Full wwPDB EM Validation Report

Apr 23, 2024 – 06:11 PM EDT

PDB ID	:	8VS9
EMDB ID	:	EMD-43490
Title	:	Endogenous trans-translation complex with tmRNA*SmpB in the P site and alanyl-tRNA in the A site and deacyl-tRNA in the E site of E. coli 70S ribosome
Authors	:	Teran, D.; Zhang, Y.; Korostelev, A.A.
Deposited on	:	2024-01-23
Resolution	:	3.90 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

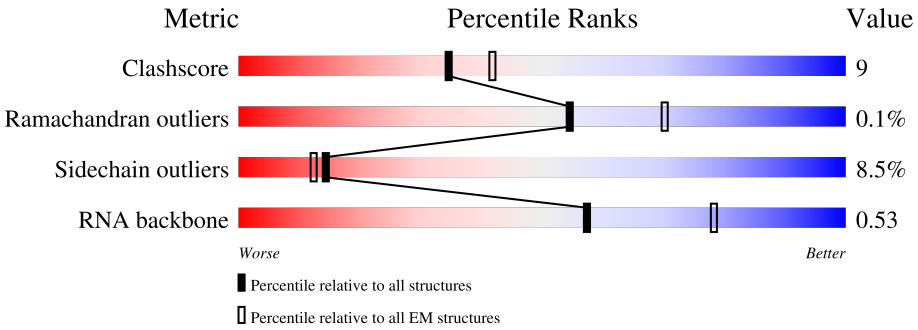
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 3.90 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	16S	1539	58% 36% 6%
2	23S	2903	55% 38% 7%
3	5S	120	53% 39% 8%
4	ATRN	76	76% 24%
5	ETRN	77	69% 31%
6	L02	273	73% 24%
7	L03	209	74% 23%

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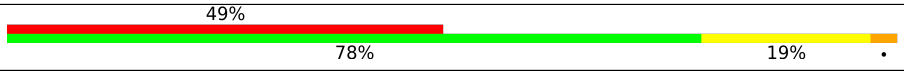
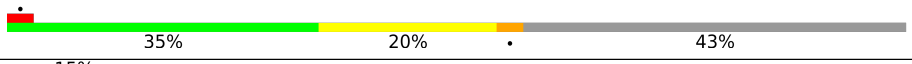
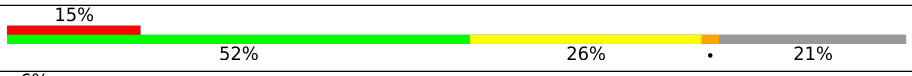
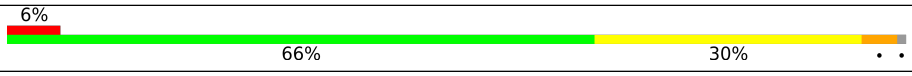
Mol	Chain	Length	Quality of chain
8	L04	201	
9	L05	179	
10	L06	177	
11	L09	149	
12	L1	234	
13	L10	165	
14	L11	142	
15	L13	142	
16	L14	123	
17	L15	144	
18	L16	136	
19	L17	127	
20	L18	117	
21	L19	115	
22	L20	118	
23	L21	103	
24	L22	110	
25	L23	100	
26	L24	104	
27	L25	94	
28	L27	85	
29	L28	78	
30	L29	63	
31	L30	59	
32	L31	45	

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Mol	Chain	Length	Quality of chain
33	L32	57	74% 19% 5%
34	L33	55	71% 16% 9%
35	L34	46	72% 26%
36	L35	65	71% 26%
37	L36	38	74% 24%
38	S02	241	74% 17% 7%
39	S03	233	63% 24% 12%
40	S04	206	63% 33%
41	S05	167	76% 16% 6%
42	S06	135	46% 24% 26%
43	S07	179	60% 23% 16%
44	S08	130	71% 24% 5%
45	S09	130	57% 36% 5%
46	S10	103	61% 32% 5%
47	S11	129	64% 24% 10%
48	S12	124	68% 28%
49	S13	118	68% 26%
50	S14	101	65% 33%
51	S15	89	69% 30%
52	S16	82	65% 33%
53	S17	84	63% 25% 7% 5%
54	S18	75	64% 20% 13%
55	S19	92	60% 22% 14%
56	S20	87	76% 22%
57	S21	71	58% 28% 6% 8%

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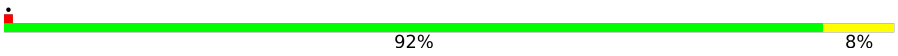
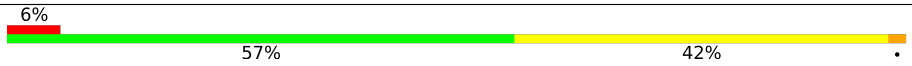
Mol	Chain	Length	Quality of chain
58	SMPB	150	
59	TMRN	363	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 157472 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	16S	1539	33012	14725	6052	10697	1538	0	0

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	23S	2903	62317	27801	11468	20146	2902	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
23S	747	C	U	variant	GB 1036415628

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	5S	120	2568	1145	471	833	119	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5S	120	A	U	conflict	GB 1370526515

- Molecule 4 is a RNA chain called A-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	ATRN	76	1621	722	289	534	76	0	0

- Molecule 5 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	ETRN	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L02	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L03	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 8 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L04	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 9 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L05	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L06	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 11 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 12 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L1	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 13 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L10	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 14 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L13	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L14	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L15	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L16	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 19 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L17	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	L18	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L19	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	L20	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 23 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L21	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L22	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	L23	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	L24	102	Total 779	C 492	N 146	O 141	0	0

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L25	94	Total 753	C 479	N 137	O 134	S 3	0	0

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L27	75	Total 575	C 356	N 116	O 102	S 1	0	0

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L28	77	Total 625	C 388	N 129	O 106	S 2	0	0

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L29	63	Total 509	C 313	N 99	O 95	S 2	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L30	58	Total 449	C 281	N 87	O 79	S 2	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	L31	45	Total 351	C 219	N 61	O 65	S 6	0	0

- Molecule 33 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L32	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 34 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	L33	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 35 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L34	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 36 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L35	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L36	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	S02	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	S03	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S04	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S05	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 42 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S06	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S07	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	S08	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 45 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	S09	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S10	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S11	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S12	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S13	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 50 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S14	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 51 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S15	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 52 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S16	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 53 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S17	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S18	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S19	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S20	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 57 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S21	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 58 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SMPB	150	Total	C	N	O	S	0	0
			1209	763	226	216	4		

- Molecule 59 is a RNA chain called TMRN.

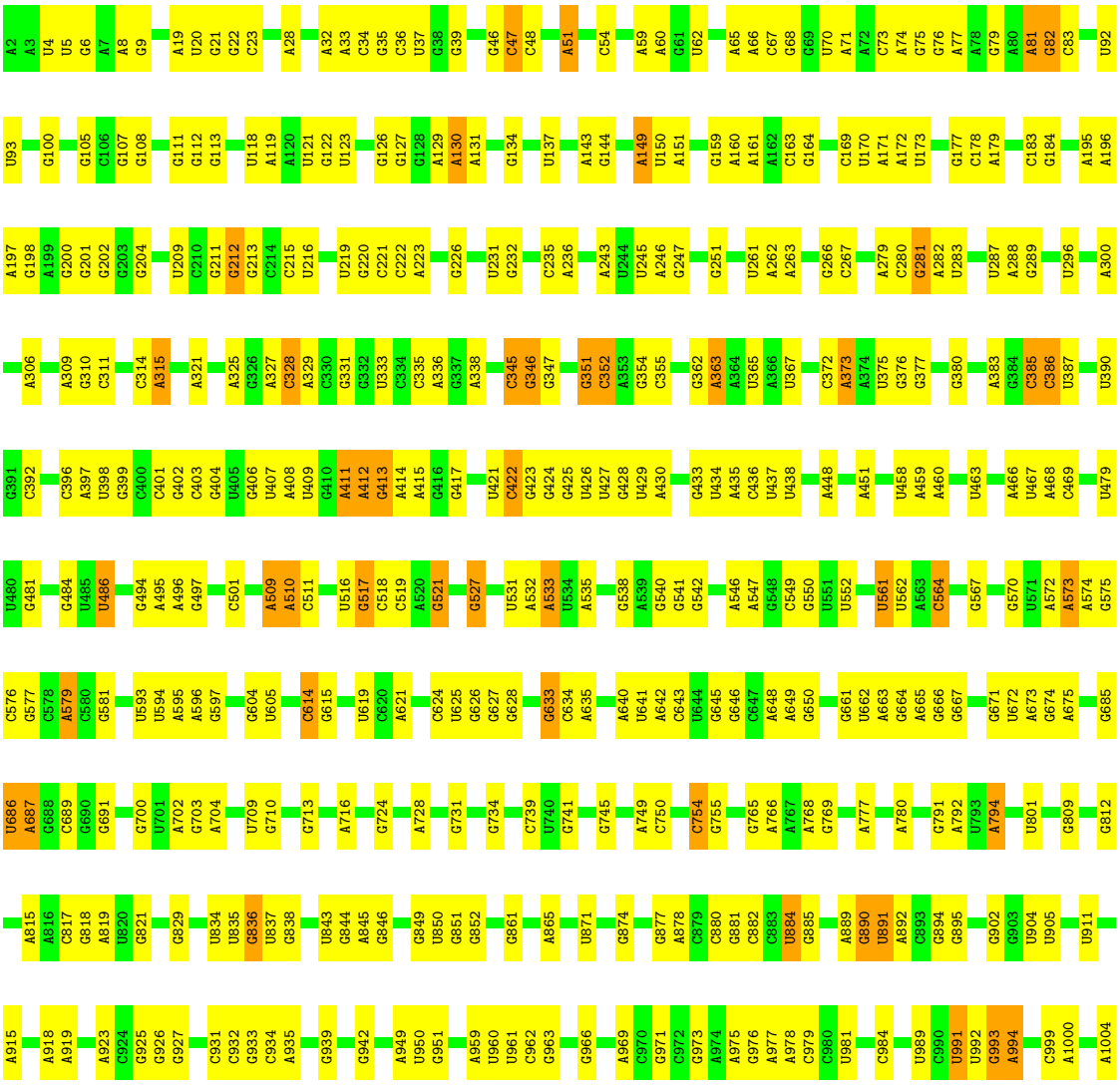
Mol	Chain	Residues	Atoms					AltConf	Trace
59	TMRN	363	Total	C	N	O	P	0	0
			7758	3465	1410	2520	363		

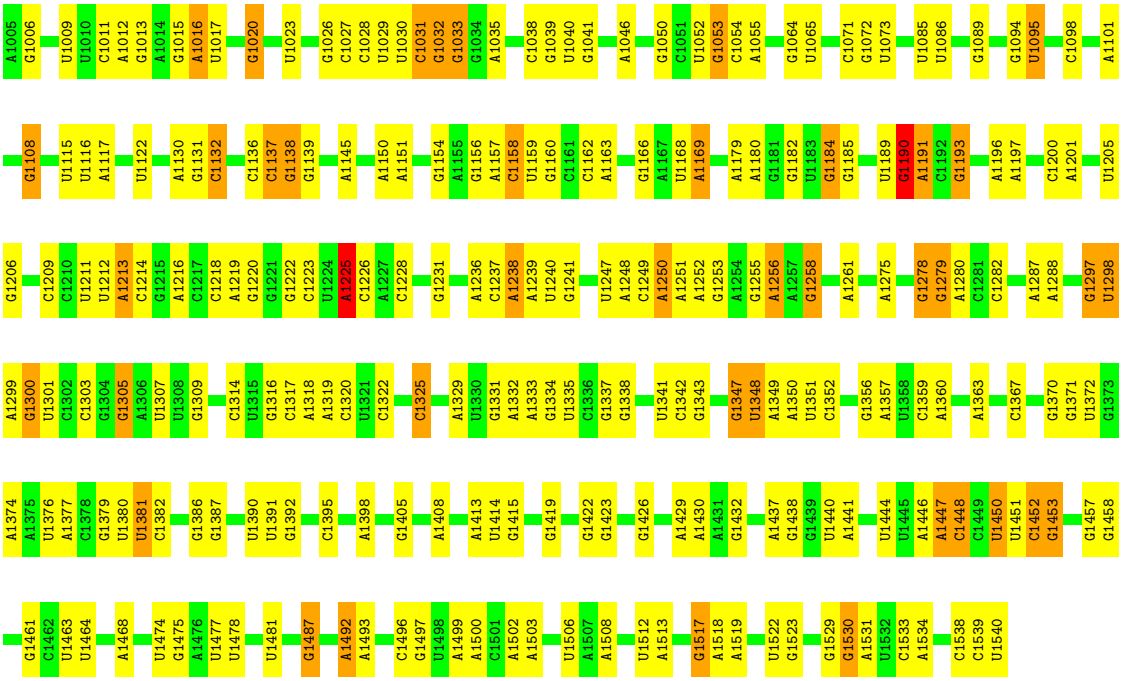
3 Residue-property plots (i)

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: 16S ribosomal RNA

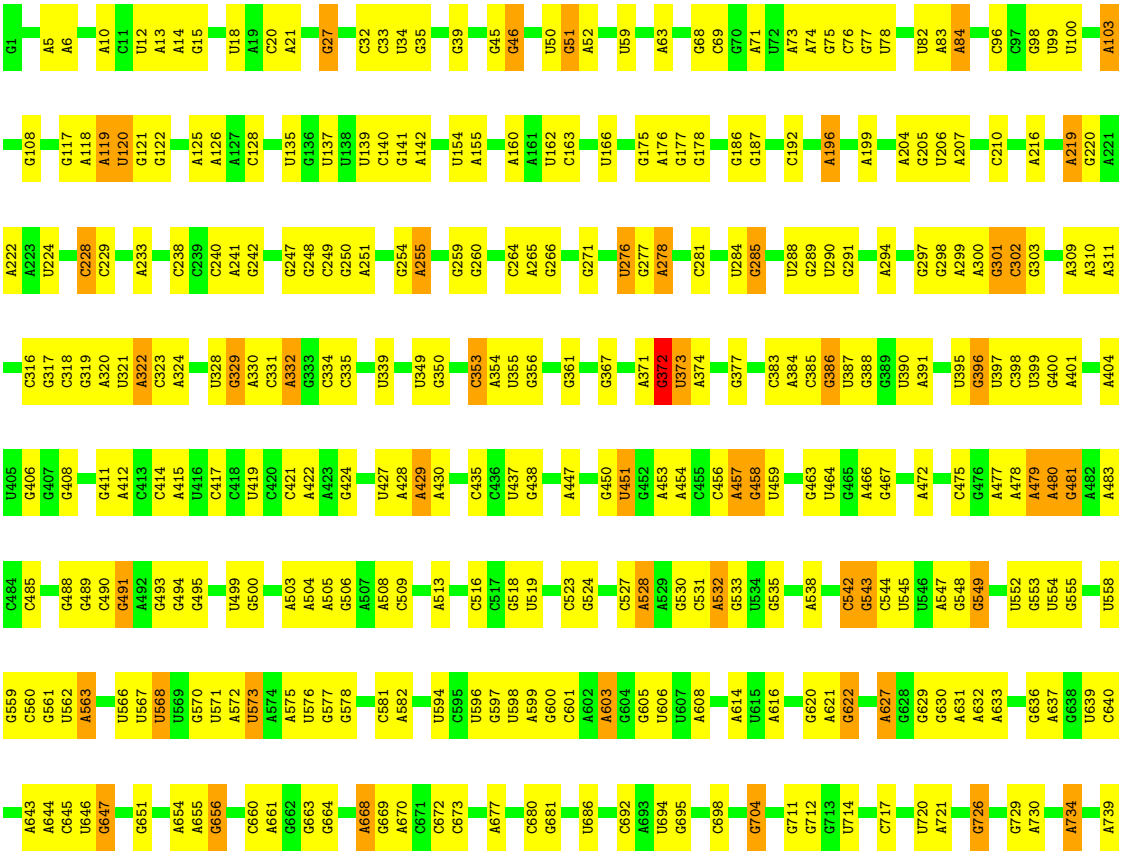
Chain 16S:

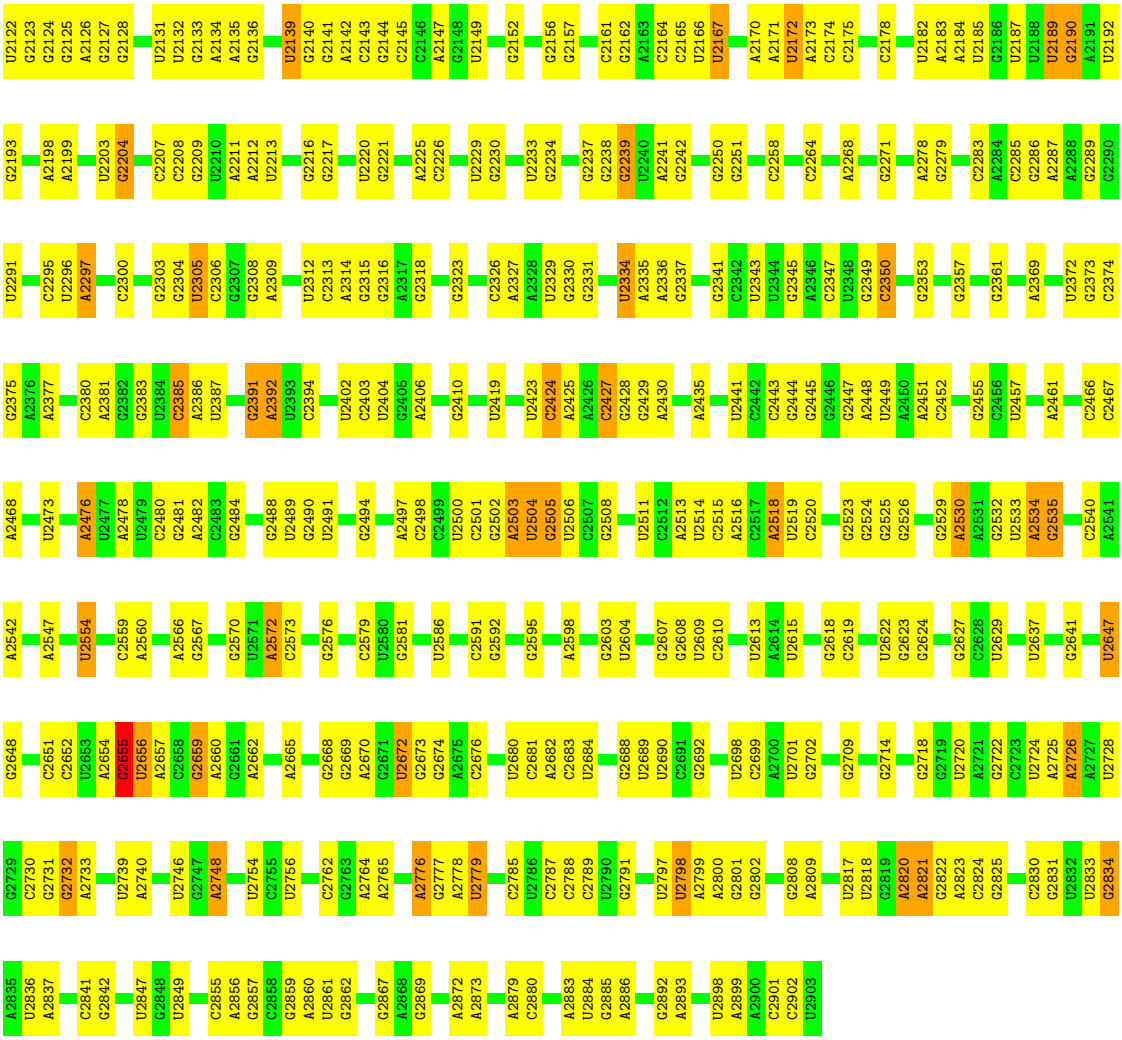




• Molecule 2: 23S ribosomal RNA

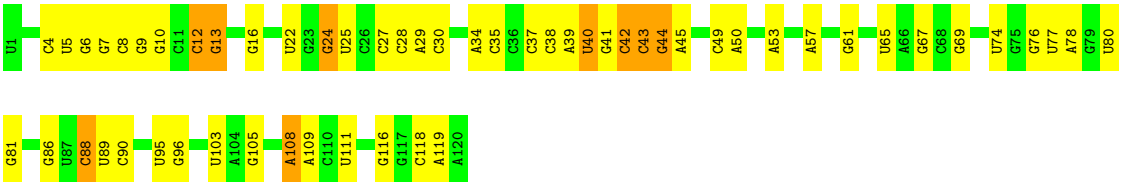
Chain 23S:





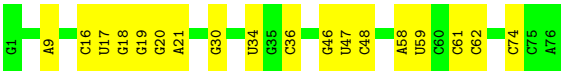
• Molecule 3: 5S ribosomal RNA

Chain 5S:



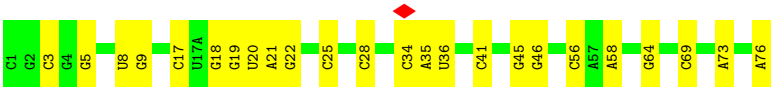
• Molecule 4: A-tRNA

Chain ATRN:



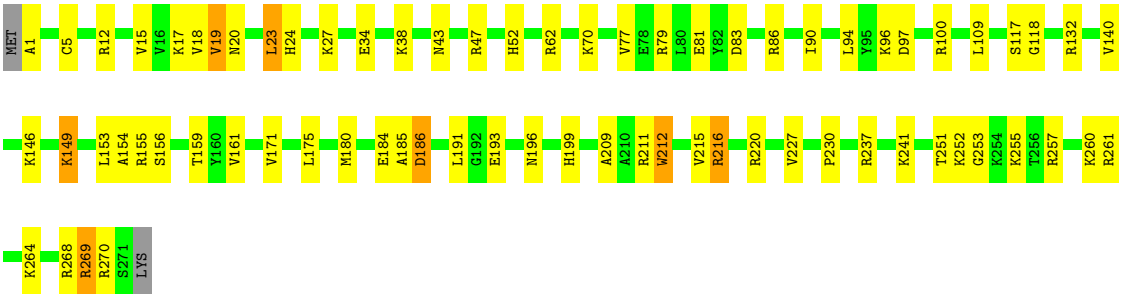
• Molecule 5: E-tRNA

Chain ETRN:



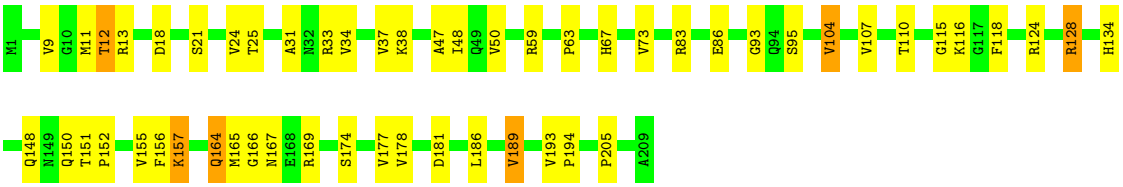
• Molecule 6: 50S ribosomal protein L2

Chain L02:



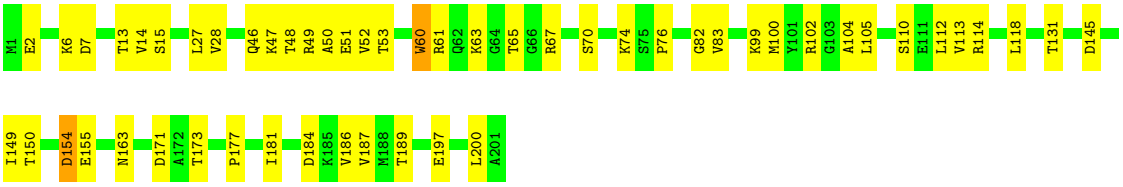
• Molecule 7: 50S ribosomal protein L3

Chain L03:



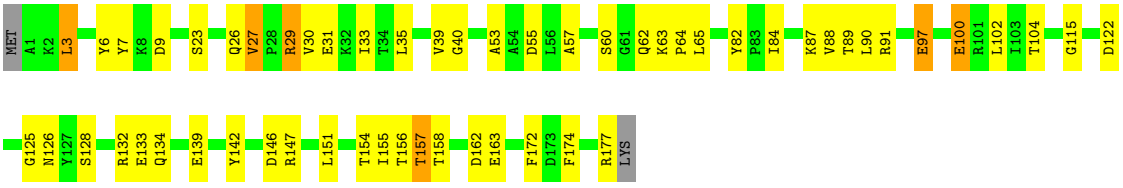
• Molecule 8: 50S ribosomal protein L4

Chain L04:



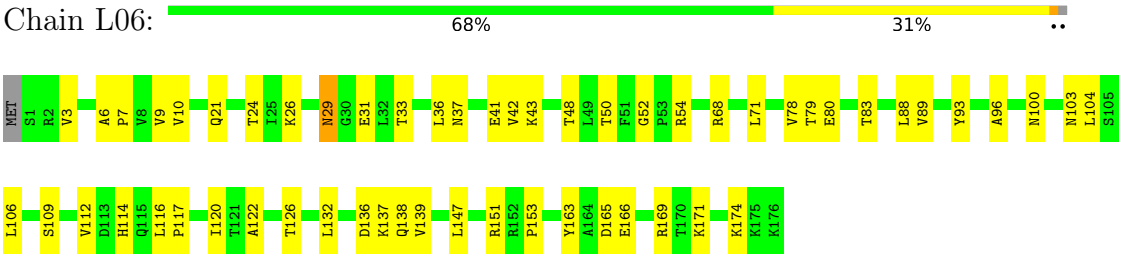
• Molecule 9: 50S ribosomal protein L5

Chain L05:



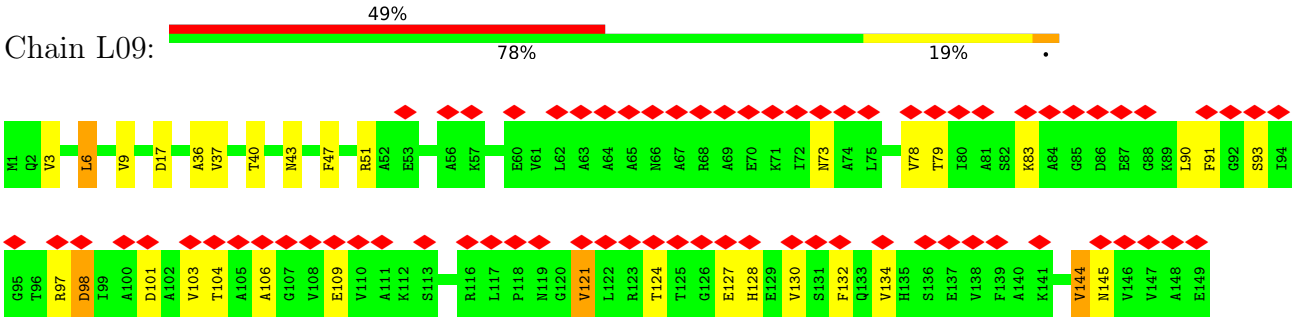
• Molecule 10: 50S ribosomal protein L6

Chain L06:



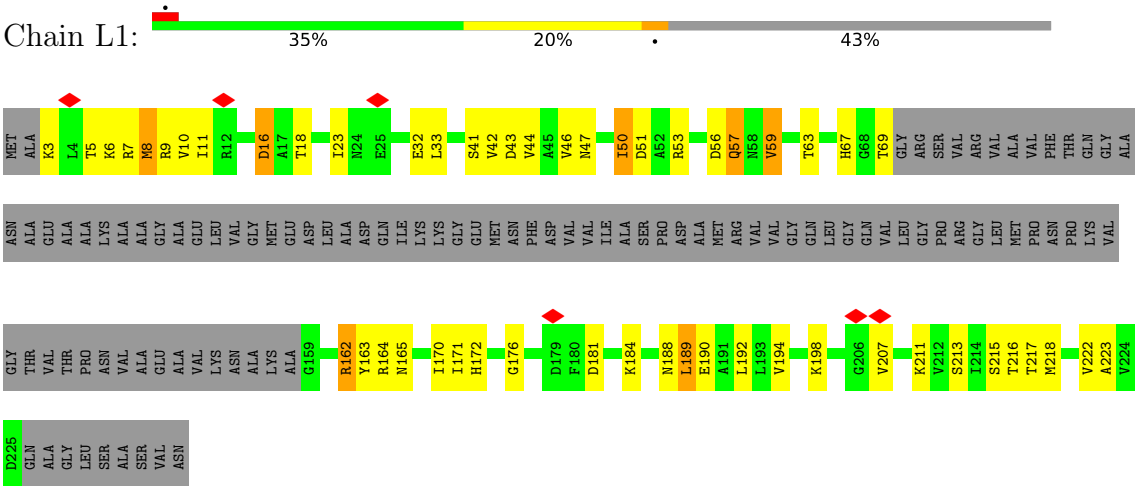
• Molecule 11: Large ribosomal subunit protein bL9

Chain L09:



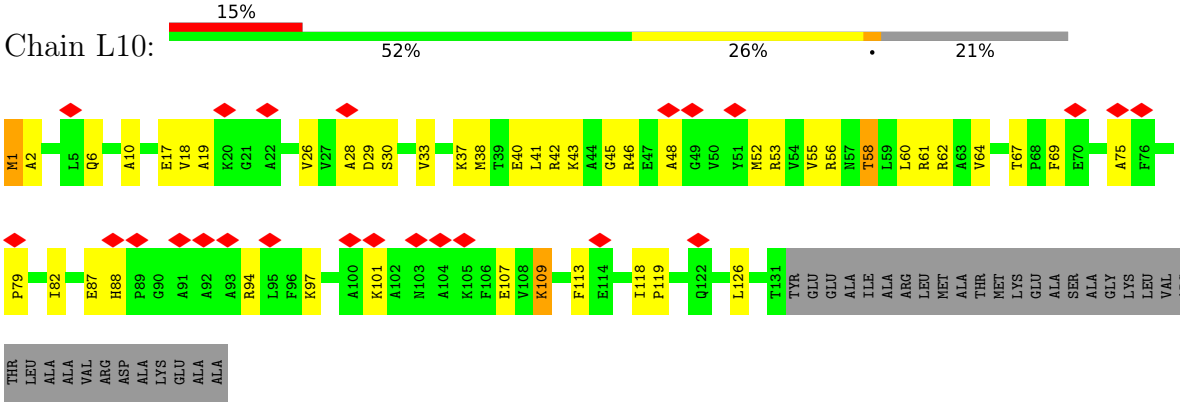
• Molecule 12: 50S ribosomal protein L1

Chain L1:



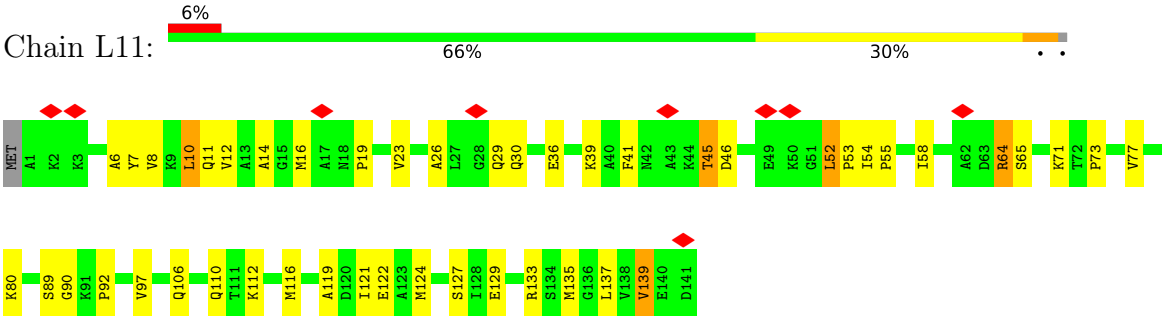
• Molecule 13: 50S ribosomal protein L10

Chain L10:



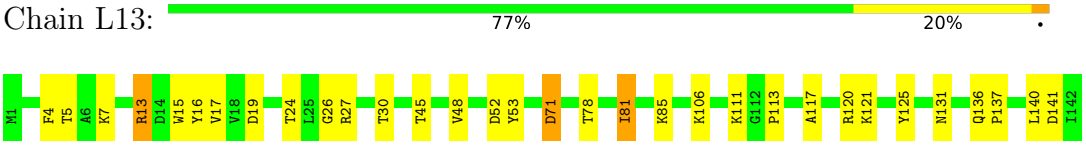
• Molecule 14: 50S ribosomal protein L11

Chain L11:



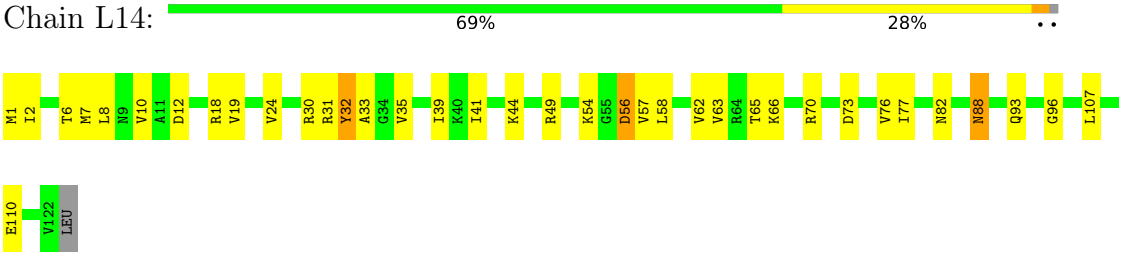
• Molecule 15: 50S ribosomal protein L13

Chain L13:



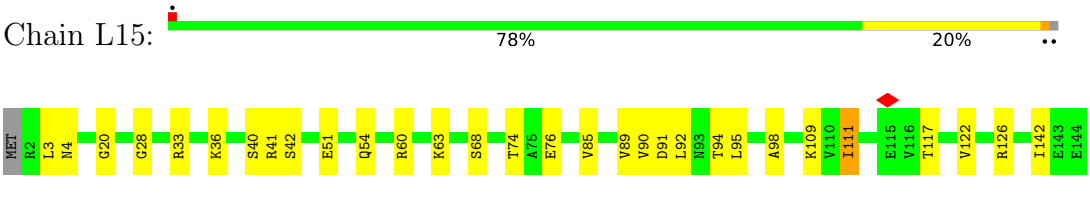
• Molecule 16: 50S ribosomal protein L14

Chain L14:



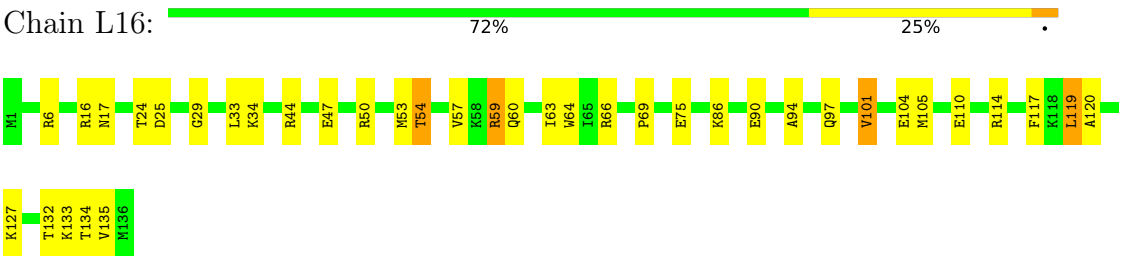
• Molecule 17: 50S ribosomal protein L15

Chain L15:



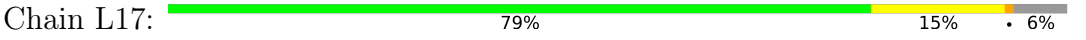
• Molecule 18: 50S ribosomal protein L16

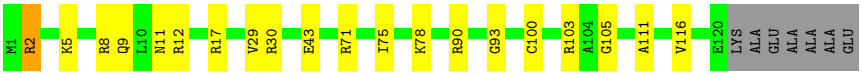
Chain L16:



• Molecule 19: Large ribosomal subunit protein bL17

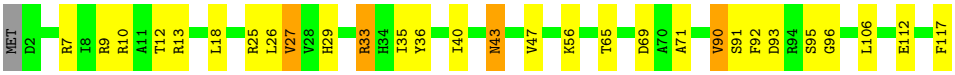
Chain L17:





• Molecule 20: 50S ribosomal protein L18

Chain L18:



• Molecule 21: 50S ribosomal protein L19

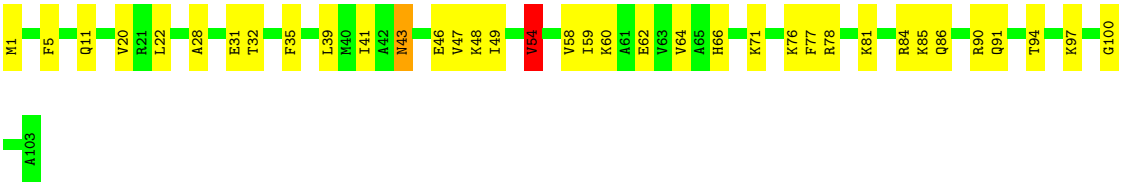
Chain L19:

• Molecule 22: 50S ribosomal protein L20

Chain L20:

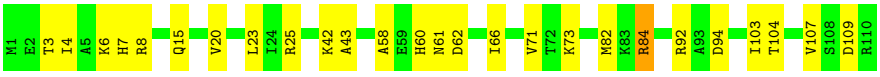
• Molecule 23: Ribosomal protein L21

Chain L21:



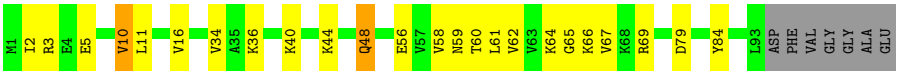
• Molecule 24: 50S ribosomal protein L22

Chain L22:



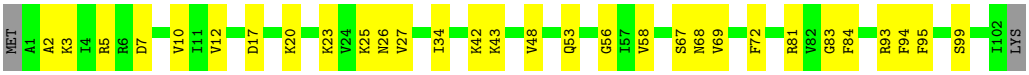
• Molecule 25: 50S ribosomal protein L23

Chain L23:



• Molecule 26: 50S ribosomal protein L24

Chain L24:

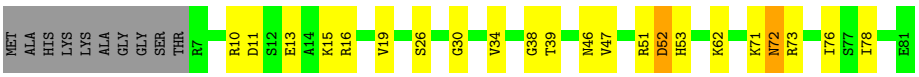


• Molecule 27: 50S ribosomal protein L25

Chain L25:

• Molecule 28: 50S ribosomal protein L27

Chain L27:



• Molecule 29: 50S ribosomal protein L28

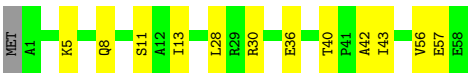
Chain L28:

• Molecule 30: 50S ribosomal protein L29

Chain L29:

• Molecule 31: Large ribosomal subunit protein uL30

Chain L30:

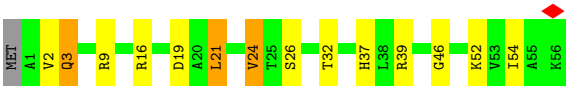


• Molecule 32: Large ribosomal subunit protein bL31

Chain L31:

• Molecule 33: 50S ribosomal protein L32

Chain L32:

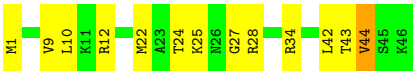


• Molecule 34: Large ribosomal subunit protein bL33

Chain L33:

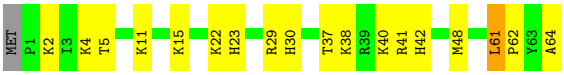
• Molecule 35: 50S ribosomal protein L34

Chain L34:



• Molecule 36: 50S ribosomal protein L35

Chain L35:

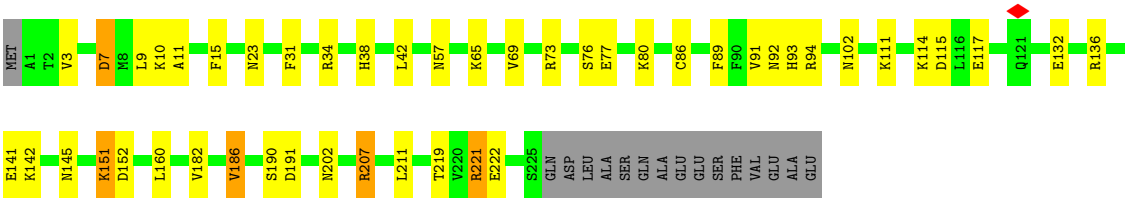


• Molecule 37: 50S ribosomal protein L36

Chain L36:

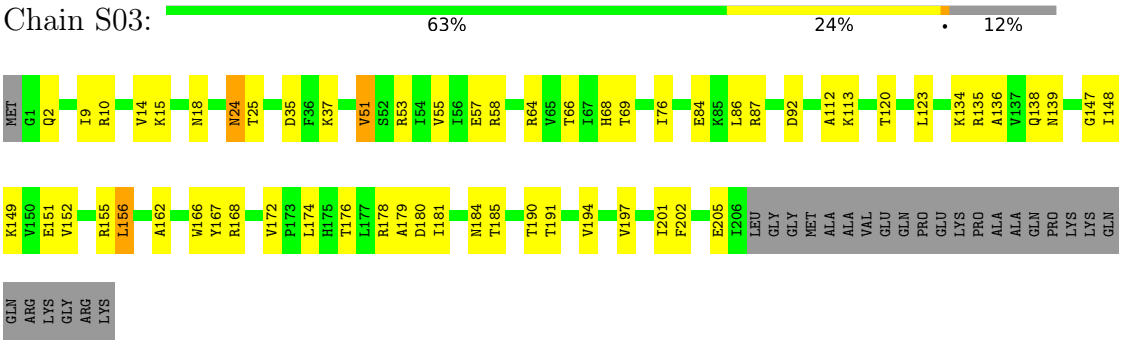
• Molecule 38: 30S ribosomal protein S2

Chain S02:



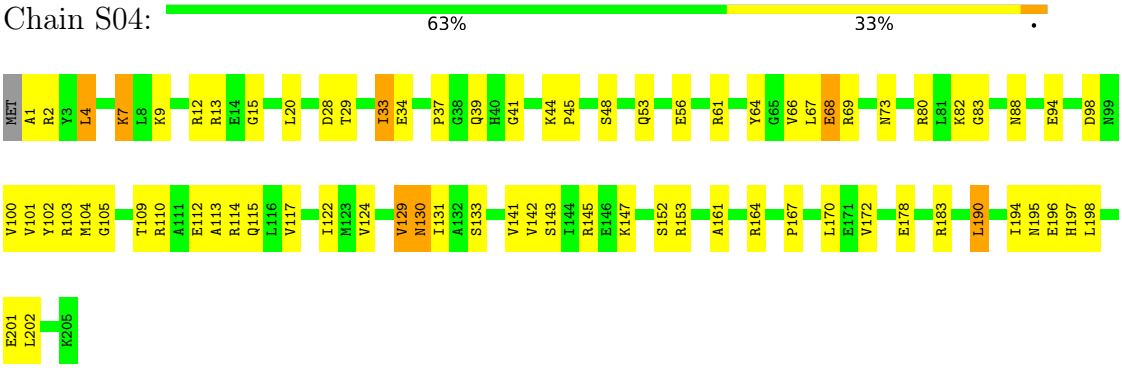
• Molecule 39: 30S ribosomal protein S3

Chain S03:



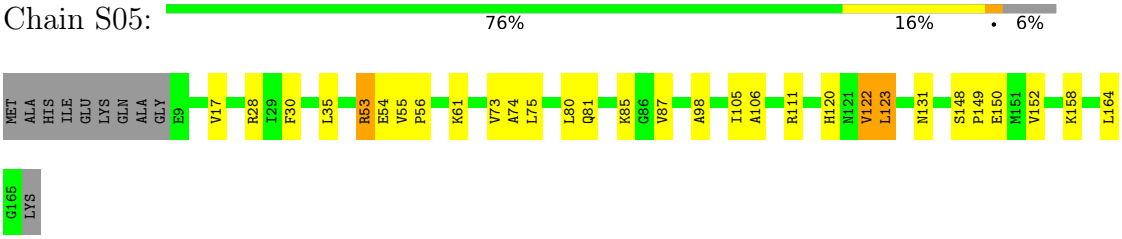
• Molecule 40: 30S ribosomal protein S4

Chain S04:



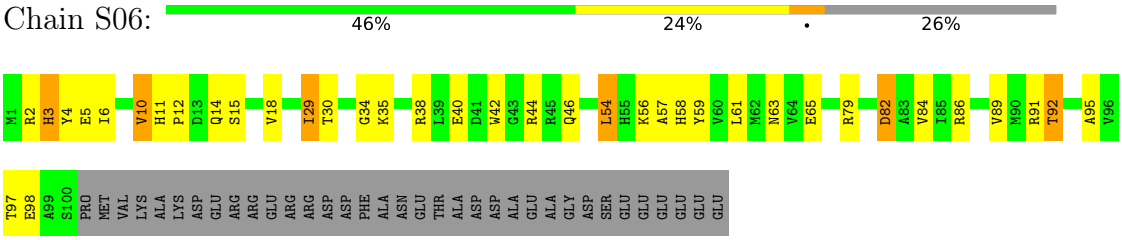
• Molecule 41: 30S ribosomal protein S5

Chain S05:



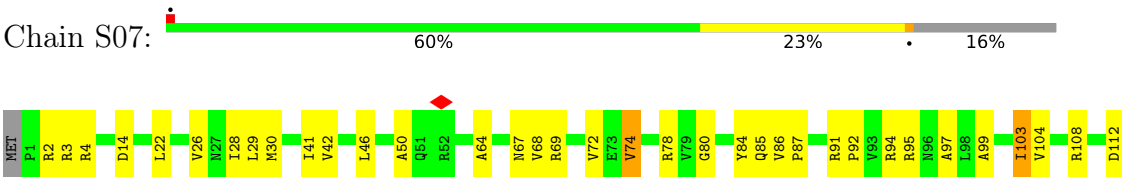
• Molecule 42: 30S ribosomal protein S6

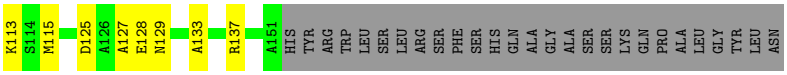
Chain S06:



• Molecule 43: 30S ribosomal protein S7

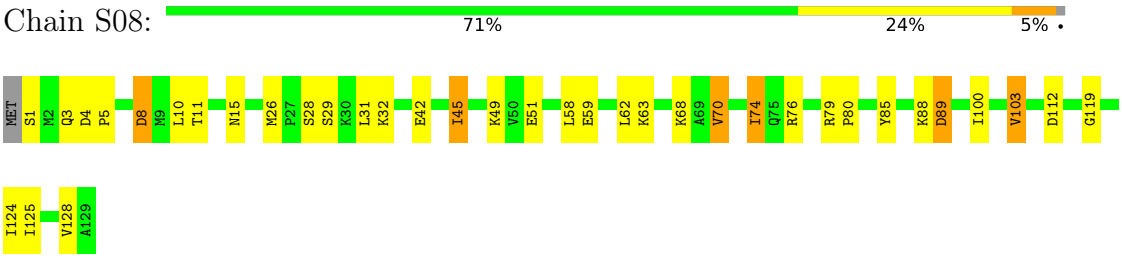
Chain S07:





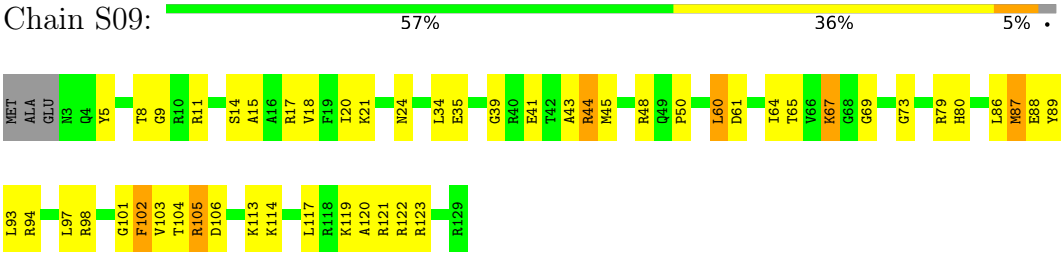
• Molecule 44: 30S ribosomal protein S8

Chain S08:



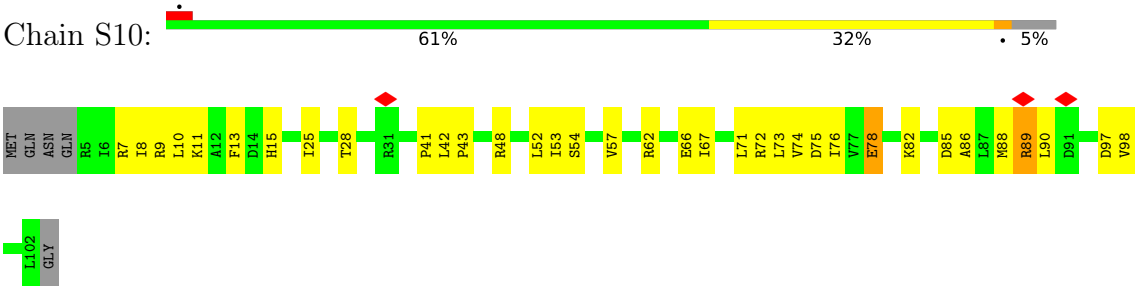
• Molecule 45: Small ribosomal subunit protein uS9

Chain S09:



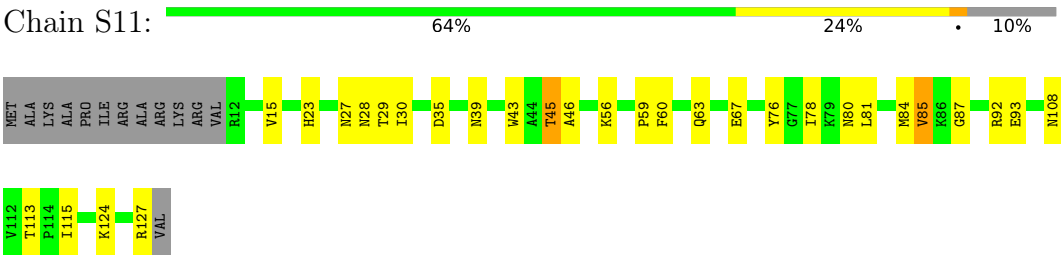
• Molecule 46: 30S ribosomal protein S10

Chain S10:



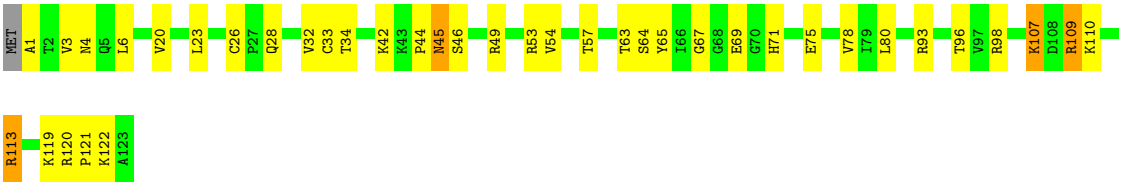
• Molecule 47: 30S ribosomal protein S11

Chain S11:



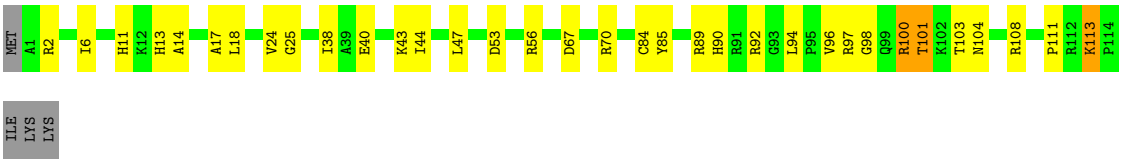
• Molecule 48: 30S ribosomal protein S12

Chain S12:



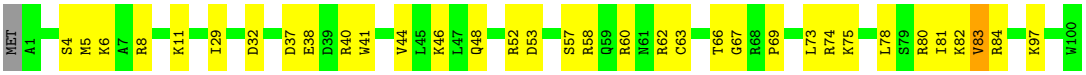
• Molecule 49: 30S ribosomal protein S13

Chain S13:



• Molecule 50: Small ribosomal subunit protein uS14

Chain S14:

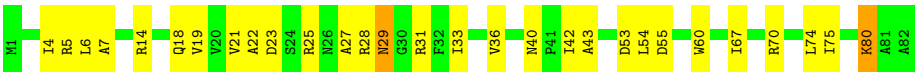


• Molecule 51: Small ribosomal subunit protein uS15

Chain S15:

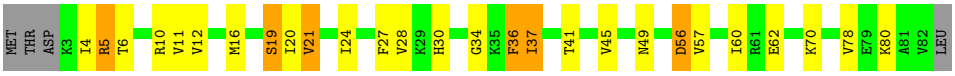
• Molecule 52: 30S ribosomal protein S16

Chain S16:



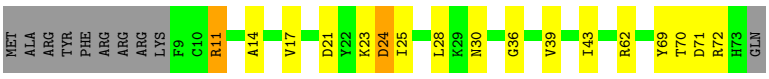
• Molecule 53: Small ribosomal subunit protein uS17

Chain S17:



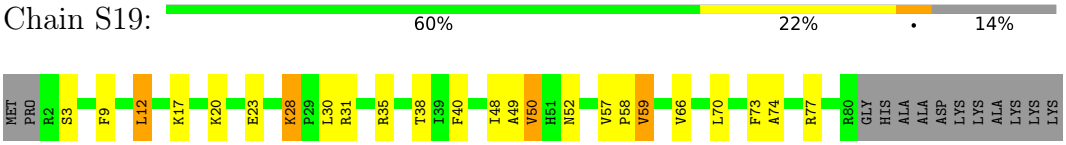
• Molecule 54: 30S ribosomal protein S18

Chain S18:



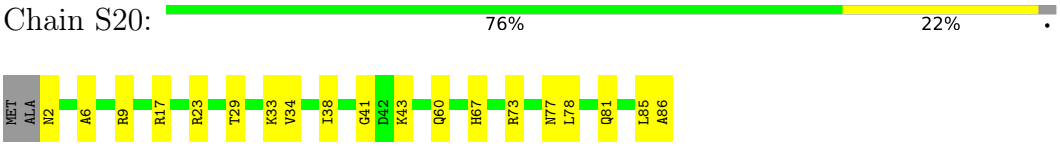
• Molecule 55: 30S ribosomal protein S19

Chain S19:



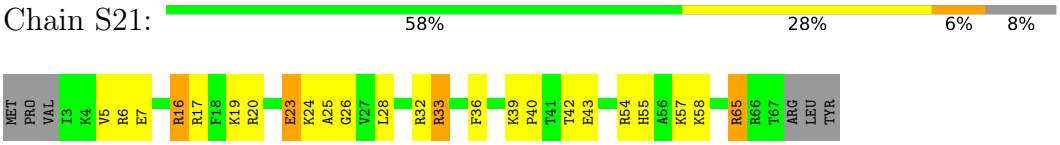
• Molecule 56: 30S ribosomal protein S20

Chain S20:



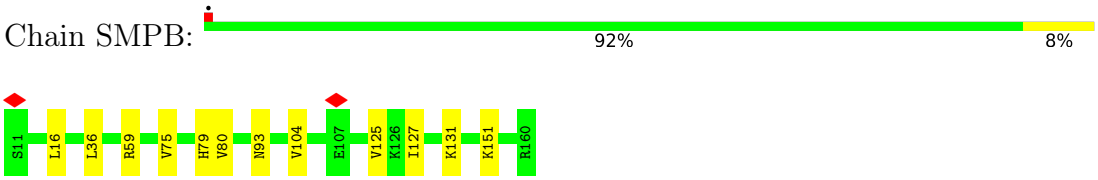
• Molecule 57: 30S ribosomal protein S21

Chain S21:



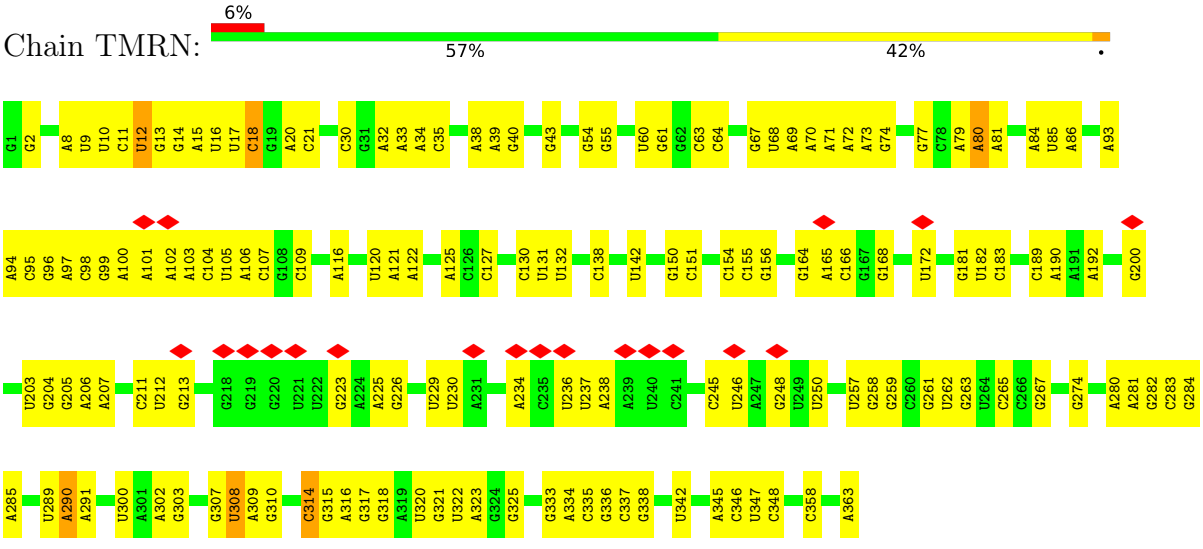
• Molecule 58: SsrA-binding protein

Chain SMPB:



• Molecule 59: TMRN

Chain TMRN:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	4215	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	29.9	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1100	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	24.205	Depositor
Minimum map value	-12.008	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.736	Depositor
Recommended contour level	3.0	Depositor
Map size (Å)	487.2, 487.2, 487.2	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.87, 0.87, 0.87	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	16S	0.27	0/36963	0.85	18/57662 (0.0%)
2	23S	0.30	0/69796	0.85	23/108888 (0.0%)
3	5S	0.28	0/2872	0.90	4/4479 (0.1%)
4	ATRN	0.28	0/1810	0.83	0/2820
5	ETRN	0.25	0/1832	0.89	2/2855 (0.1%)
6	L02	0.27	0/2121	0.57	0/2852
7	L03	0.27	0/1586	0.52	0/2134
8	L04	0.25	0/1571	0.49	0/2113
9	L05	0.26	0/1434	0.55	0/1926
10	L06	0.25	0/1343	0.53	1/1816 (0.1%)
11	L09	0.25	0/1122	0.50	0/1515
12	L1	0.24	0/1033	0.51	0/1387
13	L10	0.28	0/1001	0.59	0/1350
14	L11	0.26	0/1046	0.51	0/1410
15	L13	0.26	0/1152	0.50	0/1551
16	L14	0.26	0/947	0.57	0/1268
17	L15	0.26	0/1054	0.58	0/1403
18	L16	0.28	0/1093	0.56	0/1460
19	L17	0.25	0/973	0.60	0/1301
20	L18	0.24	0/902	0.55	0/1209
21	L19	0.26	0/929	0.56	1/1242 (0.1%)
22	L20	0.25	0/960	0.50	0/1278
23	L21	0.27	0/829	0.54	0/1107
24	L22	0.23	0/864	0.52	0/1156
25	L23	0.25	0/744	0.50	0/994
26	L24	0.27	0/787	0.55	0/1051
27	L25	0.26	0/766	0.50	0/1025
28	L27	0.27	0/582	0.54	0/769
29	L28	0.25	0/635	0.55	0/848
30	L29	0.24	0/510	0.52	0/677
31	L30	0.24	0/453	0.54	0/605
32	L31	0.28	0/358	0.59	0/480
33	L32	0.24	0/450	0.55	0/599
34	L33	0.26	0/416	0.51	0/554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	L34	0.24	0/380	0.63	0/498
36	L35	0.26	0/513	0.57	0/676
37	L36	0.26	0/303	0.57	0/397
38	S02	0.25	0/1787	0.49	0/2408
39	S03	0.24	0/1651	0.51	0/2225
40	S04	0.25	0/1665	0.55	1/2227 (0.0%)
41	S05	0.27	0/1169	0.55	0/1573
42	S06	0.25	0/835	0.57	1/1128 (0.1%)
43	S07	0.25	0/1195	0.53	0/1602
44	S08	0.26	0/989	0.50	0/1326
45	S09	0.25	0/1034	0.60	0/1375
46	S10	0.24	0/796	0.58	0/1077
47	S11	0.26	0/885	0.56	0/1195
48	S12	0.26	0/969	0.62	0/1300
49	S13	0.24	0/892	0.58	0/1193
50	S14	0.25	0/817	0.55	0/1088
51	S15	0.23	0/722	0.55	0/964
52	S16	0.25	0/659	0.59	0/884
53	S17	0.25	0/657	0.55	0/881
54	S18	0.26	0/544	0.54	0/731
55	S19	0.24	0/652	0.54	0/877
56	S20	0.24	0/671	0.49	0/888
57	S21	0.28	0/550	0.67	0/728
58	SMPB	0.25	0/1231	0.54	0/1655
59	TMRN	0.27	0/8681	0.91	12/13532 (0.1%)
All	All	0.28	0/171181	0.79	63/256212 (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
41	S05	0	1

There are no bond length outliers.

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	16S	1158	C	N1-C2-O2	10.60	125.26	118.90
1	16S	1158	C	C2-N1-C1'	9.92	129.72	118.80
1	16S	1158	C	N3-C2-O2	-8.87	115.69	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	5S	12	C	N1-C2-O2	8.64	124.08	118.90
1	16S	386	C	N3-C2-O2	-7.59	116.59	121.90
3	5S	12	C	N3-C2-O2	-7.45	116.68	121.90
2	23S	2207	C	N3-C2-O2	-7.37	116.74	121.90
2	23S	1313	U	C2-N1-C1'	7.33	126.50	117.70
1	16S	614	C	N3-C2-O2	-7.31	116.78	121.90
59	TMRN	307	G	N3-C4-C5	-7.21	125.00	128.60
1	16S	1158	C	C6-N1-C2	-7.10	117.46	120.30
1	16S	754	C	C2-N1-C1'	7.07	126.58	118.80
2	23S	1915	U	N1-C2-O2	7.03	127.72	122.80
59	TMRN	307	G	N3-C4-N9	7.03	130.22	126.00
2	23S	1915	U	C2-N1-C1'	6.86	125.93	117.70
2	23S	758	C	N3-C2-O2	-6.75	117.17	121.90
2	23S	1915	U	N3-C2-O2	-6.73	117.49	122.20
59	TMRN	307	G	C4-N9-C1'	6.67	135.17	126.50
1	16S	1158	C	C6-N1-C1'	-6.67	112.80	120.80
2	23S	758	C	N1-C2-O2	6.64	122.88	118.90
3	5S	12	C	C2-N1-C1'	6.64	126.10	118.80
59	TMRN	290	A	P-O3'-C3'	6.50	127.50	119.70
59	TMRN	308	U	P-O3'-C3'	6.47	127.47	119.70
21	L19	113	LEU	CA-CB-CG	6.28	129.75	115.30
2	23S	1020	A	P-O3'-C3'	6.24	127.19	119.70
1	16S	1347	G	P-O3'-C3'	6.22	127.17	119.70
2	23S	458	G	P-O3'-C3'	5.98	126.88	119.70
59	TMRN	314	C	P-O3'-C3'	5.88	126.75	119.70
42	S06	54	LEU	CA-CB-CG	5.82	128.68	115.30
10	L06	153	PRO	C-N-CA	5.79	136.17	121.70
1	16S	754	C	N1-C2-O2	5.74	122.35	118.90
3	5S	12	C	C6-N1-C2	-5.71	118.02	120.30
59	TMRN	307	G	C8-N9-C1'	-5.64	119.67	127.00
1	16S	1158	C	C5-C6-N1	5.57	123.79	121.00
59	TMRN	18	C	N1-C2-O2	5.56	122.24	118.90
2	23S	2300	C	N1-C2-O2	5.52	122.21	118.90
40	S04	4	LEU	CA-CB-CG	5.51	127.98	115.30
2	23S	1914	C	N1-C2-O2	5.50	122.20	118.90
1	16S	890	G	P-O3'-C3'	5.50	126.29	119.70
1	16S	1190	G	P-O3'-C3'	5.46	126.26	119.70
2	23S	859	G	P-O3'-C3'	5.43	126.21	119.70
1	16S	1325	C	N1-C2-O2	5.42	122.15	118.90
2	23S	2655	G	P-O3'-C3'	5.41	126.19	119.70
2	23S	1313	U	N1-C2-O2	5.40	126.58	122.80
59	TMRN	80	A	C2-N3-C4	5.38	113.29	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	23S	1914	C	C2-N1-C1'	5.36	124.69	118.80
2	23S	372	G	P-O3'-C3'	5.30	126.06	119.70
1	16S	1225	A	C4-N9-C1'	5.30	135.83	126.30
1	16S	221	C	N3-C2-O2	-5.29	118.19	121.90
2	23S	1092	C	C5-C6-N1	5.24	123.62	121.00
2	23S	1064	C	N1-C2-O2	5.22	122.03	118.90
5	ETRN	56	C	N3-C2-O2	-5.21	118.25	121.90
2	23S	1931	U	C5-C6-N1	5.21	125.30	122.70
59	TMRN	12	U	C2-N1-C1'	5.21	123.95	117.70
5	ETRN	56	C	N1-C2-O2	5.20	122.02	118.90
59	TMRN	18	C	C2-N1-C1'	5.19	124.51	118.80
2	23S	1313	U	C6-N1-C1'	-5.19	113.94	121.20
1	16S	1132	C	N1-C2-O2	5.15	121.99	118.90
2	23S	1730	C	P-O3'-C3'	5.14	125.87	119.70
2	23S	1075	C	N1-C2-O2	5.10	121.96	118.90
2	23S	2076	U	C2-N1-C1'	5.08	123.80	117.70
1	16S	754	C	C6-N1-C1'	-5.05	114.74	120.80
59	TMRN	12	U	N1-C2-O2	5.04	126.33	122.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
41	S05	120	HIS	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	16S	33012	0	16618	410	0
2	23S	62317	0	31346	751	0
3	5S	2568	0	1303	33	0
4	ATRN	1621	0	0	0	0
5	ETRN	1640	0	0	0	0
6	L02	2082	0	2157	51	0
7	L03	1565	0	1616	41	0
8	L04	1552	0	1619	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	L05	1410	0	1447	31	0
10	L06	1323	0	1374	26	0
11	L09	1111	0	1148	15	0
12	L1	1026	0	1092	29	0
13	L10	988	0	1025	26	0
14	L11	1032	0	1088	32	0
15	L13	1129	0	1162	24	0
16	L14	938	0	1012	22	0
17	L15	1045	0	1117	20	0
18	L16	1074	0	1157	28	0
19	L17	960	0	1000	14	0
20	L18	892	0	923	19	0
21	L19	917	0	965	33	0
22	L20	947	0	1022	23	0
23	L21	816	0	839	21	0
24	L22	857	0	922	21	0
25	L23	738	0	807	9	0
26	L24	779	0	834	19	0
27	L25	753	0	780	17	0
28	L27	575	0	592	15	0
29	L28	625	0	655	11	0
30	L29	509	0	543	14	0
31	L30	449	0	491	6	0
32	L31	351	0	350	13	0
33	L32	444	0	461	10	0
34	L33	409	0	440	5	0
35	L34	377	0	418	10	0
36	L35	504	0	574	13	0
37	L36	302	0	343	7	0
38	S02	1756	0	1787	24	0
39	S03	1624	0	1699	32	0
40	S04	1643	0	1710	50	0
41	S05	1156	0	1199	14	0
42	S06	817	0	808	25	0
43	S07	1181	0	1240	21	0
44	S08	979	0	1034	25	0
45	S09	1022	0	1070	37	0
46	S10	786	0	828	19	0
47	S11	869	0	878	17	0
48	S12	955	0	1019	27	0
49	S13	883	0	944	19	0
50	S14	805	0	847	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	S15	714	0	737	18	0
52	S16	649	0	666	17	0
53	S17	648	0	691	15	0
54	S18	535	0	552	11	0
55	S19	637	0	665	14	0
56	S20	665	0	714	15	0
57	S21	544	0	579	14	0
58	SMPB	1209	0	0	0	0
59	TMRN	7758	0	0	0	0
All	All	157472	0	98907	1953	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (1953) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:16S:978:A:C2	1:16S:1316:G:N2	2.23	1.06
2:23S:1072:C:H42	2:23S:1093:G:N2	1.54	1.04
2:23S:881:G:H1	2:23S:895:U:H3	1.04	0.99
2:23S:2834:G:H21	2:23S:2883:A:N6	1.61	0.99
2:23S:1035:U:H3	2:23S:1120:G:H1	1.09	0.98
2:23S:408:G:H1	2:23S:419:U:H3	1.07	0.98
2:23S:1215:G:H1	2:23S:1234:U:H3	1.08	0.98
2:23S:1468:U:H3	2:23S:1524:G:H1	1.08	0.97
2:23S:2452:C:H42	2:23S:2504:U:H3	1.08	0.97
2:23S:285:G:H1	2:23S:355:U:H3	0.97	0.97
2:23S:1268:A:H62	2:23S:2012:G:N2	1.63	0.97
2:23S:1072:C:N4	2:23S:1093:G:H22	1.63	0.96
2:23S:1862:G:H1	2:23S:1880:U:H3	0.98	0.96
2:23S:2847:U:H3	2:23S:2869:G:H1	1.02	0.96
2:23S:59:U:H3	2:23S:68:G:H1	0.96	0.96
2:23S:1408:G:H1	2:23S:1594:U:H3	1.10	0.96
2:23S:78:U:H3	2:23S:108:G:H1	0.96	0.95
1:16S:978:A:H2	1:16S:1316:G:N2	1.61	0.95
2:23S:1268:A:H62	2:23S:2012:G:H21	0.96	0.95
1:16S:150:U:H3	1:16S:171:A:H62	1.08	0.94
2:23S:2100:G:H1	2:23S:2189:U:H3	0.94	0.94
2:23S:2104:C:N4	2:23S:2185:U:H3	1.67	0.93
2:23S:2291:U:H3	2:23S:2341:G:H1	1.03	0.93
2:23S:1415:U:H3	2:23S:1587:G:H1	1.17	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:2452:C:N4	2:23S:2504:U:H3	1.67	0.92
1:16S:409:U:H3	1:16S:433:G:H1	1.11	0.91
2:23S:2834:G:H21	2:23S:2883:A:H62	1.13	0.91
2:23S:711:G:H1	2:23S:720:U:H3	0.93	0.90
1:16S:76:G:H1	1:16S:93:U:H3	0.94	0.89
1:16S:1438:G:H1	1:16S:1463:U:H3	1.14	0.89
1:16S:978:A:H2	1:16S:1316:G:H21	1.10	0.89
2:23S:1483:G:H1	2:23S:1506:U:H3	1.18	0.89
3:5S:9:G:H1	3:5S:111:U:H3	1.22	0.88
2:23S:2289:G:H1	2:23S:2343:U:H3	1.13	0.88
1:16S:1422:G:H1	1:16S:1478:U:H3	0.92	0.88
2:23S:1770:G:H1	2:23S:1982:U:H3	0.91	0.88
1:16S:615:G:H1	1:16S:625:U:H3	1.22	0.87
2:23S:694:U:H3	2:23S:768:G:H1	1.17	0.87
2:23S:2104:C:H42	2:23S:2185:U:H3	0.89	0.86
1:16S:1009:U:H3	1:16S:1020:G:H1	1.23	0.86
2:23S:535:G:H1	2:23S:558:U:H3	1.23	0.86
1:16S:198:G:H1	1:16S:219:U:H3	0.86	0.85
2:23S:594:U:H3	2:23S:663:G:H1	1.23	0.85
2:23S:1268:A:N6	2:23S:2012:G:H21	1.73	0.85
1:16S:895:G:H1	1:16S:904:U:H3	1.24	0.84
1:16S:1116:U:H3	1:16S:1184:G:H1	1.24	0.84
1:16S:112:G:H1	1:16S:315:A:H61	1.20	0.84
1:16S:593:U:H3	1:16S:646:G:H1	1.24	0.83
2:23S:1168:G:H1	2:23S:1181:U:H3	1.26	0.83
2:23S:1072:C:H42	2:23S:1093:G:H22	0.87	0.82
1:16S:129:A:H61	1:16S:232:G:H1	1.28	0.82
1:16S:835:U:H3	1:16S:851:G:H1	1.25	0.82
2:23S:2834:G:N2	2:23S:2883:A:H62	1.77	0.81
1:16S:1348:U:N3	1:16S:1374:A:C8	2.48	0.81
2:23S:839:U:H3	2:23S:939:G:H1	1.28	0.81
2:23S:1478:G:H1	2:23S:1513:U:H3	1.25	0.81
1:16S:925:G:H1	1:16S:1391:U:H3	0.84	0.81
1:16S:927:G:H1	1:16S:1390:U:H3	1.28	0.79
1:16S:978:A:N6	1:16S:1360:A:C2	2.50	0.79
2:23S:291:G:H1	2:23S:349:U:H3	1.29	0.79
2:23S:1282:U:H3	2:23S:1286:A:H62	1.29	0.79
1:16S:765:G:H1	1:16S:812:G:HO2'	1.28	0.78
1:16S:151:A:N6	1:16S:170:U:C2	2.51	0.78
2:23S:2107:G:H1	2:23S:2182:U:H3	1.28	0.78
1:16S:664:G:H22	1:16S:741:G:H1	1.33	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:16S:605:U:H3	1:16S:633:G:H1	1.32	0.76
1:16S:594:U:H3	1:16S:645:G:H1	1.33	0.76
1:16S:1026:G:H1	1:16S:1035:A:H2	1.25	0.75
1:16S:834:U:H3	1:16S:852:G:H1	1.35	0.74
1:16S:950:U:H3	1:16S:1231:G:H1	1.33	0.74
1:16S:1006:G:H1	1:16S:1023:U:H3	0.80	0.74
1:16S:1238:A:H62	1:16S:1301:U:H3	1.36	0.73
1:16S:151:A:N6	1:16S:170:U:N3	2.37	0.72
1:16S:62:U:H3	1:16S:105:G:H1	1.36	0.71
1:16S:201:G:H1	1:16S:216:U:H3	1.39	0.70
2:23S:1907:G:H1	2:23S:1923:U:H3	1.37	0.69
1:16S:1236:A:N6	1:16S:1337:G:C6	2.60	0.69
1:16S:150:U:H3	1:16S:171:A:N6	1.87	0.69
12:L1:181:ASP:H	12:L1:184:LYS:HD3	1.58	0.69
14:L11:14:ALA:HB3	14:L11:54:ILE:H	1.57	0.69
1:16S:129:A:N6	1:16S:232:G:H1	1.91	0.69
3:5S:80:U:H3	3:5S:96:G:H1	1.40	0.69
2:23S:2019:A:H61	2:23S:2035:G:H1	1.39	0.68
2:23S:1072:C:N3	2:23S:1093:G:N1	2.38	0.68
53:S17:30:HIS:HB3	53:S17:34:GLY:H	1.59	0.68
1:16S:672:U:H3	1:16S:734:G:H1	1.40	0.68
2:23S:2102:G:H1	2:23S:2187:U:H3	1.42	0.68
2:23S:999:U:O2	2:23S:1157:G:C2	2.47	0.68
2:23S:1430:G:H1	2:23S:1563:U:H3	1.42	0.67
43:S07:78:ARG:HH21	43:S07:80:GLY:HA2	1.59	0.66
1:16S:202:G:H21	1:16S:466:A:H61	1.43	0.66
6:L02:52:HIS:HA	6:L02:216:ARG:HG2	1.76	0.66
2:23S:1084:A:H62	13:L10:29:ASP:HB3	1.59	0.66
2:23S:2117:A:N6	2:23S:2170:A:N1	2.43	0.66
2:23S:1270:C:H5"	2:23S:1271:G:H5'	1.79	0.65
30:L29:15:ASN:HA	30:L29:18:LEU:HB3	1.78	0.65
49:S13:11:HIS:HB3	49:S13:43:LYS:HD2	1.77	0.65
14:L11:89:SER:HB2	14:L11:92:PRO:HG3	1.79	0.65
1:16S:894:G:H1	1:16S:905:U:H3	1.45	0.64
23:L21:35:PHE:HB2	23:L21:59:ILE:HB	1.79	0.64
1:16S:112:G:H1	1:16S:315:A:N6	1.93	0.64
38:S02:186:VAL:HG23	38:S02:190:SER:HB2	1.80	0.64
1:16S:401:C:O2'	1:16S:621:A:N3	2.31	0.64
20:L18:29:HIS:HB3	20:L18:36:TYR:HB2	1.80	0.64
1:16S:1236:A:N6	1:16S:1337:G:N1	2.45	0.64
14:L11:55:PRO:HG2	14:L11:71:LYS:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5S:22:U:H3	3:5S:61:G:H1	1.46	0.63
18:L16:57:VAL:HB	18:L16:60:GLN:HB2	1.78	0.63
2:23S:1478:G:N2	2:23S:1513:U:O2	2.29	0.63
2:23S:251:A:N6	2:23S:386:G:O6	2.32	0.63
27:L25:72:VAL:HG12	27:L25:93:ARG:HA	1.81	0.63
2:23S:2682:A:H61	2:23S:2728:U:H1'	1.64	0.63
12:L1:11:ILE:HG23	12:L1:33:LEU:HD22	1.80	0.63
1:16S:1115:U:H3	1:16S:1185:G:H1	1.45	0.63
14:L11:112:LYS:HB3	14:L11:116:MET:HG3	1.79	0.63
40:S04:12:ARG:HG2	40:S04:33:ILE:HA	1.80	0.62
52:S16:75:ILE:HG23	52:S16:80:LYS:HE3	1.81	0.62
1:16S:1413:A:N1	1:16S:1487:G:O6	2.32	0.62
2:23S:2514:U:H3	2:23S:2570:G:H1	1.48	0.62
10:L06:29:ASN:ND2	10:L06:78:VAL:O	2.33	0.62
12:L1:162:ARG:HE	12:L1:162:ARG:H	1.47	0.62
20:L18:90:VAL:HG23	20:L18:117:PHE:HB3	1.82	0.62
1:16S:1026:G:O6	1:16S:1035:A:N1	2.32	0.62
14:L11:11:GLN:HB3	14:L11:14:ALA:HB2	1.80	0.62
1:16S:1238:A:N7	1:16S:1301:U:O4	2.32	0.62
2:23S:45:G:H5"	2:23S:46:G:H5'	1.82	0.62
1:16S:1216:A:H5"	50:S14:4:SER:HB3	1.82	0.61
2:23S:1106:G:H4'	13:L10:56:ARG:HB2	1.81	0.61
1:16S:151:A:N7	1:16S:170:U:O4	2.33	0.61
3:5S:30:C:H1'	3:5S:57:A:H61	1.65	0.61
1:16S:363:A:N6	48:S12:26:CYS:SG	2.73	0.61
1:16S:978:A:H61	1:16S:1316:G:H1'	1.65	0.61
2:23S:377:G:N1	2:23S:397:U:N3	2.49	0.61
2:23S:1032:A:N1	2:23S:1122:G:O6	2.32	0.61
2:23S:2884:U:H3	33:L32:39:ARG:HD2	1.66	0.61
2:23S:2641:G:H5"	15:L13:78:THR:HB	1.83	0.61
16:L14:76:VAL:H	21:L19:72:VAL:HG22	1.65	0.61
38:S02:69:VAL:HG22	38:S02:91:VAL:HB	1.83	0.61
40:S04:101:VAL:HG23	40:S04:113:ALA:HB1	1.81	0.61
2:23S:33:C:O2	2:23S:447:A:N6	2.33	0.61
1:16S:1414:U:H2'	1:16S:1415:G:H8	1.66	0.61
2:23S:1072:C:N4	2:23S:1098:A:OP2	2.32	0.61
39:S03:112:ALA:HB3	39:S03:184:ASN:HD22	1.63	0.61
2:23S:276:U:O2'	2:23S:278:A:N6	2.33	0.61
2:23S:1779:U:OP2	2:23S:1784:A:N6	2.32	0.61
2:23S:2139:U:O2	2:23S:2152:G:O6	2.19	0.61
57:S21:23:GLU:HB2	57:S21:26:GLY:H	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:910:A:N3	2:23S:2264:C:O2'	2.33	0.61
21:L19:87:ARG:HH22	21:L19:109:ILE:HG13	1.65	0.61
2:23S:1819:A:H5"	6:L02:159:THR:HG21	1.82	0.61
17:L15:109:LYS:HG2	17:L15:126:ARG:HB2	1.82	0.61
30:L29:24:GLU:HA	30:L29:27:ASN:HB2	1.83	0.61
2:23S:917:A:H5"	2:23S:2268:A:H61	1.65	0.60
2:23S:1265:A:H61	2:23S:2013:A:H3'	1.66	0.60
6:L02:184:GLU:HG3	6:L02:186:ASP:H	1.66	0.60
57:S21:65:ARG:O	57:S21:65:ARG:NH1	2.34	0.60
1:16S:415:A:N7	1:16S:428:G:O6	2.34	0.60
2:23S:1791:A:N6	2:23S:1828:G:O2'	2.33	0.60
44:S08:29:SER:H	44:S08:32:LYS:HB2	1.65	0.60
2:23S:320:A:N3	8:L04:163:ASN:ND2	2.49	0.60
2:23S:1501:G:H4'	6:L02:94:LEU:HD21	1.83	0.60
43:S07:67:ASN:HB3	43:S07:129:ASN:HB3	1.83	0.60
2:23S:1071:G:N3	2:23S:1089:A:O2'	2.34	0.60
2:23S:1842:G:H1	2:23S:1898:U:H3	1.49	0.60
2:23S:2656:U:O2	2:23S:2665:A:N7	2.34	0.60
57:S21:20:ARG:HA	57:S21:24:LYS:HB2	1.83	0.60
1:16S:516:U:O2	1:16S:533:A:N7	2.35	0.60
1:16S:1447:A:OP2	1:16S:1448:C:N4	2.33	0.60
40:S04:131:ILE:HG22	40:S04:133:SER:H	1.66	0.60
1:16S:345:C:H4'	21:L19:38:ARG:HH21	1.66	0.60
2:23S:1798:U:OP2	6:L02:270:ARG:NH2	2.35	0.60
2:23S:1715:G:N2	2:23S:1744:A:OP2	2.35	0.60
43:S07:29:LEU:HD12	43:S07:108:ARG:HH21	1.67	0.60
45:S09:87:MET:N	45:S09:87:MET:SD	2.75	0.60
1:16S:978:A:N1	1:16S:1316:G:N3	2.49	0.60
2:23S:2468:A:H5'	18:L16:119:LEU:HD21	1.84	0.60
2:23S:2526:G:N3	37:L36:1:MET:N	2.50	0.60
1:16S:674:G:H1	1:16S:716:A:H61	1.49	0.60
2:23S:2391:G:H2'	2:23S:2424:C:H41	1.67	0.60
1:16S:959:A:HO2'	1:16S:984:C:HO2'	1.49	0.59
2:23S:475:C:O2	2:23S:479:A:N6	2.34	0.59
12:L1:69:THR:HA	12:L1:176:GLY:HA2	1.83	0.59
53:S17:24:ILE:HB	53:S17:41:THR:HB	1.83	0.59
1:16S:978:A:N1	1:16S:1316:G:C2	2.70	0.59
2:23S:562:U:N3	2:23S:572:A:C5	2.71	0.59
2:23S:1415:U:O2	2:23S:1587:G:N2	2.34	0.59
1:16S:1032:G:N2	1:16S:1033:G:O2'	2.36	0.59
2:23S:1063:G:N2	14:L11:90:GLY:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:1068:G:O2'	2:23S:1070:A:N7	2.32	0.59
46:S10:53:ILE:HG22	50:S14:84:ARG:HD2	1.84	0.59
2:23S:2831:G:OP2	7:L03:59:ARG:NH2	2.34	0.59
9:L05:40:GLY:HA2	9:L05:84:ILE:HG13	1.84	0.59
10:L06:79:THR:HG23	10:L06:80:GLU:HG3	1.85	0.59
1:16S:1305:G:H22	1:16S:1331:G:H2'	1.67	0.59
2:23S:457:A:N7	2:23S:472:A:N6	2.49	0.59
2:23S:1323:C:N4	2:23S:1324:G:O6	2.36	0.59
2:23S:1675:C:H2'	2:23S:1676:A:H8	1.68	0.59
2:23S:1996:C:OP1	16:L14:31:ARG:NH1	2.36	0.59
42:S06:12:PRO:O	42:S06:44:ARG:NH1	2.35	0.59
2:23S:1044:C:O2'	2:23S:1111:A:N6	2.29	0.59
2:23S:2032:G:N2	7:L03:151:THR:OG1	2.36	0.59
9:L05:115:GLY:HA3	9:L05:177:ARG:HB2	1.85	0.59
12:L1:7:ARG:NH2	12:L1:32:GLU:O	2.36	0.59
45:S09:18:VAL:HA	45:S09:64:ILE:HG23	1.84	0.59
2:23S:999:U:O2	2:23S:1157:G:N2	2.36	0.59
19:L17:100:CYS:H	19:L17:111:ALA:HA	1.68	0.59
9:L05:23:SER:HB3	9:L05:26:GLN:HB2	1.83	0.59
48:S12:32:VAL:HA	48:S12:78:VAL:HG12	1.84	0.59
2:23S:1860:G:N2	2:23S:1882:U:O2	2.33	0.58
2:23S:2046:G:H1	2:23S:2622:U:H3	1.50	0.58
3:5S:78:A:OP2	27:L25:14:LYS:NZ	2.34	0.58
42:S06:11:HIS:HB3	42:S06:14:GLN:HB2	1.84	0.58
57:S21:16:ARG:HB2	57:S21:19:LYS:HD3	1.84	0.58
1:16S:126:G:OP1	1:16S:633:G:N2	2.36	0.58
2:23S:1352:U:O2	2:23S:1380:G:C2	2.56	0.58
7:L03:148:GLN:HB2	7:L03:152:PRO:HG2	1.85	0.58
14:L11:121:ILE:HG23	14:L11:122:GLU:HG3	1.85	0.58
1:16S:150:U:N3	1:16S:171:A:N6	2.39	0.58
1:16S:1405:G:H21	1:16S:1518:A:H1'	1.67	0.58
2:23S:1070:A:OP2	2:23S:1076:C:N4	2.36	0.58
45:S09:113:LYS:HA	45:S09:120:ALA:HB2	1.84	0.58
2:23S:2449:U:O2'	2:23S:2501:C:N4	2.37	0.58
14:L11:52:LEU:HD13	14:L11:73:PRO:HB3	1.86	0.58
1:16S:362:G:N2	1:16S:365:U:OP2	2.32	0.58
1:16S:942:G:H1	1:16S:1341:U:H3	1.49	0.58
3:5S:34:A:N6	3:5S:44:G:O2'	2.37	0.58
1:16S:137:U:O2	1:16S:226:G:N2	2.35	0.58
1:16S:1348:U:C2	1:16S:1374:A:N7	2.71	0.58
2:23S:320:A:O2'	2:23S:322:A:OP2	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:400:G:N7	29:L28:56:ARG:NH2	2.52	0.58
2:23S:2618:G:H21	7:L03:155:VAL:HG21	1.69	0.58
9:L05:125:GLY:HA2	9:L05:162:ASP:HA	1.85	0.58
16:L14:35:VAL:HA	16:L14:62:VAL:HB	1.85	0.58
38:S02:76:SER:OG	38:S02:92:ASN:ND2	2.36	0.58
45:S09:50:PRO:HD3	45:S09:79:ARG:HG3	1.83	0.58
1:16S:521:G:H4'	48:S12:69:GLU:HG2	1.85	0.58
1:16S:1137:C:O2'	1:16S:1138:G:N2	2.37	0.58
2:23S:1912:A:N7	2:23S:1917:U:O2	2.37	0.58
10:L06:88:LEU:HD22	10:L06:93:TYR:HB3	1.85	0.58
13:L10:58:THR:HG21	13:L10:82:ILE:H	1.67	0.58
23:L21:49:ILE:HG22	23:L21:54:VAL:H	1.68	0.58
40:S04:103:ARG:HH21	40:S04:110:ARG:HH21	1.52	0.58
50:S14:6:LYS:NZ	50:S14:63:CYS:O	2.37	0.58
1:16S:59:A:H5"	1:16S:387:U:H5"	1.86	0.58
1:16S:1457:G:OP1	56:S20:33:LYS:NZ	2.36	0.58
2:23S:1203:U:H1'	17:L15:4:ASN:HB3	1.86	0.58
1:16S:1419:G:H1	1:16S:1481:U:H3	1.52	0.58
2:23S:254:G:N7	36:L35:4:LYS:NZ	2.49	0.58
2:23S:1069:A:H1'	2:23S:1096:A:H4'	1.86	0.58
2:23S:13:A:O2'	2:23S:15:G:N7	2.35	0.58
2:23S:857:G:N2	2:23S:921:C:O2	2.37	0.58
23:L21:76:LYS:HB2	23:L21:85:LYS:HB3	1.85	0.58
1:16S:894:G:N2	1:16S:905:U:O2	2.34	0.57
1:16S:1279:G:OP2	46:S10:9:ARG:NH2	2.37	0.57
1:16S:1379:G:N2	1:16S:1381:U:O4	2.35	0.57
1:16S:1441:A:H62	1:16S:1461:G:H21	1.51	0.57
2:23S:383:C:H2'	2:23S:385:C:H41	1.69	0.57
40:S04:7:LYS:HB2	40:S04:20:LEU:HB3	1.86	0.57
40:S04:61:ARG:NH1	40:S04:68:GLU:OE1	2.37	0.57
44:S08:89:ASP:OD1	44:S08:89:ASP:N	2.37	0.57
1:16S:414:A:OP2	1:16S:428:G:N2	2.37	0.57
1:16S:549:C:OP1	40:S04:69:ARG:NH2	2.38	0.57
2:23S:993:G:N3	23:L21:91:GLN:NE2	2.52	0.57
40:S04:37:PRO:HD2	40:S04:41:GLY:HA3	1.87	0.57
1:16S:338:A:N1	1:16S:351:G:O6	2.37	0.57
1:16S:671:G:O2'	42:S06:79:ARG:NH2	2.38	0.57
2:23S:995:C:H5"	22:L20:53:LYS:HA	1.86	0.57
28:L27:46:ASN:HB2	28:L27:78:ILE:HB	1.84	0.57
1:16S:911:U:OP1	48:S12:93:ARG:NH1	2.38	0.57
1:16S:1179:A:H4'	45:S09:104:THR:HA	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:L15:90:VAL:HG13	17:L15:95:LEU:HD21	1.86	0.57
49:S13:100:ARG:NH2	49:S13:103:THR:OG1	2.36	0.57
55:S19:17:LYS:HB3	55:S19:30:LEU:HD11	1.87	0.57
2:23S:776:G:N1	2:23S:2072:C:OP1	2.32	0.57
2:23S:2530:A:O2'	2:23S:2534:A:N6	2.37	0.57
44:S08:49:LYS:HB2	44:S08:59:GLU:HB3	1.86	0.57
2:23S:516:C:OP1	33:L32:9:ARG:NH2	2.36	0.57
2:23S:1035:U:O2	2:23S:1120:G:N2	2.34	0.57
2:23S:1306:C:N4	2:23S:1607:C:OP2	2.37	0.57
2:23S:2107:G:N2	2:23S:2182:U:O2	2.33	0.57
12:L1:184:LYS:O	12:L1:188:ASN:ND2	2.37	0.57
40:S04:117:VAL:HG22	40:S04:122:ILE:HG13	1.87	0.57
1:16S:949:A:N7	49:S13:104:ASN:ND2	2.53	0.57
2:23S:27:G:H21	2:23S:513:A:H62	1.51	0.57
2:23S:1086:A:H5"	2:23S:1087:G:H5'	1.87	0.57
2:23S:1035:U:H2'	2:23S:1036:G:H8	1.70	0.57
2:23S:1614:A:N6	24:L22:92:ARG:O	2.38	0.57
2:23S:2073:C:H5'	6:L02:227:VAL:HG23	1.86	0.57
1:16S:1298:U:OP2	43:S07:113:LYS:NZ	2.38	0.56
2:23S:993:G:OP2	22:L20:50:ARG:NH2	2.38	0.56
2:23S:2619:C:OP1	7:L03:157:LYS:NZ	2.38	0.56
3:5S:95:U:OP2	27:L25:19:ARG:NH2	2.38	0.56
17:L15:51:GLU:OE1	17:L15:60:ARG:NH2	2.38	0.56
18:L16:25:ASP:O	18:L16:66:ARG:NH1	2.37	0.56
19:L17:29:VAL:HG12	19:L17:78:LYS:HD3	1.87	0.56
26:L24:81:ARG:HE	26:L24:81:ARG:H	1.53	0.56
42:S06:35:LYS:HB2	42:S06:65:GLU:HB3	1.86	0.56
1:16S:54:C:OP1	1:16S:351:G:N2	2.35	0.56
2:23S:238:C:O2'	2:23S:608:A:N3	2.37	0.56
8:L04:110:SER:HB2	8:L04:114:ARG:HH12	1.70	0.56
9:L05:60:SER:N	32:L31:7:PRO:O	2.38	0.56
20:L18:18:LEU:HD11	20:L18:91:SER:HB2	1.86	0.56
35:L34:22:MET:O	35:L34:28:ARG:NH1	2.38	0.56
56:S20:23:ARG:NH2	56:S20:60:GLN:OE1	2.38	0.56
1:16S:835:U:O2	1:16S:851:G:N2	2.33	0.56
1:16S:993:G:O2'	1:16S:994:A:N7	2.37	0.56
1:16S:1150:A:H4'	46:S10:43:PRO:HB3	1.87	0.56
1:16S:1348:U:O2	1:16S:1374:A:N7	2.38	0.56
2:23S:228:C:N3	2:23S:417:C:O2'	2.34	0.56
2:23S:2892:G:H5"	2:23S:2893:A:H5'	1.87	0.56
6:L02:1:ALA:N	6:L02:19:VAL:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L02:86:ARG:HH12	6:L02:155:ARG:HH21	1.53	0.56
38:S02:132:GLU:OE2	38:S02:136:ARG:NH2	2.38	0.56
45:S09:45:MET:HA	45:S09:48:ARG:HE	1.69	0.56
45:S09:94:ARG:HA	45:S09:97:LEU:HB2	1.87	0.56
12:L1:42:VAL:HA	12:L1:216:THR:HA	1.87	0.56
20:L18:71:ALA:HB1	20:L18:106:LEU:HB2	1.88	0.56
42:S06:15:SER:OG	42:S06:44:ARG:NH1	2.39	0.56
44:S08:10:LEU:HD22	44:S08:74:ILE:HD11	1.86	0.56
1:16S:413:G:N2	1:16S:428:G:O3'	2.38	0.56
2:23S:284:U:H3	2:23S:356:G:H1	1.52	0.56
10:L06:7:PRO:O	10:L06:68:ARG:NH2	2.38	0.56
1:16S:380:G:N2	1:16S:383:A:OP2	2.32	0.56
1:16S:672:U:O2	1:16S:734:G:N2	2.34	0.56
2:23S:643:A:N1	2:23S:2369:A:O2'	2.34	0.56
2:23S:959:A:N3	2:23S:2457:U:O2'	2.35	0.56
2:23S:1072:C:O2	2:23S:1093:G:O6	2.23	0.56
3:5S:13:G:N2	3:5S:16:G:N3	2.52	0.56
6:L02:261:ARG:O	6:L02:264:LYS:NZ	2.39	0.56
10:L06:163:TYR:HB2	10:L06:166:GLU:HB2	1.88	0.56
1:16S:352:C:O2	1:16S:355:C:N4	2.39	0.56
1:16S:1300:G:H22	1:16S:1334:G:H2'	1.71	0.56
12:L1:47:ASN:ND2	12:L1:211:LYS:O	2.39	0.56
14:L11:77:VAL:HA	14:L11:80:LYS:HD3	1.88	0.56
15:L13:16:TYR:HB3	15:L13:140:LEU:HB2	1.88	0.56
19:L17:103:ARG:HG2	19:L17:105:GLY:H	1.70	0.56
1:16S:263:A:OP1	56:S20:73:ARG:NH1	2.39	0.56
2:23S:2345:G:H5'	2:23S:2347:C:H5'	1.87	0.56
2:23S:2884:U:OP2	33:L32:39:ARG:NH2	2.39	0.56
24:L22:6:LYS:HA	24:L22:104:THR:HA	1.87	0.56
44:S08:103:VAL:HB	44:S08:124:ILE:HG22	1.86	0.56
1:16S:542:G:O2'	40:S04:13:ARG:NH2	2.39	0.56
2:23S:328:U:O2'	26:L24:68:ASN:OD1	2.21	0.56
6:L02:5:CYS:SG	6:L02:12:ARG:NH1	2.79	0.56
1:16S:376:G:H2'	1:16S:377:G:H8	1.70	0.56
1:16S:1222:G:H5"	55:S19:77:ARG:HH11	1.71	0.56
2:23S:538:A:H4'	15:L13:7:LYS:HG2	1.87	0.56
20:L18:43:ASN:OD1	20:L18:43:ASN:N	2.37	0.56
34:L33:22:THR:OG1	34:L33:23:THR:N	2.39	0.56
38:S02:10:LYS:O	38:S02:207:ARG:NH1	2.39	0.56
39:S03:149:LYS:HA	39:S03:168:ARG:HA	1.88	0.56
41:S05:74:ALA:O	41:S05:81:GLN:NE2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:16S:1222:G:OP1	55:S19:77:ARG:NH1	2.39	0.55
1:16S:1314:C:N4	55:S19:3:SER:OG	2.38	0.55
2:23S:126:A:H61	35:L34:42:LEU:HB3	1.71	0.55
2:23S:247:G:OP2	2:23S:249:C:N4	2.35	0.55
2:23S:481:G:O2'	2:23S:506:G:N2	2.39	0.55
9:L05:87:LYS:NZ	9:L05:89:THR:OG1	2.37	0.55
54:S18:21:ASP:OD2	54:S18:23:LYS:NZ	2.37	0.55
1:16S:373:A:O2'	1:16S:451:A:N7	2.38	0.55
2:23S:355:U:H2'	2:23S:356:G:H8	1.70	0.55
2:23S:813:U:OP1	23:L21:84:ARG:NH2	2.39	0.55
7:L03:34:VAL:HG22	7:L03:50:VAL:HG12	1.87	0.55
55:S19:52:ASN:HB3	55:S19:74:ALA:HB1	1.88	0.55
1:16S:527:G:O6	48:S12:45:ASN:ND2	2.38	0.55
1:16S:834:U:O2	1:16S:852:G:N2	2.38	0.55
2:23S:290:U:O2	2:23S:350:G:N2	2.36	0.55
2:23S:1728:C:O2'	2:23S:1731:G:N2	2.39	0.55
38:S02:15:PHE:O	38:S02:202:ASN:ND2	2.39	0.55
1:16S:1238:A:N6	1:16S:1301:U:H3	2.01	0.55
2:23S:527:C:N4	2:23S:2779:U:OP2	2.39	0.55
7:L03:115:GLY:HA2	7:L03:166:GLY:HA3	1.88	0.55
13:L10:119:PRO:HB3	13:L10:126:LEU:HD12	1.89	0.55
2:23S:668:A:H2'	2:23S:670:A:H62	1.69	0.55
2:23S:1275:A:OP2	2:23S:1646:C:N4	2.39	0.55
16:L14:56:ASP:OD1	16:L14:56:ASP:N	2.39	0.55
39:S03:55:VAL:HB	39:S03:66:THR:HB	1.87	0.55
46:S10:41:PRO:O	46:S10:72:ARG:NH1	2.40	0.55
1:16S:1255:G:O2'	1:16S:1258:G:N3	2.37	0.55
2:23S:494:G:H2'	2:23S:495:G:H8	1.72	0.55
2:23S:881:G:N2	2:23S:895:U:O2	2.39	0.55
2:23S:1476:U:H3	2:23S:1515:A:H62	1.55	0.55
2:23S:2503:A:O2'	2:23S:2505:G:OP2	2.25	0.55
16:L14:24:VAL:HA	16:L14:39:ILE:HG22	1.89	0.55
34:L33:10:LEU:HD22	34:L33:48:TYR:HB3	1.89	0.55
36:L35:61:LEU:HB2	36:L35:64:ALA:HB3	1.89	0.55
1:16S:151:A:OP2	1:16S:169:C:N4	2.38	0.55
1:16S:595:A:O2'	1:16S:640:A:N6	2.40	0.55
2:23S:712:G:OP1	51:S15:88:ARG:NH1	2.40	0.55
2:23S:2010:G:H5"	24:L22:42:LYS:HB2	1.89	0.55
1:16S:780:A:N6	1:16S:801:U:OP2	2.40	0.55
7:L03:12:THR:HG22	21:L19:55:HIS:HE2	1.71	0.55
18:L16:64:TRP:HB2	18:L16:104:GLU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:2110:G:H5'	2:23S:2145:C:H41	1.71	0.55
2:23S:2312:U:H5'	9:L05:84:ILE:HD13	1.89	0.55
19:L17:9:GLN:O	19:L17:17:ARG:NH1	2.40	0.55
23:L21:77:PHE:O	23:L21:78:ARG:NH1	2.40	0.55
28:L27:71:LYS:HG3	28:L27:73:ARG:HG3	1.89	0.55
46:S10:76:ILE:HG23	46:S10:78:GLU:HG2	1.87	0.55
54:S18:36:GLY:O	54:S18:62:ARG:NH2	2.38	0.55
1:16S:979:C:OP1	1:16S:1223:C:N4	2.40	0.55
2:23S:1257:C:OP1	8:L04:67:ARG:NH2	2.38	0.55
2:23S:2615:U:H1'	33:L32:3:GLN:HB3	1.88	0.55
2:23S:2627:G:N2	2:23S:2777:G:OP2	2.40	0.55
18:L16:134:THR:OG1	27:L25:79:ARG:NH1	2.38	0.55
37:L36:14:CYS:SG	37:L36:33:HIS:ND1	2.79	0.55
49:S13:67:ASP:OD1	49:S13:70:ARG:NH1	2.40	0.55
56:S20:43:LYS:HB3	56:S20:86:ALA:HB2	1.89	0.55
1:16S:1116:U:O2	1:16S:1184:G:N2	2.36	0.54
1:16S:1496:C:O2'	1:16S:1517:G:N1	2.41	0.54
2:23S:568:U:O5'	2:23S:945:A:N6	2.40	0.54
2:23S:1215:G:N2	2:23S:1234:U:O2	2.40	0.54
2:23S:1665:A:OP1	16:L14:66:LYS:NZ	2.39	0.54
28:L27:52:ASP:OD1	28:L27:52:ASP:N	2.40	0.54
1:16S:5:U:OP1	40:S04:82:LYS:NZ	2.41	0.54
1:16S:107:G:OP1	1:16S:325:A:N6	2.39	0.54
2:23S:288:U:H2'	2:23S:289:G:H8	1.72	0.54
2:23S:328:U:O2	2:23S:332:A:N7	2.40	0.54
2:23S:2508:G:HO2'	2:23S:2554:U:HO2'	1.54	0.54
10:L06:122:ALA:HA	10:L06:132:LEU:HA	1.89	0.54
18:L16:17:ASN:OD1	18:L16:97:GLN:NE2	2.40	0.54
20:L18:10:ARG:NH2	20:L18:96:GLY:O	2.39	0.54
25:L23:11:LEU:HA	25:L23:34:VAL:HG12	1.89	0.54
40:S04:82:LYS:O	40:S04:88:ASN:ND2	2.40	0.54
40:S04:124:VAL:HG22	40:S04:142:VAL:HG23	1.89	0.54
1:16S:212:G:H2'	1:16S:213:G:H8	1.72	0.54
2:23S:869:G:O3'	18:L16:6:ARG:NH1	2.40	0.54
2:23S:2199:A:O2'	29:L28:35:HIS:NE2	2.40	0.54
2:23S:2484:G:OP1	18:L16:44:ARG:NH1	2.38	0.54
18:L16:133:LYS:NZ	18:L16:134:THR:O	2.41	0.54
48:S12:71:HIS:HA	48:S12:98:ARG:HH12	1.71	0.54
52:S16:4:ILE:HD12	52:S16:67:ILE:HG12	1.90	0.54
1:16S:119:A:N7	1:16S:287:U:O2	2.40	0.54
1:16S:624:C:H1'	52:S16:14:ARG:HH22	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:16S:1359:C:OP2	50:S14:74:ARG:NH1	2.41	0.54
2:23S:692:C:H5"	6:L02:38:LYS:HB2	1.90	0.54
2:23S:793:A:OP2	2:23S:2071:A:O2'	2.25	0.54
1:16S:28:A:O2'	1:16S:296:U:OP1	2.26	0.54
2:23S:1061:U:H1'	14:L11:12:VAL:HA	1.89	0.54
12:L1:50:ILE:HG13	12:L1:57:GLN:HE22	1.73	0.54
38:S02:7:ASP:N	38:S02:7:ASP:OD1	2.40	0.54
49:S13:108:ARG:NH1	49:S13:108:ARG:O	2.40	0.54
54:S18:11:ARG:HH11	54:S18:11:ARG:H	1.54	0.54
1:16S:597:G:N2	44:S08:85:TYR:OH	2.40	0.54
2:23S:1799:G:OP1	6:L02:257:ARG:NH1	2.40	0.54
2:23S:2031:A:N3	2:23S:2455:G:O2'	2.39	0.54
14:L11:6:ALA:HA	14:L11:30:GLN:HB3	1.89	0.54
40:S04:102:TYR:O	40:S04:164:ARG:NH1	2.40	0.54
1:16S:403:C:H5'	40:S04:131:ILE:HG23	1.89	0.54
2:23S:228:C:H42	2:23S:417:C:H1'	1.73	0.54
2:23S:2457:U:H3	2:23S:2494:G:H1	1.54	0.54
7:L03:181:ASP:HB3	7:L03:186:LEU:HB2	1.89	0.54
29:L28:5:GLN:O	29:L28:73:ARG:NH2	2.40	0.54
30:L29:49:ASP:OD1	30:L29:52:ARG:NH2	2.41	0.54
50:S14:44:VAL:O	50:S14:48:GLN:NE2	2.41	0.54
1:16S:77:A:H61	1:16S:92:U:H3	1.55	0.54
1:16S:112:G:H21	1:16S:354:G:H5'	1.71	0.54
2:23S:1800:C:N4	2:23S:1818:U:O2'	2.40	0.54
2:23S:2237:G:O2'	2:23S:2239:G:N7	2.37	0.54
2:23S:2296:U:OP2	20:L18:9:ARG:NH2	2.40	0.54
8:L04:102:ARG:NH2	8:L04:200:LEU:O	2.41	0.54
38:S02:86:CYS:HB3	38:S02:221:ARG:HH11	1.73	0.54
2:23S:83:A:O2'	2:23S:103:A:N6	2.41	0.54
2:23S:2720:U:OP1	21:L19:52:ARG:NH2	2.40	0.54
50:S14:53:ASP:OD2	50:S14:58:ARG:NH2	2.40	0.54
1:16S:614:C:OP2	40:S04:80:ARG:NH2	2.40	0.54
1:16S:674:G:H2'	1:16S:675:A:H8	1.72	0.54
1:16S:1297:G:N2	43:S07:113:LYS:O	2.40	0.54
2:23S:694:U:O4	2:23S:768:G:O6	2.26	0.54
2:23S:2124:G:N2	12:L1:217:THR:O	2.40	0.54
2:23S:2754:U:O3'	37:L36:19:ARG:NH2	2.40	0.54
22:L20:23:TYR:HB2	22:L20:28:SER:HB2	1.90	0.54
26:L24:3:LYS:O	26:L24:93:ARG:NH1	2.41	0.54
29:L28:15:ASN:HD21	29:L28:23:ALA:HB1	1.73	0.54
41:S05:106:ALA:O	41:S05:111:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:16S:1052:U:O2	1:16S:1206:G:O6	2.26	0.53
1:16S:1220:G:OP1	50:S14:52:ARG:NH2	2.41	0.53
1:16S:1329:A:H5"	49:S13:25:GLY:H	1.73	0.53
1:16S:1426:G:H1	1:16S:1474:U:H3	1.55	0.53
25:L23:10:VAL:HG13	25:L23:11:LEU:HD12	1.90	0.53
39:S03:9:ILE:HG23	39:S03:10:ARG:HG3	1.90	0.53
42:S06:2:ARG:HG2	42:S06:91:ARG:HH22	1.72	0.53
56:S20:41:GLY:O	56:S20:43:LYS:NZ	2.38	0.53
2:23S:2306:C:H5'	9:L05:132:ARG:HH12	1.73	0.53
2:23S:2698:U:H3	2:23S:2709:G:H1	1.56	0.53
11:L09:93:SER:OG	11:L09:121:VAL:O	2.27	0.53
44:S08:11:THR:O	44:S08:15:ASN:ND2	2.40	0.53
48:S12:69:GLU:O	48:S12:107:LYS:NZ	2.39	0.53
1:16S:593:U:O2	1:16S:646:G:N2	2.37	0.53
2:23S:1342:A:O2'	2:23S:1344:U:OP2	2.24	0.53
2:23S:1550:C:OP1	2:23S:1720:U:O2'	2.26	0.53
9:L05:97:GLU:OE1	32:L31:25:ARG:NH1	2.41	0.53
10:L06:21:GLN:NE2	10:L06:37:ASN:O	2.42	0.53
16:L14:8:LEU:HB2	16:L14:19:VAL:HG23	1.90	0.53
41:S05:54:GLU:HG3	41:S05:56:PRO:HD2	1.90	0.53
45:S09:15:ALA:O	45:S09:67:LYS:NZ	2.41	0.53
46:S10:28:THR:HB	46:S10:86:ALA:HB1	1.89	0.53
1:16S:745:G:OP1	1:16S:851:G:O2'	2.26	0.53
2:23S:1653:G:N1	19:L17:9:GLN:OE1	2.41	0.53
2:23S:2443:C:H2'	2:23S:2444:G:H8	1.72	0.53
47:S11:23:HIS:HB3	47:S11:30:ILE:HB	1.89	0.53
50:S14:5:MET:O	50:S14:62:ARG:NH2	2.40	0.53
1:16S:1423:G:N2	1:16S:1477:U:O2	2.37	0.53
10:L06:6:ALA:O	10:L06:68:ARG:NE	2.40	0.53
48:S12:42:LYS:HG3	48:S12:44:PRO:HD2	1.91	0.53
49:S13:89:ARG:HB2	49:S13:96:VAL:HG12	1.89	0.53
1:16S:134:G:O6	52:S16:25:ARG:NH1	2.42	0.53
1:16S:376:G:N2	1:16S:387:U:O2	2.38	0.53
1:16S:981:U:OP1	50:S14:8:ARG:NH1	2.42	0.53
2:23S:784:G:O6	2:23S:2072:C:O2'	2.27	0.53
2:23S:1952:A:N3	2:23S:2560:A:O2'	2.39	0.53
13:L10:40:GLU:HG3	13:L10:107:GLU:HG3	1.90	0.53
1:16S:1408:A:O2'	2:23S:1916:A:N1	2.41	0.53
2:23S:483:A:O2'	26:L24:56:GLY:N	2.40	0.53
2:23S:2285:C:H3'	34:L33:5:ARG:HH12	1.72	0.53
3:5S:65:U:H3'	3:5S:108:A:H61	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L1:56:ASP:OD1	12:L1:56:ASP:N	2.42	0.53
1:16S:1046:A:N6	1:16S:1211:U:O2'	2.41	0.53
1:16S:1071:C:O3'	41:S05:53:ARG:NH1	2.41	0.53
1:16S:1380:U:O2	1:16S:1382:C:N4	2.36	0.53
2:23S:210:C:H5"	35:L34:25:LYS:HE3	1.90	0.53
2:23S:1254:A:H5"	2:23S:1255:U:H5"	1.89	0.53
2:23S:1825:U:O2	6:L02:252:LYS:NZ	2.42	0.53
2:23S:1972:G:OP2	6:L02:237:ARG:NH1	2.42	0.53
2:23S:2746:U:H5"	10:L06:137:LYS:HE2	1.90	0.53
7:L03:156:PHE:HB3	15:L13:81:ILE:HB	1.90	0.53
25:L23:44:LYS:O	25:L23:48:GLN:NE2	2.42	0.53
39:S03:35:ASP:OD1	39:S03:58:ARG:NH2	2.42	0.53
42:S06:29:ILE:HD12	42:S06:30:THR:HG23	1.89	0.53
2:23S:408:G:N2	2:23S:419:U:O2	2.33	0.53
6:L02:255:LYS:HD3	6:L02:269:ARG:HH12	1.73	0.53
30:L29:28:LEU:HD22	30:L29:37:LEU:HD13	1.91	0.53
46:S10:11:LYS:HG3	46:S10:97:ASP:HB3	1.91	0.53
1:16S:1386:G:H2'	1:16S:1387:G:H8	1.73	0.53
2:23S:372:G:N2	2:23S:401:A:OP2	2.42	0.53
2:23S:499:U:H5"	26:L24:42:LYS:HE2	1.90	0.53
2:23S:647:G:N2	2:23S:2350:C:O3'	2.42	0.53
2:23S:1427:A:N6	2:23S:1571:A:OP2	2.37	0.53
8:L04:113:VAL:HG22	8:L04:118:LEU:HD22	1.91	0.53
28:L27:13:GLU:O	28:L27:15:LYS:NZ	2.40	0.53
55:S19:17:LYS:NZ	55:S19:31:ARG:O	2.40	0.53
1:16S:390:U:O3'	52:S16:28:ARG:NH1	2.42	0.52
1:16S:1191:A:OP1	39:S03:2:GLN:NE2	2.41	0.52
2:23S:2394:C:H5"	17:L15:63:LYS:HE2	1.92	0.52
2:23S:2680:U:H5'	7:L03:194:PRO:HA	1.91	0.52
1:16S:451:A:OP2	52:S16:70:ARG:NH2	2.40	0.52
2:23S:956:G:N2	2:23S:960:A:OP2	2.33	0.52
2:23S:1046:A:H2'	13:L10:62:ARG:HH21	1.74	0.52
2:23S:1047:G:O2'	2:23S:1111:A:N6	2.32	0.52
2:23S:1899:A:H4'	2:23S:1901:A:H5"	1.90	0.52
16:L14:63:VAL:HG12	16:L14:107:LEU:HD21	1.91	0.52
17:L15:51:GLU:OE2	17:L15:54:GLN:NE2	2.41	0.52
40:S04:167:PRO:HD2	40:S04:170:LEU:HD11	1.92	0.52
44:S08:88:LYS:HE2	44:S08:119:GLY:HA2	1.92	0.52
53:S17:10:ARG:HH11	53:S17:11:VAL:H	1.57	0.52
57:S21:55:HIS:HA	57:S21:58:LYS:HE2	1.89	0.52
1:16S:33:A:N6	1:16S:550:G:O6	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:16S:792:A:O2'	1:16S:794:A:N7	2.36	0.52
1:16S:973:G:O3'	50:S14:80:ARG:NH2	2.42	0.52
1:16S:1300:G:H1	1:16S:1334:G:H3'	1.74	0.52
2:23S:1111:A:H2'	2:23S:1112:G:H4'	1.91	0.52
2:23S:1328:A:H4'	2:23S:1329:U:H5	1.74	0.52
2:23S:1844:C:O3'	6:L02:255:LYS:NZ	2.40	0.52
50:S14:78:LEU:HD12	50:S14:83:VAL:HG23	1.89	0.52
2:23S:220:G:H22	2:23S:427:U:H2'	1.73	0.52
7:L03:37:VAL:HG22	7:L03:48:ILE:HG22	1.90	0.52
21:L19:30:TRP:NE1	21:L19:81:ASP:OD2	2.41	0.52
32:L31:8:LYS:HD3	32:L31:9:TYR:H	1.73	0.52
38:S02:23:ASN:ND2	38:S02:191:ASP:OD1	2.39	0.52
42:S06:10:VAL:HG12	42:S06:58:HIS:HB3	1.91	0.52
1:16S:73:C:H2'	1:16S:74:A:H8	1.73	0.52
1:16S:127:G:O2'	53:S17:5:ARG:NH1	2.42	0.52
1:16S:404:G:OP2	40:S04:1:ALA:N	2.43	0.52
1:16S:1166:G:N1	1:16S:1169:A:OP2	2.42	0.52
1:16S:1256:A:H1'	1:16S:1258:G:C4	2.45	0.52
2:23S:463:G:N2	2:23S:466:A:OP2	2.37	0.52
2:23S:1105:U:H2'	2:23S:1106:G:H8	1.74	0.52
2:23S:1682:G:OP2	2:23S:1699:G:N2	2.43	0.52
18:L16:110:GLU:OE2	18:L16:114:ARG:NH2	2.42	0.52
1:16S:1180:A:OP2	45:S09:98:ARG:NH2	2.43	0.52
2:23S:219:A:N6	2:23S:428:A:OP2	2.43	0.52
2:23S:789:A:N6	2:23S:1614:A:OP2	2.42	0.52
2:23S:2572:A:N7	7:L03:150:GLN:NE2	2.53	0.52
11:L09:104:THR:HG22	11:L09:109:GLU:HA	1.91	0.52
41:S05:98:ALA:HB3	41:S05:122:VAL:HA	1.91	0.52
1:16S:137:U:H3	1:16S:226:G:H1	1.56	0.52
1:16S:1376:U:H2'	1:16S:1377:A:H8	1.75	0.52
2:23S:494:G:OP1	24:L22:8:ARG:NH1	2.43	0.52
2:23S:1222:U:O2	2:23S:1227:G:O6	2.28	0.52
2:23S:1418:G:N1	2:23S:1579:A:OP2	2.36	0.52
2:23S:1721:G:H2'	2:23S:1738:G:H22	1.74	0.52
2:23S:2305:U:O2'	9:L05:132:ARG:NH1	2.43	0.52
21:L19:74:GLN:HB2	21:L19:77:SER:HB2	1.92	0.52
41:S05:148:SER:OG	41:S05:150:GLU:OE1	2.27	0.52
2:23S:1419:A:H61	2:23S:1495:A:H2	1.56	0.52
2:23S:1849:G:H2'	2:23S:1850:G:H8	1.75	0.52
2:23S:1869:G:H1'	2:23S:1872:A:H62	1.75	0.52
2:23S:2688:G:N1	2:23S:2720:U:OP2	2.32	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L02:180:MET:HB2	6:L02:268:ARG:H	1.73	0.52
10:L06:36:LEU:HD11	10:L06:71:LEU:HD11	1.91	0.52
26:L24:10:VAL:HA	26:L24:72:PHE:H	1.75	0.52
38:S02:11:ALA:HA	38:S02:207:ARG:HH11	1.74	0.52
46:S10:88:MET:HG3	46:S10:89:ARG:HD3	1.91	0.52
1:16S:422:C:HO2'	1:16S:423:G:N2	2.08	0.52
1:16S:749:A:O2'	51:S15:19:ASN:OD1	2.27	0.52
1:16S:1006:G:N2	1:16S:1023:U:O2	2.36	0.52
2:23S:301:G:H5'	2:23S:317:G:H21	1.74	0.52
2:23S:466:A:OP1	35:L34:34:ARG:NH2	2.43	0.52
2:23S:1310:G:H1'	2:23S:1611:C:H5"	1.91	0.52
2:23S:2102:G:N2	2:23S:2187:U:O2	2.42	0.52
3:5S:28:C:OP2	20:L18:33:ARG:NH2	2.43	0.52
3:5S:38:C:H2'	3:5S:39:A:C8	2.45	0.52
19:L17:12:ARG:O	19:L17:17:ARG:NH1	2.41	0.52
52:S16:29:ASN:OD1	52:S16:29:ASN:N	2.42	0.52
1:16S:321:A:N6	1:16S:328:C:O2'	2.43	0.52
1:16S:837:U:H3	1:16S:849:G:H1	1.57	0.52
2:23S:464:U:O2'	35:L34:12:ARG:NH1	2.42	0.52
2:23S:2656:U:C2	2:23S:2665:A:N7	2.78	0.52
13:L10:67:THR:HG21	13:L10:75:ALA:HB2	1.92	0.52
20:L18:7:ARG:HG3	20:L18:10:ARG:HH21	1.74	0.52
24:L22:3:THR:OG1	24:L22:107:VAL:O	2.28	0.52
44:S08:42:GLU:HG3	44:S08:100:ILE:HD13	1.92	0.52
45:S09:21:LYS:HB2	45:S09:61:ASP:HB2	1.92	0.52
1:16S:417:G:N2	1:16S:540:G:O2'	2.43	0.51
2:23S:698:C:O2'	2:23S:734:A:N6	2.43	0.51
2:23S:1021:A:H61	2:23S:1142:A:H61	1.58	0.51
2:23S:1143:A:OP1	15:L13:27:ARG:NH1	2.42	0.51
2:23S:1720:U:O2	2:23S:1740:G:O6	2.28	0.51
2:23S:1869:G:N2	2:23S:1872:A:OP2	2.43	0.51
10:L06:165:ASP:OD1	10:L06:165:ASP:N	2.42	0.51
18:L16:53:MET:HB2	18:L16:120:ALA:HB2	1.90	0.51
1:16S:119:A:OP2	1:16S:288:A:N6	2.35	0.51
1:16S:345:C:O2	1:16S:346:G:N1	2.43	0.51
1:16S:345:C:H5'	21:L19:38:ARG:HE	1.75	0.51
1:16S:1238:A:OP2	1:16S:1299:A:N6	2.36	0.51
2:23S:241:A:O2'	36:L35:2:LYS:NZ	2.43	0.51
2:23S:1857:G:N2	2:23S:1886:U:O4	2.43	0.51
2:23S:2183:A:H2'	2:23S:2184:A:C8	2.46	0.51
2:23S:2834:G:N2	2:23S:2883:A:N6	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:L34:24:THR:HG23	35:L34:27:GLY:H	1.75	0.51
37:L36:2:LYS:H	37:L36:35:GLN:HA	1.74	0.51
38:S02:93:HIS:ND1	38:S02:145:ASN:O	2.39	0.51
48:S12:3:VAL:HG23	48:S12:6:LEU:HD12	1.92	0.51
51:S15:13:GLU:OE2	51:S15:83:ARG:NH2	2.43	0.51
1:16S:1250:A:N3	1:16S:1370:G:O2'	2.38	0.51
1:16S:1413:A:H2	1:16S:1487:G:H1	1.58	0.51
2:23S:59:U:H1'	2:23S:73:A:H2'	1.93	0.51
2:23S:1046:A:H4'	13:L10:61:ARG:HB3	1.92	0.51
2:23S:1378:A:O2'	2:23S:1380:G:OP2	2.28	0.51
2:23S:2353:G:N2	28:L27:30:GLY:O	2.41	0.51
2:23S:2692:G:N3	2:23S:2847:U:O2'	2.43	0.51
10:L06:24:THR:HG22	10:L06:33:THR:HG23	1.93	0.51
15:L13:17:VAL:HG23	15:L13:137:PRO:HB2	1.92	0.51
43:S07:112:ASP:OD1	43:S07:112:ASP:N	2.44	0.51
49:S13:111:PRO:HB2	49:S13:113:LYS:HG2	1.92	0.51
1:16S:1209:C:O2'	1:16S:1214:C:N4	2.42	0.51
1:16S:1523:G:OP1	47:S11:127:ARG:NH2	2.43	0.51
2:23S:532:A:OP1	2:23S:561:G:N2	2.39	0.51
2:23S:881:G:H2'	2:23S:882:G:H8	1.76	0.51
2:23S:2102:G:N1	2:23S:2187:U:N3	2.49	0.51
2:23S:2118:U:O4	2:23S:2143:C:O2'	2.27	0.51
2:23S:2334:U:O2'	20:L18:13:ARG:NH2	2.44	0.51
8:L04:154:ASP:OD1	8:L04:154:ASP:N	2.43	0.51
14:L11:64:ARG:HH21	14:L11:65:SER:HB2	1.76	0.51
14:L11:135:MET:HB3	14:L11:137:LEU:HD13	1.92	0.51
17:L15:20:GLY:HA2	17:L15:28:GLY:HA2	1.91	0.51
27:L25:9:ARG:HG2	27:L25:41:GLU:HB3	1.92	0.51
32:L31:20:ASN:HD22	32:L31:37:CYS:HB2	1.75	0.51
42:S06:3:HIS:CE1	42:S06:92:THR:HG1	2.28	0.51
1:16S:1009:U:O2	1:16S:1020:G:N2	2.35	0.51
1:16S:1206:G:O2'	39:S03:191:THR:O	2.27	0.51
2:23S:18:U:O2'	2:23S:554:U:OP1	2.29	0.51
2:23S:321:U:H5"	8:L04:131:THR:HG23	1.91	0.51
2:23S:2622:U:O2'	2:23S:2824:C:N4	2.43	0.51
19:L17:90:ARG:NH1	19:L17:93:GLY:O	2.43	0.51
20:L18:25:ARG:HE	20:L18:40:ILE:HD12	1.76	0.51
26:L24:12:VAL:HA	26:L24:69:VAL:HG12	1.93	0.51
40:S04:98:ASP:OD2	40:S04:114:ARG:NH1	2.43	0.51
50:S14:37:ASP:H	50:S14:40:ARG:HB2	1.75	0.51
52:S16:40:ASN:HB3	52:S16:43:ALA:HB2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:16S:837:U:H2'	1:16S:838:G:H8	1.76	0.51
2:23S:99:U:H5"	2:23S:100:U:H5'	1.93	0.51
2:23S:1300:G:H4'	2:23S:1301:A:H5"	1.93	0.51
2:23S:1807:G:OP1	6:L02:47:ARG:NH1	2.44	0.51
2:23S:2081:U:OP1	29:L28:16:ASN:ND2	2.44	0.51
2:23S:2468:A:OP2	2:23S:2476:A:N6	2.43	0.51
2:23S:2533:U:OP1	2:23S:2665:A:O2'	2.27	0.51
39:S03:15:LYS:NZ	39:S03:181:ILE:O	2.39	0.51
1:16S:766:A:OP2	1:16S:812:G:N2	2.44	0.51
1:16S:1026:G:N1	1:16S:1035:A:C2	2.67	0.51
1:16S:1200:C:O2'	1:16S:1205:U:O4	2.28	0.51
1:16S:1530:G:H2'	1:16S:1531:A:H8	1.75	0.51
2:23S:390:U:H4'	2:23S:391:A:H5'	1.91	0.51
2:23S:535:G:N2	2:23S:558:U:O2	2.34	0.51
2:23S:1530:G:N1	2:23S:1542:U:O2	2.44	0.51
2:23S:2637:U:O2	2:23S:2776:A:N7	2.44	0.51
7:L03:31:ALA:HB1	7:L03:95:SER:HB3	1.93	0.51
42:S06:46:GLN:HA	42:S06:56:LYS:HA	1.93	0.51
1:16S:991:U:O2	1:16S:1213:A:N7	2.44	0.51
2:23S:519:U:H5"	24:L22:25:ARG:HH12	1.75	0.51
2:23S:1155:A:O3'	22:L20:54:ARG:NH1	2.43	0.51
7:L03:33:ARG:HD2	7:L03:73:VAL:HB	1.92	0.51
11:L09:6:LEU:HD21	11:L09:51:ARG:HD3	1.93	0.51
1:16S:21:G:H1'	1:16S:915:A:H61	1.75	0.51
1:16S:769:G:H4'	1:16S:1513:A:H4'	1.93	0.51
1:16S:1249:C:N4	1:16S:1288:A:OP2	2.44	0.51
2:23S:1096:A:N6	14:L11:29:GLN:OE1	2.43	0.51
2:23S:1769:U:O2	2:23S:1983:G:O6	2.28	0.51
41:S05:80:LEU:HD13	41:S05:122:VAL:HG11	1.93	0.51
43:S07:26:VAL:HG22	43:S07:42:VAL:HG11	1.93	0.51
2:23S:672:C:OP2	17:L15:42:SER:OG	2.29	0.51
2:23S:793:A:N6	2:23S:2073:C:OP1	2.43	0.51
2:23S:1066:U:H2'	2:23S:1068:G:H5"	1.93	0.51
20:L18:7:ARG:NH1	20:L18:95:SER:O	2.44	0.51
24:L22:58:ALA:HA	24:L22:62:ASP:HB2	1.93	0.51
40:S04:195:ASN:HD22	40:S04:198:LEU:HG	1.75	0.51
57:S21:5:VAL:HG22	57:S21:7:GLU:H	1.75	0.51
1:16S:1248:A:N6	1:16S:1288:A:OP2	2.44	0.50
1:16S:1278:G:N2	1:16S:1278:G:OP2	2.44	0.50
2:23S:774:G:H5"	6:L02:47:ARG:HH21	1.76	0.50
2:23S:1565:C:OP1	6:L02:17:LYS:NZ	2.38	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:2730:C:H2'	2:23S:2731:G:H8	1.76	0.50
9:L05:134:GLN:NE2	9:L05:147:ARG:O	2.41	0.50
12:L1:51:ASP:HB3	12:L1:57:GLN:HG3	1.94	0.50
15:L13:15:TRP:HB3	15:L13:137:PRO:HB3	1.93	0.50
27:L25:32:GLY:O	27:L25:93:ARG:NH1	2.42	0.50
52:S16:5:ARG:NH2	52:S16:27:ALA:O	2.41	0.50
1:16S:51:A:H61	1:16S:314:C:H1'	1.77	0.50
1:16S:417:G:O6	1:16S:426:U:O2	2.29	0.50
1:16S:1423:G:H1	1:16S:1477:U:H3	1.58	0.50
2:23S:996:A:H2'	2:23S:997:G:H8	1.77	0.50
2:23S:1141:U:O2	2:23S:1142:A:N6	2.44	0.50
11:L09:127:GLU:OE1	11:L09:145:ASN:ND2	2.44	0.50
21:L19:64:SER:OG	21:L19:65:ASN:OD1	2.29	0.50
47:S11:35:ASP:OD1	47:S11:39:ASN:N	2.44	0.50
1:16S:950:U:O2	1:16S:1231:G:N2	2.37	0.50
2:23S:851:C:O2'	31:L30:42:ALA:O	2.25	0.50
2:23S:2532:G:O2'	2:23S:2657:A:N1	2.43	0.50
2:23S:2659:G:N2	2:23S:2662:A:OP2	2.45	0.50
3:5S:13:G:H1	3:5S:69:G:HO2'	1.59	0.50
18:L16:29:GLY:N	18:L16:104:GLU:OE1	2.41	0.50
19:L17:29:VAL:HB	19:L17:75:ILE:HD12	1.93	0.50
25:L23:40:LYS:HZ3	25:L23:60:THR:HG22	1.75	0.50
1:16S:1444:U:O2	1:16S:1458:G:N2	2.39	0.50
2:23S:600:G:H1'	8:L04:100:MET:HG2	1.93	0.50
1:16S:1011:C:H2'	1:16S:1012:A:H8	1.76	0.50
1:16S:1307:U:O4	1:16S:1331:G:N2	2.44	0.50
2:23S:995:C:O2	22:L20:92:LYS:NZ	2.44	0.50
2:23S:1227:G:OP2	22:L20:15:LYS:NZ	2.43	0.50
2:23S:2684:U:OP2	21:L19:50:ARG:NH1	2.44	0.50
47:S11:92:ARG:NH2	47:S11:111:ASP:OD1	2.45	0.50
1:16S:160:A:N6	1:16S:346:G:N7	2.58	0.50
1:16S:861:G:H21	1:16S:874:G:H5'	1.76	0.50
2:23S:1619:G:O2'	35:L34:1:MET:N	2.40	0.50
6:L02:70:LYS:NZ	6:L02:97:ASP:OD2	2.45	0.50
9:L05:100:GLU:O	9:L05:104:THR:OG1	2.29	0.50
20:L18:26:LEU:HB3	20:L18:92:PHE:HA	1.92	0.50
42:S06:42:TRP:HB2	42:S06:59:TYR:HB2	1.93	0.50
44:S08:103:VAL:HA	44:S08:124:ILE:HA	1.94	0.50
1:16S:19:A:OP2	41:S05:131:ASN:ND2	2.45	0.50
1:16S:434:U:H2'	1:16S:435:A:H8	1.77	0.50
2:23S:1408:G:N2	2:23S:1594:U:O2	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:2489:U:O2'	2:23S:2518:A:N6	2.44	0.50
2:23S:2637:U:OP1	7:L03:83:ARG:NH1	2.45	0.50
6:L02:186:ASP:OD1	6:L02:186:ASP:N	2.45	0.50
11:L09:73:ASN:ND2	11:L09:106:ALA:O	2.45	0.50
24:L22:71:VAL:HA	24:L22:107:VAL:HG12	1.93	0.50
37:L36:22:VAL:HB	37:L36:37:GLN:HB3	1.94	0.50
39:S03:147:GLY:O	39:S03:202:PHE:N	2.45	0.50
52:S16:55:ASP:OD1	52:S16:55:ASP:N	2.42	0.50
1:16S:739:C:O2'	51:S15:41:HIS:ND1	2.42	0.50
1:16S:1006:G:O6	1:16S:1023:U:O4	2.30	0.50
1:16S:1367:C:H5'	46:S10:62:ARG:HH12	1.77	0.50
2:23S:479:A:H4'	2:23S:480:A:H5'	1.93	0.50
2:23S:1800:C:OP1	6:L02:257:ARG:NH1	2.42	0.50
2:23S:2135:A:N6	2:23S:2156:G:O2'	2.45	0.50
2:23S:2466:C:C4	2:23S:2467:C:N4	2.79	0.50
14:L11:36:GLU:OE2	14:L11:64:ARG:NH2	2.44	0.50
21:L19:89:GLY:O	21:L19:112:ARG:NH1	2.44	0.50
40:S04:130:ASN:OD1	40:S04:130:ASN:N	2.45	0.50
1:16S:1432:G:N2	1:16S:1468:A:OP2	2.41	0.50
2:23S:764:A:N3	6:L02:211:ARG:NH1	2.54	0.50
2:23S:1636:U:H2'	2:23S:1637:A:H8	1.77	0.50
2:23S:2581:G:OP2	2:23S:2581:G:N2	2.44	0.50
9:L05:157:THR:OG1	9:L05:158:THR:N	2.45	0.50
16:L14:1:MET:HA	16:L14:32:TYR:HB3	1.94	0.50
22:L20:89:ILE:HG12	23:L21:39:LEU:HD23	1.93	0.50
30:L29:24:GLU:HB2	30:L29:28:LEU:HG	1.94	0.50
45:S09:35:GLU:HA	45:S09:39:GLY:HA3	1.93	0.50
1:16S:310:G:H5"	52:S16:31:ARG:HB2	1.94	0.49
1:16S:933:G:O6	43:S07:2:ARG:NH2	2.45	0.49
12:L1:6:LYS:HA	12:L1:9:ARG:HH21	1.77	0.49
12:L1:8:MET:HA	12:L1:11:ILE:HD12	1.92	0.49
45:S09:8:THR:OG1	45:S09:9:GLY:N	2.43	0.49
54:S18:24:ASP:OD1	54:S18:24:ASP:N	2.35	0.49
2:23S:119:A:H4'	2:23S:120:U:H5'	1.93	0.49
2:23S:568:U:O4	23:L21:81:LYS:NZ	2.41	0.49
2:23S:1969:A:O2'	2:23S:1972:G:N3	2.37	0.49
2:23S:2139:U:H2'	2:23S:2140:G:H8	1.75	0.49
2:23S:2323:G:H21	2:23S:2337:G:H5'	1.77	0.49
12:L1:16:ASP:N	12:L1:16:ASP:OD1	2.43	0.49
13:L10:28:ALA:HA	13:L10:56:ARG:HH22	1.77	0.49
21:L19:46:VAL:HG22	21:L19:60:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:L30:5:LYS:HB2	31:L30:57:GLU:HB3	1.94	0.49
39:S03:84:GLU:OE2	39:S03:87:ARG:NH2	2.44	0.49
44:S08:100:ILE:HG13	44:S08:128:VAL:HB	1.93	0.49
1:16S:1419:G:N2	1:16S:1481:U:O2	2.39	0.49
2:23S:1223:G:N1	2:23S:1226:A:OP2	2.41	0.49
2:23S:2019:A:N6	2:23S:2035:G:H1	2.09	0.49
2:23S:2821:A:O3'	7:L03:167:ASN:ND2	2.38	0.49
30:L29:9:LYS:HB3	30:L29:12:GLU:HG2	1.93	0.49
44:S08:26:MET:O	44:S08:58:LEU:N	2.44	0.49
1:16S:1064:G:O2'	1:16S:1190:G:N2	2.36	0.49
1:16S:1239:A:H62	1:16S:1299:A:H2	1.58	0.49
2:23S:1204:A:N6	2:23S:1241:A:OP2	2.44	0.49
2:23S:2278:A:N6	28:L27:10:ARG:O	2.44	0.49
2:23S:2730:C:O3'	7:L03:174:SER:OG	2.30	0.49
3:5S:5:U:OP1	3:5S:61:G:O2'	2.29	0.49
6:L02:117:SER:OG	6:L02:118:GLY:N	2.46	0.49
10:L06:104:LEU:HD11	10:L06:147:LEU:HD12	1.95	0.49
51:S15:25:GLU:HG2	51:S15:80:LEU:HD22	1.94	0.49
1:16S:768:A:N3	1:16S:1512:U:O2'	2.40	0.49
2:23S:770:G:H5"	35:L34:10:LEU:HD23	1.94	0.49
2:23S:954:G:OP2	18:L16:16:ARG:NH1	2.36	0.49
2:23S:1022:G:N2	2:23S:1023:U:O4	2.45	0.49
2:23S:2519:U:O4'	2:23S:2542:A:N6	2.45	0.49
2:23S:2847:U:OP1	21:L19:95:LYS:NZ	2.41	0.49
8:L04:112:LEU:HD13	8:L04:186:VAL:HG21	1.94	0.49
13:L10:43:LYS:HA	13:L10:46:ARG:HH21	1.78	0.49
39:S03:135:ARG:O	39:S03:139:ASN:ND2	2.36	0.49
45:S09:21:LYS:O	45:S09:61:ASP:N	2.45	0.49
57:S21:32:ARG:HG3	57:S21:33:ARG:HG3	1.94	0.49
1:16S:689:C:OP1	47:S11:28:ASN:ND2	2.45	0.49
1:16S:1013:G:N2	1:16S:1016:A:OP2	2.37	0.49
2:23S:1012:U:O4	15:L13:30:THR:OG1	2.27	0.49
2:23S:2372:U:H2'	2:23S:2373:G:H8	1.77	0.49
2:23S:2515:C:H2'	2:23S:2516:A:H8	1.78	0.49
8:L04:145:ASP:HB3	8:L04:184:ASP:HB2	1.95	0.49
15:L13:106:LYS:O	15:L13:111:LYS:NZ	2.41	0.49
1:16S:1444:U:H3	1:16S:1458:G:H1	1.61	0.49
2:23S:196:A:H61	2:23S:831:G:H21	1.59	0.49
2:23S:578:G:OP1	2:23S:1255:U:O2'	2.28	0.49
2:23S:1428:C:OP2	6:L02:27:LYS:NZ	2.45	0.49
2:23S:2692:G:H1'	2:23S:2847:U:H1'	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:L19:112:ARG:O	21:L19:114:ASN:ND2	2.41	0.49
25:L23:65:GLY:N	25:L23:79:ASP:OD1	2.44	0.49
44:S08:11:THR:OG1	44:S08:15:ASN:ND2	2.45	0.49
53:S17:49:ASN:OD1	53:S17:49:ASN:N	2.42	0.49
2:23S:301:G:OP2	26:L24:81:ARG:NH1	2.45	0.49
2:23S:311:A:HO2'	2:23S:331:C:HO2'	1.61	0.49
2:23S:2830:C:H3'	7:L03:59:ARG:HH21	1.77	0.49
17:L15:85:VAL:HG13	17:L15:98:ALA:HB2	1.93	0.49
19:L17:8:ARG:N	19:L17:43:GLU:OE2	2.45	0.49
23:L21:41:ILE:HB	23:L21:47:VAL:HB	1.94	0.49
38:S02:57:ASN:OD1	38:S02:219:THR:OG1	2.30	0.49
54:S18:11:ARG:NH1	54:S18:11:ARG:O	2.45	0.49
2:23S:1173:U:O2	2:23S:1176:U:N3	2.37	0.49
3:5S:22:U:O2	3:5S:61:G:N2	2.46	0.49
14:L11:129:GLU:HG3	14:L11:139:VAL:HG21	1.95	0.49
21:L19:6:GLN:OE1	21:L19:9:GLN:NE2	2.46	0.49
24:L22:23:LEU:HD11	33:L32:21:LEU:HB3	1.95	0.49
49:S13:13:HIS:O	49:S13:17:ALA:N	2.45	0.49
51:S15:28:VAL:HG11	51:S15:66:LEU:HD21	1.94	0.49
1:16S:309:A:H2'	1:16S:310:G:H8	1.77	0.49
1:16S:1237:C:OP1	1:16S:1303:C:O2'	2.31	0.49
2:23S:1028:A:OP2	2:23S:1126:A:N6	2.38	0.49
2:23S:1063:G:O2'	14:L11:89:SER:N	2.46	0.49
2:23S:1131:G:N2	2:23S:1132:U:O4	2.45	0.49
2:23S:2125:G:N2	2:23S:2172:U:OP1	2.45	0.49
2:23S:2291:U:O2'	2:23S:2374:C:O2	2.31	0.49
9:L05:60:SER:HB2	32:L31:6:HIS:HB3	1.95	0.49
9:L05:146:ASP:N	9:L05:146:ASP:OD1	2.46	0.49
51:S15:63:ARG:HH21	51:S15:87:ARG:HH21	1.61	0.49
1:16S:448:A:H62	1:16S:486:U:H3	1.59	0.48
1:16S:1115:U:O2	1:16S:1185:G:N2	2.38	0.48
1:16S:1500:A:H5"	1:16S:1508:A:H5"	1.94	0.48
2:23S:2006:C:O2'	2:23S:2823:A:N3	2.46	0.48
12:L1:67:HIS:HB2	12:L1:188:ASN:HD21	1.78	0.48
40:S04:105:GLY:HA3	40:S04:161:ALA:HB2	1.95	0.48
1:16S:20:U:O2'	1:16S:573:A:N6	2.46	0.48
2:23S:1135:C:N4	2:23S:1138:G:OP2	2.39	0.48
2:23S:1173:U:O2'	2:23S:1177:G:N1	2.45	0.48
2:23S:1373:A:H5'	2:23S:2212:A:H1'	1.95	0.48
2:23S:1476:U:H2'	2:23S:1477:A:H8	1.77	0.48
2:23S:1568:G:OP2	6:L02:62:ARG:NH2	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:2139:U:C2	2:23S:2152:G:O6	2.66	0.48
2:23S:2756:U:OP2	37:L36:19:ARG:NE	2.45	0.48
8:L04:60:TRP:NE1	8:L04:70:SER:OG	2.45	0.48
31:L30:11:SER:HB3	31:L30:13:ILE:HG12	1.95	0.48
1:16S:845:A:O2'	54:S18:11:ARG:NE	2.46	0.48
1:16S:962:C:H2'	1:16S:963:G:H8	1.78	0.48
1:16S:981:U:O4	1:16S:1223:C:N4	2.41	0.48
2:23S:5:A:H2'	2:23S:6:A:C8	2.48	0.48
2:23S:1078:U:H5'	14:L11:133:ARG:HD3	1.96	0.48
2:23S:1469:A:H2'	2:23S:1470:A:C8	2.49	0.48
2:23S:1992:G:N2	2:23S:1996:C:O2'	2.45	0.48
2:23S:2530:A:OP2	2:23S:2535:G:N2	2.45	0.48
8:L04:7:ASP:OD1	8:L04:7:ASP:N	2.46	0.48
2:23S:1338:G:N7	25:L23:66:LYS:NZ	2.61	0.48
2:23S:1667:G:O2'	2:23S:1991:U:O4	2.27	0.48
11:L09:132:PHE:HB3	11:L09:134:VAL:HG23	1.94	0.48
12:L1:43:ASP:N	12:L1:215:SER:O	2.45	0.48
13:L10:97:LYS:O	13:L10:101:LYS:N	2.44	0.48
39:S03:113:LYS:NZ	39:S03:185:THR:O	2.46	0.48
43:S07:74:VAL:HA	43:S07:87:PRO:HA	1.95	0.48
46:S10:71:LEU:O	46:S10:72:ARG:NH1	2.44	0.48
47:S11:85:VAL:HG11	57:S21:16:ARG:HH22	1.79	0.48
1:16S:643:C:H5'	44:S08:31:LEU:HD13	1.94	0.48
1:16S:1031:C:H4'	1:16S:1033:G:H1'	1.96	0.48
2:23S:743:A:O2'	2:23S:1659:G:OP1	2.25	0.48
2:23S:1153:C:OP1	22:L20:91:ARG:NH2	2.45	0.48
2:23S:1319:C:C4	2:23S:1320:C:N4	2.81	0.48
2:23S:1590:A:H2'	2:23S:1591:A:C8	2.49	0.48
2:23S:1816:C:N4	6:L02:34:GLU:OE2	2.42	0.48
9:L05:35:LEU:HB3	9:L05:88:VAL:HB	1.95	0.48
1:16S:403:C:OP1	40:S04:133:SER:OG	2.31	0.48
1:16S:1073:U:O2	38:S02:102:ASN:ND2	2.37	0.48
2:23S:2291:U:OP1	2:23S:2380:C:O2'	2.31	0.48
6:L02:154:ALA:HB2	6:L02:161:VAL:HG23	1.96	0.48
18:L16:50:ARG:O	18:L16:54:THR:OG1	2.31	0.48
42:S06:5:GLU:HA	42:S06:63:ASN:HD22	1.79	0.48
1:16S:925:G:N2	1:16S:1391:U:O2	2.39	0.48
1:16S:1492:A:N6	48:S12:46:SER:OG	2.47	0.48
2:23S:447:A:OP1	22:L20:4:LYS:NZ	2.46	0.48
2:23S:2377:A:O2'	20:L18:117:PHE:O	2.32	0.48
2:23S:2623:G:H2'	2:23S:2624:G:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:2701:U:O2	19:L17:71:ARG:NH2	2.45	0.48
11:L09:6:LEU:HB2	11:L09:36:ALA:HA	1.95	0.48
27:L25:29:ILE:HG13	27:L25:39:ALA:HA	1.95	0.48
45:S09:86:LEU:HB3	45:S09:89:TYR:HB2	1.95	0.48
46:S10:52:LEU:HB2	50:S14:80:ARG:HD2	1.95	0.48
48:S12:28:GLN:HB3	48:S12:80:LEU:HG	1.95	0.48
2:23S:69:C:O2	2:23S:73:A:O2'	2.28	0.48
2:23S:1770:G:O6	2:23S:1982:U:O4	2.31	0.48
2:23S:2857:G:N2	2:23S:2860:A:OP2	2.33	0.48
6:L02:79:ARG:NH1	6:L02:81:GLU:OE2	2.40	0.48
30:L29:12:GLU:O	30:L29:15:ASN:ND2	2.46	0.48
48:S12:67:GLY:H	48:S12:96:THR:HG22	1.78	0.48
49:S13:2:ARG:O	49:S13:56:ARG:NH2	2.47	0.48
51:S15:11:VAL:HG11	51:S15:21:THR:HG22	1.96	0.48
1:16S:62:U:OP1	1:16S:385:C:O2'	2.32	0.48
1:16S:1071:C:H2'	1:16S:1072:G:C8	2.49	0.48
2:23S:2085:U:O2	2:23S:2234:G:O6	2.32	0.48
2:23S:2739:U:H2'	2:23S:2740:A:H8	1.78	0.48
53:S17:45:VAL:HG11	53:S17:60:ILE:HD12	1.95	0.48
2:23S:627:A:O2'	17:L15:76:GLU:OE2	2.32	0.48
2:23S:971:G:OP1	2:23S:989:G:N1	2.46	0.48
2:23S:1054:A:O2'	13:L10:30:SER:O	2.26	0.48
2:23S:1282:U:O4	2:23S:1286:A:N7	2.46	0.48
2:23S:1654:A:O2'	7:L03:118:PHE:O	2.28	0.48
2:23S:2134:A:OP2	2:23S:2156:G:N1	2.38	0.48
2:23S:2473:U:OP1	2:23S:2529:G:N2	2.38	0.48
2:23S:2676:C:OP1	16:L14:31:ARG:NH2	2.41	0.48
14:L11:124:MET:SD	14:L11:127:SER:OG	2.63	0.48
51:S15:6:ALA:HA	51:S15:9:LYS:HE2	1.96	0.48
2:23S:1248:G:O6	8:L04:46:GLN:NE2	2.46	0.47
2:23S:1597:A:H5"	2:23S:1598:A:H5'	1.95	0.47
2:23S:1674:G:N2	2:23S:1991:U:O2	2.47	0.47
2:23S:2122:U:O2	12:L1:172:HIS:NE2	2.46	0.47
2:23S:2167:U:N3	2:23S:2170:A:OP2	2.42	0.47
2:23S:2656:U:H2'	2:23S:2657:A:H8	1.78	0.47
10:L06:100:ASN:HA	10:L06:116:LEU:HD12	1.95	0.47
13:L10:10:ALA:HB1	13:L10:53:ARG:HH22	1.79	0.47
18:L16:47:GLU:OE2	18:L16:50:ARG:NH2	2.41	0.47
32:L31:9:TYR:OH	32:L31:11:GLU:OE1	2.28	0.47
39:S03:181:ILE:HG12	39:S03:202:PHE:HA	1.96	0.47
45:S09:11:ARG:NE	45:S09:106:ASP:OD2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:S14:29:ILE:HA	50:S14:32:ASP:HB2	1.96	0.47
53:S17:56:ASP:OD1	53:S17:56:ASP:N	2.47	0.47
1:16S:300:A:O2'	1:16S:564:C:N3	2.38	0.47
1:16S:570:G:O6	1:16S:865:A:N6	2.47	0.47
1:16S:1297:G:H1'	1:16S:1298:U:H5	1.79	0.47
2:23S:848:C:H2'	2:23S:849:A:H8	1.79	0.47
2:23S:1548:A:H2'	2:23S:1549:A:C8	2.49	0.47
6:L02:140:VAL:HG12	6:L02:191:LEU:HA	1.96	0.47
18:L16:34:LYS:HA	18:L16:101:VAL:HA	1.96	0.47
18:L16:75:GLU:N	18:L16:90:GLU:OE1	2.47	0.47
29:L28:6:VAL:HG11	29:L28:58:ILE:HD11	1.95	0.47
34:L33:29:LYS:NZ	34:L33:31:GLU:OE2	2.47	0.47
54:S18:70:THR:OG1	54:S18:71:ASP:N	2.47	0.47
1:16S:1053:G:H4'	1:16S:1054:C:H3'	1.96	0.47
1:16S:1156:G:O2'	1:16S:1180:A:N6	2.44	0.47
1:16S:1422:G:N2	1:16S:1478:U:O2	2.33	0.47
2:23S:78:U:O4	2:23S:108:G:O6	2.32	0.47
2:23S:632:A:H4'	17:L15:68:SER:HB2	1.96	0.47
2:23S:673:C:OP1	8:L04:49:ARG:NH1	2.47	0.47
2:23S:1709:U:O2'	2:23S:2859:G:N3	2.44	0.47
15:L13:19:ASP:OD1	15:L13:19:ASP:N	2.46	0.47
15:L13:71:ASP:OD1	15:L13:71:ASP:N	2.46	0.47
18:L16:64:TRP:N	18:L16:104:GLU:O	2.42	0.47
43:S07:41:ILE:HD13	43:S07:115:MET:HB2	1.96	0.47
45:S09:97:LEU:O	45:S09:101:GLY:N	2.42	0.47
47:S11:85:VAL:HG13	47:S11:111:ASP:HA	1.96	0.47
1:16S:791:G:O6	1:16S:792:A:N6	2.47	0.47
1:16S:1225:A:OP1	49:S13:101:THR:N	2.43	0.47
2:23S:250:G:O6	2:23S:386:G:N1	2.39	0.47
2:23S:740:C:N4	2:23S:758:C:O2	2.47	0.47
2:23S:1668:A:H61	2:23S:1677:A:H2	1.62	0.47
2:23S:1847:A:HO2'	2:23S:1848:A:H8	1.58	0.47
8:L04:105:LEU:HD21	8:L04:177:PRO:HG3	1.96	0.47
17:L15:33:ARG:HD3	17:L15:40:SER:HA	1.97	0.47
21:L19:64:SER:OG	21:L19:65:ASN:N	2.47	0.47
43:S07:68:VAL:HG13	43:S07:133:ALA:HB1	1.97	0.47
1:16S:66:A:O2'	1:16S:172:A:O2'	2.31	0.47
2:23S:480:A:OP2	26:L24:43:LYS:NZ	2.44	0.47
2:23S:1227:G:OP1	22:L20:12:ARG:NH1	2.46	0.47
3:5S:24:G:H1'	3:5S:27:C:H42	1.80	0.47
3:5S:42:C:H1'	9:L05:65:LEU:HD22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L03:24:VAL:HG12	7:L03:178:VAL:HG21	1.95	0.47
7:L03:116:LYS:HB2	7:L03:165:MET:HB3	1.95	0.47
13:L10:28:ALA:HB3	13:L10:109:LYS:HB2	1.96	0.47
22:L20:46:TYR:OH	23:L21:76:LYS:NZ	2.44	0.47
28:L27:47:VAL:HG21	28:L27:76:ILE:HG22	1.96	0.47
33:L32:24:VAL:HG22	33:L32:26:SER:H	1.79	0.47
39:S03:18:ASN:OD1	39:S03:53:ARG:NH2	2.47	0.47
1:16S:396:C:O2'	1:16S:398:U:OP1	2.29	0.47
2:23S:1715:G:N2	2:23S:1716:U:O4	2.43	0.47
2:23S:2048:G:H21	7:L03:118:PHE:HE1	1.61	0.47
2:23S:2143:C:H2'	2:23S:2144:G:C4	2.50	0.47
2:23S:2681:C:O2	2:23S:2683:C:N4	2.43	0.47
29:L28:70:LEU:HD22	29:L28:75:GLU:HG3	1.97	0.47
38:S02:65:LYS:HB3	38:S02:89:PHE:HE2	1.79	0.47
42:S06:4:TYR:O	42:S06:63:ASN:ND2	2.47	0.47
56:S20:77:ASN:O	56:S20:81:GLN:N	2.47	0.47
1:16S:231:U:H2'	1:16S:232:G:H8	1.79	0.47
1:16S:579:A:O2'	51:S15:53:ARG:NH1	2.44	0.47
1:16S:880:C:H2'	1:16S:881:G:H8	1.78	0.47
1:16S:1237:C:O2'	1:16S:1300:G:N2	2.40	0.47
2:23S:300:A:O5'	26:L24:81:ARG:NH1	2.47	0.47
2:23S:767:U:H2'	2:23S:768:G:C8	2.49	0.47
2:23S:941:A:O2'	2:23S:1190:G:O3'	2.31	0.47
2:23S:1305:C:N4	2:23S:1607:C:OP2	2.46	0.47
2:23S:1333:G:H2'	2:23S:1334:G:H8	1.80	0.47
2:23S:1495:A:H2'	2:23S:1496:A:C4	2.49	0.47
2:23S:1622:G:H2'	2:23S:1623:G:H8	1.77	0.47
2:23S:2124:G:H1'	12:L1:43:ASP:HB2	1.97	0.47
2:23S:2511:U:OP1	7:L03:128:ARG:NH2	2.47	0.47
2:23S:2822:G:O2'	2:23S:2825:G:N1	2.48	0.47
2:23S:2855:C:H2'	2:23S:2856:A:H8	1.79	0.47
6:L02:146:LYS:HB2	6:L02:149:LYS:HB2	1.96	0.47
11:L09:98:ASP:N	11:L09:98:ASP:OD1	2.47	0.47
14:L11:106:GLN:O	14:L11:110:GLN:N	2.48	0.47
39:S03:138:GLN:OE1	39:S03:139:ASN:ND2	2.48	0.47
39:S03:176:THR:HG22	39:S03:179:ALA:H	1.80	0.47
40:S04:9:LYS:HG3	40:S04:12:ARG:HH21	1.80	0.47
1:16S:150:U:C2	1:16S:171:A:N6	2.77	0.47
1:16S:235:C:H2'	1:16S:236:A:C8	2.50	0.47
1:16S:1452:C:H4'	1:16S:1453:G:C2	2.50	0.47
2:23S:353:C:H2'	2:23S:354:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:603:A:N6	2:23S:655:A:O4'	2.47	0.47
2:23S:711:G:N2	2:23S:720:U:O2	2.35	0.47
2:23S:953:G:H2'	2:23S:954:G:H8	1.79	0.47
2:23S:1853:A:N7	2:23S:1889:A:N6	2.63	0.47
2:23S:2684:U:O4'	16:L14:70:ARG:NH1	2.47	0.47
2:23S:2725:A:H2'	2:23S:2726:A:H2'	1.96	0.47
7:L03:13:ARG:HD2	7:L03:21:SER:HB2	1.96	0.47
7:L03:38:LYS:HB2	7:L03:47:ALA:H	1.80	0.47
12:L1:46:VAL:HB	12:L1:171:ILE:HG23	1.97	0.47
12:L1:213:SER:HA	12:L1:223:ALA:HA	1.97	0.47
14:L11:41:PHE:O	14:L11:45:THR:OG1	2.32	0.47
57:S21:54:ARG:HA	57:S21:57:LYS:HE2	1.97	0.47
1:16S:143:A:H2	1:16S:220:G:H1	1.61	0.47
1:16S:927:G:N2	1:16S:1390:U:O2	2.40	0.47
1:16S:999:C:H2'	1:16S:1000:A:H8	1.79	0.47
2:23S:220:G:O2'	2:23S:233:A:N3	2.37	0.47
2:23S:399:U:OP2	29:L28:56:ARG:NH1	2.48	0.47
2:23S:568:U:N3	2:23S:571:U:OP2	2.43	0.47
2:23S:1788:C:OP1	6:L02:220:ARG:NH2	2.47	0.47
2:23S:2748:A:H5'	10:L06:3:VAL:HG21	1.95	0.47
21:L19:23:ASP:HA	21:L19:89:GLY:H	1.80	0.47
22:L20:48:ASP:HA	22:L20:51:GLN:HB2	1.97	0.47
40:S04:109:THR:H	40:S04:112:GLU:HB3	1.79	0.47
41:S05:81:GLN:HG2	41:S05:149:PRO:HD3	1.97	0.47
42:S06:3:HIS:CD2	42:S06:95:ALA:H	2.33	0.47
1:16S:427:U:O2'	1:16S:541:G:OP1	2.32	0.47
2:23S:1154:G:OP2	22:L20:57:ARG:NH1	2.48	0.47
2:23S:1434:A:H2'	2:23S:1435:G:C8	2.50	0.47
2:23S:1796:U:H2'	2:23S:1797:G:C8	2.50	0.47
2:23S:2064:C:O2'	2:23S:2251:G:N2	2.48	0.47
7:L03:13:ARG:HH21	21:L19:55:HIS:HA	1.80	0.47
10:L06:136:ASP:HB3	10:L06:139:VAL:HB	1.97	0.47
1:16S:198:G:O6	1:16S:219:U:O4	2.32	0.46
1:16S:434:U:H2'	1:16S:435:A:C8	2.50	0.46
1:16S:463:U:H3	1:16S:469:C:H42	1.63	0.46
1:16S:754:C:OP1	51:S15:71:ARG:NH2	2.40	0.46
1:16S:1333:A:H3'	1:16S:1334:G:H8	1.80	0.46
2:23S:126:A:N6	35:L34:43:THR:OG1	2.49	0.46
2:23S:377:G:O6	2:23S:397:U:O4	2.33	0.46
14:L11:16:MET:HB2	14:L11:19:PRO:HB3	1.96	0.46
16:L14:1:MET:N	16:L14:33:ALA:O	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:L19:4:ILE:HG13	21:L19:7:LEU:HD12	1.96	0.46
22:L20:90:ASP:OD1	22:L20:90:ASP:N	2.43	0.46
38:S02:111:LYS:O	38:S02:115:ASP:N	2.46	0.46
1:16S:81:A:H2'	1:16S:82:G:C8	2.50	0.46
1:16S:436:C:O3'	40:S04:152:SER:OG	2.29	0.46
1:16S:1157:A:OP1	1:16S:1158:C:N4	2.48	0.46
2:23S:1054:A:H2'	2:23S:1055:G:C8	2.49	0.46
2:23S:1060:U:H1'	2:23S:1062:G:H5'	1.98	0.46
2:23S:1130:U:N3	2:23S:2025:C:OP1	2.44	0.46
2:23S:1601:G:OP1	25:L23:64:LYS:NZ	2.39	0.46
2:23S:2192:U:H2'	2:23S:2193:G:H8	1.80	0.46
2:23S:2374:C:N4	2:23S:2375:G:O6	2.48	0.46
55:S19:50:VAL:HG11	55:S19:70:LEU:HB3	1.96	0.46
1:16S:222:C:H2'	1:16S:223:A:H8	1.80	0.46
1:16S:401:C:H2'	1:16S:402:G:H8	1.79	0.46
2:23S:605:G:OP1	8:L04:99:LYS:NZ	2.48	0.46
2:23S:906:U:O2'	18:L16:66:ARG:NH2	2.48	0.46
2:23S:956:G:OP2	18:L16:86:LYS:NZ	2.41	0.46
2:23S:1266:G:O5'	24:L22:15:GLN:NE2	2.46	0.46
2:23S:1753:G:H5"	21:L19:92:ARG:HD3	1.98	0.46
2:23S:2010:G:H4'	24:L22:42:LYS:HD3	1.96	0.46
2:23S:2072:C:N4	2:23S:2073:C:H42	2.13	0.46
2:23S:2297:A:H62	2:23S:2318:G:N2	2.14	0.46
10:L06:117:PRO:HD2	10:L06:120:ILE:HB	1.97	0.46
30:L29:9:LYS:HE3	30:L29:11:VAL:HB	1.96	0.46
45:S09:90:ASP:N	45:S09:90:ASP:OD1	2.44	0.46
50:S14:40:ARG:HE	50:S14:40:ARG:HB3	1.60	0.46
1:16S:8:A:N6	40:S04:201:GLU:O	2.49	0.46
1:16S:23:C:OP2	1:16S:561:U:N3	2.48	0.46
1:16S:385:C:C4	1:16S:386:C:N4	2.83	0.46
1:16S:567:G:O6	48:S12:1:ALA:N	2.48	0.46
2:23S:563:A:H4'	22:L20:40:LYS:HE3	1.98	0.46
2:23S:631:A:OP2	36:L35:22:LYS:NZ	2.38	0.46
2:23S:1992:G:H5'	2:23S:1993:U:H5	1.79	0.46
7:L03:104:VAL:HG11	7:L03:205:PRO:HB3	1.98	0.46
8:L04:48:THR:HG23	8:L04:50:ALA:H	1.81	0.46
9:L05:3:LEU:HB2	9:L05:172:PHE:HE1	1.80	0.46
21:L19:91:VAL:HG21	21:L19:96:LEU:HD11	1.95	0.46
38:S02:80:LYS:HE2	38:S02:80:LYS:HB3	1.82	0.46
40:S04:100:VAL:O	40:S04:104:MET:N	2.46	0.46
42:S06:82:ASP:N	42:S06:82:ASP:OD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S07:64:ALA:HA	43:S07:127:ALA:HA	1.98	0.46
55:S19:48:ILE:O	55:S19:59:VAL:N	2.48	0.46
1:16S:59:A:H3'	1:16S:331:G:H22	1.81	0.46
1:16S:113:G:H1'	1:16S:354:G:H5"	1.97	0.46
1:16S:517:G:N2	1:16S:533:A:OP2	2.43	0.46
2:23S:807:U:OP2	17:L15:41:ARG:NH2	2.41	0.46
2:23S:2220:U:H2'	2:23S:2221:G:H8	1.80	0.46
2:23S:2656:U:H3	2:23S:2665:A:H8	1.50	0.46
10:L06:41:GLU:HA	10:L06:54:ARG:HH21	1.81	0.46
11:L09:40:THR:OG1	11:L09:43:ASN:OD1	2.33	0.46
13:L10:37:LYS:HG3	13:L10:38:MET:HE2	1.97	0.46
32:L31:3:LYS:HD3	32:L31:3:LYS:HA	1.76	0.46
48:S12:53:ARG:HG2	48:S12:63:THR:HG22	1.97	0.46
50:S14:38:GLU:HA	50:S14:41:TRP:HB3	1.96	0.46
1:16S:546:A:H3'	40:S04:67:LEU:HD11	1.98	0.46
1:16S:687:A:N1	1:16S:700:G:O2'	2.38	0.46
1:16S:884:U:H4'	1:16S:885:G:H5"	1.98	0.46
1:16S:1429:A:H2'	1:16S:1430:A:H8	1.80	0.46
2:23S:249:C:O2	36:L35:11:LYS:NZ	2.47	0.46
2:23S:259:G:H2'	2:23S:260:G:H8	1.80	0.46
2:23S:1199:U:H1'	22:L20:3:VAL:HG22	1.98	0.46
2:23S:2847:U:O4	2:23S:2869:G:O6	2.33	0.46
21:L19:26:GLU:HA	21:L19:43:GLU:HA	1.97	0.46
49:S13:14:ALA:N	49:S13:40:GLU:O	2.47	0.46
52:S16:4:ILE:HG12	52:S16:21:VAL:HG22	1.98	0.46
2:23S:154:U:H2'	2:23S:155:A:C8	2.51	0.46
2:23S:1127:A:H62	2:23S:2488:G:H1'	1.81	0.46
2:23S:1792:G:H1	2:23S:1827:U:H3	1.64	0.46
2:23S:2680:U:O2'	7:L03:11:MET:SD	2.73	0.46
2:23S:2787:C:H1'	7:L03:63:PRO:HG3	1.97	0.46
3:5S:77:U:H2'	3:5S:78:A:H8	1.80	0.46
6:L02:24:HIS:ND1	6:L02:81:GLU:OE2	2.43	0.46
10:L06:41:GLU:N	10:L06:52:GLY:O	2.47	0.46
48:S12:64:SER:OG	48:S12:65:TYR:N	2.48	0.46
2:23S:2884:U:O2	33:L32:39:ARG:NH1	2.49	0.46
18:L16:24:THR:O	18:L16:34:LYS:NZ	2.39	0.46
23:L21:32:THR:HA	23:L21:62:GLU:HA	1.98	0.46
27:L25:79:ARG:HA	27:L25:86:LEU:HA	1.98	0.46
38:S02:141:GLU:O	38:S02:145:ASN:N	2.45	0.46
39:S03:25:THR:HA	50:S14:75:LYS:HE3	1.96	0.46
46:S10:8:ILE:HB	46:S10:74:VAL:HB	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:S18:11:ARG:HE	54:S18:14:ALA:HB3	1.81	0.46
1:16S:615:G:O6	1:16S:625:U:O4	2.34	0.46
2:23S:78:U:O2	2:23S:108:G:N2	2.36	0.46
2:23S:398:C:OP1	29:L28:31:ASN:ND2	2.48	0.46
2:23S:1306:C:H2'	2:23S:1307:A:H8	1.80	0.46
2:23S:2013:A:O2'	24:L22:94:ASP:OD2	2.34	0.46
2:23S:2392:A:OP2	36:L35:30:HIS:NE2	2.49	0.46
9:L05:3:LEU:O	9:L05:7:TYR:N	2.47	0.46
9:L05:7:TYR:HB2	9:L05:172:PHE:HZ	1.81	0.46
11:L09:128:HIS:HB2	11:L09:144:VAL:HG13	1.98	0.46
14:L11:73:PRO:O	14:L11:112:LYS:NZ	2.35	0.46
28:L27:26:SER:HB2	28:L27:62:LYS:HG2	1.98	0.46
42:S06:12:PRO:HG3	42:S06:57:ALA:HA	1.98	0.46
57:S21:40:PRO:HA	57:S21:43:GLU:HG2	1.98	0.46
2:23S:2152:G:H5"	12:L1:3:LYS:HD3	1.98	0.46
15:L13:45:THR:HB	15:L13:48:VAL:HB	1.98	0.46
47:S11:28:ASN:HB2	47:S11:56:LYS:HE3	1.97	0.46
1:16S:412:A:H8	1:16S:413:G:H4'	1.81	0.45
1:16S:728:A:N7	51:S15:53:ARG:NE	2.64	0.45
1:16S:750:C:O2'	51:S15:20:ASP:OD1	2.29	0.45
1:16S:1137:C:H4'	1:16S:1138:G:C2	2.52	0.45
1:16S:1316:G:N1	1:16S:1319:A:OP2	2.40	0.45
2:23S:160:A:N3	2:23S:2208:C:O2'	2.48	0.45
2:23S:1047:G:H2'	2:23S:1110:G:N1	2.31	0.45
14:L11:10:LEU:HD12	14:L11:23:VAL:HG13	1.98	0.45
35:L34:12:ARG:HE	35:L34:44:VAL:HG21	1.81	0.45
45:S09:5:TYR:HB2	45:S09:20:ILE:HG23	1.97	0.45
1:16S:691:G:N7	47:S11:27:ASN:ND2	2.63	0.45
1:16S:1372:U:OP1	45:S09:73:GLY:N	2.48	0.45
2:23S:59:U:O2	2:23S:68:G:N2	2.45	0.45
2:23S:385:C:O2'	2:23S:388:G:N2	2.49	0.45
2:23S:451:U:O2	2:23S:453:A:N6	2.49	0.45
2:23S:1084:A:H4'	13:L10:55:VAL:HG12	1.98	0.45
2:23S:1468:U:O2	2:23S:1524:G:N2	2.49	0.45
2:23S:2315:G:H1'	9:L05:122:ASP:HB3	1.98	0.45
2:23S:2419:U:OP1	36:L35:40:LYS:NZ	2.38	0.45
12:L1:189:LEU:HD12	12:L1:190:GLU:HG2	1.99	0.45
43:S07:91:ARG:O	43:S07:95:ARG:N	2.49	0.45
48:S12:110:LYS:O	48:S12:113:ARG:NH1	2.48	0.45
1:16S:619:U:H1'	40:S04:129:VAL:HA	1.98	0.45
2:23S:290:U:H3	2:23S:350:G:H1	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:1796:U:H2'	2:23S:1797:G:H8	1.80	0.45
2:23S:1903:G:H2'	2:23S:1904:G:H8	1.81	0.45
2:23S:2032:G:N2	7:L03:151:THR:HG1	2.14	0.45
2:23S:2039:U:H2'	2:23S:2040:G:C8	2.51	0.45
2:23S:2718:G:O2'	2:23S:2847:U:OP1	2.33	0.45
42:S06:40:GLU:HB2	42:S06:61:LEU:HD23	1.98	0.45
44:S08:4:ASP:HB2	44:S08:80:PRO:HG3	1.98	0.45
44:S08:112:ASP:OD1	44:S08:112:ASP:N	2.49	0.45
49:S13:53:ASP:HA	49:S13:56:ARG:HH11	1.81	0.45
52:S16:22:ALA:HA	52:S16:33:ILE:HG13	1.99	0.45
1:16S:198:G:N2	1:16S:219:U:O2	2.34	0.45
2:23S:309:A:N3	2:23S:329:G:O2'	2.47	0.45
2:23S:395:U:H2'	2:23S:396:G:C8	2.52	0.45
2:23S:558:U:H2'	2:23S:559:G:C8	2.52	0.45
2:23S:918:A:O2'	3:5S:96:G:N2	2.49	0.45
2:23S:1827:U:H5'	2:23S:1971:U:H4'	1.98	0.45
2:23S:1889:A:N3	2:23S:2086:U:O2'	2.38	0.45
40:S04:143:SER:OG	40:S04:178:GLU:OE2	2.34	0.45
45:S09:11:ARG:O	45:S09:14:SER:OG	2.35	0.45
45:S09:20:ILE:HD11	45:S09:60:LEU:HD13	1.99	0.45
45:S09:122:ARG:HA	45:S09:122:ARG:HD2	1.78	0.45
53:S17:57:VAL:HB	53:S17:78:VAL:HG23	1.97	0.45
1:16S:1350:A:N7	45:S09:119:LYS:NZ	2.65	0.45
2:23S:598:U:H2'	2:23S:599:A:C8	2.52	0.45
2:23S:1322:A:O3'	24:L22:84:ARG:NH2	2.49	0.45
2:23S:1653:G:O6	19:L17:11:ASN:N	2.48	0.45
2:23S:1716:U:O4	2:23S:1744:A:N7	2.50	0.45
2:23S:2135:A:C5	2:23S:2136:G:H1'	2.52	0.45
26:L24:23:LYS:HE3	26:L24:23:LYS:HB2	1.82	0.45
50:S14:6:LYS:HD2	50:S14:6:LYS:HA	1.86	0.45
1:16S:243:A:H62	1:16S:281:G:H1'	1.82	0.45
1:16S:1071:C:H2'	1:16S:1072:G:H8	1.81	0.45
2:23S:606:U:O2	2:23S:622:G:O6	2.35	0.45
2:23S:1040:A:H61	2:23S:1115:G:H1	1.65	0.45
2:23S:2220:U:H2'	2:23S:2221:G:C8	2.51	0.45
8:L04:181:ILE:HB	17:L15:3:LEU:HD13	1.98	0.45
13:L10:17:GLU:O	13:L10:88:HIS:NE2	2.49	0.45
38:S02:73:ARG:HA	38:S02:76:SER:HB2	1.99	0.45
53:S17:28:VAL:HG13	53:S17:37:ILE:HG23	1.98	0.45
1:16S:34:C:H2'	1:16S:35:G:H8	1.82	0.45
2:23S:560:C:O2'	22:L20:47:ARG:NH1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:910:A:H2'	2:23S:911:A:C8	2.52	0.45
2:23S:1010:A:O2'	2:23S:1152:C:O2	2.34	0.45
2:23S:1069:A:H2	2:23S:1073:A:H5'	1.82	0.45
2:23S:1638:C:O2	2:23S:2698:U:O2'	2.35	0.45
2:23S:2264:C:N4	28:L27:11:ASP:OD2	2.43	0.45
2:23S:2271:G:H5'	28:L27:16:ARG:HG3	1.99	0.45
2:23S:2394:C:OP1	36:L35:29:ARG:NH2	2.49	0.45
26:L24:83:GLY:N	26:L24:94:PHE:O	2.49	0.45
36:L35:23:HIS:NE2	36:L35:48:MET:O	2.46	0.45
40:S04:64:TYR:HB2	40:S04:66:VAL:HG23	1.99	0.45
45:S09:18:VAL:HG13	45:S09:64:ILE:HD12	1.98	0.45
49:S13:11:HIS:HA	49:S13:44:ILE:H	1.81	0.45
1:16S:615:G:N2	1:16S:625:U:O2	2.41	0.45
1:16S:1117:A:H4'	45:S09:105:ARG:HD2	1.99	0.45
2:23S:298:G:O2'	2:23S:322:A:N1	2.41	0.45
2:23S:495:G:N3	24:L22:61:ASN:ND2	2.65	0.45
2:23S:538:A:H5"	15:L13:7:LYS:HE3	1.99	0.45
2:23S:548:G:C5	2:23S:549:G:H1'	2.52	0.45
2:23S:1934:C:H2'	2:23S:1935:G:H8	1.81	0.45
2:23S:2647:U:H2'	2:23S:2648:G:H8	1.82	0.45
3:5S:9:G:N2	3:5S:111:U:O2	2.40	0.45
3:5S:86:G:OP2	3:5S:88:C:N4	2.50	0.45
6:L02:251:THR:OG1	6:L02:252:LYS:N	2.49	0.45
17:L15:122:VAL:HG12	17:L15:142:ILE:HA	1.99	0.45
45:S09:43:ALA:H	45:S09:44:ARG:HH21	1.65	0.45
53:S17:12:VAL:HB	53:S17:21:VAL:HG13	1.99	0.45
1:16S:118:U:H3'	1:16S:288:A:H61	1.82	0.45
1:16S:931:C:C4	1:16S:932:C:N4	2.85	0.45
2:23S:644:A:H61	2:23S:2349:G:H21	1.65	0.45
2:23S:742:A:H2'	2:23S:743:A:C8	2.52	0.45
21:L19:95:LYS:HB3	21:L19:97:TYR:HD2	1.80	0.45
36:L35:37:THR:O	36:L35:41:ARG:N	2.48	0.45
39:S03:152:VAL:HG12	39:S03:197:VAL:HG22	1.99	0.45
47:S11:45:THR:OG1	47:S11:46:ALA:N	2.49	0.45
47:S11:108:ASN:OD1	47:S11:110:THR:OG1	2.35	0.45
1:16S:65:A:N7	1:16S:200:G:O2'	2.43	0.45
1:16S:574:A:O2'	1:16S:882:C:O2'	2.31	0.45
1:16S:1162:C:H2'	1:16S:1163:A:H8	1.82	0.45
2:23S:76:C:OP1	30:L29:48:ARG:NH1	2.50	0.45
2:23S:1319:C:N4	2:23S:1320:C:N4	2.65	0.45
2:23S:1423:G:H2'	2:23S:1424:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:1652:A:N6	19:L17:11:ASN:OD1	2.37	0.45
2:23S:2128:G:H4'	12:L1:218:MET:HE1	1.99	0.45
3:5S:76:G:OP1	27:L25:9:ARG:NH1	2.46	0.45
30:L29:28:LEU:HB3	30:L29:37:LEU:HD22	1.98	0.45
39:S03:24:ASN:OD1	39:S03:24:ASN:N	2.37	0.45
46:S10:54:SER:OG	46:S10:57:VAL:O	2.26	0.45
51:S15:81:ILE:O	51:S15:85:GLY:N	2.49	0.45
1:16S:741:G:OP1	51:S15:34:GLN:NE2	2.44	0.44
1:16S:836:G:O6	1:16S:850:U:O2	2.34	0.44
2:23S:414:C:O2'	2:23S:1864:U:O2	2.35	0.44
2:23S:1072:C:N4	2:23S:1093:G:N2	2.38	0.44
2:23S:1190:G:H2'	2:23S:1191:G:H8	1.82	0.44
2:23S:1819:A:N1	6:L02:270:ARG:NH1	2.65	0.44
12:L1:63:THR:HG21	12:L1:192:LEU:HA	1.99	0.44
36:L35:5:THR:HG22	36:L35:62:PRO:HD2	1.99	0.44
42:S06:30:THR:HA	42:S06:34:GLY:H	1.82	0.44
1:16S:516:U:O2'	1:16S:519:C:N3	2.42	0.44
1:16S:686:U:H1'	47:S11:43:TRP:HE1	1.81	0.44
1:16S:1250:A:H2'	1:16S:1251:A:C8	2.52	0.44
2:23S:570:G:N2	2:23S:2030:A:O4'	2.50	0.44
2:23S:992:C:OP1	23:L21:76:LYS:NZ	2.39	0.44
2:23S:1501:G:OP1	6:L02:100:ARG:NH2	2.47	0.44
2:23S:2387:U:OP1	28:L27:51:ARG:NH2	2.51	0.44
2:23S:2674:G:H4'	16:L14:30:ARG:HD2	1.99	0.44
2:23S:2683:C:OP1	21:L19:50:ARG:NH2	2.49	0.44
3:5S:49:C:H2'	3:5S:50:A:H8	1.82	0.44
23:L21:1:MET:SD	23:L21:43:ASN:ND2	2.90	0.44
23:L21:39:LEU:HG	23:L21:49:ILE:HD13	1.98	0.44
24:L22:7:HIS:N	24:L22:103:ILE:O	2.50	0.44
36:L35:38:LYS:O	36:L35:42:HIS:ND1	2.50	0.44
40:S04:195:ASN:HD21	40:S04:197:HIS:HB3	1.82	0.44
42:S06:38:ARG:HD3	42:S06:97:THR:HA	1.99	0.44
43:S07:94:ARG:HA	43:S07:97:ALA:HB3	1.99	0.44
52:S16:7:ALA:HB3	52:S16:18:GLN:HB2	1.99	0.44
54:S18:30:ASN:OD1	54:S18:30:ASN:N	2.48	0.44
1:16S:261:U:OP2	56:S20:73:ARG:NH2	2.49	0.44
1:16S:496:A:H2'	1:16S:497:G:C8	2.53	0.44
1:16S:979:C:N4	50:S14:57:SER:O	2.49	0.44
1:16S:1095:U:OP2	1:16S:1108:G:N1	2.35	0.44
2:23S:297:G:H5"	26:L24:84:PHE:HB2	1.99	0.44
2:23S:576:U:H2'	2:23S:577:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:790:U:H3	2:23S:795:C:H5'	1.82	0.44
2:23S:1012:U:OP2	22:L20:69:ARG:NH2	2.45	0.44
2:23S:2655:G:H1'	2:23S:2656:U:H5	1.82	0.44
6:L02:77:VAL:HG21	6:L02:109:LEU:HD21	1.98	0.44
56:S20:34:VAL:HG11	56:S20:78:LEU:HG	1.99	0.44
1:16S:333:U:OP1	56:S20:2:ASN:N	2.51	0.44
1:16S:1440:U:O2	1:16S:1461:G:O6	2.36	0.44
2:23S:495:G:H5"	24:L22:4:ILE:HG13	1.99	0.44
2:23S:720:U:H2'	2:23S:721:A:C8	2.52	0.44
2:23S:1827:U:OP1	2:23S:1971:U:O2'	2.32	0.44
10:L06:104:LEU:HD13	10:L06:106:LEU:HD11	2.00	0.44
13:L10:42:ARG:HH22	14:L11:119:ALA:HA	1.82	0.44
15:L13:53:TYR:HA	15:L13:121:LYS:HB3	2.00	0.44
23:L21:43:ASN:OD1	23:L21:43:ASN:N	2.48	0.44
25:L23:36:LYS:HE3	25:L23:62:VAL:HG11	1.98	0.44
38:S02:31:PHE:HD2	38:S02:34:ARG:HH12	1.63	0.44
45:S09:114:LYS:HB2	45:S09:117:LEU:HD13	1.99	0.44
49:S13:84:CYS:SG	49:S13:85:TYR:N	2.91	0.44
1:16S:67:C:H2'	1:16S:68:G:C8	2.52	0.44
1:16S:131:A:O2'	1:16S:262:A:O2'	2.28	0.44
1:16S:195:A:H2'	1:16S:196:A:C4	2.53	0.44
2:23S:629:G:N3	2:23S:639:U:O2'	2.49	0.44
2:23S:1319:C:N3	2:23S:1320:C:N3	2.65	0.44
14:L11:89:SER:HB3	14:L11:135:MET:HA	2.00	0.44
16:L14:12:ASP:HB2	16:L14:96:GLY:HA3	2.00	0.44
29:L28:34:SER:HA	29:L28:49:ARG:HA	1.98	0.44
47:S11:87:GLY:H	47:S11:113:THR:HG22	1.82	0.44
48:S12:23:LEU:HD12	48:S12:23:LEU:HA	1.86	0.44
1:16S:674:G:H1	1:16S:716:A:N6	2.15	0.44
2:23S:1028:A:N6	2:23S:1126:A:OP1	2.50	0.44
2:23S:1055:G:H21	2:23S:1085:A:H1'	1.82	0.44
2:23S:1098:A:H4'	14:L11:8:VAL:HG23	1.99	0.44
2:23S:2595:G:N2	2:23S:2598:A:OP2	2.45	0.44
16:L14:73:ASP:OD1	16:L14:73:ASP:N	2.51	0.44
41:S05:85:LYS:HE2	41:S05:85:LYS:HB2	1.89	0.44
44:S08:76:ARG:NH1	44:S08:125:ILE:O	2.51	0.44
45:S09:14:SER:OG	45:S09:73:GLY:O	2.28	0.44
50:S14:62:ARG:HG2	50:S14:69:PRO:HA	2.00	0.44
1:16S:1249:C:O2'	45:S09:69:GLY:O	2.30	0.44
2:23S:52:A:OP2	2:23S:117:G:N1	2.42	0.44
2:23S:694:U:O2	2:23S:768:G:N2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:711:G:O6	2:23S:720:U:O4	2.35	0.44
2:23S:1457:U:O2	2:23S:2702:G:O6	2.35	0.44
2:23S:1806:C:O2	6:L02:43:ASN:ND2	2.51	0.44
2:23S:2172:U:OP1	2:23S:2174:C:N4	2.40	0.44
2:23S:2204:G:O6	2:23S:2220:U:O2	2.34	0.44
2:23S:2315:G:H2'	2:23S:2316:G:C8	2.53	0.44
2:23S:2817:U:O2'	2:23S:2836:U:O2	2.26	0.44
2:23S:2820:A:OP1	19:L17:2:ARG:NH2	2.50	0.44
30:L29:23:ARG:HB3	30:L29:24:GLU:H	1.68	0.44
56:S20:38:ILE:HD13	56:S20:81:GLN:HB3	1.98	0.44
1:16S:542:G:OP1	40:S04:9:LYS:NZ	2.45	0.44
1:16S:581:G:OP1	51:S15:60:SER:OG	2.35	0.44
1:16S:878:A:OP1	44:S08:79:ARG:NH1	2.44	0.44
1:16S:1040:U:H2'	1:16S:1041:G:H8	1.83	0.44
2:23S:414:C:H1'	2:23S:1864:U:H1'	2.00	0.44
2:23S:489:G:O2'	2:23S:491:G:OP2	2.26	0.44
2:23S:500:G:N1	2:23S:503:A:OP2	2.49	0.44
2:23S:630:G:N2	2:23S:633:A:OP2	2.34	0.44
2:23S:767:U:H2'	2:23S:768:G:H8	1.83	0.44
2:23S:1070:A:H61	2:23S:1095:A:H61	1.66	0.44
2:23S:1258:U:H2'	2:23S:1259:G:C8	2.53	0.44
2:23S:2099:U:O2	2:23S:2190:G:O6	2.35	0.44
2:23S:2241:A:H2'	2:23S:2242:G:C8	2.53	0.44
2:23S:2443:C:H2'	2:23S:2444:G:C8	2.53	0.44
2:23S:2898:U:H2'	2:23S:2899:A:C8	2.52	0.44
6:L02:196:ASN:HD22	6:L02:199:HIS:HB2	1.83	0.44
8:L04:52:VAL:HB	8:L04:74:LYS:HG2	2.00	0.44
19:L17:2:ARG:HG2	19:L17:5:LYS:HB2	2.00	0.44
20:L18:9:ARG:O	20:L18:12:THR:OG1	2.33	0.44
21:L19:16:VAL:HA	21:L19:83:ILE:HD12	2.00	0.44
43:S07:46:LEU:O	43:S07:50:ALA:N	2.46	0.44
45:S09:98:ARG:HG3	45:S09:103:VAL:HG21	2.00	0.44
1:16S:1413:A:N1	1:16S:1487:G:C6	2.86	0.44
2:23S:572:A:H61	2:23S:2029:G:H21	1.65	0.44
2:23S:1483:G:N2	2:23S:1506:U:O2	2.48	0.44
2:23S:2182:U:H2'	2:23S:2183:A:C8	2.53	0.44
10:L06:43:LYS:HE2	10:L06:43:LYS:HB2	1.76	0.44
44:S08:5:PRO:HA	44:S08:8:ASP:HB3	2.00	0.44
46:S10:48:ARG:HG2	46:S10:66:GLU:HG2	2.00	0.44
53:S17:19:SER:HB3	53:S17:70:LYS:HD3	1.99	0.44
1:16S:335:C:H2'	1:16S:336:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:16S:1348:U:H2'	1:16S:1349:A:H8	1.83	0.43
2:23S:485:C:HO2'	24:L22:60:HIS:CE1	2.30	0.43
2:23S:788:A:OP1	2:23S:791:C:N4	2.48	0.43
2:23S:2057:G:H2'	2:23S:2058:A:H8	1.81	0.43
2:23S:2836:U:H2'	2:23S:2837:A:C8	2.52	0.43
3:5S:43:C:H2'	32:L31:1:MET:SD	2.57	0.43
6:L02:12:ARG:HD2	6:L02:15:VAL:HG11	2.00	0.43
7:L03:124:ARG:NH1	7:L03:164:GLN:O	2.48	0.43
8:L04:61:ARG:HH21	8:L04:65:THR:HG23	1.83	0.43
8:L04:76:PRO:HA	8:L04:82:GLY:HA2	2.00	0.43
16:L14:19:VAL:HB	16:L14:41:ILE:HD12	1.99	0.43
21:L19:86:LYS:HZ3	21:L19:86:LYS:HG2	1.70	0.43
40:S04:64:TYR:OH	40:S04:94:GLU:OE2	2.35	0.43
42:S06:6:ILE:HG12	42:S06:89:VAL:HG12	1.99	0.43
46:S10:10:LEU:HB2	46:S10:72:ARG:HB2	2.00	0.43
56:S20:43:LYS:HE2	56:S20:43:LYS:HB2	1.88	0.43
1:16S:409:U:O2	1:16S:433:G:N2	2.51	0.43
1:16S:509:A:H2'	1:16S:510:A:C4	2.53	0.43
1:16S:1464:U:OP2	21:L19:108:ARG:NH2	2.51	0.43
2:23S:32:C:N4	2:23S:447:A:OP2	2.51	0.43
2:23S:1106:G:H2'	2:23S:1107:G:C8	2.53	0.43
3:5S:8:C:O3'	20:L18:25:ARG:NH2	2.51	0.43
17:L15:117:THR:O	17:L15:117:THR:OG1	2.30	0.43
39:S03:120:THR:HA	39:S03:123:LEU:HB2	1.98	0.43
39:S03:151:GLU:HA	39:S03:166:TRP:HA	2.00	0.43
1:16S:672:U:H2'	1:16S:673:A:C8	2.54	0.43
1:16S:673:A:HO2'	54:S18:69:TYR:HH	1.65	0.43
1:16S:674:G:OP1	42:S06:86:ARG:NH2	2.37	0.43
2:23S:903:C:H2'	2:23S:904:G:C8	2.53	0.43
2:23S:1161:C:H2'	2:23S:1162:G:C8	2.54	0.43
2:23S:2451:A:OP1	2:23S:2497:A:N6	2.48	0.43
11:L09:47:PHE:HA	11:L09:51:ARG:HD2	1.99	0.43
20:L18:35:ILE:HD12	20:L18:35:ILE:HA	1.93	0.43
25:L23:59:ASN:O	25:L23:84:TYR:N	2.49	0.43
31:L30:8:GLN:HB2	31:L30:28:LEU:HD13	2.00	0.43
1:16S:634:C:H2'	1:16S:635:A:C8	2.52	0.43
1:16S:981:U:H4'	50:S14:60:ARG:HG2	2.00	0.43
2:23S:573:U:O4	2:23S:2029:G:O2'	2.27	0.43
2:23S:1049:C:H41	2:23S:1110:G:H21	1.64	0.43
2:23S:1908:C:C4	2:23S:1909:C:N4	2.85	0.43
2:23S:2100:G:O6	2:23S:2189:U:O4	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:2216:G:H2'	2:23S:2217:G:H8	1.84	0.43
2:23S:2576:G:O2'	2:23S:2579:C:OP2	2.32	0.43
6:L02:260:LYS:HE3	6:L02:260:LYS:HB2	1.87	0.43
10:L06:26:LYS:HB2	10:L06:31:GLU:HG3	2.00	0.43
47:S11:76:TYR:HB2	47:S11:78:ILE:HD11	2.00	0.43
52:S16:42:ILE:H	52:S16:42:ILE:HG13	1.67	0.43
1:16S:1300:G:N2	1:16S:1335:U:O4'	2.50	0.43
1:16S:1522:U:H2'	1:16S:1523:G:C8	2.53	0.43
2:23S:177:G:H3'	2:23S:178:G:H8	1.83	0.43
2:23S:1085:A:H5'	2:23S:1105:U:H4'	2.00	0.43
2:23S:2461:A:N6	2:23S:2488:G:O6	2.51	0.43
2:23S:2847:U:O2	2:23S:2869:G:N2	2.46	0.43
3:5S:28:C:H2'	3:5S:29:A:C8	2.53	0.43
6:L02:132:ARG:HB3	6:L02:185:ALA:HB1	2.00	0.43
9:L05:53:ALA:HB1	9:L05:64:PRO:HB2	2.00	0.43
14:L11:26:ALA:HA	14:L11:29:GLN:HB2	2.00	0.43
27:L25:72:VAL:HA	27:L25:94:ALA:H	1.84	0.43
39:S03:178:ARG:NE	39:S03:205:GLU:OE2	2.52	0.43
43:S07:92:PRO:HA	43:S07:95:ARG:HB2	1.99	0.43
45:S09:91:GLU:HA	45:S09:94:ARG:HB2	1.99	0.43
1:16S:212:G:H2'	1:16S:213:G:C8	2.54	0.43
1:16S:709:U:H2'	1:16S:710:G:H8	1.83	0.43
2:23S:285:G:N2	2:23S:355:U:O2	2.36	0.43
2:23S:450:G:N1	2:23S:454:A:OP2	2.46	0.43
2:23S:488:G:N2	2:23S:493:G:O6	2.52	0.43
2:23S:528:A:H5"	15:L13:113:PRO:HG3	2.00	0.43
2:23S:1483:G:O6	2:23S:1506:U:O4	2.37	0.43
3:5S:39:A:H2'	3:5S:40:U:C2	2.53	0.43
3:5S:80:U:O2	3:5S:96:G:N2	2.37	0.43
40:S04:145:ARG:HD2	40:S04:147:LYS:HE2	2.01	0.43
1:16S:36:C:OP1	48:S12:119:LYS:NZ	2.46	0.43
1:16S:246:A:O4'	1:16S:282:A:N6	2.52	0.43
1:16S:411:A:C4	1:16S:413:G:H1'	2.53	0.43
1:16S:1151:A:O2'	46:S10:72:ARG:NH2	2.52	0.43
2:23S:175:G:H2'	2:23S:176:A:C8	2.54	0.43
2:23S:739:A:N3	2:23S:740:C:N4	2.63	0.43
2:23S:1030:C:OP2	18:L16:127:LYS:NZ	2.47	0.43
2:23S:1229:C:H2'	2:23S:1230:A:H8	1.84	0.43
2:23S:1930:G:N2	2:23S:1969:A:O5'	2.51	0.43
2:23S:2141:G:H2'	2:23S:2142:A:H8	1.84	0.43
2:23S:2313:C:H2'	2:23S:2314:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:2329:U:H2'	2:23S:2330:G:C8	2.54	0.43
2:23S:2586:U:OP2	2:23S:2608:G:N1	2.49	0.43
7:L03:33:ARG:HH11	7:L03:73:VAL:HB	1.84	0.43
11:L09:78:VAL:HG21	11:L09:103:VAL:HA	2.00	0.43
13:L10:94:ARG:HH21	13:L10:97:LYS:HB2	1.83	0.43
23:L21:28:ALA:HB3	23:L21:31:GLU:HB2	2.01	0.43
30:L29:25:GLN:O	30:L29:29:ARG:NH1	2.51	0.43
38:S02:65:LYS:HE3	38:S02:65:LYS:HB2	1.92	0.43
38:S02:114:LYS:HA	38:S02:117:GLU:HB2	2.00	0.43
41:S05:149:PRO:HA	41:S05:152:VAL:HB	2.00	0.43
43:S07:69:ARG:HA	43:S07:99:ALA:HB2	2.00	0.43
50:S14:63:CYS:HB3	50:S14:67:GLY:H	1.84	0.43
1:16S:666:G:H2'	1:16S:667:G:H8	1.82	0.43
1:16S:1193:G:OP1	39:S03:166:TRP:NE1	2.52	0.43
1:16S:1437:A:H2'	1:16S:1438:G:H8	1.83	0.43
2:23S:1055:G:H5"	13:L10:33:VAL:HG12	2.01	0.43
2:23S:1826:G:O2'	2:23S:1971:U:OP2	2.36	0.43
3:5S:74:U:H1'	27:L25:37:PRO:HG2	2.01	0.43
9:L05:3:LEU:HA	9:L05:6:TYR:HB3	2.00	0.43
10:L06:104:LEU:HB2	10:L06:112:VAL:HB	2.01	0.43
53:S17:4:ILE:HG13	53:S17:6:THR:HG23	2.01	0.43
1:16S:1026:G:C6	1:16S:1035:A:N1	2.87	0.43
1:16S:1530:G:H2'	1:16S:1531:A:C8	2.54	0.43
2:23S:1019:U:H2'	2:23S:1020:A:H8	1.84	0.43
2:23S:1105:U:H2'	2:23S:1106:G:C8	2.52	0.43
2:23S:1426:G:OP2	2:23S:1427:A:O2'	2.31	0.43
2:23S:2291:U:O2	2:23S:2341:G:N2	2.37	0.43
2:23S:2648:G:O6	2:23S:2672:U:O2	2.36	0.43
6:L02:96:LYS:O	6:L02:96:LYS:NZ	2.45	0.43
9:L05:126:ASN:HB3	9:L05:156:THR:HA	2.01	0.43
13:L10:19:ALA:HB2	13:L10:69:PHE:HE1	1.83	0.43
37:L36:2:LYS:NZ	37:L36:32:LYS:O	2.51	0.43
1:16S:546:A:OP1	40:S04:69:ARG:N	2.49	0.43
2:23S:84:A:N1	2:23S:98:G:O2'	2.38	0.43
2:23S:373:U:H2'	2:23S:374:A:H8	1.82	0.43
2:23S:1025:G:N2	2:23S:1139:G:O6	2.41	0.43
2:23S:1038:G:H2'	2:23S:1039:A:C8	2.53	0.43
2:23S:2559:C:H2'	2:23S:2560:A:H8	1.83	0.43
2:23S:2669:G:H2'	2:23S:2670:A:C8	2.54	0.43
6:L02:20:ASN:HB3	6:L02:23:LEU:HD22	2.00	0.43
18:L16:63:ILE:HG12	18:L16:105:MET:HG3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:L25:30:ILE:HD11	27:L25:38:LEU:HD12	2.01	0.43
53:S17:56:ASP:HB3	53:S17:80:LYS:HA	2.00	0.43
1:16S:47:C:N4	1:16S:365:U:OP2	2.52	0.42
1:16S:409:U:O4	1:16S:433:G:O6	2.36	0.42
2:23S:1170:C:H2'	2:23S:1171:G:C8	2.55	0.42
2:23S:2021:C:OP1	22:L20:24:TYR:OH	2.36	0.42
39:S03:156:LEU:H	39:S03:156:LEU:HG	1.59	0.42
39:S03:190:THR:OG1	39:S03:191:THR:N	2.52	0.42
50:S14:37:ASP:O	50:S14:41:TRP:N	2.46	0.42
1:16S:37:U:OP1	48:S12:122:LYS:NZ	2.43	0.42
1:16S:1098:C:OP1	38:S02:142:LYS:NZ	2.44	0.42
1:16S:1342:C:H2'	1:16S:1343:G:H8	1.84	0.42
2:23S:581:C:H2'	2:23S:582:A:C8	2.54	0.42
2:23S:857:G:H1	2:23S:920:A:H61	1.65	0.42
2:23S:1570:A:H2'	2:23S:1571:A:C4	2.53	0.42
2:23S:2730:C:H2'	2:23S:2731:G:C8	2.54	0.42
7:L03:177:VAL:HA	7:L03:189:VAL:HG12	2.01	0.42
10:L06:96:ALA:HB3	10:L06:103:ASN:HB3	2.00	0.42
15:L13:117:ALA:HA	15:L13:120:ARG:HH11	1.84	0.42
23:L21:76:LYS:HG3	23:L21:85:LYS:HD2	2.00	0.42
24:L22:20:VAL:HG21	24:L22:43:ALA:HB3	2.00	0.42
55:S19:9:PHE:O	55:S19:38:THR:N	2.48	0.42
1:16S:34:C:H2'	1:16S:35:G:C8	2.54	0.42
1:16S:46:G:O2'	1:16S:365:U:O2	2.32	0.42
1:16S:362:G:OP1	48:S12:57:THR:OG1	2.37	0.42
1:16S:1343:G:H4'	45:S09:123:ARG:HB2	2.00	0.42
2:23S:372:G:HO2'	2:23S:373:U:P	2.42	0.42
2:23S:523:C:H2'	2:23S:524:G:H8	1.83	0.42
2:23S:562:U:C4	2:23S:572:A:N7	2.87	0.42
2:23S:601:C:O2'	8:L04:99:LYS:NZ	2.48	0.42
2:23S:1363:C:H2'	2:23S:1364:G:H8	1.85	0.42
2:23S:1748:C:H2'	2:23S:1749:A:H8	1.84	0.42
2:23S:1936:A:H2	2:23S:1943:U:H3	1.67	0.42
15:L13:78:THR:HG21	15:L13:85:LYS:HE2	1.99	0.42
27:L25:75:GLN:HB2	27:L25:92:VAL:HG23	2.01	0.42
32:L31:10:GLU:H	32:L31:27:THR:HA	1.83	0.42
32:L31:12:ILE:HG12	32:L31:26:SER:HB3	2.01	0.42
39:S03:136:ALA:HA	39:S03:139:ASN:HB2	2.01	0.42
1:16S:552:U:H1'	48:S12:28:GLN:HE22	1.84	0.42
1:16S:625:U:H2'	1:16S:626:G:H8	1.85	0.42
2:23S:974:G:O2'	2:23S:989:G:N2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:1203:U:O2'	17:L15:4:ASN:OD1	2.30	0.42
2:23S:1218:G:O6	2:23S:1231:U:O2	2.37	0.42
2:23S:2314:A:H1'	9:L05:154:THR:HG21	2.00	0.42
2:23S:2540:C:O2'	2:23S:2740:A:N3	2.44	0.42
2:23S:2724:U:H2'	2:23S:2725:A:C8	2.54	0.42
8:L04:27:LEU:HG	8:L04:104:ALA:HB2	2.01	0.42
18:L16:34:LYS:HE3	18:L16:101:VAL:HG13	2.01	0.42
40:S04:73:ASN:OD1	40:S04:73:ASN:N	2.49	0.42
46:S10:7:ARG:HA	46:S10:75:ASP:HA	2.00	0.42
1:16S:62:U:H5"	1:16S:385:C:H1'	2.01	0.42
1:16S:401:C:H2'	1:16S:402:G:C8	2.53	0.42
1:16S:424:G:H2'	1:16S:425:G:H8	1.83	0.42
2:23S:285:G:O6	2:23S:355:U:O4	2.38	0.42
2:23S:290:U:H2'	2:23S:291:G:H8	1.84	0.42
2:23S:542:C:H2'	2:23S:543:G:H8	1.84	0.42
2:23S:1319:C:N4	2:23S:1320:C:H42	2.18	0.42
2:23S:1387:A:H2'	2:23S:1388:G:C8	2.54	0.42
2:23S:1570:A:H2'	2:23S:1571:A:N3	2.35	0.42
2:23S:1689:A:H2'	2:23S:1690:A:C8	2.53	0.42
2:23S:1909:C:H2'	2:23S:1910:G:H8	1.84	0.42
6:L02:83:ASP:HB2	6:L02:90:ILE:HD13	2.00	0.42
23:L21:62:GLU:O	23:L21:97:LYS:N	2.48	0.42
23:L21:71:LYS:HA	23:L21:90:ARG:HG2	2.01	0.42
43:S07:103:ILE:H	43:S07:103:ILE:HG12	1.58	0.42
49:S13:92:ARG:HG3	49:S13:94:LEU:HG	2.01	0.42
57:S21:25:ALA:HA	57:S21:28:LEU:HB3	2.01	0.42
1:16S:501:C:OP1	48:S12:113:ARG:NE	2.38	0.42
1:16S:837:U:H2'	1:16S:838:G:C8	2.54	0.42
2:23S:224:U:O4	2:23S:419:U:O2'	2.34	0.42
2:23S:818:G:N1	2:23S:1188:U:OP2	2.37	0.42
2:23S:832:U:H2'	2:23S:833:A:C8	2.55	0.42
2:23S:1013:C:H2'	2:23S:1014:A:C8	2.55	0.42
2:23S:1278:C:H2'	2:23S:1279:G:C8	2.55	0.42
2:23S:1853:A:N3	2:23S:2233:U:O2'	2.44	0.42
2:23S:2111:U:HO2'	2:23S:2115:G:H1	1.65	0.42
2:23S:2394:C:OP2	36:L35:29:ARG:NE	2.53	0.42
2:23S:2785:C:O2'	7:L03:67:HIS:ND1	2.48	0.42
6:L02:161:VAL:HG22	6:L02:175:LEU:HA	2.01	0.42
9:L05:27:VAL:O	9:L05:29:ARG:NH1	2.53	0.42
26:L24:17:ASP:HB3	26:L24:20:LYS:HD2	2.02	0.42
28:L27:19:VAL:HA	28:L27:34:VAL:HG22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:L32:16:ARG:HA	33:L32:19:ASP:HB2	2.02	0.42
43:S07:28:ILE:HG23	43:S07:104:VAL:HG11	2.02	0.42
1:16S:5:U:O4	40:S04:83:GLY:N	2.52	0.42
1:16S:60:A:OP1	1:16S:111:G:N2	2.46	0.42
1:16S:619:U:O2	40:S04:130:ASN:N	2.50	0.42
1:16S:1414:U:H2'	1:16S:1415:G:C8	2.51	0.42
1:16S:1496:C:HO2'	1:16S:1517:G:H1	1.63	0.42
1:16S:1512:U:H2'	1:16S:1513:A:C8	2.54	0.42
2:23S:704:G:H2'	2:23S:726:G:N2	2.34	0.42
2:23S:989:G:H5"	31:L30:13:ILE:HD11	2.01	0.42
2:23S:1009:A:H2'	2:23S:1010:A:C4	2.54	0.42
2:23S:1355:G:H2'	2:23S:1356:G:H8	1.84	0.42
2:23S:1463:C:H2'	2:23S:1464:G:C8	2.55	0.42
9:L05:57:ALA:HA	32:L31:7:PRO:HB3	2.02	0.42
23:L21:66:HIS:CD2	23:L21:94:THR:HG1	2.37	0.42
27:L25:26:PHE:HE2	27:L25:89:ILE:HG13	1.85	0.42
42:S06:3:HIS:HA	42:S06:65:GLU:HA	2.01	0.42
44:S08:45:ILE:HD11	44:S08:62:LEU:HD23	2.02	0.42
44:S08:49:LYS:HB3	44:S08:51:GLU:HG3	2.00	0.42
1:16S:149:A:N6	1:16S:171:A:N7	2.66	0.42
1:16S:178:C:H2'	1:16S:179:A:H8	1.84	0.42
1:16S:375:U:H4'	52:S16:6:LEU:HD12	2.01	0.42
1:16S:1522:U:H2'	1:16S:1523:G:H8	1.84	0.42
2:23S:240:C:H3'	2:23S:241:A:H8	1.84	0.42
2:23S:603:A:N6	2:23S:655:A:OP1	2.47	0.42
2:23S:970:U:H2'	2:23S:971:G:H8	1.83	0.42
2:23S:1080:A:H1'	14:L11:127:SER:HA	2.01	0.42
2:23S:1818:U:H5'	6:L02:156:SER:HB2	2.00	0.42
2:23S:1997:C:H2'	2:23S:1998:A:C8	2.54	0.42
2:23S:2047:C:H2'	2:23S:2048:G:H8	1.84	0.42
22:L20:74:SER:HB2	22:L20:77:LYS:HE2	2.02	0.42
28:L27:71:LYS:H	28:L27:71:LYS:HG2	1.68	0.42
32:L31:23:LYS:HE2	32:L31:23:LYS:HB2	1.95	0.42
40:S04:44:LYS:NZ	40:S04:45:PRO:O	2.43	0.42
44:S08:26:MET:HG3	44:S08:58:LEU:HB3	2.02	0.42
47:S11:28:ASN:OD1	47:S11:29:THR:N	2.52	0.42
51:S15:47:LYS:HA	51:S15:47:LYS:HD3	1.88	0.42
1:16S:1450:U:N3	1:16S:1452:C:O2'	2.50	0.42
2:23S:328:U:C2	2:23S:332:A:N7	2.88	0.42
2:23S:528:A:N1	2:23S:2042:A:H2'	2.35	0.42
2:23S:814:C:H1'	2:23S:1225:G:H21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:927:A:H2'	2:23S:928:A:C8	2.55	0.42
2:23S:1412:U:H2'	2:23S:1413:A:C8	2.55	0.42
2:23S:1673:G:O6	7:L03:134:HIS:ND1	2.44	0.42
2:23S:1783:A:O2'	2:23S:2607:G:O2'	2.33	0.42
2:23S:2102:G:N1	2:23S:2187:U:C2	2.88	0.42
2:23S:2898:U:O2'	15:L13:136:GLN:OE1	2.31	0.42
26:L24:95:PHE:HB2	26:L24:99:SER:HA	2.02	0.42
31:L30:43:ILE:HD13	31:L30:43:ILE:HA	1.89	0.42
40:S04:53:GLN:HB3	40:S04:202:LEU:HB2	2.02	0.42
44:S08:63:LYS:HB2	44:S08:70:VAL:HG11	2.01	0.42
48:S12:109:ARG:HA	48:S12:109:ARG:HD2	1.75	0.42
1:16S:1122:U:H3	1:16S:1151:A:H2	1.68	0.42
1:16S:1219:A:H2'	1:16S:1220:G:C8	2.55	0.42
1:16S:1251:A:H2'	1:16S:1252:A:C8	2.54	0.42
1:16S:1301:U:OP2	1:16S:1303:C:N4	2.53	0.42
2:23S:1587:G:H2'	2:23S:1588:G:H8	1.85	0.42
2:23S:2123:G:OP1	12:L1:164:ARG:NH1	2.50	0.42
2:23S:2380:C:H2'	2:23S:2381:A:C8	2.55	0.42
6:L02:230:PRO:O	6:L02:241:LYS:NZ	2.41	0.42
7:L03:110:THR:HG21	7:L03:169:ARG:HE	1.85	0.42
13:L10:41:LEU:O	13:L10:45:GLY:N	2.53	0.42
16:L14:2:ILE:HD12	16:L14:6:THR:HG21	2.01	0.42
16:L14:88:ASN:HD21	16:L14:93:GLN:HB2	1.84	0.42
27:L25:25:LYS:HE2	27:L25:25:LYS:HB3	1.82	0.42
38:S02:151:LYS:H	38:S02:151:LYS:HG3	1.53	0.42
44:S08:1:SER:OG	44:S08:3:GLN:OE1	2.37	0.42
45:S09:90:ASP:O	45:S09:93:LEU:N	2.48	0.42
46:S10:82:LYS:O	46:S10:86:ALA:N	2.44	0.42
1:16S:509:A:OP1	40:S04:48:SER:OG	2.38	0.41
1:16S:541:G:H2'	1:16S:542:G:H8	1.85	0.41
1:16S:685:G:N2	1:16S:704:A:OP2	2.53	0.41
1:16S:1309:G:N7	49:S13:97:ARG:NH2	2.67	0.41
2:23S:414:C:H2'	2:23S:415:A:C8	2.54	0.41
2:23S:740:C:H5'	2:23S:1784:A:H2'	2.01	0.41
2:23S:1931:U:H2'	2:23S:1932:A:H8	1.84	0.41
2:23S:2372:U:H2'	2:23S:2373:G:C8	2.54	0.41
2:23S:2523:G:H2'	2:23S:2524:G:H8	1.85	0.41
3:5S:80:U:H2'	3:5S:81:G:H8	1.85	0.41
7:L03:107:VAL:HG12	7:L03:205:PRO:HA	2.02	0.41
8:L04:28:VAL:HG12	8:L04:104:ALA:HB1	2.02	0.41
18:L16:133:LYS:HE3	18:L16:133:LYS:HB3	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:L29:42:LEU:HA	30:L29:45:GLN:HE21	1.85	0.41
40:S04:33:ILE:H	40:S04:33:ILE:HG13	1.45	0.41
45:S09:121:ARG:HD3	45:S09:121:ARG:HA	1.86	0.41
1:16S:962:C:H2'	1:16S:963:G:C8	2.53	0.41
1:16S:1331:G:O2'	1:16S:1332:A:O4'	2.37	0.41
2:23S:2061:G:OP1	8:L04:63:LYS:NZ	2.48	0.41
2:23S:2106:U:H2'	2:23S:2107:G:C8	2.55	0.41
2:23S:2668:G:H1'	10:L06:109:SER:HB2	2.02	0.41
2:23S:2788:C:H2'	2:23S:2789:C:C6	2.56	0.41
28:L27:72:ASN:OD1	28:L27:72:ASN:N	2.52	0.41
39:S03:51:VAL:HA	39:S03:69:THR:HA	2.01	0.41
39:S03:57:GLU:HG3	39:S03:64:ARG:HB3	2.01	0.41
42:S06:3:HIS:CD2	42:S06:92:THR:HG1	2.37	0.41
48:S12:34:THR:HA	48:S12:75:GLU:HA	2.02	0.41
55:S19:49:ALA:HA	55:S19:58:PRO:HA	2.02	0.41
1:16S:1351:U:H3	1:16S:1371:G:H1	1.66	0.41
2:23S:242:G:N2	2:23S:255:A:OP2	2.41	0.41
2:23S:636:G:H2'	17:L15:111:ILE:HD11	2.01	0.41
2:23S:1662:U:H2'	2:23S:1663:G:C8	2.55	0.41
2:23S:1833:C:O2'	2:23S:1969:A:N1	2.43	0.41
12:L1:59:VAL:H	12:L1:165:ASN:HB3	1.84	0.41
18:L16:33:LEU:HD13	18:L16:117:PHE:HB3	2.02	0.41
22:L20:51:GLN:HG2	22:L20:54:ARG:HH21	1.84	0.41
24:L22:82:MET:HB3	24:L22:84:ARG:HH11	1.86	0.41
39:S03:10:ARG:NH2	39:S03:174:LEU:O	2.54	0.41
47:S11:111:ASP:HB2	57:S21:19:LYS:HE3	2.02	0.41
1:16S:422:C:O2'	1:16S:423:G:N2	2.53	0.41
2:23S:20:C:H2'	2:23S:21:A:C8	2.56	0.41
2:23S:186:G:H2'	2:23S:187:G:C8	2.55	0.41
2:23S:1713:A:N6	2:23S:1746:A:N1	2.68	0.41
2:23S:1738:G:HO2'	2:23S:1739:A:H8	1.67	0.41
2:23S:2087:G:H2'	2:23S:2088:A:H8	1.86	0.41
3:5S:103:U:O2'	27:L25:75:GLN:OE1	2.37	0.41
8:L04:15:SER:N	8:L04:197:GLU:OE2	2.52	0.41
11:L09:47:PHE:HA	11:L09:51:ARG:HB2	2.02	0.41
16:L14:70:ARG:HG2	16:L14:76:VAL:HG12	2.01	0.41
21:L19:29:VAL:HG22	21:L19:80:VAL:HG12	2.01	0.41
34:L33:9:LYS:O	34:L33:51:ALA:N	2.54	0.41
39:S03:148:ILE:HA	39:S03:201:ILE:HA	2.03	0.41
57:S21:39:LYS:HD3	57:S21:42:THR:HB	2.03	0.41
1:16S:877:G:H2'	1:16S:878:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:318:C:H2'	2:23S:319:G:H8	1.85	0.41
2:23S:1140:C:H5'	15:L13:26:GLY:HA3	2.01	0.41
21:L19:25:VAL:HG22	21:L19:85:VAL:HG13	2.02	0.41
40:S04:12:ARG:HA	40:S04:34:GLU:H	1.86	0.41
40:S04:115:GLN:HE21	40:S04:115:GLN:HB2	1.61	0.41
50:S14:60:ARG:HA	50:S14:60:ARG:HD2	1.75	0.41
1:16S:130:A:N3	1:16S:263:A:O2'	2.40	0.41
1:16S:891:U:H2'	1:16S:892:A:H8	1.85	0.41
1:16S:1038:C:H2'	1:16S:1039:G:C8	2.56	0.41
2:23S:633:A:O2'	2:23S:2404:U:OP1	2.30	0.41
2:23S:1161:C:H2'	2:23S:1162:G:H8	1.85	0.41
2:23S:2303:G:H2'	2:23S:2304:G:C8	2.55	0.41
2:23S:2732:G:H3'	2:23S:2733:A:H8	1.85	0.41
7:L03:34:VAL:O	7:L03:93:GLY:N	2.48	0.41
15:L13:24:THR:HB	15:L13:27:ARG:HB2	2.02	0.41
18:L16:69:PRO:HA	18:L16:94:ALA:HB2	2.02	0.41
44:S08:28:SER:HB2	44:S08:58:LEU:HB2	2.03	0.41
45:S09:79:ARG:HH11	45:S09:102:PHE:HD1	1.67	0.41
46:S10:25:ILE:O	46:S10:28:THR:OG1	2.34	0.41
50:S14:11:LYS:HE3	50:S14:11:LYS:HB2	1.83	0.41
1:16S:398:U:H2'	1:16S:399:G:C8	2.55	0.41
2:23S:186:G:H2'	2:23S:187:G:H8	1.86	0.41
2:23S:298:G:N1	2:23S:339:U:OP2	2.47	0.41
2:23S:923:G:H2'	2:23S:924:G:H8	1.86	0.41
2:23S:948:C:H2'	2:23S:949:G:C8	2.56	0.41
2:23S:2086:U:H2'	2:23S:2087:G:C8	2.56	0.41
2:23S:2515:C:H2'	2:23S:2516:A:C8	2.56	0.41
2:23S:2841:C:H2'	2:23S:2842:G:C8	2.56	0.41
3:5S:9:G:H2'	3:5S:10:G:H8	1.85	0.41
9:L05:128:SER:HA	9:L05:154:THR:HA	2.01	0.41
11:L09:79:THR:HA	11:L09:145:ASN:HB3	2.02	0.41
27:L25:21:ARG:HE	27:L25:87:GLN:HA	1.86	0.41
29:L28:36:ARG:HA	29:L28:47:THR:HA	2.03	0.41
1:16S:54:C:H2'	1:16S:352:C:H41	1.85	0.41
1:16S:458:U:H2'	1:16S:459:A:C8	2.56	0.41
1:16S:662:U:H2'	1:16S:663:A:C8	2.56	0.41
1:16S:1015:G:N3	1:16S:1218:C:O2'	2.48	0.41
2:23S:20:C:H2'	2:23S:21:A:H8	1.85	0.41
2:23S:121:G:H2'	2:23S:122:G:H8	1.84	0.41
2:23S:437:U:H2'	2:23S:438:G:C8	2.56	0.41
2:23S:620:G:H4'	2:23S:621:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:1600:C:H2'	2:23S:1601:G:H8	1.85	0.41
2:23S:1674:G:H21	2:23S:1678:A:H2	1.67	0.41
2:23S:1917:U:O4	2:23S:1918:A:N6	2.53	0.41
2:23S:1997:C:H2'	2:23S:1998:A:H8	1.86	0.41
2:23S:2208:C:H2'	2:23S:2209:G:C8	2.56	0.41
6:L02:209:ALA:HA	6:L02:212:TRP:CE2	2.55	0.41
8:L04:150:THR:HG23	8:L04:189:THR:HG21	2.03	0.41
20:L18:27:VAL:HA	20:L18:93:ASP:HB3	2.01	0.41
45:S09:80:HIS:NE2	45:S09:103:VAL:O	2.54	0.41
48:S12:120:ARG:NH2	48:S12:121:PRO:O	2.53	0.41
1:16S:108:G:H21	56:S20:6:ALA:HB1	1.86	0.41
1:16S:407:U:H2'	1:16S:408:A:H8	1.86	0.41
1:16S:1288:A:N3	1:16S:1352:C:O2'	2.40	0.41
1:16S:1463:U:OP1	21:L19:108:ARG:NE	2.54	0.41
2:23S:302:C:H2'	2:23S:303:G:C8	2.56	0.41
2:23S:335:C:O2	26:L24:67:SER:OG	2.38	0.41
2:23S:552:U:H2'	2:23S:553:G:C8	2.55	0.41
2:23S:596:U:H2'	2:23S:597:G:H8	1.86	0.41
2:23S:680:C:H2'	2:23S:681:G:C8	2.56	0.41
2:23S:970:U:H2'	2:23S:971:G:C8	2.56	0.41
2:23S:1079:C:H2'	2:23S:1080:A:C8	2.55	0.41
2:23S:1106:G:H2'	2:23S:1107:G:H8	1.85	0.41
2:23S:1252:G:OP2	22:L20:13:HIS:NE2	2.45	0.41
2:23S:1443:U:H2'	2:23S:1444:G:C8	2.56	0.41
2:23S:1730:C:H1'	2:23S:1731:G:C6	2.56	0.41
2:23S:2072:C:C4	2:23S:2073:C:N4	2.89	0.41
2:23S:2127:G:H2'	2:23S:2128:G:C8	2.56	0.41
2:23S:2229:U:H2'	2:23S:2230:G:C8	2.56	0.41
2:23S:2258:C:O2'	2:23S:2427:C:OP2	2.37	0.41
3:5S:6:G:H2'	3:5S:7:G:H8	1.86	0.41
3:5S:118:C:H2'	3:5S:119:A:H8	1.86	0.41
13:L10:58:THR:HG22	13:L10:79:PRO:HA	2.02	0.41
15:L13:13:ARG:HH11	15:L13:53:TYR:HE2	1.68	0.41
17:L15:91:ASP:OD1	17:L15:91:ASP:N	2.52	0.41
26:L24:25:LYS:N	26:L24:34:ILE:O	2.49	0.41
40:S04:190:LEU:H	40:S04:190:LEU:HG	1.61	0.41
50:S14:66:THR:H	50:S14:66:THR:HG1	1.63	0.41
1:16S:1055:A:N3	39:S03:155:ARG:NH1	2.69	0.41
1:16S:1356:G:H2'	1:16S:1357:A:C8	2.55	0.41
2:23S:828:U:H2'	2:23S:829:A:C8	2.56	0.41
2:23S:1061:U:H3	14:L11:53:PRO:HB2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:1085:A:H2'	2:23S:1086:A:C4	2.56	0.41
2:23S:1604:C:O2'	2:23S:1610:A:N1	2.48	0.41
2:23S:1921:G:H2'	2:23S:1922:G:C8	2.56	0.41
2:23S:2081:U:O2	2:23S:2239:G:O6	2.38	0.41
2:23S:2124:G:O2'	12:L1:41:SER:O	2.39	0.41
2:23S:2385:C:H2'	2:23S:2386:A:C8	2.56	0.41
13:L10:1:MET:HB2	13:L10:2:ALA:H	1.70	0.41
14:L11:46:ASP:OD1	14:L11:46:ASP:N	2.54	0.41
14:L11:116:MET:HB3	14:L11:124:MET:HE2	2.03	0.41
16:L14:77:ILE:HG12	21:L19:71:ARG:HG3	2.02	0.41
26:L24:7:ASP:OD1	26:L24:23:LYS:NZ	2.46	0.41
48:S12:33:CYS:HA	48:S12:54:VAL:HA	2.02	0.41
55:S19:12:LEU:HD22	55:S19:12:LEU:HA	1.95	0.41
56:S20:43:LYS:HG2	56:S20:85:LEU:HG	2.03	0.41
1:16S:309:A:H2'	1:16S:310:G:C8	2.56	0.40
1:16S:1029:U:O2'	1:16S:1033:G:N2	2.54	0.40
1:16S:1247:U:H2'	1:16S:1248:A:C8	2.56	0.40
2:23S:51:G:N1	2:23S:120:U:O2'	2.52	0.40
2:23S:639:U:H2'	2:23S:640:C:C6	2.55	0.40
2:23S:948:C:H2'	2:23S:949:G:H8	1.86	0.40
2:23S:1041:G:H2'	2:23S:1042:G:H8	1.85	0.40
2:23S:1713:A:N3	2:23S:1715:G:O2'	2.52	0.40
2:23S:1921:G:H2'	2:23S:1922:G:H8	1.86	0.40
8:L04:48:THR:OG1	8:L04:49:ARG:N	2.53	0.40
13:L10:42:ARG:HH21	13:L10:46:ARG:HG3	1.86	0.40
15:L13:4:PHE:HB3	22:L20:63:ARG:HH12	1.85	0.40
15:L13:125:TYR:OH	15:L13:131:ASN:OD1	2.30	0.40
21:L19:28:LYS:HA	21:L19:41:ALA:HA	2.03	0.40
26:L24:2:ALA:HB3	26:L24:5:ARG:HH21	1.86	0.40
30:L29:32:ALA:HB2	30:L29:37:LEU:HD23	2.03	0.40
42:S06:29:ILE:H	42:S06:29:ILE:HG13	1.50	0.40
53:S17:36:PHE:HD1	53:S17:36:PHE:HA	1.78	0.40
57:S21:23:GLU:OE1	57:S21:26:GLY:N	2.55	0.40
1:16S:123:U:OP1	1:16S:311:C:O2'	2.34	0.40
1:16S:200:G:H2'	1:16S:201:G:H8	1.86	0.40
1:16S:627:G:H2'	1:16S:628:G:H8	1.86	0.40
1:16S:880:C:H2'	1:16S:881:G:C8	2.56	0.40
2:23S:206:U:H2'	2:23S:207:A:H8	1.86	0.40
2:23S:485:C:O2'	24:L22:60:HIS:NE2	2.37	0.40
2:23S:552:U:H2'	2:23S:553:G:H8	1.86	0.40
2:23S:655:A:H4'	2:23S:656:G:H5'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:23S:1278:C:H2'	2:23S:1279:G:H8	1.86	0.40
2:23S:1346:G:H2'	2:23S:1347:A:H8	1.87	0.40
2:23S:2591:C:H2'	2:23S:2592:G:C8	2.57	0.40
2:23S:2801:G:H2'	2:23S:2802:G:H8	1.86	0.40
7:L03:33:ARG:H	7:L03:33:ARG:HG2	1.52	0.40
9:L05:62:GLN:HB3	9:L05:63:LYS:H	1.73	0.40
20:L18:56:LYS:HB2	20:L18:56:LYS:HE3	1.84	0.40
33:L32:9:ARG:H	33:L32:9:ARG:HG3	1.65	0.40
39:S03:155:ARG:HG3	39:S03:162:ALA:HB2	2.02	0.40
41:S05:61:LYS:HE3	41:S05:61:LYS:HB2	1.89	0.40
41:S05:123:LEU:H	41:S05:123:LEU:HG	1.57	0.40
54:S18:25:ILE:HA	54:S18:28:LEU:HB2	2.03	0.40
55:S19:35:ARG:HH21	55:S19:74:ALA:HB3	1.86	0.40
1:16S:169:C:H2'	1:16S:170:U:C6	2.56	0.40
1:16S:407:U:O2'	40:S04:112:GLU:OE1	2.34	0.40
1:16S:538:G:OP1	48:S12:109:ARG:NH1	2.54	0.40
1:16S:541:G:H2'	1:16S:542:G:C8	2.57	0.40
1:16S:648:A:H2'	1:16S:649:A:C8	2.56	0.40
1:16S:1322:C:H5"	49:S13:98:GLY:HA3	2.02	0.40
1:16S:1348:U:H2'	1:16S:1349:A:C8	2.57	0.40
2:23S:76:C:H2'	2:23S:77:G:H8	1.86	0.40
2:23S:192:C:O2'	2:23S:802:A:N3	2.53	0.40
2:23S:428:A:H3'	2:23S:429:A:C8	2.56	0.40
2:23S:567:U:H5"	17:L15:36:LYS:HE3	2.03	0.40
2:23S:660:C:H2'	2:23S:661:A:H8	1.85	0.40
2:23S:1862:G:O6	2:23S:1880:U:O4	2.38	0.40
2:23S:2651:C:H2'	2:23S:2652:C:C6	2.56	0.40
2:23S:2861:U:H2'	2:23S:2862:G:C8	2.56	0.40
9:L05:139:GLU:HA	32:L31:28:VAL:HG13	2.02	0.40
10:L06:169:ARG:HH21	10:L06:171:LYS:HB3	1.86	0.40
12:L1:53:ARG:HA	12:L1:53:ARG:HD3	1.88	0.40
13:L10:48:ALA:HB3	13:L10:52:MET:HB2	2.02	0.40
16:L14:12:ASP:OD1	16:L14:12:ASP:N	2.54	0.40
18:L16:59:ARG:HA	18:L16:59:ARG:HD3	1.83	0.40
33:L32:46:GLY:HA3	33:L32:54:ILE:HG22	2.03	0.40
43:S07:67:ASN:O	43:S07:137:ARG:NE	2.54	0.40
47:S11:59:PRO:O	47:S11:63:GLN:N	2.55	0.40
49:S13:38:ILE:HD12	49:S13:38:ILE:HA	1.87	0.40
50:S14:46:LYS:HA	50:S14:46:LYS:HD2	1.90	0.40
51:S15:17:ASP:N	51:S15:17:ASP:OD1	2.55	0.40
52:S16:21:VAL:HG11	52:S16:60:TRP:CG	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:S17:10:ARG:NH1	53:S17:11:VAL:H	2.20	0.40
55:S19:20:LYS:HD2	55:S19:28:LYS:HZ1	1.86	0.40
1:16S:437:U:O2'	40:S04:153:ARG:NH2	2.54	0.40
1:16S:459:A:H2'	1:16S:460:A:C8	2.56	0.40
1:16S:1189:U:OP1	50:S14:97:LYS:NZ	2.50	0.40
2:23S:373:U:H2'	2:23S:374:A:C8	2.56	0.40
2:23S:477:A:H2'	2:23S:478:A:C8	2.56	0.40
2:23S:2072:C:N3	2:23S:2073:C:N3	2.70	0.40
7:L03:25:THR:HG21	7:L03:193:VAL:HG22	2.03	0.40
8:L04:47:LYS:HB3	8:L04:51:GLU:HB2	2.03	0.40
9:L05:33:ILE:H	9:L05:33:ILE:HG13	1.74	0.40
15:L13:141:ASP:OD1	15:L13:141:ASP:N	2.40	0.40
24:L22:109:ASP:OD1	24:L22:109:ASP:N	2.51	0.40
38:S02:151:LYS:HD2	38:S02:152:ASP:H	1.86	0.40
40:S04:15:GLY:HA2	40:S04:34:GLU:HB3	2.02	0.40
41:S05:28:ARG:H	41:S05:28:ARG:HG2	1.68	0.40
42:S06:38:ARG:HB2	42:S06:63:ASN:HB3	2.02	0.40
43:S07:125:ASP:N	43:S07:125:ASP:OD1	2.53	0.40
56:S20:9:ARG:HD2	56:S20:9:ARG:HA	1.91	0.40
1:16S:424:G:H2'	1:16S:425:G:C8	2.57	0.40
1:16S:918:A:H2'	1:16S:919:A:C8	2.56	0.40
1:16S:923:A:N6	1:16S:1392:G:O6	2.55	0.40
1:16S:950:U:H2'	1:16S:951:G:C8	2.55	0.40
1:16S:1225:A:H1'	55:S19:77:ARG:HD2	2.04	0.40
1:16S:1360:A:C8	50:S14:57:SER:HA	2.56	0.40
2:23S:660:C:H2'	2:23S:661:A:C8	2.56	0.40
2:23S:1114:C:H2'	2:23S:1115:G:C8	2.57	0.40
2:23S:1171:G:N2	2:23S:1179:G:N7	2.69	0.40
2:23S:1386:C:H2'	2:23S:1387:A:C8	2.57	0.40
2:23S:1530:G:H22	2:23S:1542:U:H1'	1.86	0.40
2:23S:1796:U:O2'	6:L02:253:GLY:N	2.54	0.40
2:23S:1869:G:H21	2:23S:1872:A:H8	1.67	0.40
2:23S:2089:C:H2'	2:23S:2090:A:H8	1.87	0.40
2:23S:2698:U:H2'	2:23S:2699:C:C6	2.57	0.40
2:23S:2798:U:O2'	2:23S:2799:A:N7	2.52	0.40
8:L04:171:ASP:OD2	8:L04:173:THR:OG1	2.32	0.40
11:L09:124:THR:O	11:L09:128:HIS:NE2	2.53	0.40
16:L14:7:MET:HB3	16:L14:18:ARG:HD2	2.03	0.40
21:L19:103:THR:HA	21:L19:107:ALA:HB2	2.03	0.40
23:L21:60:LYS:HE2	23:L21:100:GLY:HA3	2.02	0.40
28:L27:38:GLY:O	28:L27:53:HIS:ND1	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:S09:17:ARG:NE	45:S09:65:THR:OG1	2.51	0.40
56:S20:43:LYS:NZ	56:S20:43:LYS:H	2.20	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	
6	L02	269/273 (98%)	247 (92%)	22 (8%)	0	100	100
7	L03	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
8	L04	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	29	67
9	L05	175/179 (98%)	160 (91%)	15 (9%)	0	100	100
10	L06	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
11	L09	147/149 (99%)	132 (90%)	14 (10%)	1 (1%)	22	60
12	L1	130/234 (56%)	123 (95%)	7 (5%)	0	100	100
13	L10	129/165 (78%)	111 (86%)	17 (13%)	1 (1%)	19	57
14	L11	139/142 (98%)	123 (88%)	16 (12%)	0	100	100
15	L13	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
16	L14	120/123 (98%)	111 (92%)	9 (8%)	0	100	100
17	L15	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
18	L16	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
19	L17	118/127 (93%)	104 (88%)	14 (12%)	0	100	100
20	L18	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
21	L19	112/115 (97%)	104 (93%)	8 (7%)	0	100	100
22	L20	115/118 (98%)	115 (100%)	0	0	100	100
23	L21	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	15	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	L22	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
25	L23	91/100 (91%)	84 (92%)	7 (8%)	0	100	100
26	L24	100/104 (96%)	89 (89%)	11 (11%)	0	100	100
27	L25	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
28	L27	73/85 (86%)	70 (96%)	3 (4%)	0	100	100
29	L28	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
30	L29	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
31	L30	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
32	L31	43/45 (96%)	35 (81%)	8 (19%)	0	100	100
33	L32	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
34	L33	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
35	L34	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
36	L35	62/65 (95%)	56 (90%)	6 (10%)	0	100	100
37	L36	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
38	S02	223/241 (92%)	215 (96%)	8 (4%)	0	100	100
39	S03	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
40	S04	203/206 (98%)	182 (90%)	21 (10%)	0	100	100
41	S05	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
42	S06	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
43	S07	149/179 (83%)	142 (95%)	7 (5%)	0	100	100
44	S08	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
45	S09	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
46	S10	96/103 (93%)	86 (90%)	10 (10%)	0	100	100
47	S11	114/129 (88%)	107 (94%)	7 (6%)	0	100	100
48	S12	121/124 (98%)	103 (85%)	18 (15%)	0	100	100
49	S13	112/118 (95%)	104 (93%)	8 (7%)	0	100	100
50	S14	98/101 (97%)	92 (94%)	6 (6%)	0	100	100
51	S15	86/89 (97%)	76 (88%)	10 (12%)	0	100	100
52	S16	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
53	S17	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
54	S18	63/75 (84%)	62 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	S19	77/92 (84%)	70 (91%)	7 (9%)	0	100	100
56	S20	83/87 (95%)	82 (99%)	1 (1%)	0	100	100
57	S21	63/71 (89%)	45 (71%)	18 (29%)	0	100	100
58	SMPB	148/150 (99%)	125 (84%)	22 (15%)	1 (1%)	22	60
All	All	6110/6579 (93%)	5629 (92%)	476 (8%)	5 (0%)	54	84

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	L10	118	ILE
23	L21	54	VAL
8	L04	83	VAL
58	SMPB	79	HIS
11	L09	9	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	L02	216/218 (99%)	204 (94%)	12 (6%)	21	51
7	L03	164/164 (100%)	155 (94%)	9 (6%)	21	51
8	L04	165/165 (100%)	155 (94%)	10 (6%)	18	48
9	L05	148/150 (99%)	127 (86%)	21 (14%)	3	20
10	L06	137/138 (99%)	124 (90%)	13 (10%)	8	33
11	L09	114/114 (100%)	101 (89%)	13 (11%)	5	26
12	L1	110/181 (61%)	92 (84%)	18 (16%)	2	15
13	L10	100/123 (81%)	90 (90%)	10 (10%)	7	30
14	L11	109/110 (99%)	100 (92%)	9 (8%)	11	39
15	L13	116/116 (100%)	111 (96%)	5 (4%)	29	57
16	L14	103/104 (99%)	91 (88%)	12 (12%)	5	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
17	L15	102/103 (99%)	97 (95%)	5 (5%)	25 54
18	L16	109/109 (100%)	103 (94%)	6 (6%)	21 51
19	L17	100/103 (97%)	97 (97%)	3 (3%)	41 64
20	L18	86/87 (99%)	78 (91%)	8 (9%)	9 34
21	L19	99/100 (99%)	95 (96%)	4 (4%)	31 58
22	L20	89/90 (99%)	87 (98%)	2 (2%)	52 71
23	L21	84/84 (100%)	73 (87%)	11 (13%)	4 22
24	L22	93/93 (100%)	90 (97%)	3 (3%)	39 63
25	L23	80/84 (95%)	69 (86%)	11 (14%)	3 21
26	L24	83/85 (98%)	78 (94%)	5 (6%)	19 49
27	L25	78/78 (100%)	69 (88%)	9 (12%)	5 26
28	L27	57/63 (90%)	54 (95%)	3 (5%)	22 52
29	L28	67/68 (98%)	63 (94%)	4 (6%)	19 49
30	L29	55/55 (100%)	52 (94%)	3 (6%)	21 51
31	L30	48/49 (98%)	44 (92%)	4 (8%)	11 39
32	L31	42/42 (100%)	34 (81%)	8 (19%)	1 10
33	L32	47/48 (98%)	40 (85%)	7 (15%)	3 18
34	L33	45/49 (92%)	41 (91%)	4 (9%)	9 36
35	L34	38/38 (100%)	36 (95%)	2 (5%)	22 52
36	L35	51/52 (98%)	49 (96%)	2 (4%)	32 59
37	L36	34/34 (100%)	32 (94%)	2 (6%)	19 49
38	S02	186/199 (94%)	171 (92%)	15 (8%)	11 40
39	S03	170/190 (90%)	156 (92%)	14 (8%)	11 40
40	S04	172/173 (99%)	155 (90%)	17 (10%)	8 31
41	S05	119/126 (94%)	106 (89%)	13 (11%)	6 28
42	S06	87/116 (75%)	78 (90%)	9 (10%)	7 30
43	S07	124/147 (84%)	112 (90%)	12 (10%)	8 32
44	S08	104/105 (99%)	97 (93%)	7 (7%)	16 46
45	S09	105/107 (98%)	95 (90%)	10 (10%)	8 33
46	S10	86/90 (96%)	76 (88%)	10 (12%)	5 26
47	S11	89/99 (90%)	77 (86%)	12 (14%)	4 22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
48	S12	103/104 (99%)	96 (93%)	7 (7%)	16 45
49	S13	92/96 (96%)	84 (91%)	8 (9%)	10 37
50	S14	83/84 (99%)	79 (95%)	4 (5%)	25 54
51	S15	76/77 (99%)	73 (96%)	3 (4%)	32 59
52	S16	65/65 (100%)	57 (88%)	8 (12%)	4 24
53	S17	74/78 (95%)	64 (86%)	10 (14%)	4 22
54	S18	56/65 (86%)	50 (89%)	6 (11%)	6 29
55	S19	70/79 (89%)	61 (87%)	9 (13%)	4 23
56	S20	65/66 (98%)	62 (95%)	3 (5%)	27 55
57	S21	55/61 (90%)	48 (87%)	7 (13%)	4 23
58	SMPB	125/125 (100%)	114 (91%)	11 (9%)	10 37
All	All	5075/5349 (95%)	4642 (92%)	433 (8%)	14 39

All (433) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	L02	18	VAL
6	L02	19	VAL
6	L02	23	LEU
6	L02	149	LYS
6	L02	153	LEU
6	L02	171	VAL
6	L02	186	ASP
6	L02	193	GLU
6	L02	212	TRP
6	L02	215	VAL
6	L02	216	ARG
6	L02	269	ARG
7	L03	9	VAL
7	L03	12	THR
7	L03	18	ASP
7	L03	86	GLU
7	L03	104	VAL
7	L03	128	ARG
7	L03	157	LYS
7	L03	164	GLN
7	L03	189	VAL
8	L04	2	GLU

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Mol	Chain	Res	Type
8	L04	6	LYS
8	L04	13	THR
8	L04	14	VAL
8	L04	53	THR
8	L04	60	TRP
8	L04	149	ILE
8	L04	154	ASP
8	L04	155	GLU
8	L04	187	VAL
9	L05	3	LEU
9	L05	9	ASP
9	L05	27	VAL
9	L05	29	ARG
9	L05	30	VAL
9	L05	31	GLU
9	L05	39	VAL
9	L05	55	ASP
9	L05	82	TYR
9	L05	90	LEU
9	L05	91	ARG
9	L05	97	GLU
9	L05	100	GLU
9	L05	102	LEU
9	L05	133	GLU
9	L05	142	TYR
9	L05	151	LEU
9	L05	155	ILE
9	L05	157	THR
9	L05	163	GLU
9	L05	174	PHE
10	L06	9	VAL
10	L06	10	VAL
10	L06	29	ASN
10	L06	42	VAL
10	L06	48	THR
10	L06	50	THR
10	L06	83	THR
10	L06	89	VAL
10	L06	114	HIS
10	L06	126	THR
10	L06	138	GLN
10	L06	151	ARG

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Mol	Chain	Res	Type
10	L06	174	LYS
11	L09	3	VAL
11	L09	6	LEU
11	L09	17	ASP
11	L09	37	VAL
11	L09	83	LYS
11	L09	90	LEU
11	L09	91	PHE
11	L09	97	ARG
11	L09	98	ASP
11	L09	101	ASP
11	L09	121	VAL
11	L09	130	VAL
11	L09	144	VAL
12	L1	5	THR
12	L1	8	MET
12	L1	10	VAL
12	L1	16	ASP
12	L1	18	THR
12	L1	23	ILE
12	L1	44	VAL
12	L1	50	ILE
12	L1	57	GLN
12	L1	59	VAL
12	L1	162	ARG
12	L1	163	TYR
12	L1	170	ILE
12	L1	189	LEU
12	L1	194	VAL
12	L1	198	LYS
12	L1	207	VAL
12	L1	222	VAL
13	L10	1	MET
13	L10	6	GLN
13	L10	18	VAL
13	L10	26	VAL
13	L10	58	THR
13	L10	60	LEU
13	L10	64	VAL
13	L10	87	GLU
13	L10	109	LYS
13	L10	113	PHE

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Mol	Chain	Res	Type
14	L11	7	TYR
14	L11	10	LEU
14	L11	39	LYS
14	L11	45	THR
14	L11	52	LEU
14	L11	58	ILE
14	L11	64	ARG
14	L11	97	VAL
14	L11	139	VAL
15	L13	5	THR
15	L13	13	ARG
15	L13	52	ASP
15	L13	71	ASP
15	L13	81	ILE
16	L14	10	VAL
16	L14	32	TYR
16	L14	44	LYS
16	L14	49	ARG
16	L14	54	LYS
16	L14	56	ASP
16	L14	57	VAL
16	L14	58	LEU
16	L14	65	THR
16	L14	82	ASN
16	L14	88	ASN
16	L14	110	GLU
17	L15	74	THR
17	L15	89	VAL
17	L15	92	LEU
17	L15	94	THR
17	L15	111	ILE
18	L16	54	THR
18	L16	59	ARG
18	L16	101	VAL
18	L16	119	LEU
18	L16	132	THR
18	L16	135	VAL
19	L17	2	ARG
19	L17	30	ARG
19	L17	116	VAL
20	L18	27	VAL
20	L18	33	ARG

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Mol	Chain	Res	Type
20	L18	43	ASN
20	L18	47	VAL
20	L18	65	THR
20	L18	69	ASP
20	L18	90	VAL
20	L18	112	GLU
21	L19	31	VAL
21	L19	83	ILE
21	L19	108	ARG
21	L19	111	GLU
22	L20	7	VAL
22	L20	102	LYS
23	L21	5	PHE
23	L21	11	GLN
23	L21	20	VAL
23	L21	22	LEU
23	L21	43	ASN
23	L21	46	GLU
23	L21	48	LYS
23	L21	54	VAL
23	L21	58	VAL
23	L21	64	VAL
23	L21	86	GLN
24	L22	66	ILE
24	L22	73	LYS
24	L22	84	ARG
25	L23	2	ILE
25	L23	3	ARG
25	L23	5	GLU
25	L23	10	VAL
25	L23	16	VAL
25	L23	48	GLN
25	L23	56	GLU
25	L23	58	VAL
25	L23	61	LEU
25	L23	67	VAL
25	L23	69	ARG
26	L24	26	ASN
26	L24	27	VAL
26	L24	48	VAL
26	L24	53	GLN
26	L24	58	VAL

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Mol	Chain	Res	Type
27	L25	12	GLN
27	L25	20	LEU
27	L25	34	LYS
27	L25	42	LEU
27	L25	43	ASP
27	L25	55	GLU
27	L25	64	VAL
27	L25	69	GLU
27	L25	76	ASP
28	L27	39	THR
28	L27	52	ASP
28	L27	72	ASN
29	L28	24	THR
29	L28	43	LYS
29	L28	46	VAL
29	L28	53	LYS
30	L29	7	ARG
30	L29	15	ASN
30	L29	22	LEU
31	L30	30	ARG
31	L30	36	GLU
31	L30	40	THR
31	L30	56	VAL
32	L31	4	ASP
32	L31	5	ILE
32	L31	6	HIS
32	L31	23	LYS
32	L31	25	ARG
32	L31	27	THR
32	L31	36	VAL
32	L31	44	PHE
33	L32	2	VAL
33	L32	3	GLN
33	L32	21	LEU
33	L32	24	VAL
33	L32	32	THR
33	L32	37	HIS
33	L32	52	LYS
34	L33	6	GLU
34	L33	22	THR
34	L33	29	LYS
34	L33	32	LYS

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Mol	Chain	Res	Type
35	L34	9	VAL
35	L34	44	VAL
36	L35	15	LYS
36	L35	61	LEU
37	L36	12	ARG
37	L36	37	GLN
38	S02	3	VAL
38	S02	7	ASP
38	S02	9	LEU
38	S02	38	HIS
38	S02	42	LEU
38	S02	77	GLU
38	S02	94	ARG
38	S02	151	LYS
38	S02	160	LEU
38	S02	182	VAL
38	S02	186	VAL
38	S02	207	ARG
38	S02	211	LEU
38	S02	221	ARG
38	S02	222	GLU
39	S03	14	VAL
39	S03	24	ASN
39	S03	37	LYS
39	S03	51	VAL
39	S03	68	HIS
39	S03	76	ILE
39	S03	86	LEU
39	S03	92	ASP
39	S03	134	LYS
39	S03	156	LEU
39	S03	167	TYR
39	S03	172	VAL
39	S03	180	ASP
39	S03	194	VAL
40	S04	2	ARG
40	S04	4	LEU
40	S04	7	LYS
40	S04	28	ASP
40	S04	29	THR
40	S04	33	ILE
40	S04	39	GLN

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Mol	Chain	Res	Type
40	S04	56	GLU
40	S04	68	GLU
40	S04	129	VAL
40	S04	130	ASN
40	S04	141	VAL
40	S04	172	VAL
40	S04	183	ARG
40	S04	190	LEU
40	S04	194	ILE
40	S04	196	GLU
41	S05	17	VAL
41	S05	30	PHE
41	S05	35	LEU
41	S05	53	ARG
41	S05	55	VAL
41	S05	73	VAL
41	S05	75	LEU
41	S05	87	VAL
41	S05	105	ILE
41	S05	122	VAL
41	S05	123	LEU
41	S05	158	LYS
41	S05	164	LEU
42	S06	3	HIS
42	S06	10	VAL
42	S06	18	VAL
42	S06	29	ILE
42	S06	54	LEU
42	S06	82	ASP
42	S06	84	VAL
42	S06	92	THR
42	S06	98	GLU
43	S07	3	ARG
43	S07	4	ARG
43	S07	14	ASP
43	S07	22	LEU
43	S07	30	MET
43	S07	72	VAL
43	S07	74	VAL
43	S07	84	TYR
43	S07	85	GLN
43	S07	86	VAL

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Mol	Chain	Res	Type
43	S07	103	ILE
43	S07	128	GLU
44	S08	8	ASP
44	S08	45	ILE
44	S08	68	LYS
44	S08	70	VAL
44	S08	74	ILE
44	S08	89	ASP
44	S08	103	VAL
45	S09	24	ASN
45	S09	34	LEU
45	S09	41	GLU
45	S09	44	ARG
45	S09	60	LEU
45	S09	67	LYS
45	S09	87	MET
45	S09	88	GLU
45	S09	102	PHE
45	S09	105	ARG
46	S10	13	PHE
46	S10	15	HIS
46	S10	42	LEU
46	S10	67	ILE
46	S10	73	LEU
46	S10	78	GLU
46	S10	85	ASP
46	S10	89	ARG
46	S10	90	LEU
46	S10	98	VAL
47	S11	15	VAL
47	S11	45	THR
47	S11	60	PHE
47	S11	67	GLU
47	S11	80	ASN
47	S11	81	LEU
47	S11	84	MET
47	S11	85	VAL
47	S11	93	GLU
47	S11	109	ILE
47	S11	115	ILE
47	S11	124	LYS
48	S12	4	ASN

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Mol	Chain	Res	Type
48	S12	20	VAL
48	S12	45	ASN
48	S12	49	ARG
48	S12	107	LYS
48	S12	109	ARG
48	S12	113	ARG
49	S13	6	ILE
49	S13	18	LEU
49	S13	24	VAL
49	S13	47	LEU
49	S13	90	HIS
49	S13	100	ARG
49	S13	101	THR
49	S13	113	LYS
50	S14	73	LEU
50	S14	81	ILE
50	S14	82	LYS
50	S14	83	VAL
51	S15	46	LYS
51	S15	65	LEU
51	S15	86	LEU
52	S16	19	VAL
52	S16	23	ASP
52	S16	29	ASN
52	S16	36	VAL
52	S16	53	ASP
52	S16	54	LEU
52	S16	74	LEU
52	S16	80	LYS
53	S17	5	ARG
53	S17	16	MET
53	S17	19	SER
53	S17	20	ILE
53	S17	21	VAL
53	S17	27	PHE
53	S17	36	PHE
53	S17	37	ILE
53	S17	56	ASP
53	S17	62	GLU
54	S18	11	ARG
54	S18	17	VAL
54	S18	24	ASP

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Mol	Chain	Res	Type
54	S18	39	VAL
54	S18	43	ILE
54	S18	72	ARG
55	S19	12	LEU
55	S19	23	GLU
55	S19	28	LYS
55	S19	40	PHE
55	S19	50	VAL
55	S19	57	VAL
55	S19	59	VAL
55	S19	66	VAL
55	S19	73	PHE
56	S20	17	ARG
56	S20	29	THR
56	S20	67	HIS
57	S21	6	ARG
57	S21	16	ARG
57	S21	17	ARG
57	S21	23	GLU
57	S21	33	ARG
57	S21	36	PHE
57	S21	65	ARG
58	SMPB	16	LEU
58	SMPB	36	LEU
58	SMPB	59	ARG
58	SMPB	75	VAL
58	SMPB	80	VAL
58	SMPB	93	ASN
58	SMPB	104	VAL
58	SMPB	125	VAL
58	SMPB	127	ILE
58	SMPB	131	LYS
58	SMPB	151	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
12	L1	57	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	16S	1538/1539 (99%)	251 (16%)	5 (0%)
2	23S	2902/2903 (99%)	561 (19%)	12 (0%)
3	5S	119/120 (99%)	22 (18%)	1 (0%)
4	ATRN	75/76 (98%)	18 (24%)	1 (1%)
5	ETRN	76/77 (98%)	23 (30%)	0
59	TMRN	362/363 (99%)	150 (41%)	13 (3%)
All	All	5072/5078 (99%)	1025 (20%)	32 (0%)

All (1025) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	16S	4	U
1	16S	6	G
1	16S	9	G
1	16S	22	G
1	16S	32	A
1	16S	39	G
1	16S	47	C
1	16S	48	C
1	16S	51	A
1	16S	71	A
1	16S	75	G
1	16S	79	G
1	16S	81	A
1	16S	82	G
1	16S	83	C
1	16S	100	G
1	16S	121	U
1	16S	122	G
1	16S	130	A
1	16S	144	G
1	16S	149	A
1	16S	159	G
1	16S	161	A
1	16S	163	C
1	16S	164	G
1	16S	173	U
1	16S	177	G
1	16S	183	C
1	16S	184	G
1	16S	197	A
1	16S	204	G
1	16S	209	U

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Mol	Chain	Res	Type
1	16S	211	G
1	16S	212	G
1	16S	215	C
1	16S	245	U
1	16S	247	G
1	16S	251	G
1	16S	266	G
1	16S	267	C
1	16S	279	A
1	16S	280	C
1	16S	281	G
1	16S	283	U
1	16S	289	G
1	16S	306	A
1	16S	315	A
1	16S	327	A
1	16S	328	C
1	16S	329	A
1	16S	345	C
1	16S	346	G
1	16S	347	G
1	16S	351	G
1	16S	352	C
1	16S	363	A
1	16S	367	U
1	16S	372	C
1	16S	373	A
1	16S	385	C
1	16S	392	C
1	16S	397	A
1	16S	406	G
1	16S	411	A
1	16S	412	A
1	16S	413	G
1	16S	421	U
1	16S	422	C
1	16S	429	U
1	16S	430	A
1	16S	438	U
1	16S	467	U
1	16S	468	A
1	16S	479	U

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Mol	Chain	Res	Type
1	16S	481	G
1	16S	484	G
1	16S	486	U
1	16S	494	G
1	16S	495	A
1	16S	509	A
1	16S	510	A
1	16S	511	C
1	16S	517	G
1	16S	518	C
1	16S	521	G
1	16S	527	G
1	16S	531	U
1	16S	532	A
1	16S	533	A
1	16S	535	A
1	16S	547	A
1	16S	561	U
1	16S	562	U
1	16S	564	C
1	16S	572	A
1	16S	573	A
1	16S	575	G
1	16S	576	C
1	16S	577	G
1	16S	579	A
1	16S	596	A
1	16S	604	G
1	16S	633	G
1	16S	641	U
1	16S	642	A
1	16S	650	G
1	16S	661	G
1	16S	665	A
1	16S	686	U
1	16S	687	A
1	16S	702	A
1	16S	703	G
1	16S	713	G
1	16S	724	G
1	16S	731	G
1	16S	755	G

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Mol	Chain	Res	Type
1	16S	777	A
1	16S	794	A
1	16S	809	G
1	16S	815	A
1	16S	817	C
1	16S	818	G
1	16S	819	A
1	16S	821	G
1	16S	829	G
1	16S	836	G
1	16S	843	U
1	16S	844	G
1	16S	846	G
1	16S	871	U
1	16S	884	U
1	16S	889	A
1	16S	890	G
1	16S	891	U
1	16S	902	G
1	16S	926	G
1	16S	934	C
1	16S	935	A
1	16S	939	G
1	16S	960	U
1	16S	961	U
1	16S	966	G
1	16S	969	A
1	16S	971	G
1	16S	975	A
1	16S	976	G
1	16S	977	A
1	16S	989	U
1	16S	991	U
1	16S	992	U
1	16S	993	G
1	16S	994	A
1	16S	1004	A
1	16S	1016	A
1	16S	1017	U
1	16S	1020	G
1	16S	1027	C
1	16S	1028	C

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Mol	Chain	Res	Type
1	16S	1030	U
1	16S	1031	C
1	16S	1032	G
1	16S	1033	G
1	16S	1050	G
1	16S	1053	G
1	16S	1065	U
1	16S	1085	U
1	16S	1086	U
1	16S	1089	G
1	16S	1094	G
1	16S	1095	U
1	16S	1101	A
1	16S	1108	G
1	16S	1130	A
1	16S	1131	G
1	16S	1132	C
1	16S	1136	C
1	16S	1137	C
1	16S	1138	G
1	16S	1139	G
1	16S	1145	A
1	16S	1154	G
1	16S	1159	U
1	16S	1160	G
1	16S	1168	U
1	16S	1169	A
1	16S	1182	G
1	16S	1184	G
1	16S	1191	A
1	16S	1193	G
1	16S	1196	A
1	16S	1197	A
1	16S	1201	A
1	16S	1212	U
1	16S	1213	A
1	16S	1225	A
1	16S	1226	C
1	16S	1228	C
1	16S	1238	A
1	16S	1240	U
1	16S	1241	G

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Mol	Chain	Res	Type
1	16S	1250	A
1	16S	1253	G
1	16S	1256	A
1	16S	1258	G
1	16S	1261	A
1	16S	1275	A
1	16S	1278	G
1	16S	1279	G
1	16S	1280	A
1	16S	1282	C
1	16S	1287	A
1	16S	1297	G
1	16S	1298	U
1	16S	1300	G
1	16S	1305	G
1	16S	1317	C
1	16S	1318	A
1	16S	1320	C
1	16S	1325	C
1	16S	1338	G
1	16S	1347	G
1	16S	1348	U
1	16S	1363	A
1	16S	1381	U
1	16S	1395	C
1	16S	1398	A
1	16S	1446	A
1	16S	1447	A
1	16S	1448	C
1	16S	1450	U
1	16S	1451	U
1	16S	1452	C
1	16S	1453	G
1	16S	1475	G
1	16S	1487	G
1	16S	1492	A
1	16S	1493	A
1	16S	1497	G
1	16S	1499	A
1	16S	1502	A
1	16S	1503	A
1	16S	1506	U

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Mol	Chain	Res	Type
1	16S	1517	G
1	16S	1519	A
1	16S	1529	G
1	16S	1530	G
1	16S	1533	C
1	16S	1534	A
1	16S	1538	C
1	16S	1539	C
1	16S	1540	U
2	23S	10	A
2	23S	12	U
2	23S	14	A
2	23S	27	G
2	23S	34	U
2	23S	35	G
2	23S	39	G
2	23S	46	G
2	23S	50	U
2	23S	51	G
2	23S	63	A
2	23S	71	A
2	23S	74	A
2	23S	75	G
2	23S	82	U
2	23S	84	A
2	23S	96	C
2	23S	103	A
2	23S	118	A
2	23S	119	A
2	23S	120	U
2	23S	125	A
2	23S	128	C
2	23S	135	U
2	23S	137	U
2	23S	139	U
2	23S	140	C
2	23S	141	G
2	23S	142	A
2	23S	162	U
2	23S	163	C
2	23S	166	U
2	23S	196	A

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Mol	Chain	Res	Type
2	23S	199	A
2	23S	204	A
2	23S	205	G
2	23S	216	A
2	23S	219	A
2	23S	222	A
2	23S	228	C
2	23S	229	C
2	23S	248	G
2	23S	255	A
2	23S	264	C
2	23S	265	A
2	23S	266	G
2	23S	271	G
2	23S	276	U
2	23S	277	G
2	23S	278	A
2	23S	281	C
2	23S	285	G
2	23S	294	A
2	23S	299	A
2	23S	301	G
2	23S	302	C
2	23S	310	A
2	23S	316	C
2	23S	322	A
2	23S	323	C
2	23S	324	A
2	23S	329	G
2	23S	330	A
2	23S	332	A
2	23S	334	C
2	23S	353	C
2	23S	361	G
2	23S	367	G
2	23S	371	A
2	23S	372	G
2	23S	373	U
2	23S	384	A
2	23S	386	G
2	23S	387	U
2	23S	396	G

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Mol	Chain	Res	Type
2	23S	404	A
2	23S	406	G
2	23S	411	G
2	23S	412	A
2	23S	422	A
2	23S	424	G
2	23S	429	A
2	23S	430	A
2	23S	435	C
2	23S	451	U
2	23S	456	C
2	23S	457	A
2	23S	458	G
2	23S	459	U
2	23S	467	G
2	23S	479	A
2	23S	480	A
2	23S	481	G
2	23S	490	C
2	23S	491	G
2	23S	504	A
2	23S	505	A
2	23S	508	A
2	23S	509	C
2	23S	518	G
2	23S	528	A
2	23S	530	G
2	23S	531	C
2	23S	532	A
2	23S	533	G
2	23S	542	C
2	23S	543	G
2	23S	544	C
2	23S	545	U
2	23S	547	A
2	23S	549	G
2	23S	555	G
2	23S	563	A
2	23S	566	U
2	23S	568	U
2	23S	573	U
2	23S	575	A

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Mol	Chain	Res	Type
2	23S	603	A
2	23S	614	A
2	23S	616	A
2	23S	622	G
2	23S	627	A
2	23S	637	A
2	23S	645	C
2	23S	646	U
2	23S	647	G
2	23S	651	G
2	23S	654	A
2	23S	656	G
2	23S	664	G
2	23S	668	A
2	23S	669	G
2	23S	677	A
2	23S	686	U
2	23S	695	G
2	23S	704	G
2	23S	714	U
2	23S	717	C
2	23S	726	G
2	23S	729	G
2	23S	730	A
2	23S	734	A
2	23S	747	C
2	23S	752	A
2	23S	764	A
2	23S	765	C
2	23S	772	C
2	23S	774	G
2	23S	776	G
2	23S	782	A
2	23S	784	G
2	23S	785	G
2	23S	789	A
2	23S	805	G
2	23S	811	U
2	23S	812	C
2	23S	819	A
2	23S	827	U
2	23S	828	U

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Mol	Chain	Res	Type
2	23S	830	G
2	23S	831	G
2	23S	845	A
2	23S	846	U
2	23S	847	U
2	23S	858	G
2	23S	859	G
2	23S	860	U
2	23S	869	G
2	23S	878	A
2	23S	886	A
2	23S	887	U
2	23S	890	C
2	23S	891	G
2	23S	896	A
2	23S	897	C
2	23S	910	A
2	23S	914	G
2	23S	915	C
2	23S	919	U
2	23S	932	U
2	23S	941	A
2	23S	945	A
2	23S	946	C
2	23S	959	A
2	23S	961	C
2	23S	973	A
2	23S	974	G
2	23S	983	A
2	23S	985	C
2	23S	989	G
2	23S	995	C
2	23S	996	A
2	23S	1005	C
2	23S	1009	A
2	23S	1012	U
2	23S	1013	C
2	23S	1021	A
2	23S	1022	G
2	23S	1026	G
2	23S	1033	U
2	23S	1045	C

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Mol	Chain	Res	Type
2	23S	1046	A
2	23S	1047	G
2	23S	1051	G
2	23S	1054	A
2	23S	1057	A
2	23S	1060	U
2	23S	1061	U
2	23S	1062	G
2	23S	1063	G
2	23S	1065	U
2	23S	1066	U
2	23S	1068	G
2	23S	1069	A
2	23S	1070	A
2	23S	1071	G
2	23S	1073	A
2	23S	1074	G
2	23S	1075	C
2	23S	1076	C
2	23S	1078	U
2	23S	1081	U
2	23S	1082	U
2	23S	1083	U
2	23S	1084	A
2	23S	1085	A
2	23S	1088	A
2	23S	1089	A
2	23S	1090	A
2	23S	1098	A
2	23S	1101	U
2	23S	1104	C
2	23S	1111	A
2	23S	1112	G
2	23S	1119	U
2	23S	1132	U
2	23S	1133	A
2	23S	1135	C
2	23S	1136	G
2	23S	1139	G
2	23S	1149	G
2	23S	1172	C
2	23S	1174	U

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Mol	Chain	Res	Type
2	23S	1175	A
2	23S	1176	U
2	23S	1177	G
2	23S	1178	C
2	23S	1180	U
2	23S	1186	G
2	23S	1206	G
2	23S	1212	G
2	23S	1237	A
2	23S	1252	G
2	23S	1253	A
2	23S	1256	G
2	23S	1271	G
2	23S	1272	A
2	23S	1273	U
2	23S	1294	U
2	23S	1300	G
2	23S	1301	A
2	23S	1306	C
2	23S	1314	C
2	23S	1321	A
2	23S	1329	U
2	23S	1330	C
2	23S	1343	G
2	23S	1345	C
2	23S	1360	G
2	23S	1365	A
2	23S	1368	G
2	23S	1374	G
2	23S	1378	A
2	23S	1379	U
2	23S	1380	G
2	23S	1383	A
2	23S	1395	A
2	23S	1397	U
2	23S	1416	G
2	23S	1419	A
2	23S	1420	A
2	23S	1421	G
2	23S	1427	A
2	23S	1428	C
2	23S	1453	A

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Mol	Chain	Res	Type
2	23S	1461	C
2	23S	1475	G
2	23S	1482	G
2	23S	1490	A
2	23S	1491	G
2	23S	1493	C
2	23S	1496	A
2	23S	1497	U
2	23S	1503	A
2	23S	1504	A
2	23S	1506	U
2	23S	1509	A
2	23S	1515	A
2	23S	1524	G
2	23S	1525	A
2	23S	1529	G
2	23S	1530	G
2	23S	1534	U
2	23S	1535	A
2	23S	1536	C
2	23S	1537	G
2	23S	1554	U
2	23S	1559	U
2	23S	1560	G
2	23S	1565	C
2	23S	1569	A
2	23S	1571	A
2	23S	1578	U
2	23S	1585	C
2	23S	1607	C
2	23S	1608	A
2	23S	1611	C
2	23S	1613	G
2	23S	1634	A
2	23S	1647	U
2	23S	1648	U
2	23S	1649	G
2	23S	1660	G
2	23S	1674	G
2	23S	1675	C
2	23S	1676	A
2	23S	1677	A

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Mol	Chain	Res	Type
2	23S	1678	A
2	23S	1679	A
2	23S	1693	U
2	23S	1702	G
2	23S	1703	G
2	23S	1715	G
2	23S	1729	U
2	23S	1730	C
2	23S	1731	G
2	23S	1732	C
2	23S	1733	G
2	23S	1735	A
2	23S	1738	G
2	23S	1755	A
2	23S	1756	G
2	23S	1758	U
2	23S	1759	A
2	23S	1764	C
2	23S	1773	A
2	23S	1780	A
2	23S	1784	A
2	23S	1785	A
2	23S	1800	C
2	23S	1801	A
2	23S	1802	A
2	23S	1808	A
2	23S	1816	C
2	23S	1829	A
2	23S	1833	C
2	23S	1857	G
2	23S	1866	A
2	23S	1870	C
2	23S	1871	A
2	23S	1872	A
2	23S	1884	G
2	23S	1899	A
2	23S	1901	A
2	23S	1906	G
2	23S	1907	G
2	23S	1913	A
2	23S	1918	A
2	23S	1929	G

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Mol	Chain	Res	Type
2	23S	1930	G
2	23S	1937	A
2	23S	1938	A
2	23S	1944	U
2	23S	1955	U
2	23S	1963	U
2	23S	1967	C
2	23S	1970	A
2	23S	1971	U
2	23S	1972	G
2	23S	1982	U
2	23S	1983	G
2	23S	1991	U
2	23S	1992	G
2	23S	1993	U
2	23S	1997	C
2	23S	2013	A
2	23S	2020	A
2	23S	2021	C
2	23S	2022	U
2	23S	2023	C
2	23S	2031	A
2	23S	2033	A
2	23S	2034	U
2	23S	2043	C
2	23S	2049	G
2	23S	2052	A
2	23S	2055	C
2	23S	2056	G
2	23S	2060	A
2	23S	2061	G
2	23S	2062	A
2	23S	2063	C
2	23S	2069	G
2	23S	2072	C
2	23S	2077	A
2	23S	2093	G
2	23S	2096	C
2	23S	2100	G
2	23S	2107	G
2	23S	2110	G
2	23S	2111	U

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Mol	Chain	Res	Type
2	23S	2112	G
2	23S	2113	U
2	23S	2115	G
2	23S	2116	G
2	23S	2117	A
2	23S	2118	U
2	23S	2119	A
2	23S	2120	G
2	23S	2126	A
2	23S	2131	U
2	23S	2132	U
2	23S	2133	G
2	23S	2139	U
2	23S	2147	A
2	23S	2149	U
2	23S	2157	G
2	23S	2161	C
2	23S	2162	G
2	23S	2164	C
2	23S	2165	C
2	23S	2166	U
2	23S	2167	U
2	23S	2171	A
2	23S	2172	U
2	23S	2173	A
2	23S	2175	C
2	23S	2178	C
2	23S	2189	U
2	23S	2190	G
2	23S	2198	A
2	23S	2203	U
2	23S	2204	G
2	23S	2211	A
2	23S	2213	U
2	23S	2225	A
2	23S	2226	C
2	23S	2238	G
2	23S	2239	G
2	23S	2250	G
2	23S	2279	G
2	23S	2283	C
2	23S	2286	G

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Mol	Chain	Res	Type
2	23S	2287	A
2	23S	2295	C
2	23S	2297	A
2	23S	2305	U
2	23S	2308	G
2	23S	2309	A
2	23S	2327	A
2	23S	2331	G
2	23S	2334	U
2	23S	2335	A
2	23S	2336	A
2	23S	2350	C
2	23S	2357	G
2	23S	2361	G
2	23S	2383	G
2	23S	2385	C
2	23S	2392	A
2	23S	2402	U
2	23S	2403	C
2	23S	2406	A
2	23S	2410	G
2	23S	2423	U
2	23S	2424	C
2	23S	2425	A
2	23S	2427	C
2	23S	2428	G
2	23S	2429	G
2	23S	2430	A
2	23S	2435	A
2	23S	2441	U
2	23S	2445	G
2	23S	2447	G
2	23S	2448	A
2	23S	2476	A
2	23S	2478	A
2	23S	2480	C
2	23S	2481	G
2	23S	2482	A
2	23S	2490	G
2	23S	2491	U
2	23S	2498	C
2	23S	2500	U

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Mol	Chain	Res	Type
2	23S	2502	G
2	23S	2503	A
2	23S	2504	U
2	23S	2505	G
2	23S	2506	U
2	23S	2513	A
2	23S	2518	A
2	23S	2520	C
2	23S	2525	G
2	23S	2530	A
2	23S	2534	A
2	23S	2535	G
2	23S	2547	A
2	23S	2554	U
2	23S	2566	A
2	23S	2567	G
2	23S	2572	A
2	23S	2573	C
2	23S	2603	G
2	23S	2604	U
2	23S	2609	U
2	23S	2610	C
2	23S	2613	U
2	23S	2629	U
2	23S	2647	U
2	23S	2654	A
2	23S	2655	G
2	23S	2656	U
2	23S	2659	G
2	23S	2660	A
2	23S	2672	U
2	23S	2673	G
2	23S	2689	U
2	23S	2690	U
2	23S	2714	G
2	23S	2722	G
2	23S	2726	A
2	23S	2732	G
2	23S	2748	A
2	23S	2762	C
2	23S	2764	A
2	23S	2765	A

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Mol	Chain	Res	Type
2	23S	2776	A
2	23S	2778	A
2	23S	2779	U
2	23S	2791	G
2	23S	2797	U
2	23S	2798	U
2	23S	2800	A
2	23S	2808	G
2	23S	2809	A
2	23S	2818	U
2	23S	2820	A
2	23S	2821	A
2	23S	2833	U
2	23S	2834	G
2	23S	2849	U
2	23S	2867	G
2	23S	2872	A
2	23S	2873	A
2	23S	2879	A
2	23S	2880	C
2	23S	2885	G
2	23S	2886	A
2	23S	2901	C
2	23S	2902	C
3	5S	4	C
3	5S	12	C
3	5S	13	G
3	5S	24	G
3	5S	25	U
3	5S	35	C
3	5S	37	C
3	5S	40	U
3	5S	41	G
3	5S	42	C
3	5S	43	C
3	5S	44	G
3	5S	45	A
3	5S	53	A
3	5S	67	G
3	5S	88	C
3	5S	89	U
3	5S	90	C

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Mol	Chain	Res	Type
3	5S	105	G
3	5S	108	A
3	5S	109	A
3	5S	116	G
4	ATRN	9	A
4	ATRN	16	C
4	ATRN	17	U
4	ATRN	18	G
4	ATRN	19	G
4	ATRN	20	G
4	ATRN	21	A
4	ATRN	30	G
4	ATRN	34	U
4	ATRN	36	C
4	ATRN	46	G
4	ATRN	47	U
4	ATRN	48	C
4	ATRN	58	A
4	ATRN	59	U
4	ATRN	61	C
4	ATRN	62	C
4	ATRN	74	C
5	ETRN	3	C
5	ETRN	5	G
5	ETRN	8	U
5	ETRN	9	G
5	ETRN	17	C
5	ETRN	18	G
5	ETRN	19	G
5	ETRN	20	U
5	ETRN	21	A
5	ETRN	22	G
5	ETRN	25	C
5	ETRN	28	C
5	ETRN	34	C
5	ETRN	35	A
5	ETRN	36	U
5	ETRN	41	C
5	ETRN	45	G
5	ETRN	46	G
5	ETRN	58	A
5	ETRN	64	G

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Mol	Chain	Res	Type
5	ETRN	69	C
5	ETRN	73	A
5	ETRN	76	A
59	TMRN	2	G
59	TMRN	8	A
59	TMRN	9	U
59	TMRN	10	U
59	TMRN	11	C
59	TMRN	12	U
59	TMRN	13	G
59	TMRN	14	G
59	TMRN	15	A
59	TMRN	16	U
59	TMRN	17	U
59	TMRN	18	C
59	TMRN	20	A
59	TMRN	21	C
59	TMRN	30	C
59	TMRN	32	A
59	TMRN	33	A
59	TMRN	34	A
59	TMRN	35	C
59	TMRN	39	A
59	TMRN	40	G
59	TMRN	43	G
59	TMRN	54	G
59	TMRN	55	G
59	TMRN	61	G
59	TMRN	63	C
59	TMRN	64	C
59	TMRN	67	G
59	TMRN	68	U
59	TMRN	69	A
59	TMRN	70	A
59	TMRN	71	A
59	TMRN	72	A
59	TMRN	73	A
59	TMRN	74	G
59	TMRN	77	G
59	TMRN	79	A
59	TMRN	80	A
59	TMRN	81	A

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Mol	Chain	Res	Type
59	TMRN	84	A
59	TMRN	85	U
59	TMRN	86	A
59	TMRN	94	A
59	TMRN	95	C
59	TMRN	96	G
59	TMRN	97	A
59	TMRN	98	C
59	TMRN	99	G
59	TMRN	100	A
59	TMRN	101	A
59	TMRN	102	A
59	TMRN	103	A
59	TMRN	104	C
59	TMRN	105	U
59	TMRN	106	A
59	TMRN	107	C
59	TMRN	109	C
59	TMRN	116	A
59	TMRN	120	U
59	TMRN	121	A
59	TMRN	122	A
59	TMRN	125	A
59	TMRN	127	C
59	TMRN	130	C
59	TMRN	131	U
59	TMRN	132	U
59	TMRN	138	C
59	TMRN	142	U
59	TMRN	150	G
59	TMRN	151	C
59	TMRN	154	C
59	TMRN	155	C
59	TMRN	156	G
59	TMRN	164	G
59	TMRN	165	A
59	TMRN	166	C
59	TMRN	168	G
59	TMRN	172	U
59	TMRN	181	G
59	TMRN	182	U
59	TMRN	183	C

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Mol	Chain	Res	Type
59	TMRN	189	C
59	TMRN	190	A
59	TMRN	192	A
59	TMRN	200	G
59	TMRN	203	U
59	TMRN	204	G
59	TMRN	205	G
59	TMRN	206	A
59	TMRN	207	A
59	TMRN	211	C
59	TMRN	212	U
59	TMRN	213	G
59	TMRN	223	G
59	TMRN	225	A
59	TMRN	226	G
59	TMRN	229	U
59	TMRN	230	U
59	TMRN	234	A
59	TMRN	236	U
59	TMRN	237	U
59	TMRN	238	A
59	TMRN	245	C
59	TMRN	246	U
59	TMRN	248	G
59	TMRN	250	U
59	TMRN	257	U
59	TMRN	258	G
59	TMRN	259	G
59	TMRN	262	U
59	TMRN	263	G
59	TMRN	265	C
59	TMRN	267	G
59	TMRN	274	G
59	TMRN	280	A
59	TMRN	281	A
59	TMRN	282	G
59	TMRN	283	C
59	TMRN	284	G
59	TMRN	285	A
59	TMRN	289	U
59	TMRN	291	A
59	TMRN	300	U

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Mol	Chain	Res	Type
59	TMRN	302	A
59	TMRN	303	G
59	TMRN	308	U
59	TMRN	309	A
59	TMRN	310	G
59	TMRN	315	G
59	TMRN	316	A
59	TMRN	317	G
59	TMRN	318	G
59	TMRN	320	U
59	TMRN	321	G
59	TMRN	322	U
59	TMRN	323	A
59	TMRN	325	G
59	TMRN	333	G
59	TMRN	334	A
59	TMRN	335	C
59	TMRN	336	G
59	TMRN	337	C
59	TMRN	338	G
59	TMRN	342	U
59	TMRN	345	A
59	TMRN	346	C
59	TMRN	347	U
59	TMRN	348	C
59	TMRN	358	C
59	TMRN	363	A

All (32) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	16S	70	U
1	16S	429	U
1	16S	890	G
1	16S	1190	G
1	16S	1347	G
2	23S	372	G
2	23S	421	C
2	23S	458	G
2	23S	490	C
2	23S	858	G
2	23S	859	G

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Mol	Chain	Res	Type
2	23S	1020	A
2	23S	1730	C
2	23S	2286	G
2	23S	2326	C
2	23S	2391	G
2	23S	2655	G
3	5S	42	C
4	ATRN	16	C
59	TMRN	17	U
59	TMRN	38	A
59	TMRN	60	U
59	TMRN	93	A
59	TMRN	130	C
59	TMRN	212	U
59	TMRN	229	U
59	TMRN	261	G
59	TMRN	290	A
59	TMRN	308	U
59	TMRN	314	C
59	TMRN	322	U
59	TMRN	337	C

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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.

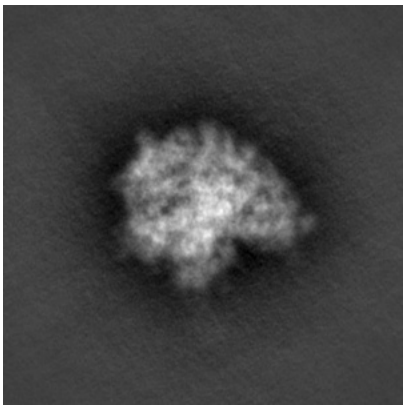
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-43490. These allow visual inspection of the internal detail of the map and identification of artifacts.

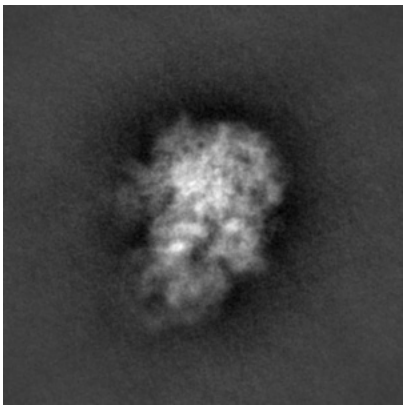
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

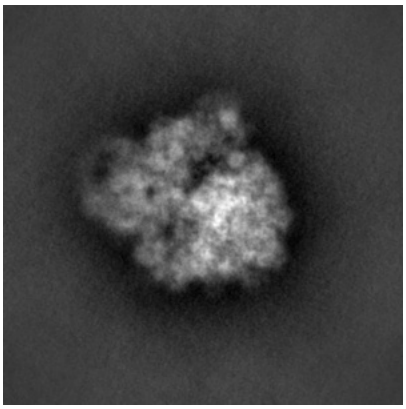
6.1.1 Primary map



X

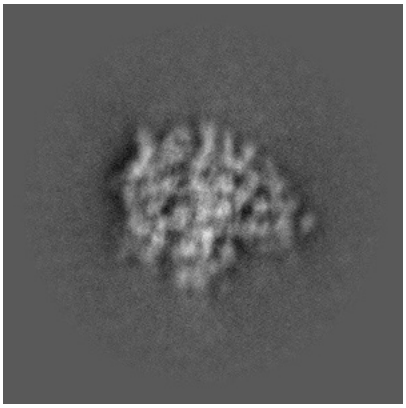


Y

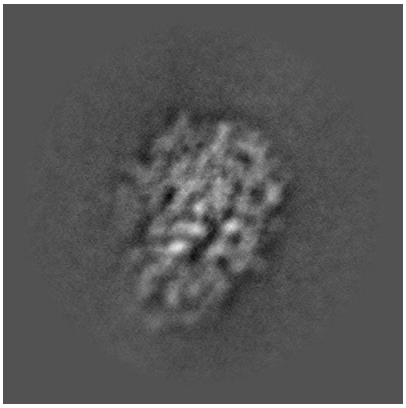


Z

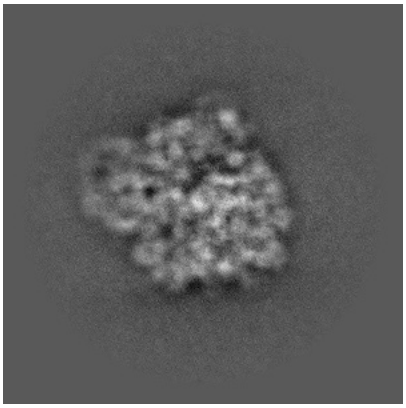
6.1.2 Raw map



X



Y

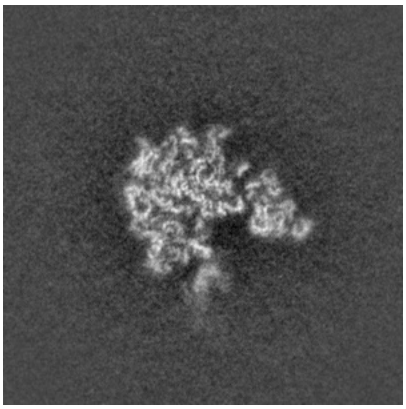


Z

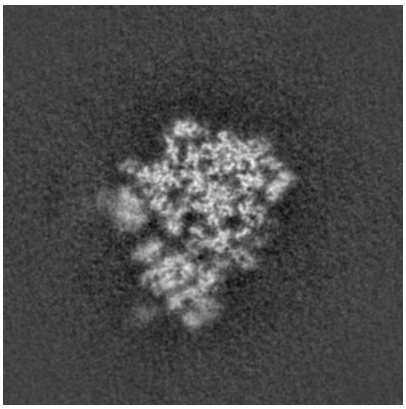
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

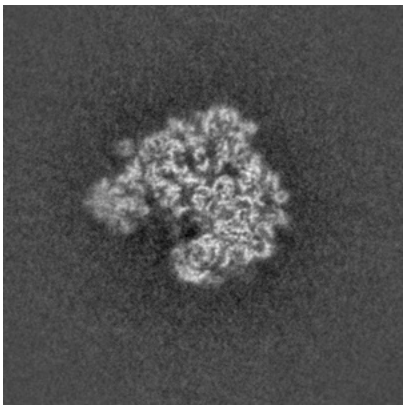
6.2.1 Primary map



X Index: 280

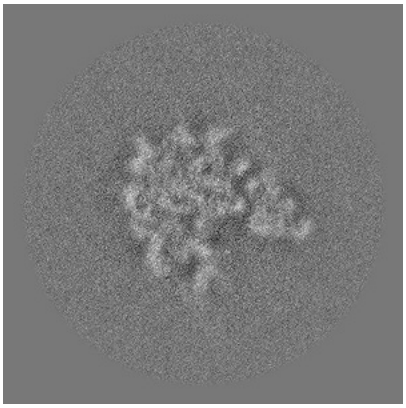


Y Index: 280

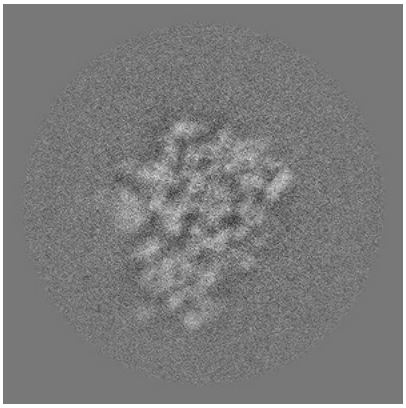


Z Index: 280

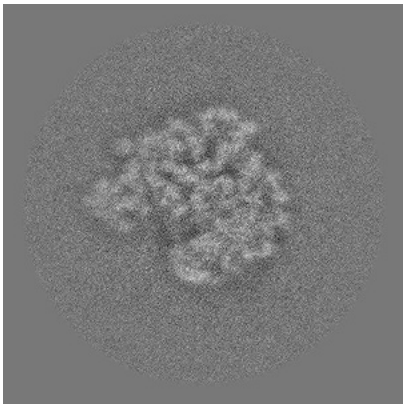
6.2.2 Raw map



X Index: 280



Y Index: 280

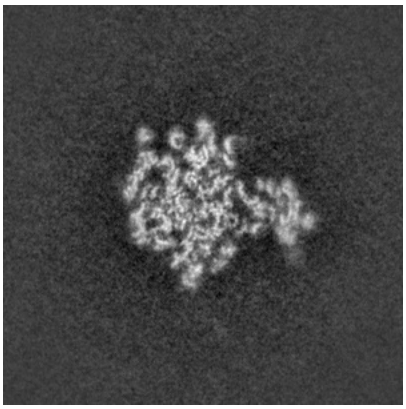


Z Index: 280

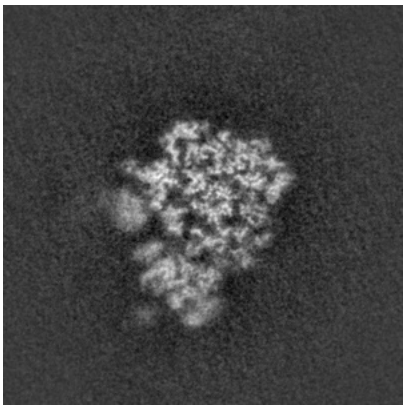
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

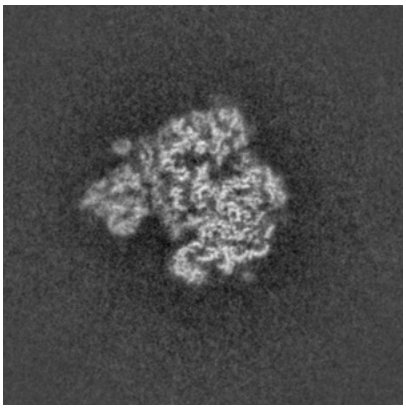
6.3.1 Primary map



X Index: 309

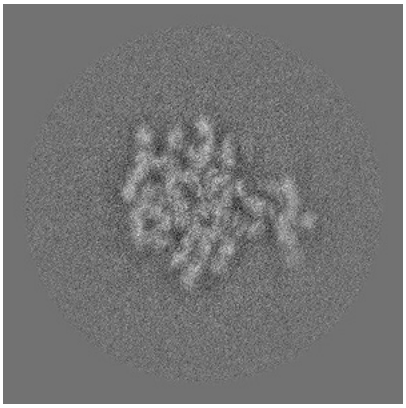


Y Index: 283

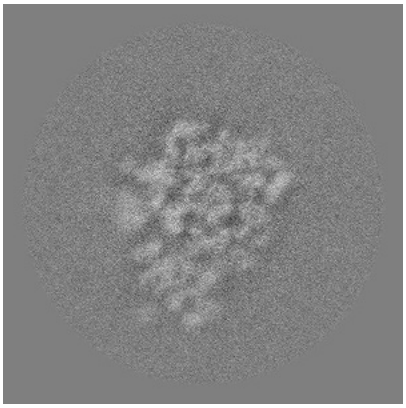


Z Index: 273

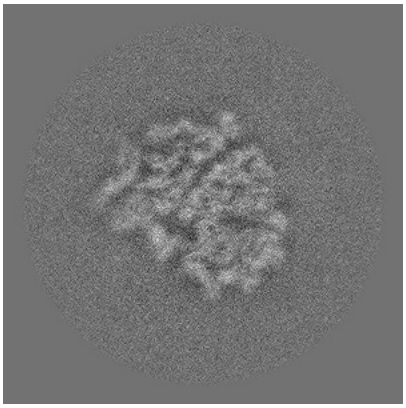
6.3.2 Raw map



X Index: 310



Y Index: 281

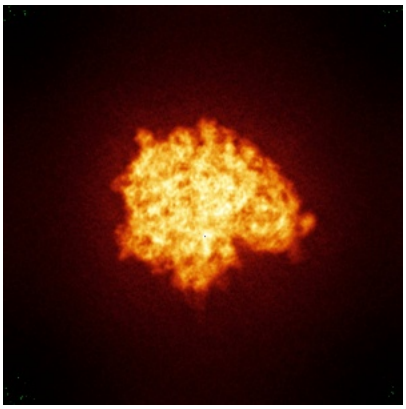


Z Index: 301

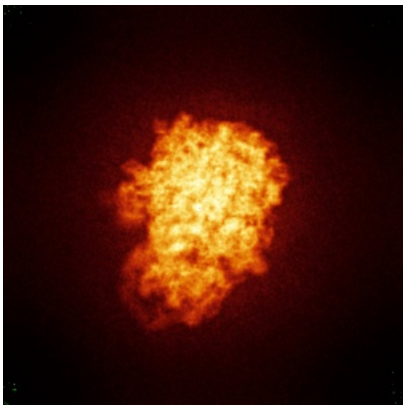
The images above show the largest variance slices of the map in three orthogonal directions.

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

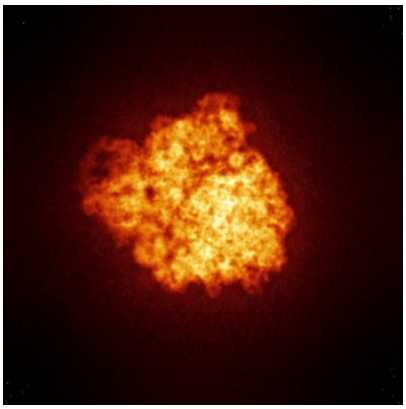
6.4.1 Primary map



X

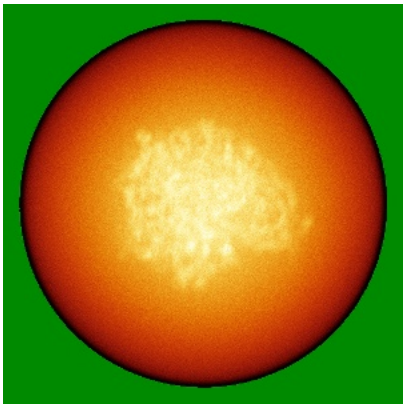


Y

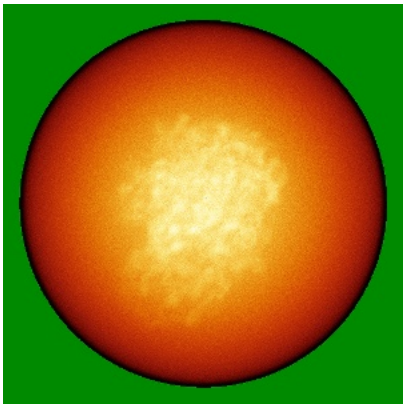


Z

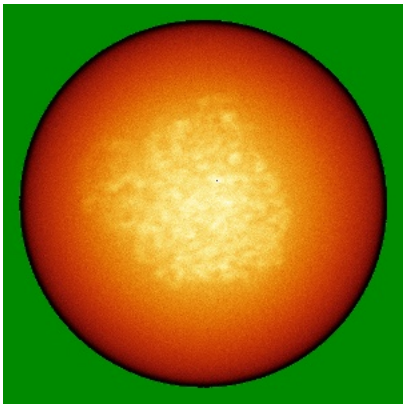
6.4.2 Raw map



X



Y



Z

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

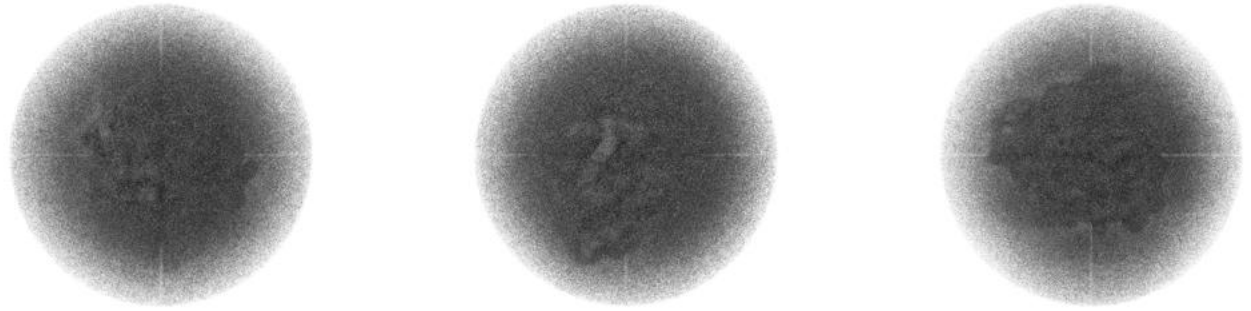
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

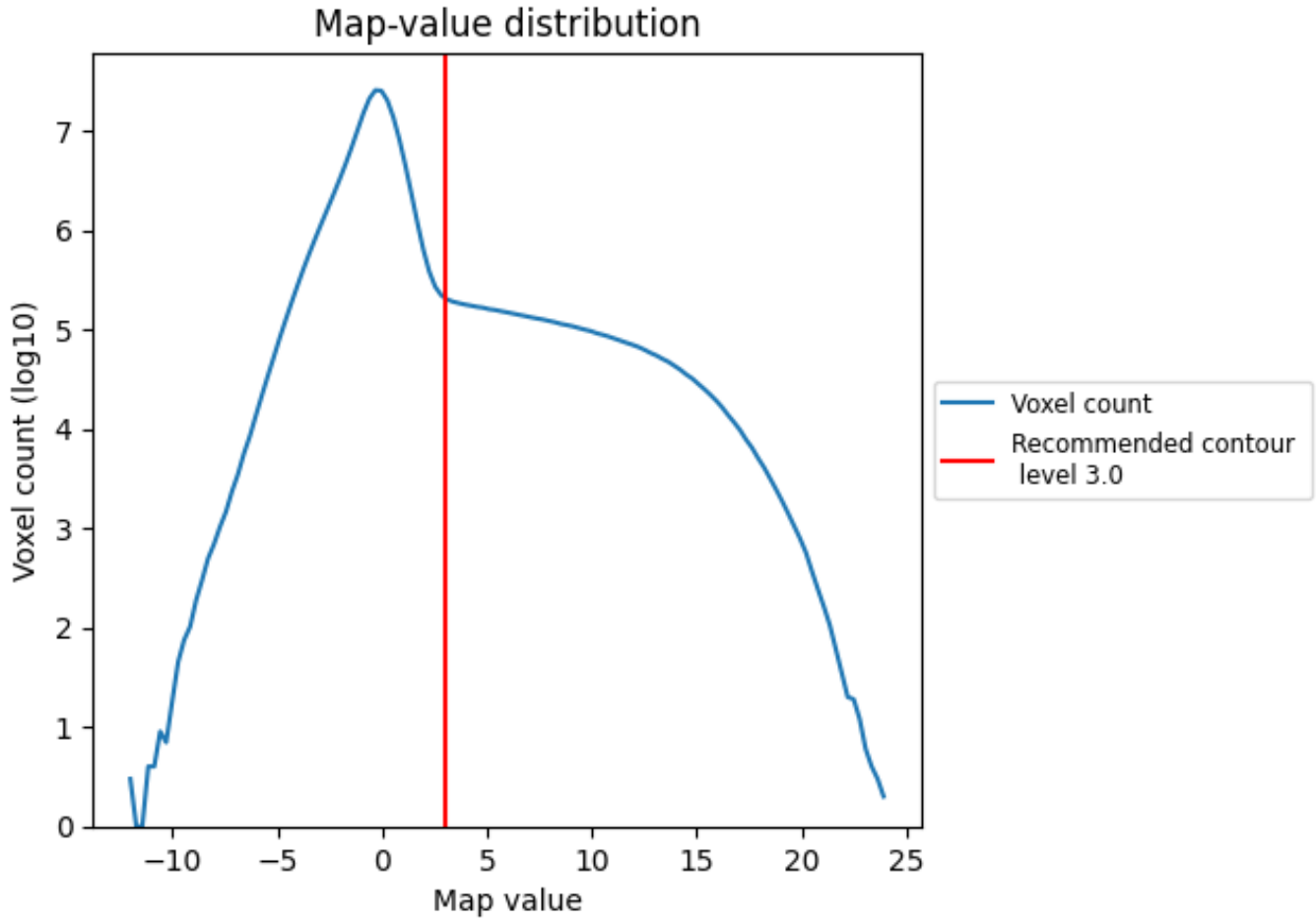
6.6 Mask visualisation (i)

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

7 Map analysis

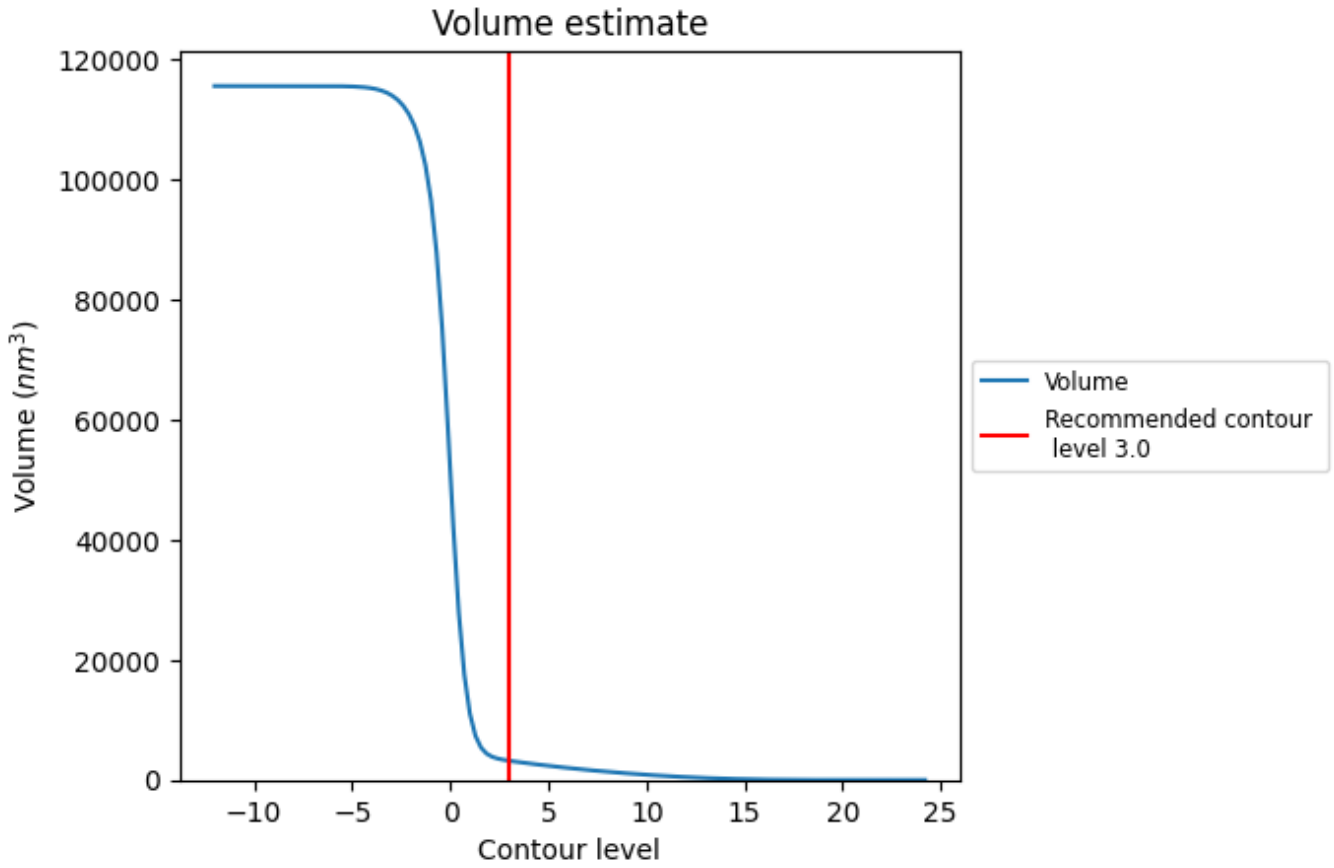
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

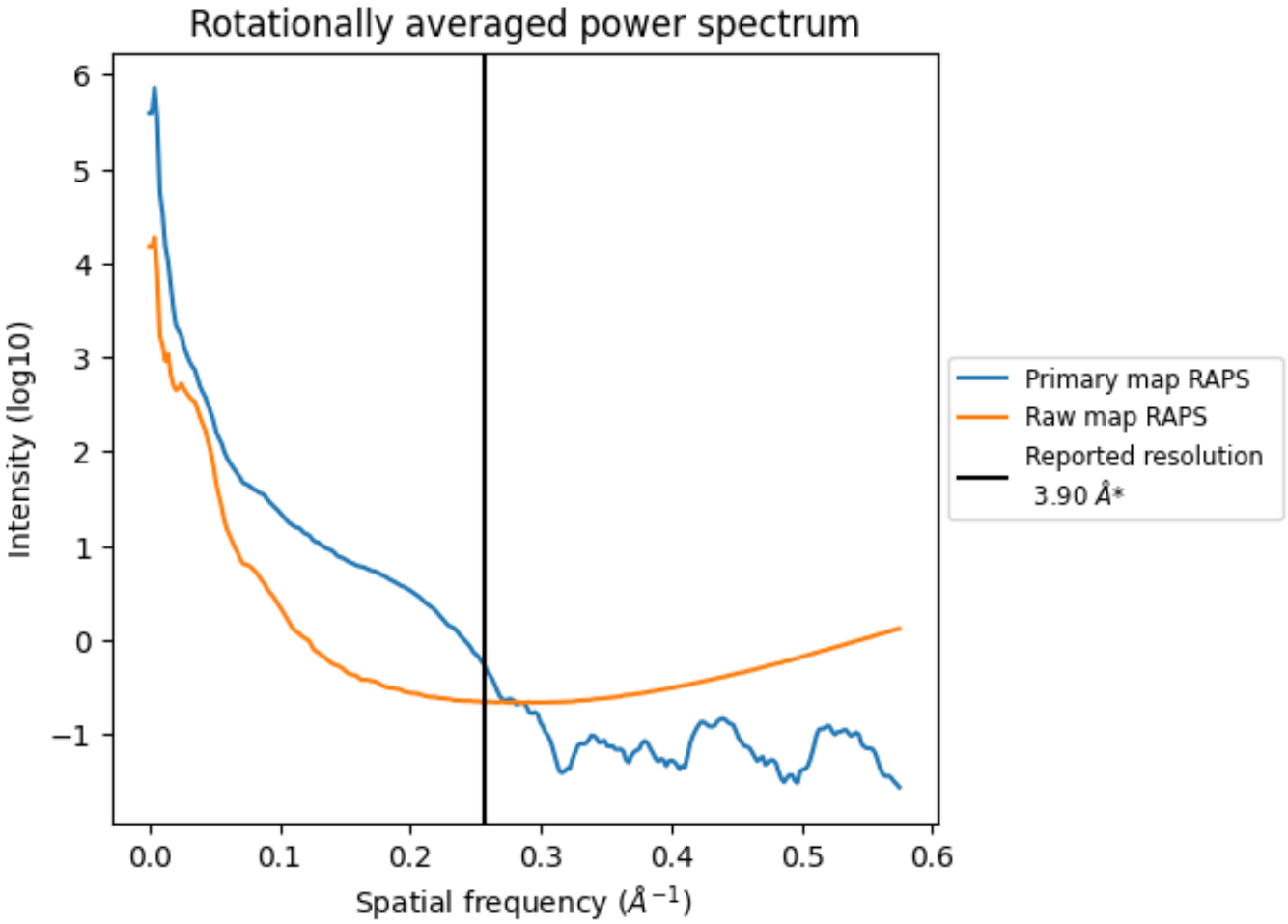
7.2 Volume estimate



The volume at the recommended contour level is 3206 nm^3; this corresponds to an approximate mass of 2896 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 (i)

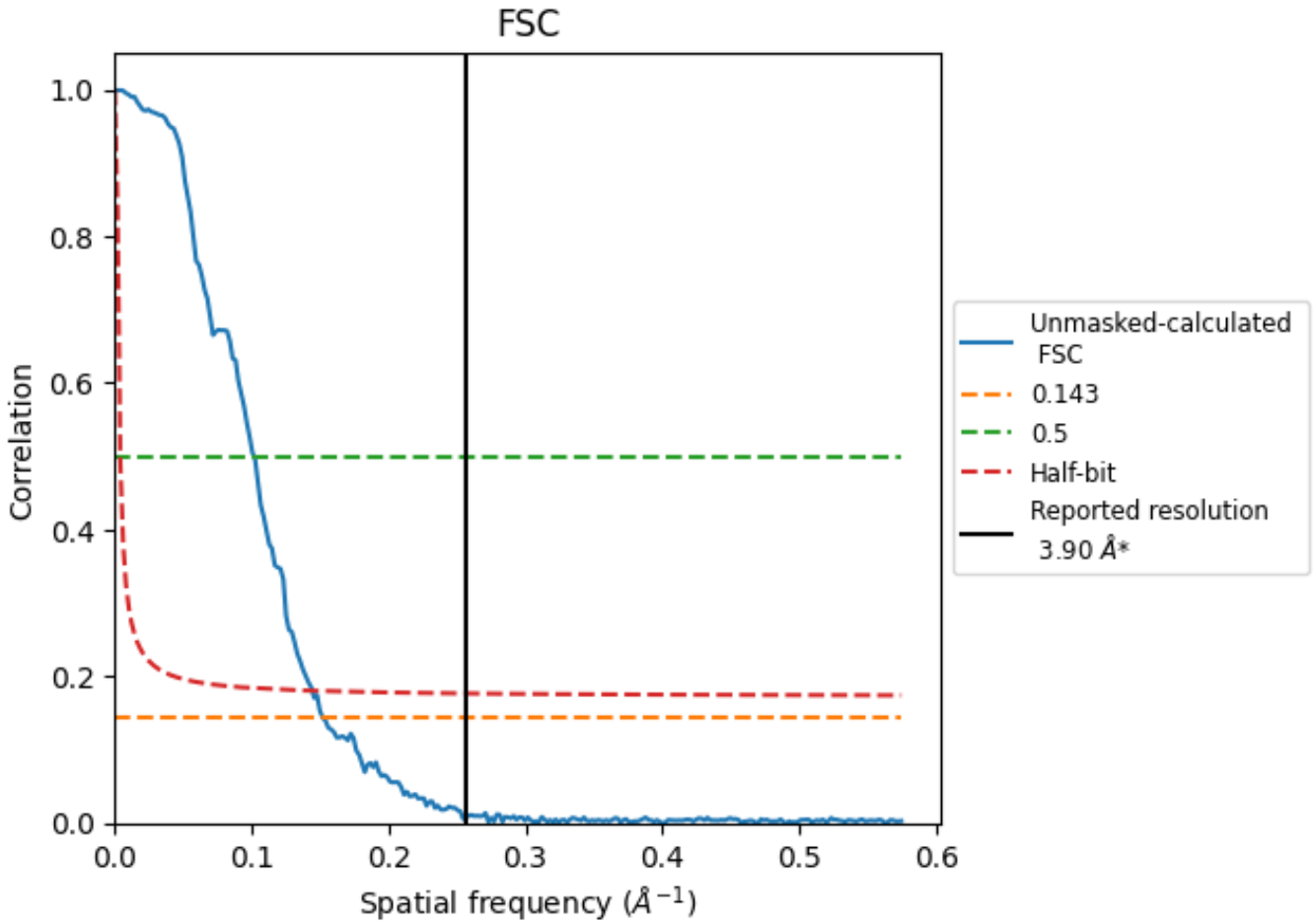


*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

8.2 Resolution estimates (i)

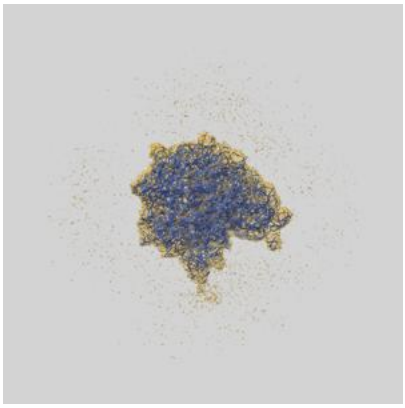
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.58	9.84	6.93

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.58 differs from the reported value 3.9 by more than 10 %

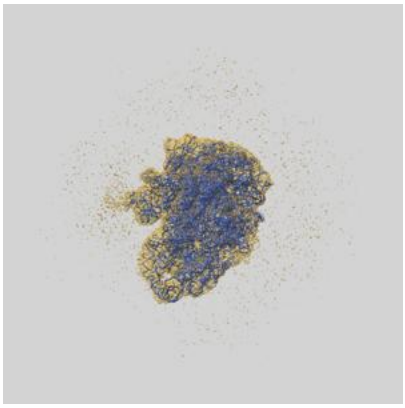
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-43490 and PDB model 8VS9. Per-residue inclusion information can be found in section 3 on page 15.

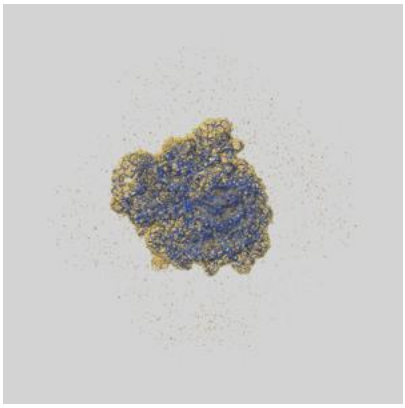
9.1 Map-model overlay



X



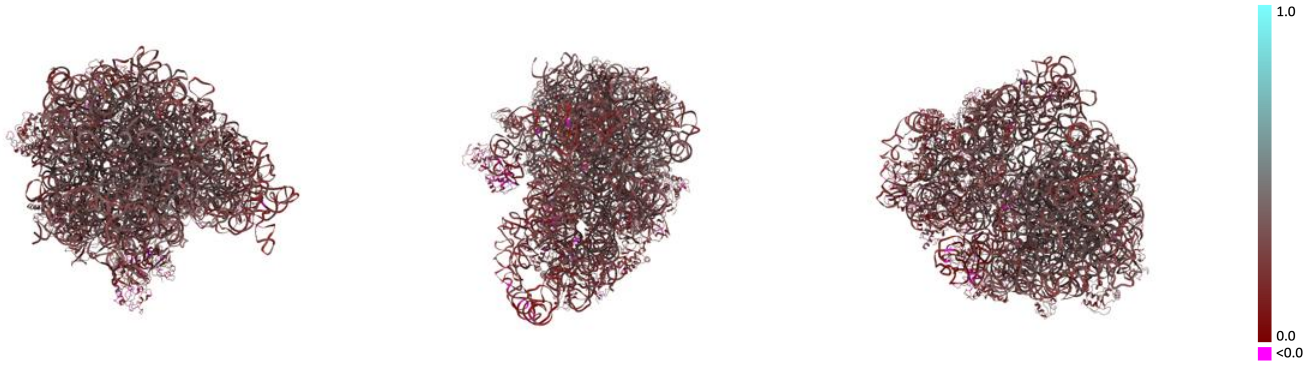
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 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.

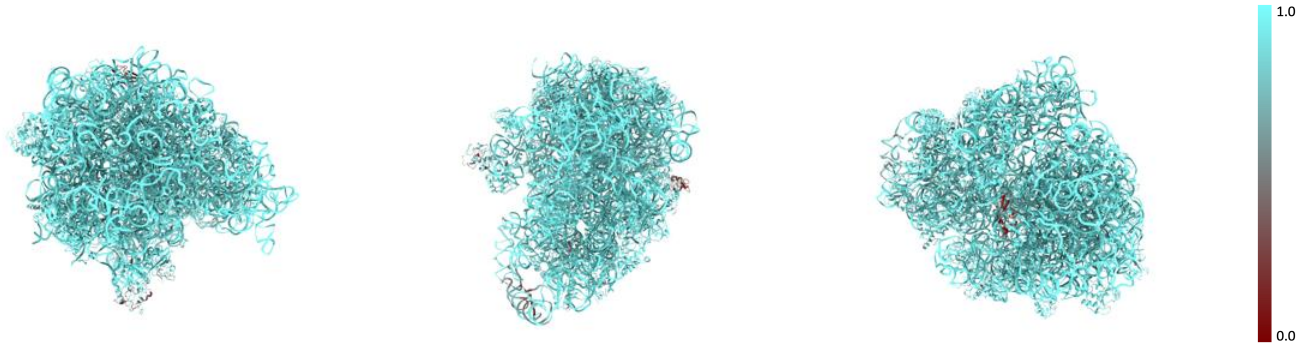
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

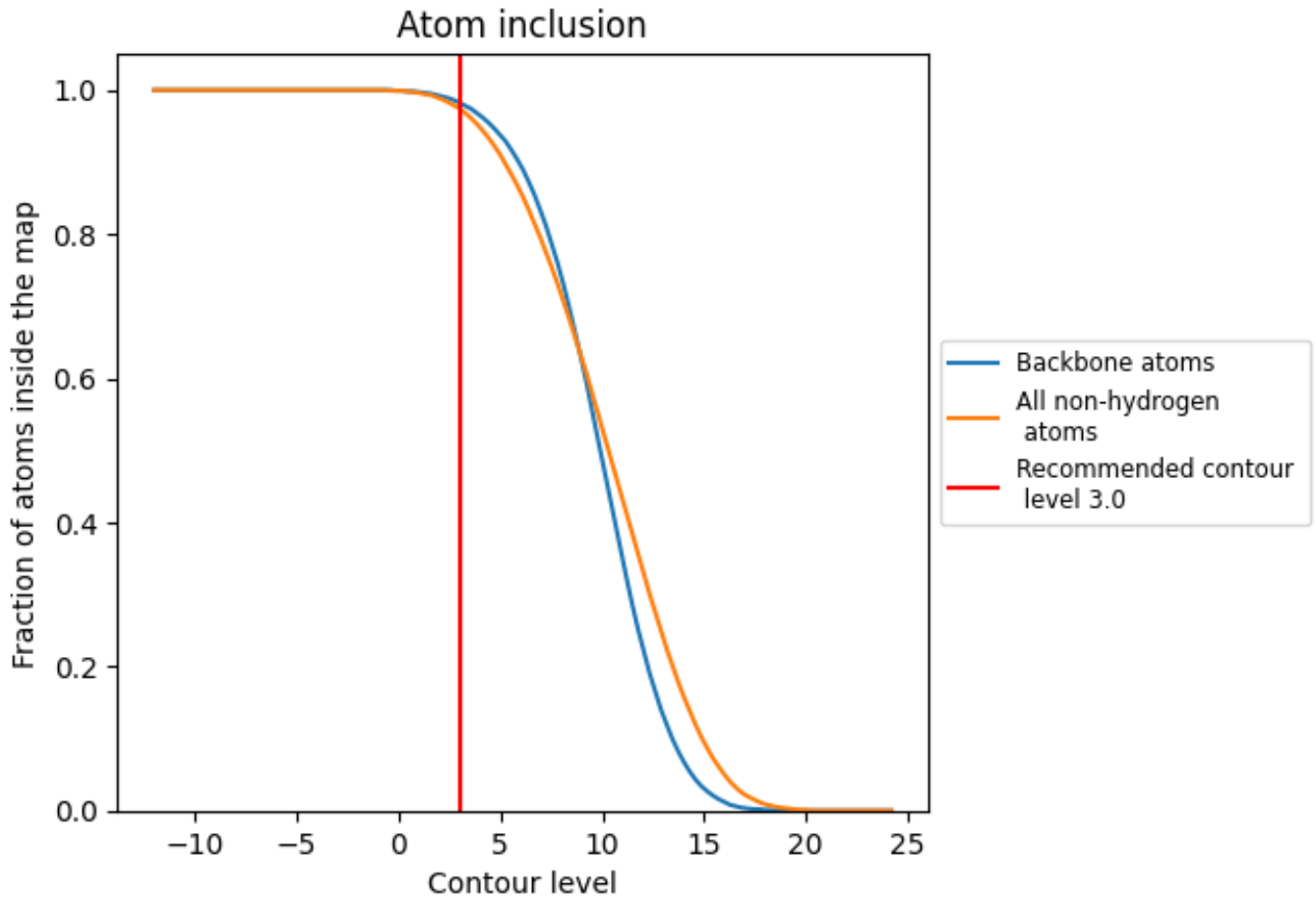
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (3.0).

9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9740	0.2890
16S	0.9980	0.2900
23S	0.9980	0.3210
5S	0.9980	0.2870
ATRN	0.9920	0.2820
ETRN	0.9500	0.1740
L02	0.9720	0.3340
L03	0.9770	0.3090
L04	0.9590	0.2930
L05	0.9640	0.2280
L06	0.9740	0.2880
L09	0.4580	0.2230
L1	0.9010	0.1460
L10	0.7180	0.1410
L11	0.8470	0.1360
L13	0.9760	0.3180
L14	0.9320	0.3300
L15	0.9680	0.3120
L16	0.9620	0.3090
L17	0.9760	0.2980
L18	0.9880	0.2670
L19	0.9480	0.3130
L20	0.9800	0.3000
L21	0.9720	0.3070
L22	0.9430	0.3060
L23	0.9560	0.2980
L24	0.9540	0.2860
L25	0.9730	0.2880
L27	0.9890	0.3040
L28	0.9670	0.3000
L29	0.9800	0.2510
L30	0.9680	0.3120
L31	0.9430	0.1960
L32	0.9490	0.3250
L33	0.9650	0.2830

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Chain	Atom inclusion	Q-score
L34	0.9860	0.3280
L35	0.9820	0.3160
L36	0.9970	0.3060
S02	0.9220	0.2510
S03	0.9530	0.2710
S04	0.9740	0.2180
S05	0.9670	0.3000
S06	0.9360	0.2690
S07	0.9150	0.2310
S08	0.9640	0.2840
S09	0.9630	0.2210
S10	0.9150	0.2380
S11	0.9460	0.2980
S12	0.9490	0.2890
S13	0.9510	0.2110
S14	0.9770	0.2270
S15	0.9740	0.2700
S16	0.9830	0.2650
S17	0.9640	0.2630
S18	0.9770	0.2760
S19	0.9920	0.2220
S20	0.9890	0.2310
S21	0.9070	0.2460
SMPB	0.8990	0.2520
TMRN	0.8820	0.1840