
50	LK	85	LYS
52	Li	16	ILE
52	Li	43	LEU
53	Lm	3	GLU
53	Lm	23	CYS
53	Lm	34	CYS
53	Lm	39	CYS
54	LT	92	HIS
55	Lo	12	CYS
55	Lo	16	CYS
55	Lo	64	THR
57	LR	70	HIS
57	LR	171	ILE
58	LE	11	ARG
58	LE	14	LYS
58	LE	38	LEU
58	LE	79	GLU
58	LE	85	LYS
58	LE	107	HIS

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Mol	Chain	Res	Type
58	LE	124	ASP
58	LE	125	PHE
58	LE	138	LYS
59	LO	32	ARG
59	LO	36	MET
59	LO	83	GLU
59	LO	198	LYS
60	LN	15	GLN
60	LN	49	ARG
60	LN	64	VAL
60	LN	121	VAL
61	Lg	26	ARG
61	Lg	57	VAL
62	Lc	51	ARG
62	Lc	95	VAL
62	Lc	226	ARG
62	Lc	227	LYS
63	LV	75	ILE
64	Ld	27	CYS
64	Ld	32	SER
65	Lp	5	THR
65	Lp	83	THR
67	Lh	32	VAL
67	Lh	74	ARG
69	LG	77	THR
69	LG	109	SER
69	LG	112	GLU
69	LG	212	PHE
70	Ln	15	MET
78	SY	1	MET
78	SY	9	VAL
78	SY	16	LYS
78	SY	27	GLN
78	SY	34	ILE
78	SY	54	LEU
78	SY	75	GLN
79	SE	25	LEU
79	SE	27	ASP
79	SE	30	SER
79	SE	43	LYS
79	SE	66	GLU
79	SE	93	MET

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Mol	Chain	Res	Type
79	SE	102	ASN
79	SE	112	LYS
79	SE	115	PHE
79	SE	118	HIS
79	SE	120	ILE
79	SE	146	VAL
79	SE	175	VAL
79	SE	177	ASP
79	SE	179	LEU
79	SE	202	VAL
79	SE	226	THR
79	SE	242	ILE
79	SE	246	LYS
79	SE	250	ILE
79	SE	254	ILE
80	Sg	30	ASP
80	Sg	42	LYS
80	Sg	51	GLN
80	Sg	94	LEU
80	Sg	99	LYS
80	Sg	105	VAL
80	Sg	118	PHE
80	Sg	121	ASP
80	Sg	123	ARG
80	Sg	137	TRP
80	Sg	149	ASN
80	Sg	176	ASP
80	Sg	184	LEU
80	Sg	192	ASN
80	Sg	208	ASP
80	Sg	249	ARG
80	Sg	254	CYS
80	Sg	255	VAL
80	Sg	279	LYS
80	Sg	282	LYS
80	Sg	295	THR
80	Sg	316	LYS
81	LF	47	LEU
81	LF	49	LYS
81	LF	85	LYS
81	LF	113	ILE
81	LF	139	VAL

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Mol	Chain	Res	Type
81	LF	140	LYS
81	LF	142	GLU
81	LF	163	CYS
81	LF	179	TYR
81	LF	187	GLU
82	Lk	16	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
1	SP	65	ASN
2	SX	70	GLN
3	SU	87	ASN
3	SU	116	ASN
3	SU	125	GLN
3	SU	136	ASN
4	SL	83	GLN
5	SR	13	HIS
6	SH	70	ASN
6	SH	89	HIS
6	SH	191	ASN
8	SA	208	GLN
12	SK	64	ASN
16	SS	17	HIS
16	SS	51	HIS
20	SB	50	HIS
21	SF	24	ASN
21	SF	41	ASN
21	SF	142	ASN
24	SO	49	HIS
29	Sf	58	HIS
30	Sc	17	HIS
30	Sc	25	ASN
33	LS	41	ASN
33	LS	102	ASN
33	LS	181	HIS
36	Lj	79	ASN
38	LB	106	GLN
39	LI	117	GLN
41	LX	71	GLN
42	La	34	GLN
43	LD	111	HIS

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Mol	Chain	Res	Type
44	LP	190	ASN
46	LU	116	HIS
46	LU	133	HIS
47	LH	81	GLN
47	LH	99	GLN
47	LH	110	HIS
47	LH	263	HIS
48	LC	163	GLN
51	LW	59	HIS
56	LI	33	HIS
59	LO	130	ASN
61	Lg	65	ASN
61	Lg	68	ASN
61	Lg	114	HIS
62	Lc	124	ASN
62	Lc	201	HIS
63	LV	70	HIS
67	Lh	33	GLN
68	LY	47	HIS
68	LY	66	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	S1	1517/1728 (87%)	366 (24%)	14 (0%)
71	L3	121/122 (99%)	39 (32%)	4 (3%)
72	L4	142/159 (89%)	23 (16%)	1 (0%)
73	L5	2854/3326 (85%)	635 (22%)	31 (1%)
74	S7	73/74 (98%)	38 (52%)	1 (1%)
75	S8	75/76 (98%)	32 (42%)	3 (4%)
76	S9	68/76 (89%)	27 (39%)	1 (1%)
77	S6	10/11 (90%)	2 (20%)	0
All	All	4860/5572 (87%)	1162 (23%)	55 (1%)

All (1162) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
31	S1	4	C
31	S1	17	C
31	S1	25	C
31	S1	30	G

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Mol	Chain	Res	Type
31	S1	31	C
31	S1	34	G
31	S1	35	U
31	S1	36	C
31	S1	38	U
31	S1	39	A
31	S1	45	U
31	S1	47	A
31	S1	57	G
31	S1	61	A
31	S1	67	A
31	S1	68	A
31	S1	69	A
31	S1	70	C
31	S1	80	U
31	S1	81	G
31	S1	102	C
31	S1	112	A
31	S1	113	G
31	S1	114	U
31	S1	125	U
31	S1	128	G
31	S1	134	C
31	S1	136	U
31	S1	139	A
31	S1	140	U
31	S1	147	G
31	S1	152	U
31	S1	155	U
31	S1	165	A
31	S1	168	A
31	S1	171	U
31	S1	172	C
31	S1	173	G
31	S1	174	A
31	S1	189	G
31	S1	194	U
31	S1	197	G
31	S1	231	C
31	S1	232	A
31	S1	234	A
31	S1	238	A

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Mol	Chain	Res	Type
31	S1	246	A
31	S1	250	G
31	S1	262	G
31	S1	265	G
31	S1	266	G
31	S1	267	A
31	S1	268	C
31	S1	274	A
31	S1	284	C
31	S1	288	U
31	S1	289	C
31	S1	291	G
31	S1	295	G
31	S1	302	G
31	S1	306	A
31	S1	310	G
31	S1	311	C
31	S1	317	G
31	S1	332	A
31	S1	333	A
31	S1	334	C
31	S1	342	U
31	S1	353	U
31	S1	361	G
31	S1	373	A
31	S1	374	A
31	S1	375	C
31	S1	377	G
31	S1	389	A
31	S1	390	A
31	S1	391	G
31	S1	392	G
31	S1	396	G
31	S1	397	C
31	S1	399	G
31	S1	412	U
31	S1	413	U
31	S1	417	C
31	S1	418	A
31	S1	421	C
31	S1	425	A
31	S1	432	G

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Mol	Chain	Res	Type
31	S1	433	A
31	S1	434	G
31	S1	437	A
31	S1	441	A
31	S1	442	C
31	S1	449	U
31	S1	450	A
31	S1	451	A
31	S1	452	C
31	S1	453	A
31	S1	456	A
31	S1	475	A
31	S1	477	U
31	S1	478	G
31	S1	480	A
31	S1	481	A
31	S1	482	U
31	S1	483	G
31	S1	484	A
31	S1	485	U
31	S1	487	G
31	S1	488	U
31	S1	491	C
31	S1	494	A
31	S1	497	C
31	S1	498	C
31	S1	501	C
31	S1	502	A
31	S1	505	A
31	S1	506	G
31	S1	507	A
31	S1	513	A
31	S1	514	A
31	S1	515	U
31	S1	520	G
31	S1	523	C
31	S1	524	A
31	S1	526	G
31	S1	527	U
31	S1	528	C
31	S1	530	G
31	S1	531	G

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Mol	Chain	Res	Type
31	S1	532	U
31	S1	533	G
31	S1	534	C
31	S1	535	C
31	S1	537	G
31	S1	547	U
31	S1	548	A
31	S1	549	A
31	S1	552	C
31	S1	557	U
31	S1	559	C
31	S1	563	A
31	S1	564	G
31	S1	575	A
31	S1	579	G
31	S1	580	U
31	S1	582	G
31	S1	588	A
31	S1	589	A
31	S1	590	A
31	S1	591	A
31	S1	592	A
31	S1	593	G
31	S1	603	G
31	S1	607	U
31	S1	608	U
31	S1	613	G
31	S1	616	G
31	S1	617	U
31	S1	618	G
31	S1	654	U
31	S1	655	U
31	S1	656	G
31	S1	657	G
31	S1	666	C
31	S1	667	C
31	S1	671	U
31	S1	680	G
31	S1	682	A
31	S1	683	A
31	S1	688	G
31	S1	689	A

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Mol	Chain	Res	Type
31	S1	690	G
31	S1	692	G
31	S1	693	U
31	S1	695	U
31	S1	702	G
31	S1	703	A
31	S1	704	C
31	S1	712	U
31	S1	713	U
31	S1	714	G
31	S1	715	A
31	S1	716	A
31	S1	718	A
31	S1	719	C
31	S1	720	U
31	S1	721	U
31	S1	736	A
31	S1	737	G
31	S1	738	A
31	S1	739	G
31	S1	743	G
31	S1	746	U
31	S1	781	A
31	S1	782	U
31	S1	784	G
31	S1	785	U
31	S1	788	A
31	S1	798	U
31	S1	801	G
31	S1	811	U
31	S1	818	C
31	S1	819	U
31	S1	820	G
31	S1	822	C
31	S1	823	A
31	S1	825	A
31	S1	826	G
31	S1	827	G
31	S1	829	G
31	S1	832	A
31	S1	833	U
31	S1	834	U

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Mol	Chain	Res	Type
31	S1	835	C
31	S1	837	U
31	S1	838	A
31	S1	839	G
31	S1	840	A
31	S1	846	U
31	S1	851	A
31	S1	857	U
31	S1	858	A
31	S1	860	U
31	S1	867	G
31	S1	885	U
31	S1	891	A
31	S1	910	G
31	S1	917	A
31	S1	918	A
31	S1	921	C
31	S1	922	G
31	S1	923	A
31	S1	924	U
31	S1	925	C
31	S1	926	A
31	S1	927	G
31	S1	929	U
31	S1	930	A
31	S1	937	U
31	S1	949	U
31	S1	951	A
31	S1	953	C
31	S1	956	U
31	S1	957	G
31	S1	964	A
31	S1	965	G
31	S1	979	U
31	S1	990	A
31	S1	1001	A
31	S1	1017	A
31	S1	1018	A
31	S1	1021	C
31	S1	1022	U
31	S1	1025	G
31	S1	1036	G

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Mol	Chain	Res	Type
31	S1	1051	G
31	S1	1063	A
31	S1	1068	A
31	S1	1075	G
31	S1	1083	C
31	S1	1092	G
31	S1	1095	G
31	S1	1110	U
31	S1	1119	A
31	S1	1121	A
31	S1	1124	G
31	S1	1125	G
31	S1	1127	A
31	S1	1142	A
31	S1	1143	G
31	S1	1151	U
31	S1	1162	G
31	S1	1167	A
31	S1	1169	A
31	S1	1170	G
31	S1	1171	C
31	S1	1194	U
31	S1	1201	U
31	S1	1212	A
31	S1	1213	G
31	S1	1216	G
31	S1	1231	C
31	S1	1232	U
31	S1	1238	A
31	S1	1239	U
31	S1	1240	U
31	S1	1245	U
31	S1	1246	A
31	S1	1250	A
31	S1	1263	C
31	S1	1265	U
31	S1	1270	A
31	S1	1271	C
31	S1	1274	G
31	S1	1286	A
31	S1	1294	C
31	S1	1297	U

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Mol	Chain	Res	Type
31	S1	1309	U
31	S1	1319	A
31	S1	1321	U
31	S1	1333	A
31	S1	1334	G
31	S1	1340	A
31	S1	1341	G
31	S1	1348	U
31	S1	1358	A
31	S1	1360	A
31	S1	1364	C
31	S1	1366	G
31	S1	1380	U
31	S1	1391	G
31	S1	1392	C
31	S1	1393	A
31	S1	1404	A
31	S1	1419	G
31	S1	1430	C
31	S1	1448	U
31	S1	1449	A
31	S1	1450	A
31	S1	1455	U
31	S1	1469	A
31	S1	1470	C
31	S1	1473	G
31	S1	1489	U
31	S1	1492	U
31	S1	1500	G
31	S1	1501	A
31	S1	1505	A
31	S1	1506	G
31	S1	1516	G
31	S1	1522	G
31	S1	1533	G
31	S1	1539	G
31	S1	1548	G
31	S1	1554	G
31	S1	1563	A
31	S1	1565	A
31	S1	1566	C
31	S1	1567	A

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Mol	Chain	Res	Type
31	S1	1569	C
31	S1	1570	G
31	S1	1589	C
31	S1	1590	G
31	S1	1591	A
31	S1	1592	G
31	S1	1612	G
31	S1	1616	G
31	S1	1617	U
31	S1	1647	G
31	S1	1683	A
31	S1	1684	A
31	S1	1685	G
31	S1	1688	G
31	S1	1691	A
31	S1	1694	A
31	S1	1695	G
31	S1	1697	U
31	S1	1708	G
31	S1	1710	A
31	S1	1720	G
31	S1	1721	G
31	S1	1722	A
31	S1	1724	C
31	S1	1725	A
31	S1	1727	U
71	L3	7	G
71	L3	17	C
71	L3	18	G
71	L3	20	C
71	L3	21	G
71	L3	22	A
71	L3	26	U
71	L3	27	A
71	L3	30	G
71	L3	31	G
71	L3	32	A
71	L3	33	U
71	L3	34	C
71	L3	35	C
71	L3	36	C
71	L3	37	A

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Mol	Chain	Res	Type
71	L3	38	U
71	L3	39	C
71	L3	41	G
71	L3	42	A
71	L3	45	U
71	L3	46	C
71	L3	47	C
71	L3	48	G
71	L3	49	A
71	L3	50	A
71	L3	51	G
71	L3	54	A
71	L3	61	G
71	L3	64	A
71	L3	72	A
71	L3	100	A
71	L3	106	U
71	L3	107	U
71	L3	108	U
71	L3	109	C
71	L3	110	G
71	L3	113	G
71	L3	122	C
72	L4	23	U
72	L4	34	A
72	L4	35	C
72	L4	52	A
72	L4	59	A
72	L4	62	A
72	L4	63	G
72	L4	75	G
72	L4	91	U
72	L4	92	A
72	L4	95	A
72	L4	104	A
72	L4	106	C
72	L4	112	A
72	L4	113	A
72	L4	114	G
72	L4	124	U
72	L4	126	U
72	L4	135	G

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Mol	Chain	Res	Type
72	L4	140	A
72	L4	150	C
72	L4	153	U
72	L4	154	G
73	L5	14	U
73	L5	26	A
73	L5	40	A
73	L5	43	A
73	L5	49	U
73	L5	57	C
73	L5	59	G
73	L5	60	A
73	L5	65	A
73	L5	66	A
73	L5	67	A
73	L5	69	U
73	L5	74	A
73	L5	92	G
73	L5	105	G
73	L5	109	A
73	L5	110	G
73	L5	111	U
73	L5	116	A
73	L5	117	G
73	L5	118	U
73	L5	121	A
73	L5	122	A
73	L5	140	U
73	L5	148	G
73	L5	156	G
73	L5	157	A
73	L5	160	G
73	L5	161	G
73	L5	162	U
73	L5	166	G
73	L5	167	C
73	L5	168	C
73	L5	178	U
73	L5	183	G
73	L5	185	A
73	L5	189	U
73	L5	190	U

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Mol	Chain	Res	Type
73	L5	198	A
73	L5	209	A
73	L5	217	G
73	L5	218	A
73	L5	219	U
73	L5	232	A
73	L5	257	U
73	L5	261	C
73	L5	262	C
73	L5	263	U
73	L5	264	G
73	L5	266	A
73	L5	267	U
73	L5	271	G
73	L5	297	A
73	L5	300	U
73	L5	307	U
73	L5	313	U
73	L5	314	C
73	L5	326	A
73	L5	331	U
73	L5	332	G
73	L5	355	G
73	L5	372	U
73	L5	376	A
73	L5	378	G
73	L5	393	U
73	L5	397	A
73	L5	399	A
73	L5	400	A
73	L5	403	A
73	L5	404	C
73	L5	405	C
73	L5	413	G
73	L5	422	G
73	L5	423	A
73	L5	439	C
73	L5	442	C
73	L5	445	C
73	L5	447	U
73	L5	482	U
73	L5	487	C

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Mol	Chain	Res	Type
73	L5	506	G
73	L5	514	C
73	L5	515	G
73	L5	516	U
73	L5	521	G
73	L5	522	G
73	L5	526	G
73	L5	539	C
73	L5	544	U
73	L5	547	U
73	L5	549	U
73	L5	557	G
73	L5	563	G
73	L5	567	G
73	L5	568	C
73	L5	569	C
73	L5	630	C
73	L5	633	A
73	L5	643	A
73	L5	649	C
73	L5	661	A
73	L5	689	A
73	L5	693	C
73	L5	694	C
73	L5	702	C
73	L5	703	A
73	L5	711	G
73	L5	715	G
73	L5	716	U
73	L5	720	G
73	L5	721	A
73	L5	724	G
73	L5	726	A
73	L5	727	A
73	L5	728	G
73	L5	729	A
73	L5	733	U
73	L5	736	U
73	L5	743	G
73	L5	745	G
73	L5	746	U
73	L5	748	A

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Mol	Chain	Res	Type
73	L5	749	G
73	L5	751	G
73	L5	752	U
73	L5	753	G
73	L5	773	A
73	L5	777	U
73	L5	778	U
73	L5	782	U
73	L5	783	U
73	L5	789	C
73	L5	790	G
73	L5	793	U
73	L5	794	G
73	L5	795	A
73	L5	808	G
73	L5	815	A
73	L5	816	A
73	L5	823	U
73	L5	826	A
73	L5	839	A
73	L5	845	A
73	L5	849	C
73	L5	850	A
73	L5	851	G
73	L5	858	G
73	L5	861	U
73	L5	864	U
73	L5	865	G
73	L5	870	U
73	L5	883	U
73	L5	889	G
73	L5	905	A
73	L5	916	G
73	L5	917	G
73	L5	923	A
73	L5	925	G
73	L5	926	A
73	L5	930	A
73	L5	933	G
73	L5	946	G
73	L5	953	U
73	L5	968	C

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Mol	Chain	Res	Type
73	L5	969	U
73	L5	971	A
73	L5	990	G
73	L5	996	U
73	L5	998	G
73	L5	1002	A
73	L5	1003	A
73	L5	1006	U
73	L5	1007	C
73	L5	1008	A
73	L5	1009	G
73	L5	1014	A
73	L5	1016	C
73	L5	1018	G
73	L5	1019	G
73	L5	1020	U
73	L5	1021	A
73	L5	1025	C
73	L5	1026	U
73	L5	1027	A
73	L5	1032	U
73	L5	1033	U
73	L5	1034	A
73	L5	1037	G
73	L5	1038	G
73	L5	1039	U
73	L5	1040	A
73	L5	1041	U
73	L5	1042	C
73	L5	1063	C
73	L5	1064	U
73	L5	1066	U
73	L5	1072	A
73	L5	1074	C
73	L5	1075	U
73	L5	1079	A
73	L5	1082	G
73	L5	1084	G
73	L5	1087	A
73	L5	1088	G
73	L5	1089	A
73	L5	1091	C

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Mol	Chain	Res	Type
73	L5	1096	U
73	L5	1097	G
73	L5	1101	G
73	L5	1104	U
73	L5	1107	G
73	L5	1108	U
73	L5	1109	U
73	L5	1110	G
73	L5	1111	A
73	L5	1114	C
73	L5	1116	U
73	L5	1122	U
73	L5	1123	G
73	L5	1124	A
73	L5	1125	A
73	L5	1127	G
73	L5	1128	U
73	L5	1129	G
73	L5	1142	G
73	L5	1156	G
73	L5	1184	A
73	L5	1188	U
73	L5	1206	U
73	L5	1207	A
73	L5	1217	C
73	L5	1219	G
73	L5	1221	U
73	L5	1226	U
73	L5	1234	G
73	L5	1237	G
73	L5	1243	U
73	L5	1332	G
73	L5	1334	U
73	L5	1341	C
73	L5	1342	A
73	L5	1356	A
73	L5	1380	A
73	L5	1381	G
73	L5	1410	G
73	L5	1415	G
73	L5	1425	G
73	L5	1440	G

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Mol	Chain	Res	Type
73	L5	1442	G
73	L5	1454	G
73	L5	1457	G
73	L5	1460	C
73	L5	1469	A
73	L5	1473	G
73	L5	1478	U
73	L5	1504	A
73	L5	1506	G
73	L5	1507	U
73	L5	1511	G
73	L5	1525	G
73	L5	1530	U
73	L5	1559	G
73	L5	1576	A
73	L5	1580	G
73	L5	1582	A
73	L5	1583	U
73	L5	1585	G
73	L5	1602	G
73	L5	1605	A
73	L5	1607	A
73	L5	1608	G
73	L5	1611	G
73	L5	1614	A
73	L5	1623	A
73	L5	1637	U
73	L5	1638	C
73	L5	1639	G
73	L5	1647	U
73	L5	1648	G
73	L5	1649	G
73	L5	1657	C
73	L5	1660	A
73	L5	1661	A
73	L5	1663	U
73	L5	1675	C
73	L5	1695	A
73	L5	1701	U
73	L5	1716	C
73	L5	1717	A
73	L5	1720	G

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Mol	Chain	Res	Type
73	L5	1722	A
73	L5	1723	A
73	L5	1726	U
73	L5	1727	U
73	L5	1730	G
73	L5	1731	U
73	L5	1732	G
73	L5	1733	G
73	L5	1734	A
73	L5	1736	U
73	L5	1737	C
73	L5	1738	A
73	L5	1739	C
73	L5	1742	U
73	L5	1743	G
73	L5	1744	C
73	L5	1745	G
73	L5	1748	G
73	L5	1750	G
73	L5	1751	A
73	L5	1752	U
73	L5	1754	C
73	L5	1755	G
73	L5	1767	G
73	L5	1770	A
73	L5	1771	U
73	L5	1776	U
73	L5	1777	C
73	L5	1793	U
73	L5	1794	C
73	L5	1795	C
73	L5	1796	G
73	L5	1801	G
73	L5	1808	A
73	L5	1809	C
73	L5	1818	A
73	L5	1828	G
73	L5	1830	A
73	L5	1842	G
73	L5	1843	C
73	L5	1860	A
73	L5	1861	C

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Mol	Chain	Res	Type
73	L5	1862	A
73	L5	1863	A
73	L5	1864	C
73	L5	1866	G
73	L5	1871	A
73	L5	1880	A
73	L5	1881	G
73	L5	1884	U
73	L5	1886	G
73	L5	1899	G
73	L5	1900	A
73	L5	1901	U
73	L5	1907	A
73	L5	1914	A
73	L5	1921	A
73	L5	1927	G
73	L5	1928	C
73	L5	1934	G
73	L5	1935	G
73	L5	1936	A
73	L5	1940	G
73	L5	1947	C
73	L5	1948	G
73	L5	1952	U
73	L5	1953	A
73	L5	1954	A
73	L5	1959	U
73	L5	1960	G
73	L5	1961	G
73	L5	1962	C
73	L5	1964	C
73	L5	1965	U
73	L5	1969	G
73	L5	1972	C
73	L5	1973	G
73	L5	2091	C
73	L5	2096	U
73	L5	2097	C
73	L5	2099	G
73	L5	2102	C
73	L5	2103	U
73	L5	2105	G

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Mol	Chain	Res	Type
73	L5	2106	A
73	L5	2107	G
73	L5	2108	C
73	L5	2110	G
73	L5	2111	A
73	L5	2112	C
73	L5	2115	G
73	L5	2116	G
73	L5	2119	A
73	L5	2125	A
73	L5	2134	U
73	L5	2138	A
73	L5	2139	A
73	L5	2144	G
73	L5	2151	G
73	L5	2152	A
73	L5	2154	G
73	L5	2187	G
73	L5	2189	C
73	L5	2190	C
73	L5	2198	U
73	L5	2200	A
73	L5	2201	A
73	L5	2203	G
73	L5	2205	C
73	L5	2206	A
73	L5	2208	C
73	L5	2214	G
73	L5	2215	A
73	L5	2217	A
73	L5	2219	U
73	L5	2224	C
73	L5	2225	A
73	L5	2229	G
73	L5	2235	A
73	L5	2236	A
73	L5	2237	A
73	L5	2239	G
73	L5	2242	G
73	L5	2245	A
73	L5	2247	U
73	L5	2248	A

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Mol	Chain	Res	Type
73	L5	2249	A
73	L5	2250	C
73	L5	2252	A
73	L5	2260	C
73	L5	2265	G
73	L5	2266	G
73	L5	2267	U
73	L5	2273	A
73	L5	2276	G
73	L5	2278	C
73	L5	2290	U
73	L5	2300	G
73	L5	2303	U
73	L5	2306	A
73	L5	2308	G
73	L5	2309	G
73	L5	2328	G
73	L5	2329	U
73	L5	2366	A
73	L5	2367	C
73	L5	2368	G
73	L5	2386	G
73	L5	2387	G
73	L5	2390	A
73	L5	2394	A
73	L5	2395	A
73	L5	2396	G
73	L5	2397	A
73	L5	2404	U
73	L5	2427	U
73	L5	2428	G
73	L5	2433	A
73	L5	2500	U
73	L5	2507	U
73	L5	2508	A
73	L5	2516	A
73	L5	2517	U
73	L5	2538	A
73	L5	2539	C
73	L5	2540	A
73	L5	2545	C
73	L5	2546	A

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Mol	Chain	Res	Type
73	L5	2547	A
73	L5	2548	G
73	L5	2566	G
73	L5	2570	A
73	L5	2583	G
73	L5	2584	G
73	L5	2591	G
73	L5	2596	G
73	L5	2603	A
73	L5	2612	A
73	L5	2614	A
73	L5	2615	A
73	L5	2625	G
73	L5	2628	G
73	L5	2629	U
73	L5	2632	C
73	L5	2633	A
73	L5	2641	C
73	L5	2642	U
73	L5	2643	C
73	L5	2645	G
73	L5	2649	G
73	L5	2650	G
73	L5	2651	A
73	L5	2652	C
73	L5	2653	A
73	L5	2654	G
73	L5	2655	A
73	L5	2661	C
73	L5	2664	G
73	L5	2665	U
73	L5	2668	A
73	L5	2669	C
73	L5	2671	A
73	L5	2680	A
73	L5	2693	U
73	L5	2705	G
73	L5	2706	U
73	L5	2729	U
73	L5	2730	G
73	L5	2735	A
73	L5	2736	U

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Mol	Chain	Res	Type
73	L5	2739	A
73	L5	2744	U
73	L5	2746	G
73	L5	2747	A
73	L5	2748	G
73	L5	2749	U
73	L5	2754	G
73	L5	2755	A
73	L5	2757	A
73	L5	2759	U
73	L5	2765	C
73	L5	2767	A
73	L5	2768	G
73	L5	2769	A
73	L5	2770	G
73	L5	2773	G
73	L5	2776	A
73	L5	2777	G
73	L5	2778	A
73	L5	2780	A
73	L5	2787	C
73	L5	2793	G
73	L5	2794	A
73	L5	2798	C
73	L5	2813	C
73	L5	2814	A
73	L5	2815	A
73	L5	2816	G
73	L5	2819	U
73	L5	2821	C
73	L5	2822	A
73	L5	2824	A
73	L5	2827	G
73	L5	2828	A
73	L5	2830	G
73	L5	2833	G
73	L5	2844	C
73	L5	2848	G
73	L5	2849	A
73	L5	2864	A
73	L5	2876	C
73	L5	2904	C

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Mol	Chain	Res	Type
73	L5	2912	U
73	L5	2913	A
73	L5	2915	G
73	L5	2924	G
73	L5	2931	U
73	L5	2932	U
73	L5	2943	G
73	L5	2945	G
73	L5	2948	A
73	L5	2949	G
73	L5	2954	G
73	L5	2960	C
73	L5	2967	G
73	L5	2973	C
73	L5	2987	A
73	L5	2988	A
73	L5	2998	G
73	L5	2999	U
73	L5	3003	A
73	L5	3004	G
73	L5	3005	A
73	L5	3008	A
73	L5	3009	A
73	L5	3033	A
73	L5	3034	U
73	L5	3035	G
73	L5	3045	G
73	L5	3046	A
73	L5	3050	G
73	L5	3054	G
73	L5	3062	A
73	L5	3068	C
73	L5	3069	C
73	L5	3075	U
73	L5	3077	G
73	L5	3092	G
73	L5	3093	C
73	L5	3098	A
73	L5	3106	A
73	L5	3107	U
73	L5	3110	A
73	L5	3118	C

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Mol	Chain	Res	Type
73	L5	3127	U
73	L5	3128	U
73	L5	3130	A
73	L5	3131	C
73	L5	3139	G
73	L5	3152	G
73	L5	3158	U
73	L5	3170	A
73	L5	3174	U
73	L5	3177	G
73	L5	3179	C
73	L5	3192	U
73	L5	3193	U
73	L5	3194	C
73	L5	3195	C
73	L5	3196	G
73	L5	3197	A
73	L5	3201	A
73	L5	3203	A
73	L5	3206	U
73	L5	3207	C
73	L5	3212	C
73	L5	3217	G
73	L5	3234	U
73	L5	3243	U
73	L5	3248	G
73	L5	3250	A
73	L5	3251	C
73	L5	3252	C
73	L5	3256	G
73	L5	3263	A
73	L5	3264	A
73	L5	3265	G
73	L5	3266	C
73	L5	3267	G
73	L5	3268	C
73	L5	3269	G
73	L5	3272	A
73	L5	3273	G
73	L5	3285	U
73	L5	3292	C
73	L5	3293	G

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Mol	Chain	Res	Type
73	L5	3294	C
73	L5	3295	U
73	L5	3296	G
73	L5	3302	C
73	L5	3305	C
73	L5	3310	A
73	L5	3311	G
73	L5	3312	U
73	L5	3326	U
74	S7	9	G
74	S7	10	G
74	S7	14	A
74	S7	16	U
74	S7	17	U
74	S7	18	G
74	S7	20	U
74	S7	22	A
74	S7	23	G
74	S7	24	C
74	S7	25	G
74	S7	29	G
74	S7	31	G
74	S7	32	U
74	S7	33	C
74	S7	34	U
74	S7	35	C
74	S7	36	A
74	S7	37	U
74	S7	39	A
74	S7	41	C
74	S7	42	C
74	S7	46	G
74	S7	53	A
74	S7	54	G
74	S7	55	U
74	S7	56	U
74	S7	57	C
74	S7	58	G
74	S7	59	A
74	S7	64	C
74	S7	66	C
74	S7	68	U

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Mol	Chain	Res	Type
74	S7	69	U
74	S7	70	A
74	S7	72	C
74	S7	73	C
74	S7	74	A
75	S8	3	C
75	S8	4	G
75	S8	5	G
75	S8	6	G
75	S8	7	G
75	S8	8	U
75	S8	9	G
75	S8	10	G
75	S8	13	C
75	S8	14	A
75	S8	16	C
75	S8	17	C
75	S8	18	G
75	S8	19	G
75	S8	21	A
75	S8	24	U
75	S8	26	G
75	S8	32	C
75	S8	33	U
75	S8	34	C
75	S8	35	A
75	S8	37	A
75	S8	47	U
75	S8	48	C
75	S8	49	G
75	S8	52	G
75	S8	59	A
75	S8	60	U
75	S8	63	G
75	S8	67	C
75	S8	74	C
75	S8	76	A
76	S9	2	C
76	S9	7	A
76	S9	8	U
76	S9	10	G
76	S9	13	C

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Mol	Chain	Res	Type
76	S9	22	G
76	S9	24	G
76	S9	27	G
76	S9	36	U
76	S9	43	C
76	S9	44	G
76	S9	46	G
76	S9	49	C
76	S9	51	U
76	S9	52	G
76	S9	57	G
76	S9	60	U
76	S9	62	C
76	S9	63	G
76	S9	64	A
76	S9	65	G
76	S9	69	G
76	S9	70	G
76	S9	71	G
76	S9	74	C
76	S9	75	C
76	S9	76	A
77	S6	43	U
77	S6	44	U

All (55) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	S1	133	C
31	S1	135	A
31	S1	249	C
31	S1	476	U
31	S1	526	G
31	S1	679	A
31	S1	694	U
31	S1	922	G
31	S1	978	G
31	S1	989	G
31	S1	1269	A
31	S1	1500	G
31	S1	1505	A
31	S1	1690	A

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Mol	Chain	Res	Type
71	L3	26	U
71	L3	50	A
71	L3	71	G
71	L3	106	U
72	L4	123	C
73	L5	117	G
73	L5	313	U
73	L5	515	G
73	L5	632	U
73	L5	642	A
73	L5	725	U
73	L5	748	A
73	L5	782	U
73	L5	925	G
73	L5	1088	G
73	L5	1735	A
73	L5	1742	U
73	L5	1744	C
73	L5	1885	A
73	L5	1934	G
73	L5	2095	C
73	L5	2106	A
73	L5	2111	A
73	L5	2200	A
73	L5	2218	U
73	L5	2234	U
73	L5	2265	G
73	L5	2277	C
73	L5	2302	A
73	L5	2614	A
73	L5	2650	G
73	L5	2748	G
73	L5	3097	U
73	L5	3191	A
73	L5	3194	C
73	L5	3266	C
74	S7	33	C
75	S8	3	C
75	S8	32	C
75	S8	34	C
76	S9	51	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 136 ligands modelled in this entry, 136 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

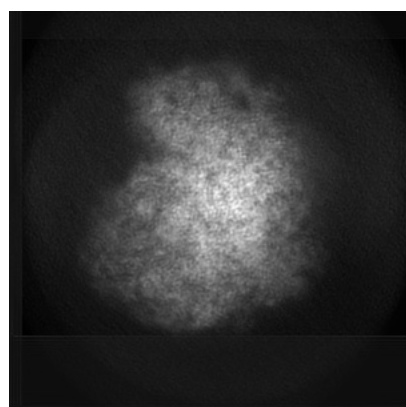
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73602. These allow visual inspection of the internal detail of the map and identification of artifacts.

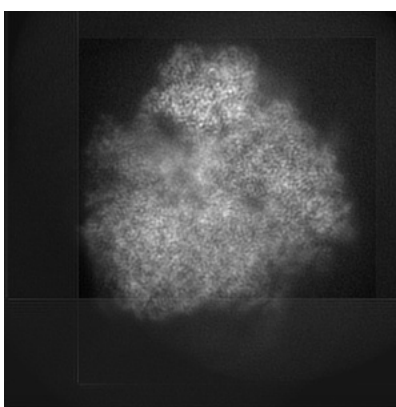
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

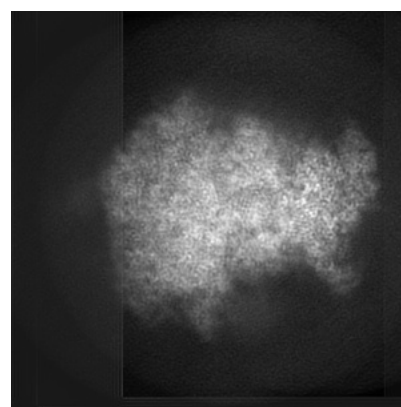
6.1.1 Primary map



X



Y

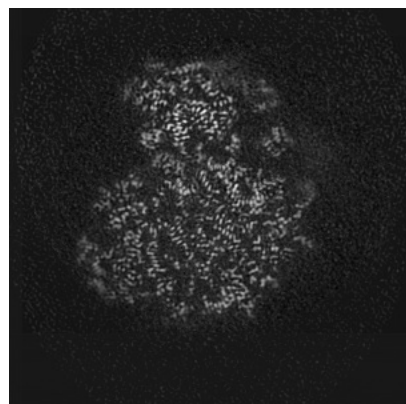


Z

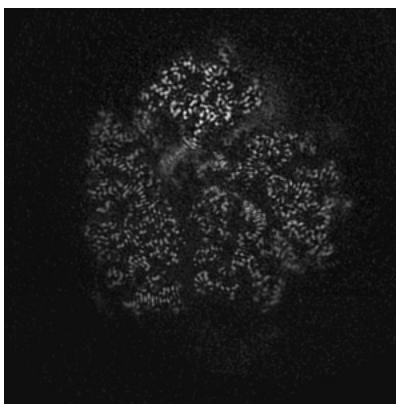
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

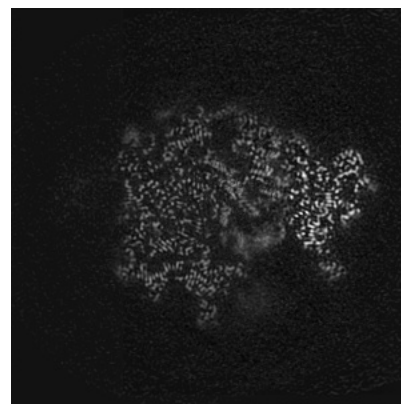
6.2.1 Primary map



X Index: 224



Y Index: 224

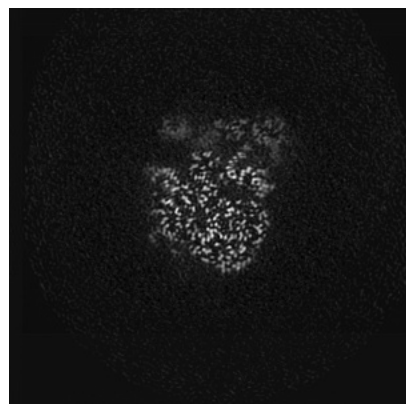


Z Index: 224

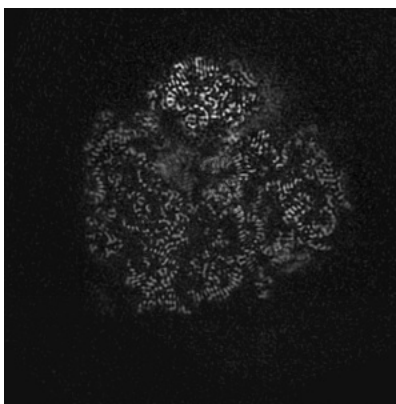
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

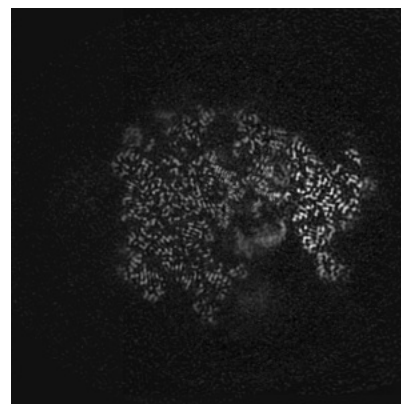
6.3.1 Primary map



X Index: 340



Y Index: 216

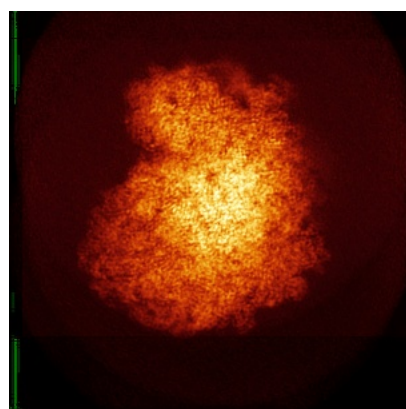


Z Index: 227

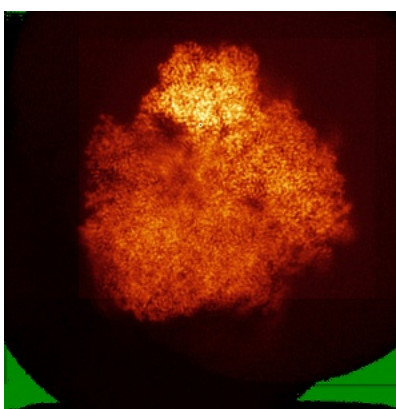
The images above show the largest variance slices of the map in three orthogonal directions.

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

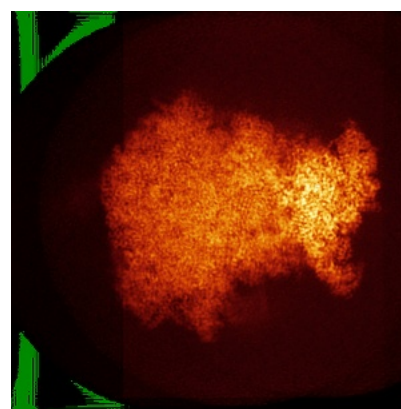
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

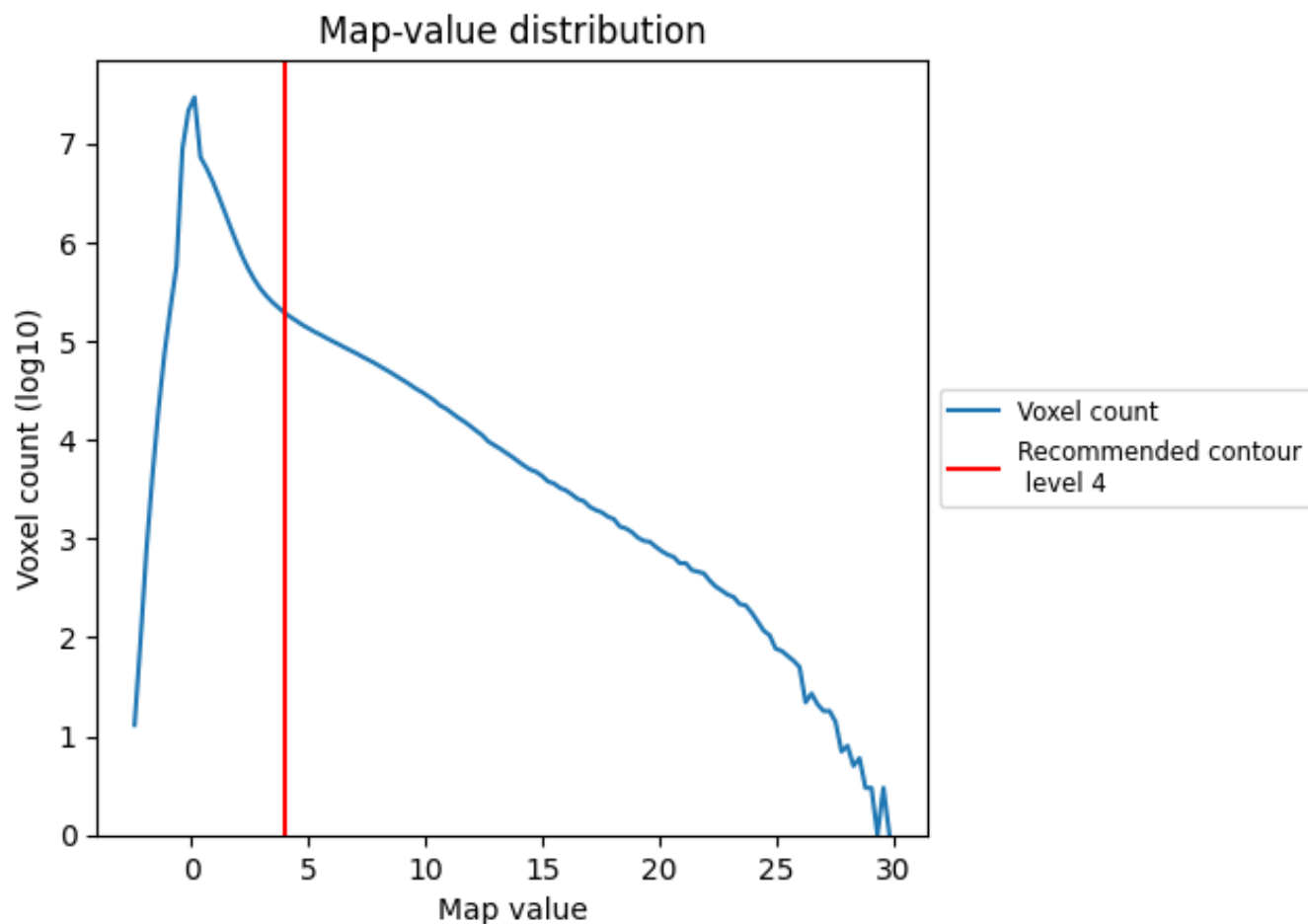
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

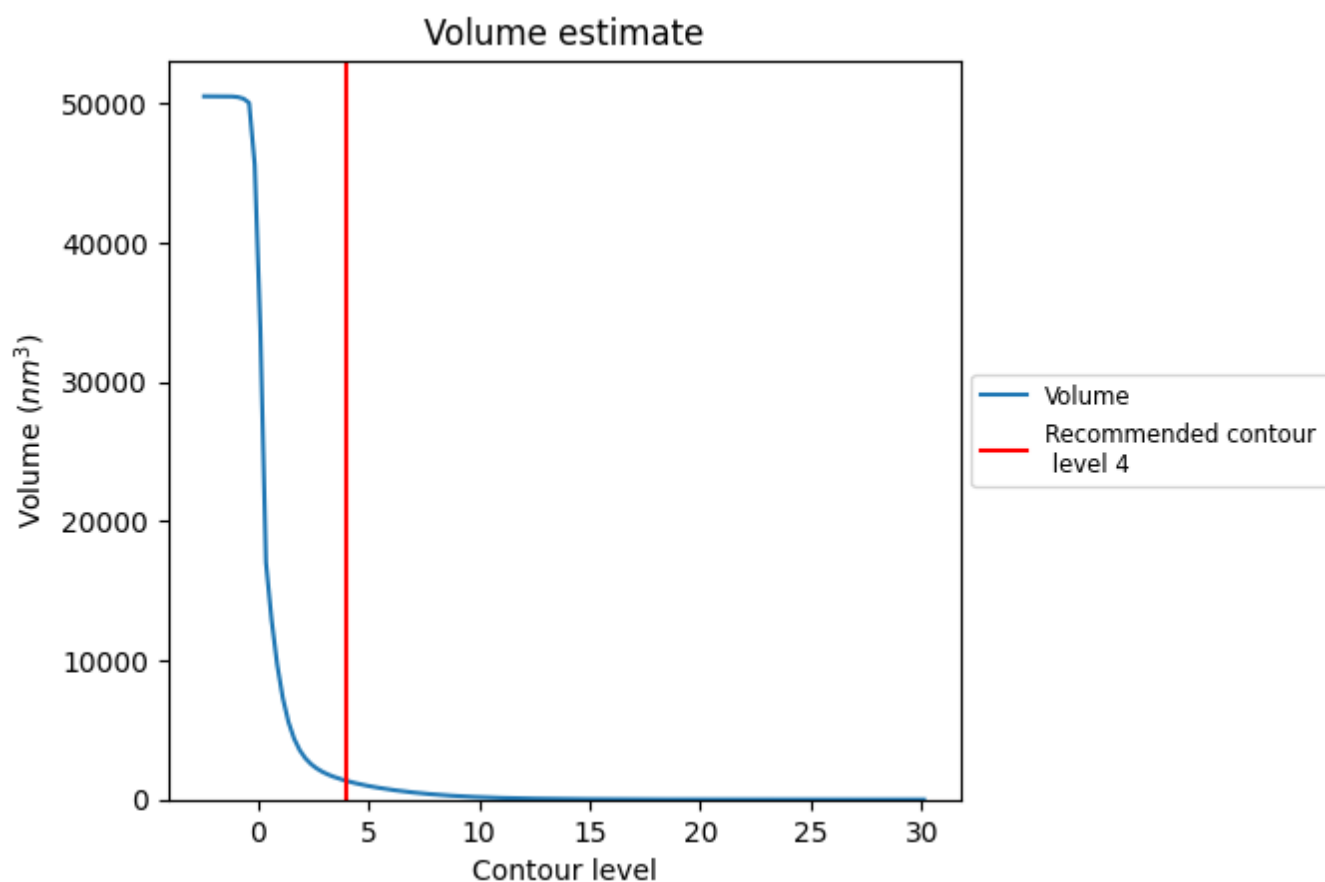
This section contains the results of statistical analysis of the map.

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.

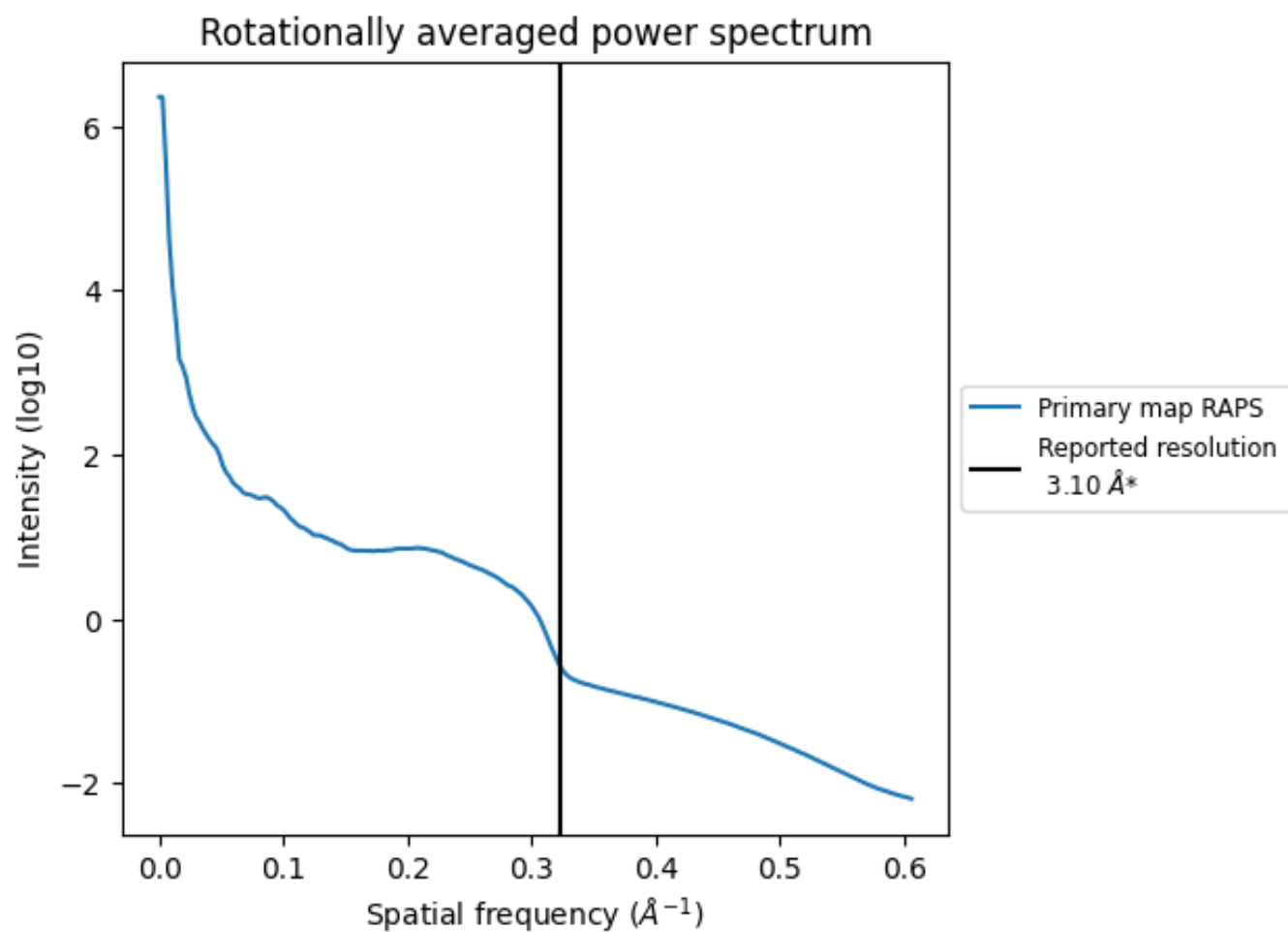
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1345 nm³; this corresponds to an approximate mass of 1215 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 0.323 Å⁻¹

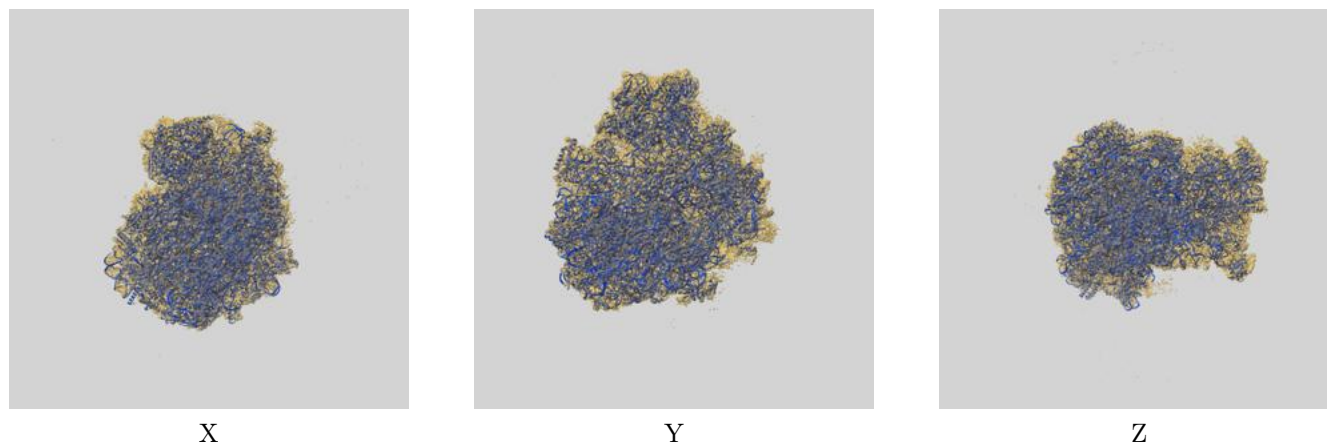
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

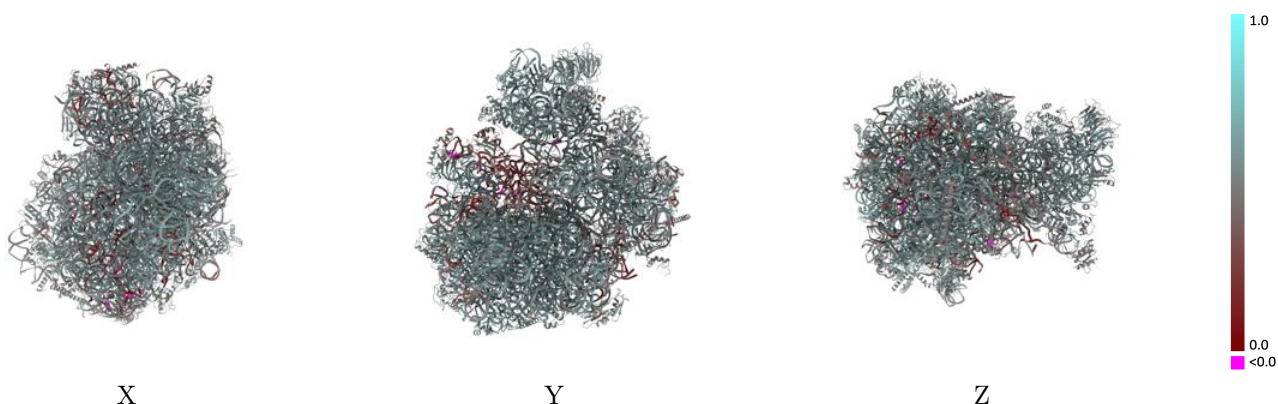
This section contains information regarding the fit between EMDB map EMD-73602 and PDB model 9YXB. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



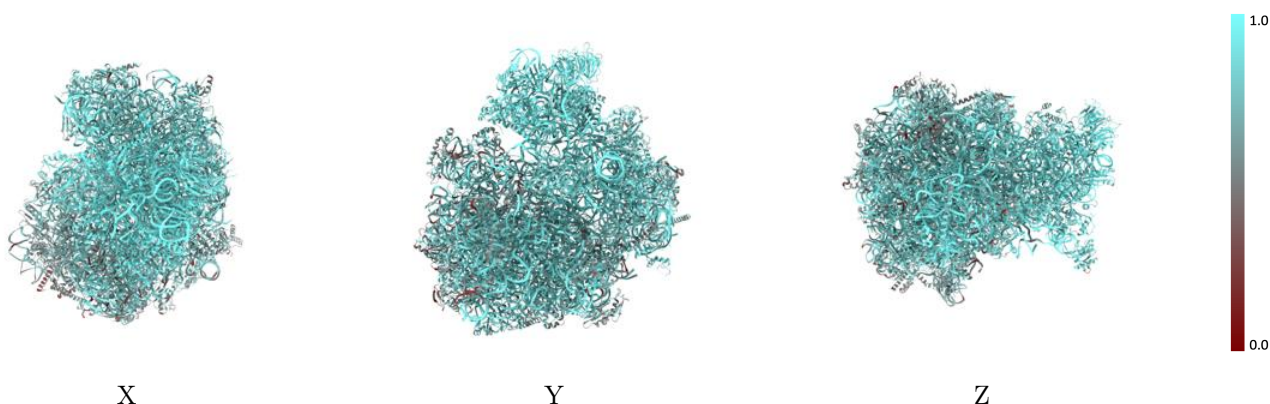
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



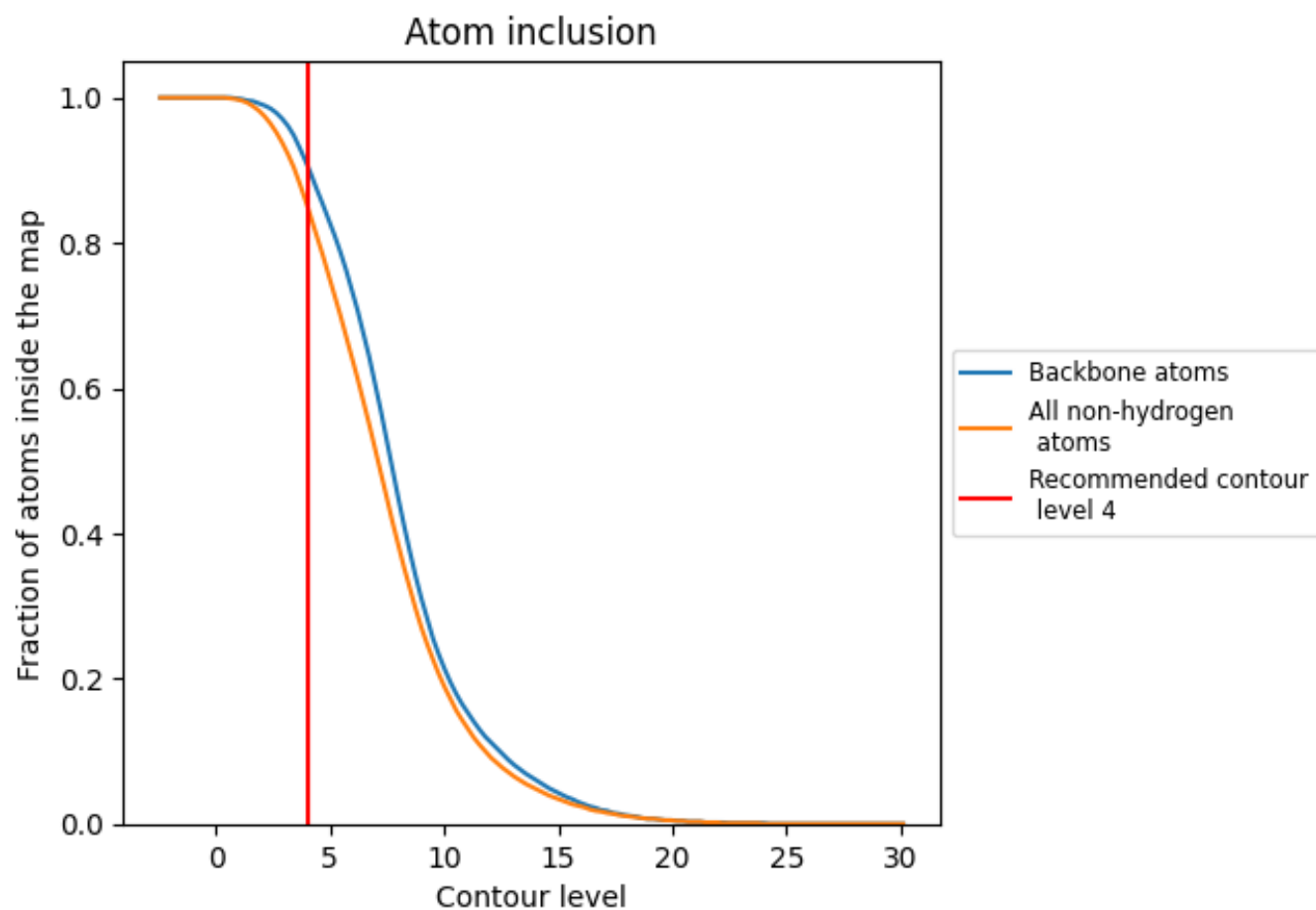
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 85% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8520	 0.5240
L3	 0.8390	 0.4830
L4	 0.9180	 0.5610
L5	 0.8700	 0.5180
LB	 0.8420	 0.5540
LC	 0.8100	 0.5730
LD	 0.6210	 0.5390
LE	 0.7170	 0.4680
LF	 0.6560	 0.5330
LG	 0.5440	 0.5120
LH	 0.6590	 0.5370
LI	 0.7490	 0.5600
LJ	 0.7490	 0.5540
LK	 0.8100	 0.5310
LL	 0.6300	 0.5360
LM	 0.8090	 0.5800
LN	 0.8300	 0.5830
LO	 0.7120	 0.5390
LP	 0.6650	 0.4930
LQ	 0.7590	 0.5640
LR	 0.7350	 0.5360
LS	 0.6920	 0.5500
LT	 0.7110	 0.5520
LU	 0.7490	 0.5640
LV	 0.6130	 0.4900
LW	 0.7230	 0.5490
LX	 0.7640	 0.5600
LY	 0.8000	 0.5430
LZ	 0.6390	 0.5390
La	 0.6850	 0.5400
Lb	 0.7770	 0.5610
Lc	 0.7160	 0.5530
Ld	 0.7440	 0.5150
Le	 0.7940	 0.5700
Lf	 0.7590	 0.5690















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Chain	Atom inclusion	Q-score
Lg	 0.7990	 0.5750
Lh	 0.7980	 0.5760
Li	 0.7300	 0.5490
Lj	 0.8500	 0.5810
Lk	 0.6690	 0.5330
Ll	 0.7850	 0.5710
Lm	 0.6730	 0.5380
Ln	 0.8910	 0.5520
Lo	 0.7850	 0.5760
Lp	 0.8640	 0.5370
S1	 0.9550	 0.5270
S6	 1.0000	 0.4930
S7	 0.8950	 0.2840
S8	 0.6840	 0.2440
S9	 0.9120	 0.3180
SA	 0.8320	 0.5280
SB	 0.8000	 0.4920
SC	 0.9420	 0.5290
SD	 0.8350	 0.4890
SE	 0.8290	 0.5250
SF	 0.9260	 0.5390
SG	 0.7980	 0.5080
SH	 0.9680	 0.5620
SI	 0.7200	 0.5110
SJ	 0.8730	 0.5490
SK	 0.8850	 0.5450
SL	 0.9700	 0.5700
SM	 0.9300	 0.5290
SN	 0.9570	 0.5410
SO	 0.8730	 0.5310
SP	 0.8670	 0.5530
SQ	 0.8260	 0.4760
SR	 0.9530	 0.5520
SS	 0.9920	 0.5820
ST	 0.8580	 0.5430
SU	 0.8840	 0.5620
SV	 0.9310	 0.5210
SW	 0.9350	 0.5500
SX	 0.9590	 0.5640
SY	 0.7910	 0.5260
SZ	 0.8100	 0.4960
Sa	 0.9360	 0.5490

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Chain	Atom inclusion	Q-score
Sb	 0.9400	 0.5570
Sc	 0.8280	 0.5310
Sd	 0.9630	 0.5740
Se	 0.8120	 0.4830
Sf	 0.8500	 0.5060
Sg	 0.9100	 0.5300