



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 03:28 AM UTC

PDB ID : 6DNC / pdb_00006dnc
EMDB ID : EMD-7970
Title : E.coli RF1 bound to E.coli 70S ribosome in response to UAU sense A-site codon
Authors : Svidritskiy, E.; Demo, G.; Korostelev, A.A.
Deposited on : 2018-06-06
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

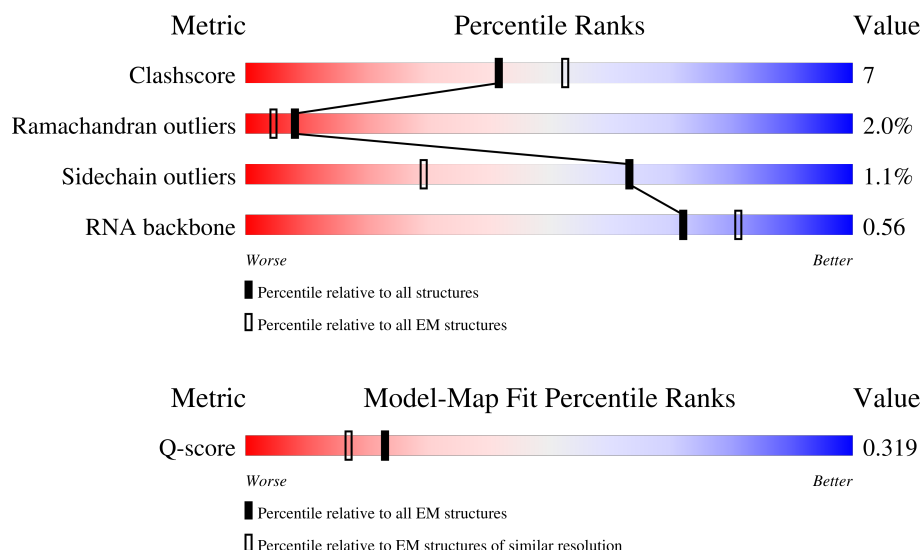
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	A	1539	
2	B	2903	
3	C	120	

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Mol	Chain	Length	Quality of chain
4	D	77	
4	LA	77	
5	E	234	
6	F	273	
7	G	209	
8	H	201	
9	I	179	
10	J	177	
11	K	149	
12	L	165	
13	M	142	
14	N	142	
15	O	123	
16	P	144	
17	Q	136	
18	R	127	
19	S	117	
20	T	115	
21	U	118	
22	V	103	
23	W	110	
24	X	100	
25	Y	104	
26	Z	94	
27	AA	85	

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Mol	Chain	Length	Quality of chain
28	BA	78	
29	CA	63	
30	DA	59	
31	EA	70	
32	FA	57	
33	GA	55	
34	HA	46	
35	IA	65	
36	JA	38	
37	KA	27	
38	MA	362	
39	OA	241	
40	PA	233	
41	QA	206	
42	RA	167	
43	SA	131	
44	TA	156	
45	UA	130	
46	VA	130	
47	WA	103	
48	XA	129	
49	YA	124	
50	ZA	118	
51	AB	102	
52	BB	89	

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Mol	Chain	Length	Quality of chain
53	CB	82	34% 71% 28% •
54	DB	84	56% 67% 26% • 5%
55	EB	75	43% 73% 12% • 13%
56	FB	92	50% 61% 23% • 14%
57	GB	87	26% 82% 13% • •
58	HB	71	68% 54% 24% 14% 8%

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 152438 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
1	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	2903	Total	C	N	O	P	0	0
			62318	27801	11468	20147	2902		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	747	C	U	conflict	GB 1036415628
B	1847	G	A	conflict	GB 1036415628

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	120	A	-	expression tag	GB 1370526515

- Molecule 4 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
4	LA	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 5 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	220	Total	C	N	O	S	0	0
			1637	1023	298	310	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	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	G	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	H	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	I	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	J	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 11 is a protein called 50S ribosomal protein L9.

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

- Molecule 12 is a protein called 50S ribosomal protein L10.

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

- Molecule 13 is a protein called 50S ribosomal protein L11.

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

- Molecule 14 is a protein called 50S ribosomal protein L13.

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

- Molecule 15 is a protein called 50S ribosomal protein L14.

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

- Molecule 16 is a protein called 50S ribosomal protein L15.

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

- Molecule 17 is a protein called 50S ribosomal protein L16.

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

- Molecule 18 is a protein called 50S ribosomal protein L17.

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

- Molecule 19 is a protein called 50S ribosomal protein L18.

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

- Molecule 20 is a protein called 50S ribosomal protein L19.

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

- Molecule 21 is a protein called 50S ribosomal protein L20.

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

- Molecule 22 is a protein called 50S ribosomal protein L21.

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

- Molecule 23 is a protein called 50S ribosomal protein L22.

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

- Molecule 24 is a protein called 50S ribosomal protein L23.

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

- Molecule 25 is a protein called 50S ribosomal protein L24.

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

- Molecule 26 is a protein called 50S ribosomal protein L25.

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

- Molecule 27 is a protein called 50S ribosomal protein L27.

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

- Molecule 28 is a protein called 50S ribosomal protein L28.

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

- Molecule 29 is a protein called 50S ribosomal protein L29.

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

- Molecule 30 is a protein called 50S ribosomal protein L30.

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

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	EA	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 32 is a protein called 50S ribosomal protein L32.

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

- Molecule 33 is a protein called 50S ribosomal protein L33.

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

- Molecule 34 is a protein called 50S ribosomal protein L34.

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

- Molecule 35 is a protein called 50S ribosomal protein L35.

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

- Molecule 36 is a protein called 50S ribosomal protein L36.

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

- Molecule 37 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	KA	19	Total	C	N	O	P	0	0
			412	186	83	125	18		

- Molecule 38 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	MA	344	Total	C	N	O	S	0	0
			2714	1656	507	538	13		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
MA	361	LEU	-	expression tag	UNP B7MKB3
MA	362	GLU	-	expression tag	UNP B7MKB3

- Molecule 39 is a protein called 30S ribosomal protein S2.

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

- Molecule 40 is a protein called 30S ribosomal protein S3.

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

- Molecule 41 is a protein called 30S ribosomal protein S4.

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

- Molecule 42 is a protein called 30S ribosomal protein S5.

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

- Molecule 43 is a protein called 30S ribosomal protein S6.

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

- Molecule 44 is a protein called 30S ribosomal protein S7.

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

- Molecule 45 is a protein called 30S ribosomal protein S8.

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

- Molecule 46 is a protein called 30S ribosomal protein S9.

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

- Molecule 47 is a protein called 30S ribosomal protein S10.

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

- Molecule 48 is a protein called 30S ribosomal protein S11.

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

- Molecule 49 is a protein called 30S ribosomal protein S12.

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

- Molecule 50 is a protein called 30S ribosomal protein S13.

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

- Molecule 51 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AB	101	Total	C	N	O	S	0	0
			810	502	165	140	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AB	35	ALA	-	insertion	UNP B7MCS2

- Molecule 52 is a protein called 30S ribosomal protein S15.

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

- Molecule 53 is a protein called 30S ribosomal protein S16.

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

- Molecule 54 is a protein called 30S ribosomal protein S17.

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

- Molecule 55 is a protein called 30S ribosomal protein S18.

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

- Molecule 56 is a protein called 30S ribosomal protein S19.

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

- Molecule 57 is a protein called 30S ribosomal protein S20.

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

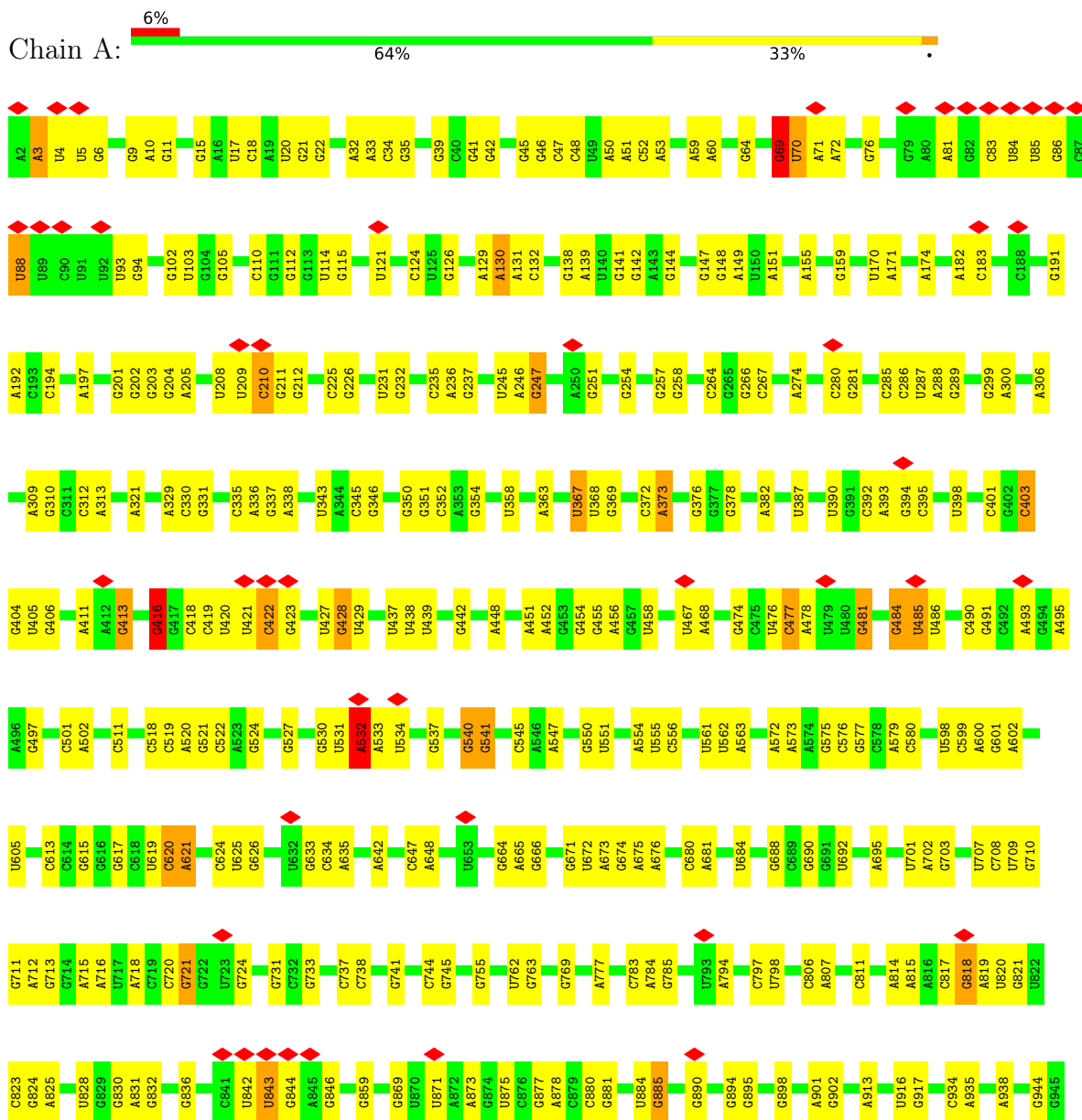
- Molecule 58 is a protein called 30S ribosomal protein S21.

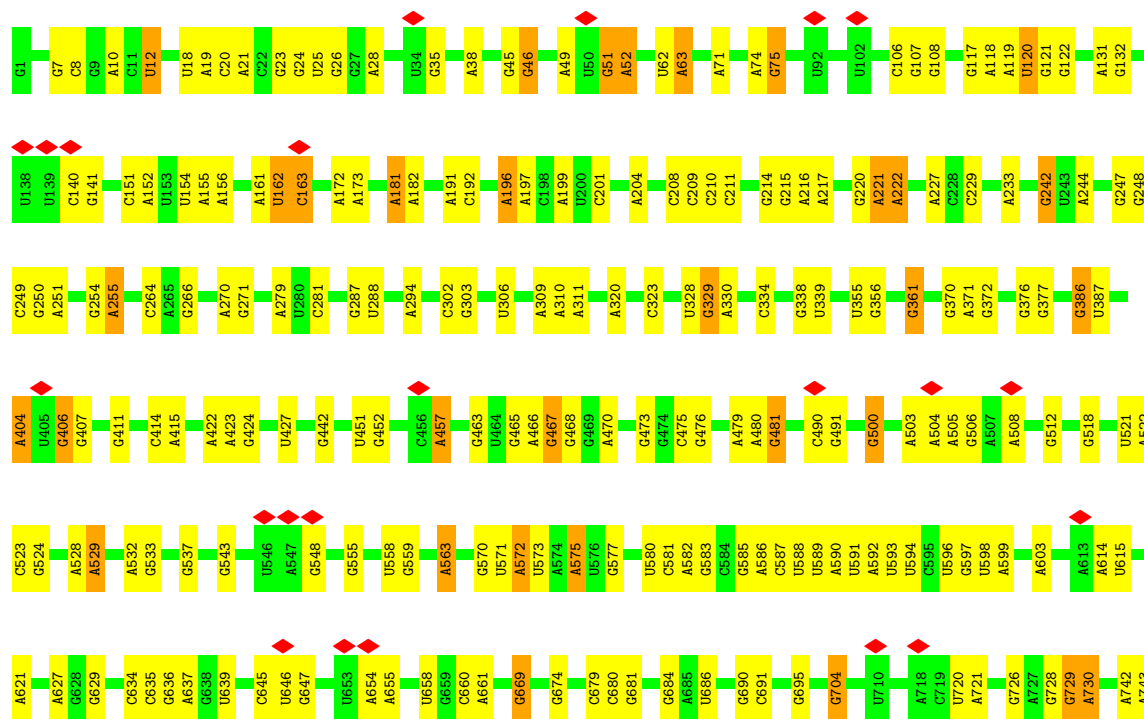
Mol	Chain	Residues	Atoms					AltConf	Trace
58	HB	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

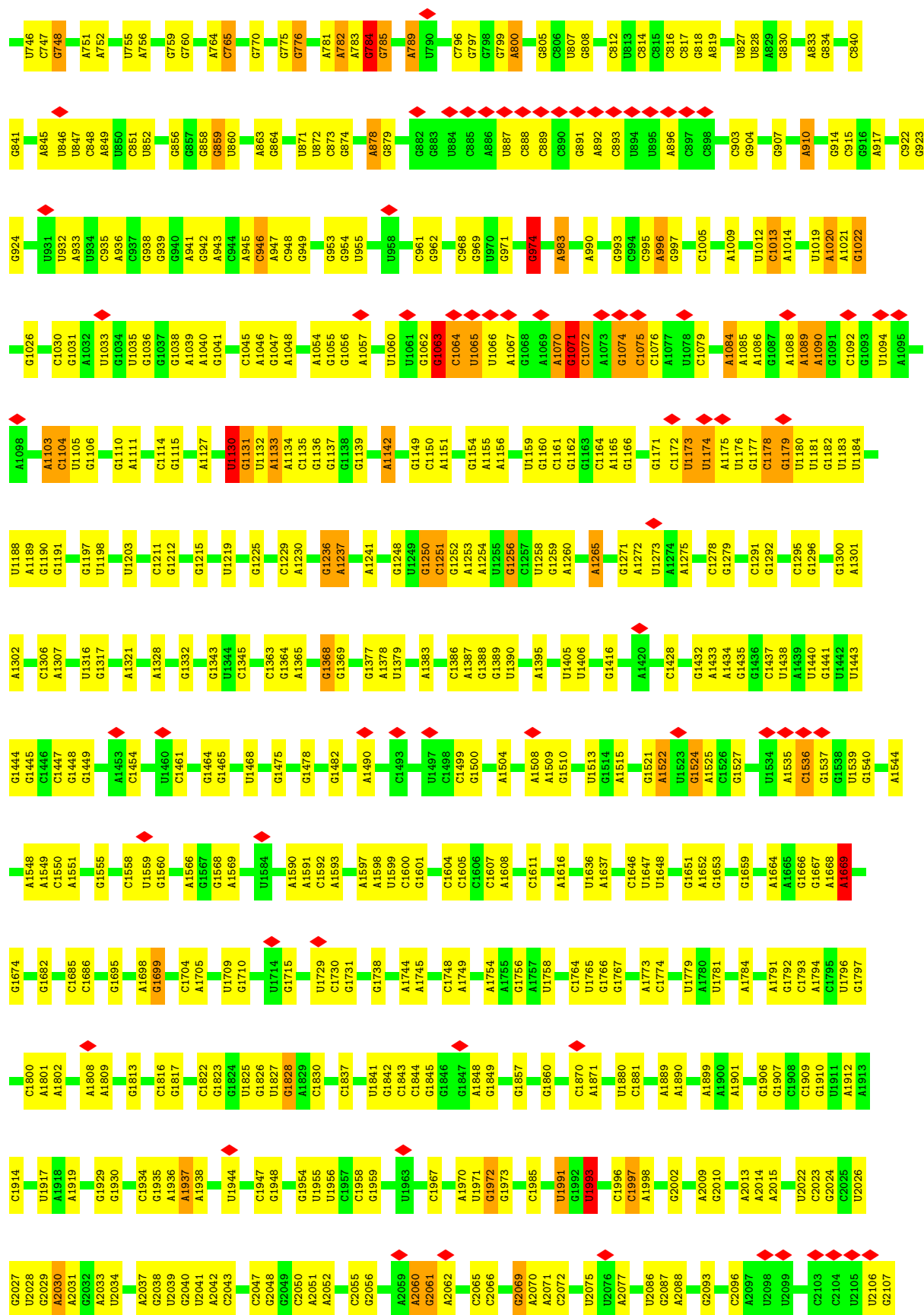
3 Residue-property plots

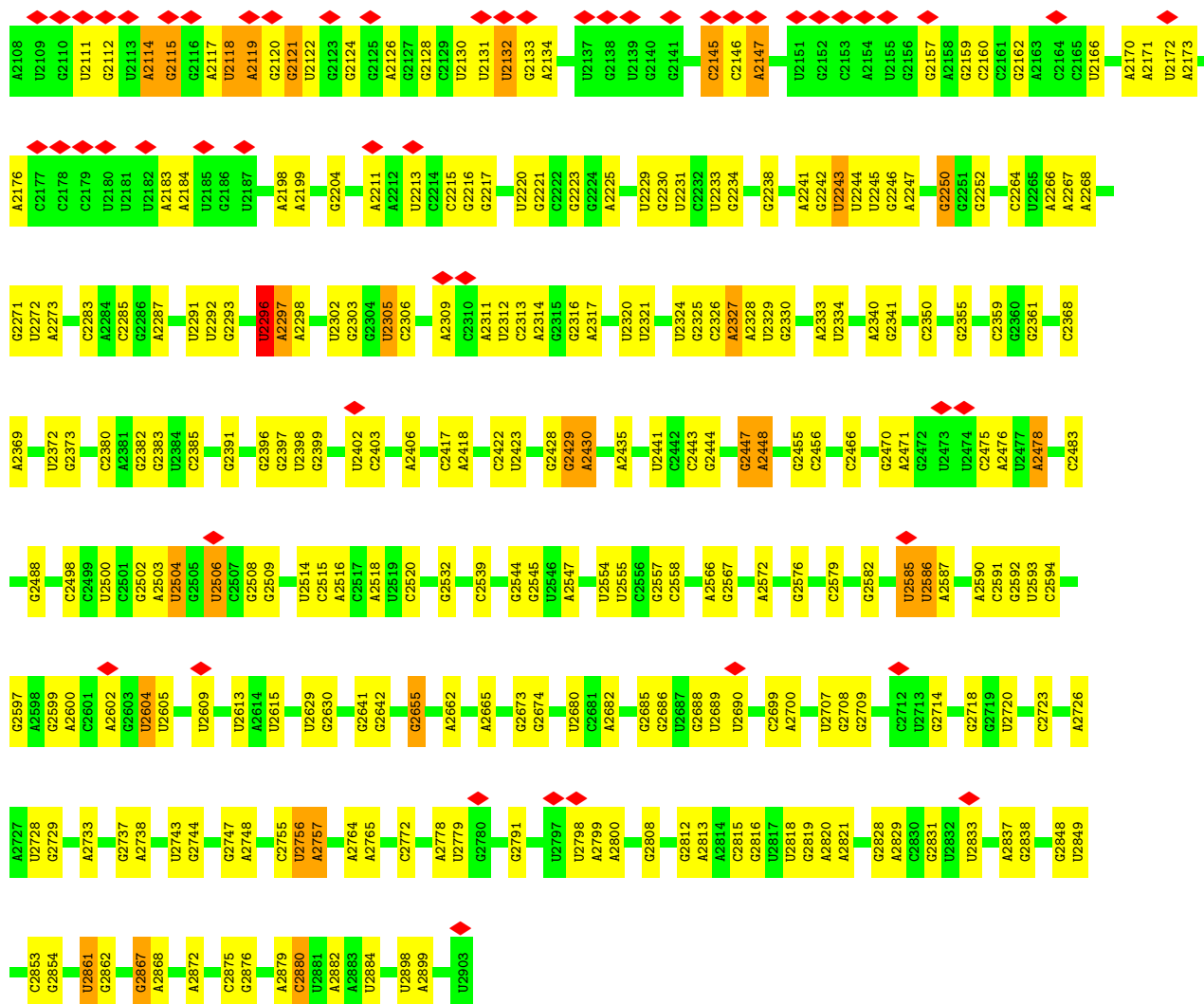
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

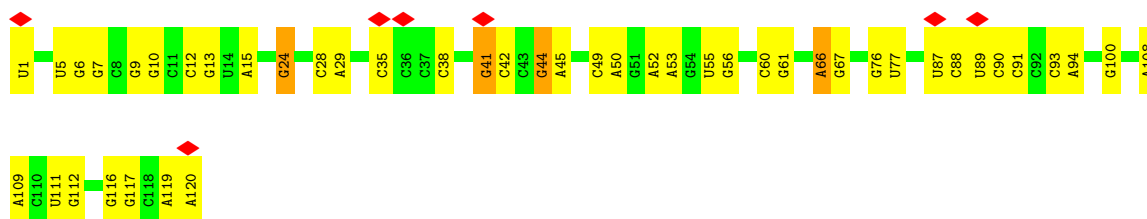




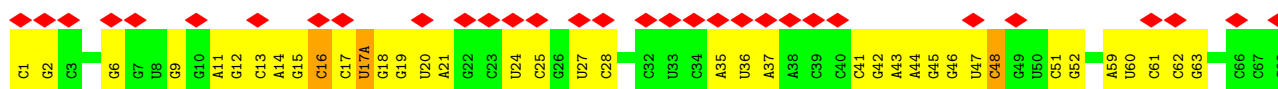


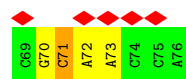


• Molecule 3: 5S ribosomal RNA

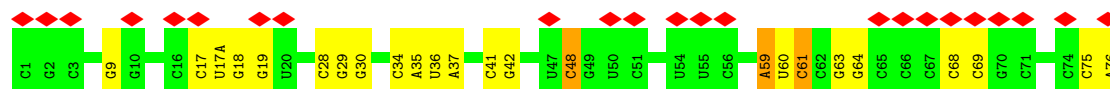
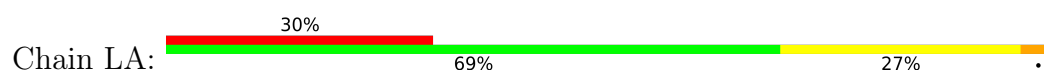


• Molecule 4: tRNA(fMet)

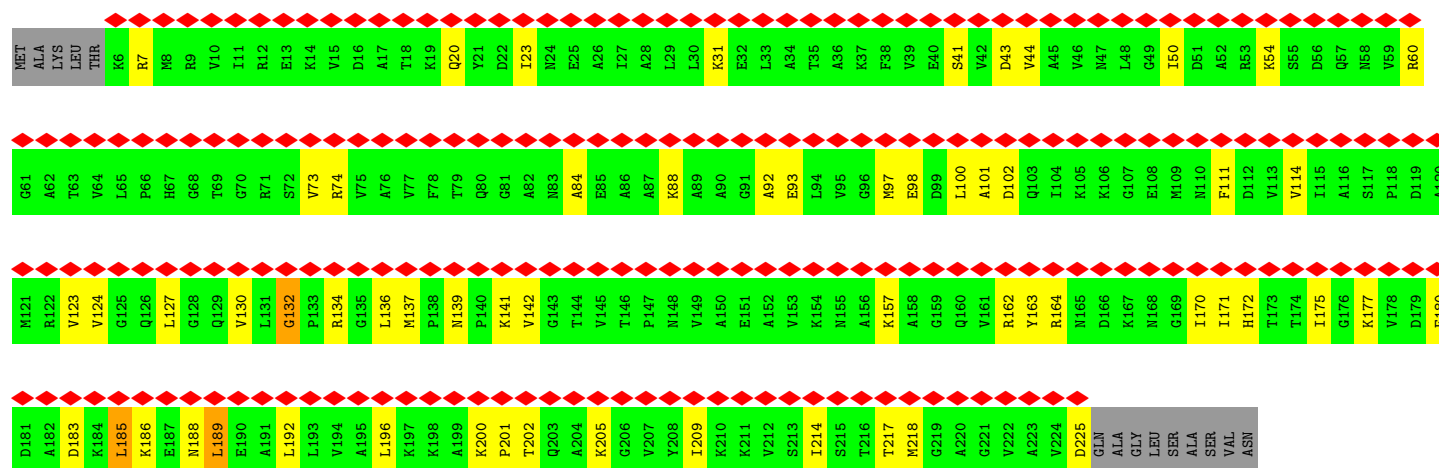




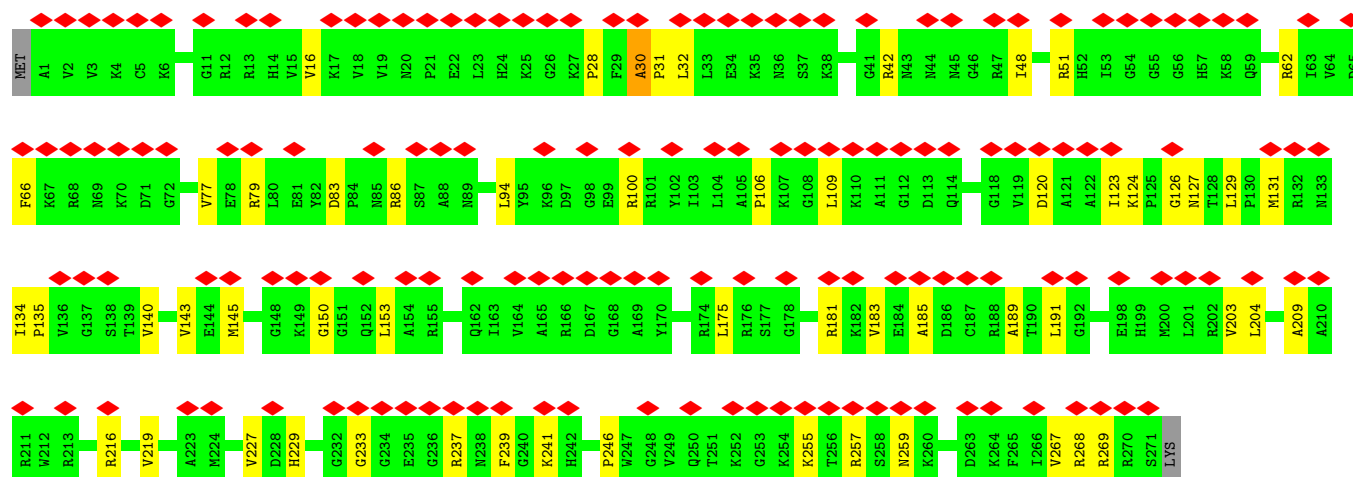
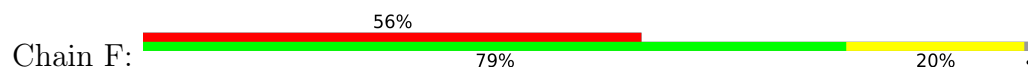
• Molecule 4: tRNA(fMet)



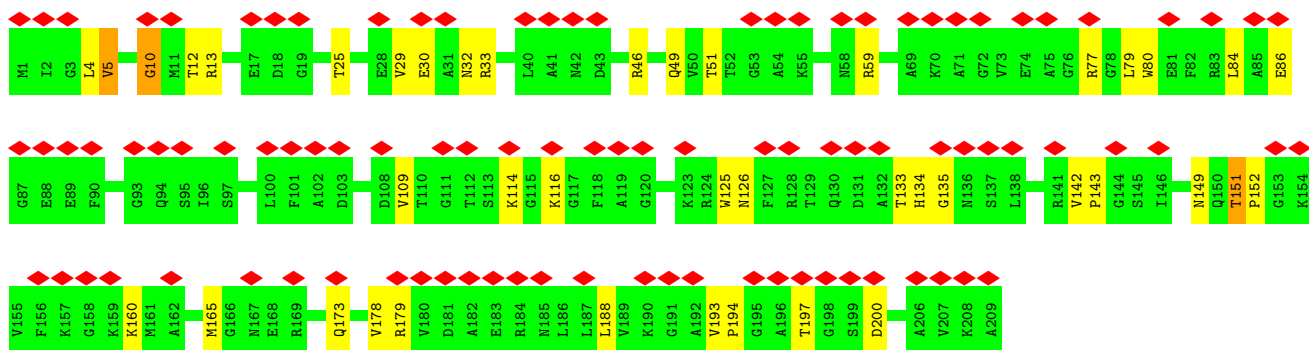
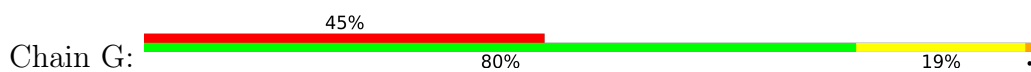
• Molecule 5: 50S ribosomal protein L1



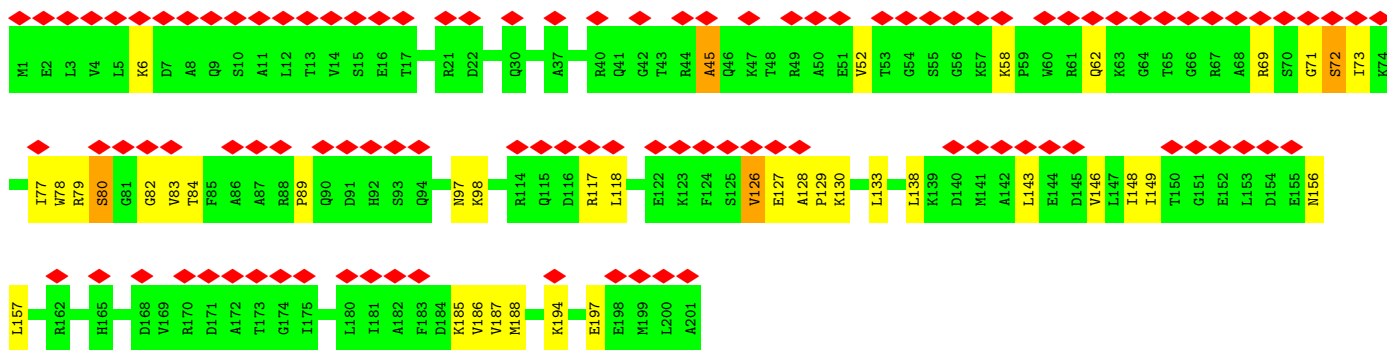
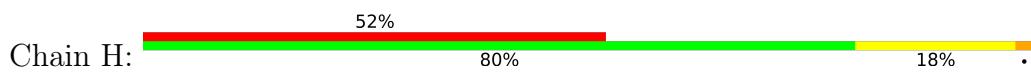
• Molecule 6: 50S ribosomal protein L2



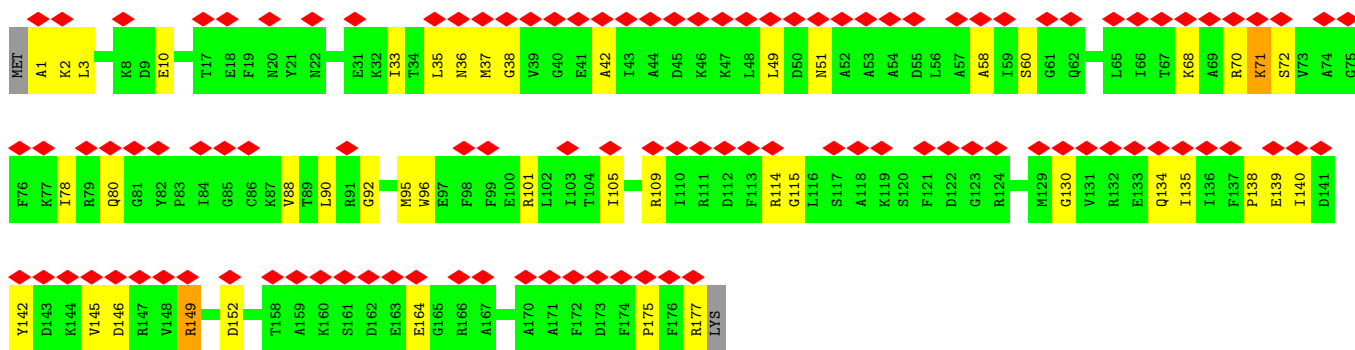
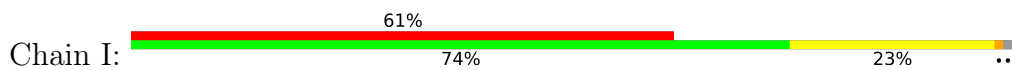
• Molecule 7: 50S ribosomal protein L3



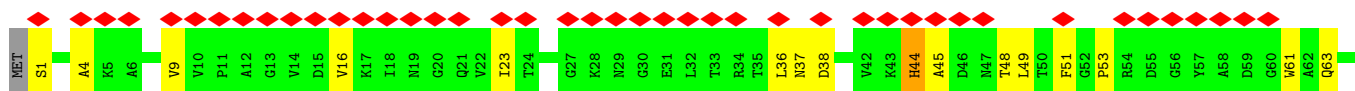
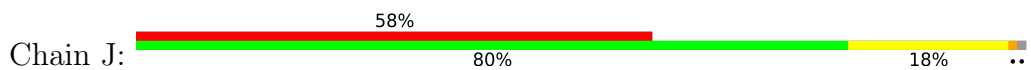
• Molecule 8: 50S ribosomal protein L4

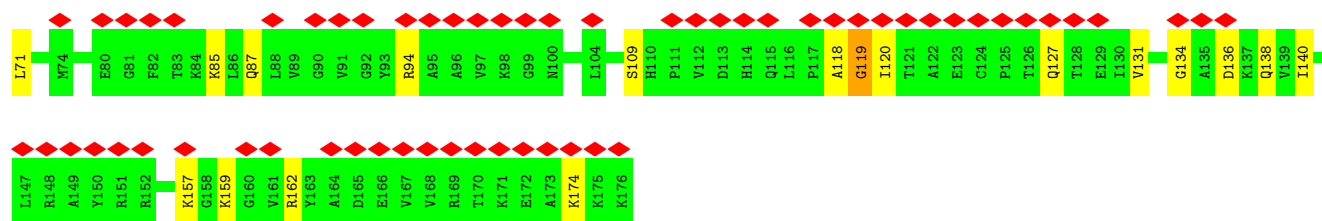


• Molecule 9: 50S ribosomal protein L5

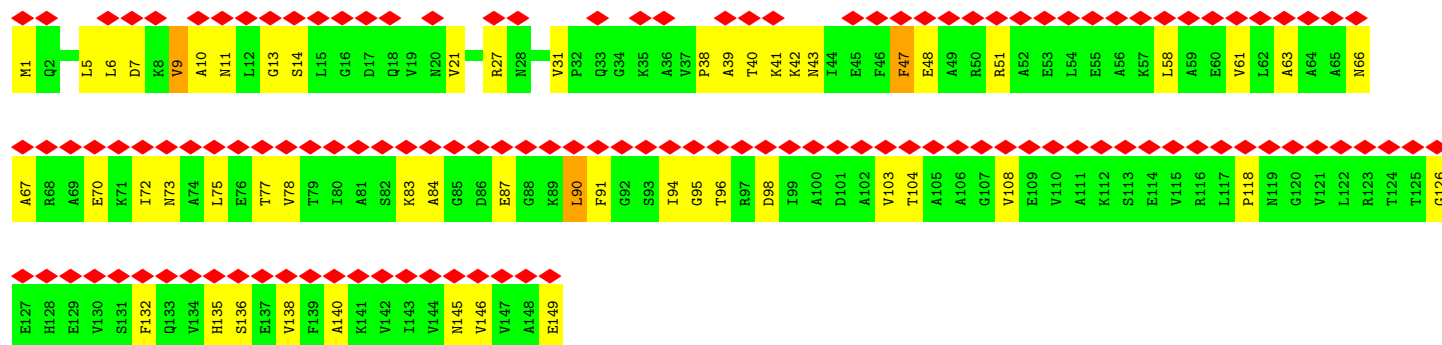
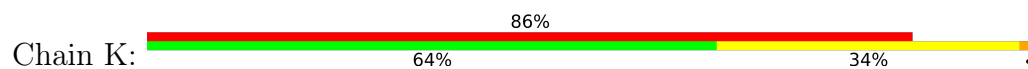


• Molecule 10: 50S ribosomal protein L6

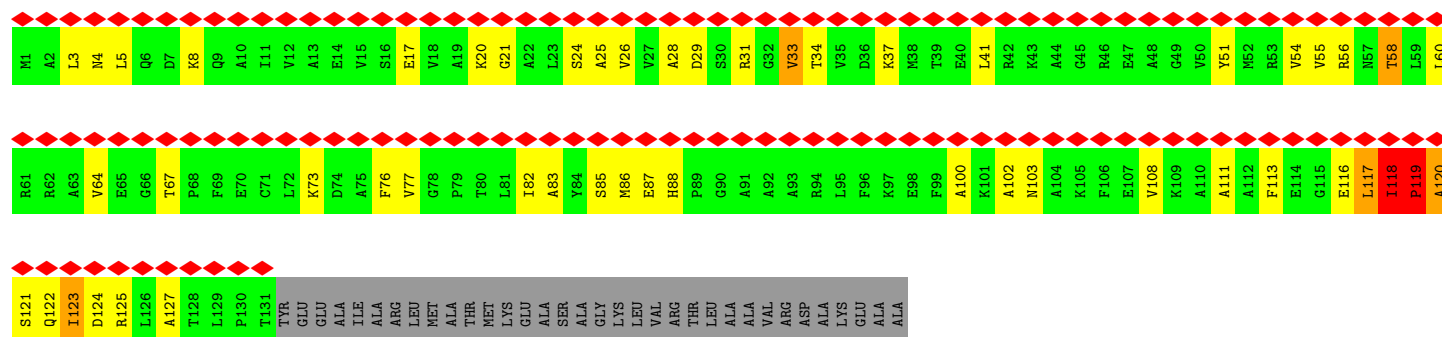
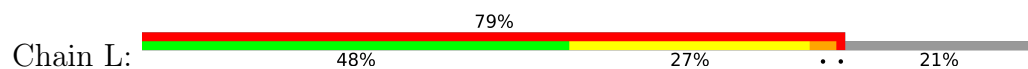




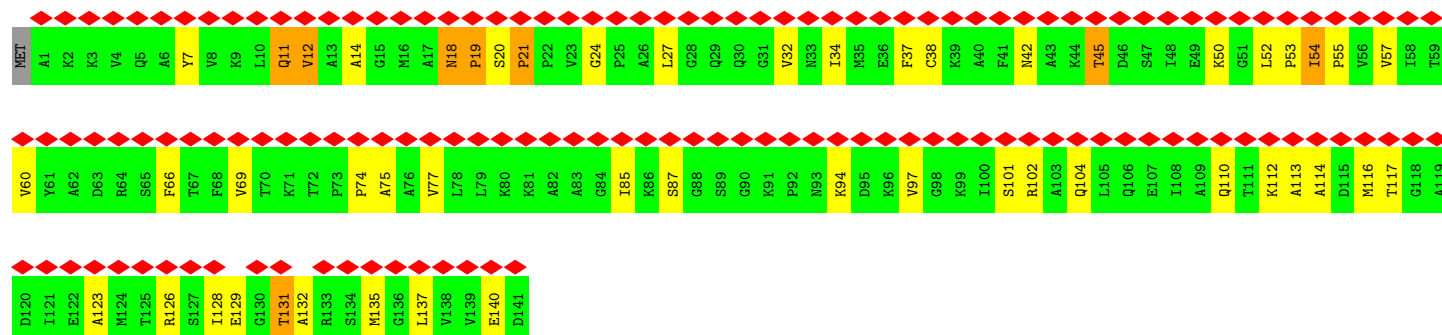
• Molecule 11: 50S ribosomal protein L9



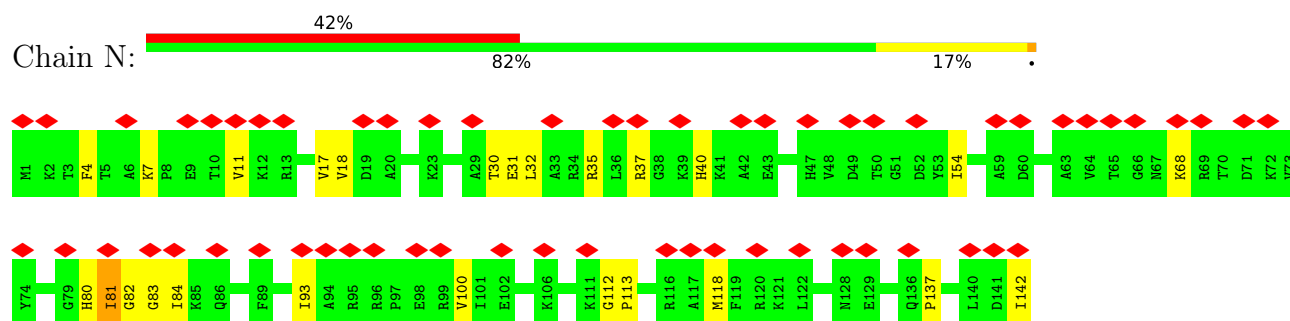
• Molecule 12: 50S ribosomal protein L10



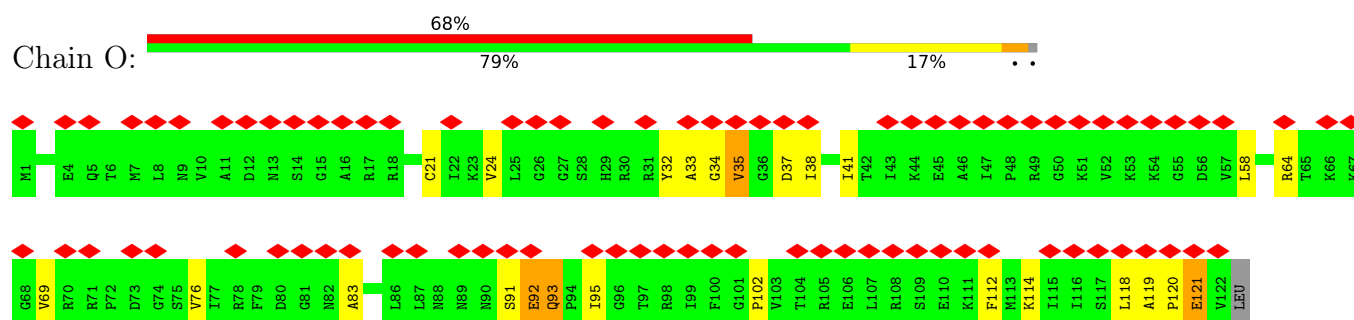
• Molecule 13: 50S ribosomal protein L11



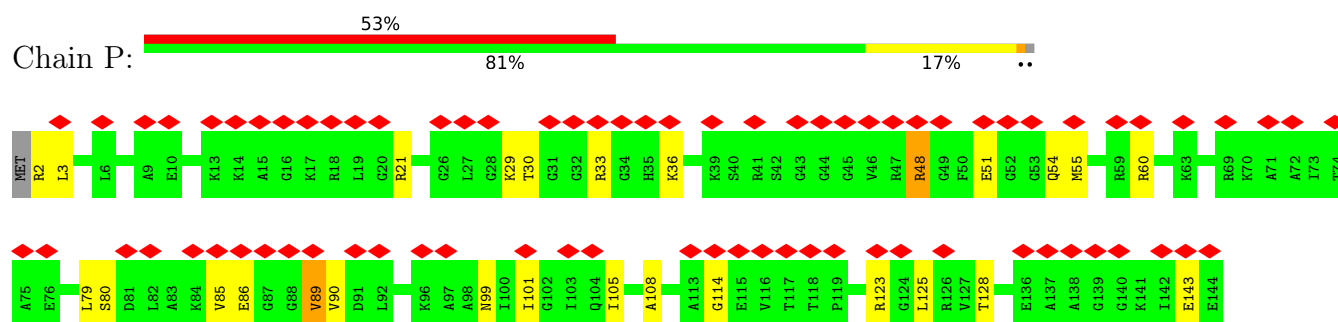
- Molecule 14: 50S ribosomal protein L13



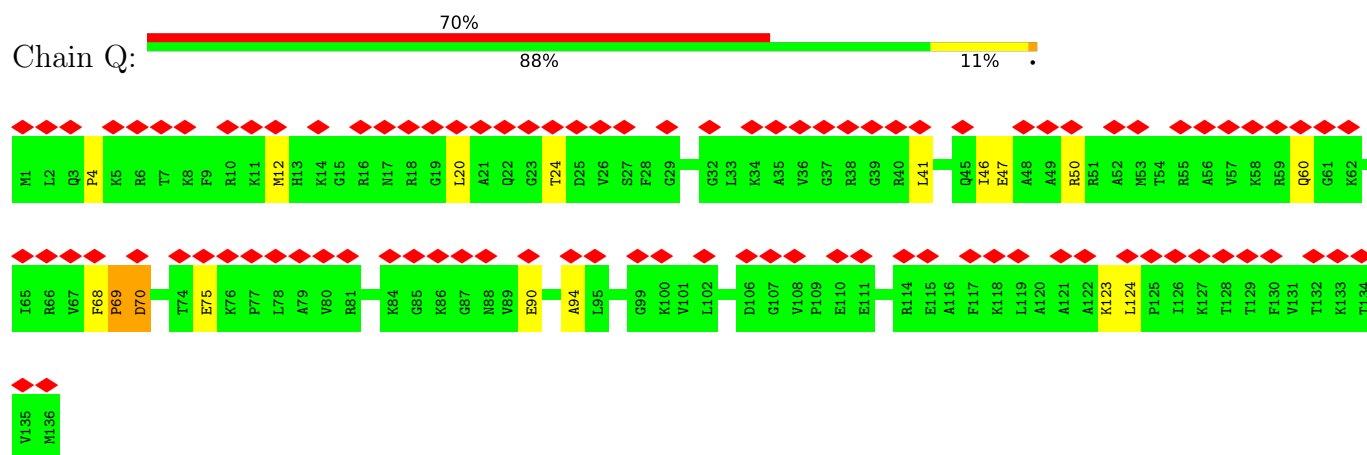
- Molecule 15: 50S ribosomal protein L14



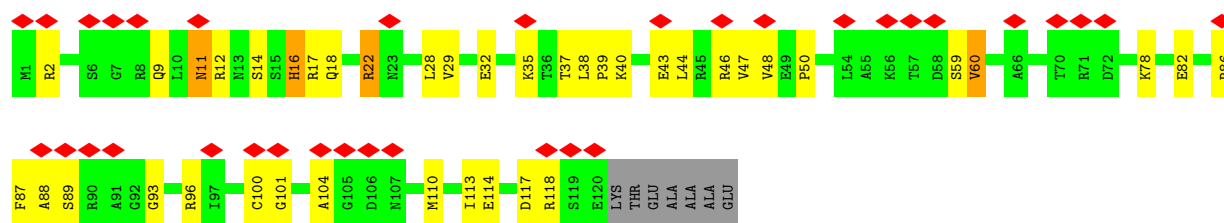
- Molecule 16: 50S ribosomal protein L15



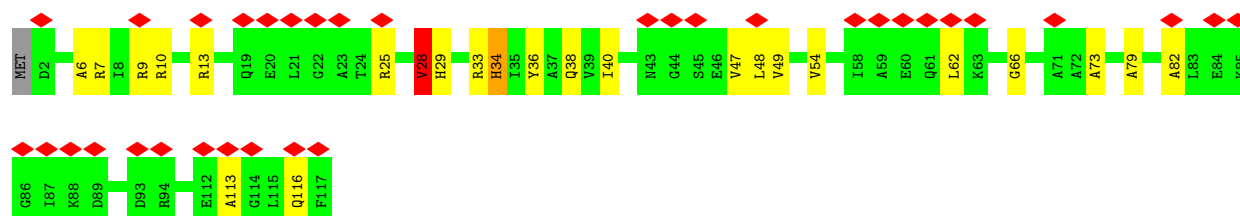
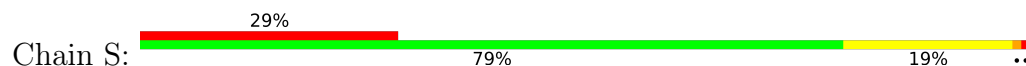
- Molecule 17: 50S ribosomal protein L16



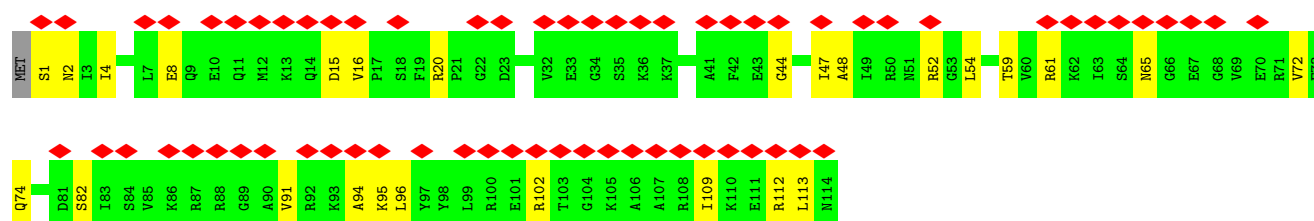
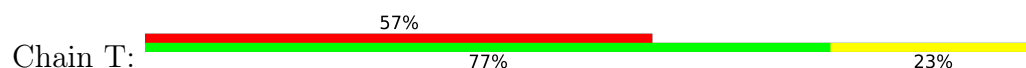
- Molecule 18: 50S ribosomal protein L17



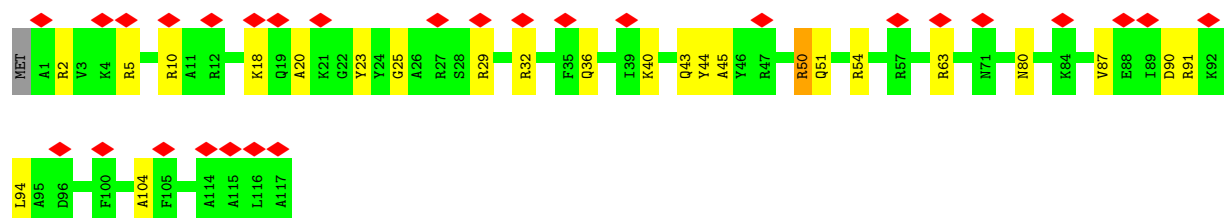
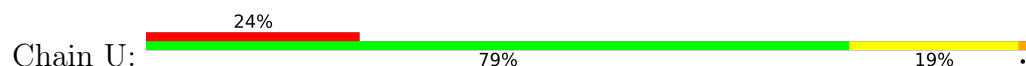
- Molecule 19: 50S ribosomal protein L18



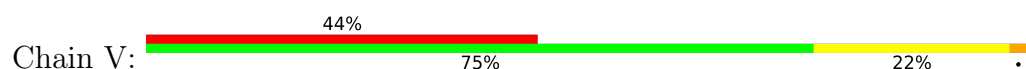
- Molecule 20: 50S ribosomal protein L19



- Molecule 21: 50S ribosomal protein L20

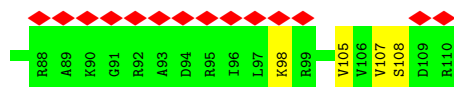
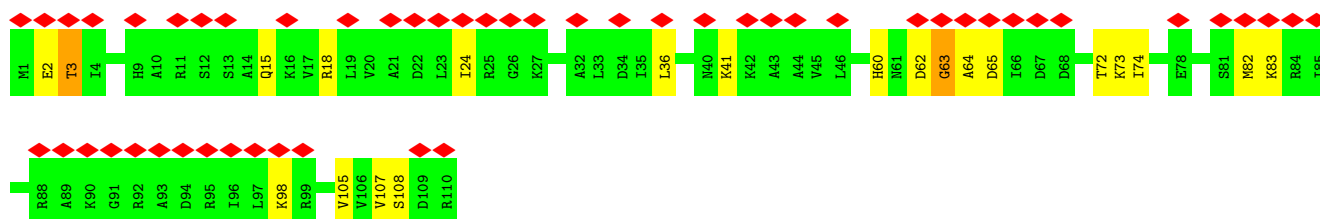
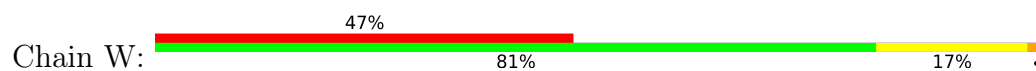


- Molecule 22: 50S ribosomal protein L21

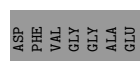
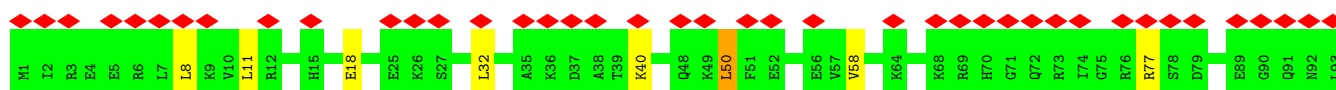
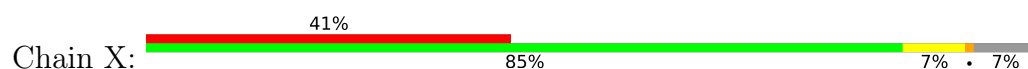




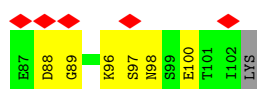
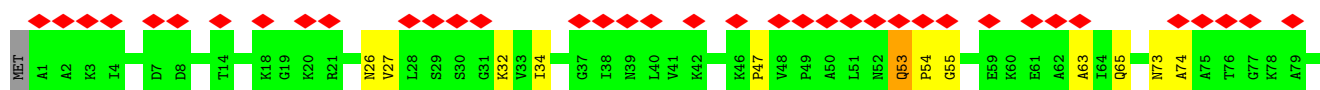
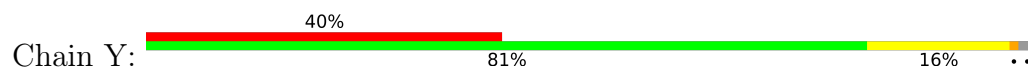
• Molecule 23: 50S ribosomal protein L22



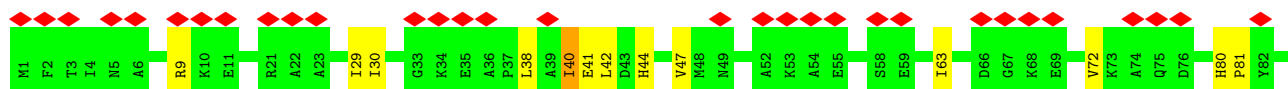
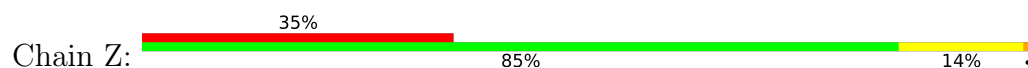
• Molecule 24: 50S ribosomal protein L23



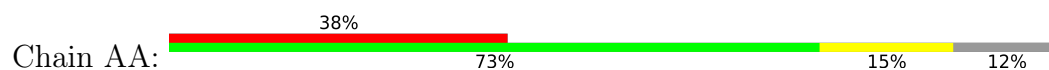
• Molecule 25: 50S ribosomal protein L24

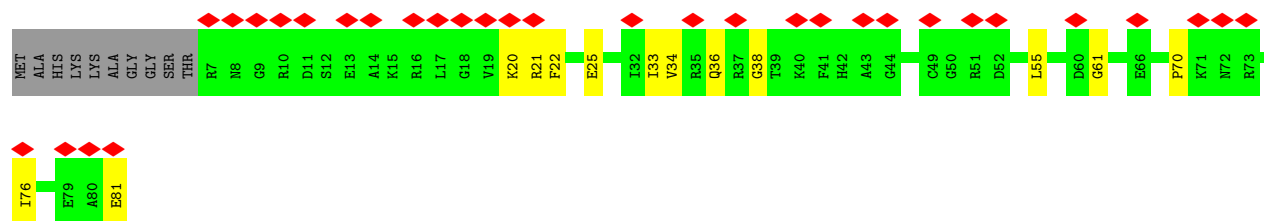


• Molecule 26: 50S ribosomal protein L25

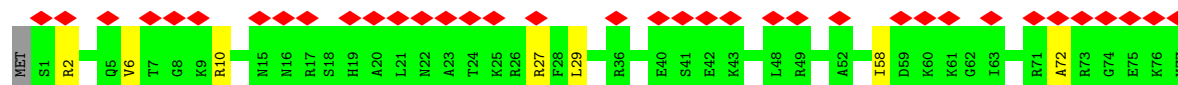
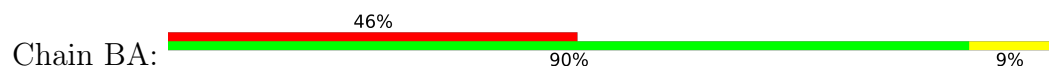


• Molecule 27: 50S ribosomal protein L27

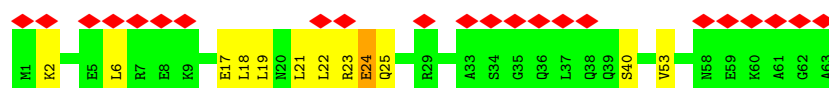
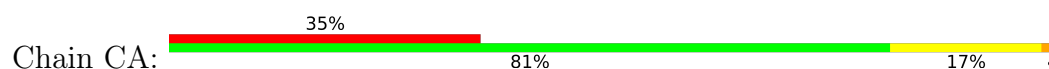




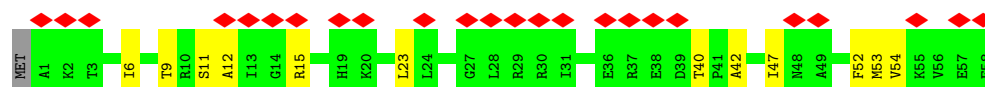
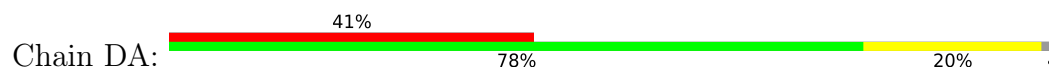
- Molecule 28: 50S ribosomal protein L28



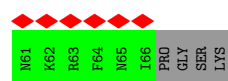
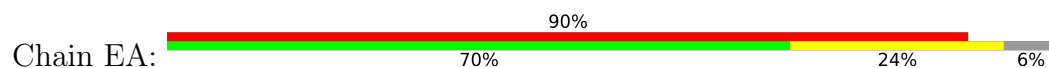
- Molecule 29: 50S ribosomal protein L29



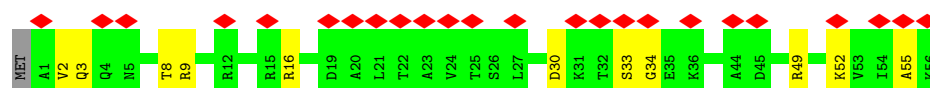
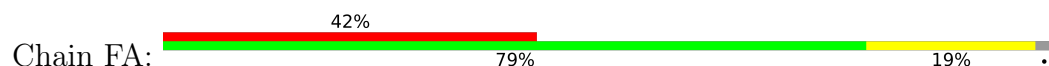
- Molecule 30: 50S ribosomal protein L30



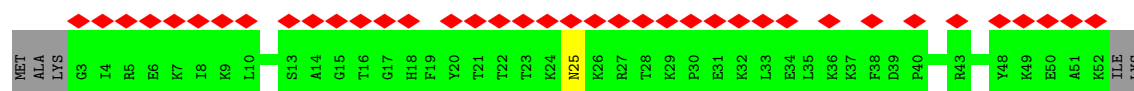
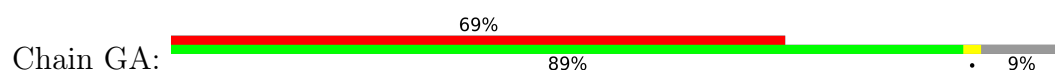
- Molecule 31: 50S ribosomal protein L31



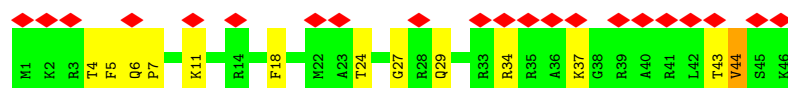
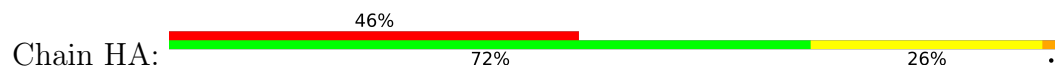
- Molecule 32: 50S ribosomal protein L32



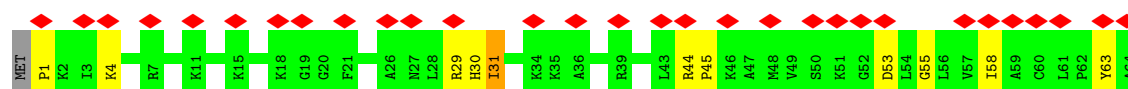
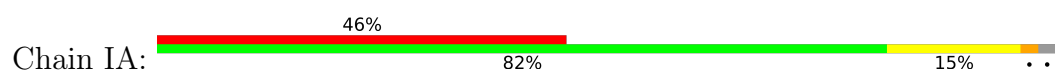
- Molecule 33: 50S ribosomal protein L33



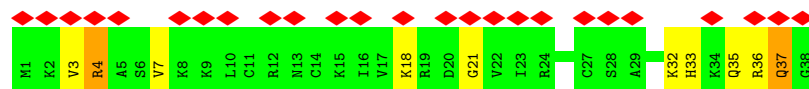
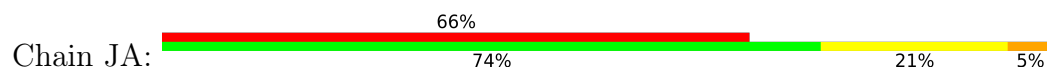
- Molecule 34: 50S ribosomal protein L34



- Molecule 35: 50S ribosomal protein L35



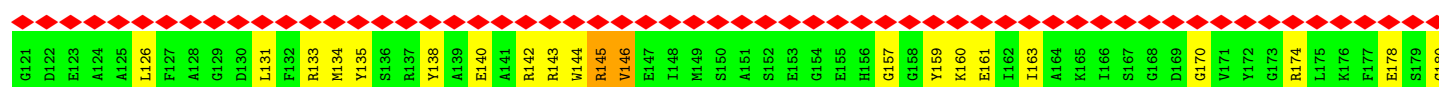
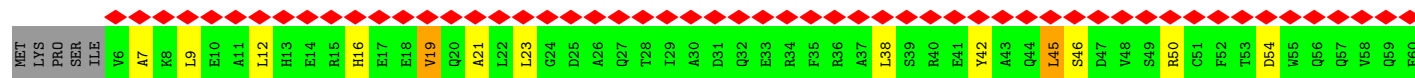
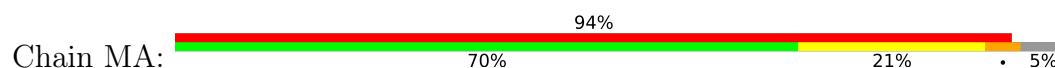
- Molecule 36: 50S ribosomal protein L36

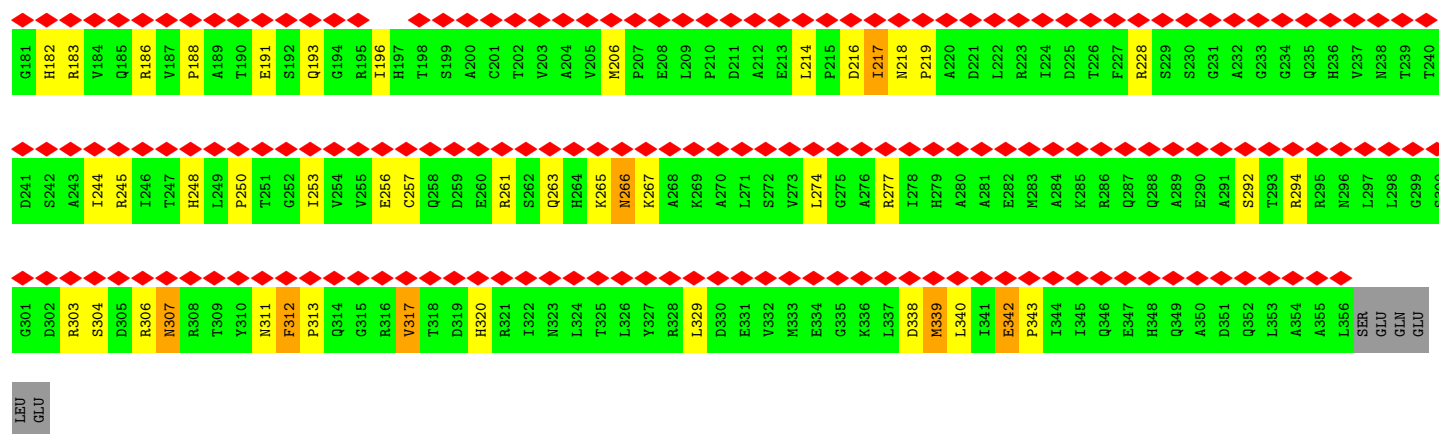


- Molecule 37: mRNA

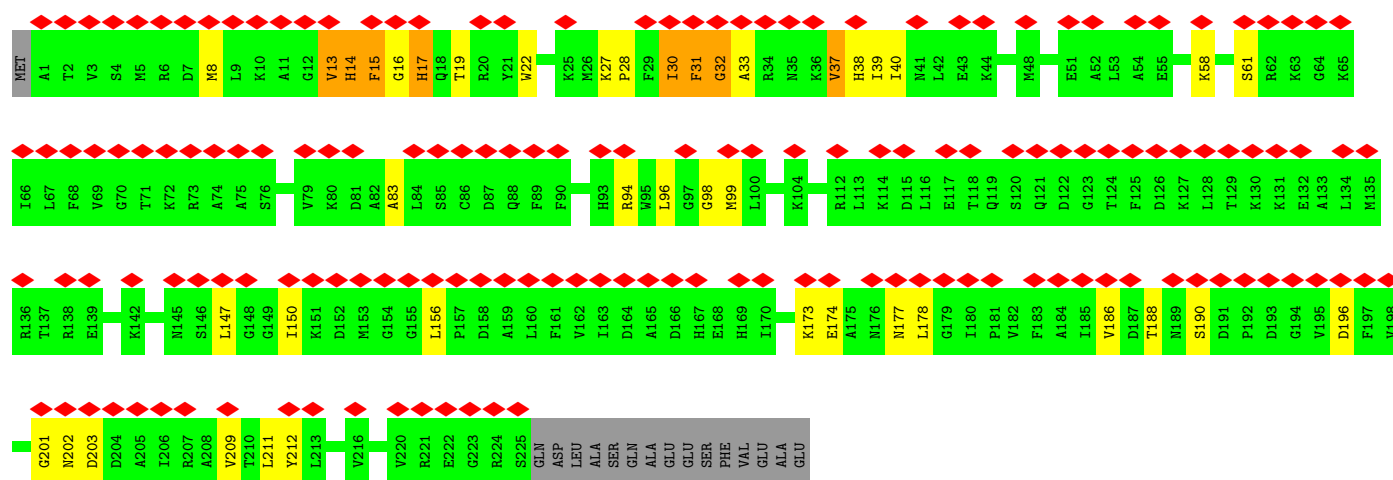
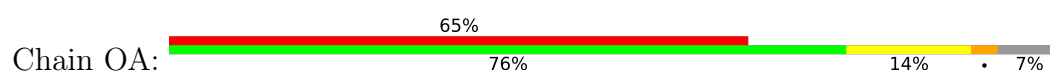


- Molecule 38: Peptide chain release factor 1

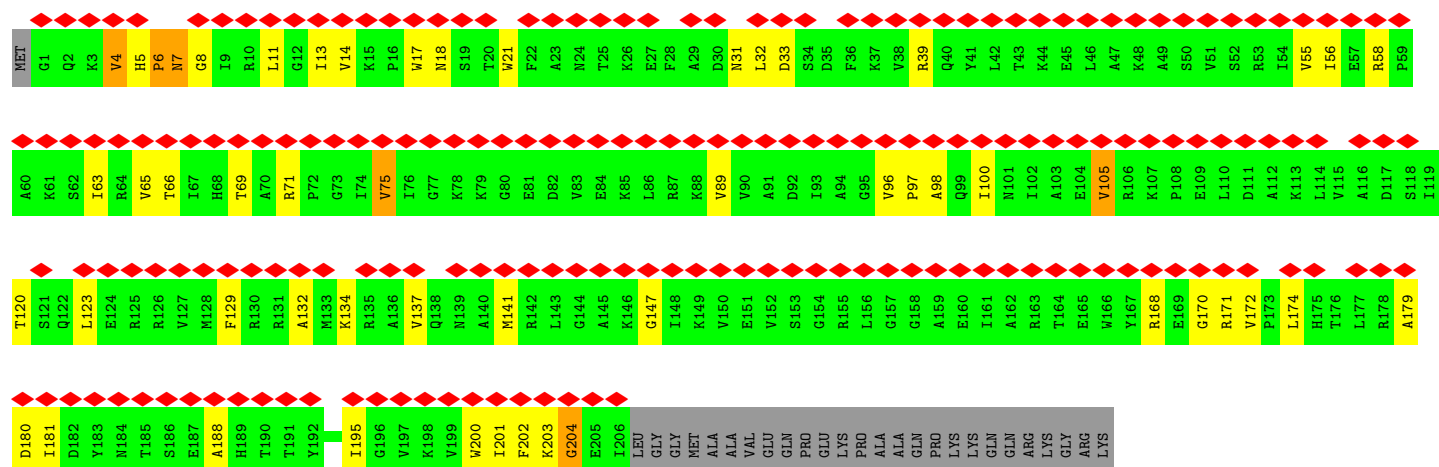
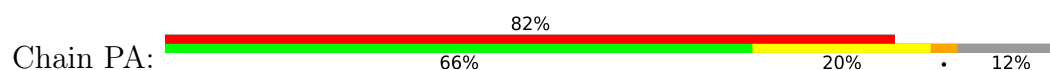




• Molecule 39: 30S ribosomal protein S2

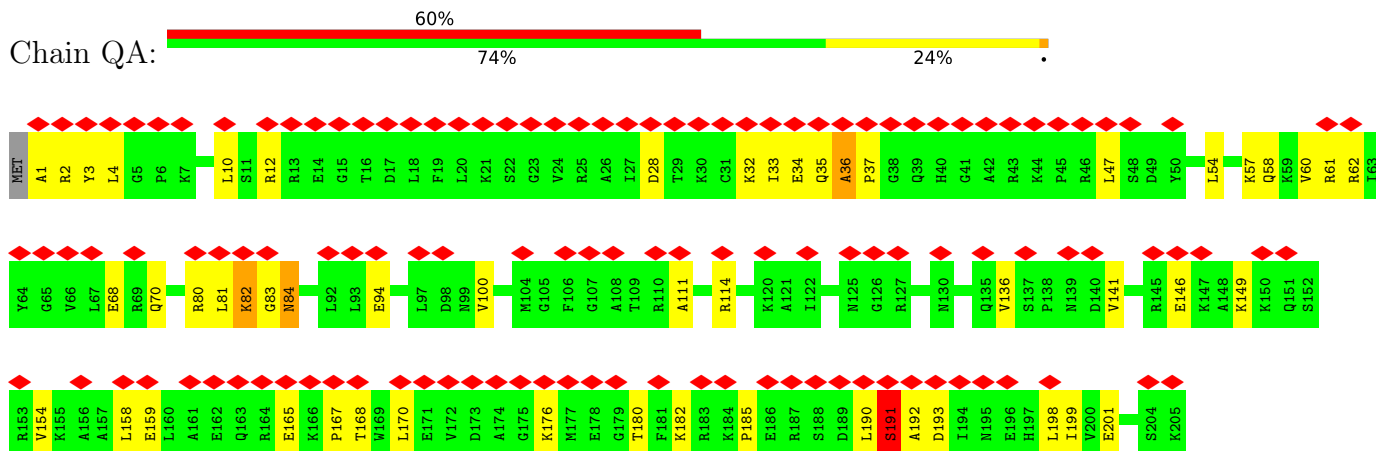


• Molecule 40: 30S ribosomal protein S3



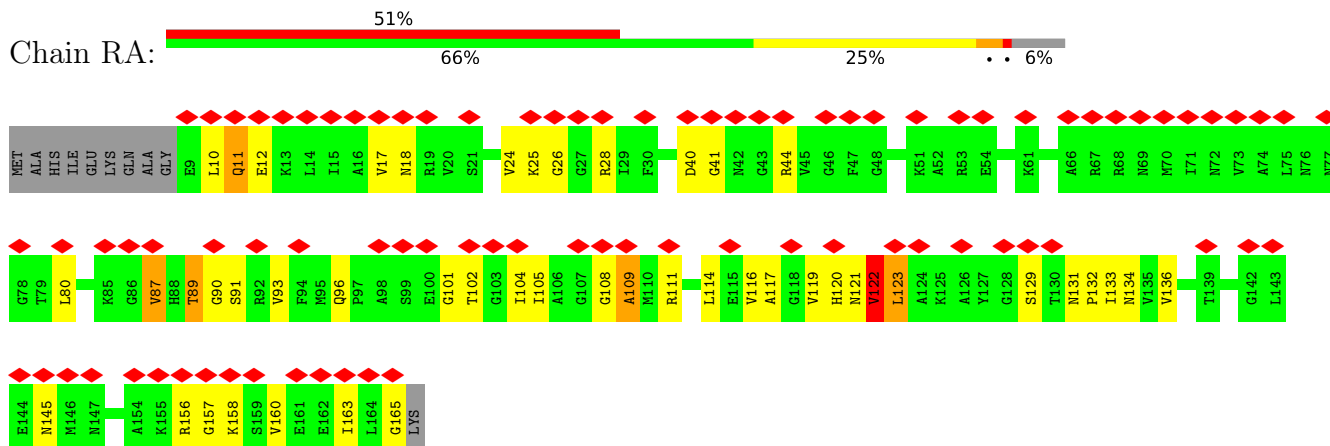
- Molecule 41: 30S ribosomal protein S4

Chain QA:



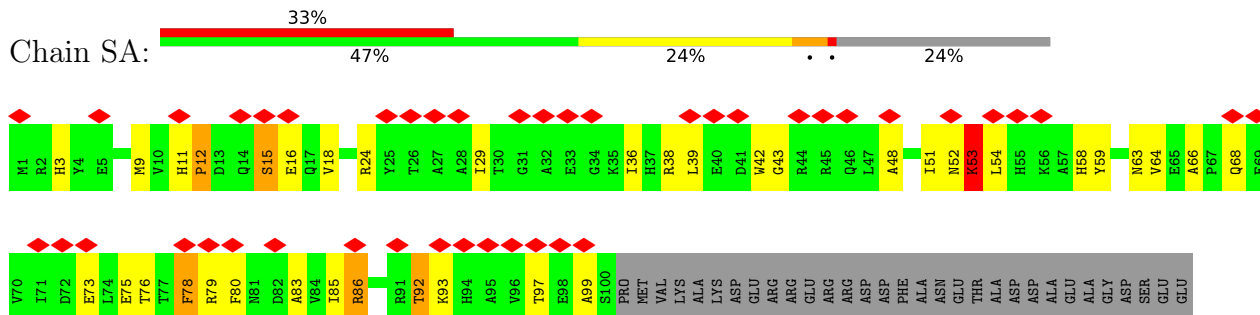
- Molecule 42: 30S ribosomal protein S5

Chain RA:



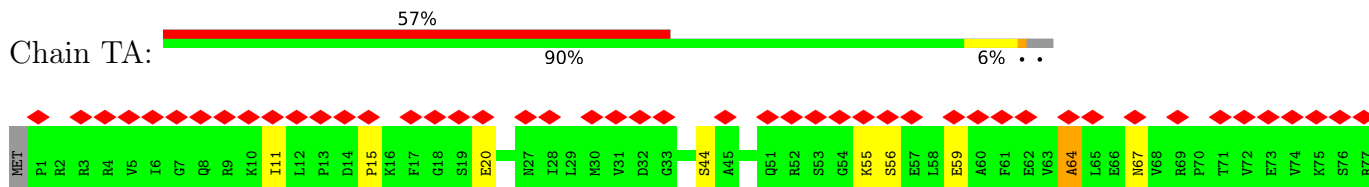
- Molecule 43: 30S ribosomal protein S6

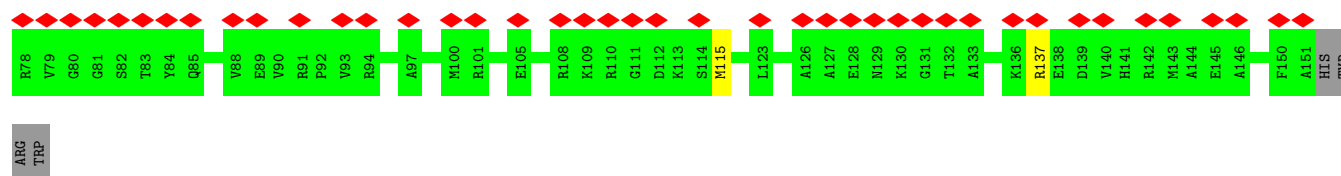
Chain SA:



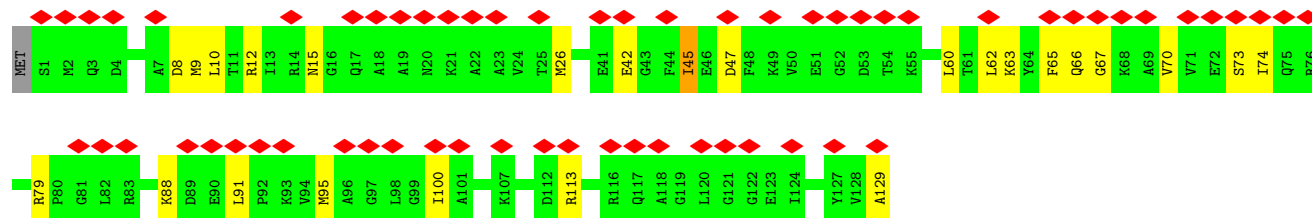
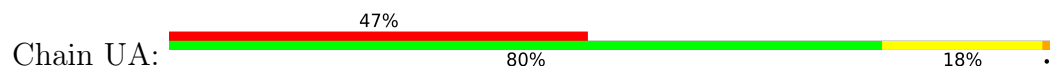
- Molecule 44: 30S ribosomal protein S7

Chain TA:

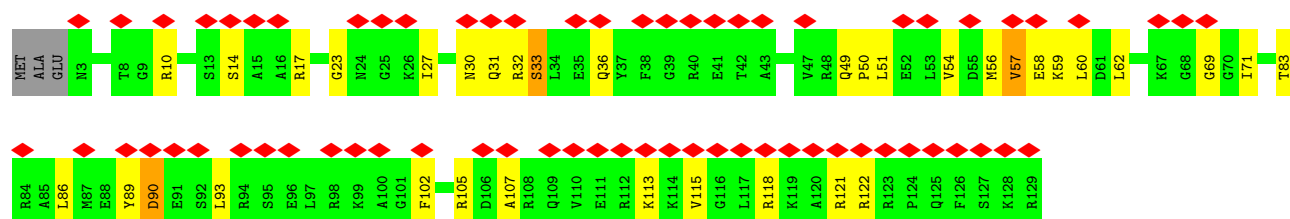
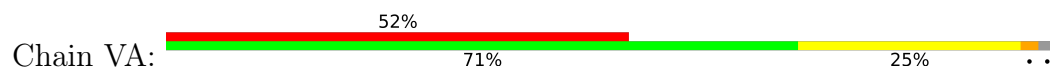




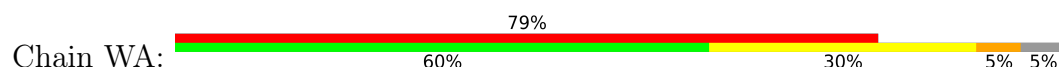
• Molecule 45: 30S ribosomal protein S8



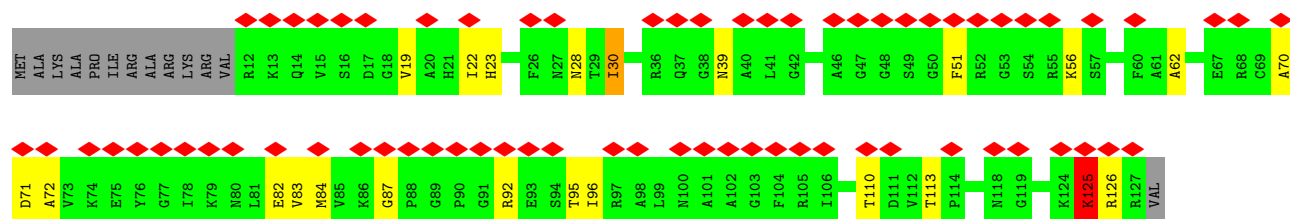
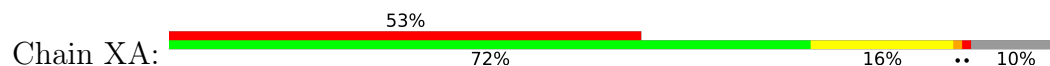
• Molecule 46: 30S ribosomal protein S9



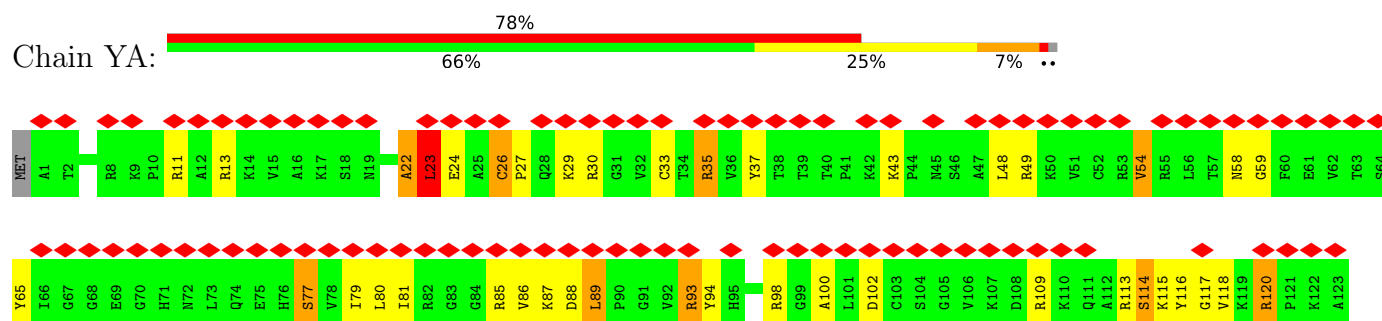
• Molecule 47: 30S ribosomal protein S10



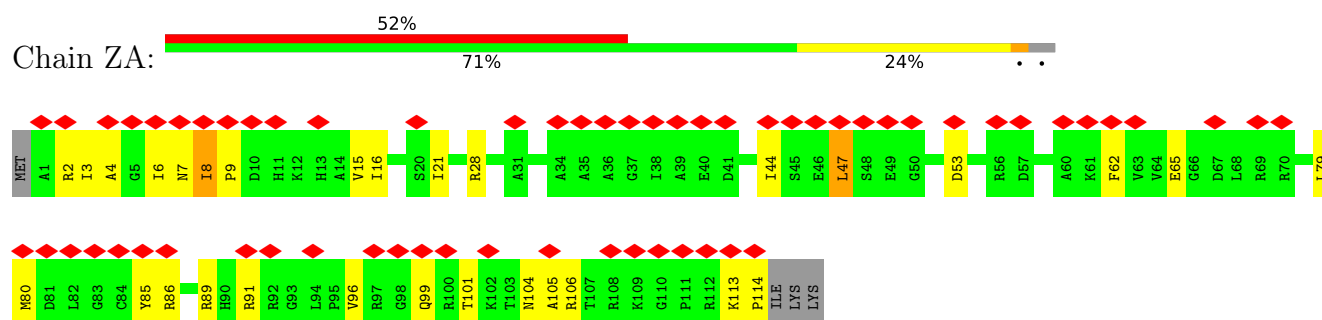
• Molecule 48: 30S ribosomal protein S11



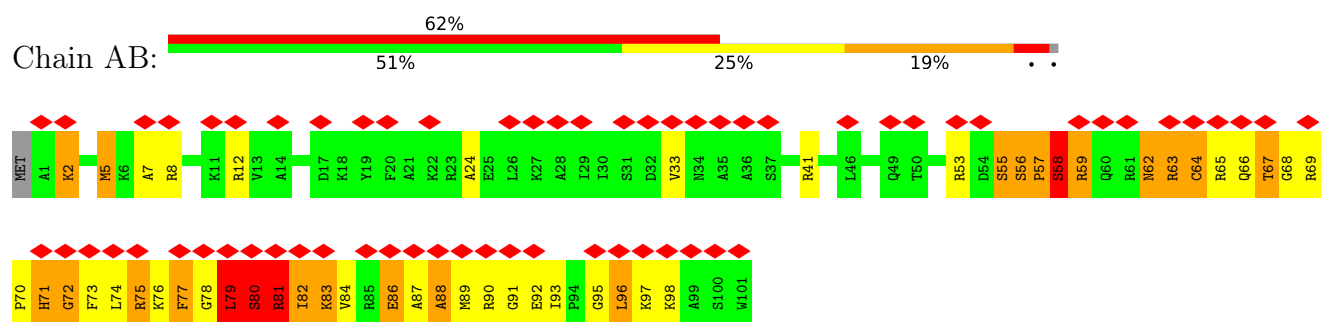
- Molecule 49: 30S ribosomal protein S12



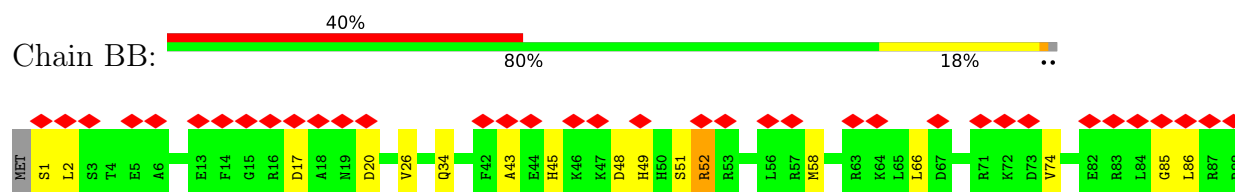
- Molecule 50: 30S ribosomal protein S13



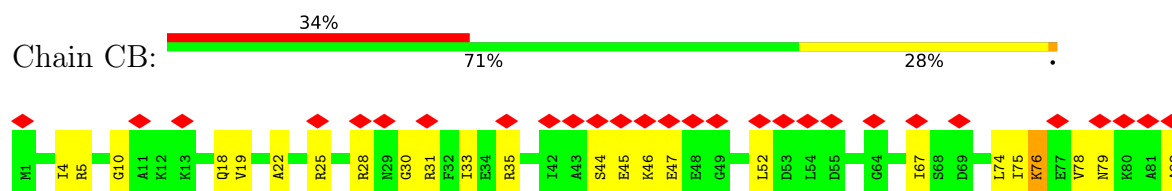
- Molecule 51: 30S ribosomal protein S14



- Molecule 52: 30S ribosomal protein S15

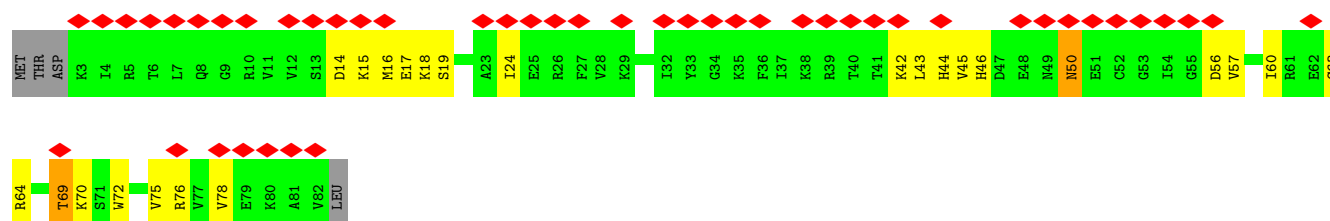


- Molecule 53: 30S ribosomal protein S16



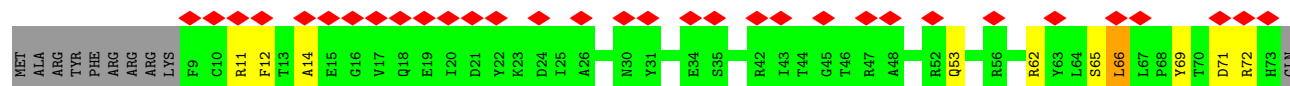
- Molecule 54: 30S ribosomal protein S17

Chain DB: 



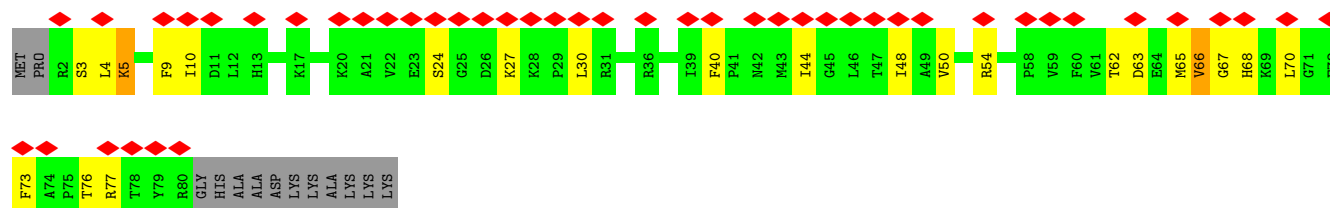
- Molecule 55: 30S ribosomal protein S18

Chain EB: 



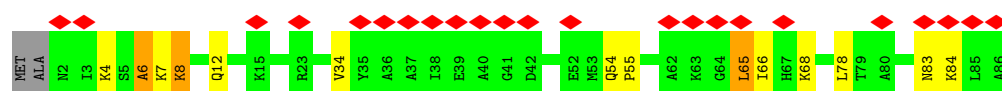
- Molecule 56: 30S ribosomal protein S19

Chain FB: 



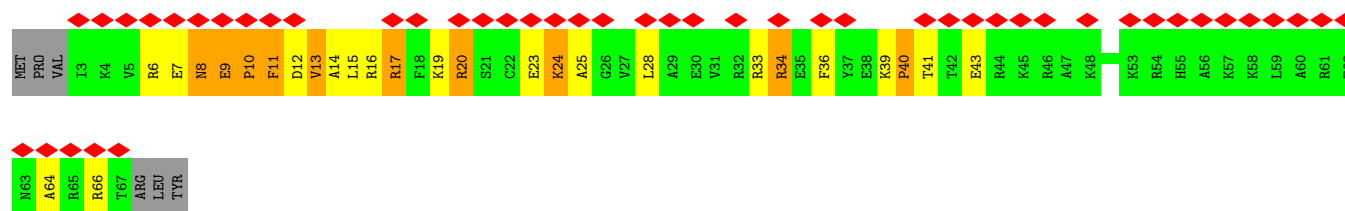
- Molecule 57: 30S ribosomal protein S20

Chain GB: 



- Molecule 58: 30S ribosomal protein S21

Chain HB: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	639088	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 ($e^-/\text{\AA}^2$)	0.5	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	22000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	16.659	Depositor
Minimum map value	-3.226	Depositor
Average map value	-0.215	Depositor
Map value standard deviation	1.283	Depositor
Recommended contour level	7	Depositor
Map size ($\text{\AA}$)	444.96, 444.96, 444.96	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.927, 0.927, 0.927	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	A	0.44	0/36963	0.58	9/57662 (0.0%)
2	B	0.44	0/69797	0.59	21/108890 (0.0%)
3	C	0.44	0/2872	0.59	2/4479 (0.0%)
4	D	0.46	0/1832	0.52	0/2855
4	LA	0.45	0/1832	0.51	0/2855
5	E	0.46	0/1652	0.98	8/2227 (0.4%)
6	F	0.42	0/2121	1.04	8/2852 (0.3%)
7	G	0.42	0/1586	0.97	3/2134 (0.1%)
8	H	0.43	0/1571	0.98	3/2113 (0.1%)
9	I	0.45	0/1434	0.98	5/1926 (0.3%)
10	J	0.43	0/1343	0.95	2/1816 (0.1%)
11	K	0.55	0/1122	1.12	9/1515 (0.6%)
12	L	0.63	0/1001	1.24	13/1350 (1.0%)
13	M	0.59	0/1046	1.15	11/1410 (0.8%)
14	N	0.39	0/1152	0.90	4/1551 (0.3%)
15	O	0.41	0/947	0.99	2/1268 (0.2%)
16	P	0.39	0/1054	0.94	1/1403 (0.1%)
17	Q	0.42	0/1093	0.99	2/1460 (0.1%)
18	R	0.46	0/973	1.06	7/1301 (0.5%)
19	S	0.44	0/902	0.94	2/1209 (0.2%)
20	T	0.37	0/929	0.99	5/1242 (0.4%)
21	U	0.45	0/960	1.09	3/1278 (0.2%)
22	V	0.41	0/829	1.02	5/1107 (0.5%)
23	W	0.43	0/864	1.03	3/1156 (0.3%)
24	X	0.43	0/744	0.90	3/994 (0.3%)
25	Y	0.40	0/787	0.93	4/1051 (0.4%)
26	Z	0.37	0/766	0.87	3/1025 (0.3%)
27	AA	0.37	0/582	0.91	1/769 (0.1%)
28	BA	0.39	0/635	0.98	1/848 (0.1%)
29	CA	0.44	0/510	1.09	5/677 (0.7%)
30	DA	0.40	0/453	0.89	1/605 (0.2%)
31	EA	0.49	0/531	1.04	3/709 (0.4%)
32	FA	0.38	0/450	0.91	0/599
33	GA	0.38	0/416	0.83	0/554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	HA	0.45	0/380	0.99	3/498 (0.6%)
35	IA	0.42	0/513	0.91	0/676
36	JA	0.51	0/303	1.07	1/397 (0.3%)
37	KA	0.43	0/464	0.60	0/723
38	MA	1.04	5/2751 (0.2%)	1.09	14/3703 (0.4%)
39	OA	0.70	2/1787 (0.1%)	1.32	13/2408 (0.5%)
40	PA	0.57	2/1651 (0.1%)	1.02	8/2225 (0.4%)
41	QA	0.44	0/1665	1.02	8/2227 (0.4%)
42	RA	0.55	1/1169 (0.1%)	1.16	12/1573 (0.8%)
43	SA	0.51	0/835	1.16	11/1128 (1.0%)
44	TA	0.42	0/1195	0.95	2/1602 (0.1%)
45	UA	0.41	0/989	0.96	2/1326 (0.2%)
46	VA	0.46	0/1034	1.02	2/1375 (0.1%)
47	WA	0.46	0/796	0.99	4/1077 (0.4%)
48	XA	0.45	0/885	0.97	3/1195 (0.3%)
49	YA	0.46	0/969	1.21	13/1300 (1.0%)
50	ZA	0.54	0/892	1.02	3/1193 (0.3%)
51	AB	1.14	10/822 (1.2%)	1.51	19/1095 (1.7%)
52	BB	0.44	0/722	1.05	5/964 (0.5%)
53	CB	0.44	0/659	1.02	2/884 (0.2%)
54	DB	0.36	0/657	0.87	1/881 (0.1%)
55	EB	0.47	0/544	0.95	2/731 (0.3%)
56	FB	0.46	0/652	0.93	1/877 (0.1%)
57	GB	0.39	0/671	0.96	6/888 (0.7%)
58	HB	0.53	0/550	1.21	7/728 (1.0%)
All	All	0.47	20/165304 (0.0%)	0.74	291/246564 (0.1%)

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
1	A	0	10
2	B	0	33
3	C	0	1
4	D	0	1
All	All	0	45

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	OA	31	PHE	C-O	12.17	1.37	1.23
38	MA	77	MET	SD-CE	10.12	2.04	1.79
51	AB	63	ARG	CA-C	9.89	1.65	1.52
51	AB	71	HIS	CA-C	8.77	1.62	1.52
38	MA	67	MET	SD-CE	8.61	2.01	1.79
51	AB	86	GLU	C-O	7.98	1.33	1.24
51	AB	77	PHE	CA-C	7.95	1.63	1.52
51	AB	77	PHE	C-O	7.09	1.32	1.24
40	PA	96	VAL	CA-C	7.04	1.60	1.52
38	MA	74	MET	SD-CE	6.96	1.97	1.79
38	MA	68	MET	SD-CE	6.79	1.96	1.79
38	MA	19	VAL	CA-CB	6.52	1.62	1.54
40	PA	97	PRO	N-CD	5.77	1.55	1.47
51	AB	77	PHE	CB-CG	5.50	1.63	1.50
51	AB	88	ALA	N-CA	5.48	1.53	1.46
51	AB	63	ARG	CB-CG	5.45	1.68	1.52
42	RA	109	ALA	CA-CB	-5.34	1.44	1.53
51	AB	90	ARG	C-O	5.30	1.30	1.24
39	OA	17	HIS	N-CA	5.10	1.52	1.45
51	AB	88	ALA	C-O	5.08	1.30	1.24

All (291) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	OA	32	GLY	N-CA-C	29.47	145.52	111.63
38	MA	342	GLU	CA-C-N	-16.08	101.59	119.28
38	MA	342	GLU	C-N-CA	-16.08	101.59	119.28
49	YA	22	ALA	N-CA-C	-12.41	97.25	111.03
39	OA	31	PHE	CA-C-N	-12.18	102.70	122.92
39	OA	31	PHE	C-N-CA	-12.18	102.70	122.92
12	L	119	PRO	N-CA-C	-11.29	89.22	112.47
2	B	1130	U	C2'-C3'-O3'	9.15	123.22	109.50
39	OA	16	GLY	CA-C-N	-8.97	108.00	122.36
39	OA	16	GLY	C-N-CA	-8.97	108.00	122.36
21	U	50	ARG	N-CA-C	-8.95	101.94	113.12
1	A	1297	G	C2'-C3'-O3'	8.73	122.60	109.50
43	SA	66	ALA	N-CA-C	8.66	115.78	108.07
49	YA	114	SER	N-CA-C	-8.62	101.83	111.14
31	EA	4	ASP	N-CA-C	8.49	123.11	111.90
42	RA	120	HIS	N-CA-C	-8.45	97.98	110.06
51	AB	62	ASN	N-CA-C	8.21	123.76	109.96
22	V	50	GLY	N-CA-C	-8.08	94.04	113.18
5	E	186	LYS	N-CA-C	-8.01	102.14	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	AB	55	SER	N-CA-C	-8.00	93.75	110.80
51	AB	92	GLU	N-CA-C	-7.99	102.98	112.89
2	B	669	G	N9-C1'-C2'	7.92	123.88	112.00
51	AB	79	LEU	CA-CB-CG	7.88	143.88	116.30
3	C	41	G	N9-C1'-C2'	7.83	123.74	112.00
43	SA	16	GLU	N-CA-C	-7.79	102.76	111.71
2	B	1020	A	C2'-C3'-O3'	7.76	121.14	109.50
41	QA	168	THR	N-CA-C	7.74	121.98	108.52
51	AB	5	MET	N-CA-C	-7.74	102.79	111.07
9	I	164	GLU	N-CA-C	-7.63	103.04	114.64
11	K	72	ILE	N-CA-C	-7.60	103.05	110.72
52	BB	52	ARG	N-CA-C	-7.58	103.09	111.36
42	RA	41	GLY	N-CA-C	-7.43	104.80	115.64
41	QA	190	LEU	N-CA-C	7.39	120.59	108.99
42	RA	116	VAL	N-CA-C	-7.20	105.58	113.43
48	XA	70	ALA	N-CA-C	-7.20	103.51	111.36
17	Q	60	GLN	N-CA-C	7.16	119.07	110.19
13	M	21	PRO	N-CA-C	7.15	119.43	110.70
46	VA	113	LYS	N-CA-C	7.14	121.10	112.38
49	YA	120	ARG	CA-C-N	-7.13	112.44	119.78
49	YA	120	ARG	C-N-CA	-7.13	112.44	119.78
18	R	14	SER	N-CA-C	-7.13	103.20	110.97
42	RA	122	VAL	N-CA-C	7.12	124.15	109.34
13	M	45	THR	N-CA-C	-7.08	103.17	111.03
2	B	12	U	N1-C1'-C2'	6.95	122.42	112.00
56	FB	5	LYS	N-CA-C	-6.90	102.91	112.30
58	HB	20	ARG	N-CA-C	-6.90	103.78	111.71
20	T	113	LEU	N-CA-C	6.89	121.00	111.90
39	OA	37	VAL	N-CA-C	-6.88	98.27	108.45
58	HB	41	THR	N-CA-C	-6.86	103.73	111.07
11	K	47	PHE	N-CA-C	6.84	118.82	111.36
12	L	118	ILE	N-CA-C	6.84	123.67	108.88
40	PA	17	TRP	CA-C-N	-6.81	108.69	122.31
40	PA	17	TRP	C-N-CA	-6.81	108.69	122.31
21	U	40	LYS	N-CA-C	-6.80	103.95	111.36
43	SA	18	VAL	N-CA-C	6.80	123.57	108.88
28	BA	72	ALA	N-CA-C	-6.79	103.95	111.36
31	EA	43	PHE	N-CA-C	-6.79	102.26	112.04
58	HB	10	PRO	N-CA-C	6.78	122.33	114.20
2	B	974	G	N9-C1'-C2'	6.71	124.07	114.00
47	WA	36	VAL	N-CA-C	-6.69	100.15	109.45
43	SA	53	LYS	N-CA-C	-6.68	96.58	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	YA	115	LYS	N-CA-C	-6.63	100.66	110.48
39	OA	94	ARG	N-CA-C	6.62	119.49	108.96
2	B	729	G	N9-C1'-C2'	6.60	121.90	112.00
42	RA	121	ASN	N-CA-C	6.58	124.81	110.80
45	UA	45	ILE	N-CA-C	6.58	116.48	108.06
1	A	1225	A	N9-C1'-C2'	6.57	121.86	112.00
29	CA	6	LEU	N-CA-C	-6.56	105.16	112.57
12	L	117	LEU	CA-C-N	6.56	134.26	122.13
12	L	117	LEU	C-N-CA	6.56	134.26	122.13
38	MA	307	ASN	N-CA-C	-6.54	106.51	114.75
29	CA	40	SER	N-CA-C	-6.51	107.20	114.62
53	CB	47	GLU	N-CA-C	-6.45	103.87	111.03
52	BB	43	ALA	N-CA-C	-6.45	105.99	114.31
8	H	73	ILE	N-CA-C	-6.43	106.86	113.10
12	L	5	LEU	N-CA-C	-6.43	104.19	111.14
5	E	84	ALA	N-CA-C	-6.43	105.40	113.18
47	WA	64	GLN	N-CA-C	6.42	119.41	109.07
57	GB	7	LYS	N-CA-C	-6.39	105.23	113.16
18	R	60	VAL	N-CA-C	-6.37	106.74	111.90
43	SA	83	ALA	N-CA-C	-6.36	104.72	113.18
42	RA	101	GLY	N-CA-C	-6.35	105.63	115.73
42	RA	134	ASN	N-CA-C	6.35	117.87	111.07
40	PA	204	GLY	N-CA-C	6.35	121.58	112.82
25	Y	53	GLN	N-CA-C	6.34	123.83	109.81
57	GB	6	ALA	N-CA-C	-6.34	105.83	112.93
39	OA	13	VAL	CB-CA-C	-6.30	103.79	112.04
51	AB	24	ALA	N-CA-C	-6.28	104.93	112.59
58	HB	9	GLU	N-CA-C	6.26	123.65	109.81
58	HB	17	ARG	N-CA-C	-6.25	104.23	113.61
7	G	151	THR	CA-C-N	-6.25	112.03	119.84
7	G	151	THR	C-N-CA	-6.25	112.03	119.84
11	K	48	GLU	N-CA-C	6.23	118.59	111.11
23	W	60	HIS	N-CA-C	-6.23	106.27	114.31
1	A	1182	G	C2'-C3'-O3'	-6.19	104.42	113.70
22	V	54	VAL	N-CA-C	6.18	122.19	109.34
20	T	44	GLY	N-CA-C	6.16	118.29	110.96
12	L	120	ALA	N-CA-C	-6.15	105.72	113.23
3	C	66	A	C2'-C3'-O3'	-6.12	104.51	113.70
13	M	14	ALA	N-CA-C	6.10	120.19	112.87
38	MA	292	SER	N-CA-C	-6.08	104.34	110.97
5	E	183	ASP	N-CA-C	-6.05	106.50	114.31
18	R	18	GLN	N-CA-C	-6.04	104.38	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	HA	6	GLN	CA-C-N	6.04	126.06	119.90
34	HA	6	GLN	C-N-CA	6.04	126.06	119.90
40	PA	17	TRP	N-CA-C	6.03	118.55	110.35
1	A	1301	U	N1-C1'-C2'	6.01	121.02	112.00
2	B	933	A	N9-C1'-C2'	6.00	121.01	112.00
6	F	30	ALA	N-CA-C	6.00	121.06	113.25
42	RA	123	LEU	N-CA-C	-6.00	100.71	110.20
50	ZA	85	TYR	N-CA-C	-6.00	104.82	111.36
51	AB	88	ALA	CA-C-O	6.00	126.76	119.38
2	B	2430	A	N9-C1'-C2'	5.96	120.95	112.00
19	S	28	VAL	N-CA-C	5.96	117.23	106.61
42	RA	117	ALA	N-CA-C	-5.96	104.90	111.82
40	PA	98	ALA	N-CA-C	5.92	118.04	107.80
42	RA	89	THR	N-CA-C	5.92	123.40	110.80
15	O	121	GLU	N-CA-C	5.89	119.42	109.76
51	AB	82	ILE	N-CA-C	-5.89	105.97	111.45
12	L	118	ILE	CA-C-N	5.87	127.17	119.84
12	L	118	ILE	C-N-CA	5.87	127.17	119.84
40	PA	75	VAL	N-CA-C	5.87	116.04	110.53
2	B	2296	U	N1-C1'-C2'	5.86	120.78	112.00
41	QA	176	LYS	N-CA-C	-5.85	105.46	113.30
18	R	22	ARG	N-CA-C	-5.85	104.59	110.97
38	MA	21	ALA	N-CA-C	5.84	117.45	111.14
49	YA	43	LYS	N-CA-C	5.83	122.69	109.81
49	YA	59	GLY	N-CA-C	5.83	123.69	115.30
2	B	1071	G	N9-C1'-C2'	5.81	120.72	112.00
46	VA	33	SER	N-CA-C	-5.81	102.70	110.55
29	CA	24	GLU	N-CA-C	5.80	123.16	110.80
13	M	104	GLN	N-CA-C	-5.80	104.87	111.14
38	MA	63	GLU	N-CA-C	5.80	117.60	111.28
6	F	239	PHE	N-CA-C	-5.79	100.89	109.86
13	M	131	THR	N-CA-C	-5.78	104.89	111.07
5	E	101	ALA	N-CA-C	5.77	117.44	111.03
58	HB	8	ASN	N-CA-C	5.77	123.09	110.80
49	YA	54	VAL	N-CA-C	5.76	116.88	108.58
52	BB	86	LEU	N-CA-C	5.76	115.62	108.19
12	L	123	ILE	N-CA-C	5.75	121.29	109.34
41	QA	191	SER	N-CA-C	5.72	122.98	110.80
2	B	1559	U	C2'-C3'-O3'	-5.72	105.12	113.70
55	EB	53	GLN	N-CA-C	-5.72	104.95	111.07
2	B	1343	G	N9-C1'-C2'	5.70	120.55	112.00
57	GB	84	LYS	N-CA-C	-5.67	105.17	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	439	U	N1-C1'-C2'	5.66	120.49	112.00
43	SA	15	SER	N-CA-C	-5.65	105.26	111.82
34	HA	7	PRO	N-CA-C	5.65	120.08	111.15
38	MA	77	MET	N-CA-C	-5.64	105.21	111.36
43	SA	68	GLN	N-CA-C	5.63	118.19	111.71
51	AB	77	PHE	CA-C-O	5.63	128.56	120.51
2	B	1669	A	N9-C1'-C2'	5.63	120.44	112.00
40	PA	141	MET	N-CA-C	5.63	117.09	111.07
5	E	132	GLY	N-CA-C	5.62	123.80	112.34
15	O	95	ILE	N-CA-C	5.62	120.30	113.00
52	BB	45	HIS	N-CA-C	5.61	117.87	111.02
11	K	31	VAL	CA-C-N	-5.61	113.90	119.56
11	K	31	VAL	C-N-CA	-5.61	113.90	119.56
7	G	5	VAL	N-CA-C	5.60	116.28	108.89
44	TA	64	ALA	N-CA-C	-5.59	98.89	110.80
25	Y	53	GLN	CA-C-N	-5.58	112.87	119.84
25	Y	53	GLN	C-N-CA	-5.58	112.87	119.84
51	AB	63	ARG	CA-CB-CG	5.58	125.26	114.10
13	M	117	THR	N-CA-C	5.55	118.65	109.94
51	AB	63	ARG	CA-C-O	-5.54	113.99	120.53
12	L	55	VAL	N-CA-C	5.54	115.63	107.15
16	P	89	VAL	N-CA-C	-5.54	100.34	108.54
1	A	69	G	C2'-C3'-O3'	5.53	122.00	113.70
2	B	1074	G	N9-C1'-C2'	5.53	120.30	112.00
5	E	185	LEU	N-CA-C	-5.52	106.05	112.89
6	F	185	ALA	N-CA-C	5.51	117.29	111.28
11	K	90	LEU	N-CA-C	5.49	117.62	110.43
26	Z	80	HIS	N-CA-C	-5.46	102.26	110.24
51	AB	86	GLU	CA-C-O	5.46	126.33	120.70
57	GB	68	LYS	N-CA-C	5.46	117.94	111.33
39	OA	83	ALA	N-CA-C	-5.46	106.30	113.12
41	QA	68	GLU	N-CA-C	5.45	117.92	111.33
23	W	63	GLY	N-CA-C	5.44	126.08	113.18
38	MA	159	TYR	N-CA-C	5.44	117.39	108.52
17	Q	24	THR	N-CA-C	5.43	118.37	111.69
49	YA	26	CYS	CA-C-N	5.43	126.63	119.84
49	YA	26	CYS	C-N-CA	5.43	126.63	119.84
55	EB	66	LEU	N-CA-C	-5.43	106.50	113.23
5	E	114	VAL	N-CA-C	5.42	116.29	108.48
53	CB	76	LYS	N-CA-C	-5.42	105.06	110.97
2	B	51	G	C2'-C3'-O3'	5.42	121.83	113.70
47	WA	34	ALA	N-CA-C	5.42	122.35	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	119	GLY	N-CA-C	5.40	125.98	113.18
38	MA	312	PHE	N-CA-C	5.40	119.59	112.35
52	BB	26	VAL	N-CA-C	5.40	116.03	110.36
41	QA	81	LEU	N-CA-C	5.40	118.31	107.41
39	OA	30	ILE	N-CA-C	5.39	116.35	108.53
51	AB	83	LYS	N-CA-C	-5.38	105.57	111.82
38	MA	265	LYS	N-CA-C	-5.38	105.50	111.36
10	J	44	HIS	N-CA-C	5.37	117.95	111.40
23	W	65	ASP	N-CA-C	5.36	122.22	110.80
39	OA	196	ASP	CA-C-N	-5.36	114.84	122.77
39	OA	196	ASP	C-N-CA	-5.36	114.84	122.77
48	XA	51	PHE	N-CA-C	5.34	119.72	107.48
51	AB	72	GLY	N-CA-C	5.34	125.84	113.18
24	X	50	LEU	N-CA-C	5.33	116.77	110.97
2	B	859	G	N9-C1'-C2'	5.32	119.98	112.00
43	SA	78	PHE	N-CA-C	-5.32	105.05	112.45
26	Z	40	ILE	N-CA-C	5.32	116.14	108.48
2	B	422	A	N9-C1'-C2'	5.31	119.97	112.00
38	MA	50	ARG	N-CA-C	-5.31	105.39	111.07
24	X	18	GLU	N-CA-C	-5.30	104.93	111.40
9	I	134	GLN	N-CA-C	-5.30	106.20	113.30
18	R	11	ASN	N-CA-C	5.30	118.74	111.54
6	F	83	ASP	CA-C-N	5.29	125.10	119.28
6	F	83	ASP	C-N-CA	5.29	125.10	119.28
22	V	58	VAL	N-CA-C	5.29	116.52	109.37
47	WA	35	GLN	N-CA-C	5.29	122.08	110.80
21	U	91	ARG	N-CA-C	5.29	117.79	111.71
43	SA	16	GLU	CA-C-N	-5.29	114.17	122.95
43	SA	16	GLU	C-N-CA	-5.29	114.17	122.95
11	K	27	ARG	N-CA-C	5.28	117.78	111.71
40	PA	89	VAL	N-CA-C	5.28	115.90	110.36
51	AB	81	ARG	CA-C-N	-5.28	113.84	121.65
51	AB	81	ARG	C-N-CA	-5.28	113.84	121.65
22	V	65	ALA	N-CA-C	5.27	116.29	108.60
42	RA	87	VAL	N-CA-C	5.27	116.20	109.30
29	CA	18	LEU	N-CA-C	-5.26	105.60	112.23
38	MA	19	VAL	N-CA-C	-5.26	105.41	110.72
57	GB	83	ASN	N-CA-C	-5.26	106.37	112.89
49	YA	117	GLY	N-CA-C	5.26	122.44	114.61
42	RA	136	VAL	N-CA-C	-5.25	105.41	110.72
6	F	241	LYS	N-CA-C	-5.25	103.47	110.55
58	HB	11	PHE	N-CA-C	5.25	117.42	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1540	U	N1-C1'-C2'	5.24	119.86	112.00
44	TA	44	SER	N-CA-C	-5.24	105.26	110.97
5	E	202	THR	N-CA-C	-5.23	106.90	113.28
36	JA	4	ARG	N-CA-C	5.23	116.23	108.86
13	M	110	GLN	N-CA-C	-5.22	105.48	111.07
41	QA	159	GLU	N-CA-C	-5.22	105.76	111.82
8	H	6	LYS	N-CA-C	5.22	116.97	111.28
14	N	83	GLY	CA-C-N	-5.22	116.85	122.59
14	N	83	GLY	C-N-CA	-5.22	116.85	122.59
13	M	54	ILE	CA-C-N	5.21	126.36	119.84
13	M	54	ILE	C-N-CA	5.21	126.36	119.84
2	B	858	G	N9-C1'-C2'	5.21	119.81	112.00
11	K	11	ASN	N-CA-C	5.21	119.11	111.04
51	AB	58	SER	O-C-N	5.19	127.20	121.85
25	Y	88	ASP	N-CA-C	5.19	121.86	110.80
2	B	892	A	N9-C1'-C2'	5.19	119.78	112.00
2	B	784	G	C2'-C3'-O3'	-5.18	105.93	113.70
49	YA	117	GLY	CA-C-N	-5.18	114.52	121.66
49	YA	117	GLY	C-N-CA	-5.18	114.52	121.66
11	K	39	ALA	N-CA-C	5.17	116.68	108.67
9	I	149	ARG	N-CA-C	5.16	116.72	108.41
8	H	82	GLY	N-CA-C	5.16	125.41	113.18
29	CA	2	LYS	N-CA-C	5.16	116.91	111.28
39	OA	31	PHE	N-CA-C	-5.16	102.48	109.54
2	B	858	G	C2'-C3'-O3'	-5.15	105.97	113.70
20	T	16	VAL	CA-C-N	-5.15	114.47	119.78
20	T	16	VAL	C-N-CA	-5.15	114.47	119.78
24	X	58	VAL	N-CA-C	5.14	115.98	108.53
1	A	1200	C	C2'-C3'-O3'	-5.13	106.00	113.70
9	I	10	GLU	N-CA-C	5.12	116.55	111.07
31	EA	3	LYS	N-CA-C	5.12	116.94	110.33
41	QA	82	LYS	N-CA-C	5.12	121.71	110.80
20	T	82	SER	N-CA-C	5.10	117.72	109.40
12	L	117	LEU	N-CA-C	5.10	116.91	110.33
54	DB	14	ASP	N-CA-C	5.09	119.11	112.13
26	Z	44	HIS	N-CA-C	5.09	116.68	111.03
27	AA	22	PHE	N-CA-C	5.08	116.50	110.19
50	ZA	8	ILE	CA-C-N	-5.08	114.56	119.90
50	ZA	8	ILE	C-N-CA	-5.08	114.56	119.90
14	N	112	GLY	CA-C-N	5.08	124.52	119.24
14	N	112	GLY	C-N-CA	5.08	124.52	119.24
45	UA	62	LEU	N-CA-C	5.08	116.89	110.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	XA	125	LYS	N-CA-C	5.07	121.61	110.80
18	R	104	ALA	N-CA-C	5.07	117.54	111.71
51	AB	59	ARG	N-CA-C	-5.07	107.60	112.97
6	F	233	GLY	N-CA-C	-5.06	103.69	111.24
9	I	96	TRP	N-CA-C	-5.06	105.42	112.45
1	A	983	A	N9-C1'-C2'	5.05	119.58	112.00
30	DA	54	VAL	N-CA-C	5.05	116.48	109.45
19	S	116	GLN	N-CA-C	5.05	117.02	109.59
6	F	183	VAL	N-CA-C	5.05	117.03	109.20
18	R	16	HIS	N-CA-C	5.04	116.47	110.97
12	L	102	ALA	N-CA-C	-5.03	106.40	112.54
43	SA	99	ALA	N-CA-C	5.03	121.52	110.80
22	V	73	LYS	N-CA-C	5.03	116.51	108.41
51	AB	90	ARG	N-CA-C	-5.03	100.08	110.80
13	M	18	ASN	CA-C-N	5.03	126.13	119.84
13	M	18	ASN	C-N-CA	5.03	126.13	119.84
38	MA	7	ALA	N-CA-C	-5.03	105.99	111.82
57	GB	8	LYS	N-CA-C	-5.03	105.99	111.82
12	L	127	ALA	N-CA-C	-5.02	106.58	113.30
38	MA	160	LYS	N-CA-C	-5.00	105.49	112.45

There are no chirality outliers.

All (45) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1167	A	Sidechain
1	A	1182	G	Sidechain
1	A	1316	G	Sidechain
1	A	159	G	Sidechain
1	A	350	G	Sidechain
1	A	416	G	Sidechain
1	A	532	A	Sidechain
1	A	563	A	Sidechain
1	A	898	G	Sidechain
1	A	938	A	Sidechain
2	B	1063	G	Sidechain
2	B	1154	G	Sidechain
2	B	1171	G	Sidechain
2	B	1215	G	Sidechain
2	B	1241	A	Sidechain
2	B	1328	A	Sidechain
2	B	1377	G	Sidechain

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Mol	Chain	Res	Type	Group
2	B	1666	G	Sidechain
2	B	1817	G	Sidechain
2	B	1828	G	Sidechain
2	B	1857	G	Sidechain
2	B	1937	A	Sidechain
2	B	196	A	Sidechain
2	B	1985	C	Sidechain
2	B	1993	U	Sidechain
2	B	201	C	Sidechain
2	B	2061	G	Sidechain
2	B	221	A	Sidechain
2	B	222	A	Sidechain
2	B	2266	A	Sidechain
2	B	2273	A	Sidechain
2	B	2447	G	Sidechain
2	B	2475	C	Sidechain
2	B	2532	G	Sidechain
2	B	26	G	Sidechain
2	B	2604	U	Sidechain
2	B	2662	A	Sidechain
2	B	370	G	Sidechain
2	B	481	G	Sidechain
2	B	500	G	Sidechain
2	B	506	G	Sidechain
2	B	512	G	Sidechain
2	B	75	G	Sidechain
3	C	1	U	Sidechain
4	D	71	C	Sidechain

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	A	33012	0	16618	277	0
2	B	62318	0	31346	529	0
3	C	2568	0	1303	25	0
4	D	1640	0	837	28	0
4	LA	1640	0	837	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1637	0	1719	40	0
6	F	2082	0	2157	36	0
7	G	1565	0	1616	33	0
8	H	1552	0	1619	28	0
9	I	1410	0	1447	26	0
10	J	1323	0	1374	22	0
11	K	1111	0	1148	25	0
12	L	988	0	1025	41	0
13	M	1032	0	1088	33	0
14	N	1129	0	1162	17	0
15	O	938	0	1012	16	0
16	P	1045	0	1117	16	0
17	Q	1074	0	1157	12	0
18	R	960	0	1000	27	0
19	S	892	0	923	16	0
20	T	917	0	965	16	0
21	U	947	0	1022	21	0
22	V	816	0	839	18	0
23	W	857	0	922	13	0
24	X	738	0	807	5	0
25	Y	779	0	834	8	0
26	Z	753	0	780	9	0
27	AA	575	0	592	8	0
28	BA	625	0	655	3	0
29	CA	509	0	543	5	0
30	DA	449	0	491	7	0
31	EA	522	0	524	9	0
32	FA	444	0	461	8	0
33	GA	409	0	440	1	0
34	HA	377	0	418	8	0
35	IA	504	0	574	11	0
36	JA	302	0	343	10	0
37	KA	412	0	207	7	0
38	MA	2714	0	2636	63	0
39	OA	1756	0	1787	27	0
40	PA	1624	0	1699	37	0
41	QA	1643	0	1710	35	0
42	RA	1156	0	1199	25	0
43	SA	817	0	808	23	0
44	TA	1181	0	1240	4	0
45	UA	979	0	1034	14	0
46	VA	1022	0	1070	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	WA	786	0	828	25	0
48	XA	869	0	878	16	0
49	YA	955	0	1019	30	0
50	ZA	883	0	944	20	0
51	AB	810	0	852	59	0
52	BB	714	0	737	7	0
53	CB	649	0	666	18	0
54	DB	648	0	691	14	0
55	EB	535	0	552	7	0
56	FB	637	0	665	16	0
57	GB	665	0	714	6	0
58	HB	544	0	579	18	0
All	All	152438	0	104230	1709	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 7.

All (1709) 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)
38:MA:77:MET:CE	38:MA:77:MET:SD	2.04	1.45
39:OA:32:GLY:O	39:OA:38:HIS:HA	1.51	1.08
39:OA:33:ALA:HA	39:OA:37:VAL:O	1.52	1.08
12:L:119:PRO:CD	12:L:120:ALA:H	1.63	1.03
51:AB:73:PHE:HA	51:AB:78:GLY:HA2	1.07	1.03
51:AB:79:LEU:O	51:AB:80:SER:O	1.76	1.01
51:AB:73:PHE:CA	51:AB:78:GLY:HA2	1.90	1.01
12:L:24:SER:O	12:L:116:GLU:HB2	1.64	0.98
39:OA:31:PHE:O	39:OA:39:ILE:HB	1.63	0.98
51:AB:55:SER:O	51:AB:56:SER:C	2.06	0.97
40:PA:4:VAL:HG13	40:PA:5:HIS:H	1.33	0.91
12:L:119:PRO:HD2	12:L:120:ALA:H	1.34	0.89
51:AB:73:PHE:HA	51:AB:78:GLY:CA	2.00	0.88
47:WA:57:VAL:HG22	47:WA:58:ASN:H	1.38	0.88
39:OA:13:VAL:O	39:OA:14:HIS:O	1.91	0.87
12:L:119:PRO:HG2	12:L:121:SER:H	1.39	0.87
4:D:71:C:H2'	4:D:72:A:C8	2.09	0.86
51:AB:56:SER:O	51:AB:58:SER:N	2.08	0.86
1:A:1399:C:H4'	1:A:1400:C:H5'	1.58	0.86
29:CA:19:LEU:O	29:CA:23:ARG:HB2	1.76	0.85
12:L:119:PRO:CD	12:L:120:ALA:N	2.38	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:1:ALA:O	9:I:3:LEU:N	2.08	0.85
51:AB:80:SER:O	51:AB:82:ILE:N	2.08	0.85
43:SA:3:HIS:H	43:SA:92:THR:HG22	1.42	0.85
13:M:11:GLN:O	13:M:54:ILE:O	1.95	0.85
1:A:376:G:H5''	53:CB:5:ARG:HB2	1.59	0.84
39:OA:14:HIS:CG	39:OA:15:PHE:H	1.93	0.84
2:B:962:G:H21	2:B:2250:G:H22	1.24	0.84
2:B:1668:A:H4'	2:B:1669:A:H5'	1.59	0.83
4:LA:75:C:OP2	38:MA:261:ARG:NH2	2.12	0.82
51:AB:79:LEU:O	51:AB:80:SER:C	2.23	0.81
38:MA:16:HIS:O	38:MA:19:VAL:HG12	1.80	0.81
1:A:484:G:H4'	1:A:485:U:H5'	1.61	0.81
9:I:142:TYR:O	9:I:145:VAL:HG22	1.79	0.80
47:WA:64:GLN:O	51:AB:98:LYS:HA	1.82	0.79
18:R:87:PHE:O	18:R:89:SER:N	2.15	0.78
51:AB:87:ALA:O	51:AB:91:GLY:N	2.18	0.77
39:OA:30:ILE:HG22	39:OA:32:GLY:H	1.48	0.77
2:B:1019:U:H3	2:B:1142:A:H62	1.33	0.77
55:EB:11:ARG:HG3	55:EB:14:ALA:HB3	1.67	0.77
41:QA:33:ILE:HG13	41:QA:34:GLU:H	1.49	0.77
13:M:101:SER:HA	13:M:140:GLU:O	1.85	0.76
1:A:1026:G:H22	1:A:1035:A:H2	1.32	0.76
13:M:54:ILE:HG23	13:M:55:PRO:HD2	1.68	0.76
12:L:118:ILE:N	12:L:119:PRO:CD	2.49	0.76
13:M:54:ILE:CG2	13:M:55:PRO:HD2	2.17	0.75
2:B:1912:A:H62	2:B:1917:U:H5	1.34	0.75
2:B:1521:G:H3'	2:B:1522:A:H5''	1.68	0.74
38:MA:339:MET:O	38:MA:343:PRO:HD3	1.87	0.74
51:AB:77:PHE:HB3	51:AB:79:LEU:HD23	1.70	0.74
51:AB:78:GLY:O	51:AB:80:SER:N	2.21	0.73
44:TA:55:LYS:HB3	44:TA:59:GLU:HG3	1.70	0.73
1:A:537:G:H5''	49:YA:109:ARG:HH12	1.53	0.73
48:XA:87:GLY:H	48:XA:113:THR:HG22	1.54	0.73
7:G:142:VAL:HG22	7:G:143:PRO:HD2	1.70	0.73
51:AB:79:LEU:HB2	51:AB:83:LYS:HB2	1.69	0.73
1:A:413:G:H1'	1:A:428:G:H22	1.53	0.72
12:L:118:ILE:O	12:L:118:ILE:HG22	1.86	0.72
43:SA:11:HIS:HD2	43:SA:12:PRO:HD2	1.53	0.72
11:K:63:ALA:HA	11:K:66:ASN:HD22	1.55	0.72
40:PA:8:GLY:HA3	51:AB:89:MET:HE3	1.71	0.72
49:YA:22:ALA:O	49:YA:23:LEU:HB2	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:38:C:H42	3:C:44:G:H1	1.38	0.71
49:YA:33:CYS:H	49:YA:54:VAL:HG13	1.55	0.71
1:A:3:A:H5''	1:A:4:U:H5'	1.73	0.71
38:MA:214:LEU:HG	38:MA:216:ASP:H	1.56	0.70
2:B:807:U:H2'	2:B:808:G:H8	1.57	0.70
53:CB:79:ASN:HB2	53:CB:82:ALA:HB3	1.71	0.70
15:O:21:CYS:HA	15:O:41:ILE:HG22	1.73	0.70
43:SA:38:ARG:HD3	43:SA:97:THR:HA	1.74	0.70
2:B:955:U:H5	2:B:962:G:H1	1.39	0.69
41:QA:36:ALA:H	41:QA:37:PRO:HD3	1.57	0.69
9:I:92:GLY:O	9:I:95:MET:HG2	1.92	0.69
49:YA:54:VAL:HG21	49:YA:79:ILE:HD11	1.74	0.69
8:H:45:ALA:HB2	8:H:89:PRO:HD3	1.74	0.69
38:MA:183:ARG:HE	38:MA:306:ARG:HD3	1.56	0.69
39:OA:30:ILE:HG22	39:OA:32:GLY:N	2.08	0.69
2:B:2478:A:H5'	36:JA:32:LYS:HD2	1.74	0.69
46:VA:83:THR:HG21	46:VA:102:PHE:HB3	1.74	0.68
2:B:1278:C:H2'	2:B:1279:G:H8	1.58	0.68
2:B:2443:C:H2'	2:B:2444:G:H8	1.59	0.68
51:AB:8:ARG:HB3	51:AB:12:ARG:HH12	1.58	0.68
13:M:20:SER:HB3	13:M:21:PRO:HD3	1.76	0.68
51:AB:93:ILE:HB	51:AB:96:LEU:HD21	1.76	0.68
2:B:953:G:H2'	2:B:954:G:H8	1.57	0.68
2:B:1064:C:O2'	2:B:1065:U:H5'	1.93	0.67
41:QA:36:ALA:N	41:QA:37:PRO:HD3	2.09	0.67
38:MA:217:ILE:HD12	38:MA:218:ASN:H	1.60	0.67
7:G:179:ARG:HB2	7:G:188:LEU:HD12	1.77	0.67
51:AB:79:LEU:HD12	51:AB:83:LYS:HB3	1.77	0.66
58:HB:40:PRO:HA	58:HB:43:GLU:HG2	1.77	0.66
1:A:367:U:C4	1:A:393:A:N1	2.63	0.66
2:B:1796:U:H2'	2:B:1797:G:H8	1.59	0.66
57:GB:65:LEU:HD13	57:GB:66:ILE:HG12	1.77	0.66
12:L:118:ILE:N	12:L:119:PRO:HD2	2.10	0.66
18:R:37:THR:HG22	18:R:39:PRO:HD2	1.78	0.66
49:YA:49:ARG:HG3	49:YA:89:LEU:HD21	1.78	0.66
40:PA:65:VAL:HB	40:PA:100:ILE:HG22	1.77	0.66
49:YA:113:ARG:HH12	49:YA:120:ARG:HA	1.60	0.66
2:B:833:A:H2'	2:B:834:G:H8	1.60	0.66
38:MA:145:ARG:HG2	38:MA:146:VAL:H	1.61	0.66
17:Q:4:PRO:HG3	17:Q:68:PHE:HE2	1.60	0.65
10:J:87:GLN:HE21	10:J:162:ARG:HD2	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:XA:23:HIS:HB3	48:XA:30:ILE:HG23	1.78	0.65
2:B:1934:C:H2'	2:B:1935:G:H8	1.60	0.65
1:A:1540:U:O4	37:KA:5:A:H2	1.80	0.64
39:OA:17:HIS:HB2	39:OA:188:THR:OG1	1.97	0.64
47:WA:6:ILE:HG22	47:WA:102:LEU:HG	1.79	0.64
23:W:82:MET:HB2	23:W:98:LYS:HB2	1.79	0.64
56:FB:62:THR:H	56:FB:65:MET:HE3	1.62	0.64
8:H:126:VAL:HG23	8:H:133:LEU:HD22	1.80	0.64
47:WA:22:THR:HG21	47:WA:39:PRO:HB3	1.80	0.64
2:B:1636:U:H2'	2:B:1637:A:H8	1.63	0.64
6:F:135:PRO:HG2	43:SA:80:PHE:HD1	1.63	0.64
1:A:413:G:H1'	1:A:428:G:N2	2.13	0.63
1:A:617:G:H4'	53:CB:46:LYS:HE3	1.80	0.63
2:B:1265:A:H61	2:B:2013:A:H5''	1.62	0.63
15:O:38:ILE:HD11	15:O:112:PHE:HZ	1.63	0.63
34:HA:18:PHE:HA	34:HA:43:THR:HG21	1.78	0.63
1:A:76:G:H1	1:A:93:U:H3	1.46	0.63
42:RA:108:GLY:O	42:RA:109:ALA:HB3	1.96	0.63
10:J:23:ILE:HD13	10:J:36:LEU:HD13	1.80	0.63
40:PA:174:LEU:HD23	40:PA:181:ILE:HD13	1.80	0.63
2:B:764:A:O2'	2:B:765:C:H5'	1.99	0.63
2:B:270:A:H5'	2:B:271:G:H5''	1.79	0.63
2:B:1316:U:H2'	2:B:1317:G:H8	1.63	0.63
11:K:83:LYS:HA	11:K:149:GLU:HB2	1.81	0.63
15:O:64:ARG:HB2	15:O:83:ALA:HB3	1.81	0.63
46:VA:89:TYR:HB2	46:VA:93:LEU:HG	1.80	0.63
4:D:17:C:H2'	4:D:17(A):U:H5	1.63	0.63
1:A:403:C:OP2	41:QA:70:GLN:NE2	2.32	0.63
2:B:586:A:H5'	8:H:84:THR:HG21	1.81	0.62
16:P:48:ARG:NH2	35:IA:4:LYS:O	2.32	0.62
2:B:910:A:H62	17:Q:12:MET:HA	1.63	0.62
2:B:581:C:H2'	2:B:582:A:C8	2.34	0.62
54:DB:46:HIS:HB2	54:DB:70:LYS:HE2	1.82	0.62
20:T:59:THR:HG22	20:T:72:VAL:HG12	1.80	0.62
47:WA:92:LEU:H	47:WA:92:LEU:HD12	1.64	0.62
49:YA:113:ARG:HB3	49:YA:118:VAL:O	1.99	0.62
51:AB:86:GLU:O	51:AB:87:ALA:C	2.43	0.62
2:B:962:G:N2	2:B:2250:G:H22	1.96	0.62
50:ZA:15:VAL:HG23	50:ZA:16:ILE:HD12	1.81	0.62
1:A:454:G:H22	1:A:478:A:H2	1.47	0.62
5:E:23:ILE:HG23	5:E:189:LEU:HD22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:AA:36:GLN:HE21	27:AA:38:GLY:H	1.47	0.62
1:A:231:U:H2'	1:A:232:G:H8	1.64	0.62
13:M:7:TYR:HE1	13:M:57:VAL:HG13	1.65	0.62
30:DA:40:THR:HG22	30:DA:42:ALA:H	1.65	0.62
46:VA:118:ARG:HB3	46:VA:122:ARG:HB3	1.82	0.61
50:ZA:3:ILE:HD11	50:ZA:21:ILE:HD11	1.82	0.61
1:A:1386:G:H2'	1:A:1387:G:H8	1.65	0.61
2:B:1070:A:OP2	2:B:1072:C:H5''	2.00	0.61
2:B:1744:A:H3'	2:B:1745:A:H8	1.65	0.61
2:B:2246:G:H2'	2:B:2247:A:C8	2.35	0.61
56:FB:50:VAL:HG21	56:FB:70:LEU:HB3	1.82	0.61
1:A:913:A:OP2	49:YA:87:LYS:NZ	2.33	0.61
38:MA:304:SER:HB2	49:YA:48:LEU:HD11	1.83	0.61
2:B:1652:A:H62	18:R:11:ASN:HD21	1.47	0.61
1:A:1279:G:N7	47:WA:45:ARG:NH2	2.48	0.61
2:B:242:G:N2	2:B:255:A:OP2	2.33	0.61
1:A:1005:A:H3'	1:A:1006:G:H8	1.64	0.61
2:B:962:G:H21	2:B:2250:G:N2	1.98	0.61
6:F:267:VAL:HG12	6:F:268:ARG:HG2	1.83	0.61
7:G:4:LEU:HD21	7:G:29:VAL:HG11	1.82	0.61
2:B:2121:G:H21	5:E:170:ILE:HD13	1.64	0.61
2:B:2267:A:H5''	2:B:2268:A:H5'	1.82	0.61
7:G:4:LEU:HG	7:G:32:ASN:HD22	1.66	0.61
20:T:1:SER:O	20:T:4:ILE:HG22	1.99	0.61
46:VA:56:MET:HA	46:VA:59:LYS:HE2	1.84	0.60
5:E:137:MET:HE3	5:E:139:ASN:HD21	1.65	0.60
10:J:118:ALA:O	10:J:120:ILE:N	2.34	0.60
39:OA:202:ASN:OD1	39:OA:203:ASP:N	2.33	0.60
36:JA:4:ARG:O	36:JA:37:GLN:O	2.19	0.60
38:MA:339:MET:O	38:MA:343:PRO:CD	2.49	0.60
2:B:807:U:H2'	2:B:808:G:C8	2.36	0.60
2:B:1386:C:H2'	2:B:1387:A:H8	1.67	0.60
2:B:2246:G:H2'	2:B:2247:A:H8	1.66	0.60
1:A:1429:A:H2'	1:A:1430:A:H8	1.67	0.60
39:OA:13:VAL:O	39:OA:14:HIS:C	2.44	0.60
39:OA:96:LEU:O	39:OA:99:MET:HG3	2.00	0.60
2:B:2743:U:OP2	2:B:2755:C:N4	2.35	0.60
1:A:1218:C:H2'	1:A:1219:A:C8	2.37	0.60
42:RA:160:VAL:O	42:RA:163:ILE:HG13	2.02	0.60
2:B:1368:G:H2'	2:B:1369:G:H8	1.66	0.59
4:D:35:A:H2'	4:D:36:U:C6	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:16:VAL:HB	6:F:203:VAL:HG22	1.84	0.59
38:MA:144:TRP:O	38:MA:145:ARG:HB2	2.02	0.59
45:UA:95:MET:SD	45:UA:129:ALA:HB1	2.42	0.59
1:A:818:G:H2'	1:A:820:U:H5	1.66	0.59
2:B:2709:G:H5'	18:R:22:ARG:HH22	1.67	0.59
15:O:114:LYS:HE3	15:O:118:LEU:HD11	1.85	0.59
43:SA:12:PRO:O	43:SA:15:SER:HB3	2.02	0.59
1:A:151:A:H62	1:A:170:U:H3	1.51	0.59
1:A:501:C:OP1	49:YA:113:ARG:NH2	2.36	0.59
1:A:540:G:H3'	1:A:541:G:H8	1.67	0.59
1:A:690:G:OP2	48:XA:28:ASN:ND2	2.33	0.59
2:B:309:A:N3	2:B:329:G:O2'	2.35	0.59
12:L:17:GLU:O	12:L:88:HIS:NE2	2.33	0.59
18:R:87:PHE:C	18:R:89:SER:H	2.10	0.59
51:AB:55:SER:O	51:AB:57:PRO:N	2.35	0.59
2:B:2500:U:O2'	2:B:2504:U:OP1	2.21	0.59
1:A:257:G:H2'	1:A:258:G:H8	1.68	0.59
1:A:880:C:H2'	1:A:881:G:H8	1.68	0.59
2:B:2673:G:H2'	2:B:2674:G:H8	1.68	0.59
40:PA:147:GLY:HA3	40:PA:171:ARG:O	2.03	0.58
2:B:1173:U:H2'	2:B:1174:U:H4'	1.85	0.58
1:A:1305:G:HO2'	1:A:1306:A:H8	1.51	0.58
2:B:2396:G:H2'	2:B:2397:G:H8	1.68	0.58
16:P:80:SER:HB3	16:P:114:GLY:HA3	1.84	0.58
43:SA:3:HIS:HB2	43:SA:92:THR:HA	1.86	0.58
56:FB:77:ARG:H	56:FB:77:ARG:HD2	1.69	0.58
4:D:1:C:H42	4:D:73:A:H61	1.49	0.58
30:DA:6:ILE:HD13	30:DA:47:ILE:HD11	1.85	0.58
2:B:2130:U:H1'	2:B:2159:G:H22	1.68	0.58
23:W:2:GLU:O	23:W:3:THR:O	2.22	0.58
37:KA:8:A:H2'	37:KA:9:G:H8	1.69	0.58
2:B:306:U:H3	2:B:310:A:H62	1.52	0.58
5:E:185:LEU:HA	5:E:188:ASN:HB2	1.86	0.58
4:D:70:G:O2'	4:D:71:C:H5'	2.04	0.58
22:V:76:LYS:HB2	22:V:85:LYS:HB3	1.86	0.58
13:M:18:ASN:ND2	13:M:38:CYS:SG	2.76	0.57
19:S:33:ARG:O	19:S:34:HIS:CB	2.52	0.57
49:YA:22:ALA:O	49:YA:23:LEU:CB	2.51	0.57
2:B:1159:U:H2'	2:B:1160:G:H8	1.69	0.57
2:B:1664:A:H61	2:B:1996:C:H42	1.52	0.57
2:B:2642:G:H5'	14:N:80:HIS:CD2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:4:PRO:HG3	17:Q:68:PHE:CE2	2.38	0.57
6:F:77:VAL:HG21	6:F:109:LEU:HD11	1.87	0.57
45:UA:45:ILE:HD11	45:UA:60:LEU:HB3	1.86	0.57
1:A:1492:A:H2	37:KA:21:U:H5''	1.68	0.57
2:B:465:G:H21	2:B:684:G:H1'	1.68	0.57
2:B:1252:G:H22	21:U:36:GLN:NE2	2.02	0.57
12:L:60:LEU:HD12	12:L:64:VAL:HG21	1.85	0.57
2:B:12:U:O2	2:B:12:U:H2'	2.05	0.57
46:VA:27:ILE:HG12	46:VA:62:LEU:HD12	1.87	0.57
41:QA:33:ILE:HG13	41:QA:34:GLU:N	2.20	0.57
1:A:674:G:H2'	1:A:675:A:H8	1.69	0.57
14:N:81:ILE:HG23	14:N:82:GLY:H	1.69	0.57
39:OA:40:ILE:HD13	39:OA:201:GLY:N	2.18	0.57
51:AB:81:ARG:HA	51:AB:84:VAL:HB	1.87	0.57
56:FB:30:LEU:HB2	56:FB:48:ILE:HG22	1.87	0.57
58:HB:6:ARG:O	58:HB:7:GLU:C	2.48	0.57
58:HB:9:GLU:HB3	58:HB:10:PRO:HD3	1.85	0.57
2:B:2443:C:H2'	2:B:2444:G:C8	2.38	0.57
43:SA:92:THR:OG1	43:SA:93:LYS:N	2.33	0.57
1:A:18:C:H1'	1:A:1079:G:H21	1.69	0.57
6:F:94:LEU:HD12	6:F:100:ARG:HE	1.70	0.57
1:A:64:G:OP1	1:A:382:A:N6	2.38	0.57
2:B:468:G:OP2	34:HA:37:LYS:NZ	2.37	0.57
4:D:36:U:H2'	4:D:37:A:O4'	2.05	0.57
17:Q:4:PRO:HG2	17:Q:70:ASP:HA	1.86	0.57
38:MA:174:ARG:NH2	38:MA:338:ASP:OD1	2.38	0.57
42:RA:80:LEU:HD13	42:RA:122:VAL:HG11	1.86	0.57
44:TA:11:ILE:HD11	44:TA:20:GLU:HB3	1.87	0.57
6:F:28:PRO:HG3	6:F:62:ARG:HH21	1.70	0.56
7:G:116:LYS:HG3	7:G:165:MET:HE3	1.87	0.56
47:WA:49:PHE:HZ	51:AB:76:LYS:HD3	1.69	0.56
2:B:1651:G:H4'	18:R:39:PRO:HG2	1.87	0.56
13:M:12:VAL:O	13:M:53:PRO:HA	2.05	0.56
19:S:33:ARG:O	19:S:34:HIS:HB2	2.05	0.56
36:JA:36:ARG:HG2	36:JA:37:GLN:H	1.70	0.56
1:A:69:G:H4'	1:A:70:U:OP1	2.05	0.56
2:B:1013:C:H2'	2:B:1014:A:H8	1.70	0.56
2:B:1390:U:H3	2:B:1395:A:H62	1.52	0.56
2:B:1447:C:H2'	2:B:1448:G:H8	1.70	0.56
34:HA:24:THR:HG23	34:HA:27:GLY:H	1.69	0.56
42:RA:114:LEU:HD12	42:RA:119:VAL:HG21	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:YA:85:ARG:HA	49:YA:93:ARG:HA	1.87	0.56
1:A:112:G:H21	1:A:354:G:H5'	1.69	0.56
53:CB:44:SER:H	53:CB:46:LYS:NZ	2.04	0.56
2:B:680:C:H2'	2:B:681:G:H8	1.70	0.56
2:B:1165:A:H2'	2:B:1166:G:H8	1.69	0.56
2:B:2688:G:N1	2:B:2720:U:OP2	2.37	0.56
5:E:7:ARG:HH22	5:E:218:MET:HB3	1.70	0.56
43:SA:42:TRP:HB2	43:SA:59:TYR:HB2	1.86	0.56
45:UA:63:LYS:O	45:UA:70:VAL:HG23	2.04	0.56
2:B:376:G:H2'	2:B:377:G:H8	1.70	0.56
2:B:2508:G:H2'	2:B:2509:G:H8	1.71	0.56
4:D:51:C:H2'	4:D:52:G:C8	2.41	0.56
7:G:142:VAL:CG2	7:G:143:PRO:HD2	2.36	0.56
27:AA:33:ILE:HG22	27:AA:34:VAL:HG23	1.88	0.56
51:AB:55:SER:O	51:AB:56:SER:O	2.22	0.56
2:B:1997:C:H2'	2:B:1998:A:H8	1.71	0.56
10:J:85:LYS:HG3	10:J:131:VAL:HG22	1.88	0.56
18:R:47:VAL:O	18:R:50:PRO:HD2	2.05	0.56
2:B:162:U:O2'	2:B:163:C:H5'	2.06	0.56
2:B:591:U:H1'	35:IA:1:PRO:HD2	1.88	0.56
2:B:1086:A:H1'	2:B:1103:A:H61	1.71	0.56
2:B:2233:U:H2'	2:B:2234:G:H8	1.71	0.56
2:B:2470:G:H2'	2:B:2471:A:H8	1.69	0.56
5:E:88:LYS:HA	5:E:92:ALA:HB3	1.87	0.56
32:FA:52:LYS:HE3	32:FA:55:ALA:HA	1.88	0.56
2:B:1278:C:H2'	2:B:1279:G:C8	2.41	0.56
2:B:1386:C:H2'	2:B:1387:A:C8	2.41	0.56
2:B:2747:G:H21	2:B:2757:A:H62	1.52	0.56
10:J:44:HIS:HA	10:J:49:LEU:HD23	1.87	0.56
38:MA:306:ARG:HE	38:MA:320:HIS:CE1	2.23	0.56
58:HB:13:VAL:HB	58:HB:15:LEU:HG	1.88	0.56
1:A:1352:C:H2'	1:A:1353:G:C8	2.41	0.56
2:B:743:A:O2'	2:B:1659:G:OP1	2.24	0.56
2:B:996:A:H2'	2:B:997:G:H8	1.70	0.56
8:H:79:ARG:HG2	8:H:80:SER:N	2.20	0.56
11:K:132:PHE:HB2	11:K:140:ALA:HB3	1.87	0.56
46:VA:51:LEU:HB3	46:VA:56:MET:HG2	1.88	0.56
58:HB:16:ARG:HH21	58:HB:19:LYS:HG2	1.71	0.56
2:B:1072:C:H42	2:B:1092:C:H41	1.53	0.55
2:B:2131:U:H5'	2:B:2132:U:H5''	1.89	0.55
42:RA:131:ASN:HD22	42:RA:132:PRO:HD2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:74:ARG:HG3	5:E:93:GLU:HG2	1.88	0.55
31:EA:28:VAL:HG11	31:EA:32:LEU:HD13	1.88	0.55
40:PA:13:ILE:HG22	40:PA:14:VAL:HG23	1.88	0.55
45:UA:9:MET:HG3	45:UA:26:MET:HE2	1.89	0.55
1:A:416:G:H22	1:A:427:U:H1'	1.71	0.55
1:A:1414:U:H2'	1:A:1415:G:H8	1.72	0.55
2:B:592:A:O2'	35:IA:63:TYR:OH	2.23	0.55
17:Q:69:PRO:HA	17:Q:94:ALA:HB2	1.88	0.55
38:MA:312:PHE:HD1	38:MA:329:LEU:HD21	1.71	0.55
2:B:1464:G:H2'	2:B:1465:G:H8	1.72	0.55
14:N:35:ARG:HB2	14:N:54:ILE:HD11	1.89	0.55
48:XA:71:ASP:O	48:XA:72:ALA:HB3	2.06	0.55
5:E:74:ARG:HD3	5:E:111:PHE:HA	1.88	0.55
40:PA:123:LEU:HD21	40:PA:129:PHE:HB3	1.88	0.55
43:SA:38:ARG:HB2	43:SA:63:ASN:HB2	1.88	0.55
1:A:246:A:H4'	1:A:247:G:OP1	2.05	0.55
1:A:692:U:H5''	48:XA:126:ARG:HH22	1.72	0.55
1:A:843:U:H5'	1:A:844:G:C8	2.42	0.55
4:LA:48:C:H2'	4:LA:59:A:H4'	1.88	0.55
1:A:235:C:H2'	1:A:236:A:C8	2.42	0.55
1:A:1506:U:O2'	1:A:1507:A:H5'	2.06	0.55
2:B:2305:U:H5''	9:I:130:GLY:HA3	1.89	0.55
2:B:2506:U:N3	2:B:2585:U:O4	2.33	0.55
2:B:2723:C:OP1	7:G:114:LYS:HD3	2.07	0.55
2:B:2882:A:H5'	18:R:96:ARG:HG3	1.89	0.55
48:XA:22:ILE:HG21	48:XA:95:THR:HG21	1.88	0.55
2:B:2818:U:H2'	2:B:2819:G:H8	1.72	0.55
4:D:62:C:O2'	5:E:54:LYS:HG2	2.07	0.55
46:VA:56:MET:C	46:VA:56:MET:SD	2.90	0.55
2:B:1447:C:H2'	2:B:1448:G:C8	2.42	0.54
9:I:33:ILE:HG12	9:I:95:MET:HE3	1.88	0.54
9:I:35:LEU:HB3	9:I:88:VAL:HB	1.89	0.54
4:LA:28:C:H2'	4:LA:29:G:H8	1.72	0.54
46:VA:10:ARG:O	46:VA:105:ARG:NH2	2.40	0.54
47:WA:65:TYR:HB3	51:AB:96:LEU:HD12	1.89	0.54
1:A:1129:C:H4'	46:VA:17:ARG:HH12	1.72	0.54
2:B:1188:U:H2'	2:B:1189:A:H8	1.71	0.54
2:B:2122:U:H2'	5:E:172:HIS:HE1	1.72	0.54
12:L:77:VAL:HG13	12:L:82:ILE:HD12	1.89	0.54
13:M:132:ALA:HA	13:M:137:LEU:HD12	1.90	0.54
14:N:37:ARG:HA	14:N:118:MET:HE3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:877:G:H2'	1:A:878:A:H8	1.73	0.54
2:B:20:C:H2'	2:B:21:A:H8	1.72	0.54
2:B:704:G:H2'	2:B:726:G:N2	2.23	0.54
2:B:974:G:H8	2:B:990:A:H62	1.55	0.54
2:B:1997:C:H2'	2:B:1998:A:C8	2.43	0.54
2:B:2292:U:H2'	2:B:2293:G:H8	1.72	0.54
4:D:41:C:H2'	4:D:42:G:C8	2.43	0.54
27:AA:61:GLY:HA2	27:AA:81:GLU:HG2	1.90	0.54
40:PA:69:THR:O	40:PA:105:VAL:HG12	2.07	0.54
2:B:558:U:OP1	14:N:113:PRO:HD2	2.07	0.54
40:PA:4:VAL:HG13	40:PA:5:HIS:N	2.10	0.54
51:AB:63:ARG:O	51:AB:64:CYS:SG	2.62	0.54
1:A:1240:U:OP1	44:TA:115:MET:HB2	2.08	0.54
10:J:120:ILE:HG21	10:J:140:ILE:HG22	1.89	0.54
11:K:73:ASN:HB2	11:K:108:VAL:HG23	1.88	0.54
38:MA:131:LEU:O	38:MA:134:MET:HG2	2.08	0.54
40:PA:6:PRO:HG2	40:PA:200:TRP:HE1	1.73	0.54
47:WA:6:ILE:HG13	47:WA:76:ILE:HB	1.90	0.54
51:AB:64:CYS:O	51:AB:65:ARG:HB2	2.07	0.54
51:AB:77:PHE:HB3	51:AB:79:LEU:CD2	2.38	0.54
56:FB:10:ILE:HD13	56:FB:40:PHE:HE2	1.72	0.54
2:B:1048:A:OP2	2:B:1110:G:N2	2.38	0.54
2:B:2297:A:N1	2:B:2321:U:H5	2.05	0.54
8:H:146:VAL:HG12	8:H:185:LYS:HB2	1.89	0.54
29:CA:17:GLU:HB3	29:CA:53:VAL:HG11	1.90	0.54
40:PA:201:ILE:HG22	40:PA:203:LYS:HG3	1.89	0.54
43:SA:36:ILE:HA	43:SA:64:VAL:HG23	1.90	0.54
2:B:570:G:C4	2:B:2030:A:N7	2.76	0.54
2:B:782:A:N7	6:F:219:VAL:HG21	2.23	0.54
47:WA:8:ILE:HB	47:WA:74:VAL:HB	1.90	0.54
47:WA:52:LEU:HB2	51:AB:81:ARG:NE	2.23	0.54
2:B:1709:U:H2'	2:B:1710:G:H8	1.72	0.54
5:E:44:VAL:HA	5:E:214:ILE:HA	1.89	0.54
13:M:74:PRO:HG2	13:M:77:VAL:HG22	1.90	0.54
38:MA:188:PRO:HG2	38:MA:191:GLU:HB2	1.89	0.54
41:QA:141:VAL:HG12	41:QA:180:THR:HG22	1.89	0.54
3:C:111:U:H2'	3:C:112:G:H8	1.72	0.54
5:E:41:SER:HA	5:E:177:LYS:HG2	1.90	0.54
1:A:948:C:H2'	1:A:949:A:H8	1.73	0.53
1:A:974:A:OP2	51:AB:81:ARG:NH1	2.41	0.53
2:B:537:G:H22	2:B:555:G:H2'	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1548:A:H2'	2:B:1549:A:H8	1.73	0.53
2:B:2837:A:H2'	2:B:2838:G:H8	1.73	0.53
7:G:151:THR:HB	7:G:152:PRO:HD3	1.90	0.53
10:J:120:ILE:HD12	10:J:134:GLY:HA3	1.90	0.53
11:K:66:ASN:HB3	11:K:138:VAL:HG21	1.89	0.53
11:K:78:VAL:HG21	11:K:103:VAL:HG22	1.88	0.53
38:MA:45:LEU:HD23	38:MA:46:SER:N	2.23	0.53
47:WA:57:VAL:HG22	47:WA:58:ASN:N	2.17	0.53
53:CB:18:GLN:NE2	53:CB:35:ARG:HH11	2.06	0.53
2:B:751:A:N7	2:B:789:A:N6	2.56	0.53
2:B:2861:U:H2'	2:B:2862:G:H8	1.73	0.53
7:G:46:ARG:HB3	7:G:84:LEU:HD12	1.88	0.53
56:FB:24:SER:HB2	56:FB:27:LYS:HD2	1.90	0.53
2:B:596:U:H2'	2:B:597:G:H8	1.73	0.53
2:B:1063:G:C8	13:M:135:MET:HE2	2.43	0.53
2:B:2329:U:H2'	2:B:2330:G:H8	1.72	0.53
31:EA:37:CYS:H	31:EA:40:CYS:HB3	1.73	0.53
6:F:66:PHE:HZ	6:F:86:ARG:HH12	1.57	0.53
15:O:35:VAL:HG13	15:O:69:VAL:HG11	1.91	0.53
16:P:30:THR:HB	16:P:33:ARG:HB2	1.89	0.53
18:R:38:LEU:HB3	18:R:39:PRO:HD3	1.90	0.53
38:MA:131:LEU:HA	38:MA:134:MET:HE3	1.90	0.53
50:ZA:89:ARG:HH22	50:ZA:101:THR:HG21	1.73	0.53
2:B:1796:U:H2'	2:B:1797:G:C8	2.42	0.53
10:J:157:LYS:HG2	10:J:159:LYS:HE3	1.90	0.53
11:K:5:LEU:HD22	11:K:13:GLY:HA3	1.89	0.53
1:A:884:U:H4'	1:A:885:G:H5''	1.89	0.53
2:B:2039:U:H2'	2:B:2040:G:C8	2.43	0.53
2:B:2422:C:H41	35:IA:30:HIS:HE2	1.57	0.53
2:B:2514:U:H2'	2:B:2515:C:C6	2.44	0.53
38:MA:257:CYS:SG	38:MA:266:ASN:ND2	2.82	0.53
2:B:197:A:H4'	2:B:2069:G:OP2	2.09	0.53
2:B:2861:U:H2'	2:B:2862:G:C8	2.44	0.53
5:E:60:ARG:HB2	5:E:141:LYS:HG3	1.90	0.53
47:WA:53:ILE:HG22	47:WA:61:ALA:O	2.08	0.53
55:EB:62:ARG:HB3	55:EB:69:TYR:CE1	2.43	0.53
1:A:312:C:H2'	1:A:313:A:C8	2.43	0.53
2:B:210:C:H2'	2:B:211:C:C6	2.44	0.53
8:H:148:ILE:HG21	8:H:157:LEU:HD21	1.90	0.53
40:PA:8:GLY:HA2	40:PA:11:LEU:HG	1.90	0.53
40:PA:55:VAL:HG13	40:PA:66:THR:HB	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:XA:84:MET:HG2	48:XA:110:THR:HB	1.91	0.53
1:A:1412:C:H2'	1:A:1413:A:C8	2.44	0.53
2:B:2243:U:H2'	2:B:2244:U:C6	2.44	0.53
2:B:121:G:H2'	2:B:122:G:H8	1.74	0.52
40:PA:56:ILE:HG23	40:PA:63:ILE:HD11	1.90	0.52
42:RA:96:GLN:HB3	42:RA:123:LEU:HB2	1.90	0.52
53:CB:19:VAL:HG21	53:CB:52:LEU:HD21	1.89	0.52
1:A:946:A:H2'	1:A:947:G:C8	2.44	0.52
1:A:1308:U:H2'	1:A:1309:G:H8	1.75	0.52
1:A:1323:G:H2'	1:A:1324:A:C8	2.44	0.52
2:B:1005:C:O2'	14:N:30:THR:HG21	2.09	0.52
2:B:1054:A:H4'	12:L:31:ARG:HA	1.90	0.52
7:G:25:THR:HG21	7:G:193:VAL:HG22	1.91	0.52
1:A:182:A:H62	1:A:194:C:H42	1.57	0.52
2:B:759:G:H2'	2:B:760:G:H8	1.73	0.52
2:B:2329:U:H2'	2:B:2330:G:C8	2.44	0.52
5:E:43:ASP:OD1	5:E:43:ASP:N	2.42	0.52
7:G:33:ARG:HD2	7:G:33:ARG:H	1.74	0.52
18:R:100:CYS:SG	18:R:101:GLY:N	2.82	0.52
1:A:149:A:H1'	1:A:1446:A:H2	1.75	0.52
5:E:50:ILE:HG12	5:E:205:LYS:H	1.74	0.52
19:S:29:HIS:HB3	19:S:36:TYR:HB2	1.90	0.52
35:IA:30:HIS:ND1	35:IA:31:ILE:HG13	2.24	0.52
1:A:1429:A:H2'	1:A:1430:A:C8	2.45	0.52
1:A:1540:U:O4	37:KA:5:A:C2	2.62	0.52
2:B:581:C:H2'	2:B:582:A:H8	1.75	0.52
51:AB:64:CYS:SG	51:AB:66:GLN:HB3	2.50	0.52
2:B:953:G:H2'	2:B:954:G:C8	2.40	0.52
25:Y:47:PRO:HG3	25:Y:55:GLY:HA3	1.92	0.52
2:B:244:A:H62	2:B:254:G:H21	1.58	0.52
12:L:118:ILE:O	12:L:118:ILE:CG2	2.55	0.52
16:P:55:MET:O	16:P:60:ARG:NH2	2.42	0.52
32:FA:30:ASP:HB3	32:FA:34:GLY:H	1.73	0.52
49:YA:81:ILE:HG23	49:YA:94:TYR:HB3	1.91	0.52
1:A:490:C:H2'	1:A:491:G:H8	1.75	0.52
2:B:38:A:H4'	8:H:45:ALA:HB3	1.92	0.52
2:B:523:C:H2'	2:B:524:G:H8	1.75	0.52
2:B:1259:G:H2'	2:B:1260:A:H8	1.75	0.52
2:B:1841:U:H2'	2:B:1842:G:H8	1.74	0.52
2:B:1848:A:H2'	2:B:1849:G:H8	1.74	0.52
2:B:2070:A:H2'	2:B:2071:A:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:9:VAL:HA	10:J:48:THR:HG22	1.91	0.52
18:R:44:LEU:HD23	18:R:113:ILE:HD13	1.92	0.52
38:MA:245:ARG:HG2	38:MA:256:GLU:HG2	1.92	0.52
38:MA:312:PHE:CD1	38:MA:329:LEU:HD21	2.44	0.52
45:UA:42:GLU:HG2	45:UA:100:ILE:HD13	1.92	0.52
2:B:2215:C:H2'	2:B:2216:G:H8	1.75	0.52
9:I:114:ARG:HD3	31:EA:47:LYS:HE2	1.92	0.52
40:PA:7:ASN:O	40:PA:8:GLY:C	2.50	0.52
51:AB:69:ARG:O	51:AB:71:HIS:N	2.36	0.52
2:B:582:A:H2'	2:B:583:G:H8	1.75	0.52
2:B:1432:G:H2'	2:B:1433:A:C8	2.45	0.52
2:B:1568:G:OP2	6:F:62:ARG:NH2	2.43	0.52
2:B:2070:A:H2'	2:B:2071:A:C8	2.45	0.52
15:O:24:VAL:HG13	15:O:33:ALA:HB2	1.91	0.52
1:A:502:A:OP1	49:YA:114:SER:N	2.41	0.51
1:A:1356:G:H2'	1:A:1357:A:C8	2.45	0.51
2:B:585:G:N7	21:U:5:ARG:NH1	2.57	0.51
2:B:1197:G:H2'	2:B:1198:U:H6	1.75	0.51
2:B:1826:G:H2'	2:B:1827:U:C6	2.45	0.51
2:B:1934:C:H2'	2:B:1935:G:C8	2.43	0.51
2:B:2050:C:N4	2:B:2051:A:N1	2.58	0.51
5:E:175:ILE:HG12	5:E:188:ASN:HB3	1.92	0.51
8:H:79:ARG:HG2	8:H:80:SER:H	1.75	0.51
12:L:33:VAL:HG12	12:L:34:THR:H	1.76	0.51
39:OA:33:ALA:CA	39:OA:37:VAL:O	2.43	0.51
12:L:56:ARG:HD3	12:L:83:ALA:HB2	1.92	0.51
14:N:84:ILE:HG23	14:N:84:ILE:O	2.10	0.51
1:A:59:A:H3'	1:A:331:G:H22	1.75	0.51
9:I:36:ASN:HB3	9:I:152:ASP:HB3	1.93	0.51
35:IA:30:HIS:O	35:IA:31:ILE:C	2.54	0.51
4:LA:41:C:H2'	4:LA:42:G:H8	1.75	0.51
41:QA:84:ASN:HA	42:RA:102:THR:HG21	1.92	0.51
42:RA:10:LEU:O	42:RA:11:GLN:O	2.28	0.51
2:B:1203:U:H5'	16:P:3:LEU:HD23	1.92	0.51
2:B:1539:U:H2'	2:B:1540:G:H8	1.75	0.51
5:E:73:VAL:HG11	5:E:157:LYS:HA	1.93	0.51
8:H:194:LYS:O	8:H:197:GLU:HB3	2.10	0.51
19:S:49:VAL:HG21	19:S:82:ALA:HA	1.91	0.51
41:QA:60:VAL:HG21	41:QA:199:ILE:HD11	1.92	0.51
2:B:45:G:H5''	2:B:46:G:H5'	1.91	0.51
2:B:2118:U:O2	2:B:2145:C:N4	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:49:LEU:HD12	10:J:71:LEU:HD21	1.93	0.51
18:R:32:GLU:HB3	18:R:118:ARG:HD2	1.92	0.51
50:ZA:3:ILE:HG12	50:ZA:7:ASN:HB2	1.92	0.51
57:GB:34:VAL:HG11	57:GB:78:LEU:HD21	1.91	0.51
1:A:451:A:H4'	1:A:452:A:N3	2.26	0.51
12:L:51:TYR:HE2	12:L:87:GLU:HA	1.75	0.51
26:Z:30:ILE:HD11	26:Z:63:ILE:HD13	1.92	0.51
1:A:337:G:H2'	1:A:338:A:C8	2.46	0.51
2:B:1251:C:O2'	2:B:1252:G:H3'	2.11	0.51
6:F:66:PHE:HB3	6:F:150:GLY:O	2.11	0.51
8:H:71:GLY:O	8:H:72:SER:HB2	2.11	0.51
38:MA:340:LEU:O	38:MA:343:PRO:HD2	2.11	0.51
41:QA:146:GLU:O	41:QA:149:LYS:HG2	2.09	0.51
42:RA:105:ILE:HG21	42:RA:123:LEU:HD23	1.93	0.51
51:AB:87:ALA:O	51:AB:91:GLY:CA	2.58	0.51
1:A:1228:C:H2'	1:A:1229:A:H8	1.76	0.51
2:B:580:U:H2'	2:B:581:C:H6	1.76	0.51
2:B:2828:G:H2'	2:B:2829:A:H8	1.75	0.51
4:D:59:A:H2'	4:D:60:U:H5'	1.92	0.51
28:BA:2:ARG:HD2	28:BA:29:LEU:HD22	1.93	0.51
1:A:1144:G:H21	1:A:1146:A:H62	1.58	0.51
1:A:1255:G:O2'	1:A:1258:G:N3	2.43	0.51
1:A:1517:G:N3	2:B:1919:A:O2'	2.43	0.51
2:B:799:G:H5''	2:B:800:A:H2'	1.92	0.51
2:B:1250:G:OP2	16:P:21:ARG:NH2	2.44	0.51
6:F:143:VAL:HB	6:F:153:LEU:HB2	1.92	0.51
10:J:94:ARG:NH1	10:J:127:GLN:OE1	2.41	0.51
15:O:76:VAL:H	20:T:72:VAL:HG22	1.76	0.51
1:A:916:U:H2'	1:A:917:G:H8	1.75	0.50
1:A:1437:A:H2'	1:A:1438:G:H8	1.74	0.50
2:B:946:C:H2'	2:B:947:A:H8	1.76	0.50
2:B:1837:C:H2'	2:B:1899:A:H61	1.76	0.50
2:B:2183:A:H2'	2:B:2184:A:C8	2.46	0.50
21:U:43:GLN:HE21	22:V:77:PHE:HB3	1.75	0.50
39:OA:14:HIS:CD2	39:OA:15:PHE:H	2.29	0.50
48:XA:62:ALA:HB1	48:XA:95:THR:HB	1.93	0.50
1:A:715:A:H2'	1:A:716:A:H8	1.76	0.50
1:A:1391:U:H2'	1:A:1392:G:C8	2.45	0.50
2:B:679:C:H2'	2:B:680:C:C6	2.47	0.50
2:B:878:A:H3'	2:B:879:G:H8	1.75	0.50
8:H:149:ILE:HG23	8:H:188:MET:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:79:ALA:HB3	19:S:113:ALA:HB3	1.94	0.50
51:AB:73:PHE:C	51:AB:78:GLY:HA2	2.35	0.50
1:A:1369:C:H2'	1:A:1370:G:C8	2.47	0.50
2:B:23:G:H2'	2:B:24:G:H8	1.76	0.50
2:B:720:U:H2'	2:B:721:A:H8	1.76	0.50
2:B:2183:A:H2'	2:B:2184:A:H8	1.77	0.50
15:O:34:GLY:N	15:O:37:ASP:OD2	2.42	0.50
40:PA:179:ALA:HB1	40:PA:202:PHE:HE1	1.76	0.50
1:A:312:C:H2'	1:A:313:A:H8	1.76	0.50
1:A:1241:G:H2'	1:A:1242:G:H8	1.76	0.50
1:A:1323:G:H2'	1:A:1324:A:H8	1.76	0.50
2:B:1057:A:H1'	12:L:34:THR:HG21	1.93	0.50
2:B:1548:A:H2'	2:B:1549:A:C8	2.46	0.50
3:C:38:C:N4	3:C:44:G:H1	2.07	0.50
1:A:208:U:H2'	1:A:210:C:H1'	1.94	0.50
1:A:624:C:H4'	53:CB:10:GLY:HA2	1.93	0.50
2:B:467:G:OP2	34:HA:34:ARG:HD3	2.12	0.50
2:B:1130:U:O2'	2:B:1131:G:H2'	2.11	0.50
2:B:1434:A:H2'	2:B:1435:G:H8	1.76	0.50
2:B:2815:C:H2'	2:B:2816:G:H8	1.76	0.50
4:D:16:C:H5'	4:D:59:A:C2	2.46	0.50
14:N:32:LEU:HD22	14:N:54:ILE:HG21	1.92	0.50
18:R:78:LYS:O	18:R:82:GLU:HB2	2.11	0.50
38:MA:244:ILE:HD11	38:MA:263:GLN:HG3	1.93	0.50
39:OA:186:VAL:HG13	39:OA:190:SER:HB2	1.93	0.50
41:QA:94:GLU:HG2	41:QA:185:PRO:HG3	1.93	0.50
2:B:587:C:OP2	16:P:21:ARG:NH1	2.45	0.50
2:B:2115:G:O2'	2:B:2117:A:N6	2.45	0.50
5:E:132:GLY:HA2	5:E:137:MET:HB2	1.94	0.50
38:MA:16:HIS:HA	38:MA:45:LEU:HD11	1.92	0.50
1:A:1158:C:C4	1:A:1160:G:C8	3.00	0.50
2:B:1219:U:OP2	21:U:18:LYS:NZ	2.44	0.50
2:B:1258:U:H2'	2:B:1259:G:H8	1.77	0.50
5:E:142:VAL:HG11	5:E:162:ARG:HH21	1.77	0.50
10:J:136:ASP:OD2	10:J:138:GLN:HB3	2.11	0.50
45:UA:8:ASP:OD2	45:UA:12:ARG:NH1	2.44	0.50
2:B:1464:G:H2'	2:B:1465:G:C8	2.47	0.50
2:B:1682:G:OP2	2:B:1699:G:N2	2.44	0.50
2:B:2114:A:H62	2:B:2119:A:H61	1.59	0.50
8:H:79:ARG:NH1	8:H:80:SER:OG	2.45	0.50
12:L:25:ALA:HB3	12:L:85:SER:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:CA:21:LEU:HA	29:CA:25:GLN:HB3	1.92	0.50
1:A:335:C:H2'	1:A:336:A:C8	2.46	0.50
2:B:18:U:H2'	2:B:19:A:H8	1.76	0.50
2:B:770:G:OP2	34:HA:11:LYS:HE3	2.11	0.50
10:J:51:PHE:HZ	10:J:71:LEU:HD22	1.75	0.50
38:MA:135:TYR:OH	38:MA:178:GLU:OE1	2.30	0.50
51:AB:53:ARG:HB3	51:AB:59:ARG:HH12	1.76	0.50
2:B:923:G:H2'	2:B:924:G:H8	1.77	0.49
2:B:1387:A:H2'	2:B:1388:G:H8	1.77	0.49
2:B:1779:U:OP2	2:B:1784:A:N6	2.44	0.49
4:D:42:G:H2'	4:D:43:A:C8	2.47	0.49
9:I:60:SER:HB2	9:I:90:LEU:HD21	1.94	0.49
13:M:57:VAL:HB	13:M:69:VAL:HB	1.94	0.49
19:S:40:ILE:HG13	19:S:47:VAL:HG12	1.94	0.49
42:RA:108:GLY:O	42:RA:109:ALA:CB	2.60	0.49
46:VA:49:GLN:HB3	46:VA:50:PRO:HD3	1.93	0.49
54:DB:63:CYS:SG	54:DB:64:ARG:N	2.81	0.49
1:A:1358:U:OP1	51:AB:75:ARG:HB2	2.12	0.49
2:B:320:A:OP1	8:H:130:LYS:NZ	2.41	0.49
2:B:563:A:OP2	22:V:79:ARG:NH2	2.43	0.49
2:B:2685:G:H2'	2:B:2686:G:H8	1.77	0.49
2:B:2812:G:H2'	2:B:2813:A:C8	2.47	0.49
13:M:52:LEU:O	13:M:54:ILE:HG13	2.12	0.49
17:Q:20:LEU:HD13	26:Z:81:PRO:HG2	1.94	0.49
1:A:110:C:O2'	53:CB:25:ARG:O	2.30	0.49
1:A:254:G:O3'	54:DB:70:LYS:NZ	2.44	0.49
1:A:419:C:H2'	1:A:420:U:O4'	2.12	0.49
2:B:457:A:H61	2:B:470:A:H5''	1.77	0.49
2:B:598:U:H2'	2:B:599:A:H8	1.76	0.49
2:B:1754:A:O2'	20:T:102:ARG:NH2	2.46	0.49
2:B:2313:C:H2'	2:B:2314:A:C8	2.48	0.49
1:A:1512:U:H2'	1:A:1513:A:C8	2.47	0.49
2:B:1164:C:H2'	2:B:1165:A:H8	1.78	0.49
2:B:1860:G:H5''	5:E:205:LYS:HD2	1.94	0.49
2:B:2126:A:H2'	2:B:2162:G:N2	2.27	0.49
4:D:24:U:H2'	4:D:25:C:C6	2.46	0.49
39:OA:58:LYS:O	39:OA:61:SER:HB3	2.13	0.49
39:OA:156:LEU:HD13	39:OA:178:LEU:HD13	1.95	0.49
1:A:958:A:C2	56:FB:54:ARG:HB3	2.47	0.49
2:B:2124:G:H21	5:E:217:THR:HA	1.78	0.49
4:D:51:C:H2'	4:D:52:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:MA:138:TYR:OH	38:MA:142:ARG:NH2	2.40	0.49
41:QA:36:ALA:H	41:QA:37:PRO:CD	2.25	0.49
53:CB:44:SER:H	53:CB:46:LYS:HZ2	1.61	0.49
56:FB:44:ILE:HD13	56:FB:63:ASP:HA	1.94	0.49
14:N:31:GLU:HG2	14:N:142:ILE:HG12	1.93	0.49
30:DA:15:ARG:HG2	30:DA:53:MET:HE3	1.94	0.49
52:BB:48:ASP:OD2	52:BB:51:SER:HB2	2.13	0.49
1:A:147:G:H2'	1:A:148:G:C8	2.48	0.49
1:A:530:G:H22	1:A:1492:A:H61	1.61	0.49
2:B:1443:U:H2'	2:B:1444:G:H8	1.78	0.49
2:B:2615:U:C2	32:FA:3:GLN:HA	2.47	0.49
47:WA:33:GLY:HA3	47:WA:83:THR:OG1	2.13	0.49
54:DB:16:MET:HG3	54:DB:19:SER:OG	2.13	0.49
1:A:1098:C:O2'	58:HB:66:ARG:HG3	2.12	0.49
2:B:181:A:H2'	2:B:182:A:C8	2.48	0.49
7:G:125:TRP:CD1	7:G:160:LYS:HB3	2.48	0.49
14:N:18:VAL:HG21	14:N:32:LEU:HD21	1.93	0.49
51:AB:72:GLY:O	51:AB:74:LEU:HD23	2.12	0.49
56:FB:76:THR:OG1	56:FB:77:ARG:N	2.46	0.49
1:A:946:A:H2'	1:A:947:G:H8	1.76	0.49
1:A:950:U:H2'	1:A:951:G:C8	2.47	0.49
1:A:1149:C:OP2	46:VA:10:ARG:NH2	2.45	0.49
2:B:2026:U:H2'	2:B:2027:G:C8	2.48	0.49
3:C:5:U:H2'	3:C:6:G:H8	1.78	0.49
5:E:130:VAL:O	5:E:134:ARG:NH1	2.46	0.49
7:G:13:ARG:HH22	20:T:74:GLN:HE21	1.59	0.49
11:K:94:ILE:HG23	11:K:98:ASP:HB2	1.95	0.49
12:L:67:THR:O	12:L:67:THR:OG1	2.31	0.49
13:M:112:LYS:O	13:M:116:MET:N	2.46	0.49
15:O:92:GLU:O	15:O:93:GLN:C	2.56	0.49
29:CA:22:LEU:HD12	29:CA:23:ARG:HE	1.76	0.49
38:MA:206:MET:HE1	38:MA:294:ARG:HH21	1.78	0.49
48:XA:28:ASN:HB3	48:XA:56:LYS:HG2	1.95	0.49
1:A:52:C:H2'	1:A:53:A:H8	1.78	0.49
1:A:674:G:H2'	1:A:675:A:C8	2.48	0.49
1:A:944:G:N1	1:A:1338:G:OP2	2.46	0.49
1:A:1203:C:H2'	1:A:1204:A:H8	1.78	0.49
2:B:863:A:H2'	2:B:864:G:H8	1.77	0.49
2:B:1161:C:H2'	2:B:1162:G:H8	1.76	0.49
2:B:1260:A:OP1	23:W:83:LYS:NZ	2.46	0.49
2:B:1592:C:H2'	2:B:1593:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:131:MET:HG2	6:F:134:ILE:HD12	1.95	0.49
8:H:127:GLU:HG2	8:H:128:ALA:H	1.77	0.49
30:DA:52:PHE:CE2	30:DA:53:MET:HG3	2.47	0.49
2:B:172:A:H2'	2:B:173:A:H8	1.78	0.48
2:B:328:U:O3'	25:Y:65:GLN:HG3	2.13	0.48
2:B:917:A:H5''	2:B:2268:A:H61	1.78	0.48
4:D:2:G:N2	4:D:72:A:C2	2.81	0.48
5:E:164:ARG:H	5:E:171:ILE:HD13	1.78	0.48
11:K:104:THR:HA	11:K:108:VAL:O	2.12	0.48
13:M:27:LEU:HD13	13:M:34:ILE:HA	1.95	0.48
18:R:47:VAL:C	18:R:50:PRO:HD2	2.38	0.48
19:S:28:VAL:O	19:S:28:VAL:HG22	2.13	0.48
38:MA:317:VAL:HB	38:MA:329:LEU:HD13	1.93	0.48
39:OA:27:LYS:HB3	39:OA:28:PRO:HD3	1.94	0.48
51:AB:97:LYS:O	51:AB:98:LYS:C	2.55	0.48
1:A:264:C:H4'	54:DB:64:ARG:HD2	1.94	0.48
1:A:299:G:C6	1:A:300:A:C6	3.01	0.48
1:A:416:G:C6	1:A:427:U:O2	2.67	0.48
1:A:562:U:H1'	49:YA:11:ARG:HD2	1.93	0.48
1:A:1538:C:O2'	58:HB:20:ARG:NH2	2.46	0.48
2:B:1181:U:H2'	2:B:1182:G:C8	2.48	0.48
20:T:8:GLU:HA	20:T:54:LEU:HD22	1.94	0.48
25:Y:73:ASN:O	25:Y:74:ALA:HB3	2.13	0.48
41:QA:191:SER:O	41:QA:193:ASP:N	2.45	0.48
43:SA:9:MET:HG3	43:SA:59:TYR:CE1	2.48	0.48
51:AB:56:SER:C	51:AB:58:SER:N	2.70	0.48
51:AB:66:GLN:O	51:AB:67:THR:OG1	2.27	0.48
2:B:7:G:H2'	2:B:8:C:C6	2.49	0.48
11:K:103:VAL:HG12	11:K:108:VAL:HB	1.96	0.48
36:JA:36:ARG:O	36:JA:37:GLN:O	2.30	0.48
1:A:367:U:N3	1:A:393:A:C2	2.81	0.48
1:A:1492:A:H2'	38:MA:303:ARG:HH12	1.79	0.48
2:B:161:A:C5	2:B:162:U:H5	2.32	0.48
2:B:742:A:H2'	2:B:743:A:C8	2.48	0.48
2:B:2002:G:OP2	18:R:9:GLN:NE2	2.46	0.48
2:B:2726:A:H4'	15:O:32:TYR:OH	2.13	0.48
7:G:13:ARG:HH12	20:T:74:GLN:HE21	1.62	0.48
7:G:77:ARG:NH2	7:G:200:ASP:OD1	2.46	0.48
2:B:107:G:H2'	2:B:108:G:H8	1.77	0.48
2:B:816:C:H2'	2:B:817:C:C6	2.49	0.48
2:B:873:C:H2'	2:B:874:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1958:C:H2'	2:B:1959:G:H8	1.79	0.48
2:B:2313:C:H2'	2:B:2314:A:H8	1.78	0.48
16:P:29:LYS:O	16:P:30:THR:OG1	2.28	0.48
36:JA:33:HIS:O	36:JA:35:GLN:HG3	2.14	0.48
38:MA:311:ASN:OD1	38:MA:313:PRO:HD2	2.13	0.48
1:A:126:G:OP1	1:A:605:U:O2'	2.28	0.48
1:A:555:U:H2'	1:A:556:C:C6	2.49	0.48
2:B:598:U:H2'	2:B:599:A:C8	2.48	0.48
2:B:1590:A:H2'	2:B:1591:A:H8	1.78	0.48
12:L:26:VAL:HG21	12:L:113:PHE:HA	1.95	0.48
35:IA:44:ARG:HB3	35:IA:45:PRO:HD3	1.94	0.48
1:A:769:G:H4'	1:A:1513:A:H4'	1.94	0.48
2:B:848:C:H2'	2:B:849:A:C8	2.49	0.48
2:B:2853:C:H2'	2:B:2854:G:H8	1.79	0.48
6:F:255:LYS:HD2	6:F:269:ARG:HH22	1.79	0.48
18:R:35:LYS:HG2	18:R:110:MET:HE2	1.96	0.48
1:A:34:C:H2'	1:A:35:G:C8	2.48	0.48
1:A:1182:G:H5'	1:A:1183:U:OP1	2.14	0.48
2:B:155:A:H2'	2:B:156:A:H8	1.79	0.48
2:B:784:G:H5'	2:B:785:G:OP1	2.12	0.48
2:B:1791:A:N6	2:B:1828:G:O2'	2.45	0.48
50:ZA:8:ILE:N	50:ZA:9:PRO:HD2	2.29	0.48
1:A:880:C:H2'	1:A:881:G:C8	2.48	0.48
2:B:817:C:H2'	2:B:818:G:H8	1.79	0.48
2:B:2039:U:H2'	2:B:2040:G:H8	1.77	0.48
4:D:21:A:H2'	4:D:46:G:O6	2.13	0.48
13:M:123:ALA:HA	13:M:126:ARG:HD2	1.95	0.48
16:P:85:VAL:HG11	16:P:90:VAL:HG22	1.96	0.48
26:Z:40:ILE:HG21	26:Z:63:ILE:HD11	1.96	0.48
1:A:367:U:O4	1:A:393:A:C6	2.67	0.48
2:B:1499:C:H2'	2:B:1500:G:H8	1.79	0.48
2:B:2122:U:H4'	5:E:164:ARG:HH12	1.78	0.48
2:B:2230:G:H2'	2:B:2231:U:C6	2.49	0.48
6:F:48:ILE:O	6:F:48:ILE:HG23	2.13	0.48
7:G:109:VAL:HG11	7:G:193:VAL:HB	1.96	0.48
12:L:119:PRO:CG	12:L:120:ALA:N	2.76	0.48
25:Y:98:ASN:O	25:Y:100:GLU:HG3	2.14	0.48
38:MA:68:MET:HG2	38:MA:74:MET:HE1	1.95	0.48
39:OA:209:VAL:HA	39:OA:212:TYR:HD2	1.79	0.48
47:WA:67:ILE:HG22	51:AB:95:GLY:O	2.13	0.48
1:A:599:C:H2'	1:A:600:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:720:C:H5''	1:A:721:G:H2'	1.96	0.47
2:B:210:C:OP1	34:HA:29:GLN:NE2	2.47	0.47
2:B:2215:C:H2'	2:B:2216:G:C8	2.49	0.47
2:B:2327:A:H2'	2:B:2328:A:C8	2.49	0.47
2:B:2728:U:H2'	2:B:2729:G:H8	1.79	0.47
3:C:55:U:H2'	3:C:56:G:C8	2.49	0.47
4:D:11:A:H2'	4:D:12:G:C8	2.48	0.47
6:F:257:ARG:HH12	6:F:259:ASN:HB2	1.78	0.47
7:G:12:THR:HG23	20:T:4:ILE:HD11	1.95	0.47
22:V:68:ARG:HH11	22:V:90:ARG:HB2	1.79	0.47
25:Y:73:ASN:HD21	25:Y:98:ASN:HD22	1.60	0.47
47:WA:36:VAL:HG23	47:WA:76:ILE:HA	1.96	0.47
1:A:1512:U:H2'	1:A:1513:A:H8	1.78	0.47
2:B:729:G:O6	2:B:1774:C:N4	2.47	0.47
2:B:1056:G:H5''	2:B:1057:A:O4'	2.15	0.47
2:B:2241:A:H2'	2:B:2242:G:C8	2.49	0.47
15:O:102:PRO:HB3	15:O:121:GLU:HB2	1.95	0.47
22:V:59:ILE:HG12	22:V:101:ILE:HG22	1.96	0.47
40:PA:69:THR:HG21	40:PA:75:VAL:HG21	1.96	0.47
56:FB:4:LEU:HD12	56:FB:9:PHE:HZ	1.78	0.47
1:A:1005:A:H3'	1:A:1006:G:C8	2.48	0.47
2:B:521:U:H2'	2:B:522:A:H8	1.79	0.47
9:I:36:ASN:OD1	9:I:37:MET:N	2.47	0.47
10:J:51:PHE:CZ	10:J:71:LEU:HD22	2.49	0.47
17:Q:41:LEU:HD22	17:Q:124:LEU:HD22	1.96	0.47
26:Z:42:LEU:HD23	26:Z:47:VAL:HG21	1.97	0.47
38:MA:9:LEU:O	38:MA:12:LEU:HB3	2.14	0.47
58:HB:23:GLU:O	58:HB:25:ALA:N	2.40	0.47
1:A:950:U:H2'	1:A:951:G:H8	1.79	0.47
2:B:406:G:H2'	2:B:407:G:H8	1.80	0.47
21:U:87:VAL:HG13	22:V:49:ILE:HD11	1.94	0.47
22:V:68:ARG:HB2	22:V:90:ARG:HH21	1.80	0.47
24:X:11:LEU:HD22	24:X:32:LEU:HD13	1.95	0.47
39:OA:19:THR:HG22	39:OA:38:HIS:CD2	2.48	0.47
39:OA:22:TRP:CE2	39:OA:38:HIS:HE1	2.31	0.47
40:PA:31:ASN:OD1	40:PA:58:ARG:NH2	2.46	0.47
46:VA:54:VAL:O	46:VA:59:LYS:NZ	2.48	0.47
2:B:2244:U:N3	2:B:2245:U:O2	2.47	0.47
8:H:77:ILE:HG13	8:H:78:TRP:HD1	1.79	0.47
13:M:38:CYS:SG	13:M:42:ASN:ND2	2.87	0.47
13:M:97:VAL:HB	13:M:137:LEU:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:76:VAL:HG12	20:T:72:VAL:HG22	1.97	0.47
17:Q:70:ASP:C	17:Q:70:ASP:OD1	2.56	0.47
40:PA:129:PHE:HA	40:PA:132:ALA:HB3	1.97	0.47
41:QA:35:GLN:O	41:QA:36:ALA:HB2	2.15	0.47
42:RA:87:VAL:HA	42:RA:91:SER:O	2.14	0.47
50:ZA:113:LYS:HA	50:ZA:114:PRO:HD3	1.72	0.47
54:DB:18:LYS:HA	54:DB:50:ASN:HD21	1.80	0.47
1:A:680:C:H2'	1:A:681:A:H8	1.80	0.47
2:B:2316:G:H2'	2:B:2317:A:C8	2.48	0.47
3:C:49:C:H2'	3:C:50:A:C8	2.50	0.47
25:Y:96:LYS:O	25:Y:97:SER:HB2	2.14	0.47
41:QA:154:VAL:HG12	41:QA:158:LEU:HD23	1.97	0.47
49:YA:109:ARG:HB3	49:YA:118:VAL:HG21	1.97	0.47
1:A:235:C:H2'	1:A:236:A:H8	1.80	0.47
1:A:741:G:OP1	52:BB:1:SER:N	2.47	0.47
2:B:452:G:OP1	8:H:52:VAL:HG13	2.14	0.47
2:B:674:G:H5''	8:H:71:GLY:H	1.79	0.47
2:B:1302:A:H5'	2:B:1608:A:OP1	2.14	0.47
2:B:1600:C:H2'	2:B:1601:G:H8	1.79	0.47
2:B:2060:A:N6	8:H:69:ARG:HH21	2.13	0.47
2:B:2544:G:H2'	2:B:2545:G:H8	1.80	0.47
2:B:2831:G:OP2	7:G:59:ARG:NH1	2.45	0.47
3:C:9:G:H2'	3:C:10:G:H8	1.79	0.47
9:I:109:ARG:HH21	9:I:138:PRO:HG3	1.79	0.47
11:K:126:GLY:O	11:K:145:ASN:ND2	2.47	0.47
13:M:45:THR:HB	13:M:50:LYS:HG2	1.97	0.47
32:FA:30:ASP:OD2	32:FA:33:SER:N	2.42	0.47
40:PA:8:GLY:O	40:PA:11:LEU:HG	2.15	0.47
41:QA:12:ARG:HD3	41:QA:36:ALA:O	2.15	0.47
49:YA:33:CYS:N	49:YA:54:VAL:HG13	2.25	0.47
51:AB:73:PHE:O	51:AB:78:GLY:N	2.47	0.47
54:DB:45:VAL:HG22	54:DB:72:TRP:HB2	1.96	0.47
1:A:81:A:H2	1:A:88:U:H3	1.63	0.47
2:B:20:C:H2'	2:B:21:A:C8	2.49	0.47
45:UA:10:LEU:HD13	45:UA:74:ILE:HD11	1.97	0.47
51:AB:80:SER:C	51:AB:82:ILE:H	2.21	0.47
2:B:404:A:H1'	2:B:406:G:C4	2.50	0.47
2:B:814:C:H1'	2:B:1225:G:H21	1.80	0.47
2:B:833:A:H2'	2:B:834:G:C8	2.46	0.47
2:B:948:C:H2'	2:B:949:G:H8	1.80	0.47
2:B:2599:G:H2'	2:B:2600:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:30:ALA:HB3	6:F:31:PRO:HD3	1.97	0.47
1:A:1254:A:OP1	47:WA:47:GLU:HG2	2.15	0.47
2:B:355:U:H2'	2:B:356:G:H8	1.80	0.47
2:B:1265:A:N6	2:B:2013:A:H5''	2.28	0.47
2:B:2087:G:H2'	2:B:2088:A:H8	1.80	0.47
2:B:2166:U:O4	2:B:2170:A:N6	2.48	0.47
6:F:229:HIS:CD2	6:F:246:PRO:HG3	2.50	0.47
8:H:118:LEU:HD12	8:H:186:VAL:O	2.15	0.47
13:M:32:VAL:HG21	13:M:60:VAL:HG21	1.96	0.47
41:QA:36:ALA:N	41:QA:37:PRO:CD	2.77	0.47
50:ZA:104:ASN:O	50:ZA:105:ALA:HB3	2.14	0.47
53:CB:78:VAL:O	53:CB:78:VAL:HG13	2.14	0.47
1:A:711:G:H2'	1:A:712:A:H8	1.81	0.46
2:B:660:C:H2'	2:B:661:A:H8	1.79	0.46
9:I:72:SER:HB3	9:I:80:GLN:HB2	1.98	0.46
13:M:87:SER:HB3	13:M:97:VAL:HG22	1.96	0.46
40:PA:134:LYS:O	40:PA:137:VAL:HG12	2.14	0.46
1:A:783:C:H2'	1:A:784:A:H8	1.80	0.46
1:A:1054:C:H42	38:MA:196:ILE:HB	1.80	0.46
2:B:161:A:H3'	2:B:162:U:H5''	1.97	0.46
2:B:1089:A:H2	2:B:1090:A:H62	1.62	0.46
2:B:2417:C:H2'	2:B:2418:A:H8	1.79	0.46
2:B:2848:G:H2'	2:B:2867:G:N2	2.30	0.46
12:L:122:GLN:O	12:L:124:ASP:N	2.48	0.46
20:T:47:ILE:HD11	20:T:61:ARG:HD2	1.97	0.46
41:QA:2:ARG:HG3	41:QA:3:TYR:N	2.30	0.46
2:B:2014:A:H2'	2:B:2015:A:C8	2.50	0.46
2:B:2340:A:H2'	2:B:2341:G:H8	1.80	0.46
2:B:2508:G:H2'	2:B:2509:G:C8	2.51	0.46
2:B:2591:C:H2'	2:B:2592:G:H8	1.80	0.46
11:K:84:ALA:HB2	11:K:90:LEU:HD23	1.96	0.46
16:P:101:ILE:HB	16:P:105:ILE:HG13	1.97	0.46
17:Q:75:GLU:HB3	17:Q:90:GLU:HG3	1.97	0.46
40:PA:180:ASP:HB3	40:PA:204:GLY:HA3	1.97	0.46
2:B:18:U:H2'	2:B:19:A:C8	2.51	0.46
2:B:121:G:H2'	2:B:122:G:C8	2.50	0.46
2:B:1909:C:H2'	2:B:1910:G:H8	1.80	0.46
2:B:2296:U:OP2	19:S:9:ARG:NH2	2.49	0.46
6:F:145:MET:HE1	6:F:181:ARG:NE	2.31	0.46
14:N:7:LYS:O	14:N:11:VAL:HG23	2.16	0.46
35:IA:55:GLY:O	35:IA:58:ILE:HG22	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:MA:114:GLU:HG2	38:MA:163:ILE:HG12	1.97	0.46
43:SA:73:GLU:O	43:SA:76:THR:OG1	2.29	0.46
58:HB:36:PHE:HB3	58:HB:39:LYS:HB2	1.97	0.46
1:A:1367:C:H5''	46:VA:115:VAL:HG23	1.97	0.46
1:A:1436:U:H2'	1:A:1437:A:C8	2.50	0.46
2:B:759:G:H2'	2:B:760:G:C8	2.50	0.46
2:B:2220:U:H2'	2:B:2221:G:H8	1.81	0.46
2:B:2470:G:H2'	2:B:2471:A:C8	2.50	0.46
2:B:2699:C:H2'	2:B:2700:A:H8	1.81	0.46
12:L:20:LYS:HB2	12:L:88:HIS:HD2	1.79	0.46
38:MA:214:LEU:C	38:MA:216:ASP:H	2.23	0.46
40:PA:168:ARG:NH2	40:PA:170:GLY:O	2.48	0.46
46:VA:56:MET:O	46:VA:58:GLU:N	2.48	0.46
49:YA:98:ARG:HB2	49:YA:116:TYR:HA	1.98	0.46
51:AB:55:SER:HB3	51:AB:56:SER:H	1.51	0.46
52:BB:66:LEU:HD23	52:BB:66:LEU:HA	1.76	0.46
1:A:647:C:H2'	1:A:648:A:H8	1.80	0.46
2:B:254:G:O2'	2:B:255:A:O4'	2.33	0.46
2:B:938:G:H2'	2:B:939:G:H8	1.80	0.46
14:N:17:VAL:HG23	14:N:137:PRO:HB2	1.97	0.46
14:N:93:ILE:HD13	14:N:100:VAL:HG21	1.98	0.46
22:V:7:SER:OG	22:V:8:GLY:N	2.49	0.46
43:SA:51:ILE:C	43:SA:53:LYS:H	2.24	0.46
45:UA:88:LYS:O	45:UA:91:LEU:HD23	2.16	0.46
53:CB:78:VAL:O	53:CB:78:VAL:HG22	2.16	0.46
1:A:673:A:H2'	1:A:674:G:C8	2.50	0.46
1:A:875:U:H1'	45:UA:15:ASN:HD21	1.81	0.46
1:A:1314:C:H2'	1:A:1315:U:C6	2.50	0.46
2:B:1114:C:H2'	2:B:1115:G:C8	2.51	0.46
2:B:2880:C:O2	18:R:93:GLY:N	2.47	0.46
5:E:163:TYR:HB2	5:E:171:ILE:HG12	1.98	0.46
11:K:95:GLY:C	11:K:96:THR:HG1	2.23	0.46
17:Q:47:GLU:OE2	17:Q:50:ARG:NH1	2.48	0.46
37:KA:8:A:H2'	37:KA:9:G:C8	2.48	0.46
39:OA:173:LYS:O	39:OA:177:ASN:ND2	2.49	0.46
43:SA:59:TYR:HE2	55:EB:66:LEU:HD21	1.81	0.46
47:WA:49:PHE:CZ	51:AB:76:LYS:HD3	2.49	0.46
55:EB:71:ASP:OD1	55:EB:72:ARG:N	2.49	0.46
1:A:52:C:H2'	1:A:53:A:C8	2.50	0.46
2:B:1190:G:H2'	2:B:1191:G:H8	1.79	0.46
2:B:1527:G:N1	2:B:1544:A:OP2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2009:A:H2'	2:B:2010:G:H8	1.80	0.46
2:B:2087:G:H2'	2:B:2088:A:C8	2.50	0.46
2:B:2359:C:O2'	35:IA:53:ASP:OD2	2.34	0.46
2:B:2483:C:N3	17:Q:123:LYS:NZ	2.62	0.46
3:C:41:G:H1	9:I:68:LYS:HE2	1.80	0.46
7:G:4:LEU:HG	7:G:32:ASN:ND2	2.30	0.46
11:K:40:THR:O	11:K:42:LYS:N	2.48	0.46
18:R:28:LEU:HD23	18:R:48:VAL:HG21	1.98	0.46
42:RA:40:ASP:OD2	42:RA:44:ARG:HB3	2.15	0.46
1:A:59:A:H5'	1:A:60:A:H5''	1.98	0.46
1:A:599:C:H2'	1:A:600:A:H8	1.81	0.46
1:A:601:G:H2'	1:A:602:A:C8	2.51	0.46
2:B:636:G:H3'	16:P:128:THR:HG21	1.97	0.46
2:B:1074:G:H3'	2:B:1075:C:H5''	1.97	0.46
2:B:1440:U:H2'	2:B:1441:G:C8	2.51	0.46
2:B:2146:C:H4'	2:B:2147:A:N7	2.31	0.46
2:B:2591:C:OP1	6:F:237:ARG:HD2	2.16	0.46
23:W:15:GLN:HE22	32:FA:16:ARG:HH22	1.62	0.46
24:X:8:LEU:HD23	24:X:50:LEU:HD21	1.98	0.46
37:KA:20:A:O2'	38:MA:303:ARG:NH2	2.49	0.46
38:MA:248:HIS:CE1	38:MA:250:PRO:HD2	2.50	0.46
41:QA:58:GLN:OE1	41:QA:62:ARG:NH1	2.49	0.46
43:SA:12:PRO:O	43:SA:15:SER:CB	2.64	0.46
1:A:363:A:H5'	49:YA:30:ARG:HB2	1.97	0.46
2:B:28:A:H2	21:U:10:ARG:HH12	1.63	0.46
6:F:123:ILE:HG23	6:F:191:LEU:HD13	1.97	0.46
13:M:75:ALA:HB3	13:M:131:THR:HG21	1.97	0.46
38:MA:42:TYR:HA	38:MA:45:LEU:HB3	1.98	0.46
41:QA:10:LEU:HD13	41:QA:62:ARG:HD3	1.99	0.46
1:A:5:U:H3	41:QA:83:GLY:N	2.14	0.45
1:A:1513:A:H2'	1:A:1514:G:H8	1.81	0.45
2:B:2398:U:H2'	2:B:2399:G:H8	1.81	0.45
5:E:31:LYS:HD2	5:E:185:LEU:HD12	1.98	0.45
6:F:48:ILE:HD11	6:F:51:ARG:HA	1.97	0.45
21:U:51:GLN:OE1	21:U:54:ARG:NH1	2.48	0.45
26:Z:72:VAL:HG12	26:Z:93:ARG:HA	1.98	0.45
28:BA:27:ARG:HE	28:BA:29:LEU:HD21	1.80	0.45
46:VA:30:ASN:O	46:VA:31:GLN:HB2	2.16	0.45
51:AB:64:CYS:HB3	51:AB:79:LEU:N	2.31	0.45
2:B:796:C:H2'	2:B:797:G:C8	2.51	0.45
2:B:1791:A:H5''	6:F:204:LEU:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2041:U:H2'	2:B:2042:A:H8	1.81	0.45
2:B:2328:A:H2'	2:B:2329:U:C6	2.51	0.45
2:B:2875:C:H2'	2:B:2876:G:H8	1.81	0.45
14:N:4:PHE:O	21:U:63:ARG:NH2	2.49	0.45
53:CB:75:ILE:O	53:CB:79:ASN:ND2	2.50	0.45
54:DB:56:ASP:OD1	54:DB:56:ASP:N	2.49	0.45
58:HB:13:VAL:HG12	58:HB:14:ALA:H	1.81	0.45
2:B:155:A:H2'	2:B:156:A:C8	2.52	0.45
2:B:1190:G:H2'	2:B:1191:G:C8	2.51	0.45
2:B:1444:G:H2'	2:B:1445:G:H8	1.82	0.45
2:B:1704:C:H2'	2:B:1705:A:C8	2.51	0.45
5:E:180:PHE:HB2	5:E:185:LEU:HG	1.97	0.45
18:R:114:GLU:OE1	18:R:118:ARG:NH2	2.49	0.45
30:DA:23:LEU:HD11	30:DA:53:MET:SD	2.57	0.45
1:A:10:A:H2'	1:A:11:G:H8	1.82	0.45
1:A:418:C:H2'	1:A:419:C:C6	2.51	0.45
1:A:977:A:O2'	1:A:979:C:OP2	2.34	0.45
1:A:1386:G:H2'	1:A:1387:G:C8	2.49	0.45
2:B:629:G:N3	2:B:639:U:O2'	2.49	0.45
2:B:2368:C:H2'	2:B:2369:A:H8	1.80	0.45
3:C:7:G:H5'	19:S:29:HIS:ND1	2.31	0.45
5:E:175:ILE:HG13	5:E:192:LEU:HD23	1.97	0.45
7:G:10:GLY:H	7:G:197:THR:HG23	1.82	0.45
12:L:21:GLY:HA3	12:L:86:MET:HE3	1.99	0.45
20:T:15:ASP:OD1	20:T:15:ASP:N	2.46	0.45
40:PA:11:LEU:HD11	51:AB:88:ALA:O	2.16	0.45
1:A:675:A:H2'	1:A:676:A:H8	1.81	0.45
2:B:302:C:H2'	2:B:303:G:H8	1.82	0.45
2:B:742:A:H2'	2:B:743:A:H8	1.82	0.45
2:B:781:A:OP1	6:F:216:ARG:NH2	2.50	0.45
2:B:2875:C:H2'	2:B:2876:G:C8	2.52	0.45
3:C:76:G:H2'	3:C:77:U:C6	2.51	0.45
3:C:93:C:H2'	3:C:94:A:H8	1.81	0.45
5:E:98:GLU:HB3	5:E:123:VAL:HG11	1.99	0.45
6:F:120:ASP:HB2	11:K:91:PHE:HE1	1.80	0.45
13:M:34:ILE:H	13:M:34:ILE:HD12	1.82	0.45
54:DB:57:VAL:HB	54:DB:78:VAL:HG21	1.97	0.45
1:A:710:G:H2'	1:A:711:G:H8	1.82	0.45
1:A:859:G:OP2	1:A:869:G:N1	2.44	0.45
1:A:1106:G:H5''	40:PA:171:ARG:HG2	1.99	0.45
1:A:1354:U:H2'	1:A:1355:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1409:C:H2'	1:A:1410:A:H8	1.81	0.45
2:B:1178:C:H2'	2:B:1179:G:C8	2.51	0.45
2:B:1765:U:H2'	2:B:1766:G:H8	1.81	0.45
2:B:1792:G:O2'	2:B:1830:C:OP1	2.35	0.45
2:B:2026:U:H2'	2:B:2027:G:H8	1.82	0.45
2:B:2417:C:H2'	2:B:2418:A:C8	2.52	0.45
2:B:2455:G:H2'	2:B:2456:C:C6	2.52	0.45
2:B:2586:U:H2'	2:B:2587:A:C8	2.51	0.45
10:J:120:ILE:HG23	10:J:134:GLY:HA3	1.98	0.45
15:O:91:SER:O	15:O:92:GLU:C	2.59	0.45
1:A:519:C:N4	1:A:520:A:C6	2.85	0.45
2:B:242:G:N7	35:IA:4:LYS:HG2	2.31	0.45
2:B:1136:G:H2'	2:B:1137:G:H8	1.81	0.45
2:B:1251:C:OP2	21:U:5:ARG:NH2	2.48	0.45
2:B:1550:C:H2'	2:B:1551:A:H8	1.82	0.45
2:B:2126:A:H2'	2:B:2162:G:H22	1.80	0.45
2:B:2229:U:H2'	2:B:2230:G:H8	1.82	0.45
2:B:2466:C:OP1	36:JA:4:ARG:HB3	2.17	0.45
5:E:97:MET:HB3	5:E:100:LEU:HB3	1.97	0.45
5:E:124:VAL:O	5:E:124:VAL:HG12	2.16	0.45
11:K:87:GLU:OE1	43:SA:24:ARG:NH1	2.44	0.45
22:V:5:PHE:HB3	22:V:59:ILE:HD12	1.98	0.45
38:MA:342:GLU:O	38:MA:343:PRO:C	2.54	0.45
51:AB:87:ALA:HB1	51:AB:93:ILE:HG13	1.99	0.45
53:CB:22:ALA:HA	53:CB:33:ILE:HD12	1.98	0.45
1:A:1479:C:H2'	1:A:1480:A:H8	1.81	0.45
2:B:1295:C:H2'	2:B:1296:G:H8	1.82	0.45
2:B:1368:G:H2'	2:B:1369:G:C8	2.49	0.45
2:B:2230:G:H2'	2:B:2231:U:H6	1.82	0.45
5:E:20:GLN:HG2	5:E:225:ASP:HB3	1.99	0.45
19:S:33:ARG:O	19:S:34:HIS:CG	2.70	0.45
21:U:20:ALA:O	21:U:23:TYR:HD2	1.99	0.45
23:W:24:ILE:HD13	23:W:36:LEU:HD11	1.99	0.45
23:W:107:VAL:HG22	23:W:108:SER:H	1.82	0.45
26:Z:9:ARG:HG2	26:Z:41:GLU:HB2	1.99	0.45
27:AA:55:LEU:HD22	27:AA:76:ILE:HD12	1.99	0.45
38:MA:54:ASP:HB3	38:MA:88:LYS:CE	2.46	0.45
46:VA:56:MET:O	46:VA:57:VAL:C	2.60	0.45
50:ZA:80:MET:O	50:ZA:91:ARG:NH1	2.49	0.45
50:ZA:86:ARG:HG3	50:ZA:96:VAL:HG13	1.99	0.45
54:DB:75:VAL:HG12	54:DB:76:ARG:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:621:A:OP2	16:P:99:ASN:ND2	2.49	0.45
2:B:2124:G:N2	5:E:217:THR:HA	2.31	0.45
2:B:2298:A:OP1	9:I:70:ARG:NH2	2.48	0.45
3:C:9:G:H2'	3:C:10:G:C8	2.51	0.45
4:D:12:G:H2'	4:D:13:C:C6	2.52	0.45
12:L:29:ASP:H	12:L:56:ARG:NH2	2.15	0.45
45:UA:65:PHE:O	45:UA:67:GLY:N	2.50	0.45
51:AB:33:VAL:HA	51:AB:41:ARG:HH22	1.82	0.45
1:A:545:C:OP2	41:QA:61:ARG:NH1	2.50	0.45
1:A:562:U:H2'	49:YA:13:ARG:HD3	1.99	0.45
1:A:987:G:H2'	1:A:988:G:H8	1.82	0.45
1:A:1507:A:H2'	1:A:1508:A:C8	2.52	0.45
1:A:1521:C:H2'	1:A:1522:U:C6	2.52	0.45
2:B:1072:C:H42	2:B:1092:C:N4	2.15	0.45
2:B:1086:A:N6	12:L:37:LYS:HZ1	2.14	0.45
2:B:1105:U:H2'	2:B:1106:G:H8	1.82	0.45
2:B:1440:U:H2'	2:B:1441:G:H8	1.81	0.45
2:B:2330:G:H21	27:AA:38:GLY:HA2	1.81	0.45
2:B:2756:U:H4'	2:B:2757:A:OP1	2.15	0.45
2:B:2898:U:H2'	2:B:2899:A:C8	2.52	0.45
2:B:2898:U:H2'	2:B:2899:A:H8	1.82	0.45
15:O:41:ILE:HG13	15:O:58:LEU:O	2.17	0.45
1:A:532:A:H62	1:A:1206:G:H21	1.65	0.44
1:A:1307:U:OP1	50:ZA:99:GLN:NE2	2.50	0.44
1:A:1496:C:O2	1:A:1517:G:N2	2.43	0.44
2:B:52:A:OP2	2:B:117:G:N1	2.46	0.44
2:B:1291:C:H2'	2:B:1292:G:H8	1.82	0.44
2:B:2555:U:O2	38:MA:228:ARG:HB2	2.17	0.44
2:B:2557:G:H2'	2:B:2558:C:C6	2.51	0.44
2:B:2590:A:C2	2:B:2604:U:H5	2.35	0.44
19:S:62:LEU:HD21	19:S:73:ALA:HB2	1.99	0.44
31:EA:45:THR:O	31:EA:48:GLN:HB2	2.17	0.44
4:LA:63:G:H2'	4:LA:64:G:H8	1.81	0.44
40:PA:18:ASN:O	40:PA:39:ARG:NH2	2.50	0.44
41:QA:165:GLU:OE2	41:QA:167:PRO:HD3	2.16	0.44
54:DB:24:ILE:HD11	54:DB:60:ILE:HD11	1.99	0.44
1:A:131:A:H2'	1:A:132:C:C6	2.51	0.44
1:A:141:G:H2'	1:A:142:G:H8	1.83	0.44
1:A:830:G:H2'	1:A:831:A:C8	2.52	0.44
1:A:977:A:H2'	1:A:978:A:H5''	1.98	0.44
2:B:1604:C:H2'	2:B:1605:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AB:62:ASN:HB2	51:AB:73:PHE:HB2	1.99	0.44
51:AB:74:LEU:C	51:AB:76:LYS:H	2.25	0.44
55:EB:62:ARG:HB3	55:EB:69:TYR:HE1	1.82	0.44
1:A:823:C:H2'	1:A:824:G:C8	2.52	0.44
2:B:658:U:O2'	8:H:97:ASN:ND2	2.51	0.44
2:B:2086:U:H2'	2:B:2087:G:H8	1.82	0.44
3:C:24:G:C6	3:C:56:G:C2	3.06	0.44
6:F:140:VAL:HG11	6:F:189:ALA:HB1	1.99	0.44
6:F:140:VAL:HG22	6:F:191:LEU:HD23	2.00	0.44
4:LA:17:C:OP1	4:LA:60:U:O2'	2.35	0.44
41:QA:146:GLU:HA	41:QA:149:LYS:HG2	1.99	0.44
49:YA:80:LEU:HD13	49:YA:100:ALA:HB1	2.00	0.44
56:FB:66:VAL:HG23	56:FB:67:GLY:H	1.82	0.44
1:A:545:C:OP1	41:QA:57:LYS:NZ	2.50	0.44
1:A:1384:C:H2'	1:A:1385:G:C8	2.53	0.44
2:B:596:U:H2'	2:B:597:G:C8	2.53	0.44
2:B:1954:G:N2	2:B:1956:U:H3	2.16	0.44
2:B:1993:U:H4'	7:G:133:THR:HG22	1.99	0.44
2:B:2655:G:N2	2:B:2665:A:OP2	2.49	0.44
3:C:5:U:H2'	3:C:6:G:C8	2.51	0.44
3:C:49:C:H2'	3:C:50:A:H8	1.83	0.44
18:R:59:SER:OG	18:R:60:VAL:N	2.50	0.44
42:RA:104:ILE:HG23	42:RA:104:ILE:O	2.17	0.44
43:SA:48:ALA:H	55:EB:65:SER:HG	1.66	0.44
47:WA:83:THR:O	47:WA:87:LEU:N	2.48	0.44
1:A:708:C:H2'	1:A:709:U:H6	1.83	0.44
1:A:1062:U:H2'	1:A:1063:C:C6	2.52	0.44
1:A:1219:A:H2'	1:A:1220:G:C8	2.53	0.44
2:B:572:A:OP2	22:V:79:ARG:NH1	2.50	0.44
2:B:1165:A:H2'	2:B:1166:G:C8	2.50	0.44
5:E:60:ARG:HG2	5:E:164:ARG:HA	1.99	0.44
21:U:104:ALA:HA	22:V:46:GLU:HG3	2.00	0.44
41:QA:201:GLU:OE1	42:RA:111:ARG:NH1	2.50	0.44
1:A:522:C:OP2	49:YA:65:TYR:OH	2.32	0.44
2:B:24:G:C2	2:B:25:U:C2	3.05	0.44
2:B:680:C:H2'	2:B:681:G:C8	2.52	0.44
2:B:1055:G:H1	2:B:1104:C:H42	1.64	0.44
2:B:1363:C:H2'	2:B:1364:G:H8	1.82	0.44
2:B:1539:U:H2'	2:B:1540:G:C8	2.53	0.44
2:B:1889:A:H2'	2:B:1890:A:H8	1.83	0.44
6:F:106:PRO:HD2	6:F:109:LEU:HD22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:50:LEU:HD12	24:X:50:LEU:N	2.33	0.44
40:PA:8:GLY:HA3	51:AB:89:MET:CE	2.46	0.44
1:A:45:G:H2'	1:A:46:G:H8	1.82	0.44
1:A:105:G:OP2	57:GB:12:GLN:NE2	2.51	0.44
1:A:708:C:H2'	1:A:709:U:C6	2.53	0.44
1:A:737:C:H2'	1:A:738:C:C6	2.53	0.44
1:A:1313:U:OP1	56:FB:5:LYS:HB3	2.18	0.44
2:B:247:G:H4'	2:B:386:G:C2	2.52	0.44
2:B:376:G:C2	2:B:377:G:N7	2.86	0.44
2:B:647:G:N2	2:B:2350:C:O2'	2.48	0.44
2:B:690:G:H2'	2:B:691:C:H6	1.83	0.44
2:B:1013:C:H2'	2:B:1014:A:C8	2.51	0.44
2:B:1509:A:H2'	2:B:1510:G:C8	2.52	0.44
2:B:2590:A:H2'	2:B:2591:C:C6	2.53	0.44
2:B:2591:C:H2'	2:B:2592:G:C8	2.52	0.44
2:B:2720:U:H5''	20:T:52:ARG:NH2	2.32	0.44
11:K:7:ASP:HB3	11:K:9:VAL:HG23	2.00	0.44
12:L:29:ASP:H	12:L:56:ARG:HH22	1.64	0.44
23:W:72:THR:HG22	23:W:73:LYS:HG3	1.99	0.44
26:Z:38:LEU:HG	26:Z:40:ILE:HD11	2.00	0.44
38:MA:54:ASP:HB3	38:MA:88:LYS:NZ	2.33	0.44
48:XA:83:VAL:HG11	48:XA:96:ILE:HG22	1.98	0.44
48:XA:126:ARG:HB3	58:HB:33:ARG:CZ	2.48	0.44
48:XA:126:ARG:O	58:HB:33:ARG:NH2	2.51	0.44
1:A:455:G:H2'	1:A:456:A:C8	2.52	0.44
1:A:797:C:H2'	1:A:798:U:C6	2.53	0.44
1:A:1198:G:H2'	1:A:1199:U:C6	2.53	0.44
2:B:1259:G:H2'	2:B:1260:A:C8	2.52	0.44
2:B:2010:G:OP1	23:W:41:LYS:HG3	2.18	0.44
2:B:2884:U:C6	32:FA:49:ARG:HG2	2.52	0.44
3:C:7:G:O2'	19:S:38:GLN:NE2	2.51	0.44
9:I:139:GLU:OE1	9:I:139:GLU:N	2.50	0.44
1:A:715:A:H2'	1:A:716:A:C8	2.51	0.44
1:A:828:U:N3	1:A:859:G:N3	2.66	0.44
2:B:463:G:N2	2:B:466:A:OP2	2.45	0.44
2:B:1030:C:H2'	2:B:1031:G:H8	1.83	0.44
2:B:1306:C:H2'	2:B:1307:A:H8	1.83	0.44
2:B:2641:G:H2'	2:B:2642:G:H8	1.83	0.44
6:F:153:LEU:HB3	6:F:175:LEU:HD11	2.00	0.44
11:K:135:HIS:CG	11:K:136:SER:H	2.36	0.44
21:U:94:LEU:HD23	21:U:94:LEU:HA	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:GB:4:LYS:C	57:GB:6:ALA:H	2.24	0.44
1:A:501:C:H2'	1:A:502:A:H8	1.83	0.43
1:A:784:A:H2'	1:A:785:G:C8	2.53	0.43
1:A:824:G:H2'	1:A:825:A:H8	1.83	0.43
2:B:914:G:H5'	2:B:915:C:OP2	2.18	0.43
2:B:968:C:H2'	2:B:969:G:C8	2.53	0.43
2:B:2024:G:OP2	2:B:2034:U:H4'	2.17	0.43
2:B:2772:C:H5'	7:G:173:GLN:HE21	1.82	0.43
7:G:178:VAL:HG12	7:G:179:ARG:HG3	2.00	0.43
10:J:37:ASN:HD22	10:J:38:ASP:H	1.65	0.43
31:EA:44:PHE:CD2	31:EA:45:THR:HG23	2.53	0.43
40:PA:4:VAL:CG1	40:PA:5:HIS:H	2.17	0.43
47:WA:67:ILE:O	47:WA:67:ILE:HG13	2.18	0.43
58:HB:11:PHE:HB2	58:HB:15:LEU:HD12	1.99	0.43
58:HB:17:ARG:HB3	58:HB:20:ARG:HH21	1.81	0.43
1:A:204:G:H2'	1:A:205:A:C8	2.53	0.43
1:A:520:A:OP1	49:YA:48:LEU:HB2	2.19	0.43
1:A:707:U:H2'	1:A:708:C:C6	2.53	0.43
1:A:1436:U:H2'	1:A:1437:A:H8	1.82	0.43
2:B:776:G:N2	2:B:2241:A:OP1	2.47	0.43
2:B:1022:G:N7	14:N:68:LYS:HD3	2.33	0.43
2:B:1592:C:H2'	2:B:1593:A:C8	2.52	0.43
2:B:1843:C:H2'	2:B:1844:C:C6	2.52	0.43
7:G:133:THR:O	7:G:134:HIS:HB2	2.18	0.43
23:W:36:LEU:HA	23:W:36:LEU:HD23	1.79	0.43
30:DA:9:THR:HG22	30:DA:53:MET:O	2.19	0.43
31:EA:24:ILE:HG22	31:EA:25:ARG:N	2.34	0.43
44:TA:67:ASN:O	44:TA:137:ARG:NH1	2.51	0.43
49:YA:77:SER:HB2	49:YA:102:ASP:HB3	2.00	0.43
51:AB:63:ARG:O	51:AB:65:ARG:N	2.52	0.43
51:AB:80:SER:C	51:AB:82:ILE:N	2.76	0.43
1:A:613:C:P	41:QA:80:ARG:HH21	2.42	0.43
2:B:871:U:H2'	2:B:872:U:C6	2.53	0.43
2:B:1161:C:H2'	2:B:1162:G:C8	2.53	0.43
2:B:1437:C:H2'	2:B:1438:U:C6	2.54	0.43
2:B:2555:U:O2'	38:MA:228:ARG:NH2	2.51	0.43
6:F:32:LEU:HD11	6:F:100:ARG:O	2.18	0.43
8:H:143:LEU:HD22	8:H:185:LYS:HG3	1.99	0.43
14:N:35:ARG:HD3	14:N:40:HIS:CD2	2.53	0.43
17:Q:68:PHE:HA	17:Q:69:PRO:HD3	1.89	0.43
27:AA:21:ARG:HB3	27:AA:25:GLU:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:FA:2:VAL:HG12	32:FA:3:GLN:O	2.18	0.43
38:MA:108:GLU:HB2	38:MA:170:GLY:HA2	2.00	0.43
39:OA:40:ILE:HD12	39:OA:201:GLY:HA2	2.00	0.43
49:YA:86:VAL:HG23	49:YA:89:LEU:HB2	1.99	0.43
1:A:1349:A:H3'	1:A:1350:A:H8	1.84	0.43
1:A:1477:U:H2'	1:A:1478:U:C6	2.53	0.43
2:B:947:A:H2'	2:B:948:C:C6	2.54	0.43
2:B:1709:U:H2'	2:B:1710:G:C8	2.53	0.43
2:B:1822:C:H2'	2:B:1823:G:H8	1.84	0.43
2:B:2291:U:OP1	2:B:2380:C:O2'	2.36	0.43
2:B:2296:U:O2'	2:B:2297:A:O5'	2.33	0.43
3:C:7:G:H5'	19:S:29:HIS:CE1	2.53	0.43
9:I:37:MET:HE3	9:I:149:ARG:HB3	2.00	0.43
18:R:29:VAL:O	18:R:29:VAL:HG12	2.18	0.43
26:Z:40:ILE:HG22	26:Z:42:LEU:HD12	2.00	0.43
38:MA:191:GLU:HG3	38:MA:193:GLN:H	1.83	0.43
38:MA:217:ILE:HD13	38:MA:219:PRO:HD3	1.99	0.43
40:PA:120:THR:HG23	40:PA:188:ALA:HB2	2.00	0.43
46:VA:86:LEU:HD23	46:VA:86:LEU:HA	1.87	0.43
1:A:335:C:H2'	1:A:336:A:H8	1.83	0.43
1:A:537:G:H5''	49:YA:109:ARG:NH1	2.27	0.43
1:A:806:C:H2'	1:A:807:A:C8	2.53	0.43
1:A:979:C:OP1	1:A:1223:C:N4	2.51	0.43
1:A:1106:G:O2'	40:PA:168:ARG:NH2	2.52	0.43
1:A:1251:A:O2'	1:A:1370:G:H5'	2.19	0.43
1:A:1425:U:H2'	1:A:1426:G:H8	1.83	0.43
1:A:1521:C:H2'	1:A:1522:U:H6	1.84	0.43
2:B:840:C:H2'	2:B:841:G:H8	1.84	0.43
2:B:993:G:OP2	21:U:50:ARG:NH2	2.51	0.43
2:B:1133:A:H4'	2:B:1134:A:H5''	2.00	0.43
2:B:1316:U:H2'	2:B:1317:G:C8	2.50	0.43
2:B:1825:U:H2'	2:B:1826:G:C8	2.54	0.43
2:B:2271:G:C5	2:B:2272:U:C4	3.06	0.43
2:B:2848:G:C8	20:T:94:ALA:HB2	2.54	0.43
13:M:54:ILE:CG2	13:M:55:PRO:CD	2.91	0.43
38:MA:304:SER:HB2	49:YA:48:LEU:CD1	2.49	0.43
43:SA:39:LEU:HD12	43:SA:39:LEU:HA	1.91	0.43
1:A:390:U:H4'	53:CB:28:ARG:HH11	1.83	0.43
1:A:392:C:O2	1:A:392:C:H2'	2.19	0.43
1:A:477:C:H2'	1:A:478:A:C8	2.53	0.43
1:A:634:C:H2'	1:A:635:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1526:G:H2'	1:A:1527:U:C6	2.53	0.43
2:B:63:A:H4'	24:X:77:ARG:NH1	2.33	0.43
2:B:1256:G:N2	8:H:77:ILE:O	2.50	0.43
2:B:2106:U:H2'	2:B:2107:G:C8	2.54	0.43
3:C:93:C:H2'	3:C:94:A:C8	2.54	0.43
9:I:58:ALA:O	9:I:139:GLU:HG2	2.19	0.43
12:L:24:SER:C	12:L:116:GLU:HB2	2.39	0.43
13:M:54:ILE:HG22	13:M:55:PRO:HD2	1.97	0.43
16:P:123:ARG:NH1	16:P:143:GLU:OE2	2.52	0.43
22:V:46:GLU:OE2	22:V:48:LYS:HB3	2.18	0.43
38:MA:214:LEU:HD23	38:MA:214:LEU:H	1.83	0.43
41:QA:111:ALA:O	41:QA:114:ARG:HG3	2.19	0.43
51:AB:2:LYS:O	51:AB:5:MET:HB2	2.18	0.43
53:CB:4:ILE:HD13	53:CB:67:ILE:HG12	2.01	0.43
1:A:202:G:H2'	1:A:203:G:H8	1.84	0.43
1:A:797:C:OP1	48:XA:125:LYS:HB2	2.19	0.43
1:A:948:C:H2'	1:A:949:A:C8	2.53	0.43
2:B:1155:A:O2'	2:B:1156:A:H2'	2.18	0.43
7:G:5:VAL:HG21	7:G:80:TRP:CG	2.53	0.43
46:VA:23:GLY:H	46:VA:60:LEU:HA	1.83	0.43
47:WA:40:ILE:HB	47:WA:73:LEU:HB3	2.00	0.43
1:A:20:U:H2'	1:A:21:G:O4'	2.19	0.43
1:A:20:U:OP2	42:RA:129:SER:OG	2.27	0.43
1:A:684:U:O2'	48:XA:39:ASN:HB3	2.19	0.43
1:A:878:A:OP1	45:UA:79:ARG:HB2	2.19	0.43
2:B:572:A:H61	2:B:2029:G:H21	1.65	0.43
2:B:660:C:H2'	2:B:661:A:C8	2.54	0.43
2:B:1071:G:H1'	2:B:1089:A:C5	2.53	0.43
2:B:1387:A:H2'	2:B:1388:G:C8	2.53	0.43
2:B:1448:G:H2'	2:B:1449:G:H8	1.82	0.43
2:B:2680:U:H5'	7:G:194:PRO:HA	2.01	0.43
9:I:71:LYS:HG2	9:I:72:SER:H	1.83	0.43
15:O:119:ALA:HA	15:O:120:PRO:HD3	1.89	0.43
20:T:91:VAL:HG21	20:T:96:LEU:HD11	2.00	0.43
46:VA:33:SER:H	46:VA:36:GLN:HE21	1.66	0.43
50:ZA:79:LEU:HD12	50:ZA:86:ARG:HB3	1.99	0.43
51:AB:63:ARG:HA	51:AB:68:GLY:O	2.19	0.43
1:A:310:G:H5''	53:CB:31:ARG:HB2	2.01	0.43
1:A:634:C:H2'	1:A:635:A:H8	1.83	0.43
1:A:1414:U:H2'	1:A:1415:G:C8	2.53	0.43
2:B:817:C:H2'	2:B:818:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2685:G:H2'	2:B:2686:G:C8	2.54	0.43
4:D:16:C:H4'	4:D:60:U:H1'	2.00	0.43
4:D:24:U:H2'	4:D:25:C:H6	1.83	0.43
6:F:124:LYS:HB3	6:F:127:ASN:OD1	2.19	0.43
9:I:135:ILE:HA	9:I:140:ILE:HG21	2.01	0.43
11:K:145:ASN:HD22	11:K:146:VAL:N	2.17	0.43
13:M:112:LYS:HD2	13:M:128:ILE:HD11	2.00	0.43
16:P:108:ALA:HB3	16:P:125:LEU:HD22	2.00	0.43
18:R:40:LYS:O	18:R:44:LEU:N	2.50	0.43
34:HA:4:THR:OG1	34:HA:5:PHE:N	2.51	0.43
35:IA:29:ARG:HD3	35:IA:29:ARG:HA	1.92	0.43
38:MA:126:LEU:HA	38:MA:157:GLY:O	2.19	0.43
45:UA:73:SER:HB2	45:UA:129:ALA:HB3	2.01	0.43
50:ZA:28:ARG:HH21	50:ZA:62:PHE:HB2	1.84	0.43
57:GB:54:GLN:N	57:GB:55:PRO:HD2	2.33	0.43
1:A:45:G:H2'	1:A:46:G:C8	2.54	0.43
1:A:1011:C:H2'	1:A:1012:A:C8	2.54	0.43
2:B:151:C:H2'	2:B:152:A:H8	1.84	0.43
2:B:582:A:H2'	2:B:583:G:C8	2.53	0.43
2:B:1248:G:C2	21:U:2:ARG:HD2	2.54	0.43
2:B:2599:G:H2'	2:B:2600:A:C8	2.54	0.43
19:S:34:HIS:CE1	19:S:54:VAL:HA	2.54	0.43
25:Y:32:LYS:HB3	25:Y:63:ALA:HB1	2.01	0.43
26:Z:29:ILE:HG13	26:Z:30:ILE:N	2.34	0.43
56:FB:4:LEU:HB3	56:FB:5:LYS:H	1.63	0.43
2:B:106:C:H2'	2:B:107:G:C8	2.54	0.42
2:B:131:A:H2'	2:B:132:G:H8	1.84	0.42
2:B:521:U:H2'	2:B:522:A:C8	2.53	0.42
2:B:851:C:H2'	2:B:852:U:C6	2.54	0.42
2:B:1667:G:H22	2:B:1991:U:H3'	1.85	0.42
2:B:2699:C:H2'	2:B:2700:A:C8	2.53	0.42
2:B:2818:U:H2'	2:B:2819:G:C8	2.53	0.42
4:D:59:A:C2'	4:D:60:U:H5'	2.48	0.42
4:D:62:C:H2'	4:D:63:G:C8	2.54	0.42
11:K:58:LEU:O	11:K:61:VAL:HG22	2.19	0.42
11:K:67:ALA:O	11:K:70:GLU:HB3	2.19	0.42
4:LA:36:U:H2'	4:LA:37:A:H8	1.84	0.42
46:VA:89:TYR:O	46:VA:90:ASP:C	2.62	0.42
50:ZA:44:ILE:HD12	50:ZA:47:LEU:HD13	1.99	0.42
51:AB:88:ALA:O	51:AB:89:MET:HE3	2.19	0.42
52:BB:34:GLN:HG2	52:BB:58:MET:HE1	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1229:C:H2'	2:B:1230:A:H8	1.83	0.42
2:B:1766:G:H2'	2:B:1767:G:H8	1.83	0.42
9:I:78:ILE:O	9:I:78:ILE:HG13	2.19	0.42
19:S:6:ALA:O	19:S:9:ARG:HG3	2.20	0.42
49:YA:23:LEU:HD12	49:YA:58:ASN:ND2	2.33	0.42
1:A:309:A:H2'	1:A:310:G:H8	1.85	0.42
1:A:1052:U:H2'	1:A:1200:C:H41	1.85	0.42
2:B:154:U:H2'	2:B:155:A:H8	1.84	0.42
2:B:945:A:C5	2:B:2448:A:C2	3.07	0.42
2:B:1183:U:H2'	2:B:1184:U:C6	2.53	0.42
2:B:1550:C:H2'	2:B:1551:A:C8	2.54	0.42
2:B:2086:U:H2'	2:B:2087:G:C8	2.53	0.42
12:L:41:LEU:HD23	12:L:41:LEU:HA	1.89	0.42
12:L:117:LEU:C	12:L:119:PRO:HD3	2.45	0.42
18:R:43:GLU:OE2	18:R:46:ARG:NH2	2.51	0.42
28:BA:6:VAL:HG21	28:BA:58:ILE:HD11	2.01	0.42
39:OA:98:GLY:N	39:OA:174:GLU:OE2	2.42	0.42
46:VA:30:ASN:C	46:VA:32:ARG:H	2.27	0.42
50:ZA:86:ARG:HG3	50:ZA:96:VAL:CG1	2.50	0.42
1:A:129:A:H1'	1:A:130:A:N7	2.34	0.42
1:A:451:A:H4'	1:A:452:A:C4	2.54	0.42
1:A:1074:G:H2'	1:A:1075:U:C6	2.55	0.42
1:A:1412:C:H2'	1:A:1413:A:H8	1.84	0.42
2:B:338:G:C2	2:B:339:U:C2	3.07	0.42
2:B:593:U:H2'	2:B:594:U:C6	2.55	0.42
2:B:784:G:C2	6:F:227:VAL:HG11	2.54	0.42
2:B:968:C:H2'	2:B:969:G:H8	1.83	0.42
2:B:2576:G:O2'	2:B:2579:C:OP2	2.26	0.42
4:D:44:A:H2'	4:D:45:G:O4'	2.20	0.42
5:E:127:LEU:HD23	5:E:127:LEU:O	2.19	0.42
8:H:129:PRO:HG3	8:H:156:ASN:HA	2.01	0.42
13:M:102:ARG:N	13:M:140:GLU:O	2.53	0.42
22:V:51:VAL:O	22:V:52:PRO:C	2.61	0.42
25:Y:26:ASN:HB2	25:Y:34:ILE:HD11	2.01	0.42
39:OA:8:MET:HG2	39:OA:211:LEU:HD21	2.01	0.42
50:ZA:2:ARG:HA	50:ZA:7:ASN:O	2.19	0.42
51:AB:97:LYS:O	51:AB:98:LYS:HB2	2.18	0.42
1:A:405:U:O4	41:QA:1:ALA:N	2.46	0.42
1:A:420:U:O2'	1:A:422:C:OP1	2.32	0.42
1:A:672:U:H2'	1:A:673:A:C8	2.55	0.42
2:B:746:U:H1'	2:B:748:G:H21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1791:A:H4'	6:F:204:LEU:HB2	2.01	0.42
2:B:1972:G:H2'	2:B:1973:G:H8	1.85	0.42
7:G:5:VAL:HG21	7:G:80:TRP:CD2	2.55	0.42
22:V:34:GLU:HG2	22:V:60:LYS:HG2	2.01	0.42
23:W:74:ILE:HD13	23:W:105:VAL:HG22	2.02	0.42
41:QA:170:LEU:HD12	41:QA:170:LEU:O	2.19	0.42
1:A:458:U:H3	1:A:474:G:H1	1.68	0.42
1:A:1071:C:H2'	1:A:1072:G:H8	1.84	0.42
2:B:571:U:N3	2:B:575:A:N7	2.67	0.42
2:B:674:G:H1'	8:H:69:ARG:NH1	2.34	0.42
2:B:1164:C:H2'	2:B:1165:A:C8	2.54	0.42
2:B:1229:C:H2'	2:B:1230:A:C8	2.55	0.42
2:B:1793:C:H2'	2:B:1794:A:H8	1.84	0.42
2:B:2291:U:H2'	2:B:2292:U:C6	2.55	0.42
2:B:2306:C:N4	9:I:38:GLY:O	2.52	0.42
10:J:37:ASN:HD22	10:J:38:ASP:N	2.17	0.42
10:J:37:ASN:OD1	10:J:63:GLN:NE2	2.53	0.42
12:L:26:VAL:HA	12:L:82:ILE:HG23	2.01	0.42
12:L:28:ALA:HB2	12:L:111:ALA:HB2	2.01	0.42
38:MA:145:ARG:HG2	38:MA:146:VAL:N	2.31	0.42
40:PA:5:HIS:O	40:PA:7:ASN:N	2.52	0.42
41:QA:3:TYR:CD2	41:QA:10:LEU:HD11	2.54	0.42
46:VA:14:SER:OG	46:VA:69:GLY:HA3	2.19	0.42
49:YA:26:CYS:SG	49:YA:29:LYS:HD3	2.60	0.42
50:ZA:6:ILE:HG22	50:ZA:8:ILE:HG12	2.00	0.42
1:A:579:A:H2'	1:A:580:C:C6	2.55	0.42
1:A:811:C:O2'	1:A:901:A:N1	2.52	0.42
1:A:1515:G:H2'	1:A:1516:G:H8	1.85	0.42
2:B:181:A:H2'	2:B:182:A:H8	1.84	0.42
2:B:922:C:H2'	2:B:923:G:H8	1.83	0.42
2:B:1653:G:H3'	18:R:2:ARG:HG2	2.01	0.42
3:C:52:A:O2'	3:C:53:A:N7	2.41	0.42
10:J:53:PRO:HG2	10:J:61:TRP:CD2	2.54	0.42
11:K:47:PHE:HA	11:K:51:ARG:HB2	2.02	0.42
13:M:126:ARG:O	13:M:129:GLU:HB3	2.19	0.42
30:DA:11:SER:OG	30:DA:12:ALA:N	2.53	0.42
42:RA:165:GLY:HA3	45:UA:113:ARG:HD2	2.01	0.42
1:A:1228:C:P	50:ZA:106:ARG:HH12	2.43	0.42
1:A:1251:A:H2'	1:A:1252:A:C8	2.55	0.42
1:A:1432:G:H1'	1:A:1468:A:H62	1.84	0.42
1:A:1458:G:H2'	1:A:1459:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:414:C:H2'	2:B:415:A:C8	2.53	0.42
2:B:948:C:H2'	2:B:949:G:C8	2.53	0.42
2:B:1685:C:H2'	2:B:1686:C:C6	2.54	0.42
2:B:2316:G:H2'	2:B:2317:A:H8	1.85	0.42
2:B:2590:A:H2'	2:B:2591:C:H6	1.85	0.42
4:D:14:A:H2'	4:D:15:G:O4'	2.19	0.42
5:E:175:ILE:O	5:E:188:ASN:ND2	2.53	0.42
12:L:33:VAL:HG12	12:L:34:THR:N	2.35	0.42
19:S:7:ARG:HA	19:S:10:ARG:HH11	1.84	0.42
21:U:20:ALA:HA	21:U:23:TYR:CE2	2.54	0.42
22:V:27:ILE:HG13	22:V:33:VAL:HG22	2.01	0.42
1:A:986:U:H2'	1:A:987:G:C8	2.54	0.42
1:A:1492:A:C2	37:KA:21:U:H5''	2.52	0.42
2:B:910:A:N3	2:B:2264:C:O2'	2.53	0.42
2:B:1405:U:H2'	2:B:1406:U:C6	2.55	0.42
2:B:2002:G:OP1	18:R:17:ARG:NH2	2.53	0.42
36:JA:18:LYS:O	36:JA:18:LYS:HG2	2.20	0.42
41:QA:12:ARG:HG2	41:QA:37:PRO:HA	2.02	0.42
41:QA:100:VAL:HG21	41:QA:136:VAL:HG21	2.01	0.42
47:WA:12:ALA:HB3	47:WA:18:ILE:HD13	2.02	0.42
51:AB:8:ARG:HB3	51:AB:12:ARG:NH1	2.28	0.42
52:BB:49:HIS:O	52:BB:52:ARG:HB3	2.20	0.42
1:A:554:A:H2'	1:A:555:U:C6	2.55	0.42
2:B:279:A:H61	2:B:361:G:H1'	1.84	0.42
2:B:287:G:H2'	2:B:288:U:C6	2.55	0.42
2:B:728:G:O2'	2:B:730:A:H8	2.02	0.42
2:B:1127:A:H62	2:B:2488:G:H1'	1.84	0.42
2:B:1748:C:H2'	2:B:1749:A:H8	1.84	0.42
2:B:1954:G:H21	2:B:1956:U:H3	1.68	0.42
2:B:2159:G:H2'	2:B:2160:C:C6	2.55	0.42
2:B:2515:C:H2'	2:B:2516:A:H8	1.84	0.42
3:C:12:C:H42	27:AA:70:PRO:HD3	1.85	0.42
10:J:1:SER:HA	10:J:4:ALA:HB3	2.02	0.42
20:T:20:ARG:HD3	20:T:112:ARG:HH11	1.85	0.42
21:U:20:ALA:HA	21:U:23:TYR:HE2	1.85	0.42
22:V:38:VAL:O	22:V:54:VAL:HG23	2.19	0.42
4:LA:17:C:H5'	4:LA:61:C:OP1	2.20	0.42
38:MA:23:LEU:HD11	38:MA:38:LEU:HB3	2.02	0.42
38:MA:263:GLN:O	38:MA:267:LYS:N	2.49	0.42
40:PA:21:TRP:CB	40:PA:58:ARG:HB3	2.49	0.42
40:PA:33:ASP:OD2	51:AB:65:ARG:NH1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:SA:43:GLY:HA2	43:SA:58:HIS:CE1	2.55	0.42
1:A:625:U:H2'	1:A:626:G:H8	1.85	0.41
1:A:1464:U:H2'	1:A:1465:A:H8	1.84	0.41
2:B:191:A:H2'	2:B:192:C:C6	2.54	0.41
2:B:528:A:C2	2:B:2042:A:H2'	2.55	0.41
2:B:720:U:H2'	2:B:721:A:C8	2.54	0.41
2:B:1258:U:H2'	2:B:1259:G:C8	2.55	0.41
7:G:125:TRP:O	7:G:126:ASN:HB2	2.19	0.41
21:U:29:ARG:HD2	32:FA:9:ARG:HH12	1.85	0.41
47:WA:17:LEU:O	47:WA:17:LEU:HD13	2.20	0.41
1:A:34:C:H2'	1:A:35:G:H8	1.86	0.41
1:A:287:U:H2'	1:A:288:A:C8	2.55	0.41
1:A:598:U:H2'	1:A:599:C:C6	2.55	0.41
1:A:986:U:H2'	1:A:987:G:H8	1.84	0.41
1:A:1023:U:H2'	1:A:1024:G:C8	2.55	0.41
1:A:1464:U:H2'	1:A:1465:A:C8	2.54	0.41
1:A:1513:A:H2'	1:A:1514:G:C8	2.55	0.41
2:B:250:G:C6	2:B:251:A:C6	3.09	0.41
2:B:589:U:H2'	2:B:590:A:C8	2.55	0.41
2:B:591:U:H2'	2:B:592:A:H8	1.84	0.41
2:B:1103:A:H5''	2:B:1104:C:C5	2.56	0.41
2:B:1434:A:H2'	2:B:1435:G:C8	2.54	0.41
2:B:2115:G:HO2'	2:B:2117:A:N6	2.18	0.41
8:H:71:GLY:O	8:H:72:SER:CB	2.68	0.41
12:L:119:PRO:O	12:L:120:ALA:HB3	2.20	0.41
38:MA:191:GLU:HG3	38:MA:193:GLN:N	2.36	0.41
40:PA:123:LEU:HD13	40:PA:195:ILE:HG21	2.00	0.41
43:SA:29:ILE:HD13	43:SA:64:VAL:HG21	2.01	0.41
1:A:420:U:H2'	1:A:422:C:H1'	2.02	0.41
1:A:671:G:O2'	43:SA:79:ARG:NH2	2.52	0.41
1:A:1515:G:H2'	1:A:1516:G:C8	2.55	0.41
2:B:923:G:H2'	2:B:924:G:C8	2.56	0.41
2:B:1388:G:H2'	2:B:1389:G:H8	1.85	0.41
2:B:2593:U:H2'	2:B:2594:C:C6	2.55	0.41
2:B:2707:U:H2'	2:B:2708:G:H8	1.85	0.41
9:I:42:ALA:HB2	9:I:49:LEU:HB2	2.01	0.41
11:K:1:MET:N	11:K:21:VAL:O	2.53	0.41
21:U:90:ASP:OD1	21:U:90:ASP:N	2.51	0.41
22:V:58:VAL:O	22:V:58:VAL:HG13	2.20	0.41
4:LA:68:C:H2'	4:LA:69:C:C6	2.56	0.41
58:HB:36:PHE:HD1	58:HB:39:LYS:HD3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:A:H2'	1:A:237:G:H8	1.85	0.41
2:B:942:G:H2'	2:B:943:A:H8	1.86	0.41
2:B:2047:C:H2'	2:B:2048:G:H8	1.86	0.41
2:B:2355:G:O2'	27:AA:20:LYS:NZ	2.53	0.41
4:D:41:C:H2'	4:D:42:G:H8	1.83	0.41
18:R:117:ASP:HB3	18:R:118:ARG:H	1.48	0.41
38:MA:186:ARG:HH11	38:MA:312:PHE:HE2	1.68	0.41
39:OA:147:LEU:HD22	39:OA:150:ILE:HD11	2.02	0.41
40:PA:4:VAL:O	40:PA:5:HIS:HB2	2.20	0.41
42:RA:10:LEU:O	42:RA:11:GLN:C	2.63	0.41
42:RA:24:VAL:O	42:RA:26:GLY:N	2.53	0.41
52:BB:17:ASP:HB2	52:BB:20:ASP:HB2	2.01	0.41
53:CB:44:SER:OG	53:CB:45:GLU:N	2.53	0.41
1:A:1001:C:H2'	1:A:1002:G:H8	1.86	0.41
1:A:1308:U:H2'	1:A:1309:G:C8	2.54	0.41
2:B:518:G:O5'	23:W:18:ARG:NH1	2.53	0.41
2:B:971:G:O2'	2:B:983:A:N3	2.50	0.41
2:B:1084:A:N6	2:B:1085:A:N1	2.68	0.41
2:B:1597:A:H5''	2:B:1598:A:H5'	2.01	0.41
3:C:116:G:H2'	3:C:117:G:H8	1.86	0.41
11:K:38:PRO:O	11:K:43:ASN:ND2	2.50	0.41
12:L:117:LEU:C	12:L:119:PRO:CD	2.93	0.41
12:L:118:ILE:N	12:L:119:PRO:HD3	2.32	0.41
20:T:48:ALA:CB	20:T:95:LYS:HG3	2.50	0.41
36:JA:18:LYS:NZ	36:JA:21:GLY:HA2	2.35	0.41
4:LA:34:C:H2'	4:LA:35:A:C8	2.56	0.41
4:LA:41:C:H2'	4:LA:42:G:C8	2.53	0.41
42:RA:87:VAL:O	42:RA:87:VAL:HG13	2.19	0.41
54:DB:18:LYS:HA	54:DB:50:ASN:ND2	2.35	0.41
1:A:762:U:H2'	1:A:763:G:C8	2.55	0.41
2:B:903:C:H2'	2:B:904:G:H8	1.85	0.41
2:B:1599:U:OP1	24:X:40:LYS:HG3	2.21	0.41
2:B:1880:U:H2'	2:B:1881:C:C6	2.55	0.41
2:B:2065:C:H2'	2:B:2066:C:C6	2.56	0.41
2:B:2673:G:H2'	2:B:2674:G:C8	2.52	0.41
3:C:28:C:H2'	3:C:29:A:C8	2.56	0.41
5:E:97:MET:HB3	5:E:100:LEU:CB	2.50	0.41
6:F:106:PRO:HG2	6:F:126:GLY:HA2	2.02	0.41
18:R:12:ARG:HD3	18:R:16:HIS:ND1	2.35	0.41
23:W:107:VAL:HG22	23:W:108:SER:N	2.35	0.41
4:LA:34:C:H2'	4:LA:35:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:MA:72:PRO:O	38:MA:75:ARG:HB2	2.19	0.41
42:RA:156:ARG:NH1	45:UA:42:GLU:OE2	2.54	0.41
54:DB:44:HIS:HB2	54:DB:69:THR:O	2.21	0.41
56:FB:65:MET:HG2	56:FB:73:PHE:CZ	2.55	0.41
2:B:208:C:H2'	2:B:209:C:H6	1.86	0.41
2:B:577:G:O2'	2:B:1254:A:OP1	2.39	0.41
2:B:755:U:H2'	2:B:756:A:C8	2.55	0.41
2:B:1038:G:H2'	2:B:1039:A:C8	2.55	0.41
2:B:2037:A:H2'	2:B:2038:G:H8	1.86	0.41
2:B:2737:G:H2'	2:B:2738:A:C8	2.56	0.41
7:G:149:ASN:O	7:G:152:PRO:HD2	2.21	0.41
9:I:105:ILE:HD12	9:I:138:PRO:HG2	2.02	0.41
12:L:73:LYS:HB2	12:L:117:LEU:HD11	2.02	0.41
22:V:49:ILE:HG22	22:V:54:VAL:HA	2.03	0.41
42:RA:156:ARG:O	42:RA:158:LYS:N	2.48	0.41
48:XA:92:ARG:HE	58:HB:24:LYS:HE2	1.85	0.41
50:ZA:53:ASP:OD1	50:ZA:53:ASP:N	2.53	0.41
57:GB:8:LYS:NZ	57:GB:12:GLN:OE1	2.53	0.41
1:A:191:G:H2'	1:A:192:A:C8	2.56	0.41
1:A:680:C:H2'	1:A:681:A:C8	2.56	0.41
2:B:154:U:H2'	2:B:155:A:C8	2.56	0.41
2:B:220:G:N2	2:B:427:U:C2	2.89	0.41
2:B:500:G:N1	2:B:503:A:OP2	2.52	0.41
2:B:634:C:H2'	2:B:635:C:C6	2.56	0.41
2:B:1508:A:H2'	2:B:1509:A:O4'	2.21	0.41
2:B:2037:A:H2'	2:B:2038:G:C8	2.56	0.41
2:B:2285:C:OP1	33:GA:25:ASN:ND2	2.54	0.41
2:B:2302:U:H2'	2:B:2303:G:H8	1.85	0.41
3:C:111:U:H2'	3:C:112:G:C8	2.53	0.41
4:D:42:G:H2'	4:D:43:A:H8	1.82	0.41
13:M:132:ALA:HA	13:M:137:LEU:HB2	2.02	0.41
4:LA:68:C:H2'	4:LA:69:C:H6	1.86	0.41
38:MA:131:LEU:HD11	38:MA:182:HIS:ND1	2.36	0.41
40:PA:8:GLY:HA2	40:PA:11:LEU:CG	2.50	0.41
55:EB:11:ARG:HG2	55:EB:12:PHE:N	2.36	0.41
1:A:114:U:H2'	1:A:115:G:C8	2.56	0.41
1:A:285:C:H2'	1:A:286:C:C6	2.56	0.41
1:A:373:A:O4'	1:A:481:G:H5'	2.20	0.41
1:A:550:G:H2'	1:A:551:U:C6	2.55	0.41
1:A:675:A:H2'	1:A:676:A:C8	2.56	0.41
1:A:830:G:H2'	1:A:831:A:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:894:G:H2'	1:A:895:G:H8	1.86	0.41
1:A:955:U:OP2	38:MA:133:ARG:NH2	2.54	0.41
1:A:994:A:O2'	51:AB:7:ALA:HB1	2.21	0.41
1:A:1002:G:C2	1:A:1003:G:H1'	2.56	0.41
1:A:1345:U:OP1	46:VA:121:ARG:NH1	2.53	0.41
1:A:1409:C:H2'	1:A:1410:A:C8	2.56	0.41
2:B:558:U:H2'	2:B:559:G:H8	1.86	0.41
2:B:1151:A:H4'	21:U:80:ASN:ND2	2.35	0.41
2:B:1236:G:O2'	2:B:1237:A:O5'	2.35	0.41
2:B:1468:U:H2'	2:B:1522:A:N6	2.36	0.41
2:B:1536:C:O2'	2:B:1537:G:N2	2.54	0.41
2:B:1947:C:H2'	2:B:1948:G:C8	2.56	0.41
2:B:2027:G:H2'	2:B:2028:U:C6	2.55	0.41
2:B:2075:U:H1'	2:B:2597:G:H21	1.86	0.41
2:B:2297:A:OP2	2:B:2297:A:H8	2.03	0.41
3:C:76:G:H2'	3:C:77:U:H6	1.85	0.41
4:D:48:C:OP2	4:D:59:A:H5'	2.21	0.41
7:G:109:VAL:HG21	7:G:193:VAL:HG12	2.02	0.41
8:H:138:LEU:HD23	8:H:138:LEU:HA	1.91	0.41
9:I:101:ARG:HB3	31:EA:24:ILE:HG21	2.03	0.41
9:I:115:GLY:HA3	9:I:177:ARG:HG3	2.03	0.41
12:L:4:ASN:OD1	12:L:8:LYS:NZ	2.52	0.41
4:LA:29:G:H2'	4:LA:30:G:H8	1.86	0.41
38:MA:180:GLY:HA3	38:MA:307:ASN:OD1	2.21	0.41
38:MA:253:ILE:HD11	38:MA:277:ARG:HD2	2.03	0.41
38:MA:306:ARG:HE	38:MA:320:HIS:HE1	1.66	0.41
42:RA:114:LEU:O	42:RA:119:VAL:HG22	2.21	0.41
42:RA:133:ILE:H	42:RA:133:ILE:HD12	1.85	0.41
48:XA:19:VAL:HG22	48:XA:82:GLU:HB2	2.03	0.41
50:ZA:8:ILE:HG13	50:ZA:9:PRO:HD3	2.03	0.41
50:ZA:86:ARG:HH22	56:FB:68:HIS:HE1	1.67	0.41
54:DB:42:LYS:C	54:DB:43:LEU:HD12	2.46	0.41
58:HB:28:LEU:HA	58:HB:28:LEU:HD23	1.85	0.41
58:HB:34:ARG:HB3	58:HB:36:PHE:CE1	2.56	0.41
1:A:17:U:H2'	1:A:18:C:C6	2.56	0.41
1:A:664:G:H22	1:A:741:G:H1	1.68	0.41
2:B:691:C:OP1	6:F:216:ARG:NH1	2.54	0.41
2:B:935:C:H2'	2:B:936:A:H8	1.86	0.41
2:B:1035:U:H2'	2:B:1036:G:H8	1.86	0.41
2:B:1448:G:H2'	2:B:1449:G:C8	2.56	0.41
7:G:49:GLN:NE2	7:G:79:LEU:HD13	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:100:ALA:O	12:L:103:ASN:HB3	2.21	0.41
13:M:18:ASN:HA	13:M:19:PRO:HD3	1.81	0.41
13:M:85:ILE:H	13:M:85:ILE:HG13	1.77	0.41
13:M:113:ALA:O	13:M:114:ALA:C	2.64	0.41
4:LA:28:C:H2'	4:LA:29:G:C8	2.55	0.41
38:MA:140:GLU:O	38:MA:143:ARG:HD2	2.21	0.41
39:OA:14:HIS:CG	39:OA:15:PHE:N	2.68	0.41
42:RA:12:GLU:O	42:RA:12:GLU:HG2	2.20	0.41
1:A:15:G:H4'	42:RA:28:ARG:HH12	1.86	0.40
1:A:287:U:H2'	1:A:288:A:H8	1.86	0.40
1:A:806:C:H2'	1:A:807:A:H8	1.86	0.40
1:A:823:C:H2'	1:A:824:G:H8	1.86	0.40
2:B:214:G:O2'	2:B:217:A:H5'	2.22	0.40
2:B:690:G:H2'	2:B:691:C:C6	2.56	0.40
2:B:863:A:H2'	2:B:864:G:C8	2.54	0.40
2:B:1844:C:H2'	2:B:1845:G:H8	1.86	0.40
2:B:2134:A:HO2'	2:B:2159:G:H21	1.66	0.40
2:B:2837:A:H2'	2:B:2838:G:C8	2.53	0.40
3:C:60:C:H2'	3:C:61:G:C8	2.56	0.40
4:D:27:U:H2'	4:D:28:C:C6	2.56	0.40
8:H:58:LYS:NZ	8:H:62:GLN:OE1	2.53	0.40
10:J:45:ALA:HB3	10:J:48:THR:O	2.21	0.40
13:M:37:PHE:HA	13:M:66:PHE:CZ	2.55	0.40
15:O:35:VAL:HG22	15:O:69:VAL:HG12	2.03	0.40
21:U:44:TYR:O	21:U:45:ALA:C	2.65	0.40
23:W:74:ILE:HG23	23:W:74:ILE:O	2.22	0.40
29:CA:19:LEU:HD23	29:CA:19:LEU:HA	1.87	0.40
31:EA:46:GLY:HA2	31:EA:49:ARG:NE	2.36	0.40
43:SA:75:GLU:HA	43:SA:78:PHE:HD2	1.86	0.40
47:WA:5:ARG:N	47:WA:77:VAL:O	2.54	0.40
53:CB:76:LYS:O	53:CB:79:ASN:OD1	2.38	0.40
2:B:873:C:H2'	2:B:874:G:C8	2.56	0.40
2:B:1252:G:H4'	21:U:32:ARG:HH11	1.86	0.40
2:B:2292:U:H2'	2:B:2293:G:C8	2.52	0.40
2:B:2428:G:H5''	2:B:2429:G:OP1	2.22	0.40
2:B:2590:A:N1	2:B:2604:U:C5	2.89	0.40
6:F:204:LEU:HB3	6:F:209:ALA:HB3	2.03	0.40
7:G:51:THR:HB	7:G:79:LEU:HD23	2.02	0.40
10:J:16:VAL:HG11	10:J:49:LEU:HD11	2.02	0.40
11:K:73:ASN:C	11:K:75:LEU:H	2.29	0.40
12:L:125:ARG:HD3	12:L:125:ARG:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:EA:20:ASN:ND2	31:EA:40:CYS:HB2	2.35	0.40
34:HA:43:THR:OG1	34:HA:44:VAL:N	2.55	0.40
38:MA:116:ARG:HB3	38:MA:161:GLU:HG3	2.02	0.40
40:PA:123:LEU:HD23	40:PA:123:LEU:HA	1.92	0.40
41:QA:28:ASP:OD1	41:QA:28:ASP:N	2.52	0.40
47:WA:42:LEU:HB2	47:WA:71:LEU:HB2	2.03	0.40
52:BB:2:LEU:HB2	52:BB:34:GLN:NE2	2.37	0.40
1:A:41:G:H2'	1:A:42:G:H8	1.87	0.40
1:A:102:G:H2'	1:A:103:U:H6	1.85	0.40
1:A:620:C:O2'	1:A:621:A:H8	2.05	0.40
1:A:985:C:H2'	1:A:986:U:C6	2.57	0.40
1:A:1038:C:H2'	1:A:1039:G:H8	1.86	0.40
2:B:62:U:O2'	2:B:63:A:N7	2.48	0.40
2:B:935:C:H2'	2:B:936:A:C8	2.56	0.40
2:B:1149:G:H2'	2:B:1150:C:C6	2.56	0.40
5:E:196:LEU:HD23	5:E:209:ILE:HG21	2.04	0.40
6:F:42:ARG:HD2	6:F:42:ARG:N	2.35	0.40
1:A:711:G:H2'	1:A:712:A:C8	2.56	0.40
2:B:172:A:H2'	2:B:173:A:C8	2.54	0.40
2:B:476:G:N1	2:B:479:A:OP2	2.53	0.40
2:B:529:A:OP2	14:N:113:PRO:HG3	2.21	0.40
2:B:743:A:OP1	7:G:135:GLY:HA2	2.21	0.40
2:B:903:C:H2'	2:B:904:G:C8	2.56	0.40
2:B:1478:G:H1	2:B:1513:U:H3	1.68	0.40
2:B:1524:G:H2'	2:B:1525:A:C8	2.56	0.40
5:E:136:LEU:HA	5:E:162:ARG:HH12	1.87	0.40
8:H:117:ARG:HH22	16:P:2:ARG:HB2	1.86	0.40
12:L:29:ASP:H	12:L:56:ARG:HH12	1.69	0.40
16:P:51:GLU:HG3	16:P:54:GLN:HE21	1.86	0.40
36:JA:7:VAL:HG11	36:JA:36:ARG:O	2.22	0.40
38:MA:206:MET:HE1	38:MA:294:ARG:NH2	2.36	0.40
41:QA:198:LEU:O	41:QA:201:GLU:HG2	2.21	0.40
43:SA:85:ILE:O	43:SA:86:ARG:O	2.40	0.40
49:YA:35:ARG:HG2	49:YA:37:TYR:HD1	1.87	0.40
56:FB:3:SER:HB3	56:FB:9:PHE:HE2	1.86	0.40
1:A:744:C:H2'	1:A:745:G:H8	1.87	0.40
1:A:1162:C:H2'	1:A:1163:A:H8	1.86	0.40
2:B:119:A:H4'	2:B:120:U:H5'	2.03	0.40
2:B:751:A:H62	2:B:789:A:H62	1.68	0.40
2:B:1040:A:H2'	2:B:1041:G:H8	1.87	0.40
2:B:1363:C:H2'	2:B:1364:G:C8	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1889:A:H2'	2:B:1890:A:C8	2.56	0.40
2:B:2216:G:H2'	2:B:2217:G:H8	1.85	0.40
2:B:2372:U:H2'	2:B:2373:G:H8	1.86	0.40
2:B:2539:C:H4'	36:JA:3:VAL:HG21	2.04	0.40
5:E:200:LYS:HA	5:E:201:PRO:HD3	1.91	0.40
9:I:51:ASN:ND2	9:I:146:ASP:OD2	2.55	0.40
41:QA:4:LEU:HD13	41:QA:4:LEU:HA	1.87	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	
5	E	218/234 (93%)	185 (85%)	32 (15%)	1 (0%)	24	56
6	F	269/273 (98%)	229 (85%)	40 (15%)	0	100	100
7	G	207/209 (99%)	177 (86%)	27 (13%)	3 (1%)	9	37
8	H	199/201 (99%)	176 (88%)	19 (10%)	4 (2%)	6	32
9	I	175/179 (98%)	150 (86%)	23 (13%)	2 (1%)	11	42
10	J	174/177 (98%)	151 (87%)	20 (12%)	3 (2%)	7	34
11	K	147/149 (99%)	123 (84%)	19 (13%)	5 (3%)	3	25
12	L	129/165 (78%)	88 (68%)	34 (26%)	7 (5%)	1	16
13	M	139/142 (98%)	114 (82%)	21 (15%)	4 (3%)	3	26
14	N	140/142 (99%)	128 (91%)	11 (8%)	1 (1%)	18	50
15	O	120/123 (98%)	97 (81%)	20 (17%)	3 (2%)	4	29
16	P	141/144 (98%)	120 (85%)	19 (14%)	2 (1%)	9	37
17	Q	134/136 (98%)	117 (87%)	15 (11%)	2 (2%)	8	36
18	R	118/127 (93%)	92 (78%)	24 (20%)	2 (2%)	7	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	S	114/117 (97%)	103 (90%)	8 (7%)	3 (3%)	4	28
20	T	112/115 (97%)	92 (82%)	19 (17%)	1 (1%)	14	45
21	U	115/118 (98%)	101 (88%)	13 (11%)	1 (1%)	14	45
22	V	101/103 (98%)	85 (84%)	14 (14%)	2 (2%)	6	32
23	W	108/110 (98%)	90 (83%)	15 (14%)	3 (3%)	4	27
24	X	91/100 (91%)	81 (89%)	10 (11%)	0	100	100
25	Y	100/104 (96%)	80 (80%)	17 (17%)	3 (3%)	3	26
26	Z	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
27	AA	73/85 (86%)	65 (89%)	8 (11%)	0	100	100
28	BA	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
29	CA	61/63 (97%)	58 (95%)	2 (3%)	1 (2%)	7	35
30	DA	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
31	EA	64/70 (91%)	52 (81%)	11 (17%)	1 (2%)	7	35
32	FA	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
33	GA	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
34	HA	44/46 (96%)	34 (77%)	9 (20%)	1 (2%)	5	30
35	IA	62/65 (95%)	50 (81%)	11 (18%)	1 (2%)	7	35
36	JA	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
38	MA	340/362 (94%)	292 (86%)	45 (13%)	3 (1%)	14	45
39	OA	223/241 (92%)	202 (91%)	19 (8%)	2 (1%)	14	45
40	PA	204/233 (88%)	177 (87%)	25 (12%)	2 (1%)	12	43
41	QA	203/206 (98%)	174 (86%)	21 (10%)	8 (4%)	2	21
42	RA	155/167 (93%)	121 (78%)	27 (17%)	7 (4%)	2	18
43	SA	98/131 (75%)	73 (74%)	20 (20%)	5 (5%)	1	17
44	TA	149/156 (96%)	125 (84%)	21 (14%)	3 (2%)	6	32
45	UA	127/130 (98%)	111 (87%)	14 (11%)	2 (2%)	7	35
46	VA	125/130 (96%)	98 (78%)	23 (18%)	4 (3%)	3	25
47	WA	96/103 (93%)	73 (76%)	19 (20%)	4 (4%)	2	20
48	XA	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	45
49	YA	121/124 (98%)	96 (79%)	19 (16%)	6 (5%)	1	17
50	ZA	112/118 (95%)	97 (87%)	13 (12%)	2 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	AB	99/102 (97%)	64 (65%)	25 (25%)	10 (10%)	0	6
52	BB	86/89 (97%)	71 (83%)	13 (15%)	2 (2%)	5	30
53	CB	80/82 (98%)	63 (79%)	16 (20%)	1 (1%)	9	38
54	DB	78/84 (93%)	63 (81%)	12 (15%)	3 (4%)	2	22
55	EB	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
56	FB	77/92 (84%)	63 (82%)	14 (18%)	0	100	100
57	GB	83/87 (95%)	79 (95%)	4 (5%)	0	100	100
58	HB	63/71 (89%)	44 (70%)	14 (22%)	5 (8%)	1	10
All	All	6412/6790 (94%)	5417 (84%)	868 (14%)	127 (2%)	8	32

All (127) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	83	VAL
9	I	2	LYS
10	J	119	GLY
11	K	9	VAL
11	K	10	ALA
11	K	41	LYS
12	L	118	ILE
12	L	119	PRO
12	L	123	ILE
13	M	11	GLN
14	N	81	ILE
15	O	35	VAL
18	R	88	ALA
19	S	34	HIS
22	V	54	VAL
29	CA	24	GLU
35	IA	31	ILE
36	JA	37	GLN
39	OA	14	HIS
39	OA	15	PHE
40	PA	4	VAL
41	QA	36	ALA
41	QA	191	SER
41	QA	192	ALA
42	RA	11	GLN
42	RA	25	LYS

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Mol	Chain	Res	Type
42	RA	89	THR
42	RA	93	VAL
42	RA	122	VAL
43	SA	86	ARG
43	SA	92	THR
45	UA	66	GLN
46	VA	57	VAL
47	WA	92	LEU
49	YA	23	LEU
49	YA	24	GLU
50	ZA	4	ALA
50	ZA	65	GLU
51	AB	64	CYS
51	AB	79	LEU
51	AB	80	SER
51	AB	81	ARG
7	G	30	GLU
8	H	72	SER
10	J	109	SER
11	K	14	SER
12	L	58	THR
18	R	86	ARG
23	W	3	THR
23	W	63	GLY
34	HA	44	VAL
41	QA	84	ASN
43	SA	54	LEU
44	TA	56	SER
44	TA	64	ALA
45	UA	47	ASP
46	VA	90	ASP
49	YA	35	ARG
51	AB	57	PRO
51	AB	75	ARG
54	DB	17	GLU
54	DB	50	ASN
58	HB	8	ASN
58	HB	24	LYS
5	E	102	ASP
8	H	45	ALA
10	J	174	LYS
12	L	54	VAL

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Mol	Chain	Res	Type
12	L	108	VAL
17	Q	70	ASP
19	S	13	ARG
20	T	65	ASN
23	W	64	ALA
31	EA	29	GLY
38	MA	145	ARG
43	SA	52	ASN
46	VA	107	ALA
47	WA	29	ALA
48	XA	125	LYS
51	AB	67	THR
54	DB	15	LYS
58	HB	12	ASP
58	HB	64	ALA
7	G	10	GLY
8	H	80	SER
9	I	175	PRO
13	M	12	VAL
15	O	92	GLU
15	O	93	GLN
17	Q	69	PRO
21	U	25	GLY
41	QA	47	LEU
43	SA	53	LYS
47	WA	14	ASP
47	WA	33	GLY
51	AB	2	LYS
58	HB	34	ARG
7	G	86	GLU
16	P	36	LYS
16	P	86	GLU
25	Y	54	PRO
41	QA	32	LYS
52	BB	74	VAL
11	K	118	PRO
12	L	76	PHE
13	M	24	GLY
25	Y	89	GLY
38	MA	45	LEU
38	MA	146	VAL
41	QA	82	LYS

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Mol	Chain	Res	Type
41	QA	182	LYS
49	YA	77	SER
49	YA	88	ASP
19	S	66	GLY
51	AB	70	PRO
40	PA	6	PRO
42	RA	90	GLY
46	VA	71	ILE
25	Y	53	GLN
49	YA	27	PRO
51	AB	56	SER
53	CB	30	GLY
13	M	19	PRO
42	RA	157	GLY
44	TA	15	PRO
52	BB	85	GLY
22	V	8	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	171/181 (94%)	170 (99%)	1 (1%)	78	79
6	F	216/218 (99%)	214 (99%)	2 (1%)	70	75
7	G	164/164 (100%)	164 (100%)	0	100	100
8	H	165/165 (100%)	162 (98%)	3 (2%)	51	67
9	I	148/150 (99%)	147 (99%)	1 (1%)	76	77
10	J	137/138 (99%)	137 (100%)	0	100	100
11	K	114/114 (100%)	112 (98%)	2 (2%)	51	67
12	L	100/123 (81%)	97 (97%)	3 (3%)	36	57
13	M	109/110 (99%)	108 (99%)	1 (1%)	70	75
14	N	116/116 (100%)	116 (100%)	0	100	100
15	O	103/104 (99%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	P	102/103 (99%)	99 (97%)	3 (3%)	37	57
17	Q	109/109 (100%)	108 (99%)	1 (1%)	70	75
18	R	100/104 (96%)	100 (100%)	0	100	100
19	S	86/87 (99%)	83 (96%)	3 (4%)	32	54
20	T	99/100 (99%)	97 (98%)	2 (2%)	48	64
21	U	89/90 (99%)	89 (100%)	0	100	100
22	V	84/84 (100%)	83 (99%)	1 (1%)	63	72
23	W	93/93 (100%)	92 (99%)	1 (1%)	65	73
24	X	80/84 (95%)	80 (100%)	0	100	100
25	Y	83/85 (98%)	82 (99%)	1 (1%)	63	72
26	Z	78/78 (100%)	78 (100%)	0	100	100
27	AA	57/63 (90%)	57 (100%)	0	100	100
28	BA	67/68 (98%)	66 (98%)	1 (2%)	57	68
29	CA	55/55 (100%)	55 (100%)	0	100	100
30	DA	48/49 (98%)	48 (100%)	0	100	100
31	EA	59/62 (95%)	59 (100%)	0	100	100
32	FA	47/48 (98%)	46 (98%)	1 (2%)	47	64
33	GA	45/49 (92%)	45 (100%)	0	100	100
34	HA	38/38 (100%)	38 (100%)	0	100	100
35	IA	51/52 (98%)	51 (100%)	0	100	100
36	JA	34/34 (100%)	34 (100%)	0	100	100
38	MA	284/302 (94%)	278 (98%)	6 (2%)	47	64
39	OA	186/199 (94%)	186 (100%)	0	100	100
40	PA	170/190 (90%)	165 (97%)	5 (3%)	37	57
41	QA	172/173 (99%)	171 (99%)	1 (1%)	78	79
42	RA	119/126 (94%)	116 (98%)	3 (2%)	42	61
43	SA	87/112 (78%)	86 (99%)	1 (1%)	65	73
44	TA	124/129 (96%)	124 (100%)	0	100	100
45	UA	104/105 (99%)	104 (100%)	0	100	100
46	VA	105/107 (98%)	105 (100%)	0	100	100
47	WA	86/90 (96%)	85 (99%)	1 (1%)	63	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	XA	89/99 (90%)	88 (99%)	1 (1%)	65	73
49	YA	103/104 (99%)	100 (97%)	3 (3%)	37	57
50	ZA	92/96 (96%)	91 (99%)	1 (1%)	65	73
51	AB	83/84 (99%)	79 (95%)	4 (5%)	23	48
52	BB	76/77 (99%)	76 (100%)	0	100	100
53	CB	65/65 (100%)	64 (98%)	1 (2%)	57	68
54	DB	74/78 (95%)	73 (99%)	1 (1%)	59	70
55	EB	56/65 (86%)	56 (100%)	0	100	100
56	FB	70/79 (89%)	69 (99%)	1 (1%)	59	70
57	GB	65/66 (98%)	64 (98%)	1 (2%)	57	68
58	HB	55/61 (90%)	53 (96%)	2 (4%)	31	54
All	All	5312/5525 (96%)	5253 (99%)	59 (1%)	63	73

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	189	LEU
6	F	79	ARG
6	F	129	LEU
8	H	98	LYS
8	H	126	VAL
8	H	187	VAL
9	I	71	LYS
11	K	6	LEU
11	K	77	THR
12	L	3	LEU
12	L	33	VAL
12	L	58	THR
13	M	94	LYS
16	P	48	ARG
16	P	79	LEU
16	P	89	VAL
17	Q	46	ILE
19	S	25	ARG
19	S	28	VAL
19	S	48	LEU
20	T	2	ASN
20	T	109	ILE

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Mol	Chain	Res	Type
22	V	54	VAL
23	W	62	ASP
25	Y	27	VAL
28	BA	10	ARG
32	FA	8	THR
38	MA	115	VAL
38	MA	217	ILE
38	MA	266	ASN
38	MA	274	LEU
38	MA	317	VAL
38	MA	339	MET
40	PA	7	ASN
40	PA	32	LEU
40	PA	71	ARG
40	PA	105	VAL
40	PA	172	VAL
41	QA	54	LEU
42	RA	17	VAL
42	RA	18	ASN
42	RA	145	ASN
43	SA	12	PRO
47	WA	73	LEU
48	XA	30	ILE
49	YA	23	LEU
49	YA	89	LEU
49	YA	93	ARG
50	ZA	47	LEU
51	AB	58	SER
51	AB	79	LEU
51	AB	80	SER
51	AB	96	LEU
53	CB	74	LEU
54	DB	69	THR
56	FB	66	VAL
57	GB	65	LEU
58	HB	13	VAL
58	HB	40	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (126) such sidechains are listed below:

Mol	Chain	Res	Type
5	E	58	ASN

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Mol	Chain	Res	Type
5	E	67	HIS
5	E	139	ASN
5	E	155	ASN
5	E	172	HIS
5	E	188	ASN
5	E	203	GLN
6	F	20	ASN
6	F	24	HIS
6	F	36	ASN
6	F	52	HIS
6	F	196	ASN
6	F	225	ASN
7	G	32	ASN
7	G	49	GLN
7	G	140	HIS
7	G	164	GLN
7	G	167	ASN
7	G	173	GLN
8	H	24	ASN
8	H	30	GLN
8	H	92	HIS
8	H	97	ASN
8	H	136	GLN
8	H	163	ASN
8	H	165	HIS
9	I	26	GLN
9	I	51	ASN
9	I	126	ASN
10	J	19	ASN
10	J	29	ASN
10	J	37	ASN
10	J	44	HIS
10	J	63	GLN
10	J	87	GLN
10	J	110	HIS
10	J	114	HIS
11	K	135	HIS
11	K	145	ASN
12	L	57	ASN
13	M	18	ASN
13	M	33	ASN
13	M	42	ASN

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Mol	Chain	Res	Type
14	N	40	HIS
16	P	38	GLN
16	P	99	ASN
17	Q	88	ASN
18	R	3	HIS
18	R	11	ASN
18	R	81	ASN
19	S	38	GLN
19	S	98	GLN
20	T	2	ASN
20	T	6	GLN
20	T	51	ASN
20	T	74	GLN
21	U	36	GLN
21	U	43	GLN
22	V	18	GLN
23	W	9	HIS
23	W	61	ASN
25	Y	45	GLN
25	Y	68	ASN
25	Y	73	ASN
26	Z	51	GLN
26	Z	78	GLN
27	AA	36	GLN
27	AA	72	ASN
29	CA	25	GLN
29	CA	27	ASN
30	DA	19	HIS
30	DA	48	ASN
31	EA	41	HIS
31	EA	61	ASN
34	HA	16	HIS
38	MA	66	GLN
38	MA	79	GLN
38	MA	156	HIS
38	MA	193	GLN
38	MA	235	GLN
38	MA	236	HIS
38	MA	238	ASN
38	MA	279	HIS
38	MA	314	GLN
38	MA	320	HIS

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Mol	Chain	Res	Type
39	OA	38	HIS
39	OA	57	ASN
39	OA	119	GLN
39	OA	176	ASN
40	PA	7	ASN
41	QA	39	GLN
41	QA	58	GLN
41	QA	73	ASN
41	QA	88	ASN
41	QA	115	GLN
41	QA	195	ASN
42	RA	18	ASN
42	RA	131	ASN
42	RA	145	ASN
43	SA	11	HIS
43	SA	17	GLN
44	TA	121	ASN
45	UA	15	ASN
46	VA	36	GLN
47	WA	56	HIS
47	WA	58	ASN
48	XA	21	HIS
48	XA	39	ASN
48	XA	63	GLN
49	YA	19	ASN
49	YA	58	ASN
49	YA	76	HIS
50	ZA	99	GLN
52	BB	19	ASN
52	BB	34	GLN
53	CB	18	GLN
53	CB	40	ASN
54	DB	30	HIS
55	EB	51	GLN
56	FB	51	HIS
56	FB	68	HIS
57	GB	2	ASN
57	GB	20	ASN
57	GB	47	GLN
57	GB	60	GLN
57	GB	81	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	223 (14%)	5 (0%)
2	B	2902/2903 (99%)	387 (13%)	8 (0%)
3	C	119/120 (99%)	18 (15%)	1 (0%)
37	KA	18/27 (66%)	3 (16%)	0
4	D	76/77 (98%)	10 (13%)	0
4	LA	76/77 (98%)	8 (10%)	0
All	All	4729/4743 (99%)	649 (13%)	14 (0%)

All (649) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	A
1	A	6	G
1	A	9	G
1	A	22	G
1	A	32	A
1	A	33	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	70	U
1	A	71	A
1	A	72	A
1	A	83	C
1	A	84	U
1	A	85	U
1	A	86	G
1	A	88	U
1	A	94	G
1	A	121	U
1	A	124	C
1	A	130	A
1	A	138	G
1	A	139	A
1	A	144	G
1	A	155	A
1	A	171	A
1	A	174	A
1	A	183	C

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Mol	Chain	Res	Type
1	A	197	A
1	A	201	G
1	A	209	U
1	A	210	C
1	A	211	G
1	A	212	G
1	A	225	C
1	A	226	G
1	A	245	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	274	A
1	A	280	C
1	A	281	G
1	A	289	G
1	A	306	A
1	A	321	A
1	A	329	A
1	A	330	C
1	A	343	U
1	A	345	C
1	A	346	G
1	A	351	G
1	A	352	C
1	A	358	U
1	A	367	U
1	A	368	U
1	A	369	G
1	A	372	C
1	A	373	A
1	A	378	G
1	A	387	U
1	A	394	G
1	A	395	C
1	A	398	U
1	A	401	C
1	A	403	C
1	A	404	G
1	A	406	G
1	A	411	A

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Mol	Chain	Res	Type
1	A	413	G
1	A	416	G
1	A	421	U
1	A	422	C
1	A	423	G
1	A	428	G
1	A	429	U
1	A	437	U
1	A	438	U
1	A	442	G
1	A	448	A
1	A	467	U
1	A	468	A
1	A	476	U
1	A	477	C
1	A	481	G
1	A	484	G
1	A	485	U
1	A	486	U
1	A	493	A
1	A	495	A
1	A	497	G
1	A	511	C
1	A	518	C
1	A	521	G
1	A	524	G
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	540	G
1	A	541	G
1	A	547	A
1	A	561	U
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	C
1	A	577	G
1	A	615	G
1	A	619	U

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Mol	Chain	Res	Type
1	A	620	C
1	A	621	A
1	A	633	G
1	A	642	A
1	A	665	A
1	A	666	G
1	A	688	G
1	A	695	A
1	A	701	U
1	A	702	A
1	A	703	G
1	A	713	G
1	A	718	A
1	A	721	G
1	A	724	G
1	A	731	G
1	A	733	G
1	A	755	G
1	A	777	A
1	A	794	A
1	A	814	A
1	A	815	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	821	G
1	A	832	G
1	A	836	G
1	A	842	U
1	A	843	U
1	A	846	G
1	A	871	U
1	A	873	A
1	A	885	G
1	A	890	G
1	A	902	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A

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Mol	Chain	Res	Type
1	A	971	G
1	A	972	C
1	A	975	A
1	A	976	G
1	A	977	A
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1028	C
1	A	1031	C
1	A	1033	G
1	A	1054	C
1	A	1055	A
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1130	A
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1159	U
1	A	1168	U
1	A	1183	U
1	A	1184	G
1	A	1196	A
1	A	1225	A
1	A	1238	A
1	A	1241	G
1	A	1258	G
1	A	1260	G
1	A	1261	A
1	A	1275	A
1	A	1278	G
1	A	1280	A
1	A	1282	C
1	A	1286	U
1	A	1287	A
1	A	1297	G
1	A	1298	U
1	A	1300	G
1	A	1317	C

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Mol	Chain	Res	Type
1	A	1323	G
1	A	1346	A
1	A	1347	G
1	A	1359	C
1	A	1378	C
1	A	1394	A
1	A	1400	C
1	A	1402	C
1	A	1419	G
1	A	1446	A
1	A	1448	C
1	A	1451	U
1	A	1452	C
1	A	1453	G
1	A	1494	G
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1506	U
1	A	1517	G
1	A	1529	G
1	A	1530	G
1	A	1534	A
1	A	1540	U
2	B	10	A
2	B	35	G
2	B	46	G
2	B	49	A
2	B	52	A
2	B	63	A
2	B	71	A
2	B	74	A
2	B	75	G
2	B	118	A
2	B	120	U
2	B	140	C
2	B	141	G
2	B	162	U
2	B	163	C
2	B	181	A
2	B	196	A

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Mol	Chain	Res	Type
2	B	199	A
2	B	204	A
2	B	215	G
2	B	216	A
2	B	221	A
2	B	222	A
2	B	227	A
2	B	229	C
2	B	233	A
2	B	242	G
2	B	248	G
2	B	249	C
2	B	255	A
2	B	264	C
2	B	266	G
2	B	281	C
2	B	294	A
2	B	311	A
2	B	323	C
2	B	329	G
2	B	330	A
2	B	334	C
2	B	361	G
2	B	371	A
2	B	372	G
2	B	386	G
2	B	387	U
2	B	404	A
2	B	406	G
2	B	411	G
2	B	423	A
2	B	424	G
2	B	442	G
2	B	451	U
2	B	457	A
2	B	467	G
2	B	473	G
2	B	475	C
2	B	480	A
2	B	481	G
2	B	490	C
2	B	491	G

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Mol	Chain	Res	Type
2	B	504	A
2	B	505	A
2	B	508	A
2	B	529	A
2	B	532	A
2	B	533	G
2	B	543	G
2	B	548	G
2	B	563	A
2	B	572	A
2	B	573	U
2	B	575	A
2	B	588	U
2	B	603	A
2	B	614	A
2	B	615	U
2	B	627	A
2	B	637	A
2	B	645	C
2	B	646	U
2	B	654	A
2	B	655	A
2	B	669	G
2	B	686	U
2	B	695	G
2	B	704	G
2	B	730	A
2	B	747	C
2	B	748	G
2	B	752	A
2	B	765	C
2	B	775	G
2	B	776	G
2	B	782	A
2	B	783	A
2	B	784	G
2	B	785	G
2	B	789	A
2	B	800	A
2	B	805	G
2	B	812	C
2	B	819	A

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Mol	Chain	Res	Type
2	B	827	U
2	B	828	U
2	B	830	G
2	B	845	A
2	B	846	U
2	B	847	U
2	B	856	G
2	B	860	U
2	B	878	A
2	B	887	U
2	B	888	C
2	B	889	C
2	B	891	G
2	B	893	C
2	B	896	A
2	B	907	G
2	B	910	A
2	B	932	U
2	B	941	A
2	B	946	C
2	B	961	C
2	B	974	G
2	B	983	A
2	B	995	C
2	B	996	A
2	B	1009	A
2	B	1012	U
2	B	1013	C
2	B	1021	A
2	B	1022	G
2	B	1026	G
2	B	1033	U
2	B	1045	C
2	B	1046	A
2	B	1047	G
2	B	1060	U
2	B	1062	G
2	B	1063	G
2	B	1064	C
2	B	1065	U
2	B	1066	U
2	B	1067	A

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Mol	Chain	Res	Type
2	B	1070	A
2	B	1071	G
2	B	1072	C
2	B	1075	C
2	B	1076	C
2	B	1079	C
2	B	1084	A
2	B	1088	A
2	B	1089	A
2	B	1090	A
2	B	1094	U
2	B	1103	A
2	B	1104	C
2	B	1111	A
2	B	1130	U
2	B	1131	G
2	B	1132	U
2	B	1133	A
2	B	1135	C
2	B	1139	G
2	B	1142	A
2	B	1172	C
2	B	1173	U
2	B	1174	U
2	B	1175	A
2	B	1176	U
2	B	1177	G
2	B	1178	C
2	B	1179	G
2	B	1180	U
2	B	1211	C
2	B	1212	G
2	B	1237	A
2	B	1250	G
2	B	1251	C
2	B	1253	A
2	B	1256	G
2	B	1265	A
2	B	1271	G
2	B	1272	A
2	B	1273	U
2	B	1275	A

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Mol	Chain	Res	Type
2	B	1300	G
2	B	1301	A
2	B	1321	A
2	B	1332	G
2	B	1345	C
2	B	1365	A
2	B	1368	G
2	B	1378	A
2	B	1379	U
2	B	1383	A
2	B	1416	G
2	B	1428	C
2	B	1454	C
2	B	1461	C
2	B	1475	G
2	B	1482	G
2	B	1490	A
2	B	1504	A
2	B	1515	A
2	B	1522	A
2	B	1524	G
2	B	1535	A
2	B	1536	C
2	B	1555	G
2	B	1558	C
2	B	1560	G
2	B	1566	A
2	B	1569	A
2	B	1607	C
2	B	1611	C
2	B	1616	A
2	B	1646	C
2	B	1647	U
2	B	1648	U
2	B	1669	A
2	B	1674	G
2	B	1695	G
2	B	1698	A
2	B	1699	G
2	B	1715	G
2	B	1729	U
2	B	1730	C

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Mol	Chain	Res	Type
2	B	1731	G
2	B	1738	G
2	B	1756	G
2	B	1758	U
2	B	1764	C
2	B	1773	A
2	B	1781	U
2	B	1800	C
2	B	1801	A
2	B	1802	A
2	B	1808	A
2	B	1809	A
2	B	1813	G
2	B	1816	C
2	B	1870	C
2	B	1871	A
2	B	1901	A
2	B	1906	G
2	B	1907	G
2	B	1914	C
2	B	1929	G
2	B	1930	G
2	B	1936	A
2	B	1937	A
2	B	1938	A
2	B	1944	U
2	B	1955	U
2	B	1967	C
2	B	1970	A
2	B	1971	U
2	B	1972	G
2	B	1991	U
2	B	1993	U
2	B	1997	C
2	B	2022	U
2	B	2023	C
2	B	2030	A
2	B	2031	A
2	B	2033	A
2	B	2043	C
2	B	2052	A
2	B	2055	C

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Mol	Chain	Res	Type
2	B	2056	G
2	B	2060	A
2	B	2061	G
2	B	2062	A
2	B	2069	G
2	B	2072	C
2	B	2077	A
2	B	2093	G
2	B	2096	C
2	B	2111	U
2	B	2112	G
2	B	2114	A
2	B	2115	G
2	B	2118	U
2	B	2119	A
2	B	2120	G
2	B	2121	G
2	B	2128	G
2	B	2132	U
2	B	2133	G
2	B	2145	C
2	B	2147	A
2	B	2157	G
2	B	2171	A
2	B	2172	U
2	B	2173	A
2	B	2176	A
2	B	2198	A
2	B	2199	A
2	B	2204	G
2	B	2211	A
2	B	2213	U
2	B	2223	G
2	B	2225	A
2	B	2238	G
2	B	2243	U
2	B	2250	G
2	B	2252	G
2	B	2283	C
2	B	2287	A
2	B	2297	A
2	B	2305	U

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Mol	Chain	Res	Type
2	B	2309	A
2	B	2311	A
2	B	2312	U
2	B	2320	U
2	B	2324	U
2	B	2325	G
2	B	2327	A
2	B	2333	A
2	B	2334	U
2	B	2361	G
2	B	2382	G
2	B	2383	G
2	B	2385	C
2	B	2391	G
2	B	2402	U
2	B	2403	C
2	B	2406	A
2	B	2423	U
2	B	2429	G
2	B	2430	A
2	B	2435	A
2	B	2441	U
2	B	2447	G
2	B	2448	A
2	B	2476	A
2	B	2478	A
2	B	2498	C
2	B	2502	G
2	B	2503	A
2	B	2504	U
2	B	2506	U
2	B	2518	A
2	B	2520	C
2	B	2547	A
2	B	2554	U
2	B	2566	A
2	B	2567	G
2	B	2572	A
2	B	2582	G
2	B	2585	U
2	B	2586	U
2	B	2602	A

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Mol	Chain	Res	Type
2	B	2605	U
2	B	2609	U
2	B	2613	U
2	B	2629	U
2	B	2630	G
2	B	2655	G
2	B	2682	A
2	B	2689	U
2	B	2690	U
2	B	2714	G
2	B	2718	G
2	B	2733	A
2	B	2744	G
2	B	2748	A
2	B	2757	A
2	B	2764	A
2	B	2765	A
2	B	2778	A
2	B	2779	U
2	B	2791	G
2	B	2798	U
2	B	2799	A
2	B	2800	A
2	B	2808	G
2	B	2820	A
2	B	2821	A
2	B	2833	U
2	B	2849	U
2	B	2861	U
2	B	2867	G
2	B	2868	A
2	B	2872	A
2	B	2879	A
2	B	2880	C
3	C	13	G
3	C	15	A
3	C	24	G
3	C	35	C
3	C	42	C
3	C	44	G
3	C	45	A
3	C	67	G

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Mol	Chain	Res	Type
3	C	87	U
3	C	88	C
3	C	89	U
3	C	90	C
3	C	91	C
3	C	100	G
3	C	108	A
3	C	109	A
3	C	119	A
3	C	120	A
4	D	6	G
4	D	9	G
4	D	16	C
4	D	17(A)	U
4	D	18	G
4	D	19	G
4	D	20	U
4	D	47	U
4	D	48	C
4	D	61	C
37	KA	12	A
37	KA	13	A
37	KA	22	A
4	LA	9	G
4	LA	17(A)	U
4	LA	18	G
4	LA	19	G
4	LA	48	C
4	LA	59	A
4	LA	61	C
4	LA	76	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	69	G
1	A	533	A
1	A	733	G
1	A	1182	G
1	A	1297	G
2	B	51	G
2	B	859	G

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Mol	Chain	Res	Type
2	B	1020	A
2	B	1130	U
2	B	1236	G
2	B	2296	U
2	B	2326	C
2	B	2756	U
3	C	66	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

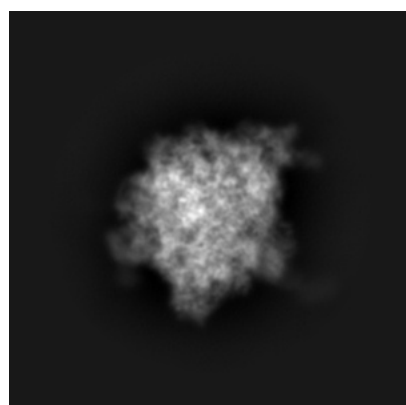
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7970. These allow visual inspection of the internal detail of the map and identification of artifacts.

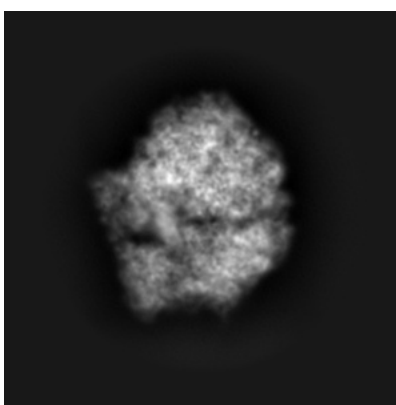
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

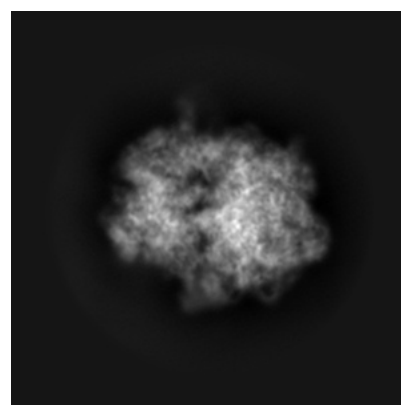
6.1.1 Primary map



X



Y

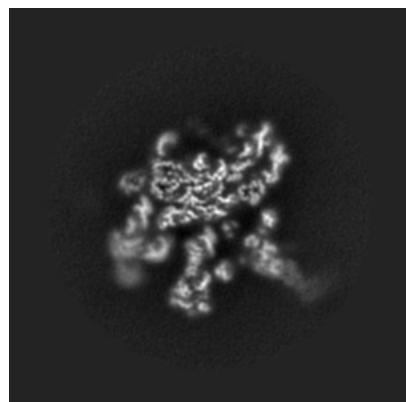


Z

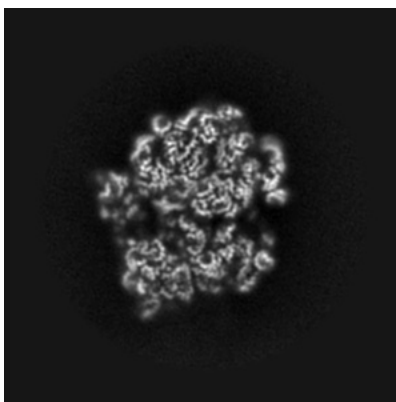
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

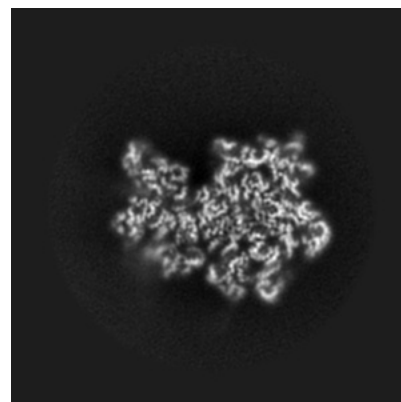
6.2.1 Primary map



X Index: 240



Y Index: 240

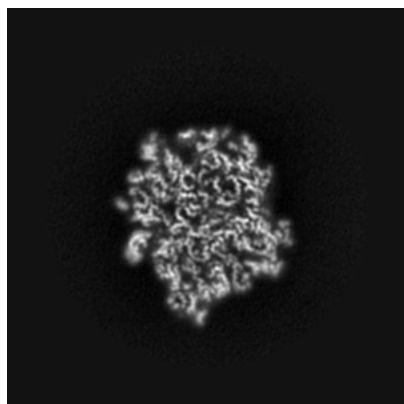


Z Index: 240

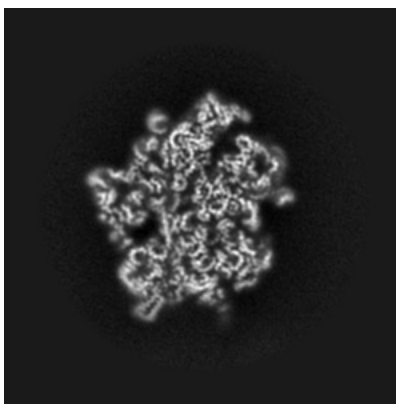
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

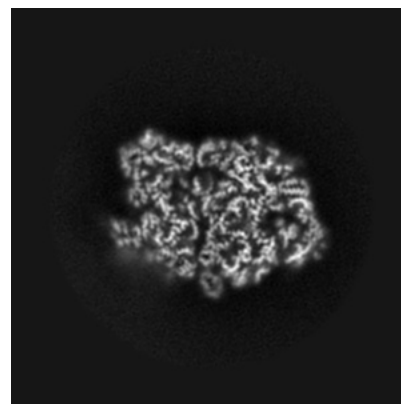
6.3.1 Primary map



X Index: 275



Y Index: 230

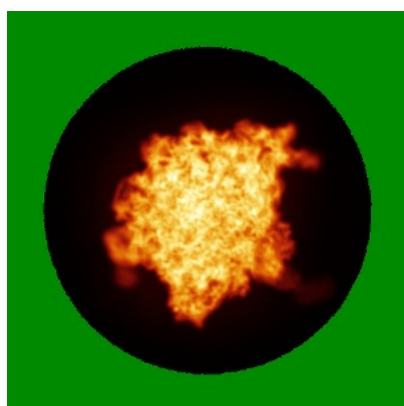


Z Index: 272

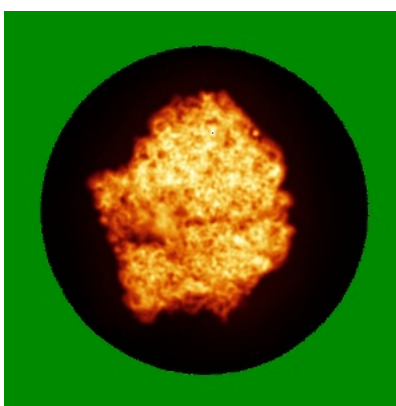
The images above show the largest variance slices of the map in three orthogonal directions.

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

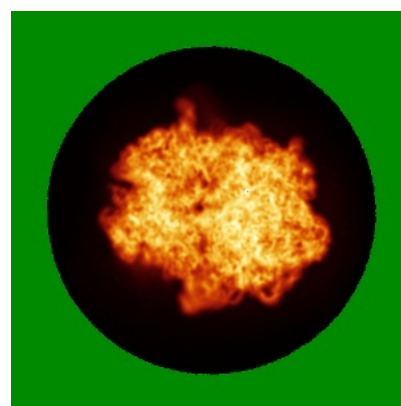
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 7.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

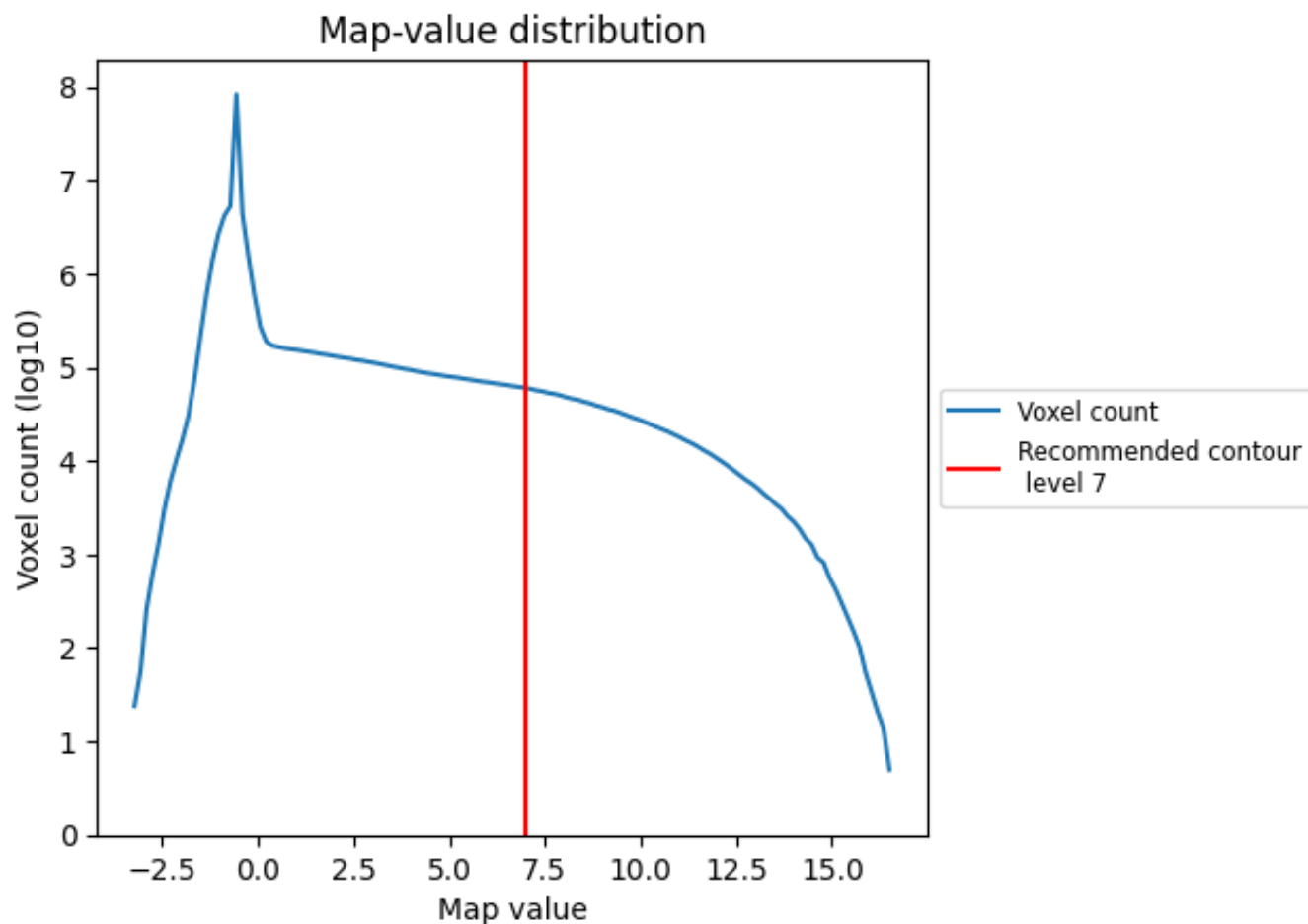
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

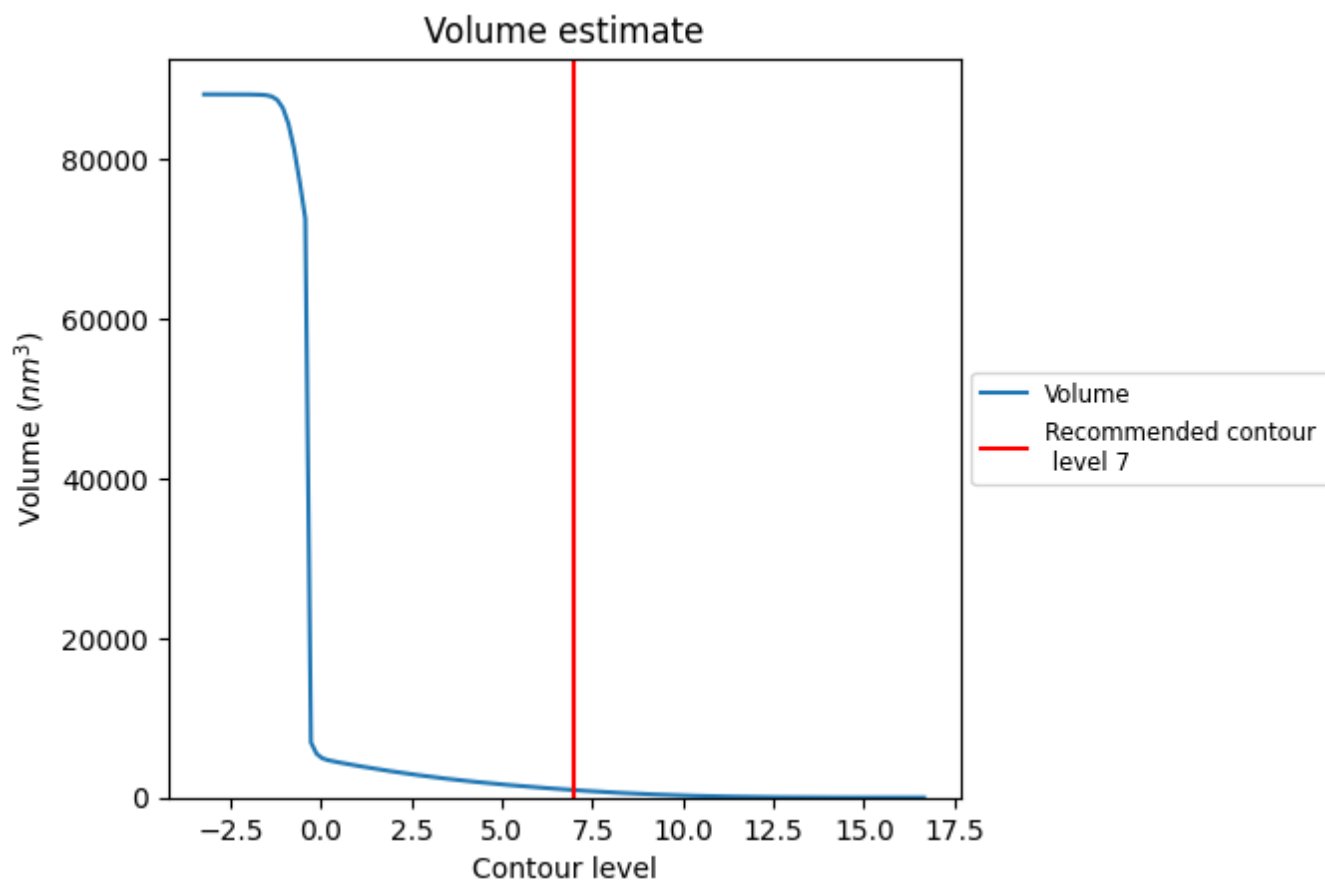
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

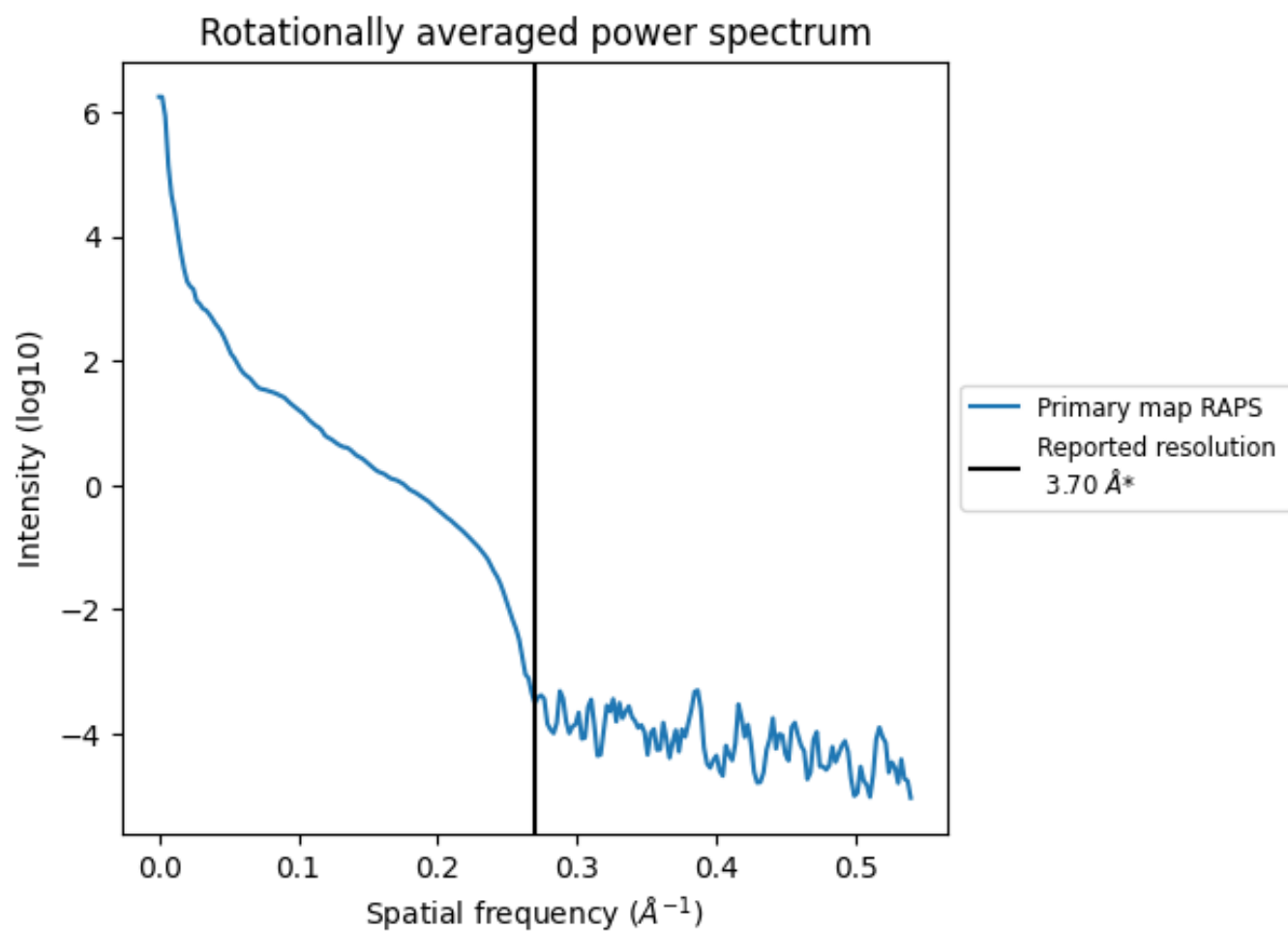
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 936 nm³; this corresponds to an approximate mass of 845 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

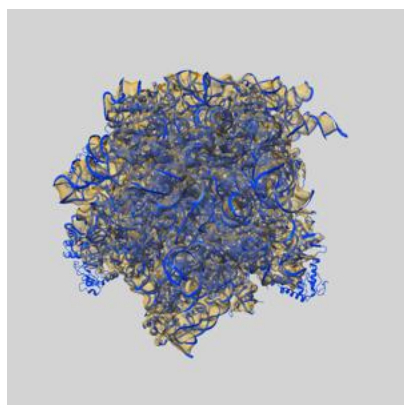
8 Fourier-Shell correlation

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

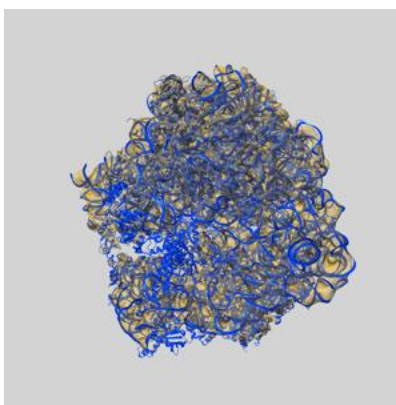
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7970 and PDB model 6DNC. Per-residue inclusion information can be found in section [3](#) on page [15](#).

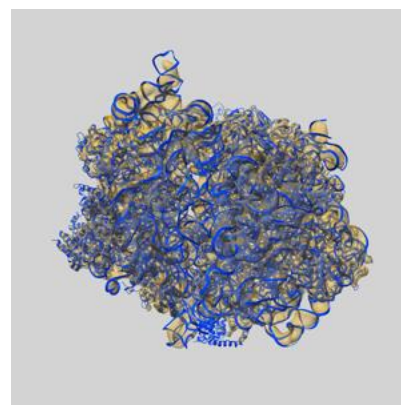
9.1 Map-model overlay [i](#)



X



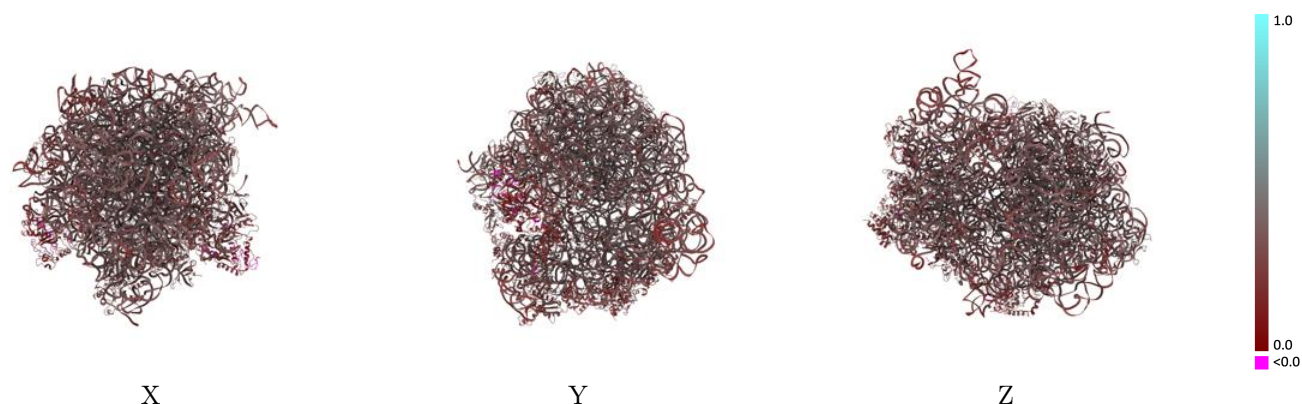
Y



Z

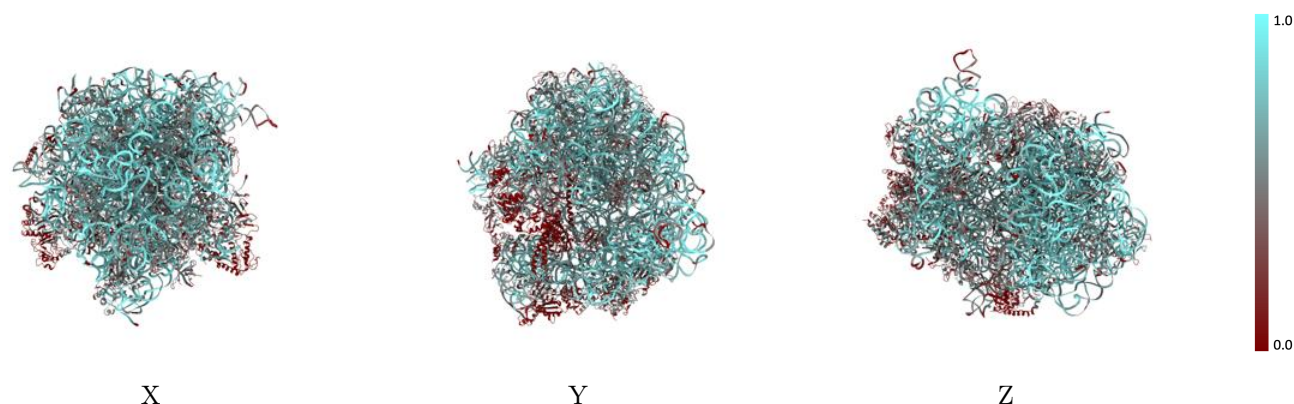
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



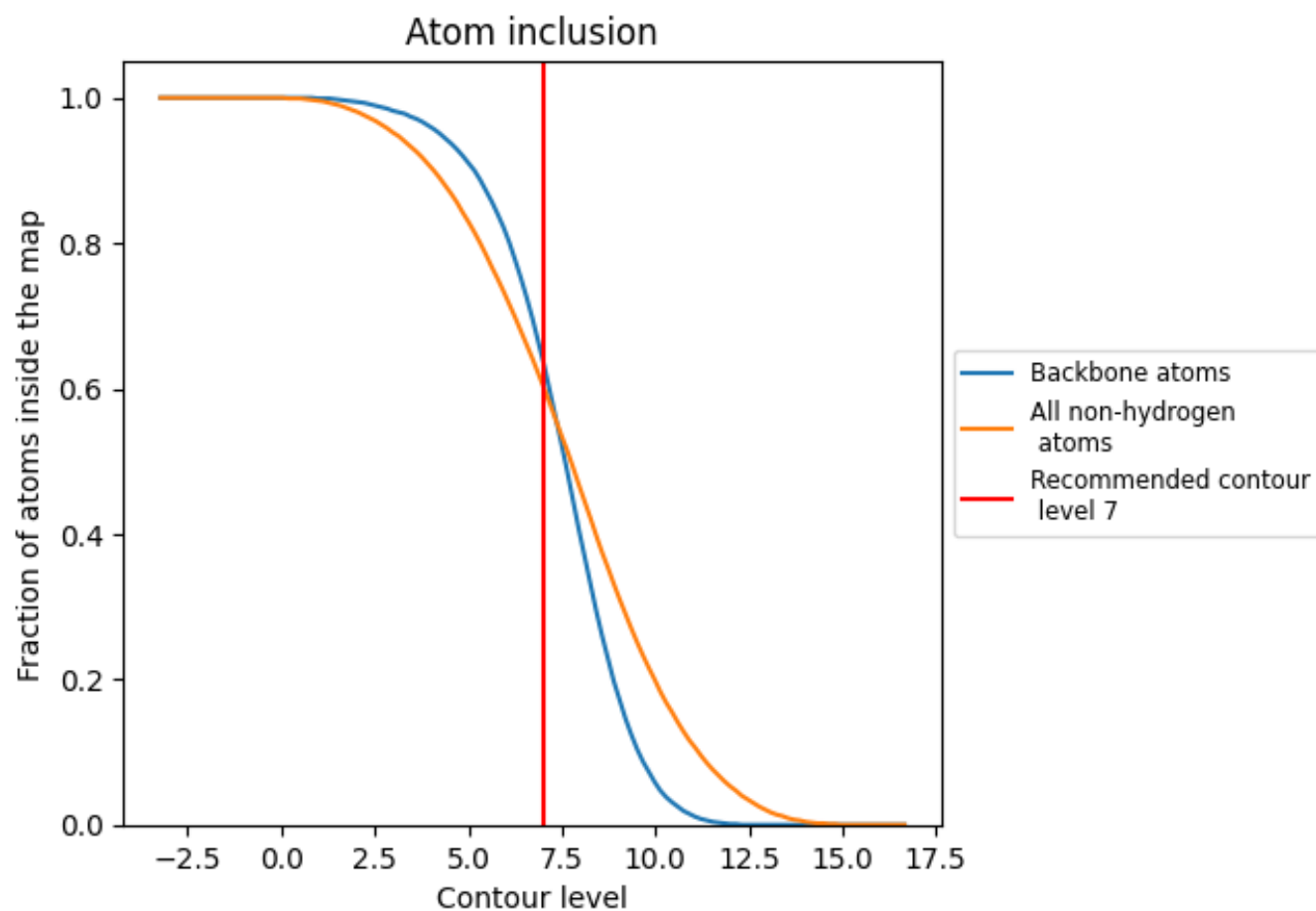
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 60% 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 (7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6040	 0.3190
A	 0.7440	 0.3290
AA	 0.4360	 0.3360
AB	 0.3150	 0.2550
B	 0.7630	 0.3420
BA	 0.4260	 0.3190
BB	 0.4300	 0.2740
C	 0.7690	 0.3270
CA	 0.4530	 0.2410
CB	 0.4560	 0.3080
D	 0.4010	 0.2220
DA	 0.4440	 0.3190
DB	 0.3560	 0.3130
E	 0.0040	 0.1350
EA	 0.0940	 0.2490
EB	 0.3600	 0.2780
F	 0.3770	 0.3440
FA	 0.4320	 0.3270
FB	 0.3250	 0.2970
G	 0.3990	 0.3420
GA	 0.2240	 0.3180
GB	 0.4740	 0.2640
H	 0.3780	 0.3140
HA	 0.4250	 0.3150
HB	 0.2300	 0.2130
I	 0.3470	 0.2760
IA	 0.4170	 0.3420
J	 0.3140	 0.2970
JA	 0.3660	 0.3080
K	 0.1190	 0.2550
KA	 0.3810	 0.3090
L	 0.0020	 0.1020
LA	 0.4850	 0.3190
M	 0.0160	 0.1590
MA	 0.0200	 0.2600



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Chain	Atom inclusion	Q-score
N	 0.4490	 0.3170
O	 0.2970	 0.3400
OA	 0.3040	 0.2650
P	 0.3970	 0.3280
PA	 0.1240	 0.2940
Q	 0.3170	 0.3280
QA	 0.3230	 0.2600
R	 0.4970	 0.3190
RA	 0.3870	 0.3040
S	 0.5030	 0.3030
SA	 0.4150	 0.2940
T	 0.3590	 0.3270
TA	 0.3160	 0.2630
U	 0.5050	 0.2980
UA	 0.4080	 0.3040
V	 0.4250	 0.3390
VA	 0.3750	 0.2720
W	 0.4160	 0.3190
WA	 0.1850	 0.2790
X	 0.4150	 0.3190
XA	 0.3560	 0.3180
Y	 0.4030	 0.3140
YA	 0.2300	 0.3170
Z	 0.4400	 0.3110
ZA	 0.3580	 0.2690